

Gut-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:0006119 oxidative phosphorylation	CG11015	FBgn0031830		1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG12400	FBgn0031505		1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG17903	FBgn0000409	Cytochrome c proximal	1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG4412	FBgn0016119	ATPase coupling factor 6	1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG4908	FBgn0032195		1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG8186	FBgn0022097		1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	CG8764	FBgn0011227	oxen	1.13E-05	140	9	6.4%
GO:0006119 oxidative phosphorylation	ND4	NA	NA	1.13E-05	140	9	6.4%
GO:0006099 tricarboxylic acid cycle	CG10219	FBgn0039112		9.78E-05	46	5	10.9%
GO:0006099 tricarboxylic acid cycle	CG11876	FBgn0039635		9.78E-05	46	5	10.9%
GO:0006099 tricarboxylic acid cycle	CG11963	FBgn0037643		9.78E-05	46	5	10.9%
GO:0006099 tricarboxylic acid cycle	CG3861	FBgn0026708		9.78E-05	46	5	10.9%
GO:0006099 tricarboxylic acid cycle	CG7010	FBgn0028325		9.78E-05	46	5	10.9%
GO:0009060 aerobic respiration	CG10219	FBgn0039112		9.78E-05	46	5	10.9%
GO:0009060 aerobic respiration	CG11876	FBgn0039635		9.78E-05	46	5	10.9%
GO:0009060 aerobic respiration	CG11963	FBgn0037643		9.78E-05	46	5	10.9%
GO:0009060 aerobic respiration	CG3861	FBgn0026708		9.78E-05	46	5	10.9%
GO:0009060 aerobic respiration	CG7010	FBgn0028325		9.78E-05	46	5	10.9%
GO:0045333 cellular respiration	CG10219	FBgn0039112		9.78E-05	46	5	10.9%
GO:0045333 cellular respiration	CG11876	FBgn0039635		9.78E-05	46	5	10.9%
GO:0045333 cellular respiration	CG11963	FBgn0037643		9.78E-05	46	5	10.9%
GO:0045333 cellular respiration	CG3861	FBgn0026708		9.78E-05	46	5	10.9%
GO:0045333 cellular respiration	CG7010	FBgn0028325		9.78E-05	46	5	10.9%
GO:0046356 acetyl-CoA catabolism	CG10219	FBgn0039112		9.78E-05	46	5	10.9%
GO:0046356 acetyl-CoA catabolism	CG11876	FBgn0039635		9.78E-05	46	5	10.9%
GO:0046356 acetyl-CoA catabolism	CG11963	FBgn0037643		9.78E-05	46	5	10.9%
GO:0046356 acetyl-CoA catabolism	CG3861	FBgn0026708		9.78E-05	46	5	10.9%
GO:0046356 acetyl-CoA catabolism	CG7010	FBgn0028325		9.78E-05	46	5	10.9%
GO:0006084 acetyl-CoA metabolism	CG10219	FBgn0039112		1.09E-04	47	5	10.6%
GO:0006084 acetyl-CoA metabolism	CG11876	FBgn0039635		1.09E-04	47	5	10.6%
GO:0006084 acetyl-CoA metabolism	CG11963	FBgn0037643		1.09E-04	47	5	10.6%
GO:0006084 acetyl-CoA metabolism	CG3861	FBgn0026708		1.09E-04	47	5	10.6%
GO:0006084 acetyl-CoA metabolism	CG7010	FBgn0028325		1.09E-04	47	5	10.6%
GO:0009109 coenzyme catabolism	CG10219	FBgn0039112		1.09E-04	47	5	10.6%
GO:0009109 coenzyme catabolism	CG11876	FBgn0039635		1.09E-04	47	5	10.6%
GO:0009109 coenzyme catabolism	CG11963	FBgn0037643		1.09E-04	47	5	10.6%
GO:0009109 coenzyme catabolism	CG3861	FBgn0026708		1.09E-04	47	5	10.6%
GO:0009109 coenzyme catabolism	CG7010	FBgn0028325		1.09E-04	47	5	10.6%
GO:0051187 cofactor catabolism	CG10219	FBgn0039112		1.20E-04	48	5	10.4%

Gut-specific age-related GO terms in Cluster 1

GO:0051187 cofactor catabolism	CG11876	FBgn0039635		1.20E-04	48	5	10.4%
GO:0051187 cofactor catabolism	CG11963	FBgn0037643		1.20E-04	48	5	10.4%
GO:0051187 cofactor catabolism	CG3861	FBgn0026708		1.20E-04	48	5	10.4%
GO:0051187 cofactor catabolism	CG7010	FBgn0028325		1.20E-04	48	5	10.4%
GO:0006732 coenzyme metabolism	CG10219	FBgn0039112		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG11876	FBgn0039635		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG11963	FBgn0037643		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG3861	FBgn0026708		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG4067	FBgn0020385	pugilist	4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG7010	FBgn0028325		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG8186	FBgn0022097		4.62E-04	226	9	4.0%
GO:0006732 coenzyme metabolism	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	4.62E-04	226	9	4.0%
GO:0006092 main pathways of carbohydrate metabolism	CG10219	FBgn0039112		5.27E-04	100	6	6.0%
GO:0006092 main pathways of carbohydrate metabolism	CG11876	FBgn0039635		5.27E-04	100	6	6.0%
GO:0006092 main pathways of carbohydrate metabolism	CG11963	FBgn0037643		5.27E-04	100	6	6.0%
GO:0006092 main pathways of carbohydrate metabolism	CG12055	FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	5.27E-04	100	6	6.0%
GO:0006092 main pathways of carbohydrate metabolism	CG3861	FBgn0026708		5.27E-04	100	6	6.0%
GO:0006092 main pathways of carbohydrate metabolism	CG7010	FBgn0028325		5.27E-04	100	6	6.0%
GO:0006725 aromatic compound metabolism	CG10449	FBgn0002022	Catecholamines up	6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG11197	NA	NA	6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG11427	FBgn0003210	ruby	6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG3140	FBgn0022708	Adenylate kinase-2	6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG4067	FBgn0020385	pugilist	6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG8186	FBgn0022097		6.41E-04	144	7	4.9%
GO:0006725 aromatic compound metabolism	CG9741	FBgn0000447	Dihydroorotate dehydrogenase	6.41E-04	144	7	4.9%
GO:0051186 cofactor metabolism	CG10219	FBgn0039112		7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG11876	FBgn0039635		7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG11963	FBgn0037643		7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG3861	FBgn0026708		7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG4067	FBgn0020385	pugilist	7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG7010	FBgn0028325		7.15E-04	240	9	3.8%
GO:0051186 cofactor metabolism	CG8186	FBgn0022097		7.15E-04	240	9	3.8%

Gut-specific age-related GO terms in Cluster 1

GO:0051186 cofactor metabolism	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	7.15E-04	240	9	3.8%
GO:0015980 energy derivation by oxidation of organic compounds	CG10219	FBgn0039112		1.05E-03	114	6	5.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG11876	FBgn0039635		1.05E-03	114	6	5.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG11963	FBgn0037643		1.05E-03	114	6	5.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG12055	FBgn0001091	Glyceraldehyde 3 phosphate dehydrogenase 1	1.05E-03	114	6	5.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG3861	FBgn0026708		1.05E-03	114	6	5.3%
GO:0015980 energy derivation by oxidation of organic compounds	CG7010	FBgn0028325		1.05E-03	114	6	5.3%
GO:0046483 heterocycle metabolism	CG11197	NA	NA	2.51E-03	135	6	4.4%
GO:0046483 heterocycle metabolism	CG11427	FBgn0003210	ruby	2.51E-03	135	6	4.4%
GO:0046483 heterocycle metabolism	CG3140	FBgn0022708	Adenylate kinase-2	2.51E-03	135	6	4.4%
GO:0046483 heterocycle metabolism	CG4067	FBgn0020385	pugilist	2.51E-03	135	6	4.4%
GO:0046483 heterocycle metabolism	CG8186	FBgn0022097		2.51E-03	135	6	4.4%
GO:0046483 heterocycle metabolism	CG9741	FBgn0000447	Dihydroorotate dehydrogenase	2.51E-03	135	6	4.4%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG11015	FBgn0031830		3.85E-03	63	4	6.3%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG12400	FBgn0031505		3.85E-03	63	4	6.3%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG8764	FBgn0011227	oxen	3.85E-03	63	4	6.3%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	ND4	NA	NA	3.85E-03	63	4	6.3%
GO:0042773 ATP synthesis coupled electron transport	CG11015	FBgn0031830		4.31E-03	65	4	6.2%
GO:0042773 ATP synthesis coupled electron transport	CG12400	FBgn0031505		4.31E-03	65	4	6.2%
GO:0042773 ATP synthesis coupled electron transport	CG8764	FBgn0011227	oxen	4.31E-03	65	4	6.2%
GO:0042773 ATP synthesis coupled electron transport	ND4	NA	NA	4.31E-03	65	4	6.2%
GO:0006752 group transfer coenzyme metabolism	CG4067	FBgn0020385	pugilist	5.34E-03	69	4	5.8%
GO:0006752 group transfer coenzyme metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	5.34E-03	69	4	5.8%
GO:0006752 group transfer coenzyme metabolism	CG8186	FBgn0022097		5.34E-03	69	4	5.8%
GO:0006752 group transfer coenzyme metabolism	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	5.34E-03	69	4	5.8%

