

Testis-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:0009894 regulation of catabolism	CG15010	FBgn0041171	archipelago	1.45E-04	27	5	18.5%
GO:0009894 regulation of catabolism	CG17161	FBgn0011598	grapes	1.45E-04	27	5	18.5%
GO:0009894 regulation of catabolism	CG2028	FBgn0015024	Casein kinase Ialpha	1.45E-04	27	5	18.5%
GO:0009894 regulation of catabolism	CG8068	FBgn0003612	Suppressor of variegation 2-10	1.45E-04	27	5	18.5%
GO:0009894 regulation of catabolism	CG9204	FBgn0025720		1.45E-04	27	5	18.5%
GO:0030162 regulation of proteolysis and peptidolysis	CG15010	FBgn0041171	archipelago	1.07E-02	24	3	12.5%
GO:0030162 regulation of proteolysis and peptidolysis	CG17161	FBgn0011598	grapes	1.07E-02	24	3	12.5%
GO:0030162 regulation of proteolysis and peptidolysis	CG2028	FBgn0015024	Casein kinase Ialpha	1.07E-02	24	3	12.5%
GO:0009968 negative regulation of signal transduction	CG12283	FBgn0015399	kekkon-1	1.17E-02	46	4	8.7%
GO:0009968 negative regulation of signal transduction	CG2028	FBgn0015024	Casein kinase Ialpha	1.17E-02	46	4	8.7%
GO:0009968 negative regulation of signal transduction	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	1.17E-02	46	4	8.7%
GO:0009968 negative regulation of signal transduction	CG8068	FBgn0003612	Suppressor of variegation 2-10	1.17E-02	46	4	8.7%
GO:0030097 hemopoiesis	CG5942	FBgn0000212	brahma	1.67E-02	51	4	7.8%
GO:0030097 hemopoiesis	CG6500	FBgn0000242	Beadex	1.67E-02	51	4	7.8%
GO:0030097 hemopoiesis	CG10894	NA	NA	1.67E-02	51	4	7.8%
GO:0030097 hemopoiesis	CG8068	FBgn0003612	Suppressor of variegation 2-10	1.67E-02	51	4	7.8%
GO:0008033 tRNA processing	CG5626	FBgn0036266		1.83E-02	11	2	18.2%
GO:0008033 tRNA processing	CG7163	FBgn0035889	monkey king protein	1.83E-02	11	2	18.2%
GO:0018991 oviposition	CG2159	NA	NA	1.83E-02	11	2	18.2%
GO:0018991 oviposition	CG8887	FBgn0005386	absent, small, or homeotic discs 1	1.83E-02	11	2	18.2%
GO:0045448 mitotic cell cycle embryonic	CG10308	FBgn0010317	Cyclin J	2.17E-02	12	2	16.7%
GO:0045448 mitotic cell cycle embryonic	CG17161	FBgn0011598	grapes	2.17E-02	12	2	16.7%
GO:0018193 peptidyl-amino acid modification	CG7265	FBgn0038272		2.54E-02	33	3	9.1%
GO:0018193 peptidyl-amino acid modification	CG7524	FBgn0003501	Src oncogene at 64B	2.54E-02	33	3	9.1%
GO:0018193 peptidyl-amino acid modification	CG8005	FBgn0035854		2.54E-02	33	3	9.1%
GO:0019221 cytokine and chemokine mediated signaling pathway	CG10535	FBgn0037926		2.54E-02	33	3	9.1%
GO:0019221 cytokine and chemokine mediated signaling pathway	CG18005	FBgn0037660		2.54E-02	33	3	9.1%
GO:0019221 cytokine and chemokine mediated signaling pathway	CG8595	FBgn0034476	Toll-7	2.54E-02	33	3	9.1%

Testis-specific age-related GO terms in Cluster 1

GO:0009966 regulation of signal transduction	CG12283	FBgn0015399	kekkon-1	3.26E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG12409	NA	NA	3.26E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG2028	FBgn0015024	Casein kinase Ialpha	3.26E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	3.26E-02	92	5	5.4%
GO:0009966 regulation of signal transduction	CG8068	FBgn0003612	Suppressor of variegation 2-10	3.26E-02	92	5	5.4%
GO:0042058 regulation of epidermal growth factor receptor signaling pathway	CG12283	FBgn0015399	kekkon-1	3.74E-02	16	2	12.5%
GO:0042058 regulation of epidermal growth factor receptor signaling pathway	CG2903	FBgn0031450	Hepatocyte growth factor regulated tyrosine kinase substrate	3.74E-02	16	2	12.5%
GO:0045893 positive regulation of transcription DNA-dependent	CG5942	FBgn0000212	brahma	3.92E-02	39	3	7.7%
GO:0045893 positive regulation of transcription DNA-dependent	CG7562	FBgn0010287	TBP-related factor	3.92E-02	39	3	7.7%
GO:0045893 positive regulation of transcription DNA-dependent	CG8887	FBgn0005386	absent, small, or homeotic discs 1	3.92E-02	39	3	7.7%
GO:0006338 chromatin remodeling	CG5942	FBgn0000212	brahma	4.17E-02	40	3	7.5%
GO:0006338 chromatin remodeling	CG10894	NA	NA	4.17E-02	40	3	7.5%
GO:0006338 chromatin remodeling	CG8887	FBgn0005386	absent, small, or homeotic discs 1	4.17E-02	40	3	7.5%
GO:0016042 lipid catabolism	CG10706	FBgn0029761	small conductance calcium-activated potassium channel	4.19E-02	17	2	11.8%
GO:0016042 lipid catabolism	CG11124	FBgn0033170	secretory Phospholipase A2	4.19E-02	17	2	11.8%
GO:0030261 chromosome condensation	CG14999	FBgn0015287	Replication-factor-C 40kD subunit	4.19E-02	17	2	11.8%
GO:0030261 chromosome condensation	CG8068	FBgn0003612	Suppressor of variegation 2-10	4.19E-02	17	2	11.8%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG10847	FBgn0004875	encore	4.66E-02	18	2	11.1%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG11254	FBgn0016034	maelstrom	4.66E-02	18	2	11.1%

