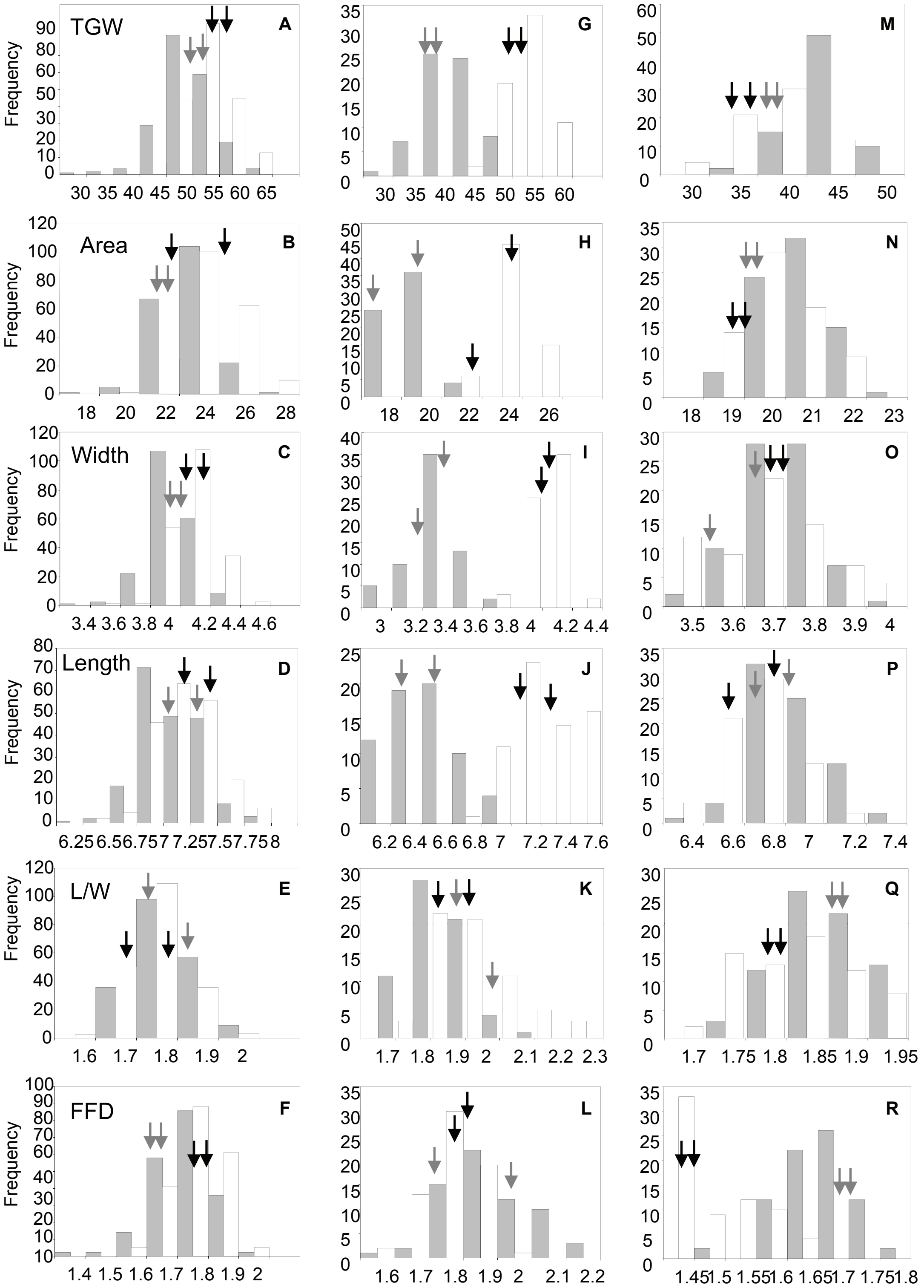
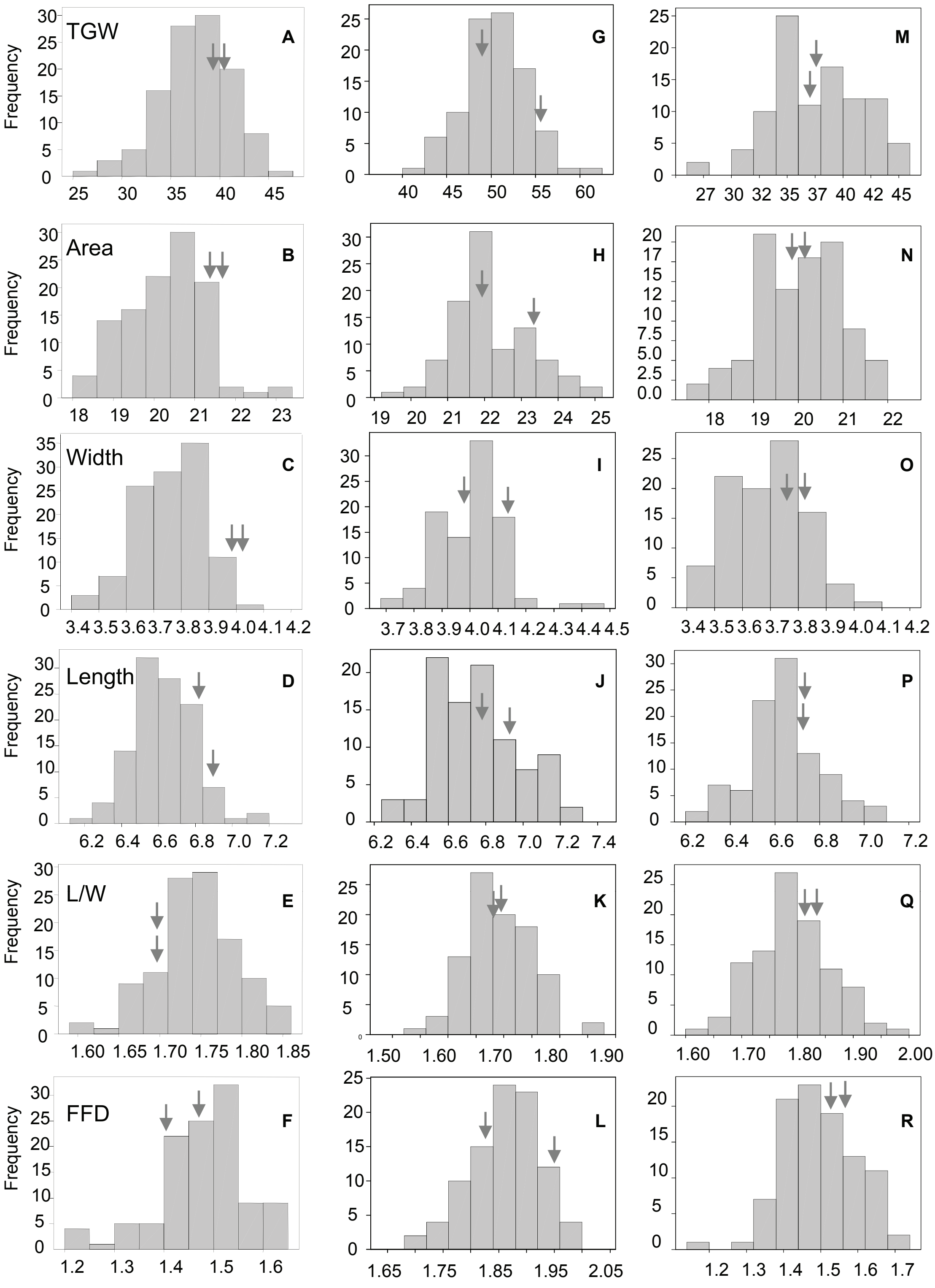
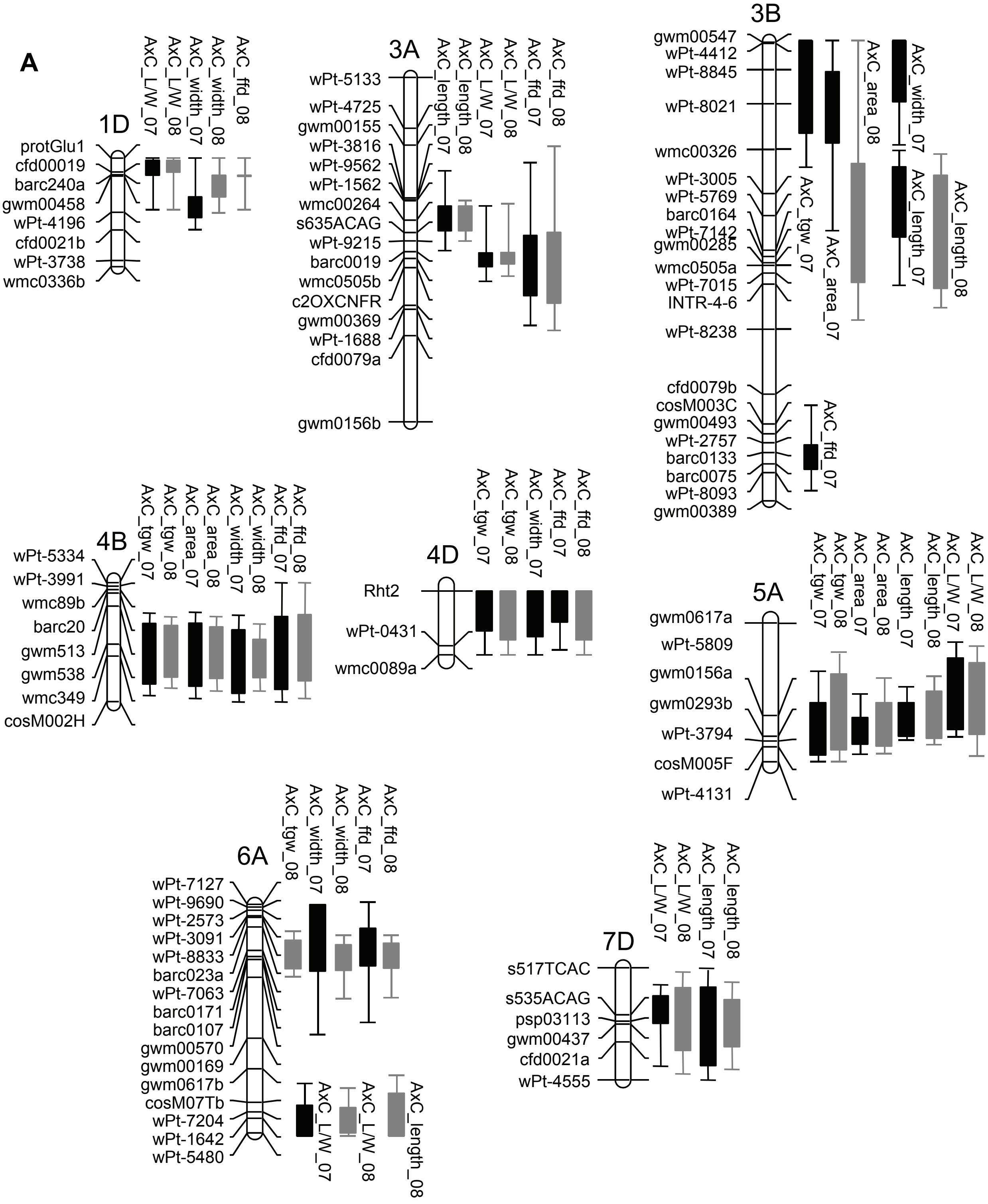


Supplemental Figure 1. Frequency distributions of the morphometric traits for AxC, BxS, and SxS. (A-F) Avalon x Candenza, (G-L) Beaver x Soissons, and (M-R) Shango x Shamrock. Mean parental values for each year are indicated by either a grey or black arrow for year 1 (grey bar) or 2 (white bar), respectively. Trait values (x-axis) are untransformed and expressed in g (TGW), mm (width, length) and mm^2 (area).