GO:0006818 hydrogen transport	CG4412	FBgn0016119	ATPase coupling factor 6	6.84E-03	74	4	5.4%
GO:0006818 hydrogen transport	CG6213	FBgn0026753	Vacuolar H[+] ATPase G-subunit	6.84E-03	74	4	5.4%
GO:0006818 hydrogen transport	CG8186	FBgn0022097		6.84E-03	74	4	5.4%
GO:0006818 hydrogen transport	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	6.84E-03	74	4	5.4%
GO:0015992 proton transport	CG4412	FBgn0016119	ATPase coupling factor 6	6.84E-03	74	4	5.4%
GO:0015992 proton transport	CG6213	FBgn0026753	Vacuolar H[+] ATPase G-subunit	6.84E-03	74	4	5.4%
GO:0015992 proton transport	CG8186	FBgn0022097		6.84E-03	74	4	5.4%
GO:0015992 proton transport	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	6.84E-03	74	4	5.4%
GO:0015672 monovalent inorganic cation transport	CG4412	FBgn0016119	ATPase coupling factor 6	7.31E-03	168	6	3.6%
GO:0015672 monovalent inorganic cation transport	CG6213	FBgn0026753	Vacuolar H[+] ATPase G-subunit	7.31E-03	168	6	3.6%
GO:0015672 monovalent inorganic cation transport	CG8178	FBgn0024319		7.31E-03	168	6	3.6%
GO:0015672 monovalent inorganic cation transport	CG8186	FBgn0022097		7.31E-03	168	6	3.6%
GO:0015672 monovalent inorganic cation transport	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	7.31E-03	168	6	3.6%
GO:0015672 monovalent inorganic cation transport	CG9903	FBgn0030756		7.31E-03	168	6	3.6%
GO:0006727 ommochrome biosynthesis	CG11197	NA	NA	1.14E-02	16	2	12.5%
GO:0006727 ommochrome biosynthesis	CG11427	FBgn0003210	ruby	1.14E-02	16	2	12.5%
GO:0008055 ocellus pigment biosynthesis	CG11197	NA	NA	1.14E-02	16	2	12.5%
GO:0008055 ocellus pigment biosynthesis	CG11427	FBgn0003210	ruby	1.14E-02	16	2	12.5%
GO:0046152 ommochrome metabolism	CG11197	NA	NA	1.14E-02	16	2	12.5%
GO:0046152 ommochrome metabolism	CG11427	FBgn0003210	ruby	1.14E-02	16	2	12.5%
GO:0046158 ocellus pigment metabolism	CG11197	NA	NA	1.14E-02	16	2	12.5%
GO:0046158 ocellus pigment metabolism	CG11427	FBgn0003210	ruby	1.14E-02	16	2	12.5%
GO:0009152 purine ribonucleotide biosynthesis	CG3140	FBgn0022708	Adenylate kinase-2	1.15E-02	86	4	4.7%
GO:0009152 purine ribonucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.15E-02	86	4	4.7%
GO:0009152 purine ribonucleotide biosynthesis	CG8186	FBgn0022097		1.15E-02	86	4	4.7%
GO:0009152 purine ribonucleotide biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.15E-02	86	4	4.7%
GO:0009150 purine ribonucleotide metabolism	CG3140	FBgn0022708	Adenylate kinase-2	1.20E-02	87	4	4.6%
GO:0009150 purine ribonucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.20E-02	87	4	4.6%
GO:0009150 purine ribonucleotide metabolism	CG8186	FBgn0022097		1.20E-02	87	4	4.6%
GO:0009150 purine ribonucleotide metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.20E-02	87	4	4.6%
GO:0006164 purine nucleotide biosynthesis	CG3140	FBgn0022708	Adenylate kinase-2	1.24E-02	88	4	4.5%

GO:0006164 purine nucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.24E-02	88	4	4.5%
GO:0006164 purine nucleotide biosynthesis	CG8186	FBgn0022097		1.24E-02	88	4	4.5%
GO:0006164 purine nucleotide biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.24E-02	88	4	4.5%
GO:0009260 ribonucleotide biosynthesis	CG3140	FBgn0022708	Adenylate kinase-2	1.24E-02	88	4	4.5%
GO:0009260 ribonucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.24E-02	88	4	4.5%
GO:0009260 ribonucleotide biosynthesis	CG8186	FBgn0022097		1.24E-02	88	4	4.5%
GO:0009260 ribonucleotide biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.24E-02	88	4	4.5%
GO:0006163 purine nucleotide metabolism	CG3140	FBgn0022708	Adenylate kinase-2	1.29E-02	89	4	4.5%
GO:0006163 purine nucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.29E-02	89	4	4.5%
GO:0006163 purine nucleotide metabolism	CG8186	FBgn0022097		1.29E-02	89	4	4.5%
GO:0006163 purine nucleotide metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.29E-02	89	4	4.5%
GO:0009108 coenzyme biosynthesis	CG4067	FBgn0020385	pugilist	1.29E-02	89	4	4.5%
GO:0009108 coenzyme biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.29E-02	89	4	4.5%
GO:0009108 coenzyme biosynthesis	CG8186	FBgn0022097		1.29E-02	89	4	4.5%
GO:0009108 coenzyme biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.29E-02	89	4	4.5%
GO:0009259 ribonucleotide metabolism	CG3140	FBgn0022708	Adenylate kinase-2	1.29E-02	89	4	4.5%
GO:0009259 ribonucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	1.29E-02	89	4	4.5%
GO:0009259 ribonucleotide metabolism	CG8186	FBgn0022097		1.29E-02	89	4	4.5%
GO:0009259 ribonucleotide metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.29E-02	89	4	4.5%
GO:0006726 eye pigment biosynthesis	CG11197	NA	NA	1.59E-02	19	2	10.5%
GO:0006726 eye pigment biosynthesis	CG11427	FBgn0003210	ruby	1.59E-02	19	2	10.5%
GO:0042441 eye pigment metabolism	CG11197	NA	NA	1.59E-02	19	2	10.5%
GO:0042441 eye pigment metabolism	CG11427	FBgn0003210	ruby	1.59E-02	19	2	10.5%
GO:0007018 microtubule-based movement	CG17192	FBgn0039472		1.91E-02	100	4	4.0%
GO:0007018 microtubule-based movement	CG17459	NA	NA	1.91E-02	100	4	4.0%
GO:0007018 microtubule-based movement	CG3761	NA	NA	1.91E-02	100	4	4.0%
GO:0007018 microtubule-based movement	CG6971	FBgn0037962		1.91E-02	100	4	4.0%
GO:0051188 cofactor biosynthesis	CG4067	FBgn0020385	pugilist	1.91E-02	100	4	4.0%
GO:0051188 cofactor biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	1.91E-02	100	4	4.0%
GO:0051188 cofactor biosynthesis	CG8186	FBgn0022097		1.91E-02	100	4	4.0%
GO:0051188 cofactor biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	1.91E-02	100	4	4.0%
GO:0048069 eye pigmentation	CG11197	NA	NA	1.92E-02	21	2	9.5%
GO:0048069 eye pigmentation	CG11427	FBgn0003210	ruby	1.92E-02	21	2	9.5%

