Supplementary Materials

Santantonio, N., Jannink, J., Sorrells, M. 2019. Homeologous epistasis in wheat: The search for an immortal hybrid. Genetics

Table S1 ANOVA table for *Rht-1B* and *Rht-1D* linked GBS markers and their epistatic interaction for plant height (cm) in 158 RIL lines derived from NY91017-8080 × Caledonia.

Source	df	SS	MS	F value	$-\log_{10}$(p-value)
SNP36427	1	7065	7065	53.5	10.9
SNP11172	1	7391	7391	56.0	11.3
SNP36427:SNP11172	1	1243	1243	9.4	2.6
Residuals	154	20323	132		

Table S2 Table of genotype frequencies for the 'perfect' *Rht-1* markers in the CNLM population. The + and − signs indicate the wildtype and mutant alleles, respectively. The margins indicate the marker allele frequencies.

	KASP_RhtD1$^-$	KASP_RhtD1$^+$	
KASP_cimRhtB1_snp$^-$	0.008	0.093	0.101
KASP_cimRhtB1_snp$^+$	0.721	0.178	0.899
	0.729	0.271	$D' = 0.89$

Table S3 Estimates of s coefficients for marker sets where both additive and the two-way interaction effects were significant at $p < 0.05$ for each of 4 traits. The expected number of non-zero additive and two-way interactions effects based on a 0.05 significance threshold by chance for each trait is 3 (i.e. 22,411 two-way interactions $\times$ 0.05^3). Coefficients have been grouped by categories related to the potential mode of epistasis, where $s < 0.5$ indicates a highly negative interaction, $0.5 \leq s < 1$ a less-than-additive interaction may be indicative of subfunctionalization for homeologous genes, and $s > 1$ which indicates positive, or greater-than-additive, epistasis. Three marker sets are shown, either across all homeologous loci (Homeo), sampled sets within (Within) and across (Across) non-syntenic subgenome regions. An additional phenotype was simulated to contain additive only phenotypes to contain no epistasis, and fit with the Homeo marker set (Simulated Additive).

Marker Set	Trait	$s < 0.5$	$0.5 \leq s < 1$	$s > 1$	Total[a]
Homeo	GY	0	0	2	2
Homeo	PH	2	8	4	14***
Homeo	TW	5	4	2	11**
Homeo	HD	1	2	0	3
Simulated Additive	PH	0	1	3	4
Simulated Additive	HD	1	0	1	2
Across	GY	2	2	1	5
Across	PH	3	0	0	3
Across	TW	2	1	0	3
Across	HD	2	4	0	6*
Within	GY	1	1	0	2
Within	PH	2	1	3	6*
Within	TW	1	1	1	3
Within	HD	2	0	0	2

[a] *, **, *** indicate significantly greater than the expected number of significant sets at p = 0.05, 10^{-4} and 10^{-6} based the binomial distribution with 22,411 trials and a probability of 0.05^3.

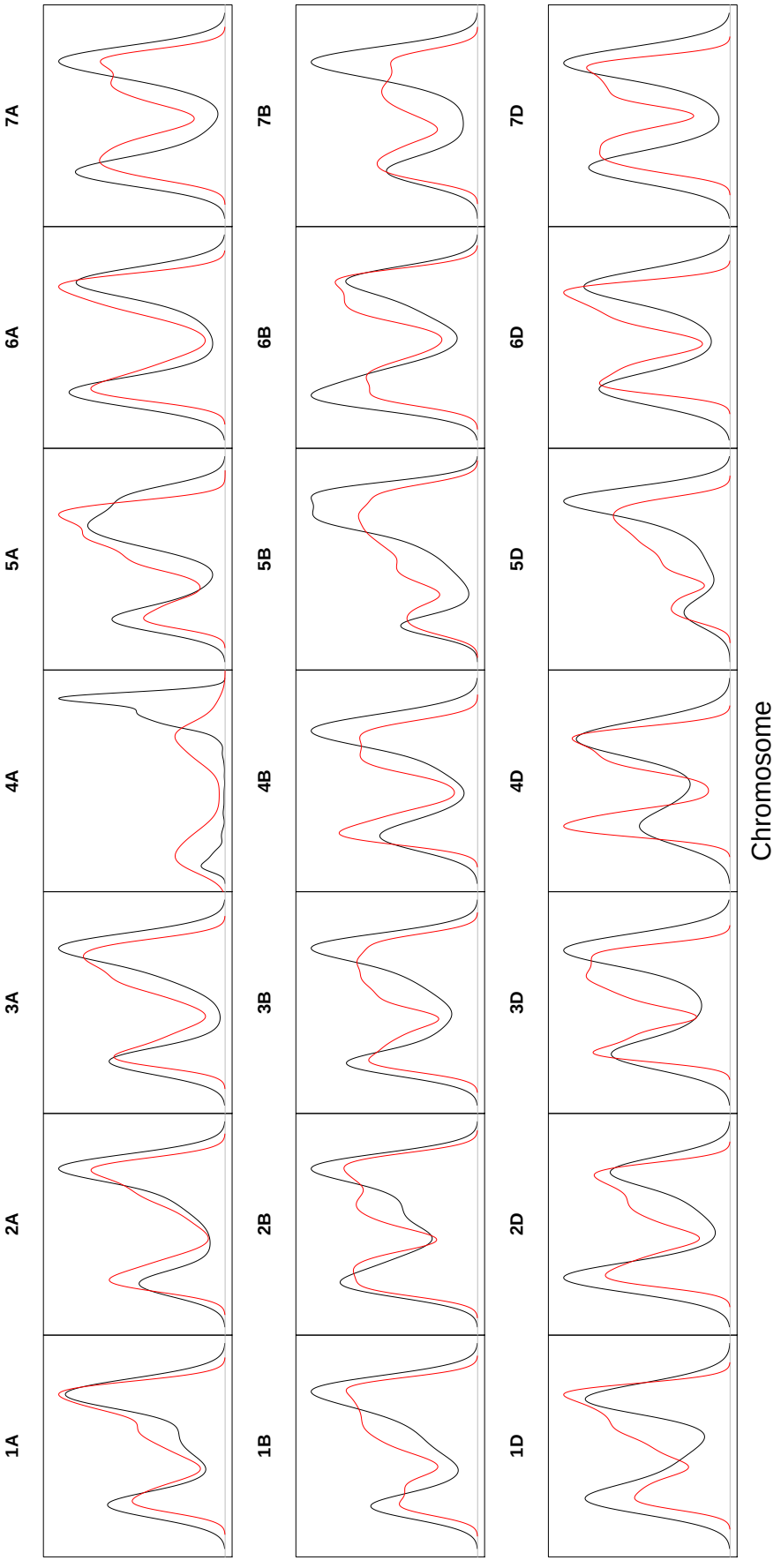

Figure S1 Smoothed densities of GBS markers (black) and genes (red) along the 21 wheat chromosomes in the CNLM population.

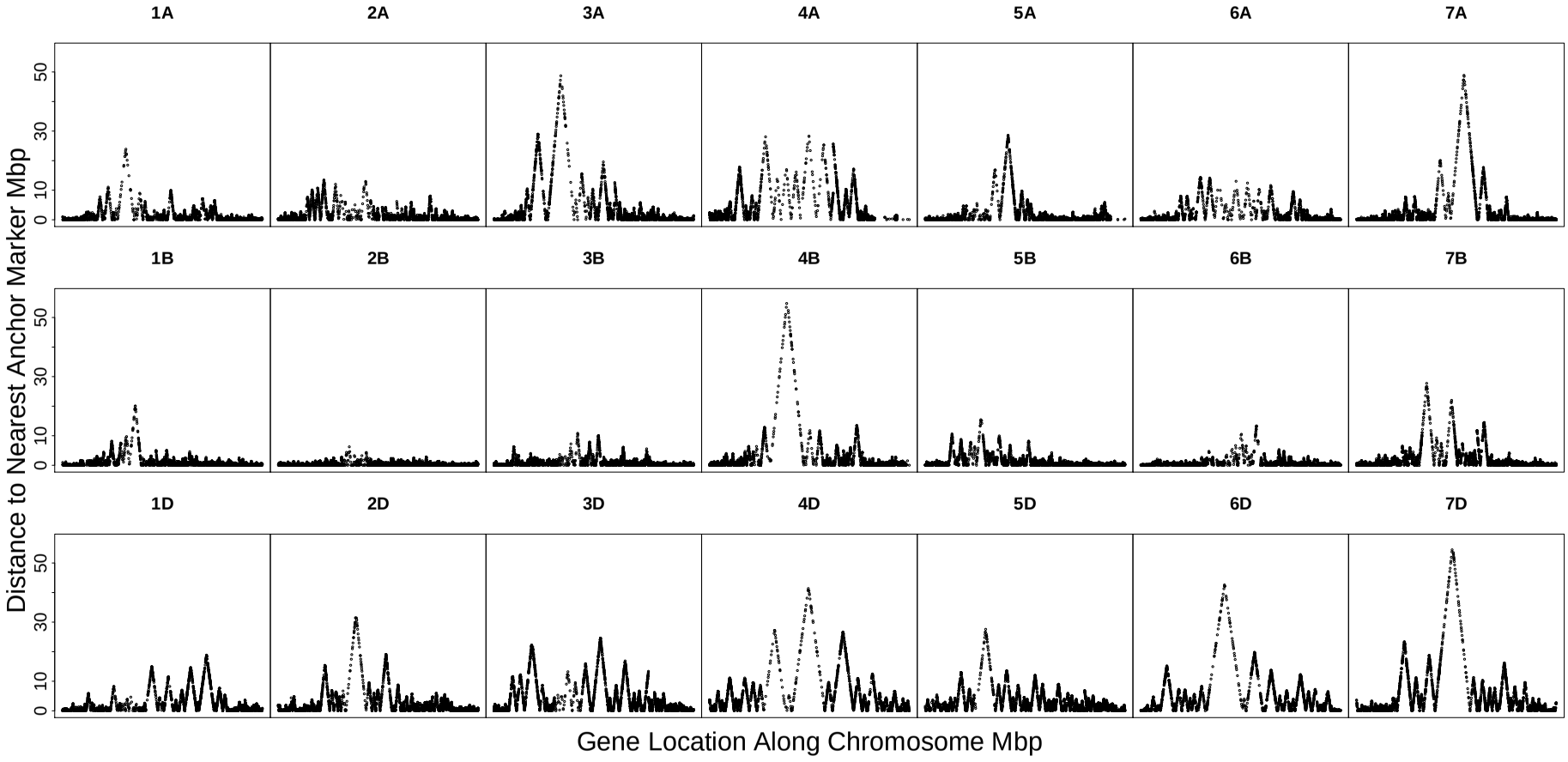

Figure S2 Distance of genes from their nearest GBS anchor marker along the 21 wheat chromosomes in the CNLM population.

