

## SUPPLEMENTARY MATERIALS

Santantonio, N., Jannink, J., Sorrells, M. 2018. A low resolution epistasis mapping approach to identify chromosome arm interactions in allohexaploid wheat. G3.

**Table S1** Table of centromere positions for the 21 chromosomes of hexaploid wheat based on the RefSeq v1.0 of ‘Chinese Spring’ (IWGSC 2018). These positions were provided by the IWGSC (IWGSC, personal communication, March 1, 2017).

Chromosome	Length <sup>a</sup>	Start <sup>b</sup>	End <sup>c</sup>	Single gap (T/F) <sup>d</sup>
1A	594,102,056	213,545,945	213,546,046	T
2A	780,798,557	340,034,816	340,034,917	T
3A	750,843,639	319,010,276	319,010,377	T
4A	744,588,157	265,465,435	343,405,303	F
5A	709,773,743	253,779,933	253,780,034	T
6A	618,079,260	285,321,675	285,321,776	T
7A	736,706,236	359,432,051	359,432,152	T
1B	689,851,870	236,742,047	236,742,148	T
2B	801,256,715	349,410,174	349,410,275	T
3B <sup>e</sup>	830,829,764	344,402,169	345,017,442	F
4B	673,617,499	319,324,823	319,324,924	T
5B	713,149,757	198,851,987	218,709,746	F
6B	720,988,478	325,245,204	325,245,305	T
7B	750,620,385	296,411,983	296,412,084	T
1D	495,453,186	172,519,511	172,519,612	T
2D	651,852,609	268,023,149	268,023,250	T
3D	615,552,423	242,690,774	242,690,875	T
4D	509,857,067	185,780,323	185,780,424	T
5D	566,080,677	188,798,562	188,798,663	T
6D	473,592,718	214,085,311	214,085,412	T
7D	638,686,055	339,371,184	339,371,285	T

