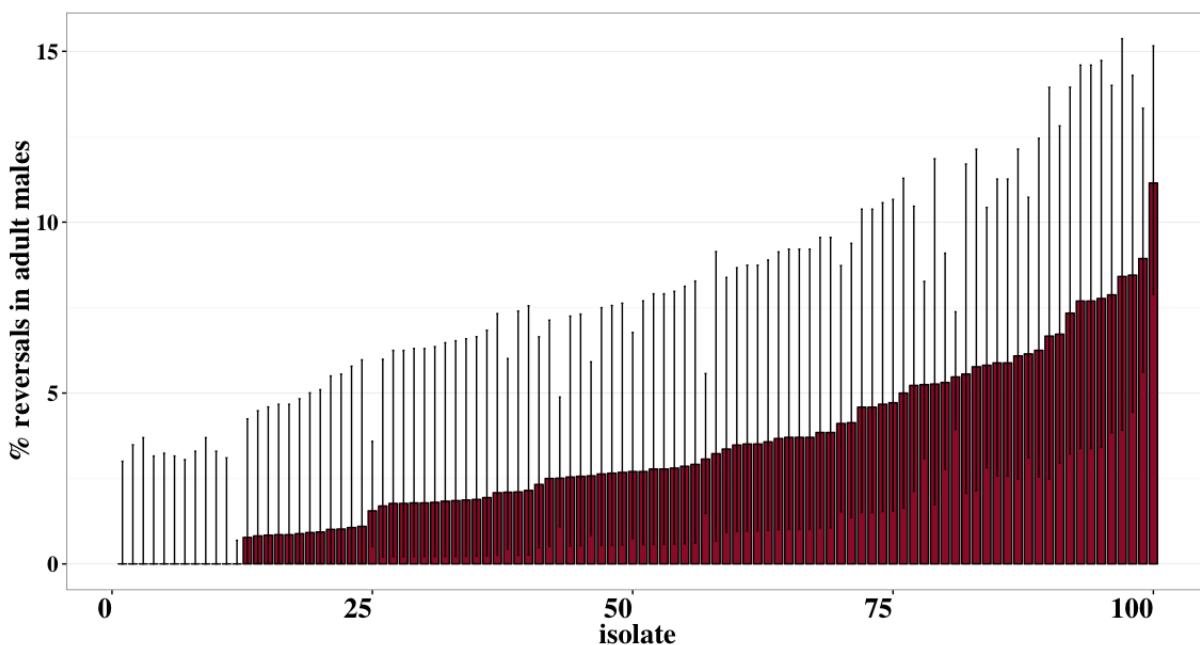


Supplementary Figure 1: The propensity for L/R gut-gonad reversals varies widely in males of *C. elegans* isolates at 20°C. In figure 2, isolates are numbered in ascending order. This figure includes lower and upper bounds for 95% Binomial proportion confidence intervals calculated using the Clopper-Pearson/Exact method (See Materials and Methods).



Supplementary Table 1: Complementary data for Figure 2: The propensity for L/R gut-gonad reversals varies widely in males of *C. elegans* isolates at 20°C. In figure 2, isolates are numbered in ascending order. This table includes isolate name, total sample size, percent reversals and the lower and upper bounds for 95% Binomial proportion confidence intervals which were calculated using the Clopper-Pearson/Exact method (See Materials and Methods). The full data set including confidence intervals is depicted in Supplemental Figure 1.

Isolate Number	Isolate	Total Sample Size	% Reversals	Lower Bound %	Upper Bound %
1	AB4	121	0.00	0.00	3.00
2	CB4857	104	0.00	0.00	3.48
3	CX11292	98	0.00	0.00	3.69
4	ED3012	115	0.00	0.00	3.16
5	JU1088	112	0.00	0.00	3.24
6	JU1440	115	0.00	0.00	3.16
7	JU1530	119	0.00	0.00	3.05
8	JU360	110	0.00	0.00	3.30