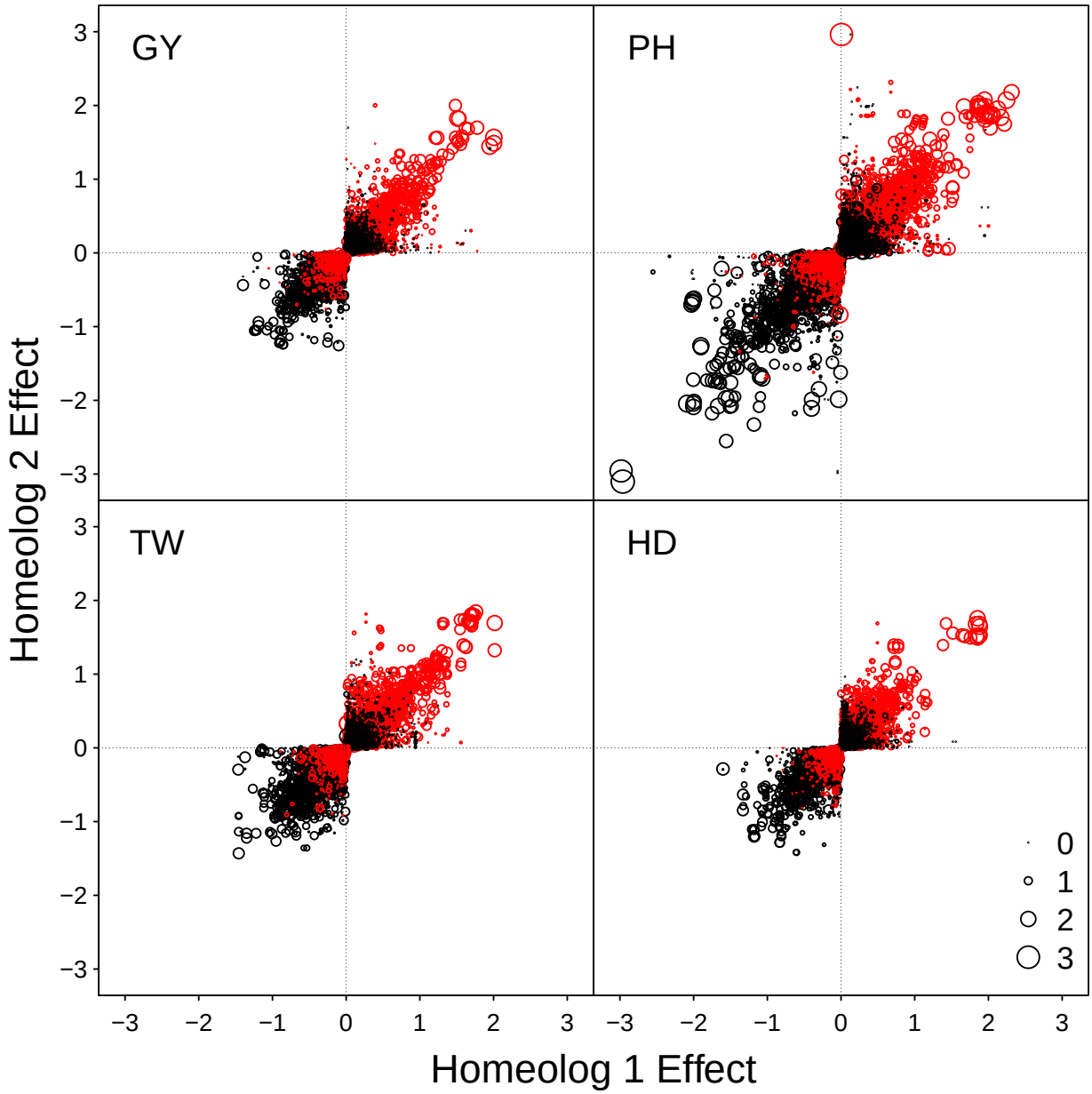

Figure S3 LAVHAE oriented homeologous marker pair additive effects with point size representing the magnitude of the two-way homeologous interaction effect, and the color denoting the direction of that effect where black is positive and red is negative. Four simulated phenotypes sampled to obtain no epistatic interactions, GY, PH, TW and HD, are shown.

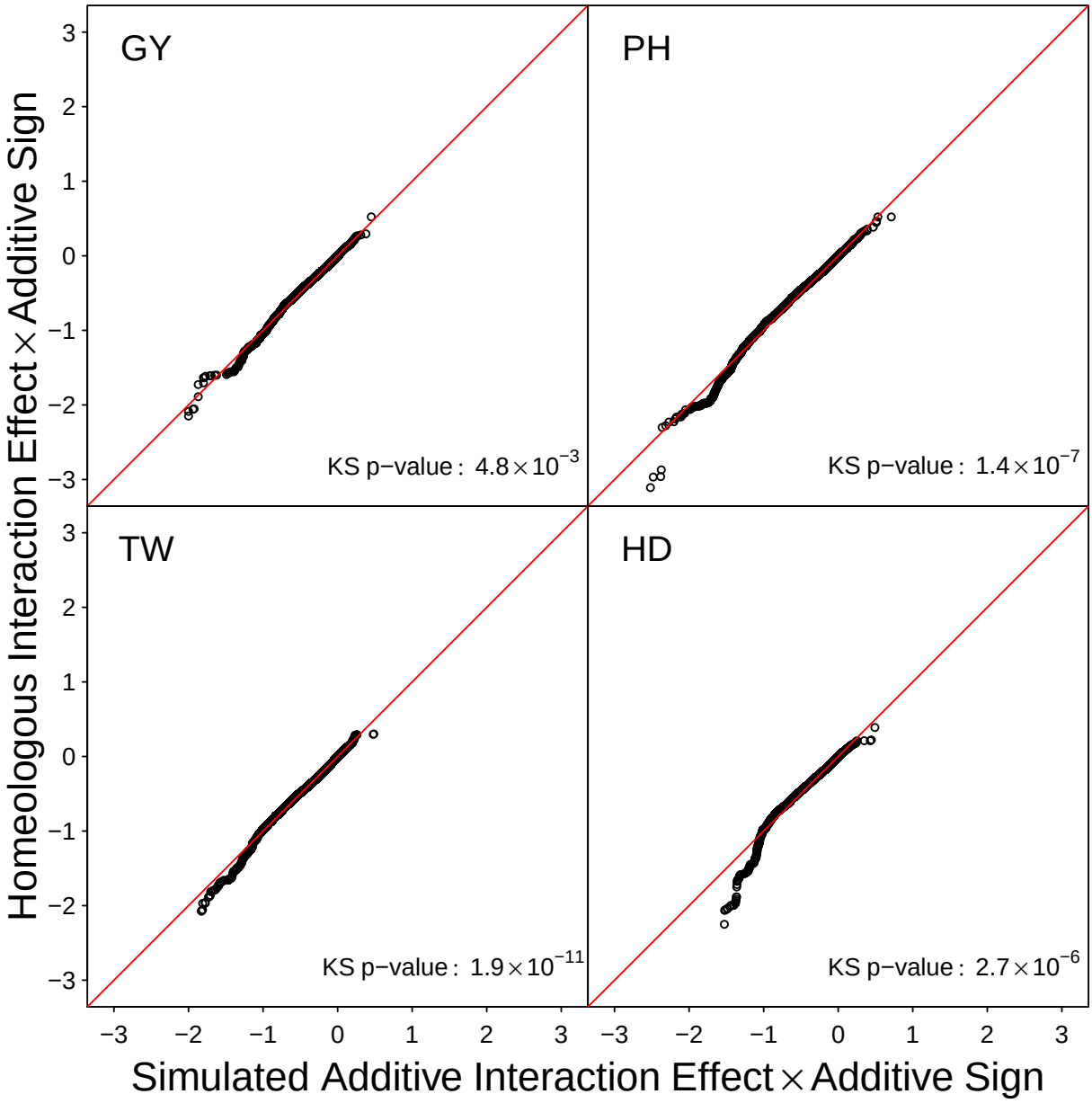

Figure S4 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from a simulated phenotype sampled to obtain no epistatic interactions using the HTEV marker orientation. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

