MOLECULAR ECOLOGY

Supplemental Information for:

Association mapping desiccation resistance within chromosomal inversions in the African malaria vector *Anopheles gambiae*

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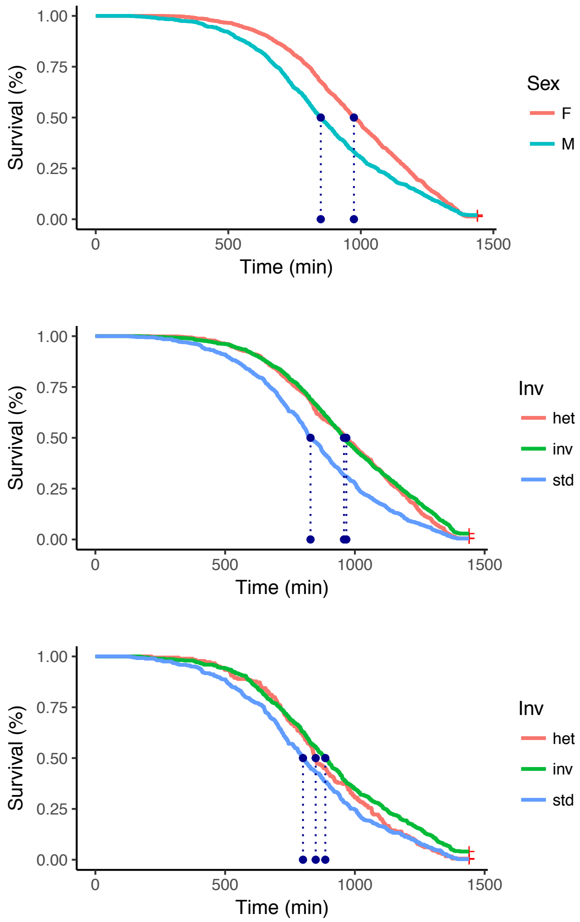

Figure S1. Survival of teneral adult *An. gambiae* under acute desiccation stress. Top, data are stratified by sex (all karyotypes combined). Middle, data are stratified by karyotype (both sexes combined). Bottom, data correspond to males only, and are stratified by karyotype (compare to Figure 1 in main text). These trends are consistent with previous measurements made using laboratory colonies of *An. gambiae*, but natural populations are more resistant to desiccation stress. For example, median survival for inverted homozygotes (both sexes combined) was 958 min (95% confidence interval: 942-981) in our samples compared to 612 min (95% confidence interval: 542-697) in a Cameroonian laboratory colony of *An. gambiae* (Fouet et al., 2012). Similarly, median survival for standard homozygotes was 829 min (95% CI: 812-863) compared to 537 min (95% CI: 506-575) in the corresponding laboratory colony (Fouet et al., 2012).