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GO:0030705 cytoskeleton-dependent intracellular transport	CG17192	FBgn0039472		1.97E-02	101	4	4.0%
GO:0030705 cytoskeleton-dependent intracellular transport	CG17459	NA	NA	1.97E-02	101	4	4.0%
GO:0030705 cytoskeleton-dependent intracellular transport	CG3761	NA	NA	1.97E-02	101	4	4.0%
GO:0030705 cytoskeleton-dependent intracellular transport	CG6971	FBgn0037962		1.97E-02	101	4	4.0%
GO:0009117 nucleotide metabolism	CG3140	FBgn0022708	Adenylate kinase-2	2.06E-02	154	5	3.2%
GO:0009117 nucleotide metabolism	CG3761	NA	NA	2.06E-02	154	5	3.2%
GO:0009117 nucleotide metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.06E-02	154	5	3.2%
GO:0009117 nucleotide metabolism	CG8186	FBgn0022097		2.06E-02	154	5	3.2%
GO:0009117 nucleotide metabolism	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	2.06E-02	154	5	3.2%
GO:0007015 actin filament organization	CG8201	FBgn0026193		2.14E-02	58	3	5.2%
GO:0007015 actin filament organization	CG5370	FBgn0010501	Death caspase-1	2.14E-02	58	3	5.2%
GO:0007015 actin filament organization	CG7793	FBgn0001965	Son of sevenless	2.14E-02	58	3	5.2%
GO:0009165 nucleotide biosynthesis	CG3140	FBgn0022708	Adenylate kinase-2	2.24E-02	105	4	3.8%
GO:0009165 nucleotide biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.24E-02	105	4	3.8%
GO:0009165 nucleotide biosynthesis	CG8186	FBgn0022097		2.24E-02	105	4	3.8%
GO:0009165 nucleotide biosynthesis	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	2.24E-02	105	4	3.8%
GO:0019748 secondary metabolism	CG11197	NA	NA	2.34E-02	60	3	5.0%
GO:0019748 secondary metabolism	CG11427	FBgn0003210	ruby	2.34E-02	60	3	5.0%
GO:0019748 secondary metabolism	CG15106	FBgn0034406	Juvenile hormone epoxide hydrolase 3	2.34E-02	60	3	5.0%
GO:0006753 nucleoside phosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.44E-02	61	3	4.9%
GO:0006753 nucleoside phosphate metabolism	CG8186	FBgn0022097		2.44E-02	61	3	4.9%
GO:0006753 nucleoside phosphate metabolism	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	2.44E-02	61	3	4.9%
GO:0006754 ATP biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.44E-02	61	3	4.9%
GO:0006754 ATP biosynthesis	CG8186	FBgn0022097		2.44E-02	61	3	4.9%
GO:0006754 ATP biosynthesis	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	2.44E-02	61	3	4.9%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG4412	FBgn0016119	ATPase coupling factor 6	2.44E-02	61	3	4.9%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG8186	FBgn0022097		2.44E-02	61	3	4.9%
GO:0015985 energy coupled proton transport down electrochemical gradient	CG8210	FBgn0010426	Vacuolar H ⁺ ATPase 14kD subunit	2.44E-02	61	3	4.9%

GO:0015986 ATP synthesis coupled proton transport	CG4412	FBgn0016119	ATPase coupling factor 6	2.44E-02	61	3	4.9%
GO:0015986 ATP synthesis coupled proton transport	CG8186	FBgn0022097		2.44E-02	61	3	4.9%
GO:0015986 ATP synthesis coupled proton transport	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.44E-02	61	3	4.9%
GO:0046034 ATP metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.55E-02	62	3	4.8%
GO:0046034 ATP metabolism	CG8186	FBgn0022097		2.55E-02	62	3	4.8%
GO:0046034 ATP metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.55E-02	62	3	4.8%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-02	65	3	4.6%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG8186	FBgn0022097		2.88E-02	65	3	4.6%
GO:0009145 purine nucleoside triphosphate biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.88E-02	65	3	4.6%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-02	65	3	4.6%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG8186	FBgn0022097		2.88E-02	65	3	4.6%
GO:0009201 ribonucleoside triphosphate biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.88E-02	65	3	4.6%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.88E-02	65	3	4.6%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG8186	FBgn0022097		2.88E-02	65	3	4.6%
GO:0009206 purine ribonucleoside triphosphate biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.88E-02	65	3	4.6%
GO:0007033 vacuole organization and biogenesis	CG11197	NA	NA	2.88E-02	26	2	7.7%
GO:0007033 vacuole organization and biogenesis	CG11427	FBgn0003210	ruby	2.88E-02	26	2	7.7%
GO:0007040 lysosome organization and biogenesis	CG11197	NA	NA	2.88E-02	26	2	7.7%
GO:0007040 lysosome organization and biogenesis	CG11427	FBgn0003210	ruby	2.88E-02	26	2	7.7%
GO:0009142 nucleoside triphosphate biosynthesis	CG4412	FBgn0016119	ATPase coupling factor 6	2.99E-02	66	3	4.5%
GO:0009142 nucleoside triphosphate biosynthesis	CG8186	FBgn0022097		2.99E-02	66	3	4.5%
GO:0009142 nucleoside triphosphate biosynthesis	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.99E-02	66	3	4.5%
GO:0009144 purine nucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.99E-02	66	3	4.5%
GO:0009144 purine nucleoside triphosphate metabolism	CG8186	FBgn0022097		2.99E-02	66	3	4.5%
GO:0009144 purine nucleoside triphosphate metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.99E-02	66	3	4.5%

GO:0009199 ribonucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.99E-02	66	3	4.5%
GO:0009199 ribonucleoside triphosphate metabolism	CG8186	FBgn0022097		2.99E-02	66	3	4.5%
GO:0009199 ribonucleoside triphosphate metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.99E-02	66	3	4.5%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	2.99E-02	66	3	4.5%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG8186	FBgn0022097		2.99E-02	66	3	4.5%
GO:0009205 purine ribonucleoside triphosphate metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	2.99E-02	66	3	4.5%
GO:0009141 nucleoside triphosphate metabolism	CG4412	FBgn0016119	ATPase coupling factor 6	3.23E-02	68	3	4.4%
GO:0009141 nucleoside triphosphate metabolism	CG8186	FBgn0022097		3.23E-02	68	3	4.4%
GO:0009141 nucleoside triphosphate metabolism	CG8210	FBgn0010426	Vacuolar H[+] ATPase 14kD subunit	3.23E-02	68	3	4.4%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG10449	FBgn0002022	Catecholamines up	3.53E-02	29	2	6.9%
GO:0007300 nurse cell to oocyte transport (sensu Insecta)	CG5370	FBgn0010501	Death caspase-1	3.53E-02	29	2	6.9%
GO:0007017 microtubule-based process	CG8201	FBgn0026193		3.77E-02	181	5	2.8%
GO:0007017 microtubule-based process	CG17192	FBgn0039472		3.77E-02	181	5	2.8%
GO:0007017 microtubule-based process	CG17459	NA	NA	3.77E-02	181	5	2.8%
GO:0007017 microtubule-based process	CG3761	NA	NA	3.77E-02	181	5	2.8%
GO:0007017 microtubule-based process	CG6971	FBgn0037962		3.77E-02	181	5	2.8%
GO:0048193 Golgi vesicle transport	CG11197	NA	NA	4.23E-02	32	2	6.3%
GO:0048193 Golgi vesicle transport	CG6625	FBgn0011712	Soluble NSF attachment protein	4.23E-02	32	2	6.3%
GO:0009112 nucleobase metabolism	CG3140	FBgn0022708	Adenylate kinase-2	4.42E-02	77	3	3.9%
GO:0009112 nucleobase metabolism	CG8186	FBgn0022097		4.42E-02	77	3	3.9%
GO:0009112 nucleobase metabolism	CG9741	FBgn0000447	Dihydroorotate dehydrogenase	4.42E-02	77	3	3.9%
GO:0046148 pigment biosynthesis	CG11197	NA	NA	4.72E-02	34	2	5.9%
GO:0046148 pigment biosynthesis	CG11427	FBgn0003210	ruby	4.72E-02	34	2	5.9%

