SupportingInformation

1. Power calculations

For power calculations we used the pwr.t2n.test package in R. Cohen's effect size *d* was calculated as follows:

$d = \frac{m_1 - m_2}{s_p}$, where $s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}$; $\mu_1$and μ_2 are the mean lifespans associated with each genotype; σ_p is the pooled standard deviation; s_1^2 and s_2^2 are variances associated with the mean lifespans within each genotype. These mean lifespans were taken from the most associated SNP (*2R*_1632386; *p*-value=5.9x10^{-08}; μ_1=56.57and μ_2=45.97; s_1^2=89.86 and s_2^2=63.57).

2. Broad sense heritability

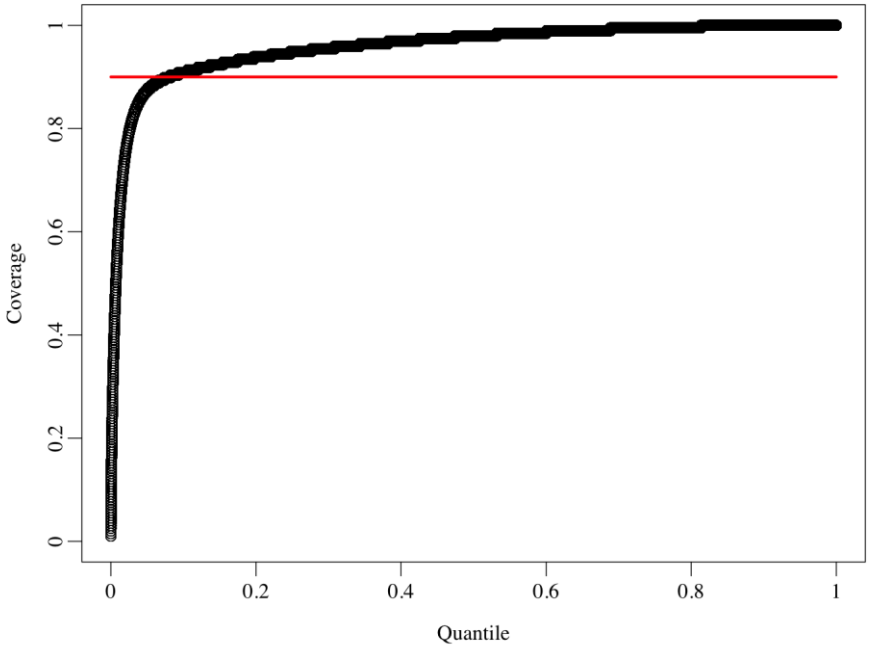
To estimate broad sense heritability (H^2) we partitioned the phenotypic variance between lines and the error variance for each line using ANOVA. Broad sense heritability was estimated by $H^2 = \frac{s_L^2}{s_L^2 + s_E^2}$, where s_L^2 is the among-line variance and s_E^2 is the within-line variance.

3. *Drosophila melanogaster*lines

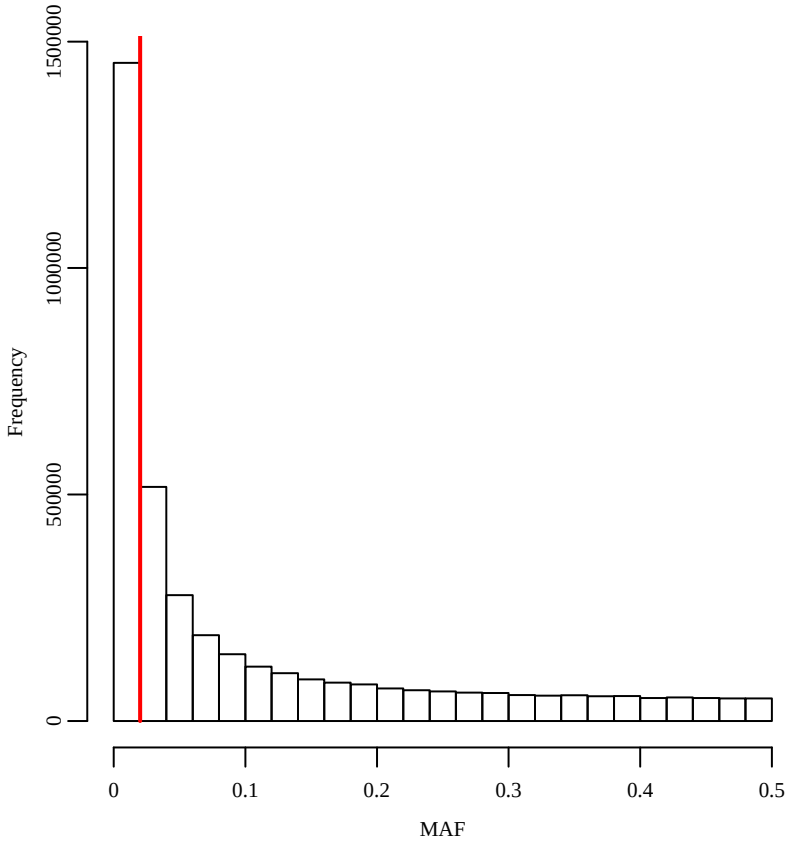
The Drosophila Genetic Reference Panel, Freeze 2.0 (1, 2), comprises 205 *D. melanogaster*lines derived by 20 generations of full-sib mating from wild-type caught females from Raleigh, North Carolina. Longevity was assayed as previously described (3, 4). All flies were reared from egg to adult on 10 ml standard cornmealagar-molasses medium at 25° in shell vials. The density of thestocks was controlled for three generations prior to the startof the longevity assays by restricting egg laying to 3 days andinitiating the cultures with 10 pairs of flies. A total of 25 virgin males and females per line were collected in a 24-hr period and 2-day-old flies were housed in five replicate vials with five same-sex individuals per vial. Flies were transferred to fresh medium every 2 days and the number of live flies was recorded until all were dead. The assays were performed in three temporally overlapping blocks; no block effects were observed.

Supplementary Graphs and Tables

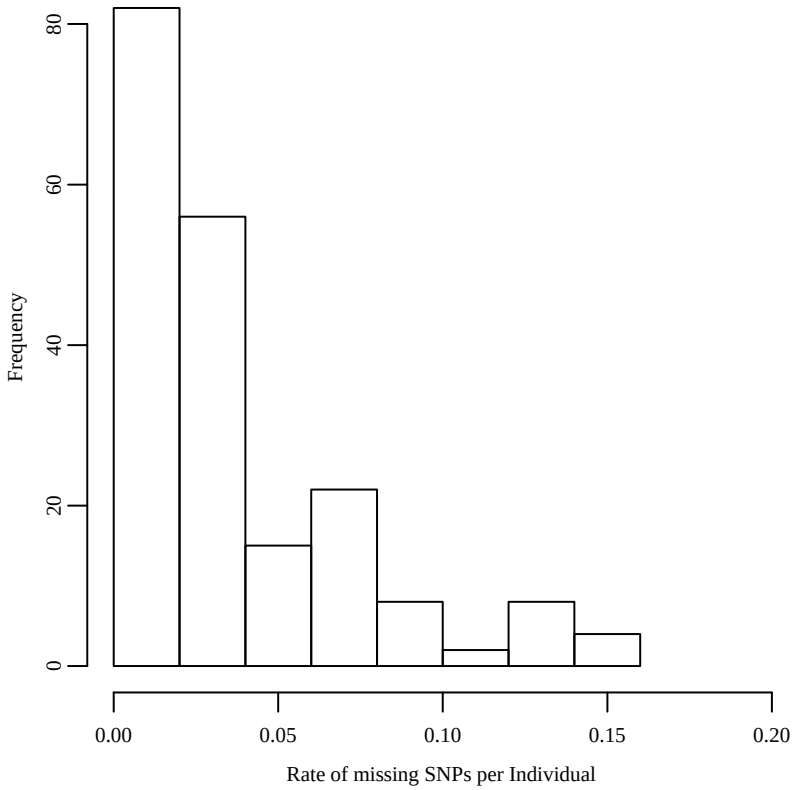
Supplementary Figure 1. SNP call rate. The red horizontal line represents the 0.9 SNP call rate. Coverage represents the proportion of genotypes present per SNP



