Suppl. Fig. 1 The gene ontology annotations of up- and down-regulated genes of *P. tricornutum* strain CCAP 1055/1.

Suppl. Table 1 Permutational MANOVA (Permutational Multivariate Analysis of Variance Using Distance Matrices) of fatty acid content per cell between the two treatment groups (control and grazing) among all strains

Suppl. Table 2 Coefficients of linear discriminants of linear discriminant analysis (LDA) on the contents in each fatty acid

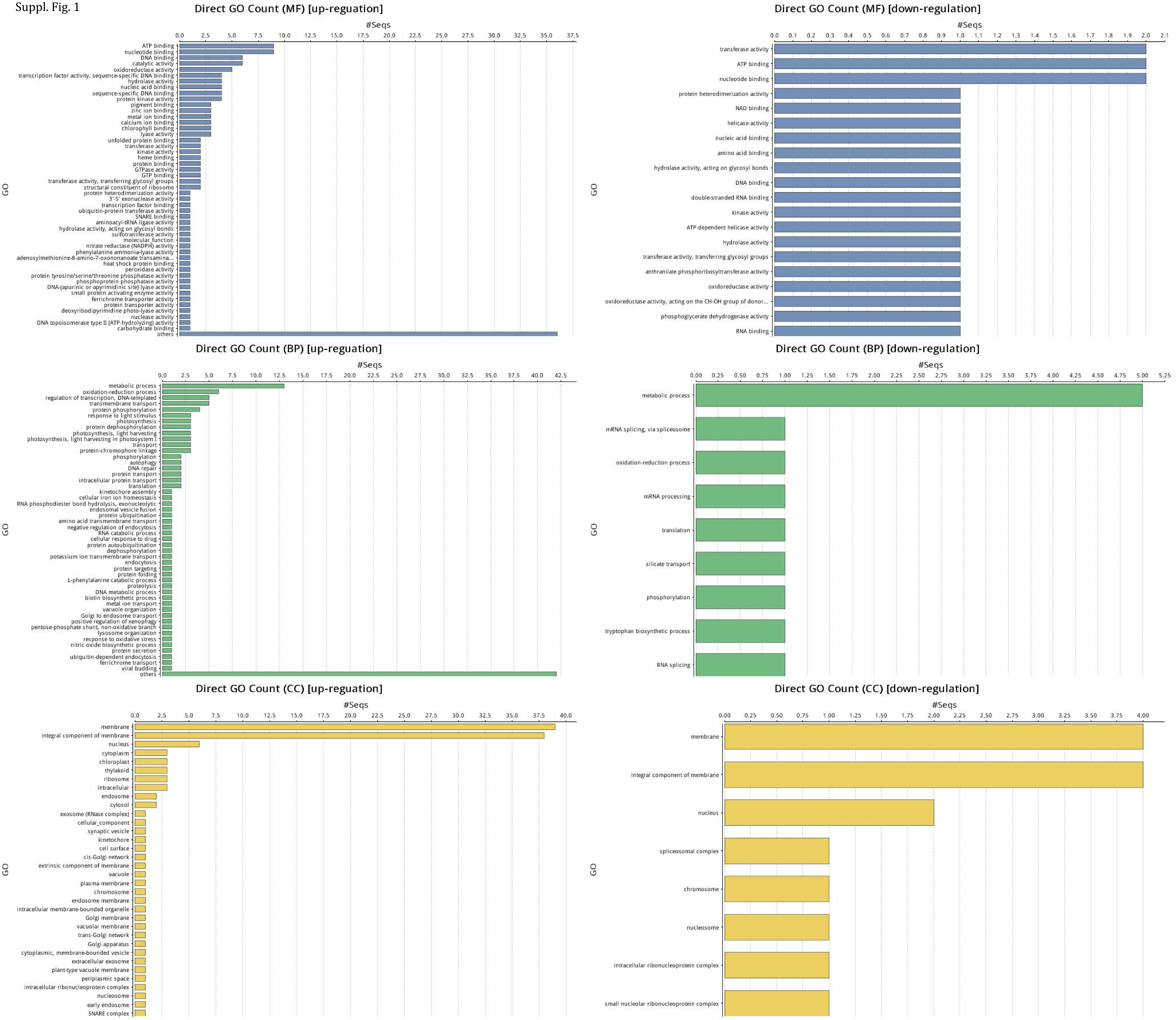
Suppl. Table 3 Two-way ANOVA on LDA results of the contents in each fatty acid

Suppl. Table 4 Statistics of clean reads alignment from paired-end sequencing on 9L cultures of strain CCAP 1055/1

Suppl. Table 5 Significantly differential expressed genes in treatment pairs of 9L cultures of strain CCAP 1055/1

Suppl. Table 6 Pathway enrichment analyses on significantly differential expressed genes

Suppl. Fig. 1



Direct GO Count (MF) [up-reguation]

Direct GO Count (MF) [down-regulation]

Direct GO Count (BP) [up-reguation]

Direct GO Count (BP) [down-regulation]

Direct GO Count (CC) [up-reguation]

Direct GO Count (CC) [down-regulation]

Suppl. Table 1

	PUFA(Polyunsaturated fatty acids)															
Strain	Permutational Multivariate Analysis of Variance Using		Number of significant different fatty acids (NSD)	Number of significant different total amount of fatty acid(NSDT)	16:2n4			16:3n4			18:2n6t			18:2n6c (LA)			18
	R2	P value			x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
9L Sets of CCAP 1055/1	R2(1,5)=0.25745	0.3	1	0	NAN	1	NA	3.9706	1	0.0463	NAN	1	NA	2.3333	1	0.1266	0
150 ml Sets of CCAP 1055/1	R2(1,5)=0.27538	0.2	3	1	1	1	0.3173	0	1	1	1	1	0.3173	2.3333	1	0.1266	1.3441
CCAP 632	R2(1,5)=0.39474	0.2	4	0	2.4	1	0.1213	NAN	1	NA	NAN	1	NA	1.1905	1	0.2752	3.8571
CCAP 2557	R2(1,5)=0.19544	0.6	0	0	NAN	1	NA	0.066667	1	0.7963	NAN	1	NA	1.1905	1	0.2752	1
CCAP 2558	R2(1,5)=0.52364	0.1	4	0	NAN	1	NA	NAN	1	NA	NAN	1	NA	0.42857	1	0.5127	2.3333
CCAP 2560	R2(1,5)=0.1466	0.8	2	0	NAN	1	NA	0.053763	1	0.8166	NAN	1	NA	0.047619	1	0.8273	1
MACC B228	R2(1,5)=0.13402	0.7	0	0	NAN	1	NA	1	1	0.3173	NAN	1	NA	0.047619	1	0.8273	1

	SFA(Saturated fatty acids)																
Strain	Permutational Multivariate Analysis of Variance Using		Number of significant different fatty acids (NSD)	Number of significant different total amount of fatty acid(NSDT)										Kruskal-Wallis rank sum test			
					C12			C13			C14			C15			
	R2	P value			x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
9L Sets of CCAP 1055/1	R2(1,5)=0.25745	0.3	0	0	2.3333	1	0.1266	0	1	1	1.1905	1	0.2752	2.3333	1	0.1266	2.3333
150 ml Sets of CCAP 1055/1	R2(1,5)=0.27538	0.2	3	1	0.78431,	1	0.3758	0.78431,	1	0.3758	1.1905	1	0.2752	0.42857	1	0.5127	3.8571
CCAP 632	R2(1,5)=0.39474	0.2	3	0	2.3333	1	0.1266	NAN	1	NA	3.8571	1	0.04953	2.3333	1	0.1266	1.1905
CCAP 2557	R2(1,5)=0.19544	0.6	0	0	0.047619	1	0.8273	1	1	0.3173	0.42857	1	0.5127	0.19608	1	0.6579	0.047619
CCAP 2558	R2(1,5)=0.52364	0.1	5	1	3.8571	1	0.04953	1	1	0.3173	3.8571	1	0.04953	2.3333	1	0.1266	3.8571
CCAP 2560	R2(1,5)=0.1466	0.8	2	0	0.047619	1	0.8273	1.1905	1	0.2752	0.047619	1	0.8273	0.047619	1	0.8273	2.3333
MACC B228	R2(1,5)=0.13402	0.7	2	0	3.8571	1	0.04953	1.3441	1	0.2463	0.42857	1	0.5127	1.1905	1	0.2752	0.047619

	TFA(Trans fatty acid)													
Strain	Permutational Multivariate Analysis of Variance Using		Number of significant different fatty acids (NSD)	Number of significant different total amount of fatty acid(NSDT)	Kruskal-Wallis rank sum test									
					18:1n9t			18:2n6t			TOTAL			
	R2	P value			x^2	df	P value	x^2	df	P value	x^2	df	P value	
9L Sets of CCAP 1055/1	R2(1,5)=NAN	NAN	0	0	2.4	1	0.1213	NAN	1	NA	2.4	1	0.1213	
150 ml Sets of CCAP 1055/1	R2(1,5)=NAN	NAN	0	0	NAN	1	NA	1	1	0.3173	1	1	0.3173	
CCAP 632	R2(1,5)=0.68139	0.1	2	1	3.8571	1	0.04953	NAN	1	NA	3.8571	1	0.04953	
CCAP 2557	R2(1,5)=0.18598	1	0	0	0.42857	1	0.5127	NAN	1	NA	0.42857	1	0.5127	
CCAP 2558	R2(1,5)=0.35744	0.2	0	0	2.3333	1	0.1266	NAN	1	NA	2.3333	1	0.1266	
CCAP 2560	R2(1,5)=0.28016	0.3	0	0	1.1905	1	0.2752	NAN	1	NA	1.1905	1	0.2752	
MACC B228	R2(1,5)=0.28016	0.3	0	0	0.42857	1	0.5127	NAN	1	NA	0.42857	1	0.5127	

	MUFA(Mono-unsaturated fatty acids)																
Strain	Permutational Multivariate Analysis of Variance Using		Number of significant different fatty acids (NSD)	Number of significant different total amount of fatty acid(NSDT)										Kruskal-Wallis rank sum test			
					16:1			17:1			18:1n9c			18:1n9t			
	R2	P value			x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
9L Sets of CCAP 1055/1	R2(1,5)=0.41862	0.2	0	0	0.42857	1	0.5127	0.42857	1	0.5127	2.3333	1	0.1266	2.4	1	0.1213	NAN
150 ml Sets of CCAP 1055/1	R2(1,5)=0.18738	0.4	0	0	1.1905	1	0.2752	0.047619	1	0.8273	0.78431,	1	0.3758	NAN	1	NA	0.066667
CCAP 632	R2(1,5)=0.31093	0.3	1	0	1.1905	1	0.2752	1.1905	1	0.2752	1.1905	1	0.2752	3.8571	1	0.04953	1.1905
CCAP 2557	R2(1,5)=0.15971	0.8	0	0	0.047619	1	0.8273	0.42857	1	0.5127	2.3333	1	0.1266	0.42857	1	0.5127	0.78431
CCAP 2558	R2(1,5)=0.21446	0.5	2	0	3.8571	1	0.04953	3.8571	1	0.04953	2.3333	1	0.1266	2.3333	1	0.1266	0.42857
CCAP 2560	R2(1,5)=0.11559	0.9	0	0	0.047619	1	0.8273	1.1905	1	0.2752	0.42857	1	0.5127	1.1905	1	0.2752	0.047619
MACC B228	R2(1,5)=0.19289	0.5	1	1	0.42857	1	0.5127	1.1905	1	0.2752	1.1905	1	0.2752	0.42857	1	0.5127	1.1905

	LC-PUFA(Long chain polyunsaturated fatty acids)																
Strain	Permutational Multivariate Analysis of Variance Using		Number of significant different fatty acids (NSD)	Number of significant different total amount of fatty acid(NSDT)	Kruskal-Wallis rank sum test												
					18:2n6c (LA)			18:3n6 (GLA)			18:3n3 (ALA)			18:4n3 (SDA)			20:
	R2	P value			x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
9L Sets of CCAP 1055/1	R2(1,5)=0.09233	0.7	0	0	2.3333	1	0.1266	0	1	1	0.047619	1	0.8273	2.3333	1	0.1266	1.1905
150 ml Sets of CCAP 1055/1	R2(1,5)=0.26983	0.2	3	0	2.3333	1	0.1266	1.3441	1	0.2463	3.8571	1	0.04953	0.78431,	1	0.3758	1.3441
CCAP 632	R2(1,5)=0.59557	0.1	2	0	1.1905	1	0.2752	3.8571	1	0.04953	0.047619	1	0.8273	3.8571	1	0.04953	2.3333
CCAP 2557	R2(1,5)=0.35087	0.4	0	0	1.1905	1	0.2752	1	1	0.3173	1.1905	1	0.2752	0.047619	1	0.8273	0.42857
CCAP 2558	R2(1,5)=0.36633	0.2	3	1	0.42857	1	0.5127	2.3333	1	0.1266	0.053763	1	0.8166	3.8571	1	0.04953	0.42857
CCAP 2560	R2(1,5)=0.1192	0.9	1	0	0.047619	1	0.8273	1	1	0.3173	0.053763	1	0.8166	3.8571	1	0.04953	1.1905
MACC B228	R2(1,5)=0.09801	0.8	0	0	0.047619	1	0.8273	1	1	0.3173	1.1905	1	0.2752	1.1905	1	0.2752	0.42857

Kruskal-Wallis rank sum test

:3n6 (GLA)		18:3n3 (ALA)			18:4n3 (SDA)			20:2n6c			20:3n6 (DGLA)			20:4n6c (AA)			20:3n3			20:4n3			20
df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
1	1	0.047619	1	0.8273	2.3333	1	0.1266	1.1905	1	0.2752	1.1905	1	0.2752	0.047619	1	0.8273	0.42857	1	0.5127	2.3333	1	0.1266	1.1905
1	0.2463	3.8571	1	0.04953	0.78431,	1	0.3758	0.78431,	1	0.3758	1.3441	1	0.2463	3.8571	1	0.04953	0.066667	1	0.7963	1.1905	1	0.2752	1.1905
1	0.04953	0.047619	1	0.8273	3.8571	1	0.04953	0.047619	1	0.8273	2.3333	1	0.1266	0.047619	1	0.8273	4.3548	1	0.0369	0.42857	1	0.5127	0.42857
1	0.3173	1.1905	1	0.2752	0.047619	1	0.8273	0.42857	1	0.5127	0.42857	1	0.5127	0.42857	1	0.5127	0	1	1	0.42857	1	0.5127	0.047619
1	0.1266	0.053763	1	0.8166	3.8571	1	0.04953	2.3333	1	0.1266	0.42857	1	0.5127	1.1905	1	0.2752	1.1905	1	0.2752	3.8571	1	0.04953	3.8571
1	0.3173	0.053763	1	0.8166	3.8571	1	0.04953	2.3333	1	0.1266	1.1905	1	0.2752	4.3548	1	0.0369	0.047619	1	0.8273	0.047619	1	0.8273	0.047619
1	0.3173	1.1905	1	0.2752	1.1905	1	0.2752	1.1905	1	0.2752	0.42857	1	0.5127	0.047619	1	0.8273	0.047619	1	0.8273	2.3333	1	0.1266	0.047619

C16		cis9,10-C17			C17			2OH-C14			C18			cis9,10-C19			3OH-C14			C20			
df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2
1	0.1266	1.1905	1	0.2752	1.1905	1	0.2752	1.1905	1	0.2752	2.3333	1	0.1266	1.1905	1	0.2752	0.48387	1	0.4867	2.3333	1	0.1266	0.42857
1	0.04953	0	1	1	0.78431,	1	0.3758	NAN	1	NA	3.8571	1	0.04953	NAN	1	NA	2.3333	1	0.1266	2.3333	1	0.1266	2.3333
1	0.2752	0.44118	1	0.5066	1.1905	1	0.2752	NAN	1	NA	1.1905	1	0.2752	NAN	1	NA	NAN	1	NA	3.8571	1	0.04953	3.8571
1	0.8273	0.053763	1	0.8166	0.42857	1	0.5127	NAN	1	NA	0.047619	1	0.8273	NAN	1	NA	0.42857	1	0.5127	2.3333	1	0.1266	0.047619
1	0.04953	3.8571	1	0.04953	3.8571	1	0.04953	NAN	1	NA	1.1905	1	0.2752	1.1905	1	0.2752	NAN	1	NA	2.3333	1	0.1266	0.42857
1	0.1266	1.1905	1	0.2752	2.3333	1	0.1266	4.3548	1	0.0369	3.8571	1	0.04953	0.047619	1	0.8273	1.1905	1	0.2752	0.047619	1	0.8273	1.1905
1	0.8273	0.42857	1	0.5127	0.047619	1	0.8273	1	1	0.3173	0.42857	1	0.5127	1	1	0.3173	0.42857	1	0.5127	3.8571	1	0.04953	0.42857

18:1n7		20:1n9c			22:1n9c			TOTAL		
df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value
1	NA	2.3333	1	0.1266	0.42857	1	0.5127	2.3333	1	0.1266
1	0.7963	1.1905	1	0.2752	1.1905	1	0.2752	1.1905	1	0.2752
1	0.2752	1	1	0.3173	0.48387	1	0.4867	0.42857	1	0.5127
1	0.3758	0.047619	1	0.8273	0.047619	1	0.8273	0.047619	1	0.8273
1	0.5127	0.066667	1	0.7963	0.047619	1	0.8273	2.3333	1	0.1266
1	0.8273	0.42857	1	0.5127	0.42857	1	0.5127	0.047619	1	0.8273
1	0.2752	1	1	0.3173	3.9706	1	0.0463	0.42857	1	0.5127

3n6 (DGLA)		20:4n6c (AA)			20:5n3c (EPA)			22:5n3 (DPA)			22:6n3c (DHA)			TOTAL		
df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value
1	0.2752	0.047619	1	0.8273	1.1905	1	0.2752	2.3333	1	0.1266	1.1905	1	0.2752	2.3333	1	0.1266
1	0.2463	3.8571	1	0.04953	1.1905	1	0.2752	3.8571	1	0.04953	0.42857	1	0.5127	3.8571	1	0.04953
1	0.1266	0.047619	1	0.8273	0.42857	1	0.5127	0.047619	1	0.8273	2.3333	1	0.1266	0.047619	1	0.8273
1	0.5127	0.42857	1	0.5127	0.047619	1	0.8273	2.3333	1	0.1266	0.047619	1	0.8273	2.3333	1	0.1266
1	0.5127	1.1905	1	0.2752	3.8571	1	0.04953	3.8571	1	0.04953	2.3333	1	0.1266	3.8571	1	0.04953
1	0.2752	4.3548	1	0.0369	0.047619	1	0.8273	1.1905	1	0.2752	0.42857	1	0.5127	0.42857	1	0.5127
1	0.5127	0.047619	1	0.8273	0.047619	1	0.8273	0.42857	1	0.5127	1.1905	1	0.2752	0.42857	1	0.5127

:5n3c(EPA)		22:2n6c			22:5n3 (DPA)			22:6n3c(DHA)			TOTAL		
df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value	x^2	df	P value
1	0.2752	1	1	0.3173	2.3333	1	0.1266	1.1905	1	0.2752	1.1905	1	0.2752
1	0.2752	1	1	0.3173	3.8571	1	0.04953	0.42857	1	0.5127	3.8571	1	0.04953
1	0.5127	3.8571	1	0.04953	0.047619	1	0.8273	2.3333	1	0.1266	0.42857	1	0.5127
1	0.8273	NAN	1	NA	2.3333	1	0.1266	0.047619	1	0.8273	0.42857	1	0.5127
1	0.04953	NAN	1	NA	3.8571	1	0.04953	2.3333	1	0.1266	1.1905	1	0.2752
1	0.8273	NAN	1	NA	1.1905	1	0.2752	0.42857	1	0.5127	2.3333	1	0.1266
1	0.8273	NAN	1	NA	0.42857	1	0.5127	1.1905	1	0.2752	2.3333	1	0.1266

C22		C24			TOTAL		
df	P value	x^2	df	P value	x^2	df	P value
1	0.5127	0.047619	1	0.8273	2.3333	1	0.1266
1	0.1266	3.8571	1	0.04953	3.8571	1	0.04953
1	0.04953	0.047619	1	0.8273	0.42857	1	0.5127
1	0.8273	0.047619	1	0.8273	1.1905	1	0.2752
1	0.5127	0.047619	1	0.8273	3.8571	1	0.04953
1	0.2752	1.1905	1	0.2752	0.42857	1	0.5127
1	0.5127	0.42857	1	0.5127	1.1905	1	0.2752

Suppl. Table 2

	LD1	LD2	LD3	LD4	LD5	LD6	LD7
C12	14.49105	-22.2587	5.811709	9.573937	3.391811	-0.28518	5.116211
C13	32.51399	-26.7666	17.11213	-18.959	10.23693	2.457432	-8.2451
C14	2.553575	0.971219	-0.10417	-0.94957	0.143863	-0.18319	-0.14442
C15	-3.13374	7.031682	-4.75279	6.448512	-3.85071	-0.91704	0.762923
C16	-1.27761	1.054629	-0.28682	0.053251	0.168011	-0.23735	-0.11693
16:1	-0.29595	-0.22704	0.059719	-0.60291	-0.41063	0.149705	-0.19481
cis9,10-C17	-7.61566	-1.29584	-0.10696	0.871737	0.197262	-0.42636	-1.59244
C17	12.77624	-4.24477	-0.78667	8.710588	4.634673	-1.1795	1.467389
16:2n4	-13.723	-2.51979	2.051914	-3.6727	-0.57488	-1.86366	-1.52301
17:1	3.755957	-0.52885	0.629161	1.300787	-0.44193	0.943529	1.261207
16:3n4	4.449487	9.957232	0.303263	1.057194	2.401536	0.745007	2.36478
2OH-C14	-12.7233	-52.5801	7.224994	-16.4646	1.47812	-12.4677	-7.59406
C18	-0.21694	-0.22458	0.119087	-0.67619	-0.38869	-0.09866	-0.22652
18:1n9t	-0.14994	0.267426	-0.03121	0.8397	-0.10019	0.268843	-0.05347
18:1n9c	-1.8803	0.282013	-0.45134	-0.27676	-0.36495	0.172557	-0.18966
18:1n7	9.109241	0.173377	1.868532	2.250919	3.132917	-1.57061	0.35796
18:2n6t	0.61541	-1.61874	-0.0884	4.056558	0.685783	1.146568	0.85849
18:2n6c	9.39188	1.951437	-2.23532	5.743098	6.840373	-2.18053	1.371716
cis9,10-C19	42.02591	-29.9142	0.593049	-6.19803	3.069588	-0.98603	3.984968
18:3n6	-2.44211	0.530818	-0.84236	-0.13848	-0.22919	-0.39163	-0.19479
3OH-C14	-0.66724	0.638147	-0.04099	0.554187	0.328912	0.0209	-0.18
18:3n3	1.501798	-1.65764	0.252298	-1.13111	-0.84552	-0.28553	-0.24332
18:4n3	-8.58904	-6.58209	8.216734	-4.48159	-3.73657	-2.46936	-2.89291
C20	-12.5762	8.313856	-2.48293	-0.605	7.933842	5.08102	1.203214
20:1n9c	-0.35706	0.140058	-0.06809	0.087516	-0.23616	0.274027	0.093089
20:2n6c	-5.7016	-0.84628	-0.24727	-9.12563	0.464893	-3.43187	-2.59285
20:3n6	1.195224	-0.36007	0.062026	0.670393	0.376295	0.01609	0.266896
20:4n6c	-0.87479	0.687985	0.261716	0.353199	0.376225	-0.49479	0.101204
20:3n3	-7.98813	7.931199	-1.48108	2.372653	-2.6122	0.803777	0.176822
20:4n3	6.062705	-5.8221	3.095607	-0.35649	-3.39511	1.247672	1.442959
C22	0.847434	0.495539	-0.15047	-0.15643	0.029631	-0.04603	-0.07144
20:5n3c	-0.46747	-0.03597	0.070945	-0.40302	-0.27494	0.117588	0.015023
22:1n9c	-6.19042	1.10861	2.554015	5.495938	1.694108	4.212103	1.326738
22:2n6c	14.09503	3.30075	-2.40437	-0.09108	0.594781	1.497575	-1.74961
C24	-0.85978	0.534853	-0.23358	0.287939	0.295964	-0.49483	0.171524
22:5n3;24:1n9c	0.562989	0.256052	0.347279	0.061257	-0.31923	0.321932	0.314558
22:6n3c	-1.18846	-2.34807	0.203136	-1.90791	-0.99188	-0.42618	-0.47955

Suppl. Table 3

LD8	LD9	LD10	LD11	LD12	LD13
-8.59715	-9.98368	1.63946	1.463759	2.3333	-1.95954
5.686075	3.828363	0.530999	-3.58088	-3.16767	0.550467
0.357397	-0.30187	0.07678	0.139032	0.019186	-0.16589
-2.04859	2.512023	-0.3143	1.511132	-0.01673	0.653623
0.113091	-0.04355	0.205637	0.04144	-0.15944	0.018905
0.279736	-0.18464	-0.14895	-0.15591	-0.12616	0.016289
-2.71902	-1.06692	0.521451	0.476492	0.149014	0.401026
0.837262	2.378531	0.75466	0.219682	1.104332	-1.87205
-0.53386	-3.4151	0.529332	-1.38289	-1.36149	2.647924
0.588391	1.376693	-0.08894	0.12861	0.049835	-0.27858
2.577477	0.807914	1.887015	0.123557	-1.50378	-0.73922
11.16081	6.625679	-10.9388	-14.9969	-7.28261	0.923944
-0.00101	0.073989	-0.05229	0.088851	-0.01592	0.025094
0.028885	0.083625	0.085144	-0.18752	0.087118	-0.01325
-0.0184	-0.33704	-0.00326	-0.07144	-0.19977	0.226869
-0.84298	-0.53435	0.385623	0.013819	0.721355	-2.63021
-0.0402	1.249092	0.307066	-0.19365	-0.30865	-0.40142
-3.4449	-1.85979	1.56835	-0.00214	2.535355	0.934867
5.800495	-1.57363	7.653144	-0.87893	9.762765	-1.63319
0.192941	0.099617	0.118119	-0.05858	-0.20162	0.030639
0.135254	0.142427	0.214474	-0.0683	-0.09025	0.073822
0.462423	-0.05292	-0.41199	-0.00014	0.426429	0.273512
-6.67217	3.670517	-1.92484	-3.27284	1.667635	-1.49299
1.798091	-2.6867	1.196861	0.563678	1.44607	-1.40704
-0.10588	-0.19791	-0.11671	0.108372	-0.03108	0.029718
3.842197	2.666174	-4.25184	1.95884	-2.17275	0.419232
0.305875	0.252796	0.09451	-0.01411	-0.0781	-0.16964
-0.07099	0.202676	0.241276	-0.10365	-0.08467	-0.07067
-1.59994	-1.30627	-1.83789	0.666654	-0.79656	1.289762
-3.38091	-2.20005	-2.04874	-0.86444	1.282445	0.008535
-0.06741	0.046674	0.02257	0.03408	0.184336	0.007921
0.067374	-0.04162	-0.1479	-0.0299	-0.07334	0.052993
-4.22489	0.169704	0.195021	-2.30302	0.971221	-1.71911
-0.55499	1.914841	1.482239	0.584759	0.060613	-1.98846
0.001227	-0.05219	0.168202	-0.07249	0.046998	0.096823
0.282443	0.281325	-0.11901	0.204931	-0.4209	-0.2729
-1.71927	-0.32883	-1.11825	-0.04622	0.238457	0.269077

Suppl. Table 3

	All strains				9L set of		150 ml set of		150 ml set of CCAP		150 ml set of CCAP		150 ml set of CCAP		150 ml set of CCAP		150 ml set of MACC	
	Strains	Treatment	Strains:Tre	Residuals	Treatment	Residuals	Treatment	Residuals	Treatment	Residuals	Treatment	Residuals	Treatment	Residuals	Treatment	Residuals	Treatment	Residuals
LD1.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD1.Sum.Sq	19950.17	376.3263	612.7248	28	121.0838	0.217762	4.087225	2.535626	355.9152	18.58878	71.43069	1.038511	188.147	2.449919	7.19324	0.189879	241.194	2.979525
LD1.Mean.Sq	3325.029	376.3263	102.1208	1	121.0838	0.054441	4.087225	0.633906	355.9152	4.647194	71.43069	0.259628	188.147	0.61248	7.19324	0.04747	241.194	0.744881
LD1.F.value	3325.029	376.3263	102.1208	#N/A	2224.144	#N/A	6.447679	#N/A	76.58712	#N/A	275.1274	#N/A	307.1889	#N/A	151.5329	#N/A	323.8019	#N/A
LD1.Pr..F.	1.35E-38	9.01E-18	1.02E-17	#N/A	1.21E-06	#N/A	0.064033	#N/A	0.00094	#N/A	7.74E-05	#N/A	6.22E-05	#N/A	0.00025	#N/A	5.61E-05	#N/A
LD2.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD2.Sum.Sq	3311.837	0.208232	322.0228	28	9.948667	1.403518	0.129606	0.189229	25.69517	14.38625	214.5716	1.934335	9.257703	5.734995	53.71028	0.588288	8.917999	3.763383
LD2.Mean.Sq	551.9728	0.208232	53.67046	1	9.948667	0.35088	0.129606	0.047307	25.69517	3.596563	214.5716	0.483584	9.257703	1.433749	53.71028	0.147072	8.917999	0.940846
LD2.F.value	551.9728	0.208232	53.67046	#N/A	28.35351	#N/A	2.739655	#N/A	7.144369	#N/A	443.7114	#N/A	6.456992	#N/A	365.1971	#N/A	9.478704	#N/A
LD2.Pr..F.	1E-27	0.651677	4.52E-14	#N/A	0.005986	#N/A	0.173228	#N/A	0.055638	#N/A	3E-05	#N/A	0.063909	#N/A	4.42E-05	#N/A	0.036977	#N/A
LD3.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD3.Sum.Sq	1330.846	4.200283	123.6996	28	23.32929	2.534025	12.59215	2.228098	6.547096	1.133153	60.12063	9.393419	7.532846	3.736222	5.284592	1.809478	12.49332	7.165605
LD3.Mean.Sq	221.8077	4.200283	20.61661	1	23.32929	0.633506	12.59215	0.557025	6.547096	0.283288	60.12063	2.348355	7.532846	0.934055	5.284592	0.45237	12.49332	1.791401
LD3.F.value	221.8077	4.200283	20.61661	#N/A	36.82566	#N/A	22.60609	#N/A	23.11108	#N/A	25.60117	#N/A	8.064667	#N/A	11.68202	#N/A	6.974048	#N/A
LD3.Pr..F.	2.87E-22	0.04989	4.38E-09	#N/A	0.003724	#N/A	0.008941	#N/A	0.008602	#N/A	0.007182	#N/A	0.046875	#N/A	0.026832	#N/A	0.05753	#N/A
LD4.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD4.Sum.Sq	502.9906	243.5305	286.5201	28	60.06704	1.70946	248.1928	0.379034	39.84771	9.532782	180.3063	1.590167	1.273421	8.00581	0.265489	1.694948	0.097879	5.087799
LD4.Mean.Sq	83.83177	243.5305	47.75335	1	60.06704	0.427365	248.1928	0.094759	39.84771	2.383196	180.3063	0.397542	1.273421	2.001452	0.265489	0.423737	0.097879	1.27195
LD4.F.value	83.83177	243.5305	47.75335	#N/A	140.5521	#N/A	2619.211	#N/A	16.72029	#N/A	453.5532	#N/A	0.636249	#N/A	0.626542	#N/A	0.076952	#N/A
LD4.Pr..F.	1.39E-16	2.42E-15	1.98E-13	#N/A	0.00029	#N/A	8.72E-07	#N/A	0.014987	#N/A	2.87E-05	#N/A	0.469744	#N/A	0.472919	#N/A	0.795218	#N/A
LD5.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD5.Sum.Sq	439.7389	78.76387	77.89294	28	3.298496	1.226791	3.656123	0.228727	5.111706	0.573671	94.32335	0.998528	24.29139	4.455174	2.778826	11.41735	23.19693	9.099763
LD5.Mean.Sq	73.28982	78.76387	12.98216	1	3.298496	0.306698	3.656123	0.057182	5.111706	0.143418	94.32335	0.249632	24.29139	1.113793	2.778826	2.854337	23.19693	2.274941
LD5.F.value	73.28982	78.76387	12.98216	#N/A	10.75488	#N/A	63.93874	#N/A	35.64208	#N/A	377.8497	#N/A	21.8096	#N/A	0.973545	#N/A	10.19672	#N/A
LD5.Pr..F.	8.12E-16	1.25E-09	5.56E-07	#N/A	0.030516	#N/A	0.001326	#N/A	0.003954	#N/A	4.13E-05	#N/A	0.009518	#N/A	0.379656	#N/A	0.033114	#N/A
LD6.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD6.Sum.Sq	228.8559	3.866659	75.75467	28	4.978244	0.229648	64.8676	3.315532	0.998205	0.921976	4.745817	0.539689	3.367705	18.64109	0.352297	0.930032	0.311464	3.422034
LD6.Mean.Sq	38.14266	3.866659	12.62578	1	4.978244	0.057412	64.8676	0.828883	0.998205	0.230494	4.745817	0.134922	3.367705	4.660272	0.352297	0.232508	0.311464	0.855508
LD6.F.value	38.14266	3.866659	12.62578	#N/A	86.71085	#N/A	78.25905	#N/A	4.330722	#N/A	35.17446	#N/A	0.722641	#N/A	1.515205	#N/A	0.364069	#N/A
LD6.Pr..F.	3.24E-12	0.059239	7.3E-07	#N/A	0.00074	#N/A	0.000901	#N/A	0.105898	#N/A	0.004051	#N/A	0.443168	#N/A	0.285777	#N/A	0.578799	#N/A
LD7.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD7.Sum.Sq	103.165	25.06489	90.41066	28	0.290682	1.355846	23.75752	3.352534	83.96275	10.67244	0.341974	2.030605	0.687521	2.357702	3.20348	2.978071	3.231615	5.252803
LD7.Mean.Sq	17.19417	25.06489	15.06844	1	0.290682	0.338962	23.75752	0.838133	83.96275	2.66811	0.341974	0.507651	0.687521	0.589426	3.20348	0.744518	3.231615	1.313201
LD7.F.value	17.19417	25.06489	15.06844	#N/A	0.857565	#N/A	28.34575	#N/A	31.469	#N/A	0.67364	#N/A	1.166425	#N/A	4.302759	#N/A	2.460869	#N/A
LD7.Pr..F.	3.14E-08	2.72E-05	1.25E-07	#N/A	0.406835	#N/A	0.005989	#N/A	0.004961	#N/A	0.457882	#N/A	0.340908	#N/A	0.106708	#N/A	0.191793	#N/A
LD8.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD8.Sum.Sq	34.09137	27.6853	87.70943	28	0.959742	0.873954	11.09505	4.834813	47.79713	7.04595	2.096866	1.263596	35.85273	7.662154	0.462757	2.339805	17.13044	3.979728
LD8.Mean.Sq	5.681895	27.6853	14.61824	1	0.959742	0.218489	11.09505	1.208703	47.79713	1.761488	2.096866	0.315899	35.85273	1.915538	0.462757	0.584951	17.13044	0.994932
LD8.F.value	5.681895	27.6853	14.61824	#N/A	4.392641	#N/A	9.179303	#N/A	27.13453	#N/A	6.637777	#N/A	18.71679	#N/A	0.791103	#N/A	17.2177	#N/A
LD8.Pr..F.	0.00058	1.36E-05	1.7E-07	#N/A	0.104139	#N/A	0.038791	#N/A	0.006476	#N/A	0.061562	#N/A	0.012386	#N/A	0.424025	#N/A	0.014267	#N/A
LD9.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD9.Sum.Sq	5.933463	0.150814	66.81116	28	13.07052	1.527205	7.811291	2.053096	0.003023	1.6385	9.674978	0.357913	0.090346	3.857286	34.59781	15.08671	1.714009	3.479292
LD9.Mean.Sq	0.988911	0.150814	11.13519	1	13.07052	0.381801	7.811291	0.513274	0.003023	0.409625	9.674978	0.089478	0.090346	0.964321	34.59781	3.771677	1.714009	0.869823
LD9.F.value	0.988911	0.150814	11.13519	#N/A	34.23383	#N/A	15.21856	#N/A	0.00738	#N/A	108.1267	#N/A	0.093689	#N/A	9.173057	#N/A	1.970526	#N/A
LD9.Pr..F.	0.451629	0.700696	2.42E-06	#N/A	0.004257	#N/A	0.017525	#N/A	0.935667	#N/A	0.000483	#N/A	0.774808	#N/A	0.03883	#N/A	0.233064	#N/A
LD10.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD10.Sum.Sq	10.87871	8.178141	21.80373	28	9.157899	5.857883	0.090862	0.717949	5.694297	3.635091	6.227976	3.912486	4.541741	2.139769	0.402794	7.175557	3.8663	4.561264
LD10.Mean.Sq	1.813119	8.178141	3.633954	1	9.157899	1.464471	0.090862	0.179487	5.694297	0.908773	6.227976	0.978121	4.541741	0.534942	0.402794	1.793889	3.8663	1.140316
LD10.F.value	1.813119	8.178141	3.633954	#N/A	6.253384	#N/A	0.506232	#N/A	6.26592	#N/A	6.367282	#N/A	8.490151	#N/A	0.224537	#N/A	3.390551	#N/A
LD10.Pr..F.	0.132674	0.007923	0.00859	#N/A	0.066718	#N/A	0.516068	#N/A	0.06654	#N/A	0.065124	#N/A	0.043513	#N/A	0.660311	#N/A	0.139381	#N/A
LD11.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD11.Sum.Sq	2.693558	2.545603	25.97007	28	1.469313	3.22502	1.694994	1.411646	0.260299	0.988865	3.708867	1.899794	3.34654	6.290727	10.905	5.784017	7.130666	8.399932
LD11.Mean.Sq	0.448926	2.545603	4.328345	1	1.469313	0.806255	1.694994	0.352911	0.260299	0.247216	3.708867	0.474948	3.34654	1.572682	10.905	1.446004	7.130666	2.099983
LD11.F.value	0.448926	2.545603	4.328345	#N/A	1.822392	#N/A	4.802888	#N/A	1.052921	#N/A	7.808988	#N/A	2.127919	#N/A	7.541469	#N/A	3.395583	#N/A
LD11.Pr..F.	0.839512	0.121828	0.00328	#N/A	0.248363	#N/A	0.09353	#N/A	0.362833	#N/A	0.049088	#N/A	0.218395	#N/A	0.051577	#N/A	0.13916	#N/A
LD12.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD12.Sum.Sq	2.068268	0.022559	22.04903	28	7.941842	1.669572	3.865028	6.92486	1.42932	0.364538	1.294122	5.349991	5.908439	6.363824	0.014451	3.568815	1.61839	3.7584
LD12.Mean.Sq	0.344711	0.022559	3.674839	1	7.941842	0.417393	3.865028	1.731215	1.42932	0.091134	1.294122	1.337498	5.908439	1.590956	0.014451	0.892204	1.61839	0.9396
LD12.F.value	0.344711	0.022559	3.674839	#N/A	19.02726	#N/A	2.232552	#N/A	15.68364	#N/A	0.967569	#N/A	3.713766	#N/A	0.016197	#N/A	1.722424	#N/A
LD12.Pr..F.	0.906975	0.881687	0.008105	#N/A	0.012043	#N/A	0.209437	#N/A	0.016674	#N/A	0.380978	#N/A	0.126234	#N/A	0.904871	#N/A	0.259622	#N/A
LD13.Df	6	1	6	28	1	4	1	4	1	4	1	4	1	4	1	4	1	4
LD13.Sum.Sq	0.440005	0.164573	10.99399	28	1.257514	6.940161	0.322275	3.22848	0.120018	5.344673	0.870672	3.848733	2.587168	1.322054	1.426086	3.835361	4.57483	3.480537
LD13.Mean.Sq	0.073334	0.164573	1.832332	1	1.257514	1.73504	0.322275	0.80712	0.120018	1.336168	0.870672	0.962183	2.587168	0.330514	1.426086	0.95884	4.57483	0.870134
LD13.F.value	0.073334	0.164573	1.832332	#N/A	0.724775	#N/A	0.39929	#N/A	0.089822	#N/A	0.904892	#N/A	7.827721	#N/A	1.487304	#N/A	5.257614	#N/A
LD13.Pr..F.	0.998217	0.688064	0.128792	#N/A	0.442548	#N/A	0.56177	#N/A	0.779331	#N/A	0.39534	#N/A	0.048921	#N/A	0.289626	#N/A	0.083585	#N/A

Suppl. Table 4

	control1	control2	control3	grazing1	grazing2	grazing3
CATEGORY	PAIR	PAIR	PAIR	PAIR	PAIR	PAIR
TOTAL_READS	14126316	13631488	14424014	14608614	13581456	14215780
PF_READS	14126316	13631488	14424014	14608614	13581456	14215780
PCT_PF_READS	1	1	1	1	1	1
PF_NOISE_READS	31	27	17	32	25	28
PF_READS_ALIGNED	9556951	8889665	11842342	11567028	8379063	10202334
PCT_PF_READS_ALIGNED	0.676535	0.652142	0.821016	0.791795	0.616949	0.717677
PF_ALIGNED_BASES	8.49E+08	7.97E+08	1.06E+09	1.03E+09	7.47E+08	9.09E+08
PF_HQ_ALIGNED_READS	9177614	8574229	11564499	11267668	8026894	9848824
PF_HQ_ALIGNED_BASES	8.16E+08	7.69E+08	1.03E+09	1E+09	7.16E+08	8.78E+08
PF_HQ_ALIGNED_Q20_BASES	7.86E+08	7.42E+08	9.97E+08	9.73E+08	6.94E+08	8.47E+08
PF_HQ_MEDIAN_MISMATCHES	0	64	0	0	0	0
PF_MISMATCH_RATE	0.003548	0.732	0.003728	0.003525	0.00382	0.004008
PF_HQ_ERROR_RATE	0.003185	0.73188	0.003648	0.003408	0.00335	0.003761
PF_INDEL_RATE	0.000183	0.001259	0.000187	0.000159	0.000203	0.000146
MEAN_READ_LENGTH	90	90	90	90	90	90
READS_ALIGNED_IN_PAIRS	4712026	8429131	11748855	11467735	8260268	10090101
PCT_READS_ALIGNED_IN_PAIRS	0.982879	0.948194	0.992106	0.991416	0.985822	0.988999
BAD_CYCLES	0	0	0	0	0	0
STRAND_BALANCE	0.498189	0.500276	0.500109	0.500042	0.499766	0.499891
PCT_CHIMERAS	0.000931	0.001063	0.000933	0.000907	0.000936	0.000995
PCT_ADAPTER	0.000005	0.000003	0.000006	0.000005	0.000064	0.00001

Suppl. Table 5

control1 vs grazing1													
geneID	Pt-control-1-Expression	Pt-grazing-1-Expression	Pt-control-1-FPKM	Pt-grazing-1-FPKM	log2 Ratio(Pt-grazing-1/Pt-control-1)	P-value	Symbol	KEGG Orthology	GO Component	GO Function	GO Process		GO Process
7199224	0	38.68	0.001	55.78	15.76746031	1.26E-11	PHATRDRAFT_24069	-	GO:0016020//membrane;GO:0005739//mitochondrion	GO:0003824//catalytic activity	-		-
7198882	0	27	0.001	18.82	14.19997901	1.82E-08	PHATRDRAFT_50208	-	-	-	-		-
7196052	0	5	0.001	16.5	14.0101784	0.0378518	PHATRDRAFT_9319	K12827|1|7e-27|116|cre:CHLREDRAFT_115043|splicing factor 3A subunit 3	GO:0044464	GO:0046914//transition metal ion binding	-		-
7202473	0	6	0.001	13.86	13.75863964	0.01954026	PHATRDRAFT_6789	-	-	GO:0003824//catalytic activity	-		-
7196933	0	13.8	0.001	12.6	13.62113611	0.000190911	PHATRDRAFT_9211	-	-	GO:0016787//hydrolase activity	-		-
7199713	0	6	0.001	10.12	13.30492167	0.01954026	PHATRDRAFT_34230	-	-	-	-		-
7205113	0	5.97	0.001	9.7	13.24376903	0.0378518	PHATRDRAFT_bd1537	-	-	-	-		-
7202956	0	7	0.001	9.58	13.22580994	0.01008726	PHATRDRAFT_38110	-	-	-	-		-
7203148	0	5	0.001	9.44	13.20457114	0.0378518	PHATRDRAFT_38312	K15153|1|9e-20|94.0|vvi:100247653|mediator of RNA polymerase II transcription subunit 31	GO:0043231//intracellular membrane-bounded organelle;GO:0043234//protein complex	GO:0001076//RNA polymerase II transcription factor binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199942	0	5	0.001	9.37	13.19383333	0.0378518	Rab5c	K07976|1|4e-23|105|osa:4348725|Rab family, other;K07888|5|2e-20|96.3|ppp:PHYPADRAFT_179911|Ras-related protein Rab-5B	-	GO:0032550	GO:0035556//intracellular signal transduction		GO:0035556//intracellular signal transduction
7199478	0	15	0.001	8.42	13.03960452	5.09E-05	PHATRDRAFT_50641	-	-	-	-		-
7199176	0	17.69	0.001	7.1	12.79360331	1.36E-05	PHATRDRAFT_50348	K00995|1|3e-23|108|cme:CMN196C|CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5];K08744|2|2e-21|102|pop:POPTR_856644|cardiolipin synthase [EC:2.7.8.-]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006644//phospholipid metabolic process		GO:0006644//phospholipid metabolic process
7200568	0	9.56	0.001	6.95	12.76279726	0.00268818	PHATRDRAFT_45465	-	-	-	-		-
7205157	0	5	0.001	6.54	12.67507492	0.0378518	PHATRDRAFT_bd1248	-	-	-	-		-
7200693	0	8.12	0.001	6.23	12.60501645	0.00520734	PHATRDRAFT_35176	-	-	-	-		-
7200044	0	8	0.001	6.19	12.59572369	0.00520734	PHATRDRAFT_35048	-	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding	-		-
7202848	0	8	0.001	5	12.28771238	0.00520734	PHATRDRAFT_28937	K00766|1|1e-81|301|vvi:100255305|anthranilate phosphoribosyltransferase [EC:2.4.2.18]	-	GO:0016763//transferase activity, transferring pentosyl groups	GO:0006568//tryptophan metabolic process		GO:0006568//tryptophan metabolic process
7196932	0	11.05	0.001	4.87	12.24970606	0.000716382	PHATRDRAFT_54051	-	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7199511	0	7	0.001	3.71	11.85720347	0.01008726	PHATRDRAFT_44993	-	-	-	-		-
7197305	0	7	0.001	3.52	11.78135971	0.01008726	PHATRDRAFT_43570	-	-	-	-		-
7200092	0	6	0.001	2.76	11.43045255	0.01954026	PHATRDRAFT_45206	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204009	0	5	0.001	2.67	11.38262403	0.0378518	PHATR_44055	K00599|1|2e-44|178|ath:AT3G27180|[EC:2.1.1.-]	-	-	-		-
7201769	0	7	0.001	2.66	11.37721053	0.01008726	PHATRDRAFT_46394	-	-	-	-		-
7197950	0	8	0.001	2.52	11.29920802	0.00520734	PHATRDRAFT_44275	-	-	-	-		-
7194703	0	5	0.001	2.06	11.00842862	0.0378518	PHATRDRAFT_39006	-	-	-	-		-
7198783	0	6	0.001	1.93	10.91438513	0.01954026	PHATRDRAFT_50006	K05941|1|6e-12|71.6|aly:ARALYDRAFT_333720|glutathione gamma-glutamylcysteinyltransferase [EC:2.3.2.15]	-	GO:0043169//cation binding;GO:0016755	GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process		GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process
7200946	0	5	0.001	1.7	10.73131903	0.0378518	PHATRDRAFT_35640	-	-	-	-		-

7202341	0	6	0.001	1.46	10.51175265	0.01954026	PHATRDRAFT_37404	-	-	GO:0060089;GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication		GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication
7196633	0	5	0.001	1.14	10.15481811	0.0378518	PHATRDRAFT_42932	K11293|1|4e-13|75.9|zma:732736|protein HIRA/HIR1;K14963|2|6e-12|72.0|mtr:MTR_4g119620|COMPASS component SWD3	-	-	-		-
7204966	0.94	39.44	0.46	18.28	5.312488399	6.53E-12	PHATRDRAFT_bd1252	-	-	GO:0003824//catalytic activity	-		-
7198322	1	13	0.49	5.97	3.606877277	0.00148391	PHATRDRAFT_49693	-	-	-	-		-
7196945	1	12	0.46	5.2	3.498805857	0.0026956	PHATRDRAFT_43218	-	-	-	-		-
7198469	2.17	21.62	2.21	20.65	3.224023507	6.82E-05	PHATRDRAFT_40594	-	-	-	-		-
7203319	2	20	0.59	5.5	3.220644759	0.000121652	PHATRDRAFT_48186	K01609|1|6e-22|105|sbi:SORBI_06g019430|indole-3-glycerol phosphate synthase [EC:4.1.1.48]	-	GO:0016831//carboxy-lyase activity	-		-
7202769	2	19	0.83	7.39	3.154391123	0.000216148	PHATRDRAFT_47526	K14546|1|3e-06|52.4|ppp:PHYPADRAFT_234339|U3 small nucleolar RNA-associated protein 5	-	-	-		-
7201878	1	9	2.44	20.61	3.078391452	0.01569284	PHATRDRAFT_12985	K15033|1|6e-18|87.4|vcn:VOLCADRAFT_104814|peptidyl-tRNA hydrolase ICT1 [EC:3.1.1.29]	-	GO:0008079//translation termination factor activity	GO:0006412//translation		GO:0006412//translation
7204460	1	9	0.81	6.83	3.075891765	0.01569284	PHATR_46930	-	-	-	-		-
7200374	1	9	0.59	4.96	3.071553261	0.01569284	PHATRDRAFT_27166	K00058|1|2e-95|348|olu:OSTLU_39000|D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7204949	1	8.44	3.31	26.25	2.987414301	0.0278798	PHATRDRAFT_bd1491	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7197626	1	8	0.55	4.15	2.915607813	0.0278798	PHATRDRAFT_44622	K13076|1|3e-12|72.0|bdi:100826592|delta8-fatty-acid desaturase [EC:1.14.19.4]	-	-	GO:0044238		GO:0044238
7197668	1	8	0.41	3.08	2.909234536	0.0278798	PHATRDRAFT_33858	-	-	-	-		-
7199819	3	22	1.63	11.23	2.784414058	0.000167574	PHATRDRAFT_19427	K00833|1|4e-37|154|cme:CMG023C|adenosylmethionine-8-amino-7-oxononanoate aminotransferase [EC:2.6.1.62];K00819|2|8e-36|150|sbi:SORBI_01g013600|ornithine--oxo-acid transaminase [EC:2.6.1.13]	-	GO:0043168//anion binding;GO:0008483//transaminase activity	GO:0006768//biotin metabolic process		GO:0006768//biotin metabolic process
7195157	1	7	0.67	4.43	2.725073698	0.0491266	PHATRDRAFT_48871	-	-	-	-		-
7199635	1	7	1.23	8.1	2.719263592	0.0491266	PHATRDRAFT_11438	K11778|1|6e-43|172|pop:POPTR_172325|ditrans,polycis-polyprenyl diphosphate synthase [EC:2.5.1.87]	-	GO:0016740//transferase activity	-		-
7199907	1	7	0.57	3.75	2.717856771	0.0491266	PHATRDRAFT_44803	-	-	-	-		-
7197502	1	7	1.18	7.76	2.717269793	0.0491266	PHATRDRAFT_32906	-	-	-	-		-
7195876	1	7	1.72	11.31	2.717118459	0.0491266	PHATRDRAFT_4593	K03593|1|6e-40|161|gmx:100817299|ATP-binding protein involved in chromosome partitioning	-	GO:0032550	-		-
7202523	1	7	1.01	6.64	2.716827949	0.0491266	PHATRDRAFT_37569	-	-	-	-		-
7198564	1	7	2.77	18.19	2.715187662	0.0491266	PHATRDRAFT_6066	-	-	-	-		-
7202317	1	7	1.25	8.2	2.713695815	0.0491266	PHATRDRAFT_37441	K07018|1|8e-11|65.5|sbi:SORBI_04g029880|	-	-	-		-

7201027	1	7	0.42	2.74	2.70571466	0.0491266	PHATRDRAFT_20335	K12818|1|4e-123|440|cre:CHLREDRAFT_127996|ATP-dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13];K12813|2|1e-122|439|ppp:PHYPADRAFT_180557|pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 [EC:3.6.4.13]	-	GO:0042623//ATPase activity, coupled;GO:0032550	-		-
7197003	1	7	0.77	5.02	2.704757013	0.0491266	PHATRDRAFT_1990	K01529|1|4e-70|263|olu:OSTLU_50012|[EC:3.6.1.-];K03257|3|8e-63|239|pop:POPTR_716781|translation initiation factor 4A	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7200155	1.22	8	2.87	17.71	2.62544157	0.0278798	H3-1a	K11253|1|6e-69|256|smo:SELMODRAFT_103546|histone H3	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7201777	2	13	1.18	7.18	2.605196984	0.00617528	Albino3	K03217|1|2e-52|205|vvi:100260431|preprotein translocase subunit YidC	GO:0031224//intrinsic component of membrane	-	-		-
7204472	1.83	11.87	1.07	6.51	2.605046747	0.00487516	PHATR 46952	-	-	-	-		-
7201488	2	12	10.27	57.97	2.496870304	0.01057166	PHATRDRAFT_12737	K09250|1|2e-20|95.1|zma:100857032|cellular nucleic acid-binding protein	-	GO:0046914//transition metal ion binding;GO:0003676//nucleic acid binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196293	3	17	2.6	13.83	2.411217628	0.00242416	PHATRDRAFT 42611	-	-	-	-		-
7203619	3	16	2.23	11.15	2.321928095	0.00406408	PHATRDRAFT_14962	K01760|1|3e-51|201|olu:OSTLU_88245|cystathionine beta-lyase [EC:4.4.1.8]	-	GO:0043168//anion binding;GO:0003824//catalytic activity	-		-
7195052	3	16	2.4	12	2.321928095	0.00406408	PHATRDRAFT 39329	-	-	-	-		-
7200413	3	16	3.08	15.39	2.320990976	0.00406408	PHATRDRAFT 35406	-	-	-	-		-
7199617	4	21	2.31	11.39	2.30180299	0.000956022	PHATRDRAFT_708	K14780|1|2e-112|404|ota:Ot05g03840|ATP-dependent RNA helicase DHX37/DHR1 [EC:3.6.4.13];K12818|2|3e-78|290|bdi:100842452|ATP-dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550;GO:0042623//ATPase activity, coupled	GO:0009987//cellular process		GO:0009987//cellular process
7201332	2	10	1.89	8.89	2.233797185	0.0302076	PHATRDRAFT_35973	-	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7201578	2	10	1.35	6.34	2.231523433	0.0302076	PHATRDRAFT 46491	-	-	-	-		-
7203022	5	25	9.16	42.97	2.229910274	0.000379078	PHATRDRAFT_14549	K06639|1|3e-10|62.8|ppp:PHYPADRAFT_88026|cell division cycle 14 [EC:3.1.3.48]	-	GO:0004721//phosphoprotein phosphatase activity	GO:0006470//protein dephosphorylation		GO:0006470//protein dephosphorylation
7200878	2	10	3.32	15.56	2.228586914	0.0302076	PHATRDRAFT_27286	K09578|1|5e-25|112|ppp:PHYPADRAFT_108242|peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 [EC:5.2.1.8]	-	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7197264	2	10	0.9	4.21	2.225823327	0.0302076	PHATRDRAFT 43742	-	-	-	-		-
7203446	3	14	1.32	5.78	2.130531563	0.01116904	PHATRDRAFT 48061	-	-	-	-		-
7197536	6	27	4.56	19.24	2.07700307	0.000397742	PHATRDRAFT 43478	-	-	-	-		-
7196021	3	13	5.75	23.39	2.024258001	0.0182795	PHATRDRAFT_9251	-	-	GO:0016787//hydrolase activity;GO:0097159//organic cyclic compound binding	-		-
7198927	3	13	1.4	5.67	2.017921908	0.0182795	PHATRDRAFT 50125	-	-	-	-		-
7202585	4	17	1.98	7.9	1.996352223	0.00686868	PHATRDRAFT 47469	-	-	-	-		-
7204946	26.13	110.31	14.06	55.66	1.985044314	1.57E-12	PHATRDRAFT_bd1806	K13862|1|3e-19|95.1|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7200872	6.43	26.86	2.52	9.88	1.971087308	0.0006402	PHATRDRAFT_45715	-	GO:0044424	GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0032550	GO:0006412//translation		GO:0006412//translation
7194976	7	29	5.18	20.15	1.959755836	0.000402462	PHATRDRAFT 48903	-	-	-	-		-

7201329	3	12	1.96	7.37	1.910810965	0.0296226	PHATRDRAFT_46085	K04040|1|2e-114|410|vcn:VOLCADRAFT_80530|chlorophyll synthase [EC:2.5.1.62]	GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0004659//prenyltransferase activity	GO:0006351//transcription, DNA-templated;GO:0016109;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0009668;GO:0015995//chlorophyll biosynthetic process;GO:0048869//cellular developmental process;GO:0009658//chloroplast organization;GO:0009887//organ morphogenesis;GO:0000097//sulfur amino acid		GO:0006351//transcription, DNA-templated;GO:0016109;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0009668;GO:0015995//chlorophyll biosynthetic process;GO:0048869//cellular developmental process;GO:0009658//chloroplast organization;GO:0009887//organ morphogenesis;GO:0000097//sulfur amino acid
7197074	5	19	2.81	10	1.831357964	0.00666778	PHATRDRAFT_32487	-	-	-	-		-
7194685	26	98	11.69	41.32	1.821565324	3.24E-10	PHATRDRAFT_48701	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196434	3	11	2.8	9.65	1.785102115	0.0474758	PHATRDRAFT_31927	K13337|1|2e-27|121|aly:ARALYDRAFT_477595|peroxin-19	GO:0042579//microbody	GO:0005515//protein binding	GO:0006996//organelle organization		GO:0006996//organelle organization
7203168	3	11	3.93	13.54	1.784626521	0.0474758	PHATRDRAFT_38235	-	-	-	-		-
7201708	3	11	2.59	8.92	1.784091612	0.0474758	PHATRDRAFT_46570	-	-	GO:0003824//catalytic activity	GO:0044238		GO:0044238
7204992	3	11	2.52	8.67	1.78260826	0.0474758	PHATRDRAFT_bd1539	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7199525	6	22	4.73	16.27	1.782302162	0.00403834	PHATRDRAFT_45011	K11982|1|8e-07|53.1|bdi:100833984|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19];K10601|2|1e-06|52.4|zma:100217233|E3 ubiquitin-protein ligase synoviolin [EC:6.3.2.19];K05283|4|7e-06|50.1|aly:ARALYDRAFT_354960|phosphatidylinositol glycan, class W [EC:2.3.-.-]	-	GO:0046914//transition metal ion binding	-		-
7202849	3	11	1.82	6.26	1.782224207	0.0474758	PHATRDRAFT_37927	-	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0018130;GO:0044710		GO:0018130;GO:0044710
7198858	3	11	0.93	3.19	1.778253803	0.0474758	PHATRDRAFT_50164	-	-	-	-		-
7204081	8	29	6.84	23.26	1.765782867	0.000964946	PHATR_44152	-	-	-	-		-
7202544	5	18	1.7	5.74	1.755515991	0.01048118	RAD4	K10838|1|2e-30|133|ath:AT5G16630|xeroderma pigmentosum group C-complementing protein	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding	GO:0006281//DNA repair		GO:0006281//DNA repair
7201486	7	25	7.68	25.74	1.744833837	0.00245178	PHATRDRAFT_20677	K13606|1|2e-12|70.9|vvi:100259397|chlorophyll(ide) b reductase [EC:1.1.1.294];K09841|5|4e-11|66.6|vvi:100265470|xanthoxin dehydrogenase [EC:1.1.1.288]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7197316	4	14	1.18	3.88	1.717269793	0.0276868	PHATRDRAFT_43587	K12855|1|1e-09|64.3|smo:SELMODRAFT_172051|pre-mRNA-processing factor 6;K12869|5|4e-09|62.4|gmx:100791616|crooked neck	GO:0044464	-	GO:0010467//gene expression		GO:0010467//gene expression

7203383	6.31	21.8	3.08	9.99	1.697554327	0.00628786	PHATRDRAFT_22332	K05656|1|7e-56|216|mtr:MTR_5g033080|ATP-binding cassette, subfamily B (MDR/TAP), member 9;K05657|2|2e-45|182|smo:SELMODRAFT_445846|ATP-binding cassette, subfamily B (MDR/TAP), member 10;K05658|4|1e-38|159|vvi:100248698|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7197229	5	17	1.45	4.63	1.674959293	0.01632922	PHATRDRAFT_18335	K01408|1|1e-136|486|ath:AT2G41790|insulysin [EC:3.4.24.56]	-	GO:0043169//cation binding;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0008152//metabolic process		GO:0008152//metabolic process
7201522	4.54	14.94	4.25	13.15	1.629528053	0.0276868	PHATRDRAFT_35903	-	-	-	-		-
7201224	4	13	21.29	65.11	1.612703189	0.043166	PHATRDRAFT_12578	K12160|1|4e-15|77.8|olu:OSTLU_42569|small ubiquitin-related modifier	-	-	-		-
7199333	7.86	25.6	8.17	24.98	1.612365493	0.00245178	PHATRDRAFT_16982	K00799|1|5e-32|136|rcu:RCOM_0360880|glutathione S-transferase [EC:2.5.1.18]	-	-	-		-
7197273	4	13	7.77	23.71	1.609509159	0.043166	PHATRDRAFT_33045	-	-	-	-		-
7198423	9	29	3.22	9.72	1.593895625	0.00211386	PHATRDRAFT_23444	K06207|1|0.0|666|bdi:100827491|GTP-binding protein	GO:0009536//plastid	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7198132	6	19	5.1	15.16	1.571700601	0.01487022	PHATRDRAFT_19191	K15456|1|1e-32|139|vvi:100250833|protein KTI12	-	-	-		-
7201461	7	22	2.87	8.47	1.561311233	0.00884932	PHATRDRAFT_27757	K00366|1|6e-122|436|gmx:100775519|ferredoxin-nitrite reductase [EC:1.7.7.1]	-	GO:0046906//tetrapyrrole binding;GO:0051540;GO:0016664	GO:0044710		GO:0044710
7195339	10.86	33.96	3.35	9.81	1.550092041	0.000846796	PHATRDRAFT_49118	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7202298	1976	6054	6117.03	17603.74	1.524978712	0	PHATRDRAFT_37403	-	-	-	-		-
7201411	8	24	3.4	9.58	1.49449091	0.0079692	PHATRDRAFT_46048	-	-	-	-		-
7198005	6	18	3.43	9.66	1.493814613	0.022557	PHATRDRAFT_33692	-	-	-	-		-
7199271	6	18	4.73	13.32	1.493681994	0.022557	PHATRDRAFT_55206	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7199905	5	15	5	14.08	1.493647334	0.0384656	PHATRDRAFT_44801	-	-	-	-		-
7202836	5	15	4.92	13.85	1.493155756	0.0384656	PHATRDRAFT_21791	K12492|1|2e-21|101|pop:POPTR_717441|ADP-ribosylation factor GTPase-activating protein 1;K12486|3|7e-21|99.4|bdi:100832113|stromal membrane-associated protein	-	GO:0005083//small GTPase regulator activity;GO:0046914//transition metal ion binding	GO:0032012//regulation of ARF protein signal transduction		GO:0032012//regulation of ARF protein signal transduction
7198992	10	30	8.76	24.65	1.492584872	0.00288334	PHATRDRAFT_55177	K00797|1|3e-91|333|cme:CMP329C|spermidine synthase [EC:2.5.1.16]	-	GO:0003824//catalytic activity	-		-
7201156	6	18	4.46	12.54	1.491421733	0.022557	RAD51-g1	K04482|1|7e-110|395|cre:CHLREDRAFT_190735|DNA repair protein RAD51	GO:0043231//intracellular membrane-bounded organelle	GO:0032550;GO:0042623//ATPase activity, coupled;GO:0003677//DNA binding	GO:0006281//DNA repair;GO:0007127//meiosis I		GO:0006281//DNA repair;GO:0007127//meiosis I
7194706	12	35	21.84	59.78	1.452690041	0.001568808	PHATRDRAFT_15134	-	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7195799	7	20	2.84	7.62	1.423900068	0.0199832	PHATRDRAFT_49433	-	-	-	-		-
7200741	32	90	16.49	43.5	1.399424002	6.41E-07	PHATRDRAFT_45560	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated

7197928	8	22	4.57	11.79	1.367297648	0.01757712	PHATRDRAFT_44700	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204806	27	74	10.99	28.26	1.362570079	1.00E-05	PHATRDRAFT_bd1329	-	-	-	-		-
7194965	7	19	6.46	16.45	1.348481514	0.0296088	PHATRDRAFT_39469	-	-	-	-		-
7201032	10	27	8.59	21.76	1.34094852	0.00923896	PHATRDRAFT_35809	-	-	-	-		-
7202592	12	32	14.01	35.05	1.322957488	0.00490246	PHATRDRAFT_14054	K06889|1|8e-07|52.4|rcu:RCOM_1047030|	-	-	-		-
7197596	24	64	18.61	46.55	1.322703112	6.03E-05	PHATRDRAFT_43293	-	-	-	-		-
7202713	14	37	12.88	31.93	1.309779959	0.00262036	PHATRDRAFT_21868	K01495|1|3e-52|203|cme:CMF055C|GTP cyclohydrolase I [EC:3.5.4.16]	GO:0044424	GO:0003933//GTP cyclohydrolase activity	GO:0009396//folic acid-containing compound biosynthetic process		GO:0009396//folic acid-containing compound biosynthetic process
7201672	13	34	3.51	8.6	1.292865629	0.00429928	PHATRDRAFT_46516	K14521|1|0.0|761|cre:CHLREDRAFT_137045|N-acetyltransferase 10 [EC:2.3.1.-]	-	GO:0016407//acetyltransferase activity	-		-
7201013	10	26	18.71	45.66	1.287121301	0.01341546	PHATRDRAFT_45933	-	-	-	-		-
7200617	12	31	11.07	26.84	1.277729449	0.00707218	CDH1	K03364|1|5e-124|442|ppp:PHYPADRAFT_58645|cell division cycle 20-like protein 1, cofactor of APC complex	GO:0043231//intracellular membrane-bounded organelle	-	GO:0042023//DNA endoreduplication		GO:0042023//DNA endoreduplication
7204001	48	124	26.67	64.63	1.276986167	4.89E-08	PHATR_44046	-	-	-	-		-
7200184	9.16	23.6	7.16	17.31	1.273574232	0.0223318	PHATRDRAFT_34724	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202980	7	18	2.65	6.4	1.272079545	0.0434208	PHATRDRAFT_47846	-	-	-	-		-
7198421	7	18	4.19	10.11	1.270760848	0.0434208	PHATRDRAFT_49728	-	-	-	-		-
7204195	7	18	3.08	7.42	1.268488836	0.0434208	PHATR_43981	-	-	-	-		-
7195022	9	23	8.09	19.39	1.261101196	0.0223318	PHATRDRAFT_22677	K04712|1|1e-88|324|smo:SELMODRAFT_94775|sphingolipid delta-4 desaturase [EC:1.14.-.-]	GO:0031224//intrinsic component of membrane	GO:0016491//oxidoreductase activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7195028	9	23	5.09	12.19	1.259960565	0.0223318	PHATRDRAFT_29821	K01206|1|4e-07|54.7|gmx:100775293|alpha-L-fucosidase [EC:3.2.1.51]	-	GO:0015928//fucosidase activity	GO:0019318//hexose metabolic process		GO:0019318//hexose metabolic process
7195700	15	38	9.51	22.6	1.248805526	0.00328456	PHATRDRAFT_49237	-	-	-	-		-
7195287	17	43	5.21	12.35	1.245155764	0.001761248	PHATRDRAFT_54983	K00360|1|0.0|782|ppp:PHYPADRAFT_184973|nitrate reductase (NADH) [EC:1.7.1.1];K00387|4|1e-95|349|olu:OSTLU_3554|sulfite oxidase [EC:1.8.3.1]	-	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016661;GO:0000166//nucleotide binding;GO:0050662//coenzyme binding	GO:0042126//nitrate metabolic process		GO:0042126//nitrate metabolic process
7204747	8	20	33.87	79.6	1.232760444	0.0373748	PHATR_13253	-	-	-	-		-
7197195	10	25	6.85	16.07	1.230194036	0.01931924	PHATRDRAFT_43503	-	-	-	-		-
7203897	12	30	8.27	19.4	1.230097418	0.01012892	PHATR_44147	-	-	-	-		-
7204088	8	20	8.09	18.97	1.229508071	0.0373748	PHATR_10362	K06889|1|1e-48|191|cme:CMT218C|	-	-	-		-
7195952	8	20	3.86	9.05	1.229316945	0.0373748	PHATRDRAFT_42569	-	-	-	-		-
7198721	8	20	6.01	14.09	1.229234716	0.0373748	PHATRDRAFT_50022	-	-	-	-		-
7197953	8	20	6.77	15.87	1.229074389	0.0373748	PHATRDRAFT_54217	-	-	-	-		-
7196655	12	30	5.1	11.95	1.228441466	0.01012892	PHATRDRAFT_42451	-	-	-	-		-
7200327	21	52	6.83	15.85	1.214525357	0.000724726	PHATRDRAFT_45142	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197279	17	42	18.03	41.8	1.213103546	0.00249364	PHATRDRAFT_43766	K00876|1|9e-10|62.4|pop:POPTR_815577|uridine kinase [EC:2.7.1.48]	GO:0009536//plastid	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7198258	11	27	12.69	29.21	1.202770289	0.01668706	PHATRDRAFT_16067	K13412|1|5e-51|199|pop:POPTR_256143|calcium-dependent protein kinase [EC:2.7.11.1];K00908|4|7e-49|192|cme:CMF051C|Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17]	-	GO:0004674//protein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7196194	36	88	24.41	55.97	1.197181453	1.29E-05	PHATRDRAFT_8678	-	-	-	-		-
7202633	58.31	140	32.83	73.93	1.171145163	5.13E-08	PHATRDRAFT_47569	-	-	-	-		-

7204230	18	43	10.56	23.67	1.164449871	0.00304252	PHATR_44047	K11806|1|1e-103|375|pop:POPTR_836650|WD repeat and SOF domain-containing protein 1	–	–	–		–
7197512	14	33	11.68	25.82	1.144448726	0.01069626	PHATRDRAFT_9855	K03086|1|6e-39|159|olu:OSTLU_41331|RNA polymerase primary sigma factor;K03093|3|1e-23|108|pop:POPTR_819521|RNA polymerase sigma factor	–	GO:0003676//nucleic acid binding;GO:0000996;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197193	49	115	17.19	37.83	1.137961232	1.61E-06	PHATRDRAFT_43498	–	GO:0043231//intracellular membrane-bounded organelle	–	GO:0015031//protein transport		GO:0015031//protein transport
7200959	50	117	25.88	56.79	1.133799294	1.41E-06	PHATRDRAFT_45852	K03834|1|2e-19|95.9|cre:CHLREDRAFT_205979|tyrosine-specific transport protein	–	–	–		–
7200294	9	21	4.82	10.56	1.131504783	0.0457492	PHATRDRAFT_34698	–	–	–	–		–
7195664	9	21	21.34	46.75	1.131406189	0.0457492	PHATRDRAFT_49172	–	GO:0043231//intracellular membrane-bounded organelle;GO:0019866//organelle inner membrane	GO:0043169//cation binding	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7203780	9	21	7.69	16.84	1.130836635	0.0457492	Lhcr5	K08907|1|5e-18|90.1|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08916|2|7e-15|79.7|gmx:100789786|light-harvesting complex II chlorophyll a/b binding protein 5	GO:0009536//plastid	–	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7197555	18	42	9.8	21.45	1.130123993	0.00424324	PHATRDRAFT_25298	K06874|1|3e-76|284|ppp:PHYPADRAFT_165148|zinc finger protein	–	GO:0046914//transition metal ion binding	–		–
7200056	13	30	7.34	15.89	1.114267157	0.01741808	PHATRDRAFT_45385	–	–	–	–		–
7200504	10	23	5.38	11.61	1.109689894	0.0390074	PHATRDRAFT_45412	–	–	GO:0070011//peptidase activity, acting on L-amino acid peptides	–		–
7199868	92	210	34.88	74.67	1.098128691	2.79E-10	PHATRDRAFT_44742	–	–	–	–		–
7205009	11	25	5.83	12.43	1.092258508	0.0332736	PHATRDRAFT_bd462	K08176|1|1e-32|139|zma:732717|MFS transporter, PHS family, inorganic phosphate transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7200897	11	25	5.64	12.02	1.091669828	0.0332736	PHATRDRAFT_45748	K08857|1|2e-10|66.2|cre:CHLREDRAFT_194082|NIMA (never in mitosis gene a)-related kinase [EC:2.7.11.1];K06228|2|2e-09|62.8|bdi:100843914|fused [EC:2.7.11.1];K04688|5|2e-09|62.4|smo:SELMODRAFT_181752|p70 ribosomal S6 kinase [EC:2.7.11.1]	–	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7202959	31	70	20.91	44.28	1.08246216	0.000338696	PHATRDRAFT_47807	–	–	–	–		–
7195828	12	27	37.15	78.51	1.079514214	0.0283974	PHATRDRAFT_15913	K11422|1|1e-14|76.3|cme:CMG025C|histone-lysine N-methyltransferase SETD1 [EC:2.1.1.43];K09188|2|3e-12|68.2|cme:CMD005C|histone-lysine N-methyltransferase MLL3 [EC:2.1.1.43];K11430|5|2e-07|52.0|mtr:MTR_5g016870|enhancer of zeste [EC:2.1.1.43]	GO:0043231//intracellular membrane-bounded organelle	GO:0016279//protein-lysine N-methyltransferase activity	GO:0016571//histone methylation		GO:0016571//histone methylation
7199481	12	27	9.02	19.04	1.07783414	0.0283974	PHATRDRAFT_50623	–	GO:0031231//intrinsic component of peroxisomal membrane	–	GO:0006996//organelle organization		GO:0006996//organelle organization
7202564	13	29	9.49	19.86	1.065385631	0.024249	PHATRDRAFT_37655	K10308|1|6e-06|50.4|zma:100272728|F-box protein 31	–	–	–		–
7204175	13	29	8.43	17.64	1.065246025	0.024249	PHATR_43948	–	–	–	–		–
7197535	13	29	7.82	16.35	1.064050123	0.024249	PHATRDRAFT_32692	–	–	–	–		–
7203160	14	31	9.99	20.75	1.054554753	0.020718	PHATRDRAFT_51092	K01915|1|8e-122|435|pop:POPTR_725763|glutamine synthetase [EC:6.3.1.2]	–	GO:0016211;GO:0032550	GO:0006541//glutamine metabolic process		GO:0006541//glutamine metabolic process

7197523	14	31	2.79	5.79	1.053298226	0.020718	PHATRDRAFT_43454	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	-		-
7203266	391	864	211.54	438.42	1.051383126	3.51E-35	PHATRDRAFT_48096	-	-	-	-		-
7204571	15	33	6.98	14.4	1.04476987	0.01771086	PHATR_46643	-	-	-	-		-
7199225	11	24	9.42	19.29	1.034054178	0.0463506	PHATRDRAFT_50419	-	-	-	-		-
7200688	11	24	4.02	8.23	1.033696929	0.0463506	FRE4	K13447|1|9e-25|114|ppp:PHYPADRAFT_204103|respiratory burst oxidase [EC:1.6.3.- 1.11.1.-]	GO:0031224//intrinsic component of membrane	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7205087	11	24	5.54	11.34	1.033462759	0.0463506	PHATRDRAFT_bd18	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0015103//inorganic anion transmembrane transporter activity	GO:0044763;GO:0015698//inorganic anion transport		GO:0044763;GO:0015698//inorganic anion transport
7195951	11	24	5.22	10.68	1.032789935	0.0463506	PHATRDRAFT_31584	K11841|1|2e-11|69.3|ppp:PHYPADRAFT_189047|ubiquitin carboxyl-terminal hydrolase 10 [EC:3.1.2.15];K11855|2|6e-11|67.8|pop:POPTR_262703|ubiquitin carboxyl-terminal hydrolase 36/42 [EC:3.1.2.15];K12493|4|1e-09|63.5|vvi:100252326|ADP-ribosylation factor GTPase-activating protein 2/3	-	GO:0016790//thiolester hydrolase activity	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7203240	17	37	8.6	17.55	1.029062466	0.01296326	PHATRDRAFT_38362	K01649|1|3e-125|447|cme:CMO208C|2-isopropylmalate synthase [EC:2.3.3.13]	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0006551//leucine metabolic process		GO:0006551//leucine metabolic process
7201854	12	26	10.86	22.08	1.023716069	0.0393714	PHATRDRAFT_36566	-	-	-	-		-
7197232	12	26	9.83	19.98	1.023293261	0.0393714	PHATRDRAFT_43681	-	-	-	-		-
7197993	12	26	4.69	9.53	1.022888291	0.0393714	PHATRDRAFT_25974	K06276|1|7e-27|120|ppp:PHYPADRAFT_144576|3-phosphoinositide dependent protein kinase-1 [EC:2.7.11.1];K04688|4|2e-26|119|aly:ARALYDRAFT_478175|p70 ribosomal S6 kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195650	12	26	5.41	10.99	1.022490887	0.0393714	PHATRDRAFT_49150	K11714|1|3e-06|52.4|vvi:100244803|rhamnogalacturonan II specific xylosyltransferase [EC:2.4.2.-]	-	-	-		-
7204722	19	41	9.54	19.31	1.017286993	0.00950718	PHATR_46877	-	-	-	-		-
7202418	13	28	2.51	5.08	1.017141133	0.0334806	PHATRDRAFT_47369	K10730|1|3e-63|243|smo:SELMODRAFT_100480|ATP-dependent DNA helicase Q4 [EC:3.6.4.12]	-	GO:0046914//transition metal ion binding;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7195595	19	41	12.59	25.47	1.016520677	0.00950718	PHATRDRAFT_30246	K00083|1|2e-60|231|pop:POPTR_667694|cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]	-	GO:0046914//transition metal ion binding;GO:0036094//small molecule binding;GO:0016614//oxidoreductase activity, acting on CH-OH group of donors	GO:0044710		GO:0044710
7195739	13	28	9.84	19.88	1.014587536	0.0334806	PHATRDRAFT_40239	-	-	-	-		-
7197010	27	58	14.03	28.27	1.010756874	0.0020762	PHATRDRAFT_43720	-	-	-	-		-
7196638	14	30	8.19	16.47	1.007905198	0.0285006	PHATRDRAFT_31407	-	-	-	-		-
7198338	38.82	82.92	25.44	50.97	1.002549683	0.000224266	PHATRDRAFT_49750	-	-	-	-		-
7203077	15	32	10.89	21.8	1.001324181	0.0242844	PHATRDRAFT_47849	-	-	-	-		-
7198781	14.9	31.72	18.67	37.27	0.997292892	0.020718	PHATRDRAFT_49996	-	-	-	-		-
7203793	46	97	17.52	34.66	0.98426888	9.29E-05	PHATRDRAFT_48325	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198863	19	40	13.8	27.25	0.981587963	0.01290364	PHATRDRAFT_50170	-	-	-	-		-
7201955	21	44	11.72	23.02	0.973915264	0.0094441	PHATRDRAFT_47175	-	-	-	-		-

7194891	34	71	14.42	28.25	0.970179703	0.000974628	PHATRDRAFT_48640	-	-	-	-		-
7203569	13	27	7.07	13.78	0.962793768	0.0458284	PHATRDRAFT_38794	-	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7197099	13	27	9.95	19.39	0.962544373	0.0458284	PHATRDRAFT_43348	-	-	-	-		-
7196255	31	64	26.63	51.58	0.953759345	0.0020408	myst	K11308|1|3e-100|363|smo:SELMODRAFT_84658|histone acetyltransferase MYST1 [EC:2.3.1.48]	GO:0043231//intracellular membrane-bounded organelle	GO:0016746//transferase activity, transferring acyl groups	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7194905	16	33	10.73	20.76	0.952156368	0.0281032	PHATRDRAFT_48667	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7205138	18	37	8.66	16.7	0.947409173	0.0203964	PHATRDRAFT_bd972	K03320|1|1e-87|322|cre:CHLREDRAFT_156131|ammonium transporter, Amt family	GO:0031224//intrinsic component of membrane	GO:0008509//anion transmembrane transporter activity	GO:0015696//ammonium transport		GO:0015696//ammonium transport
7204565	103	211	56.83	109.2	0.942248236	2.47E-08	PHATR_46841	-	-	-	-		-
7200642	21	43	13.75	26.41	0.941652683	0.01269176	PHATRDRAFT_45592	K00058|1|6e-87|319|olu:OSTLU_39000|D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7198595	786	1598	485.82	926.43	0.931260089	2.39E-52	PHATRDRAFT_49880	-	-	-	-		-
7196204	54	109	54.78	103.73	0.921112029	8.76E-05	dsCYC5	K06627|1|2e-14|78.2|pop:POPTR_548650|cyclin A	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7199105	15	30	2.95	5.54	0.909171022	0.044585	PHATRDRAFT_41167	K13026|1|2e-103|366|ota:Ot03g04590|ATP-dependent RNA helicase DHX57 [EC:3.6.4.13]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7202229	20	40	27.62	51.84	0.908352399	0.01986638	PHATRDRAFT_37077	K04554|1|1e-52|204|rcu:RCOM_0333490|ubiquitin-conjugating enzyme E2 J2 [EC:6.3.2.19]	-	GO:0016881//acid-amino acid ligase activity	-		-
7201829	21	42	17.74	33.29	0.908082861	0.01695036	PHATRDRAFT_46501	-	-	-	-		-
7204931	17	34	13.78	25.85	0.907588392	0.03216	PHATRDRAFT_bd559	K00981|1|1e-64|245|aly:ARALYDRAFT_492631|phosphatidate cytidylyltransferase [EC:2.7.7.41]	-	GO:0070567	-		-
7204694	19	38	12.36	23.18	0.907201823	0.023304	PHATR_46843	-	-	-	-		-
7205070	19.07	37.77	59.04	109.82	0.89537619	0.0309948	PHATRDRAFT_bd375	K01624|1|9e-33|136|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	-	GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7195487	54	107	35.2	65.42	0.894156331	0.000150175	PHATRDRAFT_49323	-	-	-	-		-
7201999	35	69	31.99	59.16	0.88700106	0.00256764	PHATRDRAFT_47077	-	-	GO:0036094//small molecule binding	-		-
7200002	69	136	28.2	52.13	0.886418697	2.17E-05	PHATRDRAFT_45377	K01510|1|3e-18|92.4|vcn:VOLCADRAFT_91259|apyrase [EC:3.6.1.5]	-	GO:0003824//catalytic activity	-		-
7203162	64	126	11.99	22.14	0.884823563	4.50E-05	PHATRDRAFT_47896	K12600|1|4e-16|86.3|rcu:RCOM_1602530|superkiller protein 3	-	-	-		-
7199321	29	57	26.15	48.21	0.882521483	0.00642862	PHATRDRAFT_50481	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197377	27.66	54.29	22	40.51	0.880774561	0.0066353	PHATRDRAFT_43314	-	-	-	-		-
7198294	22	43	14.01	25.69	0.874749934	0.01918708	PHATRDRAFT_49640	-	-	-	-		-

7195493	22	43	11.86	21.74	0.87424793	0.01918708	TYR1	-	-	GO:0043169//cation binding;GO:0016716//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, another compound as one donor, and incorporation of one atom of oxygen	GO:0044710		GO:0044710
7200138	87	170	32.1	58.83	0.873978739	2.67E-06	PHATRDRAFT_45275	-	-	-	-		-
7195995	50	97	23.35	42.48	0.863361216	0.000460178	PHATRDRAFT_17344	K06901|1|1e-102|372|smo:SELMODRAFT_419524|putative MFS transporter, AGZA family, xanthine/uracil permease	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7204097	30	58	13.07	23.7	0.858627918	0.00722736	PHATR_44177	-	-	GO:0008252//nucleotidase activity;GO:0046872//metal ion binding	GO:0009117//nucleotide metabolic process		GO:0009117//nucleotide metabolic process
7198324	400	771	214.78	388.29	0.854274895	8.45E-23	PHATRDRAFT_55087	-	-	-	-		-
7197265	66	127	51.18	92.38	0.852000399	7.30E-05	PHATRDRAFT_43744	-	-	-	-		-
7200104	25	48	21.04	37.89	0.848682435	0.01572874	PHATRDRAFT_54365	-	-	GO:0097159//organic cyclic compound binding	-		-
7203960	25	48	10.18	18.33	0.848469224	0.01572874	PHATR_43828	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7195444	48	92	87.9	158.13	0.847176027	0.000803182	PHATRDRAFT_15619	K02873|1|2e-27|119|cme:CMP006C|large subunit ribosomal protein L13e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7195454	86	165	14.35	25.81	0.846879405	6.61E-06	PHATRDRAFT_49102	-	-	-	-		-
7197814	33	63	19.37	34.68	0.840279945	0.00594578	PHATRDRAFT_44253	-	-	GO:0036094//small molecule binding	-		-
7202536	19	36	12.06	21.43	0.829401943	0.040927	PHATRDRAFT_14032	K13181|1|4e-118|423|ppp:PHYPADRAFT_119582|ATP-dependent RNA helicase DDX27 [EC:3.6.4.13]	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7202226	18	34	44.27	78.51	0.826547052	0.0481622	PHATRDRAFT_13633	-	-	-	-		-
7199345	18	34	11.64	20.62	0.824953274	0.0481622	PHATRDRAFT_50542	K15111|1|3e-17|88.2|gmx:100800051|solute carrier family 25 (mitochondrial S-adenosylmethionine transporter), member 26	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7195443	445	840	605.87	1073.15	0.824771567	2.53E-23	PHATRDRAFT_49088	-	-	-	-		-
7203940	554	1046	432.71	766.38	0.82465945	1.15E-28	HSP20B	K13993|1|9e-06|49.7|ath:AT4G10250|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7200544	44	83	49.03	86.78	0.823697825	0.001886206	PHATRDRAFT_45432	-	-	-	-		-
7200827	34	64	22.89	40.42	0.820351859	0.00662206	PHATRDRAFT_27447	-	-	-	-		-
7197484	25	47	15.79	27.85	0.818666156	0.020558	CPNE1b	-	-	-	-		-
7195792	24	45	9.61	16.89	0.813560992	0.0240704	PHATRDRAFT_30334	K03456|1|7e-117|419|bdi:100846752|protein phosphatase 2 (formerly 2A), regulatory subunit A	-	-	-		-
7204748	77	144	132.54	232.63	0.811609334	5.12E-05	HSP20C	-	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7202061	23	43	4.25	7.45	0.809777584	0.028204	PHATRDRAFT_47168	-	-	-	-		-
7197819	55	102	27.86	48.46	0.798599147	0.000778794	PHATRDRAFT_44339	K05531|1|2e-26|119|bdi:100846699|mannan polymerase II complex MNN10 subunit [EC:2.4.1.-];K08238|2|4e-08|58.2|osa:4329539|xyloglucan 6-xylosyltransferase [EC:2.4.2.39]	GO:0031224//intrinsic component of membrane	GO:0016757//transferase activity, transferring glycosyl groups	-		-
7194720	26	48	9.72	16.82	0.791149487	0.0228242	PHATRDRAFT_48552	-	-	-	-		-
7201431	181	333	73.59	126.97	0.786906023	1.79E-09	PHATRDRAFT_46086	K06184|1|6e-41|167|gmx:100806226|ATP-binding cassette, subfamily F, member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7201548	24	44	16.72	28.76	0.782488828	0.031277	PHATRDRAFT_46447	-	-	-	-		-
7195585	24	44	6.82	11.73	0.782359369	0.031277	PHATRDRAFT_49310	-	-	-	-		-
7201346	58	106	46.23	79.25	0.777581573	0.000814886	PHATRDRAFT_46116	-	-	-	-		-

7204122	23	42	11.71	20.06	0.77658053	0.0366538	PHATR_33590	K03762|1|1e-50|199|cre:CHLREDRAFT_54232|MFS transporter, MHS family, proline/betaine transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization; GO:0044763		GO:0051234//establishment of localization; GO:0044763
7198520	528	964	354.4	606.93	0.77615153	4.44E-24	dsCYC7	K06627|1|1e-10|65.9|ath:AT5G43080|cyclin A;K14505|4|2e-09|62.4|vvi:100264093|cyclin D3, plant	-	-	-		-
7199147	22	40	13.42	22.89	0.770332791	0.0429902	PHATRDRAFT 50371	-	-	-	-		-
7200169	38	69	9.96	16.97	0.768768917	0.00767282	PHATRDRAFT 45083	-	-	-	-		-
7196276	38	69	13.61	23.18	0.7682135	0.00767282	PHATRDRAFT 42586	-	-	-	-		-
7200905	276	501	182.27	310.33	0.767726044	5.01E-13	PHATRDRAFT 45763	-	-	-	-		-
7197029	89	161	113.11	191.99	0.763304686	4.82E-05	PHATRDRAFT 33028	-	-	-	-		-
7201499	25	45	31.59	53.35	0.756020334	0.0344872	PHATRDRAFT 46309	-	-	-	-		-
7201449	30	54	19.86	33.53	0.75558686	0.0203212	PHATRDRAFT 46117	-	-	-	-		-
7202292	68	122	15.92	26.79	0.750854245	0.000489474	PHATRDRAFT 47518	-	GO:0044464	GO:0016837	GO:0042120		GO:0042120
7198691	24	43	7.1	11.94	0.749911907	0.0403814	PHATRDRAFT 50095	-	-	-	-		-
7204856	45.16	80.92	25	42.02	0.749148067	0.00553652	PHATRDRAFT bd1127	-	-	-	-		-
7204529	33	59	22.66	38.01	0.746231164	0.01639466	PHATR 46763	-	-	-	-		-
7203028	35.98	64.3	10.91	18.28	0.744614969	0.00944402	PHATRDRAFT 48040	-	-	-	-		-
7195676	23	41	51.69	86.51	0.742981706	0.0473182	PHATRDRAFT_6433	K12191|1|1e-16|83.2|ppp:PHYPADRAFT_181789|charged multivesicular body protein 2A;K12192|2|2e-16|82.4|smo:SELMODRAFT_266789|charged multivesicular body protein 2B	-	-	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7203505	23	41	13.53	22.63	0.742074745	0.0473182	PHATRDRAFT_54869	K14319|1|1e-20|99.4|osa:4339487|Ran GTPase-activating protein 1	GO:0044464	-	-		-
7195271	1468	2614	1252.52	2092.19	0.740180234	1.36E-57	PHATRDRAFT 49007	-	-	-	-		-
7197689	36	64	7.88	13.14	0.737697741	0.01323616	PHATRDRAFT 33888	-	-	-	-		-
7196408	90	160	9.41	15.69	0.737578724	8.31E-05	PHATRDRAFT 42793	-	-	-	-		-
7197457	27	48	11.91	19.85	0.736965594	0.032359	PHATRDRAFT 32815	-	-	-	-		-
7204683	36	64	12.96	21.6	0.736965594	0.01323616	PHATR 46827	-	-	-	-		-
7200416	62	110	14.36	23.9	0.734954869	0.001165864	MSH4	K08740|1|2e-57|223|rcu:RCOM_1389090|DNA mismatch repair protein MSH4	-	GO:0003690//double-stranded DNA binding;GO:0032550	GO:0006281//DNA repair		GO:0006281//DNA repair
7196265	26	46	14.29	23.72	0.731098093	0.0378282	PHATRDRAFT_42565	K13348|1|5e-08|57.8|gmx:100796872|protein Mpv17;K13347|5|4e-07|54.7|ppp:PHYPADRAFT_161687|peroxisomal membrane protein 2	GO:0031224//intrinsic component of membrane	-	-		-
7204371	104	184.01	97.23	161.39	0.731077763	2.83E-05	PHATR_33278	K01641|1|2e-12|55.5|ppp:PHYPADRAFT_219750|hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0006720//isoprenoid metabolic process		GO:0006720//isoprenoid metabolic process
7203001	26	46	3.75	6.22	0.730023985	0.0378282	PHATRDRAFT 48002	-	-	-	-		-
7199534	43	76	34.59	57.35	0.729438473	0.00745116	PHATRDRAFT 45027	-	-	-	-		-
7195005	64	113	25.75	42.64	0.727635006	0.001098052	PHATRDRAFT_48747	K11446|1|5e-70|264|ota:Ot08g01100|histone demethylase JARID1 [EC:1.14.11.-]	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7195190	25	44	10.19	16.83	0.723881125	0.044249	PHATRDRAFT_48717	K09651|1|3e-09|62.4|gmx:100794217|rhomboid domain-containing protein 1 [EC:3.4.21.-]	GO:0031224//intrinsic component of membrane	GO:0004175//endopeptidase activity	-		-
7202708	41	72	10.05	16.55	0.719635716	0.01003504	PHATRDRAFT_47704	K11835|1|8e-84|310|pop:POPTR_798230|ubiquitin carboxyl-terminal hydrolase 4/11/15 [EC:3.1.2.15]	-	GO:0070011//peptidase activity, acting on L-amino acid peptides;GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7198906	36	63	28.09	46.12	0.715335889	0.01678988	RRP	K12589|1|9e-14|76.3|smo:SELMODRAFT_102800|exosome complex component RRP42;K12586|3|1e-10|65.9|vcn:VOLCADRAFT_86657|exosome complex component RRP43	-	-	-		-
7198601	48	84	19.54	32.07	0.714793886	0.005664	PHATRDRAFT 49896	-	-	-	-		-
7199434	122	213	68.55	112.25	0.711486874	1.07E-05	PHATRDRAFT 50619	-	-	-	-		-
7197172	97	169	9.63	15.74	0.708827838	9.42E-05	PHATRDRAFT_43464	K14772|1|1e-69|265|aly:ARALYDRAFT_353720|U3 small nucleolar RNA-associated protein 20	-	-	-		-
7196268	31	54	14.1	23.03	0.707819249	0.0283136	PHATRDRAFT 42568	-	-	-	-		-

7200506	347	604	148.76	242.84	0.707019425	1.52E-13	PHATRDRAFT_45416	K03363|1|5e-27|121|ath:AT4G33270|cell division cycle 20, cofactor of APC complex	-	-	-		-
7201709	710	1235	249.67	407.28	0.705998491	4.96E-26	PHATRDRAFT_54602	K09667|1|2e-18|93.2|bdi:100846315|polypeptide N-acetylglucosaminyltransferase [EC:2.4.1.-]	-	-	-		-
7205167	69	120	25.46	41.53	0.705921453	0.001052838	PHATRDRAFT_bd1749	-	-	GO:0004620//phospholipase activity	-		-
7196026	49	85	19.36	31.5	0.702272876	0.00614628	PHATRDRAFT_42688	K15336|1|7e-09|61.2|vvi:100259391|tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	-	-		-
7204096	30	52	41.04	66.75	0.701737106	0.0329992	PHATR_44176	K01519|1|1e-64|244|cre:CHLREDRAFT_179025|inosine triphosphate pyrophosphatase [EC:3.6.1.19]	-	GO:0005488//binding;GO:0016787//hydrolase activity	-		-
7203579	1307	2266	667.98	1086.18	0.701386391	7.72E-46	PHATRDRAFT_54892	-	-	-	-		-
7204209	26	45	20.68	33.58	0.699366045	0.0482484	PHATR_25739	K13070|1|9e-24|109|osa:4335093|momilactone-A synthase [EC:1.1.1.295];K00059|2|5e-23|107|bdi:100826298|3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202801	36	62	50.04	80.87	0.692522822	0.0211956	PHATRDRAFT_21744	K02183|1|1e-13|74.3|ppp:PHYPADRAFT_180168|calmodulin	-	GO:0046872//metal ion binding	-		-
7196574	83	143	37.04	59.85	0.692267149	0.000434538	PHATRDRAFT_43209	-	-	-	-		-
7197937	36	62	30.12	48.66	0.69201455	0.0211956	PHATRDRAFT_33651	-	-	-	-		-
7198104	136	234	85.29	137.64	0.690451292	6.94E-06	PHATRDRAFT_44607	-	-	-	-		-
7202519	39	67	33.71	54.33	0.68857242	0.01702906	PHATRDRAFT_2037	-	-	-	-		-
7198519	53	91	49.23	79.29	0.687601186	0.00538084	PHATRDRAFT_16341	K15275|1|9e-36|149|ota:Ot07g01570|solute carrier family 35 (UDP-galactose transporter), member B1	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7203333	223	382	69.38	111.46	0.683934313	1.19E-08	CYCP1	-	-	-	-		-
7203507	55	94	44.12	70.74	0.681093428	0.0050292	PHATRDRAFT_48179	-	-	GO:0003676//nucleic acid binding	-		-
7201310	86	147	47.3	75.83	0.680928539	0.000439064	PHATRDRAFT_46063	-	-	-	-		-
7202737	55	94	23.57	37.77	0.680289025	0.0050292	PHATRDRAFT_47752	-	-	-	-		-
7197418	51	87	21.41	34.26	0.678240356	0.00718688	PHATRDRAFT_25217	K05681|1|9e-64|243|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|6e-49|194|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K05643|4|6e-15|81.3|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7195534	185	315	130.07	207.74	0.675490782	3.09E-07	PHATRDRAFT_49236	-	-	-	-		-
7196800	1061	1796	446.59	708.99	0.666814332	1.05E-33	HSP70A	K03283|1|0.0|904|rcu:RCOM_1442270|heat shock 70kDa protein 1/8	-	GO:0032550	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7196590	34.74	58.79	18.76	29.78	0.666683926	0.0286284	PHATRDRAFT_32401	-	-	-	-		-
7198460	48	81	14.91	23.59	0.661895161	0.0110957	PHATRDRAFT_49793	K05349|1|7e-41|167|rcu:RCOM_1903090|beta-glucosidase [EC:3.2.1.21];K15920|4|1e-33|143|osa:4337166|beta-D-xylosidase 4 [EC:3.2.1.37]	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7204697	245	413	78.71	124.43	0.660715515	8.86E-09	NLTF	-	-	-	-		-
7199669	38	64	25.17	39.77	0.659975346	0.0247468	PHATRDRAFT_1631	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7198274	63	106	23.31	36.78	0.657972475	0.0038167	sufD	K09015|1|5e-29|128|olu:OSTLU_10147|Fe-S cluster assembly protein SufD	-	-	GO:0009058//biosynthetic process		GO:0009058//biosynthetic process
7200379	44	74	33.48	52.82	0.657784774	0.01594188	PHATRDRAFT_3137	-	GO:0044424	GO:0005543//phospholipid binding	GO:0044763		GO:0044763
7204278	138	232	82.51	130.1	0.656980076	1.84E-05	PHATR_43850	K03539|1|4e-07|54.7|bdi:100830772|ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5];K12127|2|9e-07|53.5|pop:POPTR_784463|pseudo-response regulator 1	-	-	-		-

7195917	185	311	104.57	164.87	0.65685989	6.97E-07	PHATRDRAFT_49430	-	-	-	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7201250	84	141	41.59	65.48	0.654817637	0.000884014	PHATRDRAFT_36063	-	-	-	-		-
7200016	255	428	126.63	199.34	0.654611998	6.40E-09	PHATRDRAFT_45314	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197852	62	104	21.22	33.38	0.653559298	0.00439594	PHATRDRAFT_44383	-	-	-	GO:0044260		GO:0044260
7195265	37	62	22.75	35.76	0.652480191	0.0286972	PHATRDRAFT_22909	K10206|1|8e-146|515|cme:CMN323C|LL-diaminopimelate aminotransferase [EC:2.6.1.83]	-	GO:0070546;GO:0043168//anion binding	GO:0009085//lysine biosynthetic process		GO:0009085//lysine biosynthetic process
7198241	157	263	50.34	79.09	0.651790078	5.89E-06	PHATRDRAFT_30461	K00213|1|2e-126|451|sbi:SORBI_04g017400|7-dehydrocholesterol reductase [EC:1.3.1.21]	GO:0016020//membrane	GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors	GO:0044710		GO:0044710
7201394	175	292	93.44	146.23	0.64612714	2.16E-06	PHATRDRAFT_2097	K11594|1|2e-133|474|osa:4350856|ATP-dependent RNA helicase [EC:3.6.4.13]	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7200488	99	165	61.1	95.52	0.644630457	0.000387308	PHATRDRAFT_45392	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198594	33	55	16.6	25.95	0.644551297	0.0416994	PHATRDRAFT_49878	-	-	GO:0046872//metal ion binding	-		-
7204338	69	115	26.42	41.29	0.644161952	0.00308986	PHATR_43879	-	-	-	-		-
7204358	95	158	31.55	49.2	0.64101831	0.000545296	PHATR_43917	-	-	-	GO:0046488//phosphatidylinositol metabolic process		GO:0046488//phosphatidylinositol metabolic process
7205019	41	68	24.81	38.59	0.637305309	0.0246902	PHATRDRAFT_bd36	K01230|1|5e-106|383|bdi:100824763|mannosyl-oligosaccharide alpha-1,2-mannosidase [EC:3.2.1.113]	-	GO:0046872//metal ion binding;GO:0015924	-		-
7201888	181	300	64.33	100	0.636436406	2.15E-06	PHATRDRAFT_28056	K00549|1|1e-156|551|ppp:PHYPADRAFT_205352|5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]	-	GO:0046914//transition metal ion binding;GO:0008172	GO:0000097//sulfur amino acid biosynthetic process		GO:0000097//sulfur amino acid biosynthetic process
7204389	32	53	7.43	11.53	0.633958397	0.0484424	PHATR_43975	-	-	-	-		-
7197919	40	66	44	68.12	0.630574911	0.0285678	PHATRDRAFT_10893	K08794|1|4e-49|192|vcn:VOLCADRAFT_79621|calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17];K00908|2|7e-44|175|cme:CMF051C|Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17];K00924|4|1e-38|157|ath:AT5G39440|[EC:2.7.1.-];K13412|5|7e-38|155|pop:POPTR_835420|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7203864	54	89	19.67	30.4	0.628074366	0.01103712	PHATR_44097	-	-	-	-		-
7198068	71	117	15.87	24.52	0.627656851	0.0035346	PHATRDRAFT_44535	K04886|1|3e-13|76.6|cre:CHLREDRAFT_144354|potassium voltage-gated channel Shab-related subfamily B member 2	GO:0005887//integral component of plasma membrane	GO:0005267//potassium channel activity	GO:0044763;GO:0030001//metal ion transport		GO:0044763;GO:0030001//metal ion transport
7200332	82	135	39.55	61.08	0.627022367	0.001753656	PHATRDRAFT_45149	-	-	-	-		-
7198500	62	102	46.52	71.79	0.625931801	0.00667524	PHATRDRAFT_49867	K10249|1|4e-10|64.3|ota:Ot09g02550|elongation of very long chain fatty acids protein 4;K10244|2|4e-10|64.3|ppp:PHYPADRAFT_195959|elongation of very long chain fatty acids protein 5 [EC:2.3.1.-]	GO:0031224//intrinsic component of membrane	-	-		-
7199983	91	149	50.73	77.91	0.618969354	0.001148184	PHATRDRAFT_45352	-	-	-	-		-

7198080	168	275	75.29	115.58	0.618361611	9.81E-06	PHATRDRAFT_54257	K00967|1|2e-06|53.1|zma:100382955|ethanolamine-phosphate cytidylyltransferase [EC:2.7.7.14]	-	GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7199959	55	90	27.75	42.58	0.617688178	0.01179324	PHATRDRAFT_45312	-	-	-	-		-
7196972	41	67	24.88	38.13	0.615940046	0.0305764	PHATRDRAFT_43261	-	-	-	-		-
7201361	180	294	127.92	195.98	0.615464589	5.33E-06	PHATRDRAFT_46143	-	-	-	-		-
7195337	49	80	16.98	26	0.614675164	0.01820794	PHATRDRAFT_49117	-	-	-	-		-
7201267	38	62	30.63	46.88	0.614027203	0.0382476	PHATRDRAFT_46195	-	-	-	-		-
7201671	38	62	22.21	33.99	0.613900969	0.0382476	PHATRDRAFT_46511	-	-	-	-		-
7197140	35	57	20.95	32.01	0.611572433	0.0479542	PHATRDRAFT_43410	-	-	-	-		-
7205056	41.52	67.63	23.39	35.73	0.611244052	0.0305764	PHATRDRAFT_bd1874	K01689|1|1e-134|478|olu:OSTLU_28765|enolase [EC:4.2.1.11]	GO:0043234//protein complex	GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7201066	40	65	12.71	19.37	0.607859924	0.0353386	PHATRDRAFT_46005	-	GO:0005737//cytoplasm	-	-		-
7203091	37	60	60.42	91.95	0.605823391	0.0442556	PHATRDRAFT_47876	-	-	-	-		-
7204830	74	120	34.11	51.87	0.604705615	0.00428026	PHATRDRAFT_bd1374	-	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199521	85	137	120.9	182.85	0.596846382	0.00257752	PHATRDRAFT_34586	-	-	-	-		-
7199490	107	172	41.61	62.73	0.592225274	0.000779006	PHATRDRAFT_44963	-	-	GO:0060089;GO:0005515//protein binding	GO:0006351//transcription, DNA-templated;GO:0007154//cell communication		GO:0006351//transcription, DNA-templated;GO:0007154//cell communication
7197902	53	85	29.64	44.59	0.589174752	0.01911746	PHATRDRAFT_44704	K14662|1|6e-12|70.9|vvi:100245927|protein N-terminal asparagine amidohydrolase [EC:3.5.1.-]	-	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	-		-
7200963	102	163	21.13	31.66	0.583368488	0.001245214	FRE1	K13447|1|5e-11|69.3|pop:POPTR_581871|respiratory burst oxidase [EC:1.6.3.-1.11.1.-]	GO:0031224//intrinsic component of membrane	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201602	47	75	40.87	61.18	0.582017864	0.0296294	PHATRDRAFT_46526	-	GO:0031224//intrinsic component of membrane	-	GO:0044093;GO:0051604//protein maturation		GO:0044093;GO:0051604//protein maturation
7196403	69	110	50.89	76.1	0.580514262	0.00843978	GEL1	K05768|1|1e-42|172|vvi:100254775|gelsolin	-	GO:0008092//cytoskeletal protein binding	GO:0044763		GO:0044763
7202917	49	78	41.72	62.31	0.578724559	0.0273496	PHATRDRAFT_47748	-	-	-	-		-
7198638	44	70	24.11	35.97	0.577162509	0.0369778	PHATRDRAFT_49945	-	-	GO:0016782//transferase activity, transferring sulfur-containing groups	-		-
7199963	44	70	12	17.9	0.576925182	0.0369778	PHATRDRAFT_45319	K12852|1|0.0|918|cre:CHLREDRAFT_24423|116 kDa U5 small nuclear ribonucleoprotein component	GO:0044464	GO:0032550;GO:0017111//nucleoside-triphosphatase activity	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7196670	166	264	94.83	141.45	0.576876736	4.72E-05	PGP_1	K13752|1|4e-35|147|ota:Ot11g02640|solute carrier family 24 (sodium/potassium/calcium exchanger), member 4;K13754|3|1e-15|82.8|smo:SELMODRAFT_89075|solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding	GO:0044763		GO:0044763
7201690	974	1544	423.03	628.93	0.572139475	1.32E-22	PHATRDRAFT_46547	-	-	-	-		-
7198282	169	267	129.3	191.62	0.567525873	5.55E-05	PHATRDRAFT_49620	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203199	47	74	42.24	62.39	0.562704975	0.0361486	PHATRDRAFT_47951	K11364|1|2e-11|68.6|osa:4352010|SAGA-associated factor 29	-	-	-		-
7203370	110	173	43.87	64.71	0.560753971	0.001337466	PHATRDRAFT_48267	-	-	-	-		-