Gut-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:0006120 mitochondrial electron transport NADH to ubiquinone	CG8680	FBgn0031684		7.64E-03	40	2	5.0%
GO:0006120 mitochondrial electron transport NADH to ubiquinone	ND4	NA	NA	7.64E-03	40	2	5.0%
GO:0006119 oxidative phosphorylation	CG2934	FBgn0028665		1.07E-02	140	3	2.1%
GO:0006119 oxidative phosphorylation	CG8680	FBgn0031684		1.07E-02	140	3	2.1%
GO:0006119 oxidative phosphorylation	ND4	NA	NA	1.07E-02	140	3	2.1%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	CG8680	FBgn0031684		1.83E-02	63	2	3.2%
GO:0042775 ATP synthesis coupled electron transport (sensu Eukaryota)	ND4	NA	NA	1.83E-02	63	2	3.2%
GO:0042773 ATP synthesis coupled electron transport	CG8680	FBgn0031684		1.94E-02	65	2	3.1%
GO:0042773 ATP synthesis coupled electron transport	ND4	NA	NA	1.94E-02	65	2	3.1%
GO:0006470 protein amino acid dephosphorylation	CG10376	FBgn0032702		2.73E-02	78	2	2.6%
GO:0006470 protein amino acid dephosphorylation	CG7042	FBgn0035105		2.73E-02	78	2	2.6%
GO:0006399 tRNA metabolism	CG7042	FBgn0035105		2.86E-02	80	2	2.5%
GO:0006399 tRNA metabolism	CG8431	FBgn0027091	Cysteinyl-tRNA synthetase	2.86E-02	80	2	2.5%
GO:0009152 purine ribonucleotide biosynthesis	CG2934	FBgn0028665		3.27E-02	86	2	2.3%
GO:0009152 purine ribonucleotide biosynthesis	CG8761	NA	NA	3.27E-02	86	2	2.3%
GO:0009150 purine ribonucleotide metabolism	CG2934	FBgn0028665		3.34E-02	87	2	2.3%
GO:0009150 purine ribonucleotide metabolism	CG8761	NA	NA	3.34E-02	87	2	2.3%
GO:0006164 purine nucleotide biosynthesis	CG2934	FBgn0028665		3.41E-02	88	2	2.3%
GO:0006164 purine nucleotide biosynthesis	CG8761	NA	NA	3.41E-02	88	2	2.3%
GO:0009260 ribonucleotide biosynthesis	CG2934	FBgn0028665		3.41E-02	88	2	2.3%
GO:0009260 ribonucleotide biosynthesis	CG8761	NA	NA	3.41E-02	88	2	2.3%
GO:0006163 purine nucleotide metabolism	CG2934	FBgn0028665		3.48E-02	89	2	2.2%
GO:0006163 purine nucleotide metabolism	CG8761	NA	NA	3.48E-02	89	2	2.2%
GO:0009259 ribonucleotide metabolism	CG2934	FBgn0028665		3.48E-02	89	2	2.2%
GO:0009259 ribonucleotide metabolism	CG8761	NA	NA	3.48E-02	89	2	2.2%
GO:0007307 chorion gene amplification	CG3938	FBgn0010382	Cyclin E	3.60E-02	11	1	9.1%
GO:0007616 long-term memory	CG6072	FBgn0020250	sarah	3.60E-02	11	1	9.1%
GO:0008033 tRNA processing	CG7042	FBgn0035105		3.60E-02	11	1	9.1%
GO:0016311 dephosphorylation	CG10376	FBgn0032702		4.22E-02	99	2	2.0%
GO:0016311 dephosphorylation	CG7042	FBgn0035105		4.22E-02	99	2	2.0%
GO:0009312 oligosaccharide biosynthesis	CG6394	FBgn0030930	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	4.24E-02	13	1	7.7%

Gut-specific age-related GO terms in Cluster 2

GO:0000082 G1 S transition of mitotic cell cycle	CG3938	FBgn0010382	Cyclin E	4.56E-02	14	1	7.1%
GO:0018208 peptidyl-proline modification	CG15542	FBgn0051371		4.56E-02	14	1	7.1%
GO:0018401 peptidyl-proline hydroxylation to 4-hydroxy-L-proline	CG15542	FBgn0051371		4.56E-02	14	1	7.1%
GO:0019471 4-hydroxyproline metabolism	CG15542	FBgn0051371		4.56E-02	14	1	7.1%
GO:0019511 peptidyl-proline hydroxylation	CG15542	FBgn0051371		4.56E-02	14	1	7.1%
GO:0009165 nucleotide biosynthesis	CG2934	FBgn0028665		4.70E-02	105	2	1.9%
GO:0009165 nucleotide biosynthesis	CG8761	NA	NA	4.70E-02	105	2	1.9%
GO:0009311 oligosaccharide metabolism	CG6394	FBgn0030930	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	4.88E-02	15	1	6.7%

Gut-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:0006936 muscle contraction	CG11713	NA	NA	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG12915	NA	NA	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG12968	NA	NA	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG17927	FBgn0002741	Myosin heavy chain	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG4839	FBgn0032187		1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG4843	FBgn0004117	Tropomyosin 2	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG13413	NA	NA	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG6992	FBgn0004620	Glutamate receptor IIA	1.45E-06	88	9	10.2%
GO:0006936 muscle contraction	CG8604	FBgn0027356	Amphiphysin	1.45E-06	88	9	10.2%
GO:0006030 chitin metabolism	CG10287	FBgn0026077		9.38E-05	59	6	10.2%
GO:0006030 chitin metabolism	CG10725	FBgn0036362		9.38E-05	59	6	10.2%
GO:0006030 chitin metabolism	CG6004	FBgn0036203		9.38E-05	59	6	10.2%
GO:0006030 chitin metabolism	CG8473	NA	NA	9.38E-05	59	6	10.2%
GO:0006030 chitin metabolism	CG8756	FBgn0036901		9.38E-05	59	6	10.2%
GO:0006030 chitin metabolism	CG9357	FBgn0034580		9.38E-05	59	6	10.2%
GO:0006040 amino sugar metabolism	CG10287	FBgn0026077		1.24E-04	62	6	9.7%
GO:0006040 amino sugar metabolism	CG10725	FBgn0036362		1.24E-04	62	6	9.7%
GO:0006040 amino sugar metabolism	CG6004	FBgn0036203		1.24E-04	62	6	9.7%
GO:0006040 amino sugar metabolism	CG8473	NA	NA	1.24E-04	62	6	9.7%
GO:0006040 amino sugar metabolism	CG8756	FBgn0036901		1.24E-04	62	6	9.7%
GO:0006040 amino sugar metabolism	CG9357	FBgn0034580		1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG10287	FBgn0026077		1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG10725	FBgn0036362		1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG6004	FBgn0036203		1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG8473	NA	NA	1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG8756	FBgn0036901		1.24E-04	62	6	9.7%
GO:0006041 glucosamine metabolism	CG9357	FBgn0034580		1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG10287	FBgn0026077		1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG10725	FBgn0036362		1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG6004	FBgn0036203		1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG8473	NA	NA	1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG8756	FBgn0036901		1.24E-04	62	6	9.7%
GO:0006044 N-acetylglucosamine metabolism	CG9357	FBgn0034580		1.24E-04	62	6	9.7%
GO:0044264 cellular polysaccharide metabolism	CG10287	FBgn0026077		2.08E-04	68	6	8.8%
GO:0044264 cellular polysaccharide metabolism	CG10725	FBgn0036362		2.08E-04	68	6	8.8%
GO:0044264 cellular polysaccharide metabolism	CG6004	FBgn0036203		2.08E-04	68	6	8.8%
GO:0044264 cellular polysaccharide metabolism	CG8473	NA	NA	2.08E-04	68	6	8.8%
GO:0044264 cellular polysaccharide metabolism	CG8756	FBgn0036901		2.08E-04	68	6	8.8%
GO:0044264 cellular polysaccharide metabolism	CG9357	FBgn0034580		2.08E-04	68	6	8.8%
GO:0005976 polysaccharide metabolism	CG10287	FBgn0026077		3.09E-03	152	7	4.6%
GO:0005976 polysaccharide metabolism	CG10725	FBgn0036362		3.09E-03	152	7	4.6%
GO:0005976 polysaccharide metabolism	CG3797	FBgn0036842		3.09E-03	152	7	4.6%

