Supplemental Table 3. Genes exclusively upregulated under permissive growth conditions.

Gene Name	**Fold Change**	**Description**[1]
Mediator complex subunit 22	4.453	RNA polymerase II transcription mediator activity; regulation of transcription from RNA polymerase II promoter.
ryan express	3.998	General RNA polymerase II transcription factor activity; transcription initiation factor activity. transcription initiation from RNA polymerase II promoter
CG14806	3.859	Unknown at this time.
mitochondrial ribosomal protein L54	3.832	Structural constituent of ribosome.
CG33276	3.743	trypsin activity; proteolysis
CG9373	3.7	mRNA binding; nucleotide binding.
Modifier67.2	3.7	Protein binding; chromatin binding; RNA polymerase II transcription factor activity; phosphatidate phosphatase activity. regulation of chromatin assembly or disassembly; i
CG9362	3.407	glutathione transferase activity; maleylacetoacetate isomerase activity; L-phenylalanine catabolic process; tyrosine catabolic process; aromatic amino acid family metabolic process
GAGA factor	3.31	DNA binding; specific RNA polymerase II transcription factor activity; protein binding; RNA polymerase II transcription factor activity; zinc ion binding; nucleic acid binding.
CG14434	3.302	adenylate cyclase activity; cAMP biosynthetic process
CG12018	3.19	DNA-directed DNA polymerase activity; DNA binding; DNA replication
CDC2 kinase	3.154	Cyclin-dependent protein kinase activity; protein binding; protein serine/threonine kinase activity; ATP binding.
CG9596	3.131	translation initiation factor activity; regulation of translational initiation

CG15881	3.12	Unknown at this time.
CG11858	3.105	peptidyl-prolyl cis-trans isomerase activity
CG9938	3.015	mitotic metaphase plate congression; chromosome segregation; mitotic spindle organization and biogenesis
Nckx30C	3.015	Calcium, potassium:sodium antiporter activity; calcium ion transport; compound eye development.
CG11875	3.013	Unknown at this time.
cinnamon	3.011	Cysteine-type endopeptidase activity; embryonic development via the syncytial blastoderm; Mo-molybdopterin cofactor biosynthetic process; proteolysis.
CG30381	2.924	Unknown at this time.
Centrosome associated protein 60	2.885	Microtubule binding.
CG11555	2.832	Unknown at this time.
separation anxiety	2.831	N-acetyltransferase activity; fatty acid binding ; mitotic sister chromatid cohesion; metabolic process.
CG31381	2.829	tRNA isopentenyltransferase activity; ATP binding; zinc ion binding; tRNA processing
CG4730	2.818	zinc ion binding
CG32817 /// CG3176	2.817	Unknown at this time.
lethal3Des	2.768	Biological processes: mRNA cleavage; RNA metabolic process. 47 alleles are reported.
CG4627	2.763	Unknown at this time.
CG31453	2.741	Its molecular function is described as: ATP binding; nucleoside-triphosphatase activity. The biological processes in which it is involved are not known. 4 alleles are reported. No phenotypic data is available. It has one annotated transcript and one annotated polypeptide.
CG14550	2.739	Unknown at this time.
CG7942	2.732	RNA lariat debranching enzyme activity; RNA processing; RNA splicing, via transesterification reactions; mRNA processing

Translocase of outer membrane 40	2.719	P-P-bond-hydrolysis-driven protein transmembrane transporter activity; transmembrane transporter activity; voltage-gated anion channel activity. It is involved in the biological processes: protein targeting to mitoc
CG11980	2.708	Unknown at this time.
lethal(2)34Df	2.682	DNA binding; nucleoside-triphosphatase activity; nucleotide binding; DNA-dependent DNA replication; DNA replication initiation; DNA replication; mitotic chromosome condens
CG16865	2.666	Unknown at this time.
mitochondrial ribosomal protein S18A	2.641	Structural constituent of ribosome; translation.
CG4743	2.627	transmembrane transporter activity; binding. It is involved in the biological process transport
CG9018	2.623	Unknown at this time.
CG31229	2.619	P-P-bond-hydrolysis-driven protein transmembrane transporter activity; protein targeting to mitochondrion
CG7054	2.619	phosphatidylethanolamine binding
CG14440	2.617	Unknown at this time.
CstF-50	2.608	Biological process mRNA cleavage.
CG8207	2.602	mannose-1-phosphate guanylyltransferase activity; acyltransferase activity; biosynthetic process
lethal (2) k14505	2.602	Unknown at this time
CG11837	2.6	rRNA (adenine-N6,N6-)-dimethyltransferase activity; rRNA modification
frataxin-like	2.593	Biological process cellular iron ion homeostasis
CG10222	2.585	nucleotide binding
CG8366	2.58	DNA binding; nuclease activity; magnesium ion binding
COQ7	2.579	Oxidoreductase activity; transition metal ion binding ; ubiquinone metabolic process; protein metabolic process; ubiquinone biosynthetic process.

Batman	2.578	Specific RNA polymerase II transcription factor activity; protein binding. It is involved in the biological processes: regulation of transcription from RNA polymerase II promoter; chromatin silencing.
CG14270	2.565	Unknown at this time.
CG14803	2.545	Unknown at this time.
CG3709	2.538	Unknown at this time.
CG7747	2.532	peptidyl-prolyl cis-trans isomerase activity
CG11170	2.519	ATP binding; ATPase activity
CG3542	2.518	FH1 domain binding; nuclear mRNA splicing, via spliceosome
zero population growth	2.516	Gap junction channel activity; germ cell development.
CG4951	2.51	Unknown at this time.
Mtr3	2.506	3'-5'-exoribonuclease activity; RNA binding; RNA processing. One allele is reported.
CG6388	2.49	tRNA (guanine-N2-)-methyltransferase activity; RNA binding; tRNA modification
CG6637	2.479	Unknown at this time.
semiphorin	2.478	
CG10473	2.471	nucleotide binding; apoptosis; protein targeting to lysosome. 22 alleles are reported. The phenotype of these alleles is annotated with melanotic mass. It has 2 annotated transcripts and 2 annotated polypeptides.
CG17286	2.468	mitotic spindle organization and biogenesis
CG14781	2.458	mitotic spindle elongation
Origin recognition complex subunit 4	2.452	Nucleoside-triphosphatase activity; nucleotide binding; DNA replication initiation.
CG32736	2.445	Unknown at this time.
altered disjunction	2.443	Protein kinase activity; protein serine/threonine kinase activity; ATP binding; mitotic centrosome separation; mitotic cell cycle; protein amino acid phosphorylation; mito
CG14544	2.431	Unknown at this time.