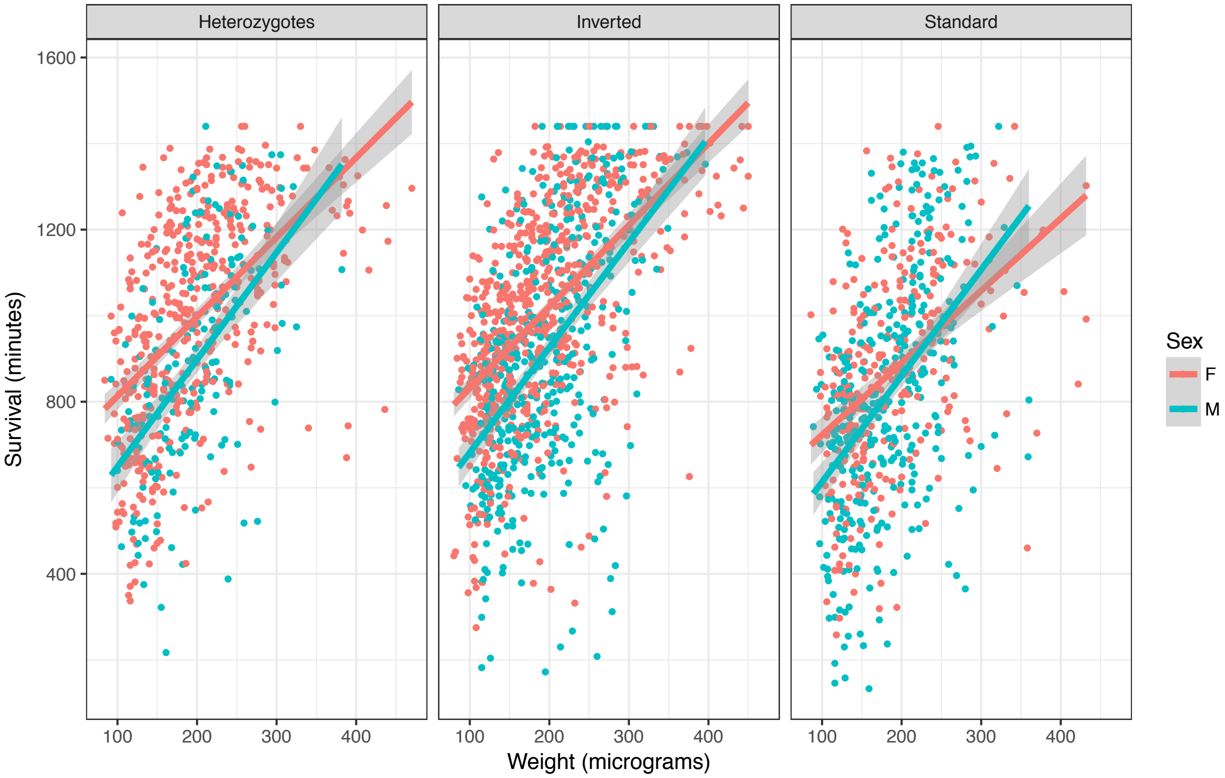

Figure S2. Survival of teneral adult *An. gambiae* under acute desiccation stress is influenced by body mass. Correlation between weight and survival in males and females of all three karyotypes was significant (*F*-statistic, $P < 0.001$).

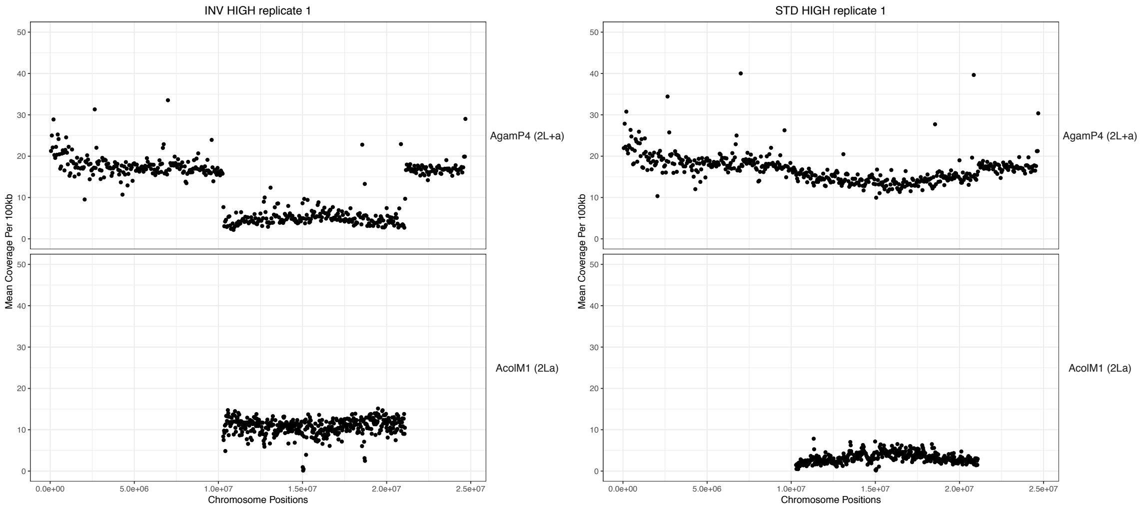

Figure S3. Chromosome 2L read-mapping coverage depends on karyotype of the reference assembly. We examined coverage on chromosome 2L using non-overlapping sliding windows (100 kb). Each point represents the average coverage of each 100-kb window. Left: Pseudo-chromosome 2La (derived from the AcolM1 reference assembly) retained twice as many reads from the INV HIGH pool (=10.8) compared to the 2L+^{a} counterpart from the AgamP4 reference assembly (=5.1). Right: The opposite pattern was observed with the STD HIGH pool. In this case, the 2La pseudo-reference retained a mean coverage of 3.2 compared with 14.5 for the 2L+^{a} reference. The sum of mean coverage across the two arrangements (15.9 and 17.7 for INV HIGH and STD HIGH, respectively) was comparable to the mean coverage for the rest of chromosome 2L (17.6 and 18.6 for INV HIGH and STD HIGH). The replicate pools further confirmed these observations.