7203640	81	127	19.31	28.39	0.556034685	0.00641222	PHATRDRAFT_48375	K12319|1|3e-32|139|cre:CHLREDRAFT_142791|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|8e-23|108|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K13755|5|3e-13|76.3|vcn:VOLCADRAFT_59941|calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7198636	547	857	145.39	213.61	0.555051144	1.32E-12	PHATRDRAFT_23629	K05853|1|4e-98|358|olu:OSTLU_14777|Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [EC:3.6.3.8];K01537|2|7e-98|357|sbi:SORBI_01g038990|Ca2+-transporting ATPase [EC:3.6.3.8]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0019829//cation-transporting ATPase activity	GO:0006811//ion transport		GO:0006811//ion transport
7197750	53	83	26.94	39.57	0.554657215	0.0283116	PHATRDRAFT_44463	K11339|1|1e-11|70.1|aly:ARALYDRAFT_912618|mortality factor 4-like protein 1	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7203379	84	131	15.49	22.66	0.548810717	0.00625734	PHATRDRAFT_48282	-	-	-	-		-
7204693	126	196	78.33	114.29	0.545062315	0.00087448	PHATR_46842	-	-	-	-		-
7198189	63	98	38.47	56.13	0.54503823	0.01891118	PHATRDRAFT_49566	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197515	47	73	28.3	41.22	0.542542452	0.043912	PHATRDRAFT_43665	-	-	GO:0042578//phosphoric ester hydrolase activity	GO:0044238		GO:0044238
7199071	49	76	12.64	18.39	0.540925016	0.0404104	PHATRDRAFT_50332	-	-	-	-		-
7195567	71	110	37.22	54.08	0.539017096	0.01373562	PHATRDRAFT_49277	K07466|1|7e-08|57.4|aly:ARALYDRAFT_329623|replication factor A1	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7202978	179	277	83.03	120.51	0.537448264	9.23E-05	PHATRDRAFT_47842	-	-	-	-		-
7202635	264.22	408.36	169.79	246.13	0.535669022	2.21E-06	PHATRDRAFT_47571	-	-	-	-		-
7204955	88	136	31.99	46.37	0.535570734	0.00641606	PHATRDRAFT_bd1748	K05389|1|1e-07|57.0|olu:OSTLU_41153|potassium channel subfamily K, other eukaryote	-	GO:0004620//phospholipase activity	-		-
7196649	182	281	83.21	120.5	0.534204323	9.00E-05	PHATRDRAFT_31433	K05681|1|2e-78|292|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|1e-58|226|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K05663|4|6e-14|77.8|rcu:RCOM_0261010|mitochondrial ABC transporter ATM;K05643|5|8e-14|77.4|olu:OSTLU_42103|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7195408	249	384	73.66	106.53	0.532306464	4.94E-06	PHATRDRAFT_49026	-	-	-	-		-
7196688	167	257	126.86	183.13	0.529630903	0.000203576	PHATRDRAFT_42510	-	-	-	-		-
7197826	69	106	31.3	45.09	0.526644853	0.01785678	PHATRDRAFT_44347	-	-	-	-		-
7197303	83	127	30.26	43.43	0.521279965	0.01020418	PHATRDRAFT_32803	K01551|1|3e-46|185|cre:CHLREDRAFT_132949|arsenite-transporting ATPase [EC:3.6.3.16]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process		GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process
7201035	284	434	224.89	322.38	0.519542732	2.07E-06	PHATRDRAFT_45968	K09272|1|5e-11|67.0|aly:ARALYDRAFT_905150|structure-specific recognition protein 1;K10802|2|1e-10|65.9|vcn:VOLCADRAFT_72419|high mobility group protein B1	-	-	-		-
7197141	78	119	45.9	65.68	0.516959973	0.01360464	PHATRDRAFT_43412	-	-	-	-		-
7198928	65	99	52.84	75.49	0.51465508	0.0251508	PHATRDRAFT_50127	-	-	-	-		-
7199326	130	198	84.36	120.51	0.514521867	0.001500212	PHATRDRAFT_50492	-	-	-	-		-
7203527	182	277	58.84	83.99	0.513420322	0.000176319	PHATRDRAFT_48215	-	-	-	-		-

7196841	56	85	32.38	46.09	0.509350782	0.0399034	MARK3	K07198|1|5e-145|512|aly:ARALYDRAFT_317081|5’-AMP-activated protein kinase, catalytic alpha subunit [EC:2.7.11.11]	GO:0043231//intracellular membrane-bounded organelle;GO:0000151//ubiquitin ligase complex	GO:0032550;GO:0004672//protein kinase activity	GO:0048364//root development;GO:0009756//carbohydrate mediated signaling;GO:0009755//hormone-mediated signaling pathway;GO:0007568//aging;GO:0009791//post-embryonic development;GO:0006796//phosphate-containing compound metabolic process;GO:0006006//glucose metabolic process;GO:0006464//cellular protein modification process;GO:0022414//reprod		GO:0048364//root development;GO:0009756//carbohydrate mediated signaling;GO:0009755//hormone-mediated signaling pathway;GO:0007568//aging;GO:0009791//post-embryonic development;GO:0006796//phosphate-containing compound metabolic process;GO:0006006//glucose metabolic process;GO:0006464//cellular protein modification process;GO:0022414//reprod
7199672	57	86	107.82	152.7	0.502075247	0.041873	PHATRDRAFT_11271	K03453|1|1e-12|70.5|vcn:VOLCADRAFT_102664|bile acid:Na+ symporter, BASS family	-	-	-		-
7204013	178	268	20.68	29.19	0.497238025	0.000335104	PHATR_44062	K14442|1|2e-60|234|bdi:100834725|ATP-dependent RNA helicase DHX36 [EC:3.6.4.13]	-	GO:0042623//ATPase activity, coupled;GO:0032550	-		-
7196277	129	194	35.3	49.79	0.496187832	0.00236668	PHATRDRAFT_42587	K01404|1|6e-28|125|bdi:100831389|leishmanolysin [EC:3.4.24.36]	-	GO:0046914//transition metal ion binding;GO:0004175//endopeptidase activity	GO:0022610;GO:0019538//protein metabolic process		GO:0022610;GO:0019538//protein metabolic process
7198662	1351	2027	1073.78	1511.25	0.493043901	1.26E-22	PHATRDRAFT_49834	-	-	-	-		-
7198685	62	93	41.65	58.6	0.492584169	0.0371318	PHATRDRAFT_2032	K02575|1|2e-62|238|smo:SELMODRAFT_136730|MFS transporter, NNP family, nitrate/nitrite transporter	GO:0031224//intrinsic component of membrane	-	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7198069	912	1363	175.97	246.61	0.486901808	2.00E-15	PHATRDRAFT_44539	-	-	-	-		-
7199730	1058	1578	256.52	358.78	0.484028158	1.93E-17	PHATRDRAFT_44761	K15172|1|1e-08|60.8|vcn:VOLCADRAFT_106802|transcription elongation factor SPT5	-	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress		GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress
7198661	102	152	56.35	78.77	0.483230665	0.00871004	PHATRDRAFT_49833	-	-	-	-		-
7198752	74	110	57.85	80.67	0.479715297	0.026866	PHATRDRAFT_23709	K15100|1|7e-41|166|ota:Ot07g03360|solute carrier family 25 (mitochondrial citrate transporter), member 1	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7200567	204	303	115.38	160.74	0.478335819	0.000236586	PHATRDRAFT_45464	-	-	-	-		-
7196138	70	104	26.72	37.22	0.478158048	0.031668	PHATRDRAFT_42762	-	-	-	-		-
7196238	95	141	48.55	67.59	0.477338519	0.01249146	PHATRDRAFT_32173	K13342|1|2e-58|225|gmx:100789878|peroxin-5	-	-	-		-
7198186	290	430	161.16	224.12	0.475777687	1.29E-05	PHATRDRAFT_49559	-	-	-	-		-
7202283	101	149	38.34	53.05	0.468502414	0.01156924	DYN1	K01528|1|2e-156|551|vvi:100243718|dynamin GTPase [EC:3.6.5.5]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7200308	167.84	247.4	105.79	146.27	0.467430642	0.001041132	PHATRDRAFT_45112	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204500	95	140	21.94	30.32	0.466706228	0.01470078	PHATR_46708	-	-	-	-		-
7204379	70	103	18.22	25.14	0.464461691	0.0374594	PHATR_43957	-	-	-	-		-
7203007	68	100	30.28	41.77	0.464101938	0.0407036	PHATRDRAFT_48012	K02218|1|6e-12|71.2|vvi:100261234|casein kinase 1 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204346	113	166	41.36	56.98	0.462219436	0.00843556	PHATR_43891	K03539|1|4e-07|55.5|bdi:100830772|ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5]	-	-	-		-
7203705	269	395	130.2	179.31	0.4617265	4.79E-05	PHATRDRAFT_48482	-	-	-	-		-
7196990	90	132	91.95	126.52	0.460443981	0.01948166	PHATRDRAFT_43687	-	-	-	-		-
7201450	1060	1555	461.79	635.34	0.46029192	8.14E-16	PHATRDRAFT_46118	-	-	-	-		-

7197898	16660.19	24373.59	4355.31	5975.27	0.456228495	1.20E-219	SMP1	–	–	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7205013	67	98	19.09	26.19	0.456198957	0.0461076	PHATRDRAFT_bd1616	–	–	–	–		–
7203355	713	1043	185.55	254.53	0.456027708	6.17E-11	PHATRDRAFT_48245	–	–	–	–		–
7202319	843	1231	703.2	963.25	0.45397521	1.57E-12	PHATRDRAFT_47279	–	–	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198724	163	238	48.87	66.92	0.453488341	0.001924028	PHATRDRAFT_50026	–	GO:0031224//intrinsic component of membrane	–	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7200942	68	99	20.99	28.66	0.449336443	0.0480052	PHATRDRAFT_45828	K14856|1|1e-71|270|olu:OSTLU_785|protein SDA1	–	–	GO:0000054//ribosomal subunit export from nucleus;GO:0007010//cytoskeleton organization		GO:0000054//ribosomal subunit export from nucleus;GO:0007010//cytoskeleton organization
7196331	338	490	345.72	470.2	0.443670473	1.29E-05	PHATRDRAFT_53967	–	–	–	–		–
7199289	177	256	68.4	92.78	0.439817521	0.001763484	PHATRDRAFT_50513	–	–	–	–		–
7194780	81	117	23.83	32.28	0.437861627	0.0356566	PHATRDRAFT_48542	–	–	–	–		–
7201627	938	1349	456.31	615.49	0.431721146	1.58E-12	PHATRDRAFT_27877	K03320|1|2e-83|308|cre:CHLREDRAFT_157754|ammonium transporter, Amt family	GO:0031224//intrinsic component of membrane	GO:0008509//anion transmembrane transporter activity	GO:0015696//ammonium transport		GO:0015696//ammonium transport
7202862	80	115	36.52	49.23	0.430850974	0.0401746	PHATRDRAFT_47657	–	–	–	–		–
7198795	179	257	99.93	134.56	0.429259851	0.00218706	PHATRDRAFT_30810	K14617|1|2e-58|224|pop:POPTR_831922|LMBR1 domain-containing protein 1	GO:0031224//intrinsic component of membrane	–	–		–
7199700	255	366	66.78	89.89	0.428744536	0.000257654	MYT1	K06632|1|2e-30|133|ppp:PHYPADRAFT_193308|wee1-like protein kinase [EC:2.7.11.1]	–	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204695	221	317	270.86	364.54	0.428529771	0.000689644	HSP20	K13993|1|2e-07|54.3|rcu:RCOM_0497910|HSP20 family protein	–	–	–		–
7205020	110.7	158.73	52.11	70.08	0.42744252	0.01629576	PHATRDRAFT_bd1646	–	–	–	–		–
7204521	377	539	249.73	334.9	0.423361234	1.17E-05	PHATR_46747	–	–	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7202954	77	110	56.5	75.7	0.422042433	0.0491218	PHATRDRAFT_47803	–	–	–	–		–
7198447	159	227	69.59	93.17	0.420985486	0.00468828	PHATRDRAFT_49769	K00924|1|6e-15|81.3|osa:4341290|[EC:2.7.1.-];K08286|2|4e-14|78.6|ath:AT4G28490|protein-serine/threonine kinase [EC:2.7.11.-];K13415|3|3e-12|72.4|pop:POPTR_650846|protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1];K13420|4|3e-11|68.9|ath:AT5G46330|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	–	–	–		–
7205067	252	359	218.92	292.57	0.418378082	0.000408284	PHATRDRAFT_bd706	K06693|1|8e-24|109|vvi:100258659|26S proteasome non-ATPase regulatory subunit 9	–	–	–		–
7205129	151	215	37.66	50.29	0.417238553	0.00637138	PHATRDRAFT_bd1636	K12319|1|2e-28|126|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|1e-23|110|vcn:VOLCADRAFT_106794|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K01120|5|2e-16|86.7|cre:CHLREDRAFT_101278|3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	–	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction

7202861	1334.54	1900.23	323.57	432.05	0.417120428	4.10E-16	PHATRDRAFT_47656	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7197991	133	189	171.31	228.42	0.415079606	0.01106064	PHATRDRAFT_33664	-	-	-	-		-
7198010	143	203	68.1	90.67	0.412970487	0.00866856	PHATRDRAFT_44301	-	-	-	-		-
7204040	93	132	24.41	32.49	0.412523449	0.034636	SMC5	K06674|1|9e-16|84.7|pop:POPTR_826684|structural maintenance of chromosome 2;K06669|5|2e-13|76.6|ath:AT2G27170|structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	GO:0000793//condensed chromosome	-	GO:0000725//recombinational repair		GO:0000725//recombinational repair
7194878	201	285	76.34	101.51	0.411110766	0.001931682	GOX	K11517|1|5e-77|287|ppp:PHYPADRAFT_159377|(S)-2-hydroxy-acid oxidase [EC:1.1.3.15]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0003973//(S)-2-hydroxy-acid oxidase activity;GO:0032553	GO:0044710		GO:0044710
7194947	118	167	108.55	144.12	0.408910831	0.01848354	PHATRDRAFT_15479	K13412|1|4e-60|229|pop:POPTR_256143|calcium-dependent protein kinase [EC:2.7.11.1];K00924|5|1e-57|221|osa:4327560|[EC:2.7.1.-]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7200471	123	174	32.6	43.25	0.407828168	0.01632852	ACS1	K01897|1|7e-95|347|gmx:100803126|long-chain acyl-CoA synthetase [EC:6.2.1.3]	-	GO:0015645//fatty acid ligase activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7199816	504	712	72.17	95.6	0.405611363	1.25E-06	PHATRDRAFT_44901	K11380|1|1e-18|95.1|ppp:PHYPADRAFT_27586|NuA3 HAT complex component NTO1	-	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding	-		-
7204759	182	257	34.83	46.13	0.405374819	0.00368326	PHATR_46935	K13427|1|7e-16|85.5|vvi:100265605|nitric-oxide synthase, plant [EC:1.14.13.39]	GO:0005789//endoplasmic reticulum membrane	GO:0016787//hydrolase activity	GO:0015031//protein transport;GO:0006664//glycolipid metabolic process		GO:0015031//protein transport;GO:0006664//glycolipid metabolic process
7202732	85	120	78.28	103.67	0.405282807	0.0478984	PHATRDRAFT_47747	-	-	-	-		-
7198131	258	364	305.75	404.73	0.404607292	0.00056433	PHATRDRAFT_44648	-	-	-	-		-
7199114	190	268	52.33	69.22	0.403550683	0.00312728	PHATRDRAFT_50272	-	-	-	-		-
7204133	171	241	57.99	76.65	0.402481654	0.00520966	PHATR_44229	-	-	-	-		-
7199755	664	935	470.7	621.71	0.401433931	3.89E-08	PHATRDRAFT_44800	-	-	-	-		-
7203457	268	377	186.29	245.81	0.399993376	0.0005107	PHATRDRAFT_48087	-	-	-	-		-
7194915	104	146	67.13	88.4	0.397088727	0.0321198	PHATRDRAFT_48683	-	-	-	-		-
7195887	110	154	160.44	210.77	0.393635664	0.0292032	PHATRDRAFT_40068	-	-	-	-		-
7204921	148.5	207.5	56.9	74.57	0.390166689	0.0116644	PHATRDRAFT_bd1601	-	-	-	-		-
7204950	148.5	207.5	56.9	74.57	0.390166689	0.0116644	PHATRDRAFT_bd1249	-	-	-	-		-
7200205	126	176	95.8	125.53	0.389934629	0.020661	PHATRDRAFT_45155	-	-	-	-		-
7198429	121	169	113.99	149.36	0.389886566	0.0234138	PHATRDRAFT_49735	-	-	GO:0003824//catalytic activity	-		-
7202075	457	638	299.26	391.88	0.389012489	1.05E-05	PHATRDRAFT_13587	-	-	-	-		-
7195582	130	181	21.27	27.76	0.384187535	0.0203084	PHATRDRAFT_49307	-	-	-	-		-
7197299	141	196	86.84	113.22	0.382697198	0.01631648	PHATRDRAFT_43560	K10766|1|1e-15|83.2|smo:SELMODRAFT_403903|alkylated DNA repair protein alkB homolog 4 [EC:1.14.11.-];K10770|4|9e-06|50.1|smo:SELMODRAFT_112315|alkylated DNA repair protein alkB homolog 8 [EC:1.14.11.- 2.1.1.229]	-	GO:0016703	GO:0044710		GO:0044710
7197815	128	177	54.52	70.7	0.374924653	0.0251258	PHATRDRAFT_44256	K12133|1|2e-10|65.9|aly:ARALYDRAFT_470177|LATE ELONGATED HYPOCOTYL;K12134|3|9e-10|63.9|aly:ARALYDRAFT_904154|circadian clock associated 1	-	GO:0003676//nucleic acid binding	-		-
7201500	139	192	31.25	40.48	0.3733531	0.0201398	PHATRDRAFT_46310	K07178|1|1e-41|171|sbi:SORBI_07g026240|RIO kinase 1 [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7197013	184	254	57.58	74.55	0.372640564	0.00761902	PHATRDRAFT_43724	K08286|1|4e-24|112|ath:AT4G28490|protein-serine/threonine kinase [EC:2.7.11.-]	-	-	-		-

7205029	171	236	40.48	52.39	0.372082172	0.0101803	PHATRDRAFT_bd1767	-	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710		GO:0044710
7203868	1397	1927	1002.72	1297.39	0.371693421	2.08E-13	ANXA1	-	-	GO:0005543//phospholipid binding;GO:0046872//metal ion binding	-		-
7203113	198	273	130.96	169.36	0.370966948	0.00587078	PHATRDRAFT_47912	K15692|1|6e-12|70.5|ppp:PHYPADRAFT_16563|E3 ubiquitin-protein ligase RNF13 [EC:6.3.2.19];K11982|2|1e-09|63.2|ath:AT3G56580|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	-		-
7199548	250	344	220.76	284.96	0.368280631	0.00213446	PHATRDRAFT_11217	K03544|1|8e-90|328|pop:POPTR_250938|ATP-dependent Clp protease ATP-binding subunit ClpX	-	GO:0005515//protein binding;GO:0016462//pyrophosphatase activity;GO:0032550	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7196796	104	143	115.74	149.32	0.367519865	0.0488076	PHATRDRAFT_42977	-	-	-	-		-
7202926	115	158	27.33	35.22	0.365909449	0.0388554	OGD1	K00164|1|0.0|993|rcu:RCOM_0465620|2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0016624//oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;GO:0019842//vitamin binding	GO:0009060//aerobic respiration;GO:0006089//lactate metabolic process;GO:0010038//response to metal ion		GO:0009060//aerobic respiration;GO:0006089//lactate metabolic process;GO:0010038//response to metal ion
7201234	262	359	93.12	119.66	0.361778005	0.00201038	PHATRDRAFT_46135	-	-	-	-		-
7198355	1017	1393	504.17	647.68	0.36137092	1.18E-09	PHATRDRAFT_52619	K03458|1|6e-116|416|cre:CHLREDRAFT_169264|nucleobase:cation symporter-2, NCS2 family	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7198835	196	268	100.23	128.54	0.358902989	0.00813924	PHATRDRAFT_55150	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203366	109	149	41.77	53.54	0.358149995	0.0490806	PHATRDRAFT_29423	-	-	-	-		-
7199251	173	236	92.49	118.34	0.355568505	0.01386914	PHATRDRAFT_50437	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7205098	3775.87	5148.69	1625.17	2078.33	0.354834107	1.27E-30	PHATRDRAFT_bd1677	K13862|1|8e-20|97.4|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7202798	160.84	218.96	97.94	125.05	0.352534956	0.01859926	PHATRDRAFT_47573	-	-	-	-		-
7204572	122	166	64.38	82.16	0.351823605	0.041212	PHATR_46645	-	-	-	-		-
7202936	482.46	655.77	570.96	728.14	0.350826188	5.23E-05	PHATRDRAFT_47653	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7203500	362	491	128.93	164	0.347107819	0.000510038	PHATRDRAFT_48163	K13118|1|4e-08|58.9|cre:CHLREDRAFT_17930|protein DGCR14;K06694|2|6e-06|51.6|cre:CHLREDRAFT_140415|26S proteasome non-ATPase regulatory subunit 10	-	-	-		-
7196153	132	179	78.21	99.48	0.347053424	0.0363872	PHATRDRAFT_42786	-	-	-	-		-
7203356	141	191	41.78	53.08	0.345355878	0.0313254	PHATRDRAFT_48248	-	-	-	-		-
7201018	787.58	1066.01	629.46	799.21	0.344459932	3.46E-07	PHATRDRAFT_45944	-	-	-	-		-
7195081	525.42	710.99	382.24	485.18	0.344041322	3.59E-05	PHATRDRAFT_48827	-	-	-	-		-
7199578	221	299	112.61	142.9	0.343670969	0.0072884	PHATRDRAFT_44873	-	-	-	GO:0044238		GO:0044238

7200245	205	277	137.71	174.53	0.341841716	0.01018886	PHATRDRAFT_51806	-	GO:0031224//intrinsic component of membrane	-	-		-
7202915	276	372	173.08	218.81	0.338239647	0.00318634	Fba3	K01624|1|4e-116|416|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13];K00120|3|2e-15|82.0|aly:ARALYDRAFT_472044|[EC:1.1.-.-]	-	GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7196500	476	639	206.84	260.42	0.33232504	0.000141725	PHATRDRAFT_42846	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-
7203024	155	208	58.43	73.53	0.331623696	0.030485	PHATRDRAFT_29260	K00615|1|2e-174|611|vcn:VOLCADRAFT_75893|transketolase [EC:2.2.1.1]	-	GO:0016744	-		-
7197763	993	1332	512.69	645.01	0.331234769	4.29E-08	PHATRDRAFT_44488	-	-	-	-		-
7202190	607	814	196.77	247.46	0.330685063	1.90E-05	PHATRDRAFT_47203	-	-	-	-		-
7201155	179	240	95.05	119.52	0.330493521	0.0205134	PHATRDRAFT_20547	K01687|1|0.0|741|olu:OSTLU_34354|dihydroxy-acid dehydratase [EC:4.2.1.9]	GO:0009536//plastid	GO:0003676//nucleic acid binding;GO:0016836//hydro-lyase activity	GO:0008652//cellular amino acid biosynthetic process		GO:0008652//cellular amino acid biosynthetic process
7197519	764	1024	244.8	307.71	0.329967771	1.69E-06	PHATRDRAFT_43674	-	-	-	-		-
7197173	150	201	104.02	130.74	0.329839659	0.0345	PHATRDRAFT_43465	-	-	-	-		-
7195494	377	505	157.99	198.48	0.329160395	0.000803032	ISIP1	-	-	-	-		-
7199926	148	198	160.96	202.03	0.327867328	0.0371408	PHATRDRAFT_11792	-	-	-	-		-
7200331	322	430	82.1	102.82	0.32466679	0.00226764	RAT1	K11267|1|6e-07|55.5|mtr:MTR_2g027090|sister chromatid cohesion protein PDS5	GO:0032991//macromolecular complex	GO:0097159//organic cyclic compound binding	-		-
7202349	173	231	44.34	55.52	0.324398798	0.0254846	PHATRDRAFT_47258	K04460|1|8e-09|61.6|smo:SELMODRAFT_182535|protein phosphatase 5 [EC:3.1.3.16];K09553|2|7e-08|58.5|gmx:100780296|stress-induced-phosphoprotein 1;K09523|4|7e-08|58.5|smo:SELMODRAFT_100291|DnaJ homolog subfamily C member 3	-	GO:0046914//transition metal ion binding	-		-
7198931	368	491	141.7	177.31	0.323434146	0.001151458	PHATRDRAFT_50133	-	-	-	-		-
7197233	179	238	107.85	134.49	0.318472729	0.0259348	PHATRDRAFT_43685	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202236	227	301	276.25	343.69	0.315133411	0.0132656	PHATRDRAFT_13553	K15377|1|7e-11|65.9|cre:CHLREDRAFT_189789|solute carrier family 44 (choline transporter-like protein), member 2/4/5	GO:0031224//intrinsic component of membrane	-	-		-
7202235	267	354	116.67	145.08	0.31441501	0.0072486	PHATRDRAFT_47001	-	-	GO:0008289//lipid binding	-		-
7202147	369	489	81.01	100.67	0.313461907	0.001628784	PHATRDRAFT_54686	-	-	-	-		-
7197405	152	201	117.23	145.42	0.310883888	0.0457396	PHATRDRAFT_43364	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199399	218	288	149.36	185.08	0.309355171	0.01715914	PHATRDRAFT_50576	-	-	-	-		-
7202251	262	346	252.08	312.3	0.30905091	0.00908538	PHATRDRAFT_47020	-	-	-	-		-
7196474	269	355	54.78	67.8	0.307636007	0.00842434	PHATRDRAFT_42902	K01164|1|4e-09|63.2|bdi:100822676|ribonuclease P/MRP protein subunit POP1 [EC:3.1.26.5]	-	GO:0004549//tRNA-specific ribonuclease activity	GO:0008033//tRNA processing		GO:0008033//tRNA processing
7195807	166	219	41.77	51.68	0.307138927	0.0389942	PHATRDRAFT_49445	-	-	-	-		-
7194713	179	236	49.55	61.27	0.306295794	0.0325846	PHATRDRAFT_48538	-	-	-	-		-
7199772	1840	2425	757.78	936.63	0.305700184	7.18E-12	PHATRDRAFT_44828	-	-	-	-		-
7202689	170	224	110.23	136.24	0.305633421	0.0378688	ISIP3	-	-	-	-		-
7197047	338	445	226.7	279.95	0.304384789	0.00350754	PHATRDRAFT_43771	-	-	-	-		-
7199139	177	233	65.71	81.12	0.30394471	0.0349744	GPI_3	K01810|1|0.0|664|cme:CMO124C|glucose-6-phosphate isomerase [EC:5.3.1.9]	GO:0044444//cytoplasmic part	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0050896//response to stimulus;GO:0006007//glucose catabolic process		GO:0050896//response to stimulus;GO:0006007//glucose catabolic process
7197808	844	1110	573.23	707.14	0.302881754	4.39E-06	GEL3	K05768|1|9e-40|162|vvi:100254775|gelsolin	GO:0044424	GO:0008092//cytoskeletal protein binding	GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization		GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization

7195651	5047	6624	3015.37	3711.97	0.299850012	1.03E-28	PHATRDRAFT_49151	-	-	GO:0036094//small molecule binding	-		-
7203006	379	497	300.67	369.86	0.298798356	0.00244334	PHATRDRAFT_48011	-	-	-	-		-
7195902	209	274	53.05	65.23	0.298182877	0.0247566	PHATRDRAFT_49408	-	-	-	-		-
7195296	258	338	214.38	263.46	0.297413621	0.0129008	PHATRDRAFT_52498	-	-	-	-		-
7201454	172	225	280.88	344.83	0.295931392	0.0441044	PHATRDRAFT_12887	-	-	GO:0046914//transition metal ion binding	-		-
7204158	519	678	601.77	737.57	0.293567791	0.00050465	PHATR_43797	-	-	-	-		-
7195420	495	646	617.24	755.82	0.292211136	0.000727242	CREG1	-	GO:0043231//intracellular membrane-bounded organelle	GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7200896	167	218	54.84	67.14	0.291943966	0.0497716	PHATRDRAFT_45746	-	-	-	-		-
7204707	629	821	400.6	490.44	0.291914228	0.000137391	PHATR_54658	-	-	-	-		-
7196665	769	1001	306.42	374.07	0.287797803	3.23E-05	PHATRDRAFT_42467	K06119|1|2e-34|145|ota:Ot15g01120|sulfoquinovosyltransferase [EC:2.4.1.-]	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7198226	946	1230	589.81	719.3	0.286343321	4.59E-06	PHATRDRAFT_49557	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199471	3014.51	3913.55	566.99	690.26	0.283816593	4.73E-16	PHATRDRAFT_50642	-	-	-	-		-
7197969	259	335	83.49	101.27	0.278531542	0.0198821	PHATRDRAFT_44307	-	-	-	-		-
7203872	240	310	91.03	110.27	0.27662636	0.026115	PHATR_44112	-	-	GO:0015291//secondary active transmembrane transporter activity	GO:0015893//drug transport;GO:0044763		GO:0015893//drug transport;GO:0044763
7198208	1566	2021	1069.52	1294.67	0.275620953	1.48E-08	PHATRDRAFT_49596	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199817	201	259	121.1	146.36	0.273322456	0.0446338	PHATRDRAFT_44902	-	GO:0044424	GO:0032550;GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0016211	GO:0006412//translation;GO:0006528//asparagine metabolic process		GO:0006412//translation;GO:0006528//asparagine metabolic process
7195163	5945	7659	5287.65	6390.42	0.273284068	7.98E-28	Lhcf15	K08907|1|9e-09|59.3|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08910|2|3e-07|54.3|cme:CMQ142C|light-harvesting complex I chlorophyll a/b binding protein 4	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7201748	431	555	265.82	321.06	0.272393279	0.00335424	PHATRDRAFT_13078	-	-	-	-		-
7203867	219	282	96.14	116.1	0.272159264	0.0367564	PHATR_44106	K13367|1|5e-27|121|ath:AT3G59050|non-specific polyamine oxidase [EC:1.5.3.17];K11450|3|1e-23|110|ota:Ot20g00660|lysine-specific histone demethylase 1 [EC:1.-.-.-]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7203870	1204	1549	938.7	1132.85	0.271220783	1.05E-06	PHATR_44109	-	-	GO:0005543//phospholipid binding;GO:0046872//metal ion binding	-		-
7202332	1931	2484	1270.32	1532.75	0.27093044	6.48E-10	PHATRDRAFT_13951	K00262|1|2e-95|347|ppp:PHYPADRAFT_179243|glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	-	GO:0016638//oxidoreductase activity, acting on the CH-NH2 group of donors;GO:0036094//small molecule binding	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7195819	404	519	131.11	157.96	0.268781546	0.00507556	PHATRDRAFT_40174	K14319|1|1e-15|84.0|mtr:MTR_1g105040|Ran GTPase-activating protein 1	-	-	-		-
7197899	2227.81	2853.41	518.62	622.92	0.26436905	9.03E-11	PHATRDRAFT_44695	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202989	560	717	109.55	131.53	0.26380241	0.001204088	PHATRDRAFT_47863	-	-	-	-		-
7197959	983	1256	324.91	389.33	0.260953369	2.23E-05	PHATRDRAFT_44296	-	-	-	-		-
7204894	257	328	96.29	115.25	0.259308868	0.0314686	PHATRDRAFT_bd1686	-	-	-	-		-

7203267	286	364	80.05	95.55	0.25535447	0.0255568	GDCP	K00281|1|0.0|994|ppp:PHYPADRAFT_171132|glycine dehydrogenase [EC:1.4.4.2]	-	GO:0043168//anion binding;GO:0016642	GO:0006544//glycine metabolic process		GO:0006544//glycine metabolic process
7196146	251	319	117.83	140.45	0.253349722	0.0381104	PF2K1	K01103|1|1e-112|405|ota:Ot01g00020|6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase [EC:2.7.1.105 3.1.3.46]	-	GO:0008443//phosphofructokinase activity;GO:0032550;GO:0050308//sugar-phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0019318//hexose metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0019318//hexose metabolic process
7199932	1144	1453	472.05	562.29	0.25237471	1.00E-05	PHATRDRAFT_45060	K13177|1|3e-07|55.8|olu:OSTLU_41294|ATP-dependent RNA helicase DDX1 [EC:3.6.4.13]	-	-	-		-
7201053	474	602	169.03	201.33	0.252282839	0.00450452	PHATRDRAFT_45988	-	-	GO:0046914//transition metal ion binding;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202607	230	292	48.48	57.72	0.251681601	0.0486016	PHATRDRAFT_37731	K11978|1|3e-17|90.1|ppp:PHYPADRAFT_127907|E3 ubiquitin-protein ligase UBR3 [EC:6.3.2.19];K10625|2|2e-14|80.5|ppp:PHYPADRAFT_90626|E3 ubiquitin-protein ligase UBR1 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation		GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation
7204593	321	407	63.9	75.98	0.249803781	0.0207282	PHATR_46676	-	-	-	-		-
7195570	463	586	455.68	541.06	0.247767537	0.00597528	PHATRDRAFT_49281	-	-	-	-		-
7204094	305	386	62.04	73.63	0.247095015	0.025803	PHATR_44174	-	-	GO:0008252//nucleotidase activity;GO:0046872//metal ion binding	GO:0009117//nucleotide metabolic process		GO:0009117//nucleotide metabolic process
7198997	292.02	369.18	98.34	116.59	0.245593793	0.0306786	PHATRDRAFT_50346	-	-	-	-		-
7195458	373	471	142.35	168.58	0.243990895	0.01501402	PHATRDRAFT_49268	-	-	-	-		-
7195677	10426	13136	7630.09	9017.44	0.241017844	6.14E-37	PHATRDRAFT_49202	-	-	-	-		-
7202224	404	508	334.4	394.44	0.238231015	0.01368698	H3.3	K11253|1|7e-69|259|olu:OSTLU_32891|histone H3	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7196698	290	364	107.85	126.95	0.235234218	0.0390164	PHATRDRAFT_24374	K00392|1|5e-167|586|cme:CMG021C|sulfite reductase (ferredoxin) [EC:1.8.7.1]	-	GO:0016673;GO:0051536//iron-sulfur cluster binding;GO:0046906//tetrapyrrole binding	GO:0044710		GO:0044710
7199468	2129	2671	812.88	956.42	0.234601906	2.35E-08	PHATRDRAFT_55230	K04079|1|0.0|832|sbi:SORBI_07g028270|molecular chaperone HtpG	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process		GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process
7203012	416	520	934.93	1097.17	0.230856823	0.01604308	PHATRDRAFT_14646	-	-	-	-		-
7195023	860	1075	302.04	354.08	0.229335734	0.000531552	PHATRDRAFT_48735	-	-	-	-		-
7196682	384	480	105.02	123.11	0.229283853	0.0207098	PHATRDRAFT_42501	-	-	-	-		-
7200964	468	584	111.21	130.14	0.226777938	0.01154894	CDKA1	K02206|1|5e-105|381|osa:4331415|cyclin-dependent kinase 2 [EC:2.7.11.22]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0044763;GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0044763;GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7199933	346	431	293.46	342.92	0.224708178	0.0319224	PHATRDRAFT_45061	-	-	-	-		-
7195877	328.98	408.82	110.1	128.31	0.220819144	0.038564	PHATRDRAFT_49357	-	-	-	-		-
7201549	756	939	479	558.04	0.220342881	0.001857418	PHATRDRAFT_46448	K13993|1|2e-09|62.4|zma:100282088|HSP20 family protein	-	-	-		-
7204866	389	483	195.67	227.86	0.219725107	0.0260262	PHATRDRAFT_bd1645	K00434|1|1e-08|59.7|gmx:100170727|L-ascorbate peroxidase [EC:1.11.1.11]	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7200157	453	562	284.92	331.54	0.218626045	0.01690426	PHATRDRAFT_34965	-	-	-	-		-
7205026	772	956	1092.61	1269.64	0.216640954	0.00206674	PHATRDRAFT_bd176	K00540|1|9e-43|171|ath:AT3G27620|[EC:1.-.-.-]	GO:0016020//membrane	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710;GO:0044707		GO:0044710;GO:0044707

7197954	683	845	671.43	779.3	0.214941817	0.0039969	PHATRDRAFT_44281	-	-	-	-		-
7195379	413	511	299.19	347.23	0.214829643	0.0251932	PHATRDRAFT_39627	K03183|1|1e-07|56.2|zma:100384459|ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.163 2.1.1.201]	GO:0044444//cytoplasmic part	GO:0008757//S-adenosylmethionine-dependent methyltransferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7200426	358	443	139.29	161.65	0.214781821	0.0370396	PHATRDRAFT_45679	K13420|1|9e-20|97.4|vvi:100253808|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1];K00924|4|2e-19|95.9|aly:ARALYDRAFT_489442|[EC:2.7.1.-]	-	-	-		-
7204769	356.13	439.87	137.19	158.92	0.212125374	0.0424586	PHATR_46953	-	-	-	-		-
7204344	419	517	254.58	294.64	0.210834218	0.0270196	PHATR_10378	K00654|1|2e-145|513|smo:SELMODRAFT_108076|serine palmitoyltransferase [EC:2.3.1.50]	-	GO:0043168//anion binding;GO:0003824//catalytic activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7198442	1414	1744	612.28	708.25	0.210067138	5.04E-05	PHATRDRAFT_49759	-	-	-	-		-
7204215	609	751	230.17	266.19	0.209756567	0.00791244	PHATR_25752	-	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	-	-		-
7195026	390.89	481.84	267.18	308.92	0.209421259	0.0334812	PHATRDRAFT_29812	K05692|1|1e-177|620|cre:CHLREDRAFT_24392|actin beta/gamma 1;K10355|2|1e-176|617|ath:AT3G12110|actin, other eukaryote	GO:0043232	GO:0032550	-		-
7199234	957	1180	119.99	138.73	0.209365624	0.000876698	ACC2	K11262|1|0.0|1371|ppp:PHYPADRAFT_115301|acetyl-CoA carboxylase / biotin carboxylase [EC:6.4.1.2 6.3.4.14]	-	GO:0016421//CoA carboxylase activity;GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7201080	389	479	183.02	211.36	0.20770106	0.0357972	MS	K01638|1|8e-159|558|cre:CHLREDRAFT_196328|malate synthase [EC:2.3.3.9]	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0044262//cellular carbohydrate metabolic process;GO:0009060//aerobic respiration		GO:0044262//cellular carbohydrate metabolic process;GO:0009060//aerobic respiration
7197079	666.34	819.71	332.83	384.01	0.206358402	0.00648958	PHATRDRAFT_43313	-	-	-	-		-
7202293	5854.49	7192.45	1071.13	1233.99	0.204197117	1.06E-15	PHATRDRAFT_47520	-	-	-	-		-
7200682	500.86	615.09	158.65	182.72	0.203787035	0.0181954	PHATRDRAFT_54405	K13862|1|1e-22|107|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0004620//phospholipase activity;GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7197404	940	1153	656.07	754.83	0.20230201	0.001501886	PHATRDRAFT_43363	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197075	7683.02	9423.08	5857.2	6738.56	0.202229169	1.16E-19	PHATRDRAFT_43305	-	-	-	-		-
7198250	1347	1652	738.04	848.96	0.201997572	0.000146627	HSF2	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus		GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus
7195309	4750	5822	956.01	1098.82	0.200857461	1.25E-12	PHATRDRAFT_49064	-	GO:0031224//intrinsic component of membrane	-	-		-

7198225	522	639	124.8	143.26	0.199017913	0.01984964	PHATRDRAFT_49555	K12319|1|5e-25|115|cre:CHLREDRAFT_142791|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|3e-21|102|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K01120|5|1e-14|80.9|cre:CHLREDRAFT_101278|3’,5’-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7197862	496	605	97.07	111.04	0.193982076	0.027172	PHATRDRAFT_44399	K11684|1|1e-13|78.2|sbi:SORBI_03g001920|bromodomain-containing factor 1;K06062|3|4e-07|56.6|mtr:MTR_8g062330|histone acetyltransferase [EC:2.3.1.48];K11723|4|3e-06|53.5|vvi:100267501|bromodomain-containing protein 7/9	-	-	-		-
7203865	2996	3651	1752.21	2002.76	0.192813856	6.84E-08	HSF1	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus		GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus
7203434	530	643	729.69	830.68	0.187009137	0.0286172	PHATRDRAFT_48086	-	-	-	-		-
7197434	713	865	108.07	122.95	0.186105645	0.01111966	PHATRDRAFT_43423	-	-	-	-		-
7195907	672	813	241.14	273.6	0.182197247	0.01596468	PHATRDRAFT_49414	-	-	-	-		-
7202869	746	901.79	352.33	399.46	0.181123724	0.01228532	VTE1	-	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0009975//cyclase activity	-		-
7203405	2959.14	3574.6	378.69	428.96	0.1798258	5.98E-07	PHATRDRAFT_48047	-	-	-	-		-
7197367	689	832	388.16	439.63	0.179638382	0.01629	CCL1	K01904|1|8e-80|296|rcu:RCOM_1325310|4-coumarate--CoA ligase [EC:6.2.1.12]	-	GO:0016874//ligase activity	-		-
7204256	871.51	1051.69	678.25	767.75	0.178819465	0.00725342	PHATR_54153	-	-	-	-		-
7203456	610	734	279.64	315.59	0.174480752	0.0282714	PHATRDRAFT_48084	-	-	-	-		-
7200037	1972	2364	1596.9	1795.74	0.169304509	0.000133451	PHATRDRAFT_45349	-	-	-	-		-
7199762	1081	1289	223.48	249.9	0.161205176	0.00704864	PHATRDRAFT_19329	K01969|1|0.0|638|ppp:PHYPADRAFT_208593|3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	-	GO:0003824//catalytic activity	-		-
7197429	716	852	475.76	531.02	0.158532218	0.031537	PHATRDRAFT_43413	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202762	774	921	129.9	144.95	0.158153903	0.0253918	PHATRDRAFT_47538	-	-	-	-		-
7197739	775	918	185.34	205.87	0.151559335	0.0322838	PHATRDRAFT_44445	K08860|1|2e-26|120|smo:SELMODRAFT_83492|eukaryotic translation initiation factor 2-alpha kinase [EC:2.7.11.1];K08282|3|3e-24|112|aly:ARALYDRAFT_486408|non-specific serine/threonine protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195518	2049	2423	1023.45	1135.09	0.14936607	0.000613896	PHATRDRAFT_49209	K10990|1|3e-08|58.9|sbi:SORBI_06g014000|RecQ-mediated genome instability protein 1;K12471|3|4e-06|51.6|vvi:100267012|epsin	-	-	-		-
7199811	710	838	214.99	237.96	0.146449527	0.0480536	PHATRDRAFT_44889	-	GO:0031224//intrinsic component of membrane	GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044763;GO:0006811//ion transport		GO:0044763;GO:0006811//ion transport
7200919	1221	1440	468.69	518.4	0.145431705	0.0100851	PHATRDRAFT_45782	K15377|1|4e-25|115|bdi:100828458|solute carrier family 44 (choline transporter-like protein), member 2/4/5	GO:0031224//intrinsic component of membrane	-	-		-
7195008	2675	3144	624.93	688.78	0.140348653	0.000237134	PHATRDRAFT_48753	-	-	-	-		-
7204974	886	1041	577.55	636.5	0.140214664	0.0351136	PHATRDRAFT_bd1714	-	-	-	-		-
7203797	1437	1686	1356.76	1493.36	0.138396452	0.00820058	PHATRDRAFT_38760	-	-	-	-		-

7198249	1827	2110	936.53	1014.43	0.115272202	0.01331488	PHATRDRAFT_49594	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203043	1986	2293	322.18	348.82	0.114615823	0.01012134	CHC	K04646|1|0.0|1461|rcu:RCOM_0838580|clathrin heavy chain	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7195281	3085	3557	902.33	975.66	0.11272333	0.001639988	FRE5	K13447|1|4e-25|115|vvi:100262614|respiratory burst oxidase [EC:1.6.3.-1.11.1.-]	GO:0031224//intrinsic component of membrane	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7194723	1699	1946	899.36	966.15	0.103348473	0.0329586	PHATRDRAFT_48554	-	-	GO:0003676//nucleic acid binding	-		-
7203359	2415	2760	860.49	922.27	0.100030744	0.01380242	PHATRDRAFT_48252	-	-	GO:0046914//transition metal ion binding	-		-
7198417	2998	3402	1490.53	1586.34	0.089876604	0.01409648	PHATRDRAFT_49722	-	-	-	-		-
7203738	3456	3892	1136.2	1199.97	0.07878153	0.0211548	PHATRDRAFT_48315	-	-	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7197940	6098	6740	2309.81	2394.28	0.051817695	0.0466638	PHATRDRAFT_44259	-	-	-	-		-
7199082	15.05	0	27.21	0.001	-14.73184934	1.80E-05	PHATRDRAFT_41282	K02838|1|3e-47|185|pop:POPTR_710069|ribosome recycling factor	-	-	GO:0010467//gene expression		GO:0010467//gene expression
7205068	21.6	0	25.42	0.001	-14.63367641	2.31E-07	PHATRDRAFT_bd1622	-	-	-	-		-
7197863	5	0	24.38	0.001	-14.57341051	0.025637	PHATRDRAFT_10821	K03007|1|1e-30|129|gmx:100778887|DNA-directed RNA polymerases I, II, and III subunit RPABC5	GO:0016591//DNA-directed RNA polymerase II, holoenzyme	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding;GO:0034062//RNA polymerase activity	GO:0010467//gene expression		GO:0010467//gene expression
7204123	5	0	18.22	0.001	-14.15323534	0.025637	PHATR_7763	K04427|1|9e-09|56.6|olu:OSTLU_42011|mitogen-activated protein kinase kinase kinase 7 [EC:2.7.11.25];K04424|2|3e-08|55.1|aly:ARALYDRAFT_909157|sterile alpha motif and leucine zipper containing kinase AZK [EC:2.7.11.25];K00870|3|1e-07|52.8|cme:CMO051C|protein kinase [EC:2.7.1.37];K14510|4|3e-07|51.6|vvi:100240856|serine/threonine-protein kinase CTR1 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204849	21	0	15.61	0.001	-13.93018292	2.31E-07	PHATRDRAFT_bd1556	-	-	-	-		-
7202285	5	0	11.99	0.001	-13.54954404	0.025637	PHATRDRAFT_13944	K11145|1|2e-16|82.4|vvi:100242891|ribonuclease III family protein [EC:3.1.26.-]	-	GO:0016891//endoribonuclease activity, producing 5’-phosphomonoesters;GO:0003676//nucleic acid binding	GO:0010467//gene expression		GO:0010467//gene expression
7197545	5	0	10.5	0.001	-13.35810171	0.025637	PHATRDRAFT_9684	-	GO:0005622//intracellular	-	GO:0016482//cytoplasmic transport		GO:0016482//cytoplasmic transport
7202538	7	0	9.44	0.001	-13.20457114	0.0059999	PHATRDRAFT_37602	-	GO:0044464;GO:0016020//membrane	-	-		-
7199170	6.36	0	7.37	0.001	-12.8474489	0.01240238	PHATRDRAFT_41374	K14319|1|2e-11|67.4|mtr:MTR_1g105040|Ran GTPase-activating protein 1	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7197587	6	0	7.24	0.001	-12.82177398	0.01240238	PHATRDRAFT_32792	-	-	-	-		-
7202294	11	0	7.03	0.001	-12.77930897	0.000328626	PHATRDRAFT_37756	-	-	-	-		-
7197704	5	0	6.06	0.001	-12.56510208	0.025637	PHATRDRAFT_33921	-	-	-	-		-
7196781	6	0	6.04	0.001	-12.56033283	0.01240238	PHATRDRAFT_32071	-	-	-	-		-
7197948	6	0	5.12	0.001	-12.32192809	0.01240238	PHATRDRAFT_33675	-	-	-	-		-

7202822	5	0	5.07	0.001	-12.30777003	0.025637	PHATRDRAFT_37877	K00943|1|4e-11|67.0|ota:Ot07g01210|dTMP kinase [EC:2.7.4.9];K15450|2|2e-09|61.2|ota:Ot09g02370|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-];K00476|3|1e-08|58.9|ota:Ot10g00170|aspartate beta-hydroxylase [EC:1.14.11.16];K07055|4|1e-08|58.9|vcn:VOLCADRAFT_121064|tRNA wybutosine-synthesizing protein 2 [EC:2.1.1.-]	-	-	-		-
7202846	6	0	5.02	0.001	-12.29347165	0.01240238	PHATRDRAFT_14230	K00766|1|9e-82|301|vvi:100255305|anthranilate phosphoribosyltransferase [EC:2.4.2.18]	-	GO:0016763//transferase activity, transferring pentosyl groups	GO:0006568//tryptophan metabolic process		GO:0006568//tryptophan metabolic process
7195944	5.41	0	4.02	0.001	-11.97297979	0.025637	PHATRDRAFT_40189	-	-	-	-		-
7195775	5	0	2.61	0.001	-11.34983409	0.025637	PHATRDRAFT_49384	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7200495	5	0	2.33	0.001	-11.18611424	0.025637	PHATRDRAFT_54396	-	-	-	-		-
7196445	9	1	29.45	3.07	-3.261957073	0.00865296	PHATRDRAFT_9649	K03872|1|4e-17|84.3|cre:CHLREDRAFT_159711|transcription elongation factor B, polypeptide 1	-	-	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7202248	8	1	5.31	0.62	-3.09837174	0.01638812	PHATRDRAFT_47014	K02357|1|2e-11|68.6|gmx:100797166|elongation factor Ts;K14792|5|1e-08|59.7|osa:4342673|rRNA biogenesis protein RRP5	GO:0009536//plastid	GO:0003676//nucleic acid binding	-		-
7196724	8	1	29.92	3.51	-3.09156724	0.01638812	PHATRDRAFT_9259	-	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7200777	15	2	10.17	1.27	-3.001419277	0.000819022	PHATRDRAFT_45752	-	-	-	-		-
7205135	7	1	8.2	1.1	-2.898120386	0.0307786	PHATRDRAFT_bd1185	-	-	-	-		-
7198700	9.08	1.78	15.92	2.92	-2.446800062	0.00865296	PHATRDRAFT_40842	-	-	-	-		-
7204252	15	3	11.63	2.18	-2.415451057	0.0028396	PHATR_33118	-	-	GO:0036094//small molecule binding	-		-
7197392	10	2	6.17	1.16	-2.411145684	0.01648462	PHATRDRAFT_54080	-	-	GO:0046872//metal ion binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7204439	14	3	20.84	4.19	-2.314333129	0.00499576	PHATR_13458	-	GO:0009536//plastid	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7199910	9	2	6.02	1.25	-2.267835392	0.0292342	PHATRDRAFT_44807	-	GO:0043231//intracellular membrane-bounded organelle	GO:0000989//transcription factor binding transcription factor activity;GO:0046914//transition metal ion binding;GO:0008080//N-acetyltransferase activity	GO:0016570//histone modification;GO:0006351//transcription, DNA-templated		GO:0016570//histone modification;GO:0006351//transcription, DNA-templated
7204011	9	2	8.91	1.86	-2.26012281	0.0292342	PHATR_2432	K10862|1|2e-47|187|aly:ARALYDRAFT_488358|tyrosyl-DNA phosphodiesterase 1 [EC:3.1.4.-]	GO:0043231//intracellular membrane-bounded organelle	GO:0042578//phosphoric ester hydrolase activity	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203436	17.69	4	30.45	6.46	-2.236836158	0.00268646	DP2	K04683|1|9e-39|157|gmx:100800599|transcription factor Dp-1	GO:0043231//intracellular membrane-bounded organelle;GO:0043234//protein complex	GO:0003676//nucleic acid binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202373	13	3	6.94	1.5	-2.209973162	0.00870992	PHATRDRAFT_47291	K10838|1|2e-20|99.4|ota:Ot14g02880|xeroderma pigmentosum group C-complementing protein	-	-	-		-
7195797	13	3	11.27	2.44	-2.207534463	0.00870992	PHATRDRAFT_40124	-	-	GO:0016787//hydrolase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200706	13	3	62.34	13.53	-2.203996316	0.00870992	PHATRDRAFT_11934	K02518|1|6e-13|70.5|aly:ARALYDRAFT_327268|translation initiation factor IF-1	GO:0009536//plastid	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7202972	17	4	24.22	5.35	-2.178588068	0.00268646	PHATRDRAFT_47833	-	-	-	-		-
7204736	12	3	5.01	1.17	-2.098302074	0.01503258	PHATR_46901	-	-	-	-		-
7194786	12	3	12.53	2.94	-2.091498354	0.01503258	PHATRDRAFT_39038	-	-	-	-		-

7203427	23	6	22.28	5.45	-2.031421098	0.000771662	PHATRDRAFT_22166	K07238|1|2e-57|221|olu:OSTLU_42358|zinc transporter, ZIP family	-	GO:0008324//cation transmembrane transporter activity	GO:0006812//cation transport;GO:0044763		GO:0006812//cation transport;GO:0044763
7199770	11	3	8.18	2.09	-1.968597901	0.0256516	PHATRDRAFT_44822	-	-	-	-		-
7204083	11	3	14.23	3.64	-1.966925306	0.0256516	PHATR_33523	-	GO:0005622//intracellular	-	-		-
7196261	25	7	32.49	8.54	-1.927687769	0.000686068	PHATRDRAFT_5762	-	-	GO:0016491//oxidoreductase activity	GO:0071704;GO:0044710;GO:0044237//cellular metabolic process		GO:0071704;GO:0044710;GO:0044237//cellular metabolic process
7197707	17	5	69.92	19.33	-1.854863547	0.0067534	PHATRDRAFT_7893	K02956|1|3e-13|71.2|mtr:MTR_4g006090|small subunit ribosomal protein S15	GO:0005840//ribosome;GO:0043231//intracellular membrane-bounded organelle;GO:0044446	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7196856	10	3	6.09	1.71	-1.832445903	0.043212	PHATRDRAFT_32202	K04567|1|7e-166|582|cme:CMO044C|lysyl-tRNA synthetase, class II [EC:6.1.1.6]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7199831	20	6	14.48	4.07	-1.830960903	0.00351824	PHATRDRAFT_44927	-	-	-	-		-
7204592	10	3	12.02	3.38	-1.830341744	0.043212	PHATR_13244	K00428|1|2e-81|300|ota:Ot09g01570|cytochrome c peroxidase [EC:1.11.1.5]	-	GO:0004601//peroxidase activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7204957	10	3	4.16	1.17	-1.830074999	0.043212	PHATRDRAFT_bd1446	-	-	-	-		-
7197897	13	4	36.33	10.5	-1.790772038	0.0217094	PHATRDRAFT_34177	-	-	-	-		-
7195930	16	5	14.77	4.33	-1.770230896	0.01109322	PHATRDRAFT_15960	K15452|1|4e-40|163|olu:OSTLU_3606|tRNA pseudouridine synthase 2 [EC:5.4.99.-]	-	GO:0016866//intramolecular transferase activity;GO:0003676//nucleic acid binding	GO:0009451//RNA modification		GO:0009451//RNA modification
7204206	19	6	14.24	4.22	-1.754634242	0.00573582	PHATR_44003	-	-	GO:0016787//hydrolase activity	-		-
7202397	22	7	22.56	6.73	-1.745088658	0.00299174	PHATRDRAFT_47337	-	-	-	-		-
7198753	28	9	43.65	13.17	-1.728726308	0.000829396	PHATRDRAFT_50065	-	-	-	-		-
7204415	31	10	22.8	6.9	-1.724365557	0.00043979	PHATR_1864	K13412|1|2e-67|254|gmx:100816157|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7196931	27	9.2	26.27	8.4	-1.644954967	0.001323924	PHATRDRAFT_9308	-	-	GO:0016787//hydrolase activity	-		-
7205043	26	9	10.26	3.33	-1.623436649	0.00209752	PHATRDRAFT_bd1316	-	-	-	-		-
7199536	20	7	17.08	5.61	-1.606235299	0.00765616	PHATRDRAFT_44712	-	-	-	-		-
7204365	20	7	36.62	12.03	-1.605995149	0.00765616	PHATR_10458	K01522|1|5e-37|151|ath:AT5G58240|bis(5’-adenosyl)-triphosphatase [EC:3.6.1.29]	GO:0044444//cytoplasmic part	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;GO:0016819	GO:0008152//metabolic process		GO:0008152//metabolic process
7196715	17	6	11.73	3.88	-1.596074456	0.0148014	PHATRDRAFT_43079	K02731|1|6e-11|67.0|gmx:100790481|20S proteasome subunit alpha 4 [EC:3.4.25.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0000502//proteasome complex;GO:0044444//cytoplasmic part	GO:0004175//endopeptidase activity	GO:0044237//cellular metabolic process;GO:0006950//response to stress;GO:0006508//proteolysis		GO:0044237//cellular metabolic process;GO:0006950//response to stress;GO:0006508//proteolysis
7202429	14	5	8.06	2.7	-1.577820431	0.0289426	PHATRDRAFT_28689	K14807|1|3e-76|284|smo:SELMODRAFT_174931|ATP-dependent RNA helicase DDX51/DBP6 [EC:3.6.4.13]	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7196892	19	7	14.67	5.07	-1.532811219	0.01207172	GPH	-	-	GO:0016791//phosphatase activity	-		-
7202724	19	7	7.46	2.58	-1.531804565	0.01207172	PHATRDRAFT_47734	-	-	-	-		-
7202149	16	6	9.42	3.31	-1.508895843	0.0233894	PHATRDRAFT_47059	-	-	-	-		-
7203483	26	10	9.02	3.25	-1.472687715	0.0041862	PHATRDRAFT_48135	K02603|1|1e-07|57.4|sbi:SORBI_10g005910|origin recognition complex subunit 1	-	GO:0046914//transition metal ion binding	-		-
7204731	13	5	20.87	7.53	-1.47070883	0.0458682	PHATR_13470	K03470|1|3e-28|122|smo:SELMODRAFT_450428|ribonuclease HII [EC:3.1.26.4];K10743|5|1e-06|51.2|cme:CMK297C|ribonuclease H2 subunit A [EC:3.1.26.4]	-	GO:0016891//endoribonuclease activity, producing 5’-phosphomonoesters;GO:0003676//nucleic acid binding	GO:0090304		GO:0090304
7200337	13	5	10.97	3.96	-1.46999119	0.0458682	PHATRDRAFT_19647	K14847|1|1e-44|178|vvi:100252891|ribosome production factor 2	-	-	-		-

7200859	17.47	6.79	23.13	8.43	-1.45616073	0.0148014	PHATRDRAFT_35858	-	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	-	GO:0009987//cellular process;GO:0050896//response to stimulus		GO:0009987//cellular process;GO:0050896//response to stimulus
7202703	18	7	11.65	4.25	-1.454795209	0.01883276	PHATRDRAFT_47695	K01718|1|2e-12|72.0|cme:CMD024C|pseudouridylate synthase [EC:4.2.1.70];K15452|3|9e-08|56.6|rcu:RCOM_1298450|tRNA pseudouridine synthase 2 [EC:5.4.99.-]	-	GO:0003676//nucleic acid binding;GO:0016866//intramolecular transferase activity	GO:0009451//RNA modification		GO:0009451//RNA modification
7195250	18	7	16.09	5.87	-1.454731918	0.01883276	PHATRDRAFT_30019	K07179|1|8e-75|278|osa:4324901|RIO kinase 2 [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199045	23	9	18.28	6.71	-1.445881399	0.00793752	PHATRDRAFT_16674	K15336|1|7e-48|189|smo:SELMODRAFT_98974|tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	GO:0003676//nucleic acid binding;GO:0016741	GO:0006305		GO:0006305
7198487	34	13.31	15.17	5.57	-1.445471853	0.00096674	PHATRDRAFT_49826	K00995|1|2e-23|108|cme:CMN196C|CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5];K08744|2|2e-21|102|pop:POPTR_856644|cardiolipin synthase [EC:2.7.8.-]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006644//phospholipid metabolic process		GO:0006644//phospholipid metabolic process
7196797	28	11	18.38	6.77	-1.440909028	0.00340242	Tpt3	K15283|1|2e-72|271|cme:CMK114C|solute carrier family 35, member E1	GO:0044444//cytoplasmic part;GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	-	-		-
7198176	15	6	13.71	5.14	-1.415388307	0.0365106	PHATRDRAFT_40467	-	-	-	-		-
7196388	20	8	16.8	6.3	-1.415037499	0.01513258	PHATRDRAFT_17487	K00020|1|7e-53|206|olu:OSTLU_45774|3-hydroxyisobutyrate dehydrogenase [EC:1.1.1.31];K00120|2|2e-20|98.6|ppp:PHYPADRAFT_189760|[EC:1.1.-.-]	-	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0036094//small molecule binding;GO:0048037//cofactor binding	GO:0006007//glucose catabolic process;GO:0009081//branched-chain amino acid metabolic process		GO:0006007//glucose catabolic process;GO:0009081//branched-chain amino acid metabolic process
7204198	15	6	12.12	4.55	-1.413451248	0.0365106	PHATR_43987	-	-	-	-		-
7201207	30	12	42.67	16.02	-1.413347963	0.00276064	SOD1	K04564|1|4e-56|215|cme:CMN023C|superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	-	GO:0003824//catalytic activity;GO:0016209//antioxidant activity;GO:0043169//cation binding	GO:0044710;GO:0072593//reactive oxygen species metabolic process		GO:0044710;GO:0072593//reactive oxygen species metabolic process
7203609	15	6	23.3	8.75	-1.412975033	0.0365106	PHATRDRAFT_14915	K02863|1|1e-26|117|cme:CMJ235C|large subunit ribosomal protein L1	GO:0044391	GO:0003676//nucleic acid binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197150	25	10	64.24	24.13	-1.412643977	0.00641502	PHATRDRAFT_32634	-	-	-	-		-
7201347	34.54	14.06	39.35	15.04	-1.387559069	0.001811126	PHATRDRAFT_36006	-	-	-	-		-
7196270	22	9	22.4	8.6	-1.381090167	0.01214554	PHATRDRAFT_9444	K15276|1|2e-49|194|olu:OSTLU_37524|solute carrier family 35 (adenosine 3'-phospho 5'-phosphosulfate transporter), member B2	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7202345	31	13	14.94	5.87	-1.34774774	0.00336596	PHATRDRAFT_47253	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7202593	19	8	11.74	4.63	-1.34234831	0.0231106	PHATRDRAFT_47489	-	-	-	-		-
7195638	19	8	8.29	3.27	-1.342081466	0.0231106	PHATRDRAFT_49132	-	-	-	-		-
7198974	38	16	24.26	9.58	-1.340481989	0.001184854	TAL	K00616|1|2e-31|135|ppp:PHYPADRAFT_110503|transaldolase [EC:2.2.1.2]	-	GO:0016744	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7195718	19	8	12.35	4.88	-1.339557989	0.0231106	PHATRDRAFT_49488	K08994|1|1e-35|149|olu:OSTLU_27908|putative membrane protein	-	-	-		-

7195231	33	14	38.11	15.17	-1.328948523	0.00271216	PHATRDRAFT_30003	K02735|1|2e-72|270|ppp:PHYPADRAFT_166946|20S proteasome subunit beta 3 [EC:3.4.25.1]	GO:0000502//proteasome complex	GO:0004175//endopeptidase activity	GO:0006508//proteolysis		GO:0006508//proteolysis
7197277	49	21	29.01	11.66	-1.314982507	0.000277256	PHATRDRAFT_43763	-	-	-	-		-
7201515	21	9	48.72	19.6	-1.313660479	0.01839748	H2A-m2	K11251|1|1e-49|192|olu:OSTLU_13304|histone H2A	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7200512	21	9	21	8.45	-1.313366081	0.01839748	PHATRDRAFT_35460	K00100|1|3e-19|94.0|olu:OSTLU_36252|[EC:1.1.1.-];K00218|2|9e-19|92.4|vvi:100255647|protochlorophyllide reductase [EC:1.3.1.33]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7195071	16	7	10.72	4.4	-1.284729477	0.044246	PHATRDRAFT_15374	K01875|1|6e-55|213|ppp:PHYPADRAFT_137980|seryl-tRNA synthetase [EC:6.1.1.11]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7197131	25	11	17.96	7.41	-1.277241902	0.01168316	PHATRDRAFT_43396	-	-	-	-		-
7204929	18.89	8.31	16.94	6.99	-1.277069514	0.0348902	PHATRDRAFT_bd977	K02930|1|2e-104|377|cre:CHLREDRAFT_195598|large subunit ribosomal protein L4e	GO:0030312;GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0015934//large ribosomal subunit;GO:0005911//cell-cell junction;GO:0031090//organelle membrane	GO:0005198//structural molecule activity	GO:0009451//RNA modification;GO:0071555//cell wall organization;GO:0006221//pyrimidine nucleotide biosynthetic process;GO:0010467//gene expression		GO:0009451//RNA modification;GO:0071555//cell wall organization;GO:0006221//pyrimidine nucleotide biosynthetic process;GO:0010467//gene expression
7198623	16.47	7.31	9.03	3.76	-1.263993326	0.044246	PHATRDRAFT_49922	-	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710		GO:0044710
7201327	18	8	15.89	6.63	-1.261038349	0.0348902	sDer1-2	K13989|1|3e-22|103|vcn:VOLCADRAFT_33117|Derlin-2/3	-	-	-		-
7199140	20	9	10.52	4.44	-1.244503123	0.027569	SQD2	K06119|1|9e-99|359|cme:CMR015C|sulfoquinovosyltransferase [EC:2.4.1.-]	GO:0043231//intracellular membrane-bounded organelle	GO:0003824//catalytic activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7195411	20	9	28.59	12.07	-1.244084944	0.027569	PHATRDRAFT_39652	-	-	-	-		-
7203719	37.28	16.87	20.52	8.71	-1.236286107	0.001760068	PHATRDRAFT_48496	K01362|1|3e-12|72.0|olu:OSTLU_44226|[EC:3.4.21.-]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199009	46	21	14.55	6.23	-1.223715085	0.000869812	PHATRDRAFT_50228	K03130|1|1e-35|150|pop:POPTR_561983|transcription initiation factor TFIID subunit 5	-	-	-		-
7199377	24	11	46.32	19.93	-1.216693543	0.01730476	PHATRDRAFT_41518	-	-	-	-		-
7201658	28	13	23.84	10.38	-1.199577792	0.0109272	PHATRDRAFT_36356	-	-	GO:0003824//catalytic activity	-		-
7202138	30	14	12.18	5.33	-1.192306695	0.00869968	PHATRDRAFT_28431	K00297|1|1e-146|518|ppp:PHYPADRAFT_161370|methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	-	GO:0016646//oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	GO:0000096//sulfur amino acid metabolic process		GO:0000096//sulfur amino acid metabolic process
7195423	30	14	27.33	11.97	-1.191062308	0.00869968	HAD2	K00074|1|8e-56|215|smo:SELMODRAFT_171538|3-hydroxybutyryl-CoA dehydrogenase [EC:1.1.1.157]	-	GO:0036094//small molecule binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0048037//cofactor binding;GO:0043168//anion binding	GO:0032787//monocarboxylic acid metabolic process		GO:0032787//monocarboxylic acid metabolic process
7199221	41	19.32	63.01	27.86	-1.177385552	0.001956004	PHATRDRAFT_16840	-	GO:0016020//membrane;GO:0005739//mitochondrion	GO:0003824//catalytic activity	-		-
7201047	19	9	16.32	7.25	-1.170588157	0.0408396	PHATRDRAFT_45980	K00729|1|1e-43|175|cre:CHLREDRAFT_18353|dolichyl-phosphate beta-glucosyltransferase [EC:2.4.1.117]	-	GO:0016740//transferase activity	-		-

7204730	19	9	17.94	7.97	-1.170528261	0.0408396	PHATR_4286	K03453|1|4e-61|233|ota:Ot06g04280|bile acid:Na+ symporter, BASS family	-	GO:0005343//organic acid:sodium symporter activity	GO:0030001//metal ion transport		GO:0030001//metal ion transport
7197334	19	9	25.99	11.55	-1.170063782	0.0408396	PHATRDRAFT_32866	-	-	-	-		-
7197996	21	10	22.41	10.01	-1.162700675	0.0321518	PHATRDRAFT_44273	-	-	-	-		-
7195810	21	10	16.07	7.18	-1.16231418	0.0321518	PHATRDRAFT_49451	K03437|1|2e-15|82.0|ota:Ot08g01510|RNA methyltransferase, TrmH family	-	GO:0003676//nucleic acid binding;GO:0008168//methyltransferase activity	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7201177	23.21	11.09	8.66	3.88	-1.158310373	0.0253744	PHATRDRAFT_36115	-	-	GO:0046914//transition metal ion binding	-		-
7195649	46	22	23.72	10.64	-1.156605859	0.00145157	PHATRDRAFT_49149	K03512|1|8e-28|123|aly:ARALYDRAFT_312091|DNA polymerase lambda subunit [EC:2.7.7.7 4.2.99.-];K02330|5|2e-25|115|olu:OSTLU_34689|DNA polymerase beta subunit [EC:2.7.7.7 4.2.99.-]	-	GO:0003676//nucleic acid binding;GO:0034061	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200220	23	11	39.12	17.56	-1.155613525	0.0253744	PHATRDRAFT_45181	-	-	-	-		-
7198276	25	12	11.03	4.96	-1.153020765	0.0200684	PHATRDRAFT_49610	-	-	GO:0008422//beta-glucosidase activity	GO:0044238		GO:0044238
7202859	27	13	27.78	12.55	-1.146359235	0.01590158	PHATRDRAFT_21829	K00991|1|1e-53|208|zma:100272499|2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [EC:2.7.7.60]	-	-	GO:0006720//isoprenoid metabolic process		GO:0006720//isoprenoid metabolic process
7194787	27	13	14.52	6.56	-1.146273733	0.01590158	PHATRDRAFT_48556	-	-	GO:0016740//transferase activity	-		-
7203638	29	14	23.42	10.6	-1.143676811	0.01262054	PHATRDRAFT_48371	-	GO:0009534//chloroplast thylakoid	-	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7199353	29	14	61.79	28	-1.141946546	0.01262054	PHATRDRAFT_41541	-	-	-	-		-
7200199	33	16	14.88	6.77	-1.136146788	0.0079834	PHATRDRAFT_45140	-	-	-	-		-
7202539	35	17	26.59	12.11	-1.134684912	0.00636118	PHATRDRAFT_47395	K00434|1|9e-83|305|smo:SELMODRAFT_108251|L-ascorbate peroxidase [EC:1.11.1.11]	GO:0044424	GO:0046906//tetrapyrrole binding;GO:0004601//peroxidase activity	GO:0006950//response to stress;GO:0044710		GO:0006950//response to stress;GO:0044710
7203660	37	18	16.5	7.53	-1.131744254	0.00507398	PHATRDRAFT_54899	-	GO:0044464	GO:0005099//Ras GTPase activator activity	GO:0032313//regulation of Rab GTPase activity		GO:0032313//regulation of Rab GTPase activity
7200159	33.61	16.61	108.72	50.47	-1.107119369	0.0079834	H4-1a	K11254|1|6e-40|160|olu:OSTLU_44220|histone H4	GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0000785//chromatin;GO:0016020//membrane	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization;GO:0006950//response to stress		GO:0034728//nucleosome organization;GO:0006950//response to stress
7201792	24	12	15.85	7.43	-1.093048724	0.0290164	AroB	K01735|1|1e-127|454|smo:SELMODRAFT_131934|3-dehydroquinate synthase [EC:4.2.3.4]	GO:0009532//plastid stroma	GO:0016838//carbon-oxygen lyase activity, acting on phosphates	GO:0008652//cellular amino acid biosynthetic process;GO:0006743//ubiquinone metabolic process		GO:0008652//cellular amino acid biosynthetic process;GO:0006743//ubiquinone metabolic process
7204930	48.47	24.23	20.32	9.53	-1.092352283	0.001883532	PHATRDRAFT_bd1635	K12319|1|3e-30|132|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|1e-24|113|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K13755|5|5e-12|71.6|vcn:VOLCADRAFT_64696|calcium/calmodulin-dependent 3’,5’-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7198824	22	11	24.11	11.31	-1.092032722	0.0368128	PHATRDRAFT_50111	-	-	-	-		-
7196777	20	10	17.2	8.07	-1.091767986	0.046829	PHATRDRAFT_42946	-	GO:0031224//intrinsic component of membrane	-	GO:0006810//transport		GO:0006810//transport
7204891	37.57	19.14	15.12	7.23	-1.064390587	0.00815984	PHATRDRAFT_bd1569	-	GO:0044424	GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0032550	GO:0006412//translation		GO:0006412//translation

7205095	36.75	18.79	48.87	23.45	-1.059361182	0.0072382	PtRabX1	K07901|1|1e-44|177|zma:100273222|Ras-related protein Rab-8A;K07976|2|2e-44|176|osa:4334590|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7195480	35	18	27.82	13.42	-1.051737748	0.01024774	PHATRDRAFT_49308	-	-	-	-		-
7196824	39	20	248.39	119.97	-1.049933406	0.0065046	PHATRDRAFT_8802	-	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197755	31	16	38.21	18.5	-1.046424987	0.01622552	PHATRDRAFT_33920	-	-	-	-		-
7199544	110	57	69.85	33.95	-1.040848541	5.62E-06	PHATRDRAFT_44821	-	-	-	-		-
7195850	27	14	20.49	9.97	-1.039254575	0.0258504	PHATRDRAFT_15917	K01758|1|8e-92|335|cme:CMT389C|cystathionine gamma-lyase [EC:4.4.1.1];K01760|2|2e-70|264|vcn:VOLCADRAFT_68235|cystathionine beta-lyase [EC:4.4.1.8]	GO:0009532//plastid stroma	GO:0043168//anion binding;GO:0016846//carbon-sulfur lyase activity	GO:0000097//sulfur amino acid biosynthetic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901605//alpha-amino acid metabolic process		GO:0000097//sulfur amino acid biosynthetic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901605//alpha-amino acid metabolic process
7195916	25	13	23	11.22	-1.035561185	0.0327218	PHATRDRAFT_3183	K01505|1|1e-28|125|olu:OSTLU_28382|1-aminocyclopropane-1-carboxylate deaminase [EC:3.5.99.7]	GO:0009536//plastid	GO:0046914//transition metal ion binding;GO:0016846//carbon-sulfur lyase activity;GO:0016810//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	GO:0009093//cysteine catabolic process;GO:1901135;GO:1901576;GO:0009692;GO:0010038//response to metal ion;GO:0006006//glucose metabolic process;GO:0006950//response to stress;GO:0044249//cellular biosynthetic process		GO:0009093//cysteine catabolic process;GO:1901135;GO:1901576;GO:0009692;GO:0010038//response to metal ion;GO:0006006//glucose metabolic process;GO:0006950//response to stress;GO:0044249//cellular biosynthetic process
7194843	25	13	21.48	10.48	-1.035355276	0.0327218	PHATRDRAFT_39159	-	-	-	-		-
7204065	46	24	29.65	14.51	-1.030984585	0.00370908	PHATR_10257	K15849|1|4e-36|150|pop:POPTR_819830|bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase [EC:2.6.1.1 2.6.1.78 2.6.1.79]	-	GO:0043168//anion binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7195312	38	20	18.13	8.95	-1.018419338	0.00912264	PHATRDRAFT_49069	-	-	-	-		-
7200517	27.48	14.5	14.3	7.07	-1.016233027	0.0258504	PHATRDRAFT_45712	-	-	GO:0016740//transferase activity	-		-
7201205	51	27	23.21	11.52	-1.010605806	0.00264538	PHATRDRAFT_46251	K08202|1|2e-21|102|cre:CHLREDRAFT_103526|MFS transporter, OCT family, solute carrier family 22 (organic cation transporter), member 4/5;K08150|3|2e-12|72.4|zma:100285429|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7199030	30	16	17.44	8.72	-1	0.0228356	PHATRDRAFT_50263	-	-	-	-		-
7200769	56	30	111.06	55.85	-0.991710115	0.001884758	PHATRDRAFT_35516	-	-	-	-		-
7199127	26	14	12.7	6.41	-0.986432235	0.0364666	GPI_2	K01810|1|5e-151|533|osa:4340677|glucose-6-phosphate isomerase [EC:5.3.1.9]	GO:0044424	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7201158	26	14	21.69	10.95	-0.986099183	0.0364666	PHATRDRAFT_36081	K02835|1|5e-109|392|gmx:100805037|peptide chain release factor 1	GO:0044424	GO:0003747//translation release factor activity	GO:0006412//translation		GO:0006412//translation
7200702	26	14	21.84	11.03	-0.985540065	0.0364666	PHATRDRAFT_45477	-	-	-	-		-
7202819	115	62	39.9	20.17	-0.984177662	9.35E-06	PHATRDRAFT_47612	-	-	-	-		-
7204690	24	13	7	3.55	-0.979535897	0.046224	PHATR_46837	K14766|1|5e-57|221|olu:OSTLU_16944|nucleolar protein 14	GO:0030684//preribosome	-	-		-
7197366	61	33	55.05	27.94	-0.978410543	0.001342176	PHATRDRAFT_43658	-	-	-	-		-
7194858	48	26	29.93	15.2	-0.977520955	0.00456122	PHATRDRAFT_15212	K05643|1|6e-45|180|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3;K05641|5|2e-42|171|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1	GO:0044464	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process

7199136	72	39	32.15	16.33	-0.977293947	0.000499152	PHATRDRAFT_50353	-	-	GO:0016703	GO:0044710		GO:0044710
7197694	24	13	47.27	24.03	-0.976088216	0.046224	PHATRDRAFT_10781	K00889|1|1e-31|133|osa:4331188|1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7199024	35	19	18.48	9.41	-0.973698129	0.01595004	PHATRDRAFT_50253	K08342|1|7e-29|127|ppp:PHYPADRAFT_43119|autophagy-related protein 4 [EC:3.4.22.-]	GO:0044424	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0044248//cellular catabolic process;GO:0019538//protein metabolic process;GO:0045184//establishment of protein localization		GO:0044248//cellular catabolic process;GO:0019538//protein metabolic process;GO:0045184//establishment of protein localization
7198268	35	19	37.5	19.1	-0.973317957	0.01595004	PHATRDRAFT_40382	-	-	GO:0043168//anion binding;GO:0046914//transition metal ion binding	-		-
7200797	53	29	100.26	51.49	-0.961381964	0.00322596	PHATRDRAFT_35573	-	-	-	-		-
7196543	38	21	21.3	11.04	-0.948113258	0.01398472	PHATRDRAFT_42913	-	-	-	-		-
7203909	27	15	15.98	8.32	-0.941611975	0.0402306	PHATR_44170	-	-	-	-		-
7203695	27	15	89.36	46.64	-0.938061397	0.0402306	PHATRDRAFT_38928	-	-	-	-		-
7204868	36	20.03	44.96	23.47	-0.937824194	0.0175446	PHATRDRAFT_bd1125	-	-	-	-		-
7196979	52	29	41.06	21.48	-0.934739634	0.00440562	PHATRDRAFT_43270	-	-	-	-		-
7195027	88.11	49.16	64.64	33.83	-0.934124021	0.00019891	ACT1	K05692|1|1e-177|620|cre:CHLREDRAFT_24392|actin beta/gamma 1;K10355|2|9e-177|617|ath:AT3G12110|actin, other eukaryote	GO:0043232	GO:0032550	-		-
7203566	34	19	12.12	6.35	-0.932561202	0.022035	PHATRDRAFT_48352	-	-	-	-		-
7198994	60.86	34.03	70.18	36.82	-0.930570321	0.00271974	PHATRDRAFT_16669	-	-	-	GO:0044248//cellular catabolic process		GO:0044248//cellular catabolic process
7201083	32	18	14.77	7.79	-0.922974593	0.0277082	PHATRDRAFT_35637	K00059|1|4e-20|98.2|rcu:RCOM_1081890|3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7204650	32	18	38.78	20.47	-0.921801701	0.0277082	PHATR_28202	K02729|1|5e-89|325|osa:4350922|20S proteasome subunit alpha 5 [EC:3.4.25.1]	GO:0005840//ribosome;GO:0005839//proteasome core complex;GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane	GO:0004175//endopeptidase activity	GO:0019941//modification-dependent protein catabolic process;GO:0010038//response to metal ion		GO:0019941//modification-dependent protein catabolic process;GO:0010038//response to metal ion
7195749	42	24	45.97	24.64	-0.89969041	0.01331942	PHATRDRAFT_49537	-	-	-	-		-
7203531	28	16	41.9	22.47	-0.898950119	0.043997	PHATRDRAFT_38627	-	-	-	-		-
7198843	54	31	21.74	11.7	-0.893843411	0.0052188	PHATRDRAFT_50140	-	-	GO:0016301//kinase activity	-		-
7194911	73	42	26.42	14.25	-0.890668547	0.001185634	PHATRDRAFT_48678	K12319|1|5e-31|134|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|4e-27|122|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15]	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7202445	40	23	43.01	23.2	-0.890547326	0.0166503	hDer1-2	K13989|1|4e-30|129|sbi:SORBI_09g005900|Derlin-2/3	-	-	-		-
7202316	40	23	14.62	7.89	-0.889846106	0.0166503	APC2	K03349|1|3e-94|344|smo:SELMODRAFT_79209|anaphase-promoting complex subunit 2	GO:0000151//ubiquitin ligase complex	GO:0044389	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7198602	33	19	11.88	6.42	-0.887889634	0.0301874	PHATRDRAFT_49898	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7199001	51	29.44	36.85	19.96	-0.884552899	0.00598174	PHATRDRAFT_50215	-	-	-	-		-
7197146	45	26	24.5	13.28	-0.883526603	0.01157496	PHATRDRAFT_43421	-	-	-	-		-
7194739	43	25	27.76	15.14	-0.874642363	0.01443932	PHATRDRAFT_48579	-	-	-	-		-
7203103	48	28	14.24	7.79	-0.870253913	0.01004728	PHATRDRAFT_47891	-	-	-	-		-
7204380	41	24	10.02	5.5	-0.865378985	0.01802314	PHATR_33295	K11293|1|5e-52|205|aly:ARALYDRAFT_665139|protein HIRA/HIR1	GO:0043231//intracellular membrane-bounded organelle	-	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197717	41	24	30.47	16.73	-0.864952055	0.01802314	PHATRDRAFT_10723	K08869|1|1e-84|311|cme:CMG161C|aarF domain-containing kinase	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7194962	29	17	9.5	5.22	-0.863877707	0.0477514	PHATRDRAFT_48886	K14724|1|8e-07|54.7|smo:SELMODRAFT_144857|solute carrier family 9 (sodium/hydrogen exchanger), member 8	GO:0031224//intrinsic component of membrane	GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044763;GO:0030001//metal ion transport		GO:0044763;GO:0030001//metal ion transport
7199341	29	17	20.09	11.05	-0.862431194	0.0477514	PHATRDRAFT_50535	-	-	-	-		-
7202259	75	44	26.86	14.78	-0.861813035	0.001380698	PHATRDRAFT_47034	-	-	-	-		-
7195561	34	20	34.25	18.9	-0.857717754	0.0326836	PHATRDRAFT_49267	-	-	-	-		-

7195321	34	20	56.71	31.31	-0.856979648	0.0326836	PHATRDRAFT_49086	-	-	-	-		-
7198101	78	46	101.69	56.27	-0.853739946	0.00120293	PHATRDRAFT_44603	K02137|1|5e-26|115|ppp:PHYPADRAFT_110216|F-type H+-transporting ATPase oligomycin sensitivity conferral protein [EC:3.6.3.14]	-	GO:0019829//cation-transporting ATPase activity	GO:0006754//ATP biosynthetic process		GO:0006754//ATP biosynthetic process
7201582	54	32	32.26	17.93	-0.84737095	0.00755212	PHATRDRAFT_13093	K14437|1|2e-129|460|cme:CMQ215C|chromodomain-helicase-DNA-binding protein 7 [EC:3.6.4.12];K11367|2|4e-107|386|gmx:100792398|chromodomain-helicase-DNA-binding protein 1 [EC:3.6.4.12]	-	GO:0003676//nucleic acid binding;GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7200778	32	19	25.29	14.09	-0.843895425	0.040998	PHATRDRAFT_3052	K06941|1|1e-58|225|ppp:PHYPADRAFT_149959|23S rRNA (adenine2503-C2)-methyltransferase [EC:2.1.1.192]	GO:0044424	GO:0051540;GO:0008168//methyltransferase activity	GO:0042254//ribosome biogenesis;GO:0009451//RNA modification		GO:0042254//ribosome biogenesis;GO:0009451//RNA modification
7204299	37	22	38.03	21.21	-0.842393318	0.0281346	PHATR_43885	-	-	-	-		-
7204043	37	22	14.27	7.96	-0.842144999	0.0281346	PHATR_44116	K03255|1|2e-08|59.7|mtr:MTR_3g027610|protein TIF31	-	-	-		-
7201742	42	25	26.4	14.74	-0.840801405	0.01941782	PHATRDRAFT_54611	-	GO:0031224//intrinsic component of membrane	GO:0016782//transferase activity, transferring sulfur-containing groups	-		-
7197039	70	42	50.12	28.21	-0.829179749	0.00278842	PHATRDRAFT_43760	-	GO:0030119//AP-type membrane coat adaptor complex	-	GO:0015031//protein transport		GO:0015031//protein transport
7197128	40	24	21.78	12.26	-0.829044975	0.0242106	PHATRDRAFT_43391	-	-	-	-		-
7204925	107.06	64.56	45.53	25.75	-0.822245027	0.000199987	PHATRDRAFT_bd1603	-	-	GO:0003824//catalytic activity	-		-
7197052	43	26	34.72	19.69	-0.818303837	0.020831	PHATRDRAFT_43778	-	-	-	-		-
7204991	38	23	18.52	10.51	-0.817321429	0.0302022	PHATRDRAFT_bd1718	-	-	-	-		-
7196055	38	23	23.87	13.55	-0.816905715	0.0302022	PHATRDRAFT_42496	-	-	-	-		-
7202011	33	20	18.7	10.63	-0.814896673	0.0440466	PHATRDRAFT_47095	-	-	-	-		-
7195551	33	20	22.18	12.61	-0.81469109	0.0440466	PHATRDRAFT_23077	K14963|1|3e-73|273|smo:SELMODRAFT_169971|COMPASS component SWD3	-	-	-		-
7200448	51	31	13.36	7.62	-0.810057105	0.0124441	UBA1	K03178|1|3e-108|391|sbi:SORBI_02g043880|ubiquitin-activating enzyme E1 [EC:6.3.2.19]	-	GO:0003824//catalytic activity;GO:0032550	GO:0036211		GO:0036211
7202310	46	28	33.81	19.3	-0.808849169	0.0179233	RPN6	K03036|1|3e-80|297|zma:100193485|26S proteasome regulatory subunit N6	GO:0043234//protein complex	-	-		-
7203966	46	28	30.9	17.64	-0.808756277	0.0179233	PHATR_43839	-	-	-	-		-
7194854	77	47	48.11	27.55	-0.804284481	0.00223714	PHATRDRAFT_48658	-	GO:0031224//intrinsic component of membrane	-	-		-
7203699	72	44	34.19	19.6	-0.802720768	0.0031798	PHATRDRAFT_48471	-	-	-	-		-
7204598	36	22	27.84	15.96	-0.80269856	0.0376976	PHATR_1103	K13412|1|2e-65|247|gmx:100797449|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7197412	36	22	17.14	9.83	-0.802103788	0.0376976	PHATRDRAFT_56626	K11808|1|5e-132|469|ppp:PHYPADRAFT_189585|phosphoribosylaminoimidazole carboxylase [EC:4.1.1.21]	-	GO:0043169//cation binding;GO:0032550;GO:0016866//intramolecular transferase activity;GO:0016831//carboxy-lyase activity	GO:0006188//IMP biosynthetic process		GO:0006188//IMP biosynthetic process
7198303	75	46	117.57	67.67	-0.796931685	0.00275172	PHATRDRAFT_49660	K07253|1|3e-24|109|olu:OSTLU_17653|phenylpyruvate tautomerase [EC:5.3.2.1];K15923|4|3e-13|73.2|mtr:MTR_4g127370|alpha-L-fucosidase 2 [EC:3.2.1.51]	GO:0009536//plastid	-	GO:0048646//anatomical structure formation involved in morphogenesis		GO:0048646//anatomical structure formation involved in morphogenesis
7202270	44	27	49.42	28.45	-0.796666358	0.0222596	PHATRDRAFT_47485	K08907|1|1e-06|52.0|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1	-	-	-		-
7202032	39	24	23.85	13.77	-0.792460707	0.032278	PHATRDRAFT_47119	K10570|1|4e-38|157|ath:AT1G19750|DNA excision repair protein ERCC-8	GO:0044424	-	-		-
7204419	52	32	93.43	53.97	-0.791728181	0.01327372	PHATR_46858	-	-	-	-		-
7200967	47	29	20.54	11.88	-0.789901346	0.0191177	PHATRDRAFT_45867	-	-	-	-		-
7195400	136	84	239.37	138.76	-0.786650606	6.49E-05	PHATRDRAFT_54979	-	-	-	-		-

7196433	55	34	42.31	24.53	-0.786451452	0.01142628	PHATRDRAFT_42835	-	-	GO:0036094//small molecule binding	-		-
7199000	43.4	26.87	30.82	17.9	-0.783907274	0.020831	PHATRDRAFT_50214	-	-	-	-		-
7196198	42	26	14.27	8.29	-0.783541328	0.0276516	PHATRDRAFT_42955	K09291|1|2e-08|59.7|bdi:100825730|nucleoprotein TPR;K10696|2|2e-08|59.7|rcu:RCOM_1455450|E3 ubiquitin-protein ligase BRE1 [EC:6.3.2.19];K06638|4|3e-07|55.8|smo:SELMODRAFT_439954|mitotic spindle assembly checkpoint protein MAD1;K10400|5|1e-06|53.9|osa:4352674|kinesin family member 15	GO:0043229//intracellular organelle	-	-		-
7198159	134	83	67.28	39.09	-0.783378121	7.92E-05	PHATRDRAFT_40433	K14683|1|1e-66|252|zma:100501653|solute carrier family 34 (sodium-dependent phosphate cotransporter)	-	GO:0015114//phosphate ion transmembrane transporter activity	GO:0006817//phosphate ion transport		GO:0006817//phosphate ion transport
7200431	50	31	53.17	30.93	-0.781605633	0.01642486	PHATRDRAFT_12113	-	GO:0012505//endomembrane system	-	GO:0044765		GO:0044765
7202263	87	54	63.29	36.85	-0.780312948	0.001543338	PHATRDRAFT_47472	-	-	GO:0097159//organic cyclic compound binding	-		-
7204545	219	136	99.55	57.98	-0.779865983	4.93E-07	PHATR_46796	-	-	-	-		-
7196282	90	56	45.54	26.57	-0.777336064	0.001335748	PHATRDRAFT_42595	K10276|1|3e-37|154|cme:CMB046C|F-box and leucine-rich repeat protein 10/11 [EC:1.14.11.27]	-	-	-		-
7202597	40	25	20.1	11.78	-0.770855962	0.034358	PHATRDRAFT_47494	-	-	-	-		-
7203154	48	30	20.73	12.15	-0.770763803	0.0203248	PHATRDRAFT_47886	K08827|1|5e-59|227|vvi:100247382|serine/threonine-protein kinase PRP4 [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198725	40	25	59.55	34.93	-0.769634865	0.034358	PHATRDRAFT_16471	-	-	-	-		-
7199589	84	53	65.55	38.8	-0.756539128	0.00245136	PHATRDRAFT_44884	-	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0044238;GO:0006026		GO:0044238;GO:0006026
7200274	38	24	17.17	10.17	-0.75557036	0.0427008	PHATRDRAFT_45260	K14207|1|5e-23|107|pop:POPTR_580719|solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 2	GO:0031224//intrinsic component of membrane	-	-		-
7196077	38	24	19.55	11.58	-0.755533354	0.0427008	PHATRDRAFT_42527	K00864|1|3e-09|62.0|cre:CHLREDRAFT_128764|glycerol kinase [EC:2.7.1.30];K11214|2|2e-06|52.8|ppp:PHYPADRAFT_103646|sedoheptulokinase [EC:2.7.1.14]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0044238		GO:0044238
7198560	93	59	28.95	17.22	-0.749478205	0.00158009	PHATRDRAFT_49976	-	-	-	-		-
7203133	63	40	31.09	18.51	-0.748145721	0.00949826	PHATRDRAFT_47945	-	-	-	-		-
7197105	63	40	68.34	40.71	-0.747347026	0.00949826	PHATRDRAFT_43356	-	-	-	-		-
7199751	66	42	48.14	28.73	-0.744678149	0.00816896	PHATRDRAFT_44793	-	-	-	-		-
7198336	44	28	52.21	31.18	-0.743705231	0.031124	PHATRDRAFT_49747	-	-	-	-		-
7195836	50	32	26.07	15.65	-0.736227926	0.0227692	PHATRDRAFT_23260	K08150|1|2e-38|159|vvi:100268023|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0022857//transmembrane transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7201639	50	32	31.73	19.05	-0.736056524	0.0227692	PHATRDRAFT_36322	K14510|1|1e-13|76.3|vvi:100240856|serine/threonine-protein kinase CTR1 [EC:2.7.11.1];K04688|4|6e-13|73.9|smo:SELMODRAFT_181752|p70 ribosomal S6 kinase [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199573	50	32	15.42	9.26	-0.735718667	0.0227692	PHATRDRAFT_259	K12874|1|0.0|671|gmx:100778665|intron-binding protein aquarius	GO:0030529//ribonucleoprotein complex	GO:0036002//pre-mRNA binding	GO:0000377		GO:0000377
7195079	39	25	24.69	14.85	-0.733463905	0.0451862	PHATRDRAFT_42247	K01893|1|2e-151|533|olu:OSTLU_51201|asparaginyl-tRNA synthetase [EC:6.1.1.22]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7201048	53	34	45.72	27.51	-0.732869264	0.01949832	PHATRDRAFT_45982	-	-	-	-		-
7200083	42	27	9.44	5.69	-0.730358207	0.0385138	PHATRDRAFT_45161	-	-	-	-		-

7198740	56	36	22.08	13.31	-0.730229601	0.01670944	PHATRDRAFT_50045	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003700//sequence-specific DNA binding transcription factor activity;GO:0046914//transition metal ion binding	GO:0006366//transcription from RNA polymerase II promoter		GO:0006366//transcription from RNA polymerase II promoter
7202649	42	27	9.47	5.71	-0.72987368	0.0385138	PHATRDRAFT_37844	-	-	-	-		-
7196875	42	27	49.23	29.69	-0.729560646	0.0385138	PHATRDRAFT_32237	-	-	GO:0097159//organic cyclic compound binding	-		-
7196954	59	38	28.78	17.39	-0.726808659	0.01432912	PHATRDRAFT_43233	-	-	-	-		-
7204968	44.97	29	14.13	8.54	-0.726453491	0.0426432	PHATRDRAFT_bd1769	-	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0046914//transition metal ion binding	GO:0044710		GO:0044710
7201893	48	31	96.53	58.52	-0.722047609	0.0280728	PHATRDRAFT_13005	K00432|1|5e-27|118|smo:SELMODRAFT_228619|glutathione peroxidase [EC:1.11.1.9]	GO:0009507//chloroplast	GO:0004601//peroxidase activity	GO:0044710;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress		GO:0044710;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress
7198479	926	601	1178.62	717.75	-0.715545322	7.19E-22	Lhcf5	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204942	123	80	38.05	23.21	-0.713149931	0.000494882	PHATRDRAFT_bd1740	-	GO:0031224//intrinsic component of membrane	GO:0004930//G-protein coupled receptor activity;GO:0004620//phospholipase activity	GO:0007166//cell surface receptor signaling pathway		GO:0007166//cell surface receptor signaling pathway
7197437	43	28	26.93	16.45	-0.711126646	0.0405834	PHATRDRAFT_43429	K01736|1|5e-153|539|cme:CME064C|chorismate synthase [EC:4.2.3.5]	GO:0009536//plastid;GO:0031981//nuclear lumen	GO:0016838//carbon-oxygen lyase activity, acting on phosphates	GO:0008652//cellular amino acid biosynthetic process;GO:0043650;GO:0019632//shikimate metabolic process		GO:0008652//cellular amino acid biosynthetic process;GO:0043650;GO:0019632//shikimate metabolic process
7201685	46	30	26.28	16.07	-0.709595347	0.0346042	PHATRDRAFT_46540	-	-	-	-		-
7205062	158	103	120.67	73.79	-0.709569828	8.36E-05	PHATRDRAFT_bd1737	-	-	-	-		-
7203311	46	30	16.58	10.14	-0.709386354	0.0346042	PHATRDRAFT_48173	K00847|1|1e-23|110|ota:Ot07g04040|fructokinase [EC:2.7.1.4];K12586|3|7e-12|71.2|smo:SELMODRAFT_176463|exosome complex component RRP43	-	-	-		-
7204817	69	45	40.55	24.8	-0.709361794	0.00952914	PHATRDRAFT_bd1691	K16052|1|3e-11|68.2|ppp:PHYPADRAFT_119414|MscS family membrane protein YnaI	-	-	GO:0044763		GO:0044763
7197746	49	32	27.84	17.05	-0.707387472	0.0295392	PHATRDRAFT_44454	K06897|1|1e-56|219|cre:CHLREDRAFT_187976|	-	GO:0003824//catalytic activity	-		-
7198885	45.04	29.45	43	26.38	-0.704892095	0.0328644	PHATRDRAFT_50213	-	-	-	-		-
7199019	122	80	64.62	39.74	-0.701388878	0.000628448	PHATRDRAFT_50245	-	-	GO:0042623//ATPase activity, coupled	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7196217	61	40	19.54	12.02	-0.700993571	0.01583238	PHATRDRAFT_42990	-	-	GO:0046872//metal ion binding	-		-
7198910	64	42	47.48	29.23	-0.699870106	0.01357328	PHATRDRAFT_50105	-	-	-	-		-
7198497	64	42	77.55	47.75	-0.699626048	0.01357328	PHATRDRAFT_16408	-	-	-	-		-
7202531	105	69	54.21	33.41	-0.698279024	0.00158527	PHATRDRAFT_47384	K03257|1|8e-63|239|pop:POPTR_716781|translation initiation factor 4A	GO:0044464	GO:0042623//ATPase activity, coupled;GO:0032550	-		-

7205153	40.18	26.45	9.61	5.93	-0.696504326	0.0476552	PHATRDRAFT_bd1631	K12319|1|8e-29|128|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|1e-24|114|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K13755|5|2e-15|83.6|vcn:VOLCADRAFT_60471|calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7200916	44	29	60.77	37.59	-0.693010377	0.0426432	PHATRDRAFT_35566	K00760|1|2e-24|110|rcu:RCOM_0296600|hypoxanthine phosphoribosyltransferase [EC:2.4.2.8]	GO:0044424	GO:0016763//transferase activity, transferring pentosyl groups	GO:0043101//purine-containing compound salvage;GO:0055086//nucleobase-containing small molecule metabolic process		GO:0043101//purine-containing compound salvage;GO:0055086//nucleobase-containing small molecule metabolic process
7195294	47	31	57.69	35.7	-0.692397189	0.0363408	PHATRDRAFT_49040	-	-	GO:0003824//catalytic activity	-		-
7198937	47	31	64.92	40.18	-0.692185436	0.0363408	PHATRDRAFT_50142	-	-	-	-		-
7195377	59	39	13.81	8.56	-0.690030618	0.01937596	PHATRDRAFT_48962	-	-	-	-		-
7202916	65	43	63.68	39.52	-0.688257389	0.01422196	PHATRDRAFT_47746	-	-	-	-		-
7196562	96	64	43.34	27.1	-0.677406302	0.00327672	PHATRDRAFT_17895	K01792|1|1e-49|196|ppp:PHYPADRAFT_155277|glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	-	GO:0005488//binding;GO:0003824//catalytic activity	GO:0044238		GO:0044238
7204753	96	64	53.7	33.58	-0.677319858	0.00327672	PHATR_46926	-	-	-	-		-
7203526	57	38	42.47	26.56	-0.677188962	0.0237006	PHATRDRAFT_54872	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202790	45	30	66.08	41.34	-0.676675298	0.0446912	PHATRDRAFT_56446	-	-	-	-		-
7197321	91	61	32.9	20.68	-0.669851398	0.00461036	PHATRDRAFT_43598	-	-	-	-		-
7194985	91	61	77.95	49.02	-0.669178539	0.00461036	PHATRDRAFT_42255	K14521|1|2e-52|204|vcn:VOLCADRAFT_98273|N-acetyltransferase 10 [EC:2.3.1.-];K05275|2|4e-13|73.9|zma:100272747|pyridoxine 4-dehydrogenase [EC:1.1.1.65];K00064|3|7e-13|73.2|aly:ARALYDRAFT_491313|D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]	GO:0009532//plastid stroma;GO:0009526//plastid envelope	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006090//pyruvate metabolic process		GO:0006090//pyruvate metabolic process
7204386	61	41	72.09	45.46	-0.665201465	0.0211806	GLRX2	K03676|1|3e-15|80.5|aly:ARALYDRAFT_895626|glutaredoxin 3	GO:0043231//intracellular membrane-bounded organelle	GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis		GO:0019725//cellular homeostasis
7202218	58	39	39.05	24.63	-0.664905921	0.0247614	PHATRDRAFT_46970	-	-	-	-		-
7197322	58	39	56.06	35.36	-0.66485347	0.0247614	PHATRDRAFT_32841	K14026|1|7e-06|49.7|olu:OSTLU_27845|SEL1 protein	-	-	-		-
7194839	55	37	36.18	22.83	-0.664261548	0.0289742	PHATRDRAFT_48638	K04799|1|1e-87|322|aly:ARALYDRAFT_489493|flap endonuclease-1 [EC:3.-.-.-]	GO:0031981//nuclear lumen;GO:0044444//cytoplasmic part	GO:0004519//endonuclease activity;GO:0046872//metal ion binding;GO:0004527//exonuclease activity	GO:0006281//DNA repair		GO:0006281//DNA repair
7198109	46	31	35.38	22.37	-0.661368792	0.046725	PHATRDRAFT_44612	-	-	-	-		-
7197307	163	110	208.08	131.76	-0.659225844	0.000178606	Lhcr3	K08907|1|6e-13|72.4|cme:CMN234C|light-harvesting complex I chlorophyll a/b binding protein 1;K14172|3|1e-11|68.2|ota:Ot11g01060|light-harvesting complex II chlorophyll a/b binding protein 7;K08910|5|1e-11|68.2|zma:100284001|light-harvesting complex I chlorophyll a/b binding protein 4	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7197908	1809.1	1227.58	403.96	257.05	-0.652163433	3.43E-35	PHATRDRAFT_33646	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203050	100	68	43.11	27.49	-0.649115656	0.0038597	PHATRDRAFT_38112	-	-	-	-		-
7199095	50	34	36.81	23.48	-0.648665341	0.0415126	PHATRDRAFT_50239	-	-	-	-		-
7200821	47	32	12.56	8.02	-0.647162322	0.0487426	PHATRDRAFT_45814	-	-	-	-		-

