A homolog of blade-on-petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence

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SUPPLEMENTAL MATERIALS

Title: A homolog of *Blade-On-Petiole 1* and *2* (*BOP1/2*) controls internode length and homeotic changes of the barley inflorescence

Authors: Jost et al.

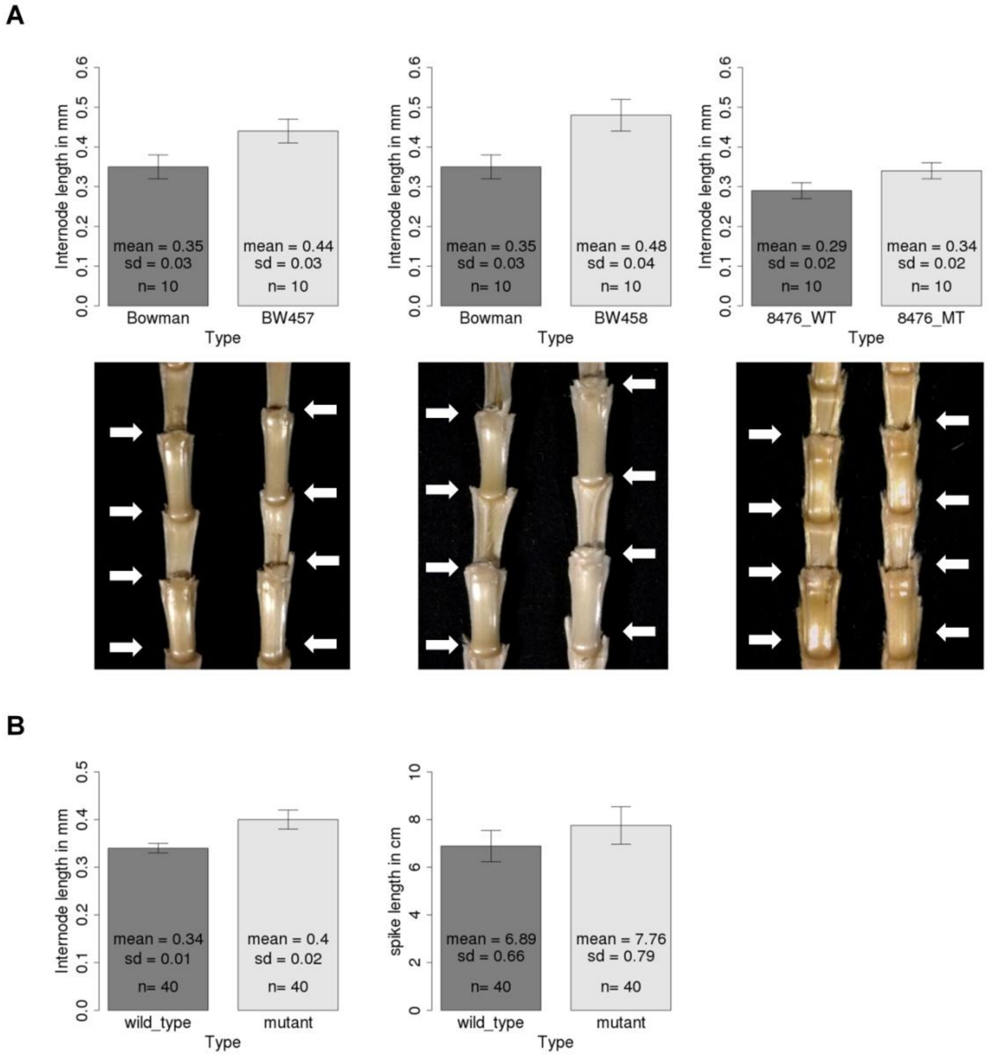

Figure S1: Rachis internode length in *lax-a* mutant and wild type plants.
Rachis internode length was determined for three spikes per plant by dividing total spike length by number of rachis nodes (number of grains). A) The average rachis internode length for Bowman spikes compared to BW457 and BW458, respectively, as well as for the TILLING mutant 8476 with wild type allele against homozygote mutant plants (upper panel) revealed extended rachis internode lengths for all mutants. The lower panel shows a detailed view from part of the rachis for each wild type (left) and mutant (right), respectively. Rachis nodes are indicated by white arrows. B) 40 wild-type plants and mutant plants, respectively, of the segregating mapping population (Bowman x BW457) were analysed for scoring segregation of the trait. While rachis internode length showed a significant difference, spike length was not significantly different between wild type and mutant plants.

