Supplemental Materials

Mitochondrial lineage assignment

To ensure the selection experiment did not confound selection between mitochondrial lineages, which are potentially cryptic species, and selection within a lineage, we determined the major and minor mitochondrial haplotypes present in our samples. This analysis follows previous COI work conducted in *A. tonsa* (1, 2), particularly Figueroa et al. (3). We used a reference COI from Figueroa et al. to align and pull out the COI region in our raw FASTQ files. Variants were called using Varscan2 (4) in the same manner as our full dataset. Because these are pooled data, we cannot determine haplotypes of individuals. Further, if two lineages were present at equal frequencies, it would be difficult to determine which two haplotypes were present; the variants of each would be mixed in these pooled data. We assessed the distribution of allele frequencies to predict the number and frequency of mitochondrial haplotypes present in these data. Given the bimodal distribution of variants, where SNPs are either nearly fixed or absent (Fig. S9), there are likely two mitochondrial lineages present in these samples; one at very high frequency, and the other at low frequency. Looking at the shift in variant frequency from F0 to F25, it is apparent that the low frequency variant drops out over time while the high frequency variant (which is nearly fixed) remains. Because of the low number of variant sites, the high frequency variant also appears to match the reference sequence, which is from an individual from clade X. All results below hold when a reference from a different clade is used instead.

We reconstruct the major and minor haplotypes present in our data. Given the bimodal distribution of variants, we can reconstruct the consensus sequence of the major haplotypes as variants that are nearly fixed, while the minor haplotype consists of the low frequency variants. We only construct the minor haplotypes for F0 samples, as these haplotypes are no longer present by F25. Variants were filtered in R and VCF files containing either the major or minor variants were created. *bcftools* was used to generate consensus sequences for each sample and haplotype and sequences were concatenated with fasta sequences from Figueroa et al. to allow for direct comparisons downstream. This fasta file was aligned with MUSCLE (5), converted to NEXUS format in R using APE (6), and a phylogenetic tree was built using MrBayes (7) using the substitution model HKY + I + G, following Figueroa et al. The plot was generated with ggtree in R (8). The resulting tree clearly shows that the major haplotype is clade X, with a low frequency of clade S present at F0 (Fig. S10). The S clade drops out by F3 and is not present in any samples at F25, including the ambient selection line. Given the low

frequency of clade S and its absence from all lines by F25, the divergence detected in our experiment is not simply due to selection for a mitochondrial clade, but due to selection within individuals of clade X.

Analysis of covariance in allele frequency change

The replicated nature of our experiment coupled with the multiple selection regimes allows us to disentangle the relative contributions of drift and selection on the genome-wide changes in allele frequencies. We use and expand upon the approach developed by Buffalo and Coop (9). This method quantifies genome-wide covariance in the change in allele frequencies between replicates of a single treatment and between treatments to determine the relative contributions of drift and selection as well as to assess the degree of shared selection between selection regimes. Finally, we can leverage the presence of the control ambient line to estimate and remove the effects of the aforementioned estimates of lab adaptation.

First, it is possible to partition the changes in allele frequencies within a treatment into selection and drift components for replicate A as:

$$\Delta P_{t,A} = \Delta_D P_t + \Delta_S P_t$$

where $\Delta_S P_t$ is the change due to selection and $\Delta_D P_t$ is drift. The proportion of change due to selection can be further defined as the allele frequency change due to lab selection common to all replicates within a treatment group, $\Delta_L P_t$, as well as the change due to selection within a specific selection regime, $\Delta_R P_t$. The change in allele frequency in replicate A can be partitioned into,

$$\Delta P_{t,A} = \Delta_D P_t + \Delta_L P + \Delta_R P_t$$

Because the terms above are uncorrelated, the variance is,

$$\mathrm{Var}(\Delta p_t) = \ \mathrm{Var}(\Delta_D P_t) + \ \mathrm{Var}(\Delta_L P_t) + \mathrm{Var}(\Delta_R P_t)$$

We estimate the shared effects of selection regime from the allele frequency changes as the covariance of allele frequency change between any two replicates,

$$\mathrm{Var}(\Delta_R P_t) = Cov(\Delta P_{t,A}, \Delta P_{t,B})$$

Where A and B indicate different replicates within a selection regime. Thus, to estimate the total shared response to selection within a selection regime, we estimate the covariance between all pairwise replicates and take their mean. Further, because of the presence of an ambient control line in our study, we can estimate the contribution of adaptation to the lab environment to the overall changes in allele frequency. The shared variance between a selection regime and the control represents the contribution of lab adaptation within a treatment group, again estimated as the mean of all pairwise comparisons between the two groups, giving $\mathrm{Var}\Delta_L P_t$. We can subtract this value from the shared response within a selection regime, $\mathrm{Var}(\Delta_R P_t)$, to get an estimate of the response to selection that is independent of estimated average lab selection effect.

After determining the contributions from selective regime and lab adaptation, the remaining variance can be attributed to the drift component. Finally, these values can be divided by the total variance to find the proportion each contributes to the overall variance in change in allele frequency.

Next, we can use similar principles to determine the shared response to selection between each selective regime. Here, the shared response to selection is again the covariance in allele frequency change between any two replicates, as above, but now from two different treatments,

$$\mathrm{Var}(\Delta_R P_t) = Cov(\Delta_{pt,A}, \Delta_{pt,B})$$

We take the mean of all possible pairwise comparisons between treatments and scale this by the total variance to determine the proportion of total variance of allele frequency change that is shared. Finally, lab adaptation can be estimated and accounted for as described above.

Accounting for shared variance due to limited F0 replication

In these data, covariances are calculated from the change in allele frequency from the same set of F0 samples for all treatments. While these F0 samples likely represent the pre-selective state of the population, replicating these samples in this way leads to a spurious increase in the covariance estimates between samples in different treatments due to shared sampling variance. This is made clear in the covariance heatmap (Fig. S3A) where along the diagonal where the same replicate is compared between treatments the covariance is increased; Fig. S3B shows these covariance calculations in a different format where the same pattern is evident. Similarly, we see the same pattern when the convergence correlation is calculated (Fig. S4). To avoid this inflation, we dropped any covariances between samples with the same F0 reference when calculating shared response to selection. For example, the covariance in allele frequency change between OWA replicate 1 and Acidification replicate 1 would not be included when quantifying the shared selection response between these treatments. While this reduces our replication to an extent, the estimates are likely much more accurate estimates of the true impact of selection on allele frequency changes as all covariances are independent as a result.

Supplemental table 1: Number of loci assigned to each functional category for each SNP set. The first value is the total number of loci, the 2nd is the proportion of the total. P-values from chi-squared tests relative to the genome-wide distribution. Underlined values are significant (Bonferroni correction: P < 0.05/15 = 0.0033). The "No Annotation" category refers to loci that were not on a scaffold with any annotated genes, indicating they are likely in fragmented regions of the genome assembly.

	All loci	OWA candidates	Warming candidates	Acidification candidates	Ambient candidates
No annotation	54,228 0.137	702 0.089 (p << 0.001)	577 0.092 (p < 0.001)	278 0.162 (p = 0.01)	431 0.134 (p=0.94)
Downstream	28,197 0.071	536 0.068 (p = 0.2)	465 0.074 (p = 0.41)	249 0.11 (p < 0.001)	276 0.088 (p=0.001)
Exon	229,898 0.583	5,198 0.656 (p < 0.001)	4,049 0.646 (p < 0.001)	885 0.517 (p = 0.0038)	1,778 0.564 (p=0.29)
Intron	46,837 0.117	809 0.102 (p < 0.001)	635 0.101 (p < 0.001)	396 0.108 (p = 0.24)	350 0.11 (p=0.24)
Promoter	35,507 0.0899	681 0.086 (p = 0.2)	544 0.087 (p = 0.42)	311 0.107 (p = 0.02)	315 0.10 (p=0.07)

Supplemental table 2: find at the end of this document.