CG10932	2.43	acetyl-CoA C-acetyltransferase activity; fatty acid biosynthetic process; pyruvate metabolic process
CG6543	2.429	enoyl-CoA hydratase activity; fatty acid beta-oxidation
CG3587	2.425	Unknown at this time.
CG14749	2.418	poly(A)+ mRNA export from nucleus
Rad1	2.417	Damaged DNA binding; exonuclease activity; exodeoxyribonuclease III activity; DNA repair
CG8378	2.411	zinc ion binding
CG2656	2.402	purine nucleotide binding
CG3402	2.399	protein binding
CG11103	2.398	Unknown at this time.
CG32554	2.391	Unknown at this time.
CG33340	2.391	Unknown at this time.
tex	2.389	Unknown at this time
CG12343	2.386	RNA splicing factor activity, transesterification mechanism
lethal (3) 01239	2.374	chaperone binding; unfolded protein binding; 'de novo' protein folding; phagocytosis, engulfment; oogenesis; protein folding
CG2685	2.364	Unknown at this time.
RfC3	2.364	DNA binding; ATP binding; DNA clamp loader activity; DNA replication.
mitochondrial ribosomal protein L11	2.36	structural constituent of ribosome; translation.
CG8159	2.352	zinc ion binding; nucleic acid binding
Xeroderma pigmentosum group A-like	2.348	Damaged DNA binding; nucleotide binding. Nucleotide-excision repair.
CG9754	2.345	Unknown at this time.
Mapmodulin	2.345	Microtubule binding; phosphatase inhibitor activity; protein binding; microtubule-based process; nucleocytoplasmic transport.
RNA polymerase III	2.336	DNA-directed RNA polymerase activity; DNA binding; RNA polymerase III promoter.
lethal (1) G0020	2.332	N-acetyltransferase activity.
CG1134	2.328	protein binding; zinc ion binding
CG7172	2.328	Unknown at this time.
CG5285	2.323	single-strand selective uracil DNA N-glycosylase activity

CG6294	2.314	metallopeptidase activity; zinc ion binding; proteolysis
CG6833	2.314	exonuclease activity; nucleic acid binding.
DNA polymerase gamma	2.309	DNA-directed DNA polymerase activity; ATP binding; glycine-tRNA ligase activity; mitochondrial genome maintenance; mitochondrion organization and biogenesis; DNA-dependent
CG11722	2.302	Unknown at this time.
CG9300	2.299	transporter activity; transport
CG34125	2.292	Unknown at this time.
CG2614	2.291	ATP binding; methyltransferase activity; metabolic process
lethal(3)88Ab	2.289	DNA binding ;DNA-dependent DNA replication; DNA replication initiation; DNA replication; eggshell chorion gene amplification; mitotic chromosome condensation; mitotic spind
CG3625	2.282	Unknown at this time.
CG5585	2.271	Unknown at this time.
thoc6	2.271	mRNA export from nucleus.
tRNA-guanine transglycosylase	2.265	Queuine tRNA-ribosyltransferase activity; queuosine biosynthetic process.
CG9867	2.257	Unknown at this time.
gluon	2.255	DNA binding; nucleotide binding; ATP binding; protein binding; ATPase activity; mitotic chromosome condensation; mitosis; mitotic sister chromatid segregation
CG32721	2.254	mRNA binding; negative regulation of transcription from RNA polymerase II promoter, mitotic
CG10672	2.252	oxidoreductase activity, acting on CH-OH group of donors; binding; metabolic process
CG31278	2.242	peptide deformylase activity; iron ion binding; translation
kappaB-Ras	2.232	GTP binding; protein binding; negative regulation of I-kappaB kinase/NF-kappaB cascade; small GTPase mediated signal transduction.
lethal (3) S147910	2.229	Unknown at this time

actin-related protein	2.228	
CG31917	2.228	Unknown at this time.
ecdysoneless	2.217	13 unique terms, many of which group under: anatomical structure development; embryonic development via the syncytial blastoderm;
Translocase of outer membrane 70	2.216	P-P-bond-hydrolysis-driven protein transmembrane transporter activity; transmembrane transporter activity; protein targeting to mitochondrion.
CG11788	2.208	Unknown at this time.
HP1b	2.206	Chromatin binding; chromatin assembly or disassembly.
CG32320	2.197	Unknown at this time.
CG8435	2.195	Unknown at this time.
NF-YC-like	2.194	
casein kinase 2	2.191	
CG2100	2.19	polynucleotide adenylyltransferase activity; RNA binding; RNA processing
CG34039	2.184	Unknown at this time.
Sirt6	2.184	NAD-dependent histone deacetylase activity; DNA binding; NAD binding; zinc ion binding; chromatin silencing; protein amino acid deacetylation.
CG32736	2.18	Unknown at this time.
CG2931	2.177	mRNA binding; nucleic acid binding; nucleotide binding
CG11808	2.176	Unknown at this time.
DNA polymerase 180K	2.175	
CG9951 /// GA22148	2.174	Unknown at this time.
ORMDL	2.174	Unknown at this time
CG13142	2.171	Unknown at this time.
Use1	2.171	Golgi organization and biogenesis.
CG7772	2.168	carbonate dehydratase activity; zinc ion binding; carbon utilization
CG11125	2.166	Unknown at this time.
5' gene	2.161	Glycerol-3-phosphate dehydrogenase (NAD+) activity; NAD binding; glycerol-3-phosphate metabolic process; flight behavior; triacylglycerol metabolic process; glycerophospha
CG5188	2.16	methionyl aminopeptidase activity; proteolysis