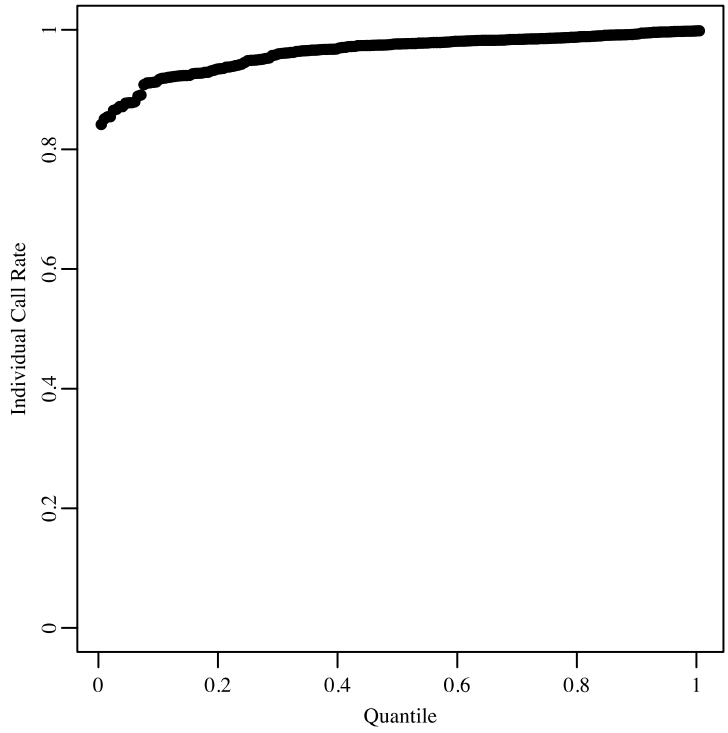
Supplementary Figure 2. Minor allele frequency (MAF). The red verticalline represents MAF=0.02



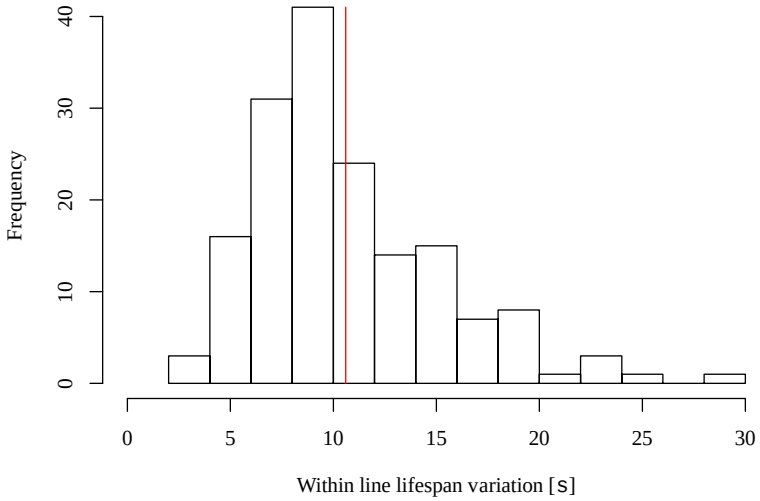
Supplementary Figure 3. Histogram of individual call rate



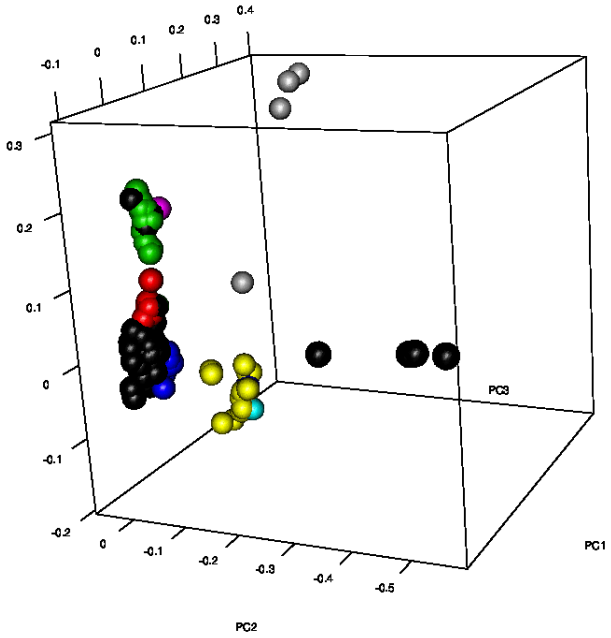
Supplementary Figure 4. Individual call rate. Individual call rate represents the proportion of genotypes present per fly



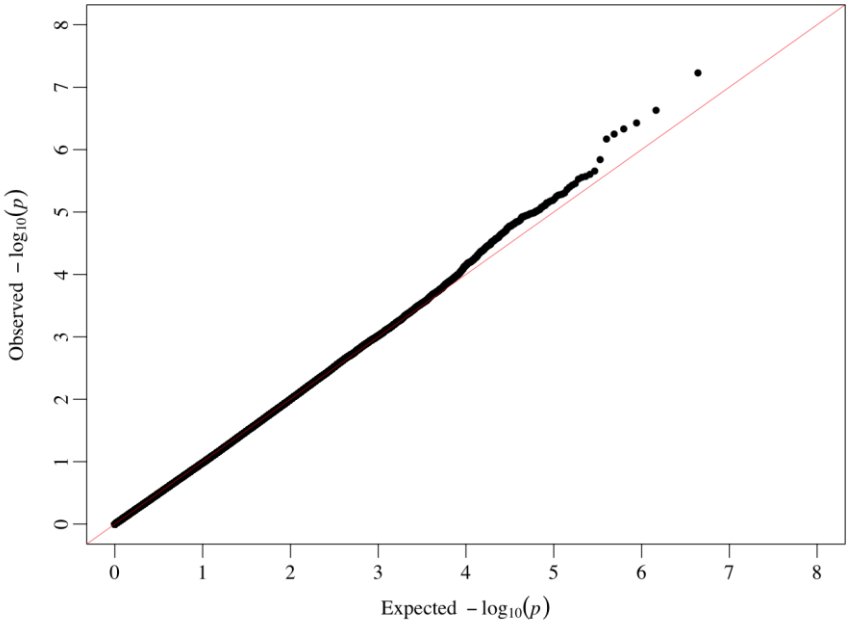
Supplementary Figure 5. Lifespan variation within individual fly lines (165 lines). The red vertical line represents the mean of the standard deviation between the fly lines (10.6)



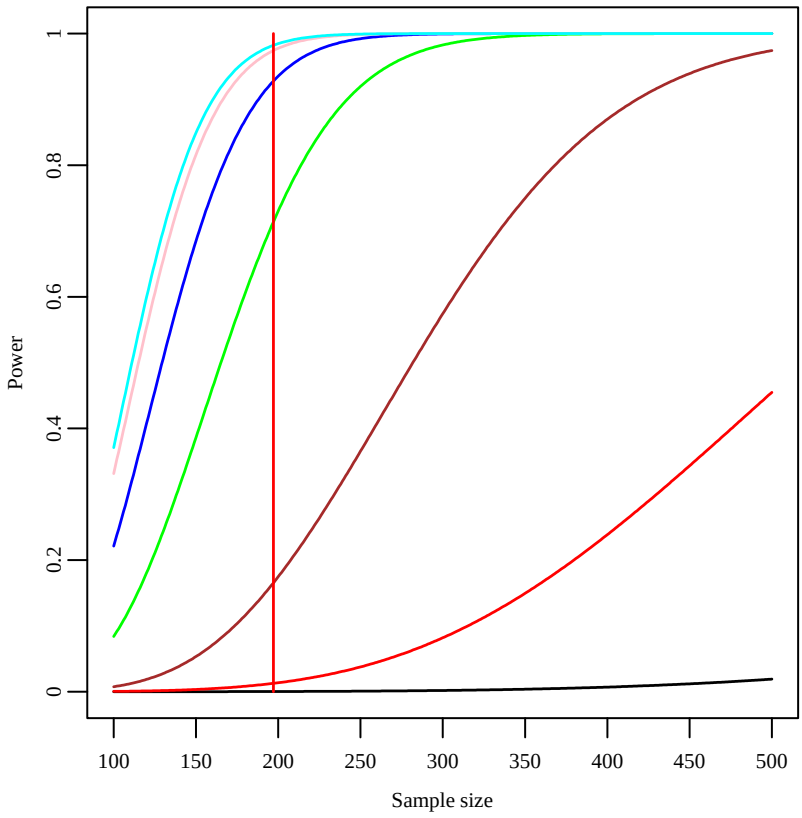
Supplementary Figure 6. Principal component analysis (PCA), 197 lines. PC1- principal component 1; PC2- principal component 2; PC3- principal component 3; Colours represent the inversion haplotype for *In(3R)Mo* and *In(2L)t*. 00- black, 01- red, 11- light blue, 12- pink, 22- grey, 10- blue, 20- yellow, 02- green



