

Fat-specific age-related GO terms in Cluster 1 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0000165 MAPKKK cascade	CG5031	NA	NA	9.83E-03	100	3	3.0%
GO:0000165 MAPKKK cascade	CG18409	NA	NA	9.83E-03	100	3	3.0%
GO:0000165 MAPKKK cascade	CG7392	FBgn0044323	Connector of kinase to AP-1	9.83E-03	100	3	3.0%
GO:0006096 glycolysis	CG11249	FBgn0037115		1.17E-02	37	2	5.4%
GO:0006096 glycolysis	CG8251	FBgn0003074	Phosphoglucose isomerase	1.17E-02	37	2	5.4%
GO:0007254 JNK cascade	CG5031	NA	NA	1.71E-02	45	2	4.4%
GO:0007254 JNK cascade	CG7392	FBgn0044323	Connector of kinase to AP-1	1.71E-02	45	2	4.4%
GO:0031098 stress-activated protein kinase signaling pathway	CG5031	NA	NA	1.71E-02	45	2	4.4%
GO:0031098 stress-activated protein kinase signaling pathway	CG7392	FBgn0044323	Connector of kinase to AP-1	1.71E-02	45	2	4.4%
GO:0007243 protein kinase cascade	CG5031	NA	NA	1.72E-02	123	3	2.4%
GO:0007243 protein kinase cascade	CG18409	NA	NA	1.72E-02	123	3	2.4%
GO:0007243 protein kinase cascade	CG7392	FBgn0044323	Connector of kinase to AP-1	1.72E-02	123	3	2.4%
GO:0006007 glucose catabolism	CG11249	FBgn0037115		1.93E-02	48	2	4.2%
GO:0006007 glucose catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	1.93E-02	48	2	4.2%
GO:0019320 hexose catabolism	CG11249	FBgn0037115		1.93E-02	48	2	4.2%
GO:0019320 hexose catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	1.93E-02	48	2	4.2%
GO:0046164 alcohol catabolism	CG11249	FBgn0037115		1.93E-02	48	2	4.2%
GO:0046164 alcohol catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	1.93E-02	48	2	4.2%
GO:0046365 monosaccharide catabolism	CG11249	FBgn0037115		1.93E-02	48	2	4.2%
GO:0046365 monosaccharide catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	1.93E-02	48	2	4.2%
GO:0051242 positive regulation of cellular physiological process	CG12653	FBgn0000233	buttonhead	2.41E-02	140	3	2.1%
GO:0051242 positive regulation of cellular physiological process	CG1401	FBgn0039632	cullin-5	2.41E-02	140	3	2.1%
GO:0051242 positive regulation of cellular physiological process	CG5031	NA	NA	2.41E-02	140	3	2.1%
GO:0043119 positive regulation of physiological process	CG12653	FBgn0000233	buttonhead	2.50E-02	142	3	2.1%
GO:0043119 positive regulation of physiological process	CG1401	FBgn0039632	cullin-5	2.50E-02	142	3	2.1%
GO:0043119 positive regulation of physiological process	CG5031	NA	NA	2.50E-02	142	3	2.1%

Fat-specific age-related GO terms in Cluster 1

GO:0006006 glucose metabolism	CG11249	FBgn0037115		2.66E-02	57	2	3.5%
GO:0006006 glucose metabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	2.66E-02	57	2	3.5%
GO:0006753 nucleoside phosphate metabolism	CG1271	FBgn0035392		3.02E-02	61	2	3.3%
GO:0006753 nucleoside phosphate metabolism	CG14909	FBgn0038458		3.02E-02	61	2	3.3%
GO:0006754 ATP biosynthesis	CG1271	FBgn0035392		3.02E-02	61	2	3.3%
GO:0006754 ATP biosynthesis	CG14909	FBgn0038458		3.02E-02	61	2	3.3%
GO:0006917 induction of apoptosis	CG1401	FBgn0039632	cullin-5	3.02E-02	61	2	3.3%
GO:0006917 induction of apoptosis	CG5031	NA	NA	3.02E-02	61	2	3.3%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG1271	FBgn0035392		3.02E-02	61	2	3.3%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG14909	FBgn0038458		3.02E-02	61	2	3.3%
GO:0015986 ATP synthesis coupled proton transport	CG1271	FBgn0035392		3.02E-02	61	2	3.3%
GO:0015986 ATP synthesis coupled proton transport	CG14909	FBgn0038458		3.02E-02	61	2	3.3%
GO:0046034 ATP metabolism	CG1271	FBgn0035392		3.11E-02	62	2	3.2%
GO:0046034 ATP metabolism	CG14909	FBgn0038458		3.11E-02	62	2	3.2%
GO:0048522 positive regulation of cellular process	CG12653	FBgn0000233	buttonhead	3.14E-02	155	3	1.9%
GO:0048522 positive regulation of cellular process	CG1401	FBgn0039632	cullin-5	3.14E-02	155	3	1.9%
GO:0048522 positive regulation of cellular process	CG5031	NA	NA	3.14E-02	155	3	1.9%
GO:0043065 positive regulation of apoptosis	CG1401	FBgn0039632	cullin-5	3.21E-02	63	2	3.2%
GO:0043065 positive regulation of apoptosis	CG5031	NA	NA	3.21E-02	63	2	3.2%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG1271	FBgn0035392		3.40E-02	65	2	3.1%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG14909	FBgn0038458		3.40E-02	65	2	3.1%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG1271	FBgn0035392		3.40E-02	65	2	3.1%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG14909	FBgn0038458		3.40E-02	65	2	3.1%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG1271	FBgn0035392		3.40E-02	65	2	3.1%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG14909	FBgn0038458		3.40E-02	65	2	3.1%
GO:0009142 nucleoside triphosphate biosynthesis	CG1271	FBgn0035392		3.49E-02	66	2	3.0%
GO:0009142 nucleoside triphosphate biosynthesis	CG14909	FBgn0038458		3.49E-02	66	2	3.0%
GO:0009144 purine nucleoside triphosphate metabolism	CG1271	FBgn0035392		3.49E-02	66	2	3.0%
GO:0009144 purine nucleoside triphosphate metabolism	CG14909	FBgn0038458		3.49E-02	66	2	3.0%
GO:0009199 ribonucleoside triphosphate metabolism	CG1271	FBgn0035392		3.49E-02	66	2	3.0%