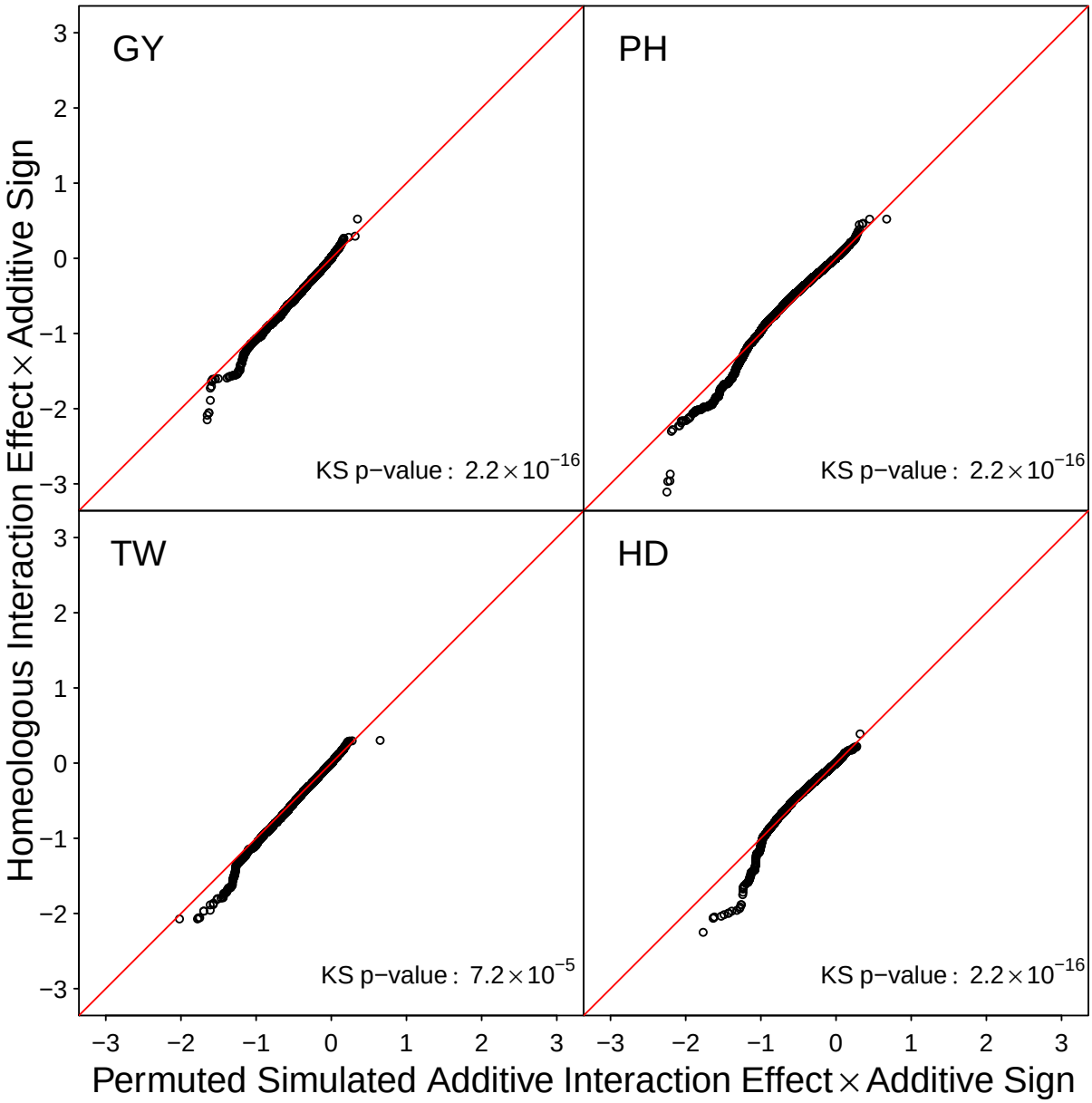

Figure S5 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from a simulated phenotype sampled to obtain no epistatic interactions using the HTEV marker orientation. Markers scores were permuted before simulation of the phenotype to remove LD between markers. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

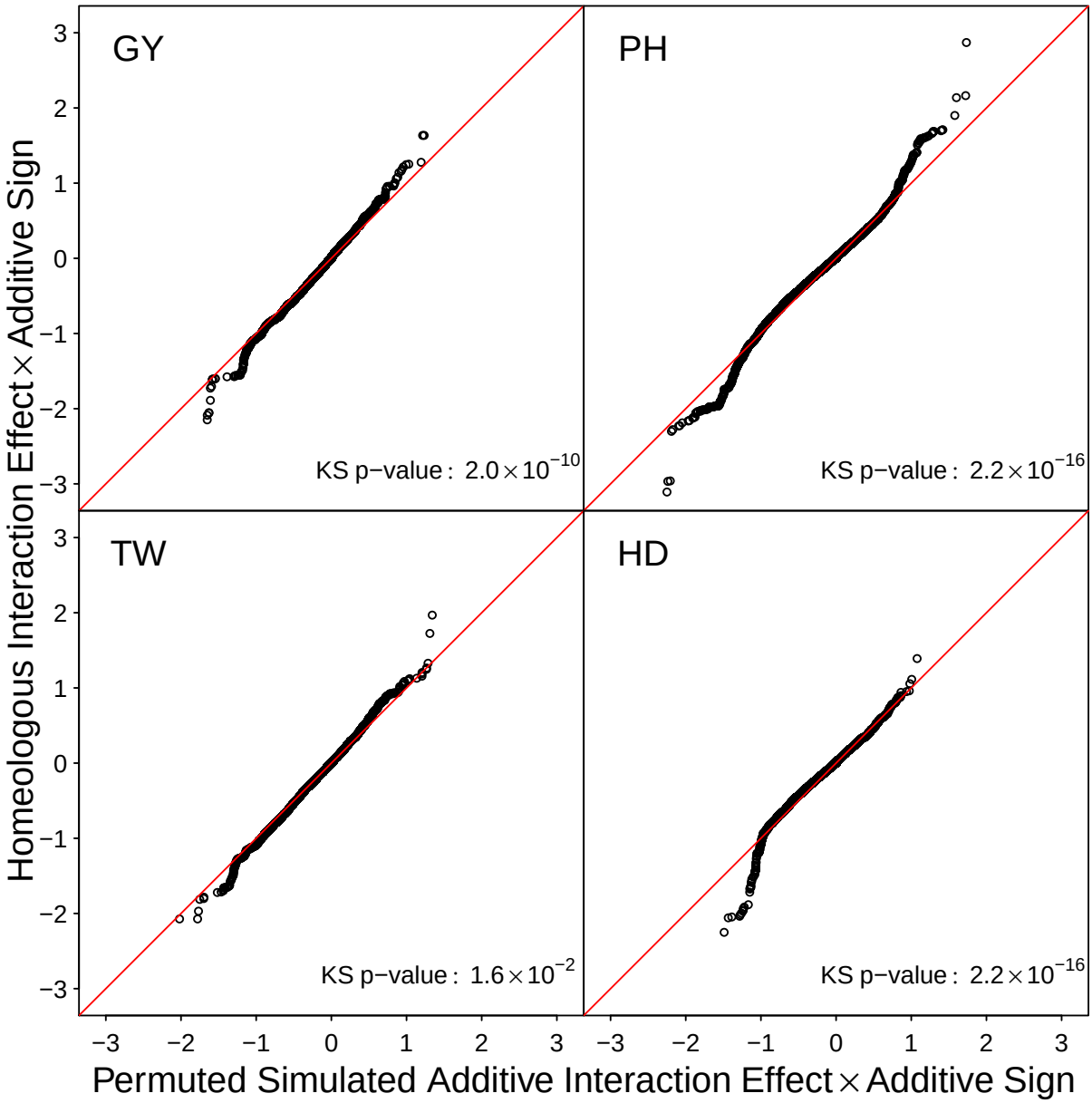

Figure S6 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from a simulated phenotype sampled to obtain no epistatic interactions using the LAVHAE marker orientation. Markers scores were permuted before simulation of the phenotype to remove LD between markers. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