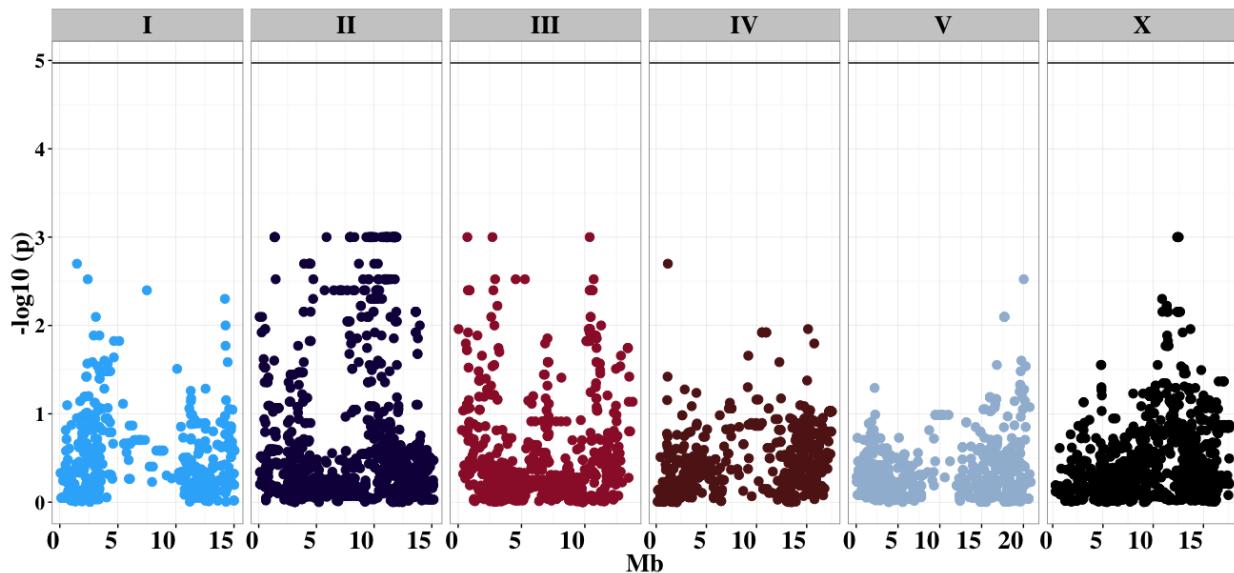
9	JU394	98	0.00	0.00	3.69
10	JU561	110	0.00	0.00	3.30
11	MY10	117	0.00	0.00	3.10
12	N2	533	0.00	0.00	0.69
13	JU363	129	0.78	0.02	4.24
14	JU1409	122	0.82	0.02	4.48
15	JU1200	119	0.84	0.02	4.59
16	JU1242	117	0.85	0.02	4.67
17	JU751	117	0.85	0.02	4.67
18	JU440	113	0.88	0.02	4.83
19	EG4349	109	0.92	0.02	5.01
20	MY14	107	0.93	0.02	5.10
21	JU1652	99	1.01	0.03	5.50
22	PB303	98	1.02	0.03	5.55
23	ED3046	94	1.06	0.03	5.79
24	JU346	91	1.10	0.03	5.97
25	JU830	322	1.55	0.51	3.59
26	ED3049	118	1.69	0.21	5.99
27	CB4852	113	1.77	0.22	6.25
28	JU642	113	1.77	0.22	6.25
29	JU1400	112	1.79	0.22	6.30
30	JU322	112	1.79	0.22	6.30
31	JU1896	111	1.80	0.22	6.36
32	JU323	109	1.83	0.22	6.47
33	CX11285	108	1.85	0.23	6.53
34	DL238	107	1.87	0.23	6.59

