

MT-specific age-related GO terms in Cluster 1 (Upregulated)							
GO term	CG ID	FB ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0006820 anion transport	CG11340	FBgn0039840		1.66E-03	93	3	3.2%
GO:0006820 anion transport	CG17646	FBgn0031362		1.66E-03	93	3	3.2%
GO:0006820 anion transport	CG9717	FBgn0039789		1.66E-03	93	3	3.2%
GO:0006869 lipid transport	CG17646	FBgn0031362		9.38E-03	57	2	3.5%
GO:0006869 lipid transport	CG9622	NA	NA	9.38E-03	57	2	3.5%
GO:0016082 synaptic vesicle priming	CG17762	FBgn0030412		3.08E-02	12	1	8.3%
GO:0006457 protein folding	CG4538	FBgn0038745		3.75E-02	119	2	1.7%
GO:0006457 protein folding	CG7182	FBgn0035878		3.75E-02	119	2	1.7%
GO:0006887 exocytosis	CG17762	FBgn0030412		3.93E-02	122	2	1.6%
GO:0006887 exocytosis	CG2095	FBgn0037373		3.93E-02	122	2	1.6%
GO:0006510 ATP-dependent proteolysis	CG4538	FBgn0038745		4.84E-02	19	1	5.3%

MT-specific age-related GO terms in Cluster 2 (Upregulated)							
GO term	CG ID	FB ID	Full name	P-value	Total gene	Changed gene	% of change
GO:0006875 metal ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	3.13E-03	20	3	15.0%
GO:0006875 metal ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	3.13E-03	20	3	15.0%
GO:0006875 metal ion homeostasis	CG3743	FBgn0040305		3.13E-03	20	3	15.0%
GO:0006873 cell ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	5.97E-03	25	3	12.0%
GO:0006873 cell ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	5.97E-03	25	3	12.0%
GO:0006873 cell ion homeostasis	CG3743	FBgn0040305		5.97E-03	25	3	12.0%
GO:0030003 cation homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	5.97E-03	25	3	12.0%
GO:0030003 cation homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	5.97E-03	25	3	12.0%
GO:0030003 cation homeostasis	CG3743	FBgn0040305		5.97E-03	25	3	12.0%
GO:0050801 ion homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	5.97E-03	25	3	12.0%
GO:0050801 ion homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	5.97E-03	25	3	12.0%
GO:0050801 ion homeostasis	CG3743	FBgn0040305		5.97E-03	25	3	12.0%
GO:0006399 tRNA metabolism	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	6.88E-03	80	5	6.3%
GO:0006399 tRNA metabolism	CG1307	FBgn0026566		6.88E-03	80	5	6.3%
GO:0006399 tRNA metabolism	CG6335	FBgn0027087	Histidyl-tRNA synthetase	6.88E-03	80	5	6.3%
GO:0006399 tRNA metabolism	CG6778	FBgn0027088	Glycyl-tRNA synthetase	6.88E-03	80	5	6.3%
GO:0006399 tRNA metabolism	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	6.88E-03	80	5	6.3%
GO:0006418 tRNA aminoacylation for protein translation	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0006418 tRNA aminoacylation for protein translation	CG6335	FBgn0027087	Histidyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0006418 tRNA aminoacylation for protein translation	CG6778	FBgn0027088	Glycyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0006418 tRNA aminoacylation for protein translation	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0043039 tRNA aminoacylation	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0043039 tRNA aminoacylation	CG6335	FBgn0027087	Histidyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0043039 tRNA aminoacylation	CG6778	FBgn0027088	Glycyl-tRNA synthetase	9.74E-03	56	4	7.1%