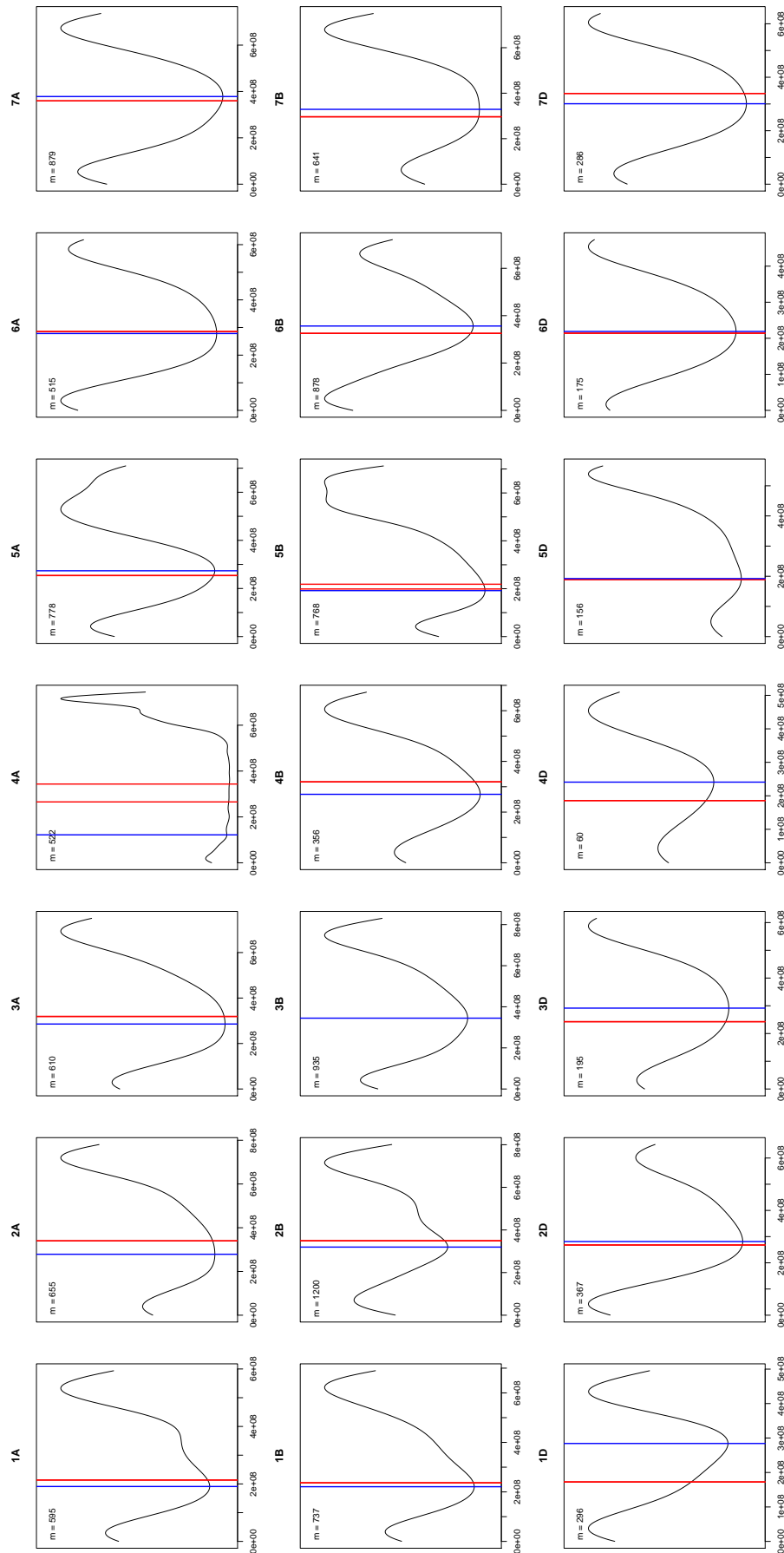
<sup>a</sup> Total chromosome length

<sup>b</sup> Centromere start address

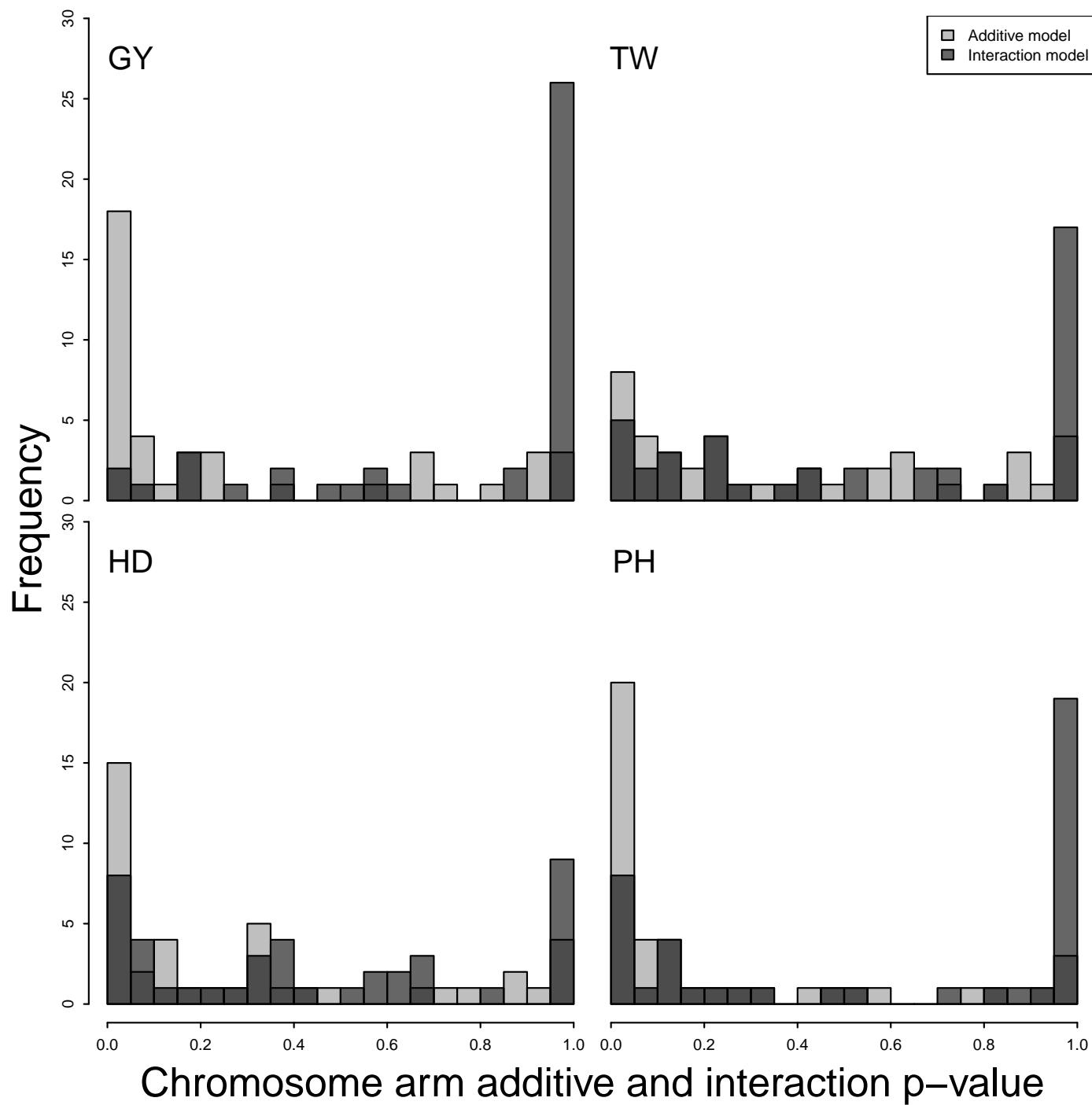
<sup>c</sup> Centromere end address

<sup>d</sup> Single gap is a boolean indicator referring to whether a clear position was determined for the centromere of each chromosome