35	ED3073	106	1.89	0.23	6.65
36	JU847	103	1.94	0.24	6.84
37	JU258	96	2.08	0.25	7.32
38	ED3048	143	2.10	0.43	6.01
39	JU1580	95	2.11	0.26	7.40
40	CB4851	93	2.15	0.26	7.55
41	CB4932	129	2.33	0.48	6.65
42	ED3005	120	2.50	0.52	7.13
43	JU345	319	2.51	1.09	4.88
44	JT11398	118	2.54	0.53	7.25
45	PS2025	117	2.56	0.53	7.31
46	ED3077	194	2.58	0.84	5.91
47	LKC34	114	2.63	0.55	7.50
48	JU397	113	2.65	0.55	7.56
49	ED3017	112	2.68	0.56	7.63
50	CX11276	148	2.70	0.74	6.78
51	PX174	111	2.70	0.56	7.70
52	JU1491	108	2.78	0.58	7.90
53	MY18	108	2.78	0.58	7.90
54	JU774	107	2.80	0.58	7.98
55	LSJ1	105	2.86	0.59	8.12
56	DL226	103	2.91	0.60	8.28
57	ED3052	326	3.07	1.48	5.57
58	ED3011	93	3.23	0.67	9.14
59	CX11264	119	3.36	0.92	8.38
60	JU1395	115	3.48	0.96	8.67

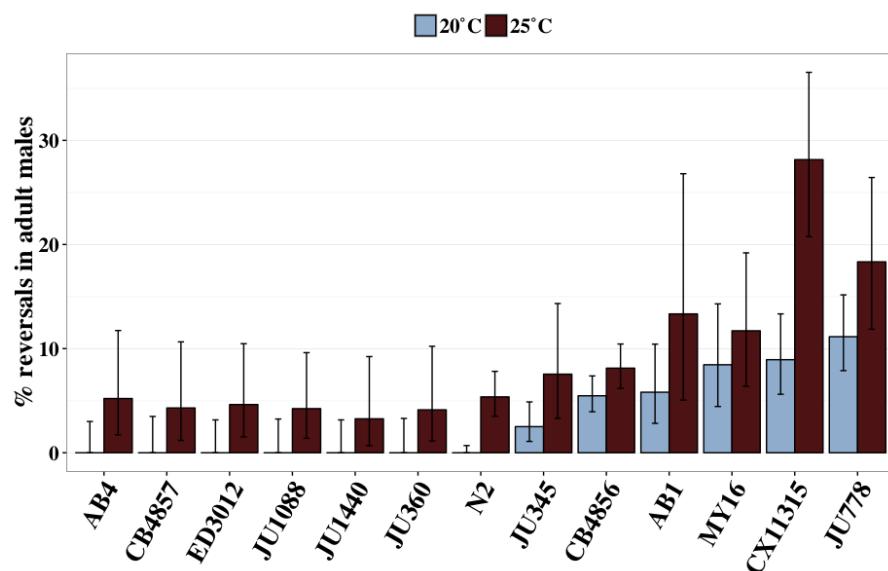
61	CX11307	114	3.51	0.96	8.74
62	CX11314	114	3.51	0.96	8.74
63	ED3040	112	3.57	0.98	8.89
64	JU1172	109	3.67	1.01	9.13
65	CB4853	108	3.70	1.02	9.21
66	JU406	108	3.70	1.02	9.21
67	JU775	108	3.70	1.02	9.21
68	MY23	104	3.85	1.06	9.56
69	RC301	104	3.85	1.06	9.56
70	CB4858	146	4.11	1.52	8.73
71	PX179	121	4.13	1.36	9.38
72	EG4724	109	4.59	1.51	10.38
73	EG4725	109	4.59	1.51	10.38
74	PB306	107	4.67	1.53	10.57
75	EG4946	106	4.72	1.55	10.67
76	WN2002	100	5.00	1.64	11.28
77	JU1213	134	5.22	2.13	10.47
78	QX1211	324	5.25	3.09	8.27
79	JU367	95	5.26	1.73	11.86
80	JU1212	226	5.31	2.77	9.09
81	CB4856	731	5.47	3.94	7.38
82	EG4347	108	5.56	2.07	11.70
83	QX1233	104	5.77	2.15	12.13
84	AB1	172	5.81	2.82	10.43
85	JU1568	136	5.88	2.57	11.26
86	MY1	136	5.88	2.57	11.26