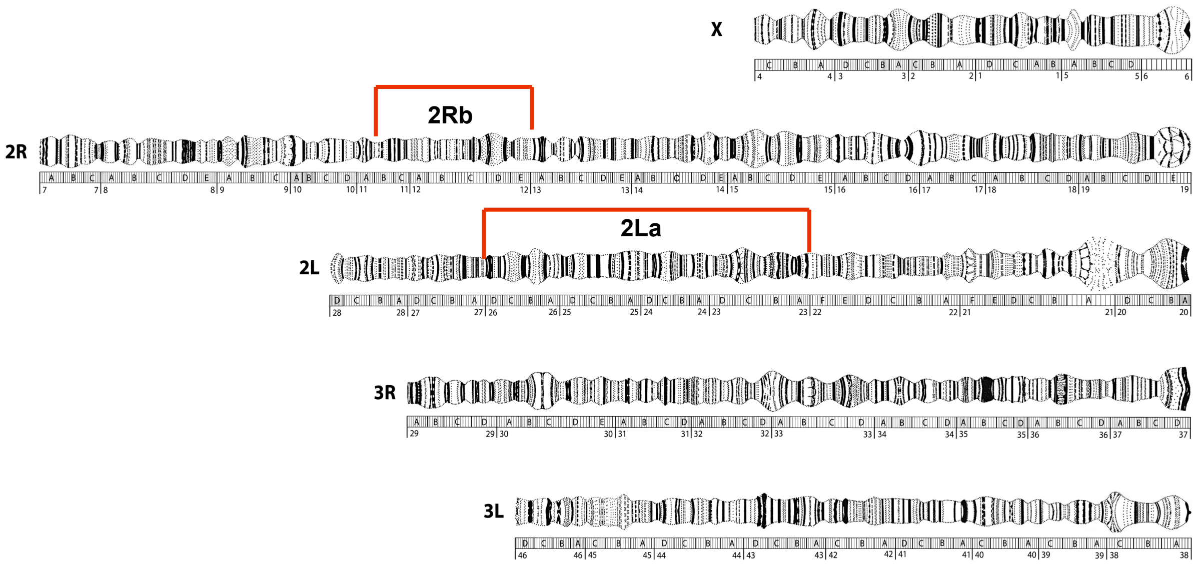

Figure S4. Genomic extent of In(2La) and In(2Rb). Polytene chromosomes of the five major chromosomal arms in *An. gambiae*, with the location of inversions 2Rb and 2La shown. For more information on the location of all common and rare inversions in *An. gambiae*, see Pombi et al. (2008), which is also the source for the polytene chromosomes shown here.

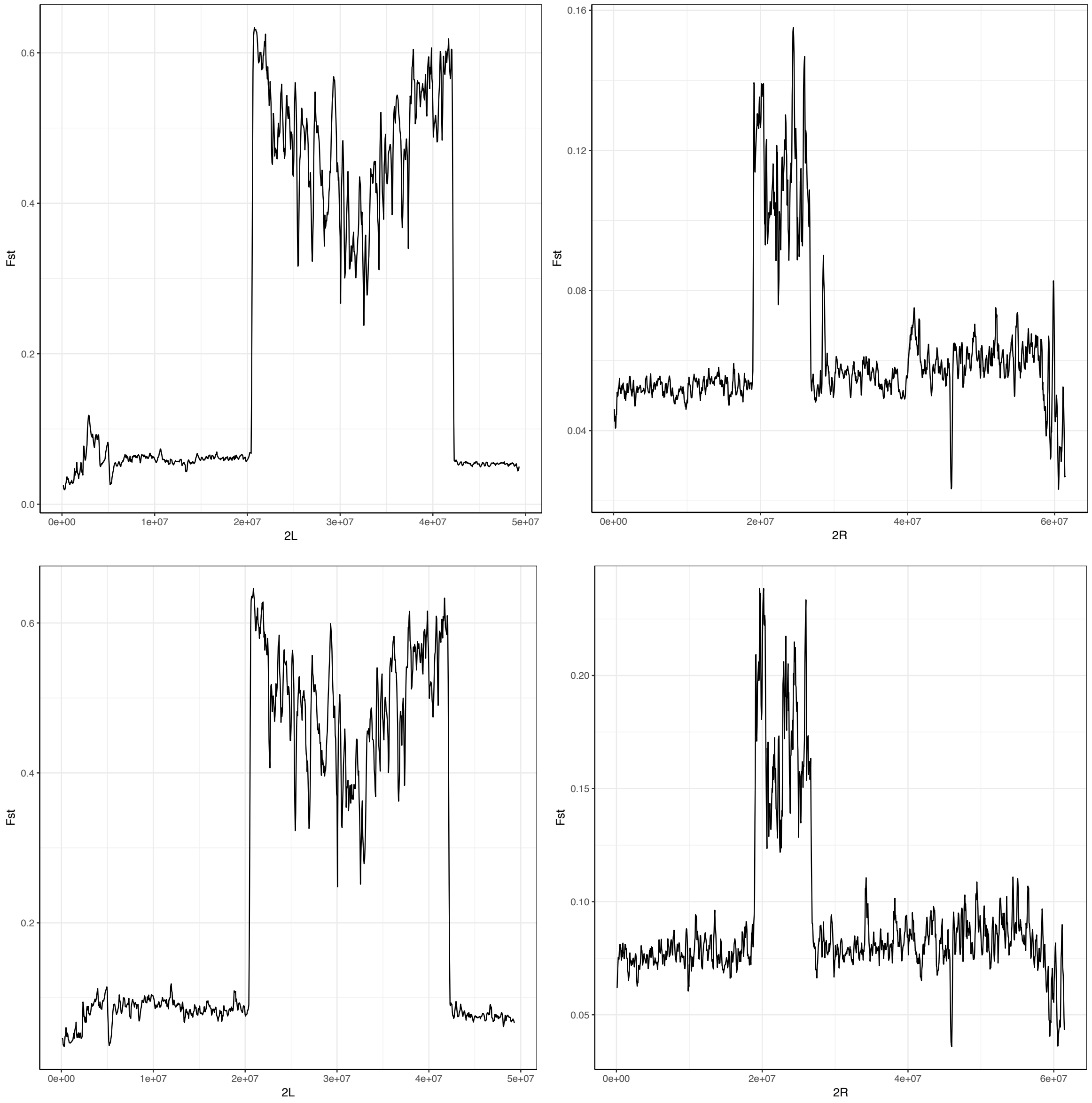

Figure S5. Sequence differentiation within inversions. Left, top: Differentiation (F_{ST}) between INV HIGH and STD HIGH pools on chromosome 2L. Left, bottom: Differentiation (F_{ST}) between INV HIGH and STD LOW pools on chromosome 2L. Right, top: Differentiation (F_{ST}) between INV HIGH and STD HIGH pools on chromosome 2R. Right, bottom: Differentiation (F_{ST}) between INV HIGH and STD LOW pools on chromosome 2R. In all cases, sharply higher differentiation corresponds to the rearranged region on each arm, regardless of phenotypes. Note the different scales on the y-axis of the left and right graphs.

