

Supplementary Table S1 Features of the Norin 61 genome assembly. Main statistics of the Norin 61 assembly at different stages. The number of bases includes unassigned (N) bases. In the 1.1 version with sequences assigned to pseudochromosomes, all the unanchored sequences were concatenated in a single fasta.

	v1.0 scaffolds	v1.1 scaffolds
Total bases (Mb)	14,157	14,910
Total scaffolds (#)	4,135	22,838
Scaffold N50 (Mb)	23.7	21.9
Scaffold N90 (Mb)	4.3	2.6
Scaffold L50 (#)	146	162
Scaffold L90 (#)	684	881
Gap sequence (Mb)	113.3	113.3
% of gaps	0.8	0.8

Supplementary Table S2 Chromosomal positions and gene content of putative alien introgressions in
Norin 61

Chr	Beg [Mb]	End [Mb]	Size [Mb]	Genes	Private ^a	Private [%] ^b
1A	0	41.7	41.7	660	103	15.6
1A	292.8	462.1	169.3	1076	70	6.5
1A	493.7	535.7	42	557	35	6.2
1A	562.7	591.5	28.8	500	55	11
2A	726.8	781.2	54.4	1089	113	10.3
3A	42.6	77.5	34.9	449	39	8.6
3A	89	111.6	22.6	183	17	9.2
3A	526.3	567.6	41.3	286	22	7.6
3A	696.9	751	54.1	872	136	15.5
4A	11.3	43.5	32.2	357	24	6.7
5A	449.3	474.4	25.1	251	12	4.7
6A	14.9	41.5	26.6	448	39	8.7
7A	0	34	34	697	50	7.1
7A	67.3	97.4	30.1	372	22	5.9
7A	705.2	731.7	26.5	477	35	7.3
1B	174	223.7	49.7	150	19	12.6
1B	320	350.1	30.1	199	17	8.5
1B	541	580.7	39.7	377	28	7.4
1B	615.9	649.5	33.6	458	36	7.8
2B	12.9	57.4	44.5	733	65	8.8
2B	203.6	238.4	34.8	206	6	2.9
2B	489.2	522.9	33.7	269	14	5.2
2B	572.3	601.1	28.8	189	9	4.7
2B	644.4	667.8	23.4	214	13	6
2B	700.9	798.5	97.6	1328	113	8.5
3B	25	46.3	21.3	271	38	14
3B	75.3	101	25.7	252	21	8.3
3B	114.8	136.3	21.5	133	3	2.2
3B	567.1	666.9	99.8	758	47	6.2

3B	700.5	734.2	33.7	260	16	6.1
5B	0	25.7	25.7	252	21	8.3
5B	457	484	27	306	20	6.5
5B	508.9	610.2	101.3	1240	99	7.9
6B	149.5	176.1	26.6	205	19	9.2
6B	420.4	442.6	22.2	75	5	6.6
6B	531	567.6	36.6	263	21	7.9
6B	615.3	651.4	36.1	306	23	7.5
7B	19.9	69	49.1	448	39	8.7
7B	542.4	669.6	127.2	1076	62	5.7
1D	407.3	433.4	26.1	374	38	10.1
2D	64	111.4	47.4	567	46	8.1
2D	524	548.6	24.6	330	19	5.7
5D	199.4	219.5	20.1	100	7	7
5D	249.3	315.2	65.9	514	23	4.4
6D	156.8	178.4	21.6	98	10	10.2

^a Genes without homologs in corresponding regions in Chinese Spring

^b Percentage of genes without homologs in corresponding regions in Chinese Spring

Supplementary Table S3 Summary of homologous search of *FT-B1* gene against CS RefSeq v2.0

Query	Chr	Start_query	End_query	Start_subject	End_subject	Length	Evalue	Bitscore	Mismatch	%Identity
TraesCS7B02G13100.1	Chr7B	1	203	10073960	10073758	203	4.80E-101	375	0	100
	Chr7B	202	264	10073132	10073070	63	3.21E-23	117	0	100
	Chr7B	263	534	10072974	10072703	272	2.11E-139	503	0	100
	Chr7B	1	203	10086304	10086102	203	4.80E-101	375	0	100
	Chr7B	202	264	10085476	10085414	63	3.21E-23	117	0	100
	Chr7B	263	534	10085318	10085047	272	2.11E-139	503	0	100
	Chr7B	1	203	10098658	10098456	203	4.80E-101	375	0	100
	Chr7B	202	264	10097831	10097769	63	3.21E-23	117	0	100
	Chr7B	263	534	10097673	10097401	273	9.81E-138	497	0	99.634
	Chr7D	1	203	70131685	70131483	203	2.25E-94	353	4	98.03
	Chr7D	202	264	70131083	70131021	63	3.21E-23	117	0	100
	Chr7D	263	534	70130931	70130660	272	9.95E-128	464	7	97.426
	Chr7A	1	203	74957656	74957858	203	2.25E-94	353	4	98.03
	Chr7A	202	264	74958248	74958310	63	3.21E-23	117	0	100
	Chr7A	263	534	74958417	74958688	272	4.63E-126	459	8	97.059

Supplementary Table S4 Variation at *Rht8* and the FHB-QTL on 2DS

Cultivar	<i>Rht8</i> (GWM261)*	FHB-QTL on 2DS** (<i>TaMRP-D1</i>)
Norin 61	194	susceptible
Arina <i>LrFor</i>	161	resistant
Chinese Spring	192	susceptible
Jagger	210	resistant
Julius	170	resistant
LongReach lancer	161	resistant
CDC Landmark	161	resistant
Mace	192	susceptible
CDC Stanley	161	resistant
SY Mattis	170	resistant
PI190962 (Spelt wheat)	170	resistant

*; amplification size of a diagnostic SSR marker *Xgwm261* for *Rht8*, a QTL showing pleiotropic effects on reducing plant height and spike length with 192bp allele (Korzun et al. 1998, Chai et al. 2019)

**; alleles of *TaMRP-D1*, a candidate gene for the FHB-QTL on 2DS (Niwa et al. 2018)

Supplementary Table S5 Summary of genes responsible for adaptation to East Asian environments and the corresponding gene ID in Chinese Spring (CS) and Norin 61. When the Norin 61 annotation was lacking the homolog gene, the assembly region with sequence homology was reported.

Gene symbol	GenBank accession	CS	Norin 61
<i>Ppd-A1</i>	AB646973.1	TraesCS2A02G081900	TraesNOR2A01G096300
<i>Ppd-D1</i>	KJ147477.1	TraesCS2D02G079600	TraesNOR2D01G091900
<i>TaRHC-R</i>	MK450312	NA	TraesNOR3B01G031400
<i>TaRHC-S</i>	MK450309	TraesCS3B02G019900	NA
<i>Rht-B1</i>	FR668586.2	TraesCS4B02G043100	TraesNOR4B01G049000
<i>Rht-D1</i>	HE585643.1	TraesCS4D02G040400	chrUn_341124423-341126675
<i>Tamyb10-A1</i>	AB599721.1	Chr3A:703904380-703906112	Chr3A:704333801-704335747
<i>Tamyb10-B1</i>	AB191459.1	TraesCS3B02G515900	TraesNOR3B01G571000
<i>Tamyb10-D1</i>	AB191460.1	TraesCS3D02G468400	TraesNOR3D01G503600