GO:0043039 tRNA aminoacylation	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	9.74E-03	56	4	7.1%
GO:0043038 amino acid activation	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	1.04E-02	57	4	7.0%
GO:0043038 amino acid activation	CG6335	FBgn0027087	Histidyl-tRNA synthetase	1.04E-02	57	4	7.0%
GO:0043038 amino acid activation	CG6778	FBgn0027088	Glycyl-tRNA synthetase	1.04E-02	57	4	7.0%
GO:0043038 amino acid activation	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	1.04E-02	57	4	7.0%
GO:0007568 aging	CG3979	FBgn0036816	I'm not dead yet	1.30E-02	33	3	9.1%
GO:0007568 aging	CG6536	FBgn0034219	methuselah-like 4	1.30E-02	33	3	9.1%
GO:0007568 aging	CG6871	FBgn0000261	Catalase	1.30E-02	33	3	9.1%
GO:0008340 determination of adult life span	CG3979	FBgn0036816	I'm not dead yet	1.30E-02	33	3	9.1%
GO:0008340 determination of adult life span	CG6536	FBgn0034219	methuselah-like 4	1.30E-02	33	3	9.1%
GO:0008340 determination of adult life span	CG6871	FBgn0000261	Catalase	1.30E-02	33	3	9.1%
GO:0006400 tRNA modification	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	1.38E-02	62	4	6.5%
GO:0006400 tRNA modification	CG6335	FBgn0027087	Histidyl-tRNA synthetase	1.38E-02	62	4	6.5%
GO:0006400 tRNA modification	CG6778	FBgn0027088	Glycyl-tRNA synthetase	1.38E-02	62	4	6.5%
GO:0006400 tRNA modification	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	1.38E-02	62	4	6.5%
GO:0016358 dendrite morphogenesis	CG11387	FBgn0004198	cut	1.41E-02	34	3	8.8%
GO:0016358 dendrite morphogenesis	CG8416	FBgn0014020		1.41E-02	34	3	8.8%
GO:0016358 dendrite morphogenesis	CG9755	FBgn0003165	pumilio	1.41E-02	34	3	8.8%
GO:0030030 cell projection organization and biogenesis	bnl	FBgn0014135	branchless	1.41E-02	34	3	8.8%
GO:0030030 cell projection organization and biogenesis	CG7103	FBgn0030964	PDGF- and VEGF-related factor 1	1.41E-02	34	3	8.8%
GO:0030030 cell projection organization and biogenesis	CG8416	FBgn0014020		1.41E-02	34	3	8.8%
GO:0043037 translation	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	1.89E-02	181	7	3.9%
GO:0043037 translation	CG1873	FBgn0000557	Elongation factor 1alpha100E	1.89E-02	181	7	3.9%
GO:0043037 translation	CG2238	FBgn0000559	Elongation factor 2b	1.89E-02	181	7	3.9%
GO:0043037 translation	CG6335	FBgn0027087	Histidyl-tRNA synthetase	1.89E-02	181	7	3.9%
GO:0043037 translation	CG6778	FBgn0027088	Glycyl-tRNA synthetase	1.89E-02	181	7	3.9%
GO:0043037 translation	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	1.89E-02	181	7	3.9%
GO:0043037 translation	CG9755	FBgn0003165	pumilio	1.89E-02	181	7	3.9%
GO:0009451 RNA modification	CG11471	FBgn0027086	Isoleucyl-tRNA synthetase	1.98E-02	69	4	5.8%

GO:0009451 RNA modification	CG6335	FBgn0027087	Histidyl-tRNA synthetase	1.98E-02	69	4	5.8%
GO:0009451 RNA modification	CG6778	FBgn0027088	Glycyl-tRNA synthetase	1.98E-02	69	4	5.8%
GO:0009451 RNA modification	CG9735	FBgn0010803	Tryptophanyl-tRNA synthetase	1.98E-02	69	4	5.8%
GO:0051276 chromosome organization and biogenesis	CG11290	FBgn0034975	enoki mushroom	2.37E-02	148	6	4.1%
GO:0051276 chromosome organization and biogenesis	CG14941	FBgn0000588	extra sexcombs	2.37E-02	148	6	4.1%
GO:0051276 chromosome organization and biogenesis	CG14999	FBgn0015287	Replication-factor-C 40kD subunit	2.37E-02	148	6	4.1%
GO:0051276 chromosome organization and biogenesis	CG3733	FBgn0016132	Chromodomain-helicase-DNA-binding protein	2.37E-02	148	6	4.1%
GO:0051276 chromosome organization and biogenesis	CG4817	FBgn0010278	Structure specific recognition protein	2.37E-02	148	6	4.1%
GO:0051276 chromosome organization and biogenesis	CG5825	FBgn0014857	Histone H3.3A	2.37E-02	148	6	4.1%
GO:0006333 chromatin assembly or disassembly	CG11290	FBgn0034975	enoki mushroom	2.83E-02	77	4	5.2%
GO:0006333 chromatin assembly or disassembly	CG3733	FBgn0016132	Chromodomain-helicase-DNA-binding protein	2.83E-02	77	4	5.2%
GO:0006333 chromatin assembly or disassembly	CG4817	FBgn0010278	Structure specific recognition protein	2.83E-02	77	4	5.2%
GO:0006333 chromatin assembly or disassembly	CG5825	FBgn0014857	Histone H3.3A	2.83E-02	77	4	5.2%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG1469	FBgn0015221	Ferritin 2 light chain homologue	2.93E-02	18	2	11.1%
GO:0030005 di- tri-valent inorganic cation homeostasis	CG2216	FBgn0015222	Ferritin 1 heavy chain homologue	2.93E-02	18	2	11.1%
GO:0006334 nucleosome assembly	CG11290	FBgn0034975	enoki mushroom	3.24E-02	19	2	10.5%
GO:0006334 nucleosome assembly	CG5825	FBgn0014857	Histone H3.3A	3.24E-02	19	2	10.5%
GO:0006414 translational elongation	CG1873	FBgn0000557	Elongation factor 1alpha100E	3.57E-02	20	2	10.0%
GO:0006414 translational elongation	CG2238	FBgn0000559	Elongation factor 2b	3.57E-02	20	2	10.0%
GO:0016318 ommatidial rotation	CG8056	FBgn0052177		3.57E-02	20	2	10.0%
GO:0016318 ommatidial rotation	CG8416	FBgn0014020		3.57E-02	20	2	10.0%
GO:0006100 tricarboxylic acid cycle intermediate metabolism	CG10160	FBgn0001258	Ecdysone-inducible gene L3	3.91E-02	21	2	9.5%
GO:0006100 tricarboxylic acid cycle intermediate metabolism	CG5320	FBgn0001098	Glutamate dehydrogenase	3.91E-02	21	2	9.5%
GO:0035152 regulation of tracheal tube architecture	bnl	FBgn0014135	branchless	3.91E-02	21	2	9.5%
GO:0035152 regulation of tracheal tube architecture	CG8416	FBgn0014020		3.91E-02	21	2	9.5%
GO:0042221 response to chemical substance	CG14268	NA	NA	4.05E-02	168	6	3.6%
GO:0042221 response to chemical substance	CG3797	FBgn0036842		4.05E-02	168	6	3.6%
GO:0042221 response to chemical substance	bnl	FBgn0014135	branchless	4.05E-02	168	6	3.6%
GO:0042221 response to chemical substance	CG5224	FBgn0034354		4.05E-02	168	6	3.6%
GO:0042221 response to chemical substance	CG5789	FBgn0039207		4.05E-02	168	6	3.6%

