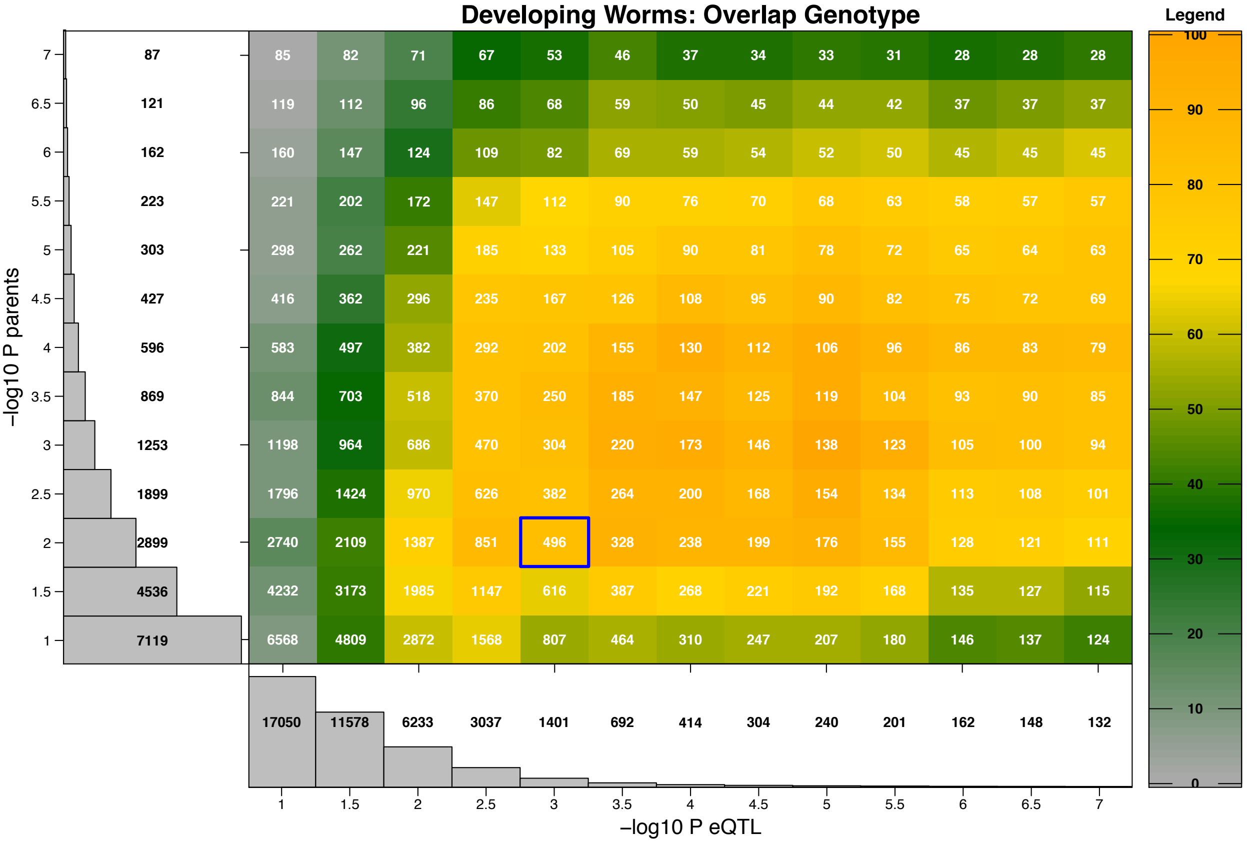