CG6364	2.158	uridine kinase activity; ATP binding; phosphotransferase activity, alcohol group as acceptor; phagocytosis, engulfment; metabolic process
CG10584	2.157	Unknown at this time.
CG15027	2.154	Unknown at this time.
CG5451	2.154	Unknown at this time.
CG6479	2.154	phagocytosis, engulfment
fragment H	2.149	Carboxylesterase activity.
ECSIT	2.147	Protein binding; innate immune response; Toll signaling pathway; defense response; signal transduction
CG11920	2.144	Unknown at this time.
CG11679	2.142	Unknown at this time.
CG12765	2.14	Unknown at this time.
CG6712	2.139	RNA binding
CG17665	2.137	Unknown at this time.
mitochondrial ribosomal protein S2	2.135	Structural constituent of ribosome; translation
CG7845	2.132	Unknown at this time.
CG15653	2.127	Unknown at this time.
CG6812	2.124	cation transmembrane transporter activity; sequence-specific DNA binding; cation transport
Origin recognition complex subunit 1	2.122	DNA binding; ATP binding; nucleoside-triphosphatase activity; DNA-dependent DNA replication; DNA replication initiation; chromatin silencing
Wsck	2.122	Protein-tyrosine kinase activity; ATP binding' protein amino acid phosphorylation.
Odorant receptor 67b	2.117	Olfactory receptor activity; odorant binding; Sensory perception of smell; detection of chemical stimulus involved in sensory perception of smell
mitochondrial ribosomal protein S31	2.115	Structural constituent of ribosome; Translation
CG31873	2.113	diacylglycerol kinase activity; activation of protein kinase C activity
snf5-related 1	2.112	RNA polymerase II transcription factor activity; transcription coactivator activity; general RNA polymerase II transcription factor activity; regulation of transcription;

SMC2	2.111	DNA binding; ATP binding; protein binding; ATPase activity; Sister chromatid cohesion; mitotic spindle organization and biogenesis; mitotic chromosome condensation;
CG3044	2.109	chitinase activity; cation binding; chitin catabolic process
Lobe	2.103	Negative regulation of programmed cell death; eye-antennal disc development; negative regulation of Wnt receptor signaling pathway; compound eye development
mitochondrial transcription termination factor	2.102	Transcription termination factor activity; DNA binding; Termination of mitochondrial transcription
CG17230	2.101	Unknown at this time.
septin	2.099	
germline transcription factor	2.093	DNA binding; ATP binding; DNA clamp loader activity; DNA replication
gamma-tubulin ring protein 84	2.092	Microtubule binding; gamma-tubulin binding; tubulin binding; microtubule minus-end binding; microtubule nucleation; microtubule-based process; regulation of cell cycle
CG12935	2.086	Unknown at this time.
modifier of rudimentary	2.083	Unknown at this time
CG7853	2.082	3'-phosphoadenosine 5'-phosphosulfate transmembrane transporter activity
CG7338	2.078	ribosome biogenesis and assembly
CG12854	2.076	Unknown at this time.
MrgBP	2.07	DNA binding; Transcription.
CG8067	2.062	methyltransferase activity; metabolic process
CG2709	2.061	protein binding; zinc ion binding
CG18428	2.06	Unknown at this time.
Serine/arginine rich protein 55	2.06	ImRNA binding; RNA splicing factor activity, transesterification mechanism; protein binding; nucleotide binding. Nuclear mRNA splicing, via spliceosome
CG8939	2.059	rRNA methyltransferase activity; rRNA processing
interference Hedgehog	2.052	Heparin binding; protein homodimerization activity; protein binding; hedgehog receptor activity;

		smoothened signaling pathway; positive regulation of smoothened signaling
phenoloxidase	2.052	
CG5705	2.051	translation release factor activity, codon specific; translational termination
Transport and Golgi organization 4	2.05	Golgi organization and biogenesis.
CG11820	2.047	protein binding.
presenilin enhancer	2.047	Endopeptidase activity
Smc5	2.047	ATP binding; mitosis; mitotic sister chromatid segregation; DNA metabolic process
CG13850	2.044	ATP binding; protein kinase activity; apoptosis
CG32250	2.043	transporter activity; transmembrane transporter activity; binding; transport
CG11035	2.041	chaperone binding; unfolded protein binding; heat shock protein binding; response to heat; protein folding
CG2611	2.038	Unknown at this time.
Brd8	2.034	Unknown at this time
CG10265	2.032	Unknown at this time.
CG6204	2.032	Unknown at this time.
CG33213	2.028	nucleic acid binding; zinc ion binding
CG12942	2.027	zinc ion binding
CG6444	2.027	Unknown at this time.
CG8060	2.027	protein binding
CG3732	2.023	zinc ion binding
CG7878	2.012	helicase activity; ATP-dependent RNA helicase activity; ATP binding; RNA binding.
CG31120	2.011	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors; iron ion binding; protein metabolic process
CG3639	2.01	protein binding; zinc ion binding; peroxisome organization and biogenesis; protein targeting to peroxisome
CG32786 /// CG32783 /// CG2941	2.008	Unknown at this time.

5' gene	2.005	Glycerol-3-phosphate dehydrogenase (NAD+) activity; NAD binding; glycerol-3-phosphate metabolic process; flight behavior; triacylglycerol metabolic process; glycerophospha
CG17508	2.004	Unknown at this time.
CG13919	2.001	Unknown at this time.
Tetraspanin 3A	2.001	Phagocytosis, engulfment
p47	1.999	nuclear envelope reassembly; rhabdomere development.
CG30094	1.996	zinc ion binding
mitochondrial ribosomal protein L13	1.995	Structural constituent of ribosome. Translation
Alpha 3 glucosyltransferase	1.991	Oligosaccharyl transferase activity; glucosyltransferase activity; protein amino acid N-linked glycosylation
CG14777	1.991	Unknown at this time.
scaf6	1.991	mRNA binding; nuclear mRNA splicing, via spliceosom
Elongation factor Tu mitochondrial	1.99	Translation elongation factor activity; GTP binding; GTPase activity.
CG8828	1.987	protein binding; mitotic spindle organization and biogenesis; regulation of mitosis; vesicle-mediated transport
CG7842	1.986	[acyl-carrier-protein] S-malonyltransferase activity; binding; fatty acid biosynthetic process
CG10107	1.985	cysteine-type peptidase activity; proteolysis
CG5104	1.982	Unknown at this time.
cyclin A	1.981	Cyclin-dependent protein kinase regulator activity; regulation of mitosis; peripheral nervous system development; mitosis; mitotic sister chromatid segregation
CG13339	1.974	Unknown at this time.
CG7705	1.974	Unknown at this time.
anon-fast-evolving-1A3	1.973	Unknown at this time
Drosophila cleavage and polyadenylation stimulation factor-160	1.973	Protein binding; mRNA 3'-UTR binding; mRNA binding; mRNA cleavage; mRNA polyadenylation.
CG5846	1.97	Unknown at this time.
CG32772	1.965	nucleic acid binding; zinc ion binding