GO:0009199 ribonucleoside triphosphate metabolism	CG14909	FBgn0038458		3.49E-02	66	2	3.0%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG1271	FBgn0035392		3.49E-02	66	2	3.0%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG14909	FBgn0038458		3.49E-02	66	2	3.0%
GO:0016052 carbohydrate catabolism	CG11249	FBgn0037115		3.49E-02	66	2	3.0%
GO:0016052 carbohydrate catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	3.49E-02	66	2	3.0%
GO:0044275 cellular carbohydrate catabolism	CG11249	FBgn0037115		3.49E-02	66	2	3.0%
GO:0044275 cellular carbohydrate catabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	3.49E-02	66	2	3.0%
GO:0009141 nucleoside triphosphate metabolism	CG1271	FBgn0035392		3.69E-02	68	2	2.9%
GO:0009141 nucleoside triphosphate metabolism	CG14909	FBgn0038458		3.69E-02	68	2	2.9%
GO:0006752 group transfer coenzyme metabolism	CG1271	FBgn0035392		3.79E-02	69	2	2.9%
GO:0006752 group transfer coenzyme metabolism	CG14909	FBgn0038458		3.79E-02	69	2	2.9%
GO:0012502 induction of programmed cell death	CG1401	FBgn0039632	cullin-5	3.79E-02	69	2	2.9%
GO:0012502 induction of programmed cell death	CG5031	NA	NA	3.79E-02	69	2	2.9%
GO:0015672 monovalent inorganic cation transport	CG1271	FBgn0035392		3.85E-02	168	3	1.8%
GO:0015672 monovalent inorganic cation transport	CG14909	FBgn0038458		3.85E-02	168	3	1.8%
GO:0015672 monovalent inorganic cation transport	CG9907	FBgn0003036	paralytic	3.85E-02	168	3	1.8%
GO:0043068 positive regulation of programmed cell death	CG1401	FBgn0039632	cullin-5	4.09E-02	72	2	2.8%
GO:0043068 positive regulation of programmed cell death	CG5031	NA	NA	4.09E-02	72	2	2.8%
GO:0048518 positive regulation of biological process	CG12653	FBgn0000233	buttonhead	4.20E-02	174	3	1.7%
GO:0048518 positive regulation of biological process	CG1401	FBgn0039632	cullin-5	4.20E-02	174	3	1.7%
GO:0048518 positive regulation of biological process	CG5031	NA	NA	4.20E-02	174	3	1.7%
GO:0006818 hydrogen transport	CG1271	FBgn0035392		4.30E-02	74	2	2.7%
GO:0006818 hydrogen transport	CG14909	FBgn0038458		4.30E-02	74	2	2.7%
GO:0015992 proton transport	CG1271	FBgn0035392		4.30E-02	74	2	2.7%
GO:0015992 proton transport	CG14909	FBgn0038458		4.30E-02	74	2	2.7%
GO:0019318 hexose metabolism	CG11249	FBgn0037115		4.51E-02	76	2	2.6%
GO:0019318 hexose metabolism	CG8251	FBgn0003074	Phosphoglucose isomerase	4.51E-02	76	2	2.6%
GO:0008543 fibroblast growth factor receptor signaling pathway	CG13414	NA	NA	4.82E-02	11	1	9.1%
GO:0035146 tube fusion	CG14553	NA	NA	4.82E-02	11	1	9.1%
GO:0035147 tracheal branch fusion	CG14553	NA	NA	4.82E-02	11	1	9.1%
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Fat-specific age-related GO terms in Cluster 1