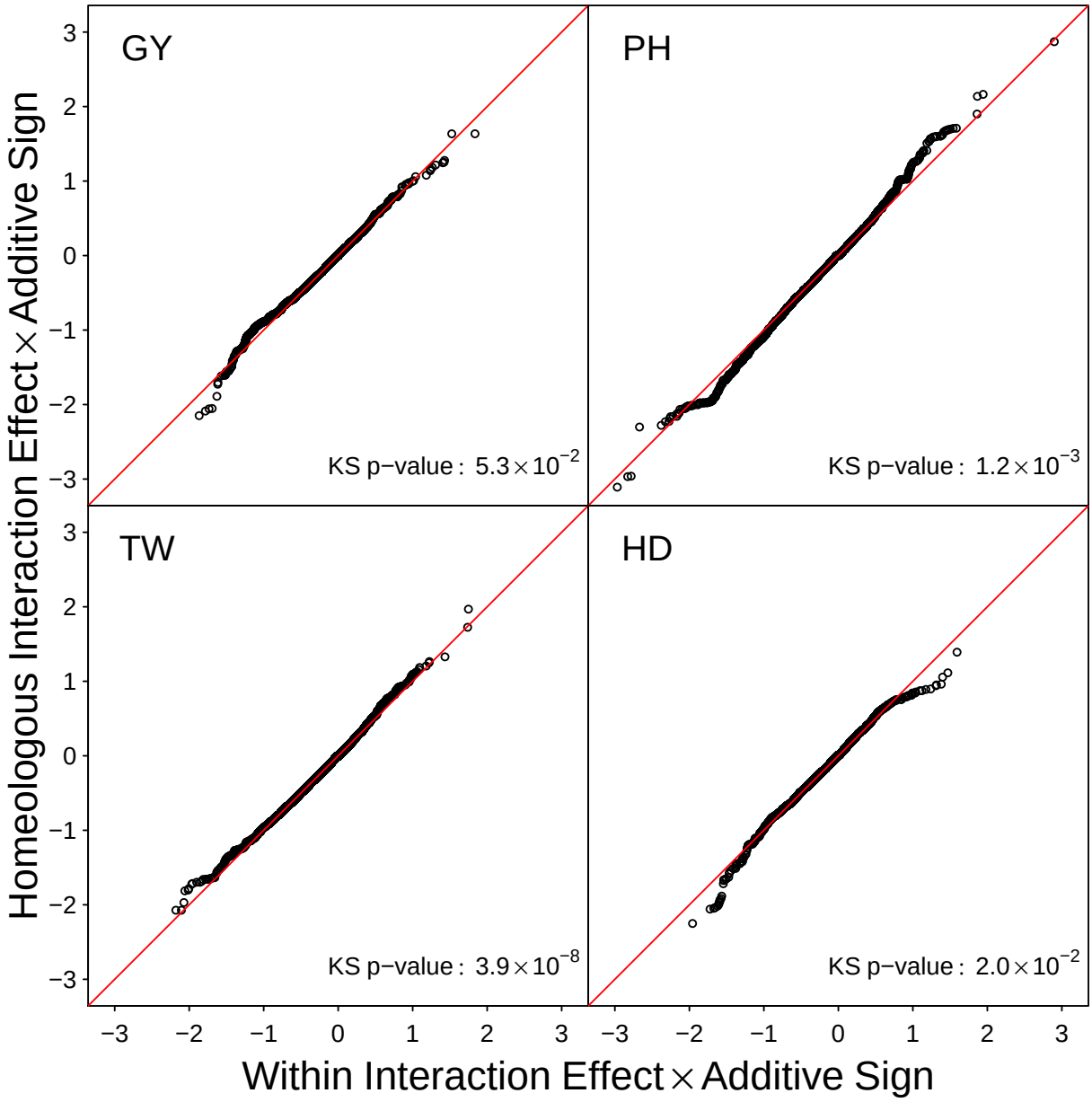

Figure S7 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets sampled within subgenome chromosomes (Within) using the LAVHAE . Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

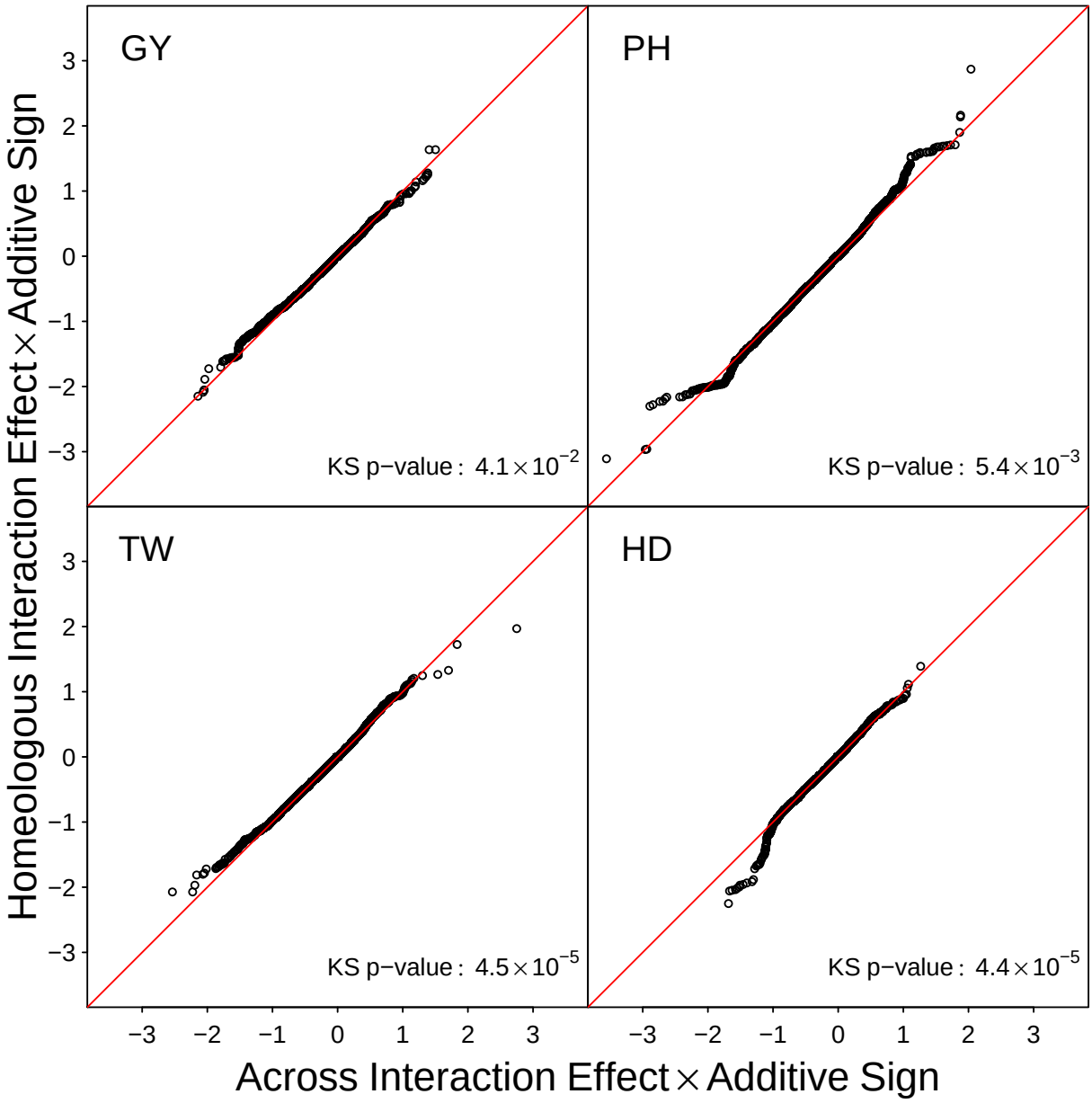

Figure S8 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets sampled across non-syntenic subgenome chromosomes (Across) using the LAVHAE marker orientation. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

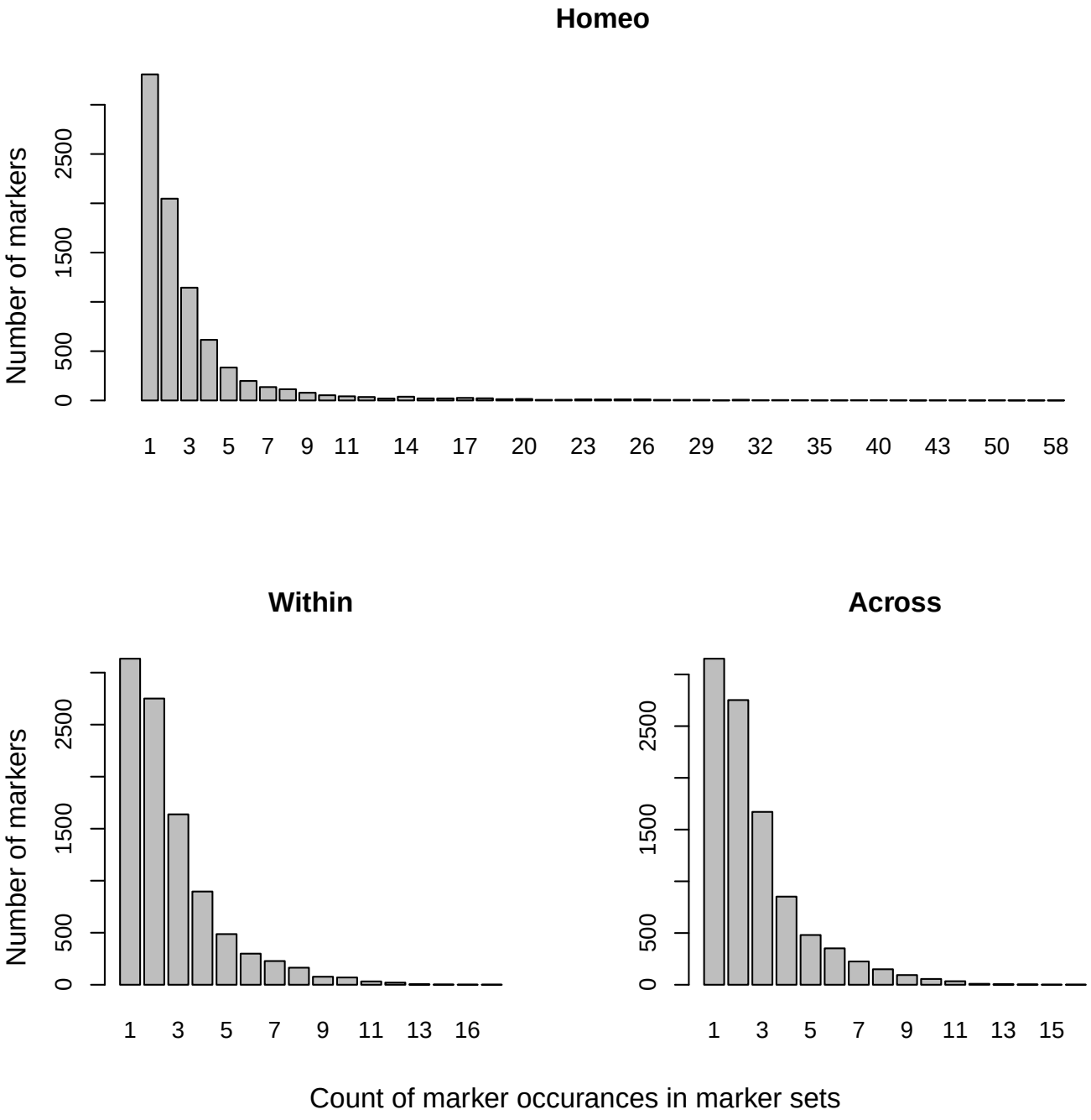

Figure S9 Distribution of the number of marker occurrences in marker sets. An occurrence of 1 indicates that a marker was only included in one marker set, whereas an occurrence of 10 would indicate that the marker was included in 10 marker sets.