Table S1. Gene candidates with significant SNPs mapped within 2La inversion.

P-value	SNP position	Gene	Variant Type	Drosophila	Gene Description†
9.00E-08	25195489	AGAP006026	5' UTR	FBgn0004619	Glutamate receptor IA
1.22E-06	40273766	AGAP006961	downstream	FBgn0001233	Hsp83
1.22E-06	40273766	AGAP006962	upstream	FBgn0026061	Multiple inositol polyphosphate phosphatase
1.22E-06	40273766	AGAP006963	downstream	FBgn0027786	Mitochondrial solute carrier
9.02E-06	34876498	AGAP006633	intron	FBgn0034135	Syntrophin-like
1.01E-05	25834778	AGAP006059	intron	FBgn0052206	LDL receptor-like
2.57E-05	34101580	AGAP028608	upstream		
2.57E-05	34101580	AGAP006546	upstream	FBgn0035360	
2.59E-05	29813359	AGAP006330	intron	FBgn0042185	Mitochondrial calcium uniporter
2.59E-05	29813359	AGAP006339	downstream	FBgn0263973	javelin
3.01E-05	34271622	AGAP028458	synonymous		
3.01E-05	34271622	AGAP006581	upstream		
3.01E-05	34271622	AGAP006582	upstream		
3.01E-05	34271622	AGAP006583	upstream		
3.01E-05	34271622	AGAP028459	downstream		
3.01E-05	34271622	AGAP006584	downstream		
3.01E-05	34271622	AGAP006585	downstream		
3.01E-05	34271622	AGAP006586	downstream		
3.40E-05	34101581	AGAP028608	upstream		
3.40E-05	34101581	AGAP006546	intron		
3.83E-05	24907183	AGAP006020	downstream	FBgn0035187	tryptophan 5-monooxygenase
5.03E-05	28601340	AGAP029069	upstream		
5.03E-05	28601340	AGAP006244	downstream	FBgn0035523	Choline transporter-like
5.03E-05	28601340	AGAP006245	downstream	FBgn0035520	spliceosome complex B
5.03E-05	28601340	AGAP006246	downstream	FBgn0033529	calcium-binding
5.45E-05	33888255	AGAP006526	intron	FBgn0063485	lasp (nebulin)
5.45E-05	33888255	AGAP006527	upstream		
5.58E-05	28779803	AGAP006264	upstream	FBgn0035922	peroxin 7
6.98E-05	34957673	AGAP006634	intron	FBgn0011260	Semaphorin-2A
8.26E-05	28487138	AGAP006218	intron	FBgn0035132	GPRMTH4 (methuselah-like receptor)
8.37E-05	41040683	AGAP007027	upstream	FBgn0033785	Scaffold protein containing ankyrin repeats and SAM domain
8.76E-05	35730362	AGAP006654	upstream	FBgn0036698	3-betahydroxysteroid dehydrogenase
8.83E-05	34270037	AGAP006580	downstream	FBgn0041100	parkin (E3 ubiquitin ligase)
8.83E-05	34270037	AGAP006581	upstream		
8.83E-05	34270037	AGAP006582	5' UTR/synonymous		
8.83E-05	34270037	AGAP006583	downstream		
8.83E-05	34270037	AGAP006584	downstream		
8.83E-05	34270037	AGAP006585	downstream		
8.83E-05	34270037	AGAP028458	downstream		
8.83E-05	34270037	AGAP028459	downstream		
9.63E-05	28713879	AGAP006260	downstream/intron	Zasp66	alpha actinin-binding
1.04E-04	28542644	AGAP006225	downstream	FBgn0038350	aldehyde oxidase
1.04E-04	28542644	AGAP006226	synonymous	FBgn003835	aldehyde oxidase
1.04E-04	28542644	AGAP006227	downstream	gasoline	carboxylesterase
1.12E-04	41032872	AGAP007025	downstream	FBgn0050001	Fanconi anaemia group A protein
1.12E-04	41032872	AGAP007026	upstream	FBgn0010531	copper chaperone for superoxide dismutase (Ccs)
1.12E-04	41032872	AGAP007027	downstream		
1.20E-04	28065761	AGAP006188	intron	FBgn0035802	Puratrophin-1-like; RhoGEF
1.40E-04	30510772	AGAP006364	synonymous	FBgn0035244	ATP binding cassette transporter (ABCB4)
1.40E-04	30510772	AGAP006365	upstream	tsunagi	spliceosome complex C
1.40E-04	30510772	AGAP013401	downstream	FBgn0053230	peptidyl-lysine methylation
1.75E-04	28942266	AGAP006270	intron	FBgn0264959	SRC tyrosine kinase
1.84E-04	40247869	AGAP006956	intron	FBgn0034972	COE10O
1.91E-04	22289023	AGAP005832	intron	FBgn0034075	Aspartyl beta-hydroxylase
1.97E-04	32232683	AGAP006448	intron	FBgn0259243	PKA-R1
2.17E-04	23141642	AGAP005883	downstream	FBgn0036685	
2.17E-04	23141642	AGAP005884	upstream	FBgn0052380	sphingomyelin synthase
2.21E-04	34077483	AGAP006540	downstream	FBgn0013751	arrowhead (LIM homeobox protein)
2.21E-04	34077483	AGAP006541	upstream/intron	FBgn0036117	aminotransferase
2.21E-04	34077483	AGAP006542	downstream	FBgn0031114	Cactin (spliceosome complex C)