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Fat-specific age-related GO terms in Cluster 2 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0006511 ubiquitin-dependent protein catabolism	CG10938	FBgn0016697	Proteasome alpha subunit	8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG11981	FBgn0026380		8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG12323	FBgn0029134		8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG17331	FBgn0032596		8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG18495	FBgn0026781	Proteasome alpha6 subunit	8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG3329	FBgn0023174	Proteasome beta2 subunit	8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG4097	FBgn0002284	Proteasome 26kD subunit	8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG5289	FBgn0015282	Proteasome 26S subunit subunit 4 ATPase	8.08E-13	74	9	12.2%
GO:0006511 ubiquitin-dependent protein catabolism	CG8392	FBgn0010590		8.08E-13	74	9	12.2%
GO:0019941 modification-dependent protein catabolism	CG10938	FBgn0016697	Proteasome alpha subunit	1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG11981	FBgn0026380		1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG12323	FBgn0029134		1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG17331	FBgn0032596		1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG18495	FBgn0026781	Proteasome alpha6 subunit	1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG3329	FBgn0023174	Proteasome beta2 subunit	1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG4097	FBgn0002284	Proteasome 26kD subunit	1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG5289	FBgn0015282	Proteasome 26S subunit subunit 4 ATPase	1.04E-12	76	9	11.8%
GO:0019941 modification-dependent protein catabolism	CG8392	FBgn0010590		1.04E-12	76	9	11.8%
GO:0006510 ATP-dependent proteolysis	CG10938	FBgn0016697	Proteasome alpha subunit	3.49E-07	19	4	21.1%
GO:0006510 ATP-dependent proteolysis	CG11981	FBgn0026380		3.49E-07	19	4	21.1%
GO:0006510 ATP-dependent proteolysis	CG4097	FBgn0002284	Proteasome 26kD subunit	3.49E-07	19	4	21.1%
GO:0006510 ATP-dependent proteolysis	CG5289	FBgn0015282	Proteasome 26S subunit subunit 4 ATPase	3.49E-07	19	4	21.1%

Fat-specific age-related GO terms in Cluster 2

GO:0006807 nitrogen compound metabolism	CG5112	FBgn0039341		3.28E-03	26	2	7.7%
GO:0006807 nitrogen compound metabolism	CG7910	FBgn0037547		3.28E-03	26	2	7.7%
GO:0006631 fatty acid metabolism	CG16904	FBgn0037763		4.09E-03	99	3	3.0%
GO:0006631 fatty acid metabolism	CG6660	FBgn0039030		4.09E-03	99	3	3.0%
GO:0006631 fatty acid metabolism	CG7400	FBgn0021953	Fatty acid (long chain) transport protein	4.09E-03	99	3	3.0%
GO:0030307 positive regulation of cell growth	CG1389	FBgn0003733	torso	3.60E-02	11	1	9.1%
GO:0045793 positive regulation of cell size	CG1389	FBgn0003733	torso	3.92E-02	12	1	8.3%
GO:0035264 body growth	CG1389	FBgn0003733	torso	4.24E-02	13	1	7.7%
GO:0040014 regulation of body size	CG1389	FBgn0003733	torso	4.24E-02	13	1	7.7%
GO:0051246 regulation of protein metabolism	CG1389	FBgn0003733	torso	4.38E-02	101	2	2.0%
GO:0051246 regulation of protein metabolism	CG4124	FBgn0053526		4.38E-02	101	2	2.0%

Fat-specific age-related GO terms in Cluster 3 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0009966 regulation of signal transduction	CG10491	FBgn0003984	vein	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG11960	NA	NA	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG2028	FBgn0015024	Casein kinase Ialpha	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG2849	FBgn0015286	Ras-related protein	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG3143	FBgn0038197	forkhead box, sub-group O	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG9484	FBgn0002431	hyperplastic discs	1.07E-04	92	7	7.6%
GO:0009966 regulation of signal transduction	CG9653	FBgn0024250	brinker	1.07E-04	92	7	7.6%
GO:0048519 negative regulation of biological process	CG10491	FBgn0003984	vein	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG2028	FBgn0015024	Casein kinase Ialpha	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG2849	FBgn0015286	Ras-related protein	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG3143	FBgn0038197	forkhead box, sub-group O	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG3878	FBgn0053525		1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG4114	FBgn0004583	expanded	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG5580	FBgn0010575	scribbler	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG8238	FBgn0040491	Buffy	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG8411	FBgn0005695	germ cell-less	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG9484	FBgn0002431	hyperplastic discs	1.54E-04	246	11	4.5%
GO:0048519 negative regulation of biological process	CG9653	FBgn0024250	brinker	1.54E-04	246	11	4.5%
GO:0009968 negative regulation of signal transduction	CG2028	FBgn0015024	Casein kinase Ialpha	2.05E-04	46	5	10.9%
GO:0009968 negative regulation of signal transduction	CG2849	FBgn0015286	Ras-related protein	2.05E-04	46	5	10.9%
GO:0009968 negative regulation of signal transduction	CG3143	FBgn0038197	forkhead box, sub-group O	2.05E-04	46	5	10.9%
GO:0009968 negative regulation of signal transduction	CG9484	FBgn0002431	hyperplastic discs	2.05E-04	46	5	10.9%
GO:0009968 negative regulation of signal transduction	CG9653	FBgn0024250	brinker	2.05E-04	46	5	10.9%
GO:0048523 negative regulation of cellular process	CG10491	FBgn0003984	vein	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG2028	FBgn0015024	Casein kinase Ialpha	3.30E-04	225	10	4.4%