GO:0005976 polysaccharide metabolism	CG6004	FBgn0036203		3.09E-03	152	7	4.6%
GO:0005976 polysaccharide metabolism	CG8473	NA	NA	3.09E-03	152	7	4.6%
GO:0005976 polysaccharide metabolism	CG8756	FBgn0036901		3.09E-03	152	7	4.6%
GO:0005976 polysaccharide metabolism	CG9357	FBgn0034580		3.09E-03	152	7	4.6%
GO:0012502 induction of programmed cell death	CG11261	FBgn0036332		1.13E-02	69	4	5.8%
GO:0012502 induction of programmed cell death	CG11491	FBgn0000210	broad	1.13E-02	69	4	5.8%
GO:0012502 induction of programmed cell death	CG11713	NA	NA	1.13E-02	69	4	5.8%
GO:0012502 induction of programmed cell death	CG4551	FBgn0016930	smell impaired 35A	1.13E-02	69	4	5.8%
GO:0008064 regulation of actin polymerization and or depolymerization	CG15112	FBgn0000578		1.14E-02	13	2	15.4%
GO:0008064 regulation of actin polymerization and or depolymerization	CG4012	FBgn0023081	genghis khan	1.14E-02	13	2	15.4%
GO:0030832 regulation of actin filament length	CG15112	FBgn0000578	enabled	1.14E-02	13	2	15.4%
GO:0030832 regulation of actin filament length	CG4012	FBgn0023081	genghis khan	1.14E-02	13	2	15.4%
GO:0043068 positive regulation of programmed cell death	CG11261	FBgn0036332		1.31E-02	72	4	5.6%
GO:0043068 positive regulation of programmed cell death	CG11491	FBgn0000210	broad	1.31E-02	72	4	5.6%
GO:0043068 positive regulation of programmed cell death	CG11713	NA	NA	1.31E-02	72	4	5.6%
GO:0043068 positive regulation of programmed cell death	CG4551	FBgn0016930	smell impaired 35A	1.31E-02	72	4	5.6%
GO:0043067 regulation of programmed cell death	CG11261	FBgn0036332		1.38E-02	112	5	4.5%
GO:0043067 regulation of programmed cell death	CG11491	FBgn0000210	broad	1.38E-02	112	5	4.5%
GO:0043067 regulation of programmed cell death	CG11713	NA	NA	1.38E-02	112	5	4.5%
GO:0043067 regulation of programmed cell death	CG4551	FBgn0016930	smell impaired 35A	1.38E-02	112	5	4.5%
GO:0043067 regulation of programmed cell death	CG7788	FBgn0019972	Ice	1.38E-02	112	5	4.5%
GO:0048489 synaptic vesicle transport	CG1467	FBgn0031106	Syntaxin 16	1.78E-02	79	4	5.1%
GO:0048489 synaptic vesicle transport	CG1618	FBgn0000346	comatose	1.78E-02	79	4	5.1%
GO:0048489 synaptic vesicle transport	CG13413	NA	NA	1.78E-02	79	4	5.1%
GO:0048489 synaptic vesicle transport	CG8604	FBgn0027356	Amphiphysin	1.78E-02	79	4	5.1%
GO:0016079 synaptic vesicle exocytosis	CG1467	FBgn0031106	Syntaxin 16	1.92E-02	45	3	6.7%
GO:0016079 synaptic vesicle exocytosis	CG1618	FBgn0000346	comatose	1.92E-02	45	3	6.7%
GO:0016079 synaptic vesicle exocytosis	CG13413	NA	NA	1.92E-02	45	3	6.7%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG10563	FBgn0032760		2.18E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG12225	FBgn0028982		2.18E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG3606	FBgn0011571	cabeza	2.18E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG3695	FBgn0034795	Mediator complex subunit 23	2.18E-02	84	4	4.8%
GO:0006352 transcription initiation	CG10563	FBgn0032760		2.36E-02	86	4	4.7%
GO:0006352 transcription initiation	CG12225	FBgn0028982		2.36E-02	86	4	4.7%
GO:0006352 transcription initiation	CG3606	FBgn0011571	cabeza	2.36E-02	86	4	4.7%

Gut-specific age-related GO terms in Cluster 3

GO:0006352 transcription initiation	CG3695	FBgn0034795	Mediator complex subunit 23	2.36E-02	86	4	4.7%
GO:0051128 regulation of cell organization and biogenesis	CG15112	FBgn0000578	enabled	2.62E-02	20	2	10.0%
GO:0051128 regulation of cell organization and biogenesis	CG4012	FBgn0023081	genghis khan	2.62E-02	20	2	10.0%
GO:0008154 actin polymerization and depolymerization	CG15112	FBgn0000578	enabled	2.87E-02	21	2	9.5%
GO:0008154 actin polymerization and depolymerization	CG4012	FBgn0023081	genghis khan	2.87E-02	21	2	9.5%
GO:0016081 synaptic vesicle docking during exocytosis	CG1467	FBgn0031106	Syntaxin 16	2.87E-02	21	2	9.5%
GO:0016081 synaptic vesicle docking during exocytosis	CG13413	NA	NA	2.87E-02	21	2	9.5%
GO:0051246 regulation of protein metabolism	CG12413	FBgn0039588		3.93E-02	101	4	4.0%
GO:0051246 regulation of protein metabolism	CG15112	FBgn0000578	enabled	3.93E-02	101	4	4.0%
GO:0051246 regulation of protein metabolism	CG1691	FBgn0030235	IGF-II mRNA-binding protein	3.93E-02	101	4	4.0%
GO:0051246 regulation of protein metabolism	CG4012	FBgn0023081	genghis khan	3.93E-02	101	4	4.0%
GO:0006917 induction of apoptosis	CG11261	FBgn0036332		4.22E-02	61	3	4.9%
GO:0006917 induction of apoptosis	CG11713	NA	NA	4.22E-02	61	3	4.9%
GO:0006917 induction of apoptosis	CG4551	FBgn0016930	smell impaired 35A	4.22E-02	61	3	4.9%
GO:0007269 neurotransmitter secretion	CG1467	FBgn0031106	Syntaxin 16	4.31E-02	104	4	3.8%
GO:0007269 neurotransmitter secretion	CG1618	FBgn0000346	comatose	4.31E-02	104	4	3.8%
GO:0007269 neurotransmitter secretion	CG13413	NA	NA	4.31E-02	104	4	3.8%
GO:0007269 neurotransmitter secretion	CG8604	FBgn0027356	Amphiphysin	4.31E-02	104	4	3.8%
GO:0045055 regulated secretory pathway	CG1467	FBgn0031106	Syntaxin 16	4.31E-02	104	4	3.8%
GO:0045055 regulated secretory pathway	CG1618	FBgn0000346	comatose	4.31E-02	104	4	3.8%
GO:0045055 regulated secretory pathway	CG13413	NA	NA	4.31E-02	104	4	3.8%
GO:0045055 regulated secretory pathway	CG8604	FBgn0027356	Amphiphysin	4.31E-02	104	4	3.8%
GO:0043065 positive regulation of apoptosis	CG11261	FBgn0036332		4.58E-02	63	3	4.8%
GO:0043065 positive regulation of apoptosis	CG11713	NA	NA	4.58E-02	63	3	4.8%
GO:0043065 positive regulation of apoptosis	CG4551	FBgn0016930	smell impaired 35A	4.58E-02	63	3	4.8%
GO:0007268 synaptic transmission	CG12915	NA	NA	4.87E-02	208	6	2.9%
GO:0007268 synaptic transmission	CG1467	FBgn0031106	Syntaxin 16	4.87E-02	208	6	2.9%
GO:0007268 synaptic transmission	CG1618	FBgn0000346	comatose	4.87E-02	208	6	2.9%
GO:0007268 synaptic transmission	CG13413	NA	NA	4.87E-02	208	6	2.9%
GO:0007268 synaptic transmission	CG6992	FBgn0004620	Glutamate receptor IIA	4.87E-02	208	6	2.9%
GO:0007268 synaptic transmission	CG8604	FBgn0027356	Amphiphysin	4.87E-02	208	6	2.9%
GO:0006260 DNA replication	CG17142	FBgn0035113		4.97E-02	109	4	3.7%
GO:0006260 DNA replication	CG5247	FBgn0011774	Inverted repeat-binding protein	4.97E-02	109	4	3.7%
GO:0006260 DNA replication	CG5371	FBgn0011703	Ribonucleoside diphosphate reductase large subunit	4.97E-02	109	4	3.7%

