

Table S11

sd::Gal4>UAS::Rpl12-Myc		Down-regulated genes					
GO ID	Description	Category	GO Rpl12 down	GO total	padj dh	Enrichment	
GO:0006468	protein phosphorylation	Biological process	57	545	4.69367E-23	5.22337	
GO:0006355	regulation of transcription, DNA-dependent	Biological process	32	520	6.74682E-07	3.07340	
GO:0006470	protein dephosphorylation	Biological process	19	181	2.56991E-07	5.24261	
GO:0007411	axon guidance	Biological process	19	278	6.72468E-05	3.41335	
GO:0048477	oogenesis	Biological process	17	367	6.03879E-03	2.31342	
GO:0007391	dorsal closure	Biological process	15	222	5.75198E-04	3.37451	
GO:0006413	translational initiation	Biological process	13	92	1.66781E-06	7.05713	
GO:0016055	Wnt receptor signaling pathway	Biological process	12	117	8.31679E-05	5.12233	
GO:0007476	imaginal disc-derived wing morphogenesis	Biological process	12	173	1.87101E-03	3.46424	
GO:0007173	epidermal growth factor receptor signaling pathway	Biological process	11	51	2.77660E-07	10.77200	
GO:0000381	regulation of alternative nuclear mRNA splicing, via spliceosome	Biological process	11	72	6.55709E-06	7.63014	
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Biological process	11	81	1.83948E-05	6.78235	
GO:0007155	cell adhesion	Biological process	11	141	1.34620E-03	3.89624	
GO:0007314	oocyte anterior/posterior axis specification	Biological process	10	38	2.29308E-07	13.14280	
GO:0007399	nervous system development	Biological process	10	133	2.92065E-03	3.75509	
GO:0006915	apoptosis	Biological process	10	136	3.26456E-03	3.67226	
GO:0000910	cytokinesis	Biological process	10	144	4.28099E-03	3.46825	
GO:0008045	motor axon guidance	Biological process	9	58	5.54803E-05	7.74974	
GO:0007224	smoothed signaling pathway	Biological process	9	82	5.75198E-04	5.48152	
GO:0007298	border follicle cell migration	Biological process	9	130	7.16409E-03	3.45757	
GO:0048749	compound eye development	Biological process	9	134	8.07655E-03	3.35436	
GO:0016339	calcium-dependent cell-cell adhesion	Biological process	8	43	5.25417E-05	9.29167	
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Biological process	8	62	5.40715E-04	6.44423	
GO:0007602	phototransduction	Biological process	8	85	2.87563E-03	4.70049	
GO:0016319	mushroom body development	Biological process	8	88	3.23070E-03	4.54025	
GO:0008360	regulation of cell shape	Biological process	8	100	5.86915E-03	3.95542	
GO:0007623	circadian rhythm	Biological process	8	106	7.71901E-03	3.76926	
GO:0007064	mitotic sister chromatid cohesion	Biological process	7	10	1.42119E-08	34.95990	
GO:0016199	axon midline choice point recognition	Biological process	7	29	3.97220E-05	12.05510	
GO:0045746	negative regulation of Notch signaling pathway	Biological process	7	33	8.03797E-05	10.59390	
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	Biological process	7	37	1.59120E-04	9.48863	
GO:0008293	torso signaling pathway	Biological process	7	43	3.82851E-04	8.13021	
GO:0007268	synaptic transmission	Biological process	7	62	2.42711E-03	5.63870	
GO:0030707	ovarian follicle cell development	Biological process	7	65	2.92065E-03	5.37845	
GO:0048096	chromatin-mediated maintenance of transcription	Biological process	6	21	6.72468E-05	14.26940	
GO:0008284	positive regulation of cell proliferation	Biological process	6	32	5.89399E-04	9.36427	
GO:0007279	pole cell formation	Biological process	6	36	1.01318E-03	8.32379	
GO:0008587	imaginal disc-derived wing margin morphogenesis	Biological process	6	38	1.23771E-03	7.88570	
