

Online Supplementary Material

A genome-wide scan for pleiotropic fitness effects on sexes and age classes in *Drosophila*, by Luke Holman and Heidi Wong.

The figures and tables in this document, along with the with the R code used to generate them, can also be viewed online at lukeholman.github.io/fitnessGWAS.

Table S1: Recipe for *Drosophila* food used in this study.

Ingredients	Quantity
Water	1000 mL
Dextrose	75g
Cornmeal	73g
Yeast	35g
Soy flour	20g
Agar	6g
Tegosept	17mL
Acid mix (4mL orthophosphoric acid, 41mL propionic acid, 55mL water per 100mL)	14mL

Table S2: Proportion of variance (R) in fitness explained by ‘DGRP line’, with associated standard errors and 95% confidence intervals estimated using parametric bootstrapping. R was calculated from univariate generalised linear mixed models of each fitness trait, which included the random effect of experimental block, and had either Poisson errors (for females) or Binomial errors (for males), using the `rpt` function from the `rptR` package for R.

Fitness trait	R	SE	Lower 95% CI	Upper 95% CI
Female fitness early	0.49	0.05	0.39	0.59
Female fitness late	0.45	0.06	0.34	0.59
Male fitness early	0.06	0.01	0.04	0.08
Male fitness late	0.17	0.03	0.12	0.22

Table S3: Pearson correlation coefficients between the DGRP line means (estimated using two Bayesian mixed models; one for each sex) for each pair of fitness traits. These correlations approximate the genetic correlations between each pair of fitness traits.

Variable 1	Variable 2	Pearson correlation	SE	Lower 95% CI	Upper 95% CI	p value
Female fitness early	Female fitness late	0.77	0.06	0.68	0.83	< 0.0001
Female fitness early	Male fitness early	0.23	0.09	0.05	0.39	0.0108
Female fitness early	Male fitness late	0.17	0.09	0.00	0.34	0.056
Female fitness late	Male fitness early	0.32	0.09	0.15	0.47	3e-04
Female fitness late	Male fitness late	0.32	0.09	0.15	0.47	3e-04
Male fitness early	Male fitness late	0.86	0.05	0.81	0.90	< 0.0001

Table S4: This table shows variants that passed the statistical significance threshold of $p < 10^{-5}$ for at least one of the four phenotypes, in a linear mixed model GWAS implemented in GEMMA. Columns 2 identifies genes that overlap the variant, and column 3 shows the site class. Columns 4-5 show the estimated effect size of the variant on the four phenotypes (where positive values mean that the minor allele is associated with higher fitness, and negative values that the minor allele is associated with lower fitness), with the p -value in parentheses ($-\log_{10}$ transformed, with significant values starred). A more readable version of this table, with extra information such as full gene names, is provided at https://lukeholman.github.io/fitnessGWAS/GWAS_tables.html.

