

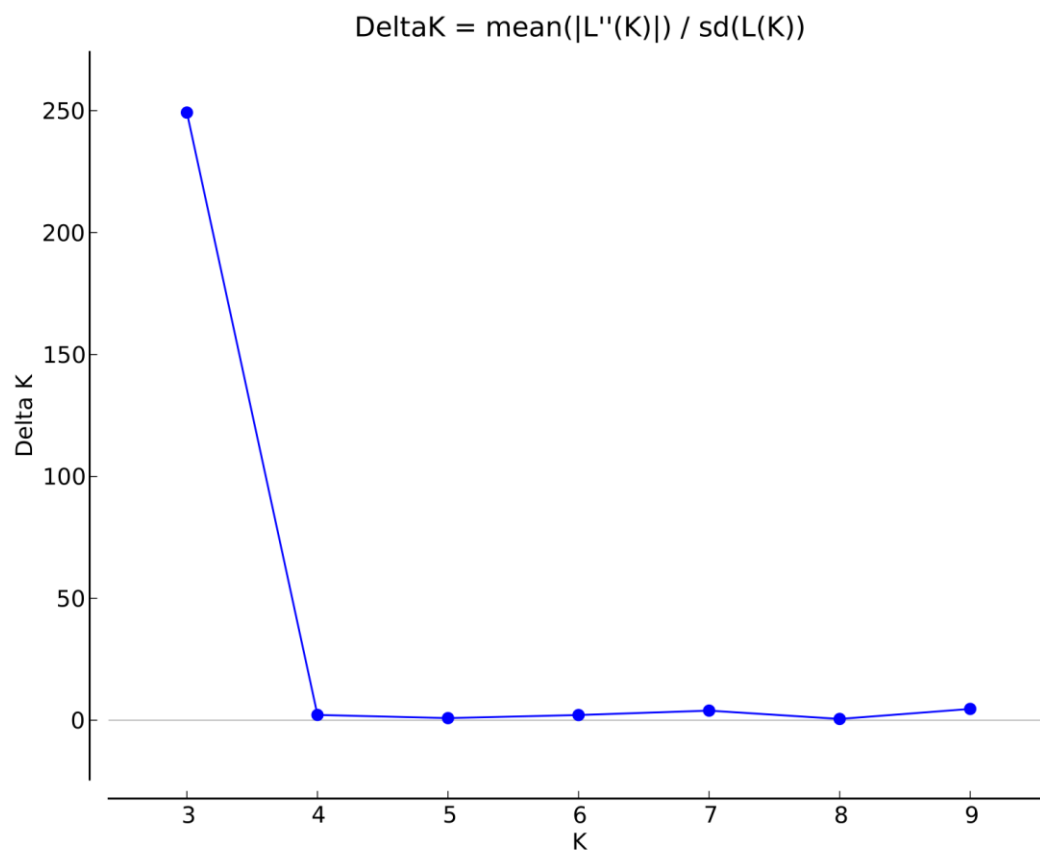


Figure S1. Estimation of the number of subpopulations (ΔK) calculated by Evanno's approach (2005) obtained in program Structure harvester and Clumpak program.