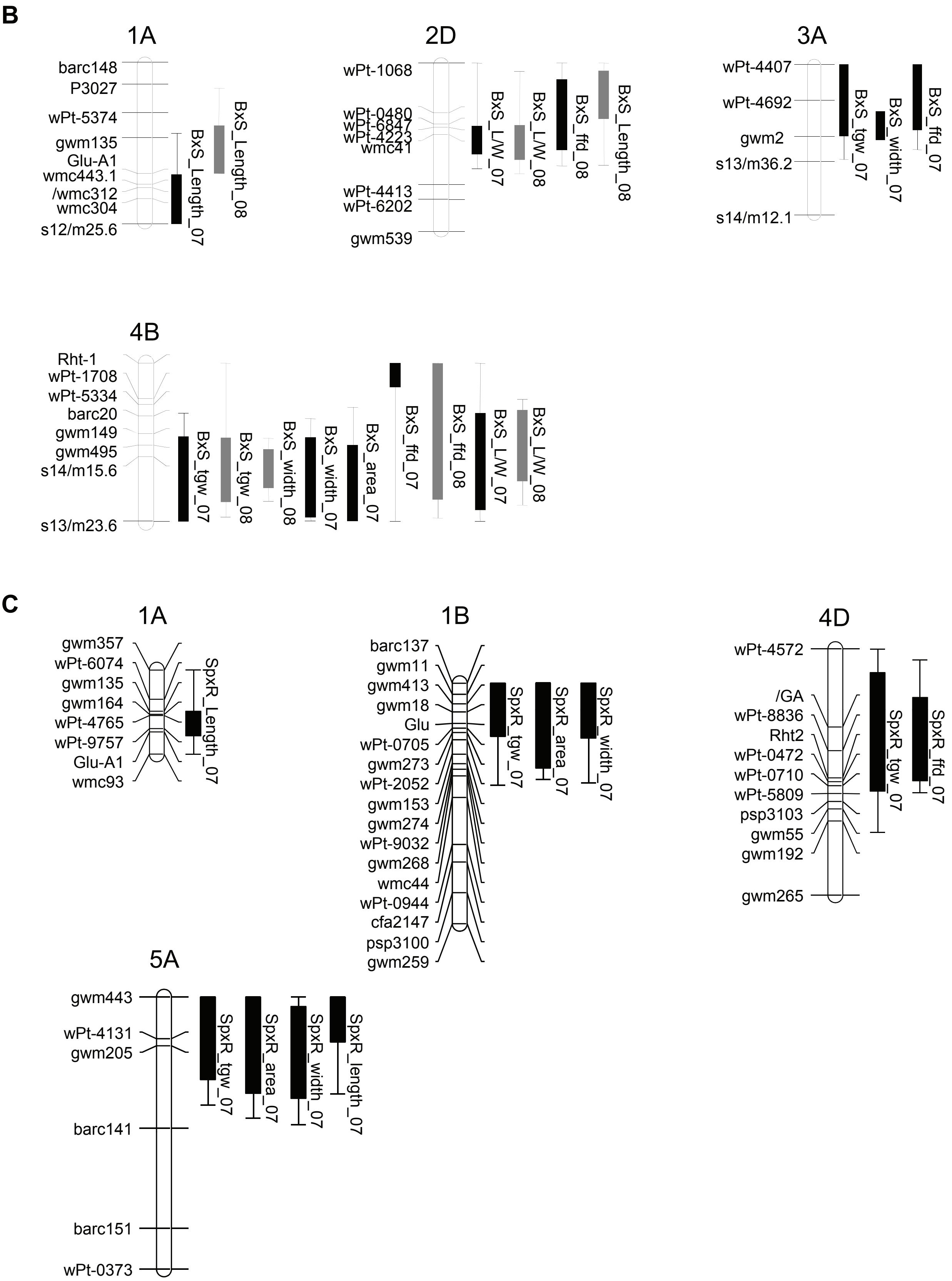


Supplemental Figure 2. Frequency distributions of the morphometric traits for Spark x Rialto, Savannah x Rialto, and Malacca x Charger. (A-F) Spark x Rialto, (G-L) Savannah x Rialto, and (M-R) Malacca x Charger. Mean parental values are indicated by a grey arrow. Trait values (x-axis) are untransformed and expressed in g (TGW), mm (width, length) and mm^2 (area).

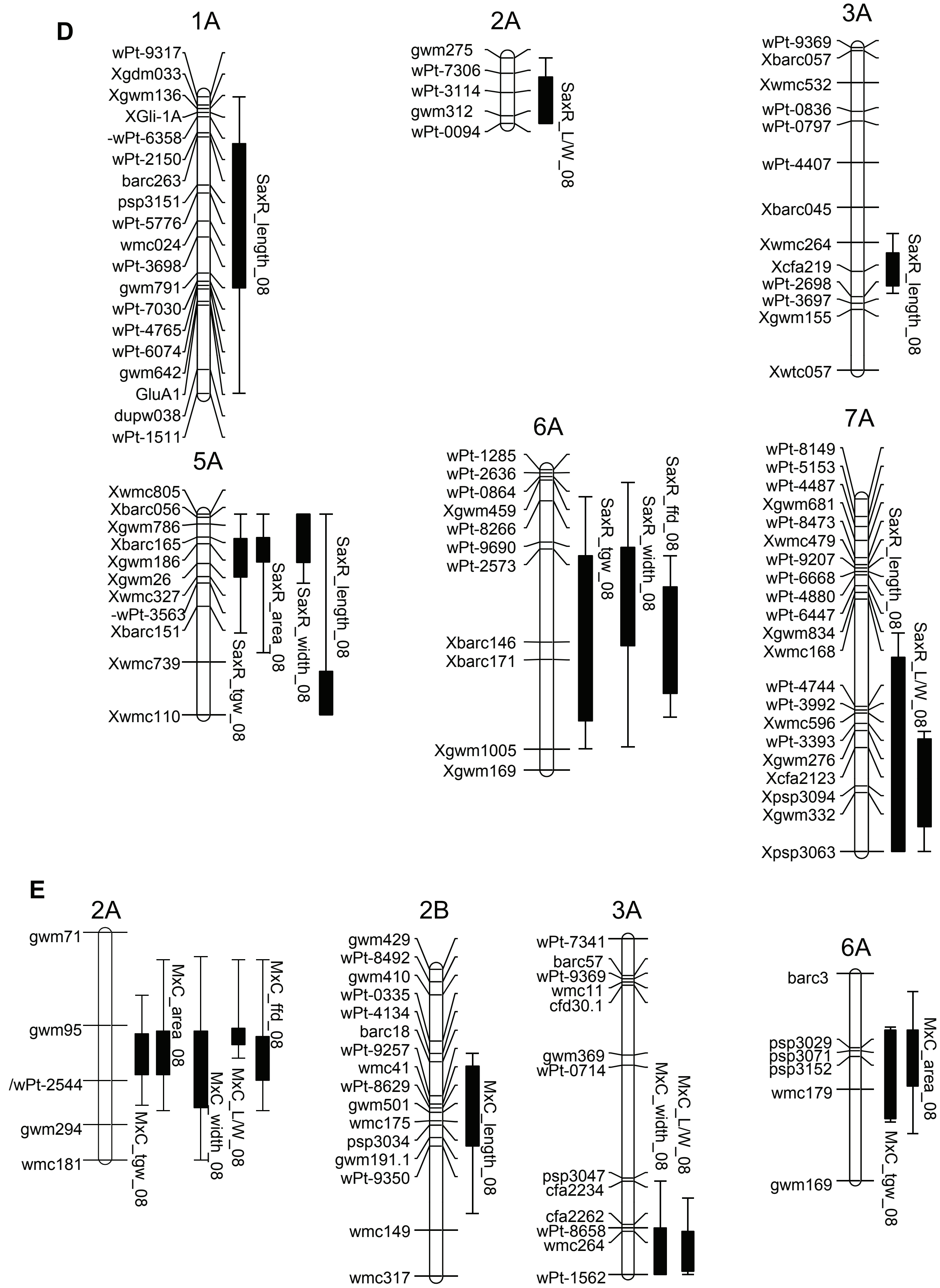


Supplemental Figure 3. QTL identified for the morphometric parameters in the six mapping populations. (A) AxC, (B) BxS, (C) SpxR, (D) SaxR, (E) MxC, and (F) SxS mapping populations. QTL are projected on the corresponding linkage maps with a solid bar and a closed line representing 1-LOD and 2-LOD mapping intervals, respectively. The numerical suffix at the end of the QTL name denotes the year of trial (i.e. 07 or 08).

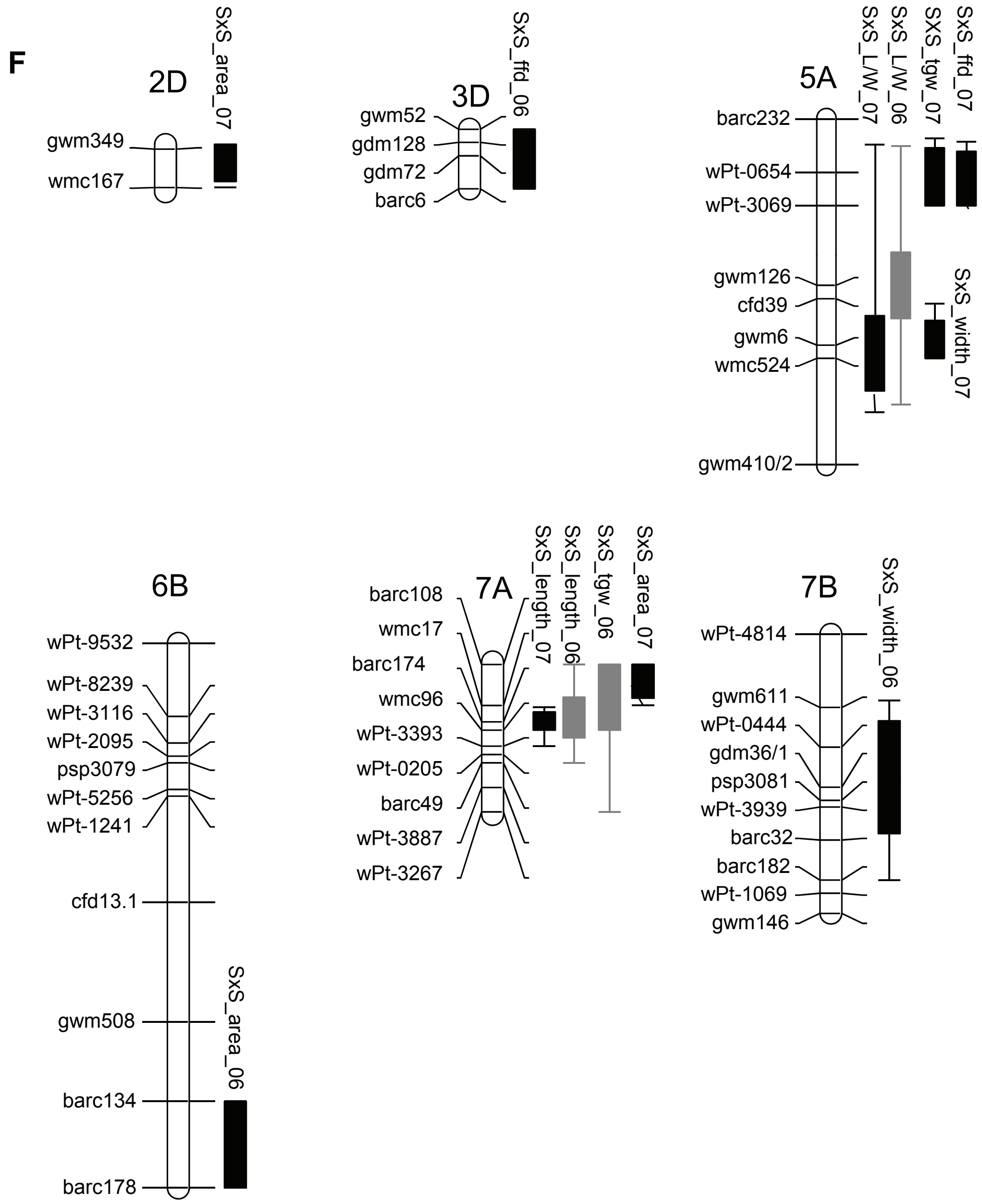
Supplemental Figure 3 cont.