Gut-specific age-related GO terms in Cluster 3

GO:0006260 DNA replication	CG9075	FBgn0001942	Eukaryotic initiation factor 4a	4.97E-02	109	4	3.7%
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Gut-specific age-related GO terms in Cluster 4 (Downregulated)							
GO term	CG_ID	FB_ID	Full_name	P-value	Total_gene	Changed_gene	% of change
GO:0035264 body growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	1.11E-03	13	2	15.4%
GO:0035264 body growth	CG3143	FBgn0038197	forkhead box, sub-group O	1.11E-03	13	2	15.4%
GO:0040014 regulation of body size	CG10539	FBgn0015806	RPS6-p70-protein kinase	1.11E-03	13	2	15.4%
GO:0040014 regulation of body size	CG3143	FBgn0038197	forkhead box, sub-group O	1.11E-03	13	2	15.4%
GO:0001558 regulation of cell growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	2.16E-03	18	2	11.1%
GO:0001558 regulation of cell growth	CG3143	FBgn0038197	forkhead box, sub-group O	2.16E-03	18	2	11.1%
GO:0016049 cell growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	4.85E-03	27	2	7.4%
GO:0016049 cell growth	CG3143	FBgn0038197	forkhead box, sub-group O	4.85E-03	27	2	7.4%
GO:0001763 branching morphogenesis	CG18138	NA	NA	5.97E-03	30	2	6.7%
GO:0001763 branching morphogenesis	CG5393	FBgn0015903	apontic	5.97E-03	30	2	6.7%
GO:0008361 regulation of cell size	CG10539	FBgn0015806	RPS6-p70-protein kinase	5.97E-03	30	2	6.7%
GO:0008361 regulation of cell size	CG3143	FBgn0038197	forkhead box, sub-group O	5.97E-03	30	2	6.7%
GO:0040008 regulation of growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	1.60E-02	50	2	4.0%
GO:0040008 regulation of growth	CG3143	FBgn0038197	forkhead box, sub-group O	1.60E-02	50	2	4.0%
GO:0051242 positive regulation of cellular physiological process	CG10539	FBgn0015806	RPS6-p70-protein kinase	1.66E-02	140	3	2.1%
GO:0051242 positive regulation of cellular physiological process	CG3143	FBgn0038197	forkhead box, sub-group O	1.66E-02	140	3	2.1%
GO:0051242 positive regulation of cellular physiological process	CG6224	FBgn0040230	diablo	1.66E-02	140	3	2.1%
GO:0043119 positive regulation of physiological process	CG10539	FBgn0015806	RPS6-p70-protein kinase	1.73E-02	142	3	2.1%
GO:0043119 positive regulation of physiological process	CG3143	FBgn0038197	forkhead box, sub-group O	1.73E-02	142	3	2.1%
GO:0043119 positive regulation of physiological process	CG6224	FBgn0040230	diablo	1.73E-02	142	3	2.1%
GO:0006066 alcohol metabolism	CG10118	FBgn0005626	pale	2.03E-02	151	3	2.0%
GO:0006066 alcohol metabolism	CG11143	FBgn0025885		2.03E-02	151	3	2.0%
GO:0006066 alcohol metabolism	CG5103	FBgn0036784		2.03E-02	151	3	2.0%
GO:0048522 positive regulation of cellular process	CG10539	FBgn0015806	RPS6-p70-protein kinase	2.18E-02	155	3	1.9%
GO:0048522 positive regulation of cellular process	CG3143	FBgn0038197	forkhead box, sub-group O	2.18E-02	155	3	1.9%
GO:0048522 positive regulation of cellular process	CG6224	FBgn0040230	diablo	2.18E-02	155	3	1.9%
GO:0006917 induction of apoptosis	CG3143	FBgn0038197	forkhead box, sub-group O	2.33E-02	61	2	3.3%
GO:0006917 induction of apoptosis	CG6224	FBgn0040230	diablo	2.33E-02	61	2	3.3%

Gut-specific age-related GO terms in Cluster 4

GO:0043065 positive regulation of apoptosis	CG3143	FBgn0038197	forkhead box, sub-group O	2.48E-02	63	2	3.2%
GO:0043065 positive regulation of apoptosis	CG6224	FBgn0040230	diablo	2.48E-02	63	2	3.2%
GO:0035239 tube morphogenesis	CG18138	NA	NA	2.55E-02	64	2	3.1%
GO:0035239 tube morphogenesis	CG5393	FBgn0015903	apontic	2.55E-02	64	2	3.1%
GO:0012502 induction of programmed cell death	CG3143	FBgn0038197	forkhead box, sub-group O	2.93E-02	69	2	2.9%
GO:0012502 induction of programmed cell death	CG6224	FBgn0040230	diablo	2.93E-02	69	2	2.9%
GO:0048518 positive regulation of biological process	CG10539	FBgn0015806	RPS6-p70-protein kinase	2.94E-02	174	3	1.7%
GO:0048518 positive regulation of biological process	CG3143	FBgn0038197	forkhead box, sub-group O	2.94E-02	174	3	1.7%
GO:0048518 positive regulation of biological process	CG6224	FBgn0040230	diablo	2.94E-02	174	3	1.7%
GO:0035295 tube development	CG18138	NA	NA	3.17E-02	72	2	2.8%
GO:0035295 tube development	CG5393	FBgn0015903	apontic	3.17E-02	72	2	2.8%
GO:0043068 positive regulation of programmed cell death	CG3143	FBgn0038197	forkhead box, sub-group O	3.17E-02	72	2	2.8%
GO:0043068 positive regulation of programmed cell death	CG6224	FBgn0040230	diablo	3.17E-02	72	2	2.8%
GO:0009309 amine biosynthesis	CG10118	FBgn0005626	pale	3.34E-02	74	2	2.7%
GO:0009309 amine biosynthesis	CG1753	FBgn0031148		3.34E-02	74	2	2.7%
GO:0040007 growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	3.34E-02	74	2	2.7%
GO:0040007 growth	CG3143	FBgn0038197	forkhead box, sub-group O	3.34E-02	74	2	2.7%
GO:0019318 hexose metabolism	CG11143	FBgn0025885		3.50E-02	76	2	2.6%
GO:0019318 hexose metabolism	CG5103	FBgn0036784		3.50E-02	76	2	2.6%
GO:0006098 pentose-phosphate shunt	CG5103	FBgn0036784		4.21E-02	11	1	9.1%
GO:0006739 NADP metabolism	CG5103	FBgn0036784		4.21E-02	11	1	9.1%
GO:0006740 NADPH regeneration	CG5103	FBgn0036784		4.21E-02	11	1	9.1%
GO:0007005 mitochondrion organization and biogenesis	CG9878	FBgn0027360		4.21E-02	11	1	9.1%
GO:0030307 positive regulation of cell growth	CG10539	FBgn0015806	RPS6-p70-protein kinase	4.21E-02	11	1	9.1%
GO:0035146 tube fusion	CG18138	NA	NA	4.21E-02	11	1	9.1%
GO:0035147 tracheal branch fusion	CG18138	NA	NA	4.21E-02	11	1	9.1%
GO:0007428 primary tracheal branching (sensu Insecta)	CG5393	FBgn0015903	apontic	4.59E-02	12	1	8.3%
GO:0008286 insulin receptor signaling pathway	CG3143	FBgn0038197	forkhead box, sub-group O	4.59E-02	12	1	8.3%
GO:0045793 positive regulation of cell size	CG10539	FBgn0015806	RPS6-p70-protein kinase	4.59E-02	12	1	8.3%
GO:0006584 catecholamine metabolism	CG10118	FBgn0005626	pale	4.96E-02	13	1	7.7%
GO:0006769 nicotinamide metabolism	CG5103	FBgn0036784		4.96E-02	13	1	7.7%
GO:0007318 pole plasm protein localization	CG5393	FBgn0015903	apontic	4.96E-02	13	1	7.7%
GO:0009070 serine family amino acid biosynthesis	CG1753	FBgn0031148		4.96E-02	13	1	7.7%
GO:0042133 neurotransmitter metabolism	CG10118	FBgn0005626	pale	4.96E-02	13	1	7.7%

Gut-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:0006520 amino acid metabolism	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG10623	FBgn0032727		1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG12032	NA	NA	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG12264	FBgn0032393		1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG3487	NA	NA	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG5353	FBgn0027081	Threonyl-tRNA synthetase	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG6287	FBgn0032350		1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG6321	FBgn0036117		1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG8553	FBgn0020615	selenide,water dikinase	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG9020	FBgn0027093	Arginyl-tRNA synthetase	1.50E-04	243	12	4.9%
GO:0006520 amino acid metabolism	CG17326	NA	NA	1.50E-04	243	12	4.9%
GO:0006400 tRNA modification	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	2.25E-04	62	6	9.7%
GO:0006400 tRNA modification	CG12032	NA	NA	2.25E-04	62	6	9.7%
GO:0006400 tRNA modification	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	2.25E-04	62	6	9.7%
GO:0006400 tRNA modification	CG5353	FBgn0027081	Threonyl-tRNA synthetase	2.25E-04	62	6	9.7%
GO:0006400 tRNA modification	CG9020	FBgn0027093	Arginyl-tRNA synthetase	2.25E-04	62	6	9.7%
GO:0006400 tRNA modification	CG17326	NA	NA	2.25E-04	62	6	9.7%
GO:0009451 RNA modification	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	4.05E-04	69	6	8.7%
GO:0009451 RNA modification	CG12032	NA	NA	4.05E-04	69	6	8.7%
GO:0009451 RNA modification	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	4.05E-04	69	6	8.7%
GO:0009451 RNA modification	CG5353	FBgn0027081	Threonyl-tRNA synthetase	4.05E-04	69	6	8.7%
GO:0009451 RNA modification	CG9020	FBgn0027093	Arginyl-tRNA synthetase	4.05E-04	69	6	8.7%
GO:0009451 RNA modification	CG17326	NA	NA	4.05E-04	69	6	8.7%
GO:0006399 tRNA metabolism	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	8.96E-04	80	6	7.5%
GO:0006399 tRNA metabolism	CG12032	NA	NA	8.96E-04	80	6	7.5%
GO:0006399 tRNA metabolism	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	8.96E-04	80	6	7.5%