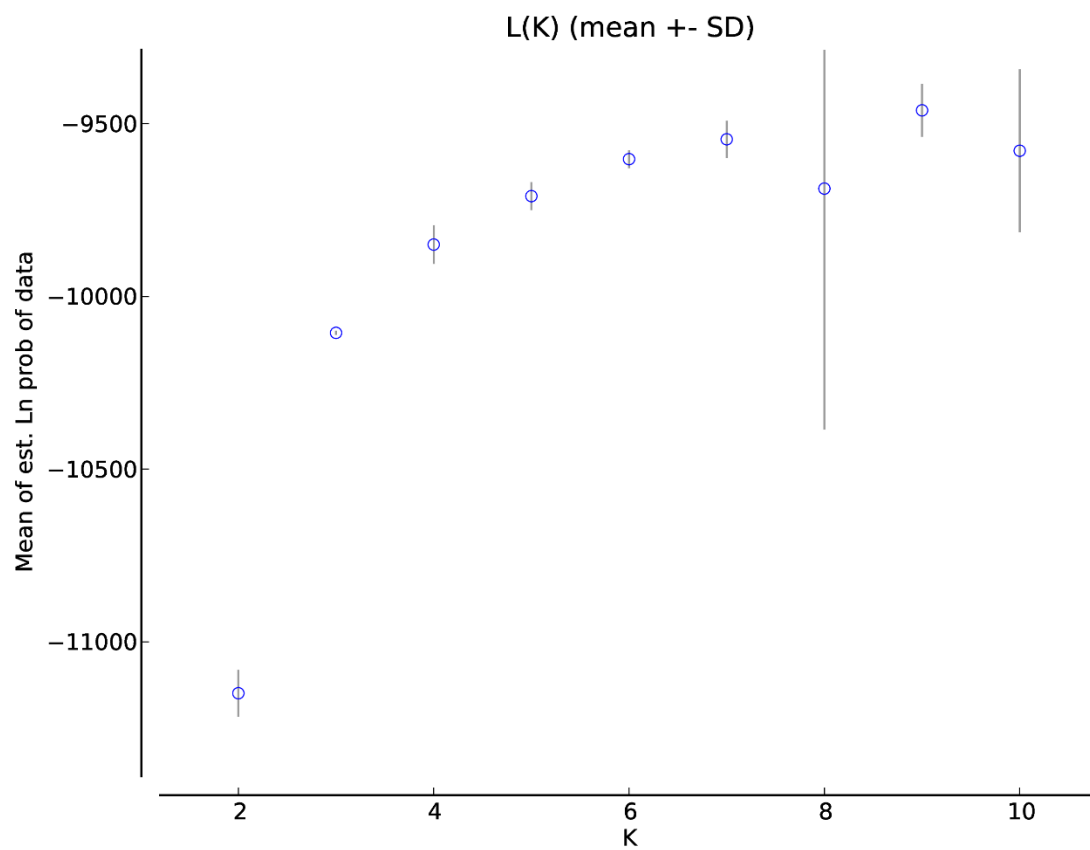


Figure S2. Probability of data (Ln) for number of clusters (K) ranging from 2 to 10 obtained by Structure harvester and Clumpak program.

Table S1. The name of markers, their forward and backward primer sequences, annealing temperatures and repeat motifs.

Marker	Forward primer/ Backward primer	Annealing temperature (°C)	Repeat motif
Bmag211	5' ATTCATCGATCTTGTATTAGTCC 3' 5' ACATCATGTCGATCAAAGC 3'	58	(CT)16
Bmag770	5' AAGCTCTTTCTTGTATTCGTG 3' 5' GTCCATACTCTTTAACATCCG 3'	55	(GT)13,(AG)19
Bmac90	5' ACATCAACCCTCCTGCTC 3' 5' CCGCACATAGTGGTTACATC 3'	58	(AC)20
Bmag0579	5' CCTAGATAAGGAACATAGCCA 3' 5' CAAAGACCCTAACTCATGTTC 3'	55	(AC)6(AG)15
GBM1234	5' TTCTTCTGACGGCGCTTATT 3' 5' TATGGGTACCCGCACTTAGC 3'	60	-
Bmac399	5' CGATGCTTTACTATGAGAGGT 3' 5' GGGTCTGAAGCCTGAAC 3'	62	(AC)21
EBmac0501	5' ACTTAAGTGCCATGCAAAG 3' 5' AGGGACAAAAATGGCTAAG 3'	58	(AC)13
Bmac0093	5' CGTTTGGGACGTATCAAT 3' 5' GGGAGTCTTGAGCCTACTG 3'	55	(AC)24
Bmac0134	5' CCAACTGAGTCGATCTCG 3' 5' CTTCGTTGCTTCTCTACCTT 3'	55	(AC)28
Bmag0720	5' AAACCGTTTGTATAGCACG 3' 5' ATAAGTGAATGCTTCTGAGGA 3'	55	(GT)6,(AG)49
AWBMS56	5' GGAGATTGTGGCTGCTGCTTTG 3' 5' GGCGACGGGTAGCTTGTATTTG 3'	58	-
Bmag692	5' GCAAGGTATCTCTTGTATTTTG 3' 5' TGGCATCTACAATCTAAAACA 3'	55	(CT)19
GBM1251	5' CCAGCAATAACAACGTGTGG 3' 5' TGTCTTTTATTTCCGGAGCG 3'	60	-
Bmag0125	5' AATTAGCGAGAACAAAATCAC 3' 5' AGATAACGATGCACCACC 3'	55	(AG)19