Supplemental Figures

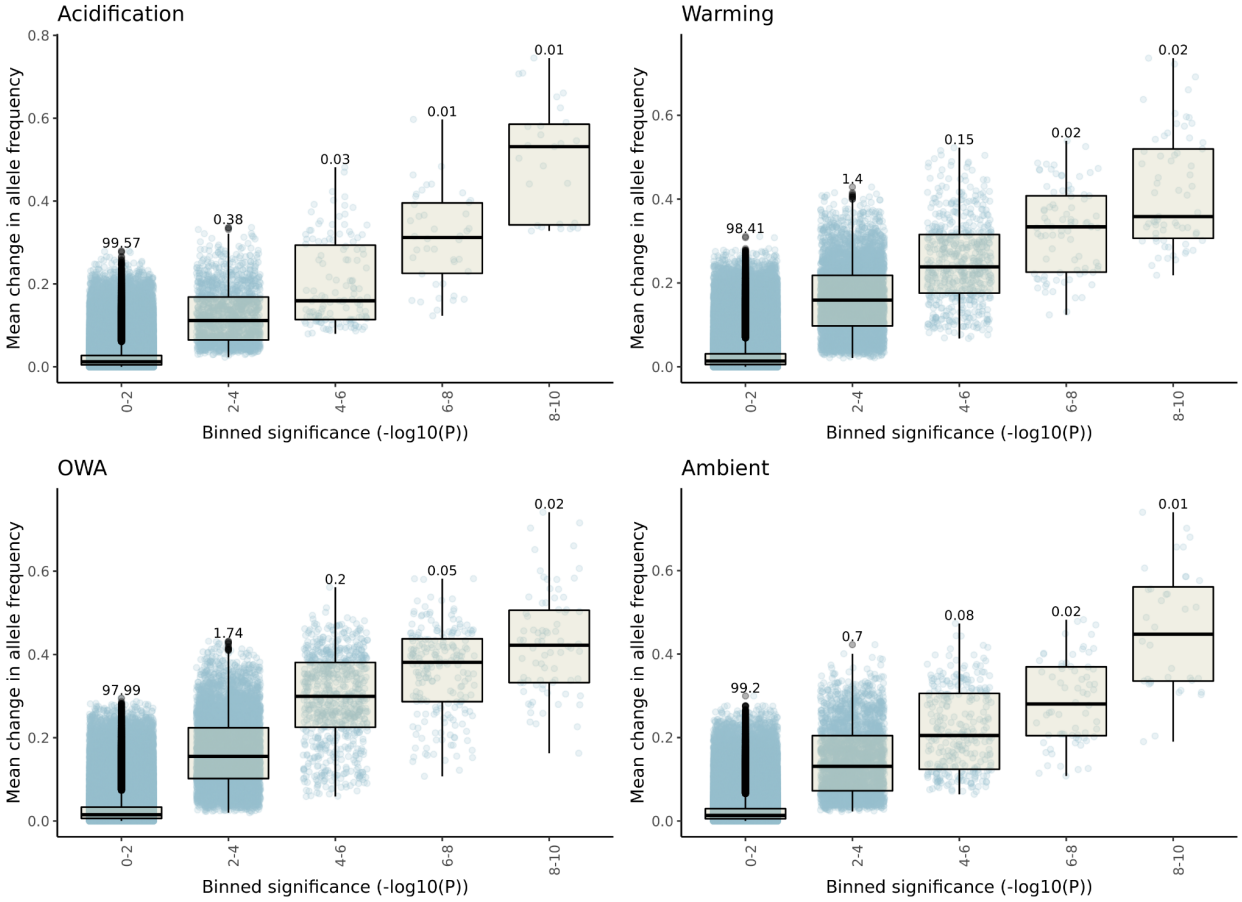

Figure S1: Empirical p-values from drift simulations. Points are individual loci with Tukey's boxplots. Values above each boxplot indicate the proportion of total loci in that bin.

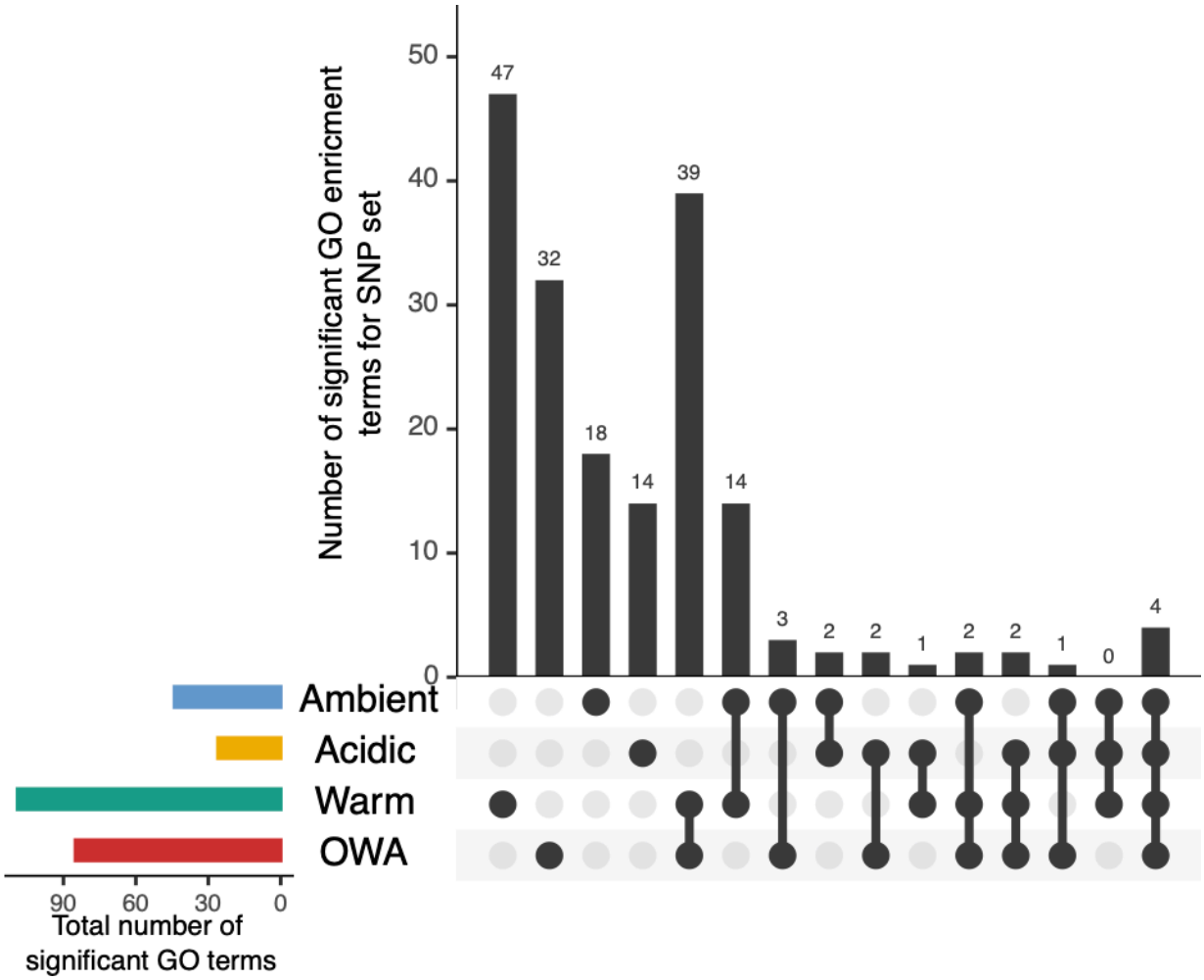

Figure S2. Number of significant go terms per category. Conducted with the same snps as the similar plot in the main text (Fig. 2).

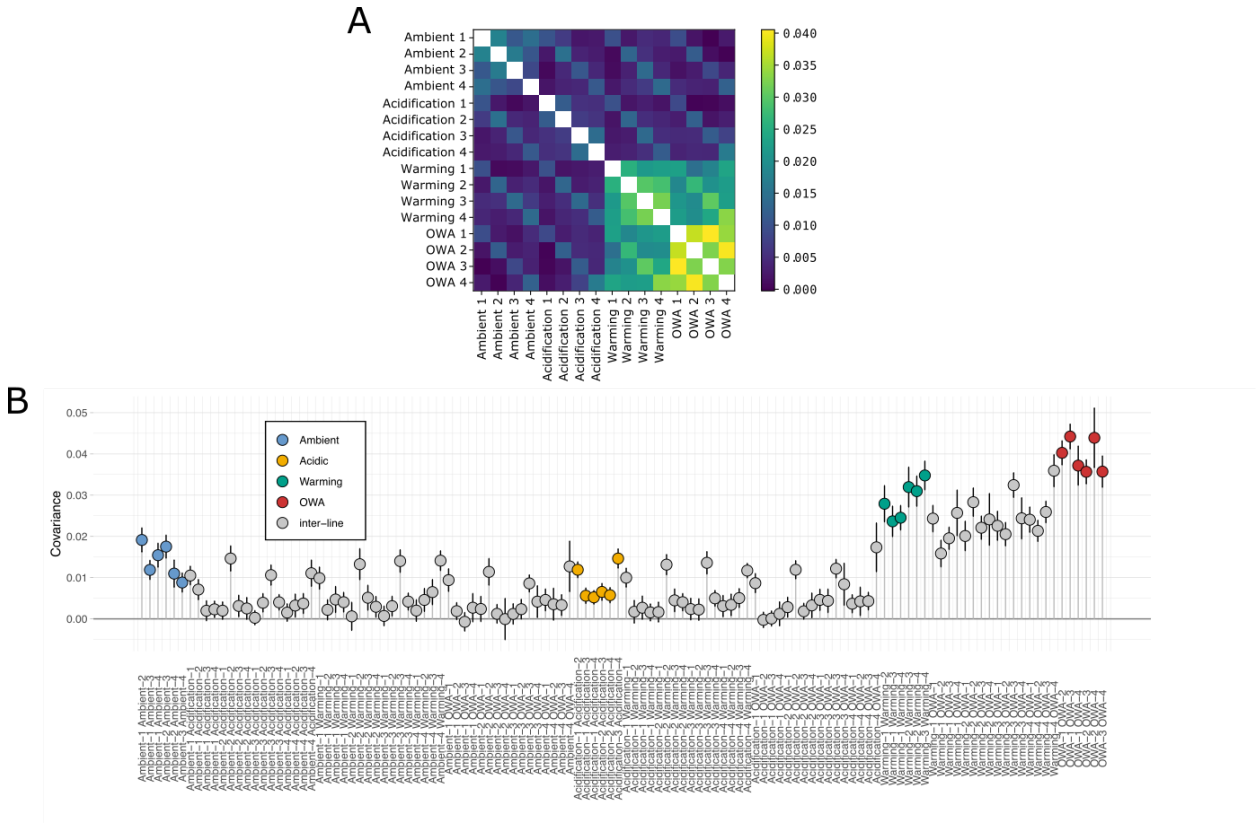

Figure S3: Pairwise covariance in allele frequency change between samples from F0 to F25. A) Each square and color indicate the covariance between two samples. Above the diagonal is a mirror of below. B) The same covariance estimates as in A, but with 95% bootstrap confidence intervals. Color indicates the group comparison. Note the increase in covariance between samples sharing the same replicate number due to an artifact from calculating allele frequency change from the same F0 sample. Samples with shared F0 samples (i.e., the same replicate number) were dropped from further calculations to avoid this bias.

