Supplementary Table 1: Gene expression changes induced by dASF or B52 overexpression in the larval developing eye

Gene expression modifications in GMR/GFP-dASF#1 and in GMR/GFP-B52#6 transgenics compared to control GMR/GFP-NLS (fold change factor threshold: 2x)
Gene molecular functions were annotated from http://flybase.bio.indiana.edu

Gene expression variation in GFP-dASF/SF2 overexpressing larvae	**Flybase-ID**	**Fold Change**	**molecular functions**
epsilonTrypsin	FBgn0010425	7.73	proteolysis
CG13323	FBgn0033788	5.45	
betaTrypsin	FBgn0010357	5.39	proteolysis
Jonah 25Biii	FBgn0031653	5.25	proteolysis
yippee interacting protein 7	FBgn0040060	5.06	proteolysis
Jonah 65Aiii	FBgn0035665	4.93	proteolysis
CG10912	FBgn0034296	4.83	
CG6277	FBgn0039475	4.35	lipid metabolism
CG31789	FBgn0051789	4.35	
Jonah 25Bii	FBgn0031654	4.14	proteolysis
CG15818	FBgn0031910	4.12	development;spermatogenesis;gametogenesis
CG14302	FBgn0038647	4.00	
Drosomycin	FBgn0010381	4.00	defense response to fungi; antibacterial humoral response
Antigen 5-related 2	FBgn0020508	3.90	defense response
Jonah 65Aiv	FBgn0035664	3.88	proteolysis
Frost	FBgn0037724	3.86	response to cold
CG17150	FBgn0035581	3.75	microtubule-based movement;cell motility;proteolysis
CG7916	FBgn0028534	3.67	
CG32302	FBgn0052302	3.61	chitin metabolism
Peritrophin-15b	FBgn0040958	3.56	chitin metabolism
CG8661	FBgn0030837	3.53	
CG6947	FBgn0036233	3.52	chitin metabolism
Jonah 44E	FBgn0001285	3.52	proteolysis
CG9672	FBgn0030777	3.52	proteolysis
CG7953	FBgn0028533	3.50	
CG4734	FBgn0033826	3.48	
CG5765	FBgn0034294	3.42	
γTrypsin	FBgn0010359	3.37	
CG7567	FBgn0039670	3.23	
CG8290	FBgn0026573	3.22	
CG13324	FBgn0033789	3.16	
CG8997	FBgn0028920	3.15	
CG6839	FBgn0036831	3.08	endonuclease activity;nucleic acid binding
alphaTrypsin	FBgn0003863	3.01	proteolysis
CG9328	FBgn0032886	2.99	
CG15043	FBgn0030929	2.95	
CG7714	FBgn0038645	2.92	
CG7017	FBgn0036951	2.89	chitin metabolism
CG5399	FBgn0038353	2.87	
CG8664	FBgn0030836	2.85	
Peritrophin-15a	FBgn0040959	2.84	chitin binding
CG8952	FBgn0030688	2.81	proteolysis
Turandot A	FBgn0028396	2.76	response to stress;humoral defense mechanism; response to heat
CG7348	FBgn0036940	2.73	chitin metabolism
split ends	FBgn0016977	2.72	neuroblast fate determination; glial cell fate determination and migration; Wnt receptor signaling pathway; axon guidance
CG6933	FBgn0036952	2.69	chitin metabolism
starry night	FBgn0024836	2.66	mushroom body and dendrite morphogenesis; ommatidial polarity and rotation; R3/R4 development; signal transduction
CG7710	FBgn0038644	2.62	

CG7298	FBgn0036948	2.62	chitin metabolism
unc-115	FBgn0037733	2.61	
CG32158	FBgn0052158	2.59	G-protein coupled receptor protein signaling pathway; cyclic nucleotide metabolism; intracellular signaling cascade
CG7715	FBgn0038646	2.59	
CG31451	FBgn0051451	2.54	
Ccp84Ag	FBgn0004777	2.52	
CG18030	FBgn0039778	2.50	
CG10910	FBgn0034289	2.50	
piwi	FBgn0004872	2.49	cell fate determination; RNA interference; chromatin silencing; posttranscriptional gene silencing; germ-line stem cell division
CG5084	FBgn0034288	2.49	
CG40077	FBgn0058077	2.46	
CG4341	FBgn0028481	2.44	
l(1)G0168	FBgn0027287	2.39	cytoskeleton organization and biogenesis; nucleobase, nucleotide and nucleic acid metabolism
CG40437	FBgn0058437	2.34	
CG32017	FBgn0052017	2.31	
CG8342	FBgn0002578	2.31	
CG6283	FBgn0039474	2.28	lipid metabolism
CG12934	FBgn0033541	2.26	
CG5604	FBgn0032208	2.25	protein modification; proteolysisprotein metabolism; ubiquitin cycle
CG12115	FBgn0030097	2.24	
PIP5K59B	FBgn0034789	2.24	G-protein coupled receptor protein signaling pathway; phosphorylation
CG16996	FBgn0032412	2.22	proteolysis
CG8193	FBgn0033367	-2.20	transport; metabolism; defense response
CG8483	FBgn0038126	-2.22	defense response
Connector of kinase to AP-1	FBgn0044323	-2.22	eye photoreceptor development; dorsal closure; JNK cascade
CG13461	FBgn0036468	-2.22	
CG5284	FBgn0036566	-2.22	anion transport; chloride transport
CG17107	FBgn0032281	-2.24	
Peritrophin A	FBgn0022770	-2.25	chitin metabolism
Myosin 61F	FBgn0010246	-1.96	mesoderm development; visual perception; intracellular protein transport; sensory perception of sound
Hsc70Cb	FBgn0026418	-2.25	protein folding; defense response; response to stress
CG11347	FBgn0035542	-2.18	
CG17838	FBgn0038826	-2.09	mRNA binding
CG5391	FBgn0038943	-2.27	
yellow-c	FBgn0041713	-2.27	
CG2924	FBgn0023528	-2.28	proteolysisubiquitin cycle
CG18812	FBgn0042135	-2.28	
Casein kinase Ialpha	FBgn0015024	-2.20	DNA repair; protein phosphorylation; Wnt and smoothened signaling pathways; regulation of proteolysis; intracellular signaling cascade
liquid facets	FBgn0028582	-2.25	synaptic vesicle endocytosis; neurotransmitter secretion; receptor mediated endocytosis; visual perception; intracellular signaling cascade
frizzled 2	FBgn0016797	-2.29	signal transduction; cell-cell signaling; cell motility and polarity; frizzled-2 and Wnt receptor signaling pathway
CG9449	FBgn0036875	-2.29	phosphate metabolism
fat facets	FBgn0005632	-2.30	negative regulation of proteolysis; germ cell migration; eye development; endocytosis; embryonic development nuclear migration
CG14998	FBgn0035500	-2.30	
CG1674	FBgn0039897	-2.30	
Muscle LIM protein at 84B	FBgn0014863	-2.31	mesoderm development; cell proliferation; cell differentiation; striated muscle development
Tropomyosin 2	FBgn0004117	-2.31	muscle contraction
ebony	FBgn0000527	-2.33	locomotor and circadian rhythm; cuticle pigmentation; pigmentation during development; defense response; dopamine metabolism
PRL-1	FBgn0024734	-2.35	protein amino acid dephosphorylation
CG10777	FBgn0029979	-2.37	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
Larval cuticle protein 2	FBgn0002533	-2.38	structural constituent of larval cuticle
dpr3	FBgn0053516	-2.09	
polyA-binding protein	FBgn0003031	-2.41	positive regulation of translation; histone mRNA 3'-end processing
CG14258	FBgn0039482	-2.42	
CG9821	FBgn0037636	-2.43	
CG14460	FBgn0037161	-2.44	
bunched	FBgn0010460	-2.45	Dpp signaling pathway; regulation of transcription; photoreceptor cell differentiation; salivary gland cell death; peripheral nervous system development

