

Table S4**Genes preferentially expressed in regenerating cells**

CG #	Synonym	median (log2)	p-value	Molecular Function
CG4250	CG4250	-6.03	3.00E-04	/
CG13053	CG13053	-4.40	4.80E-03	/
CG10112	CG10112	-4.39	6.00E-05	/
CG8846	Thor, Phas1	-3.95	5.00E-04	eukaryotic initiation factor 4E binding; ; GO:0008190; ; ; GO:0008190; ; ; GO:0008190; ; ; GO:0008190
CG15212	CG15212	-3.77	1.50E-03	/
CG1148	Osi2	-3.30	6.90E-03	/
CG9812	CG9812	-3.08	1.00E-04	/
CG15532	hdc	-2.87	1.39E-02	cell differentiation; GO:0030154; negative regulation of terminal cell fate specification; GO:0035155; terminal branching of trachea, cytoplasmic projection extension (sensu Insecta); GO:0007430; tracheal branch fusion; GO:0035147; tracheal system development (sensu Insecta); GO:0007424
CG10131	CG10131	-2.72	2.48E-02	structural molecule activity; ; GO:0005198; oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.- ; ; GO:0005198 ; ; GO:0016491 ; EC:1.-.-.-
CG3752	CG3752	-2.62	8.70E-03	aldehyde dehydrogenase (NAD) activity; ; GO:0004029 ; EC:1.2.1.3; ; ; GO:0004029 ; EC:1.2.1.3; ; ; GO:0004029 ; EC:1.2.1.3
CG1803	regucalcin	-2.59	6.00E-03	anterior/posterior axis specification; ; GO:0009948; calcium-mediated signaling; ; GO:0019722,
CG3699	CG3699	-2.41	8.80E-03	oxidoreductase activity, acting on CH-OH group of donors; ; GO:0016614 ; EC:1.1.-.-.- ; ; GO:0016614 ; EC:1.1.-.-.-
CG5575	ken	-2.37	2.00E-03	nucleic acid binding; ; GO:0003676; transcription factor activity; ; GO:0003700; ; ; GO:0003676; ; ; GO:0003700; protein binding; ; GO:0005515; ; ; GO:0005515
CG4822	CG4822	-2.26	3.36E-02	anion channel activity; ; GO:0005253; ATPase activity, coupled to transmembrane movement of substances; ; GO:0042626; ; ; GO:0005253; transporter activity; ; GO:0005215; ; ; GO:0042626; ; ; GO:0005
CG4145	Cg25C	-2.24	1.61E-02	structural molecule activity; ; GO:0005198; extracellular matrix structural constituent; ; GO:0005201; ; ; GO:0005198; ; ; GO:0005201
CG1102	CG1102	-2.12	1.77E-02	trypsin activity; GO:0004295 ; EC:3.4.21.4; monophenol monooxygenase activator activity; GO:0008439; serine-type endopeptidase activity; GO:0004252 ; EC:3.4.21.-; ; GO:0004252 ; EC:3.4.
CG2150	CG2150	-2.01	5.00E-02	/
CG1762	betaInt-nu	-1.94	3.97E-02	receptor activity; ; GO:0004872; ; ; GO:0004872; cell adhesion molecule binding; ; GO:0050839; ; ; GO:0050839; ; ; GO:0004872; ; ; GO:0050839
CG8788	CG8788	-1.92	9.70E-03	/
ND3	ND3	-1.89	3.42E-02	NADH dehydrogenase subunit 3, mitochondrial NADH-ubiquinone oxidoreductase chain 3 , abbreviated as mt:ND3
CG6899	Ptp4E	-1.81	2.40E-03	protein tyrosine phosphatase activity; ; GO:0004725 ; EC:3.1.3.48; transmembrane receptor protein tyrosine phosphatase activity; ; GO:0005001; ; ; GO:0004725 ; EC:3.1.3.48; ; ; GO:0005001
CG17245	plexB	-1.81	4.00E-04	semaphorin receptor activity; ; GO:0017154; transmembrane receptor protein tyrosine kinase activity; ; GO:0004714 ; EC:2.7.1.-; ; ; GO:0004714 ; EC:2.7.1.-; ; ; GO:0017154