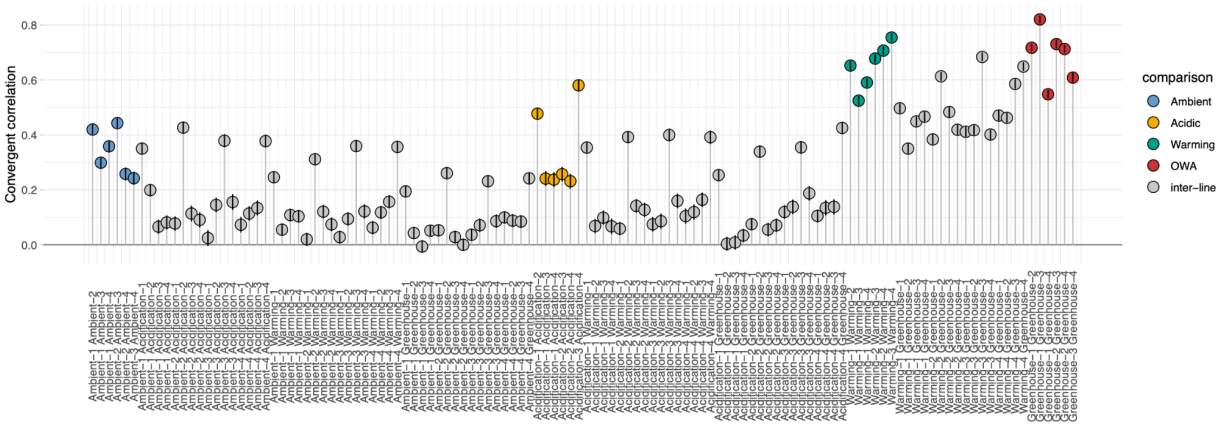

Figure S4: Convergent correlations of allele frequency change from F0 to F25 between samples. Black lines for each point show the 95% bootstrap confidence interval. Note the increase in convergent correlation between samples sharing the same replicate number due to an artifact from calculating allele frequency change from the same F0 sample. Samples with shared F0 samples (i.e., the same replicate number) were dropped from further calculations.

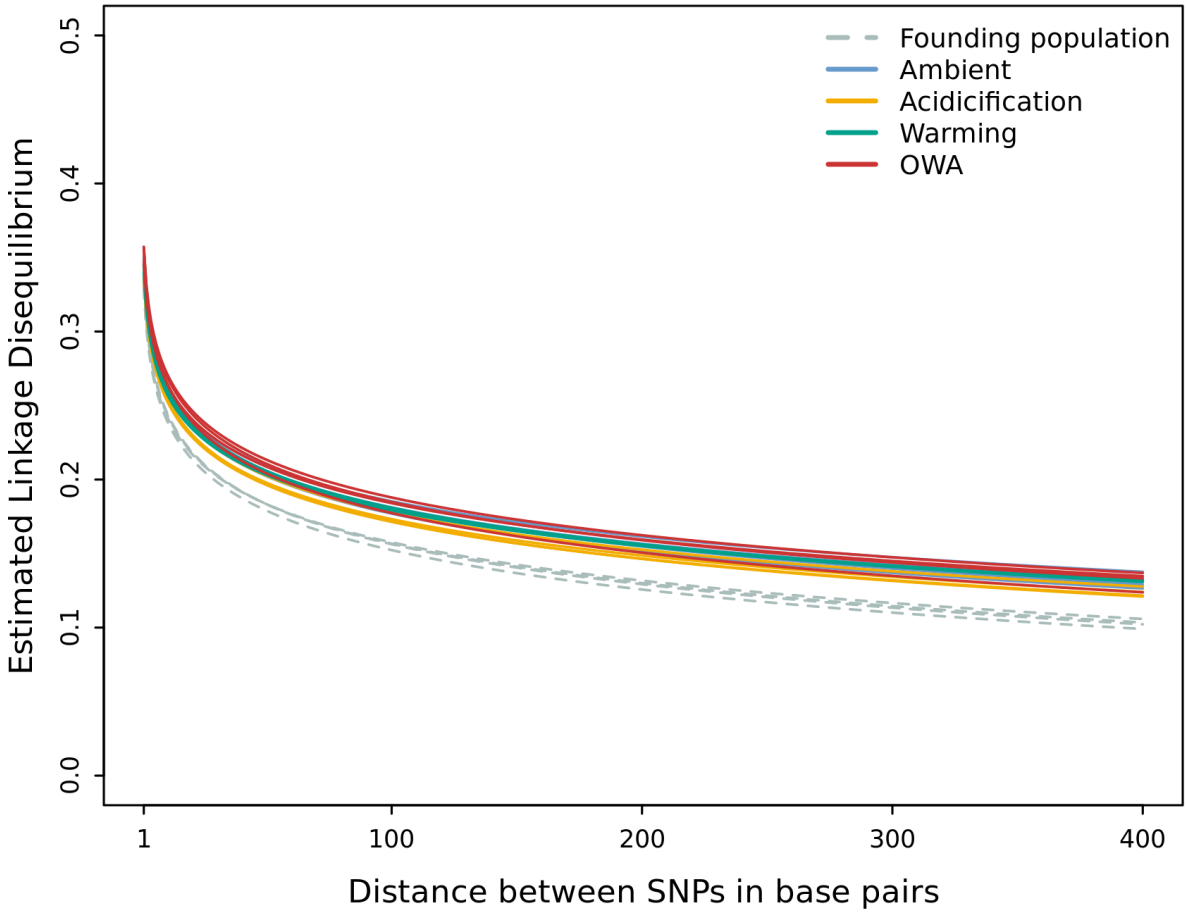

Figure S5: Linkage disequilibrium estimates. Decay curves were fit by regressing the log of the physical distance with LD between base pairs. LD estimates increased with the strength of selection relative to the F0 founding population ($P < 0.001$). Founding population: intercept = 0.212 ± 0.001, slope = -0.0497 ± 0.0003; Ambient: 0.245 ± 0.002, -0.0562 ± 0.0003; Acidification: 0.235 ± 0.001, -0.0549 ± 0.0003; Warming: 0.242 ± 0.001, -0.0556 ± 0.0003; OWA: 0.251 ± 0.002, -0.058 ± 0.0003

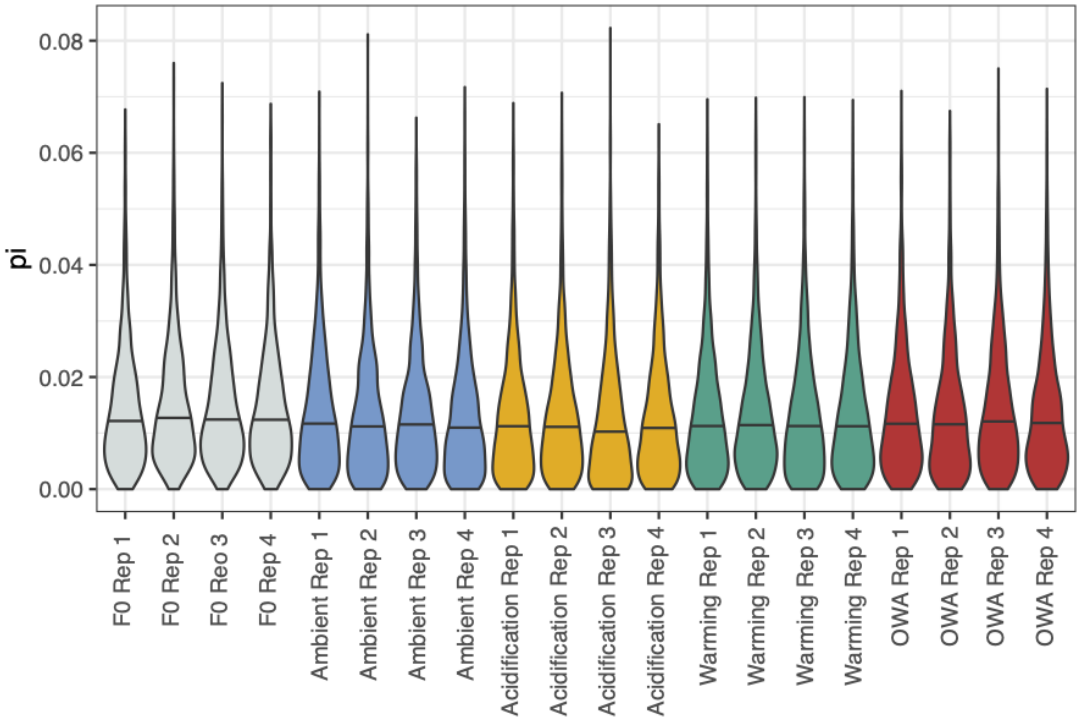

Fig. S6: Genetic diversity estimates. All treatment groups lost genetic diversity relative to the founding F0 population (Wilcoxon signed-rank test, $P < 0.0001$). Estimates for each group: F0 founding population: 0.0148 ± 0.0111; ambient: 0.0133 ± 0.0111; acidification: 0.0127 ± 0.0111; warming: 0.0133 ± 0.0110; OWA: 0.0138 ± 0.0112. Between the F25 treatments, only acidification lines were significantly lower than other lines ($P < 0.001$).