CG13403	FBgn0030544	-2.45	
CG8502	FBgn0033725	-2.46	structural constituent of larval cuticle
twins	FBgn0004889	-2.47	MAPKKK cascade; chromosome segregation; response to stress; imaginal disc formation; protein dephosphorylation; sensory organ development
Cyclin G	FBgn0039858	-2.48	DNA repair
CG1516	FBgn0027580	-2.17	pyruvate metabolism; gluconeogenesis; fatty acid biosynthesis
CG10237	FBgn0032783	-2.40	transport; prosthetic group metabolism; coenzyme metabolism
CG9759	FBgn0038160	-2.52	
CG14752	FBgn0033307	-2.52	
CG13606	FBgn0039161	-2.55	
CG30457	FBgn0050457	-2.56	
CG40196	FBgn0058196	-2.57	
Mob1	FBgn0036172	-2.57	learning and/or memory; olfactory learning
CG7906	FBgn0036417	-2.58	
CG8888	FBgn0033679	-2.58	metabolism; visual perception
tungus	FBgn0050084	-2.58	cell motility; muscle contraction; cytoskeleton organization and biogenesis
CG8317	FBgn0034140	-2.59	
CamKII	FBgn0004624	-2.59	
Zeelin1	FBgn0038294	-2.70	muscle thick filament assembly
CG17108	FBgn0032285	-2.75	transport
CG7778	FBgn0032025	-2.75	
Larval cuticle protein 3	FBgn0002534	-2.76	structural constituent of larval cuticle
CG11349	FBgn0035550	-2.76	
CG10570	FBgn0040992	-2.77	
Argonaute 1	FBgn0026611	-2.77	RNA interference; miRNA-mediated gene silencing, production of miRNAs and of siRNA; translational initiation; synaptogenesis; mRNA cleavage
squid	FBgn0003498	-2.79	mRNA export from nucleus; regulation of translation; dorsal/ventral pattern formation; intracellular mRNA localization; nonsense-mediated decay
yellow-e	FBgn0041711	-2.82	
CG16884	FBgn0028544	-2.86	
Lcp65Ag1	FBgn0020638	-2.87	
Dopamine N acetyltransferase	FBgn0019643	-2.88	behavior; serotonin, octopamine and dopamine catabolism; regulation of circadian sleep/wake cycle, pigmentation during development
hnRNP 27C	FBgn0004838	-2.89	mRNA processing; RNA localization
Calcium ATPase at 60A	FBgn0004551	-2.93	metabolism; calcium ion transport; calcium ion homeostasis
cap-n-collar	FBgn0000338	-2.72	response to stress; regulation of transcription; microtubule cytoskeleton polarization; defense response; bicoid and oskar mRNA localization
CG30029	FBgn0050029	-2.96	
CG11854	FBgn0039299	-2.98	
Dopa decarboxylase	FBgn0000422	-3.02	courtship behavior; cuticle biosynthesis; melanin and dopamine biosynthesis from tyrosine; pigmentation during development; learning and/or memory
Akt1	FBgn0010379	-3.05	regulation of cell and organ size and shape; insulin signaling pathway; regulation of protein import into nucleus; anti-apoptosis; protein phosphorylation
CG16970	FBgn0032504	-3.05	
CG9486	FBgn0031791	-3.10	N-acetyltransferase activity
murashka	FBgn0037705	-3.13	learning and/or memory; olfactory learning
Larval cuticle protein 9	FBgn0025578	-3.16	larval cuticle biosynthesis
CG7924	FBgn0036416	-3.18	
Glutamine synthetase 2	FBgn0001145	-3.22	synaptogenesis; nitrogen fixation; glutamate biosynthesis; neurotransmitter receptor metabolism
Punch	FBgn0003162	-3.24	ommochrome biosynthesis;purine base metabolism; tetrahydrobiopterin biosynthesis
CG16885	FBgn0032538	-3.29	
CG9452	FBgn0036877	-3.37	phosphate metabolism
CG3244	FBgn0031629	-3.37	sugar binding
CG18777	FBgn0042118	-3.44	
CG4847	FBgn0034229	-3.50	proteolysis
CG13722	FBgn0035553	-3.51	
Lcp65Ac	FBgn0020642	-3.67	structural constituent of larval cuticle
Larval cuticle protein 4	FBgn0002535	-3.71	structural constituent of larval cuticle
Cht3	FBgn0022701	-3.73	
CG7300	FBgn0032286	-3.88	
CG32000	FBgn0052000	-4.24	metabolism; cation transport; cell homeostasis; calcium ion homeostasis
Lcp65Aa	FBgn0020645	-4.34	
Peroxiredoxin 2540	FBgn0033520	-4.42	

yellow-d2	FBgn0034856	-4.46	
Phosphoglyceromutase	FBgn0014869	-4.50	
Dlg-interacting metalloprotease	FBgn0034903	-4.33	cell proliferation
Lcp65Ab2	FBgn0020643	-4.65	structural constituent of larval cuticle
Peroxiredoxin 2540	FBgn0033518	-4.71	
Ankyrin	FBgn0011747	-4.90	signal transduction; cytoskeletal anchoring
pale	FBgn0005626	-5.05	catecholamine biosynthesis; locomotory and courtship behavior; signal transduction; regulation of dopamine metabolism

Gene expression variation in GFP-B52 overexpressing larvae	**Flybase-ID**	**Fold Change**	**molecular functions**
CG10912	FBgn0034296	2.86	
CG15818	FBgn0031910	2.84	sugar binding; development
osa	FBgn0003013	2.82	brahma complex, regulation of transcription; photoreceptor cell differentiation; wing margin morphogenesis; Wnt receptor signaling pathway
B52	FBgn0004587	2.81	mRNA splice site selection; nuclear mRNA splicing, via spliceosome
CG14850	FBgn0038239	2.79	
CG1662	FBgn0030481	2.69	receptor signaling protein activity
kismet	FBgn0001309	2.68	chromatin assembly or disassembly; regulation of transcription from RNA polymerase II promoter; segment specification
CG13323	FBgn0033788	2.46	
CG13532	FBgn0034788	2.45	
CG9192	FBgn0035193	2.42	
beta amyloid protein precursor-like	FBgn0000108	2.38	nervous system development; cell surface receptor linked signal transduction; induction of apoptosis; nerve-nerve synaptic transmission
CG32017	FBgn0052017	2.36	
CG32634	FBgn0052634	2.32	
split ends	FBgn0016977	2.21	mRNA binding; neuroblast and glial cell fate determination and migration; Wnt receptor signaling pathway; regulation of transcription; axon guidance
PIP5K59B	FBgn0034789	2.20	G-protein coupled receptor protein signaling pathway; phosphorylation
CG15784	FBgn0029766	2.18	
CG31451	FBgn0051451	2.18	
CG9416	FBgn0034438	2.12	
Dynein heavy chain 64C	FBgn0010349	2.12	dendrite morphogenesis; mushroom body development; microtubule-based movement; intracellular mRNA localization; cell motility
Nipped-A	FBgn0053554	2.09	histone acetyltransferase complex; serine/threonine kinase activity; regulation of progression through cell cycle; regulation of transcription
starry night	FBgn0024836	2.06	dendrite morphogenesis; ommatidial polarity and rotation; mushroom body development; neuropeptide signaling pathway; R3/R4 development
CG33105	FBgn0053105	2.05	intracellular protein transport; protein carrier activity;
CG4341	FBgn0028481	2.04	
CG31224	FBgn0051224	2.02	regulation of transcription by RNA pol II; cell proliferation
CG6654	FBgn0038301	2.00	regulation of transcription by RNA pol II; cell proliferation;
Misexpression suppressor of KSR 2	FBgn0043070	-2.00	
CG5835	FBgn0038682	-2.01	
Aldolase	FBgn0000064	-2.02	fructose-bisphosphate aldolase activity; mesoderm development
drongo	FBgn0020304	-2.02	transport; regulation of GTPase activity; nucleotide and nucleic acid transport
CG17738	FBgn0038009	-2.02	
cAMP-dependent protein kinase 1	FBgn0000273	-2.02	serine/threonine kinase activity; regulation of oskar and bicoid mRNA localization; eye development; imaginal disc; learning and/or memory
CG8547	FBgn0033919	-2.02	
CG7587	FBgn0038523	-2.02	
CG11345	FBgn0035546	-2.03	
Pox meso	FBgn0003129	-2.04	nervous system development; mesoderm and endoderm development; signal transduction; regulation of transcription by RNA pol II; cell proliferation
CG12483	FBgn0040688	-2.04	
CG9914	FBgn0030737	-2.04	fatty acid metabolism; cytoskeleton organization and biogenesis; lipid metabolism
CG2781	FBgn0037534	-2.04	fatty acid metabolism; very-long-chain fatty acid biosynthesis
Basigin	FBgn0011219	-2.04	spermatid development
Odorant-binding protein 56d	FBgn0034470	-2.04	olfactory behavior; sensory perception of chemical stimulus; response to pheromone;
CG2950	FBgn0031637	-2.04	nucleic acid binding
CG7611	FBgn0037094	-2.04	
CG30497	FBgn0050497	-2.04	
CG13228	FBgn0033588	-2.04	