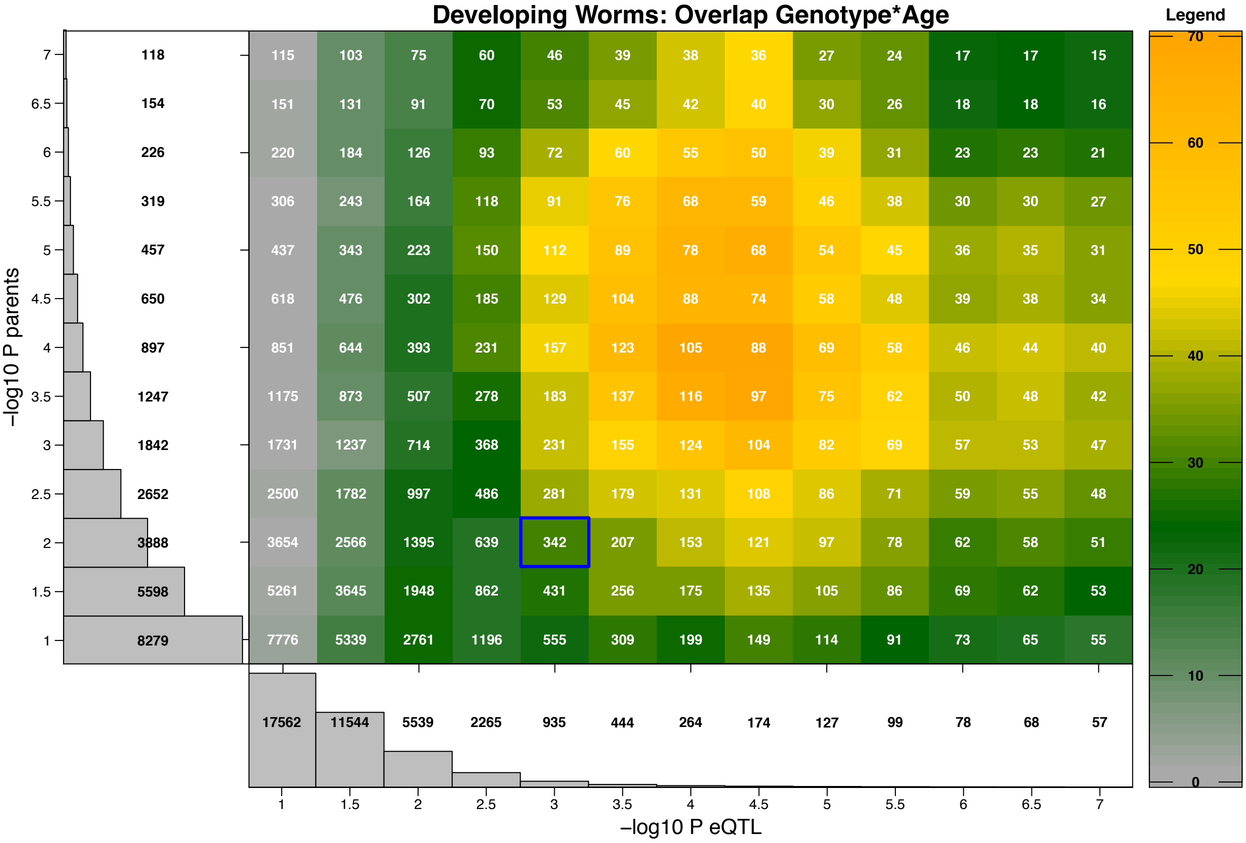