EBmac0415	5' GAAACCCATCATAGCAGC 3'	55	(AC)17
	5' AAACAGCAGCAAGAGGAG 3'		
Bmag0225	5' AACACACCAAAAAATATTACATCA 3'	58	(AG)26
	5' CGAGTAGTTCCCATGTGAC 3'		
Bmag0013	5' AAGGGGAATCAAAATGGGAG 3'	58	(CT)21
	5' TCGAATAGGTCTCCGAAGAAA 3'		
Bmac0067	5' AACGTACGAGCTCTTTTCTA 3'	55	(AC)18
	5' ATGCCAACTGCTTGTTTAG 3'		
EBmac541	5' ACGGATCTACTTTAGCTAGCA 3'	58	(AC)9
	5' AAACAACCCACACAATC 3'		
GMS116	5' GAAAGACTGACAGGCGGAAG 3'	55	(CA)16CTG(CA)4
	5' TTTCTTTGTGTGTGTGCAGTG 3'		
EBmac0871	5' TGCCTCTGTTGTGTTATTGT 3'	55	(TG)13
	5' CCCCAAGTGAACATTGAC 3'		
Bmac0701	5' ATGATGAGAACTCTTCACCC 3'	55	(AC)23
	5' TGGCACTAAAGCAAAAGAC 3'		
Bmag0808	5' TCATAGACTACGACGAAGATG 3'	55	(GA)16
	5' TCTTTGGATGTGTGTTTACTG 3'		
GBM1388	5' ACGCACAGATACGTACACGC 3'	60	-
	5' GCCCCTCCTAGAACACAACA 3'		
Bmac0030	5' CCCAATCGGAGTTACAGATG 3'	60	(AC)22
	5' GCCTCTCTGAGAATGGATC 3'		
Bmac181	5' ATAGATCACCAAGTGAACCAC 3'	55	(AC)20
	5' GGTTATCACTGAGGCAAATAC 3'		
GBM1221	5' ACCAGCAATCCAAGTTACGG 3'	55	-
	5' TGCCTTGGTCTTGGTGTGTA 3'		
GBM1323	5' GCTCTCCAGGGTTCGTTTC 3'	60	-
	5' CACCGTCTTGCAGTTGAGAC 3'		
Bmac0096	5' GCTATGGCGTACTATGTATGGTTG 3'	58	(AT)6(AC)16
	5' TCACGATGAGGTATGATCAAAGA 3'		
GMS001	5' CTGACCCTTTGCTTAACATGC 3'	60	(CT)7TTT(CT)2
	5' TCAGCGTGACAAACAATAAAGG 3'		
Bmag0223	5' TTAGTCACCCTCAACGGT 3'	58	(AG)16

