
Figure 6 - Figure Supplement 2: Gene set enrichment analysis for the most abundant trophallactic fluid proteins

(Next two pages) Gene set enrichment analysis results for the *D. melanogaster* orthologs of the 60 most abundant trophallactic fluid proteins. Observed gene count indicates how many proteins in the network are annotated with the term. Background gene count indicates how many proteins in total have this term, in this network and in the background. Strength describes how large the enrichment effect is: $\log_{10}(\text{observed proteins} / \text{expected proteins in a random network of this size})$. False Discovery Rate describes how significant the enrichment is. P-values are corrected for multiple testing within each category using the Benjamini–Hochberg procedure.

60 most abundant proteins						
Description	Observed gene count	Background gene count	Strength	False discovery rate	#term ID	Matching proteins in the network
carbohydrate metabolic process	8	236	1.06	0.00025	GO:0005975	Idgf4, Hexo1, LM408, Mal-B1, Gld, smp-30, tobi, Amy-d
lipid transport	5	75	1.36	0.00095	GO:0006869	Npc2a, Npc2g, Rfabg, Npc2e, CG30503
sterol transport	3	22	1.67	0.0071	GO:0015918	Npc2a, Npc2g, Npc2e
metabolic process	26	4926	0.25	0.022	GO:0008152	Idgf4, PHGPx, Hexo1, RNaseX25, Rpl40, Npc2a, DhpD, CG4017, LM408, Mal-B1, Gld, Act87E, smp-30, DNaseII, CG4572, tobi, CG14516, Amy-d, epsilon Try, CG30016, cathD, His4, CG31269, CG30503, Sod, CG9449
intracellular cholesterol transport	2	7	1.99	0.0235	GO:0032367	Npc2a, Npc2g
primary metabolic process	23	4093	0.28	0.0235	GO:0044238	Idgf4, Hexo1, RNaseX25, Rpl40, Npc2a, DhpD, CG4017, LM408, Mal-B1, Gld, Act87E, smp-30, DNaseII, CG4572, tobi, CG14516, Amy-d, epsilon Try, CG30016, cathD, His4, CG31269, CG30503
monosaccharide metabolic process	3	55	1.27	0.0323	GO:0005996	LM408, Gld, smp-30
nurse cell apoptotic process	2	13	1.72	0.0395	GO:0045476	DNaseII, cathD
protein deglycosylation	2	14	1.69	0.0416	GO:0006517	Hexo1, LM408
organic substance metabolic process	23	4432	0.25	0.0418	GO:0071704	Idgf4, Hexo1, RNaseX25, Rpl40, Npc2a, DhpD, CG4017, LM408, Mal-B1, Gld, Act87E, smp-30, DNaseII, CG4572, tobi, CG14516, Amy-d, epsilon Try, CG30016, cathD, His4, CG31269, CG30503
organic substance catabolic process	8	735	0.57	0.0423	GO:1901575	Idgf4, RNaseX25, Rpl40, DhpD, DNaseII, CG4572, CG14516, cathD
hydrolase activity	21	1685	0.63	2.37E-07	GO:0016787	CG6414, Idgf4, Hexo1, RNaseX25, DhpD, CG4017, LM408, Mal-B1, smp-30, DNaseII, CG4572, tobi, CG14516, Vha16-1, Amy-d, epsilon Try, CG30016, cathD, CG31269, CG30503, CG9449
hydrolase activity, hydrolyzing O-glycosyl compounds	6	97	1.32	4.32E-05	GO:0004553	Idgf4, Hexo1, LM408, Mal-B1, tobi, Amy-d
catalytic activity	24	3739	0.34	0.00066	GO:0003824	CG6414, Idgf4, PHGPx, Hexo1, RNaseX25, DhpD, CG4017, LM408, Mal-B1, Gld, smp-30, DNaseII, CG4572, tobi, CG14516, Vha16-1, Amy-d, epsilon Try, CG30016, cathD, CG31269, CG30503, Sod, CG9449
sterol binding	3	14	1.86	0.00066	GO:0032934	Npc2a, Npc2g, Npc2e
lipid antigen binding	2	3	2.36	0.002	GO:0030882	Npc2a, Npc2e
lipoteichoic acid binding	2	3	2.36	0.002	GO:0070891	Npc2a, Npc2e
lipopolysaccharide binding	2	6	2.05	0.004	GO:0001530	Npc2a, Npc2e

GO: Molecular function	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters	2	8	1.93	0.0058	GO:0016894	RNaseX25, DNaseII
	lipid binding	4	140	0.99	0.0116	GO:0008289	Npc2a,Npc2g,Rfabg,Npc2e
	peptidoglycan binding	2	18	1.58	0.0203	GO:0042834	Npc2a,Npc2e
	hydrolase activity, acting on ester bonds	6	435	0.67	0.0206	GO:0016788	CG6414,RNaseX25,smp-30, DNaseII, CG30503, CG9449
	carboxylic ester hydrolase activity	3	96	1.03	0.0345	GO:0052689	CG6414,smp-30, CG30503
	exopeptidase activity	3	100	1.01	0.0362	GO:0008238	CG4017,CG4572,CG14516
	carboxypeptidase activity	2	29	1.37	0.0372	GO:0004180	CG4017,CG4572
	peptidase activity, acting on L-amino acid peptides	6	533	0.58	0.0434	GO:0070011	CG4017,CG4572,CG14516,epsilonTry,cathD,CG31269
	extracellular space	11	454	0.92	5.81E-06	GO:0005615	Lsp1gamma,RNaseX25,Npc2a,Lsp1beta,CG4017,Spn43Aa,Rfabg,Lsp2,Npc2e,Sod,CG9449
	larval serum protein complex	3	4	2.41	3.74E-05	GO:0005616	Lsp1gamma,Lsp1beta,Lsp2
GO:CC	extracellular region	13	953	0.67	6.65E-05	GO:0005576	Idgf4,Lsp1gamma,RNaseX25,Npc2a,Lsp1beta,CG4017,smp-30,Spn43Aa,Rfabg,Lsp2,Npc2e,Sod,CG9449
	Neutrophil degranulation	10	408	0.92	3.05E-05	DME-6798695	Hexo1,RNaseX25,Npc2a,LM408,CG14516,Vha16-1,CG30016,cathD,CREG,CG9449
	Innate Immune System	11	574	0.81	3.83E-05	DME-168249	Hexo1,RNaseX25,Npc2a,CG4017,LM408,CG14516,Vha16-1,CG30016,cathD,CREG,CG9449
	Lysosome	9	117	1.42	2.03E-09	dme04142	Hexo1,Npc2a,LM408,DNaseII,Npc2g,Vha16-1,Tsp42Ea,cathD,Npc2e
KEGG pathway	Starch and sucrose metabolism	3	33	1.49	0.002	dme00500	Mal-B1,tobi,Amy-d
	Metabolic pathways	10	994	0.53	0.0042	dme01100	Hexo1,DhpD,Mal-B1,Gld,tobi,CG14516,Vha16-1,Amy-d,CG30016,CG30503
	Arachidonic acid metabolism	2	17	1.6	0.0087	dme00590	PHGPx,CG30503
	Other glycan degradation	2	22	1.49	0.0111	dme00511	Hexo1,LM408
	Galactose metabolism	2	37	1.26	0.0242	dme00052	Mal-B1,tobi