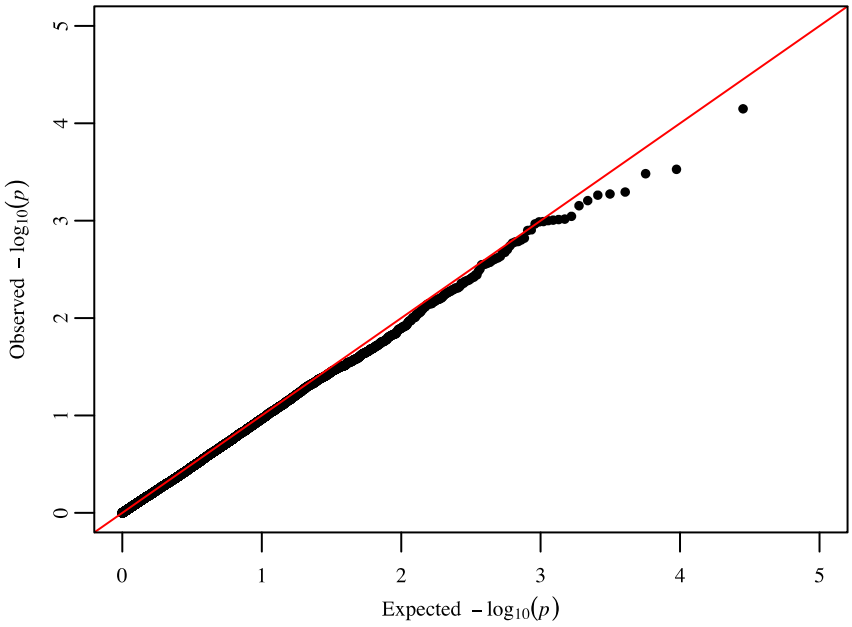
Supplementary Figure 7. SNP-based QQ-plot



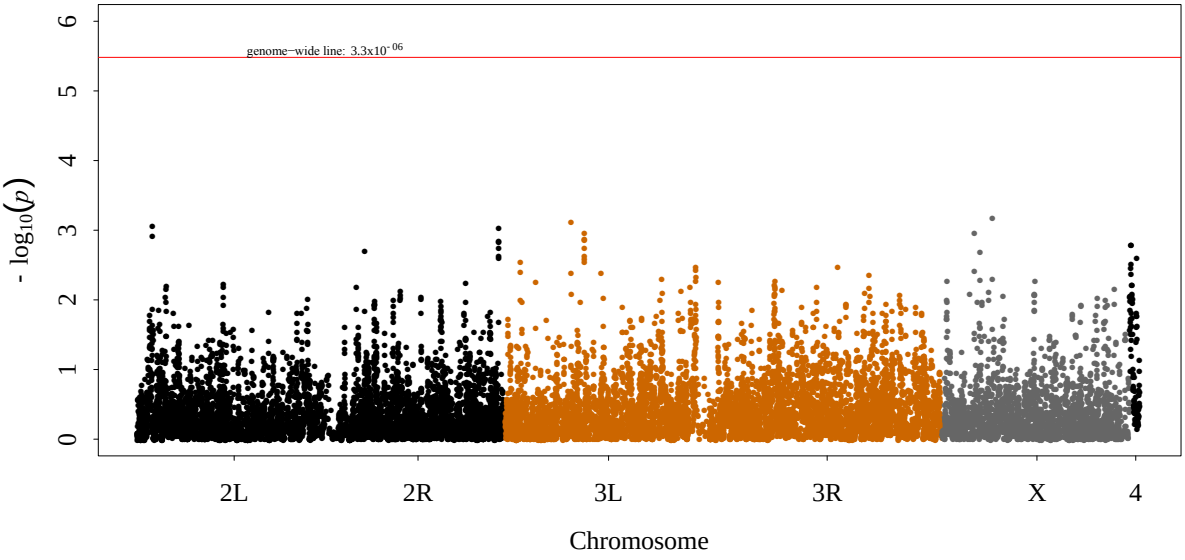
Supplementary Figure 8. Power to detect single-SNP association. Effect size = 10days (Cohen's *d*=1.15), pooled standard deviation = 9.25, μ_1=56.57, μ_2=45.97; red line represent MAF 0.1, brown line 0.2, green line 0.3, blue line 0.4 and pink line 0.5. The red vertical line represents the DGRP sample size (197 lines)



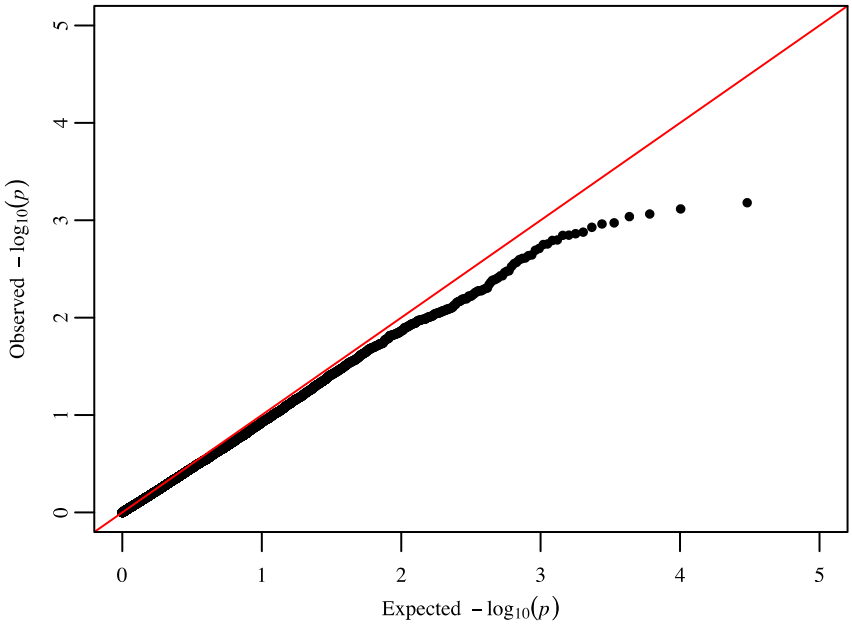
Supplementary Figure 9. Gene-based QQ-plot