7198991	47	32	28.26	18.05	-0.646762629	0.0487426	PHATRDRAFT_41268	-	-	GO:0004673//protein histidine kinase activity;GO:0032550	GO:0007165//signal transduction		GO:0007165//signal transduction
7201484	85	58	31.68	20.27	-0.644226247	0.0081766	PHATRDRAFT_46282	-	-	-	-		-
7197570	60	41	13.74	8.8	-0.642806575	0.0268878	PHATRDRAFT_18197	K05666|1|0.0|663|olu:OSTLU_35503|ATP-binding cassette, subfamily C (CFTR/MRP), member 2;K05658|2|1e-54|214|ath:AT3G28345|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7199464	73	50	31.51	20.24	-0.638600464	0.0150383	PHATRDRAFT_41639	-	-	-	-		-
7200528	108	74	77.98	50.12	-0.63771774	0.00309366	PHATRDRAFT_45403	-	-	-	-		-
7204631	105	72	22.48	14.46	-0.636574483	0.0035889	PHATR_46726	K09313|1|8e-06|52.0|gmx:100780863|homeobox protein cut-like	-	-	-		-
7202542	51	35	49.46	31.84	-0.635421904	0.0432182	PHATRDRAFT_37608	-	-	-	-		-
7204611	113	78	78.29	50.69	-0.62712688	0.00287014	PHATR_21030	K02146|1|8e-83|305|sbi:SORBI_03g026290|V-type H+-transporting ATPase subunit AC39 [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex	GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0003824//catalytic activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7203375	84	58	51.73	33.5	-0.626840096	0.01025666	PHATRDRAFT_48273	-	-	-	-		-
7196162	461.18	318.6	732.26	474.75	-0.62518799	1.55E-09	PHATRDRAFT_31876	-	GO:0043231//intracellular membrane-bounded organelle	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7194975	52	36	29.31	19.03	-0.623117406	0.0449124	PHATRDRAFT_48900	K00254|1|3e-72|271|ppp:PHYPADRAFT_70715|dihydroorotate dehydrogenase [EC:1.3.5.2]	-	GO:0004152//dihydroorotate dehydrogenase activity	GO:0009174;GO:0019856//pyrimidine nucleobase biosynthetic process		GO:0009174;GO:0019856//pyrimidine nucleobase biosynthetic process
7198917	91	63	57.49	37.33	-0.622975522	0.00786204	PHATRDRAFT_50115	K13099|1|2e-08|58.9|pop:POPTR_712237|CD2 antigen cytoplasmic tail-binding protein 2	-	-	-		-
7203675	72	50	37	24.1	-0.618492124	0.01889074	PHATRDRAFT_29561	K15498|1|1e-105|382|ath:AT3G19980|serine/threonine-protein phosphatase 6 catalytic subunit [EC:3.1.3.16]	GO:0043231//intracellular membrane-bounded organelle;GO:0008287//protein serine/threonine phosphatase complex	GO:0004672//protein kinase activity;GO:0016791//phosphatase activity	GO:0009908//flower development;GO:0009404//toxin metabolic process		GO:0009908//flower development;GO:0009404//toxin metabolic process
7197250	92	64	64	41.76	-0.615950193	0.00814476	RPN7	K03037|1|5e-70|263|smo:SELMODRAFT_267709|26S proteasome regulatory subunit N7	GO:0016020//membrane;GO:0043231//intracellular membrane-bounded organelle;GO:0000502//proteasome complex;GO:0044444//cytoplasmic part	-	GO:0006865//amino acid transport;GO:0006261//DNA-dependent DNA replication;GO:0009639//response to red or far red light;GO:0000338//protein deneddylation;GO:0010467//gene expression;GO:0001558//regulation of cell growth;GO:0009062//fatty acid catabolic process;GO:0035966//response to topologically incorrect protein;GO:0016482//cytopl		GO:0006865//amino acid transport;GO:0006261//DNA-dependent DNA replication;GO:0009639//response to red or far red light;GO:0000338//protein deneddylation;GO:0010467//gene expression;GO:0001558//regulation of cell growth;GO:0009062//fatty acid catabolic process;GO:0035966//response to topologically incorrect protein;GO:0016482//cytopl
7203666	56	39	18.89	12.34	-0.614280307	0.0397472	PHATRDRAFT_48414	K01930|1|4e-53|208|bdi:100828805|folylpolyglutamate synthase [EC:6.3.2.17]	-	GO:0032550;GO:0016881//acid-amino acid ligase activity	GO:0009059//macromolecule biosynthetic process;GO:0006760//folic acid-containing compound metabolic process		GO:0009059//macromolecule biosynthetic process;GO:0006760//folic acid-containing compound metabolic process
7196537	53	37	27.01	17.68	-0.611375365	0.0465938	PHATRDRAFT_42904	-	-	-	-		-
7197169	63	44	31.02	20.32	-0.610298284	0.030076	PHATRDRAFT_43460	-	-	-	-		-

7202891	60	42	14.02	9.2	-0.607780583	0.0351768	PHATRDRAFT_47709	K12319|1|6e-31|135|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|3e-24|112|vcn:VOLCADRAFT_106794|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K01120|5|2e-14|80.1|cre:CHLREDRAFT_101278|3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7196435	80	56	63.76	41.87	-0.606734711	0.01491592	PHATRDRAFT_42836	K15450|1|5e-12|70.5|vvi:100257307|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-];K14966|2|4e-11|67.4|vcn:VOLCADRAFT_121332|host cell factor;K12116|4|1e-08|59.3|aly:ARALYDRAFT_475919|flavin-binding kelch repeat F-box protein 1	-	-	-		-
7201376	74	52	104.22	68.72	-0.600830218	0.0202502	PHATRDRAFT_27659	K02879|1|7e-27|118|ppp:PHYPADRAFT_142580|large subunit ribosomal protein L17	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7195747	54	38	52.19	34.45	-0.599269419	0.0482614	PHATRDRAFT_40261	-	GO:0016020//membrane;GO:0044464	GO:0003824//catalytic activity;GO:0005488//binding	GO:0051716//cellular response to stimulus;GO:0018130;GO:1901362;GO:0009628//response to abiotic stimulus;GO:0046283//anthocyanin-containing compound metabolic process;GO:0050794//regulation of cellular process;GO:0006950//response to stress;GO:1901700;GO:0009725//response to hormone;GO:0019438//aromatic compound biosynthetic		GO:0051716//cellular response to stimulus;GO:0018130;GO:1901362;GO:0009628//response to abiotic stimulus;GO:0046283//anthocyanin-containing compound metabolic process;GO:0050794//regulation of cellular process;GO:0006950//response to stress;GO:1901700;GO:0009725//response to hormone;GO:0019438//aromatic compound biosynthetic
7201278	88	62	29.12	19.24	-0.597901556	0.01177642	PHATRDRAFT_36118	-	GO:0044464	GO:0016837	GO:0042120		GO:0042120
7200361	61	43	108.92	72.06	-0.595998331	0.0364054	PHATRDRAFT_35304	-	-	GO:0003824//catalytic activity	-		-
7199674	68	48	69.72	46.17	-0.594616837	0.0275626	PHATRDRAFT_34584	-	-	-	-		-
7194716	72	51	25.23	16.76	-0.590118057	0.024405	PHATRDRAFT_48543	-	-	-	-		-
7197242	55	39	27.54	18.31	-0.588896768	0.0499142	HemA	K02492|1|1e-109|395|cme:CMJ054C|glutamyl-tRNA reductase [EC:1.2.1.70]	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0006779//porphyrin-containing compound biosynthetic process;GO:0044710		GO:0006779//porphyrin-containing compound biosynthetic process;GO:0044710
7202255	55	39	36.02	23.95	-0.588772525	0.0499142	PHATRDRAFT_47027	K15030|1|3e-27|121|aly:ARALYDRAFT_488406|translation initiation factor 3 subunit M	GO:0044424	-	GO:0007126//meiotic nuclear division;GO:0044260;GO:0090304		GO:0007126//meiotic nuclear division;GO:0044260;GO:0090304
7201315	93	66	125.04	83.26	-0.58669422	0.01080122	PHATRDRAFT_46071	-	-	-	-		-
7204951	73	52	42.15	28.16	-0.581885297	0.0251928	L-SD	K01754|1|2e-19|95.9|olu:OSTLU_39224|threonine dehydratase [EC:4.3.1.19];K12235|3|4e-18|91.3|gmx:100799758|serine racemase [EC:5.1.1.18]	GO:0044464	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0043168//anion binding;GO:0016841//ammonia-lyase activity	GO:0019752//carboxylic acid metabolic process;GO:0009154//purine ribonucleotide catabolic process		GO:0019752//carboxylic acid metabolic process;GO:0009154//purine ribonucleotide catabolic process
7200674	146	104	81.08	54.17	-0.581851998	0.00152282	PHATRDRAFT_45427	-	-	-	-		-
7198817	84	60	115.28	77.27	-0.577161938	0.01696618	PHATRDRAFT_50195	-	-	-	-		-

7201458	81	58	78.82	52.94	-0.574203555	0.01974034	SCS-alpha	K01899|1|6e-106|382|gmx:100815484|succinyl-CoA synthetase alpha subunit [EC:6.2.1.4 6.2.1.5]	GO:0043231//intracellular membrane-bounded organelle	GO:0036094//small molecule binding;GO:0004774//succinate-CoA ligase activity;GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer;GO:1901363;GO:0097159//organic cyclic compound binding	GO:0009060//aerobic respiration;GO:0006637//acyl-CoA metabolic process;GO:0043648//dicarboxylic acid metabolic process		GO:0009060//aerobic respiration;GO:0006637//acyl-CoA metabolic process;GO:0043648//dicarboxylic acid metabolic process
7204537	74	53	41.5	27.88	-0.573880775	0.0259798	PHATR_46780	K14709|1|1e-23|109|ota:Ot16g02530|solute carrier family 39 (zinc transporter), member 1/2/3	-	GO:0008324//cation transmembrane transporter activity	GO:0006812//cation transport;GO:0044763		GO:0006812//cation transport;GO:0044763
7196320	74	53	69.03	46.38	-0.573720664	0.0259798	PHATRDRAFT_42659	-	-	GO:0036094//small molecule binding	-		-
7195771	1520.34	1089.51	311.39	209.26	-0.573426047	4.92E-24	PHATRDRAFT_49379	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7197270	138	99	285.54	192.29	-0.570409123	0.00241878	PHATRDRAFT_9697	K01527|1|1e-23|107|vcn:VOLCADRAFT_104715|nascent polypeptide-associated complex subunit beta	-	-	-		-
7196870	82	59	18.57	12.53	-0.567587401	0.020334	PHATRDRAFT_43088	K15305|1|4e-34|145|sbi:SORBI_01g042440|vacuole morphology and inheritance protein 14	-	GO:0008047//enzyme activator activity	GO:0016310//phosphorylation		GO:0016310//phosphorylation
7203135	86	62	69.25	46.83	-0.564381033	0.0179995	PHATRDRAFT_47950	-	-	-	-		-
7198221	61	44	26.59	17.99	-0.563688591	0.0468198	PHATRDRAFT_49551	-	-	-	-		-
7196374	159	115	266.23	180.71	-0.558996807	0.001392574	PHATRDRAFT_42746	-	-	-	-		-
7196728	87	63	104.54	71.03	-0.557554674	0.01851736	PHATRDRAFT_9576	K12581|1|1e-75|280|cre:CHLREDRAFT_184772|CCR4-NOT transcription complex subunit 7/8	GO:0043231//intracellular membrane-bounded organelle	GO:0097159//organic cyclic compound binding	-		-
7199188	98	71	57.55	39.11	-0.557278392	0.01251048	PHATRDRAFT_50364	-	-	-	-		-
7205108	62	45	39.52	26.9	-0.554976774	0.0482014	PHATRDRAFT_bd475	K14272|1|2e-121|434|ppp:PHYPADRAFT_226033|glutamate--glyoxylate aminotransferase [EC:2.6.1.4 2.6.1.2 2.6.1.44 2.6.1.-]	-	GO:0043168//anion binding;GO:0047635	GO:0008152//metabolic process		GO:0008152//metabolic process
7200997	73	53	26.83	18.27	-0.554370421	0.0320938	PHATRDRAFT_45908	-	-	-	-		-
7203664	73	53	68.85	46.89	-0.554176375	0.0320938	PHATRDRAFT_48411	K02981|1|1e-86|317|zma:100382980|small subunit ribosomal protein S2e	GO:0044391	GO:0003676//nucleic acid binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7194764	77	56	40.34	27.51	-0.552254944	0.0283324	PHATRDRAFT_48512	K10582|1|1e-12|73.2|ppp:PHYPADRAFT_168742|ubiquitin-conjugating enzyme E2 Q [EC:6.3.2.19]	-	GO:0016879//ligase activity, forming carbon-nitrogen bonds	-		-
7196315	88	64	124.96	85.28	-0.551187015	0.0190357	PHATRDRAFT_17362	K07304|1|2e-23|107|aly:ARALYDRAFT_492320|peptide-methionine (S)-S-oxide reductase [EC:1.8.4.11]	GO:0044444//cytoplasmic part	GO:0016671//oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	GO:0044763;GO:0044710;GO:0009628//response to abiotic stimulus		GO:0044763;GO:0044710;GO:0009628//response to abiotic stimulus
7202482	81	59	25.37	17.33	-0.549851865	0.0250254	PHATRDRAFT_37484	K10589|1|3e-10|65.9|smo:SELMODRAFT_89794|ubiquitin-protein ligase E3 C [EC:6.3.2.19];K10588|2|3e-10|65.9|smo:SELMODRAFT_104652|ubiquitin-protein ligase E3 B [EC:6.3.2.19]	-	-	-		-
7203209	92	67	57.53	39.3	-0.549785158	0.01684372	PHATRDRAFT_47972	-	-	-	-		-
7198179	70	51	83.07	56.78	-0.548944705	0.0374092	PHATRDRAFT_40470	-	-	-	-		-

7195855	74	54	35.96	24.61	-0.547148363	0.0329908	PHATRDRAFT_49523	K00472|1|1e-17|90.1|smo:SELMODRAFT_431327|prolyl 4-hydroxylase [EC:1.14.11.2]	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7195770	85	62	114.28	78.22	-0.5469635	0.022116	PHATRDRAFT_49377	-	-	-	-		-
7201261	133	97	257.83	176.5	-0.546751956	0.0041595	Trx-h1	K03671|1|3e-19|92.4|olu:OSTLU_26095|thioredoxin 1	-	GO:0015036//disulfide oxidoreductase activity	GO:0018904;GO:0019725//cellular homeostasis		GO:0018904;GO:0019725//cellular homeostasis
7204947	82	60	38.41	26.36	-0.543131594	0.0257054	PHATRDRAFT_bd1812	K03650|1|6e-58|223|ota:Ot03g05310|tRNA modification GTPase [EC:3.6.-.-]	GO:0044464	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process;GO:0008033//tRNA processing		GO:0009154//purine ribonucleotide catabolic process;GO:0008033//tRNA processing
7197014	324	237	451.86	310.15	-0.542909726	8.77E-06	PHATRDRAFT_43725	-	-	-	-		-
7198787	187	137	129.88	89.25	-0.541255215	0.000770568	FABB	K09458|1|9e-58|222|gmx:100790019|3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	-	GO:0016740//transferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7204672	102	75	62.46	43.08	-0.535914319	0.01390086	PHATR_46808	K09571|1|1e-17|89.4|pop:POPTR_824273|FK506-binding protein 4/5 [EC:5.2.1.8]	-	-	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7204192	72	53	36.78	25.39	-0.534661085	0.0394578	PHATR_43976	-	-	GO:0003677//DNA binding	-		-
7198055	110	81	55.43	38.28	-0.534076178	0.01090324	PHATRDRAFT_44391	-	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7204584	148	109	102.22	70.61	-0.533733075	0.00314564	PHATR_46663	-	-	GO:0016829//lyase activity	-		-
7197583	91	67	79.94	55.22	-0.533726685	0.0205916	PHATRDRAFT_54105	-	-	-	-		-
7196402	96	71	47.7	33.09	-0.527593975	0.01865986	PHATRDRAFT_42781	-	-	-	-		-
7196405	146	108	240.25	166.79	-0.526503637	0.00371346	PHATRDRAFT_42790	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7196291	89	66	84.68	58.91	-0.523508716	0.0244848	PHATRDRAFT_42608	-	-	-	-		-
7204713	74	55	56.62	39.47	-0.52055523	0.0414798	PHATR_13361	K02925|1|7e-136|481|ppp:PHYPADRAFT_190959|large subunit ribosomal protein L3e	GO:0005840//ribosome;GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane;GO:0044446;GO:0071944//cell periphery	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197968	142	106	46.02	32.21	-0.514752323	0.00516126	PHATRDRAFT_44306	K14497|1|2e-13|76.6|bdi:100838998|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0032550;GO:0004672//protein kinase activity	GO:0050896//response to stimulus;GO:0006464//cellular protein modification process		GO:0050896//response to stimulus;GO:0006464//cellular protein modification process
7196853	71	53	74.21	51.97	-0.513934548	0.048277	CacyBP	K04507|1|6e-12|69.7|gmx:100527228|calcyclin binding protein	-	-	-		-
7200223	119	89	180.93	126.99	-0.510716747	0.01085872	H2B-1b	K11252|1|3e-38|156|ota:Ot12g01070|histone H2B	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7195192	72	54	28.13	19.78	-0.508067127	0.049413	PHATRDRAFT_48724	-	-	-	-		-
7203049	212	159	90.84	63.89	-0.507737566	0.000730686	PHATRDRAFT_47805	K14686|1|5e-06|51.6|vvi:100245585|solute carrier family 31 (copper transporter), member 1	GO:0031224//intrinsic component of membrane	GO:0022890//inorganic cation transmembrane transporter activity	GO:0006825//copper ion transport		GO:0006825//copper ion transport
7204656	96	72	61.87	43.53	-0.507230014	0.0231764	PHATR_46783	-	-	-	-		-
7199929	80	60	86.24	60.68	-0.507136093	0.0382788	PHATRDRAFT_45053	-	-	-	-		-
7196829	129	97	72.34	51.02	-0.503730699	0.00890294	PHATRDRAFT_43023	K02144|1|8e-27|120|ota:Ot05g04010|V-type H+-transporting ATPase 54 kD subunit [EC:3.6.3.14]	GO:0016471//vacuolar proton-transporting V-type ATPase complex	GO:0019829//cation-transporting ATPase activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7199556	140.82	105.91	44.15	31.14	-0.503644493	0.0060763	PHATRDRAFT_44839	-	-	-	-		-

7201731	109	82	125.2	88.37	-0.502605973	0.01635766	CLC	-	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7199385	190	143	143.2	101.09	-0.502391202	0.001532748	MDH	K00026|1|3e-101|366|pop:POPTR_822907|malate dehydrogenase [EC:1.1.1.37]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0016615//malate dehydrogenase activity;GO:0036094//small molecule binding	GO:0043648//dicarboxylic acid metabolic process;GO:0009628//response to abiotic stimulus;GO:0005975//carbohydrate metabolic process;GO:0009060//aerobic respiration;GO:0006950//response to stress		GO:0043648//dicarboxylic acid metabolic process;GO:0009628//response to abiotic stimulus;GO:0005975//carbohydrate metabolic process;GO:0009060//aerobic respiration;GO:0006950//response to stress
7201365	89	67	45.46	32.1	-0.502024387	0.030411	PHATRDRAFT_46148	-	-	GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203119	91	69	29.97	21.31	-0.491988491	0.031732	PHATRDRAFT_47924	-	-	-	-		-
7203628	86.96	65.95	39.95	28.42	-0.491288949	0.035242	PHATRDRAFT_22453	K14445|1|7e-07|54.3|gmx:100790349|solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0030001//metal ion transport;GO:0044763		GO:0030001//metal ion transport;GO:0044763
7202979	87	66	36.09	25.68	-0.490953941	0.0359908	PHATRDRAFT_47845	K01133|1|4e-13|75.1|zma:100192008|choline-sulfatase [EC:3.1.6.6]	-	GO:0016788//hydrolase activity, acting on ester bonds	-		-
7200130	87	66	48.16	34.27	-0.4908892	0.0359908	PHATRDRAFT_11843	-	GO:0031224//intrinsic component of membrane	GO:0036094//small molecule binding;GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044763;GO:0030001//metal ion transport		GO:0044763;GO:0030001//metal ion transport
7202688	153	116	295.27	210.13	-0.490752635	0.00530428	PHATRDRAFT_14260	K03941|1|2e-74|275|ppp:PHYPADRAFT_165114|NADH dehydrogenase (ubiquinone) Fe-S protein 8 [EC:1.6.5.3 1.6.99.3]	GO:0005746//mitochondrial respiratory chain	GO:0043169//cation binding;GO:0051536//iron-sulfur cluster binding;GO:0050136//NADH dehydrogenase (quinone) activity	GO:0044710		GO:0044710
7196689	87	66	85.04	60.52	-0.490729609	0.0359908	PHATRDRAFT_42514	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198686	141	107	73.82	52.54	-0.490595537	0.00759546	PHATRDRAFT_50090	-	-	-	-		-
7198463	79	60	48.83	34.78	-0.489509845	0.0464034	PHATRDRAFT_16262	K14437|1|9e-126|448|cme:CMQ215C|chromodomain-helicase-DNA-binding protein 7 [EC:3.6.4.12];K11367|2|6e-120|429|vvi:100261898|chromodomain-helicase-DNA-binding protein 1 [EC:3.6.4.12]	GO:0043231//intracellular membrane-bounded organelle	GO:0046872//metal ion binding;GO:0003676//nucleic acid binding;GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7205033	79.33	60.32	36.56	26.07	-0.487875488	0.0464034	PHATRDRAFT_bd1554	K01362|1|3e-12|72.0|olu:OSTLU_44226|[EC:3.4.21.-]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7201705	105.69	80.46	19.29	13.77	-0.486324584	0.022731	PHATRDRAFT_46565	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7197189	100.24	76.33	44.3	31.64	-0.485557099	0.0252254	PHATRDRAFT_43493	-	-	-	-		-
7203723	534.11	406.9	277.93	198.59	-0.484928591	2.29E-07	PHATRDRAFT_38713	-	GO:0043231//intracellular membrane-bounded organelle	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7202701	21110.3	16093.56	4521.03	3232.09	-0.484184119	5.86E-229	PHATRDRAFT_47693	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200170	114	87	36.61	26.2	-0.482670962	0.01811442	PHATRDRAFT_19579	K03495|1|1e-99|362|cme:CMB092C|tRNA uridine 5-carboxymethylaminomethyl modification enzyme	-	GO:0000166//nucleotide binding	GO:0002097		GO:0002097

7199607	164	125	496.98	355.79	-0.482161832	0.00443114	PHATRDRAFT_11235	-	GO:0009534//chloroplast thylakoid	GO:0005488//binding	-		-
7200412	119	91	60.24	43.21	-0.479356539	0.01633546	PHATRDRAFT_45653	-	-	-	-		-
7201867	99	76	96.11	69.22	-0.473497606	0.030294	PHATRDRAFT_46593	-	-	GO:0046914//transition metal ion binding;GO:0051540	GO:0009058//biosynthetic process		GO:0009058//biosynthetic process
7194967	105	81	63.13	45.68	-0.4667631	0.0277492	PHATRDRAFT_39471	K07735|1|3e-18|91.7|ota:Ot13g00420|putative transcriptional regulator	-	-	-		-
7197315	193	149	49.59	35.9	-0.466065381	0.0028862	PHATRDRAFT_43585	-	-	-	-		-
7196462	613	473	900.18	651.8	-0.46578416	1.03E-07	PHATRDRAFT_42882	-	-	-	-		-
7202493	101	78	35.04	25.38	-0.465310706	0.0314268	PHATRDRAFT_47327	K07195|1|4e-14|79.0|zma:100281424|exocyst complex component 7	GO:0043234//protein complex	-	GO:0016192//vesicle-mediated transport		GO:0016192//vesicle-mediated transport
7201470	132	102	96.27	69.78	-0.464272693	0.01402186	AtpC	K02115|1|3e-98|357|cme:CMQ087C|F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]	GO:0009526//plastid envelope;GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain;GO:0009535//chloroplast thylakoid membrane	GO:0019829//cation-transporting ATPase activity	GO:0006633//fatty acid biosynthetic process;GO:0044093;GO:0042254//ribosome biogenesis;GO:0006470//protein dephosphorylation;GO:0006996//organelle organization;GO:0009694//jasmonic acid metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0006351//transcription, DNA-templated;GO:0006754//ATP biosynthetic process;GO:0006090//pyruva		GO:0006633//fatty acid biosynthetic process;GO:0044093;GO:0042254//ribosome biogenesis;GO:0006470//protein dephosphorylation;GO:0006996//organelle organization;GO:0009694//jasmonic acid metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0006351//transcription, DNA-templated;GO:0006754//ATP biosynthetic process;GO:0006090//pyruva
7199402	110	85	100.22	72.65	-0.46413574	0.0249582	PHATRDRAFT_17029	K03086|1|1e-64|244|olu:OSTLU_41331|RNA polymerase primary sigma factor;K03093|3|1e-33|142|gmx:100802522|RNA polymerase sigma factor	-	GO:0003676//nucleic acid binding;GO:0000996;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7200371	97	75	44.4	32.19	-0.4639471	0.0356132	PHATRDRAFT_45589	K11294|1|1e-05|50.4|bdi:100836665|nucleolin	-	-	-		-
7198142	235	182	158.73	115.31	-0.461057191	0.001118742	PHATRDRAFT_49648	-	-	-	-		-
7204570	90	70	23.61	17.22	-0.455312899	0.0466294	PHATR_46641	K15631|1|1e-106|386|vcn:VOLCADRAFT_40621|molybdenum cofactor sulfurtransferase [EC:2.8.1.9]	-	GO:0043168//anion binding;GO:0046914//transition metal ion binding	GO:0006950//response to stress		GO:0006950//response to stress
7202384	167	130	44.01	32.12	-0.454359479	0.00681124	PHATRDRAFT_21513	K01873|1|0.0|1003|ppp:PHYPADRAFT_128528|valyl-tRNA synthetase [EC:6.1.1.9]	GO:0009532//plastid stroma	GO:0032550;GO:0052689//carboxylic ester hydrolase activity;GO:0004812//aminoacyl-tRNA ligase activity	GO:0003006//developmental process involved in reproduction;GO:0006418//tRNA aminoacylation for protein translation;GO:0006605//protein targeting;GO:0009668;GO:0009886//post-embryonic morphogenesis;GO:0009451//RNA modification;GO:0042254//ribosome biogenesis;GO:0006448//regulation of translational elongation		GO:0003006//developmental process involved in reproduction;GO:0006418//tRNA aminoacylation for protein translation;GO:0006605//protein targeting;GO:0009668;GO:0009886//post-embryonic morphogenesis;GO:0009451//RNA modification;GO:0042254//ribosome biogenesis;GO:0006448//regulation of translational elongation
7195359	122	95	57.43	41.94	-0.4534777	0.0208996	PHATRDRAFT_51174	K06184|1|1e-142|504|pop:POPTR_655628|ATP-binding cassette, subfamily F, member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7197415	95	74	125.18	91.49	-0.452318113	0.0418066	PHATRDRAFT_43384	K03671|1|3e-08|56.6|cre:CHLREDRAFT_136383|thioredoxin 1	-	GO:0015036//disulfide oxidoreductase activity	GO:0018904;GO:0019725//cellular homeostasis		GO:0018904;GO:0019725//cellular homeostasis
7204205	793	618	852.73	623.48	-0.451745731	4.05E-09	PHATR_44000	-	-	-	-		-

7203681	100	78	109.17	79.89	-0.450489623	0.037502	PHATRDRAFT_56578	K03386|1|4e-27|119|ath:AT1G60740|peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15];K11187|2|4e-25|113|cre:CHLREDRAFT_196639|peroxiredoxin 5, atypical 2-Cys peroxiredoxin [EC:1.11.1.15]	GO:0044464	GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7197761	669	522	1265.52	926.84	-0.449338094	7.32E-08	PHATRDRAFT_44484	-	GO:0043231//intracellular membrane-bounded organelle	GO:0030234//enzyme regulator activity	GO:0006140;GO:0044092//negative regulation of molecular function		GO:0006140;GO:0044092//negative regulation of molecular function
7197784	106	83	51.48	37.81	-0.445244204	0.0342064	PHATRDRAFT_44525	-	-	-	-		-
7197015	1670	1309	1952.14	1435.65	-0.443352447	4.78E-17	PHATRDRAFT_43726	-	-	-	-		-
7196882	121	95	56.77	41.81	-0.441280698	0.024778	PHATRDRAFT_43106	K09584|1|1e-15|83.2|bdi:100827673|protein disulfide-isomerase A6 [EC:5.3.4.1];K01829|3|5e-15|81.3|zma:606413|protein disulfide-isomerase [EC:5.3.4.1]	-	GO:0015036//disulfide oxidoreductase activity	GO:0018904;GO:0019725//cellular homeostasis		GO:0018904;GO:0019725//cellular homeostasis
7201368	121	95	117.34	86.43	-0.441090831	0.024778	GLXI	K01759|1|5e-32|136|ppp:PHYPADRAFT_107013|lactoylglutathione lyase [EC:4.4.1.5]	-	GO:0016846//carbon-sulfur lyase activity;GO:0043169//cation binding	-		-
7200390	408	321	596.09	440.09	-0.437731581	4.13E-05	PHATRDRAFT_45617	-	-	-	-		-
7204184	132	104	49.76	36.77	-0.436457309	0.0203292	PHATR_43964	-	-	-	-		-
7199645	142	112	54.31	40.18	-0.434740299	0.01645002	PHATRDRAFT_44968	K01510|1|1e-39|163|smo:SELMODRAFT_94922|apyrase [EC:3.6.1.5]	-	GO:0003824//catalytic activity	-		-
7200713	341	269	378.53	280.15	-0.434208151	0.000200804	PHATRDRAFT_19954	-	-	GO:0046914//transition metal ion binding;GO:0046906//tetrapyrrole binding	GO:0015669		GO:0015669
7195143	182	144	100.43	74.52	-0.43049071	0.00713808	PHATRDRAFT_48851	-	-	-	-		-
7198561	157	125	71.21	53.18	-0.421196075	0.01428824	PHATRDRAFT_49978	K03453|1|9e-10|63.9|ppp:PHYPADRAFT_142102|bile acid:Na+ symporter, BASS family	-	GO:0005343//organic acid:sodium symporter activity	GO:0030001//metal ion transport		GO:0030001//metal ion transport
7204353	163	130	248.71	186.14	-0.418076403	0.01303384	PHATR_18516	K00236|1|1e-13|74.7|ota:Ot06g03360|succinate dehydrogenase (ubiquinone) cytochrome b560 subunit	GO:0043234//protein complex	GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors	GO:0009060//aerobic respiration		GO:0009060//aerobic respiration
7201545	273	218	135.89	101.77	-0.417126951	0.001365878	PHATRDRAFT_56588	K00218|1|8e-61|233|zma:100283531|protochlorophyllide reductase [EC:1.3.1.33]	GO:0009534//chloroplast thylakoid	GO:0036094//small molecule binding;GO:0016491//oxidoreductase activity	GO:1901362;GO:1901135;GO:0008610//lipid biosynthetic process;GO:0019438//aromatic compound biosynthetic process;GO:0006796//phosphate-containing compound metabolic process;GO:0019637//organophosphate metabolic process;GO:0009416//response to light stimulus;GO:0044255//cellular lipid metabolic process;GO:0016070//RNA metabolic process;GO:00		GO:1901362;GO:1901135;GO:0008610//lipid biosynthetic process;GO:0019438//aromatic compound biosynthetic process;GO:0006796//phosphate-containing compound metabolic process;GO:0019637//organophosphate metabolic process;GO:0009416//response to light stimulus;GO:0044255//cellular lipid metabolic process;GO:0016070//RNA metabolic process;GO:00
7202246	125	100	34.43	25.83	-0.414618537	0.0313702	PHATRDRAFT_54681	-	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7200405	216	174	277.8	209.98	-0.403794677	0.00564682	FtrB	-	-	GO:0016731	GO:0044710		GO:0044710
7194869	197	159	108.63	82.23	-0.401685849	0.00863708	PHATRDRAFT_48600	-	GO:0044424;GO:0031224//intrinsic component of membrane	GO:0016491//oxidoreductase activity	GO:0044238		GO:0044238
7202403	244	197	106.35	80.53	-0.401221795	0.0035027	PHATRDRAFT_54726	-	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process

7195302	174	141	74	56.24	-0.395928676	0.01489792	PHATRDRAFT_49053	-	GO:0005753//mitochondrial proton-transporting ATP synthase complex	GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0006754//ATP biosynthetic process		GO:0006754//ATP biosynthetic process
7202045	169	137	55.43	42.14	-0.395476693	0.01655306	PHATRDRAFT_47142	-	-	-	-		-
7204852	148	120	50.33	38.27	-0.395204697	0.0250338	PHATRDRAFT_bd1578	K06694|1|5e-10|65.1|ath:AT2G03430|26S proteasome non-ATPase regulatory subunit 10;K14423|3|6e-09|61.6|aly:ARALYDRAFT_329352|4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase [EC:1.14.13.72]	-	GO:0046914//transition metal ion binding	-		-
7202399	387	314	84.57	64.34	-0.394430043	0.000297592	PHATRDRAFT_37523	-	-	GO:0046914//transition metal ion binding	-		-
7197024	252	205	41.83	31.91	-0.390529389	0.00382188	PHATRDRAFT_54143	K13462|1|2e-25|117|rcu:RCOM_0708240|guanine nucleotide-exchange factor	-	GO:0005083//small GTPase regulator activity	GO:0032011//ARF protein signal transduction		GO:0032011//ARF protein signal transduction
7196929	242	197	117.53	89.73	-0.389366741	0.00468704	PHATRDRAFT_43183	K00791|1|1e-41|169|cme:CMS475C|tRNA dimethylallyltransferase [EC:2.5.1.75]	-	GO:0032550	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process
7204169	226	184	225.79	172.46	-0.388719807	0.00630798	PHATR_43939	-	-	-	-		-
7201495	136	111	71.9	55.04	-0.385511301	0.035743	PHATRDRAFT_46301	-	-	-	-		-
7203360	158	129	74.01	56.67	-0.385135014	0.0237622	PHATRDRAFT_38668	-	-	-	-		-
7195988	193	158	30.4	23.34	-0.381266763	0.013292	PHATRDRAFT_42624	-	-	-	-		-
7195597	127	104	39.27	30.16	-0.380791169	0.0449082	PHATRDRAFT_49335	K00620|1|1e-17|90.5|ota:Ot08g02650|glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]	-	-	-		-
7198454	144	118	124.72	95.87	-0.379541496	0.0331074	PHATRDRAFT_49782	-	-	GO:0003824//catalytic activity;GO:0046914//transition metal ion binding	-		-
7196347	339	278	130.3	100.21	-0.378810601	0.00110446	PHATRDRAFT_17427	K00121|1|7e-128|456|vcn:VOLCADRAFT_82410|S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	-	GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0052689//carboxylic ester hydrolase activity;GO:0036094//small molecule binding	GO:0044282;GO:0006067//ethanol metabolic process		GO:0044282;GO:0006067//ethanol metabolic process
7204508	135	111	52.36	40.37	-0.37518151	0.0415208	PHATR_46729	-	-	GO:0036094//small molecule binding	-		-
7200156	208	171	134.87	104	-0.374985948	0.01133678	PHATRDRAFT_45297	-	GO:0009536//plastid	-	-		-
7196660	135	111	80.38	61.99	-0.374801073	0.0415208	PHATRDRAFT_42457	-	-	-	-		-
7201798	478	393	427.8	329.96	-0.374645341	0.000123534	PHATRDRAFT_46444	-	-	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	-		-
7197546	215	177	136.63	105.5	-0.373031294	0.01041728	PHATRDRAFT_43494	-	-	-	-		-
7194763	453	373	219.26	169.32	-0.372890249	0.000201394	PHATRDRAFT_48511	K07240|1|6e-53|207|olu:OSTLU_89366|chromate transporter	-	GO:0015103//inorganic anion transmembrane transporter activity	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7203884	217	179	55.2	42.7	-0.370432197	0.01061204	PHATR_44131	-	GO:0031224//intrinsic component of membrane	GO:0004930//G-protein coupled receptor activity;GO:0003824//catalytic activity	GO:0007166//cell surface receptor signaling pathway;GO:0009117//nucleotide metabolic process		GO:0007166//cell surface receptor signaling pathway;GO:0009117//nucleotide metabolic process

7196967	143	118	44.11	34.13	-0.370065346	0.0383624	PGAM_2	K01834|1|2e-55|216|zma:100273347|2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.1]	-	GO:0016868//intramolecular transferase activity, phosphotransferases	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7201485	172	142	200.79	155.53	-0.368494533	0.0233562	PHATRDRAFT_12655	K04345|1|3e-29|127|smo:SELMODRAFT_440463|protein kinase A [EC:2.7.11.11];K04739|2|2e-24|110|vcn:VOLCADRAFT_31307|cAMP-dependent protein kinase regulator	GO:0043234//protein complex	GO:0003824//catalytic activity;GO:0019887//protein kinase regulator activity	GO:0006468//protein phosphorylation		GO:0006468//protein phosphorylation
7199266	138	114	78.78	61.04	-0.368074455	0.0427454	FbaC5	K01623|1|4e-106|383|cme:CMI049C|fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	GO:0044434	GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process;GO:0050896//response to stimulus		GO:0006007//glucose catabolic process;GO:0050896//response to stimulus
7197497	167	138	116.94	90.64	-0.36754873	0.025964	GMD1	K01711|1|1e-105|381|ath:AT5G66280|GDPmannose 4,6-dehydratase [EC:4.2.1.47]	GO:0044464	GO:0036094//small molecule binding;GO:0048037//cofactor binding;GO:0016836//hydro-lyase activity	GO:0009225//nucleotide-sugar metabolic process		GO:0009225//nucleotide-sugar metabolic process
7197714	151	125	51.21	39.76	-0.365107802	0.035425	PHATRDRAFT_44485	-	-	-	-		-
7195968	151	125	124.03	96.31	-0.36493161	0.035425	PHATRDRAFT_42600	-	-	-	-		-
7201661	227	188	122.5	95.16	-0.364354572	0.01001102	PHATRDRAFT_20787	K01412|1|1e-136|485|ppp:PHYPADRAFT_185217|mitochondrial processing peptidase [EC:3.4.24.64]	-	GO:0004175//endopeptidase activity;GO:0043169//cation binding	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7197844	4083	3383	2169.34	1685.82	-0.36380568	1.02E-27	PHATRDRAFT_18911	-	GO:0044424	GO:0032550;GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0016211	GO:0006412//translation;GO:0006528//asparagine metabolic process		GO:0006412//translation;GO:0006528//asparagine metabolic process
7196392	544	451	575.61	447.71	-0.362527114	7.09E-05	PHATRDRAFT_42765	K08902|1|3e-22|103|cme:CMK176C|photosystem II Psb27 protein	-	-	-		-
7197797	2436	2024	179.28	139.67	-0.360192379	7.40E-17	PHATRDRAFT_44551	-	-	-	-		-
7200382	154	128	54.96	42.84	-0.359423524	0.036385	PHATRDRAFT_45604	-	-	-	-		-
7205158	218.19	181.4	85.2	66.43	-0.359018516	0.01240542	PHATRDRAFT_bd387	K01534|1|1e-139|495|ppp:PHYPADRAFT_125099|Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0008324//cation transmembrane transporter activity;GO:0016787//hydrolase activity	GO:0006812//cation transport		GO:0006812//cation transport
7194860	202	168	60.32	47.04	-0.358748368	0.01677762	PHATRDRAFT_29758	K08776|1|4e-163|573|aly:ARALYDRAFT_491378|puromycin-sensitive aminopeptidase [EC:3.4.11.-]	GO:0044424	GO:0046914//transition metal ion binding;GO:0008238//exopeptidase activity	GO:0009987//cellular process;GO:0044699;GO:0019538//protein metabolic process		GO:0009987//cellular process;GO:0044699;GO:0019538//protein metabolic process
7200500	137	114	59.14	46.16	-0.357491019	0.0494048	PHATRDRAFT_50885	K01880|1|7e-56|217|cme:CMC037C|glycyl-tRNA synthetase [EC:6.1.1.14]	GO:0044424	GO:0004812//aminoacyl-tRNA ligase activity;GO:0032550	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7204036	310	258	187.43	146.31	-0.357323511	0.00312036	PHATR_44101	-	-	GO:0003824//catalytic activity	GO:0009987//cellular process		GO:0009987//cellular process
7197473	173	144	145.3	113.45	-0.356978094	0.0273754	PHATRDRAFT_25379	K00286|1|2e-59|228|vcn:VOLCADRAFT_80899|pyrroline-5-carboxylate reductase [EC:1.5.1.2]	-	GO:0016646//oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;GO:0036094//small molecule binding	GO:0006561//proline biosynthetic process		GO:0006561//proline biosynthetic process
7199311	149	124	219.55	171.46	-0.356677486	0.040503	PHATRDRAFT_16962	-	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7198789	673	561	242.21	189.35	-0.355203009	1.49E-05	PHATRDRAFT_30786	K01805|1|9e-124|442|aly:ARALYDRAFT_918943|xylose isomerase [EC:5.3.1.5]	GO:0043231//intracellular membrane-bounded organelle;GO:0031090//organelle membrane	GO:0043169//cation binding;GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006007//glucose catabolic process;GO:0019321//pentose metabolic process		GO:0006007//glucose catabolic process;GO:0019321//pentose metabolic process

7200761	1028	857	1191.95	932.3	-0.354457547	8.81E-08	PHATRDRAFT_20167	K11098|1|1e-25|115|vcn:VOLCADRAFT_109863|small nuclear ribonucleoprotein F	GO:0044444//cytoplasmic part;GO:0030529//ribonucleoprotein complex;GO:0031981//nuclear lumen	GO:0097159//organic cyclic compound binding	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7201972	253	211	113.5	88.78	-0.354385684	0.00807582	PHATRDRAFT_51040	K04728|1|1e-102|372|sbi:SORBI_03g008670|ataxia telangiectasia mutated family protein [EC:2.7.11.1]	-	GO:0032550;GO:0004672//protein kinase activity	GO:0009314//response to radiation;GO:0006468//protein phosphorylation;GO:0006259//DNA metabolic process;GO:0007569//cell aging;GO:0006974//cellular response to DNA damage stimulus		GO:0009314//response to radiation;GO:0006468//protein phosphorylation;GO:0006259//DNA metabolic process;GO:0007569//cell aging;GO:0006974//cellular response to DNA damage stimulus
7204792	590.93	494.23	272.94	214.1	-0.350299045	6.74E-05	FbaC1	K01624|1|1e-116|419|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13];K00120|3|2e-16|86.3|aly:ARALYDRAFT_472044|[EC:1.1.-.-]	-	GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7202394	1809	1514	1318.27	1034.9	-0.349154514	2.73E-12	PHATRDRAFT_47332	-	-	GO:0046906//tetrapyrrole binding	-		-
7196060	160	134	68.59	53.87	-0.34851619	0.0382442	PHATRDRAFT_42507	-	-	-	-		-
7197026	253	212	214.37	168.51	-0.347268813	0.00929118	TPT2	K15283|1|7e-37|152|cme:CMK114C|solute carrier family 35, member E1	GO:0031224//intrinsic component of membrane	-	-		-
7199284	1901	1593	2532.08	1990.97	-0.346851504	9.90E-13	PHATRDRAFT_50499	-	-	-	-		-
7195042	149	125	128.79	101.36	-0.345532149	0.046986	PHATRDRAFT_48766	-	-	GO:0016646//oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;GO:0032553	GO:0044710		GO:0044710
7197033	188	158	36.54	28.79	-0.343908845	0.026684	PHATRDRAFT_43751	-	-	-	-		-
7199894	157	132	85.86	67.71	-0.342617254	0.0432066	DLDH	K00382|1|2e-163|574|ppp:PHYPADRAFT_106783|dihydrolipoamide dehydrogenase [EC:1.8.1.4]	GO:0044424	GO:0016668//oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor;GO:0000166//nucleotide binding	GO:0044710;GO:0019725//cellular homeostasis		GO:0044710;GO:0019725//cellular homeostasis
7204273	278	234	214.22	169.14	-0.340875295	0.00738462	PHATR_43841	-	GO:0005753//mitochondrial proton-transporting ATP synthase complex	GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0006754//ATP biosynthetic process		GO:0006754//ATP biosynthetic process
7198311	152	128	228.28	180.4	-0.33960513	0.048075	PHATRDRAFT_49673	-	-	-	-		-
7200985	367	310	143.44	113.63	-0.336103615	0.00240128	PHATRDRAFT_54493	K12447|1|1e-137|488|ppp:PHYPADRAFT_196551|UDP-sugar pyrophosphorylase [EC:2.7.7.64]	-	GO:0051748//UTP-monosaccharide-1-phosphate uridylyltransferase activity	GO:0009225//nucleotide-sugar metabolic process		GO:0009225//nucleotide-sugar metabolic process
7197883	355	300	354.67	281.18	-0.334983323	0.0028827	PHATRDRAFT_44428	-	-	-	-		-
7196961	163	138	69.91	55.51	-0.332751142	0.0451222	PHATRDRAFT_25067	K13412|1|7e-85|313|vvi:100265650|calcium-dependent protein kinase [EC:2.7.11.1];K00924|2|3e-84|311|ath:AT5G12180|[EC:2.7.1.-]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199217	241	204	195.9	155.55	-0.332739003	0.01474826	PHATRDRAFT_16870	K00021|1|3e-97|353|mtr:MTR_5g026470|hydroxymethylglutaryl-CoA reductase (NADPH) [EC:1.1.1.34]	GO:0031224//intrinsic component of membrane	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding;GO:0048037//cofactor binding	GO:0008610//lipid biosynthetic process;GO:0006732//coenzyme metabolic process;GO:0006720//isoprenoid metabolic process		GO:0008610//lipid biosynthetic process;GO:0006732//coenzyme metabolic process;GO:0006720//isoprenoid metabolic process

7200676	203	172	49.74	39.52	-0.331823561	0.0258118	PHATRDRAFT_45431	K11407|1|2e-20|100|ppp:PHYPADRAFT_138277|histone deacetylase 6/10 [EC:3.5.1.98]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0003824//catalytic activity	-		-
7203883	203	172	86.85	69.01	-0.331720416	0.0258118	PHATR_33493	K01868|1|0.0|811|ppp:PHYPADRAFT_130801|threonyl-tRNA synthetase [EC:6.1.1.3]	GO:0044424	GO:0004812//aminoacyl-tRNA ligase activity;GO:0032550	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7201525	357.86	303.47	47.19	37.52	-0.330821344	0.00332428	PHATRDRAFT_54510	-	GO:0043234//protein complex	GO:0008092//cytoskeletal protein binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7196473	217	184	87.28	69.4	-0.330715439	0.0215826	Hsp70_1	K04043|1|0.0|802|cme:CML205C|molecular chaperone DnaK;K03283|2|0.0|791|olu:OSTLU_31330|heat shock 70kDa protein 1/8	GO:0043231//intracellular membrane-bounded organelle;GO:0071944//cell periphery;GO:0044444//cytoplasmic part	GO:0032550;GO:0005515//protein binding;GO:0043167//ion binding	GO:0044267//cellular protein metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress		GO:0044267//cellular protein metabolic process;GO:0009628//response to abiotic stimulus;GO:0006950//response to stress
7205100	401	340	172.08	136.83	-0.330694854	0.001779252	PHATRDRAFT_bd714	K13862|1|1e-23|110|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7196480	218	185	116.4	92.65	-0.329228177	0.0217236	PHATRDRAFT_31906	K00294|1|9e-175|611|ppp:PHYPADRAFT_207743|1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7196866	502	426	490.13	390.2	-0.328950676	0.000493638	PHATRDRAFT_9316	K03921|1|4e-98|355|vvi:100853715|acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2]	GO:0009536//plastid	GO:0046872//metal ion binding;GO:0016717//oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7198614	386	328	337.73	269.21	-0.327138336	0.00237992	PHATRDRAFT_16401	K15275|1|1e-20|98.6|ath:AT1G14360|solute carrier family 35 (UDP-galactose transporter), member B1	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7201366	3234	2754	237.68	189.79	-0.324616531	2.84E-18	PHATRDRAFT_36043	K10592|1|7e-32|140|ppp:PHYPADRAFT_137606|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	-	-	-		-
7196652	1999	1704	1207.76	965.64	-0.322776454	8.78E-12	Fba4	K00640|1|7e-35|146|cme:CMA007C|serine O-acetyltransferase [EC:2.3.1.30]	GO:0005737//cytoplasm	GO:0016832//aldehyde-lyase activity;GO:0016412//serine O-acyltransferase activity	GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process		GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process
7203170	633	540	800.94	641.1	-0.321144763	0.000129276	Lhcf10	-	GO:0043234//protein complex;GO:0034357;GO:0009507//chloroplast;GO:0044425//membrane part	-	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7196891	753	644	96.81	77.61	-0.318913524	3.62E-05	BGS1	K11000|1|0.0|740|gmx:100806685|callose synthase [EC:2.4.1.-]	GO:0043234//protein complex;GO:0043234//protein complex	GO:0035251//UDP-glucosyltransferase activity;GO:0035251//UDP-glucosyltransferase activity	GO:0006074//(1->3)-beta-D-glucan metabolic process;GO:0006074//(1->3)-beta-D-glucan metabolic process		GO:0006074//(1->3)-beta-D-glucan metabolic process;GO:0006074//(1->3)-beta-D-glucan metabolic process

7195416	330	282	364.44	292.18	-0.318823887	0.00608098	PHATRDRAFT_49037	K02927|1|1e-35|147|cme:CMC045C|large subunit ribosomal protein L40e;K08770|2|2e-35|147|ppp:PHYPADRAFT_208425|ubiquitin C	GO:0030529//ribonucleoprotein complex	GO:0016209//antioxidant activity;GO:0046914//transition metal ion binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203388	272	233	48.46	38.93	-0.31591206	0.01370776	PHATRDRAFT_48253	K10406|1|2e-09|63.9|gmx:100800016|kinesin family member C2/C3	-	-	-		-
7194998	182	156	218.09	175.39	-0.314357126	0.0443742	Lhcf13	K08907|1|2e-07|54.7|cme:CMN234C|light-harvesting complex I chlorophyll a/b binding protein 1	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7195448	200	172	97.63	78.74	-0.310227818	0.0377598	PK3	K00873|1|3e-126|450|cre:CHLREDRAFT_136854|pyruvate kinase [EC:2.7.1.40]	-	GO:0031420;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process
7202035	243	209	92.62	74.71	-0.310022395	0.0220706	PHATRDRAFT_47129	-	-	-	-		-
7199098	201	173	121.27	97.9	-0.308841933	0.037963	PHATRDRAFT_55162	-	-	-	-		-
7201082	196	169	113.78	92.02	-0.306227625	0.0420482	PHATRDRAFT_45833	-	-	-	-		-
7201729	309	267	82.64	66.96	-0.303540726	0.01143706	sCdc48	K13525|1|0.0|832|osa:4331645|transitional endoplasmic reticulum ATPase	GO:0043232;GO:0044446;GO:0005737//cytoplasm;GO:0005634//nucleus	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0044763		GO:0044763
7202002	280	242	190.77	154.66	-0.302734197	0.01618232	PHATRDRAFT_47079	-	-	-	-		-
7200601	1082	936	131.14	106.38	-0.301880858	2.49E-06	PHATRDRAFT_19982	K12856|1|0.0|3457|ppp:PHYPADRAFT_200564|pre-mRNA-processing factor 8	GO:0030529//ribonucleoprotein complex	-	GO:0000377		GO:0000377
7196666	238	206	168.3	136.64	-0.300655297	0.0276338	PHATRDRAFT_50645	K06269|1|2e-152|536|ppp:PHYPADRAFT_95594|protein phosphatase 1, catalytic subunit [EC:3.1.3.16]	-	GO:0016791//phosphatase activity	-		-
7198310	269	233	162.64	132.13	-0.299724054	0.01959836	PHATRDRAFT_49670	K13420|1|2e-21|102|aly:ARALYDRAFT_356368|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7203437	354	307	53.75	43.71	-0.298301377	0.00775058	PHATRDRAFT_48121	-	-	-	-		-
7197960	483	419	381.07	310.09	-0.297369034	0.001895162	PHATRDRAFT_44297	-	-	-	-		-
7199502	478	415	265.29	216.03	-0.296338622	0.00208012	PHATRDRAFT_44980	-	-	GO:0016746//transferase activity, transferring acyl groups	-		-
7195333	387	336	556.89	453.71	-0.295621929	0.00561092	PHATRDRAFT_49109	-	-	-	-		-
7199375	465	404	87.17	71.02	-0.295606349	0.00247426	PHATRDRAFT_50537	K01689|1|5e-145|514|olu:OSTLU_28765|enolase [EC:4.2.1.11]	GO:0043234//protein complex	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity	GO:0006007//glucose catabolic process;GO:0009154//purine ribonucleotide catabolic process		GO:0006007//glucose catabolic process;GO:0009154//purine ribonucleotide catabolic process
7204815	314.48	273.37	165.14	134.64	-0.294582529	0.01318532	PHATRDRAFT_bd1572	K01689|1|6e-148|522|olu:OSTLU_28765|enolase [EC:4.2.1.11]	GO:0043234//protein complex	GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7199203	228	199	98.08	80.29	-0.288738666	0.0380804	PHATRDRAFT_50390	K14007|1|7e-10|64.3|sbi:SORBI_06g001240|protein transport protein SEC24	-	-	-		-
7202185	246	215	78.18	64.08	-0.286925437	0.0323028	PHATRDRAFT_47193	-	-	-	-		-
7195545	311	272	71.83	58.92	-0.285829085	0.01643958	PHATRDRAFT_49250	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7198263	256	224	133.38	109.46	-0.285138593	0.0298806	SKT1	-	GO:0043231//intracellular membrane-bounded organelle	GO:0008410//CoA-transferase activity	GO:0044248//cellular catabolic process		GO:0044248//cellular catabolic process
7201241	337	295	261.32	214.58	-0.284301929	0.01289028	PHATRDRAFT_12562	K10592|1|3e-119|426|aly:ARALYDRAFT_684483|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7199832	241	211	192.44	158.04	-0.284118953	0.0356348	sUbi	K08770|1|6e-13|73.6|aly:ARALYDRAFT_915730|ubiquitin C	-	-	-		-

7195586	995	872	168.05	138.1	-0.283177223	2.14E-05	MER3	K15271|1|3e-94|345|ppp:PHYPADRAFT_122688|ATP-dependent DNA helicase HFM1/MER3 [EC:3.6.4.12]	-	GO:0032550;GO:0042623//ATPase activity, coupled	GO:0006259//DNA metabolic process;GO:0007129//synapsis		GO:0006259//DNA metabolic process;GO:0007129//synapsis
7199388	294	258	556.15	458.09	-0.279842977	0.0217384	UPL1	K10592|1|3e-17|85.9|mtr:MTR_5g066710|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7198329	222	195	47.19	38.87	-0.279824064	0.047156	PHATRDRAFT_49706	-	-	-	-		-
7199056	235	207	89.69	74.09	-0.275668307	0.0439932	PHATRDRAFT_50310	K12842|1|1e-49|196|smo:SELMODRAFT_85327|U2-associated protein SR140	-	GO:0036094//small molecule binding;GO:0003676//nucleic acid binding	GO:0010467//gene expression		GO:0010467//gene expression
7196256	1114	982	453.78	375.15	-0.274525467	1.24E-05	PHATRDRAFT_17265	K08176|1|5e-25|114|osa:4331542|MFS transporter, PHS family, inorganic phosphate transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0044763		GO:0044763
7196470	1996	1761	140.06	115.87	-0.273537907	5.72E-09	PHATRDRAFT_42892	K08874|1|6e-81|303|aly:ARALYDRAFT_480691|transformation/transcription domain-associated protein	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7198037	310	274	243.68	202.04	-0.2703469	0.0229548	PHATRDRAFT_3296	K14606|1|5e-59|226|aly:ARALYDRAFT_482188|lycopene cyclase CruP	-	-	-		-
7198474	398.64	352.9	37.19	30.87	-0.268709265	0.0102043	PHATRDRAFT_40606	-	-	-	-		-
7204835	1249	1105	2394.27	1988.25	-0.268086682	5.53E-06	PHATRDRAFT_bd719	-	-	-	-		-
7200783	420	373	92.63	77.14	-0.264000368	0.0097853	PHATRDRAFT_45758	K00327|1|2e-29|130|sbi:SORBI_07g007640|NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	GO:0046914//transition metal ion binding;GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202589	398	354	134.56	112.24	-0.261662697	0.01260084	PHATRDRAFT_28794	K02154|1|6e-137|486|ppp:PHYPADRAFT_113417|V-type H+-transporting ATPase subunit I [EC:3.6.3.14]	GO:0016471//vacuolar proton-transporting V-type ATPase complex	GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7197684	334	297	272.26	227.11	-0.261593808	0.022111	PHATRDRAFT_11022	-	GO:0009536//plastid	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7203220	2978	2650	187.62	156.55	-0.261190117	9.85E-12	PHATRDRAFT_47968	-	-	-	-		-
7195464	637.55	567.95	152.85	127.69	-0.259471007	0.001665926	PHATRDRAFT_49287	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7198707	824	734	946.47	791.02	-0.258842606	0.000368152	PHATRDRAFT_50007	-	-	-	-		-
7200638	317	283	311.99	261.29	-0.255847877	0.0290162	PHATRDRAFT_45582	-	-	-	-		-
7204654	525	469	85.3	71.45	-0.25561173	0.00511128	PHATR_46779	-	-	-	-		-
7197249	2213	1977	1222.68	1024.48	-0.255155051	9.02E-09	PHATRDRAFT_43716	-	-	-	-		-
7198586	556	497	71.47	59.91	-0.254540955	0.00408056	PHATRDRAFT_40677	-	-	-	-		-
7204323	368	329	250.73	210.26	-0.253960209	0.01957568	PHATR_33260	-	-	-	-		-
7204086	325	291	146.03	122.63	-0.251952822	0.0295794	PHATR_10354	K12604|1|9e-124|442|ath:AT1G02080|CCR4-NOT transcription complex subunit 1	GO:0044444//cytoplasmic part	-	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7202897	3637	3259	5242.38	4408.08	-0.250071526	4.20E-13	PHATRDRAFT_47715	-	-	-	-		-
7203234	1643	1474	1081.68	910.23	-0.248970719	1.30E-06	PHATRDRAFT_47994	-	-	-	-		-
7200719	2297	2061	1565.03	1317.15	-0.24877066	1.07E-08	PHATRDRAFT_45514	-	-	-	-		-
7196122	312	280	163.15	137.32	-0.248657225	0.0352812	PHATRDRAFT_42728	-	GO:0009536//plastid	GO:0016462//pyrophosphatase activity;GO:0032550	-		-
7204463	1135	1020	1136.57	958.24	-0.246227598	6.75E-05	PHATR_46937	-	-	-	-		-
7203599	317	285	75.68	63.81	-0.246129555	0.035658	PHATRDRAFT_48415	-	GO:0044464	GO:0005099//Ras GTPase activator activity	GO:0032313//regulation of Rab GTPase activity		GO:0032313//regulation of Rab GTPase activity
7200102	630	567	158.24	133.55	-0.244734355	0.00323602	PHATRDRAFT_45221	-	-	-	GO:0044763		GO:0044763
7203859	2468	2222	196.45	165.84	-0.244370146	6.02E-09	PHATR_44084	-	-	-	-		-
7201122	1694	1529	163.51	138.39	-0.240639173	2.03E-06	PHATRDRAFT_45889	-	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7204214	2093	1890	1591.38	1347.97	-0.239489984	1.39E-07	PHATR_44015	-	-	-	-		-
7202755	447	404	272.18	230.73	-0.238355462	0.01546786	PHATRDRAFT_47528	-	-	-	-		-
7199661	407	368	457.71	388.28	-0.237336415	0.0211758	PHATRDRAFT_44987	-	-	-	-		-
7204137	1146	1040	941.32	801.34	-0.232270755	0.000153439	PHATR_44234	-	GO:0031224//intrinsic component of membrane	-	-		-
7201330	515	468	165.26	140.84	-0.230680441	0.01183132	PHATRDRAFT_46087	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199921	987	897	1819.06	1551.68	-0.229362066	0.000495854	PHATRDRAFT_45040	-	-	-	-		-
7195512	422	384	258.79	220.87	-0.228584395	0.0238	PHATRDRAFT_49200	-	-	-	-		-

7195587	1242	1132	199.9	170.85	-0.226548224	0.000123112	PHATRDRAFT_49312	K08333|1|3e-130|465|ppp:PHYPADRAFT_144257|phosphoinositide-3-kinase, regulatory subunit 4, p150 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195681	17966	16374	9192.97	7858.06	-0.226357849	2.47E-48	PHATRDRAFT_49211	-	-	-	-		-
7197776	1085	989	639.79	546.99	-0.226083985	0.000334704	PHATRDRAFT_44510	-	-	GO:0036094//small molecule binding	-		-
7195399	1300	1186	763.42	653.25	-0.224841763	9.40E-05	PHATRDRAFT_49003	K13076|1|1e-06|52.8|olu:OSTLU_15110|delta8-fatty-acid desaturase [EC:1.14.19.4]	-	GO:0046906//tetrapyrrole binding	-		-
7194773	999	913	1152.1	987.89	-0.221843631	0.000707392	PHATRDRAFT_48527	-	-	-	-		-
7201038	403	369	105	90.16	-0.219829907	0.0335106	PHATRDRAFT_54505	K04498|1|1e-165|582|ppp:PHYPADRAFT_10108|E1A/CREB-binding protein [EC:2.3.1.48]	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0000989//transcription factor binding transcription factor activity;GO:0008080//N-acetyltransferase activity	GO:0048731;GO:0006351//transcription, DNA-templated;GO:0016570//histone modification;GO:0003006//developmental process involved in reproduction;GO:0009791//post-embryonic development;GO:0044767;GO:0043543		GO:0048731;GO:0006351//transcription, DNA-templated;GO:0016570//histone modification;GO:0003006//developmental process involved in reproduction;GO:0009791//post-embryonic development;GO:0044767;GO:0043543
7204105	402	369	72.11	62.07	-0.216303196	0.0366068	PHATR_44189	K13356|1|4e-12|73.2|bdi:100842081|fatty acyl-CoA reductase [EC:1.2.1.-]	-	GO:0036094//small molecule binding;GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0043168//anion binding;GO:0016740//transferase activity	-		-
7198299	463	425	143.17	123.25	-0.216141574	0.0249062	PHATRDRAFT_49652	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202950	10843	9974	3276.34	2826.29	-0.213175574	9.32E-27	PHATRDRAFT_54800	K09835|1|7e-12|71.6|rcu:RCOM_0422660|prolycopene isomerase [EC:5.2.1.13]	-	GO:0003824//catalytic activity	-		-
7199263	491	452	170.15	146.89	-0.212070968	0.0233778	HSP70F	K09489|1|2e-104|378|smo:SELMODRAFT_124091|heat shock 70kDa protein 4	-	GO:0032550	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7203094	736	678	105.98	91.55	-0.211160241	0.00571838	PHATRDRAFT_47879	K11292|1|2e-75|283|smo:SELMODRAFT_164675|transcription elongation factor SPT6	-	GO:0003676//nucleic acid binding;GO:0016787//hydrolase activity	GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter		GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter
7197986	654	603	364.62	315.31	-0.209622772	0.0096037	PHATRDRAFT_44260	-	-	-	-		-
7203381	4620.89	4268.61	3188.84	2763.07	-0.2067596	1.08E-11	GapC2b	K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0044710;GO:0019318//hexose metabolic process		GO:0044710;GO:0019318//hexose metabolic process
7196272	711	657	267.78	232.06	-0.206550345	0.00778948	PHATRDRAFT_42577	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated

7200158	512	474	208.17	180.74	-0.203846345	0.0257564	PHATRDRAFT_51830	-	-	GO:0019842//vitamin binding;GO:0043169//cation binding;GO:0016866//intramolecular transferase activity	-		-
7199835	596	554	847.71	739.41	-0.197196251	0.01929594	PHATRDRAFT_44934	-	-	-	-		-
7199988	1812	1686	896.21	782.1	-0.196483741	5.10E-05	PHATRDRAFT_45361	-	GO:0044424;GO:0031224//intrinsic component of membrane	GO:0016491//oxidoreductase activity	GO:0044238		GO:0044238
7194914	651	607	149.84	131.02	-0.193635751	0.01674076	TPS2	K16055|1|8e-101|367|sbi:SORBI_09g025660|trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	-	-	GO:0005991//trehalose metabolic process		GO:0005991//trehalose metabolic process
7201574	682	636	286.64	250.7	-0.193277952	0.01444432	PHATRDRAFT_46484	K10405|1|5e-06|51.6|smo:SELMODRAFT_84710|kinesin family member C1	-	-	-		-
7204619	448	418	130.28	113.99	-0.192708358	0.0482526	PHATR_46709	-	-	-	-		-
7204536	718	670	412.34	360.89	-0.192275252	0.01248124	PHATR_54643	K06694|1|6e-06|50.8|ath:AT2G03430|26S proteasome non-ATPase regulatory subunit 10	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7198435	1301	1215	128.56	112.59	-0.191363138	0.000827744	PHATRDRAFT_49748	K03235|1|3e-40|167|olu:OSTLU_36160|elongation factor 3	-	-	-		-
7203627	690	648	97.59	85.94	-0.183403546	0.01948588	Pt-separase	K02365|1|3e-26|120|olu:OSTLU_119551|separase [EC:3.4.22.49]	GO:0043231//intracellular membrane-bounded organelle	GO:0016787//hydrolase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7198808	818	768	508.9	448.15	-0.183400495	0.01081004	PHATRDRAFT_16430	K03885|1|2e-67|254|cme:CMF056C|NADH dehydrogenase [EC:1.6.99.3]	-	GO:0003824//catalytic activity;GO:0000166//nucleotide binding	GO:0044710		GO:0044710
7203656	4137	3886	1349.76	1189.01	-0.182942057	1.12E-08	PHATRDRAFT_51134	K03695|1|0.0|846|bdi:100825913|ATP-dependent Clp protease ATP-binding subunit ClpB	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0043170		GO:0006950//response to stress;GO:0043170
7197722	907	852	362.92	319.72	-0.18284257	0.00750968	BiP	K09490|1|0.0|867|vcn:VOLCADRAFT_109722|heat shock 70kDa protein 5	GO:0030312;GO:0031981//nuclear lumen;GO:0009536//plastid;GO:0016020//membrane	GO:0032550;GO:0016628//oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	GO:0043161//proteasome-mediated ubiquitin-dependent protein catabolic process;GO:0010038//response to metal ion;GO:0044710;GO:0000741//karyogamy;GO:0033554//cellular response to stress;GO:0000904//cell morphogenesis involved in differentiation		GO:0043161//proteasome-mediated ubiquitin-dependent protein catabolic process;GO:0010038//response to metal ion;GO:0044710;GO:0000741//karyogamy;GO:0033554//cellular response to stress;GO:0000904//cell morphogenesis involved in differentiation
7199425	1483	1394	631.65	556.84	-0.181862527	0.000671308	PHATRDRAFT_50604	-	-	-	-		-
7194897	526	495	149.47	131.91	-0.180302013	0.0446532	PHATRDRAFT_48652	-	-	-	-		-
7197557	698	658	91.79	81.14	-0.177923686	0.022482	PHATRDRAFT_32738	-	-	-	-		-
7197727	544	513	201.87	178.53	-0.177260003	0.0444962	PHATRDRAFT_26173	K03695|1|0.0|707|smo:SELMODRAFT_159833|ATP-dependent Clp protease ATP-binding subunit ClpB	-	GO:0032550;GO:0016462//pyrophosphatase activity	-		-
7204535	2732	2579	732.94	648.84	-0.175832339	7.98E-06	PHATR_46775	K13211|1|9e-10|64.7|smo:SELMODRAFT_161477|GC-rich sequence DNA-binding factor	-	-	-		-
7197646	713	675	209.33	185.84	-0.171718026	0.0257546	Tkl	K00615|1|1e-130|466|osa:4340025|transketolase [EC:2.2.1.1]	-	GO:0016744	-		-
7199205	3006	2850	211.51	188.04	-0.169686289	6.08E-06	DHC1	K10414|1|0.0|1176|cre:CHLREDRAFT_24009|dynein heavy chain 2, cytosolic;K10413|3|0.0|1164|cre:CHLREDRAFT_60432|dynein heavy chain 1, cytosolic	GO:0005875//microtubule associated complex	GO:0032550;GO:0003774//motor activity	GO:0009154//purine ribonucleotide catabolic process;GO:0006928//cellular component movement		GO:0009154//purine ribonucleotide catabolic process;GO:0006928//cellular component movement
7198801	1095	1039	577.85	514.26	-0.168197099	0.00667998	PHATRDRAFT_50049	K03260|1|5e-11|67.8|ppp:PHYPADRAFT_20993|translation initiation factor 4G	-	-	GO:0044260		GO:0044260

7203862	2311	2194	1991.55	1773.65	-0.167170354	8.76E-05	PHATR_44092	-	-	-	-		-
7200457	871	828	247.59	220.73	-0.165670323	0.0172279	PHATRDRAFT_45673	K12309|1|8e-45|181|aly:ARALYDRAFT_485655|beta-galactosidase [EC:3.2.1.23];K01190|3|5e-29|128|cme:CMP078C|beta-galactosidase [EC:3.2.1.23]	-	GO:0015925	GO:0044238		GO:0044238
7202590	924	879	436.64	389.58	-0.164524685	0.01473918	PHATRDRAFT_47483	-	-	-	-		-
7199362	1792	1708	398.48	356.16	-0.161981818	0.000834902	PHATRDRAFT_31339	K05917|1|1e-113|409|cme:CMS319C|cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]	GO:0044464	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016741;GO:0016712//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one	GO:0044710		GO:0044710
7195918	1763	1681	1842.76	1648.42	-0.160784315	0.000956744	PHATRDRAFT_49431	-	-	-	-		-
7198717	2000	1908	526.37	470.91	-0.160625907	0.000462408	PHATRDRAFT_50019	-	-	-	-		-
7202471	9205	8779	7525	6732.19	-0.160615688	5.03E-14	PHATRDRAFT_37667	-	-	GO:0036094//small molecule binding	-		-
7202587	643	614	62.96	56.38	-0.159252063	0.0489024	PHATRDRAFT_21660	K07203|1|0.0|1245|vcn:VOLCADRAFT_65073|FKBP12-rapamycin complex-associated protein	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7199925	1494	1426	2100.63	1881.43	-0.158992458	0.00258552	PHATRDRAFT_45046	-	-	-	-		-
7204038	667	638	137.73	123.54	-0.156864602	0.0481506	PHATR_18693	K05666|1|5e-135|481|olu:OSTLU_35503|ATP-binding cassette, subfamily C (CFTR/MRP), member 2;K05658|2|1e-46|187|smo:SELMODRAFT_184079|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7205140	1273	1218	301.75	270.74	-0.156445719	0.00647396	PHATRDRAFT_bd1613	K05658|1|5e-82|305|rcu:RCOM_1598590|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7201728	7383	7066	7969.06	7155.51	-0.155354963	6.14E-11	PHATRDRAFT_46597	-	-	-	-		-
7200555	1883	1802	3633.91	3264.23	-0.154779975	0.000947888	HSP20A	K13993|1|2e-09|59.7|aly:ARALYDRAFT_489869|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7198446	2100	2016	224.44	202.04	-0.151688871	0.000692334	PHATRDRAFT_49767	K10691|1|2e-25|117|ppp:PHYPADRAFT_206047|E3 ubiquitin-protein ligase UBR4 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0048731;GO:0032446//protein modification by small protein conjugation;GO:0009791//post-embryonic development;GO:0009653//anatomical structure morphogenesis		GO:0048731;GO:0032446//protein modification by small protein conjugation;GO:0009791//post-embryonic development;GO:0009653//anatomical structure morphogenesis
7197752	1151	1106	166.75	150.25	-0.15032177	0.01277358	PHATRDRAFT_44467	-	-	-	-		-
7200113	3574	3440	888.87	802.3	-0.147830639	1.56E-05	PHATRDRAFT_45239	K00261|1|3e-07|56.6|pop:POPTR_828764|glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7195554	1404	1354	160.99	145.58	-0.145158908	0.00787212	PHATRDRAFT_49264	-	-	-	-		-
7196924	2373	2288	2393.02	2164.62	-0.144718673	0.000536298	PHATRDRAFT_43175	-	-	-	-		-

7200165	1491	1439	726.98	658.05	-0.143718468	0.0065589	PHATRDRAFT_34685	K05681|1|3e-77|288|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|2e-57|221|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K02065|4|8e-15|80.5|pop:POPTR_275971|putative ABC transport system ATP-binding protein	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7204993	1732.1	1678.15	1049.46	953.67	-0.13808514	0.00478714	PHATRDRAFT_bd1770	-	-	-	-		-
7202857	11335	11016	5009.21	4565.74	-0.133734388	2.79E-12	PHATRDRAFT_47667	K14683|1|1e-59|229|zma:100501653|solute carrier family 34 (sodium-dependent phosphate cotransporter)	-	GO:0015114//phosphate ion transmembrane transporter activity	GO:0006817//phosphate ion transport		GO:0006817//phosphate ion transport
7204518	1734	1691	1769.4	1618.82	-0.12831765	0.00840832	PHATR_46743	-	-	-	-		-
7203517	2087	2035	2993.15	2738.73	-0.128157537	0.00379428	PHATRDRAFT_48195	-	-	-	-		-
7199280	4840	4741	2336.02	2146.1	-0.122335324	2.79E-05	PHATRDRAFT_50491	-	-	-	-		-
7196230	1895	1858	1534.54	1411.37	-0.120710003	0.0095047	PHATRDRAFT_43020	-	-	-	-		-
7203991	1676	1646	628.46	578.84	-0.118656303	0.01674726	PHATR_44028	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7203376	4418.11	4344.39	3058.73	2821.19	-0.116628932	0.000128152	GapC2a	K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0044710;GO:0019318//hexose metabolic process		GO:0044710;GO:0019318//hexose metabolic process
7205031	2045	2011	1640.55	1513.33	-0.116452945	0.00926882	PHATRDRAFT_bd1693	-	-	-	-		-
7201200	3231	3187	1324.29	1225.07	-0.112354899	0.001629364	PHATRDRAFT_46243	-	-	GO:0008233//peptidase activity	-		-
7195574	2289.45	2258.05	1814.62	1678.85	-0.112194129	0.00806314	PHATRDRAFT_49286	-	-	-	-		-
7202922	2060.9	2046.85	1169.48	1089.41	-0.102320174	0.0214864	PHATRDRAFT_47758	-	-	-	-		-
7200210	4692	4675	3625.23	3388.27	-0.097523686	0.000905842	Fru3	-	-	-	-		-
7199411	5909	5916	2267.22	2128.8	-0.090883975	0.000527298	PHATRDRAFT_50525	-	-	GO:0036094//small molecule binding	-		-
7195549	6627	6635	2882.65	2706.79	-0.090812717	0.000242778	PEPCK1	K01610|1|1e-125|448|vcn:VOLCADRAFT_106350|phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	-	GO:0004611//phosphoenolpyruvate carboxykinase activity;GO:0032550;GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0000166//nucleotide binding	GO:0006796//phosphate-containing compound metabolic process;GO:0006006//glucose metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006006//glucose metabolic process
7200902	4090	4095	2183.86	2050.77	-0.090714675	0.0039466	PHATRDRAFT_12416	-	GO:0044424	GO:0051540;GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7197211	6069	6113	2398.24	2265.48	-0.082159287	0.001447086	PHATRDRAFT_43531	-	-	-	-		-
7200932	3269	3301	359.57	340.47	-0.078744975	0.0252732	PHATRDRAFT_45802	K10590|1|2e-18|68.9|ppp:PHYPADRAFT_188237|E3 ubiquitin-protein ligase TRIP12 [EC:6.3.2.19]	GO:0044464	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7196502	3480	3515	1602.19	1517.77	-0.07809206	0.0216024	PHATRDRAFT_42850	K14510|1|8e-22|103|sbi:SORBI_02g011690|serine/threonine-protein kinase CTR1 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7203153	11643	11769	2292.82	2173.35	-0.077202572	3.41E-05	PPdK	K01006|1|0.0|857|vvi:100247690|pyruvate,orthophosphate dikinase [EC:2.7.9.1]	-	GO:0032550;GO:0016781//phosphotransferase activity, paired acceptors	GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process
7199146	4788	4885	3262.23	3121.92	-0.063424933	0.0273014	PHATRDRAFT_50366	K11498|1|1e-06|52.8|aly:ARALYDRAFT_478343|centromeric protein E	-	-	-		-

control2 vs grazing2

geneID	Pt-control-2-Expression	Pt-grazing-2-Expression	Pt-control-2-FPKM	Pt-grazing-2-FPKM	log2 Ratio(Pt-grazing-2/Pt-control-2)	P-value	Symbol	KEGG Orthology	GO Component	GO Function	GO Process		GO Process
7205113	0	8.72	0.001	19.85	14.27685139	0.000247672	PHATRDRAFT_bd1537	-	-	-	-		-
7203694	0	4	0.001	17.01	14.05409552	0.01350174	PHATRDRAFT_7656	-	-	-	-		-

7202846	0	6	0.001	6.6	12.68825031	0.001828664	PHATRDRAFT_14230	K00766|1|9e-82|301|vvi:100255305|anthranilate phosphoribosyltransferase [EC:2.4.2.18]	-	GO:0016763//transferase activity, transferring pentosyl groups	GO:0006568//tryptophan metabolic process		GO:0006568//tryptophan metabolic process
7199078	0	4.91	0.001	4.18	12.02928723	0.01350174	PHATRDRAFT_50342	-	-	-	-		-
7194928	0	3	0.001	3	11.55074679	0.0366874	PHATRDRAFT_48703	K05302|1|1e-10|66.2|rcu:RCOM_1176880|SET domain-containing protein 6	-	-	-		-
7201063	0	3	0.001	2.9	11.50183718	0.0366874	PHATRDRAFT_46000	-	-	-	-		-
7204962	0	7.53	0.001	2.46	11.2644426	0.000672986	PHATRDRAFT_bd1200	-	-	GO:0016740//transferase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7201615	0	3	0.001	1.95	10.92925841	0.0366874	PHATRDRAFT_46345	-	-	-	-		-
7197584	0	3	0.001	1.75	10.77313921	0.0366874	PHATRDRAFT_32786	K02999|1|2e-18|92.4|bdi:100821444|DNA-directed RNA polymerase I subunit RPA1 [EC:2.7.7.6];K15450|3|7e-13|74.3|ppp:PHYPADRAFT_149655|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-];K12115|4|2e-11|69.7|pop:POPTR_809263|clock-associated PAS protein ZTL	-	-	-		-
7203522	0	3	0.001	1.45	10.50183718	0.0366874	PHATRDRAFT_48206	K10746|1|2e-27|123|smo:SELMODRAFT_138122|exonuclease 1 [EC:3.1.-.-]	-	GO:0016788//hydrolase activity, acting on ester bonds	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203044	1	5	0.55	4.72	3.101283336	0.0238104	PHATRDRAFT_21922	K03595|1|9e-50|196|bdi:100839087|GTP-binding protein Era	GO:0044464	GO:0003676//nucleic acid binding;GO:0032550	-		-
7197001	1	5	0.71	6.09	3.100551298	0.0238104	PHATRDRAFT_32976	-	-	-	-		-
7204805	1	5	0.55	4.7	3.095157233	0.0238104	MPDC	K01597|1|2e-82|304|bdi:100830501|diphosphomevalonate decarboxylase [EC:4.1.1.33]	-	GO:0016831//carboxy-lyase activity;GO:0032550	GO:0006720//isoprenoid metabolic process		GO:0006720//isoprenoid metabolic process
7202298	1467	6951	3448.47	28291.75	3.036353097	0	PHATRDRAFT_37403	-	-	-	-		-
7195575	2	8	1.02	7.05	2.789054105	0.00610778	PHATRDRAFT_49288	-	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7200139	2	7	2.15	12.96	2.591657153	0.0137519	PHATRDRAFT_34931	-	-	-	-		-
7195759	3.7	12.14	1.25	7.04	2.493647334	0.000728772	PHATRDRAFT_49354	-	-	-	-		-
7199059	2	6	1.33	6.88	2.370982319	0.0303686	PHATRDRAFT_41234	-	-	-	-		-
7202058	2	6	1.25	6.45	2.367371066	0.0303686	PHATRDRAFT_47163	-	-	-	-		-
7202436	2	6	0.76	3.92	2.366782331	0.0303686	PHATRDRAFT_47389	K00889|1|3e-29|128|aly:ARALYDRAFT_478317|1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]	-	GO:0016301//kinase activity	GO:0046488//phosphatidylinositol metabolic process		GO:0046488//phosphatidylinositol metabolic process
7197666	2	6	1.48	7.62	2.364193822	0.0303686	PHATRDRAFT_33853	K00599|1|4e-28|123|olu:OSTLU_50535|[EC:2.1.1.-]	-	-	-		-
7204966	11.74	33.43	4.44	21.72	2.290392521	2.76E-07	PHATRDRAFT_bd1252	-	-	GO:0003824//catalytic activity	-		-
7200006	1.77	5	0.88	4.27	2.278660641	0.0238104	PHATRDRAFT_45386	-	-	-	-		-
7205041	4	11	1.68	7.95	2.242493627	0.00431284	PHATRDRAFT_bd1655	K14994|1|2e-06|52.4|ppp:PHYPADRAFT_168793|solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 7/8	GO:0031224//intrinsic component of membrane	-	-		-
7204609	5	13	16.11	72.73	2.174594082	0.00240192	PHATR_28147	K02980|1|2e-10|62.4|vcn:VOLCADRAFT_74966|small subunit ribosomal protein S29e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203429	2.72	6.92	4.29	18.83	2.133983447	0.0303686	PHATRDRAFT_38448	K01255|1|4e-23|105|cme:CMI185C|leucyl aminopeptidase [EC:3.4.11.1]	GO:0044424	GO:0046914//transition metal ion binding;GO:0008238//exopeptidase activity;GO:0008237//metallopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process

7202038	4	10	2.42	10.42	2.106276325	0.00892888	MSH5	K08741|1|8e-58|222|smo:SELMODRAFT_88713|DNA mismatch repair protein MSH5	-	GO:0032550;GO:0003690//double-stranded DNA binding	GO:0006281//DNA repair		GO:0006281//DNA repair
7201737	4	10	1	4.28	2.097610797	0.00892888	PHATRDRAFT_36611	-	-	-	-		-
7199579	3	7	8.85	35.81	2.016613158	0.0341362	PHATRDRAFT_11308	K12900|1|8e-10|60.1|aly:ARALYDRAFT_892527|FUS-interacting serine-arginine-rich protein 1;K13091|3|3e-09|58.2|ppp:PHYPADRAFT_198566|RNA-binding protein 39;K13095|4|1e-08|55.8|ppp:PHYPADRAFT_189930|splicing factor 1	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding	-		-
7204387	3	7	5.47	22.07	2.012473891	0.0341362	PHATR_7544	-	-	-	-		-
7200966	3	7	3.93	15.84	2.010971118	0.0341362	RNAP-II_3	K03015|1|1e-32|137|olu:OSTLU_37948|DNA-directed RNA polymerase II subunit RPB7	-	GO:0034062//RNA polymerase activity;GO:0003676//nucleic acid binding	GO:0010467//gene expression		GO:0010467//gene expression
7201384	3	7	1.33	5.34	2.005413496	0.0341362	PHATRDRAFT_46315	-	-	-	-		-
7195841	5.2	11.78	1.23	4.78	1.958352303	0.009749	PHATRDRAFT_40219	-	-	-	-		-
7201899	4	9	3.78	14.65	1.954442525	0.018127	PHATRDRAFT_12972	K01823|1|1e-72|270|vcn:VOLCADRAFT_84296|isopentenyl-diphosphate delta-isomerase [EC:5.3.3.2]	-	GO:0016863//intramolecular oxidoreductase activity, transposing C=C bonds	GO:0006720//isoprenoid metabolic process		GO:0006720//isoprenoid metabolic process
7200767	5	11	4.98	18.88	1.922641117	0.009749	PHATRDRAFT_35513	K02935|1|3e-06|50.4|ppp:PHYPADRAFT_27419|large subunit ribosomal protein L7/L12	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203488	6	13	4.89	18.24	1.899199359	0.00529218	PHATRDRAFT_48144	-	-	-	-		-
7196302	5	10	10.94	37.85	1.790680562	0.01908418	PHATRDRAFT_8877	K14510|1|3e-11|64.7|sbi:SORBI_02g011690|serine/threonine-protein kinase CTR1 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204557	4	8	8.26	28.56	1.789782293	0.0359794	PHATR_13534	-	-	-	-		-
7197117	10	20	4.45	15.31	1.782597042	0.000922654	PHATRDRAFT_43372	-	-	-	-		-
7196916	4	8	1.64	5.64	1.781999348	0.0359794	PHATRDRAFT_43163	-	-	-	-		-
7199001	14.75	29.33	8.14	27.86	1.775094558	4.73E-05	PHATRDRAFT_50215	-	-	-	-		-
7201108	10	19	19.71	64.77	1.716397968	0.001724286	PHATRDRAFT_12368	K11320|1|9e-52|199|rcu:RCOM_0342920|E1A-binding protein p400 [EC:3.6.4.-]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0003676//nucleic acid binding;GO:0032550	-		-
7204946	75.93	144.3	31.22	102.05	1.70873374	4.13E-18	PHATRDRAFT_bd1806	K13862|1|3e-19|95.1|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7203372	6	11	3.23	10.19	1.657547981	0.01948302	PHATRDRAFT_1484	K08869|1|2e-76|284|vcn:VOLCADRAFT_40547|aarF domain-containing kinase	-	GO:0016740//transferase activity	-		-
7202894	5	9	1.67	5.17	1.630316178	0.0365232	PHATRDRAFT_47712	-	-	GO:0016881//acid-amino acid ligase activity	GO:0036211		GO:0036211
7204084	9	16	5.64	17.25	1.612829294	0.00577844	PHATR_33525	K04083|1|6e-49|192|cme:CMR268C|molecular chaperone Hsp33	GO:0044424	GO:0005515//protein binding	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7204409	7.36	12.88	8.76	26.45	1.594264947	0.01947298	PHATR_36690	-	-	-	-		-
7200336	8	14	5.28	15.91	1.591324001	0.01057066	PHATRDRAFT_34775	-	-	GO:0036094//small molecule binding	-		-
7197256	11	19	7.96	23.66	1.571609738	0.0031818	PHATRDRAFT_43729	-	-	-	-		-
7195616	7	12	17	50.47	1.56989134	0.01947298	PHATRDRAFT_39807	-	-	-	-		-
7194791	13	22	11.77	34.32	1.543935232	0.001756458	PHATRDRAFT_15239	K09602|1|5e-31|132|aly:ARALYDRAFT_473019|ubiquitin thioesterase protein OTUB1 [EC:3.4.-.-]	-	-	-		-
7201807	6	10	16.18	46.74	1.530446126	0.0361986	PHATRDRAFT_12984	K08679|1|4e-13|70.9|cme:CMR075C|UDP-glucuronate 4-epimerase [EC:5.1.3.6]	-	GO:0036094//small molecule binding;GO:0048037//cofactor binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7204166	6	10	11.16	32.15	1.52648171	0.0361986	CBP	K02183|1|3e-32|134|zma:100281919|calmodulin	-	GO:0046872//metal ion binding	-		-
7197681	6	10	3.09	8.86	1.519699861	0.0361986	PHATRDRAFT_44440	-	-	-	-		-
7196241	9	15	3.83	10.98	1.519461757	0.01048036	CRTISO5	K09835|1|7e-36|150|sbi:SORBI_05g022240|prolycopene isomerase [EC:5.2.1.13]	-	-	-		-

7196038	9	15	2.97	8.5	1.51699991	0.01048036	PHATRDRAFT_31465	K02111|1|2e-18|92.8|olu:OSTLU_30441|F-type H+-transporting ATPase subunit alpha [EC:3.6.3.14]	-	GO:0032550; GO:0003824//catalytic activity	GO:0006810//transport		GO:0006810//transport
7198687	50	82	152.21	433.17	1.508870185	3.78E-09	PHATRDRAFT_23748	K02979|1|6e-15|77.0|cme:CMO024C|small subunit ribosomal protein S28e	GO:0030312;GO:0015935//small ribosomal subunit;GO:0016020//membrane	GO:0005198//structural molecule activity	GO:0042254//ribosome biogenesis;GO:0010467//gene expression		GO:0042254//ribosome biogenesis;GO:0010467//gene expression
7200751	11	18	9.67	27.25	1.494668435	0.0056847	PHATRDRAFT_45716	-	-	-	-		-
7199415	8	13	11.09	31.1	1.487655215	0.01916876	PHATRDRAFT_17109	K00888|1|1e-35|146|cme:CMI125C|phosphatidylinositol 4-kinase [EC:2.7.1.67]	-	GO:0052742	GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0046474//glycerophospholipid biosynthetic process		GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0046474//glycerophospholipid biosynthetic process
7201923	16	26	8.85	24.76	1.484261954	0.000957832	PHATRDRAFT_37253	-	-	GO:0046914//transition metal ion binding	-		-
7201777	8	13	3.6	10.06	1.482561493	0.01916876	Albino3	K03217|1|2e-52|205|vvi:100260431|preprotein translocase subunit YidC	GO:0031224//intrinsic component of membrane	-	-		-
7201275	8	13	1.41	3.94	1.482500467	0.01916876	PHATRDRAFT_46203	-	-	-	-		-
7196720	8	13	2.71	7.56	1.480093383	0.01916876	SAS1	K14767|1|4e-12|71.6|cre:CHLREDRAFT_148918|U3 small nucleolar RNA-associated protein 3	-	-	-		-
7199858	10	16	14.54	40.15	1.465372718	0.01027748	PHATRDRAFT_44724	-	-	-	-		-
7200604	10	16	4.27	11.76	1.461580085	0.01027748	PHATRDRAFT_35250	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7196791	21	33	12.93	34.97	1.435395521	0.000287868	PHATRDRAFT_42971	-	-	-	-		-
7197452	7	11	4.15	11.21	1.433603037	0.0353016	PHATRDRAFT_43683	-	-	-	-		-
7204070	7	11	1.32	3.55	1.427281095	0.0353016	PHATR_44239	-	-	-	-		-
7195812	11	17	6.61	17.58	1.411212894	0.00999198	PHATRDRAFT_49454	-	-	-	-		-
7198994	31.69	47.94	27.89	72.69	1.382008971	2.63E-05	PHATRDRAFT_16669	-	-	-	GO:0044248//cellular catabolic process		GO:0044248//cellular catabolic process
7201837	10	15	28.23	73.44	1.37933693	0.01800342	PHATRDRAFT_46545	-	-	-	-		-
7203048	31	46	64.58	165.79	1.360197644	4.39E-05	PHATRDRAFT_47804	K02921|1|4e-32|134|smo:SELMODRAFT_146258|large subunit ribosomal protein L37Ae	GO:0015934//large ribosomal subunit	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7196715	15	22	7.91	19.96	1.335362121	0.00501736	PHATRDRAFT_43079	K02731|1|6e-11|67.0|gmx:100790481|20S proteasome subunit alpha 4 [EC:3.4.25.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0000502//proteasome complex;GO:0044444//cytoplasmic part	GO:0004175//endopeptidase activity	GO:0044237//cellular metabolic process;GO:0006950//response to stress;GO:0006508//proteolysis		GO:0044237//cellular metabolic process;GO:0006950//response to stress;GO:0006508//proteolysis
7199052	11	16	6.29	15.74	1.323303619	0.0172565	PHATRDRAFT_50302	-	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7200189	9	13	3.76	9.35	1.314233703	0.0325436	PHATRDRAFT_45124	-	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7197492	9	13	5.77	14.34	1.3134018	0.0325436	PHATRDRAFT_43623	-	-	-	-		-
7195791	21	30	15.65	38.51	1.299070466	0.00137863	PHATRDRAFT_40111	K10684|1|1e-19|95.1|ppp:PHYPADRAFT_160897|ubiquitin-like 1-activating enzyme E1 A [EC:6.3.2.19]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0036211		GO:0036211
7199888	15	21	28.06	67.9	1.274896566	0.00842876	PHATRDRAFT_11313	-	GO:0009579//thylakoid	-	-		-
7194744	10	14	8.15	19.64	1.268922965	0.0309224	PHATRDRAFT_4423	K11407|1|1e-25|114|ppp:PHYPADRAFT_71876|histone deacetylase 6/10 [EC:3.5.1.98]	-	GO:0003824//catalytic activity	-		-
7196933	11.46	16	8.51	20.47	1.266280065	0.0172565	PHATRDRAFT_9211	-	-	GO:0016787//hydrolase activity	-		-
7195085	13	18	31.92	76.56	1.262130178	0.01561986	PHATRDRAFT_15286	-	GO:0044444//cytoplasmic part	-	-		-
7201271	17.45	24.04	8.5	20.16	1.245960892	0.00458348	PHATRDRAFT_46198	-	-	-	-		-
7196515	11	15	7.46	17.52	1.231755239	0.0292412	PHATRDRAFT_31968	-	-	-	-		-
7199798	11	15	9.31	21.86	1.231440328	0.0292412	PHATRDRAFT_44871	K09874|1|1e-17|88.6|aly:ARALYDRAFT_911337|aquaporin NIP	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization

7197453	14	19	5.08	11.86	1.223203608	0.01477744	NTT5	-	GO:0031224//intrinsic component of membrane	GO:0015297//antiporter activity;GO:0032550	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7194691	17	23	7.1	16.51	1.217449191	0.0075707	Sit4	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7199070	15	20	16.03	36.85	1.200890194	0.0139404	PHATRDRAFT_4708	-	-	GO:0032550	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process
7204164	12	16	4.6	10.54	1.196169101	0.0275478	PHATR_33266	K14683|1|6e-56|217|zma:100501653|solute carrier family 34 (sodium-dependent phosphate cotransporter)	-	GO:0015114//phosphate ion transmembrane transporter activity	GO:0006817//phosphate ion transport		GO:0006817//phosphate ion transport
7204516	19	25	11.15	25.26	1.179810929	0.0067367	PHATR_46740	K03004|1|2e-07|55.5|ota:Ot14g01850|DNA-directed RNA polymerase I subunit RPA43;K03506|2|2e-06|52.0|olu:OSTLU_19031|DNA polymerase epsilon subunit 4 [EC:2.7.7.7]	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding	-		-
7204223	16	21	4.13	9.32	1.174188173	0.01311944	PHATR_54178	-	-	-	-		-
7204905	83	108	17.05	38.13	1.161154792	3.02E-08	PHATRDRAFT_bd1548	-	-	GO:0097159//organic cyclic compound binding	-		-
7199628	25	32	54.14	119.91	1.147185186	0.00290626	PHATRDRAFT_11401	-	-	-	-		-
7196569	14	18	8.1	17.91	1.144771524	0.024247	PHATRDRAFT_9355	K15015|1|5e-55|213|smo:SELMODRAFT_152799|solute carrier family 32 (vesicular inhibitory amino acid transporter)	GO:0031224//intrinsic component of membrane	-	-		-
7195723	25	32	16.49	36.33	1.139569967	0.00290626	PHATRDRAFT_49495	-	-	GO:0046906//tetrapyrrole binding	-		-
7195983	11	14	9.72	21.31	1.132502374	0.048539	PHATRDRAFT_31649	K15382|1|4e-19|93.2|cre:CHLREDRAFT_134242|solute carrier family 50 (sugar transporter)	GO:0031224//intrinsic component of membrane	-	GO:0044765		GO:0044765
7201103	11	14	10.56	23.15	1.132402359	0.048539	RAD14	-	-	GO:0005488//binding	-		-
7200167	11	14	9.02	19.77	1.132113532	0.048539	PHATRDRAFT_45080	-	-	-	-		-
7203256	30.66	39	29.64	64.96	1.132006185	0.000850656	Lhcf6	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7205034	32.1	40.87	12.75	27.92	1.130801694	0.001180594	PHATRDRAFT_bd1571	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7198002	11	14	5.58	12.21	1.129726173	0.048539	PHATRDRAFT_44285	-	-	-	-		-
7204620	46	57	15.9	33.88	1.091407109	0.000128175	PHATR_46710	K14306|1|2e-10|66.2|rcu:RCOM_1609340|nuclear pore complex protein Nup62	-	-	-		-
7201370	17	21	15.27	32.49	1.089295682	0.01974576	PHATRDRAFT_4413	-	GO:0009536//plastid	GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7203895	24	29	14.03	29.17	1.055970377	0.00766398	PHATR_33511	-	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7199224	26.5	31.68	31.04	64.01	1.044168751	0.00664386	PHATRDRAFT_24069	-	GO:0016020//membrane;GO:0005739//mitochondrion	GO:0003824//catalytic activity	-		-
7198659	25.85	30.89	6	12.31	1.036796356	0.00713762	PHATRDRAFT_49830	-	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0044710		GO:0006259//DNA metabolic process;GO:0044710

7195833	16	19	5.04	10.29	1.029747343	0.033597	PHATRDRAFT_40200	K13427|1|7e-35|147|vvi:100265605|nitric-oxide synthase, plant [EC:1.14.13.39]	-	GO:0032550	-		-
7197355	27	32	9.48	19.32	1.02713613	0.00618134	PHATRDRAFT_43641	-	-	-	GO:0009987//cellular process;GO:0044699		GO:0009987//cellular process;GO:0044699
7199377	17	20	24.99	50.75	1.022056921	0.0311248	PHATRDRAFT_41518	-	-	-	-		-
7203414	24	28	12.73	25.55	1.005090872	0.01183818	PHATRDRAFT_48055	-	-	-	-		-
7195068	18	21	8.38	16.81	1.004297576	0.0288192	PHATRDRAFT_39360	-	-	-	-		-
7204605	19	22	41.14	82.44	1.002802711	0.026673	PHATR_13254	K12604|1|2e-21|99.0|vcn:VOLCADRAFT_108387|CCR4-NOT transcription complex subunit 1	-	GO:0016670//oxidoreductase activity, acting on a sulfur group of donors, oxygen as acceptor	GO:0044710		GO:0044710
7198615	19	22	13.91	27.73	0.995325196	0.026673	PHATRDRAFT_49917	-	-	-	-		-
7196291	51	59	37.05	73.8	0.994147274	0.000318002	PHATRDRAFT_42608	-	-	-	-		-
7196019	21	24	38.62	76.3	0.982334893	0.0228266	Trx-o	K03671|1|2e-15|79.0|vcn:VOLCADRAFT_85222|thioredoxin 1	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0015036//disulfide oxidoreductase activity	GO:0050896//response to stimulus;GO:0019725//cellular homeostasis;GO:0018904		GO:0050896//response to stimulus;GO:0019725//cellular homeostasis;GO:0018904
7201072	49	56	10.69	21	0.974127475	0.000548066	PHATRDRAFT_46017	-	-	-	-		-
7204376	36	41	22.16	43.44	0.971066222	0.00318388	PHATR_41785	K13025|1|2e-152|536|cre:CHLREDRAFT_608|ATP-dependent RNA helicase [EC:3.6.4.13]	GO:0043234//protein complex;GO:0016604//nuclear body	GO:0032550;GO:0042623//ATPase activity, coupled;GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation;GO:0006396//RNA processing;GO:0006950//response to stress		GO:0006412//translation;GO:0006396//RNA processing;GO:0006950//response to stress
7200401	29	33	24.07	47.18	0.970939277	0.00811312	PHATRDRAFT_45638	-	-	-	-		-
7202653	43	49	11.35	22.23	0.969815651	0.00126723	PHATRDRAFT_47597	-	GO:0044464	GO:0016837	GO:0042120		GO:0042120
7196686	22	25	12.28	24.01	0.967324843	0.0211094	PHATRDRAFT_42506	-	-	-	-		-
7205104	76.15	86.11	15.31	29.76	0.958900244	2.41E-05	PHATRDRAFT_bd1762	-	-	GO:0060089;GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication		GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication
7199881	26	29	28.2	54.23	0.943396008	0.01541814	PHATRDRAFT_5537	K03086|1|4e-20|96.3|ota:Ot06g01190|RNA polymerase primary sigma factor;K03093|3|3e-14|76.6|osa:4339759|RNA polymerase sigma factor	-	GO:0003676//nucleic acid binding;GO:0000996;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199530	18	20	8.19	15.65	0.9342273	0.0444002	PHATRDRAFT_45021	-	-	-	-		-
7197841	27	30	2.71	5.17	0.931871429	0.0142508	PHATRDRAFT_54229	-	-	GO:0008092//cytoskeletal protein binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7195224	19	21	11.85	22.55	0.928240374	0.040891	PHATRDRAFT_54969	-	-	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	GO:0008152//metabolic process		GO:0008152//metabolic process
7195339	27.87	30.8	6.57	12.48	0.925652659	0.0142508	PHATRDRAFT_49118	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7197746	31	34	13.46	25.4	0.916150087	0.01039876	PHATRDRAFT_44454	K06897|1|1e-56|219|cre:CHLREDRAFT_187976|	-	GO:0003824//catalytic activity	-		-
7196498	21	23	6.68	12.59	0.914358275	0.0346894	PHATRDRAFT_42844	K15332|1|9e-43|173|smo:SELMODRAFT_440228|tRNA (uracil-5-)-methyltransferase	-	GO:0008168//methyltransferase activity	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7201294	34	37	39.62	74.36	0.90829789	0.00821066	AP1sigma	K12394|1|4e-34|142|pop:POPTR_731013|AP-1 complex subunit sigma 1/2;K11827|2|1e-28|124|bdi:100835474|AP-2 complex subunit sigma-1	-	GO:0022892	GO:0015031//protein transport		GO:0015031//protein transport
7195691	78	85	21.46	40.2	0.905545425	6.44E-05	PHATRDRAFT_49225	-	-	-	-		-

7201917	34	37	18.88	35.36	0.90525951	0.00821066	PHATRDRAFT_47115	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-
7202383	25	27	16.65	30.96	0.894883294	0.0249952	PHATRDRAFT_42123	K10589|1|2e-78|290|ath:AT3G17205|ubiquitin-protein ligase E3 C [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7201452	25.19	27.17	21.82	40.54	0.893694987	0.0249952	PHATRDRAFT_36008	-	-	-	-		-
7204596	69	74	11.38	20.97	0.881826304	0.00026311	CHLH	K03403|1|0.0|1733|ppp:PHYPADRAFT_226175|magnesium chelatase subunit H [EC:6.6.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0051003	GO:0006779//porphyrin-containing compound biosynthetic process		GO:0006779//porphyrin-containing compound biosynthetic process
7201320	30	32	12.12	22.23	0.87511825	0.01663994	PHATRDRAFT_20445	K00130|1|9e-64|243|mtr:MTR_4g106510|betaine-aldehyde dehydrogenase [EC:1.2.1.8]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors	GO:0044710		GO:0044710
7199151	67	71	111.4	203.93	0.872324792	0.000439692	PHATRDRAFT_31133	K02151|1|4e-27|118|ppp:PHYPADRAFT_203227|V-type H+-transporting ATPase subunit F [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex	GO:0019829//cation-transporting ATPase activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7205003	32	34	10.69	19.52	0.8686912	0.01415352	PHATRDRAFT_bd1633	K11723|1|3e-06|52.4|ath:AT5G55040|bromodomain-containing protein 7/9	-	-	-		-
7202332	1815	1926	912.32	1665.72	0.868534061	1.58E-74	PHATRDRAFT_13951	K00262|1|2e-95|347|ppp:PHYPADRAFT_179243|glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	-	GO:0016638//oxidoreductase activity, acting on the CH-NH2 group of donors;GO:0036094//small molecule binding	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7198073	39	41	24.77	44.83	0.855870631	0.0080639	PHATRDRAFT_44546	K05275|1|1e-23|108|zma:100272747|pyridoxine 4-dehydrogenase [EC:1.1.1.65];K00064|2|6e-11|66.6|ath:AT4G33670|D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7197628	42	44	17.7	31.9	0.849807064	0.00634716	PHATRDRAFT_11009	K15192|1|2e-101|367|ppp:PHYPADRAFT_184534|TATA-binding protein-associated factor [EC:3.6.4.-]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0003676//nucleic acid binding	-		-
7204478	23	24	17.83	32.04	0.845567445	0.0437436	PHATR_46636	-	-	GO:0046872//metal ion binding	-		-
7195698	25	26	6.89	12.32	0.838426368	0.0369316	PHATRDRAFT_49233	-	-	-	-		-
7198097	27	28	29.14	52.1	0.838282495	0.0312178	PHATRDRAFT_6052	-	-	-	-		-
7199666	26	27	10.51	18.77	0.836665981	0.0339498	PHATRDRAFT_26649	K03341|1|6e-103|373|cre:CHLREDRAFT_117639|O-phospho-L-seryl-tRNASec:L-selenocysteinyl-tRNA synthase [EC:2.9.1.2]	-	GO:0043168//anion binding;GO:0016740//transferase activity	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process
7196825	27	28	17.77	31.72	0.83594909	0.0312178	PHATRDRAFT_9529	K10902|1|6e-72|269|smo:SELMODRAFT_41328|ATP-dependent DNA helicase Q5 [EC:3.6.4.12];K10899|4|3e-68|256|cre:CHLREDRAFT_128016|ATP-dependent DNA helicase Q1 [EC:3.6.4.12]	-	GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7197023	26	27	6.71	11.97	0.835038481	0.0339498	PHATRDRAFT_50740	K03404|1|1e-90|332|cme:CMM270C|magnesium chelatase subunit D [EC:6.6.1.1]	-	GO:0032550;GO:0051003;GO:0016462//pyrophosphatase activity	GO:0006779//porphyrin-containing compound biosynthetic process		GO:0006779//porphyrin-containing compound biosynthetic process
7197558	29	30	5.03	8.95	0.831329282	0.0264168	PHATRDRAFT_43517	-	-	GO:0046914//transition metal ion binding	-		-
7197956	37	38	15.03	26.54	0.820323361	0.01367028	PHATRDRAFT_44288	-	-	-	-		-
7198346	41	42	13.73	24.18	0.816482619	0.00987876	PHATRDRAFT_49763	-	-	-	-		-
7201335	45	46	11.95	21.01	0.814065544	0.0071565	PHATRDRAFT_46093	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process