Fat-specific age-related GO terms in Cluster 3

GO:0048523 negative regulation of cellular process	CG2849	FBgn0015286	Ras-related protein	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG3143	FBgn0038197	forkhead box, sub-group O	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG3878	FBgn0053525		3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG5580	FBgn0010575	scribbler	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG8238	FBgn0040491	Buffy	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG8411	FBgn0005695	germ cell-less	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG9484	FBgn0002431	hyperplastic discs	3.30E-04	225	10	4.4%
GO:0048523 negative regulation of cellular process	CG9653	FBgn0024250	brinker	3.30E-04	225	10	4.4%
GO:0040007 growth	CG16987	FBgn0031461	Activin Like Protein at 23B	1.86E-03	74	5	6.8%
GO:0040007 growth	CG3143	FBgn0038197	forkhead box, sub-group O	1.86E-03	74	5	6.8%
GO:0040007 growth	CG4114	FBgn0004583	expanded	1.86E-03	74	5	6.8%
GO:0040007 growth	CG9484	FBgn0002431	hyperplastic discs	1.86E-03	74	5	6.8%
GO:0040007 growth	CG9653	FBgn0024250	brinker	1.86E-03	74	5	6.8%
GO:0007224 smoothened signaling pathway	CG2028	FBgn0015024	Casein kinase Ialpha	2.48E-03	23	3	13.0%
GO:0007224 smoothened signaling pathway	CG3848	FBgn0023518	trithorax-related	2.48E-03	23	3	13.0%
GO:0007224 smoothened signaling pathway	CG9484	FBgn0002431	hyperplastic discs	2.48E-03	23	3	13.0%
GO:0006457 protein folding	CG12240	FBgn0020129	DnaJ-like-60	2.94E-03	119	6	5.0%
GO:0006457 protein folding	CG12279	FBgn0038080		2.94E-03	119	6	5.0%
GO:0006457 protein folding	CG14715	FBgn0037930		2.94E-03	119	6	5.0%
GO:0006457 protein folding	CG1866	FBgn0039581		2.94E-03	119	6	5.0%
GO:0006457 protein folding	CG7409	FBgn0035817		2.94E-03	119	6	5.0%
GO:0006457 protein folding	CG9828	FBgn0032474		2.94E-03	119	6	5.0%
GO:0042127 regulation of cell proliferation	CG3143	FBgn0038197	forkhead box, sub-group O	3.17E-03	25	3	12.0%
GO:0042127 regulation of cell proliferation	CG4114	FBgn0004583	expanded	3.17E-03	25	3	12.0%
GO:0042127 regulation of cell proliferation	CG9484	FBgn0002431	hyperplastic discs	3.17E-03	25	3	12.0%
GO:0051243 negative regulation of cellular physiological process	CG10491	FBgn0003984	vein	6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG3143	FBgn0038197	forkhead box, sub-group O	6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG3878	FBgn0053525		6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG5580	FBgn0010575	scribbler	6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG8238	FBgn0040491	Buffy	6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG8411	FBgn0005695	germ cell-less	6.36E-03	184	7	3.8%
GO:0051243 negative regulation of cellular physiological process	CG9653	FBgn0024250	brinker	6.36E-03	184	7	3.8%
GO:0043118 negative regulation of physiological process	CG10491	FBgn0003984	vein	8.20E-03	193	7	3.6%

Fat-specific age-related GO terms in Cluster 3

GO:0043118 negative regulation of physiological process	CG3143	FBgn0038197	forkhead box, sub-group O	8.20E-03	193	7	3.6%
GO:0043118 negative regulation of physiological process	CG3878	FBgn0053525		8.20E-03	193	7	3.6%
GO:0043118 negative regulation of physiological process	CG5580	FBgn0010575	scribbler	8.20E-03	193	7	3.6%
GO:0043118 negative regulation of physiological process	CG8238	FBgn0040491	Buffy	8.20E-03	193	7	3.6%
GO:0043118 negative regulation of physiological process	CG8411	FBgn0005695	germ cell-less	8.20E-03	193	7	3.6%
GO:0043118 negative regulation of physiological process	CG9653	FBgn0024250	brinker	8.20E-03	193	7	3.6%
GO:0045926 negative regulation of growth	CG3143	FBgn0038197	forkhead box, sub-group O	1.18E-02	14	2	14.3%
GO:0045926 negative regulation of growth	CG4114	FBgn0004583	expanded	1.18E-02	14	2	14.3%
GO:0016331 morphogenesis of embryonic epithelium	CG15112	FBgn0000578	enabled	1.40E-02	78	4	5.1%
GO:0016331 morphogenesis of embryonic epithelium	CG2849	FBgn0015286	Ras-related protein	1.40E-02	78	4	5.1%
GO:0016331 morphogenesis of embryonic epithelium	CG4145	FBgn0000299	Collagen type IV	1.40E-02	78	4	5.1%
GO:0016331 morphogenesis of embryonic epithelium	CG6383	FBgn0000368	crumbs	1.40E-02	78	4	5.1%
GO:0002009 morphogenesis of an epithelium	CG10579	FBgn0005640	Ecdysone-induced protein 63E	1.53E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG15112	FBgn0000578	enabled	1.53E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG2849	FBgn0015286	Ras-related protein	1.53E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG4145	FBgn0000299	Collagen type IV	1.53E-02	122	5	4.1%
GO:0002009 morphogenesis of an epithelium	CG6383	FBgn0000368	crumbs	1.53E-02	122	5	4.1%
GO:0045892 negative regulation of transcription DNA-dependent	CG3878	FBgn0053525		1.87E-02	85	4	4.7%
GO:0045892 negative regulation of transcription DNA-dependent	CG5580	FBgn0010575	scribbler	1.87E-02	85	4	4.7%
GO:0045892 negative regulation of transcription DNA-dependent	CG8411	FBgn0005695	germ cell-less	1.87E-02	85	4	4.7%
GO:0045892 negative regulation of transcription DNA-dependent	CG9653	FBgn0024250	brinker	1.87E-02	85	4	4.7%
GO:0007548 sex differentiation	CG11129	FBgn0004047	Yolk protein 3	1.96E-02	48	3	6.3%
GO:0007548 sex differentiation	CG13201	FBgn0001276	intersex	1.96E-02	48	3	6.3%
GO:0007548 sex differentiation	CG9484	FBgn0002431	hyperplastic discs	1.96E-02	48	3	6.3%
GO:0040008 regulation of growth	CG3143	FBgn0038197	forkhead box, sub-group O	2.18E-02	50	3	6.0%
	CG4114	FBgn0004583	expanded	2.18E-02	50	3	6.0%
GO:0040008 regulation of growth	CG9653	FBgn0024250	brinker	2.18E-02	50	3	6.0%
GO:0007446 imaginal disc growth	CG4114	FBgn0004583	expanded	2.81E-02	22	2	9.1%