as indicated by the IWGSC (personal communication, March 1, 2017). The number of markers, *m*, used to estimate the density is shown for each chromosome.

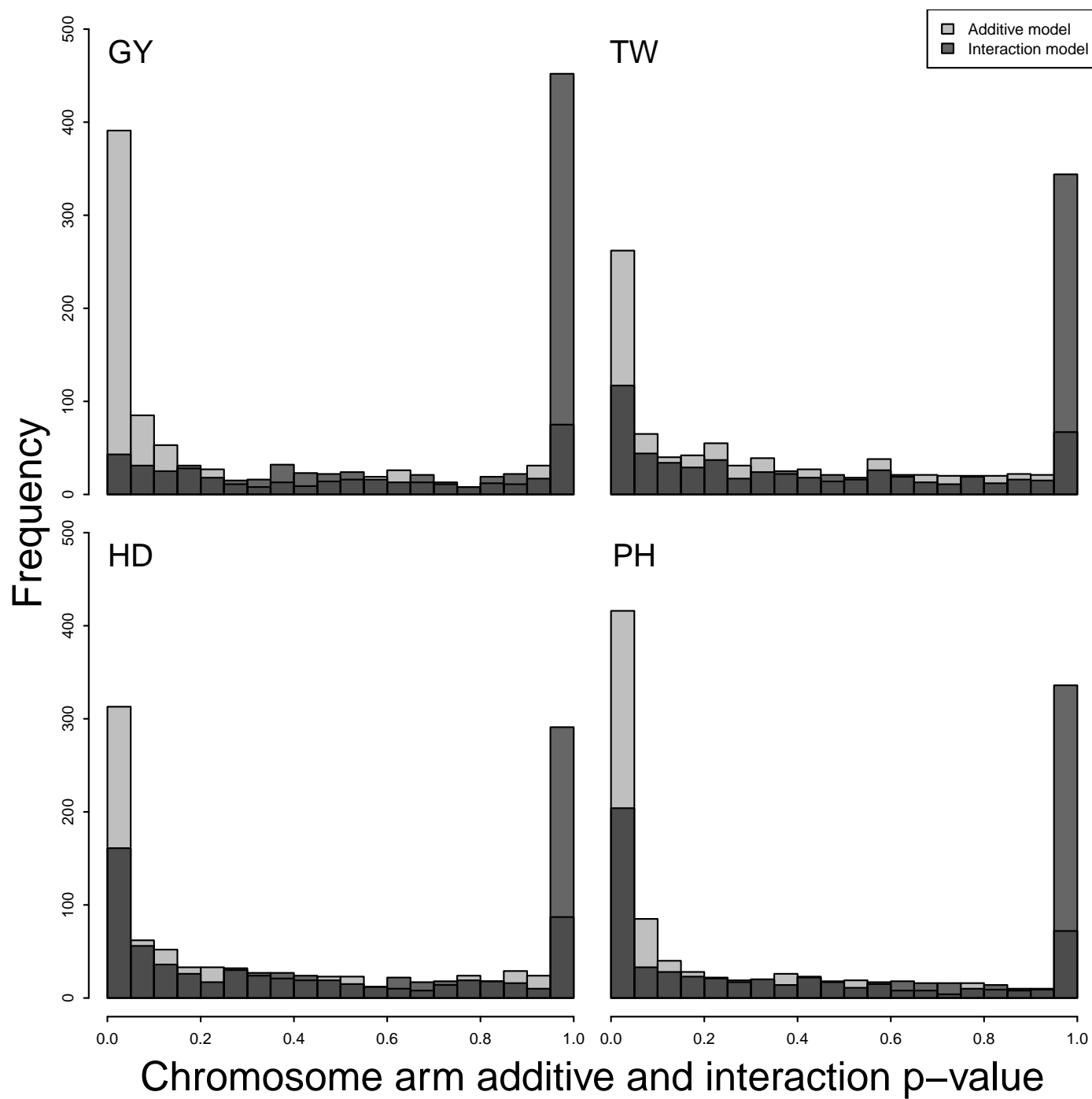
<sup>e</sup> The chromosome 3B centromere position was estimated using a kernel density estimate of GBS marker positions on 3B.