87	JU311	115	6.09	2.48	12.14
88	CX11262	179	6.15	3.11	10.73
89	JU792	112	6.25	2.55	12.45
90	JU782	90	6.67	2.49	13.95
91	JU1581	119	6.72	2.95	12.82
92	CX11271	109	7.34	3.22	13.95
93	CB4854	104	7.69	3.38	14.60
94	JU1586	104	7.69	3.38	14.60
95	JU1246	103	7.77	3.41	14.73
96	DL200	127	7.87	3.84	14.00
97	JU310	107	8.41	3.92	15.37
98	MY16	142	8.45	4.44	14.30
99	CX11315	235	8.94	5.62	13.34
100	JU778	314	11.15	7.89	15.16

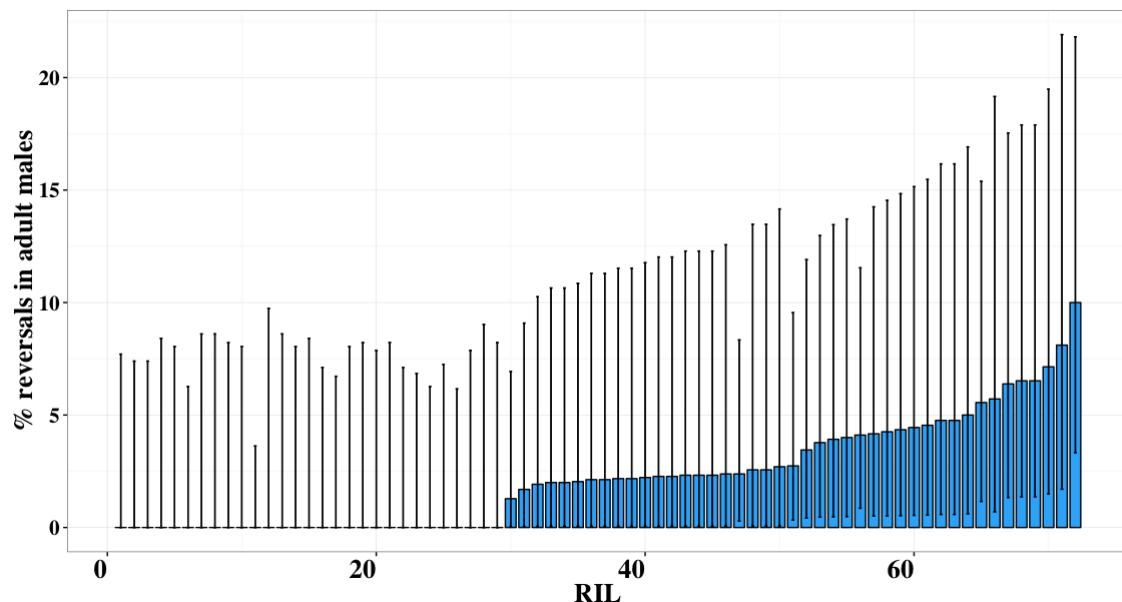
Supplementary Figure 2: Permutated *P* values from Genome-Wide Association Study (GWAS). N = 10,000 permutations. Permutated *p* values for each SNP were calculated using a linear model that associates the genotypes of each strain (N = 100 isolates representing 97 unique haplotypes) with permuted, categorical phenotype. Chromosomes are indicated by the numbered boxes (I-V, X) and genomic position along the chromosome is represented in Megabasepairs (Mb) on the x-axis. $-\log_{10}$ of each *p* value is represented on the y-axis.



Supplementary Figure 3: Frequency of Heterotaxy in *C. elegans* natural isolates is a temperature-sensitive trait in males. Reversals in males of *C. elegans* isolates cultured at 20°C and 25°C. Sample size per isolate ranges from 90 < n < 750 at 20°C and 40 < n < 700 at 25°C. Black bars represent 95% Binomial proportion confidence intervals calculated using Clopper-Pearson/Exact method (See Materials and Methods).



Supplemental Figure 4: Complementary data for Figure 7: The propensity for L/R gut-gonad reversals varies widely in adult males of RILs at 20°C. RILs are in ascending order. Black bars represent lower and upper bounds for 95% Binomial proportion confidence intervals calculated using the Clopper-Pearson/Exact method (See Materials and Methods).



