

## 1 Additional file 5

Section and responses	Gene set name	Gene set term	Set size	Observed hits	Adjusted p-value
Proximal (Linear)	GO:0006631	fatty acid metabolic process	68	19	<0.01
	GO:0006629	lipid metabolic process	184	33	<0.01
	GO:0006635	fatty acid beta-oxidation	21	9	<0.01
	GO:0042632	cholesterol homeostasis	33	11	<0.01
	GO:0030301	cholesterol transport	15	7	<0.01
	GO:0033344	cholesterol efflux	17	7	<0.01
	GO:0006695	cholesterol biosynthetic process	18	7	<0.01
	GO:0006637	acyl-CoA metabolic process	19	7	<0.01
	GO:0006694	steroid biosynthetic process	42	11	<0.01
	GO:0016126	sterol biosynthetic process	16	6	<0.01
	GO:0022900	electron transport chain	69	14	<0.01
	GO:0016192	vesicle-mediated transport	134	21	0.01
	GO:0010718	positive regulation of epithelial to mesenchymal transition	15	5	0.01
	GO:0015031	protein transport	386	45	0.01
	GO:0042157	lipoprotein metabolic process	15	5	0.01
	GO:0008203	cholesterol metabolic process	50	10	0.02
	GO:0034968	histone lysine methylation	22	6	0.02
	GO:0071300	cellular response to retinoic acid	17	5	0.02
	GO:0007040	lysosome organization	18	5	0.03
	GO:0055085	transmembrane transport	390	42	0.07
	GO:0006665	sphingolipid metabolic process	15	4	0.08
	GO:0006953	acute-phase response	22	5	0.09
Proximal (Logithm)	GO:0006917	induction of apoptosis	131	16	0.06
Middle (Linear)	GO:0006631	fatty acid metabolic process	67	28	<0.01
	GO:0006629	lipid metabolic process	183	46	<0.01
	GO:0006635	fatty acid beta-oxidation	21	11	<0.01
	GO:0005975	carbohydrate metabolic process	141	32	<0.01
	GO:0022900	electron transport chain	69	18	<0.01
	GO:0015031	protein transport	387	60	<0.01
	GO:0042542	response to hydrogen peroxide	18	7	0.01
	GO:0009058	biosynthetic process	39	11	0.01
	GO:0043154	negative regulation of caspase activity	36	10	0.02
	GO:0055085	transmembrane transport	391	57	0.02
	GO:0050796	regulation of insulin secretion	21	7	0.02
	GO:0006006	glucose metabolic process	38	10	0.03
	GO:0007040	lysosome organization	18	6	0.04
	GO:0045471	response to ethanol	29	8	0.04
	GO:0006637	acyl-CoA metabolic process	19	6	0.04
	GO:0045444	fat cell differentiation	24	7	0.04
	GO:0016042	lipid catabolic process	69	14	0.05
	GO:0032091	negative regulation of protein binding	15	5	0.05
	GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	32	8	0.07