	5' CCCCTAACTGCTGTGATG 3'		
Bmag337	5' ACAAAGAGGGAGTAGTACGC 3'	55	(AG)22
	5' GACCCATGATATATGAAGATCA 3'		
EBmac824	5' GCAAGCTTCCTAAATCCTTA 3'	55	(TG)4,(TG)4,(TG)4,(G T)4,(GT)4
	5' TGCAGACAGTTTTTCATATACA 3'		
GBM1164	5' TGAGTTTATTCGGTCTCGCC 3'	60	-
	5' ACGAACACCTTCATCCATCC 3'		
Bmac0113	5' TCAAAAGCCGGTCTAATGCT 3'	58	(AT)7(AC)18
	5' GTGCAAAGAAAATGCACAGATAG 3'		
Bmag0496	5' AGTATAACCAACAGCCGTCTA 3'	55	(CT)20
	5' CTATAGCACGCCTTTGAGA 3'		
Bmag0613	5' AAGAACACCATATGATCCAAC 3'	55	(GA)17
	5' CTCCATGACTATGAGGAGAAG 3'		
Bmag0500	5' GGGAAGTTGCTAATGAAGAG 3'	58	(AG)6CG(AG)29(AG AGGG)3(AG)6
	5' AATGTAAGGGAGTGTCCATAG 3'		
EBmac639	5' TTGAGGCCTACTGGTATGTAT 3'	58	(TG)5,(TG)8
	5' TAGTCCCTCATGCACAAGT 3'		
GBMS180	5' GGAAGTAATGCTTCGGTCCA 3'	58	(GA)30
	5' TGGTGCAAGTGAGCACCTAC 3'		
EBmac0602	5' GATTGGAGCTTCGGATCAC 3'	58	(AC)9AT(AC)7(AG)9
	5' CCGTCTAGGGAGAGGTTCTC 3'		
Bmag0009	5' AAGTGAAGCAAGCAAACAAACA 3'	58	(AG)13
	5' ATCCTTCCATATTTTGATTAGGCA 3'		
HVPLASC1B	5' GTGCATGCATCATATTGATTA 3'	55	(TCTAC)4
	5' ACGTACGTACTTATCACGAAGA 3'		
Bmag0369	5' CACTAGGCACCAATGACTG 3'	58	(CT)16
	5' ATCGAAAATCTTAGCTTTGG 3'		
Bmag0120	5' ATTCATCCCAAAGGAGAC 3'	58	(AG)15
	5' GTCACATAGACAGTTGTCTTCC 3'		
HvACL3	5' CCGTCTAGTAGGAGGAGTTATGG 3'	62	(AT)10
	5' CAAATCTTGTTCTCGCGGTCG 3'		
HVCMA	5' GCCTCGGTTTGGACATATAAAG 3'	60	(AT)9
	5' GTAAAGCAAATGTTGAGCAACG 3'		

HVSS1	5' TGGCCTTGGTGAATGTTTCG 3'	55	(AT)20
	5' TGTGGAGGCGAGTCAGCTTG 3'		
Bmag0011	5' ACAAAAACACCGCAAAGAAGA 3'	58	(AG)25
	5' GCTAGTACCTAGATGACCCCC 3'		
EBmac0603	5' ACCGAAACTAAATGAACTACTTCG 3'	58	(CA)10
	5' TGCAAACTGTGCTATTAAGGG 3'		

Table S2. The name of markers, their position on the chromosome, size range of detected alleles and basic molecular diversity parameters.