Testis-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:0007417 central nervous system development	CG13281	FBgn0022213	CAS/CSE1 segregation protein	1.08E-02	103	5	4.9%
GO:0007417 central nervous system development	CG2189	FBgn0000439	Deformed	1.08E-02	103	5	4.9%
GO:0007417 central nervous system development	CG10036	FBgn0015524	orthopedia	1.08E-02	103	5	4.9%
GO:0007417 central nervous system development	CG3388	FBgn0001148	gooseberry	1.08E-02	103	5	4.9%
GO:0007417 central nervous system development	CG4926	FBgn0010407		1.08E-02	103	5	4.9%
GO:0007263 nitric oxide mediated signal transduction	CG14552	NA	NA	1.38E-02	14	2	14.3%
GO:0007263 nitric oxide mediated signal transduction	CG5719	FBgn0034316		1.38E-02	14	2	14.3%
GO:0009112 nucleobase metabolism	CG11654	FBgn0014455	Adenosylhomocysteinase at 13	1.76E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG17146	FBgn0022709	Adenylate kinase-1	1.76E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG2277	FBgn0035204		1.76E-02	77	4	5.2%
GO:0009112 nucleobase metabolism	CG6951	FBgn0036959		1.76E-02	77	4	5.2%
GO:0046483 heterocycle metabolism	CG11654	FBgn0014455	Adenosylhomocysteinase at 13	3.09E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG12286	FBgn0001296	karmoisin	3.09E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG17146	FBgn0022709	Adenylate kinase-1	3.09E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG2277	FBgn0035204		3.09E-02	135	5	3.7%
GO:0046483 heterocycle metabolism	CG6951	FBgn0036959		3.09E-02	135	5	3.7%
GO:0006144 purine base metabolism	CG11654	FBgn0014455	Adenosylhomocysteinase at 13	3.28E-02	54	3	5.6%
GO:0006144 purine base metabolism	CG17146	FBgn0022709	Adenylate kinase-1	3.28E-02	54	3	5.6%
GO:0006144 purine base metabolism	CG2277	FBgn0035204		3.28E-02	54	3	5.6%
GO:0009582 detection of abiotic stimulus	CG15779	FBgn0003747	Trehalose-sensitivity	3.44E-02	55	3	5.5%
GO:0009582 detection of abiotic stimulus	CG2174	FBgn0030252	unconventional myosin class XV	3.44E-02	55	3	5.5%
GO:0009582 detection of abiotic stimulus	CG5279	FBgn0014019	Rhodopsin 5	3.44E-02	55	3	5.5%
GO:0006790 sulfur metabolism	CG2151	FBgn0020653	Thioredoxin reductase-1	3.77E-02	57	3	5.3%
GO:0006790 sulfur metabolism	CG7280	FBgn0030966		3.77E-02	57	3	5.3%
GO:0006790 sulfur metabolism	CG8517	FBgn0034472		3.77E-02	57	3	5.3%
GO:0007419 ventral cord development	CG13281	FBgn0022213	CAS/CSE1 segregation protein	3.84E-02	24	2	8.3%
GO:0007419 ventral cord development	CG3388	FBgn0001148	gooseberry	3.84E-02	24	2	8.3%
GO:0006725 aromatic compound metabolism	CG11654	FBgn0014455	Adenosylhomocysteinase at 13	3.92E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG12286	FBgn0001296	karmoisin	3.92E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG17146	FBgn0022709	Adenylate kinase-1	3.92E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG2277	FBgn0035204		3.92E-02	144	5	3.5%
GO:0006725 aromatic compound metabolism	CG6951	FBgn0036959		3.92E-02	144	5	3.5%
GO:0007517 muscle development	CG5980	NA	NA	3.96E-02	99	4	4.0%

Testis-specific age-related GO terms in Cluster 2

GO:0007517 muscle development	CG14552	NA	NA	3.96E-02	99	4	4.0%
GO:0007517 muscle development	CG3388	FBgn0001148	gooseberry	3.96E-02	99	4	4.0%
GO:0007517 muscle development	CG7178	FBgn0004028	wings up A	3.96E-02	99	4	4.0%
GO:0007379 segment specification	CG2189	FBgn0000439	Deformed	4.45E-02	26	2	7.7%
GO:0007379 segment specification	CG10036	FBgn0015524	orthopedia	4.45E-02	26	2	7.7%
GO:0016485 protein processing	CG11110	FBgn0034535		4.45E-02	26	2	7.7%
GO:0016485 protein processing	CG7996	FBgn0003450	snake	4.45E-02	26	2	7.7%
GO:0006633 fatty acid biosynthesis	CG13844	NA	NA	4.76E-02	27	2	7.4%
GO:0006633 fatty acid biosynthesis	CG3524	FBgn0042627		4.76E-02	27	2	7.4%
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Testis-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:0000902 cellular morphogenesis	CG10334	FBgn0005672	spitz	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG10798	FBgn0000472	diminutive	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG15112	FBgn0000578	enabled	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG1856	FBgn0003870	tramtrack	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG3320	FBgn0016700	Rab-protein 1	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG3637	FBgn0025865	Cortactin	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG5179	FBgn0019949	Cyclin-dependent kinase 9	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG6147	FBgn0026317		4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG8056	FBgn0052177		4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG9375	FBgn0003205	Ras oncogene at 85D	4.09E-03	215	11	5.1%
GO:0000902 cellular morphogenesis	CG9623	FBgn0001250	inflated	4.09E-03	215	11	5.1%
GO:0001558 regulation of cell growth	CG10798	FBgn0000472	diminutive	5.30E-03	18	3	16.7%
GO:0001558 regulation of cell growth	CG6147	FBgn0026317		5.30E-03	18	3	16.7%
GO:0001558 regulation of cell growth	CG9375	FBgn0003205	Ras oncogene at 85D	5.30E-03	18	3	16.7%
GO:0051325 interphase	CG10334	FBgn0005672	spitz	8.27E-03	21	3	14.3%
GO:0051325 interphase	CG7281	FBgn0004597	Cyclin C	8.27E-03	21	3	14.3%
GO:0051325 interphase	CG9375	FBgn0003205	Ras oncogene at 85D	8.27E-03	21	3	14.3%
GO:0051329 interphase of mitotic cell cycle	CG10334	FBgn0005672	spitz	8.27E-03	21	3	14.3%
GO:0051329 interphase of mitotic cell cycle	CG7281	FBgn0004597	Cyclin C	8.27E-03	21	3	14.3%
GO:0051329 interphase of mitotic cell cycle	CG9375	FBgn0003205	Ras oncogene at 85D	8.27E-03	21	3	14.3%
GO:0048518 positive regulation of biological process	CG10334	FBgn0005672	spitz	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG10798	FBgn0000472	diminutive	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG12919	FBgn0033483	eiger	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG4275	NA	NA	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG5927	FBgn0030899	HES-related	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG7508	FBgn0010433	atonal	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG7959	FBgn0013753	Big brother	8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG8056	FBgn0052177		8.57E-03	174	9	5.2%
GO:0048518 positive regulation of biological process	CG9375	FBgn0003205	Ras oncogene at 85D	8.57E-03	174	9	5.2%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	8.68E-03	63	5	7.9%

GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG10334	FBgn0005672	spitz	8.68E-03	63	5	7.9%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG1856	FBgn0003870	tramtrack	8.68E-03	63	5	7.9%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG7508	FBgn0010433	atonal	8.68E-03	63	5	7.9%
GO:0001751 eye photoreceptor cell differentiation (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	8.68E-03	63	5	7.9%
GO:0001754 eye photoreceptor cell differentiation	CG1007	FBgn0000575	extra macrochaetae	9.27E-03	64	5	7.8%
GO:0001754 eye photoreceptor cell differentiation	CG10334	FBgn0005672	spitz	9.27E-03	64	5	7.8%
GO:0001754 eye photoreceptor cell differentiation	CG1856	FBgn0003870	tramtrack	9.27E-03	64	5	7.8%
GO:0001754 eye photoreceptor cell differentiation	CG7508	FBgn0010433	atonal	9.27E-03	64	5	7.8%
GO:0001754 eye photoreceptor cell differentiation	CG9375	FBgn0003205	Ras oncogene at 85D	9.27E-03	64	5	7.8%
GO:0007409 axonogenesis	CG14347	NA	NA	1.23E-02	95	6	6.3%
GO:0007409 axonogenesis	CG15112	FBgn0000578	enabled	1.23E-02	95	6	6.3%
GO:0007409 axonogenesis	CG18657	FBgn0015773	Netrin-A	1.23E-02	95	6	6.3%
GO:0007409 axonogenesis	CG2005	FBgn0004369	Protein tyrosine phosphatase 99A	1.23E-02	95	6	6.3%
GO:0007409 axonogenesis	CG3359	FBgn0024211	midline fasciclin	1.23E-02	95	6	6.3%
GO:0007409 axonogenesis	CG7147	FBgn0015954	kuzbanian	1.23E-02	95	6	6.3%
GO:0048522 positive regulation of cellular process	CG10334	FBgn0005672	spitz	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG10798	FBgn0000472	diminutive	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG12919	FBgn0033483	eiger	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG4275	NA	NA	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG5927	FBgn0030899	HES-related	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG7959	FBgn0013753	Big brother	1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG8056	FBgn0052177		1.31E-02	155	8	5.2%
GO:0048522 positive regulation of cellular process	CG9375	FBgn0003205	Ras oncogene at 85D	1.31E-02	155	8	5.2%
GO:0007411 axon guidance	CG14347	NA	NA	1.34E-02	70	5	7.1%
GO:0007411 axon guidance	CG15112	FBgn0000578	enabled	1.34E-02	70	5	7.1%
GO:0007411 axon guidance	CG18657	FBgn0015773	Netrin-A	1.34E-02	70	5	7.1%
GO:0007411 axon guidance	CG2005	FBgn0004369	Protein tyrosine phosphatase 99A	1.34E-02	70	5	7.1%
GO:0007411 axon guidance	CG7147	FBgn0015954	kuzbanian	1.34E-02	70	5	7.1%
GO:0016477 cell migration	CG14347	NA	NA	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG15112	FBgn0000578	enabled	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG18657	FBgn0015773	Netrin-A	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG2005	FBgn0004369	Protein tyrosine phosphatase 99A	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG3637	FBgn0025865	Cortactin	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG7147	FBgn0015954	kuzbanian	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG9375	FBgn0003205	Ras oncogene at 85D	1.41E-02	157	8	5.1%
GO:0016477 cell migration	CG9623	FBgn0001250	inflated	1.41E-02	157	8	5.1%
GO:0016049 cell growth	CG10798	FBgn0000472	diminutive	1.66E-02	27	3	11.1%
GO:0016049 cell growth	CG6147	FBgn0026317		1.66E-02	27	3	11.1%

Testis-specific age-related GO terms in Cluster 3

GO:0016049 cell growth	CG9375	FBgn0003205	Ras oncogene at 85D	1.66E-02	27	3	11.1%
GO:0007467 photoreceptor cell differentiation (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	1.85E-02	76	5	6.6%
GO:0007467 photoreceptor cell differentiation (sensu Endopterygota)	CG10334	FBgn0005672	spitz	1.85E-02	76	5	6.6%
GO:0007467 photoreceptor cell differentiation (sensu Endopterygota)	CG1856	FBgn0003870	tramtrack	1.85E-02	76	5	6.6%
GO:0007467 photoreceptor cell differentiation (sensu Endopterygota)	CG7508	FBgn0010433	atonal	1.85E-02	76	5	6.6%
GO:0007467 photoreceptor cell differentiation (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	1.85E-02	76	5	6.6%
GO:0007594 puparial adhesion	CG18087	FBgn0003377	Salivary gland secretion 7	1.99E-02	11	2	18.2%
GO:0007594 puparial adhesion	CG7596	FBgn0003375	Salivary gland secretion 5	1.99E-02	11	2	18.2%
GO:0030307 positive regulation of cell growth	CG10798	FBgn0000472	diminutive	1.99E-02	11	2	18.2%
GO:0030307 positive regulation of cell growth	CG9375	FBgn0003205	Ras oncogene at 85D	1.99E-02	11	2	18.2%
GO:0007591 molting cycle (sensu Insecta)	CG18087	FBgn0003377	Salivary gland secretion 7	2.02E-02	29	3	10.3%
GO:0007591 molting cycle (sensu Insecta)	CG7450	FBgn0004396	Cyclic-AMP response element binding protein A	2.02E-02	29	3	10.3%
GO:0007591 molting cycle (sensu Insecta)	CG7596	FBgn0003375	Salivary gland secretion 5	2.02E-02	29	3	10.3%
GO:0007455 eye-antennal disc metamorphosis	CG1007	FBgn0000575	extra macrochaetae	2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG10334	FBgn0005672	spitz	2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG1856	FBgn0003870	tramtrack	2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG4336	FBgn0003302	roughex	2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG7508	FBgn0010433	atonal	2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG8056	FBgn0052177		2.08E-02	137	7	5.1%
GO:0007455 eye-antennal disc metamorphosis	CG9375	FBgn0003205	Ras oncogene at 85D	2.08E-02	137	7	5.1%
GO:0035214 eye-antennal disc development	CG1007	FBgn0000575	extra macrochaetae	2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG10334	FBgn0005672	spitz	2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG1856	FBgn0003870	tramtrack	2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG4336	FBgn0003302	roughex	2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG7508	FBgn0010433	atonal	2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG8056	FBgn0052177		2.16E-02	138	7	5.1%
GO:0035214 eye-antennal disc development	CG9375	FBgn0003205	Ras oncogene at 85D	2.16E-02	138	7	5.1%
GO:0008361 regulation of cell size	CG10798	FBgn0000472	diminutive	2.21E-02	30	3	10.0%
GO:0008361 regulation of cell size	CG6147	FBgn0026317		2.21E-02	30	3	10.0%
GO:0008361 regulation of cell size	CG9375	FBgn0003205	Ras oncogene at 85D	2.21E-02	30	3	10.0%
GO:0000270 peptidoglycan metabolism	CG14704	FBgn0037906	Peptidoglycan recognition protein LB	2.35E-02	12	2	16.7%
GO:0000270 peptidoglycan metabolism	CG9681	FBgn0043578		2.35E-02	12	2	16.7%
GO:0007426 tracheal outgrowth (sensu Insecta)	CG14347	NA	NA	2.35E-02	12	2	16.7%