MT-specific age-related GO terms in Cluster 2

GO:0042221 response to chemical substance	CG6633	FBgn0040256		4.05E-02	168	6	3.6%
GO:0006323 DNA packaging	CG11290	FBgn0034975	enoki mushroom	4.08E-02	126	5	4.0%
GO:0006323 DNA packaging	CG14941	FBgn0000588	extra sexcombs	4.08E-02	126	5	4.0%
GO:0006323 DNA packaging	CG3733	FBgn0016132	Chromodomain-helicase-DNA-binding protein	4.08E-02	126	5	4.0%
GO:0006323 DNA packaging	CG4817	FBgn0010278	Structure specific recognition protein	4.08E-02	126	5	4.0%
GO:0006323 DNA packaging	CG5825	FBgn0014857	Histone H3.3A	4.08E-02	126	5	4.0%
GO:0006325 establishment and or maintenance of chromatin architecture	CG11290	FBgn0034975	enoki mushroom	4.08E-02	126	5	4.0%
GO:0006325 establishment and or maintenance of chromatin architecture	CG14941	FBgn0000588	extra sexcombs	4.08E-02	126	5	4.0%
GO:0006325 establishment and or maintenance of chromatin architecture	CG3733	FBgn0016132	Chromodomain-helicase-DNA-binding protein	4.08E-02	126	5	4.0%
GO:0006325 establishment and or maintenance of chromatin architecture	CG4817	FBgn0010278	Structure specific recognition protein	4.08E-02	126	5	4.0%
GO:0006325 establishment and or maintenance of chromatin architecture	CG5825	FBgn0014857	Histone H3.3A	4.08E-02	126	5	4.0%
GO:0007613 memory	CG14268	NA	NA	4.26E-02	22	2	9.1%
GO:0007613 memory	CG9755	FBgn0003165	pumilio	4.26E-02	22	2	9.1%

MT-specific age-related GO terms in Cluster 3 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0030001 metal ion transport	CG10706	FBgn0029761	small conductance calcium-activated potassium channel	2.84E-02	140	3	2.1%
GO:0030001 metal ion transport	CG11655	FBgn0030638		2.84E-02	140	3	2.1%
GO:0030001 metal ion transport	CG14647	FBgn0037244		2.84E-02	140	3	2.1%
GO:0006813 potassium ion transport	CG10706	FBgn0029761	small conductance calcium-activated potassium channel	2.99E-02	57	2	3.5%
GO:0006813 potassium ion transport	CG14647	FBgn0037244		2.99E-02	57	2	3.5%
GO:0000910 cytokinesis	CG6873	FBgn0030951		3.39E-02	61	2	3.3%
GO:0000910 cytokinesis	CG8817	FBgn0041111	lilliputian	3.39E-02	61	2	3.3%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG5460	FBgn0001169	Hairless	3.60E-02	63	2	3.2%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG8817	FBgn0041111	lilliputian	3.60E-02	63	2	3.2%
GO:0001754 eye photoreceptor cell differentiation	CG5460	FBgn0001169	Hairless	3.70E-02	64	2	3.1%
GO:0001754 eye photoreceptor cell differentiation	CG8817	FBgn0041111	lilliputian	3.70E-02	64	2	3.1%
GO:0015672 monovalent inorganic cation transport	CG10706	FBgn0029761	small conductance calcium-activated potassium channel	4.51E-02	168	3	1.8%
GO:0015672 monovalent inorganic cation transport	CG11655	FBgn0030638		4.51E-02	168	3	1.8%
GO:0015672 monovalent inorganic cation transport	CG14647	FBgn0037244		4.51E-02	168	3	1.8%