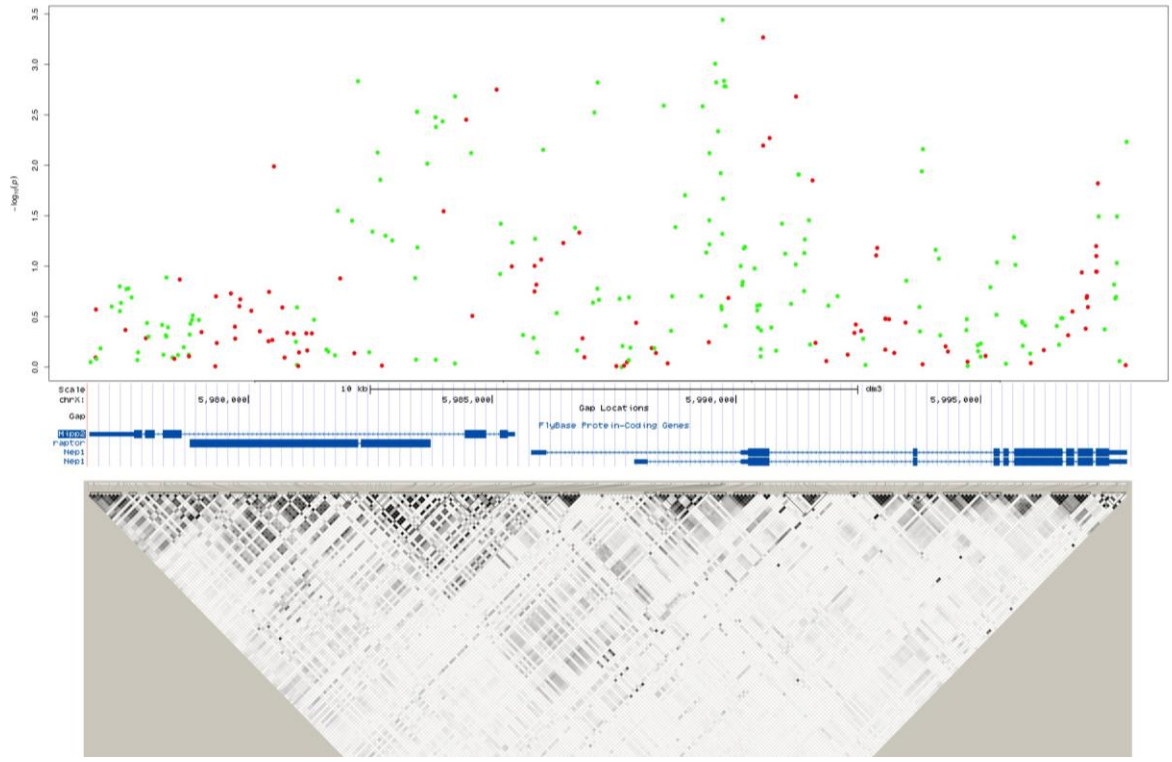
Supplementary Figure 10. Manhattan plot for gene-based analysis (genes ±5kb). Each point represents a gene. The height of the points represents the strength of association with lifespan, expressed as -log_{10}(*p*-value).The red horizontal line represents genome-wide Bonferroni significance threshold p=3.30x10^{-06}



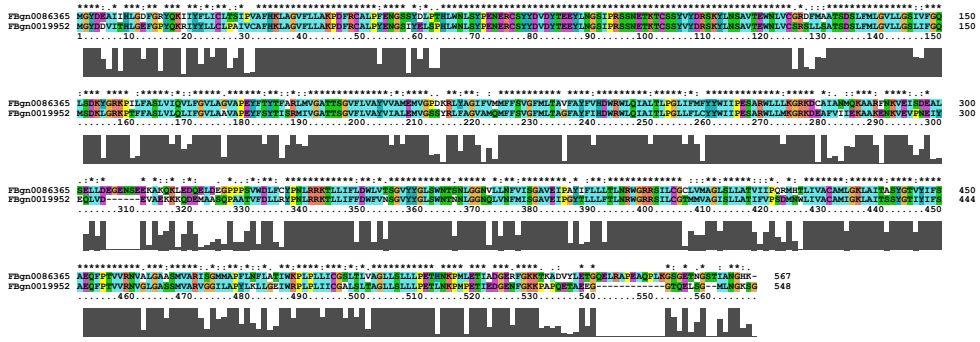
Supplementary Figure 11. Gene-based QQ-plot (genes±5kb)



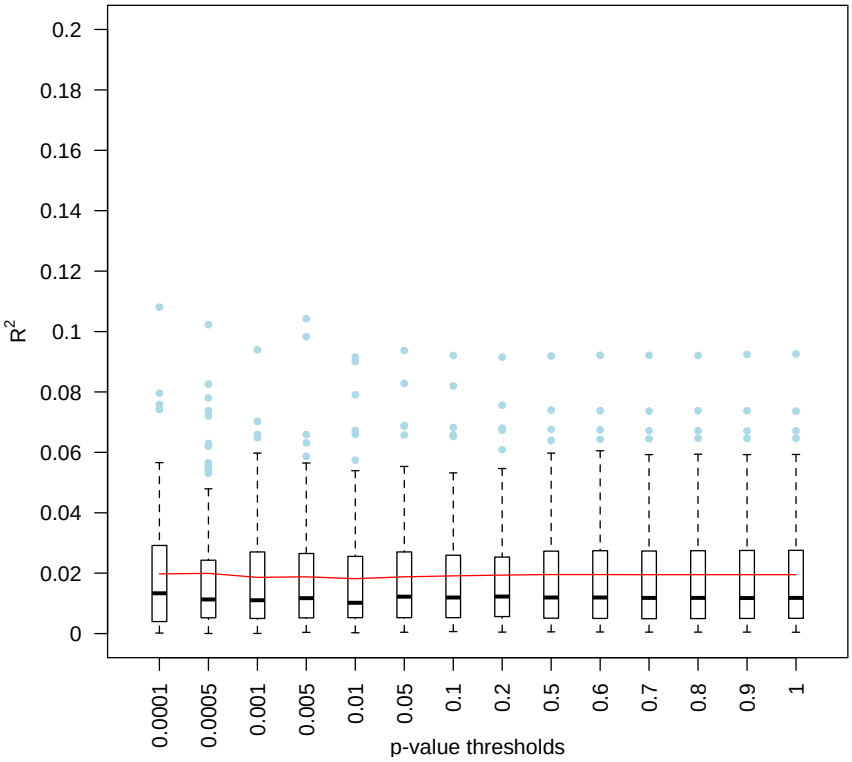
Supplementary Figure 12. LD structure of *Mipp2* and *Nep1*. Each point in the top half of the graph represents a SNP. The y-axis represents the strength of association expressed in $-log_{10}$(*p*-value). Red dots represent SNPs with negative *ß* coefficients and green dots SNPs with positive *ß* coefficients. The middle panel shows the positions of *Mipp2* and *Nep1* in the *Drosophila* genome using the UCSC genome browser http://genome-euro.ucsc.edu/cgi-bin/hgGateway; The bottom paneldepicts the LD structure within the two genes, expressed in terms of R^2. Black squares represent R^2=1. The LD structure was produced using Haploview (5)



Supplementary Figure 13. Protein alignment of *Orct* (*FBgn0019952*) and *Orct2* (*FBgn0086365*). The protein alignment was produced using ClustalX (6)



Supplementary Figure 14. Polygenic score (permuted lifespan phenotype). The lifespan data were permuted 100 times. Each box represents the interquartile range (IQR) with the median as a black horizontal line; the whiskers represent values 1.5*IQR; outliers are represented as light blue points. The orange line connects the means within each *p*-value threshold



Supplementary Table 1. DGRP lines, genotypes and phenotypes. [1]*Wolbachia* status: 1- absent, 2- present;[2]Number of flies used for determining the mean and median lifespan; The lifespan data for several lines were derived from (3), where only the mean lifespan was given, hence for standard deviation, number of flies used and median lifespan is given as NA or not assigned.