Testis-specific age-related GO terms in Cluster 3

GO:0007426 tracheal outgrowth (sensu Insecta)	CG9623	FBgn0001250	inflated	2.35E-02	12	2	16.7%
GO:0009253 peptidoglycan catabolism	CG14704	FBgn0037906	Peptidoglycan recognition protein LB	2.35E-02	12	2	16.7%
GO:0009253 peptidoglycan catabolism	CG9681	FBgn0043578		2.35E-02	12	2	16.7%
GO:0045793 positive regulation of cell size	CG10798	FBgn0000472	diminutive	2.35E-02	12	2	16.7%
GO:0045793 positive regulation of cell size	CG9375	FBgn0003205	Ras oncogene at 85D	2.35E-02	12	2	16.7%
GO:0007452 imaginal disc metamorphosis	CG1007	FBgn0000575	extra macrochaetae	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG10334	FBgn0005672	spitz	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG1856	FBgn0003870	tramtrack	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG4244	FBgn0003557	Suppressor of deltex	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG4336	FBgn0003302	roughex	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG7508	FBgn0010433	atonal	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG8056	FBgn0052177		2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG9375	FBgn0003205	Ras oncogene at 85D	2.36E-02	206	9	4.4%
GO:0007452 imaginal disc metamorphosis	CG9623	FBgn0001250	inflated	2.36E-02	206	9	4.4%
GO:0018988 molting cycle (sensu Protostomia and Nematoda)	CG18087	FBgn0003377	Salivary gland secretion 7	2.62E-02	32	3	9.4%
GO:0018988 molting cycle (sensu Protostomia and Nematoda)	CG7450	FBgn0004396	Cyclic-AMP response element binding protein A	2.62E-02	32	3	9.4%
GO:0018988 molting cycle (sensu Protostomia and Nematoda)	CG7596	FBgn0003375	Salivary gland secretion 5	2.62E-02	32	3	9.4%
GO:0042303 molting cycle	CG18087	FBgn0003377	Salivary gland secretion 7	2.62E-02	32	3	9.4%
GO:0042303 molting cycle	CG7450	FBgn0004396	Cyclic-AMP response element binding protein A	2.62E-02	32	3	9.4%
GO:0042303 molting cycle	CG7596	FBgn0003375	Salivary gland secretion 5	2.62E-02	32	3	9.4%
GO:0045465 R8 cell differentiation	CG1007	FBgn0000575	extra macrochaetae	2.74E-02	13	2	15.4%
GO:0045465 R8 cell differentiation	CG7508	FBgn0010433	atonal	2.74E-02	13	2	15.4%
GO:0046530 photoreceptor cell differentiation	CG1007	FBgn0000575	extra macrochaetae	2.85E-02	85	5	5.9%
GO:0046530 photoreceptor cell differentiation	CG10334	FBgn0005672	spitz	2.85E-02	85	5	5.9%
GO:0046530 photoreceptor cell differentiation	CG1856	FBgn0003870	tramtrack	2.85E-02	85	5	5.9%
GO:0046530 photoreceptor cell differentiation	CG7508	FBgn0010433	atonal	2.85E-02	85	5	5.9%
GO:0046530 photoreceptor cell differentiation	CG9375	FBgn0003205	Ras oncogene at 85D	2.85E-02	85	5	5.9%
GO:0031175 neurite morphogenesis	CG14347	NA	NA	2.88E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG15112	FBgn0000578	enabled	2.88E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG18657	FBgn0015773	Netrin-A	2.88E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG2005	FBgn0004369	Protein tyrosine phosphatase 99A	2.88E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG3359	FBgn0024211	midline fasciclin	2.88E-02	115	6	5.2%
GO:0031175 neurite morphogenesis	CG7147	FBgn0015954	kuzbanian	2.88E-02	115	6	5.2%
GO:0008360 regulation of cell shape	CG15112	FBgn0000578	enabled	2.98E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG3320	FBgn0016700	Rab-protein 1	2.98E-02	86	5	5.8%

Testis-specific age-related GO terms in Cluster 3

GO:0008360 regulation of cell shape	CG3637	FBgn0025865	Cortactin	2.98E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG5179	FBgn0019949	Cyclin-dependent kinase 9	2.98E-02	86	5	5.8%
GO:0008360 regulation of cell shape	CG9623	FBgn0001250	inflated	2.98E-02	86	5	5.8%
GO:0001752 eye photoreceptor fate commitment (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	3.08E-02	34	3	8.8%
GO:0001752 eye photoreceptor fate commitment (sensu Endopterygota)	CG7508	FBgn0010433	atonal	3.08E-02	34	3	8.8%
GO:0001752 eye photoreceptor fate commitment (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	3.08E-02	34	3	8.8%
GO:0042706 eye photoreceptor cell fate commitment	CG1007	FBgn0000575	extra macrochaetae	3.08E-02	34	3	8.8%
GO:0042706 eye photoreceptor cell fate commitment	CG7508	FBgn0010433	atonal	3.08E-02	34	3	8.8%
GO:0042706 eye photoreceptor cell fate commitment	CG9375	FBgn0003205	Ras oncogene at 85D	3.08E-02	34	3	8.8%
GO:0000082 G1 S transition of mitotic cell cycle	CG7281	FBgn0004597	Cyclin C	3.16E-02	14	2	14.3%
GO:0000082 G1 S transition of mitotic cell cycle	CG9375	FBgn0003205	Ras oncogene at 85D	3.16E-02	14	2	14.3%
GO:0006888 ER to Golgi transport	CG10882	FBgn0031408		3.16E-02	14	2	14.3%
GO:0006888 ER to Golgi transport	CG3320	FBgn0016700	Rab-protein 1	3.16E-02	14	2	14.3%
GO:0007539 primary sex determination soma	CG1007	FBgn0000575	extra macrochaetae	3.16E-02	14	2	14.3%
GO:0007539 primary sex determination soma	CG5927	FBgn0030899	HES-related	3.16E-02	14	2	14.3%
GO:0008587 wing margin morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	3.16E-02	14	2	14.3%
GO:0008587 wing margin morphogenesis	CG9623	FBgn0001250	inflated	3.16E-02	14	2	14.3%
GO:0016542 male courtship behavior (sensu Insecta)	CG4211	FBgn0004227	no on or off transient A	3.16E-02	14	2	14.3%
GO:0016542 male courtship behavior (sensu Insecta)	CG7508	FBgn0010433	atonal	3.16E-02	14	2	14.3%
GO:0046666 retinal programmed cell death	CG10334	FBgn0005672	spitz	3.16E-02	14	2	14.3%
GO:0046666 retinal programmed cell death	CG9375	FBgn0003205	Ras oncogene at 85D	3.16E-02	14	2	14.3%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	3.21E-02	118	6	5.1%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG10334	FBgn0005672	spitz	3.21E-02	118	6	5.1%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG1856	FBgn0003870	tramtrack	3.21E-02	118	6	5.1%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG7508	FBgn0010433	atonal	3.21E-02	118	6	5.1%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG8056	FBgn0052177		3.21E-02	118	6	5.1%
GO:0001745 compound eye morphogenesis (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	3.21E-02	118	6	5.1%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG10334	FBgn0005672	spitz	3.33E-02	119	6	5.0%

GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG12463	NA	NA	3.33E-02	119	6	5.0%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG6147	FBgn0026317		3.33E-02	119	6	5.0%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG7508	FBgn0010433	atonal	3.33E-02	119	6	5.0%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG8056	FBgn0052177		3.33E-02	119	6	5.0%
GO:0007169 transmembrane receptor protein tyrosine kinase signaling pathway	CG9375	FBgn0003205	Ras oncogene at 85D	3.33E-02	119	6	5.0%
GO:0019722 calcium-mediated signaling	CG11638	FBgn0040351		3.63E-02	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG17769	FBgn0011273	Androcam	3.63E-02	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG14281	NA	NA	3.63E-02	62	4	6.5%
GO:0019722 calcium-mediated signaling	CG6805	FBgn0034179		3.63E-02	62	4	6.5%
GO:0007173 epidermal growth factor receptor signaling pathway	CG10334	FBgn0005672	spitz	3.82E-02	37	3	8.1%
GO:0007173 epidermal growth factor receptor signaling pathway	CG7508	FBgn0010433	atonal	3.82E-02	37	3	8.1%
GO:0007173 epidermal growth factor receptor signaling pathway	CG8056	FBgn0052177		3.82E-02	37	3	8.1%
GO:0007538 primary sex determination	CG1007	FBgn0000575	extra macrochaetae	4.06E-02	16	2	12.5%
GO:0007538 primary sex determination	CG5927	FBgn0030899	HES-related	4.06E-02	16	2	12.5%
GO:0009967 positive regulation of signal transduction	CG10334	FBgn0005672	spitz	4.06E-02	16	2	12.5%
GO:0009967 positive regulation of signal transduction	CG8056	FBgn0052177		4.06E-02	16	2	12.5%
GO:0007219 Notch signaling pathway	CG1539	FBgn0082582	tropomodulin	4.09E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG4244	FBgn0003557	Suppressor of deltex	4.09E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG7147	FBgn0015954	kuzbanian	4.09E-02	38	3	7.9%
GO:0050909 perception of taste	CG14986	NA	NA	4.09E-02	38	3	7.9%
GO:0050909 perception of taste	CG17213	FBgn0032416	Gustatory receptor 33a	4.09E-02	38	3	7.9%
GO:0050909 perception of taste	CG7303	FBgn0041231	Gustatory receptor 68a	4.09E-02	38	3	7.9%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	4.33E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG10334	FBgn0005672	spitz	4.33E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG1856	FBgn0003870	tramtrack	4.33E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG4336	FBgn0003302	roughex	4.33E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG7508	FBgn0010433	atonal	4.33E-02	160	7	4.4%
GO:0007456 eye morphogenesis (sensu Endopterygota)	CG8056	FBgn0052177		4.33E-02	160	7	4.4%

GO:0007456 eye morphogenesis (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	4.33E-02	160	7	4.4%
GO:0006396 RNA processing	CG10922	FBgn0011638	La autoantigen-like	4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG11266	FBgn0031883		4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG1405	NA	NA	4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG14100	FBgn0036889		4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG4038	FBgn0011824		4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG4211	FBgn0004227	no on or off transient A	4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG6413	FBgn0039183		4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG6626	NA	NA	4.33E-02	230	9	3.9%
GO:0006396 RNA processing	CG8939	FBgn0030720		4.33E-02	230	9	3.9%
GO:0007431 salivary gland development	CG10334	FBgn0005672	spitz	4.37E-02	39	3	7.7%
GO:0007431 salivary gland development	CG7450	FBgn0004396	Cyclic-AMP response element binding protein A	4.37E-02	39	3	7.7%
GO:0007431 salivary gland development	CG9623	FBgn0001250	inflated	4.37E-02	39	3	7.7%
GO:0035272 exocrine system development	CG10334	FBgn0005672	spitz	4.37E-02	39	3	7.7%
GO:0035272 exocrine system development	CG7450	FBgn0004396	Cyclic-AMP response element binding protein A	4.37E-02	39	3	7.7%
GO:0035272 exocrine system development	CG9623	FBgn0001250	inflated	4.37E-02	39	3	7.7%
GO:0045893 positive regulation of transcription DNA-dependent	CG4275	NA	NA	4.37E-02	39	3	7.7%
GO:0045893 positive regulation of transcription DNA-dependent	CG5927	FBgn0030899	HES-related	4.37E-02	39	3	7.7%
GO:0045893 positive regulation of transcription DNA-dependent	CG7959	FBgn0013753	Big brother	4.37E-02	39	3	7.7%
GO:0016052 carbohydrate catabolism	CG14704	FBgn0037906	Peptidoglycan recognition protein LB	4.42E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG3400	FBgn0027621	6-phosphofructo-2-kinase	4.42E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG8036	FBgn0037607		4.42E-02	66	4	6.1%
GO:0016052 carbohydrate catabolism	CG9681	FBgn0043578		4.42E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG14704	FBgn0037906	Peptidoglycan recognition protein LB	4.42E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG3400	FBgn0027621	6-phosphofructo-2-kinase	4.42E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG8036	FBgn0037607		4.42E-02	66	4	6.1%
GO:0044275 cellular carbohydrate catabolism	CG9681	FBgn0043578		4.42E-02	66	4	6.1%
GO:0007167 enzyme linked receptor protein signaling pathway	CG10334	FBgn0005672	spitz	4.45E-02	161	7	4.3%
GO:0007167 enzyme linked receptor protein signaling pathway	CG12463	NA	NA	4.45E-02	161	7	4.3%
GO:0007167 enzyme linked receptor protein signaling pathway	CG6147	FBgn0026317		4.45E-02	161	7	4.3%

Testis-specific age-related GO terms in Cluster 3

GO:0007167 enzyme linked receptor protein signaling pathway	CG6890	FBgn0029114	Tollo	4.45E-02	161	7	4.3%
GO:0007167 enzyme linked receptor protein signaling pathway	CG7508	FBgn0010433	atonal	4.45E-02	161	7	4.3%
GO:0007167 enzyme linked receptor protein signaling pathway	CG8056	FBgn0052177		4.45E-02	161	7	4.3%
GO:0007167 enzyme linked receptor protein signaling pathway	CG9375	FBgn0003205	Ras oncogene at 85D	4.45E-02	161	7	4.3%
GO:0045944 positive regulation of transcription from RNA polymerase II promoter	CG5927	FBgn0030899	HES-related	4.54E-02	17	2	11.8%
GO:0045944 positive regulation of transcription from RNA polymerase II promoter	CG7959	FBgn0013753	Big brother	4.54E-02	17	2	11.8%
GO:0000122 negative regulation of transcription from RNA polymerase II promoter	CG1007	FBgn0000575	extra macrochaetae	4.65E-02	40	3	7.5%
GO:0000122 negative regulation of transcription from RNA polymerase II promoter	CG1856	FBgn0003870	tramtrack	4.65E-02	40	3	7.5%
GO:0000122 negative regulation of transcription from RNA polymerase II promoter	CG5927	FBgn0030899	HES-related	4.65E-02	40	3	7.5%
GO:0006928 cell motility	CG14347	NA	NA	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG15112	FBgn0000578	enabled	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG17769	FBgn0011273	Androcam	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG18657	FBgn0015773	Netrin-A	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG2005	FBgn0004369	Protein tyrosine phosphatase 99A	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG3637	FBgn0025865	Cortactin	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG7147	FBgn0015954	kuzbanian	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG9375	FBgn0003205	Ras oncogene at 85D	4.74E-02	234	9	3.8%
GO:0006928 cell motility	CG9623	FBgn0001250	inflated	4.74E-02	234	9	3.8%
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG1007	FBgn0000575	extra macrochaetae	4.95E-02	41	3	7.3%
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG7508	FBgn0010433	atonal	4.95E-02	41	3	7.3%
GO:0007459 photoreceptor fate commitment (sensu Endopterygota)	CG9375	FBgn0003205	Ras oncogene at 85D	4.95E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG13638	NA	NA	4.95E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG3320	FBgn0016700	Rab-protein 1	4.95E-02	41	3	7.3%
GO:0017157 regulation of exocytosis	CG9375	FBgn0003205	Ras oncogene at 85D	4.95E-02	41	3	7.3%
GO:0046552 photoreceptor cell fate commitment	CG1007	FBgn0000575	extra macrochaetae	4.95E-02	41	3	7.3%
GO:0046552 photoreceptor cell fate commitment	CG7508	FBgn0010433	atonal	4.95E-02	41	3	7.3%
GO:0046552 photoreceptor cell fate commitment	CG9375	FBgn0003205	Ras oncogene at 85D	4.95E-02	41	3	7.3%