Fat-specific age-related GO terms in Cluster 3

GO:0007446 imaginal disc growth	CG9484	FBgn0002431	hyperplastic discs	2.81E-02	22	2	9.1%
GO:0006869 lipid transport	CG15828	FBgn0032136		3.07E-02	57	3	5.3%
GO:0006869 lipid transport	CG3164	FBgn0025683		3.07E-02	57	3	5.3%
GO:0006869 lipid transport	CG4822	FBgn0031220		3.07E-02	57	3	5.3%
GO:0016481 negative regulation of transcription	CG3878	FBgn0053525		3.07E-02	99	4	4.0%
GO:0016481 negative regulation of transcription	CG5580	FBgn0010575	scribbler	3.07E-02	99	4	4.0%
GO:0016481 negative regulation of transcription	CG8411	FBgn0005695	germ cell-less	3.07E-02	99	4	4.0%
GO:0016481 negative regulation of transcription	CG9653	FBgn0024250	brinker	3.07E-02	99	4	4.0%
GO:0030162 regulation of proteolysis and peptidolysis	CG2028	FBgn0015024	Casein kinase Ialpha	3.31E-02	24	2	8.3%
GO:0030162 regulation of proteolysis and peptidolysis	CG9484	FBgn0002431	hyperplastic discs	3.31E-02	24	2	8.3%
GO:0048522 positive regulation of cellular process	CG10491	FBgn0003984	vein	3.81E-02	155	5	3.2%
GO:0048522 positive regulation of cellular process	CG13201	FBgn0001276	intersex	3.81E-02	155	5	3.2%
GO:0048522 positive regulation of cellular process	CG3143	FBgn0038197	forkhead box, sub-group O	3.81E-02	155	5	3.2%
GO:0048522 positive regulation of cellular process	CG3848	FBgn0023518	trithorax-related	3.81E-02	155	5	3.2%
GO:0048522 positive regulation of cellular process	CG8238	FBgn0040491	Buffy	3.81E-02	155	5	3.2%
GO:0007283 spermatogenesis	CG12240	FBgn0020129	DnaJ-like-60	3.92E-02	107	4	3.7%
GO:0007283 spermatogenesis	CG6963	FBgn0011253	gilgamesh	3.92E-02	107	4	3.7%
GO:0007283 spermatogenesis	CG7004	FBgn0004373	four wheel drive	3.92E-02	107	4	3.7%
GO:0007283 spermatogenesis	CG9484	FBgn0002431	hyperplastic discs	3.92E-02	107	4	3.7%
GO:0048232 male gamete generation	CG12240	FBgn0020129	DnaJ-like-60	3.92E-02	107	4	3.7%
GO:0048232 male gamete generation	CG6963	FBgn0011253	gilgamesh	3.92E-02	107	4	3.7%
GO:0048232 male gamete generation	CG7004	FBgn0004373	four wheel drive	3.92E-02	107	4	3.7%
GO:0048232 male gamete generation	CG9484	FBgn0002431	hyperplastic discs	3.92E-02	107	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG10579	FBgn0005640	Ecdysone-induced protein 63E	4.04E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG15112	FBgn0000578	enabled	4.04E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG2849	FBgn0015286	Ras-related protein	4.04E-02	108	4	3.7%
GO:0001700 embryonic development (sensu Insecta)	CG4145	FBgn0000299	Collagen type IV	4.04E-02	108	4	3.7%
GO:0006633 fatty acid biosynthesis	CG2781	FBgn0037534		4.11E-02	27	2	7.4%
GO:0006633 fatty acid biosynthesis	CG5887	FBgn0043044		4.11E-02	27	2	7.4%
GO:0009894 regulation of catabolism	CG2028	FBgn0015024	Casein kinase Ialpha	4.11E-02	27	2	7.4%
GO:0009894 regulation of catabolism	CG9484	FBgn0002431	hyperplastic discs	4.11E-02	27	2	7.4%
GO:0045934 negative regulation of nucleobase nucleoside nucleotide and nucleic acid metabolism	CG3878	FBgn0053525		4.27E-02	110	4	3.6%
GO:0045934 negative regulation of nucleobase nucleoside nucleotide and nucleic acid metabolism	CG5580	FBgn0010575	scribbler	4.27E-02	110	4	3.6%
GO:0045934 negative regulation of nucleobase nucleoside nucleotide and nucleic acid metabolism	CG8411	FBgn0005695	germ cell-less	4.27E-02	110	4	3.6%