Line	*Wolbachia* status[1]	Mean lifespan	Standard deviation	Number flies used[2]	Median lifespan	Number missing SNPs	Frequency missing SNPs
line_21	2	49.76	10.04	25	51	28607	0.0130
line_26	1	46.39	9.13	23	46	37755	0.0172
line_28	1	54.00	13.13	24	56	23626	0.0108
line_31	1	71.88	7.98	25	71	264022	0.1204
line_32	1	52.56	6.60	25	54	42210	0.0192
line_38	1	48.27	19.75	22	51	131573	0.0600
line_40	2	56.84	9.86	25	58	6940	0.0032
line_41	1	59.24	23.78	25	68	54027	0.0246
line_42	1	45.80	4.26	25	46	35373	0.0161
line_45	1	48.27	6.76	22	47	55160	0.0251
line_48	2	57.83	13.74	24	61	167964	0.0766
line_49	2	53.84	6.11	25	53	177048	0.0807
line_57	1	59.67	11.81	24	60	34166	0.0156
line_59	1	58.52	22.65	25	67	88646	0.0404
line_69	2	45.13	11.41	23	45	82957	0.0378
line_73	2	52.33	6.04	24	51	86777	0.0396
line_75	2	44.56	15.63	25	48	38276	0.0175
line_83	1	68.40	14.24	20	70	33671	0.0154
line_85	1	41.95	12.38	19	44	201093	0.0917
line_88	1	58.79	11.56	24	61	182007	0.0830
line_91	1	53.64	9.08	25	53	71934	0.0328
line_93	1	46.58	9.61	24	50	30236	0.0138
line_100	2	63.08	24.52	24	75	136767	0.0623
line_101	1	75.83	7.97	24	76	191396	0.0873
line_105	1	63.89	11.87	18	68.5	45362	0.0207
line_109	1	60.60	15.39	25	60	136599	0.0623
line_129	1	58.13	6.06	24	58	27485	0.0125
line_136	2	76.56	11.83	25	78	291551	0.1329
line_138	1	40.64	5.44	25	41	50682	0.0231
line_142	2	63.48	10.79	25	68	70638	0.0322
line_149	2	53.48	8.10	23	56	48985	0.0223
line_153	2	54.96	9.68	25	56	119735	0.0546
line_158	1	54.85	8.04	20	52.5	85662	0.0391
line_161	1	67.72	8.27	25	66	76017	0.0347
line_176	2	44.42	16.19	24	44.5	25060	0.0114
line_177	1	30.16	7.94	19	30	12027	0.0055
line_181	2	54.20	14.25	20	58	19962	0.0091
line_189	2	62.32	14.20	22	64	9351	0.0043
line_195	1	61.45	5.39	20	62.5	61031	0.0278
line_208	1	53.76	2.60	25	54	38622	0.0176
line_217	1	67.52	8.12	23	68	74816	0.0341
line_223	2	48.73	5.33	22	48	8088	0.0037
line_227	2	47.95	11.44	20	49	35679	0.0163
line_228	1	65.81	4.17	21	66	58009	0.0264
line_229	1	45.27	9.97	22	45	58098	0.0265
line_233	1	54.24	9.02	25	54	56039	0.0255
line_235	1	45.04	22.05	25	50	28884	0.0132
line_237	2	60.65	6.19	17	61	295495	0.1347
line_239	1	68.48	16.22	25	71	41365	0.0189
line_256	2	67.67	12.10	24	70	46500	0.0212
line_280	2	57.59	10.64	17	62	37967	0.0173
line_287	2	41.09	18.80	23	44	107899	0.0492
line_303	1	57.36	NA	NA	NA	347361	0.1583
line_306	2	58.78	NA	NA	NA	71315	0.0325
line_307	1	44.64	NA	NA	NA	11333	0.0052
line_309	1	52.57	4.64	23	54	167005	0.0761
line_310	2	22.13	7.82	24	21	51190	0.0233
line_313	1	80.29	NA	NA	NA	57064	0.0260
line_315	1	66.92	NA	NA	NA	39840	0.0182
line_317	2	53.76	13.29	17	56	161118	0.0734
line_318	2	49.36	NA	NA	NA	58536	0.0267

Line	*Wolbachia* status[1]	Mean lifespan	Standard deviation	Number flies used[2]	Median lifespan	Number missing SNPs	Frequency missing SNPs
line_320	2	65.70	13.07	23	69	9102	0.0041
line_321	2	49.46	21.64	24	47.5	50223	0.0229
line_324	1	48.00	NA	NA	NA	3943	0.0018
line_325	1	42.61	4.68	23	42	172915	0.0788
line_332	1	55.92	NA	NA	NA	83533	0.0381
line_335	2	67.75	NA	NA	NA	84844	0.0387
line_338	2	60.89	12.90	18	66	281675	0.1284
line_340	2	59.17	9.01	24	60	33414	0.0152
line_348	1	54.00	14.75	21	57	8446	0.0039
line_350	1	59.25	NA	NA	NA	171217	0.0781
line_352	2	46.78	11.52	23	48	194440	0.0886
line_354	1	59.83	7.32	23	58	5064	0.0023
line_355	2	52.45	8.35	22	54	5391	0.0025
line_356	2	37.96	11.63	24	41	78752	0.0359
line_357	1	58.36	NA	NA	NA	111899	0.0510
line_358	1	62.67	NA	NA	NA	71305	0.0325
line_359	1	56.28	NA	NA	NA	51370	0.0234
line_360	2	39.91	5.90	23	40	103452	0.0472
line_362	2	60.33	NA	NA	NA	76686	0.0350
line_365	2	48.24	8.40	25	47	38529	0.0176
line_367	1	64.15	8.53	20	66	57968	0.0264
line_370	2	56.82	11.05	22	57	16173	0.0074
line_371	1	39.12	3.11	25	40	8108	0.0037
line_373	1	68.24	8.05	25	68	129299	0.0589
line_374	2	66.04	8.24	23	66	12381	0.0056
line_375	1	62.60	NA	NA	NA	48611	0.0222
line_377	1	66.89	6.66	18	68	243461	0.1110
line_379	1	68.08	16.81	25	71	50561	0.0231
line_380	2	57.96	5.60	24	58	105240	0.0480
line_381	1	41.08	8.83	25	40	169648	0.0773
line_382	2	76.56	8.43	25	78	15422	0.0070
line_383	2	56.84	10.78	25	58	22528	0.0103
line_385	1	50.36	9.94	25	54	110417	0.0503
line_386	1	54.40	5.06	25	55	111546	0.0509
line_391	1	49.55	5.75	22	50	30426	0.0139
line_392	1	66.29	7.29	21	65	74115	0.0338
line_395	1	55.79	9.85	24	58.5	5285	0.0024
line_399	1	59.26	NA	NA	NA	41828	0.0191
line_405	2	50.56	9.35	25	50	174491	0.0795
line_406	1	58.00	18.10	24	64	20083	0.0092
line_409	2	23.92	9.52	24	21	267506	0.1219
line_426	1	69.84	8.58	25	70	267796	0.1221
line_427	1	52.08	7.40	24	50	40502	0.0185
line_437	1	57.76	29.40	21	72	10576	0.0048
line_439	1	57.80	12.72	25	62	52056	0.0237
line_440	2	65.00	8.25	24	68	155776	0.0710
line_441	2	65.32	17.65	25	70	19207	0.0088
line_443	1	60.64	7.87	25	60	156133	0.0712
line_461	2	36.96	8.34	24	34.5	27413	0.0125
line_486	2	65.33	8.42	24	70	61682	0.0281
line_491	1	61.13	8.06	23	62	32192	0.0147
line_492	1	62.79	5.42	24	64	17547	0.0080
line_502	1	69.91	14.05	23	72	144007	0.0656
line_505	2	56.63	13.01	19	58	6193	0.0028
line_508	1	53.60	8.08	25	56	17207	0.0078
line_509	1	62.54	6.23	24	63	31366	0.0143
line_513	2	51.38	18.29	24	52	33730	0.0154
line_517	1	63.20	5.64	25	64	39249	0.0179
line_528	2	51.08	14.87	24	54	269113	0.1227
line_530	2	46.41	7.87	22	49.5	26680	0.0122
line_531	2	53.61	19.39	23	60	61208	0.0279
line_535	2	49.32	6.00	19	50	30966	0.0141
line_551	2	59.68	8.98	25	59	158784	0.0724
line_555	2	51.44	9.70	25	53	46876	0.0214
line_559	1	59.76	6.67	25	60	159498	0.0727
line_563	1	50.25	11.23	24	56	281634	0.1284
line_566	1	65.32	10.60	25	64	109330	0.0498
line_584	2	62.48	9.08	25	65	57830	0.0264
line_589	2	65.96	15.57	24	69.5	5253	0.0024