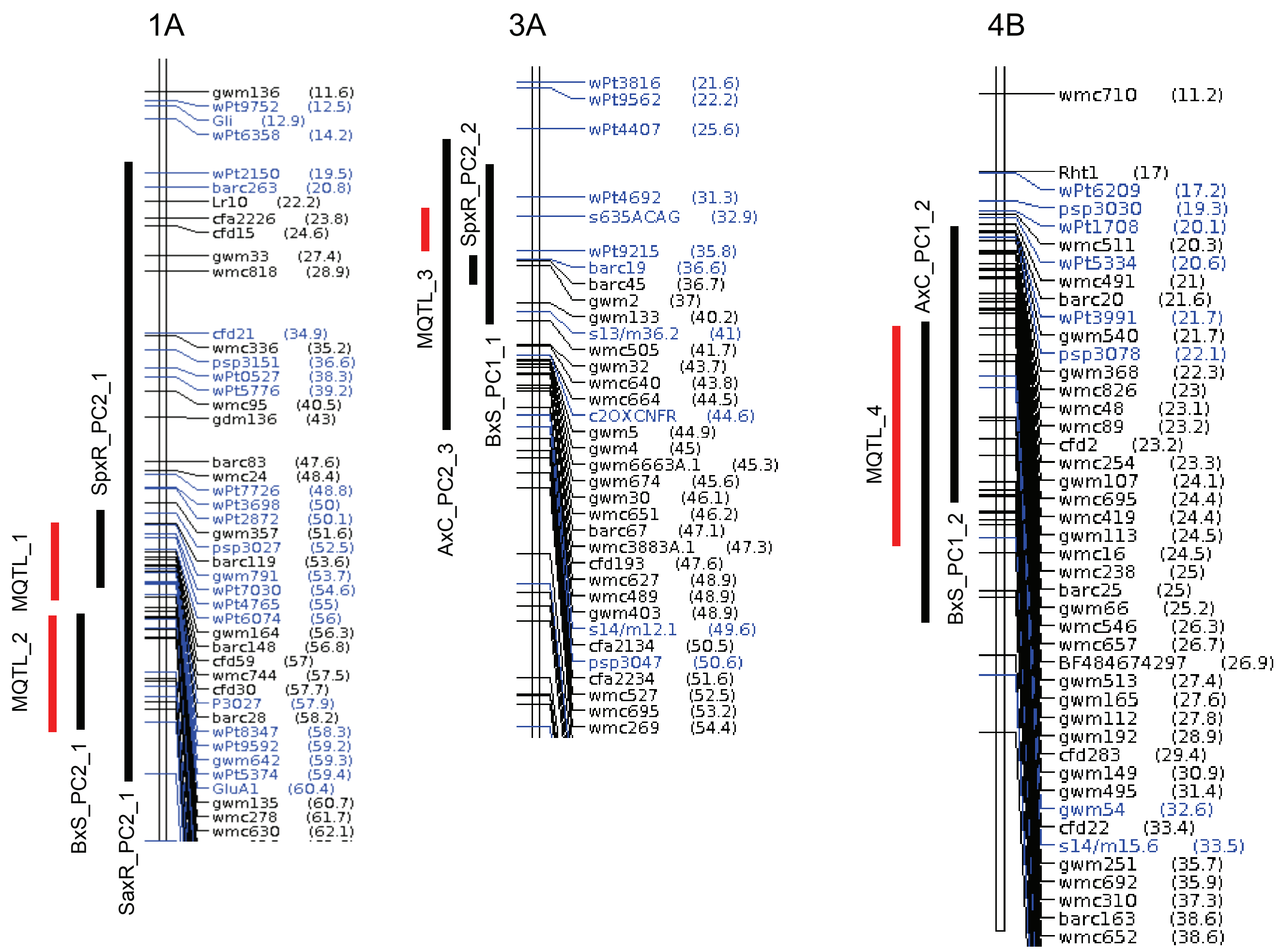


Supplemental Figure 3 cont.



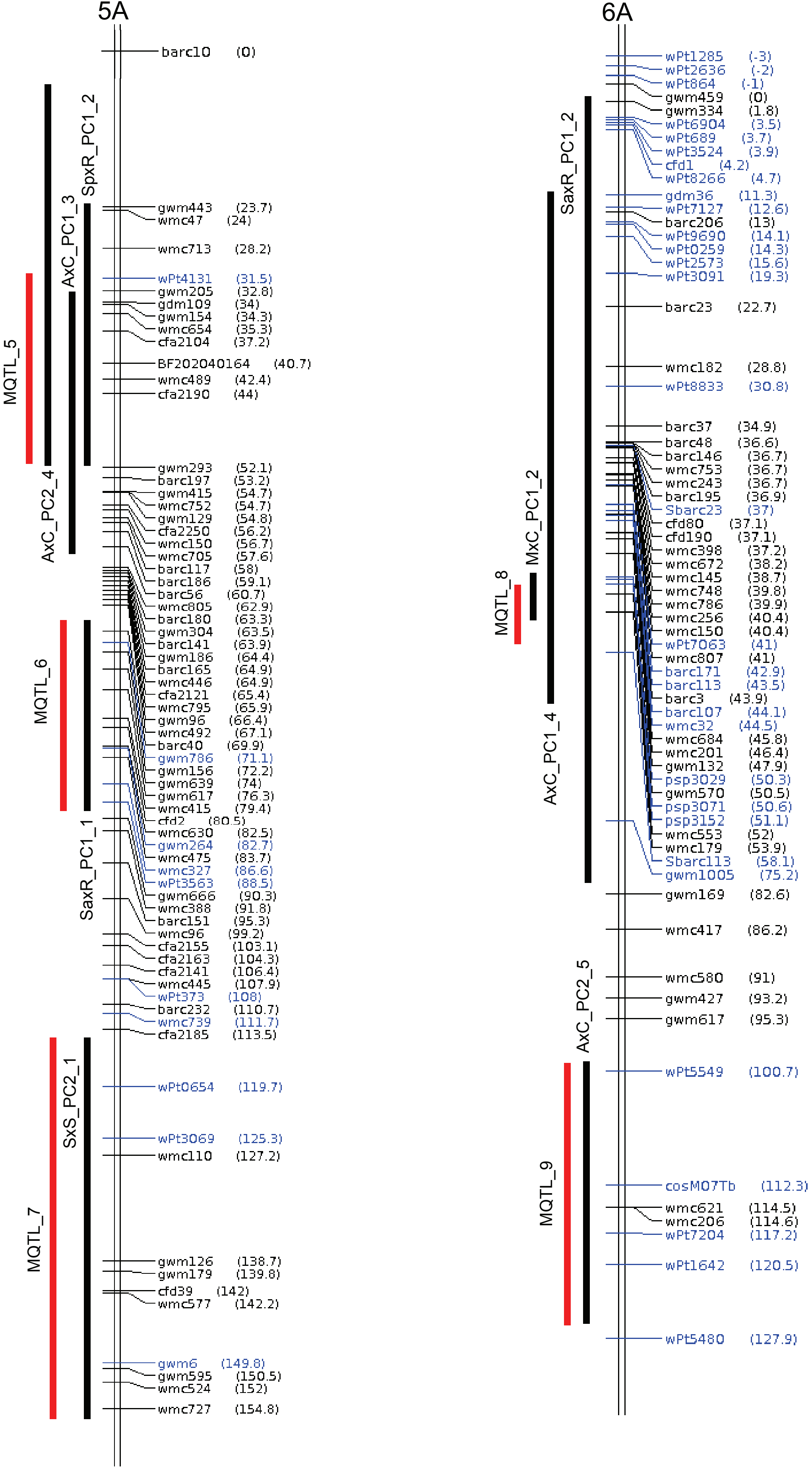
Supplemental Figure 3 cont.