7196275	49	50	8.43	14.79	0.811017516	0.00519558	CDC6	K02213|1|1e-15|84.7|rcu:RCOM_0611750|cell division control protein 6	-	-	-		-
7199456	63.99	64.67	41.49	72.19	0.799035347	0.001717016	PHATRDRAFT_41628	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7196617	28	28	31.14	53.69	0.78588446	0.0415594	PHATRDRAFT_31409	-	-	-	-		-
7204322	60	60	49.12	84.61	0.784517624	0.0030537	PHATR_18533	K12948|1|7e-26|115|cre:CHLREDRAFT_190234|signal peptidase complex subunit 3 [EC:3.4.-.-]	GO:0005789//endoplasmic reticulum membrane;GO:0031224//intrinsic component of membrane	GO:0016787//hydrolase activity	GO:0016485//protein processing		GO:0016485//protein processing
7200541	27	27	18.9	32.55	0.784271309	0.045268	PHATRDRAFT_45429	-	-	-	-		-
7201048	34	34	22.4	38.56	0.783606319	0.0250608	PHATRDRAFT_45982	-	-	-	-		-
7200732	44	44	26.18	45.06	0.783382216	0.01100776	PHATRDRAFT_45542	-	GO:0044464	GO:0097159//organic cyclic compound binding;GO:0046914//transition metal ion binding	-		-
7199826	47	47	23.59	40.59	0.782948921	0.0086322	PHATRDRAFT_44920	K00472|1|1e-13|76.3|olu:OSTLU_37102|prolyl 4-hydroxylase [EC:1.14.11.2]	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7195519	28	28	8.77	15.09	0.782944058	0.0415594	PHATRDRAFT_49212	-	-	-	-		-
7198464	28	28	9.76	16.79	0.782649177	0.0415594	PHATRDRAFT_49802	-	-	-	-		-
7201638	32	32	13.65	23.48	0.782531457	0.029627	PHATRDRAFT_46377	-	-	-	-		-
7204546	36	36	16.85	28.98	0.782309003	0.021221	PHATR_46798	K00432|1|2e-13|75.9|ath:AT2G48150|glutathione peroxidase [EC:1.11.1.9]	GO:0044464	GO:0004601//peroxidase activity	GO:0044763;GO:0003006//developmental process involved in reproduction;GO:0044710;GO:0006950//response to stress		GO:0044763;GO:0003006//developmental process involved in reproduction;GO:0044710;GO:0006950//response to stress
7196907	32	32	13.17	22.65	0.782255705	0.029627	PHATRDRAFT_17862	K12823|1|1e-156|551|cre:CHLREDRAFT_136376|ATP-dependent RNA helicase DDX5/DBP2 [EC:3.6.4.13]	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7200487	42.13	42.2	7.81	13.43	0.782064851	0.01295542	PHATRDRAFT_45390	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7195027	66.15	65.81	37.08	63.48	0.775660884	0.0026476	ACT1	K05692|1|1e-177|620|cre:CHLREDRAFT_24392|actin beta/gamma 1;K10355|2|9e-177|617|ath:AT3G12110|actin, other eukaryote	GO:0043232	GO:0032550	-		-
7196570	64	63	21.2	35.88	0.759115625	0.00310108	SLY1	K12479|1|1e-24|113|gmx:100782786|vacuolar protein sorting-associated protein 45;K15292|2|2e-24|112|smo:SELMODRAFT_234736|syntaxin-binding protein 1	-	-	GO:0006887//exocytosis		GO:0006887//exocytosis
7196929	155	152	57.54	97.05	0.754162992	5.41E-06	PHATRDRAFT_43183	K00791|1|1e-41|169|cme:CMS475C|tRNA dimethylallyltransferase [EC:2.5.1.75]	-	GO:0032550	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process
7203650	43	42	24.69	41.51	0.749532095	0.01679898	PHATRDRAFT_48389	-	-	-	-		-
7197685	79	77	12.72	21.31	0.744431922	0.001317464	PHATRDRAFT_44446	-	-	-	-		-
7198074	36	35	20.56	34.41	0.742987628	0.0300184	PHATRDRAFT_44547	-	-	-	-		-
7204743	38	37	11.76	19.68	0.742842161	0.0253994	PHATR_46912	-	-	-	-		-
7201987	36	35	18.05	30.2	0.742549712	0.0300184	PHATRDRAFT_47229	-	-	-	-		-
7202554	36	35	11.14	18.63	0.741878442	0.0300184	PHATRDRAFT_47420	K01519|1|3e-09|52.0|cre:CHLREDRAFT_179025|inosine triphosphate pyrophosphatase [EC:3.6.1.19]	-	GO:0016740//transferase activity	-		-
7204923	33	32	22.89	38.21	0.739232795	0.0386526	PHATRDRAFT_bd1626	K09553|1|8e-16|82.8|cre:CHLREDRAFT_136069|stress-induced-phosphoprotein 1	-	-	-		-
7195451	34	33	11.7	19.52	0.738444523	0.0355178	PHATRDRAFT_49097	-	-	-	-		-

7202216	33	32	13.97	23.3	0.737997934	0.0386526	PHATRDRAFT_46968	-	-	-	-		-
7202066	30	29	30.48	50.78	0.736397492	0.0499204	PHATRDRAFT_47178	-	-	-	-		-
7195968	153	147	95.98	158.74	0.725859992	1.57E-05	PHATRDRAFT_42600	-	-	-	-		-
7195825	60.43	57.95	18.48	30.47	0.721424743	0.00810476	PHATRDRAFT_49474	-	-	-	-		-
7198598	47	45	21.27	35.03	0.719770955	0.01684434	PHATRDRAFT_49887	-	-	-	-		-
7196417	41	39	45.14	74.03	0.71370361	0.0276148	PHATRDRAFT_9601	K10365|1|1e-25|114|vvi:100242539|capping protein (actin filament) muscle Z-line, beta	GO:0043234//protein complex;GO:0015629//actin cytoskeleton	GO:0008092//cytoskeletal protein binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7197943	64	61	25.88	42.42	0.712907004	0.0058913	PMI1	K01809|1|9e-72|269|osa:4325991|mannose-6-phosphate isomerase [EC:5.3.1.8]	-	GO:0046914//transition metal ion binding;GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0009226//nucleotide-sugar biosynthetic process		GO:0009226//nucleotide-sugar biosynthetic process
7203210	36	34	95.9	156.98	0.710978044	0.0419708	PHATRDRAFT_14645	-	-	-	-		-
7196312	62	59	26.82	43.9	0.710911703	0.00690838	PHATRDRAFT_50650	K10960|1|2e-152|537|cme:CMJ154C|geranylgeranyl reductase [EC:1.3.1.83]	GO:0009526//plastid envelope;GO:0009534//chloroplast thylakoid	GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors;GO:0036094//small molecule binding	GO:0044710;GO:0006779//porphyrin-containing compound biosynthetic process		GO:0044710;GO:0006779//porphyrin-containing compound biosynthetic process
7200540	97	92	38.77	63.24	0.705896633	0.000825138	PHATRDRAFT_45426	-	-	-	-		-
7202597	38	36	14.59	23.78	0.704768832	0.0354702	PHATRDRAFT_47494	-	-	-	-		-
7200820	63	59	43.88	70.75	0.689166622	0.00869864	PHATRDRAFT_45813	-	GO:0009579//thylakoid;GO:0009507//chloroplast	-	-		-
7203797	1372	1284	989.05	1593.81	0.688364293	6.90E-34	PHATRDRAFT_38760	-	-	-	-		-
7195430	47	44	17.97	28.93	0.686975914	0.023202	PHATRDRAFT_49067	-	-	-	-		-
7204187	390	365	62.45	100.43	0.685416812	9.41E-11	PHATR_43970	K01061|1|2e-12|74.3|pop:POPTR_1108355|carboxymethylenebutenolidase [EC:3.1.1.45]	-	-	-		-
7194739	45	42	22.2	35.64	0.68293766	0.0273474	PHATRDRAFT_48579	-	-	-	-		-
7200830	87	81	77.18	123.81	0.681828895	0.00241088	OEE3	-	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7196374	124	115	158.23	253.16	0.678026316	0.000339864	PHATRDRAFT_42746	-	-	-	-		-
7194718	41	38	31.75	50.68	0.674659933	0.0380928	cdc14	K06639|1|4e-75|279|smo:SELMODRAFT_91859|cell division cycle 14 [EC:3.1.3.48]	-	GO:0004721//phosphoprotein phosphatase activity	GO:0006470//protein dephosphorylation		GO:0006470//protein dephosphorylation
7203091	53	49	65.97	105.2	0.673252695	0.01941312	PHATRDRAFT_47876	-	-	-	-		-
7198726	38	35	70.48	112.21	0.670915423	0.0489702	PHATRDRAFT_50029	-	-	-	-		-
7203182	63	58	115.87	184.38	0.670175087	0.01177296	PHATRDRAFT_22027	-	GO:0019866//organelle inner membrane;GO:0005740//mitochondrial envelope	GO:0043169//cation binding	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7199043	103	95	107.29	170.59	0.669017463	0.001259918	PHATRDRAFT_50289	-	-	-	-		-
7197087	86	79	80.99	128.21	0.662693101	0.00349116	Lhcf2	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7203676	136	125	28.96	45.76	0.66002545	0.000242646	PHATRDRAFT_48434	-	-	-	-		-
7203299	72	66	16.7	26.32	0.656311386	0.00777042	PHATRDRAFT_56599	K01869|1|0.0|883|ota:Ot06g00560|leucyl-tRNA synthetase [EC:6.1.1.4]	GO:0044424	GO:0032550;GO:0052689//carboxylic ester hydrolase activity;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006448//regulation of translational elongation;GO:0006418//tRNA aminoacylation for protein translation		GO:0006448//regulation of translational elongation;GO:0006418//tRNA aminoacylation for protein translation
7195637	141	129	98.62	155.35	0.655570084	0.000220622	PHATRDRAFT_49131	-	-	-	-		-
7201276	51.94	47.45	46.77	73.62	0.654514321	0.0228332	PHATRDRAFT_46204	-	-	-	-		-
7199112	90	82	31.32	49.08	0.648051036	0.0034168	PHATRDRAFT_50268	-	-	GO:0003824//catalytic activity	-		-
7204115	344	312	439.8	688.16	0.645896432	1.77E-08	PHATR_44202	-	-	-	-		-
7203724	44	40	21.95	34.33	0.645248918	0.0405186	PHATRDRAFT_48292	-	-	-	-		-
7198740	54	49	16.28	25.4	0.641727797	0.0242096	PHATRDRAFT_50045	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003700//sequence-specific DNA binding transcription factor activity;GO:0046914//transition metal ion binding	GO:0006366//transcription from RNA polymerase II promoter		GO:0006366//transcription from RNA polymerase II promoter

7198100	63	57	55.52	86.54	0.640359553	0.01581282	Lhcr1	K08910|1|4e-25|113|cme:CMQ142C|light-harvesting complex I chlorophyll a/b binding protein 4;K08907|2|4e-21|99.8|cme:CMN234C|light-harvesting complex I chlorophyll a/b binding protein 1;K08908|4|1e-14|78.2|ppp:PHYPADRAFT_151155|light-harvesting complex I chlorophyll a/b binding protein 2	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7204536	494	447	216.82	337.48	0.638304166	1.97E-11	PHATR_54643	K06694|1|6e-06|50.8|ath:AT2G03430|26S proteasome non-ATPase regulatory subunit 10	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7198685	91	82	46.71	72.42	0.632656732	0.00419614	PHATRDRAFT_2032	K02575|1|2e-62|238|smo:SELMODRAFT_136730|MFS transporter, NNP family, nitrate/nitrite transporter	GO:0031224//intrinsic component of membrane	-	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7204948	54.48	49.07	23.55	36.49	0.631774091	0.0242096	PHATRDRAFT_bd348	K00053|1|0.0|636|vcn:VOLCADRAFT_74529|ketol-acid reductoisomerase [EC:1.1.1.86]	GO:0044435	GO:0043168//anion binding;GO:0046872//metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0042802//identical protein binding;GO:0036094//small molecule binding;GO:0048037//cofactor binding	GO:0009081//branched-chain amino acid metabolic process;GO:0008652//cellular amino acid biosynthetic process;GO:1901605//alpha-amino acid metabolic process		GO:0009081//branched-chain amino acid metabolic process;GO:0008652//cellular amino acid biosynthetic process;GO:1901605//alpha-amino acid metabolic process
7197496	313	282	49.37	76.44	0.630693133	1.26E-07	PHATRDRAFT_43627	K11373|1|4e-87|322|ppp:PHYPADRAFT_206869|elongator complex protein 1	-	-	-		-
7202934	80	72	27.39	42.4	0.630414999	0.00739788	PHATRDRAFT_29029	K01874|1|2e-113|408|aly:ARALYDRAFT_906959|methionyl-tRNA synthetase [EC:6.1.1.10]	GO:0043231//intracellular membrane-bounded organelle	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7204873	101.41	91.08	69.45	107.39	0.628813059	0.00258274	PHATRDRAFT_bd853	K07901|1|2e-44|177|zma:100273222|Ras-related protein Rab-8A;K07976|2|4e-44|176|osa:4334590|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7194955	155	139	43.22	66.63	0.624472821	0.000231946	LLA1	-	-	-	-		-
7197812	75	67	56.42	86.79	0.621322158	0.01090686	COPIepsilon	-	GO:0030120//vesicle coat	-	GO:0048193//Golgi vesicle transport		GO:0048193//Golgi vesicle transport
7199409	261.31	233.23	81.58	125.2	0.61794715	2.43E-06	PHATRDRAFT_50589	-	-	-	-		-
7202214	128	114	58.69	89.92	0.615527327	0.00100561	PHATRDRAFT_46965	-	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710

7196236	53	47	44.9	68.59	0.611282811	0.0351656	Lhcr4	K08910|1|9e-20|95.5|cme:CMQ142C|light-harvesting complex I chlorophyll a/b binding protein 4;K08907|2|3e-19|94.0|cme:CMN234C|light-harvesting complex I chlorophyll a/b binding protein 1;K08911|5|5e-09|59.7|rcu:RCOM_1590680|light-harvesting complex I chlorophyll a/b binding protein 5	-	-	-		-
7197277	53	47	23.98	36.59	0.609617757	0.0351656	PHATRDRAFT_43763	-	-	-	-		-
7199911	69	61	27.26	41.45	0.60458654	0.0174127	PHATRDRAFT_19324	K01663|1|5e-161|566|osa:4332296|glutamine amidotransferase / cyclase [EC:2.4.2.- 4.1.3.-]	GO:0005737//cytoplasm;GO:0043231//intracellular membrane-bounded organelle	GO:0016763//transferase activity, transferring pentosyl groups;GO:0016830//carbon-carbon lyase activity	GO:0006547//histidine metabolic process		GO:0006547//histidine metabolic process
7198048	58	51	40.7	61.61	0.598135741	0.031326	PHATRDRAFT_44370	K07185|1|9e-33|139|olu:OSTLU_8326|tryptophan-rich sensory protein;K05770|2|6e-10|63.2|cre:CHLREDRAFT_143874|benzodiazapine receptor	GO:0031224//intrinsic component of membrane	-	-		-
7195273	49	43	15.23	22.98	0.593462856	0.0485886	PHATRDRAFT_49011	-	-	-	-		-
7197189	94.05	82.33	31.78	47.83	0.589796667	0.00754622	PHATRDRAFT_43493	-	-	-	-		-
7199627	87	76	70.87	106.64	0.589501731	0.0098367	PHATRDRAFT_1800	-	-	-	-		-
7196502	3384	2960	1191.05	1791.59	0.58900654	6.46E-58	PHATRDRAFT_42850	K14510|1|8e-22|103|sbi:SORBI_02g011690|serine/threonine-protein kinase CTR1 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7197907	55	48	33.24	49.92	0.586697552	0.0397848	PHATRDRAFT_44711	-	-	-	-		-
7201218	179	156	124.93	187.46	0.585462828	0.00024702	PHATRDRAFT_3843	K04345|1|2e-74|277|rcu:RCOM_1050860|protein kinase A [EC:2.7.11.11]	-	GO:0043169//cation binding;GO:0004721//phosphoprotein phosphatase activity;GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7203627	686	598	74.24	111.19	0.582758428	8.01E-13	Pt-separase	K02365|1|3e-26|120|olu:OSTLU_119551|separase [EC:3.4.22.49]	GO:0043231//intracellular membrane-bounded organelle	GO:0016787//hydrolase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7198950	643	560	113	169.14	0.581895111	4.65E-12	PHATRDRAFT_50174	K10838|1|3e-23|109|ota:Ot14g02880|xeroderma pigmentosum group C-complementing protein;K00588|2|9e-09|61.6|pop:POPTR_805093|caffeoyl-CoA O-methyltransferase [EC:2.1.1.104];K13067|3|3e-07|56.6|ath:AT1G67990|putative caffeoyl-CoA 3-O-methyltransferase [EC:2.1.1.-]	-	GO:0005488//binding;GO:0008168//methyltransferase activity	-		-
7203371	90	78	125.55	187.79	0.580858212	0.0102059	PHATRDRAFT_14770	K07152|1|5e-37|151|smo:SELMODRAFT_187412|	-	-	-		-
7203749	130	113	55.43	82.88	0.580356995	0.00189942	PHATRDRAFT_48461	-	-	-	-		-
7194727	130	113	50.82	75.97	0.580033446	0.00189942	PHATRDRAFT_48558	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197270	121	104	190.6	282.92	0.569846047	0.00367408	PHATRDRAFT_9697	K01527|1|1e-23|107|vcn:VOLCADRAFT_104715|nascent polypeptide-associated complex subunit beta	-	-	-		-
7197211	5948	5124	1797.15	2661.91	0.566750965	2.27E-92	PHATRDRAFT_43531	-	-	-	-		-
7201756	302	260	122.72	181.72	0.566346823	4.33E-06	PHATRDRAFT_46370	-	-	-	-		-
7203991	1577	1357	452.17	668.95	0.565033105	1.23E-25	PHATR_44028	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7194771	120	103	74.22	109.65	0.563025906	0.0039532	PHATRDRAFT_48524	-	-	-	-		-
7198947	99	85	26.27	38.77	0.561524535	0.00871738	PHATRDRAFT_50168	-	-	-	-		-
7199104	63	54	22.85	33.68	0.559697973	0.0365502	PHATRDRAFT_50254	-	-	-	-		-
7199389	285	244	105.15	154.82	0.558143004	1.11E-05	PHATRDRAFT_50561	-	-	-	-		-

7200208	75	64	23.56	34.57	0.553181064	0.0245344	PHATRDRAFT_45164	K06980|1|2e-16|85.9|aly:ARALYDRAFT_490030|	GO:0044424	GO:0051536//iron-sulfur cluster binding;GO:0008168//methyltransferase activity	GO:0006544//glycine metabolic process;GO:0043170		GO:0006544//glycine metabolic process;GO:0043170
7201330	546	466	133.99	196.59	0.553064605	1.73E-09	PHATRDRAFT_46087	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203253	225.45	192.26	27.9	40.88	0.551130074	0.000108618	PHATRDRAFT_48038	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	-		-
7199026	200	170	162.73	238.25	0.549995971	0.00030674	PHATRDRAFT_50256	-	-	-	-		-
7204140	73	62	49.48	72.35	0.548147516	0.028579	PHATR_25956	K00390|1|7e-62|235|ppp:PHYPADRAFT_123215|phosphoadenosine phosphosulfate reductase [EC:1.8.4.8];K05907|4|3e-11|67.8|vvi:100233045|adenylyl-sulfate reductase (glutathione) [EC:1.8.4.9]	-	GO:0003824//catalytic activity	GO:0008152//metabolic process;GO:0019725//cellular homeostasis		GO:0008152//metabolic process;GO:0019725//cellular homeostasis
7203169	66	56	49.36	72.13	0.547257029	0.0377148	PHATRDRAFT_47905	K09250|1|4e-14|77.0|sbi:SORBI_04g001720|cellular nucleic acid-binding protein	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0003676//nucleic acid binding;GO:0046872//metal ion binding	GO:0048608//reproductive structure development;GO:0006351//transcription, DNA-templated;GO:0006950//response to stress		GO:0048608//reproductive structure development;GO:0006351//transcription, DNA-templated;GO:0006950//response to stress
7199737	113	96	42.09	61.5	0.547108901	0.00659608	PHATRDRAFT_44770	-	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7204479	113	96	16.51	24.1	0.545693026	0.00659608	PHATR_46639	-	-	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7203905	66	56	25.6	37.36	0.545350645	0.0377148	UGDH1	K00012|1|1e-170|598|mtr:MTR_7g012950|UDPglucose 6-dehydrogenase [EC:1.1.1.22]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0030312	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0048037//cofactor binding;GO:0000166//nucleotide binding	GO:0044710		GO:0044710
7202478	84	71	99.65	145.26	0.543695775	0.0207296	PHATRDRAFT_51066	K02966|1|1e-36|150|ath:AT3G20880|small subunit ribosomal protein S19e	GO:0030312;GO:0015935//small ribosomal subunit;GO:0031981//nuclear lumen;GO:0005911//cell-cell junction	GO:0005198//structural molecule activity	GO:0009451//RNA modification;GO:0010467//gene expression		GO:0009451//RNA modification;GO:0010467//gene expression
7201312	72	61	26.3	38.32	0.543034762	0.0308456	PHATRDRAFT_12605	K03702|1|7e-134|476|olu:OSTLU_43765|excinuclease ABC subunit B;K11594|2|1e-07|56.6|smo:SELMODRAFT_105510|ATP-dependent RNA helicase [EC:3.6.4.13];K14811|4|4e-07|55.1|cre:CHLREDRAFT_129561|ATP-dependent RNA helicase DBP3 [EC:3.6.4.13]	-	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0003676//nucleic acid binding;GO:0004520//endodeoxyribonuclease activity	GO:0006281//DNA repair		GO:0006281//DNA repair
7199337	538	454	231.64	336.25	0.537649866	7.36E-09	PHATRDRAFT_50531	-	-	-	-		-
7197633	75	63	83.69	121.22	0.534500595	0.0316996	PHATRDRAFT_26293	K02719|1|1e-21|101|cme:CMI248C|photosystem II PsbU protein	GO:0009523//photosystem II	-	GO:0042548//regulation of photosynthesis, light reaction		GO:0042548//regulation of photosynthesis, light reaction
7198250	1306	1097	546.92	790.19	0.530869769	6.77E-19	HSF2	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus		GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus
7200382	150	126	40.94	59.12	0.530135167	0.00250466	PHATRDRAFT_45604	-	-	-	-		-
7205056	82.6	69.34	35.57	51.36	0.529984228	0.0240802	PHATRDRAFT_bd1874	K01689|1|1e-134|478|olu:OSTLU_28765|enolase [EC:4.2.1.11]	GO:0043234//protein complex	GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process

7198350	131	110	19.45	28.06	0.528744854	0.0047449	PHATRDRAFT_49771	K05857|1|4e-20|99.8|ath:AT5G58670|phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	-	GO:0060089; GO:0004629//phospholipase C activity	GO:0007165//signal transduction; GO:0044238		GO:0007165//signal transduction; GO:0044238
7196094	229	192	43.68	62.94	0.527004322	0.000209276	PHATRDRAFT_83	K05681|1|6e-53|208|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|3|5e-41|168|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7194722	80	67	17.09	24.6	0.525505919	0.027971	PHATRDRAFT_48553	-	-	-	-		-
7197247	523	437	282.08	405.59	0.523917703	3.11E-08	PHATRDRAFT_43715	-	-	-	-		-
7198104	170	142	81.47	117.07	0.523030609	0.001565382	PHATRDRAFT_44607	-	-	-	-		-
7196930	513	428	301.68	433.19	0.521980884	4.84E-08	PHATRDRAFT_43184	-	-	-	-		-
7203558	100	83	119.06	170.43	0.517490509	0.01700472	PHATRDRAFT_6062	K08915|1|5e-16|82.4|smo:SELMODRAFT_149722|light-harvesting complex II chlorophyll a/b binding protein 4	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7200682	448	372.58	108.53	155.15	0.515569807	4.98E-07	PHATRDRAFT_54405	K13862|1|1e-22|107|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0004620//phospholipase activity;GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7200452	81	67	36.83	52.41	0.508960712	0.0332156	PHATRDRAFT_35419	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196297	92	76	75.79	107.85	0.508946765	0.0239646	LHL1	-	-	-	-		-
7198759	69	57	55.66	79.2	0.508859522	0.0498846	PHATRDRAFT_50078	-	-	-	-		-
7195587	1241	1026	152.81	217.09	0.506554314	1.65E-16	PHATRDRAFT_49312	K08333|1|3e-130|465|ppp:PHYPADRAFT_144257|phosphoinositide-3-kinase, regulatory subunit 4, p150 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198967	74	61	63.59	90.31	0.506085837	0.0438208	PHATRDRAFT_2819	K14648|1|3e-73|273|vcn:VOLCADRAFT_62482|poly(U)-specific endoribonuclease [EC:3.1.-.-]	-	GO:0016787//hydrolase activity	-		-
7195554	1608	1328	141.08	200.18	0.504784361	8.55E-21	PHATRDRAFT_49264	-	-	-	-		-
7204977	246	203	31.81	45.11	0.503966914	0.000253006	PHATRDRAFT_bd955	K02999|1|0.0|926|olu:OSTLU_43496|DNA-directed RNA polymerase I subunit RPA1 [EC:2.7.7.6]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding;GO:0034062//RNA polymerase activity	GO:0010467//gene expression		GO:0010467//gene expression
7202879	114	94	31.77	45.04	0.503541737	0.01261194	PHATRDRAFT_47686	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204830	108	89	38.05	53.93	0.50319158	0.01532912	PHATRDRAFT_bd1374	-	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198749	413	340	217.06	307.47	0.502351763	2.61E-06	PHATRDRAFT_50059	K10712|1|3e-20|98.2|ppp:PHYPADRAFT_196607|cysteamine dioxygenase [EC:1.13.11.19]	-	GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:0044710		GO:0044710
7198349	179	147	77.53	109.52	0.498367782	0.00208226	PHATRDRAFT_16222	K14951|1|6e-75|280|smo:SELMODRAFT_439526|cation-transporting ATPase 13A3/4/5 [EC:3.6.3.-];K14950|3|2e-38|158|pop:POPTR_269210|cation-transporting ATPase 13A1 [EC:3.6.3.-]	GO:0031224//intrinsic component of membrane	GO:0032550; GO:0008324//cation transmembrane transporter activity;GO:0003824//catalytic activity	GO:0006811//ion transport		GO:0006811//ion transport

7196256	942	769	293.38	411.81	0.489208339	5.14E-12	PHATRDRAFT_17265	K08176|1|5e-25|114|osa:4331542|MFS transporter, PHS family, inorganic phosphate transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0044763		GO:0044763
7199203	283	231	93.08	130.64	0.48905358	0.000150878	PHATRDRAFT_50390	K14007|1|7e-10|64.3|sbi:SORBI_06g001240|protein transport protein SEC24	-	-	-		-
7204174	112	91	19.29	26.94	0.481896707	0.01828314	PHATR_18549	K07204|1|1e-138|493|olu:OSTLU_41144|regulatory associated protein of mTOR	-	-	-		-
7198686	143	116	57.22	79.84	0.480592223	0.00809634	PHATRDRAFT_50090	-	-	-	-		-
7199340	147	119	84.78	118.11	0.478335247	0.00766738	PHATRDRAFT_41508	-	-	-	-		-
7202400	140	113	57.56	79.92	0.473489991	0.0099434	PHATRDRAFT_37524	-	-	-	-		-
7200866	537	432	206.47	285.67	0.468417364	6.73E-07	PHATRDRAFT_46009	-	-	GO:0046872//metal ion binding	-		-
7202868	132	106	45.72	63.14	0.465728857	0.01382268	PHATRDRAFT_47669	-	-	GO:0046914//transition metal ion binding	-		-
7194723	1923	1543	778.04	1073.78	0.464782206	1.28E-20	PHATRDRAFT_48554	-	-	GO:0003676//nucleic acid binding	-		-
7204481	166	133	109.58	151.14	0.463901019	0.00622424	PHATR_3639	K00010|1|5e-64|243|cme:CMF086C|myo-inositol 2-dehydrogenase [EC:1.1.1.18]	-	GO:0036094//small molecule binding;GO:0004022//alcohol dehydrogenase (NAD) activity	GO:0044710		GO:0044710
7194749	151	121	32.35	44.55	0.46165972	0.00900194	PHATRDRAFT_39092	-	-	-	-		-
7197702	94	75	13.83	18.97	0.455918522	0.041487	PHATRDRAFT_44469	-	-	-	-		-
7197450	228	182	34.21	46.92	0.455784909	0.001571392	PHATRDRAFT_43680	-	-	-	-		-
7202333	231.51	184.12	56.84	77.7	0.451008044	0.001586416	PHATRDRAFT_54708	-	-	-	-		-
7199848	97	77	64.61	88.3	0.450655963	0.0419106	PHATRDRAFT_11472	-	-	-	-		-
7197537	195	155	35.29	48.21	0.450073	0.00393648	PHATRDRAFT_43482	-	-	GO:0003824//catalytic activity	-		-
7200371	92	73	32.19	43.93	0.448593923	0.0477638	PHATRDRAFT_45589	K11294|1|1e-05|50.4|bdi:100836665|nucleolin	-	-	-		-
7194796	96	76	67.65	92.21	0.446833282	0.0449424	PHATRDRAFT_39066	K12818|1|4e-07|53.9|ota:Ot04g02270|ATP-dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13];K14792|3|2e-06|51.2|gmx:100797745|rRNA biogenesis protein RRP5;K02945|4|4e-06|50.4|ppp:PHYPADRAFT_122522|small subunit ribosomal protein S1	-	GO:0003676//nucleic acid binding;GO:0003824//catalytic activity	-		-
7200902	3107	2456	1268.01	1724.02	0.443210388	2.79E-29	PHATRDRAFT_12416	-	GO:0044424	GO:0051540;GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7196347	351	277	103.16	139.97	0.440233967	0.000167631	PHATRDRAFT_17427	K00121|1|7e-128|456|vcn:VOLCADRAFT_82410|S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	-	GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0052689//carboxylic ester hydrolase activity;GO:0036094//small molecule binding	GO:0044282;GO:0006067//ethanol metabolic process		GO:0044282;GO:0006067//ethanol metabolic process
7201709	1141	899	306.81	415.6	0.437850148	1.66E-11	PHATRDRAFT_54602	K09667|1|2e-18|93.2|bdi:100846315|polypeptide N-acetylglucosaminyltransferase [EC:2.4.1.-]	-	-	-		-
7194878	206	162	59.82	80.88	0.435155087	0.00432974	GOX	K11517|1|5e-77|287|ppp:PHYPADRAFT_159377|(S)-2-hydroxy-acid oxidase [EC:1.1.3.15]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0003973//(S)-2-hydroxy-acid oxidase activity;GO:0032553	GO:0044710		GO:0044710
7199977	233	183	129.06	174.43	0.434606258	0.00253826	PHATRDRAFT_45341	-	-	-	-		-
7199214	126	99	27.75	37.48	0.433633182	0.0256568	PHATRDRAFT_41359	-	-	-	-		-
7204186	124	97	81.61	109.9	0.429373539	0.0293258	PHATR_43966	-	-	-	-		-
7204185	128	100	108.16	145.56	0.4284469	0.0275924	PHATR_18559	K02991|1|6e-72|268|zma:542640|small subunit ribosomal protein S6e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression

7200033	267	209	41.56	55.9	0.427652629	0.001419484	PHATRDRAFT_45342	-	-	-	-		-
7204549	1028	802	585.18	785.68	0.425061374	6.99E-10	PHATR_36843	-	-	-	-		-
7200566	324	253	37.32	50.08	0.424285576	0.000499184	PHATRDRAFT_45463	K10777|1|3e-32|140|olu:OSTLU_26493|DNA ligase 4 [EC:6.5.1.1]	-	GO:0003676//nucleic acid binding;GO:0003909//DNA ligase activity;GO:0032550	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7198547	185	144	152.41	204.34	0.423014078	0.0091517	PHATRDRAFT_40791	-	-	-	-		-
7197752	1091	851	120.93	162.08	0.42253389	2.18E-10	PHATRDRAFT_44467	-	-	-	-		-
7199056	243	189	70.91	94.83	0.41935444	0.00293548	PHATRDRAFT_50310	K12842|1|1e-49|196|smo:SELMODRAFT_85327|U2-associated protein SR140	-	GO:0036094//small molecule binding;GO:0003676//nucleic acid binding	GO:0010467//gene expression		GO:0010467//gene expression
7205140	1397	1085	253.29	338.1	0.416659896	1.58E-12	PHATRDRAFT_bd1613	K05658|1|5e-82|305|rcu:RCOM_1598590|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7198640	151	117	50.99	67.94	0.41404688	0.0204384	PHATRDRAFT_40783	-	GO:0009526//plastid envelope	GO:0000166//nucleotide binding	-		-
7199361	186	144	76.82	102.29	0.413111243	0.01042554	PHATRDRAFT_50577	K00818|1|4e-115|413|cme:CMQ064C|acetylornithine aminotransferase [EC:2.6.1.11]	GO:0043231//intracellular membrane-bounded organelle	GO:0016769//transferase activity, transferring nitrogenous groups;GO:0043168//anion binding	GO:0009064//glutamine family amino acid metabolic process		GO:0009064//glutamine family amino acid metabolic process
7197079	651.35	503.77	248.69	330.8	0.411610738	2.18E-06	PHATRDRAFT_43313	-	-	-	-		-
7203685	145	112	101.96	135.6	0.4113539	0.024715	PHATRDRAFT_48449	-	-	GO:0016872//intramolecular lyase activity	GO:0009699//phenylpropanoid biosynthetic process		GO:0009699//phenylpropanoid biosynthetic process
7197777	110	85	55	73.12	0.410834452	0.0495434	PHATRDRAFT_26176	K03233|1|2e-74|278|ppp:PHYPADRAFT_206386|elongation factor 1-gamma	GO:0043234//protein complex	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7204631	114	88	18.67	24.77	0.407871941	0.0465016	PHATR_46726	K09313|1|8e-06|52.0|gmx:100780863|homeobox protein cut-like	-	-	-		-
7196879	162	125	20.57	27.27	0.406772906	0.01815082	PHATRDRAFT_43103	-	-	-	-		-
7197411	223	172	25.46	33.74	0.406227554	0.00573712	PHATRDRAFT_43378	-	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7201225	117.54	90.45	44.26	58.58	0.404404742	0.0466218	PHATRDRAFT_36221	-	-	-	-		-
7197033	174	134	25.87	34.24	0.404402648	0.01512548	PHATRDRAFT_43751	-	-	-	-		-
7200668	529	407	168.59	223.03	0.403718817	2.65E-05	PHATRDRAFT_45632	-	-	-	-		-
7198383	161.43	124.02	17.3	22.83	0.400158822	0.01934018	PHATRDRAFT_49814	-	-	-	-		-
7202922	1900.27	1455.52	824.13	1085.84	0.397867702	5.84E-15	PHATRDRAFT_47758	-	-	-	-		-
7198746	297	227	110.01	144.6	0.39443288	0.00211382	PHATRDRAFT_50055	-	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7194833	173	132	134.76	177.08	0.394008945	0.0194426	PHATRDRAFT_29711	K02150|1|2e-35|147|ppp:PHYPADRAFT_223748|V-type H+-transporting ATPase subunit E [EC:3.6.3.14]	GO:0016469//proton-transporting two-sector ATPase complex	GO:0019829//cation-transporting ATPase activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7197932	420	321	102.42	134.57	0.393859358	0.000261726	PHATRDRAFT_44708	K06640|1|9e-93|340|smo:SELMODRAFT_128358|serine/threonine-protein kinase ATR [EC:2.7.11.1]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7197986	749	571	319.15	418.51	0.391027448	1.43E-06	PHATRDRAFT_44260	-	-	-	-		-
7196717	888	677	190.04	249.04	0.39007437	1.54E-07	PHATRDRAFT_43085	-	-	-	-		-
7200578	163	124	113.04	148.06	0.389348563	0.0249116	PHATRDRAFT_45483	-	-	-	-		-
7203879	133	101	68.1	88.99	0.385988428	0.0438906	Prk	K00855|1|1e-117|421|zma:100279820|phosphoribulokinase [EC:2.7.1.19]	GO:0009526//plastid envelope;GO:0009579//thylakoid;GO:0044434	GO:0032550;GO:0016301//kinase activity	GO:0044238;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress		GO:0044238;GO:0006796//phosphate-containing compound metabolic process;GO:0006950//response to stress

7198226	1044	792	497.39	649.17	0.384218828	2.44E-08	PHATRDRAFT_49557	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7195586	1053	798	136.06	177.18	0.380972768	2.43E-08	MER3	K15271|1|3e-94|345|ppp:PHYPADRAFT_122688|ATP-dependent DNA helicase HFM1/MER3 [EC:3.6.4.12]	-	GO:0032550;GO:0042623//ATPase activity, coupled	GO:0006259//DNA metabolic process;GO:0007129//synapsis		GO:0006259//DNA metabolic process;GO:0007129//synapsis
7197954	724	546	543.36	705.66	0.37706487	5.73E-06	PHATRDRAFT_44281	-	-	-	-		-
7199747	989	746	213.26	276.49	0.37461391	1.14E-07	PHATRDRAFT_44788	K14445|1|6e-06|52.0|pop:POPTR_717389|solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7198249	2196	1654	860.44	1114.62	0.373405446	4.19E-15	PHATRDRAFT_49594	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197513	190	143	53.38	69.08	0.371968777	0.0205572	PHATRDRAFT_32929	K15377|1|1e-13|77.4|cre:CHLREDRAFT_189789|solute carrier family 44 (choline transporter-like protein), member 2/4/5	GO:0031224//intrinsic component of membrane	-	-		-
7204809	185.5	139.35	119.22	154.17	0.37089578	0.0232266	PHATRDRAFT_bd976	K01966|1|2e-65|248|cme:CMM132C|propionyl-CoA carboxylase beta chain [EC:6.4.1.3];K01969|2|1e-27|122|ath:AT4G34030|3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	GO:0043234//protein complex	GO:0016421//CoA carboxylase activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7196438	153	115	33.65	43.48	0.369745436	0.0384216	PHATRDRAFT_42841	K14297|1|4e-08|59.3|ath:AT1G10390|nuclear pore complex protein Nup98-Nup96	GO:0005635//nuclear envelope	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	GO:0006406//mRNA export from nucleus		GO:0006406//mRNA export from nucleus
7201876	165	124	25.3	32.68	0.369270599	0.031773	PHATRDRAFT_46608	-	-	-	-		-
7197930	168	126	25.58	32.98	0.366575135	0.0316942	PHATRDRAFT_44703	-	-	-	-		-
7200446	147	110	99.43	128.09	0.365404736	0.0462968	PHATRDRAFT_45662	K09272|1|2e-06|51.6|pop:POPTR_577589|structure-specific recognition protein 1;K09273|2|6e-06|50.1|ppp:PHYPADRAFT_210318|upstream-binding transcription factor	-	-	-		-
7204585	147	110	39.26	50.5	0.363223215	0.0462968	PHATR_46664	-	-	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0044763;GO:0032787//monocarboxylic acid metabolic process		GO:0044763;GO:0032787//monocarboxylic acid metabolic process
7199598	155	116	22.95	29.52	0.363198568	0.0407326	PHATRDRAFT_44896	-	-	GO:0046872//metal ion binding	-		-
7198619	151	113	32.06	41.23	0.362920036	0.043421	PHATRDRAFT_49919	K12874|1|5e-08|58.9|sbi:SORBI_01g033760|intron-binding protein aquarius;K10706|5|1e-06|54.3|pop:POPTR_716529|senataxin [EC:3.6.4.-]	-	-	-		-
7198840	340	254	181.89	233.82	0.362332109	0.0027549	PHATRDRAFT_50136	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated

7204023	1096	817	462.81	593.42	0.358633513	1.09E-07	PHATR_10581	K00323|1|2e-84|311|cre:CHLREDRAFT_139758|NAD(P) transhydrogenase [EC:1.6.1.2]	-	GO:0036094//small molecule binding;GO:0016652//oxidoreductase activity, acting on NAD(P)H, NAD(P) as acceptor	GO:0006818//hydrogen transport;GO:0044710		GO:0006818//hydrogen transport;GO:0044710
7204792	649.85	484.11	229.46	293.96	0.357377175	4.17E-05	FbaC1	K01624|1|1e-116|419|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13];K00120|3|2e-16|86.3|aly:ARALYDRAFT_472044|[EC:1.1.-.-]	-	GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7202870	159	118	166.69	213.25	0.355378184	0.0456068	PHATRDRAFT_47672	-	-	-	-		-
7201668	245	182	81.15	103.66	0.353196299	0.01298144	PHATRDRAFT_27923	K02145|1|0.0|772|ppp:PHYPADRAFT_114420|V-type H+-transporting ATPase subunit A [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex	GO:0032550;GO:0019829//cation-transporting ATPase activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0009150//purine ribonucleotide metabolic process		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient;GO:0009150//purine ribonucleotide metabolic process
7202278	1079	801	502.06	641.19	0.352892138	2.28E-07	PHATRDRAFT_1199	K10268|1|6e-13|73.9|smo:SELMODRAFT_410553|F-box and leucine-rich repeat protein 2/20	-	-	-		-
7205158	304.99	226.13	91.06	116.08	0.35023006	0.00554762	PHATRDRAFT_bd387	K01534|1|1e-139|495|ppp:PHYPADRAFT_125099|Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0008324//cation transmembrane transporter activity;GO:0016787//hydrolase activity	GO:0006812//cation transport		GO:0006812//cation transport
7203220	3362	2492	162.1	206.4	0.34855888	1.23E-19	PHATRDRAFT_47968	-	-	-	-		-
7201024	610	451	395.9	503.89	0.347972758	0.000130272	PsbO	K02716|1|2e-75|281|cme:CMI290C|photosystem II oxygen-evolving enhancer protein 1	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0042548//regulation of photosynthesis, light reaction		GO:0042548//regulation of photosynthesis, light reaction
7197971	208	154	42.72	54.37	0.347899181	0.0239348	PHATRDRAFT_44310	-	-	-	GO:0044763		GO:0044763
7195440	1845	1365	434.92	553.12	0.346842455	2.68E-11	PHATRDRAFT_49084	-	-	-	-		-
7202003	343	253	196.61	249.58	0.344165627	0.00445208	PHATRDRAFT_47080	-	-	-	-		-
7194859	241	178	37.32	47.37	0.344024686	0.01628268	PHATRDRAFT_22629	K05681|1|7e-47|188|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|3|4e-43|176|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7195765	364	268	73.57	93.1	0.339663576	0.00366868	SKP3	K12122|1|3e-39|162|ath:AT4G16250|phytochrome D;K12121|3|1e-38|160|smo:SELMODRAFT_161430|phytochrome B	-	GO:0004673//protein histidine kinase activity;GO:0032550;GO:0004871//signal transducer activity	GO:0009583//detection of light stimulus;GO:0006796//phosphate-containing compound metabolic process;GO:0007165//signal transduction;GO:0006351//transcription, DNA-templated		GO:0009583//detection of light stimulus;GO:0006796//phosphate-containing compound metabolic process;GO:0007165//signal transduction;GO:0006351//transcription, DNA-templated
7197464	208	153	30.57	38.64	0.337978542	0.0282654	PHATRDRAFT_43586	-	-	-	GO:0033124//regulation of GTP catabolic process		GO:0033124//regulation of GTP catabolic process
7203006	517	379	313.28	395.29	0.335458788	0.000697298	PHATRDRAFT_48011	-	-	-	-		-
7199440	470	345	76.77	96.84	0.335060431	0.001140358	PHATRDRAFT_50602	-	-	-	-		-
7204405	314	230	220.56	278.16	0.3347438	0.00835032	PHATR_4227	K07393|1|2e-82|304|cre:CHLREDRAFT_102428|putative glutathione S-transferase	-	-	-		-
7202587	863	632	64.66	81.35	0.331268838	1.33E-05	PHATRDRAFT_21660	K07203|1|0.0|1245|vcn:VOLCADRAFT_65073|FKBP12-rapamycin complex-associated protein	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process

7205026	869	633	937.9	1177.84	0.32863756	2.02E-05	PHATRDRAFT_bd176	K00540|1|9e-43|171|ath:AT3G27620|[EC:1.-.-.-]	GO:0016020//membrane	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710;GO:0044707		GO:0044710;GO:0044707
7195529	207	151	25.88	32.44	0.325936202	0.0351848	PHATRDRAFT_49228	-	-	-	-		-
7197473	228	166	146.25	183.29	0.325691452	0.0285834	PHATRDRAFT_25379	K00286|1|2e-59|228|vcn:VOLCADRAFT_80899|pyrroline-5-carboxylate reductase [EC:1.5.1.2]	-	GO:0016646//oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;GO:0036094//small molecule binding	GO:0006561//proline biosynthetic process		GO:0006561//proline biosynthetic process
7204835	1193	866	1741.74	2182.58	0.325505255	9.12E-07	PHATRDRAFT_bd719	-	-	-	-		-
7204535	2456	1790	503.96	631.31	0.325039374	7.19E-13	PHATR_46775	K13211|1|9e-10|64.7|smo:SELMODRAFT_161477|GC-rich sequence DNA-binding factor	-	-	-		-
7197142	800	582	132.72	165.93	0.322188956	4.79E-05	PHATRDRAFT_43416	K12115|1|2e-06|53.9|osa:4341923|clock-associated PAS protein ZTL	-	GO:0005488//binding	-		-
7196480	288	209	117.54	146.71	0.319815407	0.01555926	PHATRDRAFT_31906	K00294|1|9e-175|611|ppp:PHYPADRAFT_207743|1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7199325	1295	940	310.05	386.87	0.319347969	3.16E-07	PHATRDRAFT_50489	K08850|1|2e-23|109|zma:100191291|aurora kinase, other [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195107	433	314	92.4	115.17	0.317800209	0.0031723	PHATRDRAFT_48799	K14674|1|4e-52|205|ota:Ot06g03440|TAG lipase / steryl ester hydrolase / phospholipase A2 / LPA acyltransferase [EC:3.1.1.3 3.1.1.13 3.1.1.4 2.3.1.51]	-	GO:0003824//catalytic activity	GO:0044238		GO:0044238
7201323	283	205	130.02	162.03	0.317527395	0.0174314	PHATRDRAFT_46079	-	-	-	-		-
7199386	264	191	208.86	260.25	0.317361944	0.0223998	PHATRDRAFT_50556	-	-	-	-		-
7196961	196	142	64.27	80.07	0.317116334	0.047148	PHATRDRAFT_25067	K13412|1|7e-85|313|vvi:100265650|calcium-dependent protein kinase [EC:2.7.11.1];K00924|2|3e-84|311|ath:AT5G12180|[EC:2.7.1.-]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195793	203	147	51.51	64.12	0.315921885	0.043923	PHATRDRAFT_49415	-	-	-	-		-
7204105	428	310	58.73	73.1	0.315773768	0.0035391	PHATR_44189	K13356|1|4e-12|73.2|bdi:100842081|fatty acyl-CoA reductase [EC:1.2.1.-]	-	GO:0036094//small molecule binding;GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0043168//anion binding;GO:0016740//transferase activity	-		-
7202232	195	141	87.45	108.78	0.314883042	0.0498282	PHATRDRAFT_46995	K07034|1|6e-06|50.8|cme:CMM079C|	-	-	-		-
7204049	1623	1173	289.56	359.67	0.312811508	2.09E-08	PHATR_25840	K00323|1|0.0|815|cre:CHLREDRAFT_139758|NAD(P) transhydrogenase [EC:1.6.1.2]	GO:0031224//intrinsic component of membrane	GO:0008746//NAD(P)+ transhydrogenase activity;GO:0000166//nucleotide binding	GO:0006818//hydrogen transport;GO:0044710		GO:0006818//hydrogen transport;GO:0044710
7199804	227	164	26.23	32.56	0.311882892	0.0352786	PHATRDRAFT_44878	-	-	-	-		-
7202301	222	160	65.45	81.1	0.309308722	0.0396218	GPT1	-	-	GO:0008374//O-acyltransferase activity	-		-
7196946	354	255	28.85	35.7	0.307352755	0.00975508	PHATRDRAFT_43220	-	-	-	-		-

7202107	250	180	37.94	46.94	0.307098163	0.0299294	PHATRDRAFT_47011	K11654|1|0.0|760|ppp:PHYPADRAFT_216086|SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [EC:3.6.4.-]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0003682//chromatin binding;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006338//chromatin remodeling		GO:0006338//chromatin remodeling
7198789	810	582	222.91	275.36	0.304857663	0.000118093	PHATRDRAFT_30786	K01805|1|9e-124|442|aly:ARALYDRAFT_918943|xylose isomerase [EC:5.3.1.5]	GO:0043231//intracellular membrane-bounded organelle;GO:0031090//organelle membrane	GO:0043169//cation binding;GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006007//glucose catabolic process;GO:0019321//pentose metabolic process		GO:0006007//glucose catabolic process;GO:0019321//pentose metabolic process
7197075	8669.23	6217.59	5048.49	6231.58	0.303746058	1.38E-35	PHATRDRAFT_43305	-	-	-	-		-
7203735	263	188	268.86	331.27	0.301152426	0.031807	PHATRDRAFT_48309	-	-	-	-		-
7195699	257	184	131.6	162.11	0.300813599	0.0323896	PHATRDRAFT_15730	K01634|1|3e-95|347|smo:SELMODRAFT_411607|sphinganine-1-phosphate aldolase [EC:4.1.2.27]	-	GO:0016830//carbon-carbon lyase activity;GO:0043168//anion binding	GO:0043436		GO:0043436
7195545	353	253	62.37	76.82	0.300629705	0.01185354	PHATRDRAFT_49250	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7202348	218	156	94.3	116.07	0.299665459	0.0490756	PHATRDRAFT_47257	-	-	-	-		-
7202394	1429	1022	795.53	979.12	0.299569349	6.04E-07	PHATRDRAFT_47332	-	-	GO:0046906//tetrapyrrole binding	-		-
7197737	3412	2444	166.67	205.09	0.299262701	8.07E-15	PHATRDRAFT_44441	K13420|1|3e-21|105|ath:AT5G46330|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7198839	337	241	49.66	61.03	0.297434329	0.01501918	PHATRDRAFT_50132	K14327|1|4e-81|302|rcu:RCOM_1070440|regulator of nonsense transcripts 2	-	GO:0003676//nucleic acid binding	GO:0044260		GO:0044260
7199432	312	223	37.19	45.68	0.296647903	0.01957352	Sec7C	K13462|1|7e-34|145|rcu:RCOM_0708240|guanine nucleotide-exchange factor	-	GO:0005083//small GTPase regulator activity	GO:0032011//ARF protein signal transduction		GO:0032011//ARF protein signal transduction
7200761	888	633	785.69	964.93	0.296464089	0.000108745	PHATRDRAFT_20167	K11098|1|1e-25|115|vcn:VOLCADRAFT_109863|small nuclear ribonucleoprotein F	GO:0044444//cytoplasmic part;GO:0030529//ribonucleoprotein complex;GO:0031981//nuclear lumen	GO:0097159//organic cyclic compound binding	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7202857	18857	13428	6370.96	7801.33	0.292209321	3.91E-70	PHATRDRAFT_47667	K14683|1|1e-59|229|zma:100501653|solute carrier family 34 (sodium-dependent phosphate cotransporter)	-	GO:0015114//phosphate ion transmembrane transporter activity	GO:0006817//phosphate ion transport		GO:0006817//phosphate ion transport
7201331	354	252	98.58	120.65	0.291461029	0.01494848	PHATRDRAFT_35971	K09533|1|6e-08|58.2|smo:SELMODRAFT_165973|DnaJ homolog subfamily C member 13	-	-	-		-
7195771	1505.45	1071.95	235.88	288.63	0.291168161	6.05E-07	PHATRDRAFT_49379	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7199125	676	481	242.21	296.37	0.291140988	0.000817374	PHATRDRAFT_50288	-	-	-	-		-
7204210	3896	2772	1428.62	1748.07	0.291140734	1.10E-15	PHATR_44009	-	-	-	-		-
7199877	244	173	74.1	90.33	0.285731666	0.0473842	PHATRDRAFT_44756	K05681|1|1e-37|156|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|2e-34|146|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K05643|4|2e-13|76.6|olu:OSTLU_42103|ATP-binding cassette, subfamily A (ABC1), member 3;K05641|5|1e-12|73.6|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process

7200964	567	402	103.06	125.58	0.28512222	0.00261924	CDKA1	K02206|1|5e-105|381|osa:4331415|cyclin-dependent kinase 2 [EC:2.7.11.22]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0044763;GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0044763;GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7198208	2055	1455	1072.31	1306.39	0.28486361	1.40E-08	PHATRDRAFT_49596	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7201200	3509	2484	1099.64	1338.47	0.283553512	1.33E-13	PHATRDRAFT_46243	-	-	GO:0008233//peptidase activity	-		-
7203858	900	636	438.32	532.91	0.281907397	0.000199027	PHATR_10260	K00323|1|9e-88|322|vcn:VOLCADRAFT_80229|NAD(P) transhydrogenase [EC:1.6.1.2]	GO:0031224//intrinsic component of membrane	GO:0008746//NAD(P)+ transhydrogenase activity;GO:0000166//nucleotide binding	GO:0044710		GO:0044710
7195398	575	406	165.81	201.29	0.279744483	0.00303766	PHATRDRAFT_48999	-	GO:0016021//integral component of membrane	GO:0008028//monocarboxylic acid transmembrane transporter activity	GO:0015727//lactate transport		GO:0015727//lactate transport
7197434	865	611	100.31	121.75	0.279456336	0.000273838	PHATRDRAFT_43423	-	-	-	-		-
7199096	364	257	89.7	108.87	0.279426572	0.01818072	PHATRDRAFT_50241	-	-	-	-		-
7204574	476	336	117.3	142.33	0.279036769	0.00705368	PHATR_46648	-	-	-	-		-
7197557	819	578	82.4	99.92	0.27812914	0.000424548	PHATRDRAFT_32738	-	-	-	-		-
7204993	1646.73	1158.48	762.45	922.77	0.27532837	9.35E-07	PHATRDRAFT_bd1770	-	-	-	-		-
7200165	1345	944	501.3	605.1	0.271499351	1.21E-05	PHATRDRAFT_34685	K05681|1|3e-77|288|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|2e-57|221|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K02065|4|8e-15|80.5|pop:POPTR_275971|putative ABC transport system ATP-binding protein	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7204815	411.4	288.66	165.13	199.28	0.271194681	0.0161484	PHATRDRAFT_bd1572	K01689|1|6e-148|522|olu:OSTLU_28765|enolase [EC:4.2.1.11]	GO:0043234//protein complex	GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7198061	372	261	46.11	55.59	0.269745716	0.021111	PHATRDRAFT_44406	K00849|1|5e-06|53.1|cme:CMN198C|galactokinase [EC:2.7.1.6]	GO:0044424	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7199724	438	307	144.13	173.71	0.269310151	0.0129106	PHATRDRAFT_44750	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7200960	499	350	63.9	77.01	0.269229865	0.00775194	PHATRDRAFT_45854	K14297|1|1e-29|131|smo:SELMODRAFT_139717|nuclear pore complex protein Nup98-Nup96	GO:0005635//nuclear envelope	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7203517	2494	1742	2727.54	3284.64	0.268134904	6.87E-09	PHATRDRAFT_48195	-	-	-	-		-
7204137	1124	785	705.14	847.7	0.265644065	9.98E-05	PHATR_44234	-	GO:0031224//intrinsic component of membrane	-	-		-
7197797	2651	1855	149.3	179.47	0.265528539	1.59E-09	PHATRDRAFT_44551	-	-	-	-		-
7200105	1248	871	229.12	274.83	0.262436097	4.44E-05	PHATRDRAFT_45225	-	-	-	GO:0044763		GO:0044763
7202897	3690	2567	4055.76	4864.57	0.262340001	5.90E-12	PHATRDRAFT_47715	-	-	-	-		-
7199411	5901	4114	1731.23	2075.16	0.261425172	1.23E-18	PHATRDRAFT_50525	-	-	GO:0036094//small molecule binding	-		-
7201567	472	329	48.31	57.86	0.26024447	0.01243852	PHATRDRAFT_46476	-	-	GO:0016740//transferase activity	-		-
7197898	25346.62	17661.55	5068.14	6069.79	0.260190226	5.07E-74	SMP1	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7196901	322	224	144.61	173.05	0.259021621	0.0408654	PHATRDRAFT_32292	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7199707	2030	1408	1615.72	1930.14	0.256528291	5.24E-07	PHATRDRAFT_44725	-	-	-	-		-

7195918	1701	1176	1357.14	1616.03	0.251884426	6.63E-06	PHATRDRAFT_49431	-	-	-	-		-
7196652	2071	1432	956.2	1137.43	0.250393451	6.56E-07	Fba4	K00640|1|7e-35|146|cme:CMA007C|serine O-acetyltransferase [EC:2.3.1.30]	GO:0005737//cytoplasm	GO:0016832//aldehyde-lyase activity;GO:0016412//serine O-acyltransferase activity	GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process		GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process
7205121	465	321	404.36	480.89	0.250066636	0.01917664	PHATRDRAFT_bd1023	K00428|1|9e-83|304|cre:CHLREDRAFT_192806|cytochrome c peroxidase [EC:1.11.1.5]	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7198774	775	536	114.45	136.02	0.249101334	0.00227008	PHATRDRAFT_49989	-	-	GO:0046914//transition metal ion binding	-		-
7204031	1910	1320	409.43	486.36	0.248407765	1.91E-06	PHATR_44098	-	-	-	-		-
7203376	4639.11	3199.31	2453.81	2911.9	0.246937267	2.52E-13	GapC2a	K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0044710;GO:0019318//hexose metabolic process		GO:0044710;GO:0019318//hexose metabolic process
7201241	409	282	242.26	287.48	0.246905373	0.0291326	PHATRDRAFT_12562	K10592|1|3e-119|426|aly:ARALYDRAFT_684483|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7204214	1771	1217	1028.6	1216.5	0.242054261	9.54E-06	PHATR_44015	-	-	-	-		-
7196626	551	379	53.74	63.52	0.241214591	0.0127218	PHATRDRAFT_42441	-	-	-	-		-
7203723	608.17	417.91	241.9	285.89	0.241049388	0.01020122	PHATRDRAFT_38713	-	GO:0043231//intracellular membrane-bounded organelle	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7198614	405	278	270.6	319.77	0.240872756	0.0347174	PHATRDRAFT_16401	K15275|1|1e-20|98.6|ath:AT1G14360|solute carrier family 35 (UDP-galactose transporter), member B1	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7204014	627	431	51.26	60.54	0.240055197	0.00815008	PHATR_44065	-	-	-	-		-
7195310	977	671	94.04	110.97	0.238823262	0.001037452	PHATRDRAFT_49065	K12865|1|1e-14|82.0|zma:100280668|polyglutamine-binding protein 1	-	-	GO:0006901//vesicle coating		GO:0006901//vesicle coating
7196998	1063	730	83.61	98.65	0.238643548	0.000628678	PHATRDRAFT_32970	-	-	-	-		-
7197940	6168	4231	1786.44	2106.88	0.238020686	3.30E-16	PHATRDRAFT_44259	-	-	-	-		-
7197429	793	543	402.61	474.34	0.236538526	0.00372048	PHATRDRAFT_43413	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196272	870	596	250.54	295.09	0.236114076	0.00231352	PHATRDRAFT_42577	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196230	2028	1385	1254.32	1474.48	0.233300801	5.31E-06	PHATRDRAFT_43020	-	-	-	-		-
7200345	677	463	129.54	152.26	0.233139334	0.00780076	PHATRDRAFT_45171	-	-	-	-		-
7203859	2917	1995	177.68	208.76	0.232564009	3.61E-08	PHATR_44084	-	-	-	-		-
7203187	1167	798	90.83	106.7	0.232319391	0.000492398	PHATRDRAFT_47936	-	-	-	-		-
7204522	473	323	58.25	68.36	0.230894347	0.0274042	PHATR_46752	-	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7201614	604	411	492.05	576.71	0.229041115	0.01499964	PHATRDRAFT_46343	-	-	-	-		-
7198446	2639	1800	215.81	252.9	0.22880532	2.62E-07	PHATRDRAFT_49767	K10691|1|2e-25|117|ppp:PHYPADRAFT_206047|E3 ubiquitin-protein ligase UBR4 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0048731;GO:0032446//protein modification by small protein conjugation;GO:0009791//post-embryonic development;GO:0009653//anatomical structure morphogenesis		GO:0048731;GO:0032446//protein modification by small protein conjugation;GO:0009791//post-embryonic development;GO:0009653//anatomical structure morphogenesis
7196786	515	351	71.7	83.98	0.228072669	0.023112	PHATRDRAFT_25	K01529|1|0.0|1399|rcu:RCOM_1469910|[EC:3.6.1.-]	-	GO:0042623//ATPase activity, coupled;GO:0032550	-		-
7198435	1488	1014	112.52	131.73	0.227402483	0.000120318	PHATRDRAFT_49748	K03235|1|3e-40|167|olu:OSTLU_36160|elongation factor 3	-	-	-		-

7196462	644	437	721.08	843.69	0.226553674	0.01372246	PHATRDRAFT_42882	-	-	-	-		-
7205005	2839	1930	1474.38	1724.65	0.226195205	1.76E-07	PHATRDRAFT_bd1650	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7195651	6960	4718	3177.79	3705.78	0.221753447	1.09E-15	PHATRDRAFT_49151	-	-	GO:0036094//small molecule binding	-		-
7197727	621	421	176.21	205.39	0.221070141	0.01616832	PHATRDRAFT_26173	K03695|1|0.0|707|smo:SELMODRAFT_159833|ATP-dependent Clp protease ATP-binding subunit ClpB	-	GO:0032550;GO:0016462//pyrophosphatase activity	-		-
7203651	425	288	51.52	59.99	0.219589438	0.0468572	PHATRDRAFT_48390	-	-	-	-		-
7200037	2589	1751	1601.29	1864.12	0.219260125	1.47E-06	PHATRDRAFT_45349	-	-	-	-		-
7202701	22947.04	15526.5	3759.34	4371.41	0.217619296	8.57E-47	PHATRDRAFT_47693	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7204107	1856	1254	276.75	321.33	0.215472363	5.11E-05	PHATR_44192	-	-	-	-		-
7201520	478.97	323.49	44.37	51.49	0.214707717	0.0388452	PHATRDRAFT_46029	-	GO:0043234//protein complex	GO:0008092//cytoskeletal protein binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7199280	5153	3477	1901.21	2206.21	0.214652227	2.38E-11	PHATRDRAFT_50491	-	-	-	-		-
7198165	4737	3177	752.06	866.8	0.204851387	8.66E-10	PYC1	K01958|1|0.0|1176|ota:Ot08g00930|pyruvate carboxylase [EC:6.4.1.1];K01968|5|5e-91|335|gmx:548094|3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	-	GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0003676//nucleic acid binding;GO:0016885;GO:0032550	GO:0006006//glucose metabolic process		GO:0006006//glucose metabolic process
7203381	4851.89	3245.69	2558.13	2944.63	0.202996786	1.15E-09	GapC2b	K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0044710;GO:0019318//hexose metabolic process		GO:0044710;GO:0019318//hexose metabolic process
7201366	3584	2399	201.57	231.78	0.201475147	1.45E-07	PHATRDRAFT_36043	K10592|1|7e-32|140|ppp:PHYPADRAFT_137606|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	-	-	-		-
7197960	542	361	326.62	374.44	0.197121426	0.0478632	PHATRDRAFT_44297	-	-	-	-		-
7199039	668	445	335.52	384.57	0.196847457	0.0280036	PHATRDRAFT_50281	K01555|1|1e-98|358|ath:AT1G12050|fumarylacetoacetase [EC:3.7.1.2]	-	GO:0016823	GO:0006520//cellular amino acid metabolic process		GO:0006520//cellular amino acid metabolic process
7196470	2244	1497	120.49	138.09	0.196695433	4.94E-05	PHATRDRAFT_42892	K08874|1|6e-81|303|aly:ARALYDRAFT_480691|transformation/transcription domain-associated protein	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7200474	1209	806	107.93	123.63	0.19593294	0.00300596	PHATRDRAFT_45703	K04498|1|3e-80|300|vvi:100251243|E1A/CREB-binding protein [EC:2.3.1.48]	GO:0043231//intracellular membrane-bounded organelle	GO:0000989//transcription factor binding transcription factor activity;GO:0046914//transition metal ion binding;GO:0008080//N-acetyltransferase activity	GO:0016570//histone modification;GO:0006351//transcription, DNA-templated		GO:0016570//histone modification;GO:0006351//transcription, DNA-templated
7198717	2595	1727	522.37	597.52	0.193914959	1.84E-05	PHATRDRAFT_50019	-	-	-	-		-
7201728	7522	4994	6196.89	7086.78	0.193585904	8.52E-13	PHATRDRAFT_46597	-	-	-	-		-
7202471	9559	6344	5968.37	6818.13	0.192039131	9.12E-16	PHATRDRAFT_37667	-	-	GO:0036094//small molecule binding	-		-
7201046	864	573	350	399.25	0.189937486	0.01591936	PHATRDRAFT_51970	K00029|1|2e-141|501|rcu:RCOM_1489870|malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]	-	GO:0004470//malic enzyme activity;GO:0000166//nucleotide binding;GO:0043169//cation binding	GO:0043648//dicarboxylic acid metabolic process		GO:0043648//dicarboxylic acid metabolic process
7203234	1757	1163	883.84	1006.6	0.187633373	0.000726616	PHATRDRAFT_47994	-	-	-	-		-
7204205	624	412	512.15	582.46	0.185592564	0.0477582	PHATR_44000	-	-	-	-		-

7194914	757	500	133.28	151.3	0.182951682	0.0288912	TPS2	K16055|1|8e-101|367|sbi:SORBI_09g025660|trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	-	-	GO:0005991//trehalose metabolic process		GO:0005991//trehalose metabolic process
7195317	1829	1204	214.45	242.57	0.177759819	0.000985714	PHATRDRAFT_39708	K05643|1|5e-91|335|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3;K05641|5|6e-66|252|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7203656	4030	2650	1005.52	1136.64	0.176833614	1.29E-06	PHATRDRAFT_51134	K03695|1|0.0|846|bdi:100825913|ATP-dependent Clp protease ATP-binding subunit ClpB	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006950//response to stress;GO:0043170		GO:0006950//response to stress;GO:0043170
7202950	10445	6843	2413.74	2718.27	0.171418481	4.51E-14	PHATRDRAFT_54800	K09835|1|7e-12|71.6|rcu:RCOM_0422660|prolycopene isomerase [EC:5.2.1.13]	-	GO:0003824//catalytic activity	-		-
7195163	6068	3961	4121.32	4631.66	0.168422866	2.55E-08	Lhcf15	K08907|1|9e-09|59.3|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08910|2|3e-07|54.3|cme:CMQ142C|light-harvesting complex I chlorophyll a/b binding protein 4	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7200457	1019	666	221.54	248.88	0.167883093	0.0206296	PHATRDRAFT_45673	K12309|1|8e-45|181|aly:ARALYDRAFT_485655|beta-galactosidase [EC:3.2.1.23];K01190|3|5e-29|128|cme:CMP078C|beta-galactosidase [EC:3.2.1.23]	-	GO:0015925	GO:0044238		GO:0044238
7197444	868	566	337.88	378.94	0.165458479	0.0362856	PHATRDRAFT_43441	-	-	-	-		-
7199090	2500	1627	2344.41	2629.13	0.165360583	0.000500278	PHATRDRAFT_50224	-	-	-	-		-
7204391	1407	917	473.66	530.84	0.164425242	0.00807118	PHATR_43978	-	-	GO:0003824//catalytic activity	-		-
7204333	1005	655	303.51	340.12	0.164299792	0.0250136	PHATR_43872	-	-	-	-		-
7200555	1902	1232	2795.45	3125.91	0.161195701	0.00367152	HSP20A	K13993|1|2e-09|59.7|aly:ARALYDRAFT_489869|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7200644	1536	997	642.01	716.79	0.158954741	0.00771386	PHATRDRAFT_56608	K00218|1|2e-81|301|sbi:SORBI_06g033030|protochlorophyllide reductase [EC:1.3.1.33]	-	GO:0036094//small molecule binding;GO:0016628//oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7204427	2369	1537	700.64	781.57	0.157701737	0.000995088	PHATR_46872	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200113	3635	2344	691.5	766.38	0.148330661	0.000123661	PHATRDRAFT_45239	K00261|1|3e-07|56.6|pop:POPTR_828764|glutamate dehydrogenase (NAD(P)+) [EC:1.4.1.3]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7197071	3543.77	2281.41	957.62	1059.87	0.146362131	0.000192553	PHATRDRAFT_43297	-	-	-	-		-
7203865	3962	2543	1770.85	1955.25	0.14291107	0.000133564	HSF1	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus		GO:0006351//transcription, DNA-templated;GO:0050896//response to stimulus
7201122	2036	1308	150.38	165.97	0.142309783	0.00564878	PHATRDRAFT_45889	-	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7195544	7146	4582	2489.81	2745.37	0.140964945	3.92E-07	PHATRDRAFT_15815	K01507|1|0.0|655|olu:OSTLU_48479|inorganic pyrophosphatase [EC:3.6.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0016462//pyrophosphatase activity;GO:0015405	GO:0006818//hydrogen transport		GO:0006818//hydrogen transport
7197249	2175	1393	918.44	1011.8	0.139666763	0.0056367	PHATRDRAFT_43716	-	-	-	-		-
7196924	2474	1582	1904.56	2097.39	0.139137411	0.0037133	PHATRDRAFT_43175	-	-	-	-		-
7200373	2951	1883	3108.5	3419.29	0.137478208	0.001973622	PHATRDRAFT_45591	-	-	-	-		-

7199988	1636	1046	618.53	680.14	0.136988171	0.01836218	PHATRDRAFT_45361	-	GO:0044424;GO:0031224//intrinsic component of membrane	GO:0016491//oxidoreductase activity	GO:0044238		GO:0044238
7194909	1531	969	68.77	74.77	0.120680187	0.0424018	PHATRDRAFT_48676	K03254|1|1e-10|69.7|rcu:RCOM_1434190|translation initiation factor 3 subunit A	-	GO:0097159//organic cyclic compound binding	-		-
7201088	10623	6714	1503.85	1633.31	0.119137964	1.62E-07	PHATRDRAFT_45835	K12385|1|6e-18|92.4|gmx:100795551|Niemann-Pick C1 protein	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity	-		-
7194806	5037	3153	522.06	561.49	0.105044705	0.001489138	ACC1	K11262|1|0.0|2003|ota:Ot01g03240|acetyl-CoA carboxylase / biotin carboxylase [EC:6.4.1.2 6.3.4.14]	-	GO:0016421//CoA carboxylase activity;GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7200932	4264	2669	358.88	385.94	0.104875051	0.00348286	PHATRDRAFT_45802	K10590|1|2e-18|68.9|ppp:PHYPADRAFT_188237|E3 ubiquitin-protein ligase TRIP12 [EC:6.3.2.19]	GO:0044464	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7199425	2031	1269	661.37	710.57	0.103519174	0.049017	PHATRDRAFT_50604	-	-	-	-		-
7203043	3061	1904	379.91	406.06	0.096035231	0.0239512	CHC	K04646|1|0.0|1461|rcu:RCOM_0838580|clathrin heavy chain	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7197844	4165	2578	1691.4	1800.71	0.090347974	0.01497256	PHATRDRAFT_18911	-	GO:0044424	GO:0032550;GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0016211	GO:0006412//translation;GO:0006528//asparagine metabolic process		GO:0006412//translation;GO:0006528//asparagine metabolic process
7199146	5515	3384	2870.91	3031.15	0.078357143	0.0166706	PHATRDRAFT_50366	K11498|1|1e-06|52.8|aly:ARALYDRAFT_478343|centromeric protein E	-	-	-		-
7203153	12966	7889	1953.32	2042.36	0.064308872	0.00215236	PPdK	K01006|1|0.0|857|vvi:100247690|pyruvate,orthophosphate dikinase [EC:2.7.9.1]	-	GO:0032550;GO:0016781//phosphotransferase activity, paired acceptors	GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process
7199668	9	0	26.9	0.001	-14.71531855	0.0203264	PHATRDRAFT_7755	K00327|1|6e-08|53.9|mtr:MTR_4g128020|NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity;GO:0032553	GO:0044710		GO:0044710
7195292	10	0	24.83	0.001	-14.59979664	0.01284586	PHATRDRAFT_15516	K09420|1|5e-30|127|olu:OSTLU_34891|myb proto-oncogene protein;K09422|2|9e-30|126|aly:ARALYDRAFT_914801|myb proto-oncogene protein, plant	GO:0043231//intracellular membrane-bounded organelle	GO:0003712//transcription cofactor activity;GO:0001071//nucleic acid binding transcription factor activity;GO:0003676//nucleic acid binding	GO:0006351//transcription, DNA-templated;GO:0006261//DNA-dependent DNA replication;GO:0006461//protein complex assembly;GO:0034285;GO:0048446//petal morphogenesis;GO:0048868//pollen tube development;GO:0010564//regulation of cell cycle process;GO:0048447;GO:0009746;GO:0048285;GO:0009563;GO:0000086//G2/M transition of mitotic cell cycle;GO:0015851//nucleoba		GO:0006351//transcription, DNA-templated;GO:0006261//DNA-dependent DNA replication;GO:0006461//protein complex assembly;GO:0034285;GO:0048446//petal morphogenesis;GO:0048868//pollen tube development;GO:0010564//regulation of cell cycle process;GO:0048447;GO:0009746;GO:0048285;GO:0009563;GO:0000086//G2/M transition of mitotic cell cycle;GO:0015851//nucleoba

7200623	8	0	24.58	0.001	-14.5851973	0.032163	PHATRDRAFT_12221	K09503|1|5e-12|67.4|cme:CML030C|DnaJ homolog subfamily A member 2;K09531|2|8e-12|66.6|vcn:VOLCADRAFT_95730|DnaJ homolog subfamily C member 11;K09506|3|1e-11|65.9|rcu:RCOM_1469860|DnaJ homolog subfamily A member 5	-	-	-		-
7205068	25.24	0	22.67	0.001	-14.46849677	1.32E-05	PHATRDRAFT_bd1622	-	-	-	-		-
7196734	12	0	18.46	0.001	-14.17211493	0.00513062	PHATRDRAFT_51454	K03801|1|9e-44|173|cre:CHLREDRAFT_50452|lipoyl(octanoyl) transferase [EC:2.3.1.181]	GO:0043231//intracellular membrane-bounded organelle	GO:0016747//transferase activity, transferring acyl groups other than amino-acyl groups	GO:0006633//fatty acid biosynthetic process;GO:0036211		GO:0006633//fatty acid biosynthetic process;GO:0036211
7195757	28.46	0	17.93	0.001	-14.13008787	3.32E-06	PHATRDRAFT_49351	-	-	-	-		-
7200485	9	0	13.69	0.001	-13.74083483	0.0203264	PHATRDRAFT_35081	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7201891	10	0	12.96	0.001	-13.6617781	0.01284586	PHATRDRAFT_36647	-	-	-	-		-
7196521	10	0	11.97	0.001	-13.54713553	0.01284586	PHATRDRAFT_31979	-	-	-	-		-
7200193	8	0	11.16	0.001	-13.44604941	0.032163	PHATRDRAFT_11527	K01609|1|4e-25|112|zma:100382674|indole-3-glycerol phosphate synthase [EC:4.1.1.48]	-	GO:0016833//oxo-acid-lyase activity;GO:0016831//carboxy-lyase activity;GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006568//tryptophan metabolic process;GO:0008652//cellular amino acid biosynthetic process		GO:0006568//tryptophan metabolic process;GO:0008652//cellular amino acid biosynthetic process
7201059	17	0	10.29	0.001	-13.32895536	0.00051723	PHATRDRAFT_35856	-	-	-	-		-
7196931	11.54	0	8.57	0.001	-13.06507949	0.00811832	PHATRDRAFT_9308	-	-	GO:0016787//hydrolase activity	-		-
7203244	11	0	8.52	0.001	-13.05663772	0.00811832	PHATRDRAFT_14412	K03110|1|1e-47|187|smo:SELMODRAFT_77470|fused signal recognition particle receptor	-	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006613//cotranslational protein targeting to membrane		GO:0006613//cotranslational protein targeting to membrane
7200184	14.19	0	8.47	0.001	-13.04814625	0.00204916	PHATRDRAFT_34724	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202849	15	0	6.95	0.001	-12.76279726	0.001295026	PHATRDRAFT_37927	-	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0018130;GO:0044710		GO:0018130;GO:0044710
7202848	13	0	6.62	0.001	-12.6926155	0.00324244	PHATRDRAFT_28937	K00766|1|1e-81|301|vvi:100255305|anthranilate phosphoribosyltransferase [EC:2.4.2.18]	-	GO:0016763//transferase activity, transferring pentosyl groups	GO:0006568//tryptophan metabolic process		GO:0006568//tryptophan metabolic process
7196588	8	0	6.46	0.001	-12.65731845	0.032163	PHATRDRAFT_43229	-	-	-	-		-
7200863	8.25	0	6.13	0.001	-12.58167136	0.032163	PHATRDRAFT_46003	-	-	GO:0005515//protein binding	-		-
7201845	11.37	0	5.37	0.001	-12.39070637	0.00811832	PHATRDRAFT_46561	K00924|1|1e-14|79.3|ath:AT5G22850|[EC:2.7.1.-]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7201308	12	0	4.93	0.001	-12.26737193	0.00513062	PHATRDRAFT_46060	-	-	-	-		-
7199317	10	0	4.83	0.001	-12.23780747	0.01284586	PHATRDRAFT_50473	-	-	-	-		-
7199417	9	0	4.82	0.001	-12.23481743	0.0203264	PHATRDRAFT_50593	-	-	-	-		-
7201256	8	0	4.69	0.001	-12.19537221	0.032163	PHATRDRAFT_36077	-	-	-	-		-
7198487	13.57	0	4.63	0.001	-12.17679648	0.00324244	PHATRDRAFT_49826	K00995|1|2e-23|108|cme:CMN196C|CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5];K08744|2|2e-21|102|pop:POPTR_856644|cardiolipin synthase [EC:2.7.8.-]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006644//phospholipid metabolic process		GO:0006644//phospholipid metabolic process
7199782	11.48	0	3.06	0.001	-11.57931594	0.00811832	PHATRDRAFT_34367	-	-	GO:0043169//cation binding	-		-
7197264	8	0	2.75	0.001	-11.4252159	0.032163	PHATRDRAFT_43742	-	-	-	-		-
7203085	8	0	2.62	0.001	-11.3553511	0.032163	PHATRDRAFT_38186	-	-	-	-		-

7200126	8	0	2.01	0.001	-10.97297979	0.032163	PHATRDRAFT_45254	-	-	-	-		-
7198604	22	1	31.09	2.44	-3.671497564	0.00049351	PHATRDRAFT_40725	-	-	-	-		-
7199505	21	1	31.71	2.61	-3.602816166	0.00075053	PHATRDRAFT_11409	K09272|1|1e-36|149|cme:CMS034C|structure-specific recognition protein 1	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	-		-
7196066	19	1	17.3	1.57	-3.461935574	0.001727102	PHATRDRAFT_42518	-	-	-	-		-
7200512	17	1	12.98	1.31	-3.308651666	0.00394356	PHATRDRAFT_35460	K00100|1|3e-19|94.0|olu:OSTLU_36252|[EC:1.1.1.-];K00218|2|9e-19|92.4|vvi:100255647|protochlorophyllide reductase [EC:1.3.1.33]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201145	17	1	12.46	1.26	-3.30580843	0.00394356	PHATRDRAFT_35771	-	-	-	-		-
7204867	16	1	4.76	0.51	-3.222392421	0.0059388	PHATRDRAFT_bd1647	K11426|1|1e-07|57.4|ota:Ot04g04600|SET and MYND domain-containing protein	-	-	-		-
7203014	15	1	8.12	0.93	-3.126177106	0.00892056	PHATRDRAFT_22117	K01488|1|1e-52|205|smo:SELMODRAFT_138763|adenosine deaminase [EC:3.5.4.4]	-	-	-		-
7199057	15	1	10.85	1.25	-3.117695043	0.00892056	PHATRDRAFT_41231	-	-	-	-		-
7197499	15	1	25.92	2.99	-3.115848329	0.00892056	PHATRDRAFT_43635	-	-	-	-		-
7200786	14	1	4.76	0.58	-3.036836768	0.01336114	PHATRDRAFT_45765	-	-	-	-		-
7201079	14	1	12.13	1.49	-3.025195315	0.01336114	PHATRDRAFT_45827	-	-	-	-		-
7195004	14	1	16.76	2.06	-3.024305907	0.01336114	PHATRDRAFT_15393	K03809|1|1e-52|204|osa:4327039|Trp repressor binding protein	-	GO:0032553;GO:0003824//catalytic activity	GO:0044710;GO:0006351//transcription, DNA-templated		GO:0044710;GO:0006351//transcription, DNA-templated
7195592	14	1	10.62	1.31	-3.019145049	0.01336114	PHATRDRAFT_15797	K05863|1|5e-38|156|cme:CMN084C|solute carrier family 25 (mitochondrial adenine nucleotide translocator), member 4/5/6/31	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7201766	14	1	44.89	5.57	-3.010644864	0.01336114	PHATRDRAFT_13205	K11723|1|2e-08|55.1|rcu:RCOM_1302750|bromodomain-containing protein 7/9	-	GO:0016740//transferase activity	-		-
7198727	13	1	10.67	1.41	-2.919793108	0.01994842	PHATRDRAFT_16490	K00326|1|8e-51|198|olu:OSTLU_6009|cytochrome-b5 reductase [EC:1.6.2.2]	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7194786	13	1	10.36	1.37	-2.918776205	0.01994842	PHATRDRAFT_39038	-	-	-	-		-
7201603	13	1	7.48	0.99	-2.91753784	0.01994842	PHATRDRAFT_36499	-	-	-	-		-
7204618	13	1	10.1	1.34	-2.914050387	0.01994842	PHATR_46707	K08081|1|2e-07|54.7|gmx:100780806|tropine dehydrogenase [EC:1.1.1.206];K07119|2|4e-07|53.5|ath:AT1G49670|	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7200458	13	1	33.03	4.4	-2.908201541	0.01994842	PHATRDRAFT_12188	K03687|1|7e-22|100|smo:SELMODRAFT_117407|molecular chaperone GrpE	GO:0044429//mitochondrial part	GO:0042802//identical protein binding;GO:0030554//adenyl nucleotide binding	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7198738	12	1	6	0.86	-2.802553936	0.0296768	PHATRDRAFT_50043	-	-	-	-		-
7198047	12	1	9.97	1.43	-2.801578358	0.0296768	PHATRDRAFT_26035	K14775|1|1e-41|168|olu:OSTLU_15606|ribosome biogenesis protein UTP30	GO:0044391	GO:0003676//nucleic acid binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7201509	12	1	7.85	1.13	-2.796369881	0.0296768	PHATRDRAFT_36259	K15109|1|2e-08|58.5|bdi:100838576|solute carrier family 25 (mitochondrial carnitine/acylcarnitine transporter), member 20/29	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7199972	12	1	7.64	1.1	-2.796069115	0.0296768	PHATRDRAFT_45334	-	-	-	-		-
7201034	12	1	10	1.44	-2.795859283	0.0296768	PHATRDRAFT_35813	K01872|1|1e-15|81.6|cme:CMG111C|alanyl-tRNA synthetase [EC:6.1.1.7]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7200735	12	1	4.65	0.67	-2.794997716	0.0296768	PHATRDRAFT_45547	-	-	-	-		-
7200092	11	1	4.12	0.64	-2.686500527	0.0439708	PHATRDRAFT_45206	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated

7202612	11	1	5.52	0.86	-2.682259702	0.0439708	PHATRDRAFT_47510	K05275|1|4e-11|67.8|zma:100272747|pyridoxine 4-dehydrogenase [EC:1.1.1.65];K08243|2|2e-07|55.8|mtr:MTR_5g097900|6'-deoxychalcone synthase [EC:2.3.1.170];K00002|4|2e-06|52.4|osa:4338987|alcohol dehydrogenase (NADP+) [EC:1.1.1.2];K15303|5|4e-06|51.2|zma:100274478|aflatoxin B1 aldehyde reductase	GO:0043231//intracellular membrane-bounded organelle	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201620	11	1	7.15	1.12	-2.67444451	0.0439708	PHATRDRAFT_36287	-	-	-	-		-
7197985	11	1	8.8	1.38	-2.672835257	0.0439708	PHATRDRAFT_44523	-	-	-	-		-
7203463	22	2	28.35	4.45	-2.671471494	0.0024427	PHATRDRAFT_38474	K13095|1|9e-08|54.7|sbi:SORBI_01g038690|splicing factor 1;K13154|2|2e-07|53.5|bdi:100826392|U11/U12 small nuclear ribonucleoprotein 31 kDa protein	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding	-		-
7199349	11	1	10.57	1.66	-2.67072023	0.0439708	DET2	K09591|1|5e-38|155|vvi:100261294|probable steroid reductase DET2 [EC:1.3.99.-]	GO:0031224//intrinsic component of membrane;GO:0044424	GO:0016491//oxidoreductase activity	GO:0044710;GO:0044238		GO:0044710;GO:0044238
7197501	11	1	10.76	1.69	-2.670582926	0.0439708	PHATRDRAFT_32902	-	-	GO:0003824//catalytic activity	GO:0044238		GO:0044238
7200694	26.75	2.47	9.35	1.48	-2.659369189	0.00051681	PHATRDRAFT_56583	-	-	-	-		-
7205163	41.43	4.36	22.48	4.07	-2.465541336	3.01E-05	PHATRDRAFT_bd800	K04382|1|3e-139|493|pop:POPTR_547629|protein phosphatase 2 (formerly 2A), catalytic subunit [EC:3.1.3.16]	GO:0016020//membrane;GO:0031981//nuclear lumen	GO:0043169//cation binding;GO:0016791//phosphatase activity	-		-
7202034	19	2	4.08	0.74	-2.462971976	0.00760272	PHATRDRAFT_37257	-	-	GO:0003676//nucleic acid binding	-		-
7194688	18	2	12.4	2.37	-2.387381156	0.01102426	PHATRDRAFT_39235	-	-	-	-		-
7201357	18	2	12.21	2.34	-2.383482765	0.01102426	PHATRDRAFT_36026	-	-	-	-		-
7201666	43	5	32.61	6.53	-2.320159544	5.36E-05	PHATRDRAFT_1196	K13420|1|4e-47|186|sbi:SORBI_06g028760|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7201141	17	2	12.5	2.53	-2.304718805	0.01592266	PHATRDRAFT_35763	K13206|1|4e-13|73.6|bdi:100844521|coiled-coil domain-containing protein 55	-	-	-		-
7195683	17	2	21.65	4.39	-2.30207418	0.01592266	PHATRDRAFT_39869	-	-	-	-		-
7203460	17	2	16.41	3.33	-2.300981156	0.01592266	PHATRDRAFT_48093	-	-	-	-		-
7200374	17	2	7.63	1.55	-2.299414842	0.01592266	PHATRDRAFT_27166	K00058|1|2e-95|348|olu:OSTLU_39000|D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7198125	17	2	4.13	0.84	-2.297680549	0.01592266	PHATRDRAFT_44641	-	-	GO:0046914//transition metal ion binding	-		-
7196985	16.76	1.99	8.35	1.71	-2.287779872	0.0059388	PHATRDRAFT_43278	-	GO:0044424	GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0032550	GO:0006412//translation		GO:0006412//translation
7197091	25	3	13.8	2.85	-2.275634443	0.00291394	PHATRDRAFT_43339	-	-	-	-		-
7195129	16	2	2.68	0.57	-2.233199176	0.0228984	PHATRDRAFT_39392	-	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction;GO:0044764		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction;GO:0044764
7203045	24	3	8.63	1.86	-2.214057938	0.00416546	PHATRDRAFT_47802	-	-	-	-		-
7203754	16	2	11.97	2.58	-2.213980182	0.0228984	PHATRDRAFT_38930	K12251|1|3e-90|329|vvi:100260445|N-carbamoylputrescine amidase [EC:3.5.1.53]	-	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	GO:0006596//polyamine biosynthetic process		GO:0006596//polyamine biosynthetic process
7200316	23	3	19.26	4.33	-2.153168773	0.0059336	PHATRDRAFT_45123	-	-	-	-		-
7203646	38	5	22.67	5.13	-2.14375366	0.000310756	PHATRDRAFT_48383	-	-	-	-		-
7203315	15	2	11.03	2.53	-2.124223501	0.0327746	PHATRDRAFT_48182	-	-	-	-		-

7203482	15	2	3.53	0.81	-2.12367437	0.0327746	PHATRDRAFT_48134	K10400|1|8e-10|64.7|cme:CMO070C|kinesin family member 15	GO:0015630//microtubule cytoskeleton	GO:0003774//motor activity;GO:0032550	GO:0006928//cellular component movement		GO:0006928//cellular component movement
7199958	15	2	10.5	2.41	-2.123284276	0.0327746	PHATRDRAFT_34984	-	-	GO:0097159//organic cyclic compound binding;GO:0046914//transition metal ion binding	-		-
7202584	15	2	6.27	1.44	-2.122396631	0.0327746	PHATRDRAFT_47468	K15446|1|1e-31|135|ppp:PHYPADRAFT_140506|tRNA guanosine-2'-O-methyltransferase TRM13 [EC:2.1.1.-]	-	GO:0016741	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process
7196499	15	2	13.31	3.06	-2.120907013	0.0327746	PHATRDRAFT_31939	K14505|1|5e-06|49.7|vvi:100267897|cyclin D3, plant	-	-	-		-
7200940	15	2	9.96	2.29	-2.120798144	0.0327746	PHATRDRAFT_35627	-	-	GO:0048037//cofactor binding;GO:0036094//small molecule binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7201825	22	3	16.92	3.97	-2.091518656	0.00842052	PHATRDRAFT_46490	K05766|1|9e-18|89.0|ath:AT3G23610|slingshot;K14819|3|7e-08|56.2|zma:100191164|dual specificity phosphatase 12 [EC:3.1.3.16 3.1.3.48]	-	GO:0004721//phosphoprotein phosphatase activity	GO:0006470//protein dephosphorylation		GO:0006470//protein dephosphorylation
7195406	22	3	11.93	2.8	-2.091095311	0.00842052	PHATRDRAFT_49022	-	-	-	-		-
7204760	22	3	35.68	8.4	-2.086654382	0.00842052	PHATR_37006	-	-	GO:0046914//transition metal ion binding;GO:0016491//oxidoreductase activity;GO:0046906//tetrapyrrole binding	GO:0044710		GO:0044710
7200052	14	2	6.33	1.55	-2.029937284	0.0466654	PHATRDRAFT_35067	-	-	-	-		-
7195600	14	2	6.18	1.52	-2.023535514	0.0466654	PHATRDRAFT_49343	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7197235	14	2	8.05	1.98	-2.023488353	0.0466654	PHATRDRAFT_43688	-	-	-	-		-
7199443	21	3	19.92	4.9	-2.023363993	0.01190158	PHATRDRAFT_41604	K14709|1|4e-07|53.1|vcn:VOLCADRAFT_104214|solute carrier family 39 (zinc transporter), member 1/2/3;K01115|5|6e-07|52.8|vcn:VOLCADRAFT_99471|phospholipase D [EC:3.1.4.4]	-	-	-		-
7202657	21	3	10.4	2.56	-2.022367813	0.01190158	PHATRDRAFT_47601	K09833|1|1e-42|172|cme:CMN202C|homogenitisate phytyltransferase	GO:0031224//intrinsic component of membrane	GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	-		-
7204237	21	3	21.4	5.27	-2.02173593	0.01190158	PHATR_51608	K00011|1|1e-26|118|ath:AT2G37790|aldehyde reductase [EC:1.1.1.21];K00002|2|2e-25|113|osa:4338987|alcohol dehydrogenase (NADP+) [EC:1.1.1.2];K08243|3|3e-24|110|gmx:547911|6'-deoxychalcone synthase [EC:2.3.1.170]	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7195081	2262.77	323.86	1257.57	309.74	-2.021509096	3.16E-170	PHATRDRAFT_48827	-	-	-	-		-
7195780	14	2	10.19	2.51	-2.021394782	0.0466654	PHATRDRAFT_40088	-	-	-	-		-
7202248	14	2	7.1	1.75	-2.020464103	0.0466654	PHATRDRAFT_47014	K02357|1|2e-11|68.6|gmx:100797166|elongation factor Ts;K14792|5|1e-08|59.7|osa:4342673|rRNA biogenesis protein RRP5	GO:0009536//plastid	GO:0003676//nucleic acid binding	-		-
7195618	28	4	34.08	8.4	-2.020464103	0.00317024	PHATRDRAFT_42274	-	-	-	-		-
7196015	14	2	18.58	4.58	-2.020330998	0.0466654	PHATRDRAFT_5889	K02731|1|6e-27|118|cme:CMT379C|20S proteasome subunit alpha 4 [EC:3.4.25.1]	GO:0005737//cytoplasm;GO:0005839//proteasome core complex;GO:0043231//intracellular membrane-bounded organelle	GO:0004175//endopeptidase activity	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7196380	14	2	34.38	8.51	-2.014338508	0.0466654	PHATRDRAFT_31810	-	-	-	-		-

7202513	27	4	12.09	3.08	-1.972811989	0.00444638	PHATRDRAFT_47361	K10771|1|4e-53|207|ota:Ot03g02610|AP endonuclease 1 [EC:4.2.99.18];K01142|2|2e-50|198|aly:ARALYDRAFT_483223|exodeoxyribonuclease III [EC:3.1.11.2]	GO:0005622//intracellular	GO:0003676//nucleic acid binding;GO:0004518//nuclease activity	GO:0044763;GO:0006259//DNA metabolic process;GO:0050896//response to stimulus;GO:0070647//protein modification by small protein conjugation or removal		GO:0044763;GO:0006259//DNA metabolic process;GO:0050896//response to stimulus;GO:0070647//protein modification by small protein conjugation or removal
7198423	59	9	16.13	4.23	-1.93101687	2.05E-05	PHATRDRAFT_23444	K06207|1|0.0|666|bdi:100827491|GTP-binding protein	GO:0009536//plastid	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7201347	35.85	5.5	31.18	8.24	-1.919904686	0.000866234	PHATRDRAFT_36006	-	-	-	-		-
7194756	26	4	42.8	11.37	-1.912378542	0.00621322	PHATRDRAFT_6697	-	-	-	-		-
7196090	19	3	14.71	4	-1.878725341	0.02346	PHATRDRAFT_31559	K08500|1|9e-13|72.4|osa:4324558|syntaxin of plants SYP6;K08498|2|2e-10|64.3|aly:ARALYDRAFT_473066|syntaxin 6	-	-	GO:0016192//vesicle-mediated transport		GO:0016192//vesicle-mediated transport
7204698	24	4	11.48	3.29	-1.802963153	0.01198746	PHATR_46846	K14840|1|3e-13|75.1|ota:Ot03g05300|nucleolar protein 53	-	-	-		-
7200840	24	4	10.71	3.07	-1.802647919	0.01198746	PHATRDRAFT_45966	-	-	-	-		-
7194926	24	4	13.04	3.74	-1.801833694	0.01198746	PHATRDRAFT_48697	-	-	GO:0016740//transferase activity	-		-
7203790	18	3	6.38	1.83	-1.801712775	0.032694	PHATRDRAFT_48319	-	-	-	-		-
7197566	18	3	9.76	2.8	-1.801454321	0.032694	PHATRDRAFT_43528	-	-	-	-		-
7194913	18	3	17	4.88	-1.800581693	0.032694	PHATRDRAFT_15102	K02069|1|5e-24|109|cme:CMS400C|putative ABC transport system permease protein	-	-	-		-
7196863	18	3	16.86	4.84	-1.800525584	0.032694	PHATRDRAFT_32219	-	-	-	-		-
7197423	18	3	22.36	6.43	-1.798029546	0.032694	PHATRDRAFT_43398	-	-	-	-		-
7201018	2992.23	504.14	1826.64	529.72	-1.785890446	5.34E-191	PHATRDRAFT_45944	-	-	-	-		-
7204683	94	16	25.87	7.57	-1.772914849	2.99E-07	PHATR_46827	-	-	-	-		-
7198200	88	15	80.01	23.5	-1.767519569	7.44E-07	PHATRDRAFT_40322	-	-	-	-		-
7198121	23	4	10.89	3.26	-1.740060084	0.01654242	VDE	K09839|1|1e-88|325|vvi:100257865|violaxanthin de-epoxidase [EC:1.10.99.3]	GO:0009536//plastid	GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7203317	23	4	17.96	5.38	-1.739109272	0.01654242	PHATRDRAFT_48184	-	-	-	-		-
7197383	40	7	39.66	11.96	-1.729467288	0.001244148	PHATRDRAFT_43323	-	-	-	-		-
7196458	17	3	8.93	2.71	-1.720367324	0.045313	PHATRDRAFT_31982	-	-	-	-		-
7195609	17	3	12.85	3.9	-1.72022233	0.045313	PHATRDRAFT_49141	-	-	-	-		-
7201998	17	3	10.08	3.06	-1.719892081	0.045313	PHATRDRAFT_47076	-	-	-	-		-
7198214	17	3	5.6	1.7	-1.719892081	0.045313	PHATRDRAFT_49604	-	-	-	-		-
7203122	17	3	2.8	0.85	-1.719892081	0.045313	PHATRDRAFT_47929	K01411|1|2e-90|332|gmx:100797049|nardilysin [EC:3.4.24.61]	-	GO:0004175//endopeptidase activity;GO:0043169//cation binding	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7204932	17	3	10.37	3.15	-1.71899216	0.045313	PHATRDRAFT_bd1618	-	-	-	-		-
7204090	17	3	10.86	3.3	-1.718486174	0.045313	PHATR_33535	-	-	-	-		-
7203489	17	3	25.67	7.82	-1.714842783	0.045313	PHATRDRAFT_38535	-	-	-	-		-
7198945	28	5	29.21	8.99	-1.700069337	0.00849306	PHATRDRAFT_5132	-	-	-	-		-
7203642	50	9	16.16	5	-1.692427198	0.000350048	PHATRDRAFT_48378	-	GO:0044424	-	-		-
7203050	61	11	20.1	6.23	-1.689891433	7.38E-05	PHATRDRAFT_38112	-	-	-	-		-
7194829	22	4	10.11	3.16	-1.677786534	0.0227202	PHATRDRAFT_48622	-	-	-	-		-
7196116	22	4	26.77	8.4	-1.672155906	0.0227202	PHATRDRAFT_9011	K01802|1|2e-55|213|osa:4342022|peptidylprolyl isomerase [EC:5.2.1.8];K03767|4|5e-52|201|osa:4347920|peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7200643	38	7	18.34	5.81	-1.65838357	0.00230382	PHATRDRAFT_35332	-	-	-	-		-
7195960	27	5	13.3	4.24	-1.649290076	0.01159268	PHATRDRAFT_31605	K09518|1|6e-10|63.9|aly:ARALYDRAFT_494970|DnaJ homolog subfamily B member 12	-	-	-		-
7200015	27	5	21.28	6.79	-1.648014671	0.01159268	PHATRDRAFT_34985	-	-	-	-		-
7200568	48.25	8.98	28.58	9.16	-1.641586413	0.000258476	PHATRDRAFT_45465	-	-	-	-		-
7204097	75	14	24.98	8.02	-1.639099335	1.54E-05	PHATR_44177	-	-	GO:0008252//nucleotidase activity;GO:0046872//metal ion binding	GO:0009117//nucleotide metabolic process		GO:0009117//nucleotide metabolic process
7197643	101	19	21.11	6.82	-1.630082934	5.30E-07	HemE_2	K01599|1|1e-109|396|cme:CME194C|uroporphyrinogen decarboxylase [EC:4.1.1.37]	GO:0009536//plastid	GO:0016831//carboxy-lyase activity	GO:0006779//porphyrin-containing compound biosynthetic process		GO:0006779//porphyrin-containing compound biosynthetic process
7198429	428	81	307.86	100.32	-1.617665178	2.75E-25	PHATRDRAFT_49735	-	-	GO:0003824//catalytic activity	-		-
7203856	37	7	58.28	19.04	-1.613967399	0.0031196	PHATR_33436	-	-	-	-		-
7203178	21	4	8.23	2.7	-1.607933023	0.0310474	PHATRDRAFT_47923	-	-	-	-		-
7204027	26	5	9.26	3.06	-1.597480541	0.0157542	PHATR_44088	-	-	-	-		-
7196061	26	5	16.23	5.37	-1.595669007	0.0157542	PHATRDRAFT_1598	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763

7197565	26	5	32.67	10.84	-1.591601698	0.0157542	PHATRDRAFT_43526	-	-	-	-		-
7198544	31	6	10.12	3.37	-1.586388794	0.0081036	PHATRDRAFT_40779	K08214|1|9e-10|63.9|cre:CHLREDRAFT_150489|MFS transporter, OCT family, solute carrier family 22 (organic cation transporter), member 18;K08145|3|6e-07|54.7|smo:SELMODRAFT_437958|MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7197560	36	7	18.8	6.29	-1.57960074	0.00420966	PHATRDRAFT_43519	-	-	-	-		-
7201690	3587	698	1191.08	398.55	-1.579437683	5.62E-193	PHATRDRAFT_46547	-	-	-	-		-
7205037	41	8	29.17	9.8	-1.573631732	0.00220332	PHATRDRAFT_bd1463	-	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7196078	25.62	5.04	23.53	7.97	-1.561849691	0.0213102	PHATRDRAFT_42528	-	-	-	-		-
7200954	20	4	7.02	2.41	-1.542437884	0.0421966	VDL2	K09839|1|4e-11|68.6|ppp:PHYPADRAFT_139915|violaxanthin de-epoxidase [EC:1.10.99.3]	GO:0009536//plastid	GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7199912	40	8	21.77	7.49	-1.539303784	0.00295642	PHATRDRAFT_44815	K00249|1|3e-56|217|pop:POPTR_725647|acyl-CoA dehydrogenase [EC:1.3.99.3]	-	GO:0016740//transferase activity	-		-
7204515	20	4	11.33	3.9	-1.538601832	0.0421966	PHATR_36770	-	-	-	-		-
7202261	25	5	13.77	4.74	-1.538569595	0.0213102	PHATRDRAFT_37136	-	-	-	-		-
7197483	20	4	8.13	2.8	-1.537828525	0.0421966	PHATRDRAFT_25394	K14835|1|2e-116|418|smo:SELMODRAFT_437511|ribosomal RNA methyltransferase Nop2 [EC:2.1.1.-]	-	GO:0003676//nucleic acid binding;GO:0008168//methyltransferase activity	GO:0042254//ribosome biogenesis;GO:0008152//metabolic process		GO:0042254//ribosome biogenesis;GO:0008152//metabolic process
7197901	25	5	10.77	3.71	-1.537527158	0.0213102	PHATRDRAFT_50825	K11338|1|9e-162|568|smo:SELMODRAFT_80930|RuvB-like protein 2 [EC:3.6.4.12]	GO:0000790//nuclear chromatin;GO:0009536//plastid	GO:0032550;GO:0004003//ATP-dependent DNA helicase activity	GO:0032392//DNA geometric change		GO:0032392//DNA geometric change
7197983	20	4	19.56	6.74	-1.537085874	0.0421966	PHATRDRAFT_44329	-	-	-	-		-
7201123	20	4	27.72	9.57	-1.534336428	0.0421966	PHATRDRAFT_35721	-	-	-	-		-
7201524	17.44	3.5	8.71	3.01	-1.532909232	0.045313	PHATRDRAFT_46037	-	-	-	-		-
7198881	45.94	9.32	24.9	8.69	-1.51871766	0.001553976	PHATRDRAFT_30977	K09554|1|2e-35|148|ota:Ot02g05550|cell division cycle protein 37	-	GO:0019900//kinase binding	-		-
7196279	54	11	12.91	4.52	-1.514094323	0.000580462	PHATRDRAFT_42591	-	-	-	-		-
7203266	1241	254	513.16	180.66	-1.506131605	1.27E-63	PHATRDRAFT_48096	-	-	-	-		-
7202465	34	7	16.34	5.79	-1.49677273	0.00758152	PHATRDRAFT_47439	-	-	-	-		-
7198258	53	11	46.64	16.68	-1.4834485	0.000771584	PHATRDRAFT_16067	K13412|1|5e-51|199|pop:POPTR_256143|calcium-dependent protein kinase [EC:2.7.11.1];K00908|4|7e-49|192|cme:CMF051C|Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17]	-	GO:0004674//protein serine/threonine kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7195768	24	5	14.6	5.23	-1.481085518	0.0286836	RFC2	K10755|1|1e-108|391|vcn:VOLCADRAFT_84109|replication factor C subunit 2/4	-	GO:0003676//nucleic acid binding;GO:0016779//nucleotidyltransferase activity;GO:0016462//pyrophosphatase activity;GO:0032550	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200504	38	8	15.63	5.66	-1.46544382	0.00526832	PHATRDRAFT_45412	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-
7198863	80	17	44.39	16.23	-1.451571709	4.18E-05	PHATRDRAFT_50170	-	-	-	-		-
7203801	61	13	19.71	7.22	-1.448857034	0.00038295	PHATRDRAFT_48340	-	-	-	-		-
7196662	79	17	62.73	23.25	-1.431924846	5.50E-05	PHATRDRAFT_8760	K13412|1|4e-41|166|zma:100280693|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7201250	306	66	115.82	42.96	-1.430818504	1.00E-15	PHATRDRAFT_36063	-	-	-	-		-
7204238	37	8	32.96	12.28	-1.424405682	0.00699464	PHATR_33421	-	-	-	-		-
7203295	23	5	10.73	4.01	-1.419975934	0.0384064	PHATRDRAFT_48145	-	-	-	-		-
7204497	23	5	15.61	5.84	-1.418430263	0.0384064	PHATR_46702	-	-	-	-		-
7204484	23	5	8.92	3.34	-1.417195607	0.0384064	PHATR_36668	K10140|1|4e-14|78.2|mtr:MTR_5g070310|DNA damage-binding protein 2	-	-	-		-