Gut-specific age-related GO terms in Cluster 5

GO:0006399 tRNA metabolism	CG5353	FBgn0027081	Threonyl-tRNA synthetase	8.96E-04	80	6	7.5%
GO:0006399 tRNA metabolism	CG9020	FBgn0027093	Arginyl-tRNA synthetase	8.96E-04	80	6	7.5%
GO:0006399 tRNA metabolism	CG17326	NA	NA	8.96E-04	80	6	7.5%
GO:0006418 tRNA aminoacylation for protein translation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0006418 tRNA aminoacylation for protein translation	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0006418 tRNA aminoacylation for protein translation	CG5353	FBgn0027081	Threonyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0006418 tRNA aminoacylation for protein translation	CG9020	FBgn0027093	Arginyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0006418 tRNA aminoacylation for protein translation	CG17326	NA	NA	1.11E-03	56	5	8.9%
GO:0043039 tRNA aminoacylation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0043039 tRNA aminoacylation	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0043039 tRNA aminoacylation	CG5353	FBgn0027081	Threonyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0043039 tRNA aminoacylation	CG9020	FBgn0027093	Arginyl-tRNA synthetase	1.11E-03	56	5	8.9%
GO:0043039 tRNA aminoacylation	CG17326	NA	NA	1.11E-03	56	5	8.9%
GO:0043038 amino acid activation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	1.21E-03	57	5	8.8%
GO:0043038 amino acid activation	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	1.21E-03	57	5	8.8%
GO:0043038 amino acid activation	CG5353	FBgn0027081	Threonyl-tRNA synthetase	1.21E-03	57	5	8.8%
GO:0043038 amino acid activation	CG9020	FBgn0027093	Arginyl-tRNA synthetase	1.21E-03	57	5	8.8%
GO:0043038 amino acid activation	CG17326	NA	NA	1.21E-03	57	5	8.8%
GO:0008652 amino acid biosynthesis	CG10623	FBgn0032727		1.76E-03	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG12264	FBgn0032393		1.76E-03	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG3487	NA	NA	1.76E-03	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG6287	FBgn0032350		1.76E-03	62	5	8.1%
GO:0008652 amino acid biosynthesis	CG8553	FBgn0020615	selenide,water dikinase	1.76E-03	62	5	8.1%
GO:0016318 ommatidial rotation	CG17579	FBgn0003326	scabrous	2.64E-03	20	3	15.0%
GO:0016318 ommatidial rotation	CG2534	FBgn0000340	canoe	2.64E-03	20	3	15.0%
GO:0016318 ommatidial rotation	CG6667	FBgn0000462	dorsal	2.64E-03	20	3	15.0%
GO:0009309 amine biosynthesis	CG10623	FBgn0032727		3.84E-03	74	5	6.8%
GO:0009309 amine biosynthesis	CG12264	FBgn0032393		3.84E-03	74	5	6.8%
GO:0009309 amine biosynthesis	CG3487	NA	NA	3.84E-03	74	5	6.8%
GO:0009309 amine biosynthesis	CG6287	FBgn0032350		3.84E-03	74	5	6.8%

Gut-specific age-related GO terms in Cluster 5

GO:0009309 amine biosynthesis	CG8553	FBgn0020615	selenide,water dikinase	3.84E-03	74	5	6.8%
GO:0043037 translation	CG10506	FBgn0027090	Glutaminyl-tRNA synthetase	3.99E-03	181	8	4.4%
GO:0043037 translation	CG3506	FBgn0003970	vasa	3.99E-03	181	8	4.4%
GO:0043037 translation	CG3821	FBgn0002069	Aspartyl-tRNA synthetase	3.99E-03	181	8	4.4%
GO:0043037 translation	CG5353	FBgn0027081	Threonyl-tRNA synthetase	3.99E-03	181	8	4.4%
GO:0043037 translation	CG6341	FBgn0028737	Elongation factor 1 beta	3.99E-03	181	8	4.4%
GO:0043037 translation	CG9020	FBgn0027093	Arginyl-tRNA synthetase	3.99E-03	181	8	4.4%
GO:0043037 translation	CG17326	NA	NA	3.99E-03	181	8	4.4%
GO:0043037 translation	CG9124	FBgn0022023	Eukaryotic initiation factor 3 p40 subunit	3.99E-03	181	8	4.4%
GO:0001738 morphogenesis of a polarized epithelium	CG17579	FBgn0003326	scabrous	4.58E-03	48	4	8.3%
GO:0001738 morphogenesis of a polarized epithelium	CG2534	FBgn0000340	canoe	4.58E-03	48	4	8.3%
GO:0001738 morphogenesis of a polarized epithelium	CG2671	FBgn0002121	lethal (2) giant larvae	4.58E-03	48	4	8.3%
GO:0001738 morphogenesis of a polarized epithelium	CG6667	FBgn0000462	dorsal	4.58E-03	48	4	8.3%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG17579	FBgn0003326	scabrous	1.02E-02	32	3	9.4%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG2534	FBgn0000340	canoe	1.02E-02	32	3	9.4%
GO:0042067 establishment of ommatidial polarity (sensu Endopterygota)	CG6667	FBgn0000462	dorsal	1.02E-02	32	3	9.4%
GO:0040029 regulation of gene expression epigenetic	CG10279	FBgn0003261	Rm62	1.40E-02	66	4	6.1%
GO:0040029 regulation of gene expression epigenetic	CG17743	FBgn0002521	pleiohomeotic	1.40E-02	66	4	6.1%
GO:0040029 regulation of gene expression epigenetic	CG3041	FBgn0015270	Origin recognition complex subunit 2	1.40E-02	66	4	6.1%
GO:0040029 regulation of gene expression epigenetic	CG3496	FBgn0003977	virilizer	1.40E-02	66	4	6.1%
GO:0009070 serine family amino acid biosynthesis	CG6287	FBgn0032350		1.40E-02	13	2	15.4%
GO:0009070 serine family amino acid biosynthesis	CG8553	FBgn0020615	selenide,water dikinase	1.40E-02	13	2	15.4%
GO:0045465 R8 cell differentiation	CG17579	FBgn0003326	scabrous	1.40E-02	13	2	15.4%
GO:0045465 R8 cell differentiation	CG6667	FBgn0000462	dorsal	1.40E-02	13	2	15.4%
GO:0007163 establishment and or maintenance of cell polarity	CG17579	FBgn0003326	scabrous	1.62E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG2534	FBgn0000340	canoe	1.62E-02	69	4	5.8%

GO:0007163 establishment and or maintenance of cell polarity	CG2671	FBgn0002121	lethal (2) giant larvae	1.62E-02	69	4	5.8%
GO:0007163 establishment and or maintenance of cell polarity	CG6667	FBgn0000462	dorsal	1.62E-02	69	4	5.8%
GO:0007219 Notch signaling pathway	CG2534	FBgn0000340	canoe	1.63E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG2671	FBgn0002121	lethal (2) giant larvae	1.63E-02	38	3	7.9%
GO:0007219 Notch signaling pathway	CG6667	FBgn0000462	dorsal	1.63E-02	38	3	7.9%
GO:0001736 establishment of planar polarity	CG17579	FBgn0003326	scabrous	1.87E-02	40	3	7.5%
GO:0001736 establishment of planar polarity	CG2534	FBgn0000340	canoe	1.87E-02	40	3	7.5%
GO:0001736 establishment of planar polarity	CG6667	FBgn0000462	dorsal	1.87E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG17579	FBgn0003326	scabrous	1.87E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG2534	FBgn0000340	canoe	1.87E-02	40	3	7.5%
GO:0007164 establishment of tissue polarity	CG6667	FBgn0000462	dorsal	1.87E-02	40	3	7.5%
GO:0006406 mRNA-nucleus export	CG12752	FBgn0028411	NTF2-related export protein 1	2.10E-02	16	2	12.5%
GO:0006406 mRNA-nucleus export	CG7269	FBgn0014189	Helicase at 25E	2.10E-02	16	2	12.5%
GO:0051028 mRNA transport	CG12752	FBgn0028411	NTF2-related export protein 1	2.10E-02	16	2	12.5%
GO:0051028 mRNA transport	CG7269	FBgn0014189	Helicase at 25E	2.10E-02	16	2	12.5%
GO:0016458 gene silencing	CG10279	FBgn0003261	Rm62	2.26E-02	43	3	7.0%
GO:0016458 gene silencing	CG17743	FBgn0002521	pleiohomeotic	2.26E-02	43	3	7.0%
GO:0016458 gene silencing	CG3041	FBgn0015270	Origin recognition complex subunit 2	2.26E-02	43	3	7.0%
GO:0009069 serine family amino acid metabolism	CG6287	FBgn0032350		2.35E-02	17	2	11.8%
GO:0009069 serine family amino acid metabolism	CG8553	FBgn0020615	selenide,water dikinase	2.35E-02	17	2	11.8%
GO:0009968 negative regulation of signal transduction	CG2671	FBgn0002121	lethal (2) giant larvae	2.70E-02	46	3	6.5%
GO:0009968 negative regulation of signal transduction	CG3412	FBgn0023423	supernumerary limbs	2.70E-02	46	3	6.5%
GO:0009968 negative regulation of signal transduction	CG9484	FBgn0002431	hyperplastic discs	2.70E-02	46	3	6.5%
GO:0007422 peripheral nervous system development	CG17579	FBgn0003326	scabrous	2.74E-02	120	5	4.2%
GO:0007422 peripheral nervous system development	CG2671	FBgn0002121	lethal (2) giant larvae	2.74E-02	120	5	4.2%
GO:0007422 peripheral nervous system development	CG3172	FBgn0038206	twinfilin	2.74E-02	120	5	4.2%
GO:0007422 peripheral nervous system development	CG3758	FBgn0001981	escargot	2.74E-02	120	5	4.2%
GO:0007422 peripheral nervous system development	CG6667	FBgn0000462	dorsal	2.74E-02	120	5	4.2%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG1070	FBgn0037471		3.09E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG14216	FBgn0031054		3.09E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG17358	FBgn0011290	TBP-associated factor 12	3.09E-02	84	4	4.8%
GO:0006367 transcription initiation from RNA polymerase II promoter	CG8491	FBgn0001324	kohtalo	3.09E-02	84	4	4.8%