2.40E-04	39234911	AGAP006867	intron	FBgn0036880	CPR141
2.41E-04	28065781	AGAP006188	intron		
2.58E-04	22289028	AGAP005832	intron		

[†] blank gene description means no available function annotation

Table S2. Gene candidates with significant SNPs mapped within 2Rb inversion.

P-value	SNP Position	Gene	Variant Type	Drosophila	Description†
0.00000126	23164879	AGAP002578	intron	FBgn0263111	cacophony; voltage-dependent p/q type calcium channel
0.00000164	21489892	AGAP002444	downstream		GPROP2; pteropsin
0.00000264	20780850	AGAP002372	intron	FBgn0003267	rough; Hox-like homeobox transcription factor
0.00000533	26592984	AGAP002744	intron	FBgn0040359	
0.00000533	26592984	AGAP013160	downstream		
0.00000609	21934742	AGAP002487	upstream	FBgn0052532	Paired-like homeobox transcription factor
0.00000865	25505947	AGAP002677	intron	FBgn0083946	coiled-coil domain-containing protein lobo (lost boys) homolog; transglutaminase; dynein regulatory complex subunit 7
0.0000119	22873334	AGAP002562	upstream		tRNA-Ala
0.0000119	22873334	AGAP002563	downstream	FBgn0037326	Ras-like protein family member 10B precursor
0.0000119	22873334	AGAP002564	upstream	FBgn0000064	fructose-bisphosphate aldolase, class I
0.00001453	22796341	AGAP002556	upstream	FBgn0011282	Obp66; odorant-binding protein 66
0.00001453	22796341	AGAP002557	downstream	FBgn0001112	gld; glucose dehydrogenase (acceptor)
0.00001453	22796341	AGAP013111	synonymous		
0.00001453	22796341	AGAP013222	upstream		
0.0000147	20009436	AGAP002335	upstream	FBgn0005649	nucleolysin TIA-1/TIAR
0.00001871	21209074	AGAP002425	downstream	FBgn0036975	cysteine sulfinic acid decarboxylase
0.00001871	21209074	AGAP002426	upstream	FBgn0035243	Protein OPI10 homolog
0.00001871	21209074	AGAP002427	upstream	FBgn0004380	klp64D; kinesin family member 3/17
0.00001871	21209074	AGAP002428	downstream	FBgn0036433	
0.00001912	26241026	AGAP002721	upstream	FBgn0003965	v (vermilion); tryptophan 2,3-dioxygenase
0.00001912	26241026	AGAP002722	synonymous		odorant receptor (Or28)
0.00001912	26241026	AGAP002723	upstream	FBgn0052544	
0.00001987	24528329	AGAP002628	intron	FBgn0085382	Fibronectin III/immunoglobulin subtype 2
0.00001989	20385010	AGAP002342	intron		
0.00002513	21004295	AGAP002411	intron	FBgn0020278	Loco (locomotion defects); regulator of G protein signaling; in Drosophila, roles include response to stress, starvation, and temperature stimulus
0.00002957	22852527	AGAP002560	intron	FBgn0037324	odorant receptor obligate co-receptor (Orco, Or7)
0.00002957	22852527	AGAP002561	downstream		tRNA-Ala
0.00003237	19894062	AGAP002327	downstream	FBgn0042179	glucosyl/glucuronosyl transferases
0.00003237	19894062	AGAP012947	downstream	FBgn0039027	
0.00003237	19894062	AGAP002328	upstream	FBgn0030797	
0.00003701	20545039	AGAP002352	downstream/intron	FBgn0039044	p53 transcription factor
0.00003701	20545039	AGAP002353	upstream		lipase
0.00003739	26592585	AGAP002744	intron		
0.00004798	24165003	AGAP002614	intron		splicing factor, arginine/serine-rich 16
0.00004867	22445479	AGAP002530	upstream		poly(ADP-ribose) glycohydrolase ARH3
0.00004867	22445479	AGAP002531	downstream	FBgn0263602	taspase, threonine aspartase, 1
0.00004867	22445479	AGAP002532	downstream	FBgn0010317	CycJ; cyclin J
0.00004867	22445479	AGAP002533	upstream	FBgn0002283	polycomb group RING finger protein 3
0.00004867	22445479	AGAP002534	downstream	FBgn0035964	Dhpr; dihydropteridine reductase
0.00004995	21004288	AGAP002411	intron		
0.00005171	22461451	AGAP002537	downstream	FBgn0038901	Bursicon; component of bursicon neurohormone
0.0000528	23019258	AGAP002573	intron		GTPase-activating Rap/Ran-GAP domain-like protein 3
0.00005779	25208441	AGAP002657	upstream	FBgn0031094	
0.00005779	25208441	AGAP002658	downstream	FBgn0000426	small nuclear ribonucleoprotein polypeptide F; mRNA splicing
0.00005779	25208441	AGAP002659	upstream	FBgn0030756	solute carrier family 10 (sodium/bile acid cotransporter)
0.00005779	25208441	AGAP002660	downstream		tRNA-Glu
0.00005779	25208441	AGAP002661	upstream	FBgn0031092	delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase
0.00005779	25208441	AGAP002662	downstream	FBgn0038649	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
0.00006072	24970806	AGAP002647	intron	FBgn0011754	phosphorylase kinase gamma subunit
0.00007603	19393501	AGAP002315	intron	FBgn0039705	APG16L, autophagy related gene
0.00008807	25208466	AGAP002657	upstream		
0.00008807	25208466	AGAP002658	downstream		
0.00008807	25208466	AGAP002659	upstream		
0.00008807	25208466	AGAP002660	downstream		
0.00008807	25208466	AGAP002661	upstream		

