

Additional file 5: GO enrichment of biological processes for autosomal and X-linked, male and female-biased genes.

X-linked male-biased genes GO enrichment. Enriched Biological Processes GO terms of male-biased X-linked genes with unique *D. melanogaster* homologs (n=235).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0003341	cilium movement	1.82E-12	1.05E-08	19.59 (5349.13.210.10)
GO:0007018	microtubule-based movement	9.01E-07	2.60E-03	4.75 (5349.75.210.14)
GO:0007017	microtubule-based process	5.86E-05	1.13E-01	2.56 (5349.209.210.21)
GO:0006513	protein monoubiquitination	5.97E-05	8.63E-02	25.47 (5349.3.210.3)
GO:0046692	sperm competition	7.36E-05	8.52E-02	14.56 (5349.7.210.4)
GO:0044706	multi-multicellular organism process	1.43E-04	1.38E-01	12.74 (5349.8.210.4)
GO:0045814	negative regulation of gene expression. epigenetic	3.42E-04	2.83E-01	5.09 (5349.35.210.7)
GO:0040029	regulation of gene expression. epigenetic	6.23E-04	4.50E-01	3.40 (5349.75.210.10)
GO:0044703	multi-organism reproductive process	8.91E-04	5.73E-01	8.49 (5349.12.210.4)

X-linked female-biased genes GO enrichment. Enriched Biological Processes GO terms of female-biased X-linked genes with unique *D. melanogaster* homologs (n=182).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0009886	post-embryonic animal morphogenesis	3.97E-05	2.29E-01	4.56 (5349.309.38.10)
GO:0048518	positive regulation of biological process	4.02E-05	1.16E-01	2.85 (5349.790.38.16)
GO:0048583	regulation of response to stimulus	9.16E-05	1.77E-01	3.19 (5349.573.38.13)
GO:0009653	anatomical structure morphogenesis	1.22E-04	1.76E-01	2.75 (5349.768.38.15)
GO:0048522	positive regulation of cellular process	1.40E-04	1.61E-01	2.88 (5349.685.38.14)
GO:0010646	regulation of cell communication	1.45E-04	1.40E-01	3.28 (5349.515.38.12)
GO:0023051	regulation of signaling	1.45E-04	1.20E-01	3.28 (5349.515.38.12)
GO:0035120	post-embryonic appendage morphogenesis	2.87E-04	2.07E-01	5.27 (5349.187.38.7)
GO:0035114	imaginal disc-derived appendage morphogenesis	3.27E-04	2.10E-01	5.16 (5349.191.38.7)
GO:0035107	appendage morphogenesis	3.95E-04	2.28E-01	5.00 (5349.197.38.7)
GO:0002682	regulation of immune system process	4.00E-04	2.10E-01	6.03 (5349.140.38.6)
GO:0003002	regionalization	4.46E-04	2.15E-01	4.90 (5349.201.38.7)
GO:0030718	germ-line stem cell population maintenance	5.31E-04	2.36E-01	10.43 (5349.54.38.4)
GO:0009966	regulation of signal transduction	8.96E-04	3.70E-01	3.12 (5349.451.38.10)

X-linked unbiased genes GO enrichment. Enriched Biological Processes GO terms of unbiased X-linked genes with unique *D. melanogaster* homologs (n=517).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0007424	open tracheal system development	4.23E-04	1.00E+00	2.44 (5349.81.461.17)
GO:0060541	respiratory system development	4.23E-04	1.00E+00	2.44 (5349.81.461.17)
GO:0098732	macromolecule deacylation	8.14E-04	1.00E+00	5.80 (5349.10.461.5)

Autosomal male-biased genes GO enrichment. Enriched Biological Processes GO terms of male-biased autosomal genes with unique *D. melanogaster* homologs (n=598).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0006629	lipid metabolic process	8.50E-08	4.91E-04	2.21 (5349.214.532.47)
GO:0044281	small molecule metabolic process	1.34E-07	3.87E-04	1.85 (5349.374.532.69)
GO:0044710	single-organism metabolic process	1.83E-07	3.52E-04	1.54 (5349.776.532.119)
GO:0055085	transmembrane transport	7.74E-07	1.12E-03	2.14 (5349.202.532.43)
GO:0044712	single-organism catabolic process	2.96E-05	3.42E-02	2.41 (5349.100.532.24)
GO:0042445	hormone metabolic process	4.14E-05	3.99E-02	3.66 (5349.33.532.12)
GO:0055114	oxidation-reduction process	4.20E-05	3.47E-02	1.86 (5349.227.532.42)
GO:0006091	generation of precursor metabolites and energy	1.20E-04	8.67E-02	2.99 (5349.47.532.14)
GO:0006820	anion transport	1.49E-04	9.58E-02	3.26 (5349.37.532.12)
GO:0015698	inorganic anion transport	2.03E-04	1.17E-01	3.93 (5349.23.532.9)
GO:0044255	cellular lipid metabolic process	2.36E-04	1.24E-01	1.95 (5349.155.532.30)
GO:0006082	organic acid metabolic process	3.93E-04	1.90E-01	1.77 (5349.204.532.36)
GO:0044262	cellular carbohydrate metabolic process	4.15E-04	1.85E-01	3.35 (5349.30.532.10)
GO:0006865	amino acid transport	4.22E-04	1.74E-01	3.62 (5349.25.532.9)
GO:0030239	myofibril assembly	5.15E-04	1.99E-01	5.03 (5349.12.532.6)
GO:0006099	tricarboxylic acid cycle	5.72E-04	2.07E-01	3.83 (5349.21.532.8)
GO:0044282	small molecule catabolic process	5.92E-04	2.01E-01	2.61 (5349.54.532.14)
GO:0015849	organic acid transport	8.08E-04	2.60E-01	3.35 (5349.27.532.9)
GO:0006979	response to oxidative stress	8.41E-04	2.56E-01	2.43 (5349.62.532.15)
GO:0032787	monocarboxylic acid metabolic process	8.64E-04	2.50E-01	2.28 (5349.75.532.17)
GO:0043648	dicarboxylic acid metabolic process	8.77E-04	2.41E-01	4.64 (5349.13.532.6)
GO:0006121	mitochondrial electron transport. succinate to ubiquinone	9.79E-04	2.57E-01	10.05 (5349.3.532.3)