7202291	23	5	29.29	10.99	-1.414216807	0.0384064	PHATRDRAFT_37751	-	-	GO:0016881//acid-amino acid ligase activity	GO:0036211		GO:0036211
7197279	59	13	47.77	18.13	-1.397725952	0.000663774	PHATRDRAFT_43766	K00876|1|9e-10|62.4|pop:POPTR_815577|uridine kinase [EC:2.7.1.48]	GO:0009536//plastid	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7200213	27	6	21.83	8.36	-1.384737283	0.0260576	PHATRDRAFT_11866	K15102|1|7e-42|169|cme:CMT361C|solute carrier family 25 (mitochondrial phosphate transporter), member 3	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7196318	27	6	34.19	13.11	-1.382906737	0.0260576	PHATRDRAFT_8663	K00861|1|2e-28|123|cme:CMJ134C|riboflavin kinase [EC:2.7.1.26];K00995|2|4e-25|112|gmx:100784881|CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5]	GO:0031224//intrinsic component of membrane	GO:0017169//CDP-alcohol phosphatidyltransferase activity	GO:0006644//phospholipid metabolic process		GO:0006644//phospholipid metabolic process
7195658	76	17	31.55	12.14	-1.377871584	0.00012371	PHATRDRAFT_49165	K01669|1|6e-14|77.4|cme:CMH170C|deoxyribodipyrimidine photo-lyase [EC:4.1.99.3]	-	GO:0003913//DNA photolyase activity	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200642	76	17	38.03	14.64	-1.377222385	0.00012371	PHATRDRAFT_45592	K00058|1|6e-87|319|olu:OSTLU_39000|D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7196767	58	13	27.28	10.52	-1.37470894	0.000870506	PHATRDRAFT_43171	K05389|1|2e-23|108|pop:POPTR_755721|potassium channel subfamily K, other eukaryote	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding;GO:0005261//cation channel activity	GO:0034220//ion transmembrane transport		GO:0034220//ion transmembrane transport
7195823	40	9	14.73	5.7	-1.369723606	0.00638724	PHATRDRAFT_49471	-	-	-	-		-
7202486	31	7	20.08	7.81	-1.362364816	0.01777966	PHATRDRAFT_28652	K03644|1|2e-102|370|pop:POPTR_783924|lipoic acid synthetase [EC:2.8.1.8]	GO:0009536//plastid	GO:0051536//iron-sulfur cluster binding;GO:0016783//sulfurtransferase activity	GO:0006633//fatty acid biosynthetic process		GO:0006633//fatty acid biosynthetic process
7195571	53	12	47.73	18.62	-1.358043263	0.001631638	PHATRDRAFT_49282	-	-	-	-		-
7200959	119	27	47.08	18.37	-1.357762694	1.75E-06	PHATRDRAFT_45852	K03834|1|2e-19|95.9|cre:CHLREDRAFT_205979|tyrosine-specific transport protein	-	-	-		-
7201573	44	10	21.65	8.47	-1.35393315	0.0044214	PHATRDRAFT_46483	K14011|1|2e-07|55.8|osa:4347001|UBX domain-containing protein 6	-	-	-		-
7204059	74	17	36.34	14.36	-1.33950267	0.000210272	PHATR_44224	-	GO:0031224//intrinsic component of membrane	-	-		-
7201132	39	9	16.08	6.38	-1.333639077	0.0083851	PHATRDRAFT_45917	-	-	-	-		-
7203073	26	6	17.88	7.1	-1.332455807	0.034481	PHATRDRAFT_47844	-	-	-	-		-
7197449	26	6	7.95	3.16	-1.331030302	0.034481	PHATRDRAFT_43679	-	-	-	-		-
7198093	26	6	21.66	8.61	-1.3309481	0.034481	PHATRDRAFT_34059	-	-	-	-		-
7196081	95	22	62.21	24.8	-1.326806386	2.80E-05	PHATRDRAFT_42531	-	-	-	-		-
7202380	43	10	25.09	10.04	-1.321353201	0.00578758	PHATRDRAFT_54721	-	-	GO:0016407//acetyltransferase activity	-		-
7199345	43	10	21.24	8.5	-1.32124902	0.00578758	PHATRDRAFT_50542	K15111|1|3e-17|88.2|gmx:100800051|solute carrier family 25 (mitochondrial S-adenosylmethionine transporter), member 26	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7200575	30	7	20.94	8.41	-1.316083737	0.0234144	PHATRDRAFT_35196	K10632|1|1e-22|105|pop:POPTR_911570|BRCA1-associated protein [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	-		-
7201855	30	7	18.35	7.37	-1.316043539	0.0234144	PHATRDRAFT_46579	K08081|1|6e-10|63.5|ath:AT2G30670|tropine dehydrogenase [EC:1.1.1.206];K00059|3|3e-09|61.2|rcu:RCOM_1121800|3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710

7196348	30	7	22.36	8.99	-1.314527167	0.0234144	PHATRDRAFT_9277	-	-	GO:0004518//nuclease activity;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7198030	34	8	20.99	8.5	-1.30416742	0.01598782	PHATRDRAFT_44338	K05531|1|4e-26|117|bdi:100846699|mannan polymerase II complex MNN10 subunit [EC:2.4.1.-];K08238|2|5e-07|53.9|bdi:100842881|xyloglucan 6-xylosyltransferase [EC:2.4.2.39]	GO:0031224//intrinsic component of membrane	GO:0016757//transferase activity, transferring glycosyl groups	-		-
7203230	38	9	11.7	4.76	-1.297475051	0.01096576	PHATRDRAFT_47986	K15336|1|5e-10|65.1|vvi:100259391|tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	-	-		-
7199221	26.5	6.32	31.05	12.76	-1.282964939	0.034481	PHATRDRAFT_16840	-	GO:0016020//membrane;GO:0005739//mitochondrion	GO:0003824//catalytic activity	-		-
7197788	121	29	50.13	20.67	-1.278135845	4.07E-06	PHATRDRAFT_44536	-	-	-	-		-
7202715	25	6	8.75	3.61	-1.27728418	0.0453862	PHATRDRAFT_47722	-	-	-	-		-
7201349	25	6	15.79	6.52	-1.276067302	0.0453862	PHATRDRAFT_46122	K12179|1|1e-14|79.3|smo:SELMODRAFT_230963|COP9 signalosome complex subunit 6	-	-	-		-
7202580	25	6	21.68	8.96	-1.274794119	0.0453862	PHATRDRAFT_47463	K14405|1|8e-07|52.4|cme:CMR160C|pre-mRNA 3'-end-processing factor FIP1	-	-	-		-
7199225	25	6	16.35	6.76	-1.274195484	0.0453862	PHATRDRAFT_50419	-	-	-	-		-
7201749	29	7	14.57	6.05	-1.26799383	0.0306878	PHATRDRAFT_46625	-	-	-	-		-
7205146	29	7	12.06	5.01	-1.267347399	0.0306878	PHATRDRAFT_bd1481	-	-	-	-		-
7197515	128	31	58.89	24.54	-1.262887425	2.61E-06	PHATRDRAFT_43665	-	-	GO:0042578//phosphoric ester hydrolase activity	GO:0044238		GO:0044238
7196859	45	11	13.31	5.59	-1.251590383	0.0067613	PHATRDRAFT_43071	K00565|1|1e-30|133|ath:AT3G20650|mRNA (guanine-N7-)-methyltransferase [EC:2.1.1.56]	-	-	-		-
7203144	61	15	29.77	12.6	-1.240435488	0.001564882	PHATRDRAFT_47959	-	-	-	-		-
7200567	600	148	259.36	110.05	-1.236796851	5.71E-24	PHATRDRAFT_45464	-	-	-	-		-
7201053	1133	281	308.96	131.74	-1.229726614	1.88E-43	PHATRDRAFT_45988	-	-	GO:0046914//transition metal ion binding;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7198224	36	9	13.03	5.6	-1.218338352	0.01852808	PHATRDRAFT_49553	-	-	-	-		-
7194740	48	12	22.77	9.79	-1.217753527	0.00603148	PHATRDRAFT_48580	-	-	-	-		-
7195355	28	7	11	4.73	-1.217591435	0.0400194	PHATRDRAFT_39534	-	-	-	-		-
7195452	76	19	32.18	13.84	-1.217320383	0.000477546	PHATRDRAFT_49099	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204394	52	13	37.36	16.08	-1.216227049	0.00417434	PHATR_33327	-	-	-	-		-
7204482	72	18	54.98	23.67	-1.215847201	0.000682842	PHATR_36662	-	-	-	-		-
7194847	40	10	30.12	12.97	-1.21554329	0.0127003	PHATRDRAFT_29736	K00365|1|1e-46|185|bdi:100845980|urate oxidase [EC:1.7.3.3]	GO:0042579//microbody	GO:0016663//oxidoreductase activity, acting on other nitrogenous compounds as donors, oxygen as acceptor	GO:0009112;GO:0044282		GO:0009112;GO:0044282
7198928	167	42	103.68	44.88	-1.207993042	1.97E-07	PHATRDRAFT_50127	-	-	-	-		-
7199434	345	87	148.16	64.27	-1.204938626	6.86E-14	PHATRDRAFT_50619	-	-	-	-		-
7198434	106	27	47.7	20.9	-1.190486324	4.60E-05	PHATRDRAFT_40517	K14209|1|2e-49|195|gmx:100791548|solute carrier family 36 (proton-coupled amino acid transporter)	GO:0031224//intrinsic component of membrane	-	-		-
7196194	156	40	80.82	35.66	-1.180405649	8.06E-07	PHATRDRAFT_8678	-	-	-	-		-
7204904	35	9	16.45	7.28	-1.176077228	0.0239302	PHATRDRAFT_bd1746	-	-	GO:0004620//phospholipase activity	-		-
7201077	31	8	11.73	5.21	-1.170847736	0.0351394	PHATRDRAFT_45824	K14209|1|3e-14|78.6|ppp:PHYPADRAFT_144039|solute carrier family 36 (proton-coupled amino acid transporter)	GO:0031224//intrinsic component of membrane	-	-		-
7202219	31	8	17.2	7.64	-1.170764022	0.0351394	PHATRDRAFT_46972	K03839|1|3e-24|111|olu:OSTLU_87975|flavodoxin I	-	GO:0003824//catalytic activity;GO:0032553	GO:0044710		GO:0044710
7203579	3602	932	1407.14	626.2	-1.16807046	2.94E-124	PHATRDRAFT_54892	-	-	-	-		-
7204326	42	11	14.17	6.38	-1.151211429	0.0144346	PHATR_43862	-	-	-	-		-

7195093	42	11	48.17	21.76	-1.146456367	0.0144346	PHATRDRAFT_5904	K12191|1|5e-51|198|sbi:SORBI_02g007010|charged multivesicular body protein 2A	-	-	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7198638	99	26	41.46	18.73	-1.146369217	0.000133532	PHATRDRAFT_49945	-	-	GO:0016782//transferase activity, transferring sulfur-containing groups	-		-
7195144	38	10	13.11	5.93	-1.144563676	0.0210302	PHATRDRAFT_39421	-	-	GO:0005254//chloride channel activity	GO:0015698//inorganic anion transport;GO:0044763		GO:0015698//inorganic anion transport;GO:0044763
7201775	38	10	16.82	7.62	-1.142314803	0.0210302	PHATRDRAFT_27905	K14859|1|7e-52|203|ppp:PHYPADRAFT_204687|ribosome biogenesis protein SSF1/2	-	-	-		-
7200381	38	10	28.82	13.06	-1.141915439	0.0210302	PHATRDRAFT_12140	K03686|1|1e-48|191|gmx:100799735|molecular chaperone DnaJ	-	GO:0005515//protein binding	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7198024	106	28	42.57	19.34	-1.138249295	8.37E-05	PHATRDRAFT_44326	-	-	GO:0016740//transferase activity	-		-
7196276	102	27	27.94	12.72	-1.13523335	0.000118841	PHATRDRAFT_42586	-	-	-	-		-
7204168	45	12	10.01	4.59	-1.124875915	0.01269638	PHATR_43937	-	-	-	-		-
7201194	45	12	17.77	8.15	-1.124571717	0.01269638	PHATRDRAFT_46234	K11323|1|8e-39|160|cre:CHLREDRAFT_120259|histone arginine demethylase JMJD6 [EC:1.14.11.-]	-	-	-		-
7202987	60	16	33.89	15.55	-1.123945056	0.00372092	PHATRDRAFT_47857	-	GO:0031224//intrinsic component of membrane	GO:0016782//transferase activity, transferring sulfur-containing groups	GO:0044723		GO:0044723
7204180	30	8	5.23	2.4	-1.123776541	0.0452486	SMC	K06677|1|2e-121|435|ppp:PHYPADRAFT_143027|condensin complex subunit 1	-	-	GO:0000070//mitotic sister chromatid segregation		GO:0000070//mitotic sister chromatid segregation
7198009	45	12	26.23	12.04	-1.123382416	0.01269638	PHATRDRAFT_44299	-	-	-	-		-
7202367	30	8	18.84	8.65	-1.123026927	0.0452486	PHATRDRAFT_37452	-	-	-	-		-
7197837	41	11	21.77	10.05	-1.115145906	0.0184443	PHATRDRAFT_44360	-	-	-	-		-
7197139	93	25	36.42	16.84	-1.112838784	0.000303088	PHATRDRAFT_43408	-	-	-	-		-
7204955	208	56	57.82	26.76	-1.111490493	5.31E-08	PHATRDRAFT_bd1748	K05389|1|1e-07|57.0|olu:OSTLU_41153|potassium channel subfamily K, other eukaryote	-	GO:0004620//phospholipase activity	-		-
7197819	156	42	60.4	27.97	-1.110668296	2.59E-06	PHATRDRAFT_44339	K05531|1|2e-26|119|bdi:100846699|mannan polymerase II complex MNN10 subunit [EC:2.4.1.-];K08238|2|4e-08|58.2|osa:4329539|xyloglucan 6-xylosyltransferase [EC:2.4.2.39]	GO:0031224//intrinsic component of membrane	GO:0016757//transferase activity, transferring glycosyl groups	-		-
7200873	31.82	8.58	12.47	5.78	-1.109320067	0.0351394	PHATRDRAFT_45718	-	-	-	-		-
7200530	74	20	9.21	4.28	-1.10559036	0.001413754	PHATRDRAFT_45406	-	-	-	-		-
7203733	37	10	20.37	9.48	-1.103487016	0.0268912	PHATRDRAFT_48305	-	-	-	-		-
7195374	37	10	37.53	17.48	-1.102339105	0.0268912	PHATRDRAFT_48961	-	-	-	-		-
7200169	70	19	14.04	6.55	-1.099976124	0.00202152	PHATRDRAFT_45083	-	-	-	-		-
7199751	59	16	32.87	15.34	-1.099472974	0.00471556	PHATRDRAFT_44793	-	-	-	-		-
7198338	96.14	26.17	48.14	22.55	-1.094108708	0.000268562	PHATRDRAFT_49750	-	-	-	-		-
7199515	44	12	10.99	5.15	-1.093547049	0.01615256	PHATRDRAFT_44997	-	-	-	-		-
7200294	33	9	13.52	6.34	-1.092540406	0.0393762	PHATRDRAFT_34698	-	-	-	-		-
7197574	44	12	14.86	6.97	-1.092203555	0.01615256	PHATRDRAFT_43541	-	-	-	-		-
7194976	33	9	18.67	8.76	-1.091719153	0.0393762	PHATRDRAFT_48903	-	-	-	-		-
7195315	33	9	10.72	5.03	-1.091674601	0.0393762	PHATRDRAFT_49073	K14994|1|8e-20|97.4|ota:Ot03g05700|solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 7/8;K14207|2|2e-18|92.4|pop:POPTR_580719|solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 2	GO:0031224//intrinsic component of membrane	-	-		-
7200445	44	12	15.77	7.4	-1.091585484	0.01615256	PHATRDRAFT_45660	-	-	GO:0003824//catalytic activity	GO:0044238		GO:0044238
7203097	44	12	9.27	4.35	-1.091553938	0.01615256	PHATRDRAFT_47883	-	-	-	-		-
7204765	31.18	8.51	12.89	6.05	-1.091245216	0.0351394	PHATR_37020	-	-	-	-		-
7202149	33	9	14.85	6.97	-1.09123237	0.0393762	PHATRDRAFT_47059	-	-	-	-		-

7198535	179	49	34.57	16.27	-1.087306353	7.25E-07	PHATRDRAFT_49924	K13289|1|9e-32|137|ota:Ot12g01330|cathepsin A (carboxypeptidase C) [EC:3.4.16.5];K06892|2|3e-25|116|sbi:SORBI_01g031160|	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7197183	51	14	21.86	10.32	-1.08285043	0.0097798	PHATRDRAFT_43481	-	-	-	-		-
7195662	51	14	21.62	10.21	-1.082383657	0.0097798	PHATRDRAFT_49170	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197418	91	25	29.21	13.8	-1.081794091	0.000479886	PHATRDRAFT_25217	K05681|1|9e-64|243|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|6e-49|194|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K05643|4|6e-15|81.3|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7202271	40	11	25.41	12.03	-1.078759733	0.0234722	PHATRDRAFT_37711	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7204961	87	24	35.71	16.94	-1.075894259	0.000682436	PHATRDRAFT_bd1331	K03979|1|2e-89|328|cre:CHLREDRAFT_126186|GTP-binding protein	GO:0009536//plastid	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0046872//metal ion binding	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7203028	86.9	24.01	20.15	9.57	-1.074189009	0.0008557	PHATRDRAFT_48040	-	-	-	-		-
7198906	105	29	62.59	29.75	-1.073042508	0.000185975	RRP	K12589|1|9e-14|76.3|smo:SELMODRAFT_102800|exosome complex component RRP42;K12586|3|1e-10|65.9|vcn:VOLCADRAFT_86657|exosome complex component RRP43	-	-	-		-
7201056	47	13	18.77	8.93	-1.07169657	0.01413038	PHATRDRAFT_45995	-	-	GO:0046914//transition metal ion binding;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202336	45.39	12.57	18.06	8.6	-1.070389328	0.01269638	PHATRDRAFT_47245	-	-	GO:0016740//transferase activity	-		-
7196902	83	23	74.54	35.59	-1.066542886	0.000971196	PHATRDRAFT_43138	-	-	-	-		-
7204710	72	20	25.18	12.03	-1.065641641	0.00224248	PHATR_46853	-	-	-	-		-
7197905	36	10	30.98	14.82	-1.063791696	0.0342328	PSP	K01079|1|7e-59|225|sbi:SORBI_05g025180|phosphoserine phosphatase [EC:3.1.3.3]	-	GO:0016791//phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006563//L-serine metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006563//L-serine metabolic process
7200520	36	9.99	51.53	24.68	-1.062070198	0.01852808	PHATRDRAFT_11901	K12197|1|5e-35|144|olu:OSTLU_29213|charged multivesicular body protein 1	-	-	GO:0009790//embryo development;GO:0045184//establishment of protein localization		GO:0009790//embryo development;GO:0045184//establishment of protein localization
7200662	79	22	57.08	27.37	-1.0603899	0.001383242	PHATRDRAFT_45622	-	-	-	-		-
7196041	43	12	37.54	18.05	-1.056429813	0.02047	PHATRDRAFT_8934	K14510|1|8e-53|205|ppp:PHYPADRAFT_30352|serine/threonine-protein kinase CTR1 [EC:2.7.11.1];K04424|5|4e-51|199|aly:ARALYDRAFT_909157|sterile alpha motif and leucine zipper containing kinase AZK [EC:2.7.11.25]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process

7205051	71	20	46.59	22.59	-1.04433606	0.00281344	GrpE	K03687|1|2e-07|54.7|gmx:100794766|molecular chaperone GrpE	-	GO:0042802//identical protein binding;GO:0030554//adenyl nucleotide binding;GO:0019842//vitamin binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044267//cellular protein metabolic process;GO:0044710		GO:0044267//cellular protein metabolic process;GO:0044710
7196927	46	13	30	14.6	-1.038994132	0.0178415	PHATRDRAFT_32345	-	-	-	-		-
7198354	145	41	82.54	40.17	-1.038974977	1.74E-05	PHATRDRAFT_49779	-	-	-	-		-
7197814	113	32	50.68	24.69	-1.037489688	0.000159665	PHATRDRAFT_44253	-	-	GO:0036094//small molecule binding	-		-
7201764	67	19	24.8	12.1	-1.035333073	0.0040184	PHATRDRAFT_46385	-	-	-	-		-
7198212	60	17	55.48	27.08	-1.034740049	0.00656808	PHATRDRAFT_16065	K14574|1|2e-48|190|rcu:RCOM_0559400|ribosome maturation protein SDO1	-	-	GO:0010467//gene expression;GO:0022613//ribonucleoprotein complex biogenesis;GO:0016070//RNA metabolic process		GO:0010467//gene expression;GO:0022613//ribonucleoprotein complex biogenesis;GO:0016070//RNA metabolic process
7201493	123	35	60.13	29.44	-1.030307287	8.79E-05	PHATRDRAFT_54552	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0006811//ion transport;GO:0044763		GO:0006811//ion transport;GO:0044763
7197747	56	16	21.09	10.36	-1.025535092	0.00942284	PHATRDRAFT_33901	K13420|1|5e-22|104|aly:ARALYDRAFT_356368|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7196514	63	18	22.11	10.87	-1.024347085	0.00574586	PHATRDRAFT_42867	-	-	-	-		-
7198909	56	16	30.08	14.79	-1.024182515	0.00942284	PHATRDRAFT_30898	K12196|1|2e-114|410|aly:ARALYDRAFT_481753|vacuolar protein-sorting-associated protein 4	-	GO:0032550;GO:0016462//pyrophosphatase activity	-		-
7199641	42	12	41.27	20.32	-1.022193036	0.0258378	PHATRDRAFT_5532	-	-	GO:0008168//methyltransferase activity	GO:0008213		GO:0008213
7202080	42	12	63.43	31.29	-1.019463684	0.0258378	PHATRDRAFT_37052	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197852	149	43	39	19.35	-1.011140558	2.08E-05	PHATRDRAFT_44383	-	-	-	GO:0044260		GO:0044260
7200771	52	15	11.77	5.84	-1.011074046	0.01354018	PHATRDRAFT_35518	-	-	-	-		-
7201518	52	15	42.21	20.97	-1.009257968	0.01354018	PHATRDRAFT_35895	-	-	-	-		-
7195111	38	11	15.22	7.58	-1.005698605	0.0375296	PHATRDRAFT_39361	-	-	-	-		-
7203174	38	11	21.78	10.85	-1.005308911	0.0375296	PHATRDRAFT_47913	-	-	-	-		-
7198308	38	11	23.79	11.86	-1.004251262	0.0375296	PHATRDRAFT_49669	-	-	-	-		-
7194713	460	134	97.4	48.77	-0.9979278	9.53E-14	PHATRDRAFT_48538	-	-	-	-		-
7195487	147	43	73.22	36.85	-0.990573154	3.18E-05	PHATRDRAFT_49323	-	-	-	-		-
7204924	61.9	18.13	24.58	12.38	-0.989473601	0.0089445	PHATRDRAFT_bd1587	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7203077	41	12	22.75	11.46	-0.989259501	0.0324782	PHATRDRAFT_47849	-	-	-	-		-
7200244	58	17	25.52	12.87	-0.987616276	0.01027032	PHATRDRAFT_45218	-	-	-	-		-
7199601	58	17	30.63	15.45	-0.987338529	0.01027032	PHATRDRAFT_44900	-	-	GO:0008081//phosphoric diester hydrolase activity	GO:0019400		GO:0019400
7199189	136.16	40.02	77.71	39.31	-0.983203898	7.11E-05	PHATRDRAFT_50367	-	-	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation		GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation
7198118	51	15	38.36	19.43	-0.981316819	0.01693128	PHATRDRAFT_44630	K00079|1|6e-36|149|cre:CHLREDRAFT_159999|carbonyl reductase 1 [EC:1.1.1.184 1.1.1.189 1.1.1.197];K15095|2|3e-31|133|vvi:100248214|(+)-neomenthol dehydrogenase [EC:1.1.1.208]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7204702	51	15	53.98	27.37	-0.979829542	0.01693128	PHATR_46852	-	-	-	-		-

7199453	44	13	16.57	8.42	-0.976681464	0.0281162	PHATRDRAFT_41624	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7195901	64	19	34.46	17.61	-0.968527792	0.00779022	PHATRDRAFT_16032	K08790|1|3e-87|320|cre:CHLREDRAFT_116419|serine/threonine kinase 38 [EC:2.7.11.1];K08286|2|2e-86|317|osa:4339288|protein-serine/threonine kinase [EC:2.7.11.-]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7201410	37	11	18.57	9.5	-0.966974397	0.0471378	PHATRDRAFT_46046	-	-	-	-		-
7200994	37	11	11.12	5.69	-0.96665623	0.0471378	PHATRDRAFT_45906	K11407|1|1e-64|246|rcu:RCOM_1469870|histone deacetylase 6/10 [EC:3.5.1.98]	-	GO:0003824//catalytic activity	-		-
7202899	37	11	26.79	13.71	-0.96646601	0.0471378	PHATRDRAFT_47717	-	-	-	-		-
7197772	47	14	10.54	5.4	-0.964843555	0.0243494	PHATRDRAFT_44502	K13103|1|2e-21|103|rcu:RCOM_1517460|tuftelin-interacting protein 11	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198854	47	14	18.11	9.28	-0.964589836	0.0243494	PHATRDRAFT_50155	-	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds;GO:0097367//carbohydrate derivative binding	GO:0044238;GO:0006022		GO:0044238;GO:0006022
7203969	47	14	38.15	19.57	-0.963039301	0.0243494	PHATR_41778	K03062|1|1e-136|483|ath:AT4G29040|26S proteasome regulatory subunit T2	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0005838//proteasome regulatory particle	GO:0032550;GO:0017111//nucleoside-triphosphatase activity	GO:0006261//DNA-dependent DNA replication;GO:0016458//gene silencing;GO:0001558//regulation of cell growth;GO:0009062//fatty acid catabolic process;GO:0006007//glucose catabolic process;GO:0035966//response to topologically incorrect protein;GO:0043094;GO:0009791//post-embryonic development;GO:0006511//ubiquitin-		GO:0006261//DNA-dependent DNA replication;GO:0016458//gene silencing;GO:0001558//regulation of cell growth;GO:0009062//fatty acid catabolic process;GO:0006007//glucose catabolic process;GO:0035966//response to topologically incorrect protein;GO:0043094;GO:0009791//post-embryonic development;GO:0006511//ubiquitin-
7198054	37	11	51.61	26.48	-0.962747508	0.0471378	PHATRDRAFT_5546	K14570|1|8e-15|77.8|gmx:100785565|RNA exonuclease 1 [EC:3.1.-.-]	GO:0044464	GO:0097159//organic cyclic compound binding;GO:0004518//nuclease activity	-		-
7201267	57	17	35.09	18.01	-0.962261766	0.01278146	PHATRDRAFT_46195	-	-	-	-		-
7200680	67	20	31.09	15.96	-0.961989965	0.00678548	PHATRDRAFT_45439	-	-	-	-		-
7201361	439	131	238.34	122.39	-0.96153541	1.59E-12	PHATRDRAFT_46143	-	-	-	-		-
7197029	241	72	233.66	120.3	-0.957774139	1.85E-07	PHATRDRAFT_33028	-	-	-	-		-
7199672	140	42	201.71	104.46	-0.949332	8.31E-05	PHATRDRAFT_11271	K03453|1|1e-12|70.5|vcn:VOLCADRAFT_102664|bile acid:Na+ symporter, BASS family	-	-	-		-
7205095	69.59	20.92	70.6	36.58	-0.948613108	0.00439336	PtRabX1	K07901|1|1e-44|177|zma:100273222|Ras-related protein Rab-8A;K07976|2|2e-44|176|osa:4334590|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7196875	53	16	47.4	24.66	-0.942714259	0.01828444	PHATRDRAFT_32237	-	-	GO:0097159//organic cyclic compound binding	-		-
7203092	43	13	29.45	15.33	-0.941909937	0.035083	PHATRDRAFT_47877	-	-	-	-		-
7199805	46	14	17.65	9.24	-0.933703427	0.0303002	PHATRDRAFT_44879	-	-	-	-		-
7205131	46	14	25.85	13.54	-0.932936542	0.0303002	PHATRDRAFT_bd1723	-	-	-	-		-
7195032	59	18	13.28	6.96	-0.932095935	0.01375264	PHATRDRAFT_48750	-	-	-	-		-
7195788	59	18	23.09	12.12	-0.929878474	0.01375264	PHATRDRAFT_49403	-	-	-	-		-
7204965	49	15	25.19	13.27	-0.924682751	0.0261878	PHATRDRAFT_bd1759	-	-	-	-		-
7204209	49	15	29.77	15.69	-0.924013869	0.0261878	PHATR_25739	K13070|1|9e-24|109|osa:4335093|momilactone-A synthase [EC:1.1.1.295];K00059|2|5e-23|107|bdi:100826298|3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202267	101	31	140	74.16	-0.916713678	0.001224316	PHATRDRAFT_37703	-	-	-	-		-
7202651	68	21	44.35	23.58	-0.911370386	0.00899736	PHATRDRAFT_37848	-	-	-	-		-
7200192	55	17	46.36	24.68	-0.909538172	0.01959948	PHATRDRAFT_34746	-	-	-	-		-
7201848	42	13	16.11	8.58	-0.908906941	0.0435926	PHATRDRAFT_46567	-	-	-	-		-

7194715	42	13	28.09	14.97	-0.907982403	0.0435926	PHATRDRAFT_54920	-	-	-	-		-
7204681	71	22	31.5	16.79	-0.907749598	0.00781642	PHATR_1155	K00318|1|3e-86|317|cre:CHLREDRAFT_146649|proline dehydrogenase [EC:1.5.99.8]	-	GO:0046872//metal ion binding;GO:0016645//oxidoreductase activity, acting on the CH-NH group of donors	GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process		GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process
7199868	158	49	45.8	24.42	-0.907284398	6.04E-05	PHATRDRAFT_44742	-	-	-	-		-
7199960	45	14	19.98	10.69	-0.90229473	0.0375554	PHATRDRAFT_45315	-	-	-	-		-
7202558	90	28	39.29	21.03	-0.901713318	0.0027675	PHATRDRAFT_47426	-	-	GO:0046872//metal ion binding	-		-
7194844	58	18	85.82	45.98	-0.900307435	0.01697094	PHATRDRAFT_15145	K02155|1|4e-36|148|cre:CHLREDRAFT_134189|V-type H+-transporting ATPase 16kDa proteolipid subunit [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex;GO:0031224//intrinsic component of membrane	GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0003824//catalytic activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7198959	77	24	25.83	13.84	-0.9002037	0.00590522	PHATRDRAFT_23830	K14640|1|2e-77|288|cre:CHLREDRAFT_196439|solute carrier family 20 (sodium-dependent phosphate transporter)	-	GO:0015291//secondary active transmembrane transporter activity	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7200703	61	19	27.17	14.56	-0.90000421	0.01470304	PHATRDRAFT_45479	-	-	-	-		-
7202635	489.49	152.53	240.35	128.85	-0.899444266	1.42E-12	PHATRDRAFT_47571	-	-	-	-		-
7197538	428	134	282.52	152.27	-0.891721269	5.41E-11	PHATRDRAFT_43483	-	-	-	-		-
7201842	51	16	26.87	14.5	-0.889943421	0.0279524	PHATRDRAFT_36534	-	-	GO:0016407//acetyltransferase activity	-		-
7195740	51	16	19.4	10.47	-0.88979521	0.0279524	PHATRDRAFT_23292	K00225|1|6e-117|419|bdi:100840661|L-galactono-1,4-lactone dehydrogenase [EC:1.3.2.3]	GO:0043231//intracellular membrane-bounded organelle	GO:0016632;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0016899//oxidoreductase activity, acting on the CH-OH group of donors, oxygen as acceptor;GO:0000166//nucleotide binding	GO:0019852//L-ascorbic acid metabolic process;GO:0043094		GO:0019852//L-ascorbic acid metabolic process;GO:0043094
7202734	48	15	83.39	45.03	-0.888987911	0.0323856	PHATRDRAFT_14373	-	-	-	-		-
7203940	965	303	575.73	311.14	-0.887828511	8.31E-23	HSP20B	K13993|1|9e-06|49.7|ath:AT4G10250|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7195337	73	23	19.34	10.48	-0.883949078	0.00832418	PHATRDRAFT_49117	-	-	-	-		-
7204861	43.86	13.83	20.64	11.19	-0.883232934	0.035083	PHATRDRAFT_bd1101	-	-	-	-		-
7200535	57	18	12.99	7.05	-0.881706268	0.020873	PHATRDRAFT_45417	-	-	GO:0034062//RNA polymerase activity	GO:0051716//cellular response to stimulus;GO:0048519//negative regulation of biological process;GO:0051707//response to other organism;GO:0010033//response to organic substance;GO:0044237//cellular metabolic process;GO:0010468//regulation of gene expression;GO:0044238;GO:0050794//regulation of cellular process		GO:0051716//cellular response to stimulus;GO:0048519//negative regulation of biological process;GO:0051707//response to other organism;GO:0010033//response to organic substance;GO:0044237//cellular metabolic process;GO:0010468//regulation of gene expression;GO:0044238;GO:0050794//regulation of cellular process
7200234	98	31	23.14	12.58	-0.879256942	0.00223396	PHATRDRAFT_45204	K06674|1|9e-11|67.8|gmx:100788674|structural maintenance of chromosome 2;K09291|2|2e-09|63.2|gmx:100811882|nucleoprotein TPR;K06638|5|6e-07|55.1|ppp:PHYPADRAFT_40827|mitotic spindle assembly checkpoint protein MAD1	-	-	-		-

7198172	111	35	269.57	147.21	-0.872784273	0.001059748	PHATRDRAFT_7679	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7205070	47.15	14.89	110.84	60.59	-0.871327005	0.0243494	PHATRDRAFT_bd375	K01624|1|9e-33|136|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	-	GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7198864	44	14	15.11	8.27	-0.869544426	0.0463568	PHATRDRAFT_50172	K03686|1|3e-08|58.9|aly:ARALYDRAFT_490783|molecular chaperone DnaJ;K09531|2|3e-08|58.9|sbi:SORBI_01g017590|DnaJ homolog subfamily C member 11	GO:0044434	-	-		-
7204529	88	28	46.18	25.28	-0.86927171	0.00412568	PHATR_46763	-	-	-	-		-
7201823	44	14	18.59	10.18	-0.868789209	0.0463568	PHATRDRAFT_46488	-	-	-	-		-
7197613	160	51	62.39	34.21	-0.866896705	0.000100541	PHATRDRAFT_34060	K15336|1|7e-06|50.8|vvi:100259391|tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	-	-		-
7201858	69	22	24.71	13.55	-0.866802159	0.01173222	PHATRDRAFT_20899	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7196896	94	30	24.28	13.32	-0.866174339	0.003123	PHATRDRAFT_43128	-	-	-	-		-
7199191	6105	1946	3655.59	2005.55	-0.866106337	5.95E-130	PHATRDRAFT_41316	-	-	-	-		-
7195923	47	15	14.36	7.88	-0.865788214	0.0398942	PHATRDRAFT_23224	K15305|1|4e-142|503|bdi:100824122|vacuole morphology and inheritance protein 14	-	GO:0008047//enzyme activator activity	GO:0016310//phosphorylation		GO:0016310//phosphorylation
7195270	69	22	44.87	24.63	-0.865334556	0.01173222	PHATRDRAFT_22921	K15272|1|6e-20|96.7|ota:Ot16g00800|solute carrier family 35 (UDP-sugar transporter), member A1/2/3	GO:0012505//endomembrane system;GO:0031224//intrinsic component of membrane	GO:0015215//nucleotide transmembrane transporter activity;GO:0005402//cation:sugar symporter activity	GO:0006862//nucleotide transport		GO:0006862//nucleotide transport
7201281	47	15	36.92	20.29	-0.863633688	0.0398942	PHATRDRAFT_12577	K04345|1|4e-70|263|aly:ARALYDRAFT_480465|protein kinase A [EC:2.7.11.11]	-	GO:0004721//phosphoprotein phosphatase activity;GO:0043169//cation binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195904	150	48	51.05	28.09	-0.861854337	0.000182043	PHATRDRAFT_49410	-	-	-	-		-
7198378	156.1	49.99	39.66	21.83	-0.861372547	8.94E-05	PHATRDRAFT_49810	-	-	-	-		-
7197196	56	18	12.17	6.72	-0.85679603	0.0255848	PHATRDRAFT_43504	K14827|1|3e-06|53.1|olu:OSTLU_17102|pre-rRNA-processing protein IPI1	-	-	-		-
7199669	84	27	42.52	23.51	-0.854867058	0.00577662	PHATRDRAFT_1631	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7195631	53	17	65.72	36.36	-0.853980281	0.0296406	PHATRDRAFT_49186	-	-	-	-		-
7204000	174	56	73.81	40.86	-0.853127086	6.22E-05	hNpl4	K14015|1|3e-32|138|cme:CMH273C|nuclear protein localization protein 4 homolog	-	-	-		-
7204862	115	37	103.42	57.33	-0.851153026	0.001188522	PHATRDRAFT_bd1717	-	-	-	-		-
7199277	87	28	73.23	40.6	-0.850955068	0.00501966	PHATRDRAFT_50486	-	-	-	-		-
7204685	176	57	78.56	43.77	-0.843852546	6.56E-05	PHATR_13232	K00318|1|3e-91|334|vcn:VOLCADRAFT_64330|proline dehydrogenase [EC:1.5.99.8]	-	GO:0046872//metal ion binding;GO:0016645//oxidoreductase activity, acting on the CH-NH group of donors	GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process		GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process
7195776	123	40	24.26	13.56	-0.839222372	0.000952772	PHATRDRAFT_49385	K03515|1|3e-74|278|rcu:RCOM_0810900|DNA repair protein REV1 [EC:2.7.7.-]	-	GO:0003677//DNA binding;GO:0034061	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7198579	46	15	28.03	15.73	-0.833453074	0.0489464	PHATRDRAFT_49855	-	-	-	-		-
7198461	52	17	24.44	13.74	-0.830862281	0.0362536	PHATRDRAFT_49794	-	-	-	-		-
7203207	52	17	19.69	11.07	-0.830807889	0.0362536	PHATRDRAFT_47967	K15429|1|2e-39|162|smo:SELMODRAFT_128902|tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]	-	-	-		-
7203882	132	43	220.59	124.14	-0.82939934	0.000632236	CYCP6	-	-	GO:0016407//acetyltransferase activity;GO:0019900//kinase binding	GO:0051726//regulation of cell cycle		GO:0051726//regulation of cell cycle
7200444	55	18	23.73	13.36	-0.828792093	0.0312512	PHATRDRAFT_45658	-	-	-	-		-
7202842	58	19	32.02	18.05	-0.826974471	0.0269646	PHATRDRAFT_47647	-	-	-	-		-
7205020	291.66	95.72	104.96	59.24	-0.825196079	3.55E-07	PHATRDRAFT_bd1646	-	-	-	-		-
7195839	70	23	15.88	8.97	-0.824031022	0.0150644	PHATRDRAFT_49498	-	-	-	-		-
7203395	76	25	49.42	27.99	-0.820183524	0.01130436	PHATRDRAFT_54879	-	-	-	-		-
7201066	94	31	22.84	12.95	-0.818610553	0.00483392	PHATRDRAFT_46005	-	GO:0005737//cytoplasm	-	-		-

7205019	91	30	42.07	23.86	-0.818197775	0.00556324	PHATRDRAFT_bd36	K01230|1|5e-106|383|bdi:100824763|mannosyl-oligosaccharide alpha-1,2-mannosidase [EC:3.2.1.113]	-	GO:0046872//metal ion binding;GO:0015924	-		-
7204021	88	29	70.99	40.29	-0.817194008	0.0064051	PHATR_44077	-	-	GO:0036094//small molecule binding	-		-
7203399	58.5	19.33	25.71	14.61	-0.815373432	0.0269646	PHATRDRAFT_48278	-	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7198713	2086	690	1840.72	1048.99	-0.811269264	3.86E-41	PHATRDRAFT_23658	K03839|1|2e-35|147|olu:OSTLU_87975|flavodoxin I	-	GO:0003824//catalytic activity;GO:0032553	GO:0044710		GO:0044710
7202798	274.52	91	127.74	72.85	-0.810209478	1.48E-06	PHATRDRAFT_47573	-	-	-	-		-
7194957	60	20	11.33	6.49	-0.803857478	0.0282842	PHATRDRAFT_48878	-	-	-	-		-
7200291	54	18	21.53	12.34	-0.803005925	0.0380364	PHATRDRAFT_45086	-	-	-	-		-
7202491	96	32	41.31	23.68	-0.802821979	0.0050656	PHATRDRAFT_47324	-	-	-	-		-
7196766	57	19	29.84	17.11	-0.802407776	0.0327842	PHATRDRAFT_43169	K12450|1|1e-06|52.8|osa:4332425|UDP-glucose 4,6-dehydratase [EC:4.2.1.76]	GO:0009536//plastid	GO:0036094//small molecule binding;GO:0048037//cofactor binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7201309	93	31	51.86	29.75	-0.801732538	0.00583022	PHATRDRAFT_46061	-	-	-	-		-
7197916	60	20	35.54	20.39	-0.801581906	0.0282842	PHATRDRAFT_44677	-	-	-	-		-
7197733	78	26	61.93	35.56	-0.800383122	0.011851	PHATRDRAFT_44519	-	-	-	-		-
7201530	57	19	63.39	36.43	-0.799128273	0.0327842	PHATRDRAFT_12863	-	-	-	-		-
7198624	963	322	323.03	185.74	-0.798383615	2.95E-19	PHATRDRAFT_49926	-	-	-	-		-
7195494	472	158	151.23	87.05	-0.796828157	3.89E-10	ISIP1	-	-	-	-		-
7195567	191	64	76.52	44.1	-0.795058218	7.65E-05	PHATRDRAFT_49277	K07466|1|7e-08|57.4|aly:ARALYDRAFT_329623|replication factor A1	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7201316	161	54	90.94	52.49	-0.792872407	0.000294652	PHATRDRAFT_12894	K00953|1|2e-36|151|bdi:100841620|FAD synthetase [EC:2.7.7.2]	-	-	GO:0009108//coenzyme biosynthetic process		GO:0009108//coenzyme biosynthetic process
7200529	131	44	46.23	26.7	-0.791989621	0.001151646	PHATRDRAFT_45404	K02065|1|7e-07|54.3|gmx:100789283|putative ABC transport system ATP-binding protein;K05658|3|8e-06|50.8|mtr:MTR_1g025560|ATP-binding cassette, subfamily B (MDR/TAP), member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7204521	715	240	361.89	209.01	-0.791979274	1.60E-14	PHATR_46747	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7203677	113	38	71.5	41.39	-0.788660993	0.00263538	PHATRDRAFT_48436	-	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7204572	297	100	119.8	69.38	-0.788036162	9.11E-07	PHATR_46645	-	-	-	-		-
7204108	101	34	58.25	33.75	-0.787370548	0.00460186	PHATR_44195	-	-	-	-		-
7197320	77	26	22.06	12.81	-0.784162315	0.01429202	PHATRDRAFT_43596	-	-	-	-		-
7198218	74	25	32.65	18.98	-0.782602999	0.01650384	PHATRDRAFT_49547	-	-	-	-		-
7200332	201	68	74.12	43.12	-0.781505703	6.37E-05	PHATRDRAFT_45149	-	-	-	-		-
7197845	56	19	27.33	15.96	-0.776024808	0.0397206	PHATRDRAFT_44373	K15429|1|1e-63|242|vcn:VOLCADRAFT_81828|tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]	-	-	-		-
7204451	109	37	48.06	28.07	-0.775807585	0.0036295	PHATR_36976	K03834|1|9e-55|213|smo:SELMODRAFT_93357|tyrosine-specific transport protein	-	-	-		-
7197380	106	36	54.79	32.02	-0.774939296	0.00417252	PHATRDRAFT_9947	K08150|1|2e-51|201|vvi:100268023|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0015145//monosaccharide transmembrane transporter activity	GO:0044763;GO:0015749//monosaccharide transport		GO:0044763;GO:0015749//monosaccharide transport
7200514	100	34	44.94	26.28	-0.774034849	0.00551996	PHATRDRAFT_45701	-	-	GO:0043168//anion binding;GO:0003824//catalytic activity	-		-
7201431	247	84	76.78	44.9	-0.774015115	1.07E-05	PHATRDRAFT_46086	K06184|1|6e-41|167|gmx:100806226|ATP-binding cassette, subfamily F, member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7194930	80	27	221.13	129.4	-0.773057147	0.01238376	PHATRDRAFT_15217	K15919|1|4e-13|70.9|mtr:MTR_4g013100|hydroxypyruvate reductase 2	-	GO:0036094//small molecule binding;GO:0016614//oxidoreductase activity, acting on CH-OH group of donors	GO:0044710		GO:0044710

7200136	144	49	60.77	35.57	-0.772698317	0.000830202	PHATRDRAFT_26862	K08679|1|1e-58|225|vvi:100247175|UDP-glucuronate 4-epimerase [EC:5.1.3.6]	-	GO:0036094//small molecule binding;GO:0016854//racemase and epimerase activity;GO:0048037//cofactor binding	GO:0044238		GO:0044238
7201604	179	61	66.6	39.03	-0.770938715	0.000194401	PHATRDRAFT_46530	-	-	-	-		-
7194708	103	35	133.76	78.42	-0.770353206	0.00479836	UBC2	K06689|1|3e-70|262|cme:CMD152C|ubiquitin-conjugating enzyme E2 D/E [EC:6.3.2.19]	-	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7196668	85	29	22.36	13.12	-0.769152468	0.01118702	PHATRDRAFT_42478	K15732|1|1e-10|67.0|cme:CMP176C|RNA polymerase II subunit A C-terminal domain phosphatase [EC:3.1.3.16]	-	-	-		-
7196396	181	62	99.92	58.9	-0.762505843	0.000202144	PHATRDRAFT_8945	K00827|1|4e-30|130|ppp:PHYPADRAFT_178763|alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase [EC:2.6.1.44 2.6.1.40]	-	GO:0043168//anion binding;GO:0016769//transferase activity, transferring nitrogenous groups	-		-
7201626	70	24	21.61	12.74	-0.762333795	0.0229554	PHATRDRAFT_13053	K12867|1|5e-115|413|olu:OSTLU_42299|pre-mRNA-splicing factor SYF1	GO:0044464	-	GO:0010467//gene expression		GO:0010467//gene expression
7199436	76	26.01	84.53	49.87	-0.761291247	0.01718892	PHATRDRAFT_31375	K12197|1|8e-35|144|olu:OSTLU_29213|charged multivesicular body protein 1	-	-	GO:0009790//embryo development;GO:0045184//establishment of protein localization		GO:0009790//embryo development;GO:0045184//establishment of protein localization
7204292	102	35	35.3	20.83	-0.761005344	0.005742	PHATR_43878	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7202993	67	23	22.77	13.44	-0.760601153	0.0265552	PHATRDRAFT_21982	K11835|1|6e-81|300|aly:ARALYDRAFT_326514|ubiquitin carboxyl-terminal hydrolase 4/11/15 [EC:3.1.2.15]	-	GO:0008233//peptidase activity;GO:0016790//thiolester hydrolase activity	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7198447	332	114	111.08	65.59	-0.760051302	4.79E-07	PHATRDRAFT_49769	K00924|1|6e-15|81.3|osa:4341290|[EC:2.7.1.-];K08286|2|4e-14|78.6|ath:AT4G28490|protein-serine/threonine kinase [EC:2.7.11.-];K13415|3|3e-12|72.4|pop:POPTR_650846|protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1];K13420|4|3e-11|68.9|ath:AT5G46330|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7201479	99	34	39.33	23.23	-0.759641032	0.00660682	PHATRDRAFT_46275	-	-	-	GO:0044238		GO:0044238
7196335	64	22	14.43	8.53	-0.758453653	0.0307428	PHATRDRAFT_42685	-	-	-	-		-
7202370	64	22	19.63	11.61	-0.757692201	0.0307428	PHATRDRAFT_47287	-	-	-	-		-
7202965	137	47	162.23	95.99	-0.757084609	0.001301396	PHATRDRAFT_38130	K12194|1|1e-15|80.9|ath:AT2G19830|charged multivesicular body protein 4	-	-	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7204533	93	32	40.55	24	-0.756667509	0.00875688	PHATR_46770	K06185|1|1e-18|92.8|ota:Ot05g02490|ATP-binding cassette, subfamily F, member 2	GO:0009536//plastid	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7196472	145	50	45.42	26.93	-0.754113476	0.00102795	PHATRDRAFT_42896	-	-	-	-		-
7195925	110	38	36.49	21.68	-0.751136394	0.00450844	PHATRDRAFT_49443	-	-	-	-		-
7196561	90	31	129.67	77.1	-0.750041976	0.01008778	PHATRDRAFT_43181	-	-	-	-		-
7199957	81	28	47.34	28.16	-0.749412372	0.01546486	PHATRDRAFT_11735	K03063|1|9e-168|587|rcu:RCOM_1270490|26S proteasome regulatory subunit T3	GO:0043234//protein complex;GO:0044424	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0009057//macromolecule catabolic process;GO:0019538//protein metabolic process		GO:0009057//macromolecule catabolic process;GO:0019538//protein metabolic process
7202633	188.64	65.32	81.17	48.34	-0.74772914	0.000190396	PHATRDRAFT_47569	-	-	-	-		-
7204082	75	26	33.34	19.88	-0.745936347	0.0206156	PHATR_44153	-	-	-	-		-
7196500	1195	415	397.01	237.08	-0.743801384	5.01E-21	PHATRDRAFT_42846	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-

7199268	95	33	35.79	21.38	-0.743294691	0.00908338	PHATRDRAFT_50468	-	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0050694//galactose 3-O-sulfotransferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7201982	72	25	57.58	34.44	-0.741482646	0.0238242	PHATRDRAFT_37371	K07750|1|1e-10|65.1|ota:Ot05g04520|methylsterol monooxygenase [EC:1.14.13.72];K00227|3|2e-07|54.7|osa:4325687|lathosterol oxidase [EC:1.14.21.6]	GO:0031224//intrinsic component of membrane	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7201367	89	31	27.05	16.2	-0.739634781	0.01205308	PHATRDRAFT_46151	-	GO:0044464	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding	-		-
7195546	66	23	36.8	22.07	-0.737619137	0.031883	PHATRDRAFT_49251	-	-	-	-		-
7198925	63	22	18.91	11.36	-0.735186528	0.0369258	PHATRDRAFT_23798	K15450|1|1e-09|63.9|vvi:100257307|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-]	-	-	-		-
7200747	106	37	88.1	52.97	-0.733966511	0.00617442	PHATRDRAFT_54435	-	-	GO:0060089	GO:0007154//cell communication		GO:0007154//cell communication
7199258	214	75	47.63	28.69	-0.731322581	9.80E-05	ATPase2-3A	K01535|1|2e-99|362|vcn:VOLCADRAFT_103448|H+-transporting ATPase [EC:3.6.3.6]	GO:0031224//intrinsic component of membrane	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0043169//cation binding;GO:0008324//cation transmembrane transporter activity	GO:0009152//purine ribonucleotide biosynthetic process;GO:0009154//purine ribonucleotide catabolic process;GO:0006811//ion transport		GO:0009152//purine ribonucleotide biosynthetic process;GO:0009154//purine ribonucleotide catabolic process;GO:0006811//ion transport
7197303	154	54	42.94	25.89	-0.729927226	0.000996494	PHATRDRAFT_32803	K01551|1|3e-46|185|cre:CHLREDRAFT_132949|arsenite-transporting ATPase [EC:3.6.3.16]	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process		GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process
7196204	154	54	119.25	72.02	-0.727519762	0.000996494	dsCYC5	K06627|1|2e-14|78.2|pop:POPTR_548650|cyclin A	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7203405	6000.61	2110.96	587.57	355.14	-0.726372874	7.27E-95	PHATRDRAFT_48047	-	-	-	-		-
7198080	415	146	142.18	86.02	-0.724974504	6.29E-08	PHATRDRAFT_54257	K00967|1|2e-06|53.1|zma:100382955|ethanolamine-phosphate cytidylyltransferase [EC:2.7.7.14]	-	GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7203312	71	25	26.37	15.97	-0.723533258	0.0284996	PHATRDRAFT_48175	K05941|1|8e-39|160|cme:CMI111C|glutathione gamma-glutamylcysteinyltransferase [EC:2.3.2.15]	-	GO:0043169//cation binding;GO:0016755	GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process		GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process
7201649	71	25	26.83	16.25	-0.723407336	0.0284996	PHATRDRAFT_56506	-	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7198594	85	30	32.68	19.84	-0.719995958	0.01656134	PHATRDRAFT_49878	-	-	GO:0046872//metal ion binding	-		-
7196967	167	59	39.4	23.92	-0.71997824	0.00070821	PGAM_2	K01834|1|2e-55|216|zma:100273347|2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.1]	-	GO:0016868//intramolecular transferase activity, phosphotransferases	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7203985	241	85	220.04	133.72	-0.718550548	4.26E-05	PHATR_18620	K12198|1|1e-23|108|ppp:PHYPADRAFT_163299|charged multivesicular body protein 5	-	-	-		-
7203370	263	93	80.2	48.76	-0.717904111	2.05E-05	PHATRDRAFT_48267	-	-	-	-		-
7200889	65	23	16.33	9.93	-0.717659168	0.038159	PHATRDRAFT_45737	-	-	-	-		-
7198702	114.21	40.45	36.01	21.93	-0.715491788	0.00483436	PHATRDRAFT_49998	-	-	-	-		-
7199709	62	22	19.29	11.77	-0.712738823	0.0442066	PHATRDRAFT_44729	K13210|1|1e-20|100|ppp:PHYPADRAFT_80579|far upstream element-binding protein	-	GO:0003676//nucleic acid binding	-		-

7195789	76	27	26.07	15.92	-0.711550247	0.0254504	PHATRDRAFT_55040	K00102|1|5e-93|340|aly:ARALYDRAFT_487468|D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	-	GO:0004457//lactate dehydrogenase activity;GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7202375	138	49	103.22	63.11	-0.709782007	0.00232846	PHATRDRAFT_37468	-	-	-	-		-
7201656	813	290	372.23	228.42	-0.704505359	1.29E-13	PHATRDRAFT_46406	-	-	-	-		-
7199241	98	35	22.19	13.62	-0.704182964	0.0115205	PHATRDRAFT_50519	K00870|1|9e-15|81.3|cme:CMD015C|protein kinase [EC:2.7.1.37];K13430|2|9e-15|81.3|osa:4329463|serine/threonine-protein kinase PBS1 [EC:2.7.11.1];K00924|3|2e-14|80.1|aly:ARALYDRAFT_475717|[EC:2.7.1.-];K04424|4|2e-14|80.1|olu:OSTLU_6189|sterile alpha motif and leucine zipper containing kinase AZK [EC:2.7.11.25];K13414|5|2e-14|79.7|vvi:100241228|mitogen-activated protein kinase kinase kinase 1, plant [EC:2.7.11.25]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198324	1185	424	486.33	299.31	-0.700295109	5.62E-19	PHATRDRAFT_55087	-	-	-	-		-
7198479	316	113	306.83	189.09	-0.698366479	4.60E-06	Lhcf5	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7202676	209	75	129.75	80.15	-0.694960113	0.000221936	PHATRDRAFT_14345	K10592|1|2e-69|260|vcn:VOLCADRAFT_75266|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7197596	78	28	46.2	28.54	-0.694907517	0.0262088	PHATRDRAFT_43293	-	-	-	-		-
7202618	58.41	20.98	24.15	14.92	-0.694775653	0.0413084	PHATRDRAFT_47240	-	-	-	-		-
7197637	103	37	49.07	30.33	-0.694095773	0.01030736	FBPC4	K03841|1|5e-70|263|cme:CMO245C|fructose-1,6-bisphosphatase I [EC:3.1.3.11]	-	GO:0050308//sugar-phosphatase activity	GO:0044238		GO:0044238
7200422	164	59	57.57	35.62	-0.692629696	0.001159176	PHATRDRAFT_45672	K08202|1|6e-17|87.8|cre:CHLREDRAFT_103526|MFS transporter, OCT family, solute carrier family 22 (organic cation transporter), member 4/5;K08150|2|1e-13|76.6|smo:SELMODRAFT_168181|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7201170	139	50	55.42	34.29	-0.692618807	0.00282802	MMSDH	K00140|1|3e-90|330|cre:CHLREDRAFT_130434|malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27]	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7201257	89	32	49.34	30.53	-0.692530126	0.01758044	PHATRDRAFT_46182	-	-	-	-		-
7198183	103	37	115.33	71.43	-0.691165814	0.01030736	PHATRDRAFT_23324	K02868|1|9e-71|264|mtr:MTR_3g007700|large subunit ribosomal protein L11e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7201477	78	28	109.04	67.56	-0.690616234	0.0262088	PHATRDRAFT_46273	-	-	-	-		-
7204411	147	53	65.7	40.75	-0.689093311	0.00221528	PHATR_46673	-	-	-	-		-
7204670	164	59	177.88	110.33	-0.68907918	0.001159176	PHATR_36846	-	-	-	-		-
7204906	94.02	34	39.17	24.37	-0.684642877	0.01568954	PHATRDRAFT_bd1558	K01362|1|2e-13|75.5|olu:OSTLU_44226|[EC:3.4.21.-];K09566|2|7e-07|53.9|mtr:MTR_3g107660|peptidyl-prolyl isomerase G (cyclophilin G) [EC:5.2.1.8]	-	GO:0005515//protein binding;GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process;GO:0044092//negative regulation of molecular function		GO:0019538//protein metabolic process;GO:0044092//negative regulation of molecular function

7194764	94	34	37.64	23.42	-0.684525552	0.01568954	PHATRDRAFT_48512	K10582|1|1e-12|73.2|ppp:PHYPADRAFT_168742|ubiquitin-conjugating enzyme E2 Q [EC:6.3.2.19]	-	GO:0016879//ligase activity, forming carbon-nitrogen bonds	-		-
7195214	268	97	158.17	98.53	-0.682841028	3.72E-05	PHATRDRAFT_48923	-	-	-	-		-
7198752	127	46	75.84	47.28	-0.681728929	0.00488132	PHATRDRAFT_23709	K15100|1|7e-41|166|ota:Ot07g03360|solute carrier family 25 (mitochondrial citrate transporter), member 1	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization; GO:0044763		GO:0051234//establishment of localization; GO:0044763
7198794	102	37	30.32	18.91	-0.68112039	0.01217454	PHATRDRAFT_30807	K00278|1|2e-63|242|rcu:RCOM_0850500|L-aspartate oxidase [EC:1.4.3.16]	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201965	135	49	32.08	20.01	-0.680952975	0.00381336	PHATRDRAFT_47188	K14319|1|8e-13|74.7|aly:ARALYDRAFT_907895|Ran GTPase-activating protein 1	-	-	-		-
7198788	201	73	63.78	39.83	-0.679248618	0.000397974	PHATRDRAFT_50012	-	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization; GO:0044763		GO:0051234//establishment of localization; GO:0044763
7199757	124	45	64.24	40.12	-0.679150287	0.00559762	PHATRDRAFT_44804	K08506|1|4e-11|67.8|osa:4339549|syntaxin of plants SYP7	-	-	-		-
7204866	1131	411	434.85	271.78	-0.67807854	2.86E-17	PHATRDRAFT_bd1645	K00434|1|1e-08|59.7|gmx:100170727|L-ascorbate peroxidase [EC:1.11.1.11]	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7198646	66	24	20.69	12.94	-0.677096028	0.0467566	PHATRDRAFT_40792	-	-	-	-		-
7200103	192	70	100.03	62.75	-0.672745379	0.000592406	PHATRDRAFT_45223	-	-	-	-		-
7195076	74	27	29.74	18.66	-0.672455661	0.0358784	PHATRDRAFT_54954	K13412|1|4e-07|54.7|mtr:MTR_5g009830|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0046872//metal ion binding;GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7197080	175	64	94.93	59.74	-0.668166846	0.001124054	PHATRDRAFT_18029	K03644|1|1e-105|381|gmx:100775835|lipoic acid synthetase [EC:2.8.1.8]	-	-	-		-
7204925	157.26	57.57	51.13	32.19	-0.667557449	0.001782588	PHATRDRAFT_bd1603	-	-	GO:0003824//catalytic activity	-		-
7203546	90	33	19.59	12.34	-0.666775003	0.0213184	PHATRDRAFT_48242	-	-	GO:0003723//RNA binding	-		-
7202730	71	26	36.55	23.03	-0.666356995	0.041447	CCDA	K06196|1|7e-23|106|ppp:PHYPADRAFT_146798|cytochrome c-type biogenesis protein	-	-	GO:0043623//cellular protein complex assembly;GO:0044710		GO:0043623//cellular protein complex assembly;GO:0044710
7202932	71	26	63.25	39.9	-0.664676733	0.041447	Lhcr6	K08907|1|3e-17|87.0|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08916|2|7e-17|85.9|vcn:VOLCADRAFT_104309|light-harvesting complex II chlorophyll a/b binding protein 5	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7204278	329	121	150.32	95.11	-0.660368031	9.00E-06	PHATR_43850	K03539|1|4e-07|54.7|bdi:100830772|ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5];K12127|2|9e-07|53.5|pop:POPTR_784463|pseudo-response regulator 1	-	-	-		-
7195933	68	25	41.74	26.42	-0.659800134	0.0479098	PHATRDRAFT_40163	K00967|1|4e-88|323|zma:100384780|ethanolamine-phosphate cytidylyltransferase [EC:2.7.7.14]	-	GO:0016779//nucleotidyltransferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7198756	247	91	71.51	45.29	-0.658952464	0.000129551	PHATRDRAFT_23723	K13354|1|7e-28|124|smo:SELMODRAFT_160785|solute carrier family 25 (peroxisomal adenine nucleotide transporter), member 17;K00133|4|2e-19|96.7|ota:Ot01g02440|aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization

7205097	190	70	51.03	32.32	-0.658918444	0.000809586	PHATRDRAFT_bd645	K01895|1|0.0|663|rcu:RCOM_1443610|acetyl-CoA synthetase [EC:6.2.1.1]	-	GO:0016405//CoA-ligase activity;GO:0032550	GO:0006083//acetate metabolic process		GO:0006083//acetate metabolic process
7201605	125	46	78.49	49.72	-0.658682563	0.00673872	Pt-KIF11	K10406|1|3e-53|207|sbi:SORBI_01g049720|kinesin family member C2/C3	GO:0015630//microtubule cytoskeleton	GO:0032550;GO:0003777//microtubule motor activity	GO:0016458//gene silencing;GO:0048444//floral organ morphogenesis;GO:0016570//histone modification;GO:0006928//cellular component movement;GO:0043414		GO:0016458//gene silencing;GO:0048444//floral organ morphogenesis;GO:0016570//histone modification;GO:0006928//cellular component movement;GO:0043414
7197416	76	28	31.77	20.13	-0.658317918	0.0367434	PHATRDRAFT_18087	K01756|1|4e-136|483|cme:CMQ211C|adenylosuccinate lyase [EC:4.3.2.2]	-	GO:0016842	GO:0006164//purine nucleotide biosynthetic process		GO:0006164//purine nucleotide biosynthetic process
7202641	114	42	54.43	34.5	-0.657805674	0.00993002	PHATRDRAFT_47583	K00059|1|5e-27|120|rcu:RCOM_1081890|3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202989	1160	428	173.6	110.07	-0.657345637	8.96E-17	PHATRDRAFT_47863	-	-	-	-		-
7202877	138	51	60.73	38.61	-0.653434815	0.00469218	PHATRDRAFT_37960	K00464|1|8e-16|83.6|cre:CHLREDRAFT_151463|all-trans-8’-apo-beta-carotenal 15,15’-oxygenase [EC:1.14.99.41];K09840|5|6e-11|67.4|gmx:100780284|9-cis-epoxycarotenoid dioxygenase [EC:1.13.11.51]	-	-	-		-
7202420	100	37	63.16	40.22	-0.65109809	0.0168721	PHATRDRAFT_14003	K00924|1|6e-75|279|osa:4326374|[EC:2.7.1.-];K08287|2|5e-74|276|aly:ARALYDRAFT_914113|dual-specificity kinase [EC:2.7.12.1];K08823|5|3e-60|230|olu:OSTLU_50484|CDC-like kinase [EC:2.7.12.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199216	81	30	36.43	23.21	-0.650380472	0.0325788	PHATRDRAFT_50408	K15109|1|3e-11|68.2|ppp:PHYPADRAFT_220012|solute carrier family 25 (mitochondrial carnitine/acylcarnitine transporter), member 20/29	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7194992	151	56	81.44	51.97	-0.648058502	0.0032738	PHATRDRAFT_48720	-	-	-	-		-
7199750	70	26	25.46	16.26	-0.646905162	0.0489866	PHATRDRAFT_44792	-	-	-	-		-
7197616	369	137	237.15	151.57	-0.645815637	3.84E-06	chk2	K08794|1|3e-57|220|vcn:VOLCADRAFT_79621|calcium/calmodulin-dependent protein kinase I [EC:2.7.11.17];K00908|2|1e-56|218|cme:CMF051C|Ca2+/calmodulin-dependent protein kinase [EC:2.7.11.17];K13412|3|8e-54|209|cre:CHLREDRAFT_182699|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0032550;GO:0004674//protein serine/threonine kinase activity	GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process		GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process
7195308	94	35	53.6	34.35	-0.641922902	0.0222886	PHATRDRAFT_49062	-	-	-	-		-
7200448	83	31	16.64	10.68	-0.639743786	0.0332694	UBA1	K03178|1|3e-108|391|sbi:SORBI_02g043880|ubiquitin-activating enzyme E1 [EC:6.3.2.19]	-	GO:0003824//catalytic activity;GO:0032550	GO:0036211		GO:0036211
7198610	233	87	88.65	56.93	-0.638931531	0.00029511	PHATRDRAFT_16391	K08956|1|7e-163|572|osa:4339002|AFG3 family protein [EC:3.4.24.-]	GO:0016020//membrane	GO:0004175//endopeptidase activity;GO:0043167//ion binding;GO:0016462//pyrophosphatase activity;GO:0032550	GO:0009057//macromolecule catabolic process;GO:0019538//protein metabolic process		GO:0009057//macromolecule catabolic process;GO:0019538//protein metabolic process
7202109	398	149	196.75	126.73	-0.634605551	2.34E-06	PHATRDRAFT_47015	-	-	-	-		-
7204510	85	32	35.99	23.3	-0.627266147	0.033921	PHATR_46733	-	-	-	-		-
7198154	122	46	51.78	33.58	-0.624792735	0.01077848	PHATRDRAFT_49671	K13420|1|3e-25|114|vvi:100253808|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-

7202402	98	37	33.88	21.99	-0.62358627	0.023171	Rab6	K07893|1|1e-65|249|ppp:PHYPADRAFT_152083|Ras-related protein Rab-6A	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7203375	106	40	49.89	32.39	-0.623202201	0.01791766	PHATRDRAFT_48273	-	-	-	-		-
7205077	86.74	32.8	26.17	17.01	-0.621530783	0.0288924	PHATRDRAFT_bd1566	-	-	-	-		-
7201155	209	79	84.82	55.15	-0.621043597	0.000834006	PHATRDRAFT_20547	K01687|1|0.0|741|olu:OSTLU_34354|dihydroxy-acid dehydratase [EC:4.2.1.9]	GO:0009536//plastid	GO:0003676//nucleic acid binding;GO:0016836//hydro-lyase activity	GO:0008652//cellular amino acid biosynthetic process		GO:0008652//cellular amino acid biosynthetic process
7195368	418	158	366.39	238.6	-0.618786085	2.07E-06	PHATRDRAFT_48950	-	-	-	-		-
7203538	103	39	48.44	31.55	-0.61855886	0.0205528	PHATRDRAFT_48230	-	-	-	-		-
7203542	182	69	48.52	31.63	-0.617285995	0.001969746	PHATRDRAFT_48237	-	-	-	-		-
7200712	87	33	19.51	12.72	-0.617115107	0.0345352	PHATRDRAFT_45496	K03714|1|9e-31|134|ppp:PHYPADRAFT_223790|glycoprotein 2-beta-D-xylosyltransferase [EC:2.4.2.38]	-	GO:0016740//transferase activity	-		-
7202708	108	41	20.25	13.21	-0.616291441	0.01823678	PHATRDRAFT_47704	K11835|1|8e-84|310|pop:POPTR_798230|ubiquitin carboxyl-terminal hydrolase 4/11/15 [EC:3.1.2.15]	-	GO:0070011//peptidase activity, acting on L-amino acid peptides;GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7196517	92	35	31.02	20.29	-0.612429821	0.030562	PHATRDRAFT_42871	-	-	-	-		-
7199710	134	51	44.9	29.39	-0.611390086	0.00867942	PHATRDRAFT_51720	K00234|1|1e-24|113|aly:ARALYDRAFT_480752|succinate dehydrogenase (ubiquinone) flavoprotein subunit [EC:1.3.5.1]	-	GO:0046906//tetrapyrrole binding;GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors	GO:0044710		GO:0044710
7198625	84	32	19.84	12.99	-0.611010595	0.0397202	PHATRDRAFT_49927	-	-	-	-		-
7201310	181	69	76.09	49.89	-0.608956193	0.00228254	PHATRDRAFT_46063	-	-	-	-		-
7201264	110	42	20.84	13.67	-0.608342035	0.01854168	PHATRDRAFT_46192	K06694|1|5e-06|52.4|bdi:100820844|26S proteasome non-ATPase regulatory subunit 10	-	-	-		-
7201942	123	47	31	20.36	-0.606530654	0.01276458	PHATRDRAFT_47155	-	-	-	-		-
7195419	2641	1008	1578.52	1036.96	-0.606212296	8.33E-32	ISIP2B	-	-	-	-		-
7202533	217	83	42.42	27.89	-0.604996687	0.000891608	PHATRDRAFT_47388	K15172|1|2e-82|306|gmx:100801380|transcription elongation factor SPT5	GO:0005622//intracellular	-	GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter		GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter
7204695	338	129	316.06	207.86	-0.604586305	2.93E-05	HSP20	K13993|1|2e-07|54.3|rcu:RCOM_0497910|HSP20 family protein	-	-	-		-
7203433	259	99	142.98	94.05	-0.604313509	0.000272536	PHATRDRAFT_48085	-	-	-	-		-
7195563	102	39	65.75	43.27	-0.603623774	0.0239694	PHATRDRAFT_49272	-	-	-	-		-
7200249	99	38	29.36	19.38	-0.599283397	0.0274868	PHATRDRAFT_45229	-	-	-	-		-
7198662	2722	1044	1652.47	1090.88	-0.599131671	4.26E-32	PHATRDRAFT_49834	-	-	-	-		-
7199247	164	63	36.84	24.32	-0.599129833	0.00431714	PHATRDRAFT_50430	-	-	-	-		-
7198068	151	58	25.81	17.04	-0.599004806	0.0062103	PHATRDRAFT_44535	K04886|1|3e-13|76.6|cre:CHLREDRAFT_144354|potassium voltage-gated channel Shab-related subfamily B member 2	GO:0005887//integral component of plasma membrane	GO:0005267//potassium channel activity	GO:0044763;GO:0030001//metal ion transport		GO:0044763;GO:0030001//metal ion transport
7198855	117	45	99.89	66.19	-0.593726986	0.0167034	PHATRDRAFT_50156	-	-	-	-		-
7204358	249	96	63.23	41.91	-0.593314698	0.000460014	PHATR_43917	-	-	-	GO:0046488//phosphatidylinositol metabolic process		GO:0046488//phosphatidylinositol metabolic process
7199108	109	42	41.76	27.68	-0.593277769	0.0215614	PHATRDRAFT_41173	-	-	-	-		-
7196590	123.17	47.49	50.84	33.71	-0.592787403	0.01276458	PHATRDRAFT_32401	-	-	-	-		-
7200414	464	179	150.65	99.93	-0.592210913	1.65E-06	PHATRDRAFT_45657	K00469|1|2e-20|99.8|ath:AT1G14520|inositol oxygenase [EC:1.13.99.1]	GO:0044424	GO:0046914//transition metal ion binding;GO:0016701//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0006020//inositol metabolic process		GO:0006020//inositol metabolic process
7198082	96	37	118.81	78.99	-0.588914343	0.031526	PHATRDRAFT_10972	-	-	GO:0003824//catalytic activity;GO:0032553	GO:0044710		GO:0044710

<table>
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<tr><td>7202992</td><td>119</td><td>46</td><td>72.85</td><td>48.47</td><td>-0.58783689</td><td>0.01694448</td><td>PHATRDRAFT_47866</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7196953</td><td>109.83</td><td>42.51</td><td>38.99</td><td>25.95</td><td>-0.587369616</td><td>0.0215614</td><td>PHATRDRAFT_43232</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
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<tr><td>7204626</td><td>119</td><td>46</td><td>122.41</td><td>81.56</td><td>-0.58578774</td><td>0.01694448</td><td>PHATR_46718</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
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<tr><td>7201549</td><td>1199</td><td>465</td><td>580.49</td><td>387.33</td><td>-0.583707967</td><td>2.26E-14</td><td>PHATRDRAFT_46448</td><td>K13993|1|2e-09|62.4|zma:100282088|HSP20 family protein</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7198453</td><td>237</td><td>92</td><td>111.38</td><td>74.38</td><td>-0.582503545</td><td>0.000763744</td><td>PHATRDRAFT_49776</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7203907</td><td>319</td><td>124</td><td>177.89</td><td>119</td><td>-0.580023839</td><td>9.58E-05</td><td>PHATR_41807</td><td>K00654|1|4e-75|280|ppp:PHYPADRAFT_198015|serine palmitoyltransferase [EC:2.3.1.50]</td><td>-</td><td>GO:0043168//anion binding</td><td>GO:0008152//metabolic process</td><td></td><td>GO:0008152//metabolic process</td></tr>
<tr><td>7203113</td><td>347</td><td>135</td><td>175.36</td><td>117.39</td><td>-0.579010187</td><td>4.85E-05</td><td>PHATRDRAFT_47912</td><td>K15692|1|6e-12|70.5|ppp:PHYPADRAFT_16563|E3 ubiquitin-protein ligase RNF13 [EC:6.3.2.19];K11982|2|1e-09|63.2|ath:AT3G56580|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19]</td><td>-</td><td>GO:0046914//transition metal ion binding</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7200987</td><td>118</td><td>46</td><td>28.64</td><td>19.19</td><td>-0.577676781</td><td>0.01962488</td><td>PHATRDRAFT_45895</td><td>-</td><td>-</td><td>GO:0016298//lipase activity</td><td>GO:0044238</td><td></td><td>GO:0044238</td></tr>
<tr><td>7204748</td><td>139</td><td>54</td><td>182.31</td><td>122.2</td><td>-0.577149413</td><td>0.0105145</td><td>HSP20C</td><td>-</td><td>-</td><td>-</td><td>GO:0050896//response to stimulus</td><td></td><td>GO:0050896//response to stimulus</td></tr>
<tr><td>7204755</td><td>200</td><td>78</td><td>52.26</td><td>35.04</td><td>-0.57670435</td><td>0.00224826</td><td>FRE2</td><td>-</td><td>GO:0031224//intrinsic component of membrane</td><td>GO:0003824//catalytic activity</td><td>GO:0044710</td><td></td><td>GO:0044710</td></tr>
<tr><td>7195877</td><td>533.81</td><td>208.25</td><td>136.61</td><td>91.62</td><td>-0.576328626</td><td>5.42E-07</td><td>PHATRDRAFT_49357</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7203116</td><td>187</td><td>73</td><td>81.53</td><td>54.75</td><td>-0.57447205</td><td>0.00321882</td><td>MIZF</td><td>K14816|1|2e-22|105|ppp:PHYPADRAFT_147985|pre-60S factor REI1</td><td>GO:0044464</td><td>GO:0046914//transition metal ion binding</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7203030</td><td>333.56</td><td>130.29</td><td>146.4</td><td>98.37</td><td>-0.573625246</td><td>7.86E-05</td><td>PHATRDRAFT_51110</td><td>K02218|1|7e-145|512|ppp:PHYPADRAFT_141762|casein kinase 1 [EC:2.7.11.1]</td><td>-</td><td>GO:0004672//protein kinase activity;GO:0032550</td><td>GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process</td><td></td><td>GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process</td></tr>
<tr><td>7201782</td><td>92</td><td>36</td><td>24.07</td><td>16.19</td><td>-0.572133156</td><td>0.0420082</td><td>PHATRDRAFT_46419</td><td>K10268|1|6e-15|81.6|smo:SELMODRAFT_118815|F-box and leucine-rich repeat protein 2/20</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7201212</td><td>143</td><td>56</td><td>74.86</td><td>50.44</td><td>-0.569626773</td><td>0.01077792</td><td>PHATRDRAFT_46265</td><td>-</td><td>-</td><td>GO:0046914//transition metal ion binding</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7198750</td><td>176</td><td>69</td><td>37.99</td><td>25.6</td><td>-0.569475902</td><td>0.00467234</td><td>PHATRDRAFT_50061</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7201727</td><td>97</td><td>38</td><td>50.14</td><td>33.8</td><td>-0.56893875</td><td>0.0370876</td><td>PHATRDRAFT_36595</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7196339</td><td>260</td><td>102</td><td>63.31</td><td>42.7</td><td>-0.568197326</td><td>0.000570584</td><td>PHATRDRAFT_42694</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
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<tr><td>7199360</td><td>210</td><td>83</td><td>56.15</td><td>38.15</td><td>-0.557602966</td><td>0.00237868</td><td>PHATRDRAFT_50575</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
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7198134	96	38	18.32	12.46	-0.556115435	0.0429274	PHATRDRAFT_44658	K10400|1|8e-09|61.6|pop:POPTR_927223|kinesin family member 15;K10696|2|1e-06|54.3|mtr:MTR_087s0035|E3 ubiquitin-protein ligase BRE1 [EC:6.3.2.19];K06675|3|2e-06|53.9|bdi:100831033|structural maintenance of chromosome 4;K03254|4|2e-06|53.9|osa:4326038|translation initiation factor 3 subunit A	-	-	-		-
7198997	562.19	222.75	144.78	98.61	-0.554056459	5.56E-07	PHATRDRAFT_50346	-	-	-	-		-
7204420	91	36	71.22	48.53	-0.553405576	0.0486738	PHATR_13322	-	-	GO:0003824//catalytic activity	-		-
7201307	126	50	13.79	9.4	-0.552889795	0.0205052	PHATRDRAFT_46058	K01110|1|7e-06|52.8|ath:AT5G39400|phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase [EC:3.1.3.67]	GO:0043234//protein complex	GO:0008092//cytoskeletal protein binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7200041	126	50	51.26	34.99	-0.550890814	0.0205052	PHATRDRAFT_45357	K01772|1|9e-106|382|smo:SELMODRAFT_439765|ferrochelatase [EC:4.99.1.1]	GO:0009536//plastid	GO:0004672//protein kinase activity;GO:0016829//lyase activity;GO:0005488//binding	GO:0016109;GO:0006089//lactate metabolic process;GO:0006779//porphyrin-containing compound biosynthetic process;GO:0006412//translation;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0005984//disaccharide metabolic process;GO:0005982//starch metabolic process;GO:0006396//RNA processing;GO:0006468//pro		GO:0016109;GO:0006089//lactate metabolic process;GO:0006779//porphyrin-containing compound biosynthetic process;GO:0006412//translation;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0005984//disaccharide metabolic process;GO:0005982//starch metabolic process;GO:0006396//RNA processing;GO:0006468//pro
7204565	292	116	123.14	84.15	-0.549264297	0.000385812	PHATR_46841	-	-	-	-		-
7200377	98	39	26.9	18.41	-0.547116546	0.0433362	PHATRDRAFT_45596	-	-	-	-		-
7198802	435	173	346.22	237.16	-0.545828365	1.49E-05	PHATRDRAFT_50051	-	GO:0009536//plastid	-	GO:0044249//cellular biosynthetic process;GO:1901576;GO:0044238;GO:0046483//heterocycle metabolic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901360//organic cyclic compound metabolic process;GO:0006725//cellular aromatic compound metabolic process;GO:0016043//cellular component organization		GO:0044249//cellular biosynthetic process;GO:1901576;GO:0044238;GO:0046483//heterocycle metabolic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901360//organic cyclic compound metabolic process;GO:0006725//cellular aromatic compound metabolic process;GO:0016043//cellular component organization
7197793	123	49	52.55	36.01	-0.545293165	0.0233734	PHATRDRAFT_44545	-	-	-	-		-
7204753	110	44	47.02	32.35	-0.539508827	0.0340788	PHATR_46926	-	-	-	-		-
7195272	130	52	75.44	51.93	-0.538761451	0.0208758	PHATRDRAFT_49010	-	-	-	-		-
7196331	843	337	658.21	453.17	-0.538495588	2.40E-09	PHATRDRAFT_53967	-	-	-	-		-
7204610	105	42	74.47	51.29	-0.537981786	0.0385822	PHATR_36721	K04640|1|1e-44|178|sbi:SORBI_01g045320|guanine nucleotide-binding protein subunit alpha, other	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0060089;GO:0032403//protein complex binding;GO:0017076//purine nucleotide binding	GO:0009154//purine ribonucleotide catabolic process;GO:0007166//cell surface receptor signaling pathway		GO:0009154//purine ribonucleotide catabolic process;GO:0007166//cell surface receptor signaling pathway
7200506	891	357	292.03	201.2	-0.537486278	1.04E-09	PHATRDRAFT_45416	K03363|1|5e-27|121|ath:AT4G33270|cell division cycle 20, cofactor of APC complex	-	-	-		-
7199746	157	63	29.61	20.42	-0.536101624	0.01153636	PHATRDRAFT_44785	-	-	-	-		-
7199578	486	195	189.3	130.63	-0.535188152	7.33E-06	PHATRDRAFT_44873	-	-	-	GO:0044238		GO:0044238

7200403	122	49	35.13	24.26	-0.534124026	0.0268556	PHATRDRAFT_20082	K12349|1|7e-166|582|pop:POPTR_576910|neutral ceramidase [EC:3.5.1.23]	GO:0005911//cell-cell junction;GO:0031090//organelle membrane	-	-		-
7202782	152	61	98.94	68.36	-0.533401502	0.01299926	PHATRDRAFT_47546	-	-	-	-		-
7202281	199	80	52.13	36.02	-0.533315679	0.00452724	PHATRDRAFT_47504	K07752|1|3e-09|62.8|sbi:SORBI_10g003060|carboxypeptidase D [EC:3.4.17.22]	-	GO:0046914//transition metal ion binding;GO:0008235//metalloexopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202705	281	113	71.55	49.46	-0.532689527	0.000722626	PHATRDRAFT_47698	K13414|1|9e-08|57.8|aly:ARALYDRAFT_489755|mitogen-activated protein kinase kinase kinase 1, plant [EC:2.7.11.25];K04427|2|1e-07|57.4|olu:OSTLU_42011|mitogen-activated protein kinase kinase kinase 7 [EC:2.7.11.25];K14510|4|3e-07|56.2|rcu:RCOM_0382890|serine/threonine-protein kinase CTR1 [EC:2.7.11.1];K08852|5|8e-07|54.7|ppp:PHYPADRAFT_164091|serine/threonine-protein kinase/endoribonuclease IRE1 [EC:2.7.11.1 3.1.26.-]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7201253	127	51	94.13	65.09	-0.532218681	0.0237668	PHATRDRAFT_46174	-	-	-	-		-
7197233	276	111	127.07	87.92	-0.531360173	0.000809832	PHATRDRAFT_43685	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7197170	309	124	362	250.53	-0.531006326	0.000362886	Rab5a	K07887|1|1e-55|214|osa:4333662|Ras-related protein Rab-5A;K07976|2|1e-53|207|olu:OSTLU_33115|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7200717	134	54	26.01	18.02	-0.529467388	0.0212034	PHATRDRAFT_45509	K01950|1|0.0|761|smo:SELMODRAFT_267968|NAD+ synthase (glutamine-hydrolysing) [EC:6.3.5.1]	-	GO:0032550;GO:0016884//carbon-nitrogen ligase activity, with glutamine as amido-N-donor;GO:0016787//hydrolase activity	GO:0019359//nicotinamide nucleotide biosynthetic process		GO:0019359//nicotinamide nucleotide biosynthetic process
7200882	129	52	44.22	30.65	-0.528811951	0.023945	PHATRDRAFT_45731	-	-	-	-		-
7202862	161	65	56.19	39.01	-0.526469402	0.01170956	PHATRDRAFT_47657	-	-	-	-		-
7198530	131	53	39.22	27.28	-0.523745891	0.0241112	PHATRDRAFT_49908	-	-	-	-		-
7197266	131	53	48.39	33.67	-0.523245218	0.0241112	PHATRDRAFT_43747	-	-	-	-		-
7197647	168	68	48.34	33.64	-0.523039768	0.0104678	PHATRDRAFT_44656	-	-	-	GO:0007165//signal transduction		GO:0007165//signal transduction
7198661	195	79	82.34	57.38	-0.521045481	0.00584356	PHATRDRAFT_49833	-	-	-	-		-
7197965	533	216	192.97	134.49	-0.520877672	4.56E-06	PHATRDRAFT_44302	-	-	-	-		-
7202569	111	45	39.41	27.47	-0.520704839	0.0394316	PHATRDRAFT_47447	-	-	-	-		-
7202797	232.34	94.15	107.5	74.94	-0.520528777	0.0026057	PHATRDRAFT_47572	-	-	-	-		-
7199326	259	105	128.42	89.58	-0.519621333	0.001475262	PHATRDRAFT_50492	-	-	-	-		-
7195463	106	43	47.31	33.02	-0.518805041	0.0446662	PHATRDRAFT_15806	K00514|1|1e-15|82.8|cme:CMT061C|zeta-carotene desaturase [EC:1.3.5.6]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7200002	155	63	48.43	33.85	-0.516745169	0.01506476	PHATRDRAFT_45377	K01510|1|3e-18|92.4|vcn:VOLCADRAFT_91259|apyrase [EC:3.6.1.5]	-	GO:0003824//catalytic activity	-		-
7204379	118	48	23.49	16.42	-0.516592586	0.035049	PHATR_43957	-	-	-	-		-
7197801	118	48	41.09	28.74	-0.515727269	0.035049	PHATRDRAFT_50806	K00826|1|1e-51|202|vcn:VOLCADRAFT_102054|branched-chain amino acid aminotransferase [EC:2.6.1.42]	-	GO:0004084//branched-chain-amino-acid transaminase activity	-		-
7198929	113	46	64.89	45.46	-0.513398482	0.0396686	PHATRDRAFT_50130	K12848|1|2e-19|95.1|gmx:100795833|U4/U6.U5 tri-snRNP component SNU23	GO:0005622//intracellular	GO:0046872//metal ion binding	-		-
7202954	135	55	75.67	53.05	-0.512368694	0.0244094	PHATRDRAFT_47803	-	-	-	-		-
7194860	277	113	63.26	44.36	-0.51203419	0.00120217	PHATRDRAFT_29758	K08776|1|4e-163|573|aly:ARALYDRAFT_491378|puromycin-sensitive aminopeptidase [EC:3.4.11.-]	GO:0044424	GO:0046914//transition metal ion binding;GO:0008238//exopeptidase activity	GO:0009987//cellular process;GO:0044699;GO:0019538//protein metabolic process		GO:0009987//cellular process;GO:0044699;GO:0019538//protein metabolic process
7202887	365	149	100.32	70.41	-0.510757006	0.000201148	PHATRDRAFT_47701	-	-	-	-		-
7203767	120	49	35.19	24.71	-0.510070503	0.0352442	PHATRDRAFT_48485	-	-	-	-		-

7204396	169	69	85.34	59.95	-0.509462357	0.01200322	PHATR_41790	K03667|1|9e-125|445|cme:CMT122C|ATP-dependent HslUV protease ATP-binding subunit HslU	GO:0043234//protein complex;GO:0044424	GO:0008233//peptidase activity;GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0050896//response to stimulus;GO:0009154//purine ribonucleotide catabolic process		GO:0050896//response to stimulus;GO:0009154//purine ribonucleotide catabolic process
7202914	146.09	59.68	130.84	92.1	-0.506530603	0.01676938	PHATRDRAFT_29011	K02155|1|1e-46|184|vcn:VOLCADRAFT_107886|V-type H+-transporting ATPase 16kDa proteolipid subunit [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex;GO:0031224//intrinsic component of membrane	GO:0015077//monovalent inorganic cation transmembrane transporter activity;GO:0003824//catalytic activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7195887	191	78	212.42	149.57	-0.506098771	0.0075229	PHATRDRAFT_40068	-	-	-	-		-
7201139	151	62	23.57	16.63	-0.50316359	0.01946078	PHATRDRAFT_45927	-	-	-	-		-
7200810	112	46	45.23	31.95	-0.501464065	0.0453792	PHATRDRAFT_45798	-	-	-	-		-
7203640	141	58	25.71	18.17	-0.500771191	0.0247766	PHATRDRAFT_48375	K12319|1|3e-32|139|cre:CHLREDRAFT_142791|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|8e-23|108|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K13755|5|3e-13|76.3|vcn:VOLCADRAFT_59941|calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7200917	112	46	65.98	46.64	-0.500460989	0.0453792	PHATRDRAFT_45779	K03132|1|9e-09|59.7|osa:4338489|transcription initiation factor TFIID subunit 7	GO:0005667//transcription factor complex	-	GO:0006366//transcription from RNA polymerase II promoter		GO:0006366//transcription from RNA polymerase II promoter
7202999	248	102	54.4	38.46	-0.500247889	0.00272242	PHATRDRAFT_47999	K01872|1|0.0|860|ppp:PHYPADRAFT_140193|alanyl-tRNA synthetase [EC:6.1.1.7]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7198343	124	51	26.05	18.42	-0.500010311	0.0355828	PHATRDRAFT_30585	K03655|1|1e-54|213|rcu:RCOM_0843050|ATP-dependent DNA helicase RecG [EC:3.6.4.12]	-	GO:0032550;GO:0042623//ATPase activity, coupled	GO:0046483//heterocycle metabolic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901360//organic cyclic compound metabolic process;GO:0006725//cellular aromatic compound metabolic process		GO:0046483//heterocycle metabolic process;GO:0034641//cellular nitrogen compound metabolic process;GO:1901360//organic cyclic compound metabolic process;GO:0006725//cellular aromatic compound metabolic process
7204697	381	157	93.61	66.31	-0.497436201	0.000209176	NLTF	-	-	-	-		-
7203000	141	58	111.55	79.03	-0.4972182	0.0247766	Rab2	K07976|1|2e-83|306|osa:4329809|Rab family, other;K07878|2|1e-82|304|osa:4336117|Ras-related protein Rab-2B;K07877|3|3e-82|303|aly:ARALYDRAFT_493160|Ras-related protein Rab-2A	GO:0016020//membrane;GO:0009536//plastid	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7198010	284	117	103.39	73.25	-0.497195989	0.001387918	PHATRDRAFT_44301	-	-	-	-		-
7203705	517	213	191.28	135.53	-0.497073803	1.51E-05	PHATRDRAFT_48482	-	-	-	-		-
7205032	131	54	30.41	21.55	-0.496857947	0.0316066	PHATRDRAFT_bd1590	K11267|1|6e-19|95.1|gmx:100775397|sister chromatid cohesion protein PDS5	-	-	-		-
7201080	546	225	196.38	139.17	-0.496799756	8.77E-06	MS	K01638|1|8e-159|558|cre:CHLREDRAFT_196328|malate synthase [EC:2.3.3.9]	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0044262//cellular carbohydrate metabolic process;GO:0009060//aerobic respiration		GO:0044262//cellular carbohydrate metabolic process;GO:0009060//aerobic respiration
7197218	143	59	24.88	17.64	-0.496135925	0.024879	PHATRDRAFT_43544	-	-	-	-		-
7200570	182	75	106.65	75.64	-0.495662697	0.0108676	SytA	K08486|1|2e-18|92.0|olu:OSTLU_27950|syntaxin 1B/2/3	-	GO:0005515//protein binding	GO:0015031//protein transport		GO:0015031//protein transport
7204234	165	68	126.14	89.52	-0.494743897	0.01544994	PetJ	K08906|1|3e-19|94.0|cme:CMV209C|cytochrome c6	GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding	GO:0044710;GO:0006091//generation of precursor metabolites and energy		GO:0044710;GO:0006091//generation of precursor metabolites and energy
7200068	305	126	110.61	78.58	-0.493247749	0.000999198	PHATRDRAFT_45050	-	-	-	-		-
7200653	346	143	148.78	105.77	-0.492250115	0.00045871	PHATRDRAFT_45612	-	-	-	-		-
7197763	1714	709	676.42	481.24	-0.491162755	5.35E-15	PHATRDRAFT_44488	-	-	-	-		-

7196176	227	94	59.2	42.14	-0.490406862	0.00488804	PHATRDRAFT_24772	K01702|1|0.0|847|olu:OSTLU_28677|3-isopropylmalate dehydratase [EC:4.2.1.33];K01703|4|3e-33|142|aly:ARALYDRAFT_682975|3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33 4.2.1.35]	GO:0043234//protein complex	GO:0051536//iron-sulfur cluster binding;GO:0016836//hydro-lyase activity	GO:0006551//leucine metabolic process		GO:0006551//leucine metabolic process
7200053	181	75	55.25	39.36	-0.489244244	0.01232386	PHATRDRAFT_26975	K03253|1|2e-124|445|bdi:100834858|translation initiation factor 3 subunit B	GO:0044424	GO:0008135//translation factor activity, nucleic acid binding;GO:0036094//small molecule binding	GO:0006412//translation		GO:0006412//translation
7204094	571	237	88.85	63.38	-0.487344117	8.17E-06	PHATR_44174	-	-	GO:0008252//nucleotidase activity;GO:0046872//metal ion binding	GO:0009117//nucleotide metabolic process		GO:0009117//nucleotide metabolic process
7200690	159	66	52.69	37.61	-0.486412873	0.01976412	PHATRDRAFT_27039	K09540|1|5e-46|184|ath:AT1G79940|translocation protein SEC63	-	GO:0022892	GO:0006620//posttranslational protein targeting to membrane		GO:0006620//posttranslational protein targeting to membrane
7203012	704	291	1203.99	859.86	-0.485649721	5.40E-07	PHATRDRAFT_14646	-	-	-	-		-
7204338	178	74	52.11	37.24	-0.484707182	0.01391574	PHATR_43879	-	-	-	-		-
7199755	1117	464	604.94	432.42	-0.484358807	4.47E-10	PHATRDRAFT_44800	-	-	-	-		-
7200250	226	94	62.14	44.44	-0.483663425	0.00552458	PHATRDRAFT_45230	K01090|1|1e-34|147|osa:4341433|protein phosphatase [EC:3.1.3.16];K14497|2|5e-34|144|gmx:100805281|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0004721//phosphoprotein phosphatase activity;GO:0043169//cation binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7196977	120	50	23.15	16.58	-0.481568187	0.046009	PHATRDRAFT_43268	-	-	-	-		-
7199936	125	52	87.15	62.42	-0.481492307	0.0406692	PHATRDRAFT_45279	-	-	-	-		-
7200290	364	152	55.85	40.08	-0.478674772	0.000472278	PHATRDRAFT_45084	-	-	-	-		-
7197265	187	78	110.76	79.52	-0.478047297	0.0124359	PHATRDRAFT_43744	-	-	-	-		-
7199027	141	59	59.77	43.02	-0.474414018	0.0320852	PHATRDRAFT_41170	-	GO:0016020//membrane	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710;GO:0044707		GO:0044710;GO:0044707
7197398	900	377	197.63	142.3	-0.473866301	4.52E-08	PHATRDRAFT_43354	-	-	-	-		-
7195147	186	78	82.02	59.17	-0.471109849	0.0140533	PHATRDRAFT_48859	-	-	-	-		-
7198559	181	76	103.21	74.58	-0.468722058	0.01581126	PHATRDRAFT_49974	-	-	-	-		-
7200416	133	56	23.57	17.06	-0.466334112	0.0409938	MSH4	K08740|1|2e-57|223|rcu:RCOM_1389090|DNA mismatch repair protein MSH4	-	GO:0003690//double-stranded DNA binding;GO:0032550	GO:0006281//DNA repair		GO:0006281//DNA repair
7196845	190	80	67.31	48.73	-0.466010634	0.01410082	PHATRDRAFT_43044	-	-	-	-		-
7202936	815.65	342.75	736.54	533.27	-0.465897708	2.25E-07	PHATRDRAFT_47653	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7200597	434	183	98.26	71.22	-0.464321803	0.00020015	PHATRDRAFT_45518	K14674|1|6e-35|148|cre:CHLREDRAFT_183258|TAG lipase / steryl ester hydrolase / phospholipase A2 / LPA acyltransferase [EC:3.1.1.3 3.1.1.13 3.1.1.4 2.3.1.51]	-	GO:0046872//metal ion binding;GO:0003824//catalytic activity	GO:0044238		GO:0044238
7198241	313	132	76.76	55.65	-0.463973024	0.0016294	PHATRDRAFT_30461	K00213|1|2e-126|451|sbi:SORBI_04g017400|7-dehydrocholesterol reductase [EC:1.3.1.21]	GO:0016020//membrane	GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors	GO:0044710		GO:0044710
7204593	375	159	57.11	41.61	-0.456813096	0.000674558	PHATR_46676	-	-	-	-		-
7195602	168	71	180.14	131.25	-0.456801144	0.0225842	PHATRDRAFT_30262	K02885|1|5e-45|178|smo:SELMODRAFT_185317|large subunit ribosomal protein L19e	GO:0005840//ribosome	-	-		-
7197031	1040	441	230.45	167.97	-0.456250182	1.33E-08	PHATRDRAFT_43746	-	-	-	-		-

7196246	465	197	322.83	235.47	-0.455231387	0.000145291	PHATRDRAFT_43051	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196621	139	59	59.38	43.36	-0.453612337	0.0410892	PHATRDRAFT_42434	-	GO:0044464	GO:0016462//pyrophosphatase activity;GO:0032550	-		-
7196963	158	67	153.41	112.12	-0.452348878	0.0286604	PHATRDRAFT_43244	K08493|1|1e-10|65.1|cre:CHLREDRAFT_187998|vesicle transport through interaction with t-SNAREs 1	-	-	-		-
7203570	285	121	221.74	162.13	-0.451717976	0.0032094	PHATRDRAFT_48358	-	-	-	-		-
7196990	167	71	130.24	95.36	-0.449716464	0.0254614	PHATRDRAFT_43687	-	-	-	-		-
7203296	183	78	29.32	21.47	-0.449562912	0.0201136	PHATRDRAFT_48146	K11982|1|4e-07|56.2|mtr:MTR_6g079660|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	-		-
7200663	195	83	121.41	88.95	-0.448820744	0.01591592	PHATRDRAFT_45624	-	-	-	-		-
7204707	1141	486	555.28	406.92	-0.448470244	4.22E-09	PHATR_54658	-	-	-	-		-
7203788	336.25	143.38	88.57	64.93	-0.44793291	0.001468254	PHATRDRAFT_48317	-	-	-	-		-
7204615	136	58	50.4	36.97	-0.44706869	0.0463932	PHATR_46703	-	-	-	-		-
7200075	493	210	388.63	285.11	-0.446878631	0.000117443	PHATRDRAFT_11673	-	GO:0005911//cell-cell junction;GO:0031090//organelle membrane;GO:0009536//plastid	GO:0019901//protein kinase binding	-		-
7202090	171	73	58.92	43.26	-0.445723765	0.0254616	PHATRDRAFT_46983	-	GO:0005622//intracellular;GO:0031224//intrinsic component of membrane	-	-		-
7202319	1557	666	991.93	730.37	-0.441610806	1.19E-11	PHATRDRAFT_47279	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7204693	236	101	112.11	82.55	-0.441574849	0.0089258	PHATR_46842	-	-	-	-		-
7197815	254	109	82.71	61.03	-0.438543178	0.007093	PHATRDRAFT_44256	K12133|1|2e-10|65.9|aly:ARALYDRAFT_470177|LATE ELONGATED HYPOCOTYL;K12134|3|9e-10|63.9|aly:ARALYDRAFT_904154|circadian clock associated 1	-	GO:0003676//nucleic acid binding	-		-
7200229	676	289	1082.99	799.64	-0.437597375	7.92E-06	PHATRDRAFT_45193	-	-	-	-		-
7202861	2328.35	1002.25	431.81	319.46	-0.434761353	3.86E-16	PHATRDRAFT_47656	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7201731	142	61	124.47	92.12	-0.434211747	0.0462998	CLC	-	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7194869	230	99	96.94	71.77	-0.433711162	0.01120544	PHATRDRAFT_48600	-	GO:0044424;GO:0031224//intrinsic component of membrane	GO:0016491//oxidoreductase activity	GO:0044238		GO:0044238
7199690	172	74	141.88	105.14	-0.432359595	0.0285946	PHATRDRAFT_45025	-	-	-	-		-
7199266	269	116	117.36	87.06	-0.430858851	0.0063073	FbaC5	K01623|1|4e-106|383|cme:CMI049C|fructose-bisphosphate aldolase, class I [EC:4.1.2.13]	GO:0044434	GO:0016832//aldehyde-lyase activity	GO:0006007//glucose catabolic process;GO:0050896//response to stimulus		GO:0006007//glucose catabolic process;GO:0050896//response to stimulus
7204063	305	131	521.62	387.08	-0.430367419	0.00320842	PHATR_10391	-	-	GO:0016810//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	-		-
7201454	295	127	367.17	272.67	-0.429292207	0.00401298	PHATRDRAFT_12887	-	-	GO:0046914//transition metal ion binding	-		-
7205167	148	64	41.76	31.05	-0.427528443	0.0461034	PHATRDRAFT_bd1749	-	-	GO:0004620//phospholipase activity	-		-

7205100	400	173	131.23	97.6	-0.427144514	0.000933786	PHATRDRAFT_bd714	K13862|1|1e-23|110|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7203434	943	407	990.16	736.69	-0.42660401	2.87E-07	PHATRDRAFT_48086	-	-	-	-		-
7197849	402	174	257.85	192.12	-0.424524332	0.000932572	PHATRDRAFT_18927	K15109|1|2e-37|154|pop:POPTR_670402|solute carrier family 25 (mitochondrial carnitine/acylcarnitine transporter), member 20/29	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7204256	1598.72	693.41	950.37	709.45	-0.421788285	4.44E-11	PHATR_54153	-	-	-	-		-
7198029	2149	934	711.43	531.69	-0.42013648	3.18E-14	PHATRDRAFT_11014	K00253|1|1e-10|67.0|bdi:100833691|isovaleryl-CoA dehydrogenase [EC:1.3.8.4]	-	GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors;GO:0000166//nucleotide binding	GO:0006635//fatty acid beta-oxidation		GO:0006635//fatty acid beta-oxidation
7197047	536	233	274.67	205.45	-0.418912015	0.000159082	PHATRDRAFT_43771	-	-	-	-		-
7200829	156	68	70.35	52.75	-0.41537933	0.045705	PHATRDRAFT_45947	K00626|1|6e-69|259|vvi:100855181|acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	-	GO:0016408	-		-
7204756	220	96	96.37	72.33	-0.413989953	0.01754192	PHATR_46929	-	-	-	-		-
7202292	190	83	34.03	25.55	-0.41348386	0.0281106	PHATRDRAFT_47518	-	GO:0044464	GO:0016837	GO:0042120		GO:0042120
7200026	424	185	282.43	212.15	-0.412808663	0.000914952	PHATRDRAFT_19805	-	GO:0044444//cytoplasmic part;GO:0043231//intracellular membrane-bounded organelle	-	-		-
7198835	424	186	165.74	125.05	-0.40641677	0.001121766	PHATRDRAFT_55150	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197969	430	189	106	80.09	-0.40437024	0.00111273	PHATRDRAFT_44307	-	-	-	-		-
7200252	198	87	68.05	51.42	-0.404265552	0.0277868	PHATRDRAFT_26837	K01874|1|2e-150|531|olu:OSTLU_36966|methionyl-tRNA synthetase [EC:6.1.1.10]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7198675	323	142	69.17	52.27	-0.404163297	0.00482436	PHATRDRAFT_50076	-	-	GO:0004721//phosphoprotein phosphatase activity	GO:0006470//protein dephosphorylation		GO:0006470//protein dephosphorylation
7199521	171	75	185.47	140.25	-0.403185077	0.0400608	PHATRDRAFT_34586	-	-	-	-		-
7202290	343	151	133.05	100.74	-0.401331874	0.00382134	PHATRDRAFT_37749	-	-	-	-		-
7199433	311	137	101.83	77.13	-0.400798638	0.00602386	PHATRDRAFT_50618	-	-	-	-		-
7197376	177	78	53.58	40.6	-0.400214854	0.0396636	PHATRDRAFT_43312	-	-	GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7202968	211	93	68.17	51.66	-0.40008934	0.0244652	PHATRDRAFT_51088	K01637|1|1e-149|528|ppp:PHYPADRAFT_189731|isocitrate lyase [EC:4.1.3.1]	-	GO:0016833//oxo-acid-lyase activity	GO:0043436		GO:0043436
7199382	238	105	47.39	35.93	-0.399393726	0.01708472	PHATRDRAFT_50551	-	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7198248	360	159	77.8	59.07	-0.397344543	0.0033644	PHATRDRAFT_49592	-	-	-	-		-
7197519	1295	572	317.33	240.95	-0.397250117	2.31E-08	PHATRDRAFT_43674	-	-	-	-		-
7195215	509	225	159.13	120.95	-0.395795076	0.000494668	PHATRDRAFT_48924	K00685|1|2e-55|216|aly:ARALYDRAFT_478464|arginine-tRNA-protein transferase [EC:2.3.2.8]	-	GO:0016755	GO:0044699;GO:0009056//catabolic process;GO:0006464//cellular protein modification process;GO:0032502//developmental process		GO:0044699;GO:0009056//catabolic process;GO:0006464//cellular protein modification process;GO:0032502//developmental process
7196778	210	93	75.12	57.21	-0.392929719	0.0272062	PHATRDRAFT_42948	-	-	-	-		-
7203264	226	100	151.31	115.26	-0.392615413	0.0214636	PHATRDRAFT_54855	K08493|1|2e-07|54.7|olu:OSTLU_31153|vesicle transport through interaction with t-SNAREs 1	-	-	-		-
7200135	751	332	743.47	566.46	-0.392300444	2.27E-05	PHATRDRAFT_45270	-	-	-	-		-
7200809	1196	530	391.6	298.4	-0.392133229	1.10E-07	PHATRDRAFT_45797	-	-	-	-		-
7203952	301.28	133.59	138.04	105.3	-0.390580943	0.00750002	PHATR_43815	-	-	-	-		-
7203990	189	84	41.92	32.03	-0.388214919	0.0387432	PHATR_44026	-	-	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710