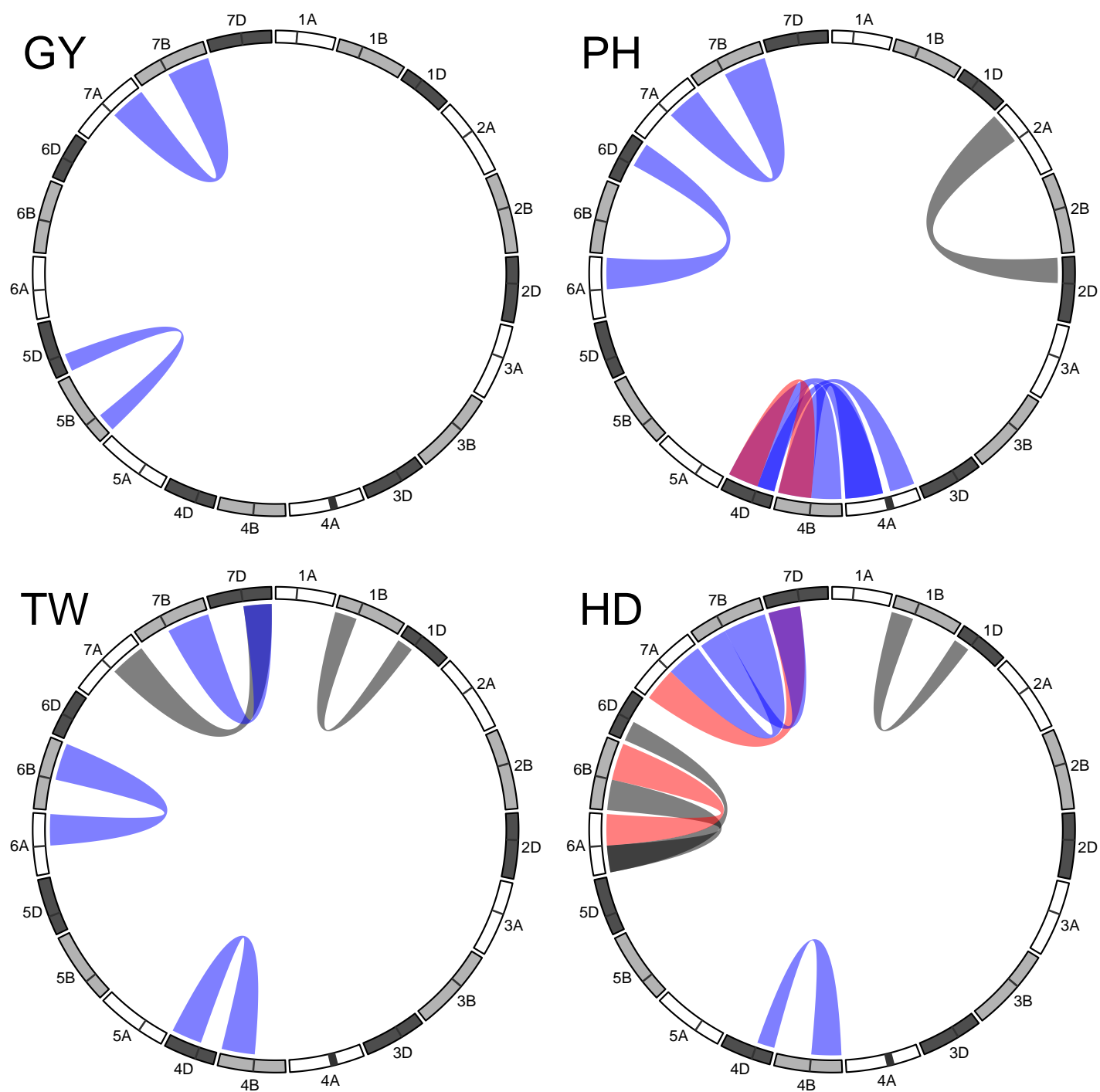
**Figure S1** Kernel density estimation of GBS marker distribution across the 21 chromosomes of wheat. Red lines indicate the centromere interval provided by IWGSC (per-sonal communication, March 1, 2017), and blue line indicate the centromere interval estimate based on the first derivative of the density estimate. No interval was provided by the IWGSC for chromosome 3B