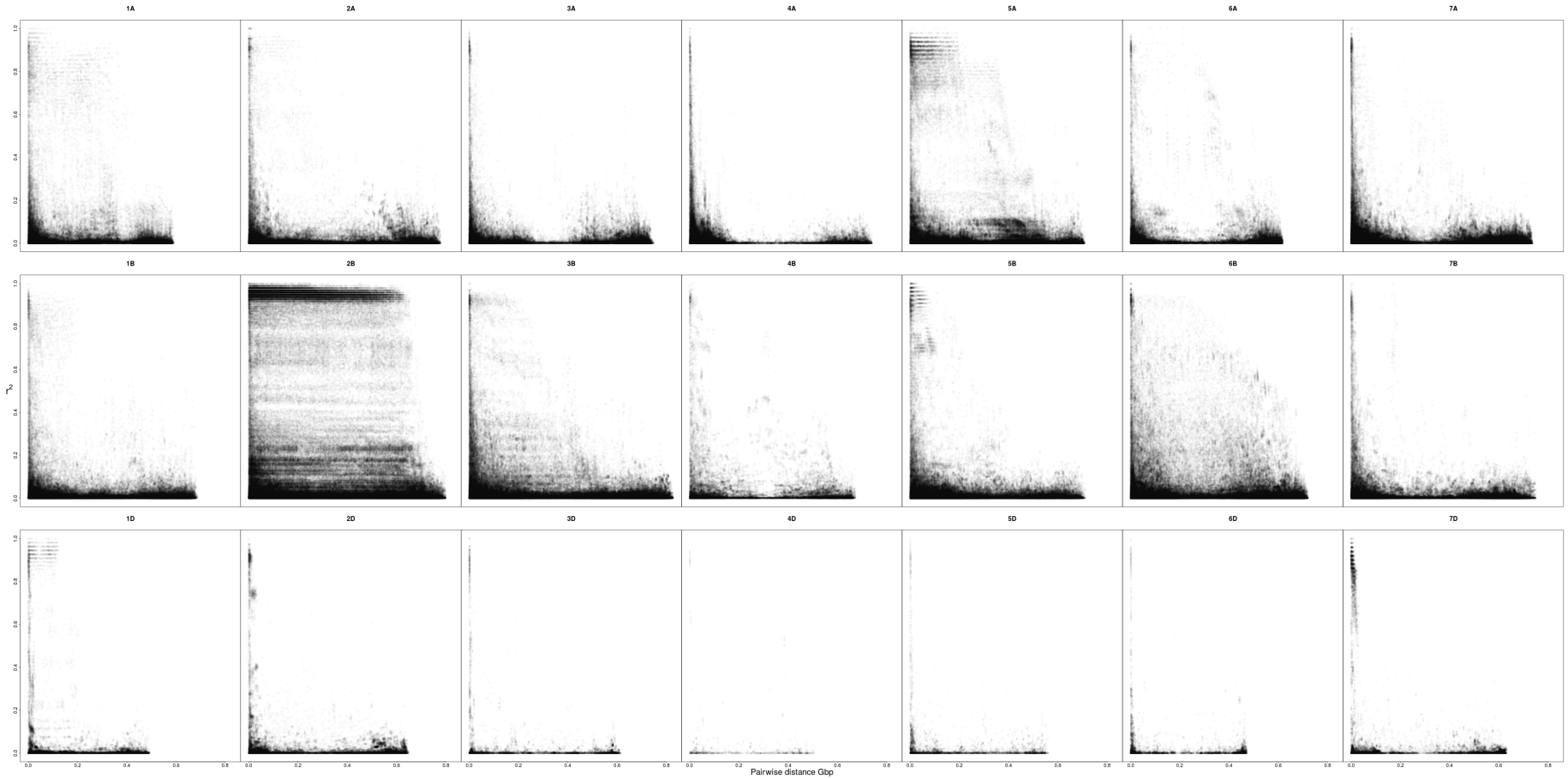

Figure S10 Pairwise linkage disequilibrium r^2 values for the 21 wheat chromosomes in the CNLM population.

Table S4 Mixed model REML fit summaries of one additive and four epistasis models for four traits (GY, PH, TW and HD) in the CNLM population based on the $\{-1, 1\}$ marker parameterization using the LAVHAE marker orientation. Plot level heritabilities assuming genotype independence (i.i.d.) for each trait are shown underneath each trait name.

Trait		Additive	Pairwise	Homeo	Within	Across
GY	$\log\mathcal{L}$	-48	-43	-42	-26	-23
$h^2 = 0.30$[a]	parameters	28	29	29	29	29
	AIC	153	144	141	110	104
	G	0.268[b] (12.59)[c]	0.203 (7.86)	0.204 (8.49)	0.133 (5.93)	0.13 (5.84)
	H		0.018 (3.04)	0.046 (3.29)***[d]	0.093 (5.64)****	0.093 (5.77)****
	R	0.324 (61.86)[e]	0.322 (61.39)	0.323 (61.68)	0.321 (61.7)	0.321 (61.7)
PH	$\log\mathcal{L}$	2237	2360	2314	2367	2374
$h^2 = 0.73$	parameters	26	27	27	27	27
	AIC	-4423	-4665	-4574	-4680	-4694
	G	3.823 (20.75)	0.889 (6.46)	1.882 (11.66)	0.986 (7.35)	1.046 (7.81)
	H		0.478 (11.95)	0.914 (8.72)****	1.277 (11.67)****	1.253 (11.62)****
	R	0.135 (56.17)	0.132 (56.5)	0.133 (56.34)	0.133 (56.45)	0.133 (56.5)
TW	$\log\mathcal{L}$	1547	1630	1608	1641	1632
$h^2 = 0.79$	parameters	28	29	29	29	29
	AIC	-3037	-3203	-3159	-3224	-3205
	G	1.067 (16.66)	0.194 (4.47)	0.442 (8.35)	0.212 (4.81)	0.221 (4.79)
	H		0.184 (11.33)	0.346 (8.39)****	0.473 (10.95)****	0.473 (10.66)****
	R	0.2 (60.12)	0.195 (60.25)	0.198 (60.24)	0.197 (60.35)	0.197 (60.31)
HD	$\log\mathcal{L}$	6343	6432	6404	6425	6444
$h^2 = 0.53$	parameters	27	28	28	28	28
	AIC	-12631	-12808	-12751	-12794	-12831
	G	3.9 (21.16)	1.121 (7.3)	2.019 (12.03)	1.483 (9.25)	1.212 (8.29)
	H		0.451 (11.13)	0.857 (8.26)****	1.091 (10.01)****	1.202 (10.97)****
	R	0.054 (58.76)	0.053 (58.98)	0.053 (58.88)	0.053 (58.93)	0.053 (58.96)

[a] h^2 is the plot level trait heritability assuming genotype independence.
[b] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[c] The variance component divided by their respective standard errors are shown in parentheses.
[d] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[e] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S5 Mixed model REML fit summaries of three epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{0,1\}$ marker parameterization using the LAVHAE marker orientation.

Trait		Homeo	Within	Across
GY	log$\mathcal{L}$	-48	-47	-42
	parameters	29	29	29
	AIC	155	152	143
	G	0.267[a] (7.6)[b]	0.207 (5.5)	0.146 (4.16)
	H	0 (0.01)	0.054 (1.73)	0.108 (3.39)***[c]
	R	0.324 (61.81)[d]	0.324 (61.77)	0.324 (61.8)
PH	log$\mathcal{L}$	2282	2268	2285
	parameters	27	27	27
	AIC	-4510	-4482	-4516
	G	1.198 (5.03)	1.766 (6.95)	1.177 (5.02)
	H	1.981 (8.36)****	1.592 (6.95)****	2.051 (8.66)****
	R	0.134 (56.23)	0.134 (56.24)	0.134 (56.24)
TW	log$\mathcal{L}$	1560	1555	1567
	parameters	29	29	29
	AIC	-3061	-3052	-3076
	G	0.553 (5.88)	0.659 (6.68)	0.498 (5.57)
	H	0.414 (5.04)****	0.331 (4.06)***	0.482 (5.85)****
	R	0.199 (60.11)	0.199 (60.1)	0.198 (60.13)
HD	log$\mathcal{L}$	6382	6364	6379
	parameters	28	28	28
	AIC	-12709	-12673	-12702
	G	1.51 (6.14)	2.077 (7.82)	1.659 (6.67)
	H	1.781 (7.73)****	1.358 (6.09)****	1.68 (7.36)****
	R	0.053 (58.84)	0.054 (58.78)	0.054 (58.81)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[d] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S6 Mixed model REML fit summaries of three epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{-1, 1\}$ marker parameterization using the POS marker orientation.

Trait		Homeo	Within	Across
GY	log$\mathcal{L}$	-48	-41	-40
	parameters	29	29	29
	AIC	154	140	138
	G	0.257[a] (10.31)[b]	0.191 (7.44)	0.186 (7.32)
	H	0.008 (0.75)	0.052 (3.45)***[c]	0.054 (3.61)***
	R	0.324 (61.7)[d]	0.323 (61.64)	0.323 (61.64)
PH	log$\mathcal{L}$	2287	2323	2326
	parameters	27	27	27
	AIC	-4521	-4593	-4598
	G	2.316 (13.04)	1.507 (9.34)	1.551 (9.59)
	H	0.705 (7.3)****	1.056 (9.85)****	1.036 (9.72)****
	R	0.134 (56.29)	0.133 (56.38)	0.133 (56.4)
TW	log$\mathcal{L}$	1589	1599	1604
	parameters	29	29	29
	AIC	-3120	-3139	-3150
	G	0.554 (9.49)	0.437 (7.44)	0.395 (7.02)
	H	0.282 (7.22)****	0.354 (8.36)****	0.368 (8.71)****
	R	0.198 (60.18)	0.197 (60.2)	0.197 (60.21)
HD	log$\mathcal{L}$	6379	6393	6415
	parameters	28	28	28
	AIC	-12701	-12730	-12774
	G	2.547 (13.61)	2.017 (10.81)	1.689 (9.94)
	H	0.601 (6.43)****	0.848 (8.04)****	0.982 (9.26)****
	R	0.053 (58.83)	0.053 (58.87)	0.053 (58.92)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[d] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S7 Mixed model REML fit summaries of three epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{-1, 1\}$ marker parameterization using the NEG marker orientation.