7196211	189	84	56.64	43.28	-0.388120766	0.0387432	PHATRDRAFT_42978	K10523|1|1e-17|90.1|osa:4344979|speckle-type POZ protein;K15450|2|5e-17|88.2|smo:SELMODRAFT_418563|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-];K02999|5|3e-16|85.9|bdi:100821444|DNA-directed RNA polymerase I subunit RPA1 [EC:2.7.7.6]	-	-	-		-
7197808	1556	691	807.44	616.99	-0.388107952	1.79E-09	GEL3	K05768|1|9e-40|162|vvi:100254775|gelsolin	GO:0044424	GO:0008092//cytoskeletal protein binding	GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization		GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization
7195875	184.6	82.02	75.62	57.79	-0.387947979	0.043438	PHATRDRAFT_49355	K08852|1|2e-11|68.9|vcn:VOLCADRAFT_107956|serine/threonine-protein kinase/endoribonuclease IRE1 [EC:2.7.11.1 3.1.26.-]	-	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding	-		-
7196267	274	122	46.13	35.3	-0.386037109	0.01302618	BGER1	-	-	GO:0052736//beta-glucanase activity	GO:0044036//cell wall macromolecule metabolic process		GO:0044036//cell wall macromolecule metabolic process
7202978	238	106	84.4	64.64	-0.384815801	0.0209546	PHATRDRAFT_47842	-	-	-	-		-
7200435	193	86	169.17	129.87	-0.381405542	0.0384056	PHATRDRAFT_12097	K10144|1|2e-51|200|sbi:SORBI_01g020210|RING finger and CHY zinc finger domain-containing protein 1 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	GO:0010035//response to inorganic substance;GO:0006811//ion transport		GO:0010035//response to inorganic substance;GO:0006811//ion transport
7196800	2131	952	685.79	526.8	-0.380511522	5.23E-12	HSP70A	K03283|1|0.0|904|rcu:RCOM_1442270|heat shock 70kDa protein 1/8	-	GO:0032550	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7198064	606	271	227.41	174.9	-0.378765407	0.000257056	PHATRDRAFT_54251	-	-	-	-		-
7195260	350	157	139.8	107.86	-0.374204422	0.00615734	PHATRDRAFT_54973	-	-	-	-		-
7198795	376	169	160.42	124.03	-0.3711649	0.00479768	PHATRDRAFT_30810	K14617|1|2e-58|224|pop:POPTR_831922|LMBR1 domain-containing protein 1	GO:0031224//intrinsic component of membrane	-	-		-
7198971	320	144	100.04	77.41	-0.369985108	0.00966354	PHATRDRAFT_16786	K09487|1|4e-150|530|bdi:100823353|heat shock protein 90kDa beta	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550;GO:0005515//protein binding	GO:0044267//cellular protein metabolic process;GO:0006950//response to stress		GO:0044267//cellular protein metabolic process;GO:0006950//response to stress
7201285	371	167	101	78.16	-0.369852921	0.00533214	PHATRDRAFT_46212	K13418|1|2e-16|86.7|pop:POPTR_913861|somatic embryogenesis receptor kinase 1 [EC:2.7.10.1 2.7.11.1]	-	-	-		-
7203186	200	90	77.03	59.62	-0.36962405	0.0417582	PHATRDRAFT_38270	K14570|1|4e-06|51.6|ath:AT5G67240|RNA exonuclease 1 [EC:3.1.-.-]	-	-	-		-
7199574	282	127	62.24	48.18	-0.369407667	0.01553802	PHATRDRAFT_44864	-	-	-	-		-
7203854	191	86	56.59	43.81	-0.369286923	0.047237	PHATR_44149	-	GO:0031224//intrinsic component of membrane	GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044763;GO:0006811//ion transport		GO:0044763;GO:0006811//ion transport
7195096	397	179	155.09	120.27	-0.366828843	0.00415472	PHATRDRAFT_42245	K00311|1|5e-153|539|ppp:PHYPADRAFT_55177|electron-transferring-flavoprotein dehydrogenase [EC:1.5.5.1]	-	GO:0051540;GO:0016649//oxidoreductase activity, acting on the CH-NH group of donors, quinone or similar compound as acceptor	GO:0044710		GO:0044710
7202122	235	106	83.07	64.43	-0.36659496	0.0283728	PHATRDRAFT_47039	K03262|1|1e-30|133|olu:OSTLU_46171|translation initiation factor 5	-	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7199569	226	102	58.13	45.1	-0.366155475	0.0320206	myoA4	K10357|1|9e-141|499|aly:ARALYDRAFT_887631|myosin V;K03165|2|9e-130|462|ota:Ot06g03550|DNA topoisomerase III [EC:5.99.1.2]	GO:0015629//actin cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7196592	304	137	215.84	167.48	-0.36597343	0.01215254	PHATRDRAFT_43237	-	-	-	-		-
7200157	840	379	403.71	313.38	-0.365406214	3.01E-05	PHATRDRAFT_34965	-	-	-	-		-

7199633	348	157	188.31	146.2	-0.365166303	0.00746842	PHATRDRAFT_11204	K13289|1|9e-76|282|zma:100273121|cathepsin A (carboxypeptidase C) [EC:3.4.16.5]	-	GO:0004180//carboxypeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200156	279	126	138.23	107.41	-0.363942441	0.0172209	PHATRDRAFT_45297	-	GO:0009536//plastid	-	-		-
7195023	1420.01	642	381.37	296.42	-0.363548568	6.98E-08	PHATRDRAFT_48735	-	-	-	-		-
7195296	755	341	479.14	372.51	-0.363168104	8.15E-05	PHATRDRAFT_52498	-	-	-	-		-
7203102	221	100	44.18	34.36	-0.362663382	0.0357582	PHATRDRAFT_47888	-	-	-	-		-
7198542	323	146	174.5	135.73	-0.362487406	0.01053436	PHATRDRAFT_49939	-	-	-	-		-
7203766	283	128	113.59	88.37	-0.362207242	0.01703786	PHATRDRAFT_48484	K01362|1|6e-18|90.9|olu:OSTLU_44226|[EC:3.4.21.-]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200393	197	89	150.95	117.44	-0.362146884	0.0464628	PHATRDRAFT_45623	-	-	-	-		-
7203351	201	91	58.27	45.35	-0.36165076	0.045936	PHATRDRAFT_48238	-	-	-	-		-
7202684	230	104	145.26	113.06	-0.361548883	0.0316714	PHATRDRAFT_47649	-	-	-	-		-
7195281	4837	2193	1082.03	843.25	-0.359708181	6.13E-23	FRE5	K13447|1|4e-25|115|vvi:100262614|respiratory burst oxidase [EC:1.6.3.-1.11.1.-]	GO:0031224//intrinsic component of membrane	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201663	504	229	82.34	64.3	-0.356774711	0.001673676	PHATRDRAFT_46420	-	-	-	-		-
7197065	227	103	143.64	112.19	-0.35651347	0.0351482	PHATRDRAFT_43684	K00011|1|9e-11|66.2|ath:AT2G37790|aldehyde reductase [EC:1.1.1.21];K00002|2|3e-10|64.3|osa:4338987|alcohol dehydrogenase (NADP+) [EC:1.1.1.2];K00085|4|7e-07|53.1|ath:AT2G21260|aldose-6-phosphate reductase (NADPH2) [EC:1.1.1.200]	-	-	-		-
7198127	271	123	153.86	120.18	-0.356421386	0.0212448	IscS	K04487|1|1e-151|534|zma:100274462|cysteine desulfurase [EC:2.8.1.7]	-	GO:0016783//sulfurtransferase activity;GO:0043168//anion binding	GO:0000096//sulfur amino acid metabolic process		GO:0000096//sulfur amino acid metabolic process
7195643	506	230	359.64	281.47	-0.353572326	0.001664682	Sec4	K07901|1|7e-65|245|ota:Ot05g02380|Ras-related protein Rab-8A	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7196145	373	170	47.87	37.49	-0.35261598	0.00764568	PHATRDRAFT_42770	K11568|1|2e-09|64.3|vcn:VOLCADRAFT_121384|DASH complex subunit DAD3;K10400|2|3e-08|60.5|cme:CMO070C|kinesin family member 15;K09291|3|4e-07|56.6|vcn:VOLCADRAFT_89403|nucleoprotein TPR;K06675|5|2e-06|54.7|vcn:VOLCADRAFT_61097|structural maintenance of chromosome 4	-	-	GO:0000301//retrograde transport, vesicle recycling within Golgi		GO:0000301//retrograde transport, vesicle recycling within Golgi
7195807	263	120	50.62	39.69	-0.350931945	0.0261804	PHATRDRAFT_49445	-	-	-	-		-
7203409	2990.39	1365.04	278.3	218.27	-0.350527055	4.33E-14	PHATRDRAFT_48048	-	-	-	-		-
7196866	575	262	428.6	336.3	-0.349883071	0.000890192	PHATRDRAFT_9316	K03921|1|4e-98|355|vvi:100853715|acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2]	GO:0009536//plastid	GO:0046872//metal ion binding;GO:0016717//oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7196277	265	121	55.47	43.53	-0.349697705	0.0260204	PHATRDRAFT_42587	K01404|1|6e-28|125|bdi:100831389|leishmanolysin [EC:3.4.24.36]	-	GO:0046914//transition metal ion binding;GO:0004175//endopeptidase activity	GO:0022610;GO:0019538//protein metabolic process		GO:0022610;GO:0019538//protein metabolic process

7199217	342	156	212.33	166.71	-0.348967577	0.01094756	PHATRDRAFT_16870	K00021|1|3e-97|353|mtr:MTR_5g026470|hydroxymethylglutaryl-CoA reductase (NADPH) [EC:1.1.1.34]	GO:0031224//intrinsic component of membrane	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding;GO:0048037//cofactor binding	GO:0008610//lipid biosynthetic process;GO:0006732//coenzyme metabolic process;GO:0006720//isoprenoid metabolic process		GO:0008610//lipid biosynthetic process;GO:0006732//coenzyme metabolic process;GO:0006720//isoprenoid metabolic process
7198943	315	144	44.12	34.66	-0.348161136	0.01553686	PHATRDRAFT_50162	K06699|1|6e-19|95.9|gmx:100781622|proteasome activator subunit 4	-	-	-		-
7201675	468	214	115.41	90.72	-0.34727569	0.00313288	PHATRDRAFT_46527	-	-	-	-		-
7199392	308	141	180.16	141.95	-0.343895883	0.01736346	PHATRDRAFT_50567	-	-	GO:0042623//ATPase activity, coupled	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7195335	430	197	171.13	134.85	-0.343737173	0.00496238	PHATRDRAFT_49112	K00451|1|5e-109|393|osa:4339844|homogentisate 1,2-dioxygenase [EC:1.13.11.5]	-	GO:0016702//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	GO:0006558//L-phenylalanine metabolic process		GO:0006558//L-phenylalanine metabolic process
7202757	637	292	260.94	205.74	-0.342895805	0.000628896	PHATRDRAFT_47530	-	-	-	-		-
7202964	388	178	89.35	70.46	-0.342663254	0.00798472	PHATRDRAFT_47817	K11804|1|1e-26|120|osa:4332480|WD repeat-containing protein 42A	-	-	-		-
7195470	244	112	136.07	107.48	-0.340280798	0.0365798	PHATRDRAFT_49296	-	-	-	-		-
7195907	1162	534	318.85	251.91	-0.339969488	4.63E-06	PHATRDRAFT_49414	-	-	-	-		-
7195306	1136	522	1289.53	1021.76	-0.335788974	5.88E-06	PHATRDRAFT_49059	-	-	GO:0004866//endopeptidase inhibitor activity	GO:0006950//response to stress		GO:0006950//response to stress
7197180	389	179	353.7	280.43	-0.334885524	0.00867916	PHATRDRAFT_4936	K08568|1|4e-82|302|ota:Ot01g04810|cathepsin X [EC:3.4.18.1]	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203145	230	106	133.47	105.86	-0.334357945	0.0459624	PHATRDRAFT_47962	K04523|1|1e-09|62.8|sbi:SORBI_01g048260|ubiquilin	-	-	-		-
7196146	379	175	136.02	108.01	-0.332653908	0.01063948	PF2K1	K01103|1|1e-112|405|ota:Ot01g00020|6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase [EC:2.7.1.105 3.1.3.46]	-	GO:0008443//phosphofructokinase activity;GO:0032550;GO:0050308//sugar-phosphatase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0019318//hexose metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0019318//hexose metabolic process
7197967	232	107	165.43	131.37	-0.332585029	0.0456436	PHATRDRAFT_44305	-	-	-	-		-
7195311	242	112	35.36	28.12	-0.33052168	0.0440568	PHATRDRAFT_49068	-	-	-	-		-
7200903	423	196	149.36	119.01	-0.327711029	0.00776224	PHATRDRAFT_45761	-	-	-	-		-
7195420	1360	629	1293.8	1031.17	-0.327332421	1.35E-06	CREG1	-	GO:0043231//intracellular membrane-bounded organelle	GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7204354	317	147	68.31	54.45	-0.327164743	0.0219	PHATR_10319	K01412|1|4e-15|82.4|sbi:SORBI_03g032670|mitochondrial processing peptidase [EC:3.4.24.64]	-	GO:0043169//cation binding	-		-
7200148	235	109	76.53	61.03	-0.326506809	0.049352	PHATRDRAFT_45285	K09291|1|6e-09|61.2|ath:AT1G79280|nucleoprotein TPR;K09313|3|8e-09|60.8|bdi:100843418|homeobox protein cut-like	GO:0044424	GO:0015631//tubulin binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7195271	3225	1494	2101.4	1675.82	-0.326483607	1.37E-13	PHATRDRAFT_49007	-	-	-	-		-
7198595	2226	1032	1051.39	838.59	-0.326260387	9.02E-10	PHATRDRAFT_49880	-	-	-	-		-
7195008	2628	1220	469.63	374.69	-0.325827096	3.57E-11	PHATRDRAFT_48753	-	-	-	-		-
7205067	397	184	263.38	210.15	-0.325726341	0.01001592	PHATRDRAFT_bd706	K06693|1|8e-24|109|vvi:100258659|26S proteasome non-ATPase regulatory subunit 9	-	-	-		-
7199381	933	434	162.92	130.24	-0.322991115	9.45E-05	PHATRDRAFT_24186	K14290|1|0.0|1047|ppp:PHYPADRAFT_163030|exportin-1	GO:0005635//nuclear envelope	GO:0022892	GO:0015031//protein transport		GO:0015031//protein transport
7199139	316	147	89.71	71.75	-0.32228998	0.023921	GPI_3	K01810|1|0.0|664|cme:CMO124C|glucose-6-phosphate isomerase [EC:5.3.1.9]	GO:0044444//cytoplasmic part	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0050896//response to stimulus;GO:0006007//glucose catabolic process		GO:0050896//response to stimulus;GO:0006007//glucose catabolic process

7203872	457	213	132.54	106.21	-0.319508218	0.0069041	PHATR_44112	-	-	GO:0015291//secondary active transmembrane transporter activity	GO:0015893//drug transport;GO:0044763		GO:0015893//drug transport;GO:0044763
7199306	553	258	81.22	65.12	-0.318734328	0.00305304	PHATRDRAFT_41409	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7203868	2495	1163	1368.13	1097.44	-0.318063256	2.28E-10	ANXA1	-	-	GO:0005543//phospholipid binding;GO:0046872//metal ion binding	-		-
7195239	843	393	493.98	396.35	-0.317677656	0.000237094	PHATRDRAFT_48957	-	-	-	-		-
7198969	255	119	68.51	54.97	-0.317670106	0.0457906	PHATRDRAFT_50305	-	-	-	-		-
7202729	257	120	46.01	36.93	-0.317154194	0.0454422	PHATRDRAFT_54789	K12397|1|5e-65|248|ppp:PHYPADRAFT_183108|AP-3 complex subunit beta	GO:0030119//AP-type membrane coat adaptor complex	-	GO:0015031//protein transport		GO:0015031//protein transport
7202762	1277	597	163.97	131.72	-0.315957466	7.62E-06	PHATRDRAFT_47538	-	-	-	-		-
7203024	306	143	88.2	70.87	-0.315603607	0.0293378	PHATRDRAFT_29260	K00615|1|2e-174|611|vcn:VOLCADRAFT_75893|transketolase [EC:2.2.1.1]	-	GO:0016744	-		-
7194758	565	264	240.9	193.62	-0.31520641	0.00292764	FABZ_1	K03686|1|3e-15|81.6|rcu:RCOM_1526580|molecular chaperone DnaJ	-	-	-		-
7200313	293	137	94.9	76.3	-0.31472503	0.033486	PHATRDRAFT_45119	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0006811//ion transport;GO:0044763		GO:0006811//ion transport;GO:0044763
7196070	263	123	170.52	137.29	-0.312714415	0.0444066	PHATRDRAFT_42523	-	-	-	-		-
7201234	401	188	108.99	87.84	-0.311245812	0.01369272	PHATRDRAFT_46135	-	-	-	-		-
7203862	2699	1264	1776.26	1432.05	-0.310760906	1.01E-10	PHATR_44092	-	-	-	-		-
7195219	1008	473	144.57	116.57	-0.310571657	9.22E-05	CPS-II	K11541|1|0.0|1449|cme:CMQ255C|carbamoyl-phosphate synthase / aspartate carbamoyltransferase [EC:6.3.5.5 2.1.3.2];K01955|2|0.0|678|smo:SELMODRAFT_440891|carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	-	GO:0043169//cation binding;GO:0032550	GO:0006541//glutamine metabolic process;GO:0044271//cellular nitrogen compound biosynthetic process		GO:0006541//glutamine metabolic process;GO:0044271//cellular nitrogen compound biosynthetic process
7204759	328	154	48.03	38.75	-0.309739498	0.0269812	PHATR_46935	K13427|1|7e-16|85.5|vvi:100265605|nitric-oxide synthase, plant [EC:1.14.13.39]	GO:0005789//endoplasmic reticulum membrane	GO:0016787//hydrolase activity	GO:0015031//protein transport;GO:0006664//glycolipid metabolic process		GO:0015031//protein transport;GO:0006664//glycolipid metabolic process
7200293	321	151	108.01	87.37	-0.305954993	0.030058	PHATRDRAFT_55575	K08679|1|3e-62|238|ota:Ot02g07320|UDP-glucuronate 4-epimerase [EC:5.1.3.6]	-	GO:0036094//small molecule binding;GO:0016854//racemase and epimerase activity;GO:0048037//cofactor binding	GO:0044238		GO:0044238
7196688	325	153	188.59	152.8	-0.303608636	0.0295904	PHATRDRAFT_42510	-	-	-	-		-
7198492	856	403	669.16	542.57	-0.302541929	0.000385678	PLS1	-	-	-	-		-
7201516	390	184	85.02	68.94	-0.30246096	0.01809812	COPbeta2	K05236|1|6e-72|271|ath:AT2G21390|coatomer protein complex, subunit alpha (xenin)	GO:0043234//protein complex	-	GO:0015031//protein transport		GO:0015031//protein transport
7200390	438	206	487.94	395.69	-0.302333151	0.01101416	PHATRDRAFT_45617	-	-	-	-		-
7203074	627	296	196.96	159.88	-0.300913189	0.0027256	PHATRDRAFT_47847	-	-	-	-		-
7195917	375	177	161.99	131.52	-0.300622551	0.0207524	PHATRDRAFT_49430	-	-	-	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7195913	362	171	138.7	112.68	-0.299736319	0.0236226	PHATRDRAFT_49425	K06694|1|1e-09|63.2|rcu:RCOM_1621740|26S proteasome non-ATPase regulatory subunit 10	-	-	-		-
7201035	519	245	313.91	255.06	-0.299514324	0.0064335	PHATRDRAFT_45968	K09272|1|5e-11|67.0|aly:ARALYDRAFT_905150|structure-specific recognition protein 1;K10802|2|1e-10|65.9|vcn:VOLCADRAFT_72419|high mobility group protein B1	-	-	-		-
7201531	592	280	129.82	105.54	-0.298722773	0.00389108	COPbeta	K12392|1|1e-13|77.4|ppp:PHYPADRAFT_224233|AP-1 complex subunit beta-1	GO:0030137//COPI-coated vesicle;GO:0030120//vesicle coat	-	GO:0015031//protein transport		GO:0015031//protein transport
7198442	2288	1082	757.45	615.94	-0.298360836	1.20E-08	PHATRDRAFT_49759	-	-	-	-		-

7199730	1891	897	350.7	285.91	-0.29467635	3.24E-07	PHATRDRAFT_44761	K15172|1|1e-08|60.8|vcn:VOLCADRAFT_106802|transcription elongation factor SPT5	-	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress		GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress
7199286	312	148	78.59	64.09	-0.294246482	0.0395554	PHATRDRAFT_50503	-	-	-	-		-
7203267	550	261	117.75	96.04	-0.294019751	0.00615518	GDCP	K00281|1|0.0|994|ppp:PHYPADRAFT_171132|glycine dehydrogenase [EC:1.4.4.2]	-	GO:0043168//anion binding;GO:0016642	GO:0006544//glycine metabolic process		GO:0006544//glycine metabolic process
7203355	1480	703	294.59	240.5	-0.292671564	7.15E-06	PHATRDRAFT_48245	-	-	-	-		-
7198365	11179	5314	1201.26	981.14	-0.292017525	7.34E-35	PHATRDRAFT_23497	K05641|1|2e-177|622|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1;K05643|3|2e-168|592|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7198069	1587	755	234.25	191.51	-0.290629321	3.92E-06	PHATRDRAFT_44539	-	-	-	-		-
7203333	555	264	132.06	107.98	-0.290429429	0.0064967	CYCP1	-	-	-	-		-
7203359	3588	1707	977.61	799.6	-0.289980571	3.74E-12	PHATRDRAFT_48252	-	-	GO:0046914//transition metal ion binding	-		-
7195408	585	279	132.35	108.5	-0.286663152	0.00576938	PHATRDRAFT_49026	-	-	-	-		-
7203900	1846	881	367.77	301.67	-0.285832567	9.31E-07	PHATR_25856	K03695|1|0.0|896|cme:CMI251C|ATP-dependent Clp protease ATP-binding subunit ClpB	GO:0009536//plastid	GO:0016462//pyrophosphatase activity;GO:0032550	GO:0043170		GO:0043170
7196682	748	357	156.47	128.36	-0.285690381	0.001843846	PHATRDRAFT_42501	-	-	-	-		-
7202321	467	223	117.1	96.12	-0.284832522	0.01433862	PHATRDRAFT_47283	-	-	-	-		-
7204974	1261	602	628.09	515.9	-0.283879853	5.23E-05	PHATRDRAFT_bd1714	-	-	-	-		-
7198397	320	153	40.05	32.9	-0.283714659	0.0445992	PHATRDRAFT_49712	K11498|1|3e-08|60.5|aly:ARALYDRAFT_478343|centromeric protein E;K10400|2|1e-07|58.5|cme:CMO070C|kinesin family member 15;K03254|3|1e-07|58.2|osa:4326038|translation initiation factor 3 subunit A;K09291|4|2e-07|57.8|smo:SELMODRAFT_444132|nucleoprotein TPR	GO:0015630//microtubule cytoskeleton	GO:0032550;GO:0003774//motor activity	GO:0006928//cellular component movement		GO:0006928//cellular component movement
7198546	495	237	107.48	88.45	-0.281134178	0.01278218	HSP70G	K09486|1|8e-88|323|ath:AT4G16660|hypoxia up-regulated 1	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550	GO:0009987//cellular process;GO:0006950//response to stress		GO:0009987//cellular process;GO:0006950//response to stress
7195443	1024	489	1063.33	875.3	-0.280739925	0.000274566	PHATRDRAFT_49088	-	-	-	-		-
7202075	946	453	473.34	389.99	-0.279439712	0.000560892	PHATRDRAFT_13587	-	-	-	-		-
7196779	1399	670	1244.52	1026.87	-0.277335865	2.70E-05	PHATRDRAFT_42949	-	-	-	-		-
7204652	825	396	213.88	176.49	-0.27721514	0.001458258	hCdc48	K13525|1|0.0|1113|bdi:100821547|transitional endoplasmic reticulum ATPase	-	GO:0032550;GO:0016462//pyrophosphatase activity	GO:0044763		GO:0044763
7202293	9945.04	4777.52	1391.99	1149.1	-0.276644494	2.17E-28	PHATRDRAFT_47520	-	-	-	-		-
7203204	703	338	232.73	192.41	-0.274473412	0.00358896	PHATRDRAFT_29174	K08332|1|6e-14|77.8|vcn:VOLCADRAFT_41528|vacuolar protein 8;K10590|4|3e-12|72.4|mtr:MTR_4g073370|E3 ubiquitin-protein ligase TRIP12 [EC:6.3.2.19]	GO:0043231//intracellular membrane-bounded organelle	GO:0022892	GO:0006886//intracellular protein transport		GO:0006886//intracellular protein transport
7204344	711	342	330.13	273.19	-0.273129572	0.0034742	PHATR_10378	K00654|1|2e-145|513|smo:SELMODRAFT_108076|serine palmitoyltransferase [EC:2.3.1.50]	-	GO:0043168//anion binding;GO:0003824//catalytic activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7198063	440	212	62.93	52.1	-0.27246457	0.0230006	PHATRDRAFT_44527	-	-	-	-		-
7197539	1548	746	349.38	289.41	-0.271682252	1.85E-05	PHATRDRAFT_232	K06972|1|0.0|877|ppp:PHYPADRAFT_232291|	GO:0009532//plastid stroma;GO:0009526//plastid envelope;GO:0005576//extracellular region	GO:0043169//cation binding;GO:0004175//endopeptidase activity	GO:0010038//response to metal ion;GO:0051604//protein maturation;GO:0009657//plastid organization;GO:0042743//hydrogen peroxide metabolic process;GO:0003006//developmental process involved in reproduction		GO:0010038//response to metal ion;GO:0051604//protein maturation;GO:0009657//plastid organization;GO:0042743//hydrogen peroxide metabolic process;GO:0003006//developmental process involved in reproduction
7197959	1586	765	400.89	332.42	-0.270199246	1.59E-05	PHATRDRAFT_44296	-	-	-	-		-
7202190	1082	522	268.24	222.46	-0.269978436	0.00037465	PHATRDRAFT_47203	-	-	-	-		-

7199943	346	167	103.26	85.69	-0.269082746	0.0461184	PHATRDRAFT_19761	K01880|1|3e-169|593|vcn:VOLCADRAFT_75635|glycyl-tRNA synthetase [EC:6.1.1.14]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7198511	543	262	409.86	340.56	-0.267222203	0.01204188	PHATRDRAFT_49879	-	GO:0009536//plastid	-	-		-
7199256	546	264	100.61	83.6	-0.26719886	0.01273268	UGP/PGM	K01835|1|0.0|654|ath:AT1G23190|phosphoglucomutase [EC:5.4.2.2]	-	GO:0046872//metal ion binding;GO:0016868//intramolecular transferase activity, phosphotransferases;GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0044238		GO:0044238
7203881	415	201	85.26	70.98	-0.264456481	0.0316458	PHATR_44128	-	GO:0031231//intrinsic component of peroxisomal membrane	-	GO:0007031//peroxisome organization		GO:0007031//peroxisome organization
7199700	477	232	95.55	79.88	-0.25842154	0.0240742	MYT1	K06632|1|2e-30|133|ppp:PHYPADRAFT_193308|wee1-like protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195772	482.29	235.04	94.06	78.79	-0.255568797	0.0251742	PHATRDRAFT_49381	-	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer;GO:0046914//transition metal ion binding	GO:0006720//isoprenoid metabolic process		GO:0006720//isoprenoid metabolic process
7204203	469	229	109.85	92.2	-0.252696214	0.0285024	PHATR_43996	-	-	-	-		-
7200478	8762	4276	3378.75	2835.88	-0.25269312	1.19E-21	ISIP2A	-	-	-	-		-
7198791	418	204	227.88	191.38	-0.251834241	0.0383252	PHATRDRAFT_40880	K01476|1|1e-21|102|bdi:100821269|arginase [EC:3.5.3.1]	-	GO:0043169//cation binding;GO:0016810//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	-		-
7203456	1009	493	353.62	297.12	-0.251154152	0.00131215	PHATRDRAFT_48084	-	-	-	-		-
7199816	822	402	90.05	75.67	-0.251004831	0.00393166	PHATRDRAFT_44901	K11380|1|1e-18|95.1|ppp:PHYPADRAFT_27586|NuA3 HAT complex component NTO1	-	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding	-		-
7199240	443	217	123.68	104.15	-0.247949385	0.0365594	PHATRDRAFT_50517	-	-	-	-		-
7202236	409	200	379.76	319.98	-0.247106221	0.04269	PHATRDRAFT_13553	K15377|1|7e-11|65.9|cre:CHLREDRAFT_189789|solute carrier family 44 (choline transporter-like protein), member 2/4/5	GO:0031224//intrinsic component of membrane	-	-		-
7200913	4383	2183	2137.07	1803.31	-0.244986738	1.84E-09	hUbi	K08770|1|0.0|715|ppp:PHYPADRAFT_222215|ubiquitin C	GO:0043231//intracellular membrane-bounded organelle	-	GO:0014070//response to organic cyclic compound;GO:0044767;GO:0036211		GO:0014070//response to organic cyclic compound;GO:0044767;GO:0036211
7195379	733	360	405.66	342.86	-0.242651452	0.00785468	PHATRDRAFT_39627	K03183|1|1e-07|56.2|zma:100384459|ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.163 2.1.1.201]	GO:0044444//cytoplasmic part	GO:0008757//S-adenosylmethionine-dependent methyltransferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7204314	1202	592	506.92	429.44	-0.239301508	0.000789046	PHATR_43911	-	-	-	-		-
7202590	1224	604	442.17	375.23	-0.236825968	0.000808114	PHATRDRAFT_47483	-	-	-	-		-
7198166	517	256	219.44	186.91	-0.23148277	0.0335666	PHATRDRAFT_49683	-	-	-	-		-
7197862	797	396	119.33	101.89	-0.227944322	0.00955436	PHATRDRAFT_44399	K11684|1|1e-13|78.2|sbi:SORBI_03g001920|bromodomain-containing factor 1;K06062|3|4e-07|56.6|mtr:MTR_8g062330|histone acetyltransferase [EC:2.3.1.48];K11723|4|3e-06|53.5|vvi:100267501|bromodomain-containing protein 7/9	-	-	-		-

7201503	741	370	151.29	129.85	-0.220470617	0.01538774	PHATRDRAFT_27838	K03235|1|0.0|797|olu:OSTLU_45865|elongation factor 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7203976	1423	712	305.14	262.43	-0.217538659	0.00089072	PHATR_43856	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7199471	4961.96	2488.48	713.98	615.31	-0.214570223	9.05E-10	PHATRDRAFT_50642	-	-	-	-		-
7198289	666.34	335	284.67	246.18	-0.209576902	0.0285102	PHATRDRAFT_49632	K12183|1|1e-17|89.7|cme:CMK136C|ESCRT-I complex subunit TSG101	-	-	GO:0045184//establishment of protein localization;GO:0036211		GO:0045184//establishment of protein localization;GO:0036211
7204057	1395	703	349.79	303.03	-0.207028418	0.001686098	PHATR_33512	K09291|1|1e-13|77.4|ath:AT1G79280|nucleoprotein TPR;K10400|3|8e-12|71.2|vvi:100255624|kinesin family member 15	GO:0043229//intracellular organelle	-	-		-
7201586	1113	562	308.63	267.92	-0.204076023	0.00567136	PHATRDRAFT_46502	-	-	-	-		-
7197961	684	346	86.51	75.2	-0.202134247	0.032573	PHATRDRAFT_44298	K03260|1|9e-37|155|smo:SELMODRAFT_30927|translation initiation factor 4G	GO:0031224//intrinsic component of membrane	GO:0003676//nucleic acid binding	GO:0044763;GO:0044260		GO:0044763;GO:0044260
7203870	1997	1011	1189.28	1036.27	-0.198688472	0.000266484	PHATR_44109	-	-	GO:0005543//phospholipid binding;GO:0046872//metal ion binding	-		-
7195734	792	402	126.5	110.35	-0.197050755	0.0245872	PHATRDRAFT_15968	K00106|1|0.0|983|vcn:VOLCADRAFT_63971|xanthine dehydrogenase/oxidase [EC:1.17.1.4 1.17.3.2]	-	GO:0046914//transition metal ion binding;GO:0051536//iron-sulfur cluster binding;GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7195006	829	423	89.14	78.15	-0.189827088	0.0267614	PHATRDRAFT_29824	K01870|1|0.0|1123|cre:CHLREDRAFT_139213|isoleucyl-tRNA synthetase [EC:6.1.1.5]	GO:0044424	GO:0032550;GO:0052689//carboxylic ester hydrolase activity;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006448//regulation of translational elongation;GO:0006418//tRNA aminoacylation for protein translation		GO:0006448//regulation of translational elongation;GO:0006418//tRNA aminoacylation for protein translation
7195518	1979	1020	755.6	669.79	-0.173913865	0.001475488	PHATRDRAFT_49209	K10990|1|3e-08|58.9|sbi:SORBI_06g014000|RecQ-mediated genome instability protein 1;K12471|3|4e-06|51.6|vvi:100267012|epsin	-	-	-		-
7196337	1820	939	217.9	193.18	-0.173720457	0.0024951	PHATRDRAFT_42689	-	-	-	-		-
7199818	7400	3818	2469.68	2191.11	-0.172662208	1.01E-09	PHATRDRAFT_54319	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199760	936	485	181.52	161.66	-0.167165761	0.0367538	PHATRDRAFT_44809	-	-	-	-		-
7197359	2551	1323	1084.88	967.8	-0.164754629	0.000595624	PHATRDRAFT_25433	K01365|1|3e-68|257|mtr:MTR_5g022560|cathepsin L [EC:3.4.22.15]	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7197015	1656	858	1477.13	1318.59	-0.163800756	0.00533336	PHATRDRAFT_43726	-	-	-	-		-
7203738	5247	2731	1319.19	1180.35	-0.160437654	1.75E-06	PHATRDRAFT_48315	-	-	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7203002	994	518	399.47	358.05	-0.157926094	0.0403242	PHATRDRAFT_48004	-	-	-	-		-
7199368	1560.21	824.93	400.22	363.78	-0.137727036	0.023321	PHATRDRAFT_50588	-	-	-	-		-
7205098	6098.07	3247.7	2006.65	1837.67	-0.126911286	3.56E-05	PHATRDRAFT_bd1677	K13862|1|8e-20|97.4|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7203948	3319	1770	717.08	657.32	-0.125538198	0.00273382	ACS3	K01897|1|3e-63|242|smo:SELMODRAFT_165130|long-chain acyl-CoA synthetase [EC:6.2.1.3]	-	GO:0015645//fatty acid ligase activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7195200	1771	945	814.26	747.45	-0.123512458	0.02991	PHATRDRAFT_49119	-	-	-	-		-
7200210	6546	3496	3863.36	3551.14	-0.12157388	3.42E-05	Fru3	-	-	-	-		-
7195309	5801	3144	893.16	831.87	-0.102560552	0.001154124	PHATRDRAFT_49064	-	GO:0031224//intrinsic component of membrane	-	-		-

7199468	3528	1929	1029.99	968.26	-0.089163929	0.0259676	PHATRDRAFT_55230	K04079|1|0.0|832|sbi:SORBI_07g028270|molecular chaperone HtpG	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process		GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process
control3 vs grazing3													
geneID	Pt-control-3-Expression	Pt-grazing-3-Expression	Pt-control-3-FPKM	Pt-grazing-3-FPKM	log2 Ratio(Pt-grazing-3/Pt-control-3)	P-value	Symbol	KEGG Orthology	GO Component	GO Function	GO Process		GO Process
7205007	0	20.74	0.001	43.48	15.40806432	2.27E-07	PHATRDRAFT_bd358	K03238|1|6e-45|177|olu:OSTLU_88846|translation initiation factor 2 subunit 2	-	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7200155	0	14.46	0.001	39.1	15.25488099	2.19E-05	H3-1a	K11253|1|6e-69|256|smo:SELMODRAFT_103546|histone H3	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7196608	0	5	0.001	21.54	14.39473063	0.020733	PHATRDRAFT_8741	K12471|1|2e-15|79.0|rcu:RCOM_0050890|epsin	-	-	-		-
7194945	0	4	0.001	17.7	14.11146174	0.0444006	PHATRDRAFT_7337	-	GO:0031224//intrinsic component of membrane	-	GO:0006810//transport		GO:0006810//transport
7199435	0	6.01	0.001	17.41	14.08762858	0.00968128	PHATRDRAFT_6282	K03773|1|1e-40|162|olu:OSTLU_30671|FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8];K09571|4|2e-20|95.5|gmx:100810243|FK506-binding protein 4/5 [EC:5.2.1.8]	-	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7204448	0	5	0.001	17.05	14.05748412	0.020733	RPC11	K03019|1|1e-27|119|ota:Ot03g03890|DNA-directed RNA polymerase III subunit RPC10	GO:0043231//intracellular membrane-bounded organelle	GO:0034062//RNA polymerase activity;GO:0046914//transition metal ion binding;GO:0003676//nucleic acid binding	GO:0010467//gene expression		GO:0010467//gene expression
7196933	0	14	0.001	15.55	13.92462696	2.19E-05	PHATRDRAFT_9211	-	-	GO:0016787//hydrolase activity	-		-
7202538	0	7	0.001	10.79	13.39740724	0.00452068	PHATRDRAFT_37602	-	GO:0044464;GO:0016020//membrane	-	-		-
7202996	0	4	0.001	9.35	13.19075065	0.0444006	PHATRDRAFT_38343	-	-	-	-		-
7200650	0	6	0.001	9.18	13.16427844	0.00968128	PHATRDRAFT_45607	-	-	-	-		-
7196922	0	4	0.001	8.33	13.02410078	0.0444006	PHATRDRAFT_9348	K01493|1|8e-45|177|rcu:RCOM_1506180|dCMP deaminase [EC:3.5.4.12]	-	GO:0016814//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;GO:0046914//transition metal ion binding	-		-
7200776	0	7	0.001	6.15	12.5863707	0.00452068	PHATRDRAFT_45751	-	-	-	-		-
7201063	0	6	0.001	5.04	12.29920802	0.00968128	PHATRDRAFT_46000	-	-	-	-		-
7204128	0	4	0.001	4.72	12.20457114	0.0444006	HemF_2	K00228|1|5e-125|445|cre:CHLREDRAFT_53583|coproporphyrinogen III oxidase [EC:1.3.3.3]	-	GO:0016634	GO:0044710;GO:0006778//porphyrin-containing compound metabolic process		GO:0044710;GO:0006778//porphyrin-containing compound metabolic process
7194808	0	4	0.001	4.54	12.14847658	0.0444006	PHATRDRAFT_2593	K13420|1|2e-40|164|ath:AT5G46330|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7202627	0	7	0.001	4.34	12.08347933	0.00452068	PHATRDRAFT_47561	-	-	-	-		-
7200737	0	7	0.001	4.23	12.04644195	0.00452068	PHATRDRAFT_45552	-	-	-	-		-
7195173	0	5.44	0.001	3.97	11.95492329	0.020733	PHATRDRAFT_39484	-	-	GO:0097159//organic cyclic compound binding	-		-
7195860	0	8.11	0.001	3.58	11.80574387	0.00211094	PHATRDRAFT_40254	-	-	-	-		-
7197002	0	4	0.001	3.5	11.77313921	0.0444006	PHATRDRAFT_43703	-	-	-	-		-
7195692	0	4	0.001	3.05	11.57459353	0.0444006	PHATRDRAFT_39888	-	-	-	-		-
7202428	0	9	0.001	3.03	11.56510208	0.000985706	PHATRDRAFT_37580	-	-	GO:0016787//hydrolase activity;GO:0097159//organic cyclic compound binding	GO:0044238		GO:0044238
7195136	0	4	0.001	2.76	11.43045255	0.0444006	PHATRDRAFT_48837	-	-	-	-		-

7196451	0	4	0.001	2.63	11.36084708	0.0444006	PHATRDRAFT_42868	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7200428	0	5.81	0.001	2.56	11.32192809	0.020733	PHATRDRAFT_35442	-	-	-	-		-
7195340	0	6.01	0.001	2.17	11.08347933	0.00968128	PHATRDRAFT_39762	-	-	GO:0016787//hydrolase activity;GO:0097159//organic cyclic compound binding	GO:0044238		GO:0044238
7194948	0	4	0.001	1.98	10.95128471	0.0444006	PHATRDRAFT_48861	-	-	GO:0003824//catalytic activity	-		-
7201946	0	4	0.001	1.87	10.86882255	0.0444006	PHATRDRAFT_37299	-	-	-	-		-
7199193	0	5	0.001	1.81	10.82177398	0.020733	PHATRDRAFT_41318	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7203386	0	5.83	0.001	1.77	10.78953364	0.020733	PHATRDRAFT_38462	-	-	GO:0060089;GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication		GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication
7204109	0	5.27	0.001	1.69	10.72280753	0.020733	PHATR_44196	-	-	GO:0060089;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0007154//cell communication		GO:0006259//DNA metabolic process;GO:0007154//cell communication
7198177	1.44	57	0.71	32.15	5.500855903	4.20E-18	Sit1	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7198393	2	26	4.95	74	3.90202484	2.89E-07	PHATRDRAFT_40475	-	-	-	-		-
7195583	1	9	1.09	11.22	3.363672636	0.00624	PHATRDRAFT_39989	-	-	-	-		-
7200154	1	9	1.07	11.01	3.363131767	0.00624	H1	K11275|1|4e-07|53.5|gmx:100785055|histone H1/5	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7198860	1	9	0.65	6.66	3.357010554	0.00624	PHATRDRAFT_41055	K15287|1|5e-15|80.9|osa:4338343|solute carrier family 35, member F1/2	-	-	-		-
7202058	1	8	0.82	7.46	3.185479816	0.01223804	PHATRDRAFT_47163	-	-	-	-		-
7205039	1	8.01	0.43	3.91	3.184760043	0.01223804	PHATRDRAFT_bd1768	-	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0016298//lipase activity;GO:0097159//organic cyclic compound binding	GO:0044710;GO:0044238		GO:0044710;GO:0044238
7203316	1	7	2.35	18.93	3.009941749	0.0237986	PHATRDRAFT_14713	K02871|1|5e-29|124|cre:CHLREDRAFT_185004|large subunit ribosomal protein L13	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7201891	1	7	1.7	13.63	3.003178911	0.0237986	PHATRDRAFT_36647	-	-	-	-		-
7195844	1	7	0.49	3.92	3	0.0237986	PHATRDRAFT_49506	-	-	-	-		-
7202648	1	7	0.51	4.05	2.989352756	0.0237986	PHATRDRAFT_37843	-	-	-	-		-
7203216	1	6	0.34	2.36	2.795180208	0.0458054	PHATRDRAFT_47987	-	-	-	-		-
7198162	1	6	3.78	26.2	2.793108672	0.0458054	PHATRDRAFT_16074	-	-	GO:0003676//nucleic acid binding	-		-
7199696	1	6	0.43	2.97	2.788054366	0.0458054	PHATRDRAFT_34625	-	-	-	-		-
7203263	1	6	0.6	4.14	2.786596362	0.0458054	PHATRDRAFT_2271	K03977|1|1e-46|186|smo:SELMODRAFT_123195|GTP-binding protein	-	GO:0032550	-		-
7197588	1	6	0.88	6.06	2.783742365	0.0458054	PHATRDRAFT_43562	-	-	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710

7199687	1	6	1.13	7.78	2.783447383	0.0458054	PHATRDRAFT_34610	K03434|1|3e-29|126|ath:AT3G58130|N-acetylglucosaminylphosphatidylinositol deacetylase [EC:3.5.1.89]	-	-	-		-
7202822	1	6	1.01	6.95	2.782657685	0.0458054	PHATRDRAFT_37877	K00943|1|4e-11|67.0|ota:Ot07g01210|dTMP kinase [EC:2.7.4.9];K15450|2|2e-09|61.2|ota:Ot09g02370|tRNA wybutosine-synthesizing protein 3 [EC:2.1.1.-];K00476|3|1e-08|58.9|ota:Ot10g00170|aspartate beta-hydroxylase [EC:1.14.11.16];K07055|4|1e-08|58.9|vcn:VOLCADRAFT_121064|tRNA wybutosine-synthesizing protein 2 [EC:2.1.1.-]	-	-	-		-
7202379	1	6	0.81	5.56	2.77909107	0.0458054	PHATRDRAFT_47300	-	-	-	-		-
7204131	1	6	0.61	4.16	2.769702381	0.0458054	Gamma-tub	K10389|1|9e-179|624|ppp:PHYPADRAFT_170153|tubulin gamma	GO:0032991//macromolecular complex;GO:0015630//microtubule cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0043623//cellular protein complex assembly		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0043623//cellular protein complex assembly
7195191	1	6	0.49	3.33	2.764668523	0.0458054	PHATRDRAFT_29793	K00599|1|2e-35|148|cme:CMJ198C|[EC:2.1.1.-];K02493|2|3e-19|95.1|smo:SELMODRAFT_99812|release factor glutamine methyltransferase [EC:2.1.1.-]	-	GO:0097159//organic cyclic compound binding;GO:0008168//methyltransferase activity	GO:0008213		GO:0008213
7195117	0.92	5.12	0.27	1.73	2.679740725	0.020733	PHATRDRAFT_52461	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7195319	2	11	1.59	10	2.652901329	0.00635314	PHATRDRAFT_49082	-	-	-	-		-
7200316	3	14	3.28	17.54	2.418881028	0.0031968	PHATRDRAFT_45123	-	-	-	-		-
7205137	2.28	10.45	0.5	2.62	2.389566812	0.01179084	PHATRDRAFT_bd1453	-	-	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7201214	2	9	1.76	9.07	2.365527122	0.0216444	ADH_2	K13953|1|2e-23|107|zma:100274539|alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1];K00121|2|3e-23|107|vvi:100245520|S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1];K00008|3|2e-22|104|vvi:100232980|L-iditol 2-dehydrogenase [EC:1.1.1.14]	-	GO:0046914//transition metal ion binding;GO:0036094//small molecule binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7202298	959	4289	2963.76	15265.21	2.364746906	0	PHATRDRAFT_37403	-	-	-	-		-
7198966	2	9	1.56	8.02	2.362056208	0.0216444	PHATRDRAFT_50299	K14648|1|3e-71|267|vcn:VOLCADRAFT_62482|poly(U)-specific endoribonuclease [EC:3.1.-.-]	-	GO:0016787//hydrolase activity	-		-
7196583	2	9	1.23	6.32	2.361266243	0.0216444	PHATRDRAFT_43221	-	-	-	-		-
7203765	2	9	1.39	7.14	2.360839191	0.0216444	PHATRDRAFT_48481	-	-	-	-		-
7201897	2	9	0.63	3.23	2.358110431	0.0216444	PHATRDRAFT_36284	K06676|1|3e-21|102|vvi:100251638|condensin complex subunit 2	-	-	-		-
7198486	1.78	7.72	1.83	9.11	2.315607406	0.0237986	PHATRDRAFT_40626	K13199|1|3e-06|50.8|gmx:100814825|plasminogen activator inhibitor 1 RNA-binding protein	-	-	-		-
7204966	9.04	36.61	4.46	20.63	2.209628206	5.55E-06	PHATRDRAFT_bd1252	-	-	GO:0003824//catalytic activity	-		-
7198642	0.99	4	0.75	3.45	2.201633861	0.0444006	PHATRDRAFT_40785	-	-	-	-		-

7197827	3	12	6.24	28.66	2.199420675	0.01030714	PHATRDRAFT_10670	-	GO:0043231//intracellular membrane-bounded organelle	-	GO:0016482//cytoplasmic transport		GO:0016482//cytoplasmic transport
7197476	4	16	1.7	7.79	2.196088582	0.00282216	PHATRDRAFT_32848	K10736|1|3e-10|65.5|mtr:MTR_3g117880|minichromosome maintenance protein 10	-	-	-		-
7202426	2	8	1.1	5.04	2.19592021	0.0392292	PHATRDRAFT_47378	-	-	-	-		-
7195237	3	12	1.92	8.78	2.193114629	0.01030714	PHATRDRAFT_15508	K14399|1|2e-54|211|osa:4328733|polyribonucleotide 5'-hydroxyl-kinase [EC:2.7.1.78]	-	-	-		-
7195736	2	8	1.09	4.97	2.188917717	0.0392292	PHATRDRAFT_49514	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7195131	3	11	2.14	9	2.072314205	0.01820246	PHATRDRAFT_2215	K09480|1|1e-76|285|osa:4329584|digalactosyldiacylglycerol synthase [EC:2.4.1.241]	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7195994	6	22	8.39	35.25	2.070880542	0.000680804	PHATRDRAFT_3171	K15731|1|8e-20|95.1|smo:SELMODRAFT_77112|carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase [EC:3.1.3.16]	-	-	-		-
7196389	3	10	4.89	18.68	1.933588085	0.031729	PHATRDRAFT_6580	-	GO:0019866//organelle inner membrane	-	GO:0007005//mitochondrion organization		GO:0007005//mitochondrion organization
7200593	3	10	1.92	7.33	1.932706887	0.031729	PHATRDRAFT_12107	K13941|1|2e-94|344|smo:SELMODRAFT_102265|2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase / dihydropteroate synthase [EC:2.7.6.3 2.5.1.15]	-	GO:0016778;GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0006760//folic acid-containing compound metabolic process		GO:0006760//folic acid-containing compound metabolic process
7204224	3	10	2.78	10.6	1.930907477	0.031729	PHATR_4821	K11418|1|1e-10|65.5|mtr:MTR_1g016440|histone deacetylase 11 [EC:3.5.1.98]	-	GO:0003824//catalytic activity	-		-
7200042	4	13	6.59	24.57	1.898547487	0.01477452	PHATRDRAFT_35042	-	-	-	-		-
7198479	277	855.95	351.6	1244.97	1.824104003	5.95E-87	Lhcf5	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7196705	4	12	6.79	23.36	1.782556795	0.025054	PHATRDRAFT_41701	-	-	-	GO:0032502//developmental process		GO:0032502//developmental process
7197092	4	12	6.71	23.08	1.782258552	0.025054	PHATRDRAFT_32531	K03232|1|8e-09|58.2|ath:AT1G30230|elongation factor 1-beta	GO:0043234//protein complex	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7200677	4	12	4.56	15.68	1.78181983	0.025054	PHATRDRAFT_12044	K08869|1|5e-36|149|pop:POPTR_1118267|aarF domain-containing kinase	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7200758	4	12	3.13	10.76	1.781443516	0.025054	PHATRDRAFT_45724	-	-	-	-		-
7199150	4	12	3.14	10.79	1.780858401	0.025054	PHATRDRAFT_16911	K00599|1|7e-22|103|ath:AT3G21300|[EC:2.1.1.-]	-	GO:0008757//S-adenosylmethionine-dependent methyltransferase activity	GO:0006399//tRNA metabolic process;GO:0010467//gene expression;GO:0009451//RNA modification		GO:0006399//tRNA metabolic process;GO:0010467//gene expression;GO:0009451//RNA modification
7202906	4	12	2.95	10.13	1.779847315	0.025054	PHATRDRAFT_47728	K09522|1|6e-13|73.6|gmx:100814414|DnaJ homolog subfamily C member 2	-	GO:0003676//nucleic acid binding	-		-
7197578	4	12	3.14	10.78	1.779520714	0.025054	PHATRDRAFT_43546	-	-	-	-		-
7198478	12	35.05	16.32	54.63	1.743052366	0.000125233	Lhcf11	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7200478	349	977	175.5	561.79	1.678559914	1.26E-88	ISIP2A	-	-	-	-		-
7195130	14	39	12.68	40.43	1.672871458	8.05E-05	PHATRDRAFT_22774	K02937|1|6e-64|242|ppp:PHYPADRAFT_158886|large subunit ribosomal protein L7e	GO:0030529//ribonucleoprotein complex	-	-		-
7197820	4	11	5.68	17.92	1.657607803	0.0418884	PHATRDRAFT_44340	-	-	-	-		-
7204850	4.4	12.11	2.6	8.2	1.657112286	0.025054	PHATRDRAFT_bd315	K08869|1|2e-108|391|mtr:MTR_5g068050|aarF domain-containing kinase	GO:0009570//chloroplast stroma	GO:0016301//kinase activity	GO:0005984//disaccharide metabolic process;GO:0005982//starch metabolic process;GO:0044093;GO:0006787		GO:0005984//disaccharide metabolic process;GO:0005982//starch metabolic process;GO:0044093;GO:0006787

7196023	4	11	3.13	9.84	1.652495658	0.0418884	APC6	K03353|1|1e-65|248|ppp:PHYPADRAFT_153829|anaphase-promoting complex subunit 6	-	-	-		-
7202307	4	11	2.3	7.22	1.650364976	0.0418884	PHATRDRAFT_37419	-	-	-	-		-
7202571	7	19	12.32	38.36	1.638600464	0.00726538	PHATRDRAFT_14064	K01522|1|4e-07|52.4|ota:Ot03g01500|bis(5'-adenosyl)-triphosphatase [EC:3.6.1.29]	GO:0044464	GO:0003824//catalytic activity	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7201983	13	35	11.18	34.45	1.623583795	0.000259564	PHATRDRAFT_47222	-	-	-	-		-
7199077	4.47	11.78	4.37	13.21	1.595925282	0.0418884	PHATRDRAFT_50340	-	-	-	-		-
7203201	5	13	14.66	43.88	1.581678422	0.0320546	PHATRDRAFT_14478	-	-	GO:0051540;GO:0043169//cation binding	-		-
7200198	5	13	8.96	26.74	1.577428828	0.0320546	PHATRDRAFT_11653	K14568|1|5e-36|148|ppp:PHYPADRAFT_46413|essential for mitotic growth 1	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7199582	5	13	3.83	11.41	1.574882494	0.0320546	PHATRDRAFT_34415	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202448	11	28	12.3	35.87	1.54411943	0.00168532	PHATRDRAFT_14067	K01718|1|5e-38|155|olu:OSTLU_4215|pseudouridylate synthase [EC:4.2.1.70];K15452|2|1e-10|65.1|rcu:RCOM_1298450|tRNA pseudouridine synthase 2 [EC:5.4.99.-]	GO:0044444//cytoplasmic part	GO:0003676//nucleic acid binding;GO:0016866//intramolecular transferase activity	GO:0019752//carboxylic acid metabolic process;GO:0009451//RNA modification		GO:0019752//carboxylic acid metabolic process;GO:0009451//RNA modification
7201523	8.37	21	10.2	29.32	1.523315951	0.0056661	PHATRDRAFT_12641	K14497|1|1e-31|134|gmx:100785905|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0004721//phosphoprotein phosphatase activity;GO:0043169//cation binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7203625	8	20	6.6	18.87	1.515556493	0.00904916	PHATRDRAFT_48450	-	-	-	-		-
7202101	8	20	6.79	19.41	1.515316638	0.00904916	PHATRDRAFT_47000	-	-	-	-		-
7199364	15	37	10.5	29.62	1.496182313	0.000398534	PHATRDRAFT_24223	K13985|1|6e-57|219|smo:SELMODRAFT_2635|N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D [EC:3.1.4.54]	-	GO:0004620//phospholipase activity;GO:0046914//transition metal ion binding	-		-
7198922	13	32	16.19	45.66	1.495827874	0.001023334	PHATRDRAFT_50120	K14965|1|5e-10|62.8|cre:CHLREDRAFT_3897|protein dpy-30	-	GO:0043168//anion binding;GO:0046914//transition metal ion binding	-		-
7202594	11	27	6.29	17.67	1.490170118	0.00265388	PHATRDRAFT_21682	K15449|1|2e-137|487|smo:SELMODRAFT_169856|tRNA wybutosine-synthesizing protein 1	-	GO:0051540;GO:0003824//catalytic activity;GO:0043167//ion binding;GO:0032553	GO:0044710		GO:0044710
7194892	9	22	7.09	19.84	1.484554493	0.00697668	PHATRDRAFT_48645	-	-	GO:0032553;GO:0016641//oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	GO:0009108//coenzyme biosynthetic process;GO:0044710		GO:0009108//coenzyme biosynthetic process;GO:0044710
7201502	6.28	15.34	3.77	10.53	1.481869008	0.0244908	PHATRDRAFT_46313	-	-	-	-		-
7203619	7	17	5.19	14.41	1.473263892	0.01870746	PHATRDRAFT_14962	K01760|1|3e-51|201|olu:OSTLU_88245|cystathionine beta-lyase [EC:4.4.1.8]	-	GO:0043168//anion binding;GO:0003824//catalytic activity	-		-
7201383	5.72	13.66	2.84	7.76	1.450165723	0.0320546	PHATRDRAFT_46314	-	-	-	-		-
7201738	6	14	14	37.55	1.423386081	0.0390114	PHATRDRAFT_13047	-	-	GO:0008092//cytoskeletal protein binding	GO:0032989;GO:0006996//organelle organization		GO:0032989;GO:0006996//organelle organization
7195618	12	28	19.11	51.14	1.420124382	0.0031929	PHATRDRAFT_42274	-	-	-	-		-
7198112	6	14	3.44	9.19	1.417656297	0.0390114	PHATRDRAFT_34085	-	-	-	-		-
7198771	9	21	8.23	21.98	1.417227051	0.01093186	PHATRDRAFT_49987	K05770|1|8e-23|105|cre:CHLREDRAFT_143874|benzodiazapine receptor;K07185|4|1e-09|62.0|olu:OSTLU_8326|tryptophan-rich sensory protein	GO:0031224//intrinsic component of membrane	-	-		-
7194817	6	14	3.63	9.69	1.416527117	0.0390114	PHATRDRAFT_48606	-	-	-	-		-
7195752	16	37	11.33	29.97	1.403371223	0.000739878	PHATRDRAFT_49542	-	-	-	-		-

7196102	10	23	9.94	26.17	1.396596167	0.00836666	PHATRDRAFT_41667	K08343|1|2e-63|240|ppp:PHYPADRAFT_183062|autophagy-related protein 3	GO:0044424	-	GO:0044248//cellular catabolic process;GO:0045184//establishment of protein localization		GO:0044248//cellular catabolic process;GO:0045184//establishment of protein localization
7195739	10	23	7.55	19.86	1.395317073	0.00836666	PHATRDRAFT_40239	-	-	-	-		-
7202040	30	69	7.59	19.95	1.394216956	4.12E-06	PHATRDRAFT_52174	K03164|1|0.0|1162|vvi:100253371|DNA topoisomerase II [EC:5.99.1.3]	GO:0043232	GO:0008094//DNA-dependent ATPase activity;GO:0003677//DNA binding;GO:0032550	GO:0071103//DNA conformation change		GO:0071103//DNA conformation change
7204891	11.97	27.44	4.8	12.59	1.391171972	0.00265388	PHATRDRAFT_bd1569	-	GO:0044424	GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0032550	GO:0006412//translation		GO:0006412//translation
7200580	7	16	3.23	8.45	1.387417176	0.0294718	CRTISO1	K09835|1|3e-43|174|smo:SELMODRAFT_174745|prolycopene isomerase [EC:5.2.1.13]	-	-	-		-
7200059	11.93	27.03	13.95	36.19	1.375325986	0.00265388	PHATRDRAFT_34632	-	-	-	-		-
7197608	8	18	18.83	48.68	1.370296168	0.0223208	PHATRDRAFT_7358	K02867|1|4e-17|84.7|olu:OSTLU_13461|large subunit ribosomal protein L11	GO:0043229//intracellular organelle;GO:0044444//cytoplasmic part;GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0044238;GO:0034645//cellular macromolecule biosynthetic process;GO:0010467//gene expression		GO:0044238;GO:0034645//cellular macromolecule biosynthetic process;GO:0010467//gene expression
7194950	12	27	6.69	17.21	1.363168981	0.00491386	PHATRDRAFT_48865	K01206|1|5e-07|54.3|gmx:100805382|alpha-L-fucosidase [EC:3.2.1.51]	-	GO:0015928//fucosidase activity	GO:0019318//hexose metabolic process		GO:0019318//hexose metabolic process
7200038	9	20	45.39	116.76	1.363099723	0.01694302	PHATRDRAFT_51837	K03676|1|1e-13|72.8|pop:POPTR_173884|glutaredoxin 3	-	GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis		GO:0019725//cellular homeostasis
7202539	27	60	20.45	52	1.34641078	2.99E-05	PHATRDRAFT_47395	K00434|1|9e-83|305|smo:SELMODRAFT_108251|L-ascorbate peroxidase [EC:1.11.1.11]	GO:0044424	GO:0046906//tetrapyrrole binding;GO:0004601//peroxidase activity	GO:0006950//response to stress;GO:0044710		GO:0006950//response to stress;GO:0044710
7204151	10	22	11.88	29.95	1.334021167	0.0128867	PHATR_10524	K03798|1|1e-56|218|bdi:100837571|cell division protease FtsH [EC:3.4.24.-]	GO:0009526//plastid envelope	GO:0070011//peptidase activity, acting on L-amino acid peptides;GO:0032550;GO:0016887//ATPase activity	-		-
7204613	11	24	18.41	46.07	1.323337971	0.0098191	PHATR_46699	K03012|1|6e-07|52.0|mtr:MTR_8g011890|DNA-directed RNA polymerase II subunit RPB4	-	GO:0034062//RNA polymerase activity;GO:0036094//small molecule binding	GO:0010467//gene expression		GO:0010467//gene expression
7202781	22	48	6.48	16.15	1.317468447	0.000240388	PHATRDRAFT_47544	-	-	-	-		-
7195267	17	37	8.55	21.29	1.316179625	0.001317846	PK5	K00873|1|2e-94|345|cre:CHLREDRAFT_136854|pyruvate kinase [EC:2.7.1.40]	-	GO:0031420;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process
7196279	23	50	7.17	17.8	1.311832217	0.000185984	PHATRDRAFT_42591	-	-	-	-		-
7196974	13	28	14.83	36.59	1.302930818	0.00572736	SybE	K08517|1|7e-33|139|vcn:VOLCADRAFT_80612|vesicle transport protein SEC22	GO:0031224//intrinsic component of membrane	-	GO:0006810//transport		GO:0006810//transport
7200983	7	15	7.77	19.07	1.29531834	0.0458008	PHATRDRAFT_45890	-	-	-	-		-
7203910	8	17	16.28	39.73	1.287128094	0.0344152	PHATR_33540	K12877|1|2e-48|189|gmx:100305742|protein mago nashi	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7201087	8	17	12.46	30.37	1.28534284	0.0344152	PHATRDRAFT_35644	-	-	-	-		-
7205014	8	17	3.89	9.46	1.282070028	0.0344152	PHATRDRAFT_bd780	K01883|1|2e-103|374|cme:CME037C|cysteinyl-tRNA synthetase [EC:6.1.1.16]	GO:0005737//cytoplasm	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7197195	9	19	6.15	14.85	1.271804615	0.0259542	PHATRDRAFT_43503	-	-	-	-		-
7204883	10	21	24.61	59.42	1.271703947	0.0196333	PHATRDRAFT_bd1340	-	-	-	-		-

7195828	12	25	37.09	88.98	1.262450831	0.01131872	PHATRDRAFT_15913	K11422|1|1e-14|76.3|cme:CMG025C|histone-lysine N-methyltransferase SETD1 [EC:2.1.1.43];K09188|2|3e-12|68.2|cme:CMD005C|histone-lysine N-methyltransferase MLL3 [EC:2.1.1.43];K11430|5|2e-07|52.0|mtr:MTR_5g016870|enhancer of zeste [EC:2.1.1.43]	GO:0043231//intracellular membrane-bounded organelle	GO:0016279//protein-lysine N-methyltransferase activity	GO:0016571//histone methylation		GO:0016571//histone methylation
7199951	20	41.54	28	66.67	1.2516109	0.001332778	H3-1b	K11253|1|5e-70|261|ota:Ot11g02340|histone H3	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7204908	10.44	21.68	2.56	6.08	1.247927513	0.0196333	PHATRDRAFT_bd1623	K12319|1|2e-29|130|vcn:VOLCADRAFT_61364|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|1e-24|114|vcn:VOLCADRAFT_106794|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K01120|5|1e-14|80.9|cre:CHLREDRAFT_101278|3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7195429	31	64	8.3	19.59	1.238934156	5.25E-05	PHATRDRAFT_49066	-	-	GO:0016740//transferase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7202653	37	76	12.73	29.88	1.230947729	1.14E-05	PHATRDRAFT_47597	-	GO:0044464	GO:0016837	GO:0042120		GO:0042120
7203240	19	39	9.58	22.48	1.230544474	0.001734434	PHATRDRAFT_38362	K01649|1|3e-125|447|cme:CMO208C|2-isopropylmalate synthase [EC:2.3.3.13]	-	GO:0046912//transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	GO:0006551//leucine metabolic process		GO:0006551//leucine metabolic process
7203329	9	18	14.49	33.25	1.198296746	0.0392632	PHATRDRAFT_4950	K00472|1|5e-26|115|bdi:100831521|prolyl 4-hydroxylase [EC:1.14.11.2]	GO:0044464	GO:0046914//transition metal ion binding;GO:0019842//vitamin binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7199430	11	22	11.99	27.46	1.195499967	0.0223378	PHATRDRAFT_50612	-	-	-	-		-
7204501	12	24	12.54	28.71	1.195015982	0.01692334	PHATR_36742	K09941|1|2e-09|61.6|olu:OSTLU_33635|hypothetical protein	-	-	-		-
7200282	13	26	9.85	22.55	1.194931804	0.01285198	PHATRDRAFT_45274	-	-	-	-		-
7202134	10	20	6.47	14.81	1.194734023	0.0295664	PHATRDRAFT_47061	-	-	-	-		-
7196324	19	38	10.97	25.1	1.194123838	0.00255564	PHATRDRAFT_42671	-	-	-	-		-
7200079	24	48	13.16	30.1	1.193603998	0.000686118	PHATRDRAFT_45068	-	-	-	-		-
7195019	23	46	13.44	30.74	1.193584027	0.000891076	PHATRDRAFT_48730	-	-	-	-		-
7200094	9	18	3.42	7.81	1.191326223	0.0392632	PHATRDRAFT_45210	-	-	-	-		-
7197554	26	51	38.95	87.59	1.169142841	0.000592792	PHATRDRAFT_43509	-	-	-	-		-
7194755	16	31	29.42	65.41	1.152713968	0.00835986	PHATRDRAFT_7018	-	-	-	GO:0009987//cellular process;GO:0051234//establishment of localization;GO:0006950//response to stress		GO:0009987//cellular process;GO:0051234//establishment of localization;GO:0006950//response to stress
7195915	29	56	21.98	48.57	1.1438741	0.000393096	PHATRDRAFT_49428	-	-	-	-		-
7197228	13	25	11.21	24.69	1.139140558	0.01896866	PHATRDRAFT_43673	K09651|1|2e-15|81.3|ppp:PHYPADRAFT_205013|rhomboid domain-containing protein 1 [EC:3.4.21.-]	GO:0031224//intrinsic component of membrane	GO:0004175//endopeptidase activity	-		-
7203697	13	25	7.83	17.22	1.13700093	0.01896866	PHATRDRAFT_48468	-	-	-	-		-
7202675	12	23	16.29	35.8	1.135972984	0.0250332	PHATRDRAFT_14191	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7197445	12	23	14.32	31.44	1.134569725	0.0250332	PHATRDRAFT_43442	-	-	-	-		-
7200119	11	21	12.65	27.66	1.128663772	0.0331266	PHATRDRAFT_34891	-	-	GO:0016407//acetyltransferase activity	-		-
7198002	11	21	7.28	15.89	1.126108769	0.0331266	PHATRDRAFT_44285	-	-	-	-		-

7197987	19	36	54.59	119.06	1.124980197	0.00542652	PHATRDRAFT_11032	K02898|1|7e-40|159|ppp:PHYPADRAFT_163662|large subunit ribosomal protein L26e	GO:0015934//large ribosomal subunit;GO:0009536//plastid	GO:0005488//binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197837	21	40	14.55	31.71	1.123918724	0.003188	PHATRDRAFT_44360	-	-	-	-		-
7196893	20	38	9.03	19.62	1.119527149	0.004157	PHATRDRAFT_43122	-	GO:0044424	GO:0015631//tubulin binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7203346	23.34	44	11.18	24.11	1.108711463	0.001880472	PHATRDRAFT_48227	K07019|1|3e-17|88.6|ppp:PHYPADRAFT_140563|	-	-	-		-
7201248	17	32	15.28	32.93	1.107757969	0.00928212	PHATRDRAFT_46163	-	-	-	-		-
7195509	15	28	41.7	89.58	1.103129283	0.01597358	PHATRDRAFT_30160	K02976|1|1e-28|122|aly:ARALYDRAFT_486074|small subunit ribosomal protein S26e	GO:0015935//small ribosomal subunit;GO:0009536//plastid;GO:0005911//cell-cell junction	GO:0005198//structural molecule activity	GO:0071555//cell wall organization;GO:0022613//ribonucleoprotein complex biogenesis;GO:0009117//nucleotide metabolic process;GO:0010467//gene expression		GO:0071555//cell wall organization;GO:0022613//ribonucleoprotein complex biogenesis;GO:0009117//nucleotide metabolic process;GO:0010467//gene expression
7203483	16	30	5.53	11.86	1.100752624	0.01216628	PHATRDRAFT_48135	K02603|1|1e-07|57.4|sbi:SORBI_10g005910|origin recognition complex subunit 1	-	GO:0046914//transition metal ion binding	-		-
7196353	15	28	29.08	62.31	1.099436448	0.01597358	PHATRDRAFT_6927	K03762|1|4e-33|138|cre:CHLREDRAFT_54232|MFS transporter, MHS family, proline/betaine transporter;K08176|3|2e-07|53.1|ath:AT5G43340|MFS transporter, PHS family, inorganic phosphate transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7195071	15	28	10.02	21.4	1.094728288	0.01597358	PHATRDRAFT_15374	K01875|1|6e-55|213|ppp:PHYPADRAFT_137980|seryl-tRNA synthetase [EC:6.1.1.11]	GO:0044424	GO:0032550;GO:0004812//aminoacyl-tRNA ligase activity	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7201592	15	28	7.98	17.03	1.093617783	0.01597358	PHATRDRAFT_46513	-	-	-	-		-
7199536	14	26	11.92	25.34	1.088032289	0.0210126	PHATRDRAFT_44712	-	-	-	-		-
7202474	14	26	8.07	17.15	1.087567998	0.0210126	PHATRDRAFT_47458	-	-	-	-		-
7204180	14	26	3.18	6.75	1.085860737	0.0210126	SMC	K06677|1|2e-121|435|ppp:PHYPADRAFT_143027|condensin complex subunit 1	-	-	GO:0000070//mitotic sister chromatid segregation		GO:0000070//mitotic sister chromatid segregation
7201618	25	46	18.38	38.7	1.0741968	0.0022864	PHATRDRAFT_46348	-	-	-	-		-
7202392	25	46	16.09	33.86	1.073417647	0.0022864	PHATRDRAFT_47328	-	-	GO:0097159//organic cyclic compound binding	-		-
7195002	12	22	11.84	24.86	1.070157215	0.0366116	PHATRDRAFT_48742	-	-	-	-		-
7198005	12	22	6.85	14.36	1.067879856	0.0366116	PHATRDRAFT_33692	-	-	-	-		-
7198006	23	42	42.93	89.98	1.067618194	0.00386478	PHATRDRAFT_18859	K02920|1|5e-22|101|ath:AT2G37600|large subunit ribosomal protein L36e	GO:0015934//large ribosomal subunit	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197548	18	33	7.77	16.28	1.067114196	0.01021832	PHATRDRAFT_43499	-	-	-	-		-
7199546	17	31	19.47	40.67	1.062712107	0.01337844	EB1	K10436|1|1e-41|168|aly:ARALYDRAFT_496428|microtubule-associated protein, RP/EB family	GO:0043231//intracellular membrane-bounded organelle;GO:0055028//cortical microtubule	GO:0015631//tubulin binding	GO:0009630//gravitropism;GO:0009612//response to mechanical stimulus		GO:0009630//gravitropism;GO:0009612//response to mechanical stimulus
7197520	11	20	16.51	34.41	1.059487772	0.0485296	PHATRDRAFT_43676	-	-	-	-		-
7196329	11	20	14.13	29.44	1.059016206	0.0485296	PHATRDRAFT_42676	-	-	-	-		-
7202614	28	51	10.75	22.39	1.058517868	0.001485838	PHATRDRAFT_47513	-	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7202689	22	40	14.22	29.58	1.056700587	0.005031	ISIP3	-	-	-	-		-
7194997	11	20	6.28	13.05	1.055213343	0.0485296	PHATRDRAFT_48732	K00472|1|5e-16|84.3|ath:AT2G43080|prolyl 4-hydroxylase [EC:1.14.11.2]	-	GO:0046914//transition metal ion binding;GO:0016491//oxidoreductase activity;GO:0019842//vitamin binding	GO:0044710		GO:0044710

7201545	102	185	50.61	104.96	1.052345246	1.52E-09	PHATRDRAFT_56588	K00218|1|8e-61|233|zma:100283531|protochlorophyllide reductase [EC:1.3.1.33]	GO:0009534//chloroplast thylakoid	GO:0036094//small molecule binding;GO:0016491//oxidoreductase activity	GO:1901362;GO:1901135;GO:0008610//lipid biosynthetic process;GO:0019438//aromatic compound biosynthetic process;GO:0006796//phosphate-containing compound metabolic process;GO:0019637//organophosphate metabolic process;GO:0009416//response to light stimulus;GO:0044255//cellular lipid metabolic process;GO:0016070//RNA metabolic process;GO:00		GO:1901362;GO:1901135;GO:0008610//lipid biosynthetic process;GO:0019438//aromatic compound biosynthetic process;GO:0006796//phosphate-containing compound metabolic process;GO:0019637//organophosphate metabolic process;GO:0009416//response to light stimulus;GO:0044255//cellular lipid metabolic process;GO:0016070//RNA metabolic process;GO:00
7195206	16	29	10.95	22.7	1.051761428	0.01754288	PHATRDRAFT_39772	-	GO:0031224//intrinsic component of membrane	GO:0042887	GO:0015840//urea transport		GO:0015840//urea transport
7196851	11	20	2.24	4.64	1.050626073	0.0485296	PHATRDRAFT_43055	-	-	GO:0003676//nucleic acid binding;GO:0034061	GO:0010467//gene expression		GO:0010467//gene expression
7199153	20	36	35.04	72.37	1.046388997	0.00854994	PHATRDRAFT_31140	K09550|1|3e-20|95.9|osa:4333507|prefoldin subunit 4	GO:0043234//protein complex	GO:0005515//protein binding	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7196607	20	36	22.37	46.12	1.043827257	0.00854994	PHATRDRAFT_32443	-	-	-	-		-
7204607	24	43	15.75	32.28	1.03528875	0.00421684	PHATR_46694	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201943	19	34	18.58	38.07	1.034904068	0.01116406	PHATRDRAFT_47157	-	-	-	-		-
7195810	14	25	10.68	21.82	1.030739455	0.0303282	PHATRDRAFT_49451	K03437|1|2e-15|82.0|ota:Ot08g01510|RNA methyltransferase, TrmH family	-	GO:0003676//nucleic acid binding;GO:0008168//methyltransferase activity	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7203968	22	39	34.09	69.29	1.023298557	0.00713488	PHATR_10593	K01358|1|8e-53|204|olu:OSTLU_119581|ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	GO:0009532//plastid stroma	GO:0004175//endopeptidase activity;GO:0016757//transferase activity, transferring glycosyl groups	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199415	13	23	23.6	47.91	1.021539954	0.0400052	PHATRDRAFT_17109	K00888|1|1e-35|146|cme:CMI125C|phosphatidylinositol 4-kinase [EC:2.7.1.67]	-	GO:0052742	GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0046474//glycerophospholipid biosynthetic process		GO:0046488//phosphatidylinositol metabolic process;GO:0048017//inositol lipid-mediated signaling;GO:0046474//glycerophospholipid biosynthetic process
7204608	35	62	18.49	37.46	1.018605675	0.000683144	VPS45	K12479|1|1e-94|345|ota:Ot04g00850|vacuolar protein sorting-associated protein 45	-	-	GO:0006887//exocytosis		GO:0006887//exocytosis
7197205	13	23	10.94	22.15	1.017693961	0.0400052	Lhcr7	K08916|1|1e-16|85.5|cre:CHLREDRAFT_184397|light-harvesting complex II chlorophyll a/b binding protein 5;K08907|2|1e-15|82.4|cme:CMN234C|light-harvesting complex I chlorophyll a/b binding protein 1;K14172|4|3e-14|77.8|cre:CHLREDRAFT_205903|light-harvesting complex II chlorophyll a/b binding protein 7;K08911|5|2e-13|75.1|vcn:VOLCADRAFT_108852|light-harvesting complex I chlorophyll a/b binding protein 5	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7195262	13	23	8.02	16.23	1.016988858	0.0400052	PHATRDRAFT_48993	-	-	-	-		-
7195258	13	23	4.85	9.8	1.014797002	0.0400052	PHATRDRAFT_48986	-	-	-	-		-
7202066	21	37	27.9	56.33	1.01363835	0.00929292	PHATRDRAFT_47178	-	-	-	-		-

7198812	29	51	47.78	96.39	1.012476628	0.0022746	PHATRDRAFT_40933	K01358|1|9e-54|207|vcn:VOLCADRAFT_80119|ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202855	25	44	15.48	31.17	1.009752683	0.0045765	PHATRDRAFT_47665	-	-	-	-		-
7205105	16.03	28.18	5.21	10.47	1.006906165	0.0250522	PHATRDRAFT_bd1563	-	-	GO:0016866//intramolecular transferase activity;GO:0003676//nucleic acid binding	GO:0009451//RNA modification		GO:0009451//RNA modification
7202573	16	28	16.66	33.38	1.002595554	0.0250522	PHATRDRAFT_37671	-	-	-	-		-
7198753	23	40	35.77	71.33	0.995758855	0.00772194	PHATRDRAFT_50065	-	-	-	-		-
7194793	15	26	21.71	43.14	0.990666451	0.0329024	PHATRDRAFT_48567	-	-	-	-		-
7195955	52	90	20.25	40.06	0.984240513	6.77E-05	PHATRDRAFT_42574	-	-	-	-		-
7203591	22	38	9.93	19.6	0.980988031	0.0100417	PK1	K00873|1|8e-61|233|ppp:PHYPADRAFT_108784|pyruvate kinase [EC:2.7.1.40]	-	GO:0031420;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process
7194826	14	24	14.16	27.8	0.973263618	0.0432958	PHATRDRAFT_39127	-	-	-	-		-
7204598	21	36	16.19	31.76	0.972107927	0.01306902	PHATR_1103	K13412|1|2e-65|247|gmx:100797449|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0046872//metal ion binding;GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7196640	21	36	11.41	22.37	0.971266465	0.01306902	PHATRDRAFT_42431	-	-	-	-		-
7199530	14	24	8.31	16.29	0.971066222	0.0432958	PHATRDRAFT_45021	-	-	-	-		-
7197351	21	36	13.85	27.15	0.971066222	0.01306902	PHATRDRAFT_43636	K00344|1|1e-19|96.3|osa:4331066|NADPH2:quinone reductase [EC:1.6.5.5];K07119|5|2e-12|72.4|pop:POPTR_1087070|	-	GO:0046914//transition metal ion binding;GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7197057	14	24	6.97	13.66	0.970726922	0.0432958	PHATRDRAFT_43785	-	-	GO:0005254//chloride channel activity	GO:0015698//inorganic anion transport;GO:0044763		GO:0015698//inorganic anion transport;GO:0044763
7199802	49	84	14.8	29	0.970455724	0.000142774	cupD	-	-	-	-		-
7199174	17	29	8.38	16.34	0.963385834	0.027031	PHATRDRAFT_41383	-	-	-	-		-
7204647	36	61	88.61	172.61	0.961974621	0.001416676	PHATR_21073	K02975|1|6e-14|73.9|osa:4347899|small subunit ribosomal protein S25e	GO:0005840//ribosome	-	-		-
7202037	17	29	4.22	8.22	0.961895395	0.027031	PHATRDRAFT_13581	K03164|1|0.0|909|olu:OSTLU_41836|DNA topoisomerase II [EC:5.99.1.3]	GO:0043232	GO:0008094//DNA-dependent ATPase activity;GO:0003677//DNA binding;GO:0032550	GO:0071103//DNA conformation change		GO:0071103//DNA conformation change
7195016	83	141	117.16	228.15	0.961502555	1.08E-06	PHATRDRAFT_48728	K03626|1|5e-31|132|vvi:100245825|nascent polypeptide-associated complex subunit alpha	-	-	-		-
7203424	26	44	22.43	43.45	0.953926557	0.00687996	PHATRDRAFT_48071	-	-	-	-		-
7202901	26	44	20.8	40.27	0.953121944	0.00687996	PHATRDRAFT_47720	K12822|1|4e-10|63.9|sbi:SORBI_07g020335|RNA-binding protein 25;K11824|2|1e-08|59.3|vcn:VOLCADRAFT_120602|AP-2 complex subunit alpha;K01115|3|9e-06|49.7|vcn:VOLCADRAFT_99471|phospholipase D [EC:3.1.4.4]	-	-	-		-
7195295	52	88	33.29	64.44	0.952867624	0.000127797	PHATRDRAFT_54986	-	-	-	-		-
7200517	19.72	33.33	10.23	19.77	0.950506726	0.0158121	PHATRDRAFT_45712	-	-	GO:0016740//transferase activity	-		-
7195857	39.24	66.33	6.86	13.25	0.949711878	0.000916572	PHATRDRAFT_49526	K11274|1|3e-37|156|bdi:100826226|chromosome transmission fidelity protein 4	-	GO:0003676//nucleic acid binding	-		-
7200226	16	27	12.83	24.78	0.949655017	0.0354158	PHATRDRAFT_26807	K15289|1|4e-37|153|bdi:100845570|solute carrier family 35, member F5	-	-	-		-
7195514	24.51	41.28	32.96	63.64	0.949217593	0.00831454	PHATRDRAFT_15699	K13348|1|2e-19|93.6|smo:SELMODRAFT_79996|protein Mpv17	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	-	-		-

7198658	16	27	8.06	15.55	0.948062836	0.0354158	PHATRDRAFT_49980	-	-	GO:0048531//beta-1,3-galactosyltransferase activity	GO:0006493//protein O-linked glycosylation		GO:0006493//protein O-linked glycosylation
7204671	35	59	24.41	47.08	0.947642025	0.001823364	PHATR_36848	-	GO:0031224//intrinsic component of membrane	-	-		-
7195480	22	37	17.43	33.55	0.944740197	0.01402166	PHATRDRAFT_49308	-	-	-	-		-
7197845	22	37	14.01	26.95	0.943828317	0.01402166	PHATRDRAFT_44373	K15429|1|1e-63|242|vcn:VOLCADRAFT_81828|tRNA (guanine37-N1)-methyltransferase [EC:2.1.1.228]	-	-	-		-
7195833	22	37	9.03	17.36	0.942969055	0.01402166	PHATRDRAFT_40200	K13427|1|7e-35|147|vvi:100265605|nitric-oxide synthase, plant [EC:1.14.13.39]	-	GO:0032550	-		-
7200192	24	40	26.43	50.45	0.932677844	0.01154702	PHATRDRAFT_34746	-	-	-	-		-
7195657	18	30	10.94	20.86	0.93112642	0.0289738	LAG1	K04710|1|6e-10|63.9|mtr:MTR_4g086150|ceramide synthetase [EC:2.3.1.24]	GO:0031224//intrinsic component of membrane	-	-		-
7197166	21	35	12.1	23.07	0.931010957	0.0182278	PHATRDRAFT_18132	K14423|1|9e-15|80.1|aly:ARALYDRAFT_329352|4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase [EC:1.14.13.72];K06674|2|2e-10|65.5|vcn:VOLCADRAFT_106052|structural maintenance of chromosome 2	-	GO:0046914//transition metal ion binding	-		-
7202048	18	30	13.48	25.7	0.930947863	0.0289738	PHATRDRAFT_13725	K14664|1|4e-82|303|aly:ARALYDRAFT_892157|IAA-amino acid hydrolase [EC:3.5.1.-]	-	GO:0003824//catalytic activity	-		-
7202657	15	25	9.69	18.47	0.930615296	0.0464754	PHATRDRAFT_47601	K09833|1|1e-42|172|cme:CMN202C|homogenitisate phytyltransferase	GO:0031224//intrinsic component of membrane	GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	-		-
7205033	29.07	48.27	13.35	25.36	0.925715004	0.0060704	PHATRDRAFT_bd1554	K01362|1|3e-12|72.0|olu:OSTLU_44226|[EC:3.4.21.-]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203422	26	43	8.33	15.75	0.918963428	0.00950948	PHATRDRAFT_48068	-	-	-	-		-
7202366	23	38	9.29	17.55	0.917720529	0.01497064	PHATRDRAFT_47281	-	-	-	-		-
7194704	17	28	9.05	17.04	0.912935638	0.0378622	PHATRDRAFT_48523	K00902|1|3e-13|75.1|mtr:MTR_117s0018|dolichol kinase [EC:2.7.1.108]	-	-	-		-
7198134	58	95	14.42	26.99	0.904353812	0.000136677	PHATRDRAFT_44658	K10400|1|8e-09|61.6|pop:POPTR_927223|kinesin family member 15;K10696|2|1e-06|54.3|mtr:MTR_087s0035|E3 ubiquitin-protein ligase BRE1 [EC:6.3.2.19];K06675|3|2e-06|53.9|bdi:100831033|structural maintenance of chromosome 4;K03254|4|2e-06|53.9|osa:4326038|translation initiation factor 3 subunit A	-	-	-		-
7198496	22	36	14.01	26.22	0.90421073	0.01941976	PHATRDRAFT_23557	K14689|1|2e-50|198|ppp:PHYPADRAFT_58387|solute carrier family 30 (zinc transporter), member 2	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0006811//ion transport;GO:0044763		GO:0006811//ion transport;GO:0044763
7204721	33	54	18.92	35.4	0.903837272	0.004136	PHATR_46875	K01362|1|2e-78|291|osa:4339651|[EC:3.4.21.-];K14810|5|8e-30|130|ota:Ot01g04880|ATP-dependent RNA helicase DDX56/DBP9 [EC:3.6.4.13]	GO:0009507//chloroplast;GO:0009579//thylakoid	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7205095	34.86	56.68	46.23	86.15	0.898021434	0.00321694	PtRabX1	K07901|1|1e-44|177|zma:100273222|Ras-related protein Rab-8A;K07976|2|2e-44|176|osa:4334590|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization

7204794	48	78	27.41	50.93	0.893813389	0.000631906	PHATRDRAFT_bd870	K15849|1|3e-94|344|vcn:VOLCADRAFT_103084|bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase [EC:2.6.1.1 2.6.1.78 2.6.1.79]	GO:0043231//intracellular membrane-bounded organelle	GO:0043168//anion binding;GO:0008483//transaminase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7204836	14.95	24.28	2.14	3.97	0.891528211	0.0432958	PHATRDRAFT_bd1883	K05356|1|2e-09|64.3|sbi:SORBI_0011s005450|all-trans-nonaprenyl-diphosphate synthase [EC:2.5.1.84 2.5.1.85]	GO:0043231//intracellular membrane-bounded organelle	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200994	21	34	8.23	15.23	0.887951606	0.0252054	PHATRDRAFT_45906	K11407|1|1e-64|246|rcu:RCOM_1469870|histone deacetylase 6/10 [EC:3.5.1.98]	-	GO:0003824//catalytic activity	-		-
7194741	32.68	52.79	23.23	42.93	0.885997019	0.00531786	PHATRDRAFT_48581	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7200859	16.51	26.61	21.8	40.26	0.885019037	0.0495394	PHATRDRAFT_35858	-	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	-	GO:0009987//cellular process;GO:0050896//response to stimulus		GO:0009987//cellular process;GO:0050896//response to stimulus
7195995	57	92	26.53	48.96	0.883978882	0.000234682	PHATRDRAFT_17344	K06901|1|1e-102|372|smo:SELMODRAFT_419524|putative MFS transporter, AGZA family, xanthine/uracil permease	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7201393	44	71	24.89	45.93	0.883870553	0.001244632	PHATRDRAFT_46335	-	-	-	-		-
7198777	59	94	17.96	32.7	0.864503286	0.000261096	PHATRDRAFT_49993	-	-	-	-		-
7203221	34	54	15.67	28.46	0.860930482	0.00593846	PHATRDRAFT_47970	-	-	-	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7198688	24	38	12.01	21.75	0.85677925	0.021758	PHATRDRAFT_50093	-	-	-	-		-
7195175	31	49	27.13	49.08	0.855246201	0.00927132	PHATRDRAFT_48901	-	-	-	-		-
7201570	62	98	22.48	40.61	0.853192992	0.000227684	PHATRDRAFT_46479	K03240|1|3e-86|318|pop:POPTR_1112738|translation initiation factor eIF-2B subunit epsilon	-	GO:0008135//translation factor activity, nucleic acid binding;GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006412//translation		GO:0006412//translation
7199116	19	30	9.7	17.51	0.852122431	0.0425374	PHATRDRAFT_50274	K02325|1|6e-44|177|ppp:PHYPADRAFT_216321|DNA polymerase epsilon subunit 2 [EC:2.7.7.7]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0034061	GO:0006260//DNA replication		GO:0006260//DNA replication
7200096	19	30	7.24	13.06	0.851093294	0.0425374	PHATRDRAFT_45212	-	-	-	-		-
7204901	19	30	7.43	13.4	0.850798885	0.0425374	PHATRDRAFT_bd29	K10357|1|1e-112|405|aly:ARALYDRAFT_887631|myosin V;K03165|2|2e-111|402|ota:Ot06g03550|DNA topoisomerase III [EC:5.99.1.2]	GO:0015629//actin cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7201808	28	44	11.37	20.43	0.84545695	0.01453448	PHATRDRAFT_27956	K02355|1|6e-36|150|ota:Ot07g03840|elongation factor G	GO:0044424	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0003747//translation release factor activity	GO:0006412//translation;GO:0009154//purine ribonucleotide catabolic process		GO:0006412//translation;GO:0009154//purine ribonucleotide catabolic process
7202916	46	72	44.94	80.53	0.841526209	0.001854048	PHATRDRAFT_47746	-	-	-	-		-
7203256	27.09	42.16	34.23	61.05	0.834730003	0.01868632	Lhcf6	-	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199300	38	59	25.98	46.14	0.828616573	0.00539108	PHATRDRAFT_50431	-	-	-	-		-
7203170	343	531	432.81	767.76	0.826921566	7.92E-17	Lhcf10	-	GO:0043234//protein complex;GO:0034357;GO:0009507//chloroplast;GO:0044425//membrane part	-	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7198575	22	34	40.71	72.21	0.826815421	0.036306	PHATRDRAFT_30670	K02971|1|8e-20|94.4|ppp:PHYPADRAFT_224961|small subunit ribosomal protein S21e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression

7200948	22	34	19.49	34.48	0.823025684	0.036306	PHATRDRAFT_35643	-	-	GO:0036094//small molecule binding	-		-
7203939	24	37	21.87	38.6	0.819647627	0.029506	PHATR_43793	-	-	-	-		-
7197021	24	37	16.26	28.68	0.818717767	0.029506	PHATRDRAFT_33014	-	-	GO:0016646//oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;GO:0032553	GO:0044710		GO:0044710
7196040	30	46	37.09	65.16	0.812956336	0.01599252	PHATRDRAFT_17187	K01725|1|4e-39|159|bdi:100834419|cyanate lyase [EC:4.2.1.104]	-	GO:0016840;GO:0003677//DNA binding	GO:0006082//organic acid metabolic process		GO:0006082//organic acid metabolic process
7197688	21	32	57.46	100.73	0.809863521	0.0469084	PHATRDRAFT_10948	K14489|1|3e-08|54.7|pop:POPTR_775135|arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3];K14509|3|5e-07|50.8|gmx:100805023|ethylene receptor [EC:2.7.13.-]	-	GO:0004871//signal transducer activity;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0007165//signal transduction;GO:0006351//transcription, DNA-templated		GO:0006796//phosphate-containing compound metabolic process;GO:0007165//signal transduction;GO:0006351//transcription, DNA-templated
7204174	66	101	14.81	25.9	0.806380457	0.000362952	PHATR_18549	K07204|1|1e-138|493|olu:OSTLU_41144|regulatory associated protein of mTOR	-	-	-		-
7202265	21	32	18.1	31.57	0.802564563	0.0469084	PHATRDRAFT_47477	-	-	-	-		-
7202110	23	35	14.46	25.18	0.800210731	0.0380168	PHATRDRAFT_51026	K06067|1|8e-166|581|smo:SELMODRAFT_114783|histone deacetylase 1/2 [EC:3.5.1.98]	GO:0043231//intracellular membrane-bounded organelle	GO:0017136//NAD-dependent histone deacetylase activity	GO:0009292//genetic transfer;GO:0009611//response to wounding;GO:0016575//histone deacetylation;GO:0050793//regulation of developmental process;GO:0006351//transcription, DNA-templated		GO:0009292//genetic transfer;GO:0009611//response to wounding;GO:0016575//histone deacetylation;GO:0050793//regulation of developmental process;GO:0006351//transcription, DNA-templated
7194736	29	44	12.45	21.59	0.794217501	0.020473	PHATRDRAFT_48573	K09422|1|6e-07|54.7|smo:SELMODRAFT_413266|myb proto-oncogene protein, plant	-	GO:0003676//nucleic acid binding	-		-
7204172	39	59	13.55	23.43	0.790064103	0.0074997	PHATR_54169	K08288|1|6e-16|84.7|rcu:RCOM_1122020|protein kinase C substrate 80K-H	-	-	GO:0006487//protein N-linked glycosylation		GO:0006487//protein N-linked glycosylation
7201135	30	45	36.93	63.47	0.78128158	0.0213442	PHATRDRAFT_45921	-	-	-	GO:0044699		GO:0044699
7200401	22	33	23.86	40.99	0.780677947	0.0489778	PHATRDRAFT_45638	-	-	-	-		-
7198861	24	36	21.31	36.58	0.779524482	0.039676	PHATRDRAFT_50167	-	-	-	-		-
7203526	26	39	19.32	33.15	0.778913776	0.0322102	PHATRDRAFT_54872	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199795	42	63	12.73	21.83	0.778079711	0.00640698	PHATRDRAFT_44863	K00962|1|4e-69|261|aly:ARALYDRAFT_488299|polyribonucleotide nucleotidyltransferase [EC:2.7.7.8]	-	GO:0016779//nucleotidyltransferase activity;GO:0003676//nucleic acid binding;GO:0008408//3’-5’ exonuclease activity	GO:0000959//mitochondrial RNA metabolic process;GO:0006401//RNA catabolic process;GO:0006606//protein import into nucleus		GO:0000959//mitochondrial RNA metabolic process;GO:0006401//RNA catabolic process;GO:0006606//protein import into nucleus
7195419	73	109	56.95	97.31	0.772892228	0.000366534	ISIP2B	-	-	-	-		-
7203065	79	117	97.95	166.22	0.762976584	0.000269762	PHATRDRAFT_47828	-	-	-	-		-
7196007	27	40	30.72	52.13	0.762935644	0.03351	PHATRDRAFT_17372	-	-	-	GO:0009966//regulation of signal transduction		GO:0009966//regulation of signal transduction
7202718	29	43	7.03	11.91	0.760576819	0.027252	PHATRDRAFT_47725	-	GO:0043232	GO:0008092//cytoskeletal protein binding	-		-
7197530	25	37	19.7	33.37	0.760356057	0.0412832	PHATRDRAFT_43469	K14457|1|1e-22|105|aly:ARALYDRAFT_485503|2-acylglycerol O-acyltransferase 2 [EC:2.3.1.22]	-	GO:0016746//transferase activity, transferring acyl groups	-		-
7200739	38	56	45.54	76.88	0.755474045	0.01255772	PHATRDRAFT_45557	K00658|1|7e-11|65.9|cme:CMJ055C|2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]	-	-	-		-
7196437	60	88	167.36	282.45	0.755040744	0.00189072	PHATRDRAFT_9035	K07390|1|2e-30|128|smo:SELMODRAFT_102863|monothiol glutaredoxin	GO:0009536//plastid	GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis		GO:0019725//cellular homeostasis
7198952	28	41	26.71	44.78	0.745474552	0.0347742	PHATRDRAFT_41069	-	GO:0009536//plastid	-	-		-

7199900	66	96	141.71	236.76	0.740483794	0.00137512	PHATRDRAFT_19314	K02962|1|2e-40|162|cme:CMT402C|small subunit ribosomal protein S17e	GO:0015935//small ribosomal subunit;GO:0031981//nuclear lumen;GO:0016020//membrane	GO:0005198//structural molecule activity	GO:0006412//translation;GO:0022618//ribonucleoprotein complex assembly		GO:0006412//translation;GO:0022618//ribonucleoprotein complex assembly
7204199	64	93	107.1	178.53	0.737208044	0.001666666	PHATR_18585	K02903|1|6e-22|101|pop:POPTR_645780|large subunit ribosomal protein L28e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7205062	125	182	95.18	158.57	0.736389492	1.00E-05	PHATRDRAFT_bd1737	-	-	-	-		-
7199372	44	64	28.92	48.12	0.73456909	0.00903406	PHATRDRAFT_41501	K13254|1|2e-49|194|smo:SELMODRAFT_271275|spastin [EC:3.6.4.3]	-	GO:0032550;GO:0016462//pyrophosphatase activity	-		-
7200769	38	55	75.19	124.94	0.732622729	0.0164494	PHATRDRAFT_35516	-	-	-	-		-
7199911	51	74	26.28	43.6	0.730362859	0.0051695	PHATRDRAFT_19324	K01663|1|5e-161|566|osa:4332296|glutamine amidotransferase / cyclase [EC:2.4.2.- 4.1.3.-]	GO:0005737//cytoplasm;GO:0043231//intracellular membrane-bounded organelle	GO:0016763//transferase activity, transferring pentosyl groups;GO:0016830//carbon-carbon lyase activity	GO:0006547//histidine metabolic process		GO:0006547//histidine metabolic process
7195880	29	42	27.03	44.82	0.729581137	0.0360024	PHATRDRAFT_49363	K00891|1|3e-35|147|cme:CMT093C|shikimate kinase [EC:2.7.1.71]	GO:0009536//plastid	GO:0032550;GO:0016301//kinase activity	GO:0008652//cellular amino acid biosynthetic process		GO:0008652//cellular amino acid biosynthetic process
7198148	105.01	152	41.1	68	0.726396352	6.46E-05	PHATRDRAFT_49659	-	-	GO:0016788//hydrolase activity, acting on ester bonds	-		-
7198465	32	46	85.91	142.06	0.725602413	0.0302648	PHATRDRAFT_7780	K13628|1|2e-11|65.1|ppp:PHYPADRAFT_178946|iron-sulfur cluster assembly protein	-	GO:0051540	GO:0009058//biosynthetic process		GO:0009058//biosynthetic process
7198040	27	39	17.23	28.47	0.724519792	0.0443416	UBA3	K10686|1|2e-96|351|smo:SELMODRAFT_106904|ubiquitin-activating enzyme E1 C [EC:6.3.2.19]	-	GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7198410	92	133	32.53	53.74	0.724225499	0.000193064	PHATRDRAFT_49707	K01415|1|1e-56|220|cme:CMP249C|endothelin-converting enzyme [EC:3.4.24.71]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200765	36	52	14.03	23.17	0.723743035	0.0201298	PDS1	K02293|1|0.0|814|olu:OSTLU_38345|15-cis-phytoene desaturase [EC:1.3.5.5]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0097159//organic cyclic compound binding;GO:0016491//oxidoreductase activity;GO:1901363;GO:0036094//small molecule binding	GO:0016109		GO:0016109
7196013	36	52	7.35	12.12	0.721573544	0.0201298	PHATRDRAFT_24514	K02519|1|1e-77|290|mtr:MTR_5g032140|translation initiation factor IF-2	-	GO:0043169//cation binding;GO:0008238//exopeptidase activity;GO:0008237//metallopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203891	34	49	19.28	31.78	0.721014073	0.024665	PHATR_44138	-	-	-	-		-
7204758	91	131	49.26	81.1	0.719285287	0.000240294	SQD1	K06118|1|2e-153|541|cme:CMR012C|UDP-sulfoquinovose synthase [EC:3.13.1.1]	GO:0043231//intracellular membrane-bounded organelle	GO:0036094//small molecule binding;GO:0048037//cofactor binding	GO:0009987//cellular process;GO:0008152//metabolic process		GO:0009987//cellular process;GO:0008152//metabolic process
7204454	32	46	36.56	60.19	0.719257746	0.0302648	PHATR_46924	K03098|1|1e-14|78.2|aly:ARALYDRAFT_918995|outer membrane lipoprotein Blc	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	-	GO:0009628//response to abiotic stimulus;GO:0006950//response to stress		GO:0009628//response to abiotic stimulus;GO:0006950//response to stress
7202813	96	138	65.16	107.15	0.717573341	0.000169988	PHATRDRAFT_54765	-	-	-	-		-
7195383	76	109	43.54	71.41	0.713784711	0.000877416	PHATRDRAFT_48972	-	-	-	-		-
7196369	53	76	30.73	50.4	0.713775967	0.005505	PHATRDRAFT_42738	-	-	-	-		-
7195783	53	76	24.91	40.84	0.713257845	0.005505	PHATRDRAFT_1048	K06174|1|0.0|884|vvi:100249488|ATP-binding cassette, sub-family E, member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0016791//phosphatase activity;GO:0051540	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process

7198409	42	60	9.85	16.09	0.707968696	0.01433334	SMC3	K06669|1|0.0|758|ppp:PHYPADRAFT_61626|structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	GO:0043232	GO:0032550	GO:0006996//organelle organization		GO:0006996//organelle organization
7198307	33	47	17.56	28.61	0.704226653	0.0312186	PHATRDRAFT_49668	-	-	-	-		-
7195155	31	44	12.34	20.02	0.69809958	0.038351	PHATRDRAFT_48869	-	-	-	-		-
7201626	43	61	17.3	28.06	0.697742971	0.01476188	PHATRDRAFT_13053	K12867|1|5e-115|413|olu:OSTLU_42299|pre-mRNA-splicing factor SYF1	GO:0044464	-	GO:0010467//gene expression		GO:0010467//gene expression
7202135	90	127	157.05	254.28	0.695194051	0.000487156	PHATRDRAFT_21323	K02974|1|2e-31|132|ppp:PHYPADRAFT_161917|small subunit ribosomal protein S24e	GO:0005840//ribosome	GO:0036094//small molecule binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7198303	51	72	79.74	129.1	0.69511349	0.00863044	PHATRDRAFT_49660	K07253|1|3e-24|109|olu:OSTLU_17653|phenylpyruvate tautomerase [EC:5.3.2.1];K15923|4|3e-13|73.2|mtr:MTR_4g127370|alpha-L-fucosidase 2 [EC:3.2.1.51]	GO:0009536//plastid	-	GO:0048646//anatomical structure formation involved in morphogenesis		GO:0048646//anatomical structure formation involved in morphogenesis
7194953	29	41	10.21	16.51	0.693357254	0.047194	PHATRDRAFT_48873	K12603|1|8e-08|57.8|smo:SELMODRAFT_418021|CCR4-NOT transcription complex subunit 6	-	-	-		-
7197496	222	314	45.62	73.72	0.692389624	3.57E-08	PHATRDRAFT_43627	K11373|1|4e-87|322|ppp:PHYPADRAFT_206869|elongator complex protein 1	-	-	-		-
7201205	34	48	15.42	24.89	0.690763465	0.032147	PHATRDRAFT_46251	K08202|1|2e-21|102|cre:CHLREDRAFT_103526|MFS transporter, OCT family, solute carrier family 22 (organic cation transporter), member 4/5;K08150|3|2e-12|72.4|zma:100285429|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7199188	71	100	41.56	66.95	0.687888401	0.0020476	PHATRDRAFT_50364	-	-	-	-		-
7198702	50.54	71.21	20.78	33.47	0.687672897	0.00839102	PHATRDRAFT_49998	-	-	-	-		-
7203718	52	73	31.68	50.86	0.682959127	0.00886742	PHATRDRAFT_48495	K01362|1|3e-19|95.1|olu:OSTLU_44226|[EC:3.4.21.-];K08653|2|1e-08|59.7|aly:ARALYDRAFT_351066|membrane-bound transcription factor site-1 protease [EC:3.4.21.112]	-	GO:0005515//protein binding;GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process;GO:0044092//negative regulation of molecular function		GO:0019538//protein metabolic process;GO:0044092//negative regulation of molecular function
7204328	30	42	40.16	64.44	0.682197225	0.0485448	PHATR_10617	K02906|1|7e-57|218|ath:AT3G17465|large subunit ribosomal protein L3	GO:0043231//intracellular membrane-bounded organelle;GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203402	34.14	47.83	19.57	31.36	0.680281803	0.0416064	PHATRDRAFT_48286	-	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7200274	40	56	18.02	28.84	0.678472153	0.0226474	PHATRDRAFT_45260	K14207|1|5e-23|107|pop:POPTR_580719|solute carrier family 38 (sodium-coupled neutral amino acid transporter), member 2	GO:0031224//intrinsic component of membrane	-	-		-
7200128	33	46	63.11	100.98	0.678129054	0.0405564	rps19	K02958|1|7e-50|194|smo:SELMODRAFT_172403|small subunit ribosomal protein S15e	GO:0009536//plastid;GO:0044391	GO:0003723//RNA binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7201917	33	46	23.91	38.14	0.673690714	0.0405564	PHATRDRAFT_47115	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-

7201753	44	61	28.02	44.43	0.665077186	0.01952066	IPMDH	K00052|1|1e-118|424|ppp:PHYPADRAFT_115152|3-isopropylmalate dehydrogenase [EC:1.1.1.85]	GO:0044424	GO:0046872//metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0008652//cellular amino acid biosynthetic process;GO:0006551//leucine metabolic process		GO:0008652//cellular amino acid biosynthetic process;GO:0006551//leucine metabolic process
7200989	39	54	37.58	59.58	0.664863057	0.0284166	PHATRDRAFT_54494	K05607|1|5e-10|63.5|ath:AT4G16800|methylglutaconyl-CoA hydratase [EC:4.2.1.18];K07511|5|1e-08|58.5|ppp:PHYPADRAFT_143267|enoyl-CoA hydratase [EC:4.2.1.17]	-	GO:0016836//hydro-lyase activity	-		-
7203080	39	54	29.51	46.76	0.664071009	0.0284166	PHATRDRAFT_38175	-	-	-	-		-
7200076	39	54	19.28	30.53	0.663122538	0.0284166	PHATRDRAFT_45064	-	-	GO:0008235//metalloexopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7204363	34	47	12.39	19.57	0.659467568	0.0416064	PHATR_33257	K15156|1|8e-08|57.8|rcu:RCOM_0484490|mediator of RNA polymerase II transcription subunit 14	-	-	-		-
7195076	58	80	30.4	47.95	0.657459492	0.00806384	PHATRDRAFT_54954	K13412|1|4e-07|54.7|mtr:MTR_5g009830|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0046872//metal ion binding;GO:0016772//transferase activity, transferring phosphorus-containing groups	-		-
7198817	48	66	65.7	103.54	0.656222948	0.01680172	PHATRDRAFT_50195	-	-	-	-		-
7196291	40	55	37.95	59.74	0.654597352	0.029112	PHATRDRAFT_42608	-	-	-	-		-
7196026	48	66	18.91	29.72	0.652284753	0.01680172	PHATRDRAFT_42688	K15336|1|7e-09|61.2|vvi:100259391|tRNA (cytosine38-C5)-methyltransferase [EC:2.1.1.204]	-	-	-		-
7196979	43	59	33.85	53.16	0.651185271	0.0243968	PHATRDRAFT_43270	-	-	-	-		-
7204200	62	85	69.26	108.75	0.650921108	0.00695992	PHATR_25714	K02877|1|4e-66|249|ppp:PHYPADRAFT_179263|large subunit ribosomal protein L15e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7196672	54	74	52.87	82.95	0.649792654	0.01188864	Rpe	K01783|1|5e-51|199|cre:CHLREDRAFT_135614|ribulose-phosphate 3-epimerase [EC:5.1.3.1]	GO:0044434	GO:0043169//cation binding;GO:0016857//racemase and epimerase activity, acting on carbohydrates and derivatives	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7200461	43	59	14.69	23.03	0.648680015	0.0243968	PHATRDRAFT_45682	K13420|1|9e-23|107|pop:POPTR_1075175|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	GO:0044464	GO:0016740//transferase activity;GO:0005488//binding	GO:0044763;GO:0071704;GO:0048513//organ development;GO:0044238;GO:0044767		GO:0044763;GO:0071704;GO:0048513//organ development;GO:0044238;GO:0044767
7196740	69	94	114.13	178.35	0.64403315	0.0050674	PHATRDRAFT_17846	K02901|1|2e-26|116|cre:CHLREDRAFT_260|large subunit ribosomal protein L27e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7196358	60	82	23.82	37.21	0.643516977	0.00843696	PHATRDRAFT_42722	-	-	-	-		-
7204525	63	86	25.76	40.2	0.642062908	0.00711436	SSD1	K00135|1|5e-120|430|zma:100280779|succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO:0050896//response to stimulus;GO:0044710		GO:0050896//response to stimulus;GO:0044710
7205108	55	75	34.95	54.51	0.641228465	0.01215362	PHATRDRAFT_bd475	K14272|1|2e-121|434|ppp:PHYPADRAFT_226033|glutamate--glyoxylate aminotransferase [EC:2.6.1.4 2.6.1.2 2.6.1.44 2.6.1.-]	-	GO:0043168//anion binding;GO:0047635	GO:0008152//metabolic process		GO:0008152//metabolic process
7200369	55	75	26.7	41.63	0.640783817	0.01215362	PHATRDRAFT_45587	-	-	-	-		-
7202533	118	161	30.06	46.86	0.640511945	0.000232294	PHATRDRAFT_47388	K15172|1|2e-82|306|gmx:100801380|transcription elongation factor SPT5	GO:0005622//intracellular	-	GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter		GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter

7202932	39	53	45.4	70.68	0.638609742	0.0364098	Lhcr6	K08907|1|3e-17|87.0|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08916|2|7e-17|85.9|vcn:VOLCADRAFT_104309|light-harvesting complex II chlorophyll a/b binding protein 5	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7203146	53	72	63.33	98.57	0.638259547	0.0147614	PHATRDRAFT_29177	K02880|1|1e-46|184|cre:CHLREDRAFT_77517|large subunit ribosomal protein L17e	GO:0009536//plastid;GO:0015934//large ribosomal subunit;GO:0005911//cell-cell junction;GO:0031090//organelle membrane	GO:0005198//structural molecule activity	GO:0009451//RNA modification;GO:0071555//cell wall organization;GO:0010467//gene expression		GO:0009451//RNA modification;GO:0071555//cell wall organization;GO:0010467//gene expression
7198420	39	53	39.87	62.05	0.638127605	0.0364098	PHATRDRAFT_16210	K15105|1|2e-46|184|ppp:PHYPADRAFT_34303|solute carrier family 25 (mitochondrial aspartate/glutamate transporter), member 12/13	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7194680	47	64	14.01	21.8	0.637871179	0.0209262	PHATRDRAFT_48695	-	-	-	-		-
7204003	67	91	43.91	68.22	0.63564522	0.00613016	PHATR_44048	-	-	-	-		-
7194985	68	92	58.08	89.93	0.630761015	0.00625638	PHATRDRAFT_42255	K14521|1|2e-52|204|vcn:VOLCADRAFT_98273|N-acetyltransferase 10 [EC:2.3.1.-];K05275|2|4e-13|73.9|zma:100272747|pyridoxine 4-dehydrogenase [EC:1.1.1.65];K00064|3|7e-13|73.2|aly:ARALYDRAFT_491313|D-threo-aldose 1-dehydrogenase [EC:1.1.1.122]	GO:0009532//plastid stroma;GO:0009526//plastid envelope	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006090//pyruvate metabolic process		GO:0006090//pyruvate metabolic process
7196477	49	66	42.1	64.91	0.624620523	0.0218132	PHATRDRAFT_9654	K00013|1|3e-52|203|cme:CMQ082C|histidinol dehydrogenase [EC:1.1.1.23]	-	GO:0046914//transition metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0000166//nucleotide binding	GO:0006547//histidine metabolic process		GO:0006547//histidine metabolic process
7201588	75	101	62.19	95.86	0.624246323	0.00454564	PHATRDRAFT_27972	K07390|1|1e-26|118|ppp:PHYPADRAFT_153882|monothiol glutaredoxin	-	GO:0015036//disulfide oxidoreductase activity	GO:0019725//cellular homeostasis		GO:0019725//cellular homeostasis
7197842	38	51	71.24	109.74	0.623330059	0.0454662	PHATRDRAFT_10774	K02876|1|2e-34|142|vcn:VOLCADRAFT_109530|large subunit ribosomal protein L15	GO:0044391	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7204039	67	90	88.86	136.8	0.622462184	0.00771472	PHATR_10655	K00472|1|1e-25|114|aly:ARALYDRAFT_472257|prolyl 4-hydroxylase [EC:1.14.11.2]	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0019842//vitamin binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	GO:0044710		GO:0044710
7196104	134	180	170.09	261.81	0.622221879	0.000163294	PHATRDRAFT_17414	K02995|1|4e-62|235|ppp:PHYPADRAFT_208398|small subunit ribosomal protein S8e	GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197968	142	191	45.86	70.51	0.620591526	9.85E-05	PHATRDRAFT_44306	K14497|1|2e-13|76.6|bdi:100838998|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0032550;GO:0004672//protein kinase activity	GO:0050896//response to stimulus;GO:0006464//cellular protein modification process		GO:0050896//response to stimulus;GO:0006464//cellular protein modification process
7201898	38	51	16.9	25.92	0.617042472	0.0454662	PHATRDRAFT_46351	-	-	-	-		-
7197297	39	52	63.17	96.6	0.612783617	0.046349	PHATRDRAFT_32791	K03152|1|2e-38|156|cme:CMS007C|4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis	-	-	-		-

7196486	65	87	15.76	24.1	0.612765612	0.00932938	PHATRDRAFT_42826	-	-	GO:0003899//DNA-directed RNA polymerase activity;GO:0046914//transition metal ion binding;GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7201902	188	251	108.57	165.78	0.610644454	1.11E-05	PHATRDRAFT_20755	K09874|1|3e-14|78.6|osa:4340558|aquaporin NIP;K09873|5|2e-12|72.4|osa:4324276|aquaporin TIP	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7201812	39	52	30.65	46.76	0.609387856	0.046349	PHATRDRAFT_46468	-	-	-	-		-
7195804	49	65	11.04	16.73	0.599697273	0.0275342	SMC2	K06674|1|0.0|920|rcu:RCOM_1500520|structural maintenance of chromosome 2	GO:0043231//intracellular membrane-bounded organelle;GO:0000793//condensed chromosome	GO:0032550	GO:0009908//flower development;GO:0070918//production of small RNA involved in gene silencing by RNA;GO:0035194//posttranscriptional gene silencing by RNA;GO:0006342//chromatin silencing;GO:0000070//mitotic sister chromatid segregation;GO:0034968//histone lysine methylation;GO:0006260//DNA replication		GO:0009908//flower development;GO:0070918//production of small RNA involved in gene silencing by RNA;GO:0035194//posttranscriptional gene silencing by RNA;GO:0006342//chromatin silencing;GO:0000070//mitotic sister chromatid segregation;GO:0034968//histone lysine methylation;GO:0006260//DNA replication
7198938	53	70	45.81	69.26	0.596359825	0.023468	PHATRDRAFT_50150	-	-	-	-		-
7203664	41	54	38.56	58.13	0.592177857	0.0480212	PHATRDRAFT_48411	K02981|1|1e-86|317|zma:100382980|small subunit ribosomal protein S2e	GO:0044391	GO:0003676//nucleic acid binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203182	58	76	139.95	210.8	0.59096338	0.02033	PHATRDRAFT_22027	-	GO:0019866//organelle inner membrane;GO:0005740//mitochondrial envelope	GO:0043169//cation binding	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7194815	102	134	28.76	43.17	0.585965417	0.001935142	PHATRDRAFT_228	K01537|1|0.0|766|sbi:SORBI_01g038990|Ca2+-transporting ATPase [EC:3.6.3.8]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0019829//cation-transporting ATPase activity	GO:0006811//ion transport		GO:0006811//ion transport
7204127	71	93	67.43	101.12	0.584605866	0.01031794	RabX2	K07910|1|2e-34|144|osa:4348795|Ras-related protein Rab-18;K07976|2|2e-34|144|cme:CMD062C|Rab family, other	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550	GO:0003006//developmental process involved in reproduction;GO:0048856//anatomical structure development;GO:0045184//establishment of protein localization;GO:0035556//intracellular signal transduction		GO:0003006//developmental process involved in reproduction;GO:0048856//anatomical structure development;GO:0045184//establishment of protein localization;GO:0035556//intracellular signal transduction
7198458	55	72	24.89	37.26	0.582061444	0.0242364	PHATRDRAFT_30620	K08145|1|2e-43|176|ppp:PHYPADRAFT_187073|MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8	GO:0031224//intrinsic component of membrane	GO:0022857//transmembrane transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7204829	75	98	26.44	39.49	0.578765191	0.00882432	DXS	K01662|1|0.0|854|cme:CMF089C|1-deoxy-D-xylulose-5-phosphate synthase [EC:2.2.1.7]	-	GO:0016744	GO:0006721//terpenoid metabolic process		GO:0006721//terpenoid metabolic process
7196371	43	56	31.83	47.44	0.575716853	0.049573	PHATRDRAFT_42740	-	GO:0044464	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7202069	109	142	25.94	38.62	0.574169685	0.00173737	PHATRDRAFT_47184	-	-	GO:0046872//metal ion binding	-		-
7196741	110	143	90.34	134.41	0.573203659	0.00176167	PHATRDRAFT_43127	-	-	-	-		-
7204373	60	78	39.32	58.47	0.57243327	0.0209462	PHATR_43945	-	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7203943	50	65	24.52	36.45	0.571959836	0.0350858	PHATR_43801	-	-	-	-		-

7199058	51	66	68.6	101.74	0.568606518	0.0355898	PHATRDRAFT_31073	K02993|1|1e-55|214|vcn:VOLCADRAFT_73479|small subunit ribosomal protein S7e	GO:0015935//small ribosomal subunit;GO:0009536//plastid;GO:0071944//cell periphery;GO:0030684//preribosome;GO:0016020//membrane	GO:0003723//RNA binding;GO:0005198//structural molecule activity	GO:0042254//ribosome biogenesis;GO:0010467//gene expression		GO:0042254//ribosome biogenesis;GO:0010467//gene expression
7202327	65	84	111.61	165.47	0.568103382	0.01808884	PHATRDRAFT_28620	K11353|1|4e-23|105|ppp:PHYPADRAFT_162309|NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 13 [EC:1.6.5.3 1.6.99.3]	-	-	-		-
7195909	48	62	20.74	30.62	0.562058389	0.0425758	PHATRDRAFT_49418	K16075|1|6e-07|54.7|cme:CMI180C|magnesium transporter	-	GO:0046873//metal ion transmembrane transporter activity	GO:0044763;GO:0070838//divalent metal ion transport		GO:0044763;GO:0070838//divalent metal ion transport
7195386	69	89	53.1	78.38	0.561773712	0.01541336	PHATRDRAFT_22896	K01551|1|2e-82|304|ppp:PHYPADRAFT_206681|arsenite-transporting ATPase [EC:3.6.3.16]	-	GO:0032550;GO:0016887//ATPase activity	GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process		GO:0009636//response to toxic substance;GO:0009154//purine ribonucleotide catabolic process
7200371	69	89	31.48	46.42	0.560310982	0.01541336	PHATRDRAFT_45589	K11294|1|1e-05|50.4|bdi:100836665|nucleolin	-	-	-		-
7204171	81	104	56.27	82.65	0.554648856	0.00957126	PHATR_43941	-	-	-	-		-
7204662	85	109	75.38	110.64	0.553619361	0.0081748	PHATR_46791	K04078|1|1e-18|92.0|vcn:VOLCADRAFT_80038|chaperonin GroES	GO:0044424	-	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7195427	75	96	60.95	89.29	0.550872389	0.01347284	PHATRDRAFT_49057	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0006811//ion transport;GO:0044763		GO:0006811//ion transport;GO:0044763
7203680	57	73	26.4	38.66	0.550303708	0.0309956	PHATRDRAFT_48439	-	-	-	-		-
7203478	108	138	107.71	157.59	0.549023792	0.00316782	PHATRDRAFT_38509	K01476|1|8e-12|69.3|ppp:PHYPADRAFT_234776|arginase [EC:3.5.3.1]	-	GO:0016813//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines;GO:0043169//cation binding	GO:0009064//glutamine family amino acid metabolic process		GO:0009064//glutamine family amino acid metabolic process
7202575	68	87	13.2	19.3	0.548062918	0.01879372	Pt-MAD1	K06638|1|4e-15|83.2|ppp:PHYPADRAFT_40827|mitotic spindle assembly checkpoint protein MAD1	-	-	GO:0045841//negative regulation of mitotic metaphase/anaphase transition		GO:0045841//negative regulation of mitotic metaphase/anaphase transition
7198601	52	66	21.1	30.62	0.537231284	0.0447572	PHATRDRAFT_49896	-	-	-	-		-
7203018	130	165	60.08	87.18	0.537112391	0.001498704	PHATRDRAFT_48025	K09540|1|2e-06|52.8|aly:ARALYDRAFT_477265|translocation protein SEC63;K09527|3|3e-06|52.0|gmx:100781496|DnaJ homolog subfamily C member 7;K03686|4|4e-06|51.6|bdi:100841335|molecular chaperone DnaJ	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7201155	164	208	86.81	125.9	0.536345136	0.000372948	PHATRDRAFT_20547	K01687|1|0.0|741|olu:OSTLU_34354|dihydroxy-acid dehydratase [EC:4.2.1.9]	GO:0009536//plastid	GO:0003676//nucleic acid binding;GO:0016836//hydro-lyase activity	GO:0008652//cellular amino acid biosynthetic process		GO:0008652//cellular amino acid biosynthetic process
7199800	77	97	208.68	302.43	0.535308918	0.01689564	PHATRDRAFT_19413	K02923|1|3e-20|94.7|cre:CHLREDRAFT_194928|large subunit ribosomal protein L38e	GO:0015934//large ribosomal subunit	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7197472	80	101	102.46	148.23	0.532776665	0.01424144	PHATRDRAFT_25375	K02872|1|1e-55|214|ppp:PHYPADRAFT_184654|large subunit ribosomal protein L13Ae	GO:0043231//intracellular membrane-bounded organelle;GO:0015934//large ribosomal subunit	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7201968	118	149	50.25	72.53	0.529454253	0.00289298	PHATRDRAFT_47192	-	-	GO:0008289//lipid binding	-		-
7196847	69	87	48.13	69.43	0.528622748	0.0233656	NAP	K11279|1|2e-40|164|gmx:100778198|nucleosome assembly protein 1-like 1	GO:0043231//intracellular membrane-bounded organelle	-	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7202684	146	184	120.37	173.62	0.528457276	0.000985488	PHATRDRAFT_47649	-	-	-	-		-

7203140	71	89	150.19	216.23	0.52577794	0.0238286	UBI1/2	K02927|1|6e-58|220|cme:CMC045C|large subunit ribosomal protein L40e	GO:0031981//nuclear lumen;GO:0015934//large ribosomal subunit	GO:0005198//structural molecule activity	GO:0032446//protein modification by small protein conjugation;GO:0003006//developmental process involved in reproduction;GO:0010467//gene expression		GO:0032446//protein modification by small protein conjugation;GO:0003006//developmental process involved in reproduction;GO:0010467//gene expression
7195211	105	132	99.61	143.37	0.525380684	0.00555688	PHATRDRAFT_48918	-	-	-	-		-
7204106	113	142	49.91	71.7	0.522644215	0.00406434	PHATR_44190	K00102|1|5e-18|91.3|gmx:100803612|D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0006629//lipid metabolic process		GO:0006629//lipid metabolic process
7204417	78	98	33.77	48.5	0.522242568	0.0170622	PHATR_46687	-	-	-	-		-
7199948	62.94	78.77	107.21	153.94	0.521928673	0.0327734	H4-1b	K11254|1|1e-39|160|olu:OSTLU_44220|histone H4	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7195168	137	172	76.19	109.39	0.521807298	0.001605494	PHATRDRAFT_48891	K00472|1|7e-23|107|gmx:100798201|prolyl 4-hydroxylase [EC:1.14.11.2]	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7199100	91	114	45.07	64.56	0.518473129	0.01065046	PHATRDRAFT_56243	K03531|1|2e-94|344|cme:CMS004C|cell division protein FtsZ	GO:0032991//macromolecular complex;GO:0015630//microtubule cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0043623//cellular protein complex assembly		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0043623//cellular protein complex assembly
7194867	84	105	55.09	78.77	0.515855813	0.01479774	PHATRDRAFT_15121	K14416|1|9e-66|249|pop:POPTR_737500|elongation factor 1 alpha-like protein	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7200462	116	145	55.72	79.63	0.5151168	0.00417648	PHATRDRAFT_45684	K05337|1|9e-12|70.5|olu:OSTLU_7956|ferredoxin	-	GO:0051540	-		-
7198740	56	70	22.01	31.45	0.514900872	0.0466356	PHATRDRAFT_50045	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003700//sequence-specific DNA binding transcription factor activity;GO:0046914//transition metal ion binding	GO:0006366//transcription from RNA polymerase II promoter		GO:0006366//transcription from RNA polymerase II promoter
7204184	69	86	25.93	36.94	0.51056166	0.0285848	PHATR_43964	-	-	-	-		-
7198459	61	76	30.55	43.52	0.510506177	0.0398028	PHATRDRAFT_49791	-	-	-	-		-
7200830	66	82	76.52	108.9	0.509095175	0.0340016	OEE3	-	GO:0009523//photosystem II	GO:0046872//metal ion binding	GO:0044237//cellular metabolic process		GO:0044237//cellular metabolic process
7200005	119	148	62.52	88.92	0.50819017	0.00428372	PHATRDRAFT_45384	K09506|1|2e-07|55.8|rcu:RCOM_1469860|DnaJ homolog subfamily A member 5;K09510|2|1e-06|53.5|vcn:VOLCADRAFT_62070|DnaJ homolog subfamily B member 4;K09523|3|2e-06|52.8|ppp:PHYPADRAFT_31787|DnaJ homolog subfamily C member 3	-	-	-		-
7197148	91	113	97.33	138.42	0.50809595	0.01293316	PHATRDRAFT_43424	-	-	-	-		-

7196530	149	185	138.44	196.78	0.507322751	0.001473508	PHATRDRAFT_42891	-	-	-	-		-
7200942	74	92	22.77	32.35	0.506631421	0.024475	PHATRDRAFT_45828	K14856|1|1e-71|270|olu:OSTLU_785|protein SDA1	-	-	GO:0000054//ribosomal subunit export from nucleus;GO:0007010//cytoskeleton organization		GO:0000054//ribosomal subunit export from nucleus;GO:0007010//cytoskeleton organization
7196876	66	82	25.32	35.96	0.506115616	0.0340016	PHATRDRAFT_43097	K01881|1|1e-144|512|cme:CMJ098C|prolyl-tRNA synthetase [EC:6.1.1.15]	GO:0044424	GO:0004812//aminoacyl-tRNA ligase activity;GO:0032550	GO:0006418//tRNA aminoacylation for protein translation		GO:0006418//tRNA aminoacylation for protein translation
7196029	87	108	44.59	63.29	0.505257368	0.0151819	PHATRDRAFT_17172	K03977|1|3e-103|374|smo:SELMODRAFT_123195|GTP-binding protein	GO:0043231//intracellular membrane-bounded organelle	GO:0032550	-		-
7204319	62	77	15.54	22.05	0.504792152	0.040148	PHATR_43922	K12616|1|1e-17|91.3|mtr:MTR_2g027690|enhancer of mRNA-decapping protein 4	-	-	-		-
7196320	72	89	66.97	94.77	0.50091547	0.0293024	PHATRDRAFT_42659	-	-	GO:0036094//small molecule binding	-		-
7197784	59	73	28.56	40.41	0.500716372	0.0478628	PHATRDRAFT_44525	-	-	-	-		-
7198704	59	73	11.89	16.8	0.498712518	0.0478628	PHATRDRAFT_50002	-	-	-	-		-
7202966	68	84	20.73	29.26	0.497209653	0.0345556	PHATRDRAFT_267	K01408|1|8e-111|400|ppp:PHYPADRAFT_136105|insulysin [EC:3.4.24.56]	-	GO:0043169//cation binding	-		-
7199626	69	85	35.68	50.27	0.494582074	0.0348182	PHATRDRAFT_44952	-	-	-	-		-
7195478	117	144	104.3	146.94	0.494488022	0.0061301	PHATRDRAFT_49306	-	-	-	-		-
7200978	346.48	426.04	136.22	191.47	0.491179827	2.37E-06	PHATRDRAFT_45886	K01966|1|6e-143|506|cme:CMM132C|propionyl-CoA carboxylase beta chain [EC:6.4.1.3];K01969|2|2e-59|229|ath:AT4G34030|3-methylcrotonyl-CoA carboxylase beta subunit [EC:6.4.1.4]	-	GO:0016421//CoA carboxylase activity	-		-
7196707	105	129	45.67	64.14	0.489977564	0.00983666	PHATRDRAFT_41702	K01696|1|2e-138|491|olu:OSTLU_32688|tryptophan synthase beta chain [EC:4.2.1.20]	-	GO:0016836//hydro-lyase activity	GO:0006568//tryptophan metabolic process		GO:0006568//tryptophan metabolic process
7201934	75	92	50.3	70.59	0.488905421	0.0299522	PHATRDRAFT_47141	K07119|1|7e-08|57.0|ath:AT1G49670|;K00344|2|3e-07|55.1|osa:4331066|NADPH2:quinone reductase [EC:1.6.5.5]	GO:0043231//intracellular membrane-bounded organelle	GO:0046914//transition metal ion binding;GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7203305	63	77	107.53	150.77	0.487610176	0.0492782	PHATRDRAFT_14715	K02864|1|6e-25|111|smo:SELMODRAFT_233811|large subunit ribosomal protein L10	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0030529//ribonucleoprotein complex	-	GO:0022613//ribonucleoprotein complex biogenesis		GO:0022613//ribonucleoprotein complex biogenesis
7195512	285	349	174.23	244.03	0.48606546	2.56E-05	PHATRDRAFT_49200	-	-	-	-		-
7196839	67	82	14.8	20.69	0.483336469	0.0416892	AP3delta	K12396|1|7e-102|370|olu:OSTLU_42302|AP-3 complex subunit delta-1	GO:0043234//protein complex	-	GO:0015031//protein transport		GO:0015031//protein transport
7196405	125	152	205.18	286.18	0.480032741	0.0064473	PHATRDRAFT_42790	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7197015	1191	1449	1388.33	1934.9	0.478908476	3.63E-17	PHATRDRAFT_43726	-	-	-	-		-
7195748	82	100	26.23	36.55	0.478653599	0.0259358	PHATRDRAFT_23306	K12585|1|3e-177|620|aly:ARALYDRAFT_480636|exosome complex exonuclease DIS3/RRP44 [EC:3.1.13.-]	-	GO:0003676//nucleic acid binding;GO:0004518//nuclease activity	-		-
7197761	489	593	922.83	1284.52	0.477092543	9.30E-08	PHATRDRAFT_44484	-	GO:0043231//intracellular membrane-bounded organelle	GO:0030234//enzyme regulator activity	GO:0006140;GO:0044092//negative regulation of molecular function		GO:0006140;GO:0044092//negative regulation of molecular function
7195574	1613.99	1963	1275.41	1775.12	0.476955458	9.87E-23	PHATRDRAFT_49286	-	-	-	-		-
7196170	130	158	129.8	180.64	0.476827008	0.0055466	PHATRDRAFT_17545	K02984|1|2e-79|293|vcn:VOLCADRAFT_109707|small subunit ribosomal protein S3Ae	GO:0005840//ribosome;GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane;GO:0071944//cell periphery	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203099	65	79	48.16	66.98	0.475894984	0.0498986	PHATRDRAFT_54813	K12606|1|9e-110|395|ppp:PHYPADRAFT_203554|CCR4-NOT transcription complex subunit 9	-	-	-		-

7199346	74	90	25.47	35.4	0.474950401	0.0359954	HSP90	K04079|1|2e-164|578|vvi:100264968|molecular chaperone HtpG;K09487|2|2e-161|568|zma:100285108|heat shock protein 90kDa beta	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process		GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process
7201196	70	85	56.68	78.76	0.474623353	0.0424764	PHATRDRAFT_46237	-	-	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0022892	GO:0015669		GO:0015669
7197441	98	119	58.33	81.01	0.473861933	0.01636296	CK2_1	K03097|1|1e-149|528|ppp:PHYPADRAFT_218940|casein kinase II subunit alpha [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7203450	94	114	85.85	119.19	0.47337316	0.01920898	PHATRDRAFT_48069	-	-	-	-		-
7201567	328	398	43.73	60.61	0.470932494	1.18E-05	PHATRDRAFT_46476	-	-	GO:0016740//transferase activity	-		-
7198389	143	173	119.39	165.31	0.469491997	0.00417588	PHATRDRAFT_30660	K02941|1|2e-72|270|olu:OSTLU_29307|large subunit ribosomal protein LP0	GO:0030529//ribonucleoprotein complex	-	GO:0022613//ribonucleoprotein complex biogenesis		GO:0022613//ribonucleoprotein complex biogenesis
7202798	93.65	113.18	56.85	78.58	0.467001819	0.01910148	PHATRDRAFT_47573	-	-	-	-		-
7197913	88	106	47.28	65.13	0.462092191	0.0268032	PHATRDRAFT_41857	K06185|1|8e-51|199|vcn:VOLCADRAFT_93958|ATP-binding cassette, subfamily F, member 2	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7197313	89	107	94.25	129.77	0.461392379	0.0269302	PHATRDRAFT_43581	-	-	-	-		-
7202549	108	130	62.58	86.16	0.461316591	0.0143895	PHATRDRAFT_47413	-	GO:0034357;GO:0009534//chloroplast thylakoid	-	GO:0009987//cellular process		GO:0009987//cellular process
7199544	113	136	71.53	98.48	0.46128232	0.01234042	PHATRDRAFT_44821	-	-	-	-		-
7204990	165.93	199.49	64.58	88.76	0.458822227	0.00232458	PHATRDRAFT_bd391	K01534|1|1e-139|495|ppp:PHYPADRAFT_125099|Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0008324//cation transmembrane transporter activity;GO:0016787//hydrolase activity	GO:0006812//cation transport		GO:0006812//cation transport
7197713	135	162	59.5	81.63	0.456209789	0.00677494	PHATRDRAFT_44482	K00387|1|6e-88|323|cre:CHLREDRAFT_59800|sulfite oxidase [EC:1.8.3.1]	-	GO:0046914//transition metal ion binding;GO:0003824//catalytic activity;GO:0046906//tetrapyrrole binding	GO:0044710		GO:0044710
7201556	121	145	23.97	32.82	0.45334533	0.01073086	PHATRDRAFT_46460	K12571|1|2e-46|187|ota:Ot01g00110|PAB-dependent poly(A)-specific ribonuclease subunit 2 [EC:3.1.13.4]	GO:0044464	GO:0004518//nuclease activity;GO:0097159//organic cyclic compound binding	-		-
7199801	138	165	81.23	111.08	0.451514533	0.00685912	PHATRDRAFT_44874	-	-	-	-		-
7199284	1064	1269	1413.39	1931.92	0.450875747	9.88E-14	PHATRDRAFT_50499	-	-	-	-		-
7202089	218	260	237.93	325	0.449902529	0.000755396	PHATRDRAFT_28359	K02865|1|7e-62|235|aly:ARALYDRAFT_662048|large subunit ribosomal protein L10Ae	GO:0044391	GO:0003676//nucleic acid binding;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7196359	145	173	89.15	121.66	0.448548206	0.00594394	PHATRDRAFT_1784	-	-	-	-		-
7196562	78	93	35.1	47.85	0.447047894	0.0441316	PHATRDRAFT_17895	K01792|1|1e-49|196|ppp:PHYPADRAFT_155277|glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	-	GO:0005488//binding;GO:0003824//catalytic activity	GO:0044238		GO:0044238
7195798	89	106	42.68	58.11	0.445226278	0.032198	PHATRDRAFT_49426	K06694|1|2e-08|59.3|rcu:RCOM_1621740|26S proteasome non-ATPase regulatory subunit 10	-	-	-		-
7199786	183	218	38.48	52.37	0.444631806	0.00211422	PHATRDRAFT_44845	-	-	-	-		-
7200615	85	101	83.13	113.09	0.444030248	0.0378788	PHATRDRAFT_20007	K02737|1|3e-82|303|vcn:VOLCADRAFT_74437|20S proteasome subunit beta 5 [EC:3.4.25.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0000502//proteasome complex	GO:0004175//endopeptidase activity	GO:0006508//proteolysis;GO:0010038//response to metal ion		GO:0006508//proteolysis;GO:0010038//response to metal ion
7205085	222	264	65.45	88.95	0.442601413	0.000765918	PtAP1/2beta	K12392|1|0.0|901|osa:4332864|AP-1 complex subunit beta-1	GO:0030119//AP-type membrane coat adaptor complex	GO:0022892	GO:0015031//protein transport		GO:0015031//protein transport
7198539	85	101	47.64	64.74	0.442483952	0.0378788	PHATRDRAFT_49931	-	-	-	-		-

7204355	80	95	47.03	63.87	0.441557118	0.0444546	PHATR_54164	-	GO:0031224//intrinsic component of membrane	GO:0015075//ion transmembrane transporter activity	GO:0044765;GO:0044763		GO:0044765;GO:0044763
7204554	87	103	91.91	124.61	0.439126106	0.0381302	rpl2	K02938|1|6e-88|322|rcu:RCOM_1544580|large subunit ribosomal protein L8e	GO:0009536//plastid;GO:0044391	GO:0003723//RNA binding;GO:0003824//catalytic activity;GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7203735	159	188	212.53	288	0.43840231	0.00526748	PHATRDRAFT_48309	-	-	-	-		-
7194874	93	110	76.97	104.19	0.436848664	0.0326328	PHATRDRAFT_48607	-	-	-	-		-
7195548	148	175	64.86	87.68	0.434918775	0.00709594	PHATRDRAFT_49253	K08232|1|3e-15|82.0|cme:CMT414C|monodehydroascorbate reductase (NADH) [EC:1.6.5.4]	GO:0044424	GO:0003824//catalytic activity;GO:0000166//nucleotide binding	GO:0044710;GO:0019725//cellular homeostasis		GO:0044710;GO:0019725//cellular homeostasis
7194833	143	168	145.5	195.73	0.427845745	0.00972838	PHATRDRAFT_29711	K02150|1|2e-35|147|ppp:PHYPADRAFT_223748|V-type H+-transporting ATPase subunit E [EC:3.6.3.14]	GO:0016469//proton-transporting two-sector ATPase complex	GO:0019829//cation-transporting ATPase activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7201614	415	487	441.67	593.57	0.426449336	1.16E-05	PHATRDRAFT_46343	-	-	-	-		-
7205097	103	121	36.06	48.41	0.424905697	0.0282536	PHATRDRAFT_bd645	K01895|1|0.0|663|rcu:RCOM_1443610|acetyl-CoA synthetase [EC:6.2.1.1]	-	GO:0016405//CoA-ligase activity;GO:0032550	GO:0006083//acetate metabolic process		GO:0006083//acetate metabolic process
7200713	192	225	212.53	285.26	0.424610961	0.00299616	PHATRDRAFT_19954	-	-	GO:0046914//transition metal ion binding;GO:0046906//tetrapyrrole binding	GO:0015669		GO:0015669
7203621	87	102	51.82	69.48	0.423088739	0.045338	PHATRDRAFT_48445	-	-	GO:0042578//phosphoric ester hydrolase activity	GO:0044238		GO:0044238
7196905	100	117	107.23	143.68	0.422150667	0.0332086	PHATRDRAFT_17860	K03521|1|3e-79|293|smo:SELMODRAFT_232605|electron transfer flavoprotein beta subunit	-	-	GO:1901565;GO:0044710;GO:0044248//cellular catabolic process		GO:1901565;GO:0044710;GO:0044248//cellular catabolic process
7197743	100	117	106.43	142.6	0.422069113	0.0332086	PHATRDRAFT_10847	K02945|1|2e-71|266|aly:ARALYDRAFT_489681|small subunit ribosomal protein S1	GO:0009532//plastid stroma;GO:0030529//ribonucleoprotein complex	GO:0005198//structural molecule activity;GO:0003676//nucleic acid binding	GO:0010467//gene expression;GO:0006779//porphyrin-containing compound biosynthetic process;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0009668;GO:0016070//RNA metabolic process;GO:0009658//chloroplast organization;GO:0042254//ribosome		GO:0010467//gene expression;GO:0006779//porphyrin-containing compound biosynthetic process;GO:0006007//glucose catabolic process;GO:0006090//pyruvate metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0009668;GO:0016070//RNA metabolic process;GO:0009658//chloroplast organization;GO:0042254//ribosome
7199304	308	361	111.05	148.77	0.421874238	0.000168811	PHATRDRAFT_50441	-	-	-	-		-
7204244	105	123	27.67	37.04	0.420761455	0.0283804	PHATR_43803	-	-	-	GO:0000301//retrograde transport, vesicle recycling within Golgi		GO:0000301//retrograde transport, vesicle recycling within Golgi
7199019	107	125	56.5	75.47	0.417652407	0.0284934	PHATRDRAFT_50245	-	-	GO:0042623//ATPase activity, coupled	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7204173	227	265	126.9	169.42	0.416912125	0.001463462	PHATR_43944	K03942|1|3e-175|613|olu:OSTLU_43184|NADH dehydrogenase (ubiquinone) flavoprotein 1 [EC:1.6.5.3 1.6.99.3]	-	GO:0051536//iron-sulfur cluster binding;GO:0050136//NADH dehydrogenase (quinone) activity;GO:0032553	GO:0044710		GO:0044710
7200783	244	285	53.63	71.58	0.41651629	0.000948148	PHATRDRAFT_45758	K00327|1|2e-29|130|sbi:SORBI_07g007640|NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	GO:0046914//transition metal ion binding;GO:0032553;GO:0003824//catalytic activity	GO:0044710		GO:0044710

7198310	265	309	159.72	213.02	0.415443911	0.000619732	PHATRDRAFT_49670	K13420|1|2e-21|102|aly:ARALYDRAFT_356368|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7195163	3732	4346	3309.55	4411.57	0.41465711	2.08E-37	Lhcf15	K08907|1|9e-09|59.3|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08910|2|3e-07|54.3|cme:CMQ142C|light-harvesting complex I chlorophyll a/b binding protein 4	GO:0009536//plastid	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7200223	93	108	141.03	187.8	0.413194977	0.0458246	H2B-1b	K11252|1|3e-38|156|ota:Ot12g01070|histone H2B	GO:0000785//chromatin;GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0046983//protein dimerization activity	GO:0034728//nucleosome organization		GO:0034728//nucleosome organization
7200116	136	158	73.44	97.57	0.40987157	0.01558376	PHATRDRAFT_45247	-	-	-	-		-
7202252	159	184	119.05	157.64	0.405066034	0.009987	PHATRDRAFT_47023	-	-	-	-		-
7199311	105	121	154.32	203.88	0.40179521	0.0393966	PHATRDRAFT_16962	-	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7198846	122	141	31.23	41.24	0.401111763	0.024729	Sec61alpha	K10956|1|0.0|700|smo:SELMODRAFT_271933|protein transport protein SEC61 subunit alpha	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	-	GO:0045184//establishment of protein localization		GO:0045184//establishment of protein localization
7196347	310	357	118.77	156.35	0.396608746	0.000415874	PHATRDRAFT_17427	K00121|1|7e-128|456|vcn:VOLCADRAFT_82410|S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	-	GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0052689//carboxylic ester hydrolase activity;GO:0036094//small molecule binding	GO:0044282;GO:0006067//ethanol metabolic process		GO:0044282;GO:0006067//ethanol metabolic process
7202290	208	239	105.22	138.24	0.393766167	0.00415402	PHATRDRAFT_37749	-	-	-	-		-
7203685	133	152	122.12	159.77	0.387697044	0.0248594	PHATRDRAFT_48449	-	-	GO:0016872//intramolecular lyase activity	GO:0009699//phenylpropanoid biosynthetic process		GO:0009699//phenylpropanoid biosynthetic process
7197850	111	127	25.26	33.02	0.386485481	0.0394944	PHATRDRAFT_26057	K15900|1|4e-126|451|gmx:100780256|tRNA threonylcarbamoyladenosine biosynthesis protein	-	-	-		-
7197497	170	194	118.67	154.94	0.38475438	0.01168836	GMD1	K01711|1|1e-105|381|ath:AT5G66280|GDPmannose 4,6-dehydratase [EC:4.2.1.47]	GO:0044464	GO:0036094//small molecule binding;GO:0048037//cofactor binding;GO:0016836//hydro-lyase activity	GO:0009225//nucleotide-sugar metabolic process		GO:0009225//nucleotide-sugar metabolic process
7197014	317	361	440.92	575.56	0.384449413	0.000640604	PHATRDRAFT_43725	-	-	-	-		-
7197899	1711.42	1954.44	397.09	518.13	0.383848089	1.05E-15	PHATRDRAFT_44695	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7201606	185	211	117.55	153.35	0.383553628	0.00868156	PHATRDRAFT_46535	K12133|1|5e-10|64.3|ath:AT1G01060|LATE ELONGATED HYPOCOTYL;K12134|3|4e-09|61.2|aly:ARALYDRAFT_904154|circadian clock associated 1	-	GO:0003676//nucleic acid binding	-		-
7195968	152	173	124.48	162.14	0.381326083	0.01833248	PHATRDRAFT_42600	-	-	-	-		-
7202002	156	177	105.96	137.54	0.376331502	0.0183057	PHATRDRAFT_47079	-	-	-	-		-

7199044	196	222	89.71	116.17	0.372896835	0.00864892	GPI_1	K01810|1|8e-136|482|vcn:VOLCADRAFT_103185|glucose-6-phosphate isomerase [EC:5.3.1.9]	GO:0044424	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006007//glucose catabolic process		GO:0006007//glucose catabolic process
7204627	173	196	59.37	76.88	0.372874223	0.01352988	PHATR_46720	-	-	GO:0036094//small molecule binding	-		-
7197221	143	162	45	58.26	0.3725807	0.0247892	PHATRDRAFT_18202	K08675|1|0.0|774|olu:OSTLU_41620|Lon-like ATP-dependent protease [EC:3.4.21.-]	-	GO:0004175//endopeptidase activity;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0051603//proteolysis involved in cellular protein catabolic process		GO:0051603//proteolysis involved in cellular protein catabolic process
7196598	119	134	192.02	248	0.369083537	0.0458482	PHATRDRAFT_17954	K03263|1|2e-36|150|zma:542537|translation initiation factor 5A	-	GO:0043021//ribonucleoprotein complex binding;GO:0008135//translation factor activity, nucleic acid binding	GO:0050896//response to stimulus;GO:0006414//translational elongation;GO:0006415//translational termination;GO:0018205//peptidyl-lysine modification		GO:0050896//response to stimulus;GO:0006414//translational elongation;GO:0006415//translational termination;GO:0018205//peptidyl-lysine modification
7202384	155	175	40.71	52.52	0.367483695	0.0212144	PHATRDRAFT_21513	K01873|1|0.0|1003|ppp:PHYPADRAFT_128528|valyl-tRNA synthetase [EC:6.1.1.9]	GO:0009532//plastid stroma	GO:0032550;GO:0052689//carboxylic ester hydrolase activity;GO:0004812//aminoacyl-tRNA ligase activity	GO:0003006//developmental process involved in reproduction;GO:0006418//tRNA aminoacylation for protein translation;GO:0006605//protein targeting;GO:0009668;GO:0009886//post-embryonic morphogenesis;GO:0009451//RNA modification;GO:0042254//ribosome biogenesis;GO:0006448//regulation of translational elongation		GO:0003006//developmental process involved in reproduction;GO:0006418//tRNA aminoacylation for protein translation;GO:0006605//protein targeting;GO:0009668;GO:0009886//post-embryonic morphogenesis;GO:0009451//RNA modification;GO:0042254//ribosome biogenesis;GO:0006448//regulation of translational elongation
7201218	134	151	122.12	157.53	0.367327107	0.0335638	PHATRDRAFT_3843	K04345|1|2e-74|277|rcu:RCOM_1050860|protein kinase A [EC:2.7.11.11]	-	GO:0043169//cation binding;GO:0004721//phosphoprotein phosphatase activity;GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7204107	1309	1475	254.29	327.36	0.364403321	3.16E-11	PHATR_44192	-	-	-	-		-
7205100	352	396	150.56	193.64	0.363038466	0.000627148	PHATRDRAFT_bd714	K13862|1|1e-23|110|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7201231	129	145	74.1	95.26	0.362397006	0.0390984	PHATRDRAFT_46131	-	-	-	-		-
7196196	122	137	84.82	108.97	0.36145462	0.0456908	PHATRDRAFT_17671	K03953|1|1e-46|185|cme:CMM267C|NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 9 [EC:1.6.5.3 1.6.99.3]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity;GO:0048037//cofactor binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7200405	191	214	244.98	314.53	0.360533655	0.01329758	FtrB	-	-	GO:0016731	GO:0044710		GO:0044710
7195448	174	195	84.67	108.49	0.357639275	0.01800598	PK3	K00873|1|3e-126|450|cre:CHLREDRAFT_136854|pyruvate kinase [EC:2.7.1.40]	-	GO:0031420;GO:0016301//kinase activity	GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0006007//glucose catabolic process
7197249	1480	1656	815.13	1043.03	0.355678585	7.40E-12	PHATRDRAFT_43716	-	-	-	-		-
7205121	359	401	407.93	521.93	0.355534719	0.0008117	PHATRDRAFT_bd1023	K00428|1|9e-83|304|cre:CHLREDRAFT_192806|cytochrome c peroxidase [EC:1.11.1.5]	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress

7200158	382	427	154.81	197.82	0.353689627	0.000529698	PHATRDRAFT_51830	-	-	GO:0019842//vitamin binding;GO:0043169//cation binding;GO:0016866//intramolecular transferase activity	-		-
7199571	213	237	205.49	261.78	0.349286691	0.01120446	PHATRDRAFT_26515	K00413|1|1e-77|287|rcu:RCOM_0897640|ubiquinol-cytochrome c reductase cytochrome c1 subunit	-	GO:0046914//transition metal ion binding;GO:0015078//hydrogen ion transmembrane transporter activity;GO:0003824//catalytic activity;GO:0046906//tetrapyrrole binding	GO:0044710		GO:0044710
7202107	218	243	43.1	54.89	0.34885547	0.00970172	PHATRDRAFT_47011	K11654|1|0.0|760|ppp:PHYPADRAFT_216086|SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 [EC:3.6.4.-]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0003682//chromatin binding;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006338//chromatin remodeling		GO:0006338//chromatin remodeling
7204036	238	265	143.45	182.68	0.348770727	0.00716484	PHATR_44101	-	-	GO:0003824//catalytic activity	GO:0009987//cellular process		GO:0009987//cellular process
7201126	197	219	85.24	108.34	0.345963498	0.01512026	PHATRDRAFT_45904	K08245|1|2e-18|92.8|olu:OSTLU_44385|phytepsin [EC:3.4.23.40]	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7197714	143	159	48.34	61.43	0.34572591	0.0382694	PHATRDRAFT_44485	-	-	-	-		-
7201381	166	184	48.1	60.93	0.341115846	0.027708	PHATRDRAFT_46307	-	-	-	-		-
7202394	1339	1481	972.8	1231.07	0.339697663	6.05E-10	PHATRDRAFT_47332	-	-	GO:0046906//tetrapyrrole binding	-		-
7198204	155	171	200.91	254	0.338279123	0.037315	PHATRDRAFT_49591	-	-	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7198787	202	223	139.87	176.65	0.33680719	0.01712202	FABB	K09458|1|9e-58|222|gmx:100790019|3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	-	GO:0016740//transferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7204522	344	380	55.19	69.65	0.335716467	0.001811406	PHATR_46752	-	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7197026	226	249	190.93	240.76	0.334551917	0.01246388	TPT2	K15283|1|7e-37|152|cme:CMK114C|solute carrier family 35, member E1	GO:0031224//intrinsic component of membrane	-	-		-
7203003	197	217	85.72	107.95	0.332659488	0.01977256	PHATRDRAFT_29223	K03083|1|9e-125|446|ppp:PHYPADRAFT_105861|glycogen synthase kinase 3 beta [EC:2.7.11.26]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process		GO:0006796//phosphate-containing compound metabolic process;GO:0006464//cellular protein modification process
7197254	193	212	115.27	144.82	0.329243768	0.0227784	PHATRDRAFT_43727	-	-	-	-		-
7200531	370	405	376.02	471.3	0.325836282	0.001931874	PHATRDRAFT_45408	-	-	-	-		-
7198785	513	562	207.41	259.74	0.324582753	0.000247218	PHATRDRAFT_51245	K01968|1|5e-96|350|bdi:100828042|3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4];K01961|3|3e-95|347|pop:POPTR_673504|acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	-	GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550;GO:0043169//cation binding	-		-
7199385	196	214	147.27	183.99	0.321163784	0.0257326	MDH	K00026|1|3e-101|366|pop:POPTR_822907|malate dehydrogenase [EC:1.1.1.37]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0016615//malate dehydrogenase activity;GO:0036094//small molecule binding	GO:0043648//dicarboxylic acid metabolic process;GO:0009628//response to abiotic stimulus;GO:0005975//carbohydrate metabolic process;GO:0009060//aerobic respiration;GO:0006950//response to stress		GO:0043648//dicarboxylic acid metabolic process;GO:0009628//response to abiotic stimulus;GO:0005975//carbohydrate metabolic process;GO:0009060//aerobic respiration;GO:0006950//response to stress
7200156	199	217	128.64	160.46	0.318874391	0.0255118	PHATRDRAFT_45297	-	GO:0009536//plastid	-	-		-

7195719	178	193	273.32	339.83	0.314222187	0.0398942	PsbM	K02714|1|2e-06|50.4|cme:CMT182C|photosystem II PsbM protein	GO:0009521;GO:0031224//intrinsic component of membrane	-	GO:0006091//generation of precursor metabolites and energy		GO:0006091//generation of precursor metabolites and energy
7201470	162	176	117.79	146.42	0.313895566	0.0477478	AtpC	K02115|1|3e-98|357|cme:CMQ087C|F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]	GO:0009526//plastid envelope;GO:0033178//proton-transporting two-sector ATPase complex, catalytic domain;GO:0009535//chloroplast thylakoid membrane	GO:0019829//cation-transporting ATPase activity	GO:0006633//fatty acid biosynthetic process;GO:0044093;GO:0042254//ribosome biogenesis;GO:0006470//protein dephosphorylation;GO:0006996//organelle organization;GO:0009694//jasmonic acid metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0006351//transcription, DNA-templated;GO:0006754//ATP biosynthetic process;GO:0006090//pyruva		GO:0006633//fatty acid biosynthetic process;GO:0044093;GO:0042254//ribosome biogenesis;GO:0006470//protein dephosphorylation;GO:0006996//organelle organization;GO:0009694//jasmonic acid metabolic process;GO:0009767//photosynthetic electron transport chain;GO:0006351//transcription, DNA-templated;GO:0006754//ATP biosynthetic process;GO:0006090//pyruva
7201260	189	205	210.3	261.26	0.313037409	0.0339198	PHATRDRAFT_46187	-	GO:0031967	GO:0015002//heme-copper terminal oxidase activity	-		-
7197429	517	561	342.47	425.11	0.311858581	0.000441726	PHATRDRAFT_43413	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196775	266	289	41.59	51.62	0.311693456	0.0111968	PHATRDRAFT_42942	-	-	GO:0005083//small GTPase regulator activity;GO:0046914//transition metal ion binding	GO:0032012//regulation of ARF protein signal transduction		GO:0032012//regulation of ARF protein signal transduction
7198260	634	688	177.4	219.99	0.310431936	9.94E-05	PHATRDRAFT_49618	-	-	-	-		-
7203615	285	309	117.79	145.99	0.309652487	0.00935604	PHATRDRAFT_48435	-	-	GO:0042623//ATPase activity, coupled	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7199083	167.24	181.24	96.85	120.03	0.309571081	0.0469818	PHATRDRAFT_50347	K00360|1|8e-06|50.4|ppp:PHYPADRAFT_184973|nitrate reductase (NADH) [EC:1.7.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0046906//tetrapyrrole binding;GO:0046872//metal ion binding;GO:0008940//nitrate reductase activity	GO:0009314//response to radiation;GO:0016042//lipid catabolic process;GO:0048588//developmental cell growth;GO:0042126//nitrate metabolic process;GO:0009608//response to symbiont;GO:0044271//cellular nitrogen compound biosynthetic process		GO:0009314//response to radiation;GO:0016042//lipid catabolic process;GO:0048588//developmental cell growth;GO:0042126//nitrate metabolic process;GO:0009608//response to symbiont;GO:0044271//cellular nitrogen compound biosynthetic process
7204214	1189	1286	901.3	1115.45	0.30754655	1.58E-07	PHATR_44015	-	-	-	-		-
7197883	248	268	247.05	305.69	0.307266303	0.01708084	PHATRDRAFT_44428	-	-	-	-		-
7198341	307	332	135.45	167.46	0.306056137	0.00774524	PHATRDRAFT_55097	-	-	GO:0046872//metal ion binding	-		-
7198435	1032	1117	101.64	125.65	0.305942391	9.48E-07	PHATRDRAFT_49748	K03235|1|3e-40|167|olu:OSTLU_36160|elongation factor 3	-	-	-		-
7198290	180	194	81.34	100.23	0.301277493	0.0449402	PHATRDRAFT_49634	K07376|1|3e-09|62.4|ota:Ot02g05760|protein kinase, cGMP-dependent [EC:2.7.11.12];K02183|3|5e-08|58.2|zma:100281919|calmodulin;K04345|4|2e-07|55.8|gmx:100799821|protein kinase A [EC:2.7.11.11]	GO:0043234//protein complex	GO:0046872//metal ion binding;GO:0016740//transferase activity;GO:0019887//protein kinase regulator activity	GO:0006468//protein phosphorylation;GO:0019725//cellular homeostasis		GO:0006468//protein phosphorylation;GO:0019725//cellular homeostasis
7202116	199	214	114.23	140.49	0.298525851	0.0371216	PHATRDRAFT_21296	K01012|1|6e-107|386|bdi:100827697|biotin synthetase [EC:2.8.1.6]	-	GO:0043169//cation binding;GO:0051536//iron-sulfur cluster binding;GO:0016783//sulfurtransferase activity	GO:0006768//biotin metabolic process		GO:0006768//biotin metabolic process
7196577	250	269	82.94	101.99	0.298287752	0.01913348	PHATRDRAFT_43213	-	-	-	-		-

7198840	274	294	191.27	234.8	0.295821798	0.01562194	PHATRDRAFT_50136	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203354	2212	2374	1151.6	1413.3	0.295428044	6.23E-12	PHATRDRAFT_51125	K00927|1|3e-78|291|vvi:100244419|phosphoglycerate kinase [EC:2.7.2.3]	GO:0005911//cell-cell junction;GO:0005576//extracellular region;GO:0009532//plastid stroma;GO:0031090//organelle membrane;GO:0030312;GO:0009526//plastid envelope	GO:0016301//kinase activity	GO:0044272//sulfur compound biosynthetic process;GO:0051707//response to other organism;GO:0006007//glucose catabolic process;GO:0046394;GO:0006091//generation of precursor metabolites and energy;GO:0044262//cellular carbohydrate metabolic process;GO:0006796//phosphate-containing compound metabolic process;GO:00		GO:0044272//sulfur compound biosynthetic process;GO:0051707//response to other organism;GO:0006007//glucose catabolic process;GO:0046394;GO:0006091//generation of precursor metabolites and energy;GO:0044262//cellular carbohydrate metabolic process;GO:0006796//phosphate-containing compound metabolic process;GO:00
7195471	455	488	295.46	362.49	0.294978368	0.001884708	PHATRDRAFT_49297	-	-	-	-		-
7197954	514	550	503.83	617.26	0.292941276	0.001101426	PHATRDRAFT_44281	-	-	-	-		-
7203502	536	573	308.92	377.7	0.290007507	0.00091376	PHATRDRAFT_48166	K07735|1|2e-26|118|smo:SELMODRAFT_102585|putative transcriptional regulator	-	-	-		-
7200165	853	912	414.58	506.82	0.289822937	2.85E-05	PHATRDRAFT_34685	K05681|1|3e-77|288|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|2e-57|221|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K02065|4|8e-15|80.5|pop:POPTR_275971|putative ABC transport system ATP-binding protein	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7200682	373.52	399.05	117.93	143.99	0.288037851	0.00550992	PHATRDRAFT_54405	K13862|1|1e-22|107|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0004620//phospholipase activity;GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7204491	435	463	371.52	452.6	0.284796707	0.00351662	PHATR_46690	-	-	-	-		-
7200373	2586	2745	3562.23	4334.12	0.282958429	2.38E-12	PHATRDRAFT_45591	-	-	-	-		-
7199921	752	797	1382.63	1681.75	0.282548124	0.000177707	PHATRDRAFT_45040	-	-	-	-		-
7196256	690	734	280.16	340.69	0.282208613	0.000248192	PHATRDRAFT_17265	K08176|1|5e-25|114|osa:4331542|MFS transporter, PHS family, inorganic phosphate transporter	GO:0031224//intrinsic component of membrane	GO:0005215//transporter activity	GO:0044763		GO:0044763
7197621	213	226	270.77	329.2	0.281896432	0.0445824	PHATRDRAFT_19152	K02896|1|1e-23|107|gmx:100499979|large subunit ribosomal protein L24e	GO:0030529//ribonucleoprotein complex	-	-		-
7198707	669	710	766.28	931.55	0.281761555	0.000367412	PHATRDRAFT_50007	-	-	-	-		-
7197460	305	324	222.34	270.24	0.281473714	0.01558108	PHATRDRAFT_25360	K10251|1|4e-71|266|pop:POPTR_821856|beta-keto reductase [EC:1.1.1.-]	-	GO:0036094//small molecule binding;GO:0016614//oxidoreductase activity, acting on CH-OH group of donors	GO:0044710		GO:0044710
7203125	205	218	64.23	78.05	0.281151336	0.0460756	PHATRDRAFT_47933	K10636|1|8e-20|97.8|ppp:PHYPADRAFT_112701|autocrine motility factor receptor [EC:6.3.2.19];K10601|2|2e-07|56.6|aly:ARALYDRAFT_897909|E3 ubiquitin-protein ligase synoviolin [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	-		-
7199283	302	321	120.62	146.56	0.281022268	0.01576596	PHATRDRAFT_50498	-	-	-	-		-
7196392	449	476	473.74	575.14	0.279817688	0.0037134	PHATRDRAFT_42765	K08902|1|3e-22|103|cme:CMK176C|photosystem II Psb27 protein	-	-	-		-
7196914	419	445	49.41	59.94	0.278716028	0.0046425	PHATRDRAFT_43159	-	-	GO:0046914//transition metal ion binding	-		-
7199389	215	228	103.44	125.42	0.277973244	0.0442128	PHATRDRAFT_50561	-	-	-	-		-

7204443	214	226	58.88	71.05	0.271056978	0.049783	G6PDH/6PGDH	K00033|1|1e-157|556|aly:ARALYDRAFT_493822|6-phosphogluconate dehydrogenase [EC:1.1.1.44]	-	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;GO:0048037//cofactor binding;GO:0000166//nucleotide binding	GO:0044710;GO:0006007//glucose catabolic process		GO:0044710;GO:0006007//glucose catabolic process
7196272	782	825	293.56	354.01	0.270134711	0.000194264	PHATRDRAFT_42577	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7200719	1926	2030	1308.22	1577.42	0.269961664	6.01E-09	PHATRDRAFT_45514	-	-	-	-		-
7200968	217	229	41.7	50.28	0.269937266	0.049138	PHATRDRAFT_45870	-	-	-	-		-
7195587	993	1046	159.28	191.67	0.267059419	3.14E-05	PHATRDRAFT_49312	K08333|1|3e-130|465|ppp:PHYPADRAFT_144257|phosphoinositide-3-kinase, regulatory subunit 4, p150 [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7196698	327	344	121.21	145.76	0.266086136	0.01769998	PHATRDRAFT_24374	K00392|1|5e-167|586|cme:CMG021C|sulfite reductase (ferredoxin) [EC:1.8.7.1]	-	GO:0016673;GO:0051536//iron-sulfur cluster binding;GO:0046906//tetrapyrrole binding	GO:0044710		GO:0044710
7197776	858	902	504.35	606.42	0.265892077	0.000130296	PHATRDRAFT_44510	-	-	GO:0036094//small molecule binding	-		-
7197751	230	242	48.86	58.74	0.265689402	0.0464076	PHATRDRAFT_44465	-	-	-	-		-
7205026	507	531	715.66	859.2	0.263719647	0.00400076	PHATRDRAFT_bd176	K00540|1|9e-43|171|ath:AT3G27620|[EC:1.-.-.-]	GO:0016020//membrane	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	GO:0044710;GO:0044707		GO:0044710;GO:0044707
7202003	244	256	182.54	219.13	0.263574374	0.043592	PHATRDRAFT_47080	-	-	-	-		-
7201798	288	302	257	308.48	0.263408597	0.0288702	PHATRDRAFT_46444	-	-	GO:0051536//iron-sulfur cluster binding;GO:0043169//cation binding	-		-
7200191	562	590	132.81	159.31	0.262473049	0.0021256	PHATRDRAFT_26742	K01188|1|3e-56|219|ath:AT3G47000|beta-glucosidase [EC:3.2.1.21]	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7199724	303	317	130	155.48	0.25821739	0.0270026	PHATRDRAFT_44750	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202332	930	972	609.92	729.21	0.257714322	0.000118152	PHATRDRAFT_13951	K00262|1|2e-95|347|ppp:PHYPADRAFT_179243|glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	-	GO:0016638//oxidoreductase activity, acting on the CH-NH2 group of donors;GO:0036094//small molecule binding	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7202457	1126	1176	1007.94	1205	0.257623385	2.47E-05	TIM_1	K01803|1|2e-67|254|zma:100194114|triosephosphate isomerase (TIM) [EC:5.3.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0006007//glucose catabolic process;GO:0050896//response to stimulus		GO:0006007//glucose catabolic process;GO:0050896//response to stimulus

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<tr><td>7203381</td><td>3183.36</td><td>3325.26</td><td>2190.08</td><td>2617.2</td><td>0.257040606</td><td>1.25E-12</td><td>GapC2b</td><td>K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]</td><td>-</td><td>GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding</td><td>GO:0044710;GO:0019318//hexose metabolic process</td><td></td><td>GO:0044710;GO:0019318//hexose metabolic process</td></tr>
<tr><td>7200638</td><td>253</td><td>264</td><td>248.28</td><td>296.63</td><td>0.256696463</td><td>0.0465812</td><td>PHATRDRAFT_45582</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7204792</td><td>524.39</td><td>547.42</td><td>241.43</td><td>288.16</td><td>0.25526513</td><td>0.00410986</td><td>FbaC1</td><td>K01624|1|1e-116|419|olu:OSTLU_94831|fructose-bisphosphate aldolase, class II [EC:4.1.2.13];K00120|3|2e-16|86.3|aly:ARALYDRAFT_472044|[EC:1.1.-.-]</td><td>-</td><td>GO:0046914//transition metal ion binding;GO:0016832//aldehyde-lyase activity</td><td>GO:0006007//glucose catabolic process</td><td></td><td>GO:0006007//glucose catabolic process</td></tr>
<tr><td>7204536</td><td>347</td><td>362</td><td>198.66</td><td>237.02</td><td>0.254707384</td><td>0.01997626</td><td>PHATR_54643</td><td>K06694|1|6e-06|50.8|ath:AT2G03430|26S proteasome non-ATPase regulatory subunit 10</td><td>-</td><td>GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen</td><td>GO:0044710</td><td></td><td>GO:0044710</td></tr>
<tr><td>7199375</td><td>476</td><td>497</td><td>88.94</td><td>106.09</td><td>0.254384365</td><td>0.00616964</td><td>PHATRDRAFT_50537</td><td>K01689|1|5e-145|514|olu:OSTLU_28765|enolase [EC:4.2.1.11]</td><td>GO:0043234//protein complex</td><td>GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0046872//metal ion binding;GO:0016836//hydro-lyase activity</td><td>GO:0006007//glucose catabolic process;GO:0009154//purine ribonucleotide catabolic process</td><td></td><td>GO:0006007//glucose catabolic process;GO:0009154//purine ribonucleotide catabolic process</td></tr>
<tr><td>7198166</td><td>308</td><td>320</td><td>170.51</td><td>202.6</td><td>0.248777822</td><td>0.0324578</td><td>PHATRDRAFT_49683</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
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<tr><td>7205005</td><td>1710</td><td>1776</td><td>1158.75</td><td>1376.77</td><td>0.248718227</td><td>5.02E-07</td><td>PHATRDRAFT_bd1650</td><td>-</td><td>GO:0043231//intracellular membrane-bounded organelle</td><td>GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity</td><td>GO:0006351//transcription, DNA-templated</td><td></td><td>GO:0006351//transcription, DNA-templated</td></tr>
<tr><td>7199997</td><td>299</td><td>310</td><td>108.21</td><td>128.24</td><td>0.245012502</td><td>0.0374908</td><td>PHATRDRAFT_26970</td><td>K03885|1|4e-95|347|cme:CMF056C|NADH dehydrogenase [EC:1.6.99.3]</td><td>-</td><td>GO:0003824//catalytic activity</td><td>GO:0044710</td><td></td><td>GO:0044710</td></tr>
<tr><td>7198839</td><td>288</td><td>298</td><td>55.3</td><td>65.37</td><td>0.241349217</td><td>0.0437322</td><td>PHATRDRAFT_50132</td><td>K14327|1|4e-81|302|rcu:RCOM_1070440|regulator of nonsense transcripts 2</td><td>-</td><td>GO:0003676//nucleic acid binding</td><td>GO:0044260</td><td></td><td>GO:0044260</td></tr>
<tr><td>7204509</td><td>719</td><td>744</td><td>79.15</td><td>93.55</td><td>0.241148303</td><td>0.001443726</td><td>PHATR_46730</td><td>K04523|1|2e-06|55.1|cre:CHLREDRAFT_179183|ubiquilin</td><td>-</td><td>GO:0008047//enzyme activator activity</td><td>GO:0043087//regulation of GTPase activity;GO:0007264//small GTPase mediated signal transduction</td><td></td><td>GO:0043087//regulation of GTPase activity;GO:0007264//small GTPase mediated signal transduction</td></tr>
<tr><td>7203517</td><td>2131</td><td>2195</td><td>3048.2</td><td>3599.33</td><td>0.239770815</td><td>1.00E-07</td><td>PHATRDRAFT_48195</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7204323</td><td>297</td><td>306</td><td>201.74</td><td>237.78</td><td>0.23713021</td><td>0.0462456</td><td>PHATR_33260</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7195266</td><td>306</td><td>315</td><td>266.4</td><td>313.89</td><td>0.236664985</td><td>0.0442356</td><td>PHATRDRAFT_49001</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7204105</td><td>311</td><td>320</td><td>55.6</td><td>65.35</td><td>0.233102353</td><td>0.0431564</td><td>PHATR_44189</td><td>K13356|1|4e-12|73.2|bdi:100842081|fatty acyl-CoA reductase [EC:1.2.1.-]</td><td>-</td><td>GO:0036094//small molecule binding;GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0043168//anion binding;GO:0016740//transferase activity</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7204115</td><td>327</td><td>335</td><td>547.22</td><td>643.1</td><td>0.23292213</td><td>0.0438862</td><td>PHATR_44202</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7204463</td><td>1302</td><td>1336</td><td>1300.04</td><td>1527.44</td><td>0.232559697</td><td>4.87E-05</td><td>PHATR_46937</td><td>-</td><td>-</td><td>-</td><td>-</td><td></td><td>-</td></tr>
<tr><td>7196142</td><td>303</td><td>311</td><td>121.59</td><td>142.66</td><td>0.230556297</td><td>0.0494998</td><td>PHATRDRAFT_8670</td><td>K01414|1|0.0|641|gmx:100780377|oligopeptidase A [EC:3.4.24.70]</td><td>GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part</td><td>GO:0004175//endopeptidase activity;GO:0043169//cation binding</td><td>GO:0019538//protein metabolic process</td><td></td><td>GO:0019538//protein metabolic process</td></tr>
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7198950	596	611	136.47	159.86	0.228225154	0.0062959	PHATRDRAFT_50174	K10838|1|3e-23|109|ota:Ot14g02880|xeroderma pigmentosum group C-complementing protein;K00588|2|9e-09|61.6|pop:POPTR_805093|caffeoyl-CoA O-methyltransferase [EC:2.1.1.104];K13067|3|3e-07|56.6|ath:AT1G67990|putative caffeoyl-CoA 3-O-methyltransferase [EC:2.1.1.-]	-	GO:0005488//binding;GO:0008168//methyltransferase activity	-		-
7195643	339	346	314.64	367.63	0.224552409	0.0453894	Sec4	K07901|1|7e-65|245|ota:Ot05g02380|Ras-related protein Rab-8A	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7202587	725	741	70.75	82.59	0.223236963	0.00315048	PHATRDRAFT_21660	K07203|1|0.0|1245|vcn:VOLCADRAFT_65073|FKBP12-rapamycin complex-associated protein	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7201122	1538	1571	147.95	172.6	0.222322768	1.85E-05	PHATRDRAFT_45889	-	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7204604	349	356	107.76	125.62	0.221244419	0.0431466	PHATR_13511	K12391|1|4e-168|590|smo:SELMODRAFT_154964|AP-1 complex subunit gamma-1	GO:0030119//AP-type membrane coat adaptor complex;GO:0005794//Golgi apparatus	GO:0005488//binding;GO:0022892	GO:0015031//protein transport		GO:0015031//protein transport
7195544	4650	4717	2112.5	2450.01	0.213836296	1.27E-12	PHATRDRAFT_15815	K01507|1|0.0|655|olu:OSTLU_48479|inorganic pyrophosphatase [EC:3.6.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part;GO:0016020//membrane	GO:0016462//pyrophosphatase activity;GO:0015405	GO:0006818//hydrogen transport		GO:0006818//hydrogen transport
7199502	356	361	196.96	228.41	0.213723148	0.0499608	PHATRDRAFT_44980	-	-	GO:0016746//transferase activity, transferring acyl groups	-		-
7200902	2292	2322	1219.96	1413.33	0.212264516	7.93E-07	PHATRDRAFT_12416	-	GO:0044424	GO:0051540;GO:0016491//oxidoreductase activity	GO:0044710		GO:0044710
7199818	5290	5352	2301.86	2662.4	0.209927248	1.11E-13	PHATRDRAFT_54319	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203094	752	760	107.92	124.59	0.207226024	0.0054365	PHATRDRAFT_47879	K11292|1|2e-75|283|smo:SELMODRAFT_164675|transcription elongation factor SPT6	-	GO:0003676//nucleic acid binding;GO:0016787//hydrolase activity	GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter		GO:0006354//DNA-templated transcription, elongation;GO:0006366//transcription from RNA polymerase II promoter
7203376	3124.64	3146.74	2156.62	2484.7	0.204299679	3.43E-08	GapC2a	K00134|1|1e-115|414|ppp:PHYPADRAFT_109421|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors;GO:0000166//nucleotide binding	GO:0044710;GO:0019318//hexose metabolic process		GO:0044710;GO:0019318//hexose metabolic process
7197367	662	666	371.78	427.75	0.202318693	0.01165428	CCL1	K01904|1|8e-80|296|rcu:RCOM_1325310|4-coumarate--CoA ligase [EC:6.2.1.12]	-	GO:0016874//ligase activity	-		-
7203497	488	491	245.4	282.33	0.202247187	0.0301728	PHATRDRAFT_48157	K14497|1|4e-25|114|gmx:100791754|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0004721//phosphoprotein phosphatase activity;GO:0043169//cation binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7204205	494	496	529.7	609.09	0.20147991	0.0317856	PHATR_44000	-	-	-	-		-
7196924	1892	1896	1902.47	2182.99	0.198431817	3.50E-05	PHATRDRAFT_43175	-	-	-	-		-
7200555	1206	1205	2321.94	2663.25	0.197857168	0.001239258	HSP20A	K13993|1|2e-09|59.7|aly:ARALYDRAFT_489869|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus

7203858	661	662	419.99	481.14	0.196101767	0.01486554	PHATR_10260	K00323|1|9e-88|322|vcn:VOLCADRAFT_80229|NAD(P) transhydrogenase [EC:1.6.1.2]	GO:0031224//intrinsic component of membrane	GO:0008746//NAD(P)+ transhydrogenase activity;GO:0000166//nucleotide binding	GO:0044710		GO:0044710
7205031	1288	1289	1030.16	1179.82	0.195698343	0.000725616	PHATRDRAFT_bd1693	-	-	-	-		-
7199292	946	939	296.81	336.7	0.181924022	0.00667272	PHATRDRAFT_50516	-	GO:0031224//intrinsic component of membrane	GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044763;GO:0006811//ion transport		GO:0044763;GO:0006811//ion transport
7197557	691	686	90.56	102.7	0.181490318	0.0202324	PHATRDRAFT_32738	-	-	-	-		-
7194806	4433	4400	598.48	678.54	0.181130829	4.41E-09	ACC1	K11262|1|0.0|2003|ota:Ot01g03240|acetyl-CoA carboxylase / biotin carboxylase [EC:6.4.1.2 6.3.4.14]	-	GO:0016421//CoA carboxylase activity;GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7199362	1377	1366	305.18	345.9	0.180694596	0.00112829	PHATRDRAFT_31339	K05917|1|1e-113|409|cme:CMS319C|cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]	GO:0044464	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016741;GO:0016712//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one	GO:0044710		GO:0044710
7199411	4223	4185	1615.07	1829.52	0.179868492	1.57E-08	PHATRDRAFT_50525	-	-	GO:0036094//small molecule binding	-		-
7201322	515	510	108.68	122.96	0.178102599	0.0495466	PHATRDRAFT_46078	-	-	GO:0003676//nucleic acid binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199747	689	682	193.61	219	0.1777774	0.0236758	PHATRDRAFT_44788	K14445|1|6e-06|52.0|pop:POPTR_717389|solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7204049	1235	1219	287.09	323.78	0.173510794	0.00311806	PHATR_25840	K00323|1|0.0|815|cre:CHLREDRAFT_139758|NAD(P) transhydrogenase [EC:1.6.1.2]	GO:0031224//intrinsic component of membrane	GO:0008746//NAD(P)+ transhydrogenase activity;GO:0000166//nucleotide binding	GO:0006818//hydrogen transport;GO:0044710		GO:0006818//hydrogen transport;GO:0044710
7201142	1044	1030	366.37	413.14	0.173329374	0.006788	PHATRDRAFT_35766	K03234|1|0.0|1011|bdi:100836272|elongation factor 2	GO:0016020//membrane;GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550;GO:0017111//nucleoside-triphosphatase activity;GO:0043167//ion binding	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7194773	955	936	1098.28	1233.04	0.166973694	0.01462314	PHATRDRAFT_48527	-	-	-	-		-
7196652	1615	1582	972.72	1089.82	0.163993386	0.001586122	Fba4	K00640|1|7e-35|146|cme:CMA007C|serine O-acetyltransferase [EC:2.3.1.30]	GO:0005737//cytoplasm	GO:0016832//aldehyde-lyase activity;GO:0016412//serine O-acyltransferase activity	GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process		GO:0006007//glucose catabolic process;GO:0000097//sulfur amino acid biosynthetic process;GO:0006563//L-serine metabolic process
7202701	21722.73	21298.78	4636.69	5194.19	0.163803514	1.62E-31	PHATRDRAFT_47693	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7204549	753	737	559.41	626.47	0.163339381	0.032279	PHATR_36843	-	-	-	-		-
7195677	6965	6817	5081.72	5690.76	0.163304451	7.65E-11	PHATRDRAFT_49202	-	-	-	-		-

7196891	810	784	103.74	114.7	0.144893117	0.0463978	BGS1	K11000|1|0.0|740|gmx:100806685|callose synthase [EC:2.4.1.-]	GO:0043234//protein complex;GO:0043234//protein complex	GO:0035251//UDP-glucosyltransferase activity;GO:0035251//UDP-glucosyltransferase activity	GO:0006074//(1->3)-beta-D-glucan metabolic process;GO:0006074//(1->3)-beta-D-glucan metabolic process		GO:0006074//(1->3)-beta-D-glucan metabolic process;GO:0006074//(1->3)-beta-D-glucan metabolic process
7200601	1015	979	122.6	135.08	0.139855105	0.0315948	PHATRDRAFT_19982	K12856|1|0.0|3457|ppp:PHYPADRAFT_200564|pre-mRNA-processing factor 8	GO:0030529//ribonucleoprotein complex	-	GO:0000377		GO:0000377
7199707	1452	1397	1509.67	1663.31	0.139823852	0.01234742	PHATRDRAFT_44725	-	-	-	-		-
7200037	2039	1962	1646.2	1812.78	0.139064227	0.00299288	PHATRDRAFT_45349	-	-	-	-		-
7204427	1634	1573	629.98	693.24	0.138048872	0.00757224	PHATR_46872	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203220	2855	2740	179.26	196.48	0.132328864	0.000644768	PHATRDRAFT_47968	-	-	-	-		-
7204993	1214.16	1162.68	733.36	803.22	0.131273614	0.0308268	PHATRDRAFT_bd1770	-	-	-	-		-
7198165	2903	2781	600.48	657.22	0.130260189	0.00075048	PYC1	K01958|1|0.0|1176|ota:Ot08g00930|pyruvate carboxylase [EC:6.4.1.1];K01968|5|5e-91|335|gmx:548094|3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	-	GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0003676//nucleic acid binding;GO:0016885;GO:0032550	GO:0006006//glucose metabolic process		GO:0006006//glucose metabolic process
7201728	5264	5002	5665.71	6165.74	0.122017295	3.83E-05	PHATRDRAFT_46597	-	-	-	-		-
7201200	2696	2551	1101.45	1191.4	0.113253858	0.0052539	PHATRDRAFT_46243	-	-	GO:0008233//peptidase activity	-		-
7203738	4467	4226	1463.79	1582.69	0.112670109	0.000338688	PHATRDRAFT_48315	-	-	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7203020	16093	15198	7568.14	8171.76	0.110708057	3.08E-11	PHATRDRAFT_48027	-	-	-	-		-
7197898	14984.58	14143.56	3904.33	4211.01	0.109091305	1.98E-10	SMP1	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7195771	1540.96	1454.18	314.56	339.15	0.108588266	0.0404432	PHATRDRAFT_49379	-	-	GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7197797	2121	2000	155.56	167.53	0.106948326	0.01813868	PHATRDRAFT_44551	-	-	-	-		-
7199280	3781	3557	1819.09	1956.68	0.105190911	0.00226962	PHATRDRAFT_50491	-	-	-	-		-
7195681	14446	13582	7368.43	7921.65	0.104443705	3.33E-09	PHATRDRAFT_49211	-	-	-	-		-
7202950	8539	7787	2571.69	2680.13	0.059586235	0.01031272	PHATRDRAFT_54800	K09835|1|7e-12|71.6|rcu:RCOM_0422660|prolycopene isomerase [EC:5.2.1.13]	-	GO:0003824//catalytic activity	-		-
7203153	9524	8655	1869.27	1940.74	0.054131885	0.01344706	PPdK	K01006|1|0.0|857|vvi:100247690|pyruvate,orthophosphate dikinase [EC:2.7.9.1]	-	GO:0032550;GO:0016781//phosphotransferase activity, paired acceptors	GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process		GO:0006796//phosphate-containing compound metabolic process;GO:0032787//monocarboxylic acid metabolic process
7198328	63.56	0	31.41	0.001	-14.93893632	6.52E-18	PHATRDRAFT_55090	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7194848	5	0	28.16	0.001	-14.78135971	0.0458808	PHATRDRAFT_7934	K09517|1|1e-12|69.7|pop:POPTR_816712|DnaJ homolog subfamily B member 11	GO:0005911//cell-cell junction;GO:0044432	GO:0005515//protein binding;GO:0003824//catalytic activity	GO:0009687//abscisic acid metabolic process;GO:0009642//response to light intensity;GO:0044267//cellular protein metabolic process;GO:0000302//response to reactive oxygen species;GO:0000904//cell morphogenesis involved in differentiation;GO:0009408//response to heat		GO:0009687//abscisic acid metabolic process;GO:0009642//response to light intensity;GO:0044267//cellular protein metabolic process;GO:0000302//response to reactive oxygen species;GO:0000904//cell morphogenesis involved in differentiation;GO:0009408//response to heat
7201517	13.63	0	24.28	0.001	-14.5674808	0.000299064	PHATRDRAFT_12786	K14497|1|2e-28|123|osa:4324182|protein phosphatase 2C [EC:3.1.3.16]	-	GO:0004721//phosphoprotein phosphatase activity;GO:0043169//cation binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7203932	5	0	16.71	0.001	-14.02842411	0.0458808	PHATR_33598	-	-	-	-		-
7205113	8.2	0	14.17	0.001	-13.79055214	0.00694914	PHATRDRAFT_bd1537	-	-	-	-		-
7199082	7.38	0	13.31	0.001	-13.70022295	0.01303658	PHATRDRAFT_41282	K02838|1|3e-47|185|pop:POPTR_710069|ribosome recycling factor	-	-	GO:0010467//gene expression		GO:0010467//gene expression

7197521	9	0	12.96	0.001	-13.6617781	0.00370422	PHATRDRAFT_10102	K10643|1|1e-54|210|mtr:MTR_2g093100|CCR4-NOT transcription complex subunit 4 [EC:6.3.2.19]	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:0046914//transition metal ion binding	-		-
7198312	5	0	12.94	0.001	-13.65955	0.0458808	PHATRDRAFT_40435	-	-	-	-		-
7200863	12.39	0	12.04	0.001	-13.55554777	0.000561044	PHATRDRAFT_46003	-	-	GO:0005515//protein binding	-		-
7196024	5	0	10.98	0.001	-13.42259043	0.0458808	PHATRDRAFT_42686	-	-	-	-		-
7199778	13.13	0	10.95	0.001	-13.41864325	0.000299064	PHATRDRAFT_11288	K07566|1|1e-33|142|vcn:VOLCADRAFT_56845|tRNA threonylcarbamoyladenosine biosynthesis protein	-	GO:0003723//RNA binding	-		-
7203525	5	0	10.47	0.001	-13.35397382	0.0458808	PHATRDRAFT_14856	K06182|1|8e-08|54.3|olu:OSTLU_10376|23S rRNA pseudouridine2604 synthase [EC:5.4.99.21]	-	GO:0016866//intramolecular transferase activity;GO:0003676//nucleic acid binding	GO:0009451//RNA modification		GO:0009451//RNA modification
7200693	12.64	0	10.3	0.001	-13.33035672	0.000561044	PHATRDRAFT_35176	-	-	-	-		-
7200184	7.37	0	5.74	0.001	-12.48683502	0.01303658	PHATRDRAFT_34724	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202507	9	0	5.31	0.001	-12.37449615	0.00370422	PHATRDRAFT_47347	-	-	-	-		-
7199273	6	0	5.29	0.001	-12.36905201	0.0244566	PHATRDRAFT_24119	-	-	-	-		-
7197206	5.66	0	5.03	0.001	-12.29634268	0.0458808	GapC4	K00134|1|2e-126|449|gmx:100810217|glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	-	GO:0016620//oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses;GO:0000166//nucleotide binding	GO:0044710;GO:0006007//glucose catabolic process		GO:0044710;GO:0006007//glucose catabolic process
7201059	6	0	4.74	0.001	-12.21067134	0.0244566	PHATRDRAFT_35856	-	-	-	-		-
7201140	6	0	4.64	0.001	-12.17990909	0.0244566	PHATRDRAFT_45928	-	-	-	-		-
7200556	5	0	4.36	0.001	-12.09011242	0.0458808	PHATRDRAFT_45451	-	-	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	GO:0008152//metabolic process		GO:0008152//metabolic process
7199452	5	0	4.3	0.001	-12.07012094	0.0458808	PHATRDRAFT_41620	-	-	-	-		-
7199782	6.29	0	2.18	0.001	-11.09011242	0.0244566	PHATRDRAFT_34367	-	-	GO:0043169//cation binding	-		-
7196962	11	1	11.37	1.18	-3.26837349	0.00695024	PHATRDRAFT_8828	K00868|1|3e-73|273|mtr:MTR_5g079730|pyridoxine kinase [EC:2.7.1.35]	-	GO:0016301//kinase activity	GO:0042823//pyridoxal phosphate biosynthetic process		GO:0042823//pyridoxal phosphate biosynthetic process
7196781	11	1	11.05	1.15	-3.264340603	0.00695024	PHATRDRAFT_32071	-	-	-	-		-
7203168	10	1	13.08	1.5	-3.124328135	0.01211664	PHATRDRAFT_38235	-	-	-	-		-
7201027	10	1	4.16	0.48	-3.115477217	0.01211664	PHATRDRAFT_20335	K12818|1|4e-123|440|cre:CHLREDRAFT_127996|ATP-dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13];K12813|2|1e-122|439|ppp:PHYPADRAFT_180557|pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 [EC:3.6.4.13]	-	GO:0042623//ATPase activity, coupled;GO:0032550	-		-
7202658	9	1	7.71	0.98	-2.975877206	0.0210012	PHATRDRAFT_37859	-	-	-	-		-
7201640	9	1	9.43	1.2	-2.974223365	0.0210012	PHATRDRAFT_46380	-	-	-	-		-
7197114	9	1	10.83	1.38	-2.972293071	0.0210012	PHATRDRAFT_43368	K01304|1|9e-19|92.0|vcn:VOLCADRAFT_62493|pyroglutamyl-peptidase [EC:3.4.19.3]	-	-	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7203946	9	1	6.58	0.84	-2.969626351	0.0210012	PHATR_33111	-	-	-	-		-

7200353	9	1	39.22	5.04	-2.960093897	0.0210012	PHATRDRAFT_7426	K05658|1|2e-14|75.5|vcn:VOLCADRAFT_103054|ATP-binding cassette, subfamily B (MDR/TAP), member 1;K12741|4|4e-09|57.8|zma:100382538|heterogeneous nuclear ribonucleoprotein A1/A3	-	GO:0097159//organic cyclic compound binding;GO:0036094//small molecule binding	-		-
7205042	17	2	11.33	1.53	-2.888544303	0.001127354	PHATRDRAFT_bd79	K03363|1|2e-121|434|ppp:PHYPADRAFT_130843|cell division cycle 20, cofactor of APC complex	-	-	-		-
7201443	8	1	10.81	1.55	-2.802026402	0.0361534	PHATRDRAFT_5702	K06927|1|1e-31|134|olu:OSTLU_6853|	-	-	-		-
7195004	8	1	12.53	1.8	-2.799317603	0.0361534	PHATRDRAFT_15393	K03809|1|1e-52|204|osa:4327039|Trp repressor binding protein	-	GO:0032553;GO:0003824//catalytic activity	GO:0044710;GO:0006351//transcription, DNA-templated		GO:0044710;GO:0006351//transcription, DNA-templated
7200057	15.07	1.97	21.81	3.28	-2.73322205	0.000719854	PHATRDRAFT_34630	-	-	-	-		-
7198935	15	2	21.6	3.3	-2.710493383	0.00323974	PHATRDRAFT_41026	-	-	-	-		-
7195339	22.55	3.36	6.93	1.18	-2.554068493	0.00031807	PHATRDRAFT_49118	-	-	GO:0097159//organic cyclic compound binding;GO:0016298//lipase activity	GO:0044238		GO:0044238
7204302	20	3	9.2	1.58	-2.541709303	0.000883142	PHATR_33218	-	GO:0031224//intrinsic component of membrane	-	GO:0044763		GO:0044763
7196889	13	2	8.41	1.48	-2.506508625	0.0091011	PHATRDRAFT_43117	-	-	GO:0003676//nucleic acid binding	GO:0006281//DNA repair		GO:0006281//DNA repair
7202991	12	2	39.65	7.62	-2.379457963	0.01509904	PHATRDRAFT_14535	K02895|1|3e-12|68.2|ppp:PHYPADRAFT_36942|large subunit ribosomal protein L24	GO:0005840//ribosome	GO:0005198//structural molecule activity	GO:0010467//gene expression		GO:0010467//gene expression
7202405	17	3	10.61	2.14	-2.309741955	0.0039299	PHATRDRAFT_47350	-	-	-	-		-
7203494	17	3	8.41	1.7	-2.306571054	0.0039299	PHATRDRAFT_38545	-	-	-	-		-
7202509	11	2	11.18	2.33	-2.262518328	0.0248508	PHATRDRAFT_21538	K14769|1|6e-51|199|olu:OSTLU_32092|U3 small nucleolar RNA-associated protein 11	GO:0030684//preribosome	-	GO:0042254//ribosome biogenesis		GO:0042254//ribosome biogenesis
7198810	11	2	20.62	4.3	-2.261635768	0.0248508	PHATRDRAFT_16545	K15437|1|7e-35|144|aly:ARALYDRAFT_483125|aminoacyl tRNA synthase complex-interacting multifunctional protein 1;K15439|5|1e-32|137|vcn:VOLCADRAFT_121172|eukaryotic translation elongation factor 1 epsilon-1	-	GO:0003723//RNA binding;GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds	-		-
7194693	16	3	15.21	3.27	-2.217657612	0.00638492	PHATRDRAFT_38977	-	-	-	-		-
7199525	46	9	36.15	8.09	-2.159784039	2.90E-06	PHATRDRAFT_45011	K11982|1|8e-07|53.1|bdi:100833984|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19];K10601|2|1e-06|52.4|zma:100217233|E3 ubiquitin-protein ligase synoviolin [EC:6.3.2.19];K05283|4|7e-06|50.1|aly:ARALYDRAFT_354960|phosphatidylinositol glycan, class W [EC:2.3.-.-]	-	GO:0046914//transition metal ion binding	-		-
7201238	20	4	18.46	4.23	-2.125672985	0.00273066	ELO6b_2	K10244|1|3e-24|110|ppp:PHYPADRAFT_195959|elongation of very long chain fatty acids protein 5 [EC:2.3.1.-];K10249|2|3e-19|94.4|ota:Ot09g02550|elongation of very long chain fatty acids protein 4;K10247|4|2e-07|55.1|pop:POPTR_593429|elongation of very long chain fatty acids protein 1	GO:0031224//intrinsic component of membrane	-	-		-
7204165	15	3	24.16	5.54	-2.124662573	0.01029972	PHATR_33267	-	-	GO:0003676//nucleic acid binding	-		-
7203918	10	2	8.46	1.94	-2.124601011	0.040532	PHATR_44188	-	-	-	-		-
7201721	10	2	26.11	6.01	-2.119165562	0.040532	PHATRDRAFT_36578	-	-	-	-		-
7204557	10	2	27.1	6.24	-2.118674917	0.040532	PHATR_13534	-	-	-	-		-

7196086	8	1.73	2.2	0.54	-2.026472211	0.0361534	PHATRDRAFT_42537	-	-	GO:0060089;GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0097159//organic cyclic compound binding	GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication		GO:0006259//DNA metabolic process;GO:0044710;GO:0007154//cell communication
7194715	18	4	15.72	4	-1.974529312	0.00687924	PHATRDRAFT_54920	-	-	-	-		-
7200375	13	3	7.2	1.9	-1.921997488	0.0261528	PHATRDRAFT_51897	K14788|1|5e-98|356|vcn:VOLCADRAFT_118613|ribosome biogenesis protein ENP2	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7202387	13	3	7.31	1.93	-1.921270559	0.0261528	PHATRDRAFT_47315	-	-	-	-		-
7204316	13	3	29.38	7.79	-1.915139162	0.0261528	PHATR_5508	K13102|1|3e-46|181|rcu:RCOM_1086480|DNA/RNA-binding protein KIN17	GO:0044464	GO:0046914//transition metal ion binding	GO:0007010//cytoskeleton organization		GO:0007010//cytoskeleton organization
7201868	24	6	11.89	3.4	-1.806142064	0.00299582	PHATRDRAFT_46595	K04710|1|1e-12|73.6|cre:CHLREDRAFT_105088|ceramide synthetase [EC:2.3.1.24]	GO:0031224//intrinsic component of membrane	-	-		-
7200838	12	3	12.01	3.44	-1.803755681	0.0410902	PHATRDRAFT_12269	K06125|1|1e-87|320|olu:OSTLU_43450|4-hydroxybenzoate hexaprenyltransferase [EC:2.5.1.-]	GO:0031224//intrinsic component of membrane	GO:0016765//transferase activity, transferring alkyl or aryl (other than methyl) groups	GO:0006743//ubiquinone metabolic process		GO:0006743//ubiquinone metabolic process
7195281	5243	1362	1528.48	453.75	-1.752128127	0	FRE5	K13447|1|4e-25|115|vvi:100262614|respiratory burst oxidase [EC:1.6.3.-1.11.1.-]	GO:0031224//intrinsic component of membrane	GO:0003824//catalytic activity	GO:0044710		GO:0044710
7198176	19	5	17.32	5.22	-1.730317218	0.0108228	PHATRDRAFT_40467	-	-	-	-		-
7204188	19	5	31.8	9.6	-1.727920455	0.0108228	PHATR_43971	-	-	-	-		-
7195157	15	4	10.09	3.08	-1.711923918	0.0259588	PHATRDRAFT_48871	-	-	-	-		-
7199595	15	4	27.23	8.33	-1.708808582	0.0259588	PHATRDRAFT_34433	-	-	-	-		-
7202667	22	6	16.25	5.07	-1.680382066	0.00697722	PHATRDRAFT_47617	K06167|1|2e-34|145|ath:AT4G03610|PhnP protein	-	GO:0003824//catalytic activity	-		-
7195859	18	5	9.38	2.98	-1.654275592	0.01649378	PHATRDRAFT_49528	-	-	-	-		-
7198783	14	4	4.78	1.56	-1.615464589	0.0396764	PHATRDRAFT_50006	K05941|1|6e-12|71.6|aly:ARALYDRAFT_333720|glutathione gamma-glutamylcysteinyltransferase [EC:2.3.2.15]	-	GO:0043169//cation binding;GO:0016755	GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process		GO:0010035//response to inorganic substance;GO:0043043//peptide biosynthetic process
7200203	14	4	10.38	3.39	-1.614449265	0.0396764	PHATRDRAFT_45150	-	-	-	-		-
7196748	14	4	18.57	6.08	-1.610830586	0.0396764	PHATRDRAFT_8763	K03648|1|8e-47|184|zma:100284406|uracil-DNA glycosylase [EC:3.2.2.27]	-	GO:0019104//DNA N-glycosylase activity	GO:0006281//DNA repair		GO:0006281//DNA repair
7200178	14	4	18.66	6.11	-1.610704701	0.0396764	PHATRDRAFT_34708	-	-	-	-		-
7195683	21	6	35.01	11.47	-1.60990167	0.01053224	PHATRDRAFT_39869	-	-	-	-		-
7202778	14	4	25.41	8.33	-1.609007975	0.0396764	PHATRDRAFT_52248	K01231|1|4e-49|191|sbi:SORBI_10g008770|alpha-mannosidase II [EC:3.2.1.114]	GO:0043231//intracellular membrane-bounded organelle	GO:0015923//mannosidase activity	GO:0006486//protein glycosylation		GO:0006486//protein glycosylation
7198423	34	10	12.12	4.07	-1.574288999	0.00123081	PHATRDRAFT_23444	K06207|1|0.0|666|bdi:100827491|GTP-binding protein	GO:0009536//plastid	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7194843	17	5	14.56	4.9	-1.571156701	0.0249162	PHATRDRAFT_39159	-	-	-	-		-
7196263	20	6	22.46	7.72	-1.540685175	0.01577234	PHATRDRAFT_31578	-	-	-	-		-
7194832	20	6	26.9	9.25	-1.540080902	0.01577234	PHATRDRAFT_48626	-	-	-	-		-
7200519	13	3.99	32.75	11.55	-1.503602055	0.0261528	PHATRDRAFT_12088	K03773|1|1e-40|162|olu:OSTLU_30671|FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8];K09571|4|2e-20|95.5|gmx:100810243|FK506-binding protein 4/5 [EC:5.2.1.8]	-	GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification
7197667	29	9	13.28	4.71	-1.495456182	0.00413348	PHATRDRAFT_44426	K12735|1|1e-62|239|cre:CHLREDRAFT_48580|peptidyl-prolyl cis-trans isomerase-like 4 [EC:5.2.1.8]	-	GO:0036094//small molecule binding;GO:0097159//organic cyclic compound binding;GO:0016859//cis-trans isomerase activity	GO:0018208//peptidyl-proline modification		GO:0018208//peptidyl-proline modification

7204498	16	5	7.57	2.7	-1.487333893	0.0372816	MCM7	K02210|1|8e-151|532|gmx:100802903|minichromosome maintenance protein 7 (cell division control protein 47)	GO:0043234//protein complex;GO:0043231//intracellular membrane-bounded organelle	GO:0004386//helicase activity;GO:0003676//nucleic acid binding;GO:0032550	GO:0032392//DNA geometric change		GO:0032392//DNA geometric change
7202772	16	5	18.78	6.72	-1.482663925	0.0372816	PHATRDRAFT_37769	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7196340	16	5	18.5	6.62	-1.482622149	0.0372816	PHATRDRAFT_31740	-	-	-	-		-
7201349	16	5	13.19	4.72	-1.4825858	0.0372816	PHATRDRAFT_46122	K12179|1|1e-14|79.3|smo:SELMODRAFT_230963|COP9 signalosome complex subunit 6	-	-	-		-
7196156	16	5	14.22	5.09	-1.482183904	0.0372816	APC3	K03350|1|1e-90|331|smo:SELMODRAFT_409868|anaphase-promoting complex subunit 3	-	-	-		-
7205076	16	5	21.35	7.65	-1.480704417	0.0372816	TRD5	-	GO:0031224//intrinsic component of membrane	GO:0022857//transmembrane transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7202291	16	5	26.67	9.56	-1.480135302	0.0372816	PHATRDRAFT_37751	-	-	GO:0016881//acid-amino acid ligase activity	GO:0036211		GO:0036211
7196124	19	6	13.79	4.98	-1.469404809	0.0234182	PHATRDRAFT_42732	K01974|1|2e-54|211|vcn:VOLCADRAFT_80268|RNA 3'-terminal phosphate cyclase [EC:6.5.1.4];K11108|4|4e-26|117|ppp:PHYPADRAFT_106207|RNA 3'-terminal phosphate cyclase-like protein	-	GO:0009975//cyclase activity	GO:0010467//gene expression		GO:0010467//gene expression
7202171	22	7	17.05	6.21	-1.457106566	0.01482792	PHATRDRAFT_47096	K15637|1|2e-20|98.6|ota:Ot11g03350|serine/threonine-protein phosphatase PGAM5 [EC:3.1.3.16]	-	-	-		-
7198871	25	8	31.27	11.47	-1.446913828	0.009447	PHATRDRAFT_41079	-	-	-	-		-
7197383	31	10	40.18	14.85	-1.436014633	0.00388848	PHATRDRAFT_43323	-	-	-	-		-
7197826	34	11	15.37	5.69	-1.433616607	0.00250826	PHATRDRAFT_44347	-	-	-	-		-
7201883	14	4.63	8.8	3.32	-1.406320282	0.0396764	PHATRDRAFT_36628	-	-	-	-		-
7197449	21	7	8.38	3.19	-1.39339382	0.0217052	PHATRDRAFT_43679	-	-	-	-		-
7195930	18	6	16.56	6.32	-1.389706209	0.0344518	PHATRDRAFT_15960	K15452|1|4e-40|163|olu:OSTLU_3606|tRNA pseudouridine synthase 2 [EC:5.4.99.-]	-	GO:0016866//intramolecular transferase activity;GO:0003676//nucleic acid binding	GO:0009451//RNA modification		GO:0009451//RNA modification
7201666	30	10	29.71	11.34	-1.389527965	0.00563604	PHATRDRAFT_1196	K13420|1|4e-47|186|sbi:SORBI_06g028760|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7195287	65	22	19.85	7.68	-1.369960791	4.67E-05	PHATRDRAFT_54983	K00360|1|0.0|782|ppp:PHYPADRAFT_184973|nitrate reductase (NADH) [EC:1.7.1.1];K00387|4|1e-95|349|olu:OSTLU_3554|sulfite oxidase [EC:1.8.3.1]	-	GO:0046906//tetrapyrrole binding;GO:0046914//transition metal ion binding;GO:0016661;GO:0000166//nucleotide binding;GO:0050662//coenzyme binding	GO:0042126//nitrate metabolic process		GO:0042126//nitrate metabolic process
7199168	72.75	25.26	28.23	11.2	-1.333730397	2.65E-05	PHATRDRAFT_50412	-	-	-	-		-
7203642	43	15	18.12	7.23	-1.325515403	0.001302412	PHATRDRAFT_48378	-	GO:0044424	-	-		-
7197675	20	7	17.45	6.99	-1.319862676	0.0314926	PHATRDRAFT_33867	-	-	-	-		-
7195982	31	11	64.93	26.46	-1.295072148	0.00744526	PHATRDRAFT_9199	K02953|1|3e-67|251|smo:SELMODRAFT_171673|small subunit ribosomal protein S13e	GO:0005840//ribosome;GO:0030312;GO:0031981//nuclear lumen;GO:0009536//plastid	GO:0005198//structural molecule activity	GO:0009887//organ morphogenesis;GO:0010467//gene expression;GO:0000904//cell morphogenesis involved in differentiation		GO:0009887//organ morphogenesis;GO:0010467//gene expression;GO:0000904//cell morphogenesis involved in differentiation
7199142	39	14	15.2	6.24	-1.284453389	0.00284192	PHATRDRAFT_41302	-	-	-	-		-
7196655	41	15	17.36	7.26	-1.257725494	0.00259786	PHATRDRAFT_42451	-	-	-	-		-
7201032	27	10	23.13	9.8	-1.238911612	0.01646778	PHATRDRAFT_35809	-	-	-	-		-
7204765	26.55	9.99	14.32	6.16	-1.217029237	0.0126831	PHATR_37020	-	-	-	-		-
7201452	27.12	10.24	30.69	13.28	-1.208513499	0.01646778	PHATRDRAFT_36008	-	-	-	-		-
7202592	37	14	43.07	18.67	-1.205961396	0.00560632	PHATRDRAFT_14054	K06889|1|8e-07|52.4|rcu:RCOM_1047030|	-	-	-		-
7202896	21	8	15.85	6.91	-1.197725225	0.0406176	PHATRDRAFT_3425	K00566|1|4e-54|210|olu:OSTLU_43910|tRNA-specific 2-thiouridylase [EC:2.8.1.-]	GO:0044424	GO:0016782//transferase activity, transferring sulfur-containing groups	GO:0006399//tRNA metabolic process		GO:0006399//tRNA metabolic process

7199453	39	15	19.15	8.42	-1.185452254	0.0050704	PHATRDRAFT_41624	-	-	GO:0016298//lipase activity	GO:0044238		GO:0044238
7201805	39	15	26.9	11.83	-1.185156099	0.0050704	PHATRDRAFT_46456	-	-	-	-		-
7200761	1000	385	1156.24	509.93	-1.181069767	5.49E-47	PHATRDRAFT_20167	K11098|1|1e-25|115|vcn:VOLCADRAFT_109863|small nuclear ribonucleoprotein F	GO:0044444//cytoplasmic part;GO:0030529//ribonucleoprotein complex;GO:0031981//nuclear lumen	GO:0097159//organic cyclic compound binding	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7198748	44	17	30.84	13.63	-1.178017203	0.00298644	PHATRDRAFT_40919	-	-	GO:0003824//catalytic activity	-		-
7199129	44	17	40.31	17.83	-1.17683108	0.00298644	PHATRDRAFT_50293	-	-	-	-		-
7197081	90	35	62.07	27.61	-1.168705258	2.14E-05	PHATRDRAFT_18036	K09517|1|1e-48|192|gmx:100807885|DnaJ homolog subfamily B member 11	-	GO:0005515//protein binding;GO:0043169//cation binding	GO:0044267//cellular protein metabolic process		GO:0044267//cellular protein metabolic process
7204394	41	16	38.47	17.19	-1.162164285	0.0045761	PHATR_33327	-	-	-	-		-
7198342	23	9	17.59	7.88	-1.158487948	0.036321	PHATRDRAFT_49755	-	-	-	-		-
7198643	23	9	25.93	11.62	-1.158012137	0.036321	PHATRDRAFT_40786	-	-	-	-		-
7197944	84	33	37.08	16.65	-1.155119067	4.84E-05	PHATRDRAFT_44266	-	-	-	-		-
7200504	28	11	15.02	6.75	-1.153925406	0.0207974	PHATRDRAFT_45412	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-
7198854	43	17	21.61	9.77	-1.145268605	0.00412274	PHATRDRAFT_50155	-	-	GO:0004553//hydrolase activity, hydrolyzing O-glycosyl compounds;GO:0097367//carbohydrate derivative binding	GO:0044238;GO:0006022		GO:0044238;GO:0006022
7199442	43	17	23.84	10.78	-1.145027058	0.00412274	PHATRDRAFT_50605	-	-	GO:0016740//transferase activity	-		-
7201410	35	14	22.92	10.49	-1.127592366	0.01079522	PHATRDRAFT_46046	-	-	-	-		-
7197506	25	10	26.81	12.28	-1.126460659	0.0323998	PHATRDRAFT_32914	K13412|1|4e-11|67.0|ota:Ot03g03430|calcium-dependent protein kinase [EC:2.7.11.1]	-	GO:0016301//kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198103	47	19	57.28	26.53	-1.110406817	0.0033324	PHATRDRAFT_44606	-	GO:0005743//mitochondrial inner membrane	-	GO:0006626//protein targeting to mitochondrion		GO:0006626//protein targeting to mitochondrion
7195571	37	15	43.55	20.22	-1.106889722	0.00966752	PHATRDRAFT_49282	-	-	-	-		-
7196185	32	13	36.36	16.92	-1.103622631	0.01662606	PHATRDRAFT_42929	-	-	-	-		-
7194706	27	11	49.01	22.91	-1.097098688	0.028852	PHATRDRAFT_15134	-	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7203646	39	16	30.37	14.26	-1.090672927	0.00864744	PHATRDRAFT_48383	-	-	-	-		-
7201461	34	14	13.92	6.55	-1.087592399	0.01483544	PHATRDRAFT_27757	K00366|1|6e-122|436|gmx:100775519|ferredoxin-nitrite reductase [EC:1.7.7.1]	-	GO:0046906//tetrapyrrole binding;GO:0051540;GO:0016664	GO:0044710		GO:0044710
7200514	114	47	66.83	31.51	-1.08468612	6.41E-06	PHATRDRAFT_45701	-	-	GO:0043168//anion binding;GO:0003824//catalytic activity	-		-
7200543	29	12	23.11	10.94	-1.078904522	0.0256608	PHATRDRAFT_35135	-	-	-	-		-
7203266	809	337	436.3	207.84	-1.069847138	7.11E-33	PHATRDRAFT_48096	-	-	-	-		-
7196555	43	18	39.48	18.92	-1.061209901	0.00690038	PHATRDRAFT_42930	K06911|1|5e-39|159|ppp:PHYPADRAFT_130782|	-	-	-		-
7202320	38	16	18.22	8.77	-1.054874211	0.01178094	PHATRDRAFT_47282	-	GO:0030176//integral component of endoplasmic reticulum membrane	-	-		-
7202618	26	11.05	14.02	6.82	-1.039642705	0.0397006	PHATRDRAFT_47240	-	-	-	-		-
7198628	61	26	54.32	26.5	-1.03549112	0.001540606	PHATRDRAFT_49930	-	-	-	-		-
7200206	28	12	13.25	6.49	-1.029701976	0.0351092	PHATRDRAFT_26775	K12585|1|1e-81|302|rcu:RCOM_0875030|exosome complex exonuclease DIS3/RRP44 [EC:3.1.13.-]	-	GO:0003676//nucleic acid binding;GO:0004518//nuclease activity	-		-
7204678	35	15	18.91	9.27	-1.028508119	0.01797402	PHATR_46821	-	-	-	-		-
7204067	28	12	13.36	6.55	-1.028353196	0.0351092	PHATR_10282	K11273|1|1e-98|358|olu:OSTLU_37740|chromosome transmission fidelity protein 1 [EC:3.6.4.13]	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding;GO:0003678//DNA helicase activity;GO:0042623//ATPase activity, coupled;GO:0032550	GO:0032392//DNA geometric change		GO:0032392//DNA geometric change
7194976	30	13	22.15	10.98	-1.012428644	0.0310418	PHATRDRAFT_48903	-	-	-	-		-
7203297	39	17	25.21	12.57	-1.004011468	0.01414962	PHATRDRAFT_48149	-	-	-	-		-