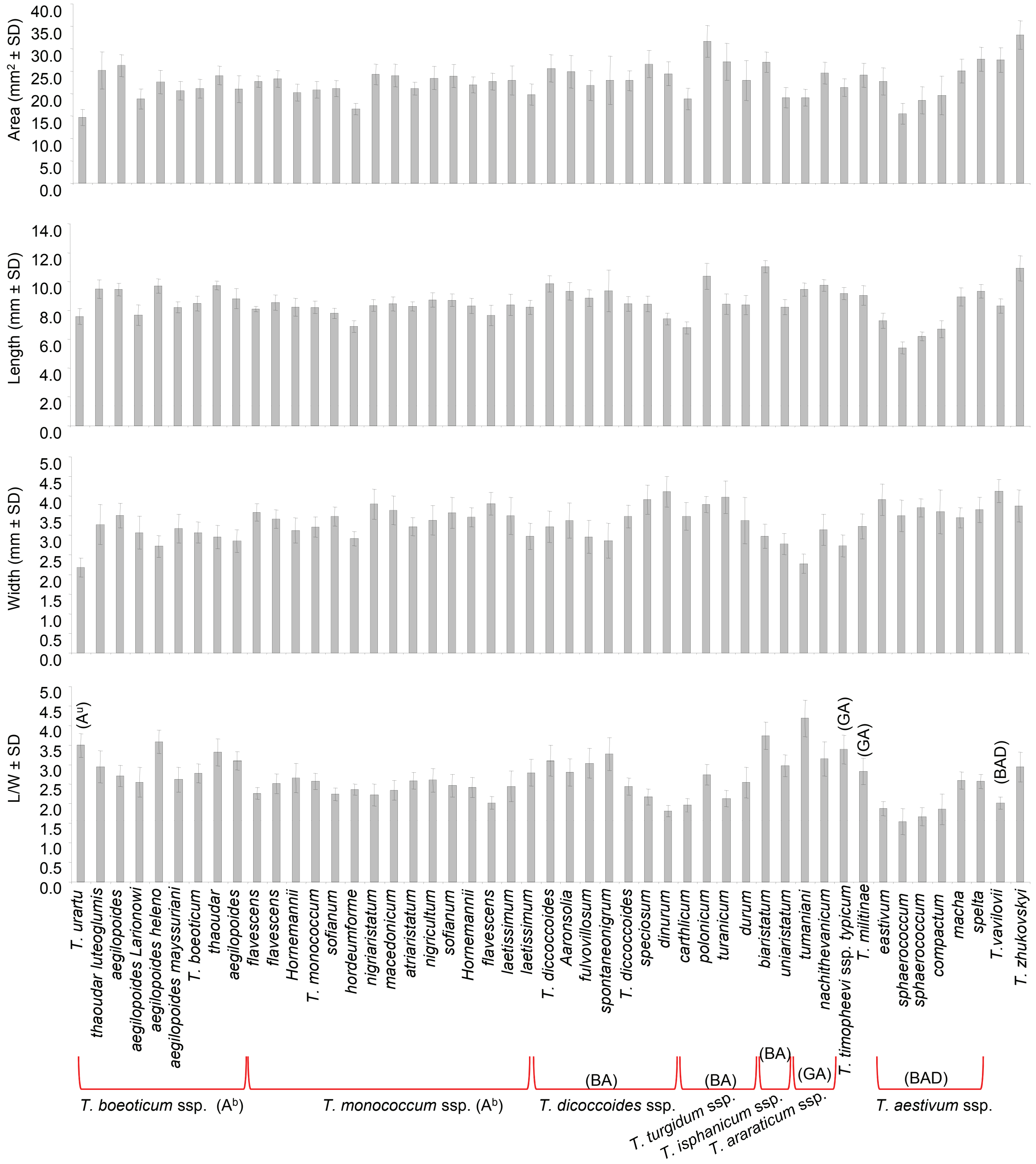




Supplemental Figure 4. Common genetic components for grain size and shape in the DH mapping populations. Schematic representation of co-located QTL identified for PC1 and PC2 on five main chromosomes, i.e. 1A, 3A, 4B, 5A, 6A, and their corresponding meta-QTL. QTL for each PC and DH population are depicted as black boxes. Meta-QTL are depicted as red boxes. The length of each QTL denotes 2-LOD confidence intervals on the wheat consensus map.

Supplemental Figure 4 cont.





Supplemental Figure 5. Morphometric traits for *Triticum* species. Values represent the mean of 20-30 grains ± standard deviation (SD). The genome type of each species is given in parenthesis. The species taxonomy follows the classification appearing in the John Innes Centre Triticeae Collection (http://data.jic.bbsrc.ac.uk/cgi-bin/germplasm/triticeae/). Entries with the same species name represent different accession number (see Supplemental Table 7).

Supplemental Table 1. Trait variation and heritability in the parental lines and DH mapping populations. (A) AxC, (B) BxS, (C) SxS, (D) SpxR, (E) SaxR, (F) MxC. Values highlighted in bold are significant different at $p<0.001$.

		year 1				year 2				
		mean ± SD				mean ± SD				
A		**Beaver**	**Soisson**	**DH (2007)**	**range (min-max)**	**Beaver**	**Soisson**	**DH (2008)**	**range (min-max)**	**h^2**
Beaver x Soisson	TGW (g)	40.4	40.9	40 ± 4.7	23 (26-49)	54.0	53.5	51.53 ± 3.81	21.6 (38.7-60.3)	0.83
	AREA (mm^2)	**19.6**	**17.7**	18.3 ± 1.0	4.6 (16-20.6)	**24**	**22.6**	23.2 ± 1	4.9 (20.7-25.6)	0.84
	WIDTH (mm)	3.4	3.3	3.3 ± 0.18	1 (2.7-3.7)	4.1	4.1	4.05 ± 0.13	0.6 (3.7-4.3)	0.86
	LENGTH (mm)	6.6	6.3	6.43 ± 0.23	0.9 (6-6.9)	7.3	7.1	7.225 ± 0.23	1 (6.7-7.7)	0.93
	L/W	**2.0**	**1.9**	1.95 ± 0.12	0.64 (1.7-2.4)	**1.8**	**1.7**	1.786 ± 0.0822	0.4 (1.6-2)	0.92
	FFD	1.8	2.0	1.9 ± 0.12	0.6 (1.5-2.1)	1.80	1.84	1.76 ± 0.089	0.6 (1.4-2)	0.78
B		**Shamrock**	**Shango**	**DH (2006)**	**range (min-max)**	**Shamrock**	**Shango**	**DH (2007)**	**range (min-max)**	**h^2**
Shamrock x Shango	TGW	41.6	42.7	43.2 ± 3.1	15.3 (34.0-49.3)	34.52	35.9	36.3 ± 4.1	19 (26.3-45.3)	0.58
	AREA	19.8	20.1	20.5 ± 0.86	4.2 (18.4-22.6)	19.3	19.8	19.9	3.8 (18.2-22.0)	0.61
	WIDTH	3.6	3.7	3.7 ± 0.1	0.5 (3.5-4.0)	3.7	3.7	3.7 ± 0.14	0.5 (3.5-4.0)	0.63
	LENGTH	6.8	6.9	6.9 ± 0.2	1.1 (6.3-7.4)	6.6	6.7	6.7 ± 0.17	0.7 (6.4-7.1)	0.82
	L/W	1.9	1.9	1.8 ± 0.06	0.3 (1.7-2.0)	1.8	1.8	1.8 ± 0.07	0.3 (1.7-2)	0.85
	FFD	1.7	1.7	1.7 ± 0.06	0.36 (1.47-1.83)	1.41	1.45	1.5 ± 0.1	0.526 (1.12-1.65)	0.52
C		**Avalon**	**Candenza**	**DH (2007)**	**range (min-max)**	**Avalon**	**Candenza**	**DH (2008)**	**range (min-max)**	**h^2**
Avalon x Cadenza	TGW	48.8	48.8	52.7 ± 4.7	27.7 (37.8-65.5)	54.4	52.3	49 ± 5.2	36.4 (28.6-65)	0.9
	AREA	23.4	22.4	22.5 ± 1.4	9.8 (16.8-26.6)	24.8	23.1	23.6 ± 1.4	7.9 (18.9-26.8)	0.93
	WIDTH	3.9	4.0	4.0 ± 0.2	1.1 (3.3-4.4)	4.1	4.2	4.1 ± 0.13	0.9 (3.6-4.5)	0.89
	LENGTH	**7.4**	**7.0**	7.1 ± 0.3	1.6 (6.2-7.8)	**7.5**	**7**	7.2 ± 0.3	1.5 (6.4-7.9)	0.95
	L/W	**1.9**	**1.8**	1.8 ± 0.08	0.4 (1.6-2.0)	**1.8**	**1.7**	1.7 ± 0.07	0.4 (1.6-2.0)	0.9
	FFD	1.69	1.74	1.7 ± 0.09	0.6 (1.4-2.0)	1.77	1.78	1.8 ± 0.08	0.5 (1.5-2.0)	0.83

Supplemental Table 1 cont.

D

		Spark	Rialto	DH (2007)	range (min-max)	h^2
Spark x Rialto	TGW	40.3	40.0	37.6 ± 3.66	18.62 (27-45.6)	0.9
	AREA	21.9	21.8	20.3 ± 0.97	5.2 (18.1-23.3)	0.93
	WIDTH	4.1	4.0	3.8 ± 0.12	0.6 (3.5-4.1)	0.89
	LENGTH	7.0	6.8	6.6 ± 0.18	1 (6.2-7.2)	0.95
	L/W	1.7	1.7	1.7 ± 0.05	0.2 (1.6-1.8)	0.9
	FFD	1.4	1.5	1.5 ± 0.09	0.4 (1.2-1.6)	0.83

E

		Rialto	Savannah	DH (2008)	range (min-max)	h^2
Savannah x Rialto	TGW	**48.3**	**55.7**	50.4 ± 3.60	19.4 (41.2-60.6)	0.90
	Area	21.9	23.3	22.2 ± 1.05	5.5 (25-19.5)	0.90
	Width	4.0	4.1	4.0 ± 0.11	0.7 (3.8-4.4)	0.84
	Length	6.7	6.9	6.7 ± 0.21	1.0 (6.25-7.25)	0.86
	L/W	1.7	1.7	1.7 ± 0.06	0.3 (1.6-1.9)	0.85
	FFD	**1.8**	**2.0**	1.9 ± 0.06	0.3 (1.7-2.0)	0.78

F

		Malacca	Charger	DH (2007)	range (min-max)	h^2
Malacca x Charger	TGW	37.8	37.0	37.49 ± 3.98	17.8 (26.8-44.5)	0.64
	Area	20.4	20.2	20 ± 0.91	4.3 (17.6-21.9)	0.52
	Width	3.8	3.7	3.7 ± 0.14	0.7 (3.4-4.1)	0.60
	Length	6.7	6.7	6.7 ± 0.17	0.8 (6.3-7.1)	0.73
	L/W	1.8	1.8	1.8 ± 0.07	0.3 (1.6-1.9)	0.67
	FFD	1.5	1.5	1.5 ± 0.1	0.5 (1.2-1.7)	0.51

Supplemental Table 2. Spearman rank correlation coefficients between morphometric traits. (A) Avalon x Candenza, (B) Beaver x Soissons, (C) Shango x Shamrock, (D) Spark x Rialto, (E) Malacca x Charger and (F) Savannah x Rialto. Values in bold represent non-significant correlations, (*) denotes p<0.05, all the other correlations are significant at p<0.01.

A (AxC)	TGW		Area		Width		Length		L/W		FFD	
TGW	year 1	year 2										
Area	0.883	0.895	year 1	year 2								
Width	0.902	0.873	0.754	0.743	year 1	year 2						
Length	0.547	0.622	0.829	0.862	0.319	0.376	year 1	year 2				
L/W	**-0.171**	**-0.043**	0.175	0.271	-0.457	-0.379	0.644	0.675	year 1	year 2		
FFD	0.848	0.789	0.537	0.477	0.781	0.684	**0.119**	**0.117**	-0.478	-0.405	year 1	year 2

B (BxS)	TGW		Area		Width		Length		L/W		FFD	
TGW	year 1	year 2										
Area	0.768	0.778	year 1	year 2								
Width	0.856	0.807	0.705	0.566	year 1	year 2						
Length	**0.194**	0.277*	0.645	0.716	**0.006**	**-0.084**	year 1	year 2				
L/W	**-0.132**	-0.284*	**-0.078**	**0.187**	**-0.156**	-0.654	**0.058**	0.774	year 1	year 2		
FFD	0.868	0.821	0.4	0.35	0.681	0.64	**-0.2**	**-0.155**	**-0.103**	-0.523	year 1	year 2

C (SxS)	TGW		Area		Width		Length		L/W		FFD	
TGW	year 1	year 2										
Area	0.907	0.904	year 1	year 2								
width	0.871	0.887	0.737	0.814	year 1	year 2						
Length	0.583	0.487	0.811	0.731	0.297*	0.294*	year 1	year 2				
L/W	**-0.171**	-0.522	**0.127**	-0.299*	-0.521	-0.756	0.626	0.359	year 1	year 2		
FFD	0.833	0.928	0.581	0.724	0.754	0.767	**0.177**	0.249*	-0.455	-0.576	year 1	year 2

D (SpxR)	TGW	Area	Width	Length	L/W	FFD
TGW	1					
Area	0.886	1				
Width	0.849	0.842	1			
Length	0.682	0.855	0.531	1		
L/W	-0.288*	**-0.137**	-0.574	0.331*	1	
FFD	0.875	0.589	0.607	0.354*	-0.336 *	1

E (MxC)	TGW	Area	Width	Length	L/W	FFD
TGW	1					
Area	0.904	1				
Width	0.868	0.85	1			
Length	0.548	0.745	0.379*	1		
L/W	-0.476	-0.336	-0.748	0.271*	1	
FFD	0.931	0.72	0.718	0.337*	-0.455	1

F (SaxR)	TGW	Area	Width	Length	L/W	FFD
TGW	1					
Area	0.908	1				
Width	0.817	0.736	1			
Length	0.674	0.845	0.375	1		
L/W	**-0.007**	**0.212**	-0.426	0.625	1	
FFD	0.728	0.471	0.473	0.203	**-0.195**	1

Supplemental Table 3. Principal components analysis. Probability loadings of principal components identified in (A) BxS, AxC, SxS, and population wide (P-W), (B) SpxR, MxC and SaxR.