Trait		Homeo	Within	Across
GY	log$\mathcal{L}$	-46	-38	-35
	parameters	29	29	29
	AIC	151	134	129
	G	0.236[a] (9.44)[b]	0.181 (7.35)	0.178 (7.35)
	H	0.022 (1.86)	0.058 (3.9)***[c]	0.06 (4.1)****
	R	0.324 (61.71)[d]	0.323 (61.68)	0.322 (61.68)
PH	log$\mathcal{L}$	2293	2336	2342
	parameters	27	27	27
	AIC	-4532	-4619	-4629
	G	2.235 (12.79)	1.428 (9.19)	1.464 (9.46)
	H	0.746 (7.52)****	1.061 (10.06)****	1.038 (10.07)****
	R	0.134 (56.3)	0.133 (56.39)	0.133 (56.42)
TW	log$\mathcal{L}$	1580	1605	1601
	parameters	29	29	29
	AIC	-3101	-3153	-3144
	G	0.614 (9.96)	0.373 (6.78)	0.388 (6.71)
	H	0.241 (6.4)****	0.374 (8.94)****	0.367 (8.59)****
	R	0.199 (60.15)	0.198 (60.22)	0.197 (60.21)
HD	log$\mathcal{L}$	6380	6402	6409
	parameters	28	28	28
	AIC	-12704	-12747	-12762
	G	2.48 (13.41)	1.88 (10.5)	1.753 (10.09)
	H	0.626 (6.71)****	0.895 (8.59)****	0.95 (9.02)****
	R	0.053 (58.83)	0.053 (58.89)	0.053 (58.9)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[d] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S8 Mixed model REML fit summaries of three epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{-1, 1\}$ marker parameterization using the HTEV marker orientation.

trait		Homeo	Within	Across
GY	$\log\mathcal{L}$	-46	-34	-30
	parameters	29	29	29
	AIC	151	127	118
	G	0.233[a] (9.23)[b]	0.165 (6.86)	0.151 (6.45)
	H	0.025 (1.97)	0.071 (4.56)****[c]	0.079 (5)****
	R	0.323 (61.65)[d]	0.322 (61.66)	0.322 (61.67)
PH	$\log\mathcal{L}$	2300	2355	2357
	parameters	27	27	27
	AIC	-4546	-4655	-4659
	G	2.052 (12.02)	1.101 (7.81)	1.142 (7.99)
	H	0.84 (8.12)****	1.227 (11.24)****	1.209 (11.09)****
	R	0.133 (56.32)	0.133 (56.43)	0.133 (56.46)
TW	$\log\mathcal{L}$	1599	1623	1623
	parameters	29	29	29
	AIC	-3140	-3189	-3187
	G	0.476 (8.51)	0.283 (5.73)	0.267 (5.4)
	H	0.335 (7.92)****	0.435 (10.13)****	0.45 (10.15)****
	R	0.198 (60.2)	0.197 (60.29)	0.197 (60.28)
HD	$\log\mathcal{L}$	6397	6410	6423
	parameters	28	28	28
	AIC	-12738	-12764	-12790
	G	2.13 (12.27)	1.62 (9.54)	1.395 (8.69)
	H	0.808 (7.9)****	1.029 (9.43)****	1.139 (10.18)****
	R	0.053 (58.88)	0.053 (58.91)	0.053 (58.94)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[d] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S9 Mixed model REML fit summaries of three epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{0,1\}$ marker parameterization using the HTEV marker orientation.

trait		Homeo	Within	Across
GY	log$\mathcal{L}$	-48	-48	-48
	parameters	29	29	29
	AIC	155	155	155
	G	0.268[a] (12.59)[b]	0.268 (12.59)	0.268 (12.59)
	H	0	0	0
	R	0.324 (61.86)[c]	0.324 (61.86)	0.324 (61.86)
PH	log$\mathcal{L}$	2260	2246	2248
	parameters	27	27	27
	AIC	-4466	-4438	-4443
	G	1.981 (7.41)	2.84 (9.98)	2.502 (8.49)
	H	1.423 (6.05)****[d]	0.806 (3.68)***	1.081 (4.44)***
	R	0.134 (56.2)	0.134 (56.19)	0.134 (56.19)
TW	log$\mathcal{L}$	1552	1547	1549
	parameters	29	29	29
	AIC	-3046	-3036	-3041
	G	0.746 (7.61)	0.992 (9.51)	0.857 (8.24)
	H	0.264 (3.38)***	0.064 (0.87)	0.183 (2.26)*
	R	0.199 (60.1)	0.199 (60.08)	0.199 (60.09)
HD	log$\mathcal{L}$	6358	6350	6356
	parameters	28	28	28
	AIC	-12660	-12643	-12656
	G	2.528 (9.24)	2.937 (10.1)	2.468 (8.5)
	H	1.052 (4.83)****	0.749 (3.44)***	1.16 (4.78)****
	R	0.054 (58.79)	0.054 (58.76)	0.054 (58.78)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).
[d] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.

Table S10 Prediction accuracies of Homeo, Within and Across genome marker sets for both $\{-1,1\}$ and $\{0,1\}$ marker coding using POS marker orientation.

POS	$\text{Homeo}_{\text{-11}}$	Homeo_{01}	$\text{Within}_{\text{-11}}$	Within_{01}	$\text{Across}_{\text{-11}}$	Across_{01}
GY	0.599[a]	0.599	0.607	0.600	0.607	0.599
PH	0.583	0.573	0.607	0.568	0.612	0.576
TW	0.535	0.518	0.543	0.514	0.547	0.524
HD	0.681	0.681	0.688	0.670	0.698	0.671

[a] Mean Pearson correlation between predicted and observed genetic values across 10 random 5-fold cross-validation replications.

Table S11 Prediction accuracies of Homeo, Within and Across genome marker sets for both $\{-1,1\}$ and $\{0,1\}$ marker coding using NEG marker orientation.

NEG	$\text{Homeo}_{\text{-11}}$	Homeo_{01}	$\text{Within}_{\text{-11}}$	Within_{01}	$\text{Across}_{\text{-11}}$	Across_{01}
GY	0.602[a]	0.599	0.612	0.599	0.615	0.600
PH	0.589	0.582	0.620	0.565	0.615	0.579
TW	0.535	0.513	0.555	0.510	0.546	0.519
HD	0.676	0.671	0.698	0.671	0.697	0.680

[a] Mean Pearson correlation between predicted and observed genetic values across 10 random 5-fold cross-validation replications.

Table S12 Prediction accuracies of Homeo, Within and Across genome marker sets for both $\{-1,1\}$ and $\{0,1\}$ marker coding using HTEV marker orientation.

HTEV	$\text{Homeo}_{\text{-11}}$	Homeo_{01}	$\text{Within}_{\text{-11}}$	Within_{01}	$\text{Across}_{\text{-11}}$	Across_{01}
GY	0.601[a]	0.601	0.616	0.600	0.621	0.600
PH	0.591	0.565	0.640	0.557	0.633	0.558
TW	0.548	0.513	0.572	0.513	0.568	0.513
HD	0.688	0.669	0.700	0.666	0.706	0.667

[a] Mean Pearson correlation between predicted and observed genetic values across 10 random 5-fold cross-validation replications.