Papilin	FBgn0003137	-2.05	signal transduction;cell-cell adhesion;proteolysis;defense response;
Peritrophin A	FBgn0022770	-2.05	chitin metabolism
capricious	FBgn0023095	-2.06	cell migration and adhesion; signal transduction; transmission of nerve impulse; apoptosis; defense response; axon guidance
new glue 3	FBgn0010295	-2.06	puparial adhesion
CG31775	FBgn0028537	-2.07	
CG31522	FBgn0051522	-2.07	acetyltransferase; fatty acid biosynthesis
lethal (2) essential for life	FBgn0011296	-2.07	protein folding; defense response; response to stress; response to heat
CG30035	FBgn0050035	-2.08	carbohydrate transport; carbohydrate metabolism
CG15414	FBgn0031542	-2.08	
CG1874	FBgn0033425	-2.09	
ced-6	FBgn0029092	-2.09	MAPKKK cascade; cell surface receptor linked signal transduction; apoptosis; protein tyrosine kinase signaling pathway; defense response
Mitochondrial assembly regulatory factor	FBgn0029870	-2.09	mitochondrion organization and biogenesis; mitochondrial fusion; protein targeting to mitochondrion; GTPase activity
squid	FBgn0003498	-2.09	3'-UTR binding; mRNA export from nucleus; negative regulation of translation;intracellular mRNA localization; nonsense-mediated decay
Gp150	FBgn0013272	-2.09	cell adhesion; transmission of nerve impulse; eye development; protein tyrosine phosphatase signaling pathway
alpha-coatomer protein	FBgn0025725	-2.10	intracellular protein transport;endocytosis; retrograde transport Golgi to ER
fau	FBgn0020439	-2.10	
CG5866	FBgn0038508	-2.11	
CG31522	FBgn0051522	-2.11	very-long-chain fatty acid metabolism; fatty acid biosynthesis; acyltransferase activity
CG2924	FBgn0023528	-2.11	proteolysis;ubiquitin cycle;
CG7378	FBgn0030976	-2.11	protein amino acid dephosphorylation; protein tyrosine/serine/threonine phosphatase activity
homer	FBgn0025777	-2.11	G-protein coupled receptor protein signaling pathway; transmission of nerve impulse; regulation of locomotion; adult behavior
pipsqueak	FBgn0004399	-2.11	gene silencing; pole plasm assembly; regulation of transcription
CG18490	FBgn0036149	-2.13	
Larval serum protein 1 alpha	FBgn0002562	-2.13	nutrient reservoir activity; oxygen transporter activity
Akt1	FBgn0010379	-2.14	protein serine/threonine/thyrosine kinase activity; regulation of cell, organ and body size; regulation of protein import into nucleus; anti-apoptosis
Myosin 61F	FBgn0010246	-2.14	mesoderm development; visual perception; vesicle-mediated transport; intracellular protein transport; sensory perception of sound
CG31217	FBgn0051217	-2.14	intracellular protein transport; proteolysis; receptor mediated endocytosis; lipid metabolism; serine-type endopeptidase and chymotrypsin activity
CG9782	FBgn0030763	-2.14	
Pupal cuticle protein	FBgn0003046	-2.14	structural constituent of pupal cuticle
CG8785	FBgn0033760	-2.14	amino acid transport
CG9153	FBgn0035207	-2.15	protein modification; proteolysis; ubiquitin cycle
CG7532	FBgn0028915	-2.16	serine-type endopeptidase activity
CG9812	FBgn0034860	-2.16	
CG11349	FBgn0035550	-2.17	
CG10237	FBgn0032783	-2.17	vitamin E binding; retinal binding; coenzyme metabolism
CG10777	FBgn0029979	-2.17	ATP-dependent RNA helicase activity
CG40374	FBgn0058374	-2.18	
new glue 2	FBgn0010294	-2.18	
CG5292	FBgn0038491	-2.18	pyrimidine base metabolism
Myosin alkali light chain 1	FBgn0002772	-2.19	mesoderm development; muscle contraction; proteolysis; microfilament motor activity
CG10211	FBgn0032685	-2.19	transport; oxygen and reactive oxygen species metabolism; defense response; DNA binding
CG1407	FBgn0033474	-2.20	
Kuzbanian-like	FBgn0039688	-2.21	proteolysis; cell surface receptor linked signal transduction
CG32603	FBgn0052603	-2.21	
Connector of kinase to AP-1	FBgn0044323	-2.22	eye photoreceptor development; dorsal closure; JNK cascade
trio	FBgn0024277	-2.22	G-protein coupled signaling pathway; transmission of nerve impulse; peripheral and central nervous system development; axon guidance
TpnC25D	FBgn0031692	-2.23	ciliary or flagellar motility; muscle contraction; calcium-mediated signaling
Tropomyosin 1	FBgn0003721	-2.23	dendrite morphogenesis; pole plasm assembly; muscle contraction; pole plasm oskar mRNA localization
CG10467	FBgn0035679	-2.23	monosaccharide metabolism; galactose metabolism
Glycogenin	FBgn0034603	-2.24	mesoderm development; carbohydrate biosynthesis
Ornithine decarboxylase antizyme	FBgn0014184	-2.24	
CG32423	FBgn0052423	-2.25	mRNA processing
CG9077	FBgn0033600	-2.26	structural constituent of cuticle
CG3672	FBgn0035985	-2.26	structural constituent of cuticle

Larval cuticle protein 1	FBgn0002531	-2.26	structural constituent of larval cuticle
biniou	FBgn0045759	-2.27	regulation of transcription by RNA pol II; mesodermal cell fate commitment; phosphoenolpyruvate-dependent sugar phosphotransferase system
CG8888	FBgn0033679	-2.27	metabolism; visual perception; oxidoreductase activity
CG3592	FBgn0029642	-2.27	
CG8502	FBgn0033725	-2.29	structural constituent of larval cuticle
CG9119	FBgn0035189	-2.30	
la costa	FBgn0028583	-2.31	
Dopa decarboxylase	FBgn0000422	-2.31	courtship behavior; cuticle biosynthesis; serotonin/dopamine biosynthesis from tyrosine; pigmentation during development; learning and memory
CG5847	FBgn0036985	-2.31	receptor activity;structural constituent of cuticle (sensu Insecta);
CG6014	FBgn0027542	-2.31	
CG9674	FBgn0036663	-2.32	disulfide oxidoreductase activity;monooxygenase activity;glutamate synthase (NADPH) activity;
CG5177	FBgn0031908	-2.32	trehalose biosynthesis; disaccharide metabolism
CG32954	FBgn0052954	-2.33	
Vha100-2	FBgn0028670	-2.33	cation transport; proton transport
CG11652	FBgn0036194	-2.33	defense response
CG13183	FBgn0033667	-2.33	regulation of transcription
CG2121	FBgn0033289	-2.35	muscle contraction
CG10845	FBgn0039246	-2.36	cytoskeleton organization and biogenesis, kinesin complex
coracle	FBgn0010434	-2.36	regulation of tracheal tube size; dorsal closure; cell polarity; protein targeting to membrane; salivary gland morphogenesis; embryonic development
Larval visceral protein H	FBgn0002570	-2.37	
polyA-binding protein	FBgn0003031	-2.37	positive regulation of translation; histone mRNA 3'-end processing; poly(A) binding
Sema-2a	FBgn0011260	-2.37	visual and flight behavior; cell adhesion; receptor linked signal transduction; synaptic target inhibition; salivary gland development; axon guidance
CG7299	FBgn0032282	-2.38	
Hrb27C	FBgn0004838	-2.38	mRNA processing; RNA localization; ribonucleoprotein complex
CG11131	FBgn0037204	-2.39	
Black cells	FBgn0000165	-2.40	transport; response to wounding; response to pest, pathogen or parasite; defense response
Cytochrome P450-4d1	FBgn0005670	-2.40	steroid metabolism; electron transport
CG8678	FBgn0032935	-2.41	
Cht3	FBgn0022701	-2.41	
CaMKII	FBgn0004624	-2.42	
CG33178	FBgn0053178	-2.42	protein modification; protein metabolism; defense response; response to toxin
CG9452	FBgn0036877	-2.43	phosphate metabolism
CG14998	FBgn0035500	-2.43	
Ecdysone-induced gene 71Ec	FBgn0004590	-2.44	
Cyclin G	FBgn0039858	-2.44	DNA repair; cyclin-dependent protein kinase regulator activity
CG13403	FBgn0030544	-2.45	
Lysozyme D	FBgn0004427	-2.47	
I'm not dead yet	FBgn0036816	-2.47	determination of adult life span; cation transport; sodium ion transport
Na pump alpha subunit	FBgn0002921	-2.47	tracheal tube architecture; calcium ion homeostasis; embryonic development; regulation of cell shape; monovalent inorganic cation transport
Dopamine N acetyltransferase	FBgn0019643	-2.48	behavior; serotonin and dopamine catabolism; regulation of circadian sleep/wake cycle, sleep; pigmentation during development
CG11486	FBgn0035397	-2.48	mRNA processing; protein amino acid phosphorylation; histone mRNA 3'-end processing; transcription and elongation by RNA pol II
Larval serum protein 1 gamma	FBgn0002564	-2.49	nutrient reservoir activity; oxygen transporter activity
CG9449	FBgn0036875	-2.51	acid phosphatase activity
Lysozyme S	FBgn0004430	-2.51	cell wall catabolism;antimicrobial humoral response
Ecdysone-induced gene 71Ee	FBgn0004592	-2.51	puparial adhesion; hemolymph coagulation
CG32207	FBgn0052207	-2.52	
CG5656	FBgn0037083	-2.53	mesoderm development; metabolism; skeletal development
CG14237	FBgn0039428	-2.53	
CG5829	FBgn0038520	-2.54	
sluggish A	FBgn0003423	-2.54	locomotory behavior; phototactic behavior; proline catabolism; glutamate biosynthesis
CG7160	FBgn0037114	-2.54	structural constituent of cuticle
CG17549	FBgn0032774	-2.55	
CG1674	FBgn0039897	-2.56	
CG18812	FBgn0042135	-2.57	

