

**Table S6. Comparison of inferred copy numbers of co-amplified X and Y genes.** Shown are inferred copy numbers of co-amplified X and Y genes, based on our analysis, and compared to high-quality genome assemblies from *D. miranda* and *D. pseudoobscura*.

Genes	<i>D. mel</i> homolog	Y copies M/F cov	X copies assembly	Y copies long read assembly					X copies long read assembly				
				Y total	0.9- >0.9	0.9- 0.5	0.5- 0.25	<0.25	X total	>0.9	0.9- 0.5	0.5- 0.25	<0.25
				>25%	>0.9	0.9- 0.5	0.5- 0.25	<0.25	>25%	>0.9	0.9- 0.5	0.5- 0.25	<0.25
<i>D. miranda</i>													
FBgn0064414	<i>thr</i>	35	2	28	20	5	3	8	1	1	0	0	0
FBgn0070787	<i>FBgn0034491</i>	8	2	4	3	1	0	0	1	1	0	0	0
FBgn0072252	<i>FBgn0033788</i>	8	2	2	0	2	0	0	2	2	0	0	0
FBgn0074335	<i>mars</i>	32	2	48	36	10	2	1	6	2	2	2	0
FBgn0074933	<i>FBgn0033860</i>	82	3	77	60	15	2	3	2	1	1	0	2
FBgn0075168	<i>FBgn0033216</i>	10	2	3	1	0	2	0	3	1	0	2	0
FBgn0075258	<i>scra</i>	289	4	9	6	1	2	2	2	1	0	1	2
FBgn0077065	<i>Drak</i>	232	2	49	0	0	0	60; 49>1kb	1	1	0	0	44
FBgn0081586	<i>Klp61F</i>	18	3	27	0	23	4	44	4	4	0	0	1
FBgn0081588	<i>PCNA</i>	8	2	4	4	0	0	0	1	1	0	0	0
FBgn0081758	<i>FBgn0026582</i>	39	2	69	1	0	68	4	1	1	0	0	0
FBgn0082139	<i>fest</i>	147	4	145	96	43	6	10	5	3	2	0	0
FBgn0245922	<i>FBgn0060296</i>	186	2	181	0	156	25	23	1	1	0	0	0
FBgn0246178	<i>FBgn0054045</i>	14	2	2	0	2	0	60	1	1	0	0	0
FBgn0246244	<i>FBgn0033354</i>	15	3	9	0	8	1	3	14	1	0	11	2; 2>1kb
<i>D. pseudoobscura</i>													
FBgn0079543	<i>S-Lap1</i>	159	2	127	21	62	18	26	2	1	0	1	0
FBgn0250028	<i>GAPsec</i>	68	2	95	6	22	22	45	2	1	0	1	0
FBgn0070269	<i>FBgn0035690</i>	19	3	4	3	1	0	0	3	1	0	2	0