A

	BxS		AxC		SxS		P-W	
	PC1	PC2	PC1	PC2	PC1	PC2	PC1	PC2
TGW	0.96963	0.09604	0.71078	0.08286	0.96980	0.01311	0.926314	0.021878
AREA	0.73682	0.62573	0.93434	0.26831	0.94781	0.14910	0.961997	0.153397
WIDTH	0.95788	0.00678	0.89958	-0.31470	0.81878	-0.47310	0.921874	-0.303075
LENGTH	0.12174	0.98159	0.68741	0.70644	0.68576	0.67865	0.818109	0.549791
L/W	-0.78478	0.54595	-0.17037	0.97113	-0.20490	0.97544	-0.190197	0.975226
FFD	0.81622	-0.30839	0.80328	-0.43154	0.83995	-0.03832	0.88659	-0.172279
% Var.	61.626	29.291	55.571	30.105	62.117	27.662	68.748	23.1315

B

	SpxR		MxC		SaxR	
	PC1	PC2	PC1	PC2	PC1	PC2
TGW	0.98184	-0.00870	0.48606	0.04296	0.52517	-0.07054
AREA	0.94195	0.24697	0.46042	0.25025	0.51221	0.15005
WIDTH	0.92316	-0.24235	0.46223	-0.18117	0.43038	-0.33131
LENGTH	0.73167	0.66244	0.25064	0.69718	0.40666	0.47400
L/W	-0.35826	0.91203	-0.29628	0.63961	0.01691	0.73721
FFD	0.81329	-0.19465	0.43301	-0.08684	0.33309	-0.30755
% Var.	67.144	23.805	68.4	24.72	59.23	29.17

Supplemental Table 4. QTL for the morphometric traits in the AxC population. QTL are annotated as follows: initials of population, year of harvest, trait, ascending number of QTL. Genome-wide LOD threshold for significant QTL was set at 3.1 after a permutation test (10,000 simulations). Position refers to the map position (cM) that corresponds to the marker with the highest LOD score with the 2-LOD confidence intervals (from-to) shown next to it.

Chromosome	QTL	LOD	% explained	position	from	to	Effect
2D	AvXC_07_Length_1	3.0	6.6	144.6	141.1	149.6	0.074
3A	AvXC_07_Length_2	6.0	12.8	55.2	35.0	67.1	0.103
3A	AvXC_08_Length_1	6.0	14.2	53.7	47.1	63.1	0.106
3B	AvXC_07_Length_3	3.8	8.7	64.7	46.0	103.1	0.085
3B	AvXC_08_Length_2	3.1	7.1	95.3	48.0	113.1	0.075
5A	AvXC_07_Length_4	18.1	35.4	23.1	16.0	29.2	-0.170
5A	AvXC_08_Length_3	16.3	35.4	25.1	13.0	30.3	-0.162
6A	AvXC_08_Length_4	3.2	7.2	85.6	69.7	94.4	-0.076
7D	AvXC_07_Length_5	3.3	7.2	27.6	1.0	42.1	-0.077
7D	AvXC_08_Length_5	3.6	8.5	21.0	5.0	37.6	-0.083
2B	AvXC_07_Area_1	3.2	7.0	111.0	105.6	120.0	-0.364
3B	AvXC_07_Area_2	3.9	10.7	26.7	0.0	83.1	0.452
3B	AvXC_08_Area_1	3.1	7.6	78.1	39.7	118.1	0.373
4B	AvXC_07_Area_3	4.5	10.8	23.4	9.5	37.4	-0.451
4B	AvXC_08_Area_2	5.1	12.4	23.4	10.5	34.4	-0.477
5A	AvXC_07_Area_4	11.7	24.2	28.2	17.0	32.7	-0.674
5A	AvXC_08_Area_3	12.2	25.6	29.2	14.0	32.7	-0.679
2B	AvXC_07_TGW_1	3.2	7.1	111.0	79.3	120.0	-1.368
3B	AvXC_07_TGW_2	4.2	10.1	7.1	0.0	54.0	1.630
4B	AvXC_07_TGW_3	6.2	14.6	23.4	3.3	38.1	-1.966
4B	AvXC_08_TGW_1	6.1	16.1	23.4	11.5	33.4	-1.791
4D	AvXC_08_TGW_2	3.1	7.4	0.0	0.0	13.1	-1.245
5A	AvXC_07_TGW_4	4.2	9.4	28.2	12.0	34.5	-1.572
5A	AvXC_08_TGW_3	4.8	11.2	25.1	2.0	34.5	-1.539
6A	AvXC_08_TGW_4	6.3	13.6	21.5	10.4	29.8	1.736
1D	AvXC_07_Width_1	3.1	6.9	21.0	8.1	27.7	-0.040
1D	AvXC_08_Width_1	3.2	7.9	19.1	0.0	34.7	-0.037
3B	AvXC_07_Width_2	3.7	8.9	7.1	0.0	43.7	0.045
4B	AvXC_07_Width_3	4.6	11.7	23.4	10.5	38.1	-0.052
4B	AvXC_08_Width_2	5.2	13.1	23.4	13.5	34.4	-0.046
6A	AvXC_07_Width_4	3.4	7.8	19.0	0.0	56.1	0.043
6A	AvXC_08_Width_3	6.3	13.6	21.5	12.4	39.0	0.049
1D	AvXC_07_L/W_1	3.1	7.0	0.0	0.0	26.0	0.020
1D	AvXC_08_L/W_1	3.24	7.2	0	0.0	16.1	0.019
2D	AvXC_07_L/W_2	6.4	14.8	144.6	136.3	151.6	0.030
3A	AvXC_07_L/W_3	8.8	18.4	70.0	49.7	78.4	0.033
3A	AvXC_08_L/W_2	8.6	18.7	69.3	48.7	77.4	0.030
5A	AvXC_07_L/W_4	7.9	20.1	23.1	4.0	29.2	-0.034
5A	AvXC_08_L/W_3	6.8	17.4	18.0	5.0	32.7	-0.029
6A	AvXC_07_L/W_5	4.6	10.8	88.3	71.7	94.4	-0.025
6A	AvXC_08_L/W_4	5.6	12.7	86.6	74.7	94.4	-0.025
7D	AvXC_07_L/W_6	4.6	10.1	20.0	6.0	36.6	-0.024
7D	AvXC_08_L/W_5	3.2	8.9	20.0	2.0	39.6	-0.019
1D	AvXC_08_FFD_1	3.3	7.8	5.5	0.0	27.7	-0.021
3A	AvXC_07_FFD_1	3.0	6.9	73.4	60.7	84.4	-0.025
3A	AvXC_08_FFD_2	3.5	8.4	63.1	27.0	97.6	-0.022
3B	AvXC_07_FFD_2	3.6	8.6	8.1	0.0	43.7	0.027
3B	AvXC_07_FFD_3	3.7	8.2	175.7	154.9	191.1	0.027
4B	AvXC_08_FFD_3	4.0	10.0	17.5	0.0	36.4	-0.025
4B	AvXC_07_FFD_4	4.8	11.5	23.4	0.0	38.1	-0.032
4D	AvXC_08_FFD_4	5.0	11.9	3.0	0.0	13.1	-0.027
4D	AvXC_07_FFD_5	3.3	7.8	0.0	0.0	12.2	-0.029
6A	AvXC_08_FFD_5	9.9	20.8	21.0	13.4	30.0	0.036
6A	AvXC_07_FFD_6	3.8	8.6	19.0	0.0	51.0	0.028

Supplemental Table 5. QTL for the morphometric traits in the SxS, and BxS populations.

Chromosome	QTL	LOD	% Var.	position	from	to	Effect
7A	SxS_06_Length_1	3.4	20.1	7.0	0.0	18.0	0.081
7A	SxS_07_Length_1	6.8	30.9	7.0	0.0	10.0	0.098
2D	SxS_07_Area_2	3.2	14.4	4.0	0.0	4.0	0.348
6B	SxS_06_Area_1	3.2	15.1	82.0	69.0	82.0	-0.297
7A	SxS_07_Area_1	4.7	23.1	0.0	0.0	5.0	0.451
5A	SxS_07_TGW_1	3.3	20.6	8.0	3.0	13.0	-1.919
7A	SxS_06_TGW_1	3.7	19.1	1.0	0.0	18.0	1.277
7B	SxS_06_Width_1	3.3	18.9	20.0	9.0	37.0	-0.041
5A	SxS_07_Width_1	3.7	18.3	34.0	27.0	36.0	-0.061
5A	SxS_06_L/W_1	3.8	30.0	20.0	4.0	43.0	0.035
5A	SxS_07_L/W_1	4.4	29.8	36.0	27.0	45.0	0.033
3D	SxS_06_FFD_1	4.0	23.6	2.0	0.0	9.0	-0.030
5A	SxS_07_FFD_1	3.6	22.9	8.0	3.0	13.0	-0.048
1A	BxS_07_Length_1	4.6	29.4	36.0	19.0	45.0	-0.118
1A	BxS_08_Length_1	2.4	15.8	25.0	17.0	31.0	-0.091
2D	BxS_08_Length_2	4.3	26.1	8.0	0.0	28.0	-0.118
4B	BxS_07_Area_1	3.6	26.9	22.0	8.0	27.0	-0.532
3A	BxS_07_TGW_1	4.2	27.9	8.0	0.0	26.0	0.919
4B	BxS_07_TGW_2	5.1	34.0	19.0	9.0	27.0	-2.606
4B	BxS_08_TGW_1	5.1	34.1	18.0	0.0	27.0	-2.241
3A	BxS_07_Width_1	3.1	21.1	17.0	0.0	42.0	-0.079
4B	BxS_07_Width_2	6.0	41.1	20.0	9.0	27.0	-0.112
4B	BxS_08_Width_1	9.3	50.2	16.0	12.0	24.0	-0.088
2D	BxS_07_L/W_1	3.8	23.5	20.0	0.0	30.0	-0.060
2D	BxS_08_L/W_1	3.3	20.9	20.0	2.0	31.0	-0.037
4B	BxS_07_L/W_2	3.9	24.1	13.0	0.0	27.0	0.062
4B	BxS_08_L/W_2	5.6	32.8	14.0	5.0	24.0	0.048
2D	BxS_08_FFD_1	3.4	21.6	14.0	0.0	29.0	0.039
3A	BxS_07_FFD_1	4.7	31.6	6.0	0.0	24.0	-0.071
4B	BxS_07_FFD_2	3.9	25.1	0.0	0.0	27.0	-0.063
4B	BxS_08_FFD_2	4.3	26.2	14.0	0.0	27.0	-0.044

Supplemental Table 6. QTL for the morphometric traits in the SpxR, MxC, and SaxR population.