Testis-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:0016079 synaptic vesicle exocytosis	CG10322	NA	NA	5.44E-05	45	3	6.7%
GO:0016079 synaptic vesicle exocytosis	CG3985	FBgn0004575	Synapsin	5.44E-05	45	3	6.7%
GO:0016079 synaptic vesicle exocytosis	CG5448	NA	NA	5.44E-05	45	3	6.7%
GO:0048489 synaptic vesicle transport	CG10322	NA	NA	2.93E-04	79	3	3.8%
GO:0048489 synaptic vesicle transport	CG3985	FBgn0004575	Synapsin	2.93E-04	79	3	3.8%
GO:0048489 synaptic vesicle transport	CG5448	NA	NA	2.93E-04	79	3	3.8%
GO:0007269 neurotransmitter secretion	CG10322	NA	NA	6.59E-04	104	3	2.9%
GO:0007269 neurotransmitter secretion	CG3985	FBgn0004575	Synapsin	6.59E-04	104	3	2.9%
GO:0007269 neurotransmitter secretion	CG5448	NA	NA	6.59E-04	104	3	2.9%
GO:0045055 regulated secretory pathway	CG10322	NA	NA	6.59E-04	104	3	2.9%
GO:0045055 regulated secretory pathway	CG3985	FBgn0004575	Synapsin	6.59E-04	104	3	2.9%
GO:0045055 regulated secretory pathway	CG5448	NA	NA	6.59E-04	104	3	2.9%
GO:0001505 regulation of neurotransmitter levels	CG10322	NA	NA	9.06E-04	116	3	2.6%
GO:0001505 regulation of neurotransmitter levels	CG3985	FBgn0004575	Synapsin	9.06E-04	116	3	2.6%
GO:0001505 regulation of neurotransmitter levels	CG5448	NA	NA	9.06E-04	116	3	2.6%
GO:0006887 exocytosis	CG10322	NA	NA	1.05E-03	122	3	2.5%
GO:0006887 exocytosis	CG3985	FBgn0004575	Synapsin	1.05E-03	122	3	2.5%
GO:0006887 exocytosis	CG5448	NA	NA	1.05E-03	122	3	2.5%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG10449	FBgn0002022	Catecholamines up	1.09E-03	29	2	6.9%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG3937	FBgn0014141	cheerio	1.09E-03	29	2	6.9%
GO:0007268 synaptic transmission	CG10322	NA	NA	4.83E-03	208	3	1.4%
GO:0007268 synaptic transmission	CG3985	FBgn0004575	Synapsin	4.83E-03	208	3	1.4%
GO:0007268 synaptic transmission	CG5448	NA	NA	4.83E-03	208	3	1.4%
GO:0045045 secretory pathway	CG10322	NA	NA	4.96E-03	210	3	1.4%
GO:0045045 secretory pathway	CG3985	FBgn0004575	Synapsin	4.96E-03	210	3	1.4%
GO:0045045 secretory pathway	CG5448	NA	NA	4.96E-03	210	3	1.4%
GO:0046903 secretion	CG10322	NA	NA	5.86E-03	223	3	1.3%
GO:0046903 secretion	CG3985	FBgn0004575	Synapsin	5.86E-03	223	3	1.3%
GO:0046903 secretion	CG5448	NA	NA	5.86E-03	223	3	1.3%
GO:0006936 muscle contraction	CG3937	FBgn0014141	cheerio	9.72E-03	88	2	2.3%
GO:0006936 muscle contraction	CG5448	NA	NA	9.72E-03	88	2	2.3%
GO:0007594 puparial adhesion	CG10781	FBgn0002933	new glue 1	1.89E-02	11	1	9.1%
GO:0019935 cyclic-nucleotide-mediated signaling	CG14268	NA	NA	1.89E-02	11	1	9.1%
GO:0006584 catecholamine metabolism	CG10449	FBgn0002022	Catecholamines up	2.23E-02	13	1	7.7%
GO:0018958 phenol metabolism	CG10449	FBgn0002022	Catecholamines up	2.40E-02	14	1	7.1%
GO:0007317 regulation of pole plasm oskar mRNA localization	CG5448	NA	NA	3.08E-02	18	1	5.6%
GO:0008355 olfactory learning	CG14268	NA	NA	3.08E-02	18	1	5.6%
GO:0010033 response to organic substance	CG14268	NA	NA	3.08E-02	18	1	5.6%
GO:0045475 locomotor rhythm	CG14268	NA	NA	3.25E-02	19	1	5.3%

GO:0007612 learning	CG14268	NA	NA	3.42E-02	20	1	5.0%
GO:0016333 morphogenesis of follicular epithelium	CG3937	FBgn0014141	cheerio	3.42E-02	20	1	5.0%
GO:0016081 synaptic vesicle docking during exocytosis	CG5448	NA	NA	3.59E-02	21	1	4.8%
GO:0007613 memory	CG14268	NA	NA	3.75E-02	22	1	4.5%
GO:0042048 olfactory behavior	CG14268	NA	NA	3.75E-02	22	1	4.5%
GO:0007635 chemosensory behavior	CG14268	NA	NA	3.92E-02	23	1	4.3%
GO:0048512 circadian behavior	CG14268	NA	NA	3.92E-02	23	1	4.3%
GO:0007349 cellularization	CG5448	NA	NA	4.26E-02	25	1	4.0%
GO:0042335 cuticle biosynthesis	CG5448	NA	NA	4.26E-02	25	1	4.0%
GO:0044274 organismal biosynthesis	CG5448	NA	NA	4.26E-02	25	1	4.0%
GO:0007622 rhythmic behavior	CG14268	NA	NA	4.42E-02	26	1	3.8%
GO:0006904 vesicle docking during exocytosis	CG5448	NA	NA	4.92E-02	29	1	3.4%
GO:0007591 molting cycle (sensu Insecta)	CG10781	FBgn0002933	new glue 1	4.92E-02	29	1	3.4%
GO:0048278 vesicle docking	CG5448	NA	NA	4.92E-02	29	1	3.4%