MT-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:0001708 cell fate specification	CG2956	FBgn0003900	twist	2.90E-02	50	2	4.0%
GO:0001708 cell fate specification	CG3411	FBgn0004101	blistered	2.90E-02	50	2	4.0%
GO:0006790 sulfur metabolism	CG17772	NA	NA	3.70E-02	57	2	3.5%
GO:0006790 sulfur metabolism	CG7408	FBgn0036765		3.70E-02	57	2	3.5%
GO:0051169 nuclear transport	CG8069	FBgn0033380	Phosphorylated adaptor for RNA export	4.43E-02	63	2	3.2%
GO:0051169 nuclear transport	CG9426	FBgn0032485		4.43E-02	63	2	3.2%
GO:0035239 tube morphogenesis	CG2956	FBgn0003900	twist	4.56E-02	64	2	3.1%
GO:0035239 tube morphogenesis	CG3411	FBgn0004101	blistered	4.56E-02	64	2	3.1%
GO:0007411 axon guidance	CG13974	NA	NA	6.03E-03	70	3	4.3%
GO:0007411 axon guidance	CG5481	FBgn0002543	leak	6.03E-03	70	3	4.3%
GO:0007411 axon guidance	CG6407	FBgn0010194	Wnt oncogene analog 5	6.03E-03	70	3	4.3%
GO:0007409 axonogenesis	CG13974	NA	NA	1.39E-02	95	3	3.2%
GO:0007409 axonogenesis	CG5481	FBgn0002543	leak	1.39E-02	95	3	3.2%
GO:0007409 axonogenesis	CG6407	FBgn0010194	Wnt oncogene analog 5	1.39E-02	95	3	3.2%
GO:0031175 neurite morphogenesis	CG13974	NA	NA	2.31E-02	115	3	2.6%
GO:0031175 neurite morphogenesis	CG5481	FBgn0002543	leak	2.31E-02	115	3	2.6%
GO:0031175 neurite morphogenesis	CG6407	FBgn0010194	Wnt oncogene analog 5	2.31E-02	115	3	2.6%
GO:0009798 axis specification	CG11513	FBgn0041164	armitage	4.77E-02	153	3	2.0%
GO:0009798 axis specification	CG14228	FBgn0013951	Merlin	4.77E-02	153	3	2.0%
GO:0009798 axis specification	CG2956	FBgn0003900	twist	4.77E-02	153	3	2.0%

MT-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:0009309 amine biosynthesis	CG1315	FBgn0026565		2.55E-03	74	4	5.4%
GO:0009309 amine biosynthesis	CG3525	FBgn0000536	easily shocked	2.55E-03	74	4	5.4%
GO:0009309 amine biosynthesis	CG4900	FBgn0024958	Iron regulatory protein 1A	2.55E-03	74	4	5.4%
GO:0009309 amine biosynthesis	CG8553	FBgn0020615	selenide,water dikinase	2.55E-03	74	4	5.4%
GO:0035146 tube fusion	CG11579	FBgn0000117	armadillo	3.15E-03	11	2	18.2%
GO:0035146 tube fusion	CG8633	NA	NA	3.15E-03	11	2	18.2%
GO:0035147 tracheal branch fusion	CG11579	FBgn0000117	armadillo	3.15E-03	11	2	18.2%
GO:0035147 tracheal branch fusion	CG8633	NA	NA	3.15E-03	11	2	18.2%
GO:0045186 zonula adherens assembly	CG11579	FBgn0000117	armadillo	3.15E-03	11	2	18.2%
GO:0045186 zonula adherens assembly	CG15339	FBgn0003349	stardust	3.15E-03	11	2	18.2%
GO:0007028 cytoplasm organization and biogenesis	CG11579	FBgn0000117	armadillo	5.39E-03	46	3	6.5%
GO:0007028 cytoplasm organization and biogenesis	CG15339	FBgn0003349	stardust	5.39E-03	46	3	6.5%
GO:0007028 cytoplasm organization and biogenesis	CG5728	FBgn0039182		5.39E-03	46	3	6.5%
GO:0043297 apical junction assembly	CG11579	FBgn0000117	armadillo	6.69E-03	16	2	12.5%
GO:0043297 apical junction assembly	CG15339	FBgn0003349	stardust	6.69E-03	16	2	12.5%
GO:0007043 intercellular junction assembly	CG11579	FBgn0000117	armadillo	7.55E-03	17	2	11.8%
GO:0007043 intercellular junction assembly	CG15339	FBgn0003349	stardust	7.55E-03	17	2	11.8%
GO:0006637 acyl-CoA metabolism	CG8199	FBgn0037709		9.40E-03	19	2	10.5%
GO:0006637 acyl-CoA metabolism	CG8814	FBgn0031478		9.40E-03	19	2	10.5%
GO:0045216 intercellular junction assembly and or maintenance	CG11579	FBgn0000117	armadillo	9.40E-03	19	2	10.5%
GO:0045216 intercellular junction assembly and or maintenance	CG15339	FBgn0003349	stardust	9.40E-03	19	2	10.5%
GO:0006413 translational initiation	CG10161	FBgn0040227	Eukaryotic initiation factor 3 p66 subunit	9.78E-03	57	3	5.3%
GO:0006413 translational initiation	CG10716	NA	NA	9.78E-03	57	3	5.3%
GO:0006413 translational initiation	CG4900	FBgn0024958	Iron regulatory protein 1A	9.78E-03	57	3	5.3%
GO:0006520 amino acid metabolism	CG1315	FBgn0026565		1.11E-02	243	6	2.5%
GO:0006520 amino acid metabolism	CG17896	FBgn0023537		1.11E-02	243	6	2.5%
GO:0006520 amino acid metabolism	CG4900	FBgn0024958	Iron regulatory protein 1A	1.11E-02	243	6	2.5%
GO:0006520 amino acid metabolism	CG8199	FBgn0037709		1.11E-02	243	6	2.5%
GO:0006520 amino acid metabolism	CG8235	FBgn0033351		1.11E-02	243	6	2.5%
GO:0006520 amino acid metabolism	CG8553	FBgn0020615	selenide,water dikinase	1.11E-02	243	6	2.5%
GO:0008652 amino acid biosynthesis	CG1315	FBgn0026565		1.23E-02	62	3	4.8%
GO:0008652 amino acid biosynthesis	CG4900	FBgn0024958	Iron regulatory protein 1A	1.23E-02	62	3	4.8%