Variant	FBID	Site class	Female early	Female late	Male early	Male late
2L_10373585_SNP	FBgn0041723	INTRON	0.21 (0.9)	0.33 (1.9)	0.62 (6.3*)	0.36 (2.4)
2L_10666944_SNP	FBgn0051871	INTRON	0.02 (0.1)	-0.04 (0.1)	-0.49 (5.3*)	-0.31 (2.2)
2L_11155919_SNP	FBgn0032350	UPSTREAM	0.32 (1.6)	0.22 (0.9)	0.59 (5.3*)	0.28 (1.5)
2L_1139426_SNP	FBgn0031306	INTRON	0.04 (0.1)	0.04 (0.1)	0.65 (5.4*)	0.21 (0.8)
2L_11398129_SNP	—	INTERGENIC	-0.40 (2.9)	-0.54 (5.2*)	0.07 (0.2)	0.01 (0.0)
2L_11900442_SNP	FBgn0264815	INTRON	-0.39 (5.1*)	-0.19 (1.4)	-0.10 (0.5)	-0.12 (0.7)
2L_12362698_SNP	FBgn0262475	INTRON	0.11 (0.7)	0.08 (0.4)	0.41 (5.4*)	0.26 (2.5)
2L_12600320_SNP	FBgn0085424	INTRON	0.13 (0.8)	0.19 (1.3)	0.19 (1.4)	0.39 (5.1*)
2L_1278985_SNP	FBgn0041097	INTRON	-0.68 (6.3*)	-0.59 (4.7)	-0.15 (0.5)	-0.20 (0.8)
2L_1279083_SNP	FBgn0041097	INTRON	-0.64 (5.9*)	-0.58 (4.8)	-0.12 (0.4)	-0.14 (0.5)
2L_13736785_SNP	FBgn0051813	UTR_3_PRIME	-0.04 (0.2)	-0.14 (0.9)	-0.40 (5.3*)	-0.14 (0.9)
2L_14031137_SNP	FBgn0028872	NON_SYNONYMOUS_CODING	0.22 (1.7)	0.42 (5.7*)	0.22 (1.8)	0.28 (2.7)
2L_15469662_SNP	FBgn0266893	UPSTREAM	-0.54 (5.2*)	-0.12 (0.5)	0.08 (0.3)	0.08 (0.3)
2L_15469663_SNP	FBgn0266893	UPSTREAM	-0.53 (5.3*)	-0.17 (0.8)	0.08 (0.3)	0.13 (0.6)
2L_16337977_SNP	FBgn0259151	DOWNSTREAM	-0.54 (5.3*)	-0.27 (1.6)	-0.33 (2.2)	-0.11 (0.4)
2L_1992654_SNP	FBgn0043539	UPSTREAM	-0.70 (5.1*)	-0.15 (0.4)	-0.05 (0.1)	-0.04 (0.1)
2L_20590123_SNP	FBgn0266214	INTRON	-0.53 (5.7*)	-0.12 (0.5)	0.02 (0.1)	0.08 (0.3)
2L_2505499_DEL	—	INTERGENIC	-0.29 (2.4)	-0.51 (6.7*)	-0.02 (0.1)	-0.15 (0.8)
2L_3585735_SNP	—	INTERGENIC	-0.57 (5.1*)	-0.22 (1.0)	0.08 (0.3)	0.03 (0.1)
2L_3958319_DEL	FBgn0051774	INTRON	-0.18 (0.7)	-0.17 (0.7)	-0.57 (5.1*)	-0.34 (2.1)
2L_7327873_SNP	—	INTERGENIC	-0.88 (6.4*)	-0.43 (1.7)	0.23 (0.7)	0.05 (0.1)
2L_7331146_SNP	—	INTERGENIC	-0.92 (6.9*)	-0.36 (1.3)	0.12 (0.3)	-0.08 (0.2)
2L_7331381_SNP	—	INTERGENIC	-0.81 (7.6*)	-0.46 (2.5)	0.28 (1.2)	0.00 (0.0)
2L_7331966_SNP	—	INTERGENIC	-0.87 (5.5*)	-0.30 (0.9)	0.25 (0.7)	0.03 (0.1)
2L_7332711_SNP	—	INTERGENIC	-0.65 (6.0*)	-0.32 (1.7)	0.05 (0.1)	-0.12 (0.4)
2L_9468802_SNP	—	INTERGENIC	0.27 (2.0)	0.46 (5.0*)	-0.16 (0.8)	-0.06 (0.2)
2R_11451981_SNP	FBgn0034032	INTRON	-0.34 (1.7)	-0.62 (5.1*)	-0.24 (0.9)	-0.22 (0.8)