GO:0030718	germ-line stem cell maintenance	Biological process	6	39	1.39728E-03	7.68350	
GO:0051726	regulation of cell cycle	Biological process	6	49	3.68634E-03	6.11544	
GO:0046843	dorsal appendage formation	Biological process	6	51	4.00089E-03	5.87562	
GO:0007474	imaginal disc-derived wing vein specification	Biological process	6	52	4.34342E-03	5.76262	
GO:0002121	inter-male aggressive behavior	Biological process	6	58	6.87108E-03	5.16649	
GO:0016325	oocyte microtubule cytoskeleton organization	Biological process	5	20	6.06526E-04	12.48570	
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	Biological process	5	20	6.06526E-04	12.48570	
GO:0030713	ovarian follicle cell stalk formation	Biological process	5	20	6.06526E-04	12.48570	
GO:0008101	decapentaplegic receptor signaling pathway	Biological process	5	23	1.06795E-03	10.85710	
GO:0007613	memory	Biological process	5	26	1.77020E-03	9.60437	
GO:0008286	insulin receptor signaling pathway	Biological process	5	36	5.36510E-03	6.93649	
GO:0007294	germarium-derived oocyte fate determination	Biological process	5	40	7.71901E-03	6.24284	
GO:0019730	antimicrobial humoral response	Biological process	5	42	8.54005E-03	5.94557	
GO:0008069	dorsal/ventral axis specification, ovarian follicular epithelium	Biological process	4	11	7.31454E-04	18.16100	
GO:0045926	negative regulation of growth	Biological process	4	11	7.31454E-04	18.16100	
GO:0010628	positive regulation of gene expression	Biological process	4	11	7.31454E-04	18.16100	
GO:0031290	retinal ganglion cell axon guidance	Biological process	4	12	1.01318E-03	16.64760	
GO:0048132	female germ-line stem cell division	Biological process	4	15	2.13635E-03	13.31810	
GO:0046331	lateral inhibition	Biological process	4	16	2.66674E-03	12.48570	
GO:0046621	negative regulation of organ growth	Biological process	4	17	3.06087E-03	11.75120	
GO:0045879	negative regulation of smoothed signaling pathway	Biological process	4	19	4.00089E-03	10.51430	
GO:0006471	protein ADP-ribosylation	Biological process	4	21	5.65133E-03	9.51290	
GO:0000165	MAPKKK cascade	Biological process	4	24	8.07655E-03	8.32379	
GO:0016360	sensory organ precursor cell fate determination	Biological process	4	25	8.78077E-03	7.99084	
GO:0008347	glial cell migration	Biological process	4	26	9.79784E-03	7.68350	
GO:0006376	mRNA splice site selection	Biological process	3	9	5.06747E-03	16.64760	
GO:0045196	establishment or maintenance of neuroblast polarity	Biological process	3	10	6.56233E-03	14.98280	
GO:0046580	negative regulation of Ras protein signal transduction	Biological process	3	10	6.56233E-03	14.98280	
GO:0030308	negative regulation of cell growth	Biological process	3	12	9.48980E-03	12.48570	
GO:0035293	chitin-based larval cuticle pattern formation	Biological process	3	12	9.48980E-03	12.48570	
GO:0006508	proteolysis	Biological process	2	767	3.24236E-04	0.13023	
GO:0004674	protein serine/threonine kinase activity	Molecular function	48	373	4.69367E-23	6.42695	
GO:0005515	protein binding	Molecular function	43	705	4.52933E-09	3.04615	
GO:0003700	sequence-specific DNA binding transcription factor activity	Molecular function	34	570	5.25573E-07	2.97904	
GO:0005524	ATP binding	Molecular function	30	714	8.99587E-04	2.09843	
GO:0003677	DNA binding	Molecular function	29	720	1.87598E-03	2.01158	
GO:0003729	mRNA binding	Molecular function	26	275	4.54822E-09	4.72186	
GO:0008137	NADH dehydrogenase (ubiquinone) activity	Molecular function	19	52	3.01023E-17	18.24830	
GO:0004672	protein kinase activity	Molecular function	16	165	6.75288E-06	4.84293	