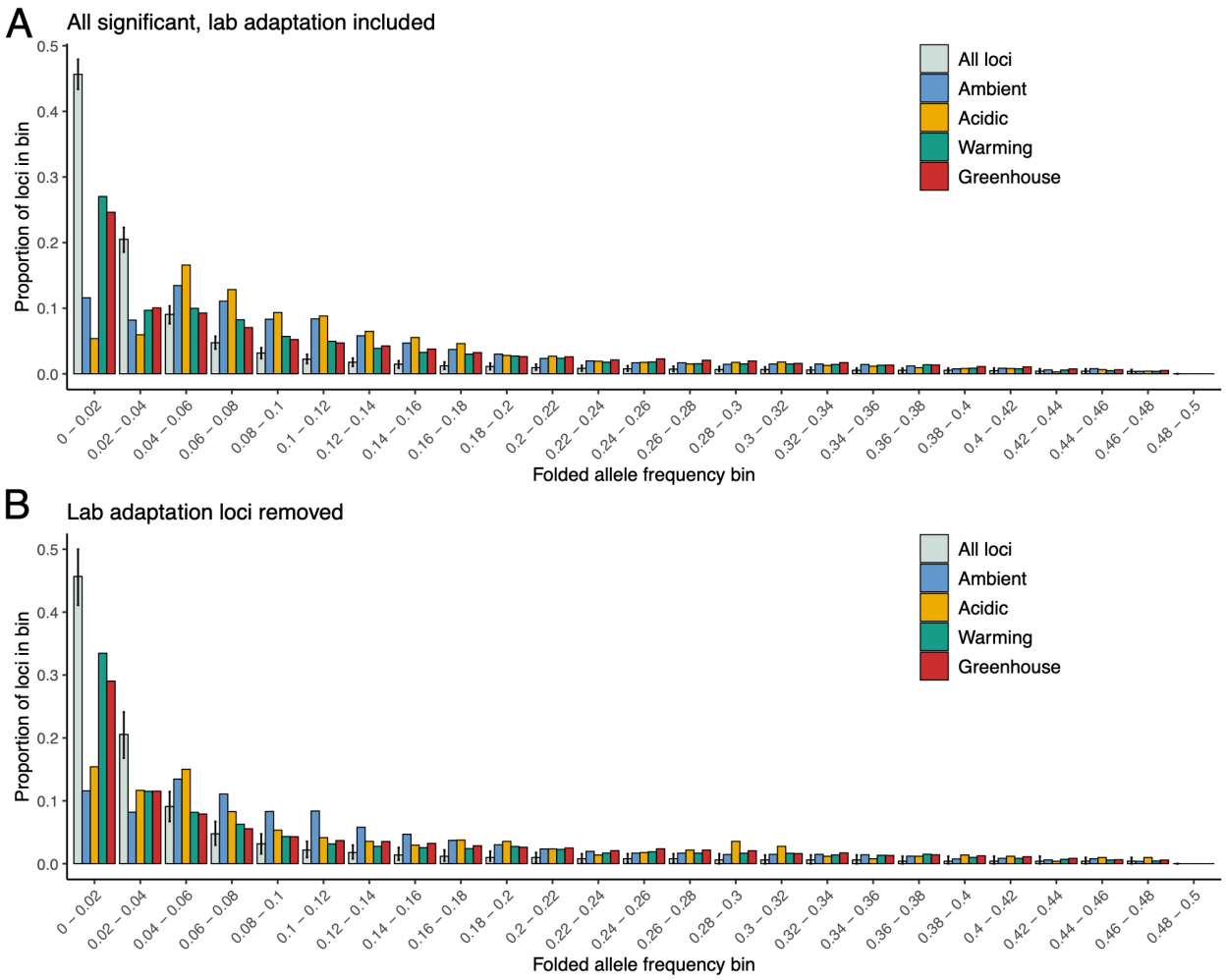

Fig. S7: Starting minor allele frequencies at F0 for loci significant for different treatments. Panel A includes lab adaptation loci in each group while these are removed in panel B. Error bars around the all loci group are 95% confidence intervals from 1000 random samples from all loci where the number of loci sampled was equal to the number of significant Acidification loci (A: 1,713, B: 506). Because the acidification group had the least number of significant loci, these confidence intervals are broader than if sampling was based on warming or OWA values.

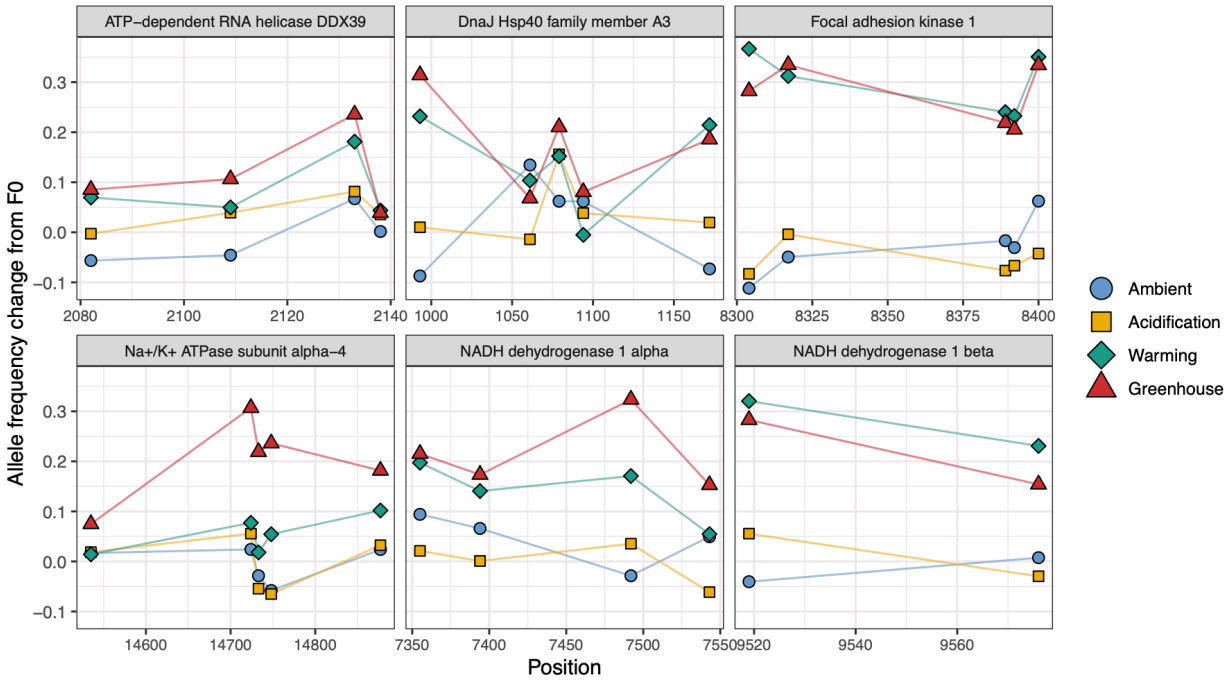

Figure S8: Representative candidate genes underlying rapid adaptation. Points represent the average allele frequency change among replicates from the starting frequencies at F0. Loci have been filtered for minor allele frequency > 0.1 at F0.

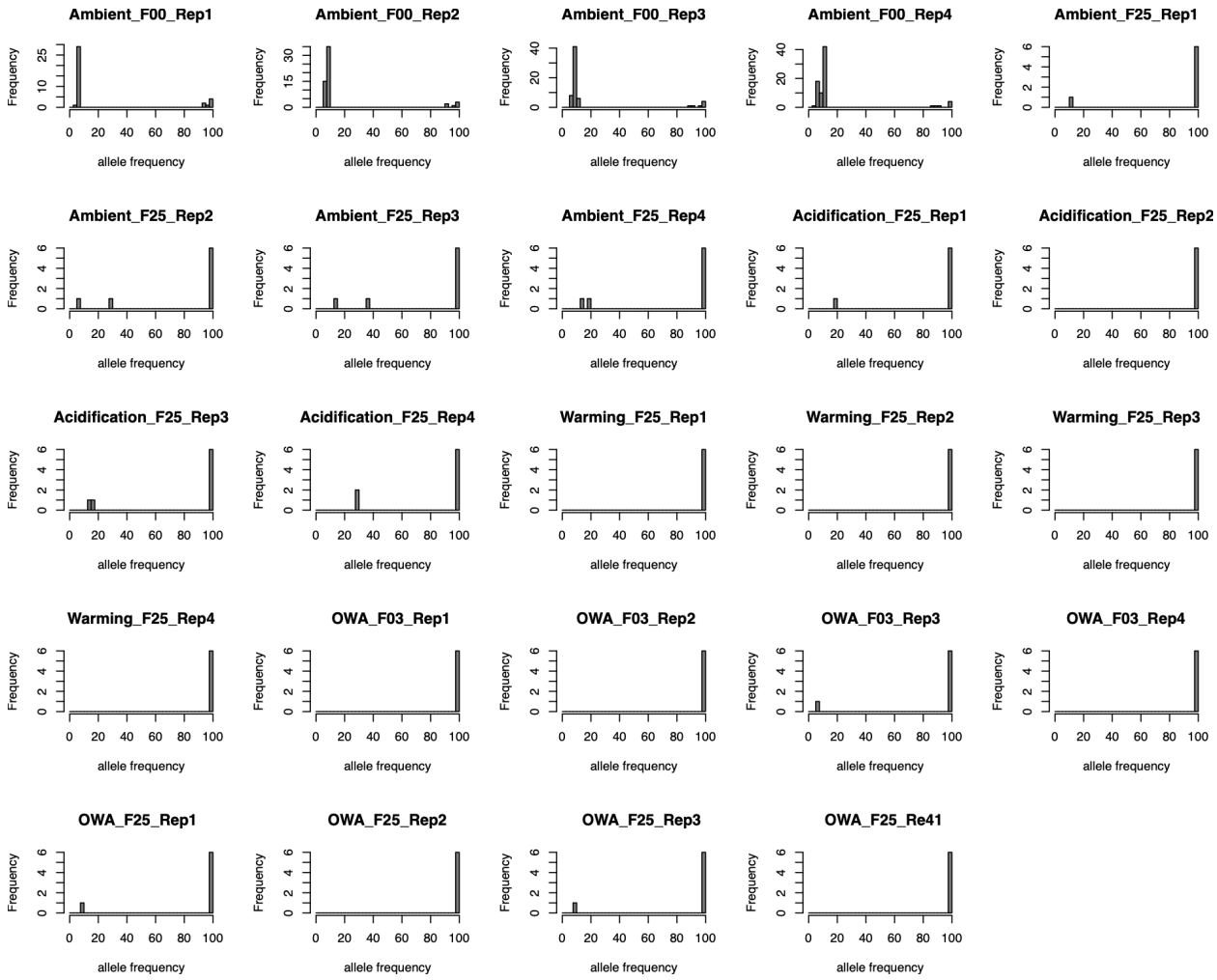

Figure S9: Frequency of mitochondrial haplotypes. Histograms show the frequency of haplotypes from variants in the pooled data. At F0, there were low frequency variants present in the data, indicating the presence of a low frequency haplotype. These minor alleles drop out by F3 and nearly absent by F25 across all samples. This indicates that the vast majority of samples matched the reference genome after 3 generations of selection. Given the low starting frequency of minor mitochondrial haplotypes, this suggests the pooled samples likely consisted of a dominant mitochondrial haplotype and selection across the rest of the genome was likely not due to shifting frequencies of mitochondrial clades.