2R_11587427_SNP	FBgn0050080	UTR_3_PRIME	-0.27 (2.2)	-0.44 (5.3*)	-0.17 (1.0)	-0.06 (0.3)
2R_13736790_SNP	FBgn0041585	INTRON	-0.39 (1.3)	-0.24 (0.7)	-0.60 (2.7)	-0.84 (5.2*)
2R_14993454_SNP	FBgn0004168	INTRON	-0.74 (5.2*)	-0.24 (0.8)	0.05 (0.1)	-0.04 (0.1)
2R_14993748_SNP	FBgn0004168	INTRON	-0.91 (7.7*)	-0.34 (1.4)	0.15 (0.4)	-0.11 (0.3)
2R_14993888_SNP	FBgn0004168	INTRON	-0.82 (6.8*)	-0.25 (0.9)	0.19 (0.6)	-0.08 (0.2)
2R_15508894_SNP	FBgn0003435	INTRON	-0.10 (0.5)	-0.14 (0.9)	-0.33 (3.8)	-0.41 (5.7*)
2R_15509740_SNP	FBgn0003435	INTRON	-0.03 (0.1)	-0.14 (0.9)	-0.42 (5.9*)	-0.19 (1.4)
2R_16248031_SNP	—	INTERGENIC	-0.75 (7.2*)	-0.27 (1.2)	0.11 (0.3)	-0.08 (0.2)
2R_16716337_SNP	FBgn0016984	SYNONYMOUS_CODING	-0.02 (0.1)	0.01 (0.0)	0.09 (0.4)	0.50 (6.3*)
2R_18582247_SNP	FBgn0005631	SYNONYMOUS_CODING	-0.63 (5.3*)	-0.23 (1.0)	0.11 (0.3)	0.11 (0.3)
3L_10151651_SNP	FBgn0052057	INTRON	-0.36 (2.0)	-0.20 (0.8)	-0.61 (5.2*)	-0.42 (2.7)
3L_10301535_SNP	—	INTERGENIC	-0.58 (5.0*)	-0.33 (1.9)	0.04 (0.1)	-0.19 (0.8)
3L_10619878_SNP	FBgn0085267	SYNONYMOUS_CODING	0.10 (0.4)	-0.17 (0.9)	-0.26 (1.6)	-0.50 (5.0*)
3L_11211699_SNP	FBgn0261553	INTRON	0.02 (0.1)	0.03 (0.1)	0.62 (6.0*)	0.27 (1.4)
3L_11350860_INS	—	INTERGENIC	-0.09 (0.5)	-0.08 (0.4)	0.13 (0.8)	0.39 (5.1*)
3L_11939100_SNP	FBgn0262401	DOWNSTREAM	-0.79 (5.7*)	-0.54 (2.8)	0.18 (0.5)	0.33 (1.3)
3L_13517615_SNP	FBgn0264001	UTR_3_PRIME	-0.52 (5.0*)	-0.27 (1.6)	-0.19 (0.9)	-0.06 (0.2)
3L_1396396_SNP	FBgn0003138	INTRON	-0.04 (0.1)	-0.12 (0.5)	-0.53 (5.2*)	-0.23 (1.3)
3L_18121280_SNP	FBgn0036778	DOWNSTREAM	-0.29 (2.4)	-0.45 (5.3*)	-0.03 (0.1)	0.07 (0.3)
3L_20120237_SNP	FBgn0036939	INTRON	-0.25 (1.2)	-0.21 (0.9)	-0.33 (2.0)	-0.54 (5.1*)
3L_2209187_DEL	—	INTERGENIC	-0.34 (2.4)	-0.56 (6.3*)	0.04 (0.1)	-0.03 (0.1)
3L_2327474_SNP	FBgn0035331	INTRON	-0.69 (6.0*)	-0.54 (3.6)	-0.23 (1.0)	-0.10 (0.3)
3L_2327987_DEL	FBgn0035331	INTRON	-0.56 (5.1*)	-0.33 (2.0)	-0.09 (0.3)	-0.14 (0.6)
3L_2328091_SNP	FBgn0035331	INTRON	-0.68 (5.8*)	-0.48 (3.0)	-0.17 (0.6)	-0.11 (0.4)
3L_2579211_SNP	FBgn0010909	INTRON	0.14 (0.6)	-0.09 (0.4)	-0.22 (1.3)	-0.47 (5.0*)
3L_3852986_SNP	FBgn0013751	INTRON	-0.78 (5.1*)	-0.12 (0.3)	-0.09 (0.2)	0.15 (0.4)