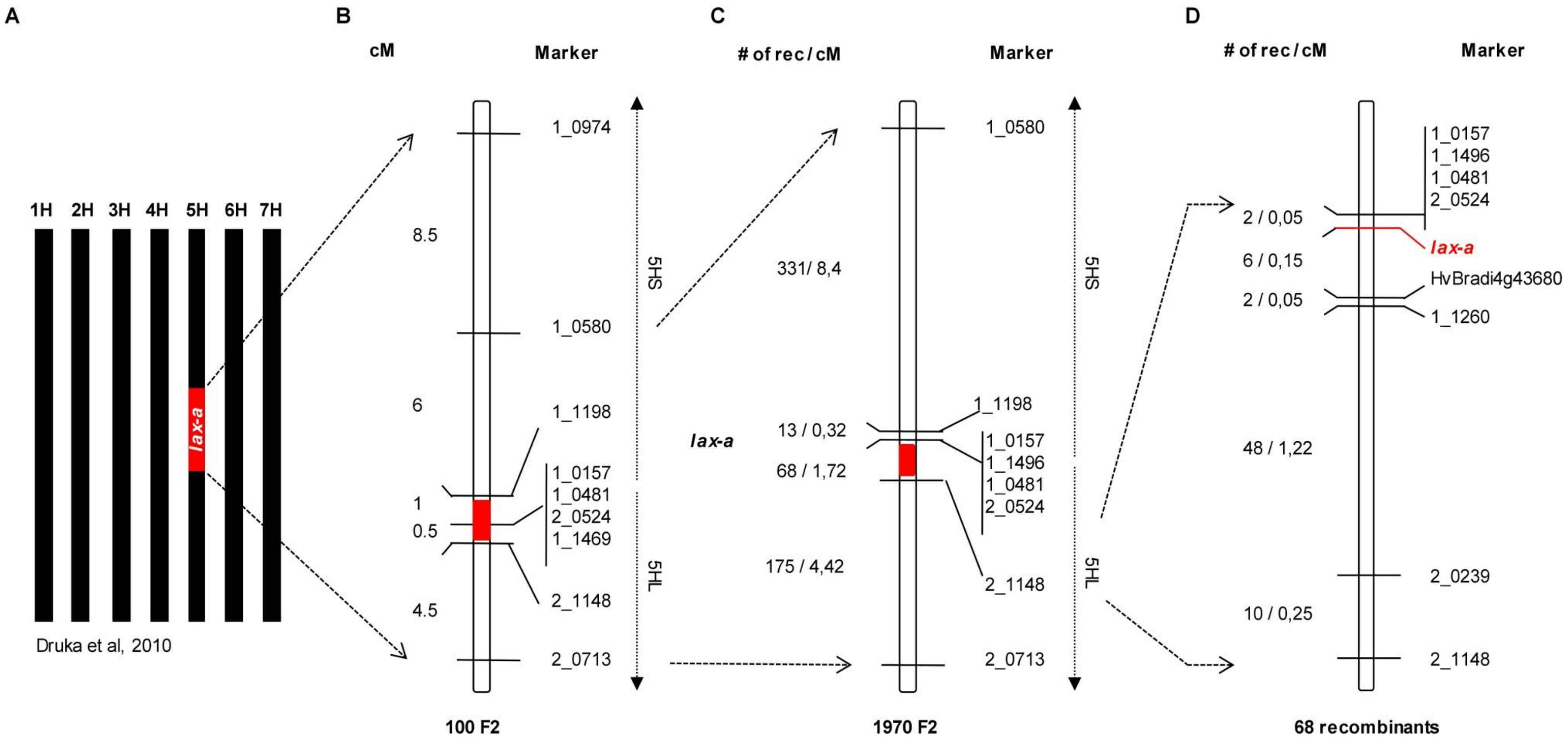

Figure S2: Genetic mapping

A) Schematic drawing of the previously localized 38.5 cM introgressed segment (red box) of the original *lax-a.8* mutant on chromosome 5H in the genetic background of Bowman (IBSC, 2012). B) Low resolution mapping in 100 F2 plants narrowed *lax-a* locus interval to 1.5 cM. The vertical arrows indicate the chromosomal assignment of markers based on sorted chromosome arm sequencing data (Mayer et al., 2011) C) High resolution mapping in 1,970 F2 plants allocated the gene to a 1.87 cM interval on long arm of 5H. D) The interval around the gene locus was narrowed by further markers to a 0.2 cM interval.