Chromosome	QTL	LOD	% Var.	position	from	to	Effect
1A	SpxR_07_Length_1	3.8	14.2	11.6	0.0	21.6	-0.067
5A	SpxR_07_Length_2	3.1	11.3	1.0	0.0	25.5	0.067
1B	SpxR_07_Area_1	4.0	15.4	20.6	0.0	24.7	-0.381
5A	SpxR_07_Area_2	3.8	16.2	7.0	0.0	30.5	0.390
1B	SpxR_07_TGW_1	3.5	14.0	0.0	0.0	26.7	-1.369
4D	SpxR_07_TGW_2	3.2	12.6	33.0	0.0	47.0	1.297
5A	SpxR_07_TGW_3	4.2	17.5	7.0	0.0	27.5	1.529
1B	SpxR_07_Width_1	3.5	14.8	1.0	0.0	25.7	-0.047
5A	SpxR_07_Width_2	3.9	15.9	13.5	0.0	32.5	0.048
4D	SpxR_07_FFD_1	3.9	17.1	24.0	3.0	39.0	0.036
2A	MxC_08_TGW_1	6.3	34.9	45.0	23.0	63.0	2.324
6A	MxC_08_TGW_2	2.9	13.2	31.0	18.0	50.0	-1.499
2A	MxC_08_Area_1	4.3	27.4	45.0	10.0	65.0	0.477
6A	MxC_08_Area_2	2.9	13.8	29.0	6.0	54.0	0.942
2A	MxC_08_Width_1	3.5	22.3	48.0	9.0	83.0	0.066
3A	MxC_08_Width_2	3.6	18.5	94.0	73.0	101.0	-0.061
2B	MxC_08_Length_1	3.1	12.5	37.0	20.0	58.0	-0.060
2A	MxC_08_L/W_1	5.5	23.9	40.0	10.0	46.0	-0.033
3A	MxC_08_L/W_2	3.7	20.8	94.0	78.0	101.0	0.031
2A	MxC_08_FFD_1	5.5	29.6	45.0	10.0	65.0	0.052
5A	SaxR_08_TGW_1	3.9	19.5	12.0	0.0	37.0	1.577
6A	SaxR_08_TGW_2	3.4	19.0	43.0	8.0	77.0	1.570
5A	SaxR_08_Area_1	4.0	19.3	10.0	0.0	42.0	0.459
5A	SaxR_08_Width_1	3.9	18.8	5.0	0.0	21.0	0.050
6A	SaxR_08_Width_2	3.0	20.9	37.0	2.0	80.0	0.053
3A	SaxR_08_Length_1	4.4	19.4	70.0	52.0	94.0	-0.097
5A	SaxR_08_Length_2	2.8	13.4	61.0	48.0	61.0	0.080
7A	SaxR_08_Length_3	3.4	15.8	60.0	39.0	102.0	-0.086
1A	SaxR_08_L/W_1	3.5	16.3	25.0	10.0	46.0	-0.023
2A	SaxR_08_L/W_2	3.2	15.1	15.0	0.0	17.0	-0.022
7A	SaxR_08_L/W_3	4.4	21.7	78.0	59.0	102.0	-0.026
6A	SaxR_08_FFD_1	3.1	14.2	50.0	25.0	72.0	0.023

Supplemental Table 7. QTL for the principal components in the AxC, SxS, BxS, SpxR, MxC and SaxR populations.

Chromosome	trait	LOD	% Var.	position	from	to	Effect
3B	AvXC_PC1_1	3.6	9.5	31.7	0.0	82.1	0.29
4B	AvXC_PC1_2	6.1	14.4	23.4	10.5	35.4	-0.36
5A	AvXC_PC1_3	7.5	16.2	28.2	13.0	33.7	-0.39
6A	AvXC_PC1_4	3.6	7.9	21.5	0.0	40.0	0.27
1D	AvXC_PC2_1	3.2	7.3	0.0	0.0	22.0	0.26
2D	AvXC_PC2_2	4.9	11.4	144.6	133.7	155.5	0.31
3A	AvXC_PC2_3	10.6	22.5	69.3	48.7	77.4	0.45
5A	AvXC_PC2_4	10.3	25.5	18.0	7.0	28.2	-0.48
6A	AvXC_PC2_5	4.9	11.6	85.6	71.7	94.4	-0.31
7A	SxS_PC1_1	3.6	23.4	1.0	0.0	18.0	0.35
5A	SxS_PC2_1	4.1	29.7	20.0	3.0	43.0	0.51
3A	BxS_PC1_1	4.0	26.8	13.0	0.0	25.0	-1.04
4B	BxS_PC1_2	5.7	36.4	18.0	8.0	27.0	-1.22
1A	BxS_PC2_1	4.6	29.2	36.0	19.0	45.0	0.72
1B	SpxR_PC1_1	3.9	14.9	20.6	0.0	25.7	-0.39
5A	SpxR_PC1_2	4.4	18.2	5.0	0.0	26.5	0.43
1A	SpxR_PC2_1	3.5	11.3	7.5	0.0	10.5	-0.34
3A	SpxR_PC2_2	2.9	9.2	58.8	54.9	60.5	-0.31
2A	MxC_PC1_1	4.3	20.6	46.0	7.0	69.0	0.93
6A	MxC_PC1_2	3.3	15.1	31.0	26.0	39.0	-0.78
2B	MxC_PC2_1	5.6	23.2	32.0	17.0	51.0	-0.58
5A	SaxR_PC1_1	4.2	20.5	11.0	0.0	22.0	0.86
6A	SaxR_PC1_2	3.1	18.3	40.0	5.0	87.0	0.82
1A	SaxR_PC2_1	4.1	18.5	24.0	7.0	67.0	-0.57
7A	SaxR_PC2_2	4.6	22.1	79.0	67.0	102.0	-0.62

Supplemental Table 8. Morphometric data on *Triticum* species.