CG17105	FBgn0032280	-2.58	
CG13461	FBgn0036468	-2.61	
lethal (2) giant larvae	FBgn0002121	-2.62	cell proliferation and differentiation; morphogenesis of imaginal disc; salivary gland cell death; neuroblast polarity; nervous system development
CG4847	FBgn0034229	-2.62	cathepsin K activity; proteolysis
held out wings	FBgn0017397	-2.63	somatic muscle development; cell differentiation; apposition of dorsal and ventral wing surfaces; apoptosis; mRNA binding
cap-n-collar	FBgn0000338	-2.64	regulation of bicoid and oskar mRNA localization; response to stress; regulation of transcription; microtubule cytoskeleton; defense response
CG17108	FBgn0032285	-2.66	transporter activity
CG1516	FBgn0027580	-2.67	pyruvate metabolism; gluconeogenesis; fatty acid biosynthesis
CG1600	FBgn0033188	-2.67	alcohol dehydrogenase activity, zinc-dependent
new glue 1	FBgn0002933	-2.68	
CG7906	FBgn0036417	-2.68	
tungus	FBgn0050084	-2.70	cell motility;muscle contraction; cytoskeleton organization and biogenesis
CG7300	FBgn0032286	-2.70	
Pheromone-binding protein-related 5	FBgn0011283	-2.72	transport; metabolism; pheromone binding
CG13606	FBgn0039161	-2.74	
Muscle LIM protein at 84B	FBgn0014863	-2.76	mesoderm development; cell proliferation; cell differentiation; striated muscle development
CG32404	FBgn0052404	-2.76	structural constituent of cuticle
Muscle LIM protein at 60A	FBgn0011643	-2.77	mesoderm development; cell proliferation; regulation of striated muscle development
kismet	FBgn0001309	-2.79	chromatin assembly or disassembly; blastoderm segmentation; regulation of transcription by RNA pol II; segment specification
Lysozyme B	FBgn0004425	-2.82	
CG9701	FBgn0036659	-2.83	carbohydrate metabolism; hydrolase activity
Heat-shock-protein-70Bc	FBgn0013279	-2.83	
Calcium ATPase at 60A	FBgn0004551	-2.84	metabolism; calcium ion transport; calcium ion homeostasis; catalyzing transmembrane movement of substances
Larval cuticle protein 4	FBgn0002535	-2.85	structural constituent of larval cuticle
Neuropeptide-like precursor 2	FBgn0040813	-2.86	neuropeptide signaling pathway
CG10962	FBgn0030073	-2.86	oxidoreductase activity
CG32081	FBgn0052081	-2.89	transport;amino acid transport; amino acid metabolism
CG33521	FBgn0053521	-2.90	
CG8157	FBgn0034010	-2.91	
CG13722	FBgn0035553	-2.92	
Zeelin1	FBgn0038294	-2.92	muscle thick filament assembly
CG15282	FBgn0028855	-2.93	
Odorant-binding protein 56a	FBgn0034468	-2.94	olfactory behavior; sensory perception of chemical stimulus; response to pheromone
CG7296	FBgn0032283	-2.95	
CG11854	FBgn0039299	-2.96	
Ecdysone-induced gene 71Ef	FBgn0004593	-2.96	salivary gland cell death; autophagic cell death
CG7778	FBgn0032025	-3.00	
wings up A	FBgn0004028	-3.01	tropomyosin binding; nervous system development; muscle contraction; muscle development
CG8193	FBgn0033367	-3.03	transport; metabolism; defense response
Ecdysone-induced gene 71Eg	FBgn0004594	-3.04	
CG9572	FBgn0031089	-3.06	
Dlg-interacting metalloprotease	FBgn0034903	-3.07	cell proliferation
CG16884	FBgn0028544	-3.09	
CG30029	FBgn0050029	-3.09	
CG16970	FBgn0032504	-3.11	
Attacin-B	FBgn0041581	-3.16	
Punch	FBgn0003162	-3.18	ommochrome and tetrahydrobiopterin biosynthesis
CG10918	FBgn0031178	-3.19	
Salivary gland secretion 1	FBgn0003372	-3.20	puparial adhesion
CG8317	FBgn0034140	-3.21	
Ccp84Aa	FBgn0004783	-3.23	structural constituent of larval cuticle
Lcp65Ac	FBgn0020642	-3.25	structural constituent of larval cuticle
CG32000	FBgn0052000	-3.25	transport; metabolism; cation transport; ion transport; cell homeostasis; calcium ion homeostasis
Troponin C at 47D	FBgn0010423	-3.26	ciliary or flagellar motility; muscle contraction; calcium-mediated signaling

CG32405	FBgn0052405	-3.29	structural constituent of larval cuticle
CG4911	FBgn0035959	-3.29	
Larval cuticle protein 2	FBgn0002533	-3.33	structural constituent of larval cuticle
CG16885	FBgn0032538	-3.35	
Gelsolin	FBgn0010225	-3.37	cytoskeleton organization and biogenesis; phosphoenolpyruvate-dependent sugar phosphotransferase system
CG31313	FBgn0051313	-3.37	cysteine protease inhibitor activity
CG40196	FBgn0058196	-3.43	
CG32118	FBgn0052118	-3.45	
CG14258	FBgn0039482	-3.50	
CG8677	FBgn0026577	-3.56	regulation of transcription
alpha actinin	FBgn0000667	-3.58	flight behavior;cell motility;actin filament bundle formation;cytoskeletal anchoring;
CG5047	FBgn0037008	-3.60	
Trehalase	FBgn0003748	-3.67	trehalose metabolism;
tropomodulin	FBgn0082582	-3.69	mesoderm development; muscle development; cytoskeleton organization and biogenesis; peripheral nervous system development
knirps	FBgn0001320	-3.71	signal transduction; regulation of mitosis; negative regulation of transcription; tracheal system development; determination of anterior/posterior axis
CG8510	FBgn0033729	-3.86	structural constituent of cuticle
Tropomyosin 2	FBgn0004117	-3.88	muscle thin filament tropomyosin
CG17107	FBgn0032281	-3.93	
Larval cuticle protein 3	FBgn0002534	-4.00	structural constituent of larval cuticle
Lcp65Aa	FBgn0020645	-4.24	
CG7924	FBgn0036416	-4.28	
Larval cuticle protein 9	FBgn0025578	-4.41	structural constituent of larval cuticle
Amylase distal	FBgn0000078	-4.43	
CG11347	FBgn0035542	-4.44	
CG9757	FBgn0003060	-4.49	
CG32249	FBgn0052249	-4.87	signal transducer activity
pale	FBgn0005626	-5.38	locomotory and courtship behavior; signal transduction; regulation of dopamine and catecholamine metabolism; pigmentation during development
yellow-d2	FBgn0034856	-5.39	
upheld	FBgn0004169	-5.43	tropomyosin binding
Phosphoglyceromutase	FBgn0014869	-5.58	
CG7941	FBgn0036108	-5.92	
Peroxiredoxin 2540	FBgn0033518	-6.01	
Peroxiredoxin 2540	FBgn0033520	-6.33	
CG17150	FBgn0035581	-7.01	microtubule-based movement; cell motility; proteolysis;
Lcp65Ab2	FBgn0020643	-11.44	structural constituent of larval cuticle

Supplementary Table 2 : Potential target genes of dASF and B52 identified by co-immunoprecipitation experiments

The enrichment factor was estimated by comparing the level of mRNA associated to GFP-SR proteins and to the GFP-NLS.

