

Supplemental Figure 1: Flowchart describing inputs, outputs, and processes in the mapping and simulation profiles of NemaScan.



Supplemental Figure 2: Effect size distribution of simulations comparing algorithm performance



Supplemental Figure 3: Distributions of simulated QTL effects expressed as the fraction of phenotypic variance explained. Horizontal panels denote the number of simulated QTL per trait and vertical panels denote the heritability of each simulated trait.



Supplemental Figure 4: Distributions of all simulated QTL minor allele frequencies among mapping populations of increasing size



Supplemental Figure 5: Manhattan plots of previous GWA mappings and NemaScan mappings. Markers exceeding the multiple testing correction threshold are colored according to the mapped trait of interest.

Figure	Number of Simulated QTL per Trait	Trait Heritability (h2)	Effect Distribution	Strain Set	Number of Strains	Simulated QTL Locations	Grouping Replicated	Approximate Replication per Group
Figure 1	1; 5	0.1; 0.2; 0.3; 0.4; 0.5; 0.6; 0.7; 0.8; 0.9	0.5-5	Hahnel et. al. 2018	203	Genome-wide	Heritability x Number of QTL	50
Figure 2	1; 5; 10; 25; 50	0.2; 0.4; 0.6; 0.8	Gamma (0.4,1.66)	CeNDR Strains	540	Genome-wide	Heritability x Number of QTL	100
Figure 3	5	0.8	Gamma (0.4,1.66)	Subsampled CeNDR Strains	100; 200; 300; 400; 500	Genome-wide	Subsampled Population	50
Figure 4	5	0.8	Gamma (0.4,1.66)	Swept Subsampled CeNDR Strains; Divergent Subsampled CeNDR Strains; Subsampled CeNDR Strains	144	Genome-wide	Subsampled Population	30
Figure 5		02-05-08	llaiform	All Divergent Strains; Select Swent Strains	183-182	Chromosome- Specific Arms and Centers; Population- specific hyperdivergent regions	Heritability x Strain Set x Chromosome Region x Divergence x Chromosome	100

Supplemental Table 1: Simulation summary

Trait Heritability	Number of Simulated QTL	Group 1	Group 2	n1	n2	Adjusted p-value	Significance
0.1	1	EMMA	fastGWA-Imm-exact	50	50	1	ns
0.1	1	EMMA	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.1	1	EMMA	fastGWA-Imm-exact-LOCO	50	50	0.78223	ns
0.1	1	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.1	- 1	fastGWA-Imm-exact	fastGWA-Imm-exact-I OCO	50	50	0.41072	ne
0.1	1	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.78223	ne
0.1	1	EMMAA	fastGWA-Imm-exact	50	50	0.78223	115
0.2	1	ENIMA	fastGWA-Imm-exact	50	50	0 44229	ns
0.2	1	ENINA	rastGWA-Imm-exact-INBRED	50	50	0.44228	ns
0.2	1	EMIMA	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.2	1	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.2	1	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.2	1	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.76257	ns
0.3	1	EMMA	fastGWA-Imm-exact	50	50	1	ns
0.3	1	EMMA	fastGWA-Imm-exact-INBRED	50	50	0.60446	ns
0.3	1	EMMA	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.3	1	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.3	1	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.3	1	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.60446	ns
0.1	5	EMMA	fastGWA-Imm-exact	50	50	1	ns
0.1	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.1	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.1	5	fastGWA-lmm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.1	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.1	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.1	5	EMMA	fastGWA-Imm-exact	50	50	1	ne
0.2	5	EMMA	factGWA-Imm.exact.INIDPED	50	50	1	ns
0.2	5	ENIMA	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.2	5		fasto WA-Imm-exact-LOCO	50	50	1	115
0.2	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.2	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.2	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.3	5	EMMA	fastGWA-Imm-exact	50	50	1	ns
0.3	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.3	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	1	ns
0.3	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	1	ns
0.3	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	0.5337	ns
0.3	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.5337	ns
0.4	5	EMMA	fastGWA-Imm-exact	50	50	0.23146	ns
0.4	5	FMMA	fastGWA-Imm-exact-INBRED	50	50	0.65345	ns
0.4	5	FMMA	fastGWA-Imm-exact-I OCO	50	50	0.3213	ns
0.4	5	fastGWA-Imm-evact	fastGWA-Imm-exact-INBRED	50	50	0.3213	ne
0.4	5	fastGWA-Imm-exact	fastGWA-Imm-exact-I/OCO	50	50	0.0271	**
0.4		fastCWA Imm suget INDDED	fastGWA-Imm-exact-LOCO	50	50	0.00271	
0.4		TastGWA-Imm-exact-INBRED	rastGWA-Imm-exact-LOCO	50	50	0.19683	ns
0.5	5	EMMA	fastGWA-Imm-exact	50	50	0.00037	
0.5	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	0.14917	ns
0.5	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	0.14917	ns
0.5	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	0.04479	•
0.5	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	0	****
0.5	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.00369	**
0.6	5	EMMA	fastGWA-Imm-exact	50	50	0	****
0.6	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	0.22415	ns
0.6	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	0.0589	ns
0.6	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	2.00E-04	***
0.6	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	0	****
0.6	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.00207	**
0.0		FMMA	fastGWA-Imm-exact	50	50	0.00207	****
0.7		EMMA	fastGWA-Imm-evact-INIRPED	50	50	0 49649	ns
0.7	D	EMMA	fastGWA-Imm.exact-INDRED	50	50	0.40048	nc
0.7		factGWA-Imm_overt	fastGWA-Imm.exact-LOCO	30	50	6.005.05	****
0.7	5	fastCWA Imm-exact	fastGWA-Imm-exact-INBRED	50	50	6.00E-05	
0.7	5	rastowA-imm-exact	rastowA-Imm-exact-LOCO	50	50	0	
0.7	5	TastGWA-Imm-exact-INBRED	rastGWA-Imm-exact-LOCO	50	50	0.01385	-
0.8	5	EMMA	rastGWA-Imm-exact	50	50	0	
0.8	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	0.9322	ns
0.8	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	0.00826	**
0.8	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	0	****
0.8	5	fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	0	****
0.8	5	fastGWA-Imm-exact-INBRED	fastGWA-Imm-exact-LOCO	50	50	0.00826	**
0.9	5	EMMA	fastGWA-Imm-exact	50	50	0	****
0.9	5	EMMA	fastGWA-Imm-exact-INBRED	50	50	0.27572	ns
0.9	5	EMMA	fastGWA-Imm-exact-LOCO	50	50	0.00501	**
0.9	5	fastGWA-Imm-exact	fastGWA-Imm-exact-INBRED	50	50	3.00F-05	****
0.5		fastGWA-Imm-exact	fastGWA-Imm-exact-LOCO	50	50	0.002-05	****
0.9		fastGWA-Imm-exact_INIBBED	fastGWA-Imm-exact-LOCO	50	50	0.00013	***
0.9	5	rasid wA-Imm-exact-INBRED	rasto wa-imm-exact-LOCO	30	20	0.00012	

Supplemental Table 2: Differences in power to detect QTL between mapping algorithms at increasing heritability for one and five underlying QTL

Heritab Number o	f S Group 1	Group 2	n1	n2	Adjusted p-v	Significan
0.1	1 EMMA	fastGWA-Im	24	27	1	ns
0.1	1 EMMA	fastGWA-Im	24	25	1	ns
0.1	1 EMMA	fastGWA-lm	24	21	1	ns
0.1	1 fastGWA-In	n fastGWA-Im	27	25	1	ns
0.1	1 fastGWA-In	n fastGWA-lm	27	21	1	ns
0.1	1 fastGWA-In	n fastGWA-Im	25	21	0.03171	ns
0.2		fastGWA-Im	48	47	0.02171	
0.2	1 EMMA	factGWA-Im	40	44	0.69477	115
0.2	1 fastGWA-In	fastGWA-Im	40	44	0.07299	115
0.2	1 fastGWA-In	fastGWA-Im	47	47	0.00097	
0.2	1 fastGWA-In	n fastGWA-lm	44	47	0.5322	ns
0.3	1 EMMA	fastGWA-Im	50	49	0.6066	ns
0.3	1 EMMA	fastGWA-Im	50	48	0.12139	ns
0.3	1 EMMA	fastGWA-Im	50	50	0.00282	••
0.3	1 fastGWA-In	n fastGWA-Im	49	48	0.6066	ns
0.3	1 fastGWA-In	n fastGWA-Im	49	50	0.12139	ns
0.3	1 fastGWA-In	n fastGWA-lm	48	50	0.6066	ns
0.4	1 EMMA	fastGWA-Im	50	50	1	ns
0.4	1 EMMA	fastGWA-Im	50	50	1	ns
0.4	1 EMMA	fastGWA-Im	50	50	1	ns
0.4	1 fastGWA-In	n fastGWA-Im	50	50	1	ns
0.4	1 fastGWA-In	n fastGWA-Im	50	50	1	ns
0.4	1 fastGWA-In	n fastGWA-Im	50	50	1	ns
0.5	1 EMMA	fastGWA-Im	50	50	0.01141	:
0.5	1 EMMA	fastGWA-Im	50	50	0.01141	
0.5	1 EMMA	fastGWA-Im	50	50	0.01141	•
0.5	1 fastGWA-In	n fastGWA-Im	50	50	1	ns
0.5	1 fastGWA-In	n fastGWA-Im	50	50	1	ns
0.5	1 TastGWA-In	fastGWA-Im	50	50	0.11091	ns
0.6	1 EMMA	fastGWA-Im	50	50	0.11581	r15
0.6	1 EMMA	fastGWA-Im	50	50	0.36002	13
0.6	1 fastGMA	fastGWA-Im	50	50	1	15
0.6	1 fastGWA	fastGWA-Im	50	50	0 1223	10
0.6	1 fact/GWA-In	factGWA-Im	50	50	0.1332	10
0.0	1 EMMA	factGWA-Im	50	50	0.36002	*
0.7	1 EMMA	fastGWA-Im	50	50	0.04518	ns
0.7	1 EMMA	factGWA-Im	50	50	0.07324	10
0.7	1 fastGWA-le	fastGWA.Jm	50	50	1	ns
0.7	1 fastGWA-In	n fastGWA-Im	50	50	0.02181	•
0.7	1 fastGWA-In	n fastGWA-Im	50	50	0.04518	•
0.8	1 EMMA	fastGWA-Im	50	50	0.10115	ns
0.8	1 EMMA	fastGWA-Im	50	50	0.60209	ns
0.8	1 EMMA	fastGWA-Im	50	50	0.60209	ns
0.8	1 fastGWA-In	n fastGWA-lm	50	50	0.59338	ns
0.8	1 fastGWA-In	n fastGWA-Im	50	50	0.0077	••
0.8	1 fastGWA-In	n fastGWA-Im	50	50	0.21354	ns
0.9	1 EMMA	fastGWA-Im	50	50	0.19981	ns
0.9	1 EMMA	fastGWA-Im	50	50	1	ns
0.9	1 EMMA	fastGWA-Im	50	50	0.26486	ns
0.9	1 fastGWA-In	n fastGWA-Im	50	50	0.19981	ns
0.9	1 fastGWA-In	n fastGWA-Im	50	50	0.00103	••
0.9	1 fastGWA-In	n fastGWA-Im	50	50	0.26486	ns
0.1	5 EMMA	fastGWA-Im	6	10	1	ns
0.1	5 EMMA	fastGWA-lm	6	8	1	ns
0.1	5 EMMA	fastGWA-Im	6	2	1	ns
0.1	5 fastGWA-In	n fastGWA-Im	10	8	1	ns
0.1	5 fastGWA-In	n fastGWA-Im	10	2	1	ns
0.1	5 fastGWA-In	n fastGWA-Im	8	2	1	ns
0.2	5 EMMA	fastGWA-Im	22	31	1	ns
0.2	5 EMMA	fastGWA-Im	22	24	1	ns
0.2	5 EMMA	fastGWA-lm	22	19	1	ns
0.2	5 fastGWA-In	n fastGWA-Im	31	24	1	ns
0.2	5 fastGWA-In	n fastGWA-Im	31	19	0.67035	ns
0.2	5 fastGWA-In	n fastGWA-Im	24	19	1	ns
0.3	5 EMMA	fastGWA-Im	36	32	0.95233	ns
0.3	5 EMMA	fastGWA-Im	36	34	1	ns
0.3	5 EMMA	fastGWA-lm	36	42	1	ns
0.3	5 fastGWA-In	n fastGWA-lm	32	34	0.95233	ns
0.3	5 fastGWA-In	n fastGWA-lm	32	42	0.17422	ns
0.3	5 fastGWA-In	n fastGWA-lm	34	42	1	ns
0.4	5 EMMA	fastGWA-lm	45	34	1	ns
0.4	5 EMMA	fastGWA-lm	45	40	1	ns
0.4	5 EMMA	fastGWA-lm	45	49	1	ns
0.4	5 fastGWA-In	n rastGWA-Im	34	40	1	ris
0.4	5 fastGWA-In	n rastoWA-lm	34	49	1	ri5
0.4	5 TASEGWA-IN	factGWA-Im	40	49	1	115
0.5		factGWA-Im	49	38	1	10
0.5	5 EMMA	fastGWA-Im	49	46	1	10
0.5	5 fastGWA la	fastGWA-Im	49	50	1	10
0.5	5 fastGWA-In	fastGWA-Im	38	40	1	10
0.5	5 fastGWA-In	n fastGWA-Im	30 46	50	1	ns
0.6	5 EMMA	fastGWA-Im	40	40	0.69605	ns
0.6	5 EMMA	fastGWA-Im	40	50	0.796	ns
0.6	5 EMMA	fastGWA-Im	49	50	0.20467	ns
0.6	5 fastGWA-In	n fastGWA-Im	40	50	0.796	ns
0.6	5 fastGWA-In	n fastGWA-Im	40	50	0.0138	•
0.6	5 fastGWA-In	n fastGWA-Im	50	50	0.02481	•
0.7	5 EMMA	fastGWA-Im	50	44	1	ns
0.7	5 EMMA	fastGWA-Im	50	50	1	ns
0.7	5 EMMA	fastGWA-lm	50	50	1	ns
0.7	5 fastGWA-In	n fastGWA-lm	44	50	1	ns
0.7	5 fastGWA-In	n fastGWA-lm	44	50	0.32848	ns
0.7	5 fastGWA-In	n fastGWA-lm	50	50	1	ns
0.8	5 EMMA	fastGWA-lm	50	46	0.28505	ns
0.8	5 EMMA	fastGWA-Im	50	50	0.77132	ns
0.8	5 EMMA	fastGWA-lm	50	50	0.87436	ns
0.8	5 fastGWA-In	n fastGWA-lm	46	50	0.87436	ns
0.8	5 fastGWA-In	n fastGWA-Im	46	50	0.04972	•
0.8	5 fastGWA-In	n fastGWA-lm	50	50	0.28505	ns
0.0	5 EMMA	fastGWA-lm	50	48	0.77541	ns
0.9			50	50	0.77541	nc
0.9	5 EMMA	fastGWA-Im	50			113
0.9	5 EMMA 5 EMMA	fastGWA-Im fastGWA-Im	50	50	0.44219	ns
0.9 0.9 0.9 0.9	5 EMMA 5 EMMA 5 fastGWA-In	fastGWA-Im fastGWA-Im fastGWA-Im	50 50 48	50	0.44219	ns ns
0.9 0.9 0.9 0.9	5 EMMA 5 EMMA 5 fastGWA-In 5 fastGWA-In	fastGWA-Im fastGWA-Im n fastGWA-Im n fastGWA-Im	50 50 48 48	50 50 50	0.44219 0.74062 0.06463	ns ns ns

Supplemental Table 3: Differences in empirical FDR between mapping algorithms at increasing heritability for one and five underlying QTL

Sample Size	0-2.5	2.5-5	5-7.5	7.5-10	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90
100	0.01 ± 0.01	0.02 ± 0.04	0.04 ± 0.05	0.07 ± 0.08	0.22 ± 0.07	0.45 ± 0.12	0.57 ± 0.14	0.73 ± 0.19	0.81 ± 0.14	0.85 ± 0.13	0.88 ± 0.11	0.91 ± 0.18
200	0.02 ± 0.02	0.06 ± 0.05	0.14 ± 0.08	0.2 ± 0.12	0.41 ± 0.1	0.53 ± 0.13	0.67 ± 0.16	0.75 ± 0.14	0.86 ± 0.12	0.92 ± 0.09	0.95 ± 0.07	0.94 ± 0.18
300	0.03 ± 0.02	0.12 ± 0.06	0.23 ± 0.12	0.36 ± 0.17	0.48 ± 0.1	0.64 ± 0.12	0.7 ± 0.15	0.82 ± 0.15	0.88 ± 0.1	0.93 ± 0.08	0.96 ± 0.06	0.96 ± 0.16
400	0.04 ± 0.02	0.15 ± 0.08	0.28 ± 0.13	0.43 ± 0.17	0.52 ± 0.13	0.68 ± 0.13	0.75 ± 0.13	0.85 ± 0.13	0.9 ± 0.1	0.94 ± 0.08	0.99 ± 0.03	0.99 ± 0.04
500	0.05 ± 0.02	0.18 ± 0.08	0.35 ± 0.13	0.49 ± 0.16	0.59 ± 0.12	0.69 ± 0.12	0.78 ± 0.14	0.86 ± 0.14	0.91 ± 0.11	0.96 ± 0.07	0.99 ± 0.03	1 ± 0

Supplemental Table 4: Average power to detect QTL explaining increasing phenotypic variance (%, columns) among subsampled populations of increasing sampling depth

Population Type	0-2.5	2.5-5	5-7.5	7.5-10	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90
Divergent	0.01 ± 0.01	0.03 ± 0.03	0.07 ± 0.07	0.12 ± 0.1	0.28 ± 0.1	0.56 ± 0.11	0.75 ± 0.14	0.87 ± 0.12	0.92 ± 0.12	0.96 ± 0.07	0.97 ± 0.07	1 ± 0
Subsampled	0.01 ± 0.02	0.04 ± 0.05	0.07 ± 0.07	0.15 ± 0.1	0.3 ± 0.1	0.52 ± 0.12	0.64 ± 0.13	0.75 ± 0.15	0.84 ± 0.13	0.88 ± 0.11	0.9 ± 0.08	0.93 ± 0.18
Swept	0 ± 0	0.01 ± 0.02	0.04 ± 0.07	0.12 ± 0.11	0.44 ± 0.11	0.85 ± 0.09	0.98 ± 0.04	1 ± 0.02	0.99 ± 0.02	1 ± 0.01	1 ± 0	1 ± 0

Supplemental Table 5: Average power to detect QTL explaining increasing phenotypic variance (%, columns) among 144 randomly sampled divergent strains, 144 randomly sampled swept strains, and 144 randomly sampled strains from the overall CeNDR population

Simulated Divergence	Simulated Chromosome Region	1	11	III	IV	v	х
Hyperdivergent	Arm	0.001170	0.028880	0.000680	0.037160	0.007740	0.075990
Non-Hyperdivergent	Arm	0.062080	0.011320	0.000220	0.005160	0.020250	0.000460
Hyperdivergent	Center	0.093920	0.191940	0.000000	0.002130	0.000730	0.001240
Non-Hyperdivergent	Center	0.250980	0.005060	0.000030	0.002930	0.000000	0.003450
Hyperdivergent	Тір	0.504990	0.595700		0.740690	0.497570	0.000010
Non-Hyperdivergent	Tip	0.077100	0.614290	0.083260	0.063850	0.000110	0.016960

Supplemental Table 6: Differences in power to detect QTL between different chromosomes controlling for hyper-divergence and historic recombination groups (tips, arms, and centers)

Strain Set	Group 1	Group 2	n1	n2	Adjusted p-value	Significance
swept.chr.sims	Hyperdivergent_Arm	Hyperdivergent_Center	1859	1038	1	ns
swept.chr.sims	Hyperdivergent_Arm	Hyperdivergent_Tip	1859	700	1	ns
swept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Arm	1859	1890	1	ns
swept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Center	1859	1009	0.69252	ns
swept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Tip	1859	695	1	ns
swept.chr.sims	Hyperdivergent_Center	Hyperdivergent_Tip	1038	700	1	ns
swept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Arm	1038	1890	1	ns
swept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Center	1038	1009	1	ns
swept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Tip	1038	695	1	ns
swept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Arm	700	1890	1	ns
swept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Center	700	1009	1	ns
swept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Tip	700	695	1	ns
swept.chr.sims	Non-Hyperdivergent_Arm	Non-Hyperdivergent_Center	1890	1009	0.35341	ns
swept.chr.sims	Non-Hyperdivergent_Arm	Non-Hyperdivergent_Tip	1890	695	1	ns
swept.chr.sims	Non-Hyperdivergent_Center	Non-Hyperdivergent_Tip	1009	695	1	ns
unswept.chr.sims	Hyperdivergent_Arm	Hyperdivergent_Center	2030	1222	0	****
unswept.chr.sims	Hyperdivergent_Arm	Hyperdivergent_Tip	2030	344	1	ns
unswept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Arm	2030	2021	1	ns
unswept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Center	2030	1285	0	****
unswept.chr.sims	Hyperdivergent_Arm	Non-Hyperdivergent_Tip	2030	291	0.6635	ns
unswept.chr.sims	Hyperdivergent_Center	Hyperdivergent_Tip	1222	344	0.00147	**
unswept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Arm	1222	2021	0	****
unswept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Center	1222	1285	0.21109	ns
unswept.chr.sims	Hyperdivergent_Center	Non-Hyperdivergent_Tip	1222	291	0.6635	ns
unswept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Arm	344	2021	1	ns
unswept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Center	344	1285	0	****
unswept.chr.sims	Hyperdivergent_Tip	Non-Hyperdivergent_Tip	344	291	0.62177	ns
unswept.chr.sims	Non-Hyperdivergent_Arm	Non-Hyperdivergent_Center	2021	1285	0	****
unswept.chr.sims	Non-Hyperdivergent_Arm	Non-Hyperdivergent_Tip	2021	291	0.6635	ns
unswept.chr.sims	Non-Hyperdivergent Center	Non-Hyperdivergent Tip	1285	291	0.03955	•

Supplemental Table 7: Power to detect simulated in hyper-divergent regions or different parts of the chromosome within the mapping populations

Supplemental Table 8: Empirical FDR of mappings as a function of whether QTL were simulated in divergent regions and different chromosomal regions

Strain Set	Simulated Divergence	Simulated Chromosome Region	Group 1	Group 2	n1	n2	Adjusted p-value	Significance
unswept.chr.sims	Hyperdivergent	Center	1	П	105	100	0.01679	•
unswept.chr.sims	Hyperdivergent	Center	11	Ш	100	230	0.002	**
unswept.chr.sims	Hyperdivergent	Center	111	v	230	387	0.0051	**
unswept.chr.sims	Hyperdivergent	Center	ш	х	230	220	0.00646	**
unswept.chr.sims	Hyperdivergent	Tip	IV	х	89	43	0.00446	**
unswept.chr.sims	Hyperdivergent	Tip	v	х	156	43	0.00749	**
swept.chr.sims	Non-Hyperdivergent	Arm	11	v	488	233	0.04509	•

Supplemental Table 9: Power to detect simulated QTL on different chromosomes, within hyperdivergent regions, historic recombination groups, and strain sets

Strain Set	Simulated Divergence	Simulated Chromosome Region	Group 1	Group 2	n1	n2	Adjusted p-value	Significance
swept.chr.sims	Hyperdivergent	Arm	1	11	168	483	0.00007	****
swept.chr.sims	Hyperdivergent	Arm	1	III	168	359	0.00001	****
swept.chr.sims	Hyperdivergent	Arm	1	IV	168	360	0.00006	****
swept.chr.sims	Hyperdivergent	Arm	1	v	168	236	0.00002	****
swept.chr.sims	Hyperdivergent	Arm	1	х	168	247	0	••••
swept.chr.sims	Hyperdivergent	Arm	11	х	483	247	0.00054	***
swept.chr.sims	Hyperdivergent	Arm	III	х	359	247	0.01327	•
swept.chr.sims	Hyperdivergent	Arm	IV	х	360	247	0.00343	••
unswept.chr.sims	Hyperdivergent	Arm	III	х	343	269	0.03806	•
unswept.chr.sims	Hyperdivergent	Center	1	11	102	99	0.00015	***
unswept.chr.sims	Hyperdivergent	Center	1	III	102	221	0	****
unswept.chr.sims	Hyperdivergent	Center	1	v	102	383	0	****
unswept.chr.sims	Hyperdivergent	Center	1	х	102	216	0.00015	***
unswept.chr.sims	Hyperdivergent	Center	III	IV	221	180	0.0002	***
unswept.chr.sims	Hyperdivergent	Center	IV	v	180	383	0.00085	***
swept.chr.sims	Hyperdivergent	Tip	III	IV	24	183	0.00191	**
swept.chr.sims	Hyperdivergent	Tip	Ш	v	24	303	0.00099	***
swept.chr.sims	Hyperdivergent	Tip	III	х	24	145	0.00002	****
unswept.chr.sims	Hyperdivergent	Tip	1	v	27	156	0.00523	**
unswept.chr.sims	Hyperdivergent	Tip	Ш	v	14	156	0.01308	•
swept.chr.sims	Non-Hyperdivergent	Arm	1	11	190	488	0.02112	•
swept.chr.sims	Non-Hyperdivergent	Arm	1	III	190	374	0.00002	****
swept.chr.sims	Non-Hyperdivergent	Arm	1	IV	190	376	0.00001	****
swept.chr.sims	Non-Hyperdivergent	Arm	1	v	190	232	0.00731	**
swept.chr.sims	Non-Hyperdivergent	Arm	1	х	190	226	0	****
swept.chr.sims	Non-Hyperdivergent	Arm	II	х	488	226	0.00004	****
swept.chr.sims	Non-Hyperdivergent	Arm	v	х	232	226	0.01199	•
unswept.chr.sims	Non-Hyperdivergent	Arm	1	v	408	404	0.04823	•
unswept.chr.sims	Non-Hyperdivergent	Arm	IV	v	289	404	0.04823	•
swept.chr.sims	Non-Hyperdivergent	Center	1	IV	15	114	0.04399	•
swept.chr.sims	Non-Hyperdivergent	Center	1	х	15	321	0.01193	•
swept.chr.sims	Non-Hyperdivergent	Center	П	х	216	321	0.00542	••
swept.chr.sims	Non-Hyperdivergent	Center	III	х	155	321	0.00028	***
unswept.chr.sims	Non-Hyperdivergent	Center	1	III	157	237	0.00608	**
unswept.chr.sims	Non-Hyperdivergent	Center	1	v	157	364	0.00018	•••
unswept.chr.sims	Non-Hyperdivergent	Center	III	х	237	185	0.00703	••
unswept.chr.sims	Non-Hyperdivergent	Center	IV	v	199	364	0.02493	•
unswept.chr.sims	Non-Hyperdivergent	Center	v	х	364	185	0.00018	***
swept.chr.sims	Non-Hyperdivergent	Tip	1	111	15	24	0.02849	•
swept.chr.sims	Non-Hyperdivergent	Tip	11	111	63	24	0.00959	**
swept.chr.sims	Non-Hyperdivergent	Tip	III	IV	24	176	0.02297	•
swept.chr.sims	Non-Hyperdivergent	Tip	III	х	24	99	0.02148	•

Supplemental Table 10: Empirical FDR of mappings as a function of whether QTL were simulated on different chromosomes, within hyper-divergent regions, historic recombination groups, and strain sets