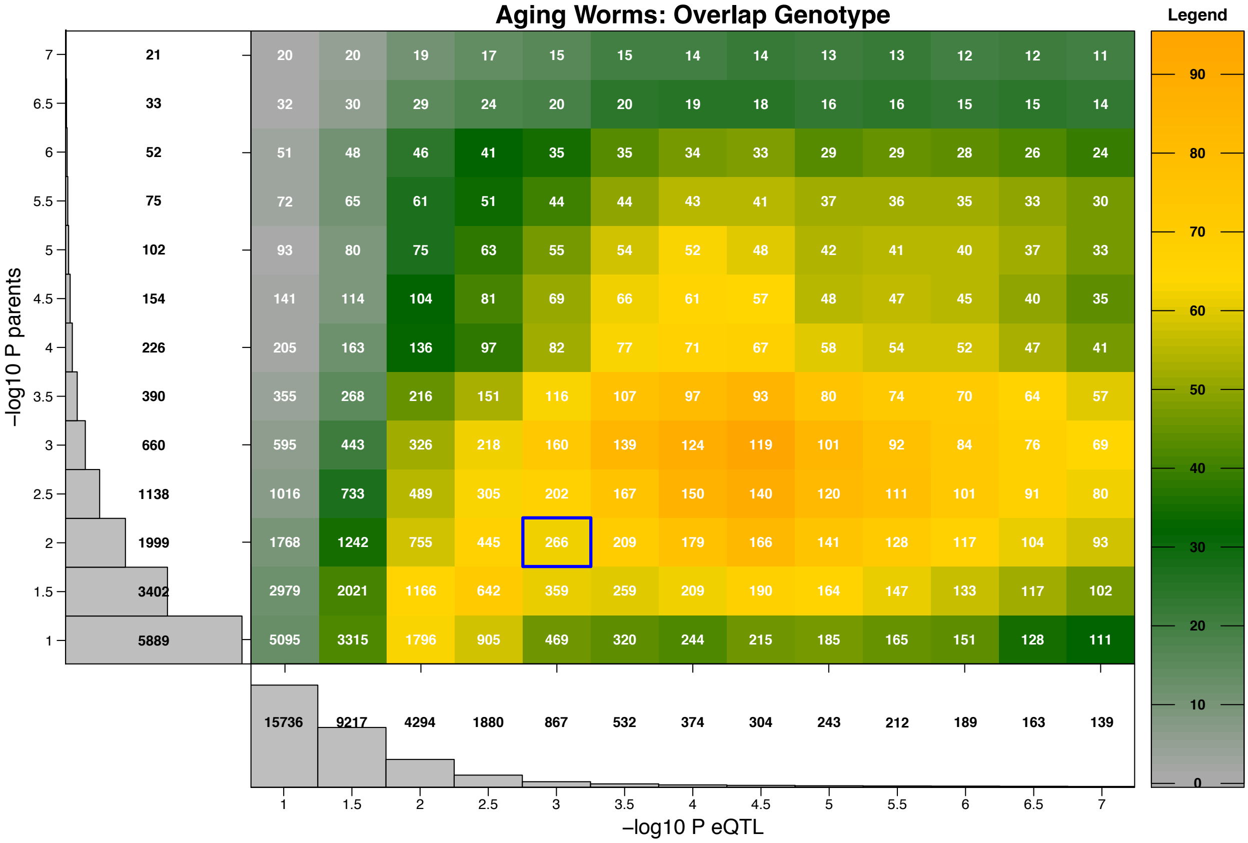
		1	1.5	2	2.5	3	3.5	4	4.5	5	5.5	6	6.5	7
7	87	85	82	71	67	53	46	37	34	33	31	28	28	28
6.5	121	119	112	96	86	68	59	50	45	44	42	37	37	37
6	162	160	147	124	109	82	69	59	54	52	50	45	45	45
5.5	223	221	202	172	147	112	90	76	70	68	63	58	57	57
5	303	298	262	221	185	133	105	90	81	78	72	65	64	63
4.5	427	416	362	296	235	167	126	108	95	90	82	75	72	69
4	596	583	497	382	292	202	155	130	112	106	96	86	83	79
3.5	869	844	703	518	370	250	185	147	125	119	104	93	90	85
3	1253	1198	964	686	470	304	220	173	146	138	123	105	100	94
2.5	1899	1796	1424	970	626	382	264	200	168	154	134	113	108	101
2	2899	2740	2109	1387	851	496	328	238	199	176	155	128	121	111
1.5	4536	4232	3173	1985	1147	616	387	268	221	192	168	135	127	115
1	7119	6568	4809	2872	1568	807	464	310	247	207	180	146	137	124
		17050	11578	6233	3037	1401	692	414	304	240	201	162	148	132