male sterile(2)46C	1.965	Small conjugating protein ligase activity; spermatid development; sperm individualization; regulation of protein metabolic process; post-translational protein modification.
CG2453	1.962	2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity
CG4685	1.962	succinate-semialdehyde dehydrogenase activity; gamma-aminobutyric acid catabolic process
anon-fast-evolving-2D12	1.961	Unknown at this time
CG12056	1.961	transition metal ion binding; heme binding
Ucp4A	1.96	Oxidative phosphorylation uncoupler activity; transmembrane transporter activity; binding; proton transport; mitochondrial transport.
CG3335	1.955	helicase activity; mRNA binding; nucleic acid binding; nucleotide binding
CG2875	1.953	Unknown at this time.
CG12022	1.948	Unknown at this time.
MAGE	1.947	Unknown at this time
CG13742	1.945	Unknown at this time.
CG1662	1.944	Unknown at this time.
yolky	1.943	Binding; nuclear mRNA splicing, via spliceosome; Malpighian tubule morphogenesis; central nervous system development; neuroblast proliferation
CG13197	1.941	protein tyrosine/serine/threonine phosphatase activity; protein tyrosine phosphatase activity; protein amino acid dephosphorylation
CG32495 /// Glutathione Synthetase	1.941	glutathione synthase activity; ATP binding; biosynthetic process
CG10688	1.94	phosphomannomutase activity; GDP-mannose biosynthetic process; mannose biosynthetic process
CG10648	1.938	mitotic spindle elongation
CG1636	1.937	Unknown at this time.

CG9597	1.937	sequence-specific DNA binding; DNA binding; bent DNA binding; protein-DNA complex assembly; snRNA transcription from RNA polymerase II promoter; snRNA transcription from RNA polymerase III promoter
CG6961 /// CG18259	1.936	mRNA binding; nucleic acid binding; nucleotide binding
CG32576	1.935	vesicle-mediated transport
Ranbp16	1.934	Ran GTPase binding; nuclear export signal receptor activity; protein transporter activity; binding; protein export from nucleus; protein import into nucleus, docking
CG11063	1.932	ligand-dependent nuclear receptor binding; thyroid hormone receptor binding; actin binding; zinc ion binding
CG32174	1.931	ubiquinone biosynthetic process
KH-domain	1.928	
CG5924	1.926	DNA helicase activity; ATP binding; mitochondrial genome maintenance; protein homooligomerization; DNA replication
CG6726	1.925	aminoacylase activity; metallopeptidase activity; protein dimerization activity; amino acid metabolic process; proteolysis
Hexosaminidase 1	1.925	Beta-N-acetylhexosaminidase activity; beta-N-acetylglucosaminidase activity; cation binding. Carbohydrate metabolic process
CG30096	1.922	Unknown at this time.
Lethal hybrid rescue	1.919	DNA binding
CG11927	1.917	Unknown at this time.
CG7639	1.917	Unknown at this time.
CG16890	1.908	Unknown at this time.
CG5199	1.908	Unknown at this time.
CG33090	1.906	beta-glucosidase activity; coenzyme binding; hydroxymethylglutaryl-CoA reductase (NADPH) activity; bile acid metabolic process; O-glycoside catabolic process; coenzyme A metabolic process

Ski-interacting protein	1.902	Embryonic development via the syncytial blastoderm; eye-antennal disc development
CG10495	1.898	FAD binding; tRNA dihydrouridine synthase activity; tRNA processing
CG12006	1.898	mannosyltransferase activity. GPI anchor biosynthetic process
CG1265	1.897	Unknown at this time.
CG7282	1.896	
CG7379	1.896	zinc ion binding; protein binding
Nobody	1.893	Endopeptidase activity; proteolysis; regulation of exit from mitosis. 4 alleles are reported
CG3011	1.891	glycine hydroxymethyltransferase activity; pyridoxal phosphate binding; L-serine biosynthetic process; glycine metabolic process
Negative elongation factor E	1.89	mRNA binding; nucleotide binding; negative regulation of transcription from RNA polymerase II promoter, mitotic. 4 alleles are reported
CG2972	1.888	Unknown at this time.
Stromalin	1.888	Binding
CG17556 /// CG3678	1.885	binding
CG32022	1.883	Unknown at this time.
mitochondrial ribosomal protein S22	1.88	Structural constituent of ribosome; Translation
vismay	1.88	Histone deacetylase binding; transcription corepressor activity; transcription factor activity; sequence-specific DNA binding' spermatogenesis; regulation of transcription
CG32344	1.877	helicase activity; ATP-dependent RNA helicase activity; ATP binding; RNA binding
Bicoid interacting protein 4	1.876	Pprotein serine/threonine kinase activity; ATP binding; protein amino acid phosphorylation.
CG11006	1.876	mitotic spindle organization and biogenesis
armitage	1.875	DNA helicase activity; embryonic axis specification; mRNA catabolic process, nonsense-mediated decay; negative regulation of oskar mRNA translation