Testis-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:0016071 mRNA metabolism	CG12749	FBgn0004237	Heterogeneous nuclear ribonucleoprotein at 87F	1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG13425	FBgn0015907	bancal	1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG17170	FBgn0003559	suppressor of forked	1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG2094	NA	NA	1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG2097	FBgn0037371		1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG2163	FBgn0005648		1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG5454	FBgn0038667		1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG5651	FBgn0035946		1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG6841	FBgn0036828		1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG7269	FBgn0014189	Helicase at 25E	1.55E-05	189	11	5.8%
GO:0016071 mRNA metabolism	CG9218	FBgn0003435	smooth	1.55E-05	189	11	5.8%
GO:0006397 mRNA processing	CG12749	FBgn0004237	Heterogeneous nuclear ribonucleoprotein at 87F	5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG13425	FBgn0015907	bancal	5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG17170	FBgn0003559	suppressor of forked	5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG2094	NA	NA	5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG2097	FBgn0037371		5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG2163	FBgn0005648		5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG5454	FBgn0038667		5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG6841	FBgn0036828		5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG7269	FBgn0014189	Helicase at 25E	5.01E-05	177	10	5.6%
GO:0006397 mRNA processing	CG9218	FBgn0003435	smooth	5.01E-05	177	10	5.6%
GO:0006396 RNA processing	CG12749	FBgn0004237	Heterogeneous nuclear ribonucleoprotein at 87F	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG13425	FBgn0015907	bancal	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG17170	FBgn0003559	suppressor of forked	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG2094	NA	NA	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG2097	FBgn0037371		9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG2109	FBgn0037330	mitochondrial ribosomal protein L44	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG2163	FBgn0005648		9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG5454	FBgn0038667		9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG6841	FBgn0036828		9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG7269	FBgn0014189	Helicase at 25E	9.45E-05	230	11	4.8%
GO:0006396 RNA processing	CG9218	FBgn0003435	smooth	9.45E-05	230	11	4.8%
GO:0035107 appendage morphogenesis	CG13425	FBgn0015907	bancal	2.64E-04	105	7	6.7%
GO:0035107 appendage morphogenesis	CG6774	NA	NA	2.64E-04	105	7	6.7%
GO:0035107 appendage morphogenesis	CG2094	NA	NA	2.64E-04	105	7	6.7%
GO:0035107 appendage morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	2.64E-04	105	7	6.7%
GO:0035107 appendage morphogenesis	CG6667	FBgn0000462	dorsal	2.64E-04	105	7	6.7%
GO:0035107 appendage morphogenesis	CG8544	FBgn0003345	scalloped	2.64E-04	105	7	6.7%

GO:0035107 appendage morphogenesis	CG8637	FBgn0003744	tricornered	2.64E-04	105	7	6.7%
GO:0007476 wing morphogenesis	CG6774	NA	NA	4.21E-04	81	6	7.4%
GO:0007476 wing morphogenesis	CG2094	NA	NA	4.21E-04	81	6	7.4%
GO:0007476 wing morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	4.21E-04	81	6	7.4%
GO:0007476 wing morphogenesis	CG6667	FBgn0000462	dorsal	4.21E-04	81	6	7.4%
GO:0007476 wing morphogenesis	CG8544	FBgn0003345	scalloped	4.21E-04	81	6	7.4%
GO:0007476 wing morphogenesis	CG8637	FBgn0003744	tricornered	4.21E-04	81	6	7.4%
GO:0007472 wing disc metamorphosis	CG6774	NA	NA	4.80E-04	83	6	7.2%
GO:0007472 wing disc metamorphosis	CG2094	NA	NA	4.80E-04	83	6	7.2%
GO:0007472 wing disc metamorphosis	CG4244	FBgn0003557	Suppressor of deltex	4.80E-04	83	6	7.2%
GO:0007472 wing disc metamorphosis	CG6667	FBgn0000462	dorsal	4.80E-04	83	6	7.2%
GO:0007472 wing disc metamorphosis	CG8544	FBgn0003345	scalloped	4.80E-04	83	6	7.2%
GO:0007472 wing disc metamorphosis	CG8637	FBgn0003744	tricornered	4.80E-04	83	6	7.2%
GO:0035220 wing disc development	CG6774	NA	NA	6.18E-04	87	6	6.9%
GO:0035220 wing disc development	CG2094	NA	NA	6.18E-04	87	6	6.9%
GO:0035220 wing disc development	CG4244	FBgn0003557	Suppressor of deltex	6.18E-04	87	6	6.9%
GO:0035220 wing disc development	CG6667	FBgn0000462	dorsal	6.18E-04	87	6	6.9%
GO:0035220 wing disc development	CG8544	FBgn0003345	scalloped	6.18E-04	87	6	6.9%
GO:0035220 wing disc development	CG8637	FBgn0003744	tricornered	6.18E-04	87	6	6.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG6774	NA	NA	1.43E-03	102	6	5.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG2094	NA	NA	1.43E-03	102	6	5.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG4244	FBgn0003557	Suppressor of deltex	1.43E-03	102	6	5.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG6667	FBgn0000462	dorsal	1.43E-03	102	6	5.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG8544	FBgn0003345	scalloped	1.43E-03	102	6	5.9%
GO:0035114 appendage morphogenesis (sensu Endopterygota)	CG8637	FBgn0003744	tricornered	1.43E-03	102	6	5.9%
GO:0008203 cholesterol metabolism	CG12390	FBgn0015582	defective in the avoidance of repellents	2.57E-03	23	3	13.0%
GO:0008203 cholesterol metabolism	CG1998	FBgn0030485		2.57E-03	23	3	13.0%
GO:0008203 cholesterol metabolism	CG5912	FBgn0000119	arrow	2.57E-03	23	3	13.0%
GO:0006457 protein folding	CG1847	FBgn0030345		3.12E-03	119	6	5.0%
GO:0006457 protein folding	CG5374	FBgn0003676	Tcp1-like	3.12E-03	119	6	5.0%
GO:0006457 protein folding	CG5525	FBgn0032444		3.12E-03	119	6	5.0%
GO:0006457 protein folding	CG8258	FBgn0033342		3.12E-03	119	6	5.0%
GO:0006457 protein folding	CG8351	FBgn0037632		3.12E-03	119	6	5.0%
GO:0006457 protein folding	CG8439	FBgn0010621	T-complex Chaperonin 5	3.12E-03	119	6	5.0%
GO:0007452 imaginal disc metamorphosis	CG12230	FBgn0000257	carnation	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG6774	NA	NA	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG2094	NA	NA	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG4244	FBgn0003557	Suppressor of deltex	3.38E-03	206	8	3.9%