GO:0043565	sequence-specific DNA binding	Molecular function	16	267	1.03752E-03	2.99282	
GO:0000166	nucleotide binding	Molecular function	15	179	6.72468E-05	4.18515	
GO:0005509	calcium ion binding	Molecular function	14	251	3.68634E-03	2.78565	
GO:0003743	translation initiation factor activity	Molecular function	13	113	1.29579E-05	5.74563	
GO:0008143	poly(A) RNA binding	Molecular function	11	13	2.66284E-15	42.25920	
GO:0004879	ligand-dependent nuclear receptor activity	Molecular function	11	65	2.78185E-06	8.45185	
GO:0005154	epidermal growth factor receptor binding	Molecular function	10	18	5.74607E-11	27.74600	
GO:0003723	RNA binding	Molecular function	10	130	2.66674E-03	3.84175	
GO:0004129	cytochrome-c oxidase activity	Molecular function	9	42	4.83721E-06	10.70200	
GO:0004714	transmembrane receptor protein tyrosine kinase activity	Molecular function	7	30	4.92600E-05	11.65330	
GO:0003730	mRNA 3'-UTR binding	Molecular function	7	34	9.45156E-05	10.28230	
GO:0005516	calmodulin binding	Molecular function	7	53	1.07070E-03	6.59621	
GO:0004722	protein serine/threonine phosphatase activity	Molecular function	7	84	8.07655E-03	4.16190	
GO:0004683	calmodulin-dependent protein kinase activity	Molecular function	6	9	3.38762E-07	33.29520	
GO:0008190	eukaryotic initiation factor 4E binding	Molecular function	6	15	9.95901E-06	19.97710	
GO:0003714	transcription corepressor activity	Molecular function	6	35	8.89303E-04	8.56161	
GO:0042393	histone binding	Molecular function	5	15	1.67326E-04	16.64760	
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	Molecular function	5	37	5.89118E-03	6.74902	
GO:0005044	scavenger receptor activity	Molecular function	5	42	8.54005E-03	5.94557	
GO:0004385	guanylate kinase activity	Molecular function	4	14	1.71959E-03	14.26940	
GO:0004708	MAP kinase kinase activity	Molecular function	4	17	3.06087E-03	11.75120	
GO:0004707	MAP kinase activity	Molecular function	4	23	7.33059E-03	8.68570	
GO:0019904	protein domain specific binding	Molecular function	3	10	6.56233E-03	14.98280	

GO:0004721	phosphoprotein phosphatase activity	Molecular function	3	12	9,48980E-03	12,48570
GO:0008601	protein phosphatase type 2A regulator activity	Molecular function	3	12	9,48980E-03	12,48570
GO:0000340	RNA 7-methylguanosine cap binding	Molecular function	3	12	9,48980E-03	12,48570
GO:0004252	serine-type endopeptidase activity	Molecular function	1	511	3,06087E-03	0,09774
GO:0005634	nucleus	Cellular component	112	1905	4,66931E-26	2,93627
GO:0005886	plasma membrane	Cellular component	40	594	1,37168E-09	3,36315
GO:0005737	cytoplasm	Cellular component	31	859	4,60124E-03	1,80236
GO:0005739	mitochondrion	Cellular component	22	333	2,39279E-05	3,29952
GO:0005921	gap junction	Cellular component	8	31	5,12663E-06	12,88850
GO:0008278	cohesin complex	Cellular component	7	20	3,42686E-06	17,48000
GO:0030529	ribonucleoprotein complex	Cellular component	7	37	1,59120E-04	9,44863
GO:0005747	mitochondrial respiratory chain complex I	Cellular component	7	71	4,00089E-03	4,92393
GO:0016028	rhabdomere	Cellular component	6	47	3,06087E-03	6,37567
GO:0043234	protein complex	Cellular component	6	58	6,87108E-03	5,16649
GO:0016281	eukaryotic translation initiation factor 4F complex	Cellular component	5	23	1,06795E-03	10,85710
GO:0005654	nucleoplasm	Cellular component	5	33	3,83253E-03	7,56708
GO:0016323	basolateral plasma membrane	Cellular component	4	16	2,66674E-03	12,48570
GO:0008287	protein serine/threonine phosphatase complex	Cellular component	3	10	6,56233E-03	14,98280