0.00008807	25208466	AGAP002662	downstream		
0.00008867	20790883	AGAP002374	3' UTR	FBgn0001215	heterogeneous nuclear ribonucleoprotein A1/A3
0.00008867	20790883	AGAP002375	downstream	FBgn0038903	DNA-directed RNA polymerase I subunit RPA12
0.00008867	20790883	AGAP002376	downstream		
0.0001082	23187621	AGAP002578	intron		_
0.00012045	19894050	AGAP002327	downstream		
0.00012045	19894050	AGAP002328	upstream		
0.00012045	19894050	AGAP012947	downstream	FBgn0039028	
0.00012982	23048372	AGAP002573	intron		
0.00014449	24942280	AGAP002644	downstream	FBgn0037989	ATP8B; phospholipid-translocating ATPase
0.00014449	24942280	AGAP002645	downstream	FBgn0011710	septin 2; GTPases involved in cytokinesis, trafficking
0.00014909	26593970	AGAP002744	intron		
0.00014909	26593970	AGAP013160	downstream		
0.00015911	23187640	AGAP002578	intron		
0.00016548	23185405	AGAP002578	intron		_
0.00016931	24564700	AGAP002629	upstream	FBgn0030999	Mur18B (mucin-related 18B); chitin-binding; chitin metabolisum
0.00017077	20969379	AGAP002403	downstream	FBgn0039632	cullin 5; nucleoside diphosphate-linked moiety X motif 18
0.00017077	20969379	AGAP002404	upstream	FBgn0039632	cullin 5; nucleoside diphosphate-linked moiety X motif 18
0.00017077	20969379	AGAP002405	downstream	FBgn0037378	
0.00017819	23048368	AGAP002573	intron		
0.00018003	23187985	AGAP002578	intron		_
0.00019025	26673777	AGAP002751	downstream		
0.00019025	26673777	AGAP002752	downstream		DnaJ (Hsp40) homolog, subfamily C, member 3
0.00019025	26673777	AGAP002753	splice region/intron		
0.00019025	26673777	AGAP002754	upstream	FBgn0037328	RpL35a; 60S ribosomal protein L35a
0.00019361	20213704	AGAP002336	upstream	FBgn0032484	kek4 (kekkon4); transmembrane leucine-rich repeat (LRR) and immunoglobulin-like protein
0.0002011	20385413	AGAP002342	intron		
0.00021119	19894069	AGAP002327	downstream		
0.00021119	19894069	AGAP002328	upstream		
0.00021119	19894069	AGAP012947	downstream		
0.00021686	23313805	AGAP002587	upstream	FBgn0031010	
0.00021686	23313805	AGAP002588	downstream		
0.00024263	19224936	AGAP002312	downstream	FBgn0051301	
0.00024263	19224936	AGAP002313	upstream	FBgn0051301	
0.00024263	19224936	AGAP002314	downstream		
0.00024378	22833655	AGAP002559	intron	FBgn0037323	alpha-tocopherol transfer protein-like
0.00024815	23108081	AGAP002575	upstream	FBgn0030357	Sclp; leucine-rich repeat
0.00024856	19290051	AGAP002315	intron	FBgn0039705	
0.00025044	25630141	AGAP029101	splice region/intron		
0.00025044	25630141	AGAP002689	downstream	FBgn0260440	Spdo (sanpodo); 4-pass transmembrane protein
0.00026453	23054521	AGAP002573	intron		
0.00027212	23167232	AGAP002578	synonymous		_
0.00027513	19614290	AGAP002325	intron	FBgn0017590	Klg (Klingon); fibronectin type III, immunoglobulin subtype 2
0.0002912	20975140	AGAP002404	downstream		
0.0002912	20975140	AGAP002405	upstream		
0.0002912	20975140	AGAP002406	intron	FBgn0038586	COMM domain-containing protein 2
0.0002912	20975140	AGAP002407	downstream	FBgn0051450	mRpS18; Mitochondrial ribosomal protein S18A
0.0002912	20975140	AGAP002408	upstream	FBgn0037652	
0.0002912	20975140	AGAP002409	downstream	FBgn0038811	tRNA pseudouridine38-40 synthase
0.00029175	20531506	AGAP002350	downstream	FBgn0004169	troponin T, fast skeletal muscle
0.00029175	20531506	AGAP002351	splice region	FBgn0039120	nuclear pore complex protein Nup98-Nup96
0.00029339	26587511	AGAP002744	downstream		
0.00029339	26587511	AGAP013298	upstream		
0.00029891	22833653	AGAP002559	intron		
0.00031556	22964231	AGAP002566	upstream	FBgn0039419	GPRHIS; putative histamine receptor
0.00032869	23586276	AGAP002591	intron	FBgn0053207	Pxb; role in memory and behavior in Drosophila
0.00034347	20860722	AGAP002382	intron		
0.00034347	20860722	AGAP002383	downstream	FBgn0027083	methionyl-tRNA synthetase
0.00043349	19074130	AGAP002309	downstream	FBgn0267449	WD repeat-containing protein

