

Table S3

Genes preferentially expressed in dorsal or ventral cell populations of wildtype and Wg over-expressing leg discs

D(wt)				
CG#	Synonym	median (log2)	p-value	Function
CG13067	CG13067	-3.23	4.66E-02	/
CG8827	Ance	-2.97	5.27E-03	zinc ion binding; ; GO:0008270; peptidyl-dipeptidase activity; ; GO:0008241 ; EC:3.4.15.-; ; GO:0008241 ; EC:3.4.15.-; peptidyl-dipeptidase A activity; ; GO:0004246 ; EC:3.4.15.1; ; GO:000424
CG4766	CG4766	-2.68	3.20E-02	/
CG18111	Obp99a	-2.63	1.90E-02	odorant binding, ; GO:0005549
CG5133	Doc1	-2.36	1.22E-02	transcription factor activity; ; GO:0003700; ; GO:0003700
CG16820	CG16820	-2.07	1.93E-02	/
CG10625	CG10625	-1.83	5.22E-03	/
CG15101	Jheh1	-1.78	7.53E-03	juvenile hormone epoxide hydrolase activity; ; GO:0008096 ; EC:3.3.2.-; ; GO:0008096 ; EC:3.3.2.-; epoxide hydrolase activity; ; GO:0004301 ; EC:3.3.2.3; ; GO:0004301 ; EC:3.3.2.3; ; GO:000
CG3935	al	-1.77	1.44E-02	specific RNA polymerase II transcription factor activity; ; GO:0003704; transcription factor activity; ; GO:0003700; ; GO:0003700; ; GO:0003704
CG5160	CG5160	-1.73	3.67E-02	GTPase activity; ; GO:0003924; ; GO:0003924
CG8333	HLHmgamma	-1.62	1.54E-02	DNA binding; GO:0003677; ; GO:0003677; transcription factor activity; GO:0003700; specific transcriptional repressor activity; GO:0016566; ; GO:0003700; ; GO:0003700; ; GO:0016566
CG1650	unpg	-1.59	4.25E-02	RNA polymerase II transcription factor activity; ; GO:0003702; ; GO:0003702
CG6906	CG6906	-1.50	2.84E-02	carbonate dehydratase activity; ; GO:0004089 ; EC:4.2.1.1; ; GO:0004089 ; EC:4.2.1.1
CG15611	CG15611	-1.49	2.10E-02	/
CG17914	yellow-b	-1.49	4.94E-02	/
CG1698	CG1698	-1.42	4.71E-02	potassium:amino acid transporter activity; ; GO:0017032; cation transporter activity; ; GO:0008324; ; GO:0008324; ; GO:0017032
CG5093	Doc3	-1.41	3.79E-03	transcription factor activity; ; GO:0003700; ; GO:0003700
CG17348	drl	-1.39	2.70E-02	transmembrane receptor protein tyrosine kinase activity; ; GO:0004714 ; EC:2.7.1.-; ; GO:0004714 ; EC:2.7.1.-; protein-tyrosine kinase activity; ; GO:0004713 ; EC:2.7.1.112; ; GO:0004713 ;
CG17045	yellow-e3	-1.37	2.11E-03	/
CG3244	CG3244	-1.36	1.91E-02	/
CG9656	grn	-1.34	3.11E-02	RNA polymerase II transcription factor activity; GO:0003702; general RNA polymerase II transcription factor activity; GO:0016251; ; GO:0003702; ; GO:0016251; ; GO:0016251
CG4914	CG4914	-1.29	2.54E-03	trypsin activity; ; GO:0004295 ; EC:3.4.21.4; serine-type endopeptidase activity; ; GO:0004252 ; EC:3.4.21.-; ; GO:0004295 ; EC:3.4.21.4; ; GO:0004252 ; EC:3.4.21.-
CG10119	LamC	-1.24	2.28E-02	structural constituent of cytoskeleton; ; GO:0005200; ; GO:0005200
CG12287	pdm2	-1.11	4.50E-02	DNA binding; ; GO:0003677; ; GO:0003677; specific RNA polymerase II transcription factor activity; ; GO:0003704; ; GO:0003704; ; GO:0003704
CG9885	dpp	-1.10	1.12E-02	signal transducer activity; ; GO:0004871; morphogen activity; ; GO:0016015; ; GO:0016015; transforming growth factor beta receptor binding; ; GO:0005160; ; GO:0005160; ; GO:0016015; ; GO:0004
CG4746	mab-2	-1.09	3.95E-02	encodes Mab-21, involved in cell fate determination
CG10200	CG10200	-1.07	2.84E-03	/