The co-immunprecipitation experiments were duplicated and genes displaying an average enrichment factor≥ 1.5 were considered as potential target of dASF/SF2 and B52

Gene molecular functions were annotated from http://flybase.bio.indiana.edu

dASF/SF2 potential target genes	**Flybase ID**	**Enrichment fold**	**Alternative splicing**	**molecular functions**	**protein activities**
Eye development					
Matrix metalloproteinase 2	FBgn0033438	5.88	+	anti-apoptosis; proteolysis and peptidolysis	metalloendopeptidase activity
karst	FBgn0004167	4.48	+	structural constituent of cytoskeleton	microtubule and actin binding
Myocyte enhancing factor 2	FBgn0011656	3.91	+	transcription regulation, cell proliferation	RNA polymerase II transcription factor
DDB1	FBgn0027049	3.74		nucleotide-excision repair	damaged DNA binding
frizzled 2	FBgn0016797	3.06	+	signal transduction, cell polarity	G-protein coupled receptor activity, Wnt receptor activity
B4	FBgn0023407	2.98	+	Imaginal disc development and circadium rythm	
grapes	FBgn0011598	2.91	+	imaginal disc development	receptor signaling protein serine/threonine kinase activity
modifier of mdg4	FBgn0002781	2.69	+	transmission of nerve impulse, transcription regulation	RNA polymerase II transcription factor
Apaf-1-related-killer	FBgn0024252	2.54		retinal programmed cell death	caspase activator
longitudinals lacking	FBgn0005630	2.44	+	axon guidance, chromatin assembly and transcription regulation	RNA polymerase II transcription factor
retinal degeneration A	FBgn0003217	2.41		photoreceptor maintenance, phototransduction, vision	diacylglycerol kinase activity
egghead	FBgn0001404	2.38	+	cell fate commitment	beta-1,4-mannosyltransferase activity
Imitation SWI	FBgn0011604	2.35	+	transcription regulation, chromatin remodeling activity	general RNA polymerase II transcription factor
Fas-associated factor	FBgn0025608	2.35	+	eye morphogenesis	ubiquitin-specific protease activity
TBP-associated factor 1	FBgn0010355	2.35	+	transcription regulation	RNA polymerase II transcription factor
polyhomeotic distal	FBgn0004860	2.19		chromatin silencing	
gartenzwerg	FBgn0033714	2.09	+	intracellular protein transport and exocytosis	
hnRNP 27C	FBgn0004838	2.04	+	mRNA processing and localization	
Rho-kinase	FBgn0026181	1.87		ommatidial rotation, cell motility and adhesion, cell cycle	receptor signaling protein serine/threonine kinase activity
Nervous system development					
Myocyte enhancing factor 2	FBgn0011656	3.91	+	cell proliferation	RNA polymerase II transcription factor
tropomodulin	FBgn0082582	3.59	+	peripheral nervous system development	structural constituent of cytoskeleton
flotillin	FBgn0024754	2.94	+	receptor binding, nervous system development	
Kinesin-like protein at 64D	FBgn0004380	2.70		kinesin complex	microtubule motor activity
Apaf-1-related-killer	FBgn0024252	2.54		retinal programmed cell death	caspase activator
chromosome bows	FBgn0021760	2.46	+	axon guidance and centrosome biogenesis	microtubule binding
longitudinals lacking	FBgn0005630	2.44	+	axon guidance, chromatin assembly and transcription regulation	RNA polymerase II transcription factor
Imitation SWI	FBgn0011604	2.35	+	transcription regulation, chromatin remodeling activity	general RNA polymerase II transcription factor
Neurotactin	FBgn0004108	2.32	+	axon guidance, central nervous system development	
Ptp52F	FBgn0034085	2.11		axon guidance	protein tyrosine phosphatase activity
mRNA processing factors					
CG6686	FBgn0032388	5.09	+	transcription regulation	RNA polymerase II transcription factor
Transcription factor IIFalpha	FBgn0010282	4.85		transcription regulation	general RNA polymerase II transcription factor
Structure specific recognition protein	FBgn0010278	4.31		transcription regulation	transcription regulator activity, RNA binding
Myocyte enhancing factor 2	FBgn0011656	3.91	+	transcription regulation, cell proliferation	RNA polymerase II transcription factor
Mi-2	FBgn0013591	3.83		transcription regulation, chromatin assembly, protein ubiquitination	ATP-dependent DNA helicase, ubiquitin ligase activity
Misexpression suppressor of ras 4	FBgn0034240	3.67		transcription regulation	
CG6227	FBgn0030631	3.28		pre-mRNA splicing	Splicing factor, RNA helicase activity
polyA-binding protein	FBgn0003031	2.89	+	regulation of translation	poly(A) mRNA binding
eIF3-S10	FBgn0037249	2.73		translation regulation	eukaryotic translation initiation factor 3 complex;
modifier of mdg4	FBgn0002781	2.69	+	transmission of nerve impulse, transcription regulation	RNA polymerase II transcription factor

no on or off transient A	FBgn0004227	2.60	+	pre-mRNA splicing, transcription regulation	poly-pyrimidine tract binding, transcription regulator
CG7757	FBgn0036915	2.55	+	pre-mRNA splicing	small nuclear ribonucleoprotein complex: snRNP U6 and U4
CG3605	FBgn0031493	2.54		pre-mRNA splicing	small nuclear ribonucleoprotein complex: snRNP U2
Rox8	FBgn0005649	2.45	+	pre-mRNA splicing	small nuclear ribonucleoprotein complex: snRNP U1
longitudinals lacking	FBgn0005630	2.44	+	axon guidance, chromatin assembly and transcription regulation	RNA polymerase II transcription factor
Chromodomain-helicase-DNA-binding protein	FBgn0016132	2.36		chromatin assembly, regulation of RNA polymerase II transcription	ATP-dependent DNA helicase activity
Imitation SWI	FBgn0011604	2.35	+	transcription regulation, chromatin remodeling	general RNA polymerase II transcription factor
TBP-associated factor 1	FBgn0010355	2.35	+	transcription regulation	RNA polymerase II transcription factor
hnRNP 27C	FBgn0004838	2.04	+	mRNA processing and localization	
Topoisomerase 1	FBgn0004924	1.89	+	DNA replication, mRNA transcription	DNA topoisomerase type I activity
Apoptosis, proteolysis					
Ubiquitin-63E	FBgn0003943	8.36	+	chromatin structure, regulation of transcription	ubiquitin-dependent protein catabolism
CG3845	FBgn0010488	3.43	+	mRNA cap complex, translation control, autophagic cell death	
modifier of mdg4	FBgn0002781	2.69	+	induction of apoptosis, chromatin and transcription regulation	RNA polymerase II transcription factor
Apaf-1-related-killer	FBgn0024252	2.54		caspase activator, retinal programmed cell death	
cul-2	FBgn0032956	2.53	+	nuclear ubiquitin ligase complex, proteolysis	
Rpn2	FBgn0028692	2.49		proteasome regulatory particle, cell cycle	
Rox8	FBgn0005649	2.45	+	small nuclear ribonucleoprotein complex: snRNP U1	
Other functions					
CG3662	FBgn0031285	113.91	+		protein tyrosine/serine/threonine phosphatase
CG18522	FBgn0038347	8.14		defense response, nucleic acid metabolism	electron transporter activity;oxidoreductase activity;
CG13917	FBgn0035237	6.81			
CG15784	FBgn0029766	5.60			
beta Spectrin	FBgn0003471	4.79		structural constituent of cytoskeleton	actin filament and microtubule binding
Cad99C	FBgn0039709	4.66		signal transduction, calcium-dependent cell-cell adhesion	
Glutathione S transferase E1	FBgn0034335	4.43		response to oxidative stress and to toxin	glutathione transferase activity
CG8492	FBgn0035813	4.40		antimicrobial humoral response	lysosome activity
Megator	FBgn0013756	4.28		Nuclear pore	
CG1703	FBgn0030321	4.02			ATP-binding cassette (ABC) transporter complex
Lysozyme S	FBgn0004430	3.91		antimicrobial humoral response	lysosome activity
CG6124	FBgn0039484	3.61		Cell communication and signal transduction	receptor binding
CG9757	FBgn0003060	3.56			
CG12505	FBgn0033926	3.55			
CG31550	FBgn0051550	3.28	+	nucleic acid binding	
CG9322	FBgn0038178	3.27			
CG5645	FBgn0036254	3.25			
CG13227	FBgn0033589	3.23			
Larval cuticle protein 9	FBgn0025578	3.09		larval cuticle biosynthesis	
CG7465	FBgn0035551	3.01			
Larval serum protein 1 alpha	FBgn0002562	2.98		extracellular nutrient metabolism and transport	nutrient reservoir and oxygen transporter activity
Troponin C at 47D	FBgn0010423	2.90		ciliary or flagellar motility, muscle contraction	calcium ion binding
CG18811	FBgn0042134	2.88			
CG10321	FBgn0034643	2.87		zinc ion and nucleic acid binding	
CG2650	FBgn0000092	2.78		circadian rhythm	
male-specific lethal 1	FBgn0005617	2.75		chromatin binding, dosage compensation complex	
genghis khan	FBgn0023081	2.67		regulation of actin polymerization, cell adhesion and motility	protein serine/threonine kinase activity
CG14850	FBgn0038239	2.67			
zipper	FBgn0005634	2.61	+	muscle attachment, head involution, mitosis	motor activity and structural constituent of cytoskeleton
CG11063	FBgn0030530	2.47		transcription regulator activity, ligand-dependent nuclear receptor binding	
Ranbp11	FBgn0053139	2.46		nuclear pore	Ran GTPase binding
Annexin X	FBgn0000084	2.41		intracellular protein transport, endocytosis, exocytosis	calcium-dependent phospholipid binding
Protein on ecdysone puffs	FBgn0004401	2.09	+	zinc ion and nucleic acid binding	