	GO:0006520	cellular amino acid metabolic process	16	5	0.07
	GO:0034612	response to tumor necrosis factor	16	5	0.07
	GO:0001890	placenta development	22	6	0.08
	GO:0006953	acute-phase response	22	6	0.08
	GO:0051262	protein tetramerization	17	5	0.09
Middle (Logarithm)	GO:0071230	cellular response to amino acid stimulus	22	7	<0.01
	GO:0007160	cell-matrix adhesion	40	8	<0.01
	GO:0051259	protein oligomerization	22	6	<0.01
	GO:0007155	cell adhesion	341	25	<0.01
	GO:0006644	phospholipid metabolic process	17	4	0.01
	GO:0018149	peptide cross-linking	17	4	0.01
	GO:0045859	regulation of protein kinase activity	16	4	0.01
	GO:0034446	substrate adhesion-dependent cell spreading	18	4	0.01
	GO:0043065	positive regulation of apoptosis	165	14	0.01
	GO:0007229	integrin-mediated signaling pathway	55	7	0.02
	GO:0006749	glutathione metabolic process	24	4	0.04
	GO:0001937	negative regulation of endothelial cell proliferation	16	3	0.06
	GO:0030574	collagen catabolic process	16	3	0.06
	GO:0009411	response to UV	29	4	0.07
	GO:0043627	response to estrogen stimulus	29	4	0.07
	GO:0045766	positive regulation of angiogenesis	57	6	0.07
	GO:0030334	regulation of cell migration	30	4	0.08
	GO:0030168	platelet activation	19	3	0.09
	GO:0007179	transforming growth factor beta receptor signaling pathway	47	5	0.10
	GO:0042632	cholesterol homeostasis	33	4	0.10
	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	47	5	0.10
	GO:0051897	positive regulation of protein kinase B signaling cascade	33	4	0.10
Middle (Exponential)	GO:0007243	intracellular protein kinase cascade	56	8	0.03
	GO:0030301	cholesterol transport	15	4	0.03
	GO:0006468	protein phosphorylation	426	27	0.08
	GO:0007049	cell cycle	411	26	0.08
	GO:0009615	response to virus	59	7	0.08
	GO:0031532	actin cytoskeleton reorganization	22	4	0.08
	GO:0006919	activation of caspase activity	50	6	0.09
	GO:0007067	mitosis	166	13	0.09
	GO:0008630	DNA damage response, signal transduction resulting in induction of apoptosis	15	3	0.09
Distal (Linear)	GO:0051260	protein homooligomerization	70	7	<0.01
	GO:0006953	acute-phase response	21	3	0.03
	GO:0016042	lipid catabolic process	69	5	0.03
	GO:0043085	positive regulation of catalytic activity	25	3	0.03
	GO:0006099	tricarboxylic acid cycle	16	2	0.05
	GO:0006520	cellular amino acid metabolic process	16	2	0.05
	GO:0006644	phospholipid metabolic process	17	2	0.05
	GO:0007200	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	17	2	0.05

	GO:0008654	phospholipid biosynthetic process	37	3	0.05
	GO:0033344	cholesterol efflux	17	2	0.05
	GO:0042157	lipoprotein metabolic process	16	2	0.05
	GO:0045859	regulation of protein kinase activity	16	2	0.05
	GO:0051262	protein tetramerization	17	2	0.05
	GO:0051402	neuron apoptosis	16	2	0.05
	GO:0060271	cilium morphogenesis	16	2	0.05
	GO:0006869	lipid transport	43	3	0.06
	GO:0006958	complement activation. classical pathway	20	2	0.06
	GO:0008202	steroid metabolic process	41	3	0.06
	GO:0030307	positive regulation of cell growth	44	3	0.06
	GO:0006888	ER to Golgi vesicle-mediated transport	22	2	0.06
	GO:0009725	response to hormone stimulus	22	2	0.06
	GO:0006749	glutathione metabolic process	24	2	0.08
	GO:0016049	cell growth	24	2	0.08
	GO:0007224	smoothened signaling pathway	25	2	0.08
	GO:0008203	cholesterol metabolic process	50	3	0.08
	GO:0045785	positive regulation of cell adhesion	25	2	0.08
Distal (Exponential)	GO:0000910	cytokinesis	31	4	<0.01
	GO:0001824	blastocyst development	16	2	0.01
	GO:0043967	histone H4 acetylation	15	2	0.01
	GO:0019882	antigen processing and presentation	18	2	0.02
	GO:0030218	erythrocyte differentiation	24	2	0.03
	GO:0032313	regulation of Rab GTPase activity	27	2	0.03
	GO:0032851	positive regulation of Rab GTPase activity	28	2	0.03
	GO:0043154	negative regulation of caspase activity	36	2	0.06

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3 **Table A5: Over-represented Gene Ontology Biological Process (GOBP) terms associated with differentially expressed genes in the**  
4 **three intestinal sections.** Genes are classified as linear, logarithmic or exponential, according to the best (i.e., with the smallest  
5 adjusted p-value) response type describing their expression pattern (as a function of fat intake). For each significant GOBP term  
6 (described by Gene set name and Gene set term) we summarize number of genes corresponding to the process (Set size), number  
7 of genes found with our analysis (Observed hits) and adjusted p-value. Universe size: proximal = 14,952; middle = 14,933; distal =  
8 14,925.