CG11784	CG11784	-1.79	2.60E-03	glutathione transferase activity; ; GO:0004364 ; EC:2.5.1.18; ; ; GO:0004364 ;

				EC:2.5.1.18
CG1368	CG1368	-1.78	4.10E-03	structural constituent of chorion (sensu Insecta); ; GO:0005213; ; ; GO:0005213
CG17299	SNF4Agamma	-1.77	1.28E-02	receptor signaling protein serine/threonine kinase activity; GO:0004702 ; EC:2.7.1.-; protein serine/threonine kinase activity; GO:0004674; ; GO:0004674; ; GO:0004702 ; EC:2.7.1.-; AMP-
CG4686	CG4686	-1.75	2.50E-03	/
CG10211	CG10211	-1.72	1.09E-02	peroxidase activity; ; GO:0004601 ; EC:1.11.1.7; ; ; GO:0004601 ; EC:1.11.1.7
CG8245	CG8245	-1.71	1.27E-02	/
CG4807	ab, abrupt	-1.70	3.60E-03	specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704
CG9358	Phk-3	-1.70	2.19E-02	diacylglycerol binding; ; GO:0019992; ; ; GO:0019992; protein serine/threonine kinase activity; ; GO:0004674; ; ; GO:0004674; protein kinase activity; ; GO:0004672 ; EC:2.7.1.37; carrier activity
CG8066	CG8066	-1.68	2.50E-02	cysteine protease inhibitor activity; GO:0004869; ; GO:0004869
CG3629	DII	-1.67	7.60E-03	specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704
CG8727	cyc	-1.65	3.45E-02	specific RNA polymerase II transcription factor activity; GO:0003704; RNA polymerase II transcription factor activity; GO:0003702; ; GO:0003702; ; GO:0003704
CG12822	CG12822	-1.64	1.32E-02	/
CG9689	CG9689	-1.61	8.20E-03	/
CG18507	CG18507	-1.58	1.05E-02	/
CG5677	CG5677	-1.56	2.64E-02	signal peptidase activity; GO:0009003; ; GO:0009003; ; GO:0009003
CG7267	CG7267	-1.55	1.05E-02	/
CG7724	CG7724	-1.55	2.45E-02	oxidoreductase activity, acting on CH-OH group of donors; ; GO:0016614 ; EC:1.1.1.-; ; ; GO:0016614 ; EC:1.1.1.-
CG15611	CG15611	-1.52	9.60E-03	/
CG6191	CG6191	-1.52	1.96E-02	/
CG5518	sda	-1.52	3.00E-04	membrane alanine aminopeptidase activity; GO:0004179 ; EC:3.4.11.2; ; GO:0004179 ; EC:3.4.11.2
CG3831	CG3831	-1.49	2.13E-02	/
CG6357	CG6357	-1.47	1.20E-03	cathepsin L activity; ; GO:0004217 ; EC:3.4.22.15; ; ; GO:0004217 ; EC:3.4.22.15
CG6247	CG32549 = new ID in v4, CG6247	-1.47	1.42E-02	CG32549, 5'-nucleotidase activity; GO:0008253 ; EC:3.1.3.5; ; GO:0008253 ; EC:3.1.3.5
CG2062	Cyp4e1	-1.44	1.71E-02	electron transporter activity; ; GO:0005489; ; ; GO:0005489; oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0005489
CG4778	CG4778	-1.43	8.30E-03	structural constituent of peritrophic membrane (sensu Insecta); ; GO:0016490; ; ; GO:0016490
CG4382	CG4382	-1.42	9.90E-03	carboxylesterase activity; ; GO:0004091 ; EC:3.1.1.1; ; ; GO:0004091 ; EC:3.1.1.1
CG8790	CG8790	-1.42	4.40E-03	carrier activity; GO:0005386; dicarboxylic acid transporter activity; GO:0005310; ; GO:0005386; ; GO:0005310
CG13044	CG13044	-1.41	4.00E-04	/
CG3704	CG3704	-1.41	2.48E-02	purine nucleotide binding; ; GO:0017076; ; ; GO:0017076
CG10126	CG10126	-1.40	2.61E-02	calcium ion binding; GO:0005509; ; GO:0005509
CG10916	CG10916	-1.39	4.90E-03	/