(continued)

Variant	FBID	Site class	Female early	Female late	Male early	Male late
3L_4337825_SNP	FBgn0035533	INTRON	0.00 (0.0)	-0.10 (0.5)	0.15 (0.9)	0.43 (5.7*)
3L_4717489_SNP	FBgn0035574	INTRON	-0.11 (0.3)	-0.04 (0.1)	-0.40 (2.0)	-0.75 (6.4*)
3L_5974927_SNP	—	INTERGENIC	0.12 (0.6)	0.03 (0.1)	0.43 (5.4*)	0.17 (1.2)
3L_7709650_SNP	FBgn0261788	INTRON	-0.09 (0.3)	0.04 (0.1)	0.61 (5.2*)	-0.02 (0.1)
3R_15069383_SNP	FBgn0038693	SYNONYMOUS_CODING	-0.47 (2.6)	-0.70 (5.3*)	0.13 (0.4)	0.09 (0.2)
3R_20857835_SNP	FBgn0039260	SYNONYMOUS_CODING	-0.16 (0.5)	-0.14 (0.4)	-0.43 (2.2)	-0.74 (6.0*)
3R_23465476_SNP	FBgn0266579	DOWNSTREAM	-0.79 (5.5*)	-0.27 (0.9)	0.36 (1.5)	0.16 (0.5)
3R_23561601_SNP	FBgn0005659	UPSTREAM	-0.20 (1.3)	-0.46 (5.3*)	-0.14 (0.8)	-0.09 (0.4)
3R_23561644_SNP	FBgn0005659	UPSTREAM	-0.32 (2.3)	-0.55 (6.6*)	-0.30 (2.1)	-0.25 (1.6)
3R_26029886_SNP	—	INTERGENIC	-0.81 (5.4*)	-0.32 (1.1)	0.02 (0.0)	0.08 (0.2)
3R_6838975_SNP	FBgn0083950	INTRON	0.27 (2.6)	0.39 (5.3*)	0.08 (0.4)	0.00 (0.0)
3R_6840122_SNP	FBgn0083950	INTRON	-0.20 (1.6)	-0.39 (5.1*)	-0.08 (0.4)	0.10 (0.6)
3R_7772970_SNP	FBgn0037963	INTRON	-0.66 (5.2*)	-0.27 (1.1)	0.05 (0.1)	-0.02 (0.1)
X_13282830_SNP	FBgn0030481	UTR_3_PRIME	-0.60 (5.3*)	-0.43 (2.9)	0.13 (0.5)	0.12 (0.4)
X_1556505_SNP	FBgn0000210	UTR_3_PRIME	0.03 (0.1)	0.01 (0.0)	0.39 (5.2*)	0.22 (1.8)
X_19894141_DEL	FBgn0031082	DOWNSTREAM	-0.70 (5.0*)	-0.58 (3.5)	-0.07 (0.2)	-0.16 (0.5)
X_19894144_SNP	FBgn0031082	DOWNSTREAM	-0.78 (5.6*)	-0.63 (3.7)	-0.07 (0.2)	-0.16 (0.5)
X_20284816_SNP	FBgn0040651	UTR_3_PRIME	-0.66 (5.2*)	-0.49 (2.9)	-0.27 (1.1)	-0.06 (0.2)
X_2319952_SNP	FBgn0052797	UPSTREAM	-0.34 (1.9)	-0.68 (6.6*)	-0.14 (0.5)	-0.09 (0.3)
X_5435183_SNP	FBgn0263512	INTRON	-0.22 (1.9)	-0.39 (5.2*)	0.06 (0.3)	-0.04 (0.2)
X_5435203_SNP	FBgn0263512	INTRON	-0.25 (2.3)	-0.41 (5.6*)	0.07 (0.3)	-0.01 (0.0)
X_5536216_SNP	FBgn0259994	INTRON	-0.47 (5.0)	-0.49 (5.3*)	-0.03 (0.1)	0.06 (0.2)
X_5536276_SNP	FBgn0259994	INTRON	-0.38 (4.0)	-0.43 (5.1*)	0.00 (0.0)	0.04 (0.2)
X_769353_SNP	FBgn0264449	INTRON	-0.21 (1.4)	-0.52 (7.5*)	-0.06 (0.3)	-0.07 (0.3)
X_8641777_SNP	—	INTERGENIC	-0.81 (5.4*)	-0.36 (1.3)	-0.04 (0.1)	0.08 (0.2)
X_889209_SNP	—	INTERGENIC	-0.75 (5.3*)	-0.32 (1.2)	-0.01 (0.0)	-0.14 (0.4)