CG12840	Tsp42EI	-1.07	2.57E-02	receptor signaling protein activity; ; GO:0005057; ; GO:0005057
CG8483	CG8483	-1.06	2.01E-02	defense response; GO:0006952
CG9593	CG9593	-1.03	7.28E-03	receptor binding; GO:0005102; ; GO:0005102
CG6868	tld	-1.02	1.24E-02	procollagen C-endopeptidase activity; GO:0017026 ; EC:3.4.24.19; metalloendopeptidase activity; GO:0004222 ; EC:3.4.24.-; ; GO:0017026 ; EC:3.4.24.19; ; GO:0004222 ; EC:3.4.24.-
CG5912	arr	-1.00	3.23E-02	low-density lipoprotein receptor activity; ; GO:0005041; ; ; GO:0005041; ; ; GO:0005041; ; ; GO:0005041
CG2125	ci	-0.97	2.15E-02	specific RNA polymerase II transcription factor activity; ; GO:0003704; transcription factor activity; ; GO:0003700; transcriptional activator activity; ; GO:0016563; transcriptional represso
CG17559	dnt	-0.96	1.06E-02	protein-tyrosine kinase activity; ; GO:0004713 ; EC:2.7.1.112; ; ; GO:0004713 ; EC:2.7.1.112; transmembrane receptor protein tyrosine kinase activity; ; GO:0004714 ; EC:2.7.1.-; ; ; GO:0004714
CG14843	CG14843	-0.96	1.32E-02	/
CG17058	Peritrophin-A	-0.95	2.24E-02	chitin binding; ; GO:0008061; ; ; GO:0008061; structural constituent of peritrophic membrane (sensu Insecta); ; GO:0016490; ; ; GO:0016490
CG7722	CG7722	-0.92	3.61E-03	serine-type endopeptidase inhibitor activity; ; GO:0004867; ; ; GO:0004867
CG7860	CG7860	-0.90	4.58E-02	asparaginase activity; ; GO:0004067 ; EC:3.5.1.1; ; ; GO:0004067 ; EC:3.5.1.1
CG14946	CG14946	-0.86	2.20E-03	oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0016491 ; EC:1.-.-.-
CG15905	CG15905	-0.86	2.21E-02	/

D(wg)

CG#	Synonym	median (log2)	p-value	Function
CG7539	Edg91	-3.03	3.18E-02	structural constituent of pupal cuticle (sensu Insecta); GO:0008011; ; GO:0008011
CG7892	nmo	-1.65	4.14E-02	protein serine/threonine kinase activity; ; GO:0004674; receptor signaling protein serine/threonine kinase activity; ; GO:0004702 ; EC:2.7.1.-; ; ; GO:0004674; ; ; GO:0004674; ; ; GO:0004674; ; G
CG14598	CG14598	-1.63	4.54E-03	/
CG6906	CG6906	-1.37	1.23E-02	carbonate dehydratase activity; ; GO:0004089 ; EC:4.2.1.1; ; ; GO:0004089 ; EC:4.2.1.1
CG8846	Thor	-1.24	3.11E-03	eukaryotic initiation factor 4E binding; ; GO:0008190; ; ; GO:0008190; ; ; GO:0008190; ; ; GO:0008190
CG1956	R	-1.23	4.42E-02	GTP binding; ; GO:0005525; ; ; GO:0005525; GDP binding; ; GO:0019003; GTPase activity; ; GO:0003924; ; ; GO:0019003; ; ; GO:0003924
CG9425	CG9425	-1.16	3.63E-02	nucleic acid binding; ; GO:0003676; ; ; GO:0003676; DNA helicase activity; ; GO:0003678; helicase activity; ; GO:0004386; ; ; GO:0004386; ; ; GO:0003678
CG13679	CG13679	-1.11	1.24E-02	/
CG1691	Imp	-1.10	1.13E-02	mRNA binding; GO:0003729; ; GO:0003729; ; GO:0003729
CG15629	CG15629	-1.05	3.19E-02	oxidoreductase activity; ; GO:0016491 ; EC:1.-.-.-; ; ; GO:0016491 ; EC:1.-.-.-
CG3935	al	-1.02	3.68E-02	specific RNA polymerase II transcription factor activity; ; GO:0003704; transcription factor activity; ; GO:0003700; ; ; GO:0003700; ; ; GO:0003704
CG9192	CG9192	-1.01	2.01E-02	/
CG14191	CG14191	-0.88	2.83E-02	/