CG13430	CG13430	-1.38	1.81E-02	trypsin activity; ; GO:0004295 ; EC:3.4.21.4; ; ; GO:0004295 ; EC:3.4.21.4; ; ; GO:0004295 ; EC:3.4.21.4
CG9338	CG9338	-1.36	4.30E-02	/
CG17035	GXIVsPLA2	-1.35	4.90E-02	phospholipase A2 activity; ; GO:0004623 ; EC:3.1.1.4; ; ; GO:0004623 ; EC:3.1.1.4
CG7860	CG7860	-1.34	9.40E-03	asparaginase activity; ; GO:0004067 ; EC:3.5.1.1; ; ; GO:0004067 ; EC:3.5.1.1
CG14812	CG14812	-1.33	1.97E-02	/
CG6667	dl	-1.32	2.85E-02	DNA binding; ; GO:0003677; ; ; GO:0003677; transcription factor activity; ; GO:0003700; transcriptional activator activity; ; GO:0016563; RNA polymerase II transcription factor activity; ; GO:000
CG12164	CG12164	-1.31	4.16E-02	/
CG1572	CG1572	-1.29	2.25E-02	/
CG11143	Inos	-1.27	4.60E-03	inositol-3-phosphate synthase activity; ; GO:0004512 ; EC:5.5.1.4; ; ; GO:0004512 ; EC:5.5.1.4; ; phosphorus-oxygen lyase activity; ; GO:0016849 ; EC:4.6.-.-; ; ; GO:00
CG4592	CG4592	-1.26	2.44E-02	hydro-lyase activity; ; GO:0016836 ; EC:4.2.1.-; ; ; GO:0016836 ; EC:4.2.1.-; dodecenoyl-CoA delta-isomerase activity; ; GO:0004165 ; EC:5.3.3.8; ; ; GO:0004165 ; EC:5.3.3.8
CG9134	CG9134	-1.25	1.52E-02	sugar binding; ; GO:0005529; ; ; GO:0005529
CG10119	LamC	-1.24	4.87E-02	structural constituent of cytoskeleton; ; GO:0005200; ; ; GO:0005200
CG8289	CG8289	-1.24	1.90E-03	/
CG3712	mRpL33	-1.23	4.54E-02	structural constituent of ribosome; ; GO:0003735; ; ; GO:0003735
CG4380	usp	-1.19	4.10E-02	DNA binding; ; GO:0003677; juvenile hormone binding; ; GO:0005500; ; ; GO:0003677; ecdysteroid hormone receptor activity; ; GO:0004884; ; ; GO:0004884; ligand-dependent nuclear receptor activity;
CG4096	CG4096	-1.18	3.12E-02	metalloendopeptidase activity; ; GO:0004222 ; EC:3.4.24.-; ; ; GO:0004222 ; EC:3.4.24.-
CG10071	RpL29	-1.18	2.99E-02	structural constituent of ribosome; ; GO:0003735; ; ; GO:0003735; ; ; GO:0003735; ; ; GO:0003735
CG12023	GV1	-1.18	2.88E-02	/
CG1516	CG1516	-1.18	2.33E-02	pyruvate carboxylase activity; ; GO:0004736 ; EC:6.4.1.1; ; ; GO:0004736 ; EC:6.4.1.1; ; ; GO:0004736 ; EC:6.4.1.1
CG11077	CG11077	-1.16	1.20E-03	development; ; GO:0007275
CG7224	CG7224	-1.16	4.58E-02	/
ND4	ND4	-1.14	3.60E-02	NADH dehydrogenase subunit 4, mitochondrial NADH-ubiquinone oxidoreductase chain 4 , abbreviated as mt:ND4
COX3	COX3	-1.14	4.90E-02	mitochondrial Cytochrome c oxidase subunit III , abbreviated as mt:CoIII
CG7291	NPC2	-1.12	4.50E-02	receptor binding; ; GO:0005102; ; ; GO:0005102
CG1402	CG1402	-1.12	1.25E-02	carbonate dehydratase activity; GO:0004089 ; EC:4.2.1.1; ; ; GO:0004089 ; EC:4.2.1.1
CG9535	CG9535	-1.11	4.58E-02	UDP-N-acetylglucosamine diphosphorylase activity; ; GO:0003977 ; EC:2.7.7.23; ; ; GO:0003977 ; EC:2.7.7.23
CG13660	CG31370 = new ID in v4, CG13660	-1.10	1.66E-02	CG31370
CG11207	feo	-1.10	3.53E-02	receptor binding; GO:0005102; ; ; GO:0005102