Marker	Chr.	Allele size	Na ¹	Ne	I	Ho	PIC	uHe	F
Bmag211	1H	178-188	6	4.50	1.60	0.000	0.778	0.782	1.000
Bmag770	1H	155-165	5	2.22	1.07	0.000	0.549	0.552	1.000
Bmac90	1H	215-230	6	2.00	1.07	0.000	0.500	0.503	1.000
Bmag0579	1H	120-142	9	6.34	1.99	0.000	0.842	0.847	1.000
GBM1234	1H	170-186	8	1.72	1.01	0.000	0.419	0.421	1.000
Bmac399	1H	145-151	3	2.89	1.08	0.000	0.655	0.658	1.000
EBmac0501	1H	145-164	4	3.57	1.32	0.000	0.720	0.724	1.000
Bmac0093	2H	154-158	3	1.78	0.78	0.000	0.438	0.441	1.000
Bmac0134	2H	140-164	8	5.51	1.85	0.000	0.819	0.823	1.000
Bmag0720	2H	169-183	6	3.80	1.54	0.000	0.737	0.741	1.000
AWBMS56	2H	190-224	12	9.53	2.36	0.000	0.895	0.900	1.000
Bmag692	2H	165-182	8	2.50	1.33	0.000	0.593	0.597	1.000
GBM1251	2H	130-144	5	1.53	0.74	0.000	0.346	0.348	1.000
Bmag0125	2H	120-142	9	6.25	1.98	0.000	0.840	0.845	1.000
EBmac0415	2H	249-263	7	3.10	1.47	0.000	0.677	0.681	1.000
Bmag0225	3H	140-169	16	4.05	1.88	0.033	0.753	0.757	0.956
Bmag0013	3H	147-161	5	2.35	1.04	0.000	0.575	0.578	1.000
Bmac0067	3H	168-181	7	4.30	1.55	0.022	0.767	0.772	0.971
EBmac541	3H	98-115	7	5.14	1.76	0.000	0.805	0.810	1.000
GMS116	3H	122-150	7	6.02	1.86	0.000	0.834	0.838	1.000
EBmac0871	3H	180-194	4	2.11	1.00	0.000	0.526	0.529	1.000
Bmac0701	4H	104-145	5	2.28	1.09	0.000	0.562	0.565	1.000
Bmag0808	4H	152-174	4	2.97	1.21	0.000	0.663	0.667	1.000
GBM1388	4H	130-154	11	7.82	2.19	0.000	0.872	0.877	1.000
Bmac0030	4H	155	1	1.00	1.00	0.000	0.000	0.000	-
Bmac181	4H	140-160	7	2.64	1.24	0.000	0.622	0.625	1.000
GBM1221	4H	143-157	6	2.55	1.22	0.000	0.607	0.611	1.000
GBM1323	4H	164-190	7	2.21	1.24	0.000	0.548	0.551	1.000
Bmac0096	5H	164-197	9	2.27	1.29	0.000	0.560	0.563	1.000

GMS001	5H	107-132	5	1.23	0.45	0.022	0.187	0.188	0.881
Bmag0223	5H	134	1	1.00	1.00	0.000	0.000	0.000	-
Bmag337	5H	139-149	5	2.19	1.09	0.000	0.543	0.546	1.000
EBmac824	5H	280-308	7	3.002	1.45	0.000	0.667	0.671	1.000
GBM1164	5H	132-140	3	1.20	0.36	0.000	0.166	0.137	1.000
Bmac0113	5H	165-189	8	5.67	1.86	0.000	0.824	0.828	1.000
Bmag0496	6H	179-211	9	3.57	1.57	0.011	0.720	0.724	0.985
Bmag0613	6H	159-195, null	9	3.13	1.48	0.022	0.681	0.685	0.967
Bmag0500	6H	140-174	11	5.96	2.04	0.000	0.832	0.837	1.000
EBmac639	6H	191-213	9	3.56	1.64	0.000	0.719	0.723	1.000
GBMS180	6H	185-197	6	2.24	1.18	0.000	0.554	0.557	1.000
EBmac0602	6H	199-223	10	6.67	2.03	0.000	0.850	0.855	1.000
Bmag0009	6H	159-183	6	5.25	1.72	0.000	0.809	0.814	1.000
HVPLASC1B	7H	97-107	4	2.03	0.93	0.067	0.506	0.509	0.868
Bmag0369	7H	171-192	5	1.62	0.75	0.000	0.383	0.385	1.000
Bmag0120	7H	207-263, null	10	3.96	1.61	0.057	0.747	0.752	0.923
HvACL3	7H	198-216	6	4.46	1.65	0.000	0.776	0.780	1.000
HVCMA	7H	133-145	4	1.40	0.56	0.000	0.287	0.289	1.000
HVSS1	7H	222-254	8	6.45	1.95	0.000	0.845	0.850	1.000
Bmag0011	7H	134-163	9	7.34	2.09	0.000	0.864	0.869	1.000
EBmac0603	7H	130-160	8	5.12	1.81	0.000	0.805	0.809	1.000
Mean			338/6.76	3.64	1.36	0.005	0.625	0.629	0.991

¹Na - number of detected alleles per locus, Ne - number of effective alleles, I - Shannon's Information Index, Ho - observed heterozygosity, PIC - polymorphism information content, uHe - unbiased expected heterozygosity, F - Wright fixation index.

Table S3. Multivariate analysis of variance (MANOVA) using Wilks' Lambda test differences between group means for a combination of the analyzed agronomical traits.