Testis-specific age-related GO terms in Cluster 5

GO:0007452 imaginal disc metamorphosis	CG5575	FBgn0011236	ken and barbie	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG6667	FBgn0000462	dorsal	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG8544	FBgn0003345	scalloped	3.38E-03	206	8	3.9%
GO:0007452 imaginal disc metamorphosis	CG8637	FBgn0003744	tricornered	3.38E-03	206	8	3.9%
GO:0016125 sterol metabolism	CG12390	FBgn0015582	defective in the avoidance of repellents	4.55E-03	28	3	10.7%
GO:0016125 sterol metabolism	CG1998	FBgn0030485		4.55E-03	28	3	10.7%
GO:0016125 sterol metabolism	CG5912	FBgn0000119	arrow	4.55E-03	28	3	10.7%
GO:0035111 leg joint morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	7.47E-03	11	2	18.2%
GO:0035111 leg joint morphogenesis	CG6667	FBgn0000462	dorsal	7.47E-03	11	2	18.2%
GO:0035285 appendage segmentation	CG4244	FBgn0003557	Suppressor of deltex	7.47E-03	11	2	18.2%
GO:0035285 appendage segmentation	CG6667	FBgn0000462	dorsal	7.47E-03	11	2	18.2%
GO:0035286 leg segmentation	CG4244	FBgn0003557	Suppressor of deltex	7.47E-03	11	2	18.2%
GO:0035286 leg segmentation	CG6667	FBgn0000462	dorsal	7.47E-03	11	2	18.2%
GO:0007219 Notch signaling pathway	CG2094	NA	NA	1.07E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG4244	FBgn0003557	Suppressor of deltex	1.07E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG6667	FBgn0000462	dorsal	1.07E-02	38	3	7.9%
GO:0006379 mRNA cleavage	CG17170	FBgn0003559	suppressor of forked	1.21E-02	14	2	14.3%
GO:0006379 mRNA cleavage	CG2097	FBgn0037371		1.21E-02	14	2	14.3%
GO:0006888 ER to Golgi transport	CG6699	FBgn0025724	beta'-coatomer protein	1.21E-02	14	2	14.3%
GO:0006888 ER to Golgi transport	CG8487	FBgn0033714	gartenzwerg	1.21E-02	14	2	14.3%
GO:0008587 wing margin morphogenesis	CG2094	NA	NA	1.21E-02	14	2	14.3%
GO:0008587 wing margin morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	1.21E-02	14	2	14.3%
GO:0016055 Wnt receptor signaling pathway	CG6774	NA	NA	2.02E-02	48	3	6.3%
GO:0016055 Wnt receptor signaling pathway	CG5912	FBgn0000119	arrow	2.02E-02	48	3	6.3%
GO:0016055 Wnt receptor signaling pathway	CG6205	FBgn0004957	porcupine	2.02E-02	48	3	6.3%
GO:0006378 mRNA polyadenylation	CG17170	FBgn0003559	suppressor of forked	2.18E-02	19	2	10.5%
GO:0006378 mRNA polyadenylation	CG2163	FBgn0005648		2.18E-02	19	2	10.5%
GO:0051128 regulation of cell organization and biogenesis	CG4012	FBgn0023081	genghis khan	2.40E-02	20	2	10.0%
GO:0051128 regulation of cell organization and biogenesis	CG15802	NA	NA	2.40E-02	20	2	10.0%
GO:0007480 leg morphogenesis (sensu Endopterygota)	CG4244	FBgn0003557	Suppressor of deltex	2.64E-02	21	2	9.5%
GO:0007480 leg morphogenesis (sensu Endopterygota)	CG6667	FBgn0000462	dorsal	2.64E-02	21	2	9.5%
GO:0006418 tRNA aminoacylation for protein translation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	3.02E-02	56	3	5.4%
GO:0006418 tRNA aminoacylation for protein translation	CG13391	FBgn0027094	Alanyl-tRNA synthetase	3.02E-02	56	3	5.4%
GO:0006418 tRNA aminoacylation for protein translation	CG17938	NA	NA	3.02E-02	56	3	5.4%
GO:0043039 tRNA aminoacylation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	3.02E-02	56	3	5.4%
GO:0043039 tRNA aminoacylation	CG13391	FBgn0027094	Alanyl-tRNA synthetase	3.02E-02	56	3	5.4%

Testis-specific age-related GO terms in Cluster 5

GO:0043039 tRNA aminoacylation	CG17938	NA	NA	3.02E-02	56	3	5.4%
GO:0007478 leg disc metamorphosis	CG4244	FBgn0003557	Suppressor of deltex	3.13E-02	23	2	8.7%
GO:0007478 leg disc metamorphosis	CG6667	FBgn0000462	dorsal	3.13E-02	23	2	8.7%
GO:0035109 limb morphogenesis (sensu Endopterygota)	CG4244	FBgn0003557	Suppressor of deltex	3.13E-02	23	2	8.7%
GO:0035109 limb morphogenesis (sensu Endopterygota)	CG6667	FBgn0000462	dorsal	3.13E-02	23	2	8.7%
GO:0043038 amino acid activation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	3.16E-02	57	3	5.3%
GO:0043038 amino acid activation	CG13391	FBgn0027094	Alanyl-tRNA synthetase	3.16E-02	57	3	5.3%
GO:0043038 amino acid activation	CG17938	NA	NA	3.16E-02	57	3	5.3%
GO:0006066 alcohol metabolism	CG12390	FBgn0015582	defective in the avoidance of repellents	3.61E-02	151	5	3.3%
GO:0006066 alcohol metabolism	CG14211	FBgn0031044		3.61E-02	151	5	3.3%
GO:0006066 alcohol metabolism	CG1998	FBgn0030485		3.61E-02	151	5	3.3%
GO:0006066 alcohol metabolism	CG5165	FBgn0003076	Phosphogluconate mutase	3.61E-02	151	5	3.3%
GO:0006066 alcohol metabolism	CG5912	FBgn0000119	arrow	3.61E-02	151	5	3.3%
GO:0006400 tRNA modification	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	3.91E-02	62	3	4.8%
GO:0006400 tRNA modification	CG13391	FBgn0027094	Alanyl-tRNA synthetase	3.91E-02	62	3	4.8%
GO:0006400 tRNA modification	CG17938	NA	NA	3.91E-02	62	3	4.8%
GO:0007379 segment specification	CG3696	FBgn0001309	kismet	3.92E-02	26	2	7.7%
GO:0007379 segment specification	CG6205	FBgn0004957	porcupine	3.92E-02	26	2	7.7%
GO:0035110 leg morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	3.92E-02	26	2	7.7%
GO:0035110 leg morphogenesis	CG6667	FBgn0000462	dorsal	3.92E-02	26	2	7.7%
GO:0035108 limb morphogenesis	CG4244	FBgn0003557	Suppressor of deltex	4.21E-02	27	2	7.4%
GO:0035108 limb morphogenesis	CG6667	FBgn0000462	dorsal	4.21E-02	27	2	7.4%
GO:0031123 RNA 3'-end processing	CG17170	FBgn0003559	suppressor of forked	4.79E-02	29	2	6.9%
GO:0031123 RNA 3'-end processing	CG2163	FBgn0005648		4.79E-02	29	2	6.9%
GO:0031124 mRNA 3'-end processing	CG17170	FBgn0003559	suppressor of forked	4.79E-02	29	2	6.9%
GO:0031124 mRNA 3'-end processing	CG2163	FBgn0005648		4.79E-02	29	2	6.9%