MT-specific age-related GO terms in Cluster 5

GO:0008652 amino acid biosynthesis	CG8553	FBgn0020615	selenide,water dikinase	1.23E-02	62	3	4.8%
GO:0001763 branching morphogenesis	CG11579	FBgn0000117	armadillo	2.26E-02	30	2	6.7%
GO:0001763 branching morphogenesis	CG8633	NA	NA	2.26E-02	30	2	6.7%
GO:0006461 protein complex assembly	CG11579	FBgn0000117	armadillo	3.28E-02	90	3	3.3%
GO:0006461 protein complex assembly	CG15339	FBgn0003349	stardust	3.28E-02	90	3	3.3%
GO:0006461 protein complex assembly	CG6022	FBgn0038925		3.28E-02	90	3	3.3%
GO:0009966 regulation of signal transduction	CG11579	FBgn0000117	armadillo	3.47E-02	92	3	3.3%
GO:0009966 regulation of signal transduction	CG12676	FBgn0000547	echinoid	3.47E-02	92	3	3.3%
GO:0009966 regulation of signal transduction	CG6523	FBgn0032509		3.47E-02	92	3	3.3%
GO:0006631 fatty acid metabolism	CG10877	FBgn0038804		4.17E-02	99	3	3.0%
GO:0006631 fatty acid metabolism	CG8199	FBgn0037709		4.17E-02	99	3	3.0%
GO:0006631 fatty acid metabolism	CG8814	FBgn0031478		4.17E-02	99	3	3.0%

MT-specific age-related GO terms in Cluster 6 (Upregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0008105 asymmetric protein localization	CG5753	FBgn0003520	staußen	1.82E-02	37	2	5.4%
GO:0008105 asymmetric protein localization	CG9326	FBgn0032885		1.82E-02	37	2	5.4%
GO:0048066 pigmentation	CG11197	NA	NA	1.92E-02	38	2	5.3%
GO:0048066 pigmentation	CG13910	NA	NA	1.92E-02	38	2	5.3%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG13910	NA	NA	1.94E-02	102	3	2.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG1500	FBgn0001083	furrowed	1.94E-02	102	3	2.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG8367	FBgn0000289	combgap	1.94E-02	102	3	2.9%
GO:0035107 appendage morphogenesis	CG13910	NA	NA	2.09E-02	105	3	2.9%
GO:0035107 appendage morphogenesis	CG1500	FBgn0001083	furrowed	2.09E-02	105	3	2.9%
GO:0035107 appendage morphogenesis	CG8367	FBgn0000289	combgap	2.09E-02	105	3	2.9%
GO:0007452 imaginal disc metamorphosis	CG11197	NA	NA	2.79E-02	206	4	1.9%
GO:0007452 imaginal disc metamorphosis	CG13910	NA	NA	2.79E-02	206	4	1.9%
GO:0007452 imaginal disc metamorphosis	CG1500	FBgn0001083	furrowed	2.79E-02	206	4	1.9%
GO:0007452 imaginal disc metamorphosis	CG8367	FBgn0000289	combgap	2.79E-02	206	4	1.9%
GO:0007067 mitosis	CG10212	FBgn0027783		3.43E-02	220	4	1.8%
GO:0007067 mitosis	CG10850	FBgn0041147	imaginal discs arrested	3.43E-02	220	4	1.8%
GO:0007067 mitosis	CG6413	FBgn0039183		3.43E-02	220	4	1.8%
GO:0007067 mitosis	CG9699	FBgn0030772		3.43E-02	220	4	1.8%
GO:0000087 M phase of mitotic cell cycle	CG10212	FBgn0027783		3.48E-02	221	4	1.8%
GO:0000087 M phase of mitotic cell cycle	CG10850	FBgn0041147	imaginal discs arrested	3.48E-02	221	4	1.8%
GO:0000087 M phase of mitotic cell cycle	CG6413	FBgn0039183		3.48E-02	221	4	1.8%
GO:0000087 M phase of mitotic cell cycle	CG9699	FBgn0030772		3.48E-02	221	4	1.8%
GO:0006144 purine base metabolism	CG2867	FBgn0004901	Phosphoribosylamidotransferase	3.69E-02	54	2	3.7%
GO:0006144 purine base metabolism	CG9326	FBgn0032885		3.69E-02	54	2	3.7%
GO:0046483 heterocycle metabolism	CG11197	NA	NA	3.99E-02	135	3	2.2%
GO:0046483 heterocycle metabolism	CG2867	FBgn0004901	Phosphoribosylamidotransferase	3.99E-02	135	3	2.2%
GO:0046483 heterocycle metabolism	CG9326	FBgn0032885		3.99E-02	135	3	2.2%
GO:0006725 aromatic compound metabolism	CG11197	NA	NA	4.68E-02	144	3	2.1%
GO:0006725 aromatic compound metabolism	CG2867	FBgn0004901	Phosphoribosylamidotransferase	4.68E-02	144	3	2.1%
GO:0006725 aromatic compound metabolism	CG9326	FBgn0032885		4.68E-02	144	3	2.1%
GO:0000278 mitotic cell cycle	CG10212	FBgn0027783		4.79E-02	245	4	1.6%
GO:0000278 mitotic cell cycle	CG10850	FBgn0041147	imaginal discs arrested	4.79E-02	245	4	1.6%
GO:0000278 mitotic cell cycle	CG6413	FBgn0039183		4.79E-02	245	4	1.6%
GO:0000278 mitotic cell cycle	CG9699	FBgn0030772		4.79E-02	245	4	1.6%