Line	*Wolbachia* status[1]	Mean lifespan	Standard deviation	Number flies used[2]	Median lifespan	Number missing SNPs	Frequency missing SNPs
line_595	2	60.00	12.18	21	60	56380	0.0257
line_596	1	37.94	11.18	16	39.5	5999	0.0027
line_627	1	65.17	8.42	23	66	239238	0.1091
line_630	1	66.08	13.17	25	67	318694	0.1453
line_634	2	52.96	14.44	25	53	141968	0.0647
line_639	2	75.82	15.23	22	79	52102	0.0238
line_642	1	62.09	12.63	23	64	35075	0.0160
line_646	2	58.00	17.57	23	64	56570	0.0258
line_703	1	32.60	4.41	25	33	38586	0.0176
line_705	2	63.67	NA	NA	NA	51922	0.0237
line_707	2	60.64	NA	NA	NA	47184	0.0215
line_712	2	45.52	7.84	25	47	42014	0.0192
line_714	1	69.28	10.04	25	72	77196	0.0352
line_716	2	60.00	14.50	25	64	48417	0.0221
line_721	2	43.36	9.37	25	42	44840	0.0204
line_727	2	39.38	10.82	21	41	18656	0.0085
line_730	2	53.28	14.39	25	55	33330	0.0152
line_732	1	66.76	NA	NA	NA	168565	0.0768
line_737	2	53.16	NA	NA	NA	113123	0.0516
line_738	2	59.88	7.98	24	60	177872	0.0811
line_748	2	58.17	6.62	24	58	8035	0.0037
line_757	1	29.65	18.25	20	29	19606	0.0089
line_761	2	46.80	5.80	25	46	35037	0.0160
line_765	1	33.96	NA	NA	NA	40839	0.0186
line_774	1	64.36	NA	NA	NA	195136	0.0890
line_776	2	59.75	6.22	24	59	66813	0.0305
line_783	2	59.46	8.96	24	60	36733	0.0167
line_786	2	53.83	NA	NA	NA	45760	0.0209
line_787	2	44.92	NA	NA	NA	55841	0.0255
line_790	2	49.48	8.66	23	52	29843	0.0136
line_796	2	42.32	2.78	25	43	74641	0.0340
line_799	1	60.00	NA	NA	NA	32325	0.0147
line_801	2	69.44	6.34	25	72	134359	0.0613
line_802	2	49.84	18.12	25	54	326828	0.1490
line_804	2	67.24	13.26	25	71	72753	0.0332
line_805	2	51.17	7.08	24	51	25221	0.0115
line_808	1	52.48	NA	NA	NA	43379	0.0198
line_810	1	49.12	15.80	25	55	18254	0.0083
line_812	1	57.04	7.27	24	59	142941	0.0652
line_818	2	60.36	8.65	25	62	71898	0.0328
line_819	2	40.40	10.23	25	40	3750	0.0017
line_820	2	38.92	NA	NA	NA	64348	0.0293
line_821	2	72.70	10.42	23	74	126181	0.0575
line_822	2	53.58	NA	NA	NA	64906	0.0296
line_837	2	60.09	13.78	23	60	18713	0.0085
line_843	1	53.38	6.96	24	56	23051	0.0105
line_849	1	58.05	16.62	20	59.5	148060	0.0675
line_850	2	44.74	5.43	23	44	5883	0.0027
line_852	2	49.88	NA	NA	NA	22057	0.0101
line_853	2	47.32	10.02	25	49	193021	0.0880
line_855	2	54.58	8.32	24	56.5	94566	0.0431
line_857	1	54.83	8.17	23	55	159737	0.0728
line_859	2	60.84	NA	NA	NA	38944	0.0178
line_861	2	55.67	14.72	24	58.5	79452	0.0362
line_879	2	59.68	7.82	19	56	35422	0.0162
line_882	2	53.54	19.83	24	58.5	25058	0.0114
line_884	2	62.17	7.62	24	62	150768	0.0687
line_887	2	48.04	10.11	23	51	24927	0.0114
line_890	2	50.79	7.41	24	51	38702	0.0176
line_892	2	51.42	16.77	24	58.5	32480	0.0148
line_894	1	61.54	8.79	24	62	38462	0.0175
line_897	2	49.60	7.80	20	52	18548	0.0085
line_900	1	46.71	10.34	21	48	49074	0.0224
line_907	1	60.44	NA	NA	NA	168053	0.0766
line_908	1	47.29	12.74	21	45	46539	0.0212
line_911	1	37.68	NA	NA	NA	92701	0.0423
line_913	2	56.61	11.17	18	58	319509	0.1456

Supplementary Table 2. Genetic variation within 165 DGRP lines. [a]Within replicate line data was available for 165 fly lines. Mean lifespan was calculated from 165 fly lines as well as the rest of the calculations; [b] Total genetic variance; [c] Variance within replicates or lines; [d] Total phenotypic variance ($s_G^2 + s_E^2$); [e] Broad sense heritability (s_G^2 / s_P^2); [f] Coefficient of genetic variation ($100 s_G$ /Mean); [g] Coefficient of environmental variation ($100 s_E$ /Mean);

Mean lifespan[a]	$s_G^{2\,b}$	$s_E^{2\,c}$	$s_P^{2\,d}$	H^{2e}	CV_G^f	CV_E^g
55.149	93.748	133.41	227.158	0.413	17.557	20.944

Supplementary Table 3. Single-SNP GWAS, genes near the top 50 SNPs; NA - not within a gene