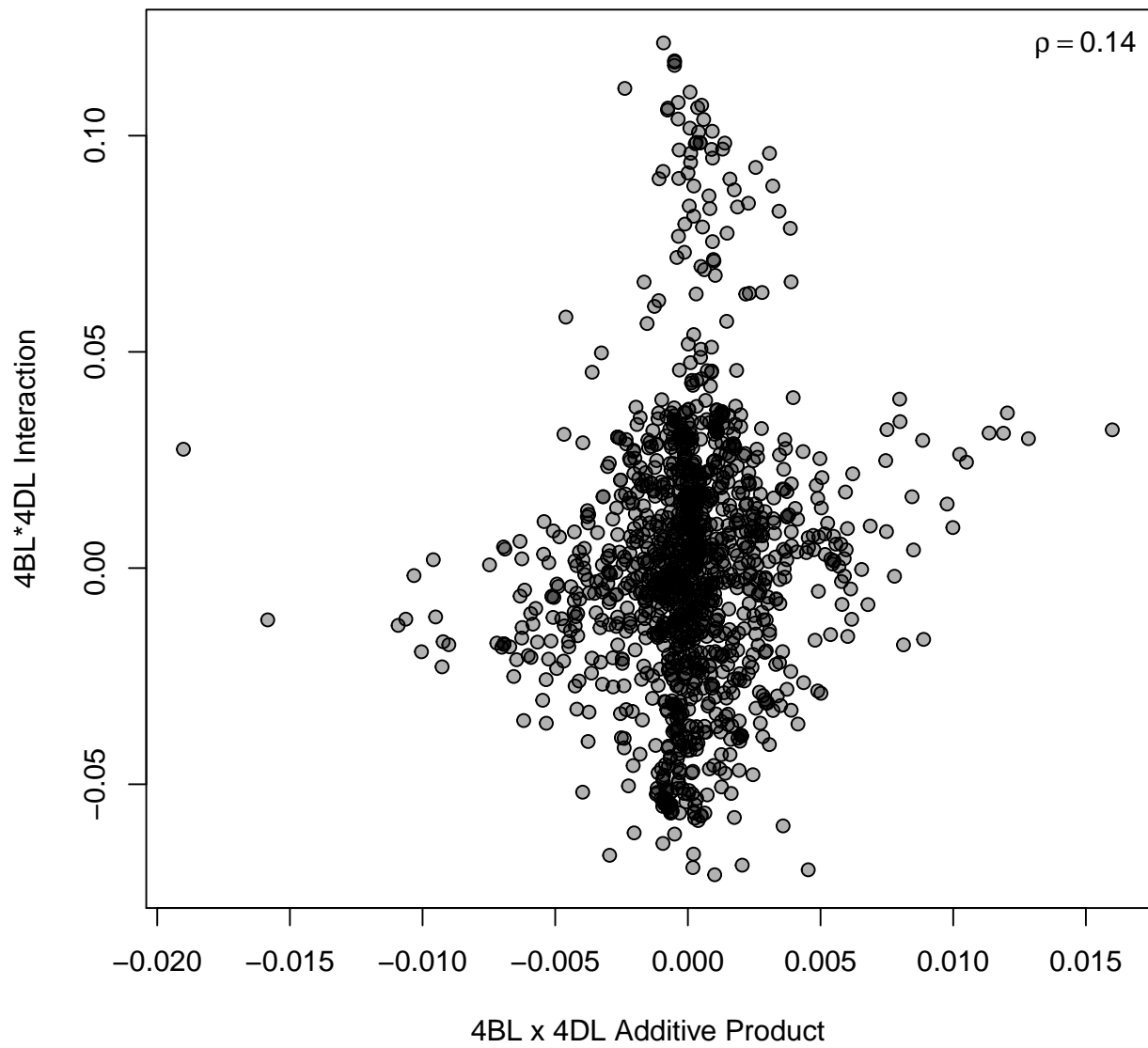
**Figure S2** Distribution of p-values for 42 homeologous chromosome arm pair models for four traits, GY, TW, PH and HD. The p-value from the likelihood ratio test for the additive chromosome arm model is plotted in light gray, whereas the p-value from the the interaction model test is shown in dark gray.