MT-specific age-related GO terms in Cluster 7 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG10363	FBgn0041180	Thiolester containing protein IV	1.24E-03	41	5	12.2%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG1165	FBgn0004430	Lysozyme S	1.24E-03	41	5	12.2%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG1180	FBgn0004428	Lysozyme E	1.24E-03	41	5	12.2%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG5680	FBgn0000229	basket	1.24E-03	41	5	12.2%
GO:0006960 antimicrobial humoral response (sensu Protostomia)	CG9116	FBgn0004429	Lysozyme P	1.24E-03	41	5	12.2%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG10363	FBgn0041180	Thiolester containing protein IV	1.71E-03	44	5	11.4%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG1165	FBgn0004430	Lysozyme S	1.71E-03	44	5	11.4%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG1180	FBgn0004428	Lysozyme E	1.71E-03	44	5	11.4%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG5680	FBgn0000229	basket	1.71E-03	44	5	11.4%
GO:0016065 humoral defense mechanism (sensu Protostomia)	CG9116	FBgn0004429	Lysozyme P	1.71E-03	44	5	11.4%
GO:0006725 aromatic compound metabolism	CG10184	FBgn0039094		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG11158	FBgn0030511		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG14681	FBgn0037820		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG17870	FBgn0004907		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG1814	FBgn0033426		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG18519	FBgn0038348		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG3390	FBgn0051773		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG5235	FBgn0036565		2.25E-03	144	9	6.3%
GO:0006725 aromatic compound metabolism	CG6612	FBgn0042094		2.25E-03	144	9	6.3%
GO:0006575 amino acid derivative metabolism	CG14681	FBgn0037820		2.53E-03	48	5	10.4%
GO:0006575 amino acid derivative metabolism	CG17870	FBgn0004907		2.53E-03	48	5	
GO:0006575 amino acid derivative metabolism	CG18238	NA	NA	2.53E-03	48	5	
GO:0006575 amino acid derivative metabolism	CG5235	FBgn0036565		2.53E-03	48	5	
GO:0006575 amino acid derivative metabolism	CG8327	FBgn0037723	Spermidine Synthase	2.53E-03	48	5	
GO:0006576 biogenic amine metabolism	CG14681	FBgn0037820		2.78E-03	30	4	
GO:0006576 biogenic amine metabolism	CG17870	FBgn0004907		2.78E-03	30	4	
GO:0006576 biogenic amine metabolism	CG5235	FBgn0036565		2.78E-03	30	4	
GO:0006576 biogenic amine metabolism	CG8327	FBgn0037723	Spermidine Synthase	2.78E-03	30	4	
GO:0019730 antimicrobial humoral response	CG10363	FBgn0041180	Thiolester containing protein IV	6.21E-03	59	5	
GO:0019730 antimicrobial humoral response	CG1165	FBgn0004430	Lysozyme S	6.21E-03	59	5	
GO:0019730 antimicrobial humoral response	CG1180	FBgn0004428	Lysozyme E	6.21E-03	59	5	