Figure S1 Number of overlapping genes between differentially expressed genes in the parental strains and with at least an eQTL at different thresholds in developing worms with genotype effect. *Bottom bar graphs* show number of genes with at least an eQTL at different thresholds (from –log10 P-value =1 to –log10 P-value = 7). *Left bar graphs* show number of differentially expressed genes between parental strains at different thresholds. The number of overlapping genes is shown in the *center graph*. The dark square indicates the number of overlapping genes at the joined-FDR (–log10 P-value =3 for eQTL analysis, –log10 P-value = 2 for parental strains analysis). A hypergeometric test was used to determine significance of the overlapping genes. The color legends for the significance are shown at the *Right graphs.*



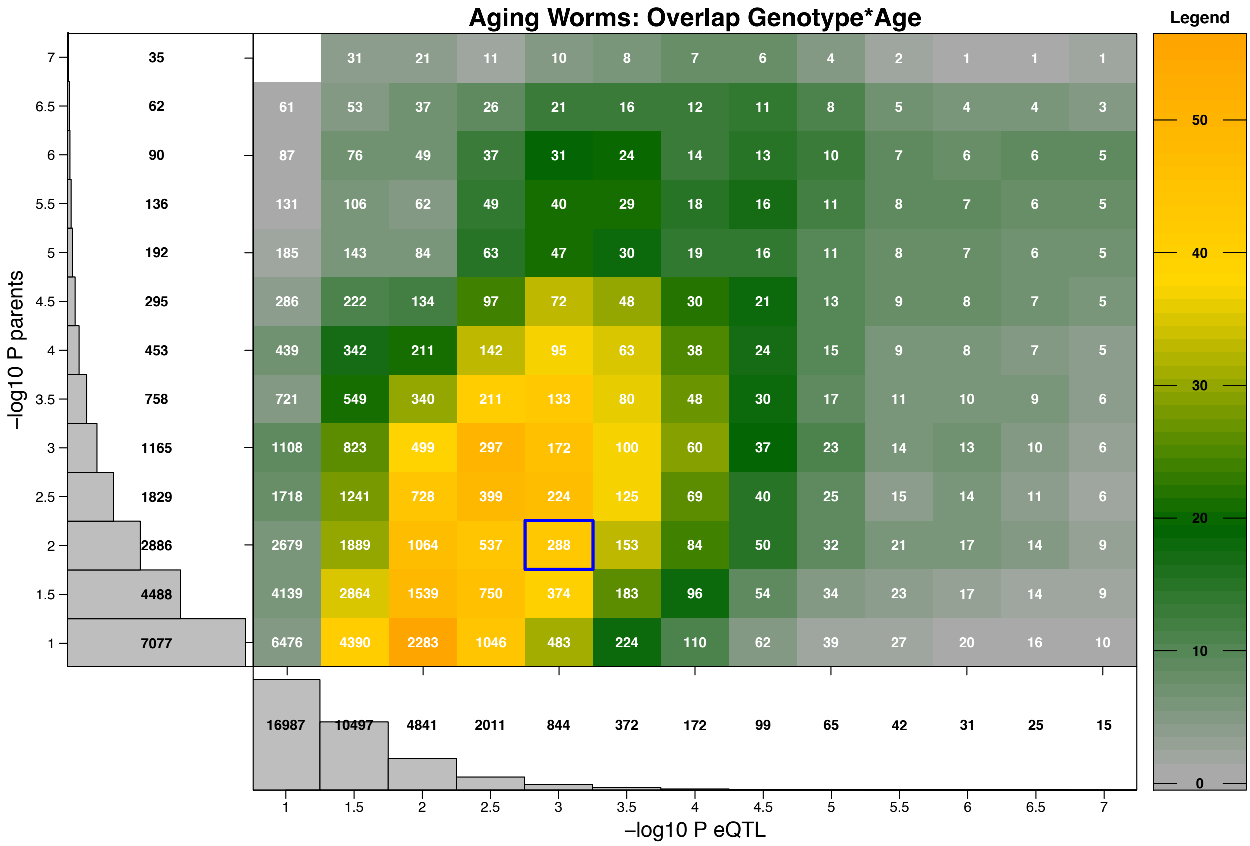
–log10 P parents		1	1.5	2	2.5	3	3.5	4	4.5	5	5.5	6	6.5	7
7	118	115	103	75	60	46	39	38	36	27	24	17	17	15
6.5	154	151	131	91	70	53	45	42	40	30	26	18	18	16
6	226	220	184	126	93	72	60	55	50	39	31	23	23	21
5.5	319	306	243	164	118	91	76	68	59	46	38	30	30	27
5	457	437	343	223	150	112	89	78	68	54	45	36	35	31
4.5	650	618	476	302	185	129	104	88	74	58	48	39	38	34
4	897	851	644	393	231	157	123	105	88	69	58	46	44	40
3.5	1247	1175	873	507	278	183	137	116	97	75	62	50	48	42
3	1842	1731	1237	714	368	231	155	124	104	82	69	57	53	47
2.5	2652	2500	1782	997	486	281	179	131	108	86	71	59	55	48
2	3888	3654	2566	1395	639	342	207	153	121	97	78	62	58	51
1.5	5598	5261	3645	1948	862	431	256	175	135	105	86	69	62	53
1	8279	7776	5339	2761	1196	555	309	199	149	114	91	73	65	55
		17562	11544	5539	2265	935	444	264	174	127	99	78	68	57