V(wt)

CG#	Synonym	median (log2)	p-value	Function
CG4889	wg	4.80	1.88E-02	frizzled-2 binding; ; GO:0005110; ; ; GO:0005110; ; ; GO:0005110; receptor binding; ; GO:0005102; Notch binding; ; GO:0005112; signal transducer activity; ; GO:0004871; morphogen activity; ; GO:00160

CG4969	Wnt6	3.83	4.55E-03	receptor binding; ; GO:0005102; ; ; GO:0005102; signal transducer activity; ; GO:0004871; ; ; GO:0005102; ; ; GO:0004871
CG6570	lbl	3.30	9.89E-03	specific RNA polymerase II transcription factor activity; GO:0003704; ; GO:0003704
CG16785	fz3	2.62	5.25E-03	Wnt-protein binding; ; GO:0017147; transmembrane receptor activity; ; GO:0004888; Wnt receptor activity; ; GO:0042813; G-protein coupled receptor activity; ; GO:0004930; ; ; GO:0004888; ; ; GO:0004
CG13857	CG13857	2.36	4.06E-02	/
CG4559	Idgf3	2.33	2.08E-02	imaginal disc growth factor activity; ; GO:0008084; NOT chitinase activity; ; GO:0004568 ; EC:3.2.1.14; hydrolase activity, hydrolyzing N-glycosyl compounds; ; GO:0016799 ; EC:3.2.2.-; ; ; GO:0
CG7777	CG7777	2.28	2.86E-03	water transporter activity; ; GO:0005372; carrier activity; ; GO:0005386; binding; ; GO:0005488; ; ; GO:0005488; ; ; GO:0005386; ; ; GO:0005372
CG8376	ap	2.18	3.36E-02	zinc ion binding; ; GO:0008270; specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704; ; ; GO:0008270
CG3388	gsb	2.16	5.58E-03	specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704
CG11922	fd96Cb	2.15	9.71E-03	transcription factor activity; GO:0003700; ; GO:0003700
CG11921	fd96Ca	1.92	1.72E-02	transcription factor activity; GO:0003700; ; GO:0003700
CG14933	CG14933	1.80	7.11E-04	/
CG1897	msh, Dr	1.75	8.12E-03	specific RNA polymerase II transcription factor activity; GO:0003704; ; GO:0003704
CG9008	CG9008	1.63	2.36E-02	isomerase activity; ; GO:0016853 ; EC:5.-.-.-; racemase and epimerase activity; ; GO:0016854 ; EC:5.1.-.-.; ; ; GO:0016853 ; EC:5.-.-.-.; ; ; GO:0016854 ; EC:5.1.-.-.
CG9747	CG9747	1.47	1.06E-03	acyl-CoA delta11-desaturase activity; GO:0017105; ; GO:0017105
CG6604	H15	1.44	1.63E-02	transcription factor activity; ; GO:0003700; ; ; GO:0003700
CG8967	otk	1.37	2.82E-03	transmembrane receptor protein tyrosine kinase activity; ; GO:0004714 ; EC:2.7.1.-; receptor activity; ; GO:0004872; ; ; GO:0004872; semaphorin receptor binding; ; GO:0030215; protein-tyrosine