	Df ¹	Wilks	approx F	num Df	den DF	Pr(>F)	partial.etasq
Season	1	0.57667	72.03	8	785	< 2.2e-16	0.507
Row type	2	0.00213	2028.15	16	1570	< 2.2e-16	0.837
Period	2	0.67233	21.55	16	1570	< 2.2e-16	0.178
Season × row type	2	0.69389	19.67	16	1570	< 2.2e-16	0.192
Season × period	2	0.95178	2.46	16	1570	0.001098	0.053
Row type × period	4	0.80772	5.40	32	2896.5	< 2.2e-16	0.057
Season × row type × period	4	0.92693	1.88	32	2896.5	0.001995	0.024
Residuals	792						

¹Df—the number of degrees of freedom, Wilks—Wilks' Lambda value, approx F—the approximate F statistic, num Df—the number of degrees of freedom in the model, den DF—the number of degrees of freedom associated with the model errors, Pr(>F)—the p-value associated with the F statistic, partial.etasq—partial eta-square value

Table S4. Analysis of variance for heading time with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	1250	43.92	< 2.2e-16	***	0.093
Row type	2	203633	7153.90	< 2.2e-16	***	0.995
Period	2	251	8.83	0.00016	***	0.085
Season × row type	4	1365	23.98	< 2.2e-16	***	0.357
Season × period	4	334	5.87	0.0001	***	0.015
Row type × period	4	168	2.95	0.0195	*	0.040
Season × row type × period	8	425	3.73	0.0003	***	0.037
Residuals	783	11144				
Genotype	89	866277	14988.78	< 2.2e-16	***	
Season	2	582	447.78	< 2.2e-16	***	
Genotype × season	178	11590	100.27	< 2.2e-16	***	
Residuals	540	351				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, *—significance at 0.05 probability level

Table S5. Analysis of variance for flowering time with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	1443	49.10	< 2.2e-16	***	0.098
Row type	2	205486	7000.00	< 2.2e-16	***	0.995
Period	2	280	9.55	8.02e-05	***	0.073
Season × row type	4	1542	26.30	< 2.2e-16	***	0.36
Season × period	4	340	5.78	0.0001	***	0.014
Row type × period	4	141	2.41	0.0481	*	0.031
Season × row type × period	8	439	3.74	0.0003	***	0.037
Residuals	783	11498				
Genotype	89	878049	14270.05	< 2.2e-16	***	
Season	2	726	525.05	< 2.2e-16	***	
Genotype × season	178	12221	99.31	< 2.2e-16	***	
Residuals	540	373				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, *—significance at 0.05 probability level

Table S6. Analysis of variance for plant height with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	6363	57.67	< 2.2e-16	***	0.452
Row type	2	4994	45.26	< 2.2e-16	***	0.464
Period	2	555	5.03	0.0067	**	0.045
Season × row type	4	581	2.63	0.0333	*	0.064
Season × period	4	1584	7.18	1.12e-05	***	0.044
Row type × period	4	289	1.31	0.2645	ns	0.023
Season × row type × period	8	910	2.06	0.0373	ns	0.021
Residuals	783	43199				
Genotype	89	24382	17.73	< 2.2e-16	***	
Season	2	566	18.33	< 2.0e-08	***	
Genotype × season	178	28356	10.31	< 2.2e-16	***	
Residuals	540	8342				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, **—significance at 0.01 probability level, *—significance at 0.05 probability level, ns—non significant.

Table S7. Analysis of variance for spike length with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	24.48	5.83	0.0031	**	0.042
Row type	2	152.36	36.31	8.33e-16	***	0.531
Period	2	6.47	1.54	0.2147	ns	0.027
Season × row type	4	24.34	2.90	0.0212	*	0.035
Season × period	4	13.3	1.58	0.1765	ns	0.018
Row type × period	4	12.82	1.53	0.1924	ns	0.025
Season × row type × period	8	30.33	1.81	0.0725	ns	0.018
Residuals	783	1642.9				
Genotype	89	1081.00	46.26	< 2.2e-16	***	
Season	2	7.74	14.73	< 5.9e-07	***	
Genotype × season	178	610.43	13.06	< 2.2e-16	***	
Residuals	540	141.77				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, **—significance at 0.01 probability level, *—significance at 0.05 probability level, ns—non significant.