Figure S2 Number of overlapping genes between differentially expressed genes in the parental strains and with at least an eQTL at different thresholds in developing worms with genotype*age interacting effect. See Figure S1 legend for details.



−log10 P parents		1	1.5	2	2.5	3	3.5	4	4.5	5	5.5	6	6.5	7
7	21	20	20	19	17	15	15	14	14	13	13	12	12	11
6.5	33	32	30	29	24	20	20	19	18	16	16	15	15	14
6	52	51	48	46	41	35	35	34	33	29	29	28	26	24
5.5	75	72	65	61	51	44	44	43	41	37	36	35	33	30
5	102	93	80	75	63	55	54	52	48	42	41	40	37	33
4.5	154	141	114	104	81	69	66	61	57	48	47	45	40	35
4	226	205	163	136	97	82	77	71	67	58	54	52	47	41
3.5	390	355	268	216	151	116	107	97	93	80	74	70	64	57
3	660	595	443	326	218	160	139	124	119	101	92	84	76	69
2.5	1138	1016	733	489	305	202	167	150	140	120	111	101	91	80
2	1999	1768	1242	755	445	266	209	179	166	141	128	117	104	93
1.5	3402	2979	2021	1166	642	359	259	209	190	164	147	133	117	102
1	5889	5095	3315	1796	905	469	320	244	215	185	165	151	128	111
		15736	9217	4294	1880	867	532	374	304	243	212	189	163	139
		1	1.5	2	2.5	3	3.5	4	4.5	5	5.5	6	6.5	7

Figure S3 Number of overlapping genes between differentially expressed genes in the parental strains and with at least an eQTL at different thresholds in old worms with genotype effect. See Figure S1 legend for details.



		1	1.5	2	2.5	3	3.5	4	4.5	5	5.5	6	6.5	7
7	35		31	21	11	10	8	7	6	4	2	1	1	1
6.5	62	61	53	37	26	21	16	12	11	8	5	4	4	3
6	90	87	76	49	37	31	24	14	13	10	7	6	6	5
5.5	136	131	106	62	49	40	29	18	16	11	8	7	6	5
5	192	185	143	84	63	47	30	19	16	11	8	7	6	5
4.5	295	286	222	134	97	72	48	30	21	13	9	8	7	5
4	453	439	342	211	142	95	63	38	24	15	9	8	7	5
3.5	758	721	549	340	211	133	80	48	30	17	11	10	9	6
3	1165	1108	823	499	297	172	100	60	37	23	14	13	10	6
2.5	1829	1718	1241	728	399	224	125	69	40	25	15	14	11	6
2	2886	2679	1889	1064	537	288	153	84	50	32	21	17	14	9
1.5	4488	4139	2864	1539	750	374	183	96	54	34	23	17	14	9
1	7077	6476	4390	2283	1046	483	224	110	62	39	27	20	16	10
		16987	10497	4841	2011	844	372	172	99	65	42	31	25	15

Figure S4 Number of overlapping genes between differentially expressed genes in the parental strains and with at least an eQTL at different thresholds in old worms with genotype*age interacting effect. See Figure S1 legend for details.