7197552	39	17	26.81	13.37	-1.003771754	0.01414962	PHATRDRAFT_10073	K15849|1|2e-31|135|pop:POPTR_760138|bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase [EC:2.6.1.1 2.6.1.78 2.6.1.79]	-	GO:0043168//anion binding;GO:0070548	GO:0008152//metabolic process		GO:0008152//metabolic process
7204096	62	27	84.59	42.22	-1.002560543	0.001839032	PHATR_44176	K01519|1|1e-64|244|cre:CHLREDRAFT_179025|inosine triphosphate pyrophosphatase [EC:3.6.1.19]	-	GO:0005488//binding;GO:0016787//hydrolase activity	-		-
7201604	136	60	65.99	33.29	-0.987158547	4.93E-06	PHATRDRAFT 46530	-	-	-	-		-
7199191	4743	2103	3706.95	1880.84	-0.97885553	9.89E-160	PHATRDRAFT 41316	-	-	-	-		-
7201848	36	16	18.01	9.15	-0.976954533	0.0214522	PHATRDRAFT 46567	-	-	-	-		-
7198636	1275	567	337.76	171.64	-0.976612678	5.73E-44	PHATRDRAFT_23629	K05853|1|4e-98|358|olu:OSTLU_14777|Ca2+ transporting ATPase, sarcoplasmic/endoplasmic reticulum [EC:3.6.3.8];K01537|2|7e-98|357|sbi:SORBI_01g038990|Ca2+-transporting ATPase [EC:3.6.3.8]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0019829//cation-transporting ATPase activity	GO:0006811//ion transport		GO:0006811//ion transport
7198347	27	12	22.43	11.41	-0.975130829	0.0476462	PHATRDRAFT_49764	K15106|1|5e-37|153|smo:SELMODRAFT_233107|solute carrier family 25 (mitochondrial carrier), member 14/30;K15104|2|6e-33|139|bdi:100827424|solute carrier family 25 (mitochondrial oxoglutarate transporter), member 11;K15112|3|1e-32|138|ppp:PHYPADRAFT_98857|solute carrier family 25 (mitochondrial uncoupling protein), member 27	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization
7200332	139	62	66.84	34.09	-0.971363134	5.19E-06	PHATRDRAFT 45149	-	-	-	-		-
7196953	125.57	56.04	58.12	29.66	-0.970516105	1.74E-05	PHATRDRAFT 43232	-	-	-	-		-
7203856	27	12	55.74	28.45	-0.97028435	0.0476462	PHATR 33436	-	-	-	-		-
7202902	47	21	20.96	10.71	-0.968680237	0.00875804	PHATRDRAFT 47724	-	-	-	-		-
7203970	49	22	24.47	12.56	-0.962177637	0.0077683	PHATR_18469	K08150|1|2e-40|165|vvi:100268023|MFS transporter, SP family, solute carrier family 2 (myo-inositol transporter), member 13	GO:0031224//intrinsic component of membrane	GO:0022857//transmembrane transporter activity	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7195190	40	18	16.26	8.36	-0.95975241	0.0167769	PHATRDRAFT_48717	K09651|1|3e-09|62.4|gmx:100794217|rhomboid domain-containing protein 1 [EC:3.4.21.-]	GO:0031224//intrinsic component of membrane	GO:0004175//endopeptidase activity	-		-
7197819	122	55	61.6	31.76	-0.955719438	2.55E-05	PHATRDRAFT_44339	K05531|1|2e-26|119|bdi:100846699|mannan polymerase II complex MNN10 subunit [EC:2.4.1.-];K08238|2|4e-08|58.2|osa:4329539|xyloglucan 6-xylosyltransferase [EC:2.4.2.39]	GO:0031224//intrinsic component of membrane	GO:0016757//transferase activity, transferring glycosyl groups	-		-
7199176	34.98	15.79	14.93	7.7	-0.955283815	0.0242626	PHATRDRAFT_50348	K00995|1|3e-23|108|cme:CMN196C|CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [EC:2.7.8.5];K08744|2|2e-21|102|pop:POPTR_856644|cardiolipin synthase [EC:2.7.8.-]	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006644//phospholipid metabolic process		GO:0006644//phospholipid metabolic process
7204965	51	23	34.21	17.65	-0.954749921	0.0068908	PHATRDRAFT bd1759	-	-	-	-		-
7198574	31	14	25.73	13.3	-0.952025211	0.0369196	PHATRDRAFT_49844	-	-	GO:0036094//small molecule binding	-		-
7195081	1480.03	669.12	1073.44	555.26	-0.951006178	8.10E-49	PHATRDRAFT 48827	-	-	-	-		-

7199241	106	48	31.27	16.18	-0.950567611	9.62E-05	PHATRDRAFT_50519	K00870|1|9e-15|81.3|cme:CMD015C|protein kinase [EC:2.7.1.37];K13430|2|9e-15|81.3|osa:4329463|serine/threonine-protein kinase PBS1 [EC:2.7.11.1];K00924|3|2e-14|80.1|aly:ARALYDRAFT_475717|[EC:2.7.1.-];K04424|4|2e-14|80.1|olu:OSTLU_6189|sterile alpha motif and leucine zipper containing kinase AZK [EC:2.7.11.25];K13414|5|2e-14|79.7|vvi:100241228|mitogen-activated protein kinase kinase kinase 1, plant [EC:2.7.11.25]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198821	33	15	15.38	7.99	-0.944788095	0.0325208	PHATRDRAFT_50103	K00620|1|1e-33|143|ota:Ot08g02650|glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]	-	-	-		-
7199554	41.7	18.94	22.98	11.94	-0.944575961	0.01255134	PHATRDRAFT_44836	-	-	-	-		-
7197181	139	63	209.68	108.97	-0.94425825	7.93E-06	PHATRDRAFT_43479	-	-	-	-		-
7202132	33	15	14.95	7.77	-0.944158981	0.0325208	PHATRDRAFT_47058	K14844|1|1e-31|136|smo:SELMODRAFT_74812|pumilio homology domain family member 6	-	GO:0003676//nucleic acid binding	-		-
7204230	44	20	25.74	13.38	-0.943933938	0.01312986	PHATR_44047	K11806|1|1e-103|375|pop:POPTR_836650|WD repeat and SOF domain-containing protein 1	-	-	-		-
7201712	33	15	15.25	7.93	-0.943416472	0.0325208	PHATRDRAFT_46577	-	-	GO:0003676//nucleic acid binding;GO:0016866//intramolecular transferase activity	GO:0009451//RNA modification		GO:0009451//RNA modification
7194713	323	147	89.12	46.35	-0.943179894	1.11E-11	PHATRDRAFT_48538	-	-	-	-		-
7195806	44	20	37.13	19.32	-0.942490221	0.01312986	PHATRDRAFT_40147	-	-	-	-		-
7200506	519	241	221.78	117.73	-0.913647275	4.74E-17	PHATRDRAFT_45416	K03363|1|5e-27|121|ath:AT4G33270|cell division cycle 20, cofactor of APC complex	-	-	-		-
7197596	84	39	64.94	34.5	-0.912511023	0.000789544	PHATRDRAFT_43293	-	-	-	-		-
7202987	43	20	31.7	16.87	-0.910022867	0.01735816	PHATRDRAFT_47857	-	GO:0031224//intrinsic component of membrane	GO:0016782//transferase activity, transferring sulfur-containing groups	GO:0044723		GO:0044723
7196977	90	42	22.62	12.06	-0.907369022	0.00055557	PHATRDRAFT_43268	-	-	-	-		-
7195251	30	14	20.43	10.9	-0.906361069	0.0492864	PHATRDRAFT_48977	K04708|1|9e-29|126|smo:SELMODRAFT_79314|3-dehydrosphinganine reductase [EC:1.1.1.102]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7198184	32	15	15.89	8.51	-0.900888088	0.0432708	PHATRDRAFT_49556	-	-	GO:0036094//small molecule binding	-		-
7199055	64	30	33.63	18.02	-0.900149768	0.00390232	PHATRDRAFT_31068	K06883|1|2e-82|304|rcu:RCOM_1775060|	-	GO:0032550;GO:0016462//pyrophosphatase activity	-		-
7196708	32	15	23.31	12.5	-0.89902091	0.0432708	E2F1	K04682|1|4e-16|84.3|smo:SELMODRAFT_445661|E2F transcription factor 4/5	GO:0043231//intracellular membrane-bounded organelle;GO:0043234//protein complex	GO:0003676//nucleic acid binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7198338	73.54	34.54	48.05	25.82	-0.89604743	0.001855434	PHATRDRAFT_49750	-	-	-	-		-
7200520	32.01	15	60.01	32.29	-0.894115489	0.0432708	PHATRDRAFT_11901	K12197|1|5e-35|144|olu:OSTLU_29213|charged multivesicular body protein 1	-	-	GO:0009790//embryo development;GO:0045184//establishment of protein localization		GO:0009790//embryo development;GO:0045184//establishment of protein localization
7195036	34	16	52.11	28.12	-0.88996366	0.038019	PHATRDRAFT_39303	-	-	-	-		-
7200850	36	17	27.51	14.86	-0.888522024	0.033429	PHATRDRAFT_45981	-	-	-	-		-
7204001	91	43	50.41	27.24	-0.887983251	0.000640588	PHATR_44046	-	-	-	-		-
7204969	42.06	19.88	36.25	19.61	-0.88639146	0.01484034	PHATRDRAFT_bd383	K10592|1|3e-70|263|gmx:100802630|E3 ubiquitin-protein ligase HUWE1 [EC:6.3.2.19]	GO:0044464	GO:0019787//small conjugating protein ligase activity	GO:0032446//protein modification by small protein conjugation		GO:0032446//protein modification by small protein conjugation
7202732	95	45	87.23	47.3	-0.882984206	0.000506334	PHATRDRAFT_47747	-	-	-	-		-
7198200	76	36	90.31	49.01	-0.881809599	0.001901514	PHATRDRAFT_40322	-	-	-	-		-

7197086	42.9	20.33	51.4	27.91	-0.880986235	0.0228116	Lhcf3	K08907|1|7e-08|55.8|cre:CHLREDRAFT_184730|light-harvesting complex I chlorophyll a/b binding protein 1;K08915|2|8e-06|48.9|zma:542478|light-harvesting complex II chlorophyll a/b binding protein 4	GO:0009521;GO:0031224//intrinsic component of membrane;GO:0009534//chloroplast thylakoid	GO:0046906//tetrapyrrole binding	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7198807	38	18	66.31	36.04	-0.879627444	0.0294126	PHATRDRAFT_23706	K02155|1|3e-15|79.3|gmx:100779290|V-type H+-transporting ATPase 16kDa proteolipid subunit [EC:3.6.3.14]	GO:0033176//proton-transporting V-type ATPase complex;GO:0031224//intrinsic component of membrane	GO:0015077//monovalent inorganic cation transmembrane transporter activity	GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient		GO:0015988//energy coupled proton transmembrane transport, against electrochemical gradient
7198024	82	39	42.95	23.36	-0.878617857	0.001330224	PHATRDRAFT_44326	-	-	GO:0016740//transferase activity	-		-
7203141	67	32	62.05	33.93	-0.87086978	0.00398598	PHATRDRAFT_47957	-	-	-	-		-
7200741	69	33	35.45	19.39	-0.870472824	0.0035322	PHATRDRAFT_45560	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7196198	54	26	18.29	10.07	-0.860991392	0.01077106	PHATRDRAFT_42955	K09291|1|2e-08|59.7|bdi:100825730|nucleoprotein TPR;K10696|2|2e-08|59.7|rcu:RCOM_1455450|E3 ubiquitin-protein ligase BRE1 [EC:6.3.2.19];K06638|4|3e-07|55.8|smo:SELMODRAFT_439954|mitotic spindle assembly checkpoint protein MAD1;K10400|5|1e-06|53.9|osa:4352674|kinesin family member 15	GO:0043229//intracellular organelle	-	-		-
7204717	143	69	39.89	22	-0.8585236	3.09E-05	PHATR_46867	K12385|1|6e-29|128|aly:ARALYDRAFT_490595|Niemann-Pick C1 protein	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity	-		-
7198429	247	119	232.02	127.97	-0.858443531	3.84E-08	PHATRDRAFT_49735	-	-	GO:0003824//catalytic activity	-		-
7204878	143	69	50.6	27.91	-0.858355261	3.09E-05	PHATRDRAFT_bd1763	K11851|1|5e-16|85.1|rcu:RCOM_0132150|ubiquitin carboxyl-terminal hydrolase 30 [EC:3.1.2.15];K11844|2|1e-14|80.5|bdi:100834637|ubiquitin carboxyl-terminal hydrolase 16/45 [EC:3.1.2.15]	-	GO:0016682//oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor;GO:0016790//thiolester hydrolase activity	GO:0019941//modification-dependent protein catabolic process;GO:0044710		GO:0019941//modification-dependent protein catabolic process;GO:0044710
7200101	50	24	189.19	104.78	-0.852472467	0.01380778	PHATRDRAFT_7629	-	-	GO:0003824//catalytic activity	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7199434	202	97.99	113.15	62.77	-0.850089471	5.96E-07	PHATRDRAFT_50619	-	-	-	-		-
7195695	70	34	30.68	17.03	-0.849220048	0.00404304	FTHFS	K01938|1|0.0|738|gmx:100806844|formate--tetrahydrofolate ligase [EC:6.3.4.3]	-	GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0006760//folic acid-containing compound metabolic process		GO:0006760//folic acid-containing compound metabolic process
7197364	35	17	15.74	8.74	-0.848730356	0.0439206	PHATRDRAFT_43654	-	-	-	-		-
7196268	74	36	33.55	18.66	-0.84636378	0.00317342	PHATRDRAFT_42568	-	-	-	-		-
7203878	37	18	37.69	21	-0.843792467	0.038561	PHATR_33484	-	-	-	-		-
7204082	82	40	47.55	26.53	-0.841820666	0.00196032	PHATR_44153	-	-	-	-		-
7197279	57	28	60.29	33.92	-0.829782559	0.01087734	PHATRDRAFT_43766	K00876|1|9e-10|62.4|pop:POPTR_815577|uridine kinase [EC:2.7.1.48]	GO:0009536//plastid	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7204866	891	439	446.75	251.69	-0.827819832	4.20E-24	PHATRDRAFT_bd1645	K00434|1|1e-08|59.7|gmx:100170727|L-ascorbate peroxidase [EC:1.11.1.11]	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress

7204277	79	39	31.54	17.8	-0.825305419	0.00283444	PHATR_18473	K05657|1|2e-101|368|smo:SELMODRAFT_445846|ATP-binding cassette, subfamily B (MDR/TAP), member 10;K05658|2|4e-97|354|ppp:PHYPADRAFT_170613|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7204552	83	41	49.16	27.77	-0.823957739	0.00222722	PHATR_46805	-	-	-	-		-
7203399	70.86	35.17	40.62	23.06	-0.816797727	0.00589372	PHATRDRAFT_48278	-	-	GO:0016209//antioxidant activity;GO:0046906//tetrapyrrole binding	GO:0044710;GO:0006950//response to stress		GO:0044710;GO:0006950//response to stress
7201690	2208	1101	955.92	544.93	-0.810818968	2.65E-55	PHATRDRAFT_46547	-	-	-	-		-
7200529	110	55	50.62	28.94	-0.806642586	0.000534028	PHATRDRAFT_45404	K02065|1|7e-07|54.3|gmx:100789283|putative ABC transport system ATP-binding protein;K05658|3|8e-06|50.8|mtr:MTR_1g025560|ATP-binding cassette, subfamily B (MDR/TAP), member 1	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7196597	40	20	23.42	13.39	-0.806585115	0.0386686	NURF-55	K10752|1|2e-121|434|cre:CHLREDRAFT_131412|histone-binding protein RBBP4	GO:0032991//macromolecular complex;GO:0009536//plastid	GO:0005488//binding	GO:0009908//flower development;GO:0048827//phyllome development;GO:0009913//epidermal cell differentiation;GO:0031497//chromatin assembly;GO:0051726//regulation of cell cycle;GO:0009887//organ morphogenesis;GO:0048229//gametophyte development;GO:0040029//regulation of gene expression, epigenetic		GO:0009908//flower development;GO:0048827//phyllome development;GO:0009913//epidermal cell differentiation;GO:0031497//chromatin assembly;GO:0051726//regulation of cell cycle;GO:0009887//organ morphogenesis;GO:0048229//gametophyte development;GO:0040029//regulation of gene expression, epigenetic
7195451	40	20	17.94	10.26	-0.806149159	0.0386686	PHATRDRAFT_49097	-	-	-	-		-
7204921	209.5	106	80.02	46.28	-0.789971764	2.85E-06	PHATRDRAFT_bd1601	-	-	-	-		-
7204950	209.5	106	80.02	46.28	-0.789971764	2.85E-06	PHATRDRAFT_bd1249	-	-	-	-		-
7200753	44	22.26	66.02	38.3	-0.785558746	0.029879	PHATRDRAFT_27282	K03238|1|8e-45|177|olu:OSTLU_88846|translation initiation factor 2 subunit 2	-	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation
7202225	55	28	14.16	8.24	-0.781105023	0.0179123	PHATRDRAFT_54677	K02327|1|0.0|1032|sbi:SORBI_04g004200|DNA polymerase delta subunit 1 [EC:2.7.7.7]	-	GO:0003676//nucleic acid binding;GO:0036094//small molecule binding;GO:0034061	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203657	55	28	34.56	20.13	-0.779756045	0.0179123	PHATRDRAFT_38849	-	-	-	-		-
7196498	49	25	20.33	11.86	-0.777506205	0.0261688	PHATRDRAFT_42844	K15332|1|9e-43|173|smo:SELMODRAFT_440228|tRNA (uracil-5-)-methyltransferase	-	GO:0008168//methyltransferase activity	GO:0010467//gene expression;GO:0009451//RNA modification		GO:0010467//gene expression;GO:0009451//RNA modification
7201018	2070.97	1057.88	1650.22	964.66	-0.77456592	2.24E-48	PHATRDRAFT_45944	-	-	-	-		-
7197814	129	66	75.47	44.16	-0.773163102	0.000293928	PHATRDRAFT_44253	-	-	GO:0036094//small molecule binding	-		-
7194718	45	23	45.52	26.64	-0.772906475	0.0337924	cdc14	K06639|1|4e-75|279|smo:SELMODRAFT_91859|cell division cycle 14 [EC:3.1.3.48]	-	GO:0004721//phosphoprotein phosphatase activity	GO:0006470//protein dephosphorylation		GO:0006470//protein dephosphorylation
7200872	44.03	22.56	17.21	10.08	-0.771751459	0.029879	PHATRDRAFT_45715	-	GO:0044424	GO:0016876//ligase activity, forming aminoacyl-tRNA and related compounds;GO:0032550	GO:0006412//translation		GO:0006412//translation
7196027	43	22	43.34	25.39	-0.771438758	0.03844	PHATRDRAFT_42672	-	-	-	-		-
7201776	41	21	28.39	16.64	-0.770727416	0.0437602	PHATRDRAFT_46408	K06173|1|1e-39|162|cme:CMQ041C|tRNA pseudouridine38-40 synthase [EC:5.4.99.12]	-	GO:0016866//intramolecular transferase activity;GO:0003676//nucleic acid binding	GO:0006399//tRNA metabolic process;GO:0009451//RNA modification		GO:0006399//tRNA metabolic process;GO:0009451//RNA modification

7198460	76	39	23.53	13.8	-0.769833054	0.0058457	PHATRDRAFT_49793	K05349|1|7e-41|167|rcu:RCOM_1903090|beta-glucosidase [EC:3.2.1.21];K15920|4|1e-33|143|osa:4337166|beta-D-xylosidase 4 [EC:3.2.1.37]	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7202889	111	57	38.34	22.5	-0.768925336	0.000849886	PHATRDRAFT_47705	-	-	-	-		-
7197788	113	58	61.06	35.84	-0.768656952	0.000754934	PHATRDRAFT_44536	-	-	-	-		-
7196574	105	54	46.71	27.46	-0.76639982	0.001213628	PHATRDRAFT_43209	-	-	-	-		-
7202708	68	35	16.61	9.77	-0.765621606	0.00954246	PHATRDRAFT_47704	K11835|1|8e-84|310|pop:POPTR_798230|ubiquitin carboxyl-terminal hydrolase 4/11/15 [EC:3.1.2.15]	-	GO:0070011//peptidase activity, acting on L-amino acid peptides;GO:0016790//thiolester hydrolase activity;GO:0046914//transition metal ion binding	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7201053	832	430	295.73	174.7	-0.759400995	1.06E-19	PHATRDRAFT_45988	-	-	GO:0046914//transition metal ion binding;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7205020	209.7	108.38	98.4	58.14	-0.759127244	5.54E-06	PHATRDRAFT_bd1646	-	-	-	-		-
7198172	109	56	348.13	206.04	-0.756701698	0.000956914	PHATRDRAFT_7679	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7200136	139	72	76.51	45.32	-0.755500462	0.000228864	PHATRDRAFT_26862	K08679|1|1e-58|225|vvi:100247175|UDP-glucuronate 4-epimerase [EC:5.1.3.6]	-	GO:0036094//small molecule binding;GO:0016854//racemase and epimerase activity;GO:0048037//cofactor binding	GO:0044238		GO:0044238
7204756	52	27	29.71	17.64	-0.752098044	0.0258872	PHATR_46929	-	-	-	-		-
7200395	56	29	97.32	57.83	-0.750918218	0.0201166	PHATRDRAFT_12233	K00411|1|1e-63|239|ota:Ot13g03160|ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	GO:0043231//intracellular membrane-bounded organelle;GO:0044425//membrane part	GO:0043169//cation binding;GO:0016491//oxidoreductase activity;GO:0051536//iron-sulfur cluster binding;GO:0015078//hydrogen ion transmembrane transporter activity	GO:0044710;GO:0006091//generation of precursor metabolites and energy		GO:0044710;GO:0006091//generation of precursor metabolites and energy
7204108	75	39	56.45	33.59	-0.748941785	0.00738492	PHATR_44195	-	-	-	-		-
7198823	46	24	13.3	7.93	-0.746033475	0.0379528	XPF	K10848|1|4e-126|451|smo:SELMODRAFT_90549|DNA excision repair protein ERCC-4 [EC:3.1.-.-]	-	GO:0016788//hydrolase activity, acting on ester bonds;GO:0003676//nucleic acid binding	GO:0044260;GO:0050896//response to stimulus;GO:0090304		GO:0044260;GO:0050896//response to stimulus;GO:0090304
7198268	48	25	51.28	30.59	-0.745336155	0.0333876	PHATRDRAFT_40382	-	-	GO:0043168//anion binding;GO:0046914//transition metal ion binding	-		-
7201888	272	142	96.36	57.5	-0.744872438	3.41E-07	PHATRDRAFT_28056	K00549|1|1e-156|551|ppp:PHYPADRAFT_205352|5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]	-	GO:0046914//transition metal ion binding;GO:0008172	GO:0000097//sulfur amino acid biosynthetic process		GO:0000097//sulfur amino acid biosynthetic process
7194905	46	24	30.76	18.36	-0.744489445	0.0379528	PHATRDRAFT_48667	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7202665	84	44	43.03	25.77	-0.739650303	0.00506042	PHATRDRAFT_37873	-	-	-	-		-
7199497	42	22	39.28	23.55	-0.73806787	0.049147	PHATRDRAFT_34538	K03237|1|6e-84|308|vvi:100250061|translation initiation factor 2 subunit 1	GO:0043234//protein complex	GO:0008135//translation factor activity, nucleic acid binding	GO:0006412//translation		GO:0006412//translation

7199902	42	22	41.31	24.78	-0.737314873	0.049147	PHATRDRAFT_11273	K08243|1|4e-11|67.0|gmx:547911|6'-deoxychalcone synthase [EC:2.3.1.170];K14521|3|2e-09|61.6|vcn:VOLCADRAFT_98273|N-acetyltransferase 10 [EC:2.3.1.-];K00085|4|5e-07|53.5|ath:AT2G21260|aldose-6-phosphate reductase (NADPH2) [EC:1.1.1.200]	-	GO:0008106//alcohol dehydrogenase (NADP+) activity	GO:0044710		GO:0044710
7198434	78	41	45.79	27.53	-0.734027955	0.00728174	PHATRDRAFT_40517	K14209|1|2e-49|195|gmx:100791548|solute carrier family 36 (proton-coupled amino acid transporter)	GO:0031224//intrinsic component of membrane	-	-		-
7203947	146	77	83.47	50.35	-0.729265993	0.000247778	PHATR_43808	-	-	-	-		-
7204925	121.96	64.39	51.7	31.2	-0.728618251	0.000911468	PHATRDRAFT_bd1603	-	-	GO:0003824//catalytic activity	-		-
7198595	1201	634	740.03	446.83	-0.727857706	6.06E-26	PHATRDRAFT_49880	-	-	-	-		-
7194858	68	36	42.26	25.59	-0.72371262	0.01342862	PHATRDRAFT_15212	K05643|1|6e-45|180|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3;K05641|5|2e-42|171|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1	GO:0044464	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7198928	122	65	98.87	60.28	-0.713853415	0.001007656	PHATRDRAFT_50127	-	-	-	-		-
7200642	58	31	37.86	23.15	-0.709662218	0.0249774	PHATRDRAFT_45592	K00058|1|6e-87|319|olu:OSTLU_39000|D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	-	GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7196571	45	24	82.21	50.32	-0.708181971	0.0481676	PHATRDRAFT_9223	-	-	GO:0016755	GO:0009057//macromolecule catabolic process		GO:0009057//macromolecule catabolic process
7201887	45	24	83.82	51.31	-0.708054496	0.0481676	PHATRDRAFT_36635	-	-	-	-		-
7195118	86	46	74.64	45.7	-0.707754821	0.00622188	PHATRDRAFT_48813	-	-	-	-		-
7202651	56	30	47.69	29.24	-0.705743471	0.0283136	PHATRDRAFT_37848	-	-	-	-		-
7200283	80	43	39.79	24.45	-0.702571434	0.00893938	PHATRDRAFT_45062	-	-	-	-		-
7195407	65	35	31.92	19.65	-0.699931339	0.0190432	hCDK4	K08829|1|1e-60|233|ppp:PHYPADRAFT_178081|male germ cell-associated kinase [EC:2.7.11.22]	-	GO:0032550;GO:0004672//protein kinase activity	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199845	61	33	31.53	19.5	-0.693251046	0.0243992	PHATRDRAFT_44950	-	-	-	-		-
7203613	48	26	21.63	13.4	-0.690800665	0.0469922	APC8	K03355|1|4e-105|380|smo:SELMODRAFT_268860|anaphase-promoting complex subunit 8	GO:0000152//nuclear ubiquitin ligase complex	-	GO:0007088//regulation of mitosis		GO:0007088//regulation of mitosis
7203764	81	44	24.05	14.93	-0.687822729	0.00985528	PHATRDRAFT_48479	-	GO:0044464	GO:0046914//transition metal ion binding	-		-
7199685	57	31	26.72	16.61	-0.685867935	0.0313116	PHATRDRAFT_45020	K12169|1|1e-12|73.2|smo:SELMODRAFT_149782|Kip1 ubiquitination-promoting complex protein 1 [EC:6.3.2.19]	-	-	-		-
7197966	57	31	36.87	22.94	-0.684582025	0.0313116	PHATRDRAFT_44303	-	-	GO:0046914//transition metal ion binding;GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;GO:0019842//vitamin binding	GO:0044710		GO:0044710
7199674	57	31	58.27	36.29	-0.683181254	0.0313116	PHATRDRAFT_34584	-	-	-	-		-
7204683	77	42	27.62	17.22	-0.681628177	0.01255348	PHATR_46827	-	-	-	-		-
7198605	64	35	25.13	15.71	-0.677727491	0.0237648	PHATRDRAFT_49903	K01739|1|5e-20|98.2|zma:541650|cystathionine gamma-synthase [EC:2.5.1.48]	-	GO:0043168//anion binding	-		-
7200567	534	292	301.08	188.28	-0.677267118	4.40E-11	PHATRDRAFT_45464	-	-	-	-		-
7201815	86	47	105.72	66.2	-0.675345208	0.00851766	PHATRDRAFT_36435	-	-	GO:0036094//small molecule binding	-		-
7201182	102	56	39.45	24.76	-0.672013986	0.00445616	PHATRDRAFT_46213	-	-	-	-		-
7201497	62	34	66.73	41.91	-0.671040982	0.026892	PHATRDRAFT_46304	-	-	-	-		-

7205037	51	28	47.39	29.78	-0.670238907	0.0456772	PHATRDRAFT_bd1463	-	-	GO:0016772//transferase activity, transferring phosphorus-containing groups;GO:0032550	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7194796	91	50	83.73	52.67	-0.668763166	0.00735816	PHATRDRAFT_39066	K12818|1|4e-07|53.9|ota:Ot04g02270|ATP-dependent RNA helicase DHX8/PRP22 [EC:3.6.4.13];K14792|3|2e-06|51.2|gmx:100797745|rRNA biogenesis protein RRP5;K02945|4|4e-06|50.4|ppp:PHYPADRAFT_122522|small subunit ribosomal protein S1	-	GO:0003676//nucleic acid binding;GO:0003824//catalytic activity	-		-
7198447	247	136	107.75	67.83	-0.667692471	9.98E-06	PHATRDRAFT_49769	K00924|1|6e-15|81.3|osa:4341290|[EC:2.7.1.-];K08286|2|4e-14|78.6|ath:AT4G28490|protein-serine/threonine kinase [EC:2.7.11.-];K13415|3|3e-12|72.4|pop:POPTR_650846|protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1];K13420|4|3e-11|68.9|ath:AT5G46330|LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	-	-	-		-
7203333	370	205	114.74	72.65	-0.65933372	8.93E-08	CYCP1	-	-	-	-		-
7201764	54	30	26.07	16.56	-0.65468791	0.044266	PHATRDRAFT_46385	-	-	-	-		-
7204596	68	38	14.61	9.33	-0.647007192	0.025286	CHLH	K03403|1|0.0|1733|ppp:PHYPADRAFT_226175|magnesium chelatase subunit H [EC:6.6.1.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0051003	GO:0006779//porphyrin-containing compound biosynthetic process		GO:0006779//porphyrin-containing compound biosynthetic process
7195604	66	37	25.75	16.5	-0.642106408	0.0285702	PHATRDRAFT_49346	-	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity	GO:0007166//cell surface receptor signaling pathway		GO:0007166//cell surface receptor signaling pathway
7199534	57	32	45.72	29.37	-0.638482138	0.0427926	PHATRDRAFT_45027	-	-	-	-		-
7205098	5592.3	3145.67	2399.25	1542.86	-0.636976336	6.69E-91	PHATRDRAFT_bd1677	K13862|1|8e-20|97.4|ota:Ot04g03190|solute carrier family 4 (sodium borate transporter), member 11	GO:0031224//intrinsic component of membrane	GO:0015301//anion:anion antiporter activity	GO:0006811//ion transport		GO:0006811//ion transport
7197029	194	109	245.89	158.3	-0.635351808	0.000169082	PHATRDRAFT_33028	-	-	-	-		-
7204358	223	126	73.81	47.66	-0.631037339	6.64E-05	PHATR_43917	-	-	-	GO:0046488//phosphatidylinositol metabolic process		GO:0046488//phosphatidylinositol metabolic process
7203886	90	51	22.7	14.7	-0.626876142	0.01212968	PHATR_44133	-	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity;GO:0003824//catalytic activity	GO:0007166//cell surface receptor signaling pathway;GO:0009117//nucleotide metabolic process		GO:0007166//cell surface receptor signaling pathway;GO:0009117//nucleotide metabolic process
7199569	210	119	70.4	45.6	-0.626541604	0.000119368	myoA4	K10357|1|9e-141|499|aly:ARALYDRAFT_887631|myosin V;K03165|2|9e-130|462|ota:Ot06g03550|DNA topoisomerase III [EC:5.99.1.2]	GO:0015629//actin cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7203298	60	34	48.35	31.35	-0.625050447	0.041283	PHATRDRAFT_48151	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7201830	113	64	133.17	86.41	-0.623998928	0.00483578	hCDK6	K08269|1|1e-61|234|smo:SELMODRAFT_268528|unc51-like kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7199053	81	46	28.13	18.26	-0.623422787	0.01792644	PHATRDRAFT_50304	-	-	GO:0046914//transition metal ion binding	-		-
7204858	73.01	41.46	61.8	40.17	-0.621488377	0.021663	PHATRDRAFT_bd1180	-	-	-	-		-
7198324	781	444	418.04	271.77	-0.621254783	1.50E-13	PHATRDRAFT_55087	-	-	-	-		-
7201049	65	37	20.22	13.15	-0.620720198	0.035194	PDH1	K00161|1|7e-53|207|pop:POPTR_755473|pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors	-		-

7195789	58	33	25.94	16.87	-0.620718506	0.0467018	PHATRDRAFT_55040	K00102|1|5e-93|340|aly:ARALYDRAFT_487468|D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]	-	GO:0004457//lactate dehydrogenase activity;GO:0000166//nucleotide binding;GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	GO:0044710		GO:0044710
7204685	160	91	93.16	60.6	-0.620392846	0.00086883	PHATR_13232	K00318|1|3e-91|334|vcn:VOLCADRAFT_64330|proline dehydrogenase [EC:1.5.99.8]	-	GO:0046872//metal ion binding;GO:0016645//oxidoreductase activity, acting on the CH-NH group of donors	GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process		GO:0006560//proline metabolic process;GO:0006536//glutamate metabolic process
7197172	142	81	14.06	9.16	-0.618177091	0.00183094	PHATRDRAFT_43464	K14772|1|1e-69|265|aly:ARALYDRAFT_353720|U3 small nucleolar RNA-associated protein 20	-	-	-		-
7204810	142	81	42.5	27.7	-0.617576865	0.00183094	PHATRDRAFT_bd1730	-	-	-	-		-
7201070	63	36	8.03	5.24	-0.615833176	0.039758	PHATRDRAFT_46012	K14550|1|3e-35|150|ath:AT3G06530|U3 small nucleolar RNA-associated protein 10	-	-	-		-
7198625	77	44	23.71	15.48	-0.615090191	0.0227528	PHATRDRAFT_49927	-	-	-	-		-
7202985	63	36	25.46	16.63	-0.614444251	0.039758	PHATRDRAFT_38174	-	-	-	-		-
7195443	597	341	810.64	530.7	-0.611164816	1.61E-10	PHATRDRAFT_49088	-	-	-	-		-
7197643	75	43	20.42	13.38	-0.60990475	0.0256392	HemE_2	K01599|1|1e-109|396|cme:CME194C|uroporphyrinogen decarboxylase [EC:4.1.1.37]	GO:0009536//plastid	GO:0016831//carboxy-lyase activity	GO:0006779//porphyrin-containing compound biosynthetic process		GO:0006779//porphyrin-containing compound biosynthetic process
7196767	61	35	37.43	24.56	-0.607884488	0.044926	PHATRDRAFT_43171	K05389|1|2e-23|108|pop:POPTR_755721|potassium channel subfamily K, other eukaryote	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding;GO:0005261//cation channel activity	GO:0034220//ion transmembrane transport		GO:0034220//ion transmembrane transport
7200016	400	230	198.01	130.18	-0.605065473	2.49E-07	PHATRDRAFT_45314	-	-	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7197266	106	61	51.06	33.59	-0.604161742	0.0083166	PHATRDRAFT_43747	-	-	-	-		-
7202801	95	55	131.71	87.4	-0.591659701	0.01372328	PHATRDRAFT_21744	K02183|1|1e-13|74.3|ppp:PHYPADRAFT_180168|calmodulin	-	GO:0046872//metal ion binding	-		-
7201367	86	50	34.08	22.65	-0.589414285	0.0202506	PHATRDRAFT_46151	-	GO:0044464	GO:0003676//nucleic acid binding;GO:0046914//transition metal ion binding	-		-
7197902	98	57	54.64	36.35	-0.588002119	0.01319456	PHATRDRAFT_44704	K14662|1|6e-12|70.9|vvi:100245927|protein N-terminal asparagine amidohydrolase [EC:3.5.1.-]	-	GO:0016811//hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	-		-
7203102	204	119	53.14	35.42	-0.585234016	0.00036318	PHATRDRAFT_47888	-	-	-	-		-
7204521	695	405	458.96	305.95	-0.585072524	3.81E-11	PHATR_46747	-	-	GO:0016741	GO:0008152//metabolic process		GO:0008152//metabolic process
7198064	487	284	238.32	158.91	-0.584690114	3.33E-08	PHATRDRAFT_54251	-	-	-	-		-
7196095	72	42	17.62	11.75	-0.584553167	0.0352324	PHATRDRAFT_42555	-	-	-	-		-
7201316	144	84	106.15	70.85	-0.583264613	0.00277548	PHATRDRAFT_12894	K00953|1|2e-36|151|bdi:100841620|FAD synthetase [EC:2.7.7.2]	-	-	GO:0009108//coenzyme biosynthetic process		GO:0009108//coenzyme biosynthetic process
7196517	97	57	42.64	28.65	-0.573672299	0.01594928	PHATRDRAFT_42871	-	-	-	-		-
7204278	240	141	143.04	96.12	-0.573510088	0.000139907	PHATR_43850	K03539|1|4e-07|54.7|bdi:100830772|ribonuclease P/MRP protein subunit RPP1 [EC:3.1.26.5];K12127|2|9e-07|53.5|pop:POPTR_784463|pseudo-response regulator 1	-	-	-		-
7199669	68	40	44.91	30.22	-0.571533062	0.0447138	PHATRDRAFT_1631	-	-	-	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7198661	112	66	61.69	41.57	-0.569493898	0.01000542	PHATRDRAFT_49833	-	-	-	-		-

7204344	565	333	342.23	230.7	-0.568948228	6.23E-09	PHATR_10378	K00654|1|2e-145|513|smo:SELMODRAFT_108076|serine palmitoyltransferase [EC:2.3.1.50]	-	GO:0043168//anion binding;GO:0003824//catalytic activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7201035	370	218	292.11	196.95	-0.568682331	2.57E-06	PHATRDRAFT_45968	K09272|1|5e-11|67.0|aly:ARALYDRAFT_905150|structure-specific recognition protein 1;K10802|2|1e-10|65.9|vcn:VOLCADRAFT_72419|high mobility group protein B1	-	-	-		-
7202636	69.1	40.87	30.42	20.57	-0.564478359	0.0367218	PHATRDRAFT_47574	-	-	-	-		-
7201478	71	42	18.81	12.72	-0.564401178	0.0427778	PHATRDRAFT_54547	-	-	GO:0016772//transferase activity, transferring phosphorus-containing groups	GO:0006796//phosphate-containing compound metabolic process		GO:0006796//phosphate-containing compound metabolic process
7199277	71	42	78.09	52.91	-0.561597395	0.0427778	PHATRDRAFT_50486	-	-	-	-		-
7197801	118	70	53.58	36.34	-0.560136162	0.00920092	PHATRDRAFT_50806	K00826|1|1e-51|202|vcn:VOLCADRAFT_102054|branched-chain amino acid aminotransferase [EC:2.6.1.42]	-	GO:0004084//branched-chain-amino-acid transaminase activity	-		-
7201867	118	70	114.23	77.58	-0.558184912	0.00920092	PHATRDRAFT_46593	-	-	GO:0046914//transition metal ion binding;GO:0051540	GO:0009058//biosynthetic process		GO:0009058//biosynthetic process
7195607	111	66	23.68	16.09	-0.557504755	0.0120174	PHATRDRAFT_49135	-	-	-	-		-
7199700	385	229	100.5	68.31	-0.557026804	2.68E-06	MYT1	K06632|1|2e-30|133|ppp:PHYPADRAFT_193308|wee1-like protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7203882	147	87	322.08	218.98	-0.556619967	0.00343424	CYCP6	-	-	GO:0016407//acetyltransferase activity;GO:0019900//kinase binding	GO:0051726//regulation of cell cycle		GO:0051726//regulation of cell cycle
7197515	74	44	44.41	30.2	-0.556336022	0.040897	PHATRDRAFT_43665	-	-	GO:0042578//phosphoric ester hydrolase activity	GO:0044238		GO:0044238
7203211	128	76	158.71	107.97	-0.555762524	0.00676476	Mob1	K06685|1|6e-32|135|osa:4333310|maintenance of ploidy protein MOB1 (MPS1 binder 1)	-	-	-		-
7204040	89	53	23.28	15.84	-0.555518723	0.0252446	SMC5	K06674|1|9e-16|84.7|pop:POPTR_826684|structural maintenance of chromosome 2;K06669|5|2e-13|76.6|ath:AT2G27170|structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	GO:0000793//condensed chromosome	-	GO:0000725//recombinational repair		GO:0000725//recombinational repair
7202246	188	112	51.61	35.13	-0.554947054	0.001106224	PHATRDRAFT_54681	-	-	GO:0016798//hydrolase activity, acting on glycosyl bonds	GO:0044238		GO:0044238
7195408	414	247	122.06	83.22	-0.552588302	1.34E-06	PHATRDRAFT_49026	-	-	-	-		-
7202147	552	330	120.78	82.5	-0.549915554	2.75E-08	PHATRDRAFT_54686	-	-	-	-		-
7204087	102	61	36.88	25.21	-0.548842538	0.01759936	myoC1	K10357|1|2e-101|369|aly:ARALYDRAFT_887631|myosin V;K03165|2|3e-99|361|ota:Ot06g03550|DNA topoisomerase III [EC:5.99.1.2]	GO:0015629//actin cytoskeleton	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	-		-
7195314	120	72	47.53	32.6	-0.543966437	0.01054446	PHATRDRAFT_49072	-	-	-	-		-
7195271	2070	1241	1760.9	1208.28	-0.543358167	1.03E-26	PHATRDRAFT_49007	-	-	-	-		-
7202917	75	45	63.67	43.73	-0.541990416	0.0438998	PHATRDRAFT_47748	-	-	-	-		-
7198624	978	588	427.74	294	-0.540917972	2.85E-13	PHATRDRAFT_49926	-	-	-	-		-
7196990	143	86	145.67	100.32	-0.538094539	0.00545682	PHATRDRAFT_43687	-	-	-	-		-
7196682	484	292	131.93	90.96	-0.536468502	3.58E-07	PHATRDRAFT_42501	-	-	-	-		-
7204140	83	50	73.45	50.65	-0.536200222	0.0356186	PHATR_25956	K00390|1|7e-62|235|ppp:PHYPADRAFT_123215|phosphoadenosine phosphosulfate reductase [EC:1.8.4.8];K05907|4|3e-11|67.8|vvi:100233045|adenylyl-sulfate reductase (glutathione) [EC:1.8.4.9]	-	GO:0003824//catalytic activity	GO:0008152//metabolic process;GO:0019725//cellular homeostasis		GO:0008152//metabolic process;GO:0019725//cellular homeostasis
7200347	169	102	94.6	65.3	-0.534757192	0.00272644	PHATRDRAFT_45173	-	-	GO:0046914//transition metal ion binding	-		-

7204870	177	107	85.59	59.16	-0.532820195	0.00224538	PHATRDRAFT_bd474	K08869|1|3e-116|417|cme:CMP122C|aarF domain-containing kinase;K13457|4|4e-78|290|vvi:100252764|disease resistance protein RPM1	-	GO:0016740//transferase activity	-		-
7197763	1249	755	642.82	444.33	-0.532783265	3.79E-16	PHATRDRAFT_44488	-	-	-	-		-
7200441	96	58	134.18	92.93	-0.529953336	0.0246812	PHATRDRAFT_12198	K14510|1|3e-34|143|ppp:PHYPADRAFT_30352|serine/threonine-protein kinase CTR1 [EC:2.7.11.1];K04424|4|6e-33|138|aly:ARALYDRAFT_909157|sterile alpha motif and leucine zipper containing kinase AZK [EC:2.7.11.25]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7195625	150	91	31.53	21.85	-0.52909189	0.00532504	PHATRDRAFT_49177	K14079|1|7e-12|72.0|mtr:MTR_005s0002|poly(A) RNA polymerase GLD2 [EC:2.7.7.19]	-	-	-		-
7198049	107	65	75.12	52.21	-0.524870904	0.0192022	hUfd1	K14016|1|2e-64|244|ath:AT2G21270|ubiquitin fusion degradation protein 1	GO:0044444//cytoplasmic part	-	GO:0019941//modification-dependent protein catabolic process;GO:0009451//RNA modification		GO:0019941//modification-dependent protein catabolic process;GO:0009451//RNA modification
7198520	528	321	353.31	245.72	-0.523919295	1.81E-07	dsCYC7	K06627|1|1e-10|65.9|ath:AT5G43080|cyclin A;K14505|4|2e-09|62.4|vvi:100264093|cyclin D3, plant	-	-	-		-
7196500	942	574	408.03	284.24	-0.521565635	4.10E-12	PHATRDRAFT_42846	-	-	GO:0070011//peptidase activity, acting on L-amino acid peptides	-		-
7201361	412	251	291.89	203.45	-0.520750505	4.57E-06	PHATRDRAFT_46143	-	-	-	-		-
7202075	615	375	401.49	280.04	-0.519731143	2.26E-08	PHATRDRAFT_13587	-	-	-	-		-
7204338	113	69	43.12	30.1	-0.518593691	0.01748788	PHATR_43879	-	-	-	-		-
7203284	282	172	294.99	206.04	-0.517741604	0.000157939	TRD1	-	-	-	-		-
7202167	88	54	19.83	13.9	-0.512599795	0.0386998	RPC157	K03018|1|0.0|1294|olu:OSTLU_24022|DNA-directed RNA polymerase III subunit RPC1 [EC:2.7.7.6]	GO:0043231//intracellular membrane-bounded organelle	GO:0034062//RNA polymerase activity;GO:0046914//transition metal ion binding;GO:0003676//nucleic acid binding;GO:0001882//nucleoside binding	GO:0010467//gene expression		GO:0010467//gene expression
7199278	105	64	357.96	251.49	-0.509297348	0.021452	PHATRDRAFT_31254	-	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	-	GO:0006007//glucose catabolic process;GO:0006996//organelle organization;GO:0010038//response to metal ion;GO:0009725//response to hormone;GO:0006972//hyperosmotic response;GO:0042044//fluid transport		GO:0006007//glucose catabolic process;GO:0006996//organelle organization;GO:0010038//response to metal ion;GO:0009725//response to hormone;GO:0006972//hyperosmotic response;GO:0042044//fluid transport
7198010	218	134	103.49	72.73	-0.508868889	0.001134558	PHATRDRAFT_44301	-	-	-	-		-
7197838	89	55	23.39	16.52	-0.501678175	0.0411854	PHATRDRAFT_44362	-	-	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	-		-
7197217	123	76	154.07	109.08	-0.498199367	0.01611792	PHATRDRAFT_43542	-	-	-	-		-
7202060	84	52	74.18	52.57	-0.496790533	0.0484292	PHATRDRAFT_47166	-	-	-	-		-
7198649	111	69	45.68	32.46	-0.492899651	0.0245508	PHATRDRAFT_49957	-	-	-	-		-
7199578	373	232	189.46	134.75	-0.491608017	3.58E-05	PHATRDRAFT_44873	-	-	-	GO:0044238		GO:0044238
7199139	305	190	112.86	80.36	-0.489984786	0.000198787	GPI_3	K01810|1|0.0|664|cme:CMO124C|glucose-6-phosphate isomerase [EC:5.3.1.9]	GO:0044444//cytoplasmic part	GO:0016861//intramolecular oxidoreductase activity, interconverting aldoses and ketoses	GO:0050896//response to stimulus;GO:0006007//glucose catabolic process		GO:0050896//response to stimulus;GO:0006007//glucose catabolic process

7199189	134.32	83.81	100.04	71.43	-0.485974936	0.0125402	PHATRDRAFT_50367	-	-	GO:0046914//transition metal ion binding;GO:0019787//small conjugating protein ligase activity	GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation		GO:0009057//macromolecule catabolic process;GO:0032446//protein modification by small protein conjugation
7198662	1675	1048	1327.29	950.33	-0.481983142	5.97E-18	PHATRDRAFT_49834	-	-	-	-		-
7204565	212	133	116.61	83.66	-0.47908161	0.00236498	PHATR_46841	-	-	-	-		-
7195667	129	81	43.1	30.93	-0.478681036	0.0182378	PHATRDRAFT_49176	K08332|1|6e-09|61.6|vcn:VOLCADRAFT_41528|vacuolar protein 8	-	-	-		-
7200552	159	100	47.5	34.14	-0.476464455	0.00900572	PHATRDRAFT_19901	K13811|1|2e-107|389|ppp:PHYPADRAFT_151174|3’-phosphoadenosine 5’-phosphosulfate synthase [EC:2.7.7.4 2.7.1.25]	GO:0044424	GO:0046872//metal ion binding;GO:0016301//kinase activity;GO:0016462//pyrophosphatase activity;GO:0032550;GO:0004779//sulfate adenylyltransferase activity	GO:0006790//sulfur compound metabolic process;GO:0006793//phosphorus metabolic process		GO:0006790//sulfur compound metabolic process;GO:0006793//phosphorus metabolic process
7200414	502	316	212.5	152.92	-0.474685736	3.42E-06	PHATRDRAFT_45657	K00469|1|2e-20|99.8|ath:AT1G14520|inositol oxygenase [EC:1.13.99.1]	GO:0044424	GO:0046914//transition metal ion binding;GO:0016701//oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	GO:0006020//inositol metabolic process		GO:0006020//inositol metabolic process
7204707	809	510	513.64	370.39	-0.471712409	4.25E-09	PHATR_54658	-	-	-	-		-
7203434	747	470	1025.7	739.7	-0.471596648	1.39E-08	PHATRDRAFT_48086	-	-	-	-		-
7201995	141	89	52.52	37.89	-0.471049776	0.01494994	PHATRDRAFT_47068	-	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity	GO:0007166//cell surface receptor signaling pathway		GO:0007166//cell surface receptor signaling pathway
7197403	114	72	55.22	39.88	-0.469525478	0.0291086	PHATRDRAFT_43361	-	-	-	-		-
7203379	109	69	20.04	14.49	-0.467824914	0.0340658	PHATRDRAFT_48282	-	-	-	-		-
7200388	275	174	124.67	90.18	-0.467234929	0.000714574	PHATRDRAFT_45610	-	-	-	-		-
7197013	248	157	77.36	55.97	-0.466934047	0.001337602	PHATRDRAFT_43724	K08286|1|4e-24|112|ath:AT4G28490|protein-serine/threonine kinase [EC:2.7.11.-]	-	-	-		-
7201138	101	64	69.21	50.17	-0.464155567	0.0420324	PHATRDRAFT_45926	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203872	397	252	150.09	108.9	-0.462823904	5.53E-05	PHATR_44112	-	-	GO:0015291//secondary active transmembrane transporter activity	GO:0015893//drug transport;GO:0044763		GO:0015893//drug transport;GO:0044763
7203272	104	66	42.75	31.02	-0.462725734	0.0398994	PHATRDRAFT_676	K01534|1|1e-120|432|ppp:PHYPADRAFT_125099|Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]	GO:0031224//intrinsic component of membrane	GO:0043169//cation binding;GO:0032550;GO:0019829//cation-transporting ATPase activity	GO:0006812//cation transport		GO:0006812//cation transport
7198703	170.68	108.43	73.6	53.45	-0.461515818	0.0086395	PHATRDRAFT_50000	-	-	-	-		-
7199730	1315	838	317.77	231.39	-0.457656413	3.73E-13	PHATRDRAFT_44761	K15172|1|1e-08|60.8|vcn:VOLCADRAFT_106802|transcription elongation factor SPT5	-	GO:0046914//transition metal ion binding;GO:0097159//organic cyclic compound binding	GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress		GO:0044763;GO:0050794//regulation of cellular process;GO:0006950//response to stress
7195917	281	179	158.33	115.34	-0.457041712	0.000791926	PHATRDRAFT_49430	-	-	-	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7203985	206	131	245.82	179.09	-0.456917516	0.00391878	PHATR_18620	K12198|1|1e-23|108|ppp:PHYPADRAFT_163299|charged multivesicular body protein 5	-	-	-		-
7200523	655	418	135.22	98.59	-0.455795326	3.33E-07	PHATRDRAFT_45399	-	-	-	-		-
7197519	934	596	298.3	217.54	-0.455483278	1.07E-09	PHATRDRAFT_43674	-	-	-	-		-
7198378	117.5	75.31	38.91	28.5	-0.449179061	0.034144	PHATRDRAFT_49810	-	-	-	-		-
7199251	284	182	151.35	110.92	-0.448369154	0.000916338	PHATRDRAFT_50437	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-

7195368	328	210	375.7	275.53	-0.447371706	0.000352058	PHATRDRAFT_48950	-	-	-	-		-
7196145	285	183	47.64	34.95	-0.446880958	0.000961162	PHATRDRAFT_42770	K11568|1|2e-09|64.3|vcn:VOLCADRAFT_121384|DASH complex subunit DAD3;K10400|2|3e-08|60.5|cme:CMO070C|kinesin family member 15;K09291|3|4e-07|56.6|vcn:VOLCADRAFT_89403|nucleoprotein TPR;K06675|5|2e-06|54.7|vcn:VOLCADRAFT_61097|structural maintenance of chromosome 4	-	-	GO:0000301//retrograde transport, vesicle recycling within Golgi		GO:0000301//retrograde transport, vesicle recycling within Golgi
7201414	105.5	67.72	35.79	26.26	-0.446689628	0.0421024	PHATRDRAFT_20424	-	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7195567	134	86	70.02	51.39	-0.44627941	0.0237712	PHATRDRAFT_49277	K07466|1|7e-08|57.4|aly:ARALYDRAFT_329623|replication factor A1	GO:0043231//intracellular membrane-bounded organelle	GO:0003676//nucleic acid binding	GO:0006259//DNA metabolic process		GO:0006259//DNA metabolic process
7203579	3056	1965	1556.91	1144.71	-0.443703396	3.77E-27	PHATRDRAFT_54892	-	-	-	-		-
7196590	144.43	92.96	77.75	57.22	-0.442323178	0.0175024	PHATRDRAFT_32401	-	-	-	-		-
7198329	211	136	44.7	32.92	-0.441310496	0.00501106	PHATRDRAFT_49706	-	-	-	-		-
7196688	275	177	208.27	153.39	-0.441250611	0.00128196	PHATRDRAFT_42510	-	-	-	-		-
7203640	169	109	40.15	29.59	-0.440290291	0.01226296	PHATRDRAFT_48375	K12319|1|3e-32|139|cre:CHLREDRAFT_142791|guanylate cyclase soluble subunit beta [EC:4.6.1.2];K11858|3|8e-23|108|cre:CHLREDRAFT_171763|ubiquitin carboxyl-terminal hydrolase 48 [EC:3.1.2.15];K13755|5|3e-13|76.3|vcn:VOLCADRAFT_59941|calcium/calmodulin-dependent 3’,5’-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0016829//lyase activity;GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7195458	529	342	201.24	148.71	-0.43641543	1.02E-05	PHATRDRAFT_49268	-	-	-	-		-
7202712	179	116	71.29	52.81	-0.43288858	0.01104996	PHATRDRAFT_47713	-	-	GO:0097159//organic cyclic compound binding;GO:0046914//transition metal ion binding	-		-
7198365	9477	6160	1326.52	984.93	-0.429553328	1.51E-75	PHATRDRAFT_23497	K05641|1|2e-177|622|ota:Ot18g01460|ATP-binding cassette, subfamily A (ABC1), member 1;K05643|3|2e-168|592|ppp:PHYPADRAFT_221752|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7197647	143	93	53.64	39.87	-0.428005632	0.0248194	PHATRDRAFT_44656	-	-	-	GO:0007165//signal transduction		GO:0007165//signal transduction
7199471	3824.52	2491.49	716.93	533.58	-0.426127672	3.98E-31	PHATRDRAFT_50642	-	-	-	-		-
7201683	135	88	28.05	20.89	-0.425188278	0.0304472	PHATRDRAFT_20872	K05666|1|0.0|697|olu:OSTLU_35503|ATP-binding cassette, subfamily C (CFTR/MRP), member 2;K05658|2|1e-59|230|ppp:PHYPADRAFT_59717|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7204179	211	138	69.78	52.16	-0.419869728	0.00730496	PHATR_43954	-	-	-	-		-
7203528	304	199	209.15	156.63	-0.417177433	0.00130722	PHATRDRAFT_54873	-	-	GO:0004175//endopeptidase activity	GO:0019538//protein metabolic process		GO:0019538//protein metabolic process
7202190	836	549	270.12	202.73	-0.414040868	1.26E-07	PHATRDRAFT_47203	-	-	-	-		-
7203705	411	270	198.29	148.94	-0.41288066	0.000217658	PHATRDRAFT_48482	-	-	-	-		-
7203113	280	184	184.62	138.79	-0.411655226	0.002317	PHATRDRAFT_47912	K15692|1|6e-12|70.5|ppp:PHYPADRAFT_16563|E3 ubiquitin-protein ligase RNF13 [EC:6.3.2.19];K11982|2|1e-09|63.2|ath:AT3G56580|E3 ubiquitin-protein ligase RNF115/126 [EC:6.3.2.19]	-	GO:0046914//transition metal ion binding	-		-
7204955	149	98	53.99	40.59	-0.411567877	0.0270498	PHATRDRAFT_bd1748	K05389|1|1e-07|57.0|olu:OSTLU_41153|potassium channel subfamily K, other eukaryote	-	GO:0004620//phospholipase activity	-		-
7199672	125	82	235.9	177.62	-0.40938138	0.041335	PHATRDRAFT_11271	K03453|1|1e-12|70.5|vcn:VOLCADRAFT_102664|bile acid:Na+ symporter, BASS family	-	-	-		-

7200002	170	112	69.26	52.16	-0.409078518	0.01877128	PHATRDRAFT_45377	K01510|1|3e-18|92.4|vcn:VOLCADRAFT_91259|apyrase [EC:3.6.1.5]	-	GO:0003824//catalytic activity	-		-
7203433	199	131	143.36	107.97	-0.409012034	0.0107443	PHATRDRAFT_48085	-	-	-	-		-
7198546	476	314	134.68	101.53	-0.40762955	8.60E-05	HSP70G	K09486|1|8e-88|323|ath:AT4G16660|hypoxia up-regulated 1	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0032550	GO:0009987//cellular process;GO:0006950//response to stress		GO:0009987//cellular process;GO:0006950//response to stress
7205144	180	119	83.5	63.12	-0.403678992	0.01678422	PHATRDRAFT_bd1656	K01120|1|9e-10|63.9|cre:CHLREDRAFT_101278|3',5'-cyclic-nucleotide phosphodiesterase [EC:3.1.4.17];K13755|2|1e-09|63.5|vcn:VOLCADRAFT_59941|calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase [EC:3.1.4.17]	-	GO:0004112//cyclic-nucleotide phosphodiesterase activity	GO:0007154//cell communication		GO:0007154//cell communication
7204572	239	158	125.73	95.05	-0.403570395	0.00580284	PHATR_46645	-	-	-	-		-
7203907	210	139	152.83	115.74	-0.401040218	0.01004472	PHATR_41807	K00654|1|4e-75|280|ppp:PHYPADRAFT_198015|serine palmitoyltransferase [EC:2.3.1.50]	-	GO:0043168//anion binding	GO:0008152//metabolic process		GO:0008152//metabolic process
7199360	181	120	63.08	47.8	-0.400172042	0.01751718	PHATRDRAFT_50575	-	-	-	-		-
7198968	233	154	407.42	308.97	-0.399050039	0.00641834	PHATRDRAFT_50303	K08341|1|1e-50|196|vcn:VOLCADRAFT_75248|GABA(A) receptor-associated protein (autophagy-related protein 8)	GO:0044437	GO:0008641//small protein activating enzyme activity;GO:0019783//small conjugating protein-specific protease activity;GO:0016879//ligase activity, forming carbon-nitrogen bonds	GO:0033554//cellular response to stress		GO:0033554//cellular response to stress
7197212	140	93	49.95	37.93	-0.397145306	0.0381592	PHATRDRAFT_43532	K06171|1|4e-18|92.0|bdi:100831865|nicastrin	GO:0031224//intrinsic component of membrane	-	GO:0051604//protein maturation		GO:0051604//protein maturation
7195781	134	89	63.51	48.23	-0.39705296	0.0424746	PHATRDRAFT_49391	K15015|1|9e-07|53.9|rcu:RCOM_0481560|solute carrier family 32 (vesicular inhibitory amino acid transporter)	GO:0031224//intrinsic component of membrane	-	-		-
7204094	531	353	107.65	81.76	-0.396881218	5.27E-05	PHATR_44174	-	-	GO:0008252//nucleotidase activity;GO:0046872//metal ion binding	GO:0009117//nucleotide metabolic process		GO:0009117//nucleotide metabolic process
7197165	218	145	54.85	41.69	-0.395790248	0.00985874	PHATRDRAFT_32665	-	-	-	-		-
7197538	379	252	326.63	248.58	-0.393947078	0.000645478	PHATRDRAFT_43483	-	-	-	-		-
7198969	234	156	81.95	62.44	-0.392273412	0.00796314	PHATRDRAFT_50305	-	-	-	-		-
7200103	147	98	99.93	76.21	-0.390937539	0.035794	PHATRDRAFT_45223	-	-	-	-		-
7199926	153	102	165.93	126.69	-0.389272095	0.0321854	PHATRDRAFT_11792	-	-	-	-		-
7196238	154	103	78.46	60	-0.386994835	0.0335568	PHATRDRAFT_32173	K13342|1|2e-58|225|gmx:100789878|peroxin-5	-	-	-		-
7197411	233	156	34.65	26.5	-0.386862993	0.00907574	PHATRDRAFT_43378	-	-	GO:0016829//lyase activity	GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction		GO:0009165//nucleotide biosynthetic process;GO:0007165//signal transduction
7204759	240	161	45.78	35.09	-0.383657515	0.00852758	PHATR_46935	K13427|1|7e-16|85.5|vvi:100265605|nitric-oxide synthase, plant [EC:1.14.13.39]	GO:0005789//endoplasmic reticulum membrane	GO:0016787//hydrolase activity	GO:0015031//protein transport;GO:0006664//glycolipid metabolic process		GO:0015031//protein transport;GO:0006664//glycolipid metabolic process
7204020	146	98	89.57	68.77	-0.381236261	0.0410336	PHATR_44074	-	-	GO:0003824//catalytic activity	-		-
7196513	247	166	38.33	29.43	-0.381186456	0.00801032	PHATRDRAFT_56605	K00284|1|0.0|1509|zma:542710|glutamate synthase (ferredoxin) [EC:1.4.7.1]	GO:0009536//plastid	GO:0005488//binding;GO:0015930//glutamate synthase activity	GO:0008652//cellular amino acid biosynthetic process;GO:0006536//glutamate metabolic process		GO:0008652//cellular amino acid biosynthetic process;GO:0006536//glutamate metabolic process
7201663	406	273	86.42	66.39	-0.380399279	0.000680096	PHATRDRAFT_46420	-	-	-	-		-
7195214	198	133	152.52	117.23	-0.379656623	0.01747252	PHATRDRAFT_48923	-	-	-	-		-

7199350	572	385	87.95	67.62	-0.379233561	5.80E-05	PHATRDRAFT_24195	K11541|1|0.0|1469|cme:CMQ255C|carbamoyl-phosphate synthase / aspartate carbamoyltransferase [EC:6.3.5.5 2.1.3.2];K01955|2|0.0|759|smo:SELMODRAFT_440891|carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	-	GO:0016884//carbon-nitrogen ligase activity, with glutamine as amido-N-donor;GO:0043169//cation binding;GO:0032550	GO:0006541//glutamine metabolic process;GO:0044271//cellular nitrogen compound biosynthetic process		GO:0006541//glutamine metabolic process;GO:0044271//cellular nitrogen compound biosynthetic process
7202293	7152.48	4836.51	1304.22	1007.53	-0.372364452	1.48E-44	PHATRDRAFT_47520	-	-	-	-		-
7204481	191	129	164.61	127.25	-0.371386325	0.022077	PHATR_3639	K00010|1|5e-64|243|cme:CMF086C|myo-inositol 2-dehydrogenase [EC:1.1.1.18]	-	GO:0036094//small molecule binding;GO:0004022//alcohol dehydrogenase (NAD) activity	GO:0044710		GO:0044710
7201394	266	180	141.58	109.56	-0.369896309	0.00723786	PHATRDRAFT_2097	K11594|1|2e-133|474|osa:4350856|ATP-dependent RNA helicase [EC:3.6.4.13]	-	GO:0032550;GO:0042623//ATPase activity, coupled	-		-
7203743	149	101	51.78	40.12	-0.368073359	0.0462574	CUL1_1	K03869|1|1e-161|568|osa:4330720|cullin 3	GO:0000151//ubiquitin ligase complex	GO:0044389	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7196681	351	238	98.6	76.4	-0.368015008	0.00217946	PHATRDRAFT_42500	-	-	-	-		-
7197934	149	101	72.25	56	-0.36757076	0.0462574	PHATRDRAFT_44709	-	-	-	-		-
7199382	168	114	43.59	33.8	-0.366973957	0.0349156	PHATRDRAFT_50551	-	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7203861	327	222	154.54	119.96	-0.365426876	0.00323798	PHATR_44091	-	-	-	-		-
7203413	505	343	265.82	206.46	-0.364587358	0.000256452	fru2	-	-	-	-		-
7203355	962	655	249.52	194.13	-0.362132375	5.62E-07	PHATRDRAFT_48245	-	-	-	-		-
7195651	4334	2953	2581.31	2011.6	-0.359759952	3.00E-26	PHATRDRAFT_49151	-	-	GO:0036094//small molecule binding	-		-
7197170	231	157	354.07	275.95	-0.359627725	0.01381478	Rab5a	K07887|1|1e-55|214|osa:4333662|Ras-related protein Rab-5A;K07976|2|1e-53|207|olu:OSTLU_33115|Rab family, other	-	GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7195907	1064	726	380.57	296.8	-0.358670748	1.78E-07	PHATRDRAFT_49414	-	-	-	-		-
7202936	694.61	473.55	819.73	640.21	-0.356603586	2.31E-05	PHATRDRAFT_47653	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7195830	162	111	36.34	28.45	-0.353129767	0.0458144	PHATRDRAFT_49478	-	-	-	-		-
7195260	241	165	125.54	98.29	-0.353030564	0.01440338	PHATRDRAFT_54973	-	-	-	-		-
7198943	299	205	54.56	42.73	-0.352594327	0.00667506	PHATRDRAFT_50162	K06699|1|6e-19|95.9|gmx:100781622|proteasome activator subunit 4	-	-	-		-
7197398	628	431	179.71	140.95	-0.350487212	8.80E-05	PHATRDRAFT_43354	-	-	-	-		-
7195379	527	362	380.61	299.13	-0.34754086	0.000344268	PHATRDRAFT_39627	K03183|1|1e-07|56.2|zma:100384459|ubiquinone/menaquinone biosynthesis methyltransferase [EC:2.1.1.163 2.1.1.201]	GO:0044444//cytoplasmic part	GO:0008757//S-adenosylmethionine-dependent methyltransferase activity	GO:0008152//metabolic process		GO:0008152//metabolic process
7198795	311	214	173.07	136.19	-0.345734895	0.00636324	PHATRDRAFT_30810	K14617|1|2e-58|224|pop:POPTR_831922|LMBR1 domain-containing protein 1	GO:0031224//intrinsic component of membrane	-	-		-
7199868	167	115	63.11	49.67	-0.345493877	0.0466874	PHATRDRAFT_44742	-	-	-	-		-
7198756	177	122	66.8	52.63	-0.343962708	0.0412614	PHATRDRAFT_23723	K13354|1|7e-28|124|smo:SELMODRAFT_160785|solute carrier family 25 (peroxisomal adenine nucleotide transporter), member 17;K00133|4|2e-19|96.7|ota:Ot01g02440|aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization		GO:0051234//establishment of localization

7199234	1572	1086	196.43	155	-0.341747068	1.43E-09	ACC2	K11262|1|0.0|1371|ppp:PHYPADRAFT_115301|acetyl-CoA carboxylase / biotin carboxylase [EC:6.4.1.2 6.3.4.14]	-	GO:0016421//CoA carboxylase activity;GO:0043169//cation binding;GO:0016879//ligase activity, forming carbon-nitrogen bonds;GO:0032550	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7200290	317	219	63.37	50.01	-0.34158341	0.00668792	PHATRDRAFT_45084	-	-	-	-		-
7204693	191	132	118.37	93.57	-0.339185528	0.0358484	PHATR_46842	-	-	-	-		-
7199433	224	155	95.62	75.64	-0.338163042	0.0236464	PHATRDRAFT_50618	-	-	-	-		-
7199306	472	327	90.32	71.49	-0.337304034	0.001056252	PHATRDRAFT_41409	-	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7201250	203	141	100.2	79.58	-0.332404704	0.0339332	PHATRDRAFT_36063	-	-	-	-		-
7196674	492	342	120.63	95.81	-0.332340594	0.000970204	PHATRDRAFT_42488	-	-	-	-		-
7197031	764	532	220.62	175.56	-0.329599407	4.42E-05	PHATRDRAFT_43746	-	-	-	-		-
7203267	495	345	138.1	109.99	-0.328340956	0.001062952	GDCP	K00281|1|0.0|994|ppp:PHYPADRAFT_171132|glycine dehydrogenase [EC:1.4.4.2]	-	GO:0043168//anion binding;GO:0016642	GO:0006544//glycine metabolic process		GO:0006544//glycine metabolic process
7199409	240.09	167.91	97.71	78.12	-0.322814271	0.0219872	PHATRDRAFT_50589	-	-	-	-		-
7202861	2094.39	1466.45	506.11	404.91	-0.321849707	3.68E-11	PHATRDRAFT_47656	-	GO:0031224//intrinsic component of membrane	GO:0015291//secondary active transmembrane transporter activity;GO:0005326//neurotransmitter transporter activity	GO:0044765		GO:0044765
7203570	230	161	233.74	187.36	-0.319091663	0.0287324	PHATRDRAFT_48358	-	-	-	-		-
7204351	263	185	52.17	41.93	-0.315237603	0.021921	PHATR_43902	-	-	GO:0097159//organic cyclic compound binding;GO:0046914//transition metal ion binding	-		-
7203405	4611.92	3245.47	588.21	472.82	-0.315040249	7.62E-22	PHATRDRAFT_48047	-	-	-	-		-
7201392	306	215	233.2	187.48	-0.314831089	0.01294352	TRD3	-	-	-	-		-
7196246	400	281	362.61	291.6	-0.314427992	0.00443686	PHATRDRAFT_43051	-	GO:0043231//intracellular membrane-bounded organelle	GO:0003677//DNA binding;GO:0001071//nucleic acid binding transcription factor activity	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7203074	570	402	233.43	188.2	-0.310723357	0.000833308	PHATRDRAFT_47847	-	-	-	-		-
7200157	709	500	444.55	358.6	-0.309970205	0.000192393	PHATRDRAFT_34965	-	-	-	-		-
7196649	248	175	113.03	91.19	-0.309758208	0.028184	PHATRDRAFT_31433	K05681|1|2e-78|292|cme:CMS467C|ATP-binding cassette, subfamily G (WHITE), member 2;K12843|2|1e-58|226|vvi:100248403|U4/U6 small nuclear ribonucleoprotein PRP3;K05663|4|6e-14|77.8|rcu:RCOM_0261010|mitochondrial ABC transporter ATM;K05643|5|8e-14|77.4|olu:OSTLU_42103|ATP-binding cassette, subfamily A (ABC1), member 3	-	GO:0017111//nucleoside-triphosphatase activity;GO:0032550	GO:0009154//purine ribonucleotide catabolic process		GO:0009154//purine ribonucleotide catabolic process
7204028	212	150	121.69	98.48	-0.305307951	0.0450584	PHATR_10531	K08832|1|3e-105|380|ppp:PHYPADRAFT_22627|serine/threonine-protein kinase SRPK3 [EC:2.7.11.1]	GO:0005911//cell-cell junction	GO:0032550;GO:0004672//protein kinase activity	GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process		GO:0006464//cellular protein modification process;GO:0006796//phosphate-containing compound metabolic process
7201748	560	397	344.31	279.19	-0.302460814	0.001207952	PHATRDRAFT_13078	-	-	-	-		-
7198248	286	203	80.55	65.34	-0.301918134	0.0215956	PHATRDRAFT_49592	-	-	-	-		-
7203868	1609	1141	1151.37	934.15	-0.301625394	4.13E-08	ANXA1	-	-	GO:0005543//phospholipid binding;GO:0046872//metal ion binding	-		-
7202989	935	664	182.3	147.91	-0.301594967	3.29E-05	PHATRDRAFT_47863	-	-	-	-		-

7196670	260	185	148.06	120.48	-0.297388259	0.0303448	PGP_1	K13752|1|4e-35|147|ota:Ot11g02640|solute carrier family 24 (sodium/potassium/calcium exchanger), member 4;K13754|3|1e-15|82.8|smo:SELMODRAFT_89075|solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	GO:0031224//intrinsic component of membrane	GO:0046872//metal ion binding	GO:0044763		GO:0044763
7198542	284	202	200.21	162.92	-0.297350316	0.023338	PHATRDRAFT_49939	-	-	-	-		-
7202109	257	183	165.75	135.01	-0.295942601	0.0318954	PHATRDRAFT_47015	-	-	-	-		-
7203867	310	221	135.65	110.56	-0.295059527	0.01901708	PHATR_44106	K13367|1|5e-27|121|ath:AT3G59050|non-specific polyamine oxidase [EC:1.5.3.17];K11450|3|1e-23|110|ota:Ot20g00660|lysine-specific histone demethylase 1 [EC:1.-.-.-]	-	GO:0036094//small molecule binding;GO:0003824//catalytic activity	GO:0044710		GO:0044710
7204314	1103	787	606.71	495.05	-0.293432846	1.01E-05	PHATR_43911	-	-	-	-		-
7196665	687	491	272.86	222.92	-0.291634859	0.00054841	PHATRDRAFT_42467	K06119|1|2e-34|145|ota:Ot15g01120|sulfoquinovosyltransferase [EC:2.4.1.-]	-	-	GO:0008152//metabolic process		GO:0008152//metabolic process
7199468	2796	2000	1064.09	870.04	-0.290466543	3.63E-12	PHATRDRAFT_55230	K04079|1|0.0|832|sbi:SORBI_07g028270|molecular chaperone HtpG	-	GO:0005515//protein binding;GO:0032550	GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process		GO:0050896//response to stimulus;GO:0044267//cellular protein metabolic process
7201827	423	303	55.75	45.62	-0.289305358	0.00733544	Sec7D	K13462|1|3e-110|399|rcu:RCOM_0708240|guanine nucleotide-exchange factor	-	GO:0005083//small GTPase regulator activity	GO:0032011//ARF protein signal transduction		GO:0032011//ARF protein signal transduction
7196337	1480	1061	230.83	189.03	-0.288215522	5.63E-07	PHATRDRAFT_42689	-	-	-	-		-
7199008	318	228	88.09	72.17	-0.287578999	0.0207258	PHATRDRAFT_16704	K12828|1|0.0|1419|mtr:MTR_2g009110|splicing factor 3B subunit 1	-	-	-		-
7198417	2790	2004	1382.72	1135.62	-0.284028879	9.85E-12	PHATRDRAFT_49722	-	-	-	-		-
7203388	314	226	55.76	45.85	-0.282308827	0.0240532	PHATRDRAFT_48253	K10406|1|2e-09|63.9|gmx:100800016|kinesin family member C2/C3	-	-	-		-
7198724	243	175	72.62	59.77	-0.280945387	0.0479674	PHATRDRAFT_50026	-	GO:0031224//intrinsic component of membrane	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7195807	247	178	61.94	51.01	-0.280091282	0.0468686	PHATRDRAFT_49445	-	-	-	-		-
7199763	248	179	66.13	54.54	-0.277990201	0.048114	PHATRDRAFT_44814	-	-	-	-		-
7194763	431	311	207.94	171.56	-0.277454085	0.0089793	PHATRDRAFT_48511	K07240|1|6e-53|207|olu:OSTLU_89366|chromate transporter	-	GO:0015103//inorganic anion transmembrane transporter activity	GO:0015698//inorganic anion transport		GO:0015698//inorganic anion transport
7199755	849	613	600.01	495.64	-0.275693922	0.000252562	PHATRDRAFT_44800	-	-	-	-		-
7195215	422	305	172	142.11	-0.275400487	0.01032574	PHATRDRAFT_48924	K00685|1|2e-55|216|aly:ARALYDRAFT_478464|arginine-tRNA-protein transferase [EC:2.3.2.8]	-	GO:0016755	GO:0044699;GO:0009056//catabolic process;GO:0006464//cellular protein modification process;GO:0032502//developmental process		GO:0044699;GO:0009056//catabolic process;GO:0006464//cellular protein modification process;GO:0032502//developmental process
7198511	435	314	428.84	354.43	-0.274938756	0.00878466	PHATRDRAFT_49879	-	GO:0009536//plastid	-	-		-
7197959	1250	904	411.82	340.39	-0.274825242	1.05E-05	PHATRDRAFT_44296	-	-	-	-		-
7204766	479.86	347.05	178.11	147.24	-0.274598864	0.00689738	PHATR_46949	-	-	-	-		-
7203524	269	196	76.93	64.05	-0.264347738	0.049642	ATPase-P4	K14802|1|7e-155|546|ath:AT1G59820|phospholipid-transporting ATPase [EC:3.6.3.1]	GO:0043231//intracellular membrane-bounded organelle;GO:0031224//intrinsic component of membrane	GO:0032550;GO:0005548//phospholipid transporter activity;GO:0016817//hydrolase activity, acting on acid anhydrides;GO:0046872//metal ion binding;GO:0008324//cation transmembrane transporter activity	GO:0006869//lipid transport;GO:0071705;GO:0022622//root system development;GO:0016192//vesicle-mediated transport;GO:0006820//anion transport;GO:0044767;GO:0046907//intracellular transport		GO:0006869//lipid transport;GO:0071705;GO:0022622//root system development;GO:0016192//vesicle-mediated transport;GO:0006820//anion transport;GO:0044767;GO:0046907//intracellular transport
7201627	1708	1244	828.26	689.75	-0.264010165	6.67E-07	PHATRDRAFT_27877	K03320|1|2e-83|308|cre:CHLREDRAFT_157754|ammonium transporter, Amt family	GO:0031224//intrinsic component of membrane	GO:0008509//anion transmembrane transporter activity	GO:0015696//ammonium transport		GO:0015696//ammonium transport
7203457	354	258	245.32	204.55	-0.262211319	0.0244038	PHATRDRAFT_48087	-	-	-	-		-
7204158	469	343	542.28	454.3	-0.255392657	0.01090842	PHATR_43797	-	-	-	-		-

7197808	1107	811	749.54	628.2	-0.254781528	0.000104688	GEL3	K05768|1|9e-40|162|vvi:100254775|gelsolin	GO:0044424	GO:0008092//cytoskeletal protein binding	GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization		GO:0044763;GO:0071704;GO:0044237//cellular metabolic process;GO:0016043//cellular component organization
7199615	371	272	187.34	157.05	-0.254435027	0.0255292	PHATRDRAFT_44931	-	-	-	-		-
7201656	558	409	333.27	279.39	-0.254411072	0.00605538	PHATRDRAFT_46406	-	-	-	-		-
7199670	293	215	111.11	93.2	-0.253586806	0.0483632	PHATRDRAFT_45002	-	-	-	-		-
7195570	585	429	574.08	482.02	-0.252158787	0.00505924	PHATRDRAFT_49281	-	-	-	-		-
7196274	672	493	625.07	524.97	-0.251782782	0.00271296	PHATRDRAFT_42406	K01673|1|8e-15|79.3|vvi:100263997|carbonic anhydrase [EC:4.2.1.1]	-	GO:0016836//hydro-lyase activity;GO:0046914//transition metal ion binding	-		-
7202762	950	699	158.91	133.57	-0.250613902	0.000447848	PHATRDRAFT_47538	-	-	-	-		-
7202742	324	238	349.16	293.74	-0.249348555	0.0389522	PHATRDRAFT_47760	-	-	-	-		-
7198931	345	254	132.42	111.44	-0.248853872	0.035316	PHATRDRAFT_50133	-	-	-	-		-
7200809	868	640	370.54	312.33	-0.246558141	0.00091145	PHATRDRAFT_45797	-	-	-	-		-
7202236	304	224	368.93	311.45	-0.244346536	0.0493024	PHATRDRAFT_13553	K15377|1|7e-11|65.9|cre:CHLREDRAFT_189789|solute carrier family 44 (choline transporter-like protein), member 2/4/5	GO:0031224//intrinsic component of membrane	-	-		-
7201052	737	545	86.37	72.95	-0.243622311	0.0026484	PHATRDRAFT_45987	-	GO:0043231//intracellular membrane-bounded organelle	-	-		-
7199932	1109	821	456.13	386.02	-0.240769464	0.00024672	PHATRDRAFT_45060	K13177|1|3e-07|55.8|olu:OSTLU_41294|ATP-dependent RNA helicase DDX1 [EC:3.6.4.13]	-	-	-		-
7200102	719	533	180	152.47	-0.239471501	0.00341718	PHATRDRAFT_45221	-	-	-	GO:0044763		GO:0044763
7200913	3957	2886	2516.35	2140.27	-0.233539794	5.73E-14	hUbi	K08770|1|0.0|715|ppp:PHYPADRAFT_222215|ubiquitin C	GO:0043231//intracellular membrane-bounded organelle	-	GO:0014070//response to organic cyclic compound;GO:0044767;GO:0036211		GO:0014070//response to organic cyclic compound;GO:0044767;GO:0036211
7204654	690	515	111.73	95.26	-0.230074154	0.00586352	PHATR_46779	-	-	-	-		-
7200591	390	291	154.97	132.18	-0.229485056	0.0381788	ACS4	K15013|1|1e-139|495|ota:Ot16g00030|long-chain-fatty-acid--CoA ligase ACSBG [EC:6.2.1.3];K01897|3|1e-62|239|cme:CML197C|long-chain acyl-CoA synthetase [EC:6.2.1.3]	-	GO:0015645//fatty acid ligase activity	GO:0006631//fatty acid metabolic process		GO:0006631//fatty acid metabolic process
7196462	543	404	795.3	678.39	-0.229384267	0.01278444	PHATRDRAFT_42882	-	-	-	-		-
7196039	714	532	719.64	613.97	-0.229107215	0.0046293	PHATRDRAFT_42469	-	-	-	-		-
7195877	402.17	300.3	134.15	114.48	-0.228751477	0.0354834	PHATRDRAFT_49357	-	-	-	-		-
7198997	430.83	321.7	144.61	123.41	-0.228708018	0.029939	PHATRDRAFT_50346	-	-	-	-		-
7195819	419	313	135.54	115.72	-0.228080448	0.0328332	PHATRDRAFT_40174	K14319|1|1e-15|84.0|mtr:MTR_1g105040|Ran GTPase-activating protein 1	-	-	-		-
7199869	467	349	123.14	105.16	-0.227713427	0.0245756	PHATRDRAFT_44745	K11366|1|4e-34|145|sbi:SORBI_06g030580|ubiquitin carboxyl-terminal hydrolase 22/27/51 [EC:3.1.2.15]	-	GO:0046914//transition metal ion binding;GO:0016790//thiolester hydrolase activity;GO:0070011//peptidase activity, acting on L-amino acid peptides	GO:0019941//modification-dependent protein catabolic process		GO:0019941//modification-dependent protein catabolic process
7195023	1021	763	357.42	305.29	-0.227440031	0.00087418	PHATRDRAFT_48735	-	-	-	-		-
7199438	515	384	742.86	635	-0.226333753	0.01668768	PHATRDRAFT_50594	-	-	-	-		-
7200229	586	437	1230.48	1053.88	-0.223510605	0.01072078	PHATRDRAFT_45193	-	-	-	-		-
7203808	957	721	103.82	89.34	-0.216706233	0.00218654	PHATRDRAFT_48348	-	-	-	-		-
7196800	1794	1355	752.7	649.91	-0.211835025	3.64E-05	HSP70A	K03283|1|0.0|904|rcu:RCOM_1442270|heat shock 70kDa protein 1/8	-	GO:0032550	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7199425	1362	1031	578.25	500.4	-0.208611571	0.00039211	PHATRDRAFT_50604	-	-	-	-		-
7195733	1229	931	885.37	767.36	-0.206376926	0.000804218	PHATRDRAFT_49510	-	-	-	-		-
7194677	748	567	485.35	420.85	-0.205719375	0.00927378	PHATRDRAFT_48691	-	-	-	-		-
7204239	672	510	373.48	324.15	-0.204369415	0.01444384	PHATR_51609	K00815|1|7e-61|233|cme:CMT533C|tyrosine aminotransferase [EC:2.6.1.5]	-	GO:0016769//transferase activity, transferring nitrogenous groups;GO:0043168//anion binding	GO:0019752//carboxylic acid metabolic process		GO:0019752//carboxylic acid metabolic process
7196835	720	548	630.02	548.86	-0.198959426	0.01301952	PHATRDRAFT_9476	K00166|1|3e-100|363|smo:SELMODRAFT_169956|2-oxoisovalerate dehydrogenase E1 component, alpha subunit [EC:1.2.4.4]	-	GO:0016903//oxidoreductase activity, acting on the aldehyde or oxo group of donors	-		-

7198211	496	378	250.9	218.64	-0.198555106	0.0412116	PHATRDRAFT_49601	-	-	GO:0043168//anion binding;GO:0008483//transaminase activity	-		-
7201628	994	758	669.85	584.36	-0.19698064	0.00397188	PHATRDRAFT_46359	-	GO:0009536//plastid	GO:0016667//oxidoreductase activity, acting on a sulfur group of donors	GO:0019725//cellular homeostasis		GO:0019725//cellular homeostasis
7195950	700	535	720.8	630.84	-0.19232487	0.01738926	PHATRDRAFT_42564	-	-	-	-		-
7199179	640	491	184.07	161.38	-0.189792718	0.0269152	PHATRDRAFT_50351	K01188|1|3e-115|415|vvi:100232900|beta-glucosidase [EC:3.2.1.21];K05350|5|2e-111|402|zma:100274288|beta-glucosidase [EC:3.2.1.21]	-	GO:0015926//glucosidase activity	GO:0030243//cellulose metabolic process		GO:0030243//cellulose metabolic process
7203012	487	372	1092.13	958.5	-0.188294258	0.0465608	PHATRDRAFT_14646	-	-	-	-		-
7204016	1242	954	785.65	690.28	-0.186705063	0.00222934	PHATR_843	K01968|1|5e-135|479|zma:100280665|3-methylcrotonyl-CoA carboxylase alpha subunit [EC:6.4.1.4]	GO:0043231//intracellular membrane-bounded organelle;GO:0044444//cytoplasmic part	GO:0043169//cation binding;GO:0032550;GO:0016879//ligase activity, forming carbon-nitrogen bonds	-		-
7202857	7941	6108	3498.07	3076.05	-0.185480205	1.87E-14	PHATRDRAFT_47667	K14683|1|1e-59|229|zma:100501653|solute carrier family 34 (sodium-dependent phosphate cotransporter)	-	GO:0015114//phosphate ion transmembrane transporter activity	GO:0006817//phosphate ion transport		GO:0006817//phosphate ion transport
7195239	770	592	588.9	518.09	-0.184819936	0.01685326	PHATRDRAFT_48957	-	-	-	-		-
7203940	1004	772	781.83	687.93	-0.184593172	0.0063828	HSP20B	K13993|1|9e-06|49.7|ath:AT4G10250|HSP20 family protein	-	-	GO:0050896//response to stimulus		GO:0050896//response to stimulus
7199054	986	758	904.36	795.88	-0.18434626	0.0067886	PHATRDRAFT_50306	-	-	-	-		-
7203409	2558.08	1972.53	310.09	273.12	-0.183152038	1.93E-05	PHATRDRAFT_48048	-	-	-	-		-
7203740	656	506	219.59	193.58	-0.18188245	0.0313982	GLNA	K01915|1|0.0|808|olu:OSTLU_39960|glutamine synthetase [EC:6.3.1.2]	-	GO:0016211	GO:0008152//metabolic process		GO:0008152//metabolic process
7195044	709	546	738.96	651.67	-0.181354692	0.0235144	Rab1a	K07874|1|9e-87|318|sbi:SORBI_04g033160|Ras-related protein Rab-1A	GO:0043231//intracellular membrane-bounded organelle;GO:0016020//membrane	GO:0003824//catalytic activity;GO:0032550	GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization		GO:0035556//intracellular signal transduction;GO:0045184//establishment of protein localization
7199146	4030	3118	2737.35	2422.86	-0.176068867	1.81E-07	PHATRDRAFT_50366	K11498|1|1e-06|52.8|aly:ARALYDRAFT_478343|centromeric protein E	-	-	-		-
7197739	806	626	192.11	170.49	-0.172245497	0.0237738	PHATRDRAFT_44445	K08860|1|2e-26|120|smo:SELMODRAFT_83492|eukaryotic translation initiation factor 2-alpha kinase [EC:2.7.11.1];K08282|3|3e-24|112|aly:ARALYDRAFT_486408|non-specific serine/threonine protein kinase [EC:2.7.11.1]	-	GO:0004672//protein kinase activity;GO:0032550	GO:0006464//cellular protein modification process		GO:0006464//cellular protein modification process
7202590	1077	837	507.32	450.79	-0.170440525	0.00929076	PHATRDRAFT_47483	-	-	-	-		-
7204256	1297.05	1008.05	1006.38	895.01	-0.16919945	0.00431114	PHATR_54153	-	-	-	-		-
7203456	720	562	329.02	293.62	-0.164225042	0.0403232	PHATRDRAFT_48084	-	-	-	-		-
7203002	836	655	438.17	392.57	-0.158540784	0.032357	PHATRDRAFT_48004	-	-	-	-		-
7202869	939	739	442.07	397.79	-0.152267824	0.0292738	VTE1	-	GO:0031224//intrinsic component of membrane;GO:0043231//intracellular membrane-bounded organelle	GO:0009975//cyclase activity	-		-
7198355	1448	1140	715.55	644.14	-0.151678297	0.00695054	PHATRDRAFT_52619	K03458|1|6e-116|416|cre:CHLREDRAFT_169264|nucleobase:cation symporter-2, NCS2 family	-	-	GO:0051234//establishment of localization;GO:0044763		GO:0051234//establishment of localization;GO:0044763
7201549	959	756	605.74	546.21	-0.149242956	0.0300424	PHATRDRAFT_46448	K13993|1|2e-09|62.4|zma:100282088|HSP20 family protein	-	-	-		-
7198209	1050	831	653.09	591.22	-0.143586744	0.0286822	PHATRDRAFT_49598	-	-	-	-		-
7198208	1422	1126	968.19	877.06	-0.142614652	0.01127364	PHATRDRAFT_49596	-	GO:0043231//intracellular membrane-bounded organelle	GO:0001071//nucleic acid binding transcription factor activity;GO:0003677//DNA binding	GO:0006351//transcription, DNA-templated		GO:0006351//transcription, DNA-templated
7199772	1986	1574	815.27	738.64	-0.142406536	0.00297982	PHATRDRAFT_44828	-	-	-	-		-
7201450	1130	897	490.7	445.31	-0.140031262	0.0274936	PHATRDRAFT_46118	-	-	-	-		-

7204057	1034	823	337.92	307.4	-0.136564575	0.0401284	PHATR_33512	K09291|1|1e-13|77.4|ath:AT1G79280|nucleoprotein TPR;K10400|3|8e-12|71.2|vvi:100255624|kinesin family member 15	GO:0043229//intracellular organelle	-	-		-
7205140	1361	1085	321.53	292.88	-0.134643674	0.0204936	PHATRDRAFT_bd1613	K05658|1|5e-82|305|rcu:RCOM_1598590|ATP-binding cassette, subfamily B (MDR/TAP), member 1	GO:0031224//intrinsic component of membrane	GO:0017111//nucleoside-triphosphatase activity;GO:0032550;GO:0015405	GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization		GO:0009154//purine ribonucleotide catabolic process;GO:0044763;GO:0051234//establishment of localization
7195399	1270	1017	743.48	680.92	-0.126808625	0.0328272	PHATRDRAFT_49003	K13076|1|1e-06|52.8|olu:OSTLU_15110|delta8-fatty-acid desaturase [EC:1.14.19.4]	-	GO:0046906//tetrapyrrole binding	-		-
7198442	1515	1217	653.91	600.52	-0.122879791	0.0243364	PHATRDRAFT_49759	-	-	-	-		-
7197075	5934.56	4789.53	4510.57	4165.44	-0.114840861	2.39E-05	PHATRDRAFT_43305	-	-	-	-		-
7203043	2607	2141	421.5	395.44	-0.09207382	0.0268668	CHC	K04646|1|0.0|1461|rcu:RCOM_0838580|clathrin heavy chain	GO:0012510//trans-Golgi network transport vesicle membrane;GO:0005905//coated pit	-	GO:0015031//protein transport		GO:0015031//protein transport
7203359	2811	2308	998.34	936.89	-0.09165156	0.0210738	PHATRDRAFT_48252	-	-	GO:0046914//transition metal ion binding	-		-
7201088	8030	6806	1480.96	1434.01	-0.04647759	0.045228	PHATRDRAFT_45835	K12385|1|6e-18|92.4|gmx:100795551|Niemann-Pick C1 protein	GO:0031224//intrinsic component of membrane	GO:0004888//transmembrane signaling receptor activity	-		-

Suppl. Table 6

#Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value	Input	Hyperlink
Biosynthesis of amino acids	KEGG PATHWAY	ko01230	41	46	4.13E-24	1.02E-21	7205056｜7203478｜7195850｜7196652｜7200374｜7195267｜7195880｜7199266｜7205108｜7203740｜7202457｜7203024｜7197905｜7204239｜7197437｜7203376｜7197206｜7203160｜7195448｜7199911｜7202848｜7196176｜7196707｜7197473｜7201792｜7203381｜7204794｜7204792｜7199350｜7198605｜7202846｜7198165｜7196967｜7202915｜7203240｜7195265｜7200642｜7197646｜7204815｜7201155｜7204951	http://www.genome.jp/kegg-bin/show_pathway?ko01230/K01079%09red/K01689%09red/K01687%09red/K01649%09red/K01624%09red/K00815%09red/K01915%09red/K00873%09red/K01702%09red/K00134%09red/K00058%09red/K01958%09red/K15849%09red/K01834%09red/K00814%09red/K00286%09red/K01623%09red/K00891%09red/K10206%09red/K01663%09red/K01694%09red/K17989%09red/K01758%09red/K01736%09red/K01735%09red/K00615%09red/K01739%09red/K01948%09red/K01803%09red/K01476%09red/K00766%09red
Carbon metabolism	KEGG PATHWAY	ko01200	41	80	1.09E-17	1.34E-15	7195267｜7205056｜7203153｜7203267｜7199127｜7199385｜7200374｜7199894｜7199266｜7205108｜7202457｜7205097｜7203024｜7197905｜7200978｜7197206｜7203376｜7202138｜7197637｜7195448｜7201458｜7198785｜7202968｜7204353｜7199139｜7203381｜7194878｜7204792｜7199350｜7202915｜7202926｜7201046｜7198165｜7196967｜7196652｜7201080｜7203879｜7200642｜7197646｜7204815｜7204951	http://www.genome.jp/kegg-bin/show_pathway?ko01200/K01079%09red/K00855%09red/K01689%09red/K11517%09red/K01638%09red/K01623%09red/K01624%09red/K01810%09red/K00873%09red/K03841%09red/K00058%09red/K01958%09red/K01834%09red/K00281%09red/K01899%09red/K01895%09red/K00236%09red/K01006%09red/K17989%09red/K01966%09red/K01965%09red/K00134%09red/K00615%09red/K01637%09red/K01948%09red/K00164%09red/K00297%09red/K01803%09red/K00029%09red/K00382%09red/K00814%09red/K00026%09red
Ribosome	KEGG PATHWAY	ko03010	36	123	5.75E-10	4.73E-08	7202135｜7196104｜7204185｜7204200｜7204713｜7197621｜7198389｜7197987｜7204328｜7199900｜7195509｜7198575｜7197472｜7202089｜7195602｜7203146｜7202478｜7203140｜7195130｜7204609｜7195982｜7204647｜7204199｜7203048｜7204554｜7199800｜7203316｜7203664｜7196740｜7198006｜7195444｜7196170｜7200128｜7198687｜7199058｜7198183	http://www.genome.jp/kegg-bin/show_pathway?ko03010/K02953%09red/K02872%09red/K02937%09red/K02885%09red/K02938%09red/K02868%09red/K02880%09red/K02958%09red/K02993%09red/K02991%09red/K02979%09red/K02995%09red/K02865%09red/K02975%09red/K02974%09red/K02976%09red/K02971%09red/K02877%09red/K02871%09red/K02923%09red/K02920%09red/K02921%09red/K02927%09red/K02898%09red/K02873%09red/K02896%09red/K02906%09red/K02925%09red/K02901%09red/K02903%09red/K02984%09red/K02980%09red/K02981%09red/K02966%09red/K02941%09red/K02962%09red
Glycolysis or Gluconeogenesis	KEGG PATHWAY	ko00010	20	38	1.72E-09	1.06E-07	7199139｜7203381｜7197206｜7204792｜7199894｜7203376｜7202915｜7205097｜7197637｜7205056｜7196967｜7199127｜7196652｜7202457｜7195267｜7201214｜7195448｜7204815｜7199266｜7199256	http://www.genome.jp/kegg-bin/show_pathway?ko00010/K03841%09red/K01623%09red/K00001%09red/K01689%09red/K01835%09red/K01834%09red/K01803%09red/K00134%09red/K01624%09red/K00382%09red/K01810%09red/K00873%09red/K01895%09red
Methane metabolism	KEGG PATHWAY	ko00680	12	14	7.24E-08	3.58E-06	7199266｜7204792｜7202915｜7205097｜7197637｜7205056｜7196967｜7196652｜7200374｜7200642｜7197905｜7204815	http://www.genome.jp/kegg-bin/show_pathway?ko00680/K01079%09red/K03841%09red/K00058%09red/K01689%09red/K01834%09red/K01623%09red/K01624%09red/K01895%09red
Pyruvate metabolism	KEGG PATHWAY	ko00620	14	28	7.70E-07	3.17E-05	7195267｜7195789｜7201368｜7205097｜7203153｜7198165｜7194806｜7195448｜7199385｜7203240｜7199894｜7199234｜7201046｜7201080	http://www.genome.jp/kegg-bin/show_pathway?ko00620/K00026%09red/K01958%09red/K01006%09red/K01759%09red/K01649%09red/K00029%09red/K00382%09red/K01638%09red/K00873%09red/K01895%09red/K11262%09red/K00102%09red
Cell cycle - yeast	KEGG PATHWAY	ko04111	17	58	1.94E-05	0.000613562	7196156｜7203613｜7195792｜7205163｜7196275｜7200964｜7204498｜7204180｜7200617｜7196023｜7205042｜7194718｜7202316｜7198409｜7203211｜7201897｜7195804	http://www.genome.jp/kegg-bin/show_pathway?ko04111/K06676%09red/K06677%09red/K06674%09red/K06669%09red/K04382%09red/K03456%09red/K02210%09red/K03353%09red/K03350%09red/K02213%09red/K03363%09red/K03355%09red/K03349%09red/K04563%09red/K06685%09red/K06639%09red/K03364%09red
Pentose phosphate pathway	KEGG PATHWAY	ko00030	10	19	2.12E-05	0.000613562	7199139｜7199266｜7204792｜7202915｜7197637｜7199127｜7196652｜7203024｜7197646｜7199256	http://www.genome.jp/kegg-bin/show_pathway?ko00030/K03841%09red/K01835%09red/K01810%09red/K01623%09red/K01624%09red/K00615%09red
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	ko00630	11	24	2.24E-05	0.000613562	7194878｜7203160｜7203267｜7203740｜7199385｜7196513｜7199894｜7198785｜7202968｜7200978｜7201080	http://www.genome.jp/kegg-bin/show_pathway?ko00630/K11517%09red/K00284%09red/K01638%09red/K00281%09red/K01966%09red/K01965%09red/K00382%09red/K01915%09red/K01637%09red/K00026%09red
Vibrio cholerae infection	KEGG PATHWAY	ko05110	12	35	9.44E-05	0.002330809	7198807｜7195027｜7195026｜7204611｜7194833｜7199151｜7202914｜7202589｜7198846｜7201668｜7194844｜7196829	http://www.genome.jp/kegg-bin/show_pathway?ko05110/K10956%09red/K05692%09red/K02144%09red/K02145%09red/K02146%09red/K02155%09red/K02154%09red/K02151%09red/K02150%09red
Selenocompound metabolism	KEGG PATHWAY	ko00450	7	11	0.000159	0.003490315	7200552｜7198605｜7200252｜7199666｜7195850｜7197552｜7204065	http://www.genome.jp/kegg-bin/show_pathway?ko00450/K01758%09red/K03341%09red/K13811%09red/K01874%09red/K00816%09red/K01739%09red
Meiosis - yeast	KEGG PATHWAY	ko04113	13	44	0.00017	0.003490315	7196156｜7203613｜7195792｜7205163｜7196275｜7204498｜7200964｜7194718｜7196666｜7202316｜7198409｜7205042｜7196023	http://www.genome.jp/kegg-bin/show_pathway?ko04113/K06639%09red/K06669%09red/K04382%09red/K03456%09red/K02210%09red/K03353%09red/K03350%09red/K02213%09red/K03363%09red/K03355%09red/K03349%09red/K04563%09red/K06269%09red
Fructose and mannose metabolism	KEGG PATHWAY	ko00051	9	21	0.000187	0.003552661	7197943｜7199266｜7204792｜7202915｜7197637｜7196652｜7198789｜7197497｜7202457	http://www.genome.jp/kegg-bin/show_pathway?ko00051/K01809%09red/K03841%09red/K01803%09red/K01805%09red/K01711%09red/K01623%09red/K01624%09red
Porphyrin and chlorophyll metabolism	KEGG PATHWAY	ko00860	9	22	0.000247	0.004278499	7197643｜7204596｜7201329｜7204128｜7197023｜7197242｜7200644｜7196312｜7200041	http://www.genome.jp/kegg-bin/show_pathway?ko00860/K02492%09red/K10960%09red/K04040%09red/K03403%09red/K03404%09red/K00228%09red/K01772%09red/K00218%09red/K01599%09red
Collecting duct acid secretion	KEGG PATHWAY	ko04966	8	17	0.00026	0.004278499	7198807｜7204611｜7194833｜7199151｜7202914｜7202589｜7201668｜7194844	http://www.genome.jp/kegg-bin/show_pathway?ko04966/K02145%09red/K02146%09red/K02155%09red/K02154%09red/K02151%09red/K02150%09red

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<tr><td>Plant-pathogen interaction</td><td>KEGG PATHWAY</td><td>ko04626</td><td>5</td><td>6</td><td>0.000626</td><td>0.009100315</td><td>7202801|7199468|7194947|7196961|7198971</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko04626/K02183%09red/K09487%09red/K13412%09red/K04079%09red</td></tr>
<tr><td>Synaptic vesicle cycle</td><td>KEGG PATHWAY</td><td>ko04721</td><td>11</td><td>40</td><td>0.000875</td><td>0.011563042</td><td>7198807|7194833|7204611|7203043|7199151|7202914|7202589|7201668|7196569|7194844|7196829</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko04721/K04646%09red/K02144%09red/K02145%09red/K02146%09red/K15015%09red/K02155%09red/K02154%09red/K02151%09red/K02150%09red</td></tr>
<tr><td>Arginine biosynthesis</td><td>KEGG PATHWAY</td><td>ko00220</td><td>7</td><td>16</td><td>0.000889</td><td>0.011563042</td><td>7199350|7205108|7203478|7203160|7203740|7202332|7200113</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00220/K00262%09red/K01948%09red/K01476%09red/K00814%09red/K01915%09red/K15371%09red</td></tr>
<tr><td>Amino sugar and nucleotide sugar metabolism</td><td>KEGG PATHWAY</td><td>ko00520</td><td>10</td><td>34</td><td>0.000969</td><td>0.011961655</td><td>7199139|7197943|7203905|7199127|7200985|7197497|7200293|7204758|7198727|7199256</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00520/K01809%09red/K00326%09red/K01835%09red/K08679%09red/K12447%09red/K01711%09red/K01810%09red/K00012%09red/K06118%09red</td></tr>
<tr><td>Fatty acid biosynthesis</td><td>KEGG PATHWAY</td><td>ko00061</td><td>5</td><td>8</td><td>0.001544</td><td>0.017334033</td><td>7194806|7199234|7196866|7200471|7200591</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00061/K01897%09red/K15013%09red/K11262%09red/K03921%09red</td></tr>
<tr><td>Sulfur metabolism</td><td>KEGG PATHWAY</td><td>ko00920</td><td>5</td><td>8</td><td>0.001544</td><td>0.017334033</td><td>7197713|7198605|7200552|7204140|7196698</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00920/K00392%09red/K00390%09red/K01739%09red/K00387%09red/K13811%09red</td></tr>
<tr><td>Starch and sucrose metabolism</td><td>KEGG PATHWAY</td><td>ko00500</td><td>8</td><td>25</td><td>0.001986</td><td>0.020443898</td><td>7199139|7200191|7194914|7203905|7199127|7199179|7200293|7199256</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00500/K01835%09red/K01188%09red/K16055%09red/K08679%09red/K01810%09red/K00012%09red/K05349%09red</td></tr>
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<tr><td>Glycine, serine and threonine metabolism</td><td>KEGG PATHWAY</td><td>ko00260</td><td>9</td><td>32</td><td>0.002228</td><td>0.022007797</td><td>7204951|7203267|7196967|7195850|7200374|7199894|7200642|7197905|7196707</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00260/K01079%09red/K00058%09red/K01694%09red/K01758%09red/K17989%09red/K00281%09red/K00382%09red/K01834%09red</td></tr>
<tr><td>Purine metabolism</td><td>KEGG PATHWAY</td><td>ko00230</td><td>21</td><td>130</td><td>0.002879</td><td>0.027348286</td><td>7200552|7204516|7197863|7204613|7200916|7199116|7202167|7204448|7200966|7195448|7204365|7204096|7203014|7199256|7195267|7204977|7197412|7195734|7194847|7197416|7202225</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00230/K01756%09red/K03007%09red/K01835%09red/K01519%09red/K00760%09red/K11808%09red/K03015%09red/K13811%09red/K03004%09red/K01488%09red/K01522%09red/K03012%09red/K02327%09red/K00106%09red/K00873%09red/K02999%09red/K00365%09red/K03019%09red/K03018%09red/K02325%09red</td></tr>
<tr><td>Aminoacyl-tRNA biosynthesis</td><td>KEGG PATHWAY</td><td>ko00970</td><td>11</td><td>48</td><td>0.003026</td><td>0.027681075</td><td>7205014|7196876|7200252|7199666|7203883|7199943|7196856|7202999|7195079|7195006|7202384</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00970/K04567%09red/K01883%09red/K01881%09red/K01880%09red/K03341%09red/K01870%09red/K01873%09red/K01872%09red/K01874%09red/K01868%09red/K01893%09red</td></tr>
<tr><td>Alanine, aspartate and glutamate metabolism</td><td>KEGG PATHWAY</td><td>ko00250</td><td>8</td><td>29</td><td>0.00427</td><td>0.036995967</td><td>7199350|7205108|7203160|7203740|7202332|7196480|7200113|7197416</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00250/K00262%09red/K01756%09red/K01948%09red/K00294%09red/K00814%09red/K01915%09red/K15371%09red</td></tr>
<tr><td>Arginine and proline metabolism</td><td>KEGG PATHWAY</td><td>ko00330</td><td>9</td><td>36</td><td>0.004344</td><td>0.036995967</td><td>7204681|7203478|7198992|7195168|7203754|7196480|7203329|7197473|7204039</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00330/K00318%09red/K00294%09red/K00286%09red/K12251%09red/K01476%09red/K00472%09red/K00797%09red</td></tr>
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<tr><td>Ascorbate and aldarate metabolism</td><td>KEGG PATHWAY</td><td>ko00053</td><td>4</td><td>7</td><td>0.005945</td><td>0.047367133</td><td>7202539|7195740|7200985|7203905</td><td>http://www.genome.jp/kegg-bin/show_pathway?ko00053/K00012%09red/K00225%09red/K00434%09red/K12447%09red</td></tr>
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