GO:0045934 negative regulation of nucleobase nucleoside nucleotide and nucleic acid metabolism	CG9653	FBgn0024250	brinker	4.27E-02	110	4	3.6%
GO:0000902 cellular morphogenesis	CG10491	FBgn0003984	vein	4.38E-02	215	6	2.8%
GO:0000902 cellular morphogenesis	CG11960	NA	NA	4.38E-02	215	6	2.8%
GO:0000902 cellular morphogenesis	CG15112	FBgn0000578	enabled	4.38E-02	215	6	2.8%
GO:0000902 cellular morphogenesis	CG3143	FBgn0038197	forkhead box, sub-group O	4.38E-02	215	6	2.8%
GO:0000902 cellular morphogenesis	CG5580	FBgn0010575	scribbler	4.38E-02	215	6	2.8%
GO:0000902 cellular morphogenesis	CG6383	FBgn0000368	crumbs	4.38E-02	215	6	2.8%
GO:0016053 organic acid biosynthesis	CG2781	FBgn0037534		4.69E-02	29	2	6.9%
GO:0016053 organic acid biosynthesis	CG5887	FBgn0043044		4.69E-02	29	2	6.9%
GO:0046394 carboxylic acid biosynthesis	CG2781	FBgn0037534		4.69E-02	29	2	6.9%
GO:0046394 carboxylic acid biosynthesis	CG5887	FBgn0043044		4.69E-02	29	2	6.9%

Fat-specific age-related GO terms in Cluster 4 (Upregulated)							
GO term	CG_ID	FB_ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0019730 antimicrobial humoral response	CG17685	NA	NA	1.96E-03	59	4	6.8%
GO:0019730 antimicrobial humoral response	CG5528	FBgn0036978		1.96E-03	59	4	6.8%
GO:0019730 antimicrobial humoral response	CG5576	FBgn0013983		1.96E-03	59	4	6.8%
GO:0019730 antimicrobial humoral response	CG18589	NA	NA	1.96E-03	59	4	6.8%
GO:0042742 defense response to bacteria	CG17685	NA	NA	2.21E-03	61	4	6.6%
GO:0042742 defense response to bacteria	CG5528	FBgn0036978		2.21E-03	61	4	6.6%
GO:0042742 defense response to bacteria	CG5576	FBgn0013983	immune deficiency	2.21E-03	61	4	6.6%
GO:0042742 defense response to bacteria	CG18589	NA	NA	2.21E-03	61	4	6.6%
GO:0009617 response to bacteria	CG17685	NA	NA	2.95E-03	66	4	6.1%
GO:0009617 response to bacteria	CG5528	FBgn0036978		2.95E-03	66	4	6.1%
GO:0009617 response to bacteria	CG5576	FBgn0013983	immune deficiency	2.95E-03	66	4	6.1%
GO:0009617 response to bacteria	CG18589	NA	NA	2.95E-03	66	4	6.1%
GO:0006959 humoral immune response	CG17685	NA	NA	3.12E-03	67	4	6.0%
GO:0006959 humoral immune response	CG5528	FBgn0036978		3.12E-03	67	4	6.0%
GO:0006959 humoral immune response	CG5576	FBgn0013983	immune deficiency	3.12E-03	67	4	6.0%
GO:0006959 humoral immune response	CG18589	NA	NA	3.12E-03	67	4	6.0%
GO:0019731 antibacterial humoral response	CG17685	NA	NA	4.49E-03	37	3	8.1%
GO:0019731 antibacterial humoral response	CG5576	FBgn0013983	immune deficiency	4.49E-03	37	3	8.1%
GO:0019731 antibacterial humoral response	CG18589	NA	NA	4.49E-03	37	3	8.1%
GO:0009613 response to pest pathogen or parasite	CG17685	NA	NA	7.30E-03	85	4	4.7%
GO:0009613 response to pest pathogen or parasite	CG5528	FBgn0036978		7.30E-03	85	4	4.7%
GO:0009613 response to pest pathogen or parasite	CG5576	FBgn0013983	immune deficiency	7.30E-03	85	4	4.7%
GO:0009613 response to pest pathogen or parasite	CG18589	NA	NA	7.30E-03	85	4	4.7%
GO:0006963 antibacterial polypeptide induction	CG17685	NA	NA	7.95E-03	15	2	13.3%
GO:0006963 antibacterial polypeptide induction	CG5576	FBgn0013983	immune deficiency	7.95E-03	15	2	13.3%
GO:0042493 response to drug	CG11537	FBgn0035400		7.95E-03	15	2	13.3%
GO:0042493 response to drug	CG5078	FBgn0037005		7.95E-03	15	2	13.3%
GO:0006955 immune response	CG17685	NA	NA	1.55E-02	106	4	3.8%
GO:0006955 immune response	CG5528	FBgn0036978		1.55E-02	106	4	3.8%
GO:0006955 immune response	CG5576	FBgn0013983	immune deficiency	1.55E-02	106	4	3.8%
GO:0006955 immune response	CG18589	NA	NA	1.55E-02	106	4	3.8%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG5576	FBgn0013983	immune deficiency	1.68E-02	22	2	9.1%
GO:0006961 antibacterial humoral response (sensu Protostomia)	CG18589	NA	NA	1.68E-02	22	2	9.1%
GO:0019748 secondary metabolism	CG12230	FBgn0000257	carnation	1.71E-02	60	3	5.0%
GO:0019748 secondary metabolism	CG15467	FBgn0003028	ovo	1.71E-02	60	3	5.0%
GO:0019748 secondary metabolism	CG6502	FBgn0000629	Enhancer of zeste	1.71E-02	60	3	5.0%