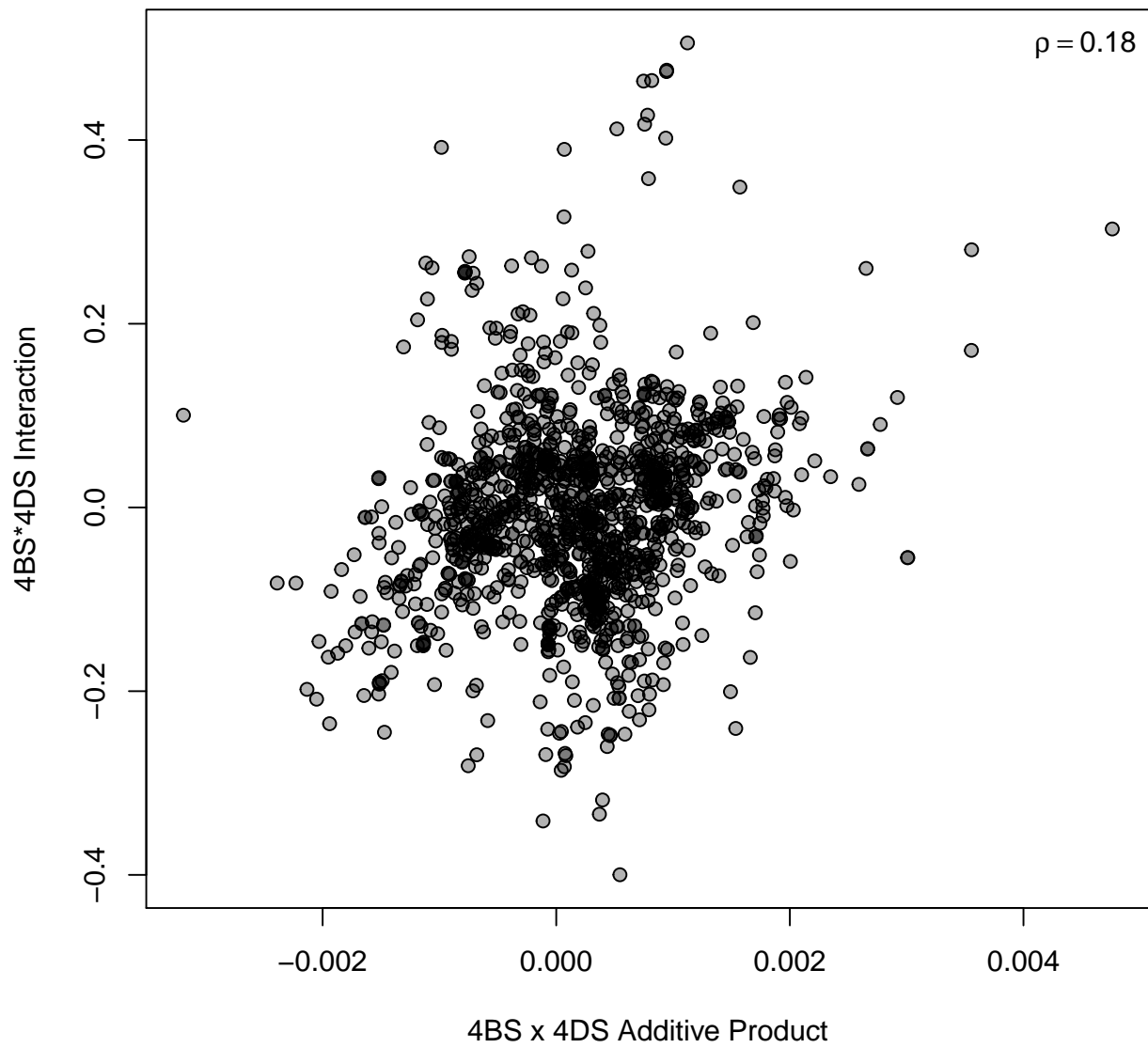
**Figure S3** Distribution of p-values for all 861 possible chromosome arm pair models for four traits, GY, TW, PH and HD. The p-value from the likelihood ratio test for the additive chromosome arm model is plotted in light gray, whereas the p-value from the the interaction model test is shown in dark gray.



**Figure S4** Homeologous chromosome arm interactions significant at  $p < 0.05$ . Blue and red bridges indicate interactions with a significant positive or negative correlation between the product of the additive effects and their interaction effect, respectively. Black bridges indicate significant interactions that did not have a significant correlation between additive products and the interaction effect.



**Figure S5** Interaction effect of chromosome 4BL by 4DL plotted against the product of the additive effects for 4BL and 4DL for TW.  $\rho$  indicates the Pearson correlation coefficient.



**Figure S6** Interaction effect of chromosome 4BS by 4DS plotted against the product of the additive effects for 4BS and 4DS for PH.  $\rho$  indicates the Pearson correlation coefficient.

■ **Table S2** Table of chromosome arm interactions for all four traits with interaction terms significant at a Bonferroni correction threshold of  $0.05/861 = 5.8 \times 10^{-5}$ . The proportion of genetic variance attributed to each arm and their corresponding interaction are shown with statistical significance from a nested likelihood ratio test.