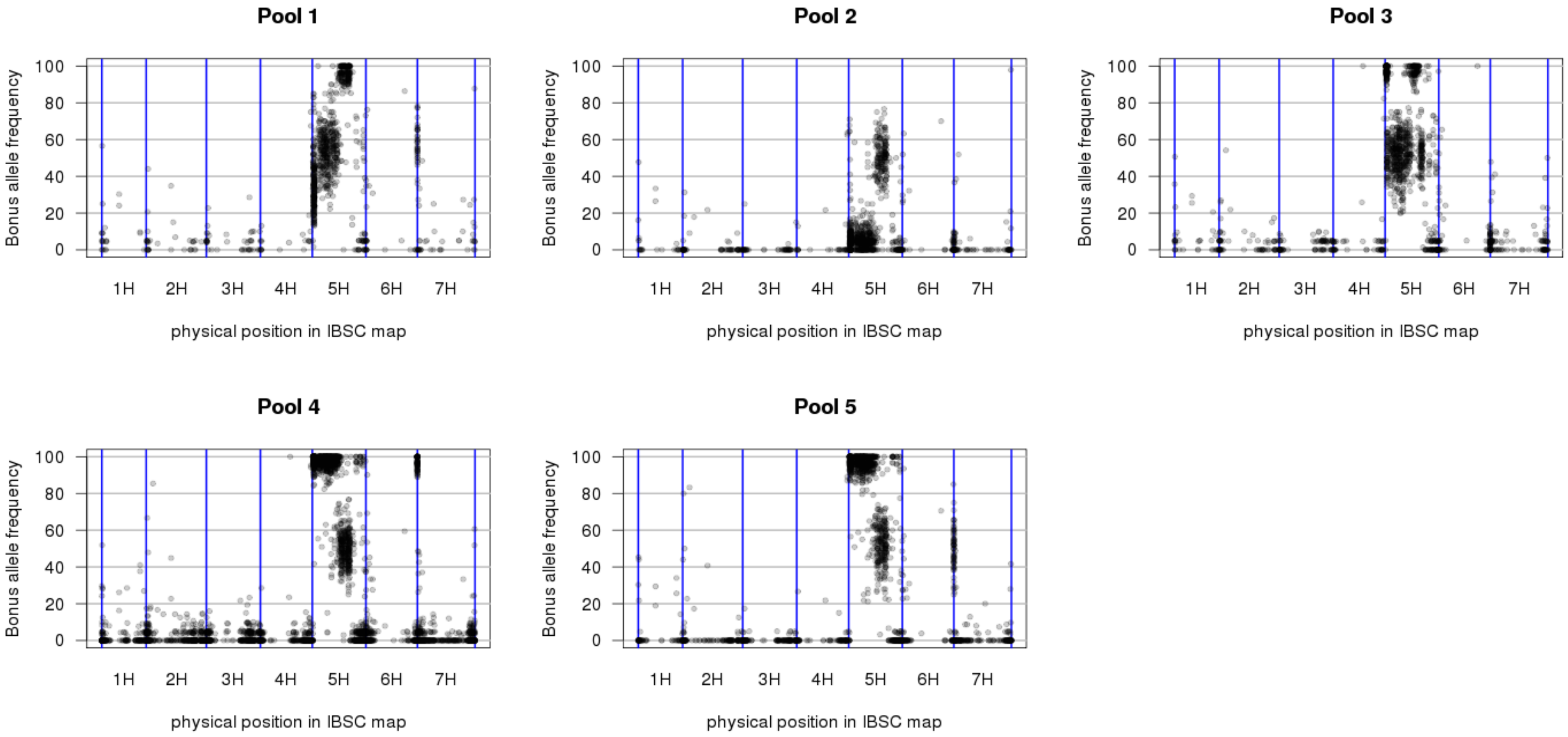

Figure S3: Exome capture SNP-Plots

Allele frequency is visualized along the seven chromosomes of barley (separated by blue lines) for each sequenced pool. Each SNP is represented by a dot and positioned by the assigned anchoring to the integrated physical and genetic map of barley (IBSC, 2012). The allele frequency was calculated as the proportion of reads supporting the BW457 allele. Allele frequencies in the neighborhood the gene locus on 5H closely reflected the recombination events detected by conventional genotyping.