Fat-specific age-related GO terms in Cluster 4

GO:0043207 response to external biotic stimulus	CG17685	NA	NA	1.76E-02	110	4	3.6%
GO:0043207 response to external biotic stimulus	CG5528	FBgn0036978		1.76E-02	110	4	3.6%
GO:0043207 response to external biotic stimulus	CG5576	FBgn0013983	immune deficiency	1.76E-02	110	4	3.6%
GO:0043207 response to external biotic stimulus	CG18589	NA	NA	1.76E-02	110	4	3.6%
GO:0006997 nuclear organization and biogenesis	CG17685	NA	NA	1.98E-02	24	2	8.3%
GO:0006997 nuclear organization and biogenesis	CG8590	FBgn0011606	Kinesin-like protein at 3A	1.98E-02	24	2	8.3%
GO:0008643 carbohydrate transport	CG11537	FBgn0035400		3.16E-02	76	3	3.9%
GO:0008643 carbohydrate transport	CG5078	FBgn0037005		3.16E-02	76	3	3.9%
GO:0008643 carbohydrate transport	CG9620	FBgn0037567		3.16E-02	76	3	3.9%
GO:0007400 neuroblast cell fate determination	CG18497	FBgn0016977	split ends	3.60E-02	33	2	6.1%
GO:0007400 neuroblast cell fate determination	CG5753	FBgn0003520	staufer	3.60E-02	33	2	6.1%

Fat-specific age-related GO terms in Cluster 5 (Upregulated)							
GO term	CG ID	FB ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0051258 protein polymerization	CG12530	FBgn0010341	Cdc42	1.84E-02	18	2	11.1%
GO:0051258 protein polymerization	CG2512	FBgn0003885	alpha-Tubulin at 84D	1.84E-02	18	2	11.1%
GO:0006875 metal ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.25E-02	20	2	10.0%
GO:0006875 metal ion homeostasis	CG3743	FBgn0040305		2.25E-02	20	2	10.0%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG12530	FBgn0010341	Cdc42	3.17E-02	24	2	8.3%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG15667	FBgn0026369	Smad anchor for receptor activation	3.17E-02	24	2	8.3%
GO:0006873 cell ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	3.42E-02	25	2	8.0%
GO:0006873 cell ion homeostasis	CG3743	FBgn0040305		3.42E-02	25	2	8.0%
GO:0007349 cellularization	CG12530	FBgn0010341	Cdc42	3.42E-02	25	2	8.0%
GO:0007349 cellularization	CG3595	FBgn0003514	spaghetti squash	3.42E-02	25	2	8.0%
GO:0030003 cation homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	3.42E-02	25	2	8.0%
GO:0030003 cation homeostasis	CG3743	FBgn0040305		3.42E-02	25	2	8.0%
GO:0050801 ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	3.42E-02	25	2	8.0%
GO:0050801 ion homeostasis	CG3743	FBgn0040305		3.42E-02	25	2	8.0%
GO:0009611 response to wounding	CG12530	FBgn0010341	Cdc42	4.21E-02	28	2	7.1%
GO:0009611 response to wounding	CG8595	FBgn0034476	Toll-7	4.21E-02	28	2	7.1%
GO:0009063 amino acid catabolism	CG17896	FBgn0023537		2.48E-03	49	4	8.2%
GO:0009063 amino acid catabolism	CG6309	NA	NA	2.48E-03	49	4	8.2%
GO:0009063 amino acid catabolism	CG6415	FBgn0032287		2.48E-03	49	4	8.2%
GO:0009063 amino acid catabolism	CG6661	FBgn0036403		2.48E-03	49	4	8.2%
GO:0009310 amine catabolism	CG17896	FBgn0023537		3.09E-03	52	4	7.7%
GO:0009310 amine catabolism	CG6309	NA	NA	3.09E-03	52	4	7.7%
GO:0009310 amine catabolism	CG6415	FBgn0032287		3.09E-03	52	4	7.7%
GO:0009310 amine catabolism	CG6661	FBgn0036403		3.09E-03	52	4	7.7%
GO:0006144 purine base metabolism	CG16758	FBgn0035348		2.50E-02	54	3	5.6%
GO:0006144 purine base metabolism	CG6767	FBgn0036030		2.50E-02	54	3	5.6%
GO:0006144 purine base metabolism	CG7642	FBgn0003308	rosy	2.50E-02	54	3	5.6%
GO:0006413 translational initiation	CG1442	FBgn0039622		2.88E-02	57	3	5.3%
GO:0006413 translational initiation	CG10840	FBgn0026259		2.88E-02	57	3	5.3%
GO:0006413 translational initiation	CG8277	FBgn0035823		2.88E-02	57	3	5.3%
GO:0019722 calcium-mediated signaling	CG10524	FBgn0030387	Protein kinase C delta	5.82E-03	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG18069	FBgn0004624	Calcium/calmodulin-dependent protein kinase II	5.82E-03	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG3595	FBgn0003514	spaghetti squash	5.82E-03	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG13413	NA	NA	5.82E-03	62	4	6.5%