Table S5: The table tallies the numbers of loci showing a particular relationship with fitness (rows), for various different p -value thresholds (columns). For example, ‘Female early only’ counts the number of loci whose genotype significantly correlated with mean female early life fitness across lines. ‘Age concordant, males’ counts loci whose genotype correlated with early- *and* late-life fitness in males, in the same direction, while ‘Age antagonistic, males’ counts loci showing significant, opposite relationships with male early- and male late-life fitness. Similarly, ‘Sex concordant, early’ counts loci showing a concordant relationship with early life fitness in both males and females, and ‘Sex antagonistic, late’ counts those showing opposing relationships with late-life fitness in males and females. All categories are mutually exclusive, such that loci are only counted towards the most specific category that applies to them. Note that this method has low power to detect loci that correlate with two or more fitness metrics, because there are two or more opportunities to make a ‘false negative’ error, and the power is low for any given locus (we therefore use a range of p -value thresholds, including some permissive ones, to illustrate general patterns of genetic covariance).

Relationship to fitness	$p < 0.01$	$p < 0.001$	$p < 1e-04$	$p < 1e-05$	$p < 1e-06$	$p < 1e-07$
Uncorrelated with fitness	1154817	1201180	1206595	1207278	1207342	1207353
Male early only	12827	1457	146	14	1	0
Female early only	12686	1753	251	35	7	3
Male late only	12315	1418	171	11	2	0
Female late only	11512	1421	185	19	5	1
Age concordant, females	1743	95	8	0	0	0
Age concordant, males	875	23	0	0	0	0
Sex concordant, early	318	6	1	0	0	0
Sex concordant, late	229	4	0	0	0	0
Sex antagonistic, early	17	0	0	0	0	0
Sex antagonistic, late	13	0	0	0	0	0
Sex concordant, both ages	5	0	0	0	0	0
Sex antagonistic, both ages	0	0	0	0	0	0
Age antagonistic, both sexes	0	0	0	0	0	0
Age concordant, both sexes	0	0	0	0	0	0
Age antagonistic, females	0	0	0	0	0	0
Age antagonistic, males	0	0	0	0	0	0

Table S6: Table showing the mean and median effect size (in standard units), across all 208,987 loci in an LD-pruned subset of the total. The average effect size is close to zero, reflecting the fact that most loci have essentially zero effect on fitness. However, the mean is significantly negative (shown by the t and p statistics, from linear models), indicating that the minor allele is most often associated with lower fitness (and the major allele with higher fitness) at loci with non-zero associations with fitness.

Fitness component	Mean (SE) variant effect	Median variant effect	t value	p
Female fitness early	-0.00168 (0.00026)	-0.00192	-6.584387	4.58e-11
Female fitness late	-0.00250 (0.00026)	-0.00285	-9.630304	6.02e-22
Male fitness early	-0.00161 (0.00025)	-0.00147	-6.350229	2.15e-10
Male fitness late	-0.00194 (0.00025)	-0.00167	-7.739391	1.00e-14

Table S7: The table showing the 517 transcripts that were associated with one or more of the four phenotypes (with a p-value less than 0.01) is too large to display here, and is provided at the following URL: https://lukeholman.github.io/fitnessGWAS/TWAS_tables.html. For each transcript, the table gives the gene name and Flybase ID, the chromosome, the extent of male bias in gene expression (as log fold change) and average expression level (calculated from the DGRP expression data from Huang et al. 2015, *PNAS*), and the average effect size and *p*-value for each fitness components (calculated using linear models relating mean expression level to mean fitness across lines).

Table S8: The table tallies the numbers of transcripts showing a particular relationship with fitness (rows) for various different p -value thresholds (columns). See Table S5 for the meanings of each row. As in Table S5, all categories are mutually exclusive, such that transcripts are only counted towards the most specific category that applies to them, and the method has low power to detect transcripts that correlate with two or more fitness metrics, because there are two or more opportunities to make a ‘false negative’ error.