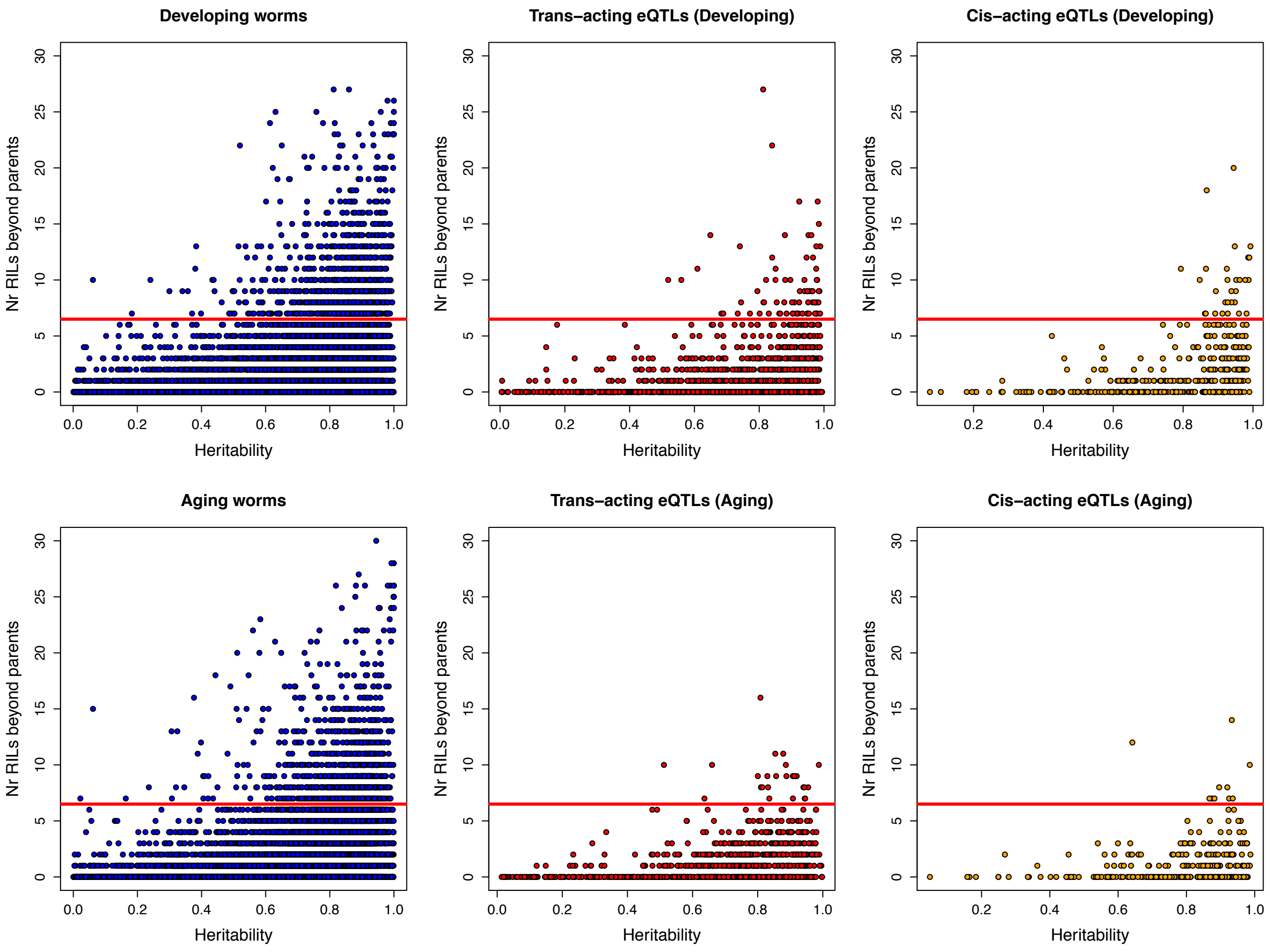


Figure S5 Transgressive segregation, heritability and eQTLs. Upper graphs show values for developing worms, lower graphs for aging worms. Left graphs (upper and lower) show the number of RILs which expression values transgress from the higher or lower parent value (*y-axis*) *versus* their heritability values (*x-axis*). Middle and right graphs plot the number of genes with eQTLs (*trans*-acting middle, *cis*-acting right) detected, their heritability values and their transgressive segregants. We detected more transgressive segregation in genes with *trans*-acting regulation and in developing worms than in aging worms and *cis*-acting eQTLs. Red line indicates the threshold for significant transgressive segregation.