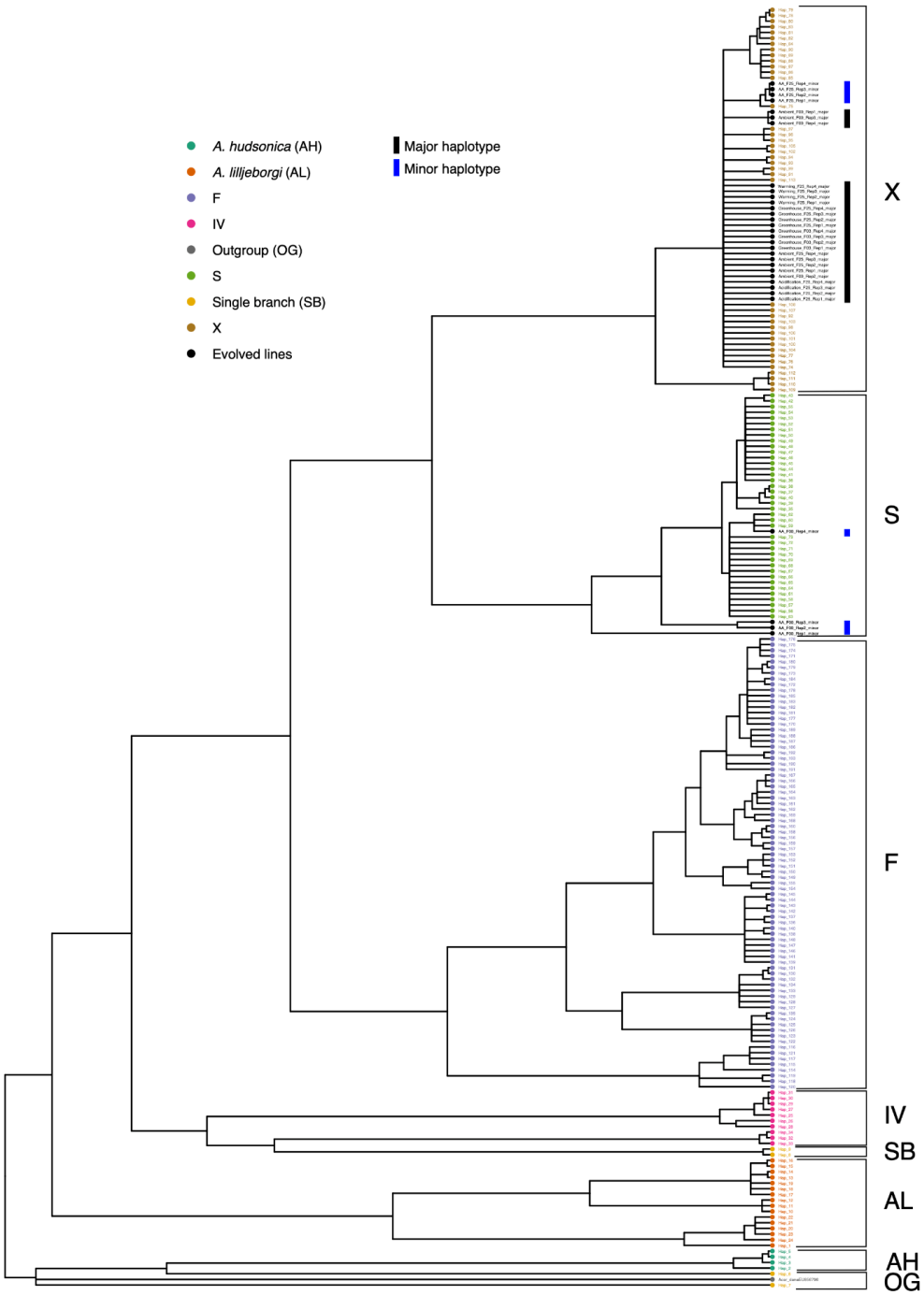

Figure S10: Phylogenetic tree from COI sequence data. We determined the clade of samples from this study using samples from Figueroa et al. (2020). Black and blue bars are the tree tips indicate major and minor haplotypes in the pooled samples, respectively. Samples in our study were predominantly clade X.

Supplemental References:

1. G. Chen, M. P. Hare, Cryptic ecological diversification of a planktonic estuarine copepod, Acartia tonsa. *Mol. Ecol.* **17**, 1451–1468 (2008).

2. G. Chen, M. P. Hare, Cryptic diversity and comparative phylogeography of the estuarine copepod Acartia tonsa on the US Atlantic coast. *Mol. Ecol.* **20**, 2425–2441 (2011).

3. N. J. Figueroa, D. F. Figueroa, D. Hicks, Phylogeography of Acartia tonsa Dana, 1849 (Calanoida: Copepoda) and phylogenetic reconstruction of the genus Acartia Dana, 1846. *Mar. Biodivers.* **50**, 23 (2020).

4. D. C. Koboldt, *et al.*, VarScan 2: somatic mutation and copy number alteration discovery in cancer by exome sequencing. *Genome Res.* **22**, 568–576 (2012).

5. R. C. Edgar, MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* **5**, 113 (2004).

6. E. Paradis, J. Claude, K. Strimmer, APE: Analyses of Phylogenetics and Evolution in R language. *Bioinformatics* **20**, 289–290 (2004).

7. F. Ronquist, *et al.*, MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Syst. Biol.* **61**, 539–542 (2012).

8. G. Yu, D. K. Smith, H. Zhu, Y. Guan, T. T. Lam, Ggtree : An r package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods Ecol. Evol.* **8**, 28–36 (2017).

9. V. Buffalo, G. Coop, Estimating the genome-wide contribution of selection to temporal allele frequency change. *Proc. Natl. Acad. Sci. U. S. A.* **117**, 20672–20680 (2020).

Supplemental table 2: Go enrichment of candidate SNPs from topGO. The group column indicates the set of SNPs in the enrichment test. "_all" means all significant loci for that treatment were tested. "_unique" means only those SNPs unique to that treatment. When multiple treatments are listed this indicates SNP sets that are significant under multiple treatments.

GO.ID	Term	Annotated	Significant	Expected	classicFisher	weight	group
GO:0019674	NAD metabolic process	8	7	1.91	0.00028	0.00028	OWA_all
GO:0006741	NADP biosynthetic process	9	7	2.15	0.00098	0.00098	OWA_all
GO:0000470	maturation of LSU-rRNA	14	11	3.35	2.40E-05	0.00316	OWA_all
GO:0000463	maturation of LSU-rRNA from tricistronic...	6	5	1.43	0.00371	0.00371	OWA_all
GO:0032786	positive regulation of DNA-templated tra...	6	5	1.43	0.00371	0.00371	OWA_all
GO:0046578	regulation of Ras protein signal transdu...	12	7	2.87	0.01087	0.01087	OWA_all
GO:0007480	imaginal disc-derived leg morphogenesis	5	4	1.19	0.01311	0.01311	OWA_all
GO:0009954	proximal/distal pattern formation	5	4	1.19	0.01311	0.01311	OWA_all
GO:0046784	viral mRNA export from host cell nucleus	5	4	1.19	0.01311	0.01311	OWA_all
GO:0061051	positive regulation of cell growth invol...	5	4	1.19	0.01311	0.01311	OWA_all
GO:1904707	positive regulation of vascular associat...	5	4	1.19	0.01311	0.01311	OWA_all
GO:2000002	negative regulation of DNA damage checkp...	5	4	1.19	0.01311	0.01311	OWA_all
GO:0098771	inorganic ion homeostasis	38	12	9.08	0.17563	0.01356	OWA_all
GO:0048872	homeostasis of number of cells	26	8	6.21	0.26785	0.01363	OWA_all
GO:0071103	DNA conformation change	27	8	6.45	0.30702	0.01365	OWA_all
GO:0006412	translation	243	61	58.07	0.34741	0.01544	OWA_all
GO:0000027	ribosomal large subunit assembly	10	6	2.39	0.0156	0.0156	OWA_all
GO:0000028	ribosomal small subunit assembly	10	6	2.39	0.0156	0.0156	OWA_all
GO:0007264	small GTPase mediated signal transductio...	53	21	12.67	0.00739	0.01888	OWA_all
GO:0006508	proteolysis	169	46	40.39	0.17002	0.02514	OWA_all
GO:0030307	positive regulation of cell growth	11	8	2.63	0.00084	0.03143	OWA_all
GO:0007005	mitochondrion organization	46	12	10.99	0.41878	0.03164	OWA_all
GO:0007447	imaginal disc pattern formation	6	4	1.43	0.03192	0.03192	OWA_all
GO:0008361	regulation of cell size	9	5	2.15	0.04058	0.04058	OWA_all