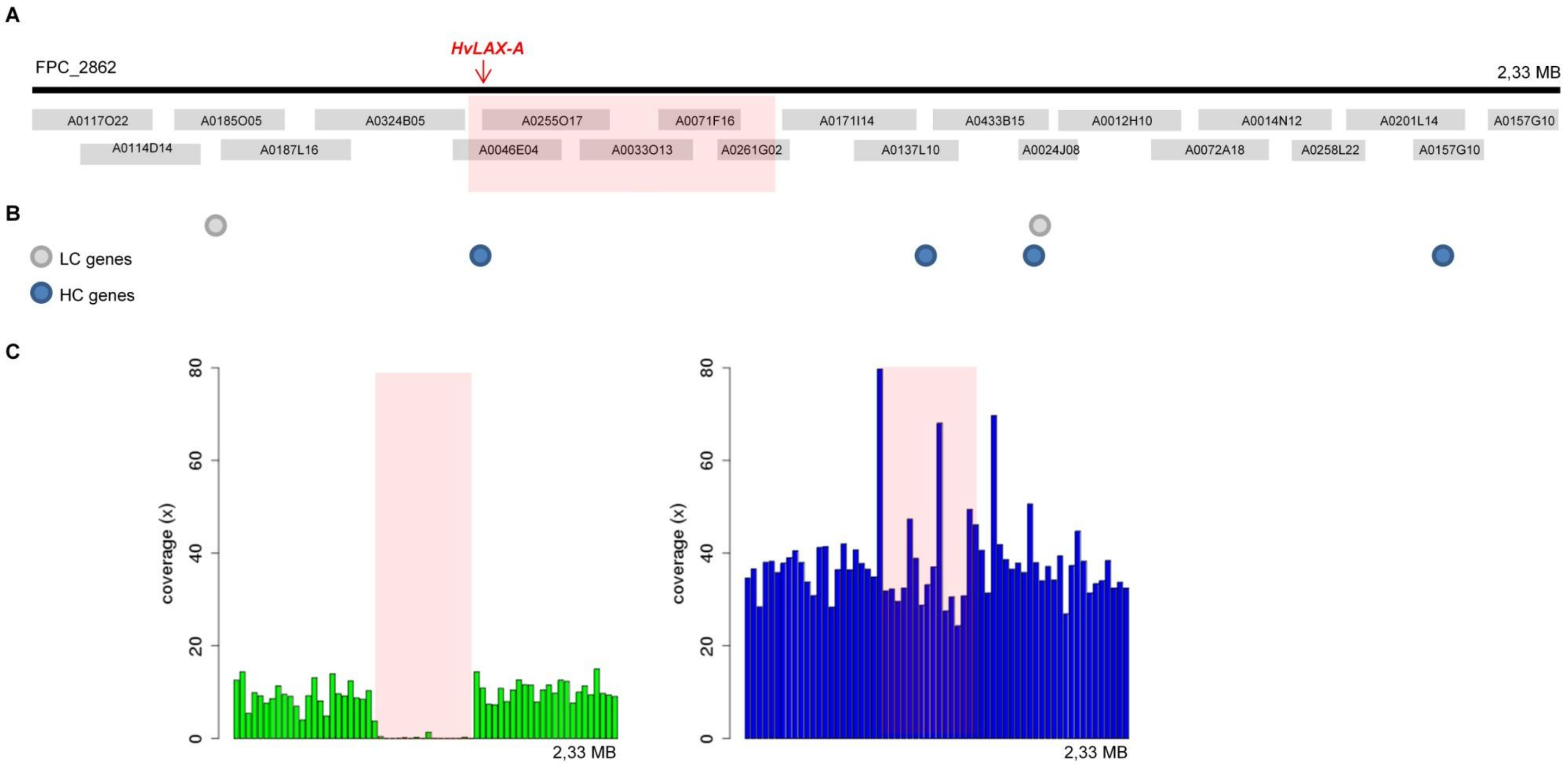

Figure S4: Sequence analysis of FPcontig_2862 containing the *HvLax-A* candidate gene