Tables S1 –S8 are available for download at

http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.002212/-/DC1.

Table S1 List of differentially expressed genes between N2 and CB4856 in juvenile (t1), reproductive (t2) and old worms (t3). Genes with a –log10 P-value > 2 in a linear model 1 (gene expression = marker (effect) + error) were considered significant. Array ID = identification number for microarray spot. CDS name = coding sequence name. Gene name = public gene name. P-value = -log10 P-value for the significant test.

Table S2 List of differentially expressed genes between N2 and CB4856 in developing (t1 vs. t2) and aging worms (t2 vs. t3). Genes with a –log10 P-value > 2 in a linear model 1 (gene expression = marker(effect) + physiological age + interaction (marker*physiological age) + error) were considered significant. *Array ID* = identification number for microarray spot. *CDS name* = coding sequence name. *Gene name* = public gene name. *P-value* = -log10 P-value for the significant test. Worksheets = *Developing (marker)* for genes differentially regulated by genotype in developing worms; *Developing (marker-age)* for genes differentially regulated by genotype*age interaction in developing worms; *Aging (marker)* for genes differentially regulated by genotype in aging worms; *Aging (marker-age)* for genes differentially regulated by genotype*age interaction in aging worms.

Table S3 Significantly enriched Gene Ontology (GO) terms and functional domains. *GO terms worksheets* contain full GO enriched analysis for differentially expressed genes between parental strains in developing and aging worms, genotype effect and genotype*age interacting effect. *GO terms* are the GO id numbers. Total genes are the total number of genes in *C. elegans* assigned to each GO term. *Number of genes* are the number of regulated genes by genotype or genotype*age in each GO term. *P-values* were calculated using hypergeometric test, values lower than 0.01 and more than two genes in a category were considered significant. The hypergeometric test compared a group of 2779 GO terms, with 18,312 annotated genes. Gene annotation with GO terms was extracted from Wormbase release WB210.

Table S4 Table with GO enrichment analysis of overlapping genes between differentially expressed genes in the parental strains with at least an eQTL in developing and aging worms.

Table S5 Table with GO enrichment analysis of highly heritable genes in developing and aging worms.

Table S6 Table summary with GO terms enrichment analysis summary for highly heritable genes in developing and aging worms. First table shows GO terms significantly enriched in both groups of genes with a P-value < 0.01. Second table shows GO terms significantly enriched (P-value < 0.01) in developing worm but not in aging worms. Third table shows GO terms significantly enriched (P-value < 0.01) in aging worms but not in developing worms.

Table S7 Excel file with genes showing signs of transgressive segregation, but without high heritability in developing worms in one spreadsheet. GO enrichment analysis of the genes is shown in the other spreadsheet.

Table S8 Excel file with genes showing signs of transgressive segregation, but without high heritability in aging worms in one spreadsheet. GO enrichment analysis of the genes is shown in the other spreadsheet.

Table S6 Table summary with GO terms enrichment analysis summary for highly heritable genes in developing and aging worms. First table shows GO terms significantly enriched in both groups of genes with a P-value < 0.01. Second table shows GO terms significantly enriched (P-value < 0.01) in developing worms genes but not in aging worms. Third table shows GO terms significantly enriched (P-value < 0.01) in aging worms genes but not in developing worms

Common Go Terms enriched in Developing and Aging worms highly heritable genes

GO terms	Genes in GO	Genes	P-value	Description
GO:0004030	4	4	0	aldehyde dehydrogenase [NAD(P)+] activity
GO:0006081	4	4	0	cellular aldehyde metabolic process
GO:0016763	6	6	0	transferase activity, transferring pentosyl groups
GO:0051020	6	6	0	GTPase binding
GO:0042302	309	191	0.00266	structural constituent of cuticle