Table S8. Analysis of variance for grain number per square meter with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	5.52e+08	1517.84	< 2.2e-16	***	0.395
Row type	2	6.42e+08	29.16	6.12e-13	***	0.433
Period	2	1.32e+08	33.90	7.59e-15	**	0.001
Season × row type	4	3.46e+08	6.95	0.0010	***	0.160
Season × period	4	4.31e+08	9.15	13.15e-07	***	0.065
Row type × period	4	2.75e+08	11.38	5.5e-09	***	0.027
Season × row type × period	8	2.69e+08	7.26	9.6e-06	***	0.035
Residuals	783	7.41e+09	3.55	0.0005		
Genotype	89	7.11e+09	32.49	< 2.2e-16	***	
Season	2	2.68e+08	54.52	< 2.2e-16	***	
Genotype × season	178	6.06e+09	13.85	< 2.2e-16	***	
Residuals	540	1.33e+09				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, **—significance at 0.01 probability level.

Table S9. Analysis of variance for thousand grain weight with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	789	26.68	6.15e-12	***	0.293
Row type	2	835	28.26	1.41e-12	***	0.460
Period	2	434	14.67	5.55e-07	***	0.166
Season × row type	4	227	3.84	0.0042	**	0.090
Season × period	4	286	4.84	0.0007	***	0.029
Row type × period	4	78	1.32	0.2589	ns	0.008
Season × row type × period	8	169	1.43	0.1816	ns	0.014
Residuals	783	11571				
Genotype	89	6686.3	25.9297	5.70e-04	***	
Season	2	43.9	7.5739	< 2.20e-16	***	
Genotype × season	178	6761.3	13.1102	< 2.20e-16	***	
Residuals	540	1564.6				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, **—significance at 0.01 probability level, ns—non significant.

Table S10. Analysis of variance for hectoliter weight with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	19	1.2688	0.2817	ns	0.147
Row type	2	417	27.7578	2.26e-12	***	0.412
Period	2	45	2.9784	0.0515	ns	0.009
Season × row type	4	127	4.2278	0.0022	**	0.061
Season × period	4	91	3.0187	0.0174	*	0.013
Row type × period	4	102	3.4016	0.0091	**	0.052
Season × row type × period	8	181	3.0042	0.0025	**	0.030
Residuals	783	5885				
Genotype	89	2501.3	19.656	< 2.0e-16	***	
Season	2	0.3	0.105	0.9003	ns	
Genotype × season	178	3630.2	14.264	< 2.0e-16	***	
Residuals	540	772.1				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, **—significance at 0.01 probability level, *—significance at 0.05 probability level, ns—non significant.

Table S11. Analysis of variance for yield with partial eta-square.

	Df ¹	Sum Sq	F value	Pr(>F)	Sig.	partial etasq
Season	2	80.26	31.0224	1.08e-13	***	0 .436
Row type	2	79.63	30.7812	1.35e-13	***	0 .569
Period	2	50.92	19.6805	4.58e-09	***	0 .089
Season × row type	4	62.5	12.0797	1.57e-09	***	0 .160
Season × period	4	46.86	9.0569	3.74e-07	***	0 .078
Row type × period	4	12.71	2.4559	0.04439	*	0 .010
Season × row type × period	8	24.93	2.409	0.01427	*	0 .024
Residuals	783	1012.84				
Genotype	89	894.56	24.659	< 2.2e-16	***	
Season	2	16.72	20.512	2.59e-09	***	
Genotype × season	178	907.02	12.501	< 2.2e-16	***	
Residuals	540	220.11				

¹Df—the number of degrees of freedom, Sum Sq — Sum of Squares, F value—the F statistic, Pr(>F)—the p-value associated with the F statistic, Sig.—the significance level, partial.etasq—partial eta-square value, ***—significance at 0.001 probability level, *—significance at 0.05 probability level.