Supplemental Table 2: Complementary data for Figure 7: The propensity for L/R gut-gonad reversals widely in adult males of RILs at 20°C. This table includes: RIL name, total sample size, percent reversals and the lower and upper bounds for 95% Binomial proportion confidence intervals calculating using the Clopper-Pearson/Exact method (See Materials and Methods).

RIL Number	RIL name	Total Sample Size	Reversals %	Lower Bound %	Upper Bound %
1	JR3703	46	0.00	0	7.71
2	JR3709	48	0.00	0	7.40
3	JR3714	48	0.00	0	7.40
4	JR3716	42	0.00	0	8.41
5	JR3720	44	0.00	0	8.04
6	JR3723	57	0.00	0	6.27
7	JR3725	41	0.00	0	8.60
8	JR3727	41	0.00	0	8.60
9	JR3728	43	0.00	0	8.22
10	JR3729	44	0.00	0	8.04

11	JR3734	100	0.00	0	3.62
12	JR3738	36	0.00	0	9.74
13	JR3739	41	0.00	0	8.60
14	JR3741	44	0.00	0	8.04
15	JR3742	42	0.00	0	8.41
16	JR3744	50	0.00	0	7.11
17	JR3745	53	0.00	0	6.72
18	JR3747	44	0.00	0	8.04
19	JR3750	43	0.00	0	8.22
20	JR3752	45	0.00	0	7.87
21	JR3753	43	0.00	0	8.22
22	JR3754	50	0.00	0	7.11
23	JR3757	52	0.00	0	6.85
24	JR3758	57	0.00	0	6.27
25	JR3763	49	0.00	0	7.25
26	JR3767	58	0.00	0	6.16
27	JR3770	45	0.00	0	7.87
28	JR3772	39	0.00	0	9.03
29	JR3774	43	0.00	0	8.22
30	JR3707	78	1.28	0.03	6.94
31	JR3731	59	1.69	0.04	9.09
32	JR3756	52	1.92	0.05	10.26
33	JR3732	50	2.00	0.05	10.65
34	JR3737	50	2.00	0.05	10.65
35	JR3748	49	2.04	0.05	10.85
36	JR3701	47	2.13	0.05	11.29

37	JR3711	47	2.13	0.05	11.29
38	JR3699	46	2.17	0.06	11.53
39	JR3724	46	2.17	0.06	11.53
40	JR3733	45	2.22	0.06	11.77
41	JR3726	44	2.27	0.06	12.02
42	JR3755	44	2.27	0.06	12.02
43	JR3708	43	2.33	0.06	12.29
44	JR3712	43	2.33	0.06	12.29
45	JR3760	43	2.33	0.06	12.29
46	JR3740	42	2.38	0.06	12.57
47	JR3743	84	2.38	0.29	8.34
48	JR3698	39	2.56	0.06	13.48
49	JR3751	39	2.56	0.06	13.48
50	JR3718	37	2.70	0.07	14.16
51	JR3722	73	2.74	0.33	9.55
52	JR3762	58	3.45	0.42	11.91
53	JR3765	53	3.77	0.46	12.98
54	JR3697	51	3.92	0.48	13.46
55	JR3736	50	4.00	0.49	13.71
56	JR3749	73	4.11	0.86	11.54
57	JR3706	48	4.17	0.51	14.25
58	JR3693	47	4.26	0.52	14.54
59	JR3746	46	4.35	0.53	14.84
60	JR3702	45	4.44	0.54	15.15
61	JR3766	44	4.55	0.56	15.47
62	JR3710	42	4.76	0.58	16.16

63	JR3735	42	4.76	0.58	16.16
64	JR3721	40	5.00	0.61	16.92
65	JR3696	54	5.56	1.16	15.39
66	JR3713	35	5.71	0.70	19.16
67	JR3695	47	6.38	1.34	17.54
68	JR3700	46	6.52	1.37	17.90
69	JR3719	46	6.52	1.37	17.90
70	JR3730	42	7.14	1.50	19.48
71	JR3764	37	8.11	1.70	21.91
72	JR3715	50	10.00	3.33	21.81