SNP	CHR	*P*-value	ß coefficient	Within Gene	5'	5' distance [bp]	3'	3'distance [bp]
2L_10068812_SNP	2L	9.41×10^{-06}	-7.41	*CG31714*				
2L_10070707_SNP	2L	6.77×10^{-06}	-6.24	*CG31714*				
2L_1632386_SNP	2L	5.90×10^{-08}	-5.85	NA	*chinmo*	18872	*RFeSP*	18204
2L_1632388_SNP	2L	3.74×10^{-07}	-5.66	NA	*chinmo*	18870	*RFeSP*	18206
2L_1696065_SNP	2L	2.49×10^{-06}	-7.09	*chinmo*				
2L_1835028_SNP	2L	1.11×10^{-05}	4.44	NA	*c-cup*	2472	*wry*	1603
2L_2279849_SNP	2L	2.21×10^{-06}	-11.63	NA	*CG17242*	10731	*CG4271*	5315
2L_3480710_SNP	2L	6.77×10^{-07}	-9.84	NA	*CG15414*	45	*Thor*	1098
2L_3746990_SNP	2L	1.14×10^{-05}	-9.63	*CG10019*				
2L_3752571_SNP	2L	2.35×10^{-07}	-12.55	*CG10019*				
2R_19786647_SNP	2R	4.66×10^{-07}	-12.29	*Lpt*				
2R_4308343_SNP	2R	8.41×10^{-06}	-7.84	NA	*CSN7*	150	*CG43296*	3132
2R_4308355_SNP	2R	7.86×10^{-06}	-7.89	NA	*CSN7*	138	*CG43296*	3144
3L_11792808_SNP	3L	5.37×10^{-06}	-3.74	*CG10361*				
3L_14778027_SNP	3L	3.71×10^{-06}	-10.20	*bmm*				
3L_14778725_SNP	3L	3.50×10^{-06}	-10.17	*bmm*				
3L_14780164_SNP	3L	4.00×10^{-06}	-10.14	*CG13472*				
3L_14781414_SNP	3L	1.45×10^{-06}	-11.72	*CG13472*				
3L_17762728_SNP	3L	1.13×10^{-05}	-9.58	NA	*Adgf-A*	5471	*CG42815*	21452
3L_18140585_SNP	3L	6.51×10^{-06}	-4.60	NA	*CG7330*	1438	*gk*	2067
3L_18810814_SNP	3L	4.36×10^{-06}	4.29	*CG14073*				
3L_18934159_SNP	3L	1.06×10^{-05}	-5.94	*CG32204*				
3L_1966180_SNP	3L	7.14×10^{-06}	-5.81	*CG1140*				
3L_4628971_SNP	3L	5.16×10^{-06}	-7.43	*Rpd3*				
3L_5319539_SNP	3L	1.12×10^{-05}	-5.30	NA	*shep*	48496	*lama*	17181
3L_5373941_SNP	3L	7.12×10^{-06}	-11.04	*Ir64a*				
3L_5636181_SNP	3L	2.69×10^{-06}	-9.57	*Blimp-1*				
3L_8650506_SNP	3L	6.13×10^{-06}	-4.02	NA	h	18353	*Pex7*	6395
3L_9507749_SNP	3L	2.97×10^{-06}	-3.42	*CG33700*				
3R_14921157_SNP	3R	1.15×10^{-05}	-7.33	*ATPsyn-d*				
3R_15338010_SNP	3R	1.08×10^{-05}	-4.16	*det*				
3R_15338014_SNP	3R	1.02×10^{-05}	-4.11	*det*				
3R_15340424_SNP	3R	6.62×10^{-06}	-4.38	*Dys*				
3R_15950064_SNP	3R	1.17×10^{-05}	-8.84	NA	*Gr92a*	2066	*CG5023*	45095
3R_18577501_SNP	3R	5.63×10^{-06}	-7.22	*CG7023*				
3R_19071977_SNP	3R	5.64×10^{-07}	-5.62	*CG4467*				
3R_20944700_SNP	3R	9.10×10^{-06}	-5.99	*CG31510*				
3R_21259405_SNP	3R	7.92×10^{-06}	-9.58	*Fur1*				
3R_21913681_SNP	3R	1.04×10^{-05}	-5.28	*dys*				
3R_23482833_SNP	3R	9.26×10^{-06}	-3.51	NA	*Mlc1*	452	*tau*	115
3R_24748071_SNP	3R	1.19×10^{-05}	-3.92	*Doa*				
3R_25189263_SNP	3R	1.05×10^{-05}	-6.41	NA	*Cnx99A*	43898	*Ptp99A*	13725
3R_25562159_SNP	3R	5.27×10^{-06}	-4.18	*CG7601*				
3R_25921654_SNP	3R	1.04×10^{-05}	-8.93	*sima*				
3R_25921693_SNP	3R	9.79×10^{-06}	-8.94	*sima*				
3R_25921696_SNP	3R	9.79×10^{-06}	-8.94	*sima*				
3R_8922024_SNP	3R	1.19×10^{-05}	-7.43	*timeout*				
X_20940365_SNP	X	4.95×10^{-06}	-14.60	*bves*				
X_604933_SNP	X	8.31×10^{-06}	-3.53	*sdk*				
X_9282626_SNP	X	2.78×10^{-06}	7.06	*mgl*				

Supplementary Table 4. Top 30 genes, gene-based analysis. *Empirical *p*-values, based on 1,000,000 permutations

FlyBaseGene ID	Gene Symbol	Chr	N SNPs	Gene-based*p*-value*
FBgn0036603	*CG13062*	3L	22	7.10×10^{-05}
FBgn0036870	*CG14095*	3L	5	2.97×10^{-04}
FBgn0037985	*ssp5*	3R	18	3.29×10^{-04}
FBgn0051956	*pgant4*	2L	74	5.08×10^{-04}
FBgn0039462	*CG14252*	3R	62	5.32×10^{-04}
FBgn0087005	*rtp*	3R	2	5.47×10^{-04}
FBgn0029843	*Nep1*	X	161	6.22×10^{-04}
FBgn0039075	*CG4393*	3R	194	7.01×10^{-04}
FBgn0037156	*CG11523*	3L	5	9.02×10^{-04}
FBgn0016120	*ATPsyn-d*	3R	10	9.63×10^{-04}
FBgn0051928	*CG31928*	2L	33	9.73×10^{-04}
FBgn0036008	*CG3408*	3L	68	9.87×10^{-04}
FBgn0050154	*CG30154*	2R	21	9.99×10^{-04}
FBgn0036208	*CG10361*	3L	70	1.02×10^{-03}
FBgn0263004	*CG43312*	3L	2	1.03×10^{-03}
FBgn0044324	*Chro*	3L	26	1.08×10^{-03}
FBgn0031596	*CG15429*	2L	46	1.24×10^{-03}
FBgn0262818	*CG43189*	2R	3	1.26×10^{-03}
FBgn0025638	*Roc1a*	X	5	1.51×10^{-03}
FBgn0036165	*chrb*	3L	137	1.58×10^{-03}
FBgn0035011	*CG13589*	2R	17	1.64×10^{-03}
FBgn0037307	*Tim17a2*	3R	9	1.65×10^{-03}
FBgn0039385	*CG5913*	3R	19	1.70×10^{-03}
FBgn0033769	*CG8768*	2R	34	1.82×10^{-03}
FBgn0039890	*CG2316*	4	25	1.98×10^{-03}
FBgn0037960	*mthl5*	3R	48	2.11×10^{-03}
FBgn0051998	*CG31998*	4	16	2.11×10^{-03}
FBgn0032217	*CG4972*	2L	52	2.32×10^{-03}
FBgn0260003	*Dys*	3R	3104	2.40×10^{-03}
FBgn0031601	*Dim1*	2L	24	2.44×10^{-03}

Supplementary Table 5. Top 30 genes, gene-based analysis (genes±5kb). *Empirical *p*-values, based on 1,000,000 permutations

FlyBaseGene ID	Gene Symbol	Chr	N SNPs	Gene-based*p*-value*
FBgn0029843	*Nep1*	X	245	6.61×10^{-04}
FBgn0035827	*CG14252*	3L	337	7.57×10^{-04}
FBgn0262275	*mir-2280*	2L	312	8.62×10^{-04}
FBgn0015300	*Ssl*	2R	224	9.17×10^{-04}
FBgn0086075	*CR34704*	3L	316	1.06×10^{-03}
FBgn0052783	*CG32783*	X	20	1.09×10^{-03}
FBgn0031367	*c-cup*	2L	349	1.18×10^{-03}
FBgn0053703	*CG33703*	3L	369	1.32×10^{-03}
FBgn0010408	*RpS9*	3L	375	1.37×10^{-03}
FBgn0017556	Prosα4T2	2R	240	1.42×10^{-03}
FBgn0029501	*Crtp*	2R	253	1.43×10^{-03}
FBgn0051998	*CG31998*	4	60	1.59×10^{-03}
FBgn0039890	*CG2316*	4	66	1.61×10^{-03}
FBgn0053702	*CG33702*	3L	371	1.75×10^{-03}
FBgn0061188	*Yu*	2R	213	1.78×10^{-03}
FBgn0262988	*CG43296*	2R	195	1.95×10^{-03}
FBgn0025387	*CG12184*	X	93	2.03×10^{-03}
FBgn0053701	*CR33701*	3L	390	2.27×10^{-03}
FBgn0035012	*CG13590*	2R	199	2.31×10^{-03}
FBgn0035011	*CG13589*	2R	188	2.44×10^{-03}
FBgn0263344	*CR43425*	4	28	2.47×10^{-03}
FBgn0036008	*CG3408*	3L	409	2.53×10^{-03}
FBgn0053700	*CG33700*	3L	701	2.80×10^{-03}
FBgn0035281	*Cpr62Bc*	3L	377	2.82×10^{-03}
FBgn0039889	*Arl4*	4	49	2.98×10^{-03}
FBgn0260003	*Dys*	3R	3271	3.30×10^{-03}
FBgn0044324	*Chro*	3L	80	3.34×10^{-03}
FBgn0053978	*CG33978*	4	91	3.45×10^{-03}
FBgn0037202	*Ssl1*	3L	69	3.72×10^{-03}
FBgn0052786	*CG32786*	X	9	3.73×10^{-03}