CG9704	Nrt	-1.07	2.10E-03	cell adhesion; ; GO:0007155; ectoderm development; ; GO:0007398; neurogenesis; ; GO:0007399, amine receptor activity; ; GO:0008227; octopamine receptor activity; ; GO:0004989; ; ; GO:0008227; ; ; GO:0004989
CG12340	CG12340	-1.07	4.89E-02	/
CG11141	CG11141	-1.06	1.15E-02	/

CG17033	CG17033	-1.06	6.40E-03	/
CG6999	CG6999	-1.06	4.09E-02	/
CG1827	CG1827	-1.05	3.70E-03	N4-(beta-N-acetylglucosaminy)-L-asparaginase activity; ; GO:0003948 ; EC:3.5.1.26; ; ; GO:0003948 ; EC:3.5.1.26
CG11562	CG11562	-1.04	1.23E-02	/
CG4860	CG4860	-1.04	1.00E-03	acyl-CoA dehydrogenase activity; GO:0003995 ; EC:1.3.99.3; ; GO:0003995 ; EC:1.3.99.3
CG12238	l(1)G0084	-1.03	3.00E-02	/
CG3937	cher	-1.02	6.50E-03	actin binding; GO:0003779; ; GO:0003779; ; GO:0003779; structural constituent of cytoskeleton; GO:0005200; ; GO:0005200; ; GO:0003779
CG18657	NetA	-1.02	4.66E-02	structural molecule activity; ; GO:0005198; ; ; GO:0005198
CG6575	glec	-1.02	1.50E-03	carbohydrate binding; GO:0030246; ; GO:0030246; ; GO:0030246
CG6073	CG6073	-1.01	1.75E-02	/
CG8980	NiPp1	-1.00	4.69E-02	RNA binding; ; GO:0003723; ; ; GO:0003723; protein phosphatase inhibitor activity; ; GO:0004864; ; ; GO:0004864; ; ; GO:0004864; type 1 serine/threonine specific protein phosphatase inhibitor act
CG15802	not found in v4, CG15802	-1.00	4.60E-03	RNA polymerase II transcription factor, ; GO:0003702
CG5753	stau	-0.99	4.20E-03	RNA binding; ; GO:0003723; double-stranded RNA binding; ; GO:0003725; ; ; GO:0003723; microtubule binding; ; GO:0008017; ; ; GO:0008017; ; ; GO:0003725; ; ; GO:0008017; ; ; GO:0003725; mRNA 3'-UTR bind
CG5571	CG5571	-0.99	6.10E-03	/
CG17059	CG17059	-0.99	1.09E-02	/
CG4260	alpha-Adaptin	-0.99	4.70E-03	asymmetric cytokinesis; ; GO:0008356; neurotransmitter secretion; ; GO:0007269; synaptic vesicle coating; ; GO:0016183; synaptic vesicle transport; ; GO:0048489; vesicle coating; ; GO:0006901; vesicle-mediated transport; ; GO:0016192
CG12874	CG12874	-0.99	3.69E-02	/
CG6695	CG6695	-0.98	1.20E-03	RNA binding; GO:0003723; ; GO:0003723
CG5887	desat1	-0.98	3.75E-02	stearoyl-CoA 9-desaturase activity; GO:0004768 ; EC:1.14.19.1; ; GO:0004768 ; EC:1.14.19.1; ; GO:0004768 ; EC:1.14.19.1
CG11025	isopeptidase-T-3	-0.97	1.69E-02	ubiquitin thiolesterase activity; ; GO:0004221 ; EC:3.1.2.15; ; ; GO:0004221 ; EC:3.1.2.15
CG8430	Got1	-0.96	1.87E-02	aspartate transaminase activity; ; GO:0004069 ; EC:2.6.1.1; ; ; GO:0004069 ; EC:2.6.1.1; ; ; GO:0004069 ; EC:2.6.1.1; ; ; GO:0004069 ; EC:2.6.1.1
CG12840	Tsp42E1	-0.96	3.80E-02	receptor signaling protein activity; ; GO:0005057; ; ; GO:0005057
CG10863	CG10863	-0.96	2.75E-02	aldehyde reductase activity; ; GO:0004032 ; EC:1.1.1.21; ; ; GO:0004032 ; EC:1.1.1.21
CG6528	not found in v4, CG6528	-0.95	6.00E-04	#N/A
CG3523	CG3523	-0.95	4.83E-02	fatty-acid synthase activity; ; GO:0004312 ; EC:2.3.1.85; ; ; GO:0004312 ; EC:2.3.1.85
CG10800	Rca1	-0.94	7.20E-03	eye-antennal disc metamorphosis; ; GO:0007455; regulation of mitosis; ; GO:0007088, structural constituent of cytoskeleton; ; GO:0005200; ; ; GO:0005200