Proteasome 26S regulatory subunit 6A	1.875	Endopeptidase activity; ATPase activity; ATP binding; ATP-dependent peptidase activity; serine-type endopeptidase activity. Proteolysis; cellular process
CG1970	1.874	NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; NAD binding; electron donor activity. mitochondrial electron transport, NADH to ubiquinone.
CG3911	1.874	Unknown at this time.
CG2617	1.873	protein binding; zinc ion binding; oxidoreductase activity; metabolic process
CG11030	1.871	Unknown at this time.
Plum	1.871	ATPase activity, coupled to transmembrane movement of substances; eye pigment precursor transporter activity; ATP binding; ommochrome biosynthetic process
Nuclear inhibitor of Protein phosphatase 1	1.87	Protein phosphatase inhibitor activity; mRNA binding; type 1 serine/threonine specific protein phosphatase inhibitor activity
rev7	1.87	Positive regulation of lyase activity; mitosis. 3 alleles are reported. No phenotypic data is available
Rpt4	1.869	ATPase activity; endopeptidase activity; ATP binding. Iproteolysis; protein catabolic process
CG11576	1.867	Unknown at this time.
CG6697	1.867	Unknown at this time.
GTPase-activating protein 69C	1.867	GTP binding; ARF GTPase activator activity; zinc ion binding; ARF GTPase activity.
dynein-related heavy chain polypeptide	1.866	
CG11123	1.865	RNA binding
CG2116	1.865	zinc ion binding
CG12237	1.863	phosphoric monoester hydrolase activity; metabolic process
CG14722	1.863	apoptotic protease activator activity
dynactin, p27 subunit /// CG17347	1.863	Acyltransferase activity; Microtubule-based movement.
CG9346	1.856	mRNA binding; RNA binding; nucleotide binding; RNA processing
CG8616	1.853	Unknown at this time.

methyltransferase-like	1.853	S-adenosylmethionine-dependent methyltransferase activity
CG13392	1.851	Unknown at this time.
almondex	1.849	Binding; ectoderm development; mesoderm development
Lysyl-tRNA synthetase	1.849	Lysine-tRNA ligase activity; ATP binding; nucleic acid binding; lysyl-tRNA aminoacylation.
CG33635	1.848	protein binding; Golgi to endosome transport
CG31301	1.847	described as nucleic acid binding
CG7828	1.847	ubiquitin activating enzyme activity; binding; metabolic process
CG3776	1.846	protein binding
toys are us	1.845	Unknown at this time
CG4925	1.839	signal transducer activity
CG6607	1.839	Unknown at this time.
Prolyl-tRNA synthetase	1.839	Proline-tRNA ligase activity; ATP binding; glycine-tRNA ligase activity; prolyl-tRNA aminoacylation; glycyl-tRNA aminoacylation
CG6299	1.838	glycolipid transporter activity; glycolipid binding.; glycolipid transport
Nipsnap	1.836	Unknown at this time
CG12360	1.835	Unknown at this time.
CG18292	1.835	Unknown at this time.
CG32649	1.833	protein kinase activity; mitochondrial electron transport, ubiquinol to cytochrome c
CG4159	1.833	pseudouridylate synthase activity; tRNA binding; tRNA-pseudouridine synthase activity; pseudouridine synthesis; tRNA processing
mutagen-sensitive 322	1.833	DNA repair
CG4291	1.832	FH1 domain binding; zinc ion binding; nucleic acid binding; nuclear mRNA splicing, via spliceosome
Signal recognition particle receptor beta	1.832	Signal recognition particle binding; GTPase activity; SRP-dependent cotranslational protein targeting to membrane; larval chitin-based cuticle development
CG8300	1.831	Unknown at this time.
lethal (1) G0255	1.831	Fumarate hydratase activity; tricarboxylic acid cycle; fumarate

		metabolic process
Aly	1.83	Transcription coactivator activity; mRNA binding; nucleic acid binding; nucleotide binding
CG7429	1.827	Unknown at this time.
CG5180	1.826	Unknown at this time.
CG16903	1.825	cyclin-dependent protein kinase regulator activity; general RNA polymerase II transcription factor activity
CG8223	1.825	Unknown at this time.
CG14290	1.824	Unknown at this time.
morula	1.821	Ubiquitin protein ligase binding; mitotic anaphase; negative regulation of synaptic growth at neuromuscular junction; regulation of synaptic transmission
supressor of Ty element 16	1.821	DNA binding; metalloexopeptidase activity; DNA unwinding during replication; regulation of chromatin assembly or disassembly; proteolysis
Cyclin-dependent kinase 8	1.819	Protein serine/threonine kinase activity; cyclin-dependent protein kinase activity; RNA polymerase II transcription mediator activity; ATP binding
lethal (1) G0232	1.818	Protein tyrosine phosphatase activity; non-membrane spanning protein tyrosine phosphatase activity; transporter activity; rhodopsin-like receptor activity.
Mediator complex subunit 27	1.818	RNA polymerase II transcription mediator activity; transcription cofactor activity; transcription initiation from RNA polymerase II promoter
CG12171	1.817	oxidoreductase activity, acting on CH-OH group of donors; binding; metabolic process
TBP-associated factor 30kD subunit beta /// Gdi-related	1.817	General RNA polymerase II transcription factor activity; DNA binding; transcription initiation from RNA polymerase II promoter; regulation of transcription, DNA-dependent
CG3571	1.816	actin binding; protein binding

CG3887	1.815	selenium binding; cell redox homeostasis
CG30373	1.814	Unknown at this time.
CG14815	1.812	peroxisome targeting sequence binding
CG11447	1.809	rRNA (uridine-2'-O-)-methyltransferase activity; rRNA processing
CG3500	1.809	Unknown at this time.
Rs1	1.809	ATP-dependent RNA helicase activity; RNA helicase activity; ATP binding; nucleic acid binding; ribosome biogenesis and assembly
S2P	1.809	Metalloendopeptidase activity; sterol regulatory element-binding protein site 2 protease activity; zinc ion binding; sterol regulatory element binding protein cleavage
CG17385	1.807	zinc ion binding; nucleic acid binding
CG8786	1.806	protein binding; zinc ion binding
lethal (2) 35Df	1.805	ATP-dependent RNA helicase activity; ATP binding; nucleic acid binding.
CG14881	1.804	oxidoreductase activity; binding; metabolic process
CG3362	1.803	Unknown at this time.
CG11859	1.802	protein kinase activity; ATP binding; protein serine/threonine kinase activity; amino acid phosphorylation
CG14881	1.802	oxidoreductase activity; binding; metabolic process
CG6689	1.798	zinc ion binding; nucleic acid binding
tumor-supressor	1.796	Transcription factor activity; sequence-specific DNA binding; negative regulation of transcription from RNA polymerase II promoter; regulation of preblastoderm mitotic cell
Grip71	1.794	Gamma-tubulin binding; mitosis; regulation of cell cycle; mitotic spindle organization and biogenesis
CG6523	1.792	thiol-disulfide exchange intermediate activity; electron carrier activity; protein disulfide oxidoreductase activity; redox homeostasis

