
Figure 6 - Figure Supplement 3: Gene set enrichment analysis for the significantly differing proteins

(Next three pages) Gene set enrichment analysis results for the *D. melanogaster* orthologs of the trophallactic fluid proteins significantly differing in two out of three of our statistical methods, first combined and then separately for the three main comparisons. 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. The significant annotations are indicated for GO: Biological process (GO:BP), GO: Molecular function (GO:MF), GO: Cellular component (GO:CC), Reactome pathways and KEGG pathways.

Significant in 2 out of 3 analysis methods in any comparison						
	Description	Observed gene count	Background gene count	Strength	False discovery rate	Matching proteins in the network
GO:BP	carbohydrate metabolic process	10	236	1.13	2.15E-06	Hexo2, Treh, Tal, Hexo1, LM408, Mdh1, Gld, tobi, Amy-d, Amy-p
	oxidation-reduction process	11	694	0.7	0.0026	blw, Tal, Mdh1, Gld, Men, CG16935, CG7737, PPO2, CG10638, GstS1, Sod
GO:MF	hydrolase activity, hydrolyzing O-glycosyl compounds	8	97	1.42	1.91E-07	Hexo2, Treh, Hexo1, LM408, tobi, Amy-d, Amy-p, CG12582
	catalytic activity	27	3739	0.36	9.88E-05	CG3097, Hexo2, Treh, blw, Tal, Hexo1, Vha26, DhpD, CG4017, LM408, Mdh1, Gld, Men, CG4572, tobi, CG14516, Amy-d, Amy-p, CG16935, ERp60, CG7737, PPO2, cathD, CG10638, CG12582, GstS1, Sod
	hydrolase activity	16	1685	0.48	0.0014	CG3097, Hexo2, Treh, blw, Hexo1, Vha26, DhpD, CG4017, LM408, CG4572, tobi, CG14516, Amy-d, Amy-p
	alpha-amylase activity	2	2	2.5	0.002	Amy-d, Amy-p
	oxidoreductase activity	9	598	0.68	0.0027	Mdh1, Gld, Men, CG16935, CG7737, PPO2, CG10638, GstS1, Sod
	carboxypeptidase activity	3	29	1.52	0.0029	CG3097, CG4017, CG4572
	beta-N-acetylglucosaminidase activity	2	4	2.2	0.0029	Hexo2, Hexo1
	exopeptidase activity	4	100	1.1	0.0045	CG3097, CG4017, CG4572, CG14516
	malate dehydrogenase activity	2	9	1.85	0.007	Mdh1, Men
	metalloexopeptidase activity	3	61	1.19	0.0132	CG3097, CG4017, CG14516
GO:CC	mannosidase activity	2	14	1.66	0.0132	LM408, CG12582
	oxidoreductase activity, acting on CH-OH group of donors	3	81	1.07	0.0253	Mdh1, Gld, Men
	metallocarboxypeptidase activity	2	24	1.42	0.0307	CG3097, CG4017
	extracellular space	11	454	0.88	1.54E-05	CG3097, CG10433, Lsp1gamma, Obp19d, Lsp1beta, CG4017, PPO2, Spn43A, Rfabg, Lsp2, Sod
	larval serum protein complex	3	4	2.38	5.56E-05	Lsp1gamma, Lsp1beta, Lsp2
	Metabolism	9	833	0.53	0.0126	Hexo2, Tal, Hexo1, DhpD, LM408, Mdh1, CG16935, CG12582, GstS1
Reactome pathway	Complement cascade	2	20	1.5	0.0129	CG3097, CG4017

KEGG pathway	Metabolic pathways	17	994	0.73	1.40E-07	dme01100	Hexo2, Treh, blw, Tal, Hexo1, Vha26, DhpD, Mdh1, Gld, Men, tobi, CG14516, Amy-d, Amy-p, CG16935, CG10638, GstS1
	Lysosome	7	117	1.28	1.97E-06	dme04142	Hexo2, Hexo1, LM408, Npc2c, Tsp42Ea, cathD, CG12582
	Other glycan degradation	4	22	1.76	1.50E-05	dme00511	Hexo2, Hexo1, LM408, CG12582
	Starch and sucrose metabolism	4	33	1.58	4.84E-05	dme00500	Treh, tobi, Amy-d, Amy-p
	Glycosphingolipid biosynthesis - ganglio series	2	5	2.1	0.0015	dme00604	Hexo2, Hexo1
	Glycosphingolipid biosynthesis - globo and isoglobo series	2	6	2.02	0.0017	dme00603	Hexo2, Hexo1
	Glycosaminoglycan degradation	2	15	1.63	0.0068	dme00531	Hexo2, Hexo1
	Pentose phosphate pathway	2	24	1.42	0.0139	dme00030	Tal, Gld
	Galactose metabolism	2	37	1.23	0.026	dme00052	tobi, CG10638
	Carbon metabolism	3	117	0.91	0.026	dme01200	Tal, Mdh1, Men
	Amino sugar and nucleotide sugar metabolism	2	47	1.13	0.0322	dme00520	Hexo2, Hexo1
	Pyruvate metabolism	2	45	1.15	0.0322	dme00620	Mdh1, Men