A) Sequencing a contig of overlapping BAC clones carrying the *lax-a* candidate gene revealed 2.33 Mbp of cumulative sequence. Sequences were used for gene prediction of high confidence genes (blue) and low confidence genes (grey) of the barley gene set (Table S7). C) Graphical visualization of the average read coverage of Bowman WGS contigs anchored to the BAC sequence contigs of FPcontig_2862. The x-axis represents anchored Bowman WGS contigs arranged along the FPcontig. Each bar represents one Bowman WGS contig. The mean read coverage of raw reads from WGS B457 (left) and Bowman (right) of each anchored WGS Bowman contig is given on the y-axis. In the center of the contig no read coverage was detected for the WGS data of the mutant indicating a large deletion of around 500 kb (marked in red in A and C).

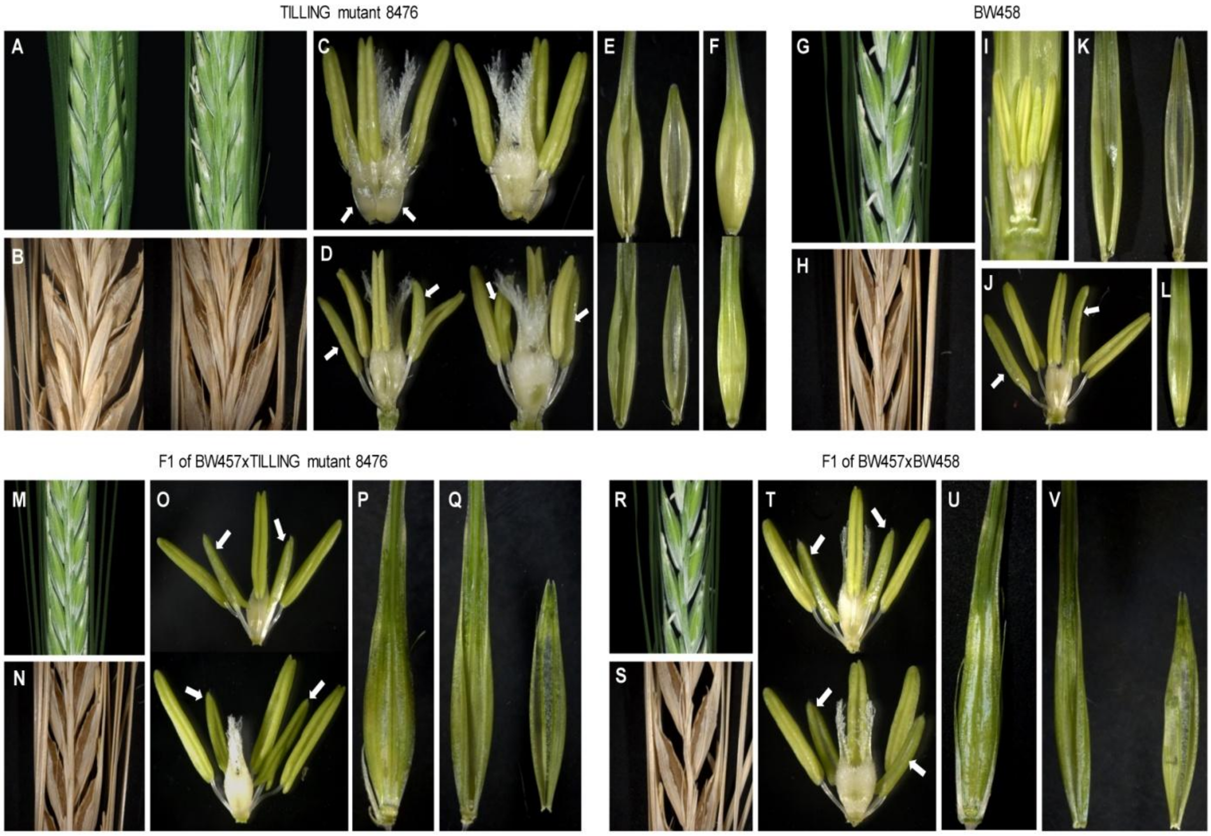

Figure S5: Independent lax-a mutant alleles and allelism test

The figure summarizes the phenotype information for TILLING mutant 8476 (A-F) and NIL BW458 (G-L) and (M-V) their respective F1 crosses with the original NIL BW457 which was used for cloning of the gene. Segregants of TILLING mutant family 8476 with either homozygous wild-type or mutant allele compared for *lax-a* characteristic traits: (A+B) exposed caryopsis of the mutant (right) to the covered grains of the wild type; five instead of three anthers in (D) mutant *vs.