Go Terms enriched only in Developing worms highly heritable genes

GO terms	Genes in GO	Genes	P-value	Description
GO:0000795	4	4	0	synaptonemal complex
GO:0006544	4	4	0	glycine metabolic process
GO:0007611	4	4	0	learning or memory
GO:0008176	4	4	0	tRNA (guanine-N7-)-methyltransferase activity
GO:0016328	4	4	0	lateral plasma membrane
GO:0016358	4	4	0	dendrite development
GO:0016471	4	4	0	vacuolar proton-transporting V-type ATPase complex
GO:0018738	4	4	0	S-formylglutathione hydrolase activity
GO:0045773	4	4	0	positive regulation of axon extension
GO:0060102	4	4	0	collagen and cuticulin-based cuticle extracellular matrix
GO:0000104	5	5	0	succinate dehydrogenase activity
GO:0005581	5	5	0	collagen
GO:0003896	6	6	0	DNA primase activity
GO:0006269	6	6	0	DNA replication, synthesis of RNA primer
GO:0030071	6	6	0	regulation of mitotic metaphase/anaphase transition
GO:0044249	6	6	0	cellular biosynthetic process
GO:0004926	9	9	0	non-G-protein coupled 7TM receptor activity
GO:0005744	8	7	0.007421	mitochondrial inner membrane presequence translocase complex
GO:0015085	8	7	0.007421	calcium ion transmembrane transporter activity
GO:0016538	8	7	0.007421	cyclin-dependent protein kinase regulator activity
GO:0032580	8	7	0.007421	Golgi cisterna membrane

GO:0005388	12	11	0.000639	calcium-transporting ATPase activity
GO:0005604	14	12	0.002407	basement membrane
GO:0000776	14	13	0.000187	kinetochore
GO:0004091	17	14	0.003357	carboxylesterase activity
GO:0008233	50	35	0.007561	peptidase activity
GO:0005198	297	181	0.007627	structural molecule activity
GO:0010171	734	428	0.009828	body morphogenesis

Go Terms enriched only in Aging worms highly heritable genes

GO terms	Genes in GO	Genes	P-value	Description
GO:0015485	4	4	0	cholesterol binding
GO:0004657	6	5	0.004131	proline dehydrogenase activity
GO:0004768	5	5	0	stearoyl-CoA 9-desaturase activity
GO:0006562	6	5	0.004131	proline catabolic process
GO:0006937	6	5	0.004131	regulation of muscle contraction
GO:0010085	6	5	0.004131	polarity specification of proximal/distal axis
GO:0032504	5	5	0	multicellular organism reproduction
GO:0006537	8	6	0.008598	glutamate biosynthetic process
GO:0004611	8	7	0.000662	phosphoenolpyruvate carboxykinase activity
GO:0005882	8	7	0.000662	intermediate filament
GO:0006505	9	7	0.00384	GPI anchor metabolic process
GO:0017076	8	7	0.000662	purine nucleotide binding
GO:0043073	9	7	0.00384	germ cell nucleus
GO:0004368	10	8	0.001697	glycerol-3-phosphate dehydrogenase activity
GO:0009331	10	8	0.001697	glycerol-3-phosphate dehydrogenase complex
GO:0034607	11	8	0.005989	turning behavior involved in mating
GO:0004652	12	9	0.002843	polynucleotide adenylyltransferase activity
GO:0006072	13	9	0.007881	glycerol-3-phosphate metabolic process
GO:0043631	12	9	0.002843	RNA polyadenylation
GO:0005262	15	10	0.009457	calcium channel activity
GO:0006094	13	11	0.000139	gluconeogenesis
GO:0016831	25	16	0.004391	carboxy-lyase activity
GO:0031625	26	16	0.007977	ubiquitin protein ligase binding
GO:0000122	27	17	0.004688	negative regulation of transcription from RNA polymerase II promoter
GO:0004518	34	23	0.000305	nuclease activity
GO:0001703	74	40	0.005349	gastrulation with mouth forming first
GO:0004713	809	359	0.004876	protein tyrosine kinase activity

GO:0004672	902	403	0.001747	protein kinase activity
GO:0004674	958	427	0.001619	protein serine/threonine kinase activity
GO:0006468	1013	452	0.001099	protein amino acid phosphorylation
GO:0005524	2060	879	0.00497	ATP binding
GO:0009790	2334	992	0.004822	embryonic development