GO:2000573	positive regulation of DNA biosynthetic ...	9	5	2.15	0.04058	0.04058	OWA_all
GO:0000460	maturation of 5.8S rRNA	10	6	2.39	0.0156	0.04438	OWA_all
GO:0000154	rRNA modification	11	5	2.63	0.09728	0.04462	OWA_all
GO:0030833	regulation of actin filament polymerizat...	11	5	2.63	0.09728	0.04462	OWA_all
GO:0045862	positive regulation of proteolysis	24	8	5.74	0.19474	0.04464	OWA_all
GO:0007088	regulation of mitotic nuclear division	15	6	1.24	0.00078	0.00035	ambient_all
GO:0007059	chromosome segregation	32	7	2.64	0.01336	0.00035	ambient_all
GO:0120036	plasma membrane bounded cell projection ...	86	9	7.1	0.2761	0.00056	ambient_all
GO:0000082	G1/S transition of mitotic cell cycle	13	5	1.07	0.00271	0.00271	ambient_all
GO:0007052	mitotic spindle organization	13	5	1.07	0.00271	0.00271	ambient_all
GO:0051225	spindle assembly	13	5	1.07	0.00271	0.00271	ambient_all
GO:0006661	phosphatidylinositol biosynthetic proces...	11	5	0.91	0.00112	0.0048	ambient_all
GO:0009168	purine ribonucleoside monophosphate bios...	5	3	0.41	0.00489	0.00489	ambient_all
GO:0006468	protein phosphorylation	163	19	13.45	0.07378	0.00659	ambient_all
GO:0007423	sensory organ development	64	9	5.28	0.07661	0.00905	ambient_all
GO:0046033	AMP metabolic process	6	3	0.5	0.00919	0.00919	ambient_all
GO:0051017	actin filament bundle assembly	6	3	0.5	0.00919	0.00919	ambient_all
GO:0043547	positive regulation of GTPase activity	24	6	1.98	0.0112	0.0112	ambient_all
GO:0048856	anatomical structure development	448	44	36.97	0.11107	0.01407	ambient_all
GO:1902600	proton transmembrane transport	26	6	2.15	0.01667	0.01667	ambient_all
GO:0045785	positive regulation of cell adhesion	11	5	0.91	0.00112	0.01884	ambient_all
GO:0022409	positive regulation of cell-cell adhesio...	8	3	0.66	0.02274	0.02274	ambient_all
GO:0003002	regionalization	46	7	3.8	0.07983	0.02961	ambient_all
GO:1902905	positive regulation of supramolecular fi...	11	4	0.91	0.00937	0.03594	ambient_all
GO:0001501	skeletal system development	12	4	0.99	0.01316	0.03597	ambient_all
GO:0110053	regulation of actin filament organizatio...	15	4	1.24	0.02981	0.03605	ambient_all
GO:0000460	maturation of 5.8S rRNA	10	3	0.83	0.04308	0.03623	ambient_all
GO:0007276	gamete generation	67	5	5.53	0.66016	0.03709	ambient_all

GO:0022412	cellular process involved in reproductio...	57	4	4.7	0.70529	0.03714	ambient_all
GO:0001701	in utero embryonic development	16	4	1.32	0.03725	0.03725	ambient_all
GO:0033365	protein localization to organelle	58	5	1.88	0.0382	0.00019	acidification_all
GO:0009060	aerobic respiration	21	4	0.68	0.0041	0.00407	acidification_all
GO:1902600	proton transmembrane transport	26	4	0.84	0.009	0.00899	acidification_all
GO:0008354	germ cell migration	5	2	0.16	0.0098	0.00979	acidification_all
GO:0010951	negative regulation of endopeptidase act...	5	2	0.16	0.0098	0.00979	acidification_all
GO:0045176	apical protein localization	5	2	0.16	0.0098	0.00979	acidification_all
GO:0006814	sodium ion transport	18	3	0.58	0.019	0.01899	acidification_all
GO:0044238	primary metabolic process	1489	49	48.37	0.4904	0.02897	acidification_all
GO:0055067	monovalent inorganic cation homeostasis	8	2	0.26	0.0257	0.0322	acidification_all
GO:0007167	enzyme linked receptor protein signaling...	43	3	1.4	0.1621	0.03225	acidification_all
GO:0007444	imaginal disc development	36	2	1.17	0.3277	0.03254	acidification_all
GO:0010248	establishment or maintenance of transmem...	10	2	0.32	0.0396	0.03963	acidification_all
GO:0007052	mitotic spindle organization	13	8	2.37	0.00064	0.00021	warming_all
GO:0051017	actin filament bundle assembly	6	5	1.1	0.00102	0.00102	warming_all
GO:0007059	chromosome segregation	32	8	5.84	0.21677	0.00188	warming_all
GO:0044238	primary metabolic process	1489	294	271.89	0.01459	0.0029	warming_all
GO:0051225	spindle assembly	13	7	2.37	0.00403	0.003	warming_all
GO:0000028	ribosomal small subunit assembly	10	6	1.83	0.00389	0.00389	warming_all
GO:0007476	imaginal disc-derived wing morphogenesis	23	10	4.2	0.00441	0.00397	warming_all
GO:0001947	heart looping	5	4	0.91	0.0047	0.0047	warming_all
GO:0007480	imaginal disc-derived leg morphogenesis	5	4	0.91	0.0047	0.0047	warming_all
GO:0009954	proximal/distal pattern formation	5	4	0.91	0.0047	0.0047	warming_all
GO:0043280	positive regulation of cysteine-type end...	5	4	0.91	0.0047	0.0047	warming_all
GO:0048872	homeostasis of number of cells	26	9	4.75	0.03471	0.00599	warming_all
GO:0072073	kidney epithelium development	10	6	1.83	0.00389	0.00599	warming_all

GO:0120036	plasma membrane bounded cell projection ...	86	16	15.7	0.51172	0.00614	warming_all
GO:0030324	lung development	8	5	1.46	0.00686	0.00686	warming_all
GO:0062012	regulation of small molecule metabolic p...	28	8	5.11	0.1226	0.0069	warming_all
GO:0042060	wound healing	11	6	2.01	0.00724	0.00724	warming_all
GO:0001934	positive regulation of protein phosphory...	23	7	4.2	0.10995	0.00734	warming_all
GO:0007447	imaginal disc pattern formation	6	4	1.1	0.01208	0.01208	warming_all
GO:0043467	regulation of generation of precursor me...	6	4	1.1	0.01208	0.01208	warming_all
GO:0007267	cell-cell signaling	106	22	19.36	0.28524	0.0121	warming_all
GO:0046578	regulation of Ras protein signal transdu...	12	6	2.19	0.01229	0.01229	warming_all
GO:0007088	regulation of mitotic nuclear division	15	6	2.74	0.04077	0.01315	warming_all
GO:0044260	cellular macromolecule metabolic process	1030	214	188.08	0.00465	0.01327	warming_all
GO:0018108	peptidyl-tyrosine phosphorylation	19	8	3.47	0.01339	0.01919	warming_all
GO:0000082	G1/S transition of mitotic cell cycle	13	6	2.37	0.01936	0.01936	warming_all
GO:0032501	multicellular organismal process	512	96	93.49	0.39616	0.01956	warming_all
GO:0043547	positive regulation of GTPase activity	24	9	4.38	0.02042	0.02042	warming_all
GO:0110053	regulation of actin filament organizatio...	15	8	2.74	0.00226	0.02056	warming_all
GO:0045862	positive regulation of proteolysis	24	9	4.38	0.02042	0.02064	warming_all
GO:1902905	positive regulation of supramolecular fi...	11	6	2.01	0.00724	0.02072	warming_all
GO:0050769	positive regulation of neurogenesis	17	7	3.1	0.02336	0.02073	warming_all
GO:0042692	muscle cell differentiation	37	6	6.76	0.69306	0.0213	warming_all
GO:0048856	anatomical structure development	448	91	81.8	0.12256	0.0228	warming_all
GO:0048546	digestive tract morphogenesis	12	7	2.19	0.0022	0.02379	warming_all
GO:0007163	establishment or maintenance of cell pol...	24	8	4.38	0.05619	0.024	warming_all
GO:0071456	cellular response to hypoxia	7	4	1.28	0.02415	0.02415	warming_all
GO:0043161	proteasome-mediated ubiquitin-dependent ...	44	12	8.03	0.09052	0.02576	warming_all
GO:0006468	protein phosphorylation	163	45	29.76	0.00159	0.02795	warming_all

GO:0032774	RNA biosynthetic process	334	73	60.99	0.04266	0.03168	warming_all
GO:0051171	regulation of nitrogen compound metaboli...	429	88	78.33	0.1066	0.03199	warming_all
GO:1902850	microtubule cytoskeleton organization in...	15	10	2.74	4.70E-05	0.03252	warming_all
GO:0042327	positive regulation of phosphorylation	26	9	4.75	0.03471	0.03293	warming_all
GO:1903533	regulation of protein targeting	7	5	1.28	0.00302	0.033	warming_all
GO:0006497	protein lipidation	8	5	1.46	0.00686	0.03303	warming_all
GO:0051270	regulation of cellular component movemen...	25	8	4.56	0.06997	0.03304	warming_all
GO:0043543	protein acylation	17	6	3.1	0.07303	0.03311	warming_all
GO:0000003	reproduction	118	23	21.55	0.39957	0.03331	warming_all
GO:0032200	telomere organization	12	3	2.19	0.37954	0.0334	warming_all
GO:0006109	regulation of carbohydrate metabolic pro...	24	5	4.38	0.4528	0.03343	warming_all
GO:0009894	regulation of catabolic process	54	10	9.86	0.53657	0.03349	warming_all
GO:0051707	response to other organism	61	11	11.14	0.57173	0.03353	warming_all
GO:0003018	vascular process in circulatory system	18	3	3.29	0.66498	0.03355	warming_all
GO:0019318	hexose metabolic process	30	5	5.48	0.66385	0.03358	warming_all
GO:1901575	organic substance catabolic process	192	34	35.06	0.61257	0.03368	warming_all
GO:0055065	metal ion homeostasis	29	4	5.3	0.80372	0.03369	warming_all
GO:0007017	microtubule-based process	68	18	12.42	0.05763	0.03427	warming_all
GO:0031647	regulation of protein stability	20	7	3.65	0.0567	0.03493	warming_all
GO:0006997	nucleus organization	14	6	2.56	0.02878	0.04119	warming_all
GO:0001708	cell fate specification	8	4	1.46	0.04144	0.04144	warming_all
GO:0006821	chloride transport	8	4	1.46	0.04144	0.04144	warming_all
GO:0043248	proteasome assembly	8	4	1.46	0.04144	0.04144	warming_all
GO:0050878	regulation of body fluid levels	8	4	1.46	0.04144	0.04144	warming_all
GO:0006954	inflammatory response	15	5	2.74	0.1218	0.04152	warming_all
GO:0006397	mRNA processing	100	21	18.26	0.27173	0.04378	warming_all
GO:0051495	positive regulation of cytoskeleton orga...	12	6	2.19	0.01229	0.04484	warming_all
GO:0006396	RNA processing	206	41	37.62	0.29006	0.0449	warming_all
GO:0007435	salivary gland morphogenesis	10	4	1.83	0.09187	0.04524	warming_all
GO:0001894	tissue homeostasis	5	3	0.91	0.04527	0.04527	warming_all