MT-specific age-related GO terms in Cluster 7

GO:0019730 antimicrobial humoral response	CG5680	FBgn0000229	basket	6.21E-03	59	5
GO:0019730 antimicrobial humoral response	CG9116	FBgn0004429	Lysozyme P	6.21E-03	59	5
GO:0007265 Ras protein signal transduction	CG13388	FBgn0027932	A kinase anchor protein 200	1.03E-02	23	3
GO:0007265 Ras protein signal transduction	CG17870	FBgn0004907		1.03E-02	23	3
GO:0007265 Ras protein signal transduction	CG9856	FBgn0016641	Protein tyrosine phosphatase-ERK/Enhancer of Ras1	1.03E-02	23	3
GO:0006959 humoral immune response	CG10363	FBgn0041180	Thiolester containing protein IV	1.06E-02	67	5
GO:0006959 humoral immune response	CG1165	FBgn0004430	Lysozyme S	1.06E-02	67	5
GO:0006959 humoral immune response	CG1180	FBgn0004428	Lysozyme E	1.06E-02	67	5
GO:0006959 humoral immune response	CG5680	FBgn0000229	basket	1.06E-02	67	5
GO:0006959 humoral immune response	CG9116	FBgn0004429	Lysozyme P	1.06E-02	67	5
GO:0016079 synaptic vesicle exocytosis	CG17762	FBgn0030412		1.20E-02	45	4
GO:0016079 synaptic vesicle exocytosis	CG1618	FBgn0000346	comatose	1.20E-02	45	4
GO:0016079 synaptic vesicle exocytosis	CG3139	FBgn0004242	synaptotagmin	1.20E-02	45	4
GO:0016079 synaptic vesicle exocytosis	CG6703	FBgn0013759	Calcium/calmodulin-dependent protein kinase	1.20E-02	45	4
GO:0016477 cell migration	CG18668	NA	NA	1.30E-02	157	8
GO:0016477 cell migration	CG14345	NA	NA	1.30E-02	157	8
GO:0016477 cell migration	CG15288	FBgn0004002	wing blister	1.30E-02	157	8
GO:0016477 cell migration	CG18381	NA	NA	1.30E-02	157	8
GO:0016477 cell migration	CG4531	FBgn0004569	argos	1.30E-02	157	8
GO:0016477 cell migration	CG11280	FBgn0010452	tartan	1.30E-02	157	8
GO:0016477 cell migration	CG7895	FBgn0004110	tinman	1.30E-02	157	8
GO:0016477 cell migration	CG9786	FBgn0001180	hunchback	1.30E-02	157	8
GO:0001708 cell fate specification	CG3956	FBgn0003448	snail	1.72E-02	50	4
GO:0001708 cell fate specification	CG4531	FBgn0004569	argos	1.72E-02	50	4
GO:0001708 cell fate specification	CG7895	FBgn0004110	tinman	1.72E-02	50	4
GO:0001708 cell fate specification	CG9786	FBgn0001180	hunchback	1.72E-02	50	4
GO:0046483 heterocycle metabolism	CG11158	FBgn0030511		1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG17870	FBgn0004907		1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG1814	FBgn0033426		1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG18238	NA	NA	1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG18519	FBgn0038348		1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG3390	FBgn0051773		1.80E-02	135	7
GO:0046483 heterocycle metabolism	CG6612	FBgn0042094	Adenylate kinase-3	1.80E-02	135	7
GO:0006333 chromatin assembly or disassembly	CG18381	NA	NA	1.85E-02	77	5
GO:0006333 chromatin assembly or disassembly	CG2252	FBgn0004656	female sterile (1) homoeotic	1.85E-02	77	5
GO:0006333 chromatin assembly or disassembly	CG5257	NA	NA	1.85E-02	77	5
GO:0006333 chromatin assembly or disassembly	CG7022	NA	NA	1.85E-02	77	5
GO:0006333 chromatin assembly or disassembly	CG7690	NA	NA	1.85E-02	77	5

MT-specific age-related GO terms in Cluster 7

GO:0007501 mesoderm cell fate specification	CG3956	FBgn0003448	snail	1.93E-02	11	2
GO:0007501 mesoderm cell fate specification	CG7895	FBgn0004110	tinman	1.93E-02	11	2
GO:0050795 regulation of behavior	CG15288	FBgn0004002	wing blister	1.93E-02	11	2
GO:0050795 regulation of behavior	CG6917	FBgn0000592	Esterase 6	1.93E-02	11	2
GO:0048489 synaptic vesicle transport	CG17762	FBgn0030412		2.04E-02	79	5
GO:0048489 synaptic vesicle transport	CG1107	FBgn0037218		2.04E-02	79	5
GO:0048489 synaptic vesicle transport	CG1618	FBgn0000346	comatose	2.04E-02	79	5
GO:0048489 synaptic vesicle transport	CG3139	FBgn0004242	synaptotagmin	2.04E-02	79	5
GO:0048489 synaptic vesicle transport	CG6703	FBgn0013759	Calcium/calmodulin-dependent protein kinase	2.04E-02	79	5
GO:0006144 purine base metabolism	CG11158	FBgn0030511		2.22E-02	54	4
GO:0006144 purine base metabolism	CG1814	FBgn0033426		2.22E-02	54	4
GO:0006144 purine base metabolism	CG18519	FBgn0038348		2.22E-02	54	4
GO:0006144 purine base metabolism	CG6612	FBgn0042094	Adenylate kinase-3	2.22E-02	54	4
GO:0016082 synaptic vesicle priming	CG17762	FBgn0030412		2.29E-02	12	2
GO:0016082 synaptic vesicle priming	CG1618	FBgn0000346	comatose	2.29E-02	12	2
GO:0048193 Golgi vesicle transport	CG10882	FBgn0031408		2.53E-02	32	3
GO:0048193 Golgi vesicle transport	CG1618	FBgn0000346	comatose	2.53E-02	32	3
GO:0048193 Golgi vesicle transport	CG3071	FBgn0023527		2.53E-02	32	3
GO:0006584 catecholamine metabolism	CG14681	FBgn0037820		2.67E-02	13	2
GO:0006584 catecholamine metabolism	CG5235	FBgn0036565		2.67E-02	13	2
GO:0009613 response to pest pathogen or parasite	CG10363	FBgn0041180	Thiolester containing protein IV	2.70E-02	85	5
GO:0009613 response to pest pathogen or parasite	CG1165	FBgn0004430	Lysozyme S	2.70E-02	85	5
GO:0009613 response to pest pathogen or parasite	CG1180	FBgn0004428	Lysozyme E	2.70E-02	85	5
GO:0009613 response to pest pathogen or parasite	CG5680	FBgn0000229	basket	2.70E-02	85	5
GO:0009613 response to pest pathogen or parasite	CG9116	FBgn0004429	Lysozyme P	2.70E-02	85	5
GO:0006888 ER to Golgi transport	CG10882	FBgn0031408		3.07E-02	14	2
GO:0006888 ER to Golgi transport	CG1618	FBgn0000346	comatose	3.07E-02	14	2
GO:0018958 phenol metabolism	CG14681	FBgn0037820		3.07E-02	14	2
GO:0018958 phenol metabolism	CG5235	FBgn0036565		3.07E-02	14	2
GO:0042401 biogenic amine biosynthesis	CG17870	FBgn0004907		3.07E-02	14	2
GO:0042401 biogenic amine biosynthesis	CG8327	FBgn0037723	Spermidine Synthase	3.07E-02	14	2
GO:0005976 polysaccharide metabolism	CG10154	FBgn0036361		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG10178	FBgn0032684		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG13837	FBgn0039042		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG17322	FBgn0027070		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG17324	FBgn0027074		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG6653	FBgn0040255		3.20E-02	152	7
GO:0005976 polysaccharide metabolism	CG8536	FBgn0027538		3.20E-02	152	7