Trait	arm <sub>i</sub>	arm <sub>j</sub>	$(h^2_{\text{arm}_i}, h^2_{\text{arm}_j})^a$	$h^2_{\text{arm}_i \times \text{arm}_j}$	$\rho^b$
PH	1AL	2AL	(0.039, 0.06)**** <sup>c</sup>	0.09****	0.37***
PH	1AL	3AS	(0.065, 0.011)**	0.076****	−0.01
PH	1AL	7AL	(0.063, 0.000)*	0.067****	0.35***
PH	1AL	4BS	(0.042, 0.024)**	0.073****	0.08**
PH	1AL	4BL	(0.066, 0.012)***	0.086****	−0.05
PH	1AL	7BL	(0.091, 0.043)***	0.059****	0.01
PH	1AL	2DS	(0.079, 0.094)****	0.065****	0.18***
PH	1AL	4DS	(0.048, 0.037)****	0.064****	−0.04
PH	1AL	4DL	(0.070, 0.002)**	0.048****	0.05
PH	2AL	7AL	(0.040, 0.000)**	0.056****	0.27***
PH	2AL	4BS	(0.060, 0.032)***	0.090****	−0.17***
PH	2AL	2DS	(0.036, 0.097)****	0.061****	−0.17***
PH	2AL	4DL	(0.039, 0.000)***	0.069****	0.23***
PH	3AS	6AS	(0.015, 0.069)**	0.084****	−0.22***
PH	3AS	6AL	(0.000, 0.086)**	0.070****	0.35***
PH	3AS	7AL	(0.008, 0.000)	0.060****	0.27***
PH	3AS	7BL	(0.001, 0.038)*	0.068****	0.01
PH	3AS	4DS	(0.020, 0.033)****	0.057****	−0.09**
PH	3AL	2DS	(0.004, 0.068)**	0.042****	−0.11***
PH	3AL	4DS	(0.008, 0.033)****	0.050****	−0.17***
PH	3AL	4DL	(0.002, 0.010)	0.023****	−0.07**
PH	6AS	7AL	(0.083, 0.000)**	0.069****	0.4***
PH	6AS	1BS	(0.078, 0.011)***	0.100****	0.02
PH	6AS	4BS	(0.054, 0.000)***	0.130****	−0.01
PH	6AS	4DS	(0.160, 0.042)****	0.052****	0.03
PH	6AS	4DL	(0.087, 0.000)**	0.073****	0.23***
PH	6AS	6DL	(0.069, 0.0077)**	0.084****	0.09**
PH	7AL	4BL	(0.000, 0.029)*	0.058****	0.29***
PH	7AL	2DS	(0.001, 0.064)**	0.054****	0.11***
PH	7AL	6DL	(0.000, 0.016)	0.051****	0.31***
PH	1BS	2DS	(0.000, 0.110)***	0.062****	0.22***
PH	1BS	4DS	(0.000, 0.035)****	0.042****	0.26***
PH	1BS	4DL	(0.023, 0.009)	0.041****	0.30***
PH	2BS	4BS	(0.027, 0.053)*	0.084****	−0.11***
PH	2BS	4DS	(0.038, 0.032)**** <sup>d</sup>	0.069****	−0.12***
PH	2BL	4DS	(0.200, 0.029)****	0.052****	0.13***
PH	4BS	4DS	(0.002, 0.031)****	0.049****	0.18***
PH	4BS	4DL	(0.000, 0.000)	0.056****	0.00

<sup>a</sup>  $h^2$  represents the proportion of the chromosome arm additive or interaction variance component estimates to the total genetic variance.

<sup>b</sup>  $\rho$  indicates the correlation between the product of the additive arm effects and their interaction effect with correlation coefficients significantly different from zero indicated by asterisks. If only one additive effect had a non-zero variance, the correlation coefficient shown is the correlation between the additive effect with the non-zero variance and the interaction effect.

<sup>c</sup> \*, \*\*, and \*\*\*\* correspond to p-values < 0.05, 0.01, 0.001, and a Bonferroni correction of  $0.05/861 = 5.8 \times 10^{-5}$ , respectively.



■ **Table S3** Continuation of Table S2 of significant chromosome arm interactions.