Autosomal female-biased genes GO enrichment. Enriched Biological Processes GO terms of female-biased autosomal genes with unique *D. melanogaster* homologs (n=1107).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0002181	cytoplasmic translation	2.75E-32	1.59E-28	4.31 (5349.74.1023.61)
GO:0006807	nitrogen compound metabolic process	1.69E-20	4.89E-17	1.52 (5349.1144.1023.332)
GO:0034641	cellular nitrogen compound metabolic process	1.80E-20	3.46E-17	1.56 (5349.1020.1023.304)
GO:0022402	cell cycle process	4.88E-17	7.05E-14	1.89 (5349.401.1023.145)
GO:0090304	nucleic acid metabolic process	1.85E-15	2.14E-12	1.62 (5349.672.1023.208)
GO:0051298	centrosome duplication	2.61E-13	2.51E-10	3.56 (5349.47.1023.32)
GO:0009059	macromolecule biosynthetic process	1.59E-12	1.32E-09	1.74 (5349.399.1023.133)
GO:0031023	microtubule organizing center organization	2.18E-12	1.58E-09	2.73 (5349.88.1023.46)
GO:0034645	cellular macromolecule biosynthetic process	2.69E-12	1.73E-09	1.79 (5349.354.1023.121)
GO:0006139	nucleobase-containing compound metabolic process	4.14E-12	2.39E-09	1.48 (5349.789.1023.224)
GO:1901360	organic cyclic compound metabolic process	4.43E-12	2.33E-09	1.45 (5349.883.1023.245)
GO:0006412	translation	7.71E-12	3.71E-09	2.16 (5349.172.1023.71)
GO:0051297	centrosome organization	1.03E-11	4.58E-09	2.71 (5349.85.1023.44)
GO:0006396	RNA processing	1.16E-11	4.79E-09	1.83 (5349.306.1023.107)
GO:0043043	peptide biosynthetic process	1.26E-11	4.87E-09	2.13 (5349.177.1023.72)
GO:0032502	developmental process	1.28E-11	4.61E-09	1.27 (5349.1787.1023.434)
GO:0016071	mRNA metabolic process	1.30E-11	4.42E-09	1.97 (5349.231.1023.87)
GO:1903047	mitotic cell cycle process	1.38E-11	4.44E-09	1.90 (5349.261.1023.95)
GO:0006725	cellular aromatic compound metabolic process	1.47E-11	4.46E-09	1.45 (5349.856.1023.237)
GO:0016070	RNA metabolic process	1.68E-11	4.87E-09	1.60 (5349.522.1023.160)
GO:0046483	heterocycle metabolic process	2.30E-11	6.32E-09	1.45 (5349.828.1023.230)
GO:0043604	amide biosynthetic process	2.39E-11	6.28E-09	2.10 (5349.179.1023.72)

Autosomal unbiased genes GO enrichment. Enriched Biological Processes GO terms of unbiased autosomal genes with unique *D. melanogaster* homologs (n=2805).

GO term	Description	P-value	FDR q-value	Enrichment (N. B. n. b)
GO:0051179	localization	7.61E-07	4.40E-03	1.14 (5349.1063.2508.569)
GO:0006810	transport	1.66E-06	4.80E-03	1.15 (5349.910.2508.491)
GO:0051234	establishment of localization	7.24E-06	1.40E-02	1.14 (5349.945.2508.504)
GO:0006898	receptor-mediated endocytosis	1.94E-05	2.80E-02	1.73 (5349.37.2508.30)
GO:0007264	small GTPase mediated signal transduction	6.54E-05	7.57E-02	1.44 (5349.89.2508.60)
GO:0072583	clathrin-dependent endocytosis	6.71E-05	6.47E-02	1.73 (5349.32.2508.26)
GO:0035556	intracellular signal transduction	1.08E-04	8.90E-02	1.26 (5349.221.2508.131)
GO:0016192	vesicle-mediated transport	1.39E-04	1.01E-01	1.20 (5349.355.2508.200)
GO:0048488	synaptic vesicle endocytosis	2.05E-04	1.32E-01	1.71 (5349.30.2508.24)
GO:0099643	signal release from synapse	3.78E-04	2.19E-01	1.40 (5349.82.2508.54)
GO:0001505	regulation of neurotransmitter levels	3.85E-04	2.02E-01	1.38 (5349.91.2508.59)
GO:0023061	signal release	4.17E-04	2.01E-01	1.40 (5349.84.2508.55)
GO:0099003	vesicle-mediated transport in synapse	4.35E-04	1.93E-01	1.55 (5349.44.2508.32)
GO:0006464	cellular protein modification process	5.41E-04	2.24E-01	1.14 (5349.601.2508.320)
GO:0036211	protein modification process	5.41E-04	2.09E-01	1.14 (5349.601.2508.320)
GO:0099531	presynaptic process involved in chemical synaptic transmission	6.48E-04	2.34E-01	1.38 (5349.85.2508.55)
GO:0070647	protein modification by small protein conjugation or removal	7.97E-04	2.71E-01	1.29 (5349.139.2508.84)
GO:0007269	neurotransmitter secretion	9.15E-04	2.94E-01	1.39 (5349.75.2508.49)