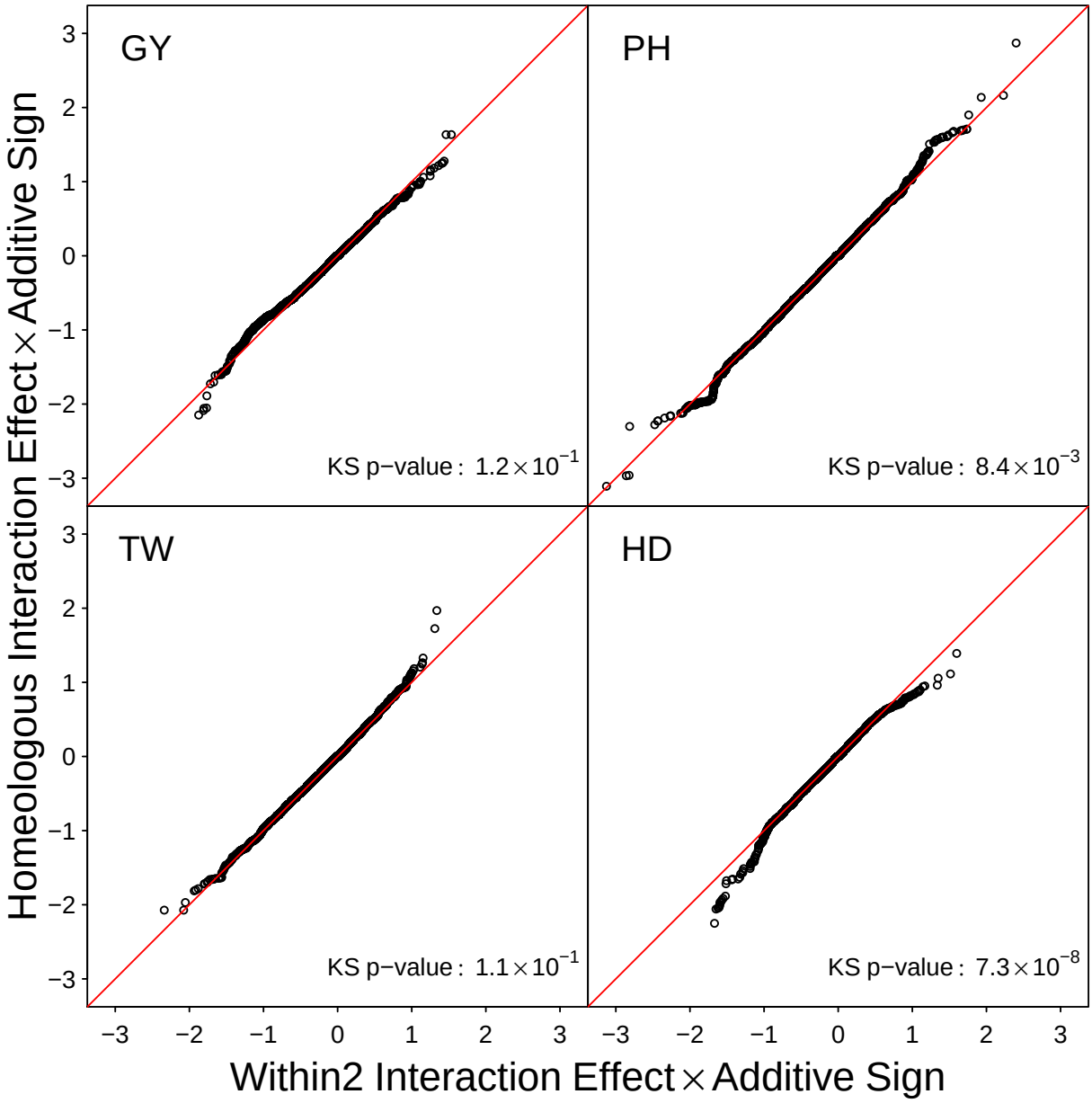

Figure S11 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets re-sampled within subgenome chromosomes (Within2) using the LAVHAE . Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

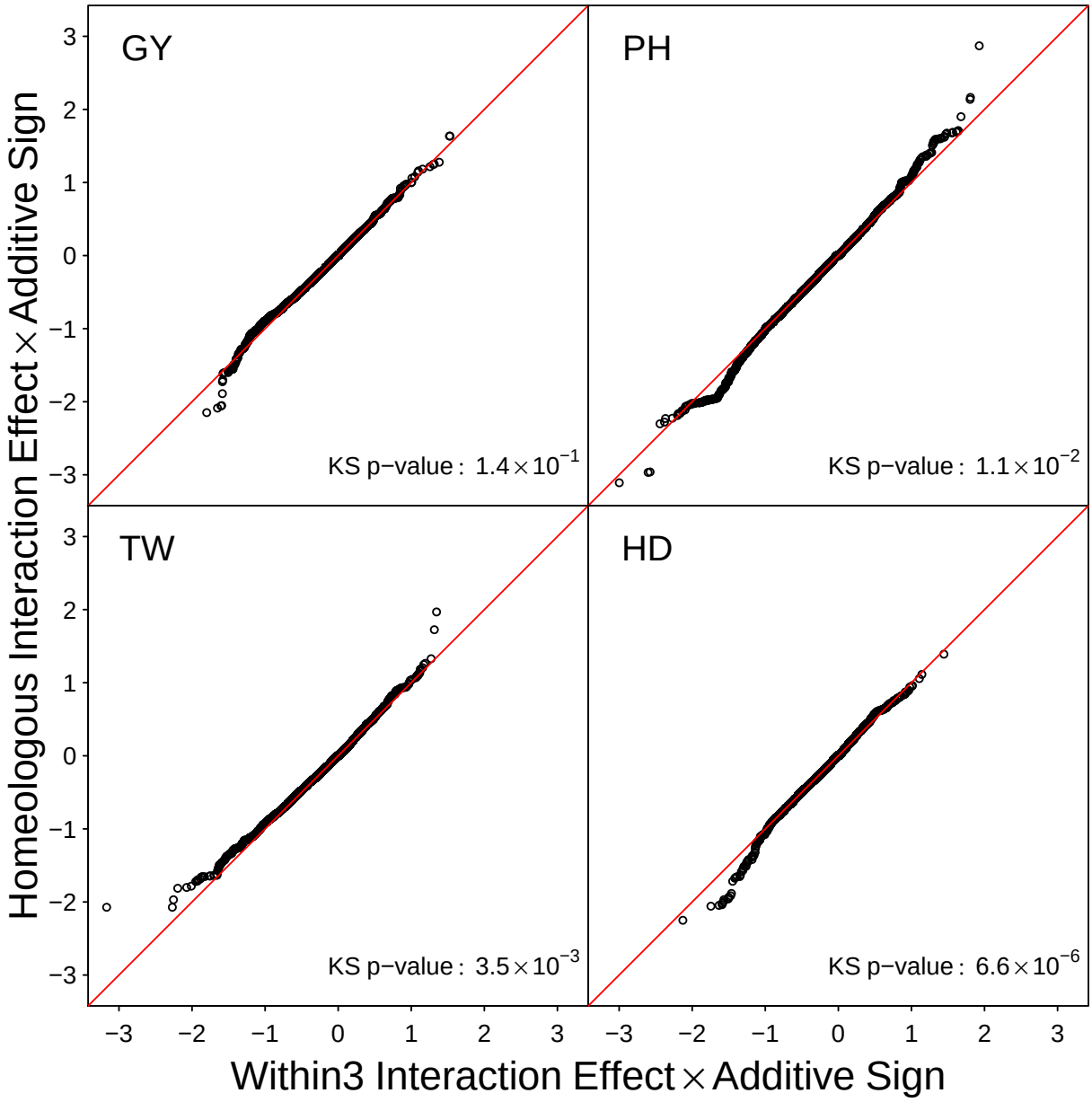

Figure S12 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets re-sampled within subgenome chromosomes (Within3) using the LAVHAE . Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

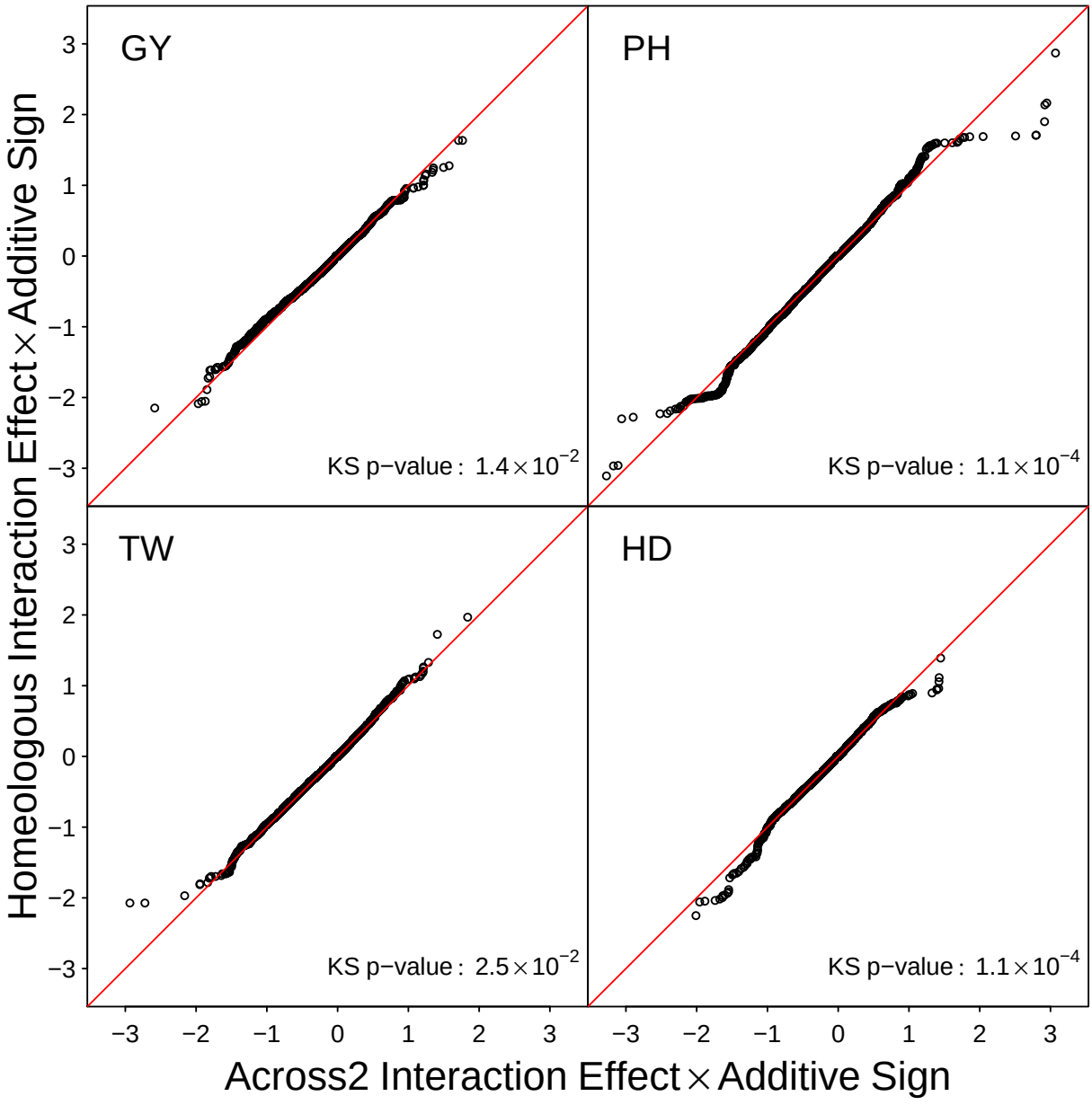

Figure S13 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets re-sampled across non-syntenic subgenome chromosomes (Across2) using the LAVHAE marker orientation. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