* (C) wild-type plants; (E, F) reduced width of lemma and palea and broadened lemma awn base in mutant (lower panels) compared to wild-type (upper panels). (G+H) BW458 carries exposed grains, (I) the wide awn base, (J) five anthers, (K) lax-a typical lemma and palea. Test of allelism: F1 generated by crossing BW457 with independent *lax-a* mutants TILLING8476 and BW458, respectively exhibited the typical *lax-a* mutant phenotype: (M, N and R, S) exposed caryopsis, (O, T) five anthers, (P,U) broad awn base and (Q,V) changed palea and lemma growth. Arrows indicating the homeotically changed organs.

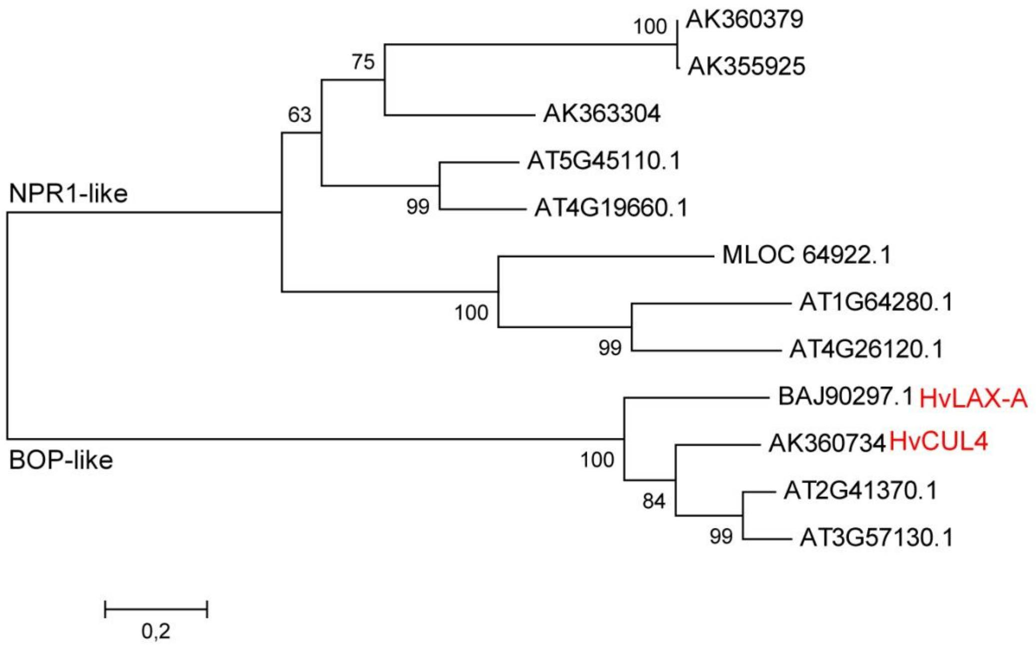

Figure S6: BOP/ANK gene family of Arabidopsis and barley

A combined phylogenetic analysis of barley and Arabidopsis *NPR1-like* and *BOP-like* genes revealed the grouping of barley and Arabidopsis genes (gene ID starts with AT) in a phylogenetic tree. *HvLAX-A* (BAJ90297.1) and the paralogous gene (*HvCUL4*) AK360734 clustered together with Arabidopsis *BOP1* (AT3G57130.1) *and BOP2* (AT3G57130.1). The published protein sequence (Matsumoto et al., 2011) (NCBI accession number: BAJ90297.1) was used instead of MLOC_61451.6 for HvLAX-A due to error in the published gene annotation (IBSC, 2012).