B52 potential target genes

Eye development					
white	FBgn0003996	5.32		eye pigment biosynthesis and transport	transmembrane receptor with ATPase activity
longitudinals lacking	FBgn0005630	2.83	+	axon guidance, chromatin assembly, transcription regulation	RNA polymerase II transcription factor
modifier of mdg4	FBgn0002781	1.94	+	transmission of nerve impulse, transcription regulation	RNA polymerase II transcription factor
DDB1	FBgn0027049	1.86		nucleotide-excision repair	damaged DNA binding
polychaetoid	FBgn0003177	1.75	+	Cellular component adherens junction, cell polarity	oxidoreductase activity, regulation of JNK cascade
Heat shock protein cognate 4	FBgn0001219	1.66	+	nervous system development, neurotransmitter secretion, axon guidance	unfolded protein binding and ATPase activity
Nervous system development					
flotillin	FBgn0024754	2.88	+	receptor binding, nervous system development	
longitudinals lacking	FBgn0005630	2.83	+	axon guidance, chromatin assembly and transcription regulation	RNA polymerase II transcription factor
Tropomyosin 1	FBgn0003721	2.57	+	dendrite morphogenesis	actin binding
Fau	FBgn0020439	1.91	+	unknown function, expressed in lamina and cortical neurons	
minibrain	FBgn0002777	1.86	+	neurogenesis and brain development, learning and memory processes	protein kinase
beta-Tubulin at 56D	FBgn0003887	1.71	+	structural constituent of microtubule cytoskeleton	tubulin binding and GTPase activity
Heat shock protein cognate 4	FBgn0001219	1.66	+	nervous system development, neurotransmitter secretion, axon guidance	unfolded protein binding and ATPase activity
Nup154	FBgn0021761	1.65	+	nucleocytoplasmic transporter activity, compenent of nuclear pore	nucleocytoplasmic transporter activity
GDP dissociation inhibitor	FBgn0004868	1.64		synaptic vesicle transport and neurotransmitter secretion	acyltransferase , Rab GDP-dissociation inhibitor activity
Dihydropteridine reductase	FBgn0035964	1.61		coenzyme metabolism, amino acid catabolism	6,7-dihydropteridine reductase activity
Imaginal disc growth factor 3	FBgn0020414	1.55	+	imaginal disc and head development, signal transduction	hydrolase and chitinase activity
C-terminal Binding Protein	FBgn0020496	1.51	+	corepressor of RNA polymerase II transcription	oxidoreductase activity
mRNA processing factors					
CG8636	FBgn0029629	2.52		translation initiation	mRNA binding, translation initiation factor
CG32068	FBgn0052068	2.34		double-stranded RNA binding	
mitochondrial ribosomal protein L49	FBgn0030433	2.33		translation initiation	translation initiation factor
polyA-binding protein	FBgn0003031	2.19	+	regulation of translation	poly(A) mRNA binding
CG1789	FBgn0030063	2.15		snRNP complex, rRNA processing	
CG6764	FBgn0037899	2.14		ribosome biogenesis and assembly	structural constituent of ribosome, nucleic acid binding
Ribosomal protein L23A	FBgn0026372	2.00		mRNA binding, structural constituent of ribosome	
Eukaryotic initiation factor 2beta	FBgn0004926	1.97		translation initiation factor	tRNA binding, GTP binding
Transcription factor IIFalpha	FBgn0010282	1.90		transcription regulation	general RNA polymerase II transcription factor
Ribosomal protein S9	FBgn0010408	1.89	+	mRNA binding, structural constituent of ribosome	
Ribosomal protein L8	FBgn0024939	1.82	+	mRNA binding, structural constituent of ribosome	
CG5941	FBgn0029833	1.79		cell cycle	mRNA binding
enhancer of rudimentary	FBgn0011586	1.78		transcription regulation	RNA polymerase II transcription factor
Ribosomal protein L22	FBgn0015288	1.76		structural constituent of ribosome, nucleic acid binding	
Ribosomal protein L6	FBgn0039857	1.75		structural constituent of ribosome, nucleic acid binding	
lark	FBgn0011640	1.73	+	actin cytoskeleton, cytoplasmic transport, regulation of eclosion	mRNA binding
Ribosomal protein L36	FBgn0002579	1.68	+	structural constituent of ribosome, nucleic acid binding	
Ribosomal protein L24	FBgn0032518	1.66		structural constituent of ribosome, nucleic acid binding	
U2AF50	FBgn0005411	1.65		splicing factor	poly-pyrimidine tract binding
Ribosomal protein S18	FBgn0010411	1.65	+	translation initiation, structural constituent of ribosome	mRNA binding
Ribosomal protein L29	FBgn0016726	1.63	+	structural constituent of ribosome	
no on or off transient A	FBgn0004227	1.61	+	splicing factor, transcription regulator	poly-pyrimidine tract binding
stubarista	FBgn0003517	1.59	+	structural constituent of ribosome, nucleic acid binding	
CG1249	FBgn0037434	1.58		splicing factor involved in trans-esterification reactions	
spenito	FBgn0027548	1.58	+	RNA binding	