CG7197	1.792	GTPase activity; GTP binding' small GTPase mediated signal transduction
Klp10A	1.792	Motor activity; microtubule motor activity; ATP binding; Mitotic sister chromatid segregation; microtubule-based movement; mitotic anaphase A; mitotic spindle organization
Anon-becker2 /// CG6171	1.789	Unknown at this time
TXBP181-like	1.789	Unknown at this time
CG9977	1.787	adenosylhomocysteinase activity; binding; one-carbon compound metabolic process
Topoisomerase IIIa	1.787	DNA topoisomerase type I activity; DNA topoisomerase activity; zinc ion binding; DNA topological change; DNA modification; DNA unwinding during replication
CG3163	1.786	Unknown at this time.
CG9839	1.786	Unknown at this time.
CG13295	1.783	Unknown at this time.
cathepsin B /// CG10992	1.782	Its molecular function is described as cathepsin B activity. It is involved in the biological processes: autophagic cell death; salivary gland cell autophagic cell death; proteolysis; regulation of catalytic activity
CG4042	1.782	sequence-specific DNA binding; transcription factor activity; regulation of transcription, DNA-dependent
Mediator complex subunit 10	1.78	RNA polymerase II transcription mediator activity; transcription coactivator activity; transcription from RNA polymerase II promoter; transcription initiator
CG31109	1.777	zinc ion binding
CG5733	1.776	Unknown at this time.
ribonucleoprotein La	1.774	5S rRNA primary transcript binding; RNA polymerase III transcription termination factor activity; mRNA binding; nucleotide binding; RNA processing
CG3925	1.772	Unknown at this time.
lethal(2) neighbour of 1(2)tid	1.772	Mannosyltransferase activity

TBP-associated factor 80	1.771	General RNA polymerase II transcription factor activity; transcription initiation from RNA polymerase II promoter; regulation of transcription, DNA-dependent; positive regulator
lethal (1) G0095	1.77	Binding
Ogg1	1.77	Oxidized purine base lesion DNA N-glycosylase activity; DNA-(apurinic or apyrimidinic site) lyase activity; damaged DNA binding; DNA repair; nucleotide-excision repair;
CG7988	1.768	circadian rhythm
CG1440	1.767	cysteine-type endopeptidase activity; proteolysis
photolyase	1.767	DNA (6-4) photolyase activity; DNA repair
CG10465	1.762	protein binding; voltage-gated potassium channel activity; potassium ion transport
CG1814	1.762	Unknown at this time.
CG7011	1.762	Unknown at this time.
CG7718	1.762	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity; phospholipid biosynthetic process
Drosophila homolog of HIRA	1.762	Transcription corepressor activity; chromatin binding; chromatin remodeling; sperm chromatin decondensation; fertilization, exchange of chromosomal proteins
mitochondrial ribosomal protein L40	1.762	Structural constituent of ribosome. Translation
Ciao1	1.761	Unknown at this time
CAS/CSE1 segregation protein	1.76	Importin-alpha export receptor activity; protein transporter activity; protein import into nucleus; protein export from nucleus; apoptosis; phagocytosis, engulfment
CG11790	1.756	Unknown at this time.
CG8257	1.754	cysteine-tRNA ligase activity; ATP binding; cysteinyl-tRNA aminoacylation
CG10466	1.752	mRNA binding; RNA binding; metallopeptidase activity; zinc ion binding; nucleotide binding; proteolysis

CG9376	1.749	GPI anchor biosynthetic process
antimeros	1.748	Kinesin binding
CG12140	1.746	electron-transferring-flavoprotein dehydrogenase activity oxidative phosphorylation
CG2246	1.746	ribose phosphate diphosphokinase activity; magnesium ion binding; nucleotide biosynthetic process; nucleoside metabolic process
CG4858	1.746	nucleotide binding; ATP binding
Cyclin-dependent kinase9 2.7	1.742	RNA polymerase subunit kinase activity; cyclin-dependent protein kinase activity; protein serine/threonine kinase activity; positive transcription elongation factor activity;
CG11847	1.74	protein export from nucleus
CG7262	1.74	transport
CG8314	1.74	zinc ion binding
CG16812	1.739	Unknown at this time.
CHORD containing protein	1.739	Zinc ion binding
mutagen-sensitive 312	1.739	Protein binding; nucleotide-excision repair, DNA damage recognition; meiotic chromosome segregation; meiotic recombination
CG12151	1.738	[pyruvate dehydrogenase (lipoamide)] phosphatase activity; protein serine/threonine phosphatase activity; phosphoprotein phosphatase activity; protein amino acid dephosphorylation; pyruvate metabolic process
CG9140	1.738	NADH dehydrogenase (ubiquinone) activity; NADH dehydrogenase activity; NAD binding; 4 iron, 4 sulfur cluster binding; FMN binding; electron donor activity; mitochondrial electron transport, NADH to ubiquinone
CG13563	1.737	Unknown at this time.
CG10563	1.736	phagocytosis, engulfment
CG11975	1.736	Unknown at this time.
CG14641	1.736	mRNA binding; zinc ion binding; nucleic acid binding; nucleotide binding; alternative nuclear mRNA splicing, via spliceosome