Accesion No	Species[a]	ssp/var	Area (mm^2)[b]			Length (mm)			Width (mm)			L/W		
			Mean	Stdev	Range (min-max)	Mean	Stdev	Range (min-max)	Mean	Stdev	Range (min-max)	Mean	Stdev	Range (min-max)
1010002	*T. urartu*		14.7	1.80	6.0(11.4-17.4)	7.6	0.55	1.9(6.5-8.4)	2.2	0.24	0.8(1.8-2.6)	3.5	0.31	1.3(3.0-4.3)
1020003	*T. boeoticum*	*thaoudar luteoglumis*	25.2	4.1	16.3 (17.1-33.4)	9.5	0.6	3.1 (8.1-11.2)	3.3	0.5	1.8 (2.4-4.2)	2.9	0.4	1.6 (2.3-3.8)
1030001	*T. boeoticum*	*aegilopoides*	26.2	2.40	8.4(22.1-30.5)	9.4	0.44	2.1(8.3-10.4)	3.5	0.31	1.5(2.5-4.0)	2.7	0.27	1.5(2.2-3.8)
1030004	*T. boeoticum*	*aegilopoides Larionowi*	18.8	2.3	9.2 (13.4-22.6)	7.7	0.7	3.1 (6.2-9.3)	3.1	0.4	1.8 (2.1-3.9)	2.5	0.4	1.7 (1.9-3.6)
1030005	*T. boeoticum*	*aegilopoides heleno*	22.6	2.6	8.2 (18.6-26.8)	9.7	0.5	1.5 (9.2-10.7)	2.7	0.3	0.9 (2.2-3.1)	3.6	0.3	1.0 (3.2-4.2)
1030022	*T. boeoticum*	*aegilopoides mayssuriani*	20.6	2.0	8.9 (15.9-24.8)	8.2	0.4	2 (7.3-9.3)	3.2	0.4	1.6 (2.4-4)	2.6	0.3	1.2 (2.1-3.3)
1020001	*T. boeoticum*		21.1	2.1	6.5 (18-24.5)	8.5	0.5	1.7 (7.7-9.4)	3.1	0.3	0.8 (2.6-3.4)	2.8	0.2	0.9 (2.4-3.3)
1020004	*T. boeoticum*	*thaoudar*	24.1	2.0	6.3 (20.1-26.4)	9.7	0.3	0.9 (9.2-10.1)	3.0	0.3	1 (2.4-3.4)	3.3	0.3	1.1 (2.9-4.0)
1030027	*T. boeoticum*	*aegilopoides*	21.0	3.0	13.9 (15.3-29.2)	8.8	0.7	3 (7.4-10.4)	2.9	0.3	1.3 (2.1-3.4)	3.1	0.2	1.0 (2.6-3.6)
1040004	*T. monococcum*	*flavescens*	22.7	1.3	4.8 (19.2-24)	8.1	0.2	0.8 (7.6-8.4)	3.6	0.2	0.9 (2.9-3.8)	2.3	0.1	0,7 (2.1-2.8)
1040005	*T. monococcum*	*flavescens*	23.3	1.9	7.3 (18.9-26.2)	8.5	0.5	2.2 (7.3-9.5)	3.4	0.2	1.1 (2.7-3.8)	2.5	0.3	1.3 (2.2-3.5)
1040008	*T. monococcum*	*Hornemannii*	20.2	1.9	6.3 (16.9-23.2)	8.2	0.6	3 (7-10)	3.1	0.3	1.2 (2.4-3.6)	2.7	0.4	1.6 (2.1-3.7)
1040011	*T. monococcum*		20.9	1.80	6.3(17.8-24.1)	8.2	0.43	2.0(7.2-9.2)	3.2	0.26	1.0(2.7-3.7)	2.6	0.20	0.8(2.1-2.9)
1040019	*T. monococcum*	*sofianum*	21.1	1.8	8.4 (16-24.4)	7.8	0.4	1.6 (7-8.6)	3.5	0.2	1.3 (2.6-3.9)	2.2	0.2	0.8 (2-2.8)
1040020	*T. monococcum*	*hordeumforme*	16.6	1.3	5.3 (13.3-18.6)	6.9	0.4	1.7 (5.9-7.6)	2.9	0.2	0.6 (2.6-3.2)	2.4	0.1	0.6 (2.1-2.7)
1040021	*T. monococcum*	*nigriaristatum*	24.3	2.3	10.7 (16.6-27.3)	8.3	0.4	1.8 (7.3-9.1)	3.8	0.4	1.6 (2.9-4.5)	2.2	0.3	1.1 (1.9-2.9)
1040022	*T. monococcum*	*macedonicum*	24.0	2.5	10.7 (18.1-28.8)	8.5	0.5	2.2 (7.3-9.5)	3.6	0.4	1.6 (2.7-4.3)	2.3	0.2	1.1 (2.0-3.1)
1040023	*T. monococcum*	*atriaristatum*	21.1	1.4	6.1 (17.1-23.2)	8.3	0.3	1.4 (7.3-8.7)	3.2	0.2	1.1 (2.5-3.6)	2.6	0.2	1.1 (2.2-3.3)
1040025	*T. monococcum*	*nigricultum*	23.5	2.6	9.7 (17.2-26.9)	8.7	0.5	2.4 (7.1-9.5)	3.4	0.4	1.6 (2.4-4)	2.6	0.3	1.3 (2.2-3.5)
1040026	*T. monococcum*	*sofianum*	23.9	2.6	11.5 (16.9-28.4)	8.7	0.4	1.9 (7.6-9.5)	3.6	0.4	1.6 (2.6-4.2)	2.5	0.3	1.2 (2.0-3.3)
1040027	*T. monococcum*	*Hornemannii*	21.9	1.8	9.3 (16.6-25.9)	8.3	0.5	2.1 (7.2-9.3)	3.5	0.2	1.5 (2.6-4.1)	2.4	0.3	1.5 (2-3.5)
1040028	*T. monococcum*	*flavescens*	22.7	1.9	8.7 (17.1-25.8)	7.7	0.7	1.4 (6.9-8.3)	3.8	0.3	1.5 (2.9-4.4)	2.0	0.2	0.8 (1.7-2.5)
1040031	*T. monococcum*	*laetissimum*	22.9	3.3	21.3 (6-27.3)	8.4	0.7	4.6 (4.8-9.4)	3.5	0.5	2.9 (1.1-4)	2.4	0.4	2.3 (2.1-4.4)
1040032	*T. monococcum*	*laetissimum*	19.8	2.3	8.7 (15.5-24.2)	8.2	0.5	2 (7.1-9.1)	3.0	0.3	1.4 (2.4-3.8)	2.8	0.3	1.6 (2.1-3.7)
1060007	*T. dicoccoides*		25.6	3.01	12.5(18.2-30.7)	9.8	0.56	3.2(7.5-10.7)	3.2	0.40	1.9(2.1-4.0)	3.1	0.39	2.0(2.4-4.4)
1060010	*T. dicoccoides*	*Aaronsolia*	24.9	3.6	18.5 (11.6-30.1)	9.3	0.6	2.8 (7.5-10.3)	3.4	0.4	2.8 (1.8-4.6)	2.8	0.3	2.1 (2.1-4.2)
1060009	*T. dicoccoides*	*fulvovillosum*	21.8	3.3	12.9 (16.8-29.7)	8.9	0.6	2.8 (7.2-10)	3.0	0.4	1.8 (2.1-3.9)	3.0	0.4	1.8 (2.3-4.1)
1060011	*T. dicoccoides*	*spontaneonigrum*	23.0	5.4	26.6 (4.7-31.3)	9.4	1.4	7.6 (3-10.6)	2.9	0.4	2.2 (1.7-3.9)	3.3	0.4	2.2 (1.8-3.9)
1070001	*T. dicoccoides*		22.9	2.18	8.7(19.5-28.2)	8.5	0.50	2.3(7.1-9.4)	3.5	0.29	1.2(3.0-4.2)	2.4	0.22	0.7(2.0-2.8)
1080060	*T. dicoccoides*	*speciosum*	26.6	3.03	14.5(20.4-34.9)	8.4	0.54	2.4(7.1-9.5)	3.9	0.38	1.6(3.2-4.8)	2.2	0.20	1.0(1.6-2.6)
1080061	*T. dicoccoides*	*dinurum*	24.4	2.63	12.9(17.1-30.0)	7.4	0.40	2.2(6.0-8.2)	4.1	0.39	1.9(3.3-5.2)	1.8	0.14	0.5(1.4-2.0)
1090007	*T. turgidum*	*carthlicum*	18.8	2.39	9.3(14.0-23.3)	6.8	0.42	2.5(5.4-7.9)	3.5	0.35	1.3(2.8-4.1)	2.0	0.17	0.6(1.6-2.3)
1100002	*T. turgidum*	*polonicum*	31.6	3.49	14.4(25.3-39.7)	10.4	0.90	4.3(8.7-13)	3.8	0.21	0.9(3.4-4.3)	2.7	0.26	1.1(2.3-3.4)
1110001	*T. turgidum*	*turanicum*	27.1	4.10	18.2(17.3-35.5)	8.4	0.70	3.0(6.8-9.8)	4.0	0.42	1.8(3.0-4.8)	2.1	0.21	0.9(1.7-2.6)
1140001	*T. turgidum*	*durum*	22.9	4.47	27.4(5.8-32.2)	8.4	0.67	5.5(4.3-9.8)	3.4	0.59	3.6(1.1-4.7)	2.5	0.39	2.0(1.8-3.9)
1120002	*T. isphanicum*	*biaristatum*	27.0	2.22	9.0(22.4-31.4)	11.0	0.41	1.7(10.0-11.7)	3.0	0.31	1.3(2.4-3.7)	3.7	0.35	1.2(3.1-4.3)
1130001	*T. isphanicum*	*uniaristatum*	19.1	2.23	9.1(13.2-22.3)	8.2	0.52	2.4(6.8-9.2)	2.8	0.27	1.1(2.1-3.2)	3.0	0.28	1.1(2.5-3.7)
1150001	*T. araraticum*	*tumaniani*	19.1	1.85	7.4(16.0-23.4)	9.4	0.45	1.7(8.4-10.1)	2.3	0.24	0.9(1.9-2.8)	4.2	0.47	1.9(3.2-5.2)
1150002	*T. araraticum*	*nachithevanicum*	24.6	2.43	7.6(19.7-27.3)	9.7	0.39	1.3(9.1-10.4)	3.1	0.40	1.2(2.5-3.7)	3.1	0.44	1.3(2.6-4.0)
1160004	*T. timopheevi*	*typicum*	21.3	1.95	8.7(16.7-25.4)	9.2	0.42	2.1(7.9-10.0)	2.7	0.28	1.1(2.3-3.4)	3.4	0.36	1.3(2.7-4.0)
1170001	*T. militinae*	*militinae*	24.1	2.68	12.4(18.5-30.9)	9.0	0.68	2.7(7.6-10.3)	3.2	0.32	1.3(2.6-3.9)	2.8	0.34	1.5(2.2-3.7)
1190844	*T. aestivum*	*eastivum*	22.7	3.01	11.9(16.4-28.3)	7.3	0.51	2.4(6.2-8.6)	3.9	0.40	1.9(3.1-5.0)	1.9	0.18	0.6(1.5-2.2)
1210001	*T. aestivum*	*sphaerococcum*	15.5	2.3	6.9(14.4-21.3)	5.4	0.42	1.9 (4.7-6.6)	3.5	0.40	2.4(2.4-4.8)	1.5	0.34	0.6(1.4-2.0)
N/A	*T. aestivum*	*sphaerococcum*	18.5	3	7.2 (16.4-23.6)	6.2	0.31	1.7(5.1-6.9)	3.7	0.23	1.2 (2.6-3.8)	1.7	0.23	0.4(1.6-2.0)
N/A	*T. aestivum*	*compactum*	19.6	4.3	10.5(15.8-26.3)	6.7	0.6	0.6(6.6-7.2)	3.6	0.56	1.9 (2.8-4.7)	1.9	0.39	0.5(1.6-2..1
1240001	*T. aestivum*	*macha*	25.1	2.65	11.8(18.7-30.5)	8.9	0.64	2.8(7.4-10.2)	3.4	0.26	1.2(2.9-4.1)	2.6	0.22	0.9(2.1-3.1)
1220007	*T. aestivum*	*spelta*	27.7	2.70	9.7(22.7-32.4)	9.3	0.47	1.9(8.3-10.2)	3.7	0.33	1.3(3.2-4.5)	2.6	0.18	0.7(2.0-2.8)
1230001	*T. vavilovii*	*var mirabile*	27.5	2.71	12.7(20.5-33.2)	8.3	0.50	2.2(7.0-9.2)	4.1	0.29	1.2(3.6-4.8)	2.0	0.15	0.6(1.7-2.3)
1260001	*T. zhukovskyi*		33.1	3.17	13.7(23.9-37.6)	10.9	0.86	3.6(8.4-12.0)	3.8	0.41	1.6(2.9-4.5)	2.9	0.38	1.4(2.2-3.7)
		Mean	22.81			8.52			3.33			2.63		
		S.D	3.58			1.10			0.43			0.55		
		Min.	14.69			5.40			2.18			1.54		
		Max.	33.08			11.03			4.12			4.19		
		Range	18.39			5.63			1.94			2.64		

Supplemental Table 8

[a] The species taxonomy follows the classification appeared in the John Innes Centre Triticeae Collection (http://data.jic.bbsrc.ac.uk/cgi-bin/germplasm/triticeae/).

[b] Values represent the mean of 20-30 grains.

Supplemental Table 9. Morphometric data on sixty one commercial varieties. Values represent the mean of 200-250 grains.