Apoptosis, proteolysis, defense response					
Drosomycin	FBgn0010381	2.44		defense response to fungi and bacteria	ion channel inhibitor activity
yippee interacting protein 7	FBgn0040060	2.11		proteolysis	serine-type endopeptidase activity
modifier of mdg4	FBgn0002781	1.94	+	induction of apotosis, chromatin and transcription regulation	RNA polymerase II transcription factor
Annexin B11	FBgn0030749	1.92	+	proteolysis, regulation of cell shape and adhesion	metallopeptidase activity
20S proteasome beta3 subunit	FBgn0026380	1.87		proteasome core complex	ubiquitin-dependent protein catabolism
minibrain	FBgn0002777	1.86	+	induction of apoptosis	protein serine/threonine/tyrosine kinase
Proteasome 29kD subunit	FBgn0003150	1.81		proteasome core complex	ubiquitin-dependent protein catabolism
CG6680	FBgn0036968	1.76		proteolysis, apoptosis	serine-type endopeptidase inhibitor activity
Odorant-binding protein 99b	FBgn0039685	1.75		autophagic cell death, sensory perception of chemical stimulus	odorant binding
CG9673	FBgn0030775	1.68		proteolysis	serine-type endopeptidase activity
Ubiquitin-63E	FBgn0003943	1.56	+	chromatin architecture, regulation of transcription	ubiquitin-dependent protein catabolism
Other functions					
CG9080	FBgn0033593	3.99			
CG12505	FBgn0033926	2.95			
NADH:ubiquinone reductase 23kD subunit	FBgn0017567	2.74		respiratory chain complex I	NADH dehydrogenase activity
CG8664	FBgn0030836	2.33			
CG9682	FBgn0039760	2.33			
CG18624	FBgn0029971	2.28	+	respiratory chain complex I	NADH dehydrogenase activity
CG6124	FBgn0039484	2.18		cell-matrix adhesion, signal transduction	receptor binding
Muscle LIM protein at 84B	FBgn0014863	2.16	+	muscle development, cell proliferation and differentiation	protein and zinc ion binding
CG14850	FBgn0038239	2.00			
CG11752	FBgn0030292	1.99			
CG7920	FBgn0039737	1.97	+	acetyl-CoA metabolism	4-hydroxybutyrate CoA-transferase activity
Larval cuticle protein 3	FBgn0002534	1.93		structural constituent of larval cuticle	
CG5325	FBgn0032407	1.93			
CG4734	FBgn0033826	1.90			
CG8206	FBgn0030679	1.88			
CG17549	FBgn0032774	1.86	+		
maggie	FBgn0035473	1.84	+	mitochondrial outer membrane translocase complex	protein translocase activity
Cyp6d5	FBgn0038194	1.83	+	steroid metabolism	monooxygenase and oxidoreductase activity
CG13499	FBgn0034680	1.80	+		
Salivary gland secretion 7	FBgn0003377	1.74		puparial adhesion	
CG40196	FBgn0058196	1.73			
CG40077	FBgn0058077	1.67			
regucalcin	FBgn0030362	1.64	+	anterior/posterior axis specification	calcium-mediated signaling
CG18066	FBgn0034517	1.61			
Phosphogluconate mutase	FBgn0003076	1.60		monosaccharide metabolism	phosphoglucomutase activity
Nucleosome assembly protein 1	FBgn0015268	1.58		regulation of transcription, nucleosome assembly	histone binding
Intronic Protein 259	FBgn0025366	1.53			

Supplementary Table 3: Gene Ontology (GO) **terms enriched respectively in the subsets of dASF and B52 target genes identified by immunoprecipitation.**

GO terms significantly enriched in the substets of dASF/SF2 and B52 potential target genes are shown in functional categories related to development, RNA, apoptosis and proteolysis. **"Count"** represents the number of target genes assigned to each category. **"Total"** represents the number of genes from the drosophila microarray assignated to each category. **"P-Value"** represents the statistical confidence of the GO annotation distribution. **"enrichment factor"** represents the ratio between the frequency of a GO term in the substets of target genes and its frequency among the genes from the drosophila array.

GO Term	GO annotation	Count	Total	P-Value	enrichment factor
dASF target genes: enrichment in GO terms related to development					
cell development	GO:0048468	9	331	7.40E-02	3.63
neuron morphogenesis during differentiation	GO:0048667	5	119	7.40E-02	5.61
axogenesis	GO:0007409	5	119	7.40E-02	5.61
neutrite morphogenesis	GO:0048812	5	119	7.40E-02	5.61
morphogenesis	GO:0009653	12	624	7.40E-02	2.57
cellular morphogenesis	GO:0000902	8	329	7.98E-02	3.25
axon guidance	GO:0007411	4	81	7.98E-02	6.59
neuron development	GO:0048666	5	140	7.98E-02	4.77
neutrite development	GO:0031175	5	140	7.98E-02	4.77
neuron differentiation	GO:0030182	5	146	8.53E-02	4.57
organ development	GO:0048513	11	628	1.04E-01	2.34
cellular morphogenesis during differentiation	GO:0000904	5	164	1.14E-01	4.07
cell differentiation	GO:0030154	9	489	1.29E-01	2.46
generation of neurons	GO:0048699	5	176	1.29E-01	3.79
oocyte microtubule cytoskeleton organization	GO:0016325	2	21	1.36E-01	12.71
ovarian follicle cell development (sensu Insecta)	GO:0030707	4	121	1.36E-01	4.41
neurogenesis	GO:0022008	5	189	1.36E-01	3.53
mystery cell fate differentiation (sensu Endopterygota)	GO:0008583	1	1	1.36E-01	133.49
establishment and/or maintenance of cell polarity	GO:0007163	3	69	1.40E-01	5.80
larval development (sensu Insecta)	GO:0002168	2	25	1.40E-01	10.68
cellularization	GO:0007349	2	28	1.41E-01	9.54
oocyte development	GO:0048599	3	77	1.41E-01	5.20
maintenance of polarity of follicular epithelium	GO:0042248	1	2	1.41E-01	66.75
sarcomere organization	GO:0045214	1	2	1.41E-01	66.75
establishment of neuroblast polarity	GO:0045200	1	2	1.41E-01	66.75
follicle cell migration (sensu Insecta)	GO:0007297	2	32	1.57E-01	8.34
oocyte differentiation	GO:0009994	3	84	1.57E-01	4.77
follicle cell adhesion (sensu Insecta)	GO:0007299	1	3	1.62E-01	44.50
dorsal closure, spreading of leading edge cells	GO:0007395	1	3	1.62E-01	44.50
organ morphogenesis	GO:0009887	6	326	1.77E-01	2.46
regulation of progression through syncytial blastoderm mitotic cell cycle	GO:0007348	1	4	1.77E-01	33.37
larval cuticle biosynthesis (sensu Insecta)	GO:0008363	1	4	1.77E-01	33.37
larval or pupal development (sensu Insecta)	GO:0002165	6	333	1.77E-01	2.41
establishment of tissue polarity	GO:0007164	2	42	1.77E-01	6.36
dorsal closure, leading edge cell differentiation	GO:0046663	1	5	1.77E-01	26.70
syncytial blastoderm mitotic cell cycle	GO:0035186	1	5	1.77E-01	26.70
larval development	GO:0002164	2	43	1.77E-01	6.21
post-embryonic development	GO:0009791	6	344	1.77E-01	2.33
sex determination	GO:0007530	2	44	1.77E-01	6.07
muscle development	GO:0007517	3	108	1.77E-01	3.71
myofibril assembly	GO:0030239	1	6	1.77E-01	22.25
regulation of progression through embryonic mitotic cell cycle	GO:0009794	1	6	1.77E-01	22.25
establishment and/or maintenance of neuroblast polarity	GO:0045196	1	6	1.77E-01	22.25
germ cell development	GO:0007281	3	110	1.77E-01	3.64
striated muscle development	GO:0007519	2	48	1.79E-01	5.56