GO:0007440	foregut morphogenesis	5	3	0.91	0.04527	0.04527	warming_all
GO:0007492	endoderm development	5	3	0.91	0.04527	0.04527	warming_all
GO:0031507	heterochromatin assembly	5	3	0.91	0.04527	0.04527	warming_all
GO:1903053	regulation of extracellular matrix organ...	5	3	0.91	0.04527	0.04527	warming_all
GO:1903955	positive regulation of protein targeting...	5	3	0.91	0.04527	0.04527	warming_all
GO:0007612	learning	12	4	2.19	0.16089	0.04534	warming_all
GO:0098660	inorganic ion transmembrane transport	71	14	12.96	0.4219	0.04553	warming_all
GO:0022904	respiratory electron transport chain	13	2	0.03	0.00045	0.00045	ambient_acidification
GO:0006119	oxidative phosphorylation	14	2	0.04	0.00053	0.00053	ambient_acidification
GO:0030218	erythrocyte differentiation	11	3	0.19	0.00071	0.00071	ambient_warming
GO:0051017	actin filament bundle assembly	6	2	0.1	0.00414	0.00414	ambient_warming
GO:0042060	wound healing	11	2	0.19	0.01439	0.01439	ambient_warming
GO:0045785	positive regulation of cell adhesion	11	2	0.19	0.01439	0.01439	ambient_warming
GO:1902905	positive regulation of supramolecular fi...	11	2	0.19	0.01439	0.01439	ambient_warming
GO:0048285	organelle fission	48	7	0.82	1.20E-05	0.0152	ambient_warming
GO:0006412	translation	243	9	4.17	0.01992	0.0157	ambient_warming
GO:0051495	positive regulation of cytoskeleton orga...	12	2	0.21	0.01708	0.01708	ambient_warming
GO:0043401	steroid hormone mediated signaling pathw...	13	2	0.22	0.01996	0.01996	ambient_warming
GO:0110053	regulation of actin filament organizatio...	15	2	0.26	0.0263	0.0263	ambient_warming
GO:0050896	response to stimulus	619	13	10.63	0.24958	0.02861	ambient_warming
GO:0006367	transcription initiation from RNA polyme...	18	2	0.31	0.03709	0.03709	ambient_warming
GO:0006814	sodium ion transport	18	2	0.31	0.03709	0.03709	ambient_warming
GO:0006979	response to oxidative stress	21	2	0.36	0.04928	0.04928	ambient_warming
GO:0009168	purine ribonucleoside monophosphate bios...	5	2	0.03	0.00025	0.00025	ambient_OWA
GO:0046033	AMP metabolic process	6	2	0.03	0.00038	0.00038	ambient_OWA
GO:0009152	purine ribonucleotide biosynthetic proce...	41	2	0.21	0.01853	0.01853	ambient_OWA
GO:0006508	proteolysis	169	2	0.25	0.022	0.022	acidification_warming
GO:0046331	lateral inhibition	13	2	0.03	0.00045	0.00045	acidification_OWA

GO:0000398	mRNA splicing, via spliceosome	77	2	0.2	0.01561	0.01561	acidification_OWA
GO:0046578	regulation of Ras protein signal transdu...	12	5	1.07	0.0025	0.0025	warming_OWA
GO:0045862	positive regulation of proteolysis	24	5	2.13	0.0557	0.0026	warming_OWA
GO:0062012	regulation of small molecule metabolic p...	28	6	2.49	0.0329	0.0032	warming_OWA
GO:0006397	mRNA processing	100	12	8.89	0.1727	0.0048	warming_OWA
GO:0007480	imaginal disc-derived leg morphogenesis	5	3	0.44	0.0061	0.0061	warming_OWA
GO:0032774	RNA biosynthetic process	334	40	29.68	0.0249	0.0072	warming_OWA
GO:0032200	telomere organization	12	3	1.07	0.0836	0.0079	warming_OWA
GO:0006109	regulation of carbohydrate metabolic pro...	24	4	2.13	0.1587	0.0079	warming_OWA
GO:0000003	reproduction	118	12	10.49	0.3551	0.0079	warming_OWA
GO:0055065	metal ion homeostasis	29	4	2.58	0.2539	0.0079	warming_OWA
GO:0019318	hexose metabolic process	30	4	2.67	0.2742	0.0079	warming_OWA
GO:0009894	regulation of catabolic process	54	6	4.8	0.3465	0.0079	warming_OWA
GO:0006355	regulation of transcription, DNA-templat...	307	36	27.28	0.0435	0.0098	warming_OWA
GO:0007447	imaginal disc pattern formation	6	3	0.53	0.0113	0.0113	warming_OWA
GO:0043467	regulation of generation of precursor me...	6	3	0.53	0.0113	0.0113	warming_OWA
GO:0045815	positive regulation of gene expression, ...	6	3	0.53	0.0113	0.0113	warming_OWA
GO:0044255	cellular lipid metabolic process	72	11	6.4	0.0502	0.0166	warming_OWA
GO:0001933	negative regulation of protein phosphory...	21	5	1.87	0.0331	0.0169	warming_OWA
GO:0007017	microtubule-based process	68	7	6.04	0.4008	0.0175	warming_OWA
GO:0006493	protein O-linked glycosylation	7	3	0.62	0.0185	0.0185	warming_OWA
GO:1901564	organonitrogen compound metabolic proces...	881	96	78.3	0.007	0.0211	warming_OWA
GO:0006643	membrane lipid metabolic process	9	3	0.8	0.0389	0.0221	warming_OWA
GO:0006612	protein targeting to membrane	13	3	1.16	0.1019	0.0222	warming_OWA
GO:1901071	glucosamine-containing compound metaboli...	18	3	1.6	0.211	0.0223	warming_OWA
GO:0016358	dendrite development	26	3	2.31	0.4108	0.0224	warming_OWA

GO:0007163	establishment or maintenance of cell pol...	24	6	2.13	0.0158	0.0225	warming_OWA
GO:0006915	apoptotic process	78	8	6.93	0.3902	0.0234	warming_OWA
GO:0043254	regulation of protein-containing complex...	31	8	2.76	0.0045	0.0268	warming_OWA
GO:0006909	phagocytosis	20	5	1.78	0.0271	0.0271	warming_OWA
GO:1902532	negative regulation of intracellular sig...	20	5	1.78	0.0271	0.0271	warming_OWA
GO:0006997	nucleus organization	14	4	1.24	0.0298	0.0276	warming_OWA
GO:0050878	regulation of body fluid levels	8	3	0.71	0.0277	0.0277	warming_OWA
GO:0015986	ATP synthesis coupled proton transport	14	4	1.24	0.0298	0.0298	warming_OWA
GO:0071704	organic substance metabolic process	1556	158	138.29	0.0038	0.0378	warming_OWA
GO:0008361	regulation of cell size	9	3	0.8	0.0389	0.0389	warming_OWA
GO:0043488	regulation of mRNA stability	9	3	0.8	0.0389	0.0389	warming_OWA
GO:0023051	regulation of signaling	151	20	13.42	0.0421	0.0401	warming_OWA
GO:0030833	regulation of actin filament polymerizat...	11	4	0.98	0.0122	0.0414	warming_OWA
GO:2000377	regulation of reactive oxygen species me...	12	4	1.07	0.017	0.0414	warming_OWA
GO:0007088	regulation of mitotic nuclear division	15	6	0.96	0.0002	0.0001	ambient_unique
GO:0007059	chromosome segregation	32	6	2.06	0.01437	0.00011	ambient_unique
GO:0000082	G1/S transition of mitotic cell cycle	13	5	0.83	0.00087	0.00087	ambient_unique
GO:0007052	mitotic spindle organization	13	5	0.83	0.00087	0.00087	ambient_unique
GO:0051225	spindle assembly	13	5	0.83	0.00087	0.00087	ambient_unique
GO:0009168	purine ribonucleoside monophosphate bios...	5	3	0.32	0.00237	0.00237	ambient_unique
GO:0043547	positive regulation of GTPase activity	24	6	1.54	0.00327	0.00327	ambient_unique
GO:0046033	AMP metabolic process	6	3	0.39	0.00451	0.00451	ambient_unique
GO:0048856	anatomical structure development	448	31	28.77	0.35119	0.00755	ambient_unique
GO:0022409	positive regulation of cell-cell adhesio...	8	3	0.51	0.01147	0.01147	ambient_unique
GO:0006468	protein phosphorylation	163	15	10.47	0.09607	0.01493	ambient_unique
GO:0000460	maturation of 5.8S rRNA	10	3	0.64	0.02234	0.02243	ambient_unique
GO:0007276	gamete generation	67	4	4.3	0.63412	0.02311	ambient_unique
GO:0071704	organic substance metabolic process	1556	95	99.94	0.80771	0.03364	ambient_unique
GO:0006661	phosphatidylinositol biosynthetic proces...	11	4	0.71	0.0038	0.03542	ambient_unique