Supplementary Table 6. Genes belonging to the IIS and TOR pathways

IIS pathway genes	*14-3-3epsilon* (*FBgn0020238*), *Akt1* (*FBgn0010379*), *B4* (*FBgn0023407*), *chico* (*FBgn0024248*), *dock* (*FBgn0010583*), *foxo* (*FBgn0038197*), *hpo* (*FBgn0261456*), *Ilp1* (*FBgn0044051*), *Ilp2* (*FBgn0036046*), *Ilp3* (*FBgn0044050*), *Ilp4* (*FBgn0044049*), *Ilp5* (*FBgn0044048*), *Ilp6* (*FBgn0044047*), *Ilp7* (*FBgn0044046*), *Ilp8* (*FBgn0036690*), *Impl2* (*FBgn0001257*), *InR* (*FBgn0013984*), *Lnk* (*FBgn0028717*), *melt* (*FBgn0023001*), *Phlpp* (*FBgn0032749*), *Pi3K21B* (*FBgn0020622*), *Pi3K92E* (*FBgn0015279*), *Pten* (*FBgn0026379*), *S6KII* (*FBgn0262866*), *sgg* (*FBgn0003371*), *step* (*FBgn0086779*), *wdb* (*FBgn0027492*), *Pdk1* (*FBgn0020386*), *B4* (*FBgn0023407*)
TOR pathway genes	*Atg1* (*FBgn0260945*), *chrb* (*FBgn0036165*), *dm* (*FBgn0262656*), *Dredd* (*FBgn0020381*), *eIF-4B* (*FBgn0020660*), *eIF-4E* (*FBgn0015218*), *eIF4G* (*FBgn0023213*), *gig* (*FBgn0005198*), *HLH106* (*FBgn0261283*), *L* (*FBgn0001332*), *lkb1* (*FBgn0038167*), *Lst8* (*FBgn0264691*), *Mipp2* (*FBgn0026060*), *Mo25* (*FBgn0017572*), *par-1* (*FBgn0260934*), *path* (*FBgn0036007*), *pgc* (*FBgn0016053*), *pico* (*FBgn0261811*), *Pka-C1* (*FBgn0000273*), *RagA* (*FBgn0037647*), *RagC* (*FBgn0033272*), *raptor* (*FBgn0029840*), *Rheb* (*FBgn0041191*), *rictor* (*FBgn0031006*), *RpS6* (*FBgn0261592*), *S6k* (*FBgn0015806*), *scyl* (*FBgn0041094*), *Sesn* (*FBgn0034897*), *Sik2* (*FBgn0025625*), *Sin1* (*FBgn0033935*), *slif* (*FBgn0037203*), *SNF1A* (*FBgn0023169*), *Thor* (*FBgn0261560*), *Tor* (*FBgn0021796*), *tor* (*FBgn0003733*), *Crtc* (*FBgn0036746*), *Tsc1* (*FBgn0026317*), *Tif-IA* (*FBgn0032988*)

Supplementary Table 7. Ranking and *p*-values of the top 20 GO categories

GO ID	Go category	*p*-value	Number of genes
GO:0046692	sperm competition	2.21×10^{-04}	22
GO:0022626	cytosolic ribosome	2.68×10^{-04}	4
GO:0046527	glucosyltransferase activity	3.04×10^{-04}	11
GO:0019318	hexose metabolic process	4.44×10^{-04}	63
GO:0006006	glucose metabolic process	4.87×10^{-04}	43
GO:0035074	pupation	5.51×10^{-04}	5
GO:0006007	glucose catabolic process	5.65×10^{-04}	33
GO:0006433	prolyl-tRNA aminoacylation	5.76×10^{-04}	2
GO:0004827	proline-tRNA ligase activity	5.76×10^{-04}	2
GO:0006096	glycolysis	8.47×10^{-04}	25
GO:0043564	Ku70:Ku80 complex	9.67×10^{-04}	3
GO:0003684	damaged DNA binding	1.10×10^{-03}	23
GO:0004197	cysteine-type endopeptidase activity	1.10×10^{-03}	28
GO:0000090	mitotic anaphase	1.25×10^{-03}	17
GO:0046365	monosaccharide catabolic process	1.29×10^{-03}	34
GO:0019320	hexose catabolic process	1.29×10^{-03}	34
GO:0045254	pyruvate dehydrogenase complex	1.42×10^{-03}	4
GO:0006085	acetyl-CoA biosynthetic process	2.11×10^{-03}	4
GO:0005996	monosaccharide metabolic process	2.27×10^{-03}	67
GO:0008534	oxidized purine nucleobase lesion DNA N-glycosylase activity	2.81×10^{-03}	2

Supplementary Table 8. Ranking and *p*-values of the top 20 GO categories (genes±5kb)

GO ID	Go category	*p*-value	Number of genes
GO:0007442	Hindgut morphogenesis	7.27×10^{-04}	19
GO:0016485	Protein processing	8.38×10^{-04}	696
GO:0051604	Protein maturation	9.21×10^{-04}	699
GO:0004165	dodecenoyl-CoA delta-isomerase activity	9.47×10^{-04}	5
GO:0035079	Polytene chromosome puffing	1.12×10^{-03}	8
GO:0007350	Blastoderm segmentation	1.21×10^{-03}	21
GO:0000090	Mitotic anaphase	1.24×10^{-03}	17
GO:0006508	proteolysis	1.44×10^{-03}	671
GO:0043564	Ku70:Ku80 complex	1.57×10^{-03}	3
GO:0070011	Peptidase activity acting on L-amino acid peptides	1.61×10^{-03}	596
GO:0004177	Aminopeptidase activity	1.81×10^{-03}	39
GO:0042600	chorion	2.14×10^{-03}	38
GO:0006426	glycyl-tRNA aminoacylation	2.39×10^{-03}	2
GO:0004820	glycine-tRNA ligase activity	2.39×10^{-03}	2
GO:0008233	Peptidase activity	2.41×10^{-03}	602
GO:0004822	isoleucine-tRNA ligase activity	2.42×10^{-03}	2
GO:0006428	isoleucyl-tRNA aminoacylation	2.42×10^{-03}	2
GO:0008527	Taste receptor activity	2.44×10^{-03}	62
GO:0045254	Pyruvate dehydrogenase complex	2.48×10^{-03}	4
GO:0004175	endopeptidase activity	2.85×10^{-03}	445

Supplementary Table 9. Polygenic score (permuted vs. original lifespan). SEM- standard error of the mean

p threshold	Mean R^2 (Lifespan)	SEM (Lifespan)	Mean R^2 (permuted lifespan)	SEM (permuted lifespan)	One-sided t-test *p*-value
≤1.0	0.042	0.0030	0.019	0.0019	$9.83x10^{-10}$
≤0.9	0.042	0.0031	0.019	0.0019	$9.18x10^{-10}$
≤0.8	0.042	0.0031	0.019	0.0019	$8.39x10^{-10}$
≤0.7	0.043	0.0031	0.019	0.0019	$7.05x10^{-10}$
≤0.6	0.043	0.0031	0.020	0.0019	$6.56x10^{-10}$
≤0.5	0.043	0.0031	0.020	0.0019	$5.88x10^{-10}$
≤0.2	0.043	0.0031	0.019	0.0019	$2.19x10^{-10}$
≤0.1	0.044	0.0031	0.019	0.0019	$5.26x10^{-11}$
≤0.05	0.044	0.0031	0.019	0.0019	$1.76x10^{-11}$
≤0.01	0.047	0.0032	0.018	0.0019	$4.57x10^{-13}$
≤0.005	0.047	0.0031	0.019	0.0002	$7.23x10^{-13}$
≤0.001	0.047	0.0032	0.019	0.0019	$1.57x10^{-12}$
≤0.0005	0.046	0.0031	0.020	0.0021	$4.79x10^{-11}$
≤0.0001	0.042	0.0030	0.020	0.0020	$4.02x10^{-09}$

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