MT-specific age-related GO terms in Cluster 7

GO:0001710 mesoderm cell fate commitment	CG3956	FBgn0003448	snail	3.95E-02	16	2	
GO:0001710 mesoderm cell fate commitment	CG7895	FBgn0004110	tinman	3.95E-02	16	2	
GO:0006839 mitochondrial transport	CG1907	FBgn0039674		3.95E-02	16	2	
GO:0006839 mitochondrial transport	CG6647	FBgn0004363	porin	3.95E-02	16	2	
GO:0042398 amino acid derivative biosynthesis	CG17870	FBgn0004907		3.95E-02	16	2	
GO:0042398 amino acid derivative biosynthesis	CG8327	FBgn0037723	Spermidine Synthase	3.95E-02	16	2	
GO:0042659 regulation of cell fate specification	CG4531	FBgn0004569	argos	3.95E-02	16	2	
GO:0042659 regulation of cell fate specification	CG9786	FBgn0001180	hunchback	3.95E-02	16	2	
GO:0048333 mesoderm cell differentiation	CG3956	FBgn0003448	snail	3.95E-02	16	2	
GO:0048333 mesoderm cell differentiation	CG7895	FBgn0004110	tinman	3.95E-02	16	2	
GO:0008202 steroid metabolism	CG10178	FBgn0032684		4.24E-02	128	6	
GO:0008202 steroid metabolism	CG1444	FBgn0029975		4.24E-02	128	6	
GO:0008202 steroid metabolism	CG17322	FBgn0027070		4.24E-02	128	6	
GO:0008202 steroid metabolism	CG17324	FBgn0027074		4.24E-02	128	6	
GO:0008202 steroid metabolism	CG6653	FBgn0040255		4.24E-02	128	6	
GO:0008202 steroid metabolism	CG7113	FBgn0021765	scully	4.24E-02	128	6	
GO:0006631 fatty acid metabolism	CG1516	FBgn0027580		4.74E-02	99	5	
GO:0006631 fatty acid metabolism	CG3394	FBgn0034999		4.74E-02	99	5	
GO:0006631 fatty acid metabolism	CG5611	FBgn0039531		4.74E-02	99	5	
GO:0006631 fatty acid metabolism	CG7113	FBgn0021765	scully	4.74E-02	99	5	
GO:0006631 fatty acid metabolism	CG7461	FBgn0034432		4.74E-02	99	5	
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG17117	FBgn0001235	homothorax	4.78E-02	41	3	
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG5680	FBgn0000229	basket	4.78E-02	41	3	
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG9856	FBgn0016641	Protein tyrosine phosphatase-ERK/Enhancer of Ras1	4.78E-02	41	3	
GO:0046552 photoreceptor cell fate commitment	CG17117	FBgn0001235	homothorax	4.78E-02	41	3	
GO:0046552 photoreceptor cell fate commitment	CG5680	FBgn0000229	basket	4.78E-02	41	3	
GO:0046552 photoreceptor cell fate commitment	CG9856	FBgn0016641	Protein tyrosine phosphatase-ERK/Enhancer of Ras1	4.78E-02	41	3	
GO:0044272 sulfur compound biosynthesis	CG12913	FBgn0033500		4.91E-02	18	2	
GO:0044272 sulfur compound biosynthesis	CG1753	FBgn0031148		4.91E-02	18	2	