Relationship to fitness	Using $p < 0.05$	Using $p < 0.01$	Using $p < 0.001$	Using $p < 1e-04$	Using $p < 1e-05$
Uncorrelated with fitness	12143	13769	14222	14280	14285
Female early only	472	123	14	1	0
Female late only	384	112	15	3	1
Age concordant, males	356	59	7	0	0
Male late only	301	76	10	1	0
Age concordant, females	292	44	3	0	0
Male early only	268	89	15	1	0
Sex concordant, early	24	5	0	0	0
Sex concordant, late	18	7	0	0	0
Sex antagonistic, early	12	2	0	0	0
Sex antagonistic, late	8	0	0	0	0
Sex concordant, both ages	6	0	0	0	0
Sex antagonistic, both ages	2	0	0	0	0
Age antagonistic, both sexes	0	0	0	0	0
Age concordant, both sexes	0	0	0	0	0
Age antagonistic, females	0	0	0	0	0
Age antagonistic, males	0	0	0	0	0

Table S9: The fourth column of the table shows the numbers of variants comprising each of the 32 coloured panels in Figures 4A and 4B. The fifth column gives these numbers as a percentage of the total number of variants, while the sixth column shows the number as a percentage among the variants that have the same association with female fitness.

Age class	Association with female fitness	Association with male fitness	Number of variants	Percentage (overall)	Percentage (given association with female fitness)
Early-life	Negative	Negative	41947	20.07	80.29
Early-life	Negative	Weakly negative	9075	4.34	17.37
Early-life	Negative	Weakly positive	1096	0.52	2.10
Early-life	Negative	Positive	129	0.06	0.25
Early-life	Weakly negative	Negative	9459	4.53	18.10
Early-life	Weakly negative	Weakly negative	31336	14.99	59.98
Early-life	Weakly negative	Weakly positive	10546	5.05	20.18
Early-life	Weakly negative	Positive	906	0.43	1.73
Early-life	Weakly positive	Negative	738	0.35	1.41
Early-life	Weakly positive	Weakly negative	10950	5.24	20.96
Early-life	Weakly positive	Weakly positive	31731	15.18	60.73
Early-life	Weakly positive	Positive	8828	4.22	16.90
Early-life	Positive	Negative	103	0.05	0.20
Early-life	Positive	Weakly negative	886	0.42	1.70
Early-life	Positive	Weakly positive	8874	4.25	16.99
Early-life	Positive	Positive	42383	20.28	81.12
Late-life	Negative	Negative	42917	20.54	82.14
Late-life	Negative	Weakly negative	8492	4.06	16.25
Late-life	Negative	Weakly positive	745	0.36	1.43
Late-life	Negative	Positive	93	0.04	0.18
Late-life	Weakly negative	Negative	8787	4.20	16.82
Late-life	Weakly negative	Weakly negative	32734	15.66	62.65
Late-life	Weakly negative	Weakly positive	10158	4.86	19.44
Late-life	Weakly negative	Positive	568	0.27	1.09
Late-life	Weakly positive	Negative	495	0.24	0.95
Late-life	Weakly positive	Weakly negative	10381	4.97	19.87
Late-life	Weakly positive	Weakly positive	33013	15.80	63.19
Late-life	Weakly positive	Positive	8358	4.00	16.00
Late-life	Positive	Negative	48	0.02	0.09
Late-life	Positive	Weakly negative	640	0.31	1.22
Late-life	Positive	Weakly positive	8331	3.99	15.95
Late-life	Positive	Positive	43227	20.68	82.74

Table S10: The fourth column of the table shows the numbers of transcripts comprising each of the 32 coloured panels in Figures 4C and 4D. The fifth column gives these numbers as a percentage of the total number of transcripts, while the sixth column shows the number as a percentage among the transcripts that have the same association with female fitness.