0.00043349	19074130	AGAP002310	downstream	FBgn0039709	protocadherin-15
0.00046668	25501338	AGAP002677	intron		
0.00046749	24934392	AGAP002644	intron		phospholipid-translocating ATPase
0.00048124	24808367	AGAP002635	upstream		GR13; gustatory receptor 13
0.0004868	25631822	AGAP002688	intron		
0.0004868	25631822	AGAP002689	downstream		
0.0004868	25631822	AGAP029101	intron		
0.00048824	19947191	AGAP002329	downstream	FBgn0039543	carnitine O-octanoyltransferase
0.00048824	19947191	AGAP002330	downstream	FBgn0039233	60S ribosome subunit biogenesis protein NIP7
0.00048824	19947191	AGAP013359	downstream		
0.00048824	19947191	AGAP013453	upstream		
0.00052752	21595437	AGAP002458	downstream		
0.00052752	21595437	AGAP013018	downstream	FBgn0053096	Abhydrolase domain-containing protein FAM108B1
0.00053027	26444854	AGAP002739	downstream	FBgn0031879	Uif (uninflatable); transmembrane protein, EGF-like; C-type lectin-like; LDL receptor class A-like
0.00053027	26444854	AGAP002740	upstream		FAD synthetase
0.00053027	26444854	AGAP002741	downstream		histone-lysine N-methyltransferase MLL1
0.00053027	26444854	AGAP013044	downstream	FBgn0015621	(clipper); cleavage and polyadenylation specificity factor subunit 4; in Drosophila, pre-mRNA cleavage required for polyadenylation
0.00053395	26677136	AGAP002752	downstream	FBgn0037718	P58IPK; DnaJ (Hsp40) homolog
0.00053395	26677136	AGAP002753	downstream		
0.00053395	26677136	AGAP002754	downstream		
0.00053792	24951815	AGAP002645	intron		
0.00053792	24951815	AGAP013050	downstream		
0.00053792	24951815	AGAP013113	downstream		
0.00053792	24951815	AGAP013264	downstream		
0.00053792	24951815	AGAP013369	upstream		
0.00053792	24951815	AGAP013448	upstream		
0.00054488	21004279	AGAP002411	intron		
0.00056482	22852328	AGAP002560	intron		
0.00056482	22852328	AGAP002561	downstream		
0.00056983	22171914	AGAP002512	downstream	FBgn0036964	Actin crosslinking; protein FRG1 family
0.00056983	22171914	AGAP002513	downstream	FBgn0036967	SCCRO4 (Squamous cell carcinoma-related oncogene 4); negative regulation of protein neddylation; positive regulation of ubiquitin-protein transferase activity
0.00056983	22171914	AGAP002514	upstream		
0.00057309	22964255	AGAP002566	upstream		
0.00057409	23187926	AGAP002578	intron		_
0.00057541	20387364	AGAP002342	intron		
0.00057973	26449098	AGAP002740	upstream		
0.00057973	26449098	AGAP002741	intron	FBgn0003862	Trx (trithorax); chromatin modification (histone methyltransferase, H3-K4 specific)
0.00060192	25507301	AGAP002677	intron		
0.00061725	20509039	AGAP002347	upstream	FBgn0031099	N-acetylglucosamine-6-phosphate deacetylase
0.00061725	20509039	AGAP002348	upstream	FBgn0030789	exosome complex component RRP45; exoribonuclease
0.00061725	20509039	AGAP002349	missense		piggyBac-derived 1
0.00063945	23005717	AGAP002569	downstream	FBgn0028399	TMS1 (Target of methylation-induced silencing 1); L-serine transmembrane transporter activity
0.00063945	23005717	AGAP002570	upstream	FBgn0036629	GluRS-m; glutamyl-tRNA synthetase
0.00063945	23005717	AGAP002571	5' UTR	FBgn0038524	Slalom (Sll); in Drosophila, transporter of 3'-phosphoadenosine 5'-phosphosulfate; sulfation of glycans and proteins, regulation of Hh, Wingless signaling pathways
0.00064663	20864882	AGAP002381	upstream	FBgn0039734	Tace; disintegrin and metalloproteinase domain-containing protein 17
0.00064663	20864882	AGAP002382	downstream		
0.00064663	20864882	AGAP002383	intron		
0.00064663	20864882	AGAP002384	downstream	FBgn0037250	tRNA (guanine10-N2)-methyltransferase
0.00065294	23822497	AGAP002601	downstream	FBgn0028999	nerfin-1 (nervous fingers); Zinc finger C2H2 transcription factor
0.00065294	23822497	AGAP002602	upstream	FBgn0024194	Rasp; acyltransferase; in Drosophila, adds essential N-terminal palmitate modifications to the secreted signaling domains of hedgehog and spitz (EGFR ligand).