CG14598	CG14598	1.33	7.87E-03	/
CG11121	so	1.18	9.97E-03	transcription factor activity; ; GO:0003700; RNA polymerase II transcription factor activity; ; GO:0003702; ; ; GO:0003700; ; ; GO:0003702
CG15209	CG15209	1.15	2.63E-02	/
CG9338	CG9338	1.12	4.47E-02	/
CG2056	CG2056	1.11	2.49E-02	trypsin activity; GO:0004295 ; EC:3.4.21.4; serine-type endopeptidase activity; GO:0004252 ; EC:3.4.21.-; ; GO:0004295 ; EC:3.4.21.4; ; GO:0004252 ; EC:3.4.21.-
CG1743	Gs2	1.09	4.24E-02	glutamate-ammonia ligase activity; ; GO:0004356 ; EC:6.3.1.2; ; ; GO:0004356 ; EC:6.3.1.2; ; ; GO:0004356 ; EC:6.3.1.2; ; ; GO:0004356 ; EC:6.3.1.2
CG3629	Dll	1.04	4.53E-02	specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704
CG4637	hh	1.00	3.45E-03	smoothened binding; GO:0005119; patched binding; GO:0005113; ; GO:0005119; ; GO:0005113; signal transducer activity; GO:0004871; morphogen activity; GO:0016015; cysteine-type endopeptid
CG8964	CG8964	0.99	1.28E-02	non-membrane spanning protein tyrosine kinase activity; ; GO:0004715 ; EC:2.7.1.-; receptor activity; ; GO:0004872; transmembrane receptor activity; ; GO:0004888; transmembrane receptor prote
CG9015	en	0.99	5.83E-03	transcription regulator activity; ; GO:0030528; transcriptional repressor activity; ; GO:0016564; specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704; ; ; GO:00
CG6206	CG6206	0.99	2.70E-02	hydrolase activity, hydrolyzing N-glycosyl compounds; ; GO:0016799 ; EC:3.2.2.-; ; ; GO:0016799 ; EC:3.2.2.-; ; alpha-mannosidase activity; ; GO:0004559 ; EC:3.2.1.24; ; ; GO:0004559 ; EC:3.2.1.2
CG9653	brk	0.96	4.18E-02	RNA polymerase II transcription factor activity; GO:0003702; specific transcriptional repressor activity; GO:0016566; ; GO:0016566; transcriptional repressor activity; GO:0016564; ; GO:
CG8927	CG8927	0.91	1.20E-02	/
CG6173	kal-1	0.89	3.93E-02	cell adhesion; GO:0007155; transmission of nerve impulse; GO:0019226
CG9614	pip	0.87	1.13E-02	heparin-sulfate 2-sulfotransferase activity; GO:0004394 ; EC:2.8.2.-; sulfotransferase activity; GO:0008146 ; EC:2.8.2.-; ; GO:0004394 ; EC:2.8.2.-; ; GO:0004394 ; EC:2.8.2.-; ; GO:0008