Age class	Association with female fitness	Association with male fitness	Number of transcripts	Percentage (overall)	Percentage (given association with female fitness)
Early-life	Negative	Negative	1578	11.05	44.18
Early-life	Negative	Weakly negative	752	5.26	21.05
Early-life	Negative	Weakly positive	551	3.86	15.43
Early-life	Negative	Positive	691	4.84	19.34
Early-life	Weakly negative	Negative	773	5.41	21.64
Early-life	Weakly negative	Weakly negative	1168	8.18	32.70
Early-life	Weakly negative	Weakly positive	1043	7.30	29.20
Early-life	Weakly negative	Positive	588	4.12	16.46
Early-life	Weakly positive	Negative	532	3.72	14.90
Early-life	Weakly positive	Weakly negative	1058	7.41	29.63
Early-life	Weakly positive	Weakly positive	1201	8.41	33.63
Early-life	Weakly positive	Positive	780	5.46	21.84
Early-life	Positive	Negative	689	4.82	19.29
Early-life	Positive	Weakly negative	594	4.16	16.63
Early-life	Positive	Weakly positive	776	5.43	21.73
Early-life	Positive	Positive	1512	10.58	42.34
Late-life	Negative	Negative	1603	11.22	44.88
Late-life	Negative	Weakly negative	758	5.31	21.22
Late-life	Negative	Weakly positive	534	3.74	14.95
Late-life	Negative	Positive	677	4.74	18.95
Late-life	Weakly negative	Negative	765	5.35	21.42
Late-life	Weakly negative	Weakly negative	1175	8.22	32.89
Late-life	Weakly negative	Weakly positive	1053	7.37	29.48
Late-life	Weakly negative	Positive	579	4.05	16.21
Late-life	Weakly positive	Negative	540	3.78	15.12
Late-life	Weakly positive	Weakly negative	1061	7.43	29.71
Late-life	Weakly positive	Weakly positive	1206	8.44	33.77
Late-life	Weakly positive	Positive	764	5.35	21.39
Late-life	Positive	Negative	664	4.65	18.59
Late-life	Positive	Weakly negative	578	4.05	16.19
Late-life	Positive	Weakly positive	778	5.45	21.79
Late-life	Positive	Positive	1551	10.86	43.43

Table S11: The table shows similar information to Table S9, except that we now tabulate the number of variants that have various associations with early- and late-life fitness (separately within each sex). Note that there are essentially no variants with opposing effects on early- and late-life fitness, in either sex.

Sex	Association with early-life fitness	Association with late-life fitness	Number of variants	Percentage (overall)	Percentage (given association with early-life fitness)
Female	Negative	Negative	50560	24.19	96.77
Female	Negative	Weakly negative	1687	0.81	3.23
Female	Negative	Weakly positive	0	0.00	0.00
Female	Negative	Positive	0	0.00	0.00
Female	Weakly negative	Negative	1687	0.81	3.23
Female	Weakly negative	Weakly negative	48453	23.18	92.74
Female	Weakly negative	Weakly positive	2107	1.01	4.03
Female	Weakly negative	Positive	0	0.00	0.00
Female	Weakly positive	Negative	0	0.00	0.00
Female	Weakly positive	Weakly negative	2107	1.01	4.03
Female	Weakly positive	Weakly positive	48489	23.20	92.81
Female	Weakly positive	Positive	1651	0.79	3.16
Female	Positive	Negative	0	0.00	0.00
Female	Positive	Weakly negative	0	0.00	0.00
Female	Positive	Weakly positive	1651	0.79	3.16
Female	Positive	Positive	50595	24.21	96.84
Male	Negative	Negative	49584	23.73	94.90
Male	Negative	Weakly negative	2661	1.27	5.09
Male	Negative	Weakly positive	1	0.00	0.00
Male	Negative	Positive	1	0.00	0.00
Male	Weakly negative	Negative	2657	1.27	5.09
Male	Weakly negative	Weakly negative	46371	22.19	88.75
Male	Weakly negative	Weakly positive	3218	1.54	6.16
Male	Weakly negative	Positive	1	0.00	0.00
Male	Weakly positive	Negative	6	0.00	0.01
Male	Weakly positive	Weakly negative	3214	1.54	6.15
Male	Weakly positive	Weakly positive	46519	22.26	89.04
Male	Weakly positive	Positive	2508	1.20	4.80
Male	Positive	Negative	0	0.00	0.00
Male	Positive	Weakly negative	1	0.00	0.00
Male	Positive	Weakly positive	2509	1.20	4.80
Male	Positive	Positive	49736	23.80	95.20

Table S12: The table shows similar information to Table S10, except that we now tabulate the number of transcripts that have various associations with early- and late-life fitness (separately within each sex). Note that there are essentially no transcripts with opposing effects on early- and late-life fitness, in either sex.