0.00065294	23822497	AGAP002603	upstream	FBgn0042712	HBS1; elongation factor 1 alpha-like protein
0.00065294	23822497	AGAP013296	downstream	FBgn0039305	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4
0.00066899	21231646	AGAP002429	upstream	FBgn0003388	Shd (shade); cytochrome P450 Halloween gene; ecdysteroid biosynthesis
0.00070341	20886116	AGAP002388	upstream	FBgn0032907	endonuclease III
0.00070341	20886116	AGAP002389	downstream	FBgn0038571	ubiquitin-like 4A
0.00070341	20886116	AGAP002390	downstream	FBgn0039730	
0.00070341	20886116	AGAP002391	upstream	FBgn0039084	COEAE5O; carboxylesterase
0.00072003	21376601	AGAP002434	downstream	FBgn0013765	centrosomin
0.00072003	21376601	AGAP002436	downstream	FBgn0013765	isopeptidase-T-3; Kip1 ubiquitination-promoting complex protein 2
0.00072738	21032768	AGAP002413	downstream	FBgn0250753	Krasavietz (Kra); translational regulator that interacts with eiF-2B; in Drosophila, involved in axon guidance, long-term memory, and alcohol addiction
0.00072738	21032768	AGAP002414	downstream	FBgn0004648	Svr (silver); carboxypeptidase D
0.00073128	25501343	AGAP002677	intron		
0.00073866	23258098	AGAP013206	upstream	FBgn0002306	Sas (stranded at second); fibronectin III-like; immunoglobulin-like fold; In Drosophila, involved in response to stimulus
0.00075762	23070605	AGAP002572	downstream		
0.00075762	23070605	AGAP002573	intron		
0.00076122	23831089	AGAP002603	downstream		
0.00076122	23831089	AGAP002604	synonymous	FBgn0085290	
0.00076122	23831089	AGAP002605	upstream	FBgn0026751	DNA-repair protein XRCC1
0.00076122	23831089	AGAP002606	downstream	FBgn0036465	26S proteasome regulatory subunit N12
0.00076122	23831089	AGAP012994	downstream		
0.00076122	23831089	AGAP013156	downstream		
0.00076122	23831089	AGAP013296	upstream		
0.00078211	23291545	AGAP002585	downstream		
0.00078211	23291545	AGAP002586	downstream	FBgn0266064	GlyS; glycogen(starch) synthase
0.00078761	21002977	AGAP002411	intron		regulator of G-protein signaling
0.0007978	22879484	AGAP002564	intron		
0.00079965	22852333	AGAP002560	intron		
0.00079965	22852333	AGAP002561	downstream		
0.00080024	21959673	AGAP002487	downstream		
0.00080024	21959673	AGAP002488	downstream	FBgn0261573	CoRest; SANT-MYB domain transcription regulator; component of chromatin remodelling complexes and co-repressors
0.0008171	25152876	AGAP002651	synonymous	FBgn0266717	Bruce; inhibitor of apoptosis (IAP6); ubiquitin-conjugating (E2) enzyme; in Drosophila, responds to nutrient levels
0.00082995	20795151	AGAP002374	upstream		
0.00082995	20795151	AGAP002375	downstream		
0.00082995	20795151	AGAP002376	downstream		
0.00082995	20795151	AGAP013161	downstream	FBgn0037548	Fatty-acid amide hydrolase 2
0.00083425	23650680	AGAP002591	intron		
0.00084014	26329251	AGAP002732	intron		
0.0008573	21317121	AGAP002431	intron	FBgn0040318	HGTX; homeodomain transcription factor; in Drosophila, major roles include neuronal specification and differentiation
0.00086079	20969364	AGAP002403	downstream		
0.00086079	20969364	AGAP002404	upstream		cullin 5
0.00086079	20969364	AGAP002405	downstream		
0.00087222	24060865	AGAP002610	downstream	FBgn0029939	
0.00088433	19317689	AGAP002315	intron	FBgn0039705	
0.0008958	24498919	AGAP002628	intron		
0.00091999	22132810	AGAP002509	3' UTR	FBgn0260049	Flr (flare); actin-interacting; promotes F-actin disassembly
0.00091999	22132810	AGAP002511	downstream	FBgn0052227	Gogo (golden goal); thromospondin; axon guidance
0.00093225	22852334	AGAP002560	intron		
0.00093225	22852334	AGAP002561	downstream		

†blank gene description means no available function annotation