Fat-specific age-related GO terms in Cluster 5

GO:0016052 carbohydrate catabolism	CG15093	FBgn0034390		4.18E-02	66	3	4.5%
GO:0016052 carbohydrate catabolism	CG17645	FBgn0011270		4.18E-02	66	3	4.5%
GO:0016052 carbohydrate catabolism	CG7496	FBgn0035806		4.18E-02	66	3	4.5%
GO:0044275 cellular carbohydrate catabolism	CG15093	FBgn0034390		4.18E-02	66	3	4.5%
GO:0044275 cellular carbohydrate catabolism	CG17645	FBgn0011270		4.18E-02	66	3	4.5%
GO:0044275 cellular carbohydrate catabolism	CG7496	FBgn0035806		4.18E-02	66	3	4.5%
GO:0009112 nucleobase metabolism	CG16758	FBgn0035348		1.24E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG17896	FBgn0023537		1.24E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG6767	FBgn0036030		1.24E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG7642	FBgn0003308	rosy	1.24E-02	77	4	5.2%
GO:0019932 second-messenger-mediated signaling	CG10524	FBgn0030387	Protein kinase C delta	1.66E-02	84	4	4.8%
GO:0019932 second-messenger-mediated signaling	CG18069	FBgn0004624	Calcium/calmodulin-dependent protein kinase II	1.66E-02	84	4	4.8%
GO:0019932 second-messenger-mediated signaling	CG3595	FBgn0003514	spaghetti squash	1.66E-02	84	4	4.8%
GO:0019932 second-messenger-mediated signaling	CG13413	NA	NA	1.66E-02	84	4	4.8%
GO:0006936 muscle contraction	CG18069	FBgn0004624	Calcium/calmodulin-dependent protein kinase II	1.94E-02	88	4	4.5%
GO:0006936 muscle contraction	CG3595	FBgn0003514	spaghetti squash	1.94E-02	88	4	4.5%
GO:0006936 muscle contraction	CG13413	NA	NA	1.94E-02	88	4	4.5%
GO:0006936 muscle contraction	CG8938	FBgn0010226	Glutathione S transferase S1	1.94E-02	88	4	4.5%
GO:0006092 main pathways of carbohydrate metabolism	CG1065	FBgn0004888	Succinyl coenzyme A synthetase alpha subunit	2.93E-02	100	4	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	2.93E-02	100	4	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG15093	FBgn0034390		2.93E-02	100	4	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG17645	FBgn0011270		2.93E-02	100	4	4.0%
GO:0015980 energy derivation by oxidation of organic compounds	CG1065	FBgn0004888	Succinyl coenzyme A synthetase alpha subunit	4.42E-02	114	4	3.5%
GO:0015980 energy derivation by oxidation of organic compounds	CG11661	FBgn0010352	Neural conserved at 73EF	4.42E-02	114	4	3.5%
GO:0015980 energy derivation by oxidation of organic compounds	CG15093	FBgn0034390		4.42E-02	114	4	3.5%
GO:0015980 energy derivation by oxidation of organic compounds	CG17645	FBgn0011270		4.42E-02	114	4	3.5%
GO:0046483 heterocycle metabolism	CG16758	FBgn0035348		2.07E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG17896	FBgn0023537		2.07E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG4067	FBgn0020385	pugilist	2.07E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG6767	FBgn0036030		2.07E-02	135	5	3.7%

Fat-specific age-related GO terms in Cluster 5

GO:0046483 heterocycle metabolism	CG7642	FBgn0003308	rosy	2.07E-02	135	5	3.7%
GO:0006725 aromatic compound metabolism	CG16758	FBgn0035348		2.64E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG17896	FBgn0023537		2.64E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG4067	FBgn0020385	pugilist	2.64E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG6767	FBgn0036030		2.64E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG7642	FBgn0003308	rosy	2.64E-02	144	5	3.5%
GO:0006732 coenzyme metabolism	CG1065	FBgn0004888	Succinyl coenzyme A synthetase alpha subunit	1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG14630	FBgn0014903		1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG15093	FBgn0034390		1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG4067	FBgn0020385	pugilist	1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG4703	FBgn0038742		1.62E-02	226	7	3.1%
GO:0006732 coenzyme metabolism	CG7026	FBgn0038276		1.62E-02	226	7	3.1%
GO:0051186 cofactor metabolism	CG1065	FBgn0004888	Succinyl coenzyme A synthetase alpha subunit	2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG11661	FBgn0010352	Neural conserved at 73EF	2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG14630	FBgn0014903		2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG15093	FBgn0034390		2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG4067	FBgn0020385	pugilist	2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG4703	FBgn0038742		2.18E-02	240	7	2.9%
GO:0051186 cofactor metabolism	CG7026	FBgn0038276		2.18E-02	240	7	2.9%
GO:0006520 amino acid metabolism	CG10621	FBgn0032726		7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG15093	FBgn0034390		7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG1607	FBgn0039844		7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG17896	FBgn0023537		7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG4067	FBgn0020385	pugilist	7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG6309	NA	NA	7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG6415	FBgn0032287		7.28E-03	243	8	3.3%
GO:0006520 amino acid metabolism	CG6661	FBgn0036403		7.28E-03	243	8	3.3%