Sex	Association with early-life fitness	Association with late-life fitness	Number of transcripts	Percentage (overall)	Percentage (given association with early life fitness)
Female	Negative	Negative	3523	24.66	98.63
Female	Negative	Weakly negative	49	0.34	1.37
Female	Negative	Weakly positive	0	0.00	0.00
Female	Negative	Positive	0	0.00	0.00
Female	Weakly negative	Negative	49	0.34	1.37
Female	Weakly negative	Weakly negative	3464	24.25	96.98
Female	Weakly negative	Weakly positive	59	0.41	1.65
Female	Weakly negative	Positive	0	0.00	0.00
Female	Weakly positive	Negative	0	0.00	0.00
Female	Weakly positive	Weakly negative	59	0.41	1.65
Female	Weakly positive	Weakly positive	3450	24.15	96.61
Female	Weakly positive	Positive	62	0.43	1.74
Female	Positive	Negative	0	0.00	0.00
Female	Positive	Weakly negative	0	0.00	0.00
Female	Positive	Weakly positive	62	0.43	1.74
Female	Positive	Positive	3509	24.56	98.26
Male	Negative	Negative	3550	24.85	99.38
Male	Negative	Weakly negative	22	0.15	0.62
Male	Negative	Weakly positive	0	0.00	0.00
Male	Negative	Positive	0	0.00	0.00
Male	Weakly negative	Negative	22	0.15	0.62
Male	Weakly negative	Weakly negative	3521	24.65	98.57
Male	Weakly negative	Weakly positive	29	0.20	0.81
Male	Weakly negative	Positive	0	0.00	0.00
Male	Weakly positive	Negative	0	0.00	0.00
Male	Weakly positive	Weakly negative	29	0.20	0.81
Male	Weakly positive	Weakly positive	3520	24.64	98.57
Male	Weakly positive	Positive	22	0.15	0.62
Male	Positive	Negative	0	0.00	0.00
Male	Positive	Weakly negative	0	0.00	0.00
Male	Positive	Weakly positive	22	0.15	0.62
Male	Positive	Positive	3549	24.84	99.38

Table S13: A list of all the GO terms with a family wise error rate (FWER) threshold of $\text{FWER} < 0.05$, when testing for GO enrichment among genes with a high evidence ratio (indicating greater likelihood of being sexually concordant, as measured in the early-life fitness assay). The results imply strong, sexually concordant selection on the expression levels of genes involved in the functions listed here, such as cytoplasmic translation and peptide metabolism.

GO	Meaning	log10 p	FWER
GO:0002181	cytoplasmic translation	13.4	0.000
GO:0006518	peptide metabolic process	11.5	0.000
GO:0043603	cellular amide metabolic process	10.6	0.000
GO:0043043	peptide biosynthetic process	9.5	0.000
GO:0006412	translation	9.3	0.000
GO:0043604	amide biosynthetic process	7.8	0.000
GO:0034641	cellular nitrogen compound metabolic process	7.4	0.000
GO:0022613	ribonucleoprotein complex biogenesis	5.8	0.002
GO:0010467	gene expression	5.1	0.010
GO:0006364	rRNA processing	5.1	0.011
GO:0042254	ribosome biogenesis	4.9	0.015
GO:0042273	ribosomal large subunit biogenesis	4.9	0.016
GO:0016072	rRNA metabolic process	4.8	0.019
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.7	0.022
GO:0042274	ribosomal small subunit biogenesis	4.5	0.038
GO:0044271	cellular nitrogen compound biosynthetic process	4.5	0.039