GO:0001894	tissue homeostasis	5	2	0.32	0.03606	0.03606	ambient_unique
GO:0010842	retina layer formation	5	2	0.32	0.03606	0.03606	ambient_unique
GO:0032006	regulation of TOR signaling	5	2	0.32	0.03606	0.03606	ambient_unique
GO:0033365	protein localization to organelle	58	4	1	0.0164	0.00052	acidification_unique
GO:0008354	germ cell migration	5	2	0.09	0.0028	0.00279	acidification_unique
GO:0045176	apical protein localization	5	2	0.09	0.0028	0.00279	acidification_unique
GO:0006814	sodium ion transport	18	3	0.31	0.0032	0.00323	acidification_unique
GO:0010248	establishment or maintenance of transmem...	10	2	0.17	0.0119	0.0119	acidification_unique
GO:0007612	learning	12	2	0.21	0.0171	0.01708	acidification_unique
GO:0035335	peptidyl-tyrosine dephosphorylation	12	2	0.21	0.0171	0.01708	acidification_unique
GO:2000377	regulation of reactive oxygen species me...	12	2	0.21	0.0171	0.01708	acidification_unique
GO:0016925	protein sumoylation	13	2	0.22	0.02	0.01996	acidification_unique
GO:0006119	oxidative phosphorylation	14	2	0.24	0.023	0.02304	acidification_unique
GO:0043066	negative regulation of apoptotic process	40	3	0.69	0.0301	0.03008	acidification_unique
GO:0048869	cellular developmental process	276	9	4.74	0.0415	0.04668	acidification_unique
GO:0009060	aerobic respiration	21	2	0.36	0.0493	0.04928	acidification_unique
GO:1901990	regulation of mitotic cell cycle phase t...	18	2	0.31	0.0371	0.04986	acidification_unique
GO:0048872	homeostasis of number of cells	26	7	2.91	0.0207	0.0014	warming_unique
GO:0044260	cellular macromolecule metabolic process	1030	131	115.38	0.029	0.0018	warming_unique
GO:0043161	proteasome-mediated ubiquitin-dependent ...	44	11	4.93	0.0074	0.0043	warming_unique
GO:0031647	regulation of protein stability	20	6	2.24	0.0187	0.0045	warming_unique
GO:0050769	positive regulation of neurogenesis	17	7	1.9	0.0015	0.005	warming_unique
GO:0042692	muscle cell differentiation	37	6	4.14	0.2281	0.0051	warming_unique
GO:0009612	response to mechanical stimulus	12	5	1.34	0.0069	0.0069	warming_unique
GO:0006997	nucleus organization	14	5	1.57	0.0145	0.0075	warming_unique
GO:0006821	chloride transport	8	4	0.9	0.0075	0.0075	warming_unique
GO:0030324	lung development	8	4	0.9	0.0075	0.0075	warming_unique
GO:0043248	proteasome assembly	8	4	0.9	0.0075	0.0075	warming_unique

GO:0032501	multicellular organismal process	512	58	57.36	0.4861	0.0107	warming_unique
GO:0007435	salivary gland morphogenesis	10	4	1.12	0.0187	0.0117	warming_unique
GO:0001947	heart looping	5	3	0.56	0.0117	0.0117	warming_unique
GO:0031507	heterochromatin assembly	5	3	0.56	0.0117	0.0117	warming_unique
GO:1903955	positive regulation of protein targeting...	5	3	0.56	0.0117	0.0117	warming_unique
GO:0006396	RNA processing	206	23	23.08	0.5429	0.012	warming_unique
GO:0098609	cell-cell adhesion	19	7	2.13	0.0032	0.012	warming_unique
GO:0006334	nucleosome assembly	9	4	1.01	0.0123	0.0123	warming_unique
GO:0035264	multicellular organism growth	9	4	1.01	0.0123	0.0123	warming_unique
GO:1902850	microtubule cytoskeleton organization in...	15	5	1.68	0.0198	0.0124	warming_unique
GO:0032200	telomere organization	12	3	1.34	0.143	0.0125	warming_unique
GO:0008360	regulation of cell shape	14	5	1.57	0.0145	0.0145	warming_unique
GO:0007286	spermatid development	10	4	1.12	0.0187	0.0187	warming_unique
GO:0008340	determination of adult lifespan	10	4	1.12	0.0187	0.0187	warming_unique
GO:0044248	cellular catabolic process	187	26	20.95	0.1377	0.0209	warming_unique
GO:0006506	GPI anchor biosynthetic process	6	3	0.67	0.0215	0.0215	warming_unique
GO:0034314	Arp2/3 complex-mediated actin nucleation	6	3	0.67	0.0215	0.0215	warming_unique
GO:0007017	microtubule-based process	68	12	7.62	0.0714	0.0264	warming_unique
GO:0042060	wound healing	11	4	1.23	0.0269	0.0269	warming_unique
GO:0048856	anatomical structure development	448	55	50.19	0.2373	0.0336	warming_unique
GO:0006325	chromatin organization	71	12	7.95	0.0928	0.034	warming_unique
GO:0006487	protein N-linked glycosylation	12	5	1.34	0.0069	0.0341	warming_unique
GO:0023014	signal transduction by protein phosphory...	29	7	3.25	0.0367	0.0343	warming_unique
GO:0006914	autophagy	37	7	4.14	0.1122	0.0344	warming_unique
GO:0060322	head development	42	8	4.71	0.0901	0.0344	warming_unique
GO:0072073	kidney epithelium development	10	4	1.12	0.0187	0.0345	warming_unique
GO:0050679	positive regulation of epithelial cell p...	7	3	0.78	0.0346	0.0346	warming_unique
GO:0007591	molting cycle, chitin-based cuticle	9	3	1.01	0.07	0.0347	warming_unique

GO:0010769	regulation of cell morphogenesis involve...	9	3	1.01	0.07	0.0347	warming_unique
GO:0030178	negative regulation of Wnt signaling pat...	11	3	1.23	0.1164	0.0347	warming_unique
GO:0035148	tube formation	15	3	1.68	0.2317	0.0348	warming_unique
GO:0034613	cellular protein localization	118	13	13.22	0.5715	0.0352	warming_unique
GO:0007424	open tracheal system development	24	6	2.69	0.0442	0.0366	warming_unique
GO:0044255	cellular lipid metabolic process	72	11	8.07	0.1759	0.0367	warming_unique
GO:0007476	imaginal disc-derived wing morphogenesis	23	7	2.58	0.0103	0.0477	warming_unique
GO:0018108	peptidyl-tyrosine phosphorylation	19	5	2.13	0.053	0.0485	warming_unique
GO:0006741	NADP biosynthetic process	9	7	1.67	0.00019	0.00019	OWA_unique
GO:0000470	maturation of LSU-rRNA	14	10	2.6	2.20E-05	0.00077	OWA_unique
GO:0032786	positive regulation of DNA-templated tra...	6	5	1.11	0.0011	0.0011	OWA_unique
GO:0006412	translation	243	51	45.1	0.17439	0.00212	OWA_unique
GO:0000028	ribosomal small subunit assembly	10	6	1.86	0.00423	0.00423	OWA_unique
GO:0046784	viral mRNA export from host cell nucleus	5	4	0.93	0.00501	0.00501	OWA_unique
GO:0061051	positive regulation of cell growth invol...	5	4	0.93	0.00501	0.00501	OWA_unique
GO:1904707	positive regulation of vascular associat...	5	4	0.93	0.00501	0.00501	OWA_unique
GO:2000002	negative regulation of DNA damage checkp...	5	4	0.93	0.00501	0.00501	OWA_unique
GO:0048872	homeostasis of number of cells	26	7	4.83	0.19349	0.00637	OWA_unique
GO:0000463	maturation of LSU-rRNA from tricistronic...	6	4	1.11	0.01282	0.01282	OWA_unique
GO:2000573	positive regulation of DNA biosynthetic ...	9	5	1.67	0.01409	0.01409	OWA_unique
GO:0000460	maturation of 5.8S rRNA	10	6	1.86	0.00423	0.02168	OWA_unique
GO:0000154	rRNA modification	11	5	2.04	0.03736	0.02183	OWA_unique
GO:0000027	ribosomal large subunit assembly	10	5	1.86	0.02395	0.02395	OWA_unique
GO:0044085	cellular component biogenesis	302	67	56.05	0.05229	0.03294	OWA_unique
GO:0051171	regulation of nitrogen compound metaboli...	429	85	79.62	0.25234	0.03376	OWA_unique
GO:0035272	exocrine system development	14	8	2.6	0.0014	0.03386	OWA_unique
GO:0035050	embryonic heart tube development	8	3	1.48	0.17198	0.0344	OWA_unique
GO:0006873	cellular ion homeostasis	34	7	6.31	0.44829	0.03452	OWA_unique

GO:0048583	regulation of response to stimulus	173	32	32.11	0.54152	0.03464	OWA_unique
GO:0006813	potassium ion transport	28	8	5.2	0.1317	0.03542	OWA_unique
GO:0000469	cleavage involved in rRNA processing	11	5	2.04	0.03736	0.03736	OWA_unique
GO:0051094	positive regulation of developmental pro...	54	14	10.02	0.11192	0.04331	OWA_unique
GO:0000245	spliceosomal complex assembly	15	6	2.78	0.0438	0.0438	OWA_unique
GO:0007435	salivary gland morphogenesis	10	5	1.86	0.02395	0.04701	OWA_unique
GO:0009954	proximal/distal pattern formation	5	3	0.93	0.04729	0.04729	OWA_unique
GO:0030166	proteoglycan biosynthetic process	5	3	0.93	0.04729	0.04729	OWA_unique
GO:0015698	inorganic anion transport	13	4	2.41	0.2093	0.04741	OWA_unique
GO:0001822	kidney development	29	5	5.38	0.64799	0.04792	OWA_unique
GO:0007264	small GTPase mediated signal transductio...	53	13	9.84	0.16964	0.048	OWA_unique
GO:0098660	inorganic ion transmembrane transport	71	9	13.18	0.93185	0.04894	OWA_unique
GO:0090304	nucleic acid metabolic process	677	3	0.76	0.016	0.0021	ambient_acidification_OWA
GO:0006367	transcription initiation from RNA polyme...	18	2	0.11	0.0048	0.0048	ambient_warming_OWA
GO:0043161	proteasome-mediated ubiquitin-dependent ...	44	2	0.26	0.0274	0.0274	ambient_warming_OWA
GO:0009260	ribonucleotide biosynthetic process	43	2	0.19	0.015	0.0083	acidification_warming_OWA
GO:0023051	regulation of signaling	151	3	0.68	0.0265	0.0235	acidification_warming_OWA
GO:0043170	macromolecule metabolic process	1313	10	7.84	0.204	0.0038	ambient_acidification_warming_OWA
GO:0090304	nucleic acid metabolic process	677	5	4.04	0.38	0.0044	ambient_acidification_warming_OWA
GO:0044238	primary metabolic process	1489	11	8.9	0.211	0.0054	ambient_acidification_warming_OWA
GO:0048869	cellular developmental process	276	3	1.65	0.224	0.0174	ambient_acidification_warming_OWA