V(wg)

CG#	Synonym	median (log2)	p-value	Function
CG4969	Wnt6	2.64	1.82E-02	receptor binding; ; GO:0005102; ; ; GO:0005102; signal transducer activity; ; GO:0004871; ; ; GO:0005102; ; ; GO:0004871
CG4889	wg	2.50	1.28E-04	frizzled-2 binding; ; GO:0005110; ; ; GO:0005110; ; ; GO:0005110; receptor binding; ; GO:0005102; Notch binding; ; GO:0005112; signal transducer activity; ; GO:0004871; morphogen activity; ; GO:00160
CG7214	CG7214	2.33	1.25E-02	/
CG6570	lbl	1.95	5.54E-03	specific RNA polymerase II transcription factor activity; GO:0003704; ; GO:0003704
CG10016	drm	1.80	2.20E-02	foregut morphogenesis; ; GO:0007440; hindgut morphogenesis; ; GO:0007442; leg joint morphogenesis (sensu Holometabola); ; GO:0016348
CG15786	CG15786	1.72	2.93E-02	/
CG6936	mth	1.60	2.02E-02	G-protein coupled receptor activity; ; GO:0004930; ; ; GO:0004930; ; ; GO:0004930
CG14648	CG14648	1.49	1.79E-02	/
CG6234	CG6234	1.48	3.30E-03	/
CG17528	CG17528	1.43	2.25E-02	microtubule binding; ; GO:0008017; ; ; GO:0008017; receptor signaling protein serine/threonine kinase activity; ; GO:0004702; EC:2.7.1.-; ; protein serine/threonine kinase activity; ; GO:0004674
CG14026	tkv	1.41	3.09E-02	protein kinase activity; ; GO:0004672; EC:2.7.1.37; type I transforming growth factor beta receptor activity; ; GO:0005025; ; ; GO:0005025; ; ; GO:0004672; EC:2.7.1.37; transforming growth fa
CG10960	CG10960	1.34	6.49E-03	glucose transporter activity; ; GO:0005355; ; ; GO:0005355
CG11107	CG11107	1.23	3.78E-02	RNA helicase activity; ; GO:0003724; EC:2.7.7.-; ; ; GO:0003724; EC:2.7.7.-; ; ; GO:0003724; EC:2.7.7.-; pre-mRNA splicing factor activity; ; GO:0008248; ; ; GO:0008248; ATP-dependent helicase
CG8798	CG8798	1.21	4.86E-02	endopeptidase La activity; GO:0008846; EC:3.4.21.53; ; GO:0008846; EC:3.4.21.53; ; GO:0008846; EC:3.4.21.53
CG10624	sinu	1.21	2.63E-02	regulation of tracheal tube size; ; GO:0035151; septate junction assembly; ; GO:0019991; tracheal system development (sensu Insecta); ; GO:0007424, nucleic acid binding; ; GO:0003676; ; ; GO:0003676; transcription regulator activity; ; GO:0030528; ; ; GO:0030528
CG17514	CG17514	1.20	2.31E-02	translation activator activity; ; GO:0008494; kinase regulator activity; ; GO:0019207; ; ; GO:0019207; ; ; GO:0008494
CG6959	CG6959	1.15	2.30E-02	/
CG8280	Ef1alpha48D	1.14	1.20E-02	translation elongation factor activity; ; GO:0003746; ; ; GO:0003746; ; ; GO:0003746; translation release factor activity; ; GO:0003747; GTPase activity; ; GO:0003924; ; ; GO:0003746; ; ; GO:0003924;
CG1374	tsh	1.11	5.65E-03	specific RNA polymerase II transcription factor activity; ; GO:0003704; ; ; GO:0003704
CG12006	CG12006	1.10	3.76E-02	transferase activity, transferring glycosyl groups; ; GO:0016757; EC:2.4.-.-; ; transferase activity; ; GO:0016740; EC:2.-.-.-; ; ; GO:0016740; EC:2.-.-.-; ; ; GO:0016757; EC:2.4.-.-
CG7254	GlyP	1.09	3.85E-02	phosphorylase activity; ; GO:0004645; EC:2.4.1.1; glycogen phosphorylase activity; ; GO:0008184; ; ; GO:0008184; ; ; GO:0008184; ; ; GO:0004645; EC:2.4.1.1
CG2791	CG2791	1.08	3.33E-02	/
CG6493	Dcr-2	1.07	2.41E-02	double-stranded RNA binding; ; GO:0003725; ; ; GO:0003725; ; ; GO:0003725; helicase activity; ; GO:0004386; ; ; GO:0004386; endonuclease activity; ; GO:0004520; RNA helicase activity; ; GO:0
CG1902	CG1902	1.05	2.85E-02	/
CG12567	CG12567	1.01	4.52E-02	thiamin diphosphokinase activity; ; GO:0004788; EC:2.7.6.2; ; ; GO:0004788; EC:2.7.6.2
CG6116	CG6116	1.01	1.87E-02	molecular_function unknown; ; GO:0005554; ; ; GO:0005554
CG6530	mthl3	1.00	2.11E-02	G-protein coupled receptor activity; ; GO:0004930; ; ; GO:0004930; ; ; GO:0004930
CG2918	CG2918	1.00	3.22E-02	defense response; ; GO:0006952; protein folding; ; GO:0006457; response to stress; ; GO:0006950
CG9915	CG9915	0.98	4.50E-02	/