CG4698	Wnt4	-0.94	8.30E-03	receptor binding; ; GO:0005102; ; ; GO:0005102; signal transducer activity; ; GO:0004871; ; ; GO:0004871; ; ; GO:0005102; ; ; GO:0004871
CG4118	nxf2	-0.93	1.58E-02	mRNA-nucleus export; ; GO:0006406, transporter activity; ; GO:0005215; ; ; GO:0005215; ; ; GO:0005215
CG6117	Pka-C3	-0.93	1.36E-02	receptor signaling protein serine/threonine kinase activity; ; GO:0004702 ; EC:2.7.1.-; ; protein serine/threonine kinase activity; ; GO:0004674; cAMP-

				dependent protein kinase activity; ; GO:00
CG6673	CG6673	-0.93	2.24E-02	glutathione transferase activity; ; GO:0004364 ; EC:2.5.1.18; ; ; GO:0004364 ; EC:2.5.1.18
CG6494	h	-0.93	2.93E-02	specific transcriptional repressor activity; ; GO:0016566; general transcriptional repressor activity; ; GO:0016565; specific RNA polymerase II transcription factor activity; ; GO:0003704; ;
CG2948	rev7	-0.91	2.19E-02	ephrin receptor binding; GO:0046875; ; GO:0046875
CG12299	CG12299	-0.91	1.20E-03	transcription regulator activity; ; GO:0030528; ; ; GO:0030528
CG5576	imd	-0.91	2.42E-02	antibacterial humoral response (sensu Protostomia); ; GO:0006961; antibacterial polypeptide induction; ; GO:0006963; antimicrobial humoral response (sensu Protostomia); ; GO:0006960; defense response; ; GO:0006952; defense response to Gram-negative bacteria; ; GO:0050829; defense response to bacteria; ; GO:0042742; humoral immune response; ; GO:0006959; immune response; ; GO:0006955; response to bacteria; ; GO:0009617; signal transduction; ; GO:0007165
CG9914	CG9914	-0.90	4.18E-02	structural molecule activity; ; GO:0005198; oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0005198; ; ; GO:0016491 ; EC:1.-.-.-
CG6454	CG6454	-0.90	4.91E-02	/
CG1618	comt	-0.89	8.90E-03	ATPase activity; ; GO:0016887; ; ; GO:0016887
CG3359	mfas	-0.89	1.10E-03	axonogenesis; GO:0007409; cell-cell adhesion; GO:0016337; ectoderm development; GO:0007398; signal transduction; GO:0007165
CG17725	Pepck	-0.89	1.65E-02	phosphoenolpyruvate carboxykinase (GTP) activity; ; GO:0004613 ; EC:4.1.1.32; ; ; GO:0004613 ; EC:4.1.1.32; ; ; GO:0004613 ; EC:4.1.1.32
CG17967	DebA	-0.88	1.37E-02	/
CG18343	CG18343	-0.88	4.40E-03	/
CG4210	CG4210	-0.87	1.29E-02	/
CG9438	Cyp6a2	-0.87	1.59E-02	electron transporter activity; ; GO:0005489; ; ; GO:0005489; oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0005489
CG9091	RpL37a	-0.87	2.80E-02	nucleic acid binding; ; GO:0003676; structural constituent of ribosome; ; GO:0003735; ; ; GO:0003735; ; ; GO:0003676; ; ; GO:0003735
CG5025	Sps2	-0.85	4.96E-02	selenide, water dikinase activity; ; GO:0004756 ; EC:2.7.9.3; ; ; ; GO:0004756 ; EC:2.7.9.3; ; ; GO:0004756 ; EC:2.7.9.3; purine nucleotide binding; ; GO:0017076; ; ; GO:0017076; ; ; GO:0004756 ; EC:
CG1093	plx	-0.85	4.28E-02	small GTPase regulatory/interacting protein activity; GO:0005083; ; GO:0005083