Trait	arm <sub>i</sub>	arm <sub>i'</sub>	( $h^2_{\text{arm}_i}, h^2_{\text{arm}_{i'}}$ ) <sup>a</sup>	$h^2_{\text{arm}_i \times \text{arm}_{i'}}$	$\rho^b$
PH	4BS	6DL	(0, 0.021)	0.11**** <sup>c</sup>	0.070**
PH	4BL	4DS	(0.063, 0.029)****	0.051****	−0.52***
PH	4BL	4DL	(0.048, 0.003)*	0.058****	−0.65***
PH	7BL	2DS	(0.030, 0.090)***	0.071****	0.00
PH	7BL	4DL	(0.031, 0.001)*	0.094****	−0.12***
PH	2DS	3DS	(0.058, 0.047)****	0.034****	0.07**
PH	2DS	4DS	(0.130, 0.038)****	0.046****	0.07**
PH	2DS	4DL	(0.110, 0.006)***	0.031****	0.04
PH	2DS	5DS	(0.080, 0.003)**	0.031****	0.11***
PH	4DS	6DL	(0.031, 0.002)****	0.036****	0.08**
PH	4DL	6DL	(0.002, 0.011)	0.026****	−0.38***
TW	1AL	1BS	(0.015, 0.000)	0.130****	0.23***
TW	1AL	7DL	(0.015, 0.061)	0.097****	−0.13***
TW	2AL	3BS	(0.013, 0.000)	0.130****	0.19***
TW	2AL	7DL	(0.032, 0.063)	0.110****	0.00
TW	3AL	7DL	(0.019, 0.072)	0.085****	0.01
TW	4AL	7DL	(0.054, 0.053)*	0.110****	−0.11***
TW	5AL	1BS	(0.031, 0.000)	0.150****	0.26***
TW	5AL	7DL	(0.026, 0.026)*	0.140****	0.06*
TW	6AS	7DL	(0.000, 0.058)	0.110****	0.04
TW	7AS	7DL	(0.007, 0.059)	0.090****	0.01
TW	7AL	7DL	(0.019, 0.030)	0.140****	−0.04
TW	1BS	7DL	(0.000, 0.018)	0.180****	0.18***
TW	2BL	7DL	(0.004, 0.063)	0.110****	−0.21***
TW	3BS	7DL	(0.000, 0.071)	0.120****	0.11***
TW	3BL	7DL	(0.003, 0.054)	0.160****	0.11***
TW	6BS	7DL	(0.000, 0.056)	0.093****	0.08**
TW	7DS	7DL	(0.000, 0.057)	0.088****	−0.02
HD	6AS	7AS	(0.004, 0.008)	0.098****	−0.03
HD	6AS	1BS	(0.007, 0.000)	0.058****	0.11***
HD	6AS	3BS	(0.012, 0.064)***	0.082****	−0.12***
HD	6AS	5BS	(0.004, 0.000)	0.051****	0.11***
HD	6AS	7BL	(0.008, 0.033)***	0.075****	0.06*
HD	7AS	7BL	(0.009, 0.037)****	0.073****	−0.05
HD	7AS	1DS	(0.013, 0.000)	0.053****	−0.09**
HD	1BS	4DS	(0.000, 0.002)	0.044****	0.00
HD	1BL	4DS	(0.000, 0.004)	0.035****	0.02
HD	7BL	3DS	(0.036, 0.002)***	0.061****	0.03
HD	7BL	4DS	(0.031, 0.003)***	0.053****	0.05*
HD	7BL	6DL	(0.035, 0.010)***	0.056****	−0.15***
HD	3DS	4DS	(0.000, 0.003)	0.029****	0.00

<sup>a</sup>  $h^2$  represents the proportion of the chromosome arm additive or interaction variance component estimates to the total genetic variance.

<sup>b</sup>  $\rho$  indicates the correlation between the product of the additive arm effects and their interaction effect with correlation coefficients significantly different from zero indicated by asterisks. If only one additive effect had a non-zero variance, the correlation coefficient shown is the correlation between the additive effect with the non-zero variance and the interaction effect.

<sup>c</sup> \*, \*\*, and \*\*\*\* correspond to p-values < 0.05, 0.01, 0.001, and a Bonferroni correction of 0.05/861 = 5.8 × 10<sup>−5</sup>, respectively.

■ **Table S4** Counts of significant homeologous chromosome arm interactions by arm and traits.

Chromosome Arm	GY	PH	TW	HD	Total
1AL	0	9	2	0	11
1BL	0	0	0	1	1
1BS	0	4	3	2	9
1DS	0	0	0	1	1
2AL	0	5	2	0	7
2BS	0	2	0	0	2
2BL	0	1	1	0	2
2DS	0	10	0	0	10
3AS	0	6	0	0	6
3AL	0	3	1	0	4
3BS	0	0	2	1	3
3BL	0	0	1	0	1
3DS	0	1	0	2	3
4AL	0	0	1	0	1
4BS	0	7	0	0	7
4BL	0	4	0	0	4
4DS	0	11	0	4	15
4DL	0	10	0	0	10
5AL	0	0	2	0	2
5BS	0	0	0	1	1
5DS	0	1	0	0	1
6AS	0	7	1	5	13
6AL	0	1	0	0	1
6BS	0	0	1	0	1
6DL	0	5	0	1	6
7AS	0	0	1	3	4
7AL	0	7	1	0	8
7BL	0	4	0	5	9
7DS	0	0	1	0	1
7DL	0	0	14	0	14
Total	0	98	34	26	158