Varieties	TGW	Area	Width	Length	L/W
ALBA	56.50	23.80	4.30	7.10	1.65
ALBATROSS	51.70	23.50	4.10	7.30	1.78
AVALON	57.02	24.90	4.10	7.50	1.83
BEAVER	48.11	23.90	4.00	7.40	1.85
CADENZA	49.93	23.60	4.10	7.30	1.78
CALIF	50.41	23.30	4.10	7.10	1.73
CAPO	49.33	22.90	3.90	7.20	1.85
CEZANNE	50.09	23.70	4.10	7.20	1.76
CHARGER	47.28	22.50	4.00	7.00	1.75
COURTOT	52.90	24.00	4.00	7.60	1.90
ELITE LEUPLE	50.70	24.10	4.10	7.30	1.78
ERLA KOLBEN	55.63	24.60	4.20	7.40	1.76
ERLA KOLBEN	54.68	24.40	4.20	7.30	1.74
ESCORIAL	52.49	24.70	4.10	7.60	1.85
ETOILE DE CHOISY	53.99	24.90	4.10	7.60	1.85
EXTREM	51.23	23.00	4.20	7.00	1.67
FANAL	56.60	24.80	4.20	7.40	1.76
FLAIR	53.76	24.90	4.10	7.40	1.80
FLAME	47.15	22.30	3.90	7.10	1.82
FLAMINGO	53.76	23.00	4.00	7.20	1.80
FLORIDA	55.27	24.70	4.10	7.50	1.83
HEREWARD	41.65	21.30	3.80	6.90	1.82
HOBBIT	48.78	24.40	4.00	7.70	1.93
HOLDFAST	41.94	20.70	3.80	6.80	1.79
JOSS CAMBIER	47.63	22.50	4.00	7.10	1.78
KAWKAS (KAVKAZ)	55.52	25.40	4.10	7.70	1.88
KONTRAST	46.17	21.40	4.00	6.70	1.68
LEDA	53.74	22.90	4.30	6.80	1.58
MAHNDORFER TEMPO	52.29	23.30	4.10	7.20	1.76
MARCO	47.04	23.10	4.10	7.20	1.76
MARIS WIDGEON	50.70	23.20	4.00	7.30	1.83
MEGA	65.71	27.40	4.30	8.10	1.88
MINISTER	49.10	23.80	4.00	7.50	1.88
MIRAS	57.53	25.70	4.20	7.70	1.83
MIRONOWSKAJA JUBILEJNAJA	62.45	27.30	4.20	8.10	1.93
MUCK	45.81	22.10	3.90	7.00	1.79
MULTIWEISS	50.39	23.40	4.00	7.20	1.80
NAUTICA	57.41	25.30	4.20	7.60	1.81
OBELISK	52.46	23.90	4.10	7.30	1.78
ORLANDO	53.09	23.90	4.20	7.20	1.71
PALUR	50.57	23.60	4.10	7.30	1.78
PERLO	57.35	24.60	4.20	7.50	1.79
RABE	51.99	22.90	4.30	6.90	1.60
RECITAL	43.47	20.80	3.90	6.60	1.69
RENAN	57.83	25.90	4.10	8.00	1.95
RIBAND	56.09	24.40	4.30	7.10	1.65
RIMPAUS BRAUN	46.29	22.60	4.00	7.20	1.80
SCHWEIGERS TACA	54.65	24.40	4.10	7.60	1.85
SLEJPNER	47.57	22.80	4.00	7.30	1.83
SOISSONS	48.95	22.30	3.90	7.20	1.85
SPERBER	52.19	23.40	4.20	7.00	1.67
STAMM 101	54.62	23.70	4.20	7.00	1.67
STARKE II	44.49	22.00	3.90	7.00	1.79
STEADFAST	53.50	24.10	4.10	7.50	1.83
SVALE	50.44	23.30	4.10	7.20	1.76
TADORNA	50.40	23.10	4.00	7.20	1.80
TARAS	55.65	24.50	4.30	7.20	1.67
TREMIE	49.88	22.90	4.10	7.00	1.71
TSCHERMAKS WEISSER	57.35	25.10	4.10	7.70	1.88
VILMORIN 27	57.45	25.10	4.20	7.50	1.79
VIRGO	49.52	23.30	4.00	7.30	1.83
WERLA	56.23	24.80	4.20	7.40	1.76
Mean	52.00	23.74	4.08	7.29	1.78
SD	4.62	1.320	0.12	0.30	0.07
Min	41.6	20.70	3.80	6.60	1.58
Max	65.71	27.40	4.30	8.10	1.95
Range	24.06	6.7	0.50	1.50	0.36

Supplemental Text 1. Details of the QTL locations and effects on each homoeologous group and their corresponding meta-QTL.

Homoeologous group 1

Grain length QTL were identified in the distal region of chromosome 1A in at least two populations. In the SpxR population a significant effect in the region of marker *wPt-4765* was found (14.2% variation explained) with the Spark allele decreasing grain length (Supplemental Figure 3C). In the BxS population a QTL was identified in both years that explained between 15.8% and 29.4% of the phenotypic variation in grain length with the Beaver allele having the decreasing effect (Supplemental Figure 3A). In the AxC population a suggestive QTL (LOD=2.46) was also present over two years at the same region of chromosome 1A with the Avalon allele decreasing grain length. Moreover, an effect was detected on 1A in the SaxR population, which explained 16.3% of the L/W variation with Savannah contributing the decreasing allele (Supplemental Figure 3E). Meta-analysis identified two meta-QTL for grain length that spanned the intervals *barc263-wPt7030* and *wPt8347-s12/m25.6*, respectively, on the wheat consensus map.

QTL for grain size parameters, i.e. TGW, grain area and width, were identified on the short arm of chromosome 1B in the SpxR population with the Spark allele decreasing the value of all three parameters (Supplemental Figure 3C). In the AxC population, small but stable effects for grain width, L/W and FFD were identified at the distal end of chromosome 1D with the Avalon allele reducing grain width and FFD, and increasing L/W (Supplemental Figure 3A). The same very distal location of these QTL suggests that these effects could be under the control of homoeoalleles.

Homoeologous group 2

Significant effects for TGW, grain area, width, and FFD were identified on the distal part of chromosome 2A in the MxC population (Supplemental Figure 3E). Specifically, all the QTL identified are around marker *gwm95* with LOD scores ranging between 3.5 and 6.3 and explaining between 22.3% and 34.9% of the trait variation. The Malacca allele increases the phenotypic value of the traits.

QTL for L/W were identified at an equivalent region of 2A in the MxC and SaxR populations (Supplemental Figure 3D and 3E). These effects explained 20.8% and 15.1% of the variation present in MxC and SaxR, respectively, with Malacca and Savannah decreasing the phenotypic value of the trait. Meta-analysis identified one meta-QTL in the interval *wmc819-gwm47.*

An effect for L/W was identified on chromosome 2D in the BxS population that was stable over two years. The QTL interval spanned around marker *wmc412* on the long arm of 2D, with an LOD ranging between 3.3 and 3.8 and explained ~22% of the phenotypic variation (Supplemental Figure 3B). In the same mapping interval, QTL for grain length and FFD were also identified, but only for one year.

QTL for grain width and TGW (Sun et al., 2009), and grain area (Breseghello, 2007) were previously identified on the sort arm of chromosome 2A at an interval approximately equivalent to the QTL reported for MxC in this study. Effects for grain length were detected on the long arm of chromosome 2B in three other populations (Campbell et al., 1999; Dholakia et al., 2003; Sun et al., 2009) at similar position as the grain length QTL in MxC. Markers associated with grain length (Campbell et al., 1999) and FFD (Dholakia et al., 2003) have been previously identified on the long arm of 2D that co-locate with the QTL for these traits in the BxS population.

Homoeologous group 3

Significant QTL for grain size and shape parameters were identified on chromosome 3A in AxC, BxS, MxC and SaxR. In the AxC population, large effects for grain length and L/W were identified around marker *wmc264* that explained ~13% and 18% of the trait variation, respectively (Supplemental Figure 3A). The Avalon allele increases the phenotypic value for both traits. Small but stable effects were also detected for FFD in the same mapping interval. Strong QTL for grain size related parameters, i.e. TGW, grain width and FFD, were detected in the BxS population around marker *wPt-4692*, each of which explained 27.9%, 21.1% and 31.6% of the variation, correspondingly (Supplemental Figure 3B). QTL for grain width and L/W were identified in the

MxC population that explained ~19% of the phenotypic variation (Supplemental Figure 3E). An effect was also found in SaxR that explained 19.4% of the variation in grain length (Supplemental Figure 3D). Three meta-QTL were identified in the following mapping intervals: *wPt1688-barc45*, *wPt9562-wPt9215*, and *barc19-cfa2262*.

Small effects for grain length, area, TGW and FFD were detected on chromosome 3B in the AxC population. The grain length and area QTL were stable in both years and explained ~8% and ~10% of the trait variation, respectively (Supplemental Figure 3A). Significant QTL for TGW and FFD were identified only in one year but suggestive QTL (LOD 2.7 and 2.4, respectively) were present in the same interval in the second year.

Homoeologous group 4

Some of the largest QTL for grain size parameters were detected on chromosome 4B in the BxS and AxC populations. Specifically, in the BxS population, significant QTL for TGW, grain area, width and FFD identified around the marker *s14/m15.6* that explained between 25.1% and 50.2% of the variation (Supplemental Figure 3B). For all the QTL, Beaver contributed the decreasing allele. Interestingly, a strong effect was also detected in the same mapping interval (around marker *s14/m15.6*) for L/W (24.1-32.8% variation explained) with Beaver increasing the trait value. In the AxC population, the 4B effect on TGW, grain width, area and FFD was identified in both years around marker *wmc349* with the Avalon allele reducing the phenotypic value of the traits (Supplemental Figure 3A). Meta-analysis identified one meta-QTL, between *s14/m15.6* and *wmc349*. QTL for TGW and FFD were identified on chromosome 4D in SpxR around the *Rht-D1* locus with the Spark allele increasing the trait value (Supplemental Figure 3C). Effects at the same region for FFD, TGW, and grain width were identified in the AxC population that also segregates for *Rht-D1*.

Homoeologous group 5

Multiple QTL for both grain size and shape parameters were identified on chromosome 5A in the AxC, SxS, SpxR, and SaxR populations. In AxC, a strong effect for grain length and L/W was detected around the marker *gwm156* that was stable in both years (Supplemental Figure 3A). Grain length QTL had a LOD ranging between 16.3 and 18.1 and explained ~35.4% of the variation, while the L/W QTL had an LOD between 6.8 and 7.9 and explained ~20% of the variation apparent in the population. Large QTL for grain area (LOD 11.7-12.2) and TGW (LOD 4.2-4.8) were identified spanning the same mapping interval, each of which explained ~25% and 10% of the phenotypic variation, correspondingly. The Avalon allele considerably decreases the value of the traits above. In the SpxR population, QTL for grain length, width, area and TGW were detected spanning the interval between markers *gwm443* and *wPt-4131* on chromosome 5A, with Spark contributing the increasing allele (Supplemental Figure 3C). QTL for the same traits were also found in the SaxR population with the Savannah allele increasing the phenotypic values of all the traits but grain length (Supplemental Figure 3D). Significant effects for TGW, FFD, grain width and L/W were identified in the same mapping interval in the SxS population (Supplemental Figure 3F). The L/W QTL was stable over the two years and explained ~30% of the variation with the Shamrock allele increasing the trait value. QTL for TGW, FFD, and grain width were detected in that interval only for one year, with Shamrock reducing the phenotypic value. This is consistent with the significant negative correlation between TGW, grain width and L/W apparent only for that specific year. Meta-analysis identified four meta-QTL that spanned the intervals *wmc443-cfa2104*, *wmc492-wmc475*, *wPt0654-wPt3069*, and *wmc110-wmc727*, respectively.

Homoeologous group 6

Two distinct clusters of QTL, i.e. one for grain size and the other for grain shape parameters, were identified on chromosome 6A in the AxC population. Effects for grain width, FFD and TGW (one year) were detected on the short arm of 6A, around marker *barc171*, with the Avalon allele conferring an increase in the trait values (Supplemental Figure 3A). A QTL for L/W was detected in both years on the long arm of 6A, around marker *wPt7204*, that explained ~12% of the trait variation with Avalon contributing the decreasing allele (Supplemental Figure 3A). Additionally, a QTL for grain length was identified only in one year spanning an interval equivalent to the L/W QTL and conferring the same negative effect on the trait. Effects for TGW and grain area in MxC and TGW, grain width, and FFD in SaxR were detected in an equivalent interval of chromosome 6A (Supplemental Figure 3D and 3E). Meta-analysis identified two meta-QTL at the proximal (*wmc6807-psp3071*) and the distal end (*cos07Tb-wPt5480*) of the chromosome, respectively.

Homoeologous group 7

A large effect controlling grain length was identified on chromosome 7A in the SxS population that was stable over the two years of trials (Supplemental Figure 3F). The LOD score of the QTL ranged between 3.4 and 6.8 and explained ~30% of the variation in grain length. QTL for grain area and TGW were detected in the same interval but only for one year. In the SaxR population, two significant QTL were detected at an equivalent chromosomal region of 7A, each of which explained 15.8% and 21.7% of the variation in grain length and L/W. In both instances, the Savannah allele decreased the trait values. Minor effects, but stable over two years, for grain length and L/W, were detected on chromosome 7D in the AxC population with Avalon decreasing the trait value.

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