CG7263	1.735	electron carrier activity; FAD binding; DNA fragmentation during apoptosis; induction of apoptosis; cell redox homeostasis
beta4GalNAcTB	1.731	Acetylgalactosaminyltransferase activit; N-acetylglucosamine metabolic process. 8 alleles are reported.
CG4673	1.731	structural constituent of nuclear pore; zinc ion binding
Rab-protein 4	1.731	GTPase activity; GTP binding; endocytosis; small GTPase mediated signal transduction; protein transport.
zeste-white 5	1.73	Transcription factor activity; chromatin insulator sequence binding; protein binding; zinc ion binding
CG5384	1.729	ubiquitin thiolesterase activity; protein modification process; ubiquitin-dependent protein catabolic process
DNA polymerase interacting tpr containing protein of 47kD	1.725	Binding
CG3040	1.724	protein binding
sec15	1.724	axon guidance; phototaxis; neurotransmitter secretion; synaptic vesicle docking during exocytosis; synaptic vesicle targeting; vesicle-mediated transport
d-spinophilin	1.723	Protein phosphatase 1 binding; protein binding; phosphopantetheine binding; olfactory behavior.
regulatory subunit A of type 2A protein phosphatase	1.721	Protein phosphatase type 2A regulator activity; protein serine/threonine phosphatase activity; binding; protein amino acid dephosphorylation; phagocytosis, engulfment; mit
tiovivo	1.718	Protein phosphatase 1 binding; microtubule motor activity; chromatin binding; plus-end-directed microtubule motor activity; ATP binding; mitotic chromosome condensation
CG4802	1.717	S-methyl-5-thioadenosine phosphorylase activity; phosphorylation

Updo	1.717	Uroporphyrinogen decarboxylase activity; heme biosynthetic process; porphyrin biosynthetic process
CG5933	1.712	mRNA (2'-O-methyladenosine-N6-)-methyltransferase activity; RNA methylation
Rrp45	1.712	3'-5'-exoribonuclease activity; RNA binding; mRNA processing
Spindle-B	1.712	Recombinase activity; ATP binding; DNA binding; DNA-dependent ATPase activity; 14 unique terms, many of which group under: primary metabolic process
zwilch	1.712	Mitosis; mitotic cell cycle spindle assembly checkpoint
CG11696	1.708	zinc ion binding
CG33681	1.708	Unknown at this time.
CG13097	1.706	rRNA processing
CG3680	1.706	catalytic activity; transcription factor activity; regulation of transcription, DNA-dependent
CG7698	1.706	hydrolase activity; mRNA cleavage; mRNA polyadenylation
CG7364	1.705	transporter activity; phagocytosis, engulfment
ribonuclease H1	1.703	Ribonuclease H activity; magnesium ion binding; nucleic acid binding
Hus1-like	1.702	DNA repair.
Sirt4	1.702	NAD-dependent histone deacetylase activity; NAD binding; DNA binding; zinc ion binding; chromatin silencing; protein amino acid deacetylation
CG3287	1.701	Unknown at this time.
CG11866	1.7	Unknown at this time.
spindle-G	1.7	Protein binding. 18 unique terms, many of which group under: oocyte axis determination; anterior/posterior axis specification; dorsal/ventral axis specification
CG15916	1.699	rRNA processing
CG11695	1.698	zinc ion binding
CG12393	1.698	Unknown at this time.
CG32038	1.698	Unknown at this time.
DNApol-eta	1.698	DNA-directed DNA polymerase activity; DNA synthesis

Spase 18/21-subunit	1.698	Signal peptidase activity; serine-type peptidase activity; signal peptide processing; proteolysis
cyclin C	1.696	Cyclin-dependent protein kinase regulator activity; RNA polymerase II transcription mediator activity; protein binding. Transcription initiation from RNA polymerase II pro
Eukaryotic initiation factor 2alpha	1.696	Translation initiation factor activity; GTP binding; tRNA binding; RNA binding; translational initiation; formation of translation initiation ternary complex; mitotic spin
CG7556	1.695	unfolded protein binding; DNA binding; heat shock protein binding; protein folding
CG3446	1.692	Its molecular function is described as NADH dehydrogenase activity; mitochondrial electron transport, NADH to ubiquinone
CG31800	1.688	Unknown at this time.
lethal (3) s1921	1.686	Deoxyhypusine monooxygenase activity; binding; peptidyl-lysine modification to hypusine
CG6672	1.684	zinc ion transmembrane transporter activity; cation transport
CG34015	1.682	Unknown at this time.
CG4813	1.681	protein binding; zinc ion binding
Dak1	1.681	Cytidylate kinase activity; uridylate kinase activity; ATP binding; nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
CG4769	1.68	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity; heme binding; iron ion binding; oxidative phosphorylation; mitochondrial electron transport, ubiquinol to cytochrome c
Polypeptide N-acetylgalactosaminyltransferase 35A	1.679	Polypeptide N-acetylgalactosaminyltransferase activity; Oligosaccharide biosynthetic process; open tracheal system development

methionine-R-sulfoxide reductase	1.678	protein-methionine-R-oxide reductase activity; zinc ion binding; peptide-methionine-(S)-S-oxide reductase activity; peptidyl-methionine modification.
CG12768	1.677	Unknown at this time.
mei-217 /// transcript c	1.677	Carboxypeptidase A activity; zinc ion binding; meiotic recombination; proteolysis
undefined 1	1.677	Transcription factor activity
CG3608	1.673	protein kinase activity; ATP binding; protein amino acid phosphorylation
fasciclin I	1.673	Cell adhesion molecule binding.; neuron recognition; axon guidance; calcium-independent cell-cell adhesion; homophilic cell adhesion; neuron adhesion
CG6995	1.67	mRNA binding; nucleic acid binding; nucleotide binding; regulation of alternative nuclear mRNA splicing, via spliceosome
CG9799	1.668	rRNA processing
Tfb2	1.668	General RNA polymerase II transcription factor activity; ttranscription initiation from RNA polymerase II promoter; regulation of transcription, DNA-dependent; DNA repair
CG13390	1.664	GTP binding; hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
CG6984	1.663	enoyl-CoA hydratase activity; metabolic process
licorne	1.663	MAP kinase kinase activity; protein kinase activity; protein serine/threonine kinase activity; receptor signaling protein serine/threonine kinase activity; ATP binding.
MICAL-like	1.663	Actin binding; zinc ion binding
ATP-dependent RNA helicase	1.661	ATP-dependent RNA helicase activity; ATP binding; nucleic acid binding; oxidoreductase activity; regulation of alternative nuclear mRNA splicing, via spliceosome
CG8818	1.656	transferase activity, transferring phosphorus-containing groups