CG7962	CdsA	0.97	1.59E-02	phosphatidate cytidyltransferase activity; ; GO:0004605 ; EC:2.7.7.41; ; ; GO:0004605 ; EC:2.7.7.41; ; ; GO:0004605 ; EC:2.7.7.41; ; ; GO:0004605 ; EC:2.7.7.41
CG3837	CG3837	0.95	6.15E-03	insulin-like growth factor receptor activity; GO:0005010; ; GO:0005010
CG1448	inx3	0.95	1.64E-02	innexin channel activity; GO:0015286; ; GO:0015286
CG9990	CG9990	0.95	4.37E-03	ATPase activity, coupled to transmembrane movement of substances; GO:0042626; transporter activity; GO:0005215; ; GO:0042626; ; GO:0005215
CG14194	CG14194	0.94	1.03E-02	/
CG9977	CG9977	0.94	4.38E-02	adenosylhomocysteinase activity; ; GO:0004013 ; EC:3.3.1.1; ; ; GO:0004013 ; EC:3.3.1.1
CG12598	Adar	0.92	3.06E-02	double-stranded RNA binding; ; GO:0003725; ; ; GO:0003725; double-stranded RNA adenosine deaminase activity; ; GO:0003726; ; ; GO:0003726
CG13252	CG13252	0.91	4.40E-02	/
CG5003	CG5003	0.91	4.51E-02	/
CG7008	Tudor-SN	0.91	3.59E-02	transcription coactivator activity; ; GO:0003713; ; ; GO:0003713
CG9735	Aats-trp	0.91	2.97E-02	tryptophan-tRNA ligase activity; GO:0004830 ; EC:6.1.1.2; ; GO:0004830 ; EC:6.1.1.2
CG5008	GNBP3	0.91	2.91E-02	Gram-negative bacterial binding; ; GO:0008368; pattern recognition receptor activity; ; GO:0008329; ; ; GO:0008329; glucosidase activity; ; GO:0015926 ; EC:3.2.1.-; ; ; GO:0008329; ; ; GO:0008368;
CG12403	Vha68-1	0.90	4.63E-02	hydrogen-exporting ATPase activity, phosphorylative mechanism; ; GO:0008553 ; EC:3.6.3.6; ; ; GO:0008553 ; EC:3.6.3.6; ; ; GO:0008553 ; EC:3.6.3.6; ; ; GO:0008553 ; EC:3.6.3.6
CG15822	CG15822	0.89	1.25E-02	/
CG3584	qkr58E-3	0.89	2.71E-02	RNA binding; ; GO:0003723; ; ; GO:0003723
CG11143	Inos	0.89	4.81E-02	inositol-3-phosphate synthase activity; ; GO:0004512 ; EC:5.5.1.4; ; ; 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
CG4027	Act5C	0.88	1.87E-02	structural constituent of cytoskeleton; ; GO:0005200; ; ; GO:0005200
CG9211	CG9211	0.88	2.90E-02	cell adhesion; ; GO:0007155; cell communication; ; GO:0007154; cell-cell adhesion; ; GO:0016337; development; ; GO:0007275; ectoderm development; ; GO:0007398; neurogenesis; ; GO:0007399; signal transduction; ; GO:0007165
CG11964	CG11964	0.87	2.26E-02	/
CG1906	CG1906	0.86	3.91E-02	protein serine/threonine phosphatase activity; GO:0004722; ; GO:0004722; ; GO:0004722
CG7070	PyK	0.86	3.01E-03	pyruvate kinase activity; GO:0004743 ; EC:2.7.1.40; carbohydrate kinase activity; GO:0019200; ; GO:0019200; ; GO:0004743 ; EC:2.7.1.40; ; GO:0004743 ; EC:2.7.1.40
CG5699	zormin	0.86	8.80E-03	zormin, structural constituent of cytoskeleton; ; GO:0005200; ; ; GO:0005200; ; ; GO:0005200
CG11228	hpo	0.86	4.61E-02	protein binding; ; GO:0005515; receptor signaling protein serine/threonine kinase activity; ; GO:0004702 ; EC:2.7.1.-; ; ; GO:0004702 ; EC:2.7.1.-; protein serine/threonine kinase activity; G
CG4567	CG4567	0.85	4.64E-02	translation elongation factor activity; ; GO:0003746; ; ; GO:0003746; ; ; GO:0003746