GO:0006405 RNA-nucleus export	CG12752	FBgn0028411	NTF2-related export protein 1	3.20E-02	20	2	10.0%
GO:0006405 RNA-nucleus export	CG7269	FBgn0014189	Helicase at 25E	3.20E-02	20	2	10.0%
GO:0006352 transcription initiation	CG1070	FBgn0037471		3.33E-02	86	4	4.7%
GO:0006352 transcription initiation	CG14216	FBgn0031054		3.33E-02	86	4	4.7%
GO:0006352 transcription initiation	CG17358	FBgn0011290	TBP-associated factor 12	3.33E-02	86	4	4.7%
GO:0006352 transcription initiation	CG8491	FBgn0001324	kohtalo	3.33E-02	86	4	4.7%
GO:0008407 bristle morphogenesis	CG17579	FBgn0003326	scabrous	3.50E-02	21	2	9.5%
GO:0008407 bristle morphogenesis	CG3172	FBgn0038206	twinfilin	3.50E-02	21	2	9.5%
GO:0009966 regulation of signal transduction	CG2534	FBgn0000340	canoe	4.11E-02	92	4	4.3%
GO:0009966 regulation of signal transduction	CG2671	FBgn0002121	lethal (2) giant larvae	4.11E-02	92	4	4.3%
GO:0009966 regulation of signal transduction	CG3412	FBgn0023423	supernumerary limbs	4.11E-02	92	4	4.3%
GO:0009966 regulation of signal transduction	CG9484	FBgn0002431	hyperplastic discs	4.11E-02	92	4	4.3%
GO:0007224 smoothened signaling pathway	CG3412	FBgn0023423	supernumerary limbs	4.15E-02	23	2	8.7%
GO:0007224 smoothened signaling pathway	CG9484	FBgn0002431	hyperplastic discs	4.15E-02	23	2	8.7%
GO:0050657 nucleic acid transport	CG12752	FBgn0028411	NTF2-related export protein 1	4.15E-02	23	2	8.7%
GO:0050657 nucleic acid transport	CG7269	FBgn0014189	Helicase at 25E	4.15E-02	23	2	8.7%
GO:0050658 RNA transport	CG12752	FBgn0028411	NTF2-related export protein 1	4.15E-02	23	2	8.7%
GO:0050658 RNA transport	CG7269	FBgn0014189	Helicase at 25E	4.15E-02	23	2	8.7%
GO:0051236 establishment of RNA localization	CG12752	FBgn0028411	NTF2-related export protein 1	4.15E-02	23	2	8.7%
GO:0051236 establishment of RNA localization	CG7269	FBgn0014189	Helicase at 25E	4.15E-02	23	2	8.7%
GO:0051049 regulation of transport	CG3204	FBgn0025806	Ras-associated protein 2-like	4.26E-02	55	3	5.5%
GO:0051049 regulation of transport	CG3412	FBgn0023423	supernumerary limbs	4.26E-02	55	3	5.5%
GO:0051049 regulation of transport	CG9994	FBgn0032782		4.26E-02	55	3	5.5%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG2671	FBgn0002121	lethal (2) giant larvae	4.48E-02	24	2	8.3%
GO:0007179 transforming growth factor beta receptor signaling pathway	CG3412	FBgn0023423	supernumerary limbs	4.48E-02	24	2	8.3%
GO:0030162 regulation of proteolysis and peptidolysis	CG3412	FBgn0023423	supernumerary limbs	4.48E-02	24	2	8.3%
GO:0030162 regulation of proteolysis and peptidolysis	CG9484	FBgn0002431	hyperplastic discs	4.48E-02	24	2	8.3%
GO:0006790 sulfur metabolism	CG12032	NA	NA	4.66E-02	57	3	5.3%
GO:0006790 sulfur metabolism	CG5554	FBgn0034914		4.66E-02	57	3	5.3%
GO:0006790 sulfur metabolism	CG8553	FBgn0020615	selenide,water dikinase	4.66E-02	57	3	5.3%
GO:0042127 regulation of cell proliferation	CG2671	FBgn0002121	lethal (2) giant larvae	4.83E-02	25	2	8.0%
GO:0042127 regulation of cell proliferation	CG9484	FBgn0002431	hyperplastic discs	4.83E-02	25	2	8.0%
GO:0051168 nuclear export	CG12752	FBgn0028411	NTF2-related export protein 1	4.83E-02	25	2	8.0%
GO:0051168 nuclear export	CG7269	FBgn0014189	Helicase at 25E	4.83E-02	25	2	8.0%

Gut-specific age-related GO terms in Cluster 5

Gut-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:0006816 calcium ion transport	CG4536	FBgn0029904		1.99E-02	28	2	7.1%
GO:0006816 calcium ion transport	CG6320	FBgn0015608	Ca[2+]-channel-protein-beta-subunit	1.99E-02	28	2	7.1%
GO:0006916 anti-apoptosis	CG4859	FBgn0035049	Matrix metalloproteinase 1	3.18E-02	36	2	5.6%
GO:0006916 anti-apoptosis	CG7901	NA	NA	3.18E-02	36	2	5.6%
GO:0015674 di- tri-valent inorganic cation transport	CG4536	FBgn0029904		3.52E-02	38	2	5.3%
GO:0015674 di- tri-valent inorganic cation transport	CG6320	FBgn0015608	Ca[2+]-channel-protein-beta-subunit	3.52E-02	38	2	5.3%
GO:0043066 negative regulation of apoptosis	CG4859	FBgn0035049	Matrix metalloproteinase 1	3.52E-02	38	2	5.3%
GO:0043066 negative regulation of apoptosis	CG7901	NA	NA	3.52E-02	38	2	5.3%
GO:0043069 negative regulation of programmed cell death	CG4859	FBgn0035049	Matrix metalloproteinase 1	3.52E-02	38	2	5.3%
GO:0043069 negative regulation of programmed cell death	CG7901	NA	NA	3.52E-02	38	2	5.3%
GO:0009416 response to light	CG18158	NA	NA	4.04E-02	41	2	4.9%
GO:0009416 response to light	CG8770	FBgn0004623	G protein beta-subunit 76C	4.04E-02	41	2	4.9%
GO:0009314 response to radiation	CG18158	NA	NA	4.78E-02	45	2	4.4%
GO:0009314 response to radiation	CG8770	FBgn0004623	G protein beta-subunit 76C	4.78E-02	45	2	4.4%
GO:0042981 regulation of apoptosis	CG11861	FBgn0001980	guftagu	4.61E-02	103	3	2.9%
GO:0042981 regulation of apoptosis	CG4859	FBgn0035049	Matrix metalloproteinase 1	4.61E-02	103	3	2.9%
GO:0042981 regulation of apoptosis	CG7901	NA	NA	4.61E-02	103	3	2.9%