Acid phosphatase 1	1.655	Acid phosphatase activity
CG10616	1.654	Unknown at this time.
CG30349	1.649	Unknown at this time.
CG18766	1.648	Unknown at this time.
Mediator complex subunit 9	1.648	Unknown at this time
Downstream of raf1	1.647	IMAP kinase kinase activity; receptor signaling protein serine/threonine kinase activity; MAP kinase activity; ATP binding; protein serine/threonine kinase activity; border
Eukaryotic initiation factor 1A	1.646	Translation initiation factor activity; RNA binding; translation; translational initiation; smoothened signaling pathway; phagocytosis, engulfment
Regena	1.646	Transcription regulator activity; regulation of transcription
CG17293	1.644	microtubule severing
Peroxisomal farnesylated protein	1.643	Unknown at this time
anonymous fast evolving gene IG5	1.639	Satellite DNA binding; telomere capping
CG6066	1.639	Unknown at this time.
lethal (1) G0156	1.639	Isocitrate dehydrogenase (NAD+) activity; tricarboxylic acid cycle
CG18853 /// photolyase	1.638	deoxyribodipyrimidine photo-lyase activity; DNA repair
CG7158	1.638	Unknown at this time.
Nucleosome assembly protein 1	1.638	Histone binding; nucleosome assembly; regulation of transcription, DNA-dependent
CG3415	1.637	estradiol 17-beta-dehydrogenase activity; binding; cysteine-type endopeptidase activity; proteolysis
CG5044	1.637	3-hydroxyisobutyryl-CoA hydrolase activity; metabolic process
Electron transfer flavoprotein	1.634	Electron carrier activity; FAD binding' Malpighian tubule morphogenesis; ectodermal gut morphogenesis; head involution; morphogenesis of an epithelium; open tracheal system
CG18508	1.633	Unknown at this time.
eukaryotic release factor 3	1.632	Translation release factor activity; translation termination factor activity; GTP binding; GTPase activity; translational termination

CG11266	1.629	mRNA binding; RNA binding; nucleotide binding; regulation of alternative nuclear mRNA splicing, via spliceosome; RNA splicing
CG32442	1.628	Unknown at this time.
CG12219	1.627	zinc ion binding; nucleic acid binding
missing imaginal precursors	1.627	Transcription activator activity; chromatin-mediated maintenance of transcription
CG9797	1.625	zinc ion binding; nucleic acid binding
Mediator complex subunit 20	1.623	RNA polymerase II transcription mediator activity; DNA-directed RNA polymerase activity; transcription coactivator activity; transcription initiation from RNA polymerase
ENL/AF9-related	1.621	General RNA polymerase II transcription factor activity; transcription initiation from RNA polymerase II promoter; regulation of transcription, DNA-dependent
bluestreak	1.62	Regulation of pole plasm oskar mRNA localization; oocyte microtubule cytoskeleton polarization; pole plasm oskar mRNA localization; protein localization
CG9849	1.617	muscle cell fate determination
Trip1	1.616	Translation initiation factor activity; translational initiation; translation
CG5317	1.612	structural constituent of ribosome; transcription regulator activity; process translation
CG14231	1.611	zinc ion binding; O-sialoglycoprotein endopeptidase activity; proteolysis
mitochondrial ribosomal protein L22	1.61	Structural constituent of ribosome; translation
CG5543	1.606	Unknown at this time.
dynactin, p25 subunit	1.605	Acyltransferase activity; microtubule-based movement
Tudor-SN	1.605	Transcription coactivator activity; nuclease activity; nucleic acid binding; RNA interference
CG17896	1.603	methylmalonate-semialdehyde dehydrogenase (acylating) activity; pyrimidine base metabolic process; valine metabolic process

CG5131	1.596	KU70 binding; metallopeptidase activity; zinc ion binding; proteolysis
Noa36	1.588	Metal ion binding; zinc ion binding
CG4140	1.587	Unknown at this time.
CG18041	1.585	magnesium ion binding; inorganic diphosphatase activity; phosphate metabolic process
CG3548	1.584	Unknown at this time.
rhomboid-7	1.579	Mitochondrial fusion
TH1	1.579	mRNA binding; negative regulation of transcription from RNA polymerase II promoter, mitotic
Int6 homologue	1.578	Translation initiation factor activity; translational initiation; phagocytosis, engulfment.
CG2056	1.577	trypsin activity; ATP binding; serine-type endopeptidase activity; protein kinase activity; proteolysis; innate immune response; defense response to Gram-positive bacterium; defense response to Gram-negative bacterium; defense response to fungus; protein amino acid phosphorylation
salvador/shar-pei	1.574	Protein binding; 13 unique terms, many of which group under: regulation of biological process; anatomical structure development; programmed cell death
Yippee	1.574	Zinc ion binding; metal ion binding
CG10306	1.572	translation initiation factor activity; ribosome binding; translational initiation; regulation of translational initiation
CG9393	1.558	P-P-bond-hydrolysis-driven transmembrane transporter activity; protein targeting to mitochondrion; mitochondrial transport; protein transport
Kisir	1.556	Larval behavior; larval locomotory behavior; spermatogenesis; peristalsis
heat shock protein 60 kDa	1.555	Unfolded protein binding; ATP binding; response to heat; protein folding; protein refolding; response to stress; 'de novo' protein folding; protein targeting to mitochondria

CG30424	1.544	Unknown at this time.
CG10585	1.531	trans-hexaprenyltranstransferase activity
CG13550	1.53	calcium ion binding; mitotic spindle organization and biogenesis
SAM methionine methyltransferase	1.525	Unknown at this time

[1] **Flybase descriptions (43)**