Significant in Nurse vs Forager

	Description	Observed gene count	Background gene count	Strength	False discovery rate	#term ID	Matching proteins in the network
GO:BP	carbohydrate metabolic process	6	236	1.27	0.00017	GO:0005975	Treh, Hexo1, Mdh1, Gld, tobi, Amy-p
	malate metabolic process	2	11	2.12	0.0198	GO:0006108	Mdh1, Men
	oxidation-reduction process	6	694	0.8	0.0234	GO:0055114	Mdh1, Gld, Men, CG7737, PPO2, CG10638
GO:MF	hydrolase activity, hydrolyzing O-glycosyl compounds	5	97	1.58	0.0000201	GO:0004553	Treh, Hexo1, tobi, Amy-p, CG12582
	catalytic activity	14	3739	0.44	0.00093	GO:0003824	Treh, Hexo1, Vha26, Mdh1, Gld, Men, CG4572, tobi, CG14516, Amy-p, CG7737, PPO2, CG10638, CG12582
	oxidoreductase activity	6	598	0.87	0.0024	GO:0016491	Mdh1, Gld, Men, CG7737, PPO2, CG10638
	malate dehydrogenase activity	2	9	2.21	0.0024	GO:0016615	Mdh1, Men
	oxidoreductase activity, acting on CH-OH group of donors	3	81	1.43	0.0031	GO:0016614	Mdh1, Gld, Men
	hydrolase activity	8	1685	0.54	0.0143	GO:0016787	Treh, Hexo1, Vha26, CG4572, tobi, CG14516, Amy-p, CG12582

	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	2	53	1.44	0.0309	GO:0016616	Mdh1, Men
KEGG pathways	Metabolic pathways	10	994	0.87	0.00000416	dme01100	Treh, Hexo1, Vha26, Mdh1, Gld, Men, tobi, CG14516, Amy-p, CG10638
	Starch and sucrose metabolism	3	33	1.82	0.00017	dme00500	Treh, tobi, Amy-p
	Lysosome	4	117	1.4	0.00017	dme04142	Hexo1, Npc2c, Tsp42Ea, CG12582
	Other glycan degradation	2	22	1.82	0.0027	dme00511	Hexo1, CG12582
	Galactose metabolism	2	37	1.6	0.0058	dme00052	tobi, CG10638
	Pyruvate metabolism	2	45	1.51	0.007	dme00620	Mdh1, Men
	Carbon metabolism	2	117	1.1	0.0369	dme01200	Mdh1, Men
	Significant in Young vs Mature						
GO:BP	carbohydrate metabolic process	4	236	1.37	0.0047	GO:0005975	Gld, tobi, Amy-d, Amy-p
GO:MF	alpha-amylase activity	2	2	3.14	0.00017	GO:0004556	Amy-d, Amy-p
	hydrolase activity, hydrolyzing O-glycosyl compounds	3	97	1.63	0.00086	GO:0004553	tobi, Amy-d, Amy-p
	calcium ion binding	3	206	1.31	0.0046	GO:0005509	Amy-d, Amy-p, Cam
	ion binding	6	1993	0.62	0.0111	GO:0043167	DhpD, Gld, Amy-d, Amy-p, Rfabg, Cam
	hydrolase activity	5	1685	0.62	0.0343	GO:0016787	DhpD, tobi, Amy-d, Amy-p, cathD
	metal ion binding	4	1027	0.73	0.0343	GO:0046872	DhpD, Amy-d, Amy-p, Cam
KEGG	Starch and sucrose metabolism	3	33	2.1	0.0000169	dme00500	tobi, Amy-d, Amy-p
	Metabolic pathways	5	994	0.85	0.0016	dme01100	DhpD, Gld, tobi, Amy-d, Amy-p
Significant in Field vs Lab							
GO:CC	extracellular space	6	454	0.96	0.0024	GO:0005615	CG3097, CG10433, Lsp1beta, CG4017, Lsp2, Sod
	larval serum protein complex	2	4	2.54	0.0024	GO:0005616	Lsp1beta, Lsp2
Reactome	Complement cascade	2	20	1.84	0.0035	DME-166658	CG3097, CG4017
	Metabolism	5	833	0.62	0.0225	DME-1430728	Hexo2, Tai, LM408, CG16935, GstS1
KEGG	Other glycan degradation	2	22	1.8	0.0127	dme00511	Hexo2, LM408
	Lysosome	3	117	1.25	0.0127	dme04142	Hexo2, LM408, cathD