morphogenesis of a polarized epithelium	GO:0001738	2	50	1.81E-01	5.34
oocyte microtubule cytoskeleton organization (sensu Insecta)	GO:0048130	1	7	1.81E-01	19.07
regulation of striated muscle development	GO:0016202	1	7	1.81E-01	19.07
axon midline choice point recognition	GO:0016199	1	7	1.81E-01	19.07
cellularization (sensu Metazoa)	GO:0009796	1	8	1.95E-01	16.69
cystoblast division	GO:0007282	1	9	2.00E-01	14.83
embryonic development (sensu Insecta)	GO:0001700	3	128	2.00E-01	3.13
morphogenesis of an epithelium	GO:0002009	3	131	2.00E-01	3.06
axonal fasciculation	GO:0007413	1	10	2.00E-01	13.35
establishment of cell polarity	GO:0030010	1	10	2.00E-01	13.35
regulation of retinal programmed cell death	GO:0046668	1	11	2.11E-01	12.14
eye morphogenesis	GO:0048592	3	141	2.15E-01	2.84
nervous system development	GO:0007399	7	493	2.17E-01	1.90
histolysis	GO:0007559	2	70	2.17E-01	3.81
dorsal closure	GO:0007391	2	74	2.27E-01	3.61
morphogenesis of embryonic epithelium	GO:0016331	2	80	2.41E-01	3.34
regulation of axogenesis	GO:0050770	1	17	2.41E-01	7.85
eye development	GO:0001654	3	169	2.57E-01	2.37
embryonic development (sensu Metazoa)	GO:0009792	3	191	2.75E-01	2.10
mesoderm development	GO:0007498	3	196	2.78E-01	2.04
embryonic morphogenesis	GO:0048598	2	104	2.78E-01	2.57
embryonic development	GO:0009790	5	346	2.78E-01	1.93
exocrine system development	GO:0035272	2	107	2.81E-01	2.50
salivary gland development	GO:0007431	2	107	2.81E-01	2.50
tissue development	GO:0009888	5	389	3.06E-01	1.72
compound eye development (sensu Endopterygota)	GO:0048749	2	127	3.26E-01	2.10
gland development	GO:0048732	2	129	3.27E-01	2.07
eye-antennal disc morphogenesis	GO:0007455	2	140	3.37E-01	1.91
imaginal disc development	GO:0007444	4	296	3.37E-01	1.80
eye-antennal disc development	GO:0035214	2	154	3.73E-01	1.73
dASF target genes: enrichment in GO terms related to RNA					
single strand RNA binding	GO:0003727	4	22	1.73E-03	24.27
transcirption from RNA polymerase II promoter	GO:0006366	13	669	8.33E-03	2.59
RNA processing	GO:0006396	8	251	8.33E-03	4.25
mRNA processing	GO:0006397	7	195	8.33E-03	4.79
mRNA metabolism	GO:0016071	7	205	8.87E-03	4.56
RNA splicing, via transesterification reactions	GO:0000375	5	148	2.74E-02	4.51
nuclear mRNA splicing	GO:0000398	5	148	2.74E-02	4.51
RNA binding	GO:0003723	8	360	2.74E-02	2.97
RNA metabolism	GO:0016070	8	362	2.74E-02	2.95
RNA splicing	GO:0008380	5	154	2.74E-02	4.33
poly(A) binding	GO:0008143	2	16	3.02E-02	16.69
RNA polymerase II transcription factor activity	GO:0003702	6	262	4.91E-02	3.06
mRNA transcription	GO:0009299	2	23	4.91E-02	11.61
mRNA cap complex	GO:0005845	1	2	6.94E-02	66.75
mRNA binding	GO:0003729	6	306	8.13E-02	2.62
transcription factor TFIIF complex	GO:0005674	1	3	8.13E-02	44.50
general RNA polymerase II transcription factor activity	GO:0016251	3	99	1.05E-01	4.05
regulation of alternative nuclear mRNA splicing, via spliceosome	GO:0000381	2	48	1.22E-01	5.56
alternative nuclear mRNA splicing, via spliceosome	GO:0000380	2	49	1.22E-01	5.45
regulation of transcription from RNA polymerase II promoter	GO:0006357	8	536	1.22E-01	1.99
regulation of mRNA processing	GO:0050684	2	53	1.22E-01	5.04
regulation of nuclear mRNA splicing, via spliceosome	GO:0048024	2	53	1.22E-01	5.04
regulation of RNA metabolism	GO:0051252	2	54	1.22E-01	4.94
poly-pyrimidine tract binding	GO:0008187	1	8	1.22E-01	16.69
DNA-directed RNA polymerase II, holoenzyme	GO:0016591	2	82	2.07E-01	3.26
transcription initiation from RNA polymerase II promoter	GO:0006367	2	82	2.07E-01	3.26

dASF target genes: enrichment in GO terms related to apoptosis					
regulation of apoptosis	GO:0042981	4	109	3.48E-02	4.90
induction of apoptosis	GO:0006917	3	61	3.48E-02	6.57
positive regulation of apoptosis	GO:0043065	3	63	3.48E-02	6.36
caspase activation via cytochrome c	GO:0008635	1	1	3.48E-02	133.49
positive regulation of caspase activity	GO:0043280	1	2	3.48E-02	66.75
regulation of caspase activity	GO:0043281	1	2	3.48E-02	66.75
caspase activation	GO:0006919	1	2	3.48E-02	66.75
apoptosis	GO:0006915	4	178	6.34E-02	3.00
ecdysone-mediated induction of salivary gland cell autophagic cell death	GO:0035072	1	9	2.00E-01	14.83
induction of programmed cell death by ecdysone	GO:0035078	1	10	2.00E-01	13.35
salivary gland cell autophagic cell death	GO:0035071	2	69	2.17E-01	3.87
dASF target genes: enrichment in GO terms related to proteolysis					
regulation of proteolysis	GO:0030162	2	29	1.54E-01	9.21
negative regulation of proteolysis	GO:0045861	1	8	1.62E-01	16.69
ubiquitin dependant catabolism	GO:0006511	2	73	1.62E-01	3.66
modification-dependent protein catabolism	GO:0019941	2	74	1.62E-01	3.61
proteolysis during cellular catabolism	GO:0051603	2	79	1.62E-01	3.38

GO annotation	**Best GOs**	**Count**	**Total**	**P-Value**	**enrichment factor**
B52 target genes: enrichment in GO terms related to development					
embryonic development (sensu insecta)	GO:0001700	4	128	3.98E-01	4.45
negative regulation of eclosion	GO:0045804	1	1	3.98E-01	142.25
larval midgut cell programmed cell death	GO:0035096	1	2	3.98E-01	71.12
eye pigment precursor transport	GO:0006856	1	3	3.98E-01	47.42
regulation of eclosion	GO:0007563	1	3	3.98E-01	47.42
larval midgut histolysis	GO:0035069	1	3	3.98E-01	47.42
sex determination	GO:0007530	2	44	3.98E-01	6.47
embryonic development (sensu metazoa)	GO:0009792	4	191	3.98E-01	2.98
axon midline choice point recognition	GO:0016199	1	7	3.98E-01	20.32
axonal fasciculation	GO:0007413	1	10	3.98E-01	14.22
neuron development	GO:0048666	3	140	3.98E-01	3.05
neuron differentiation	GO:0030182	3	146	3.98E-01	2.92
embryonic development	GO:0009790	5	346	3.98E-01	2.06
axon guidance	GO:0007411	2	81	3.99E-01	3.51
generation of neurons	GO:0048699	3	176	4.16E-01	2.42
neurogenesis	GO:0022008	3	189	4.26E-01	2.26
salvary gland development	GO:0007431	2	107	4.68E-01	2.66
exocrine system development	GO:0035272	2	107	4.68E-01	2.66
muscle development	GO:0007517	2	108	4.68E-01	2.63
anterior/posterior axis specification	GO:0009948	2	115	4.68E-01	2.47
neuron morphogenesis during differentiation	GO:0048667	2	119	4.68E-01	2.39
axonogenesis	GO:0007409	2	119	4.68E-01	2.39
organ development	GO:0048513	7	628	4.68E-01	1.59
B52 target genes: enrichment in GO terms related to RNA					
RNA binding	GO:0003723	13	360	5.55E-05	5.14
mRNA binding	GO:0003729	11	306	2.14E-04	5.11
poly-pyrimidine tract binding	GO:0008187	2	8	2.98E-02	35.56
RNA splicing factor activity, transesterification mechanism	GO:0031202	2	24	1.50E-01	11.85
transcription factor TFIIF complex	GO:0005674	1	3	2.34E-01	47.42
RNA processing	GO:0006396	5	251	2.34E-01	2.83
tRNA binding	GO:0000049	1	5	2.53E-01	28.45
mRNA processing	GO:0006397	4	195	2.68E-01	2.92
mRNA metabolism	GO:0016071	4	205	2.68E-01	2.78

RNA splicing, via transesterification reactions	GO:0000375	3	148	2.68E-01	2.88
nuclear mRNA splicing, via spliceosome	GO:0000398	3	148	2.68E-01	2.88
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	GO:0000377	3	148	2.68E-01	2.88
RNA splicing	GO:0008380	3	154	2.68E-01	2.77
spliceosome assembly	GO:0000245	1	14	2.68E-01	10.16
RNA metabolism	GO:0016070	5	362	2.68E-01	1.96
B52 target genes: enrichment in GO terms related to apoptosis					
induction of apoptosis	GO:0006917	3	61	2.71E-02	7.00
positive regulation of apoptosis	GO:0043065	3	63	2.71E-02	6.77
apoptosis	GO:0006915	4	178	5.39E-02	3.20
regulation of apoptosis	GO:0042981	3	109	5.39E-02	3.92
salvary gland cell autophagic cell death	GO:0035071	2	69	3.98E-01	4.12
ecdysone-mediated induction of salivary gland cell autophagic cell death	GO:0035072	1	9	3.98E-01	15.81
induction of programmed cell death by ecdysone	GO:0035078	1	10	3.98E-01	14.22
histolysis	GO:0007559	2	70	3.98E-01	4.06
B52 target genes: enrichment in GO terms related to proteolysis					
ATP-dependant proteolysis	GO:0006510	3	19	2.72E-03	22.46
ubiquitin-dependent protein catabolism	GO:0006511	3	73	2.91E-02	5.85
modification-dependent protein catabolism	GO:0019941	3	74	2.91E-02	5.77
proteolysis during cellular protein catabolism	GO:0051603	3	79	2.91E-02	5.40
proteolysis	GO:0006508	8	743	3.01E-01	1.53