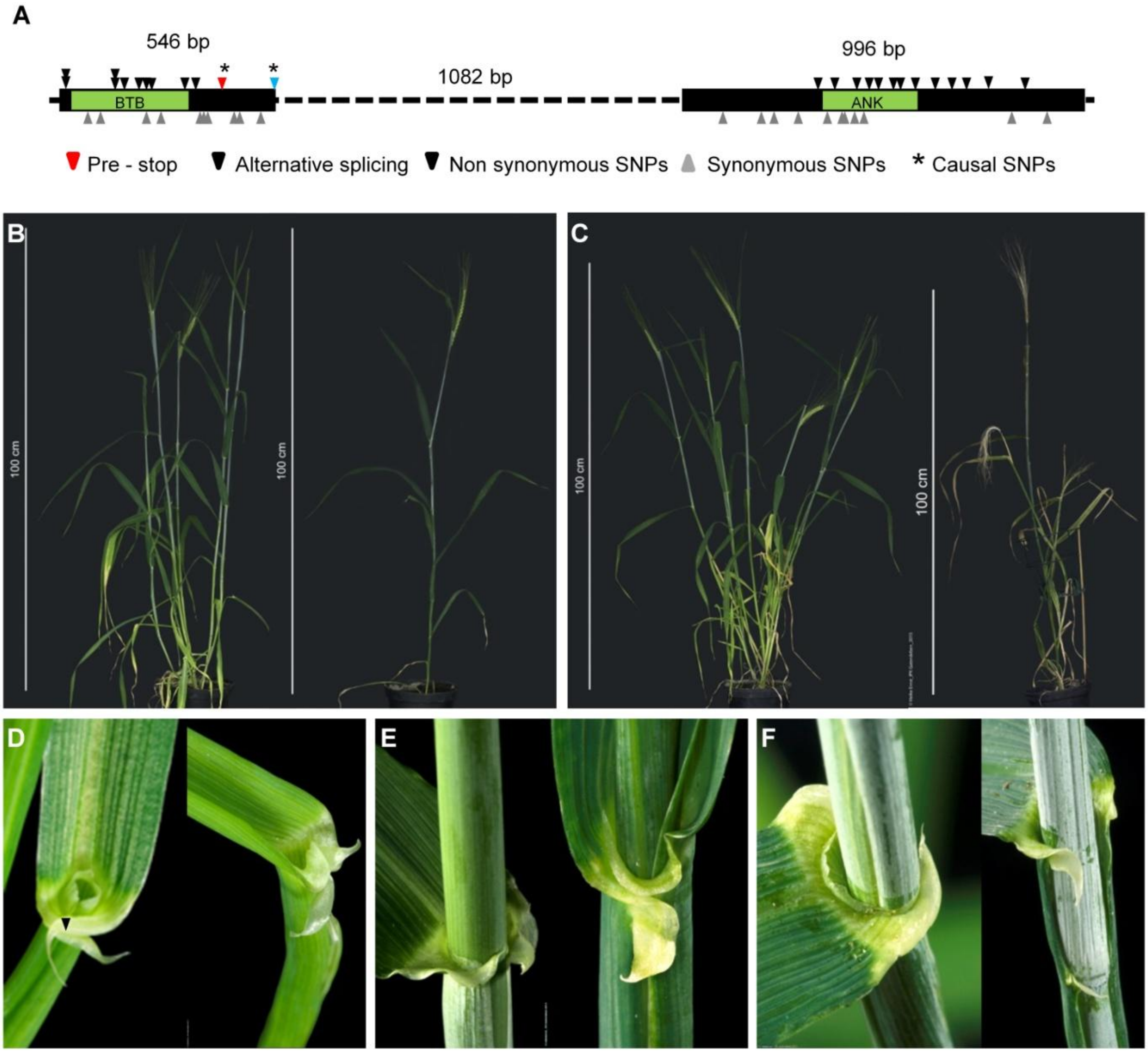

Figure S7: Phenotype of mutants obtained by TILLING of *HvCUL4*

A) Gene model of the gene *HvCUL4* represented by two exons (black boxes) spaced by a single intron (black dashed line). SNPs identified by TILLING are displayed as triangles (colored according to classification) along the gene model. B) An example of a mutant plant with splice site mutation (13391_1) and TILLING mutant 9425_1 with premature stop codons (C) developed only few tillers (right) compared to plants with wild-type allele (left). D-F) All mutant plants lacked ligules (ligule-less) but showed irregular outgrowth of