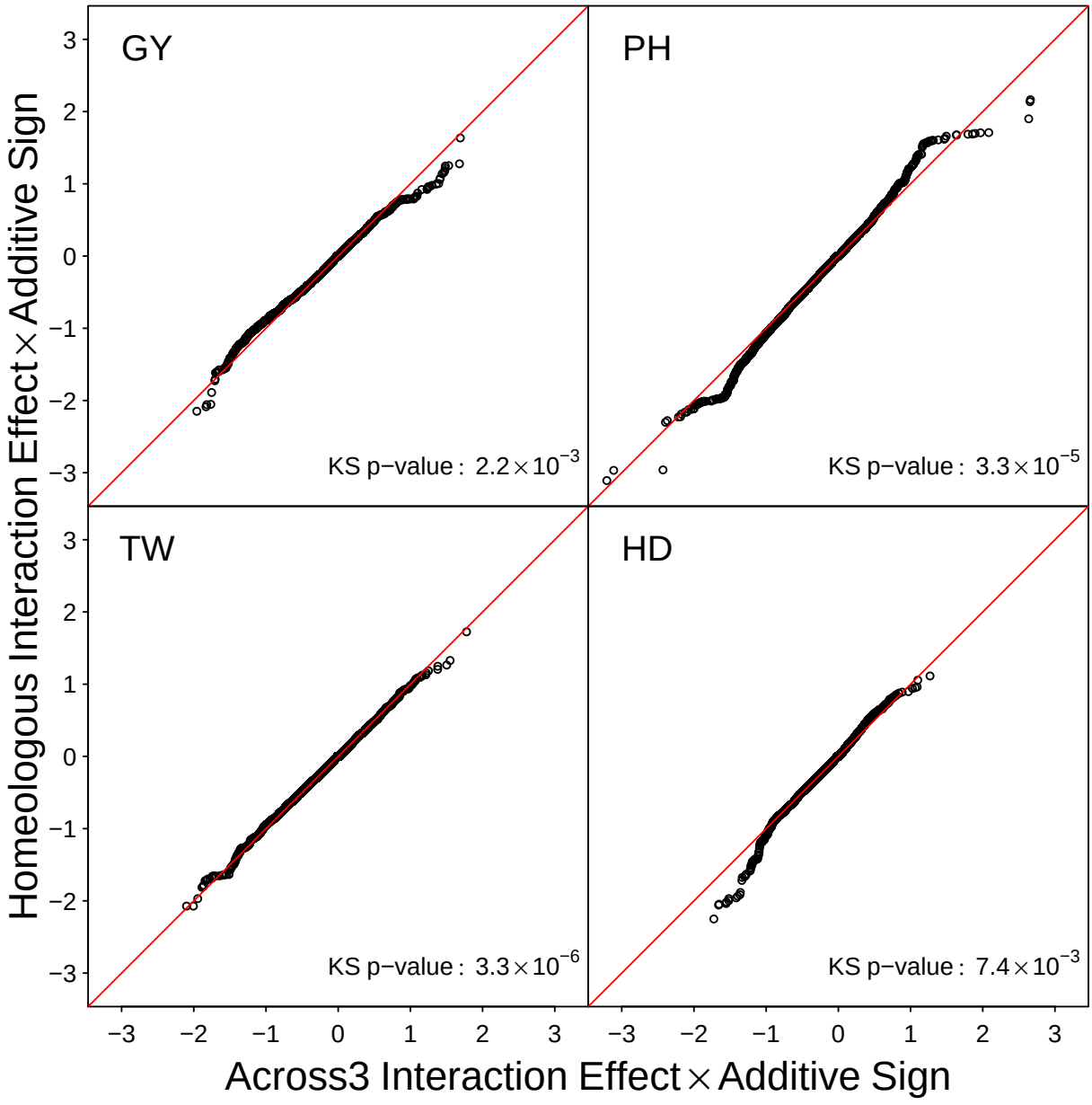

Figure S14 Quantile quantile plot of the ordered estimated homeologous interaction effects plotted against those from marker sets re-sampled across non-syntenic subgenome chromosomes (Across3) using the LAVHAE marker orientation. Interaction effects have been multiplied by the effect sign of the corresponding additive effects to emphasize the relationship between the additive and interaction effects.

Table S13 Mixed model REML fit summaries of four epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{-1, 1\}$ marker parameterization using the LAVHAE marker orientation using two additional samples of Within (Within2, Within3) and Across (Across2, Across3).

Trait		Within2	Within3	Across2	Across3
GY	log$\mathcal{L}$	-32	-29	-26	-32
	parameters	29	29	29	29
	AIC	122	115	110	121
	G	0.15[a] (6.29)[b]	0.14 (6.07)	0.134 (5.91)	0.154 (6.55)
	H	0.081 (4.97)****[c]	0.086 (5.32)****	0.092 (5.58)****	0.078 (4.89)****
	R	0.322 (61.67)[d]	0.322 (61.7)	0.321 (61.69)	0.322 (61.67)
PH	log$\mathcal{L}$	2369	2356	2357	2359
	parameters	27	27	27	27
	AIC	-4685	-4658	-4661	-4664
	G	0.979 (7.38)	1.066 (7.57)	1.083 (7.67)	1.103 (7.86)
	H	1.257 (11.59)****	1.242 (11.23)****	1.253 (11.27)****	1.23 (11.27)****
	R	0.133 (56.45)	0.133 (56.44)	0.133 (56.44)	0.133 (56.48)
TW	log$\mathcal{L}$	1647	1627	1641	1634
	parameters	29	29	29	29
	AIC	-3235	-3196	-3224	-3210
	G	0.2 (4.56)	0.267 (5.42)	0.213 (4.74)	0.233 (5)
	H	0.479 (10.94)****	0.441 (10.11)****	0.48 (10.86)****	0.472 (10.67)****
	R	0.197 (60.38)	0.197 (60.29)	0.196 (60.31)	0.196 (60.36)
HD	log$\mathcal{L}$	6455	6429	6442	6444
	parameters	28	28	28	28
	AIC	-12853	-12801	-12828	-12832
	G	1.053 (7.75)	1.366 (8.76)	1.174 (8.15)	1.173 (8.15)
	H	1.311 (11.68)****	1.15 (10.39)****	1.248 (11.19)****	1.226 (11.11)****
	R	0.053 (58.99)	0.053 (58.94)	0.053 (58.94)	0.053 (58.95)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.
[d] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).

Table S14 Mixed model REML fit summaries of four epistasis models for 4 traits (GY, PH, TW and HD) in the CNLM population based on the $\{0,1\}$ marker parameterization using the LAVHAE marker orientation using two additional samples of Within (Within2, Within3) and Across (Across2, Across3).

Trait		Within2	Within3	Across2	Across3
GY	log$\mathcal{L}$	-47	-48	-48	-48
	parameters	29	29	29	29
	AIC	153	155	154	154
	G	0.213[a] (5.66)[b]	0.25 (6.62)	0.235 (6.47)	0.248 (6.74)
	H	0.048 (1.56)	0.015 (0.53)	0.03 (1.06)	0.017 (0.62)
	R	0.324 (61.78)[c]	0.324 (61.79)	0.324 (61.75)	0.324 (61.78)
PH	log$\mathcal{L}$	2268	2273	2265	2271
	parameters	27	27	27	27
	AIC	-4482	-4491	-4476	-4487
	G	1.867 (7.5)	1.656 (6.6)	1.929 (7.38)	1.742 (6.87)
	H	1.439 (6.69)****[d]	1.682 (7.26)****	1.487 (6.49)****	1.623 (7.04)****
	R	0.134 (56.21)	0.134 (56.24)	0.134 (56.25)	0.134 (56.24)
TW	log$\mathcal{L}$	1564	1562	1557	1559
	parameters	29	29	29	29
	AIC	-3070	-3067	-3057	-3059
	G	0.49 (5.23)	0.53 (5.62)	0.657 (6.85)	0.589 (6.09)
	H	0.492 (5.67)****	0.464 (5.39)****	0.348 (4.31)***	0.401 (4.76)***
	R	0.198 (60.13)	0.198 (60.11)	0.199 (60.1)	0.199 (60.11)
HD	log$\mathcal{L}$	6381	6363	6371	6370
	parameters	28	28	28	28
	AIC	-12706	-12669	-12686	-12684
	G	1.364 (5.48)	2.291 (8.48)	1.63 (6.2)	1.994 (7.78)
	H	1.932 (8.04)****	1.194 (5.46)****	1.756 (7.18)****	1.406 (6.42)****
	R	0.054 (58.81)	0.054 (58.78)	0.054 (58.8)	0.054 (58.78)

[a] Variance component estimates reported for additive main effects (G) and epistatic interactions (H) are the ratios of the actual variance component to the residual variance component for ease of comparison.
[b] The variance component divided by their respective standard errors are shown in parentheses.
[c] The residual variance components, R, are the actual estimates from the centered and scaled data (refer to Santantonio *et al.* (2018) for scaling coefficients).
[d] *, **, ***, **** denote p-values of $p < 0.05$, $p < 0.01$, $p < 0.001$, $p < 10^{-6}$, respectively for the likelihood ratio test to determine if the epistatic variance component is zero.

Table S15 Prediction accuracies of two additional samples of Within (Within2, Within3) and Across (Across2, Across3) genome marker sets, for both $\{-1,1\}$ and $\{0,1\}$ marker coding using LAVHAE marker orientation.

LAVHAE	Within2_{01}	Within3_{01}	Across2_{01}	Across3_{01}	Within2_{-11}	Within3_{-11}	Across2_{-11}	Across3_{-11}
GY	0.600	0.599	0.600	0.600	0.620	0.624	0.623	0.618
PH	0.573	0.569	0.566	0.570	0.655	0.640	0.634	0.644
TW	0.522	0.524	0.518	0.518	0.604	0.581	0.592	0.585
HD	0.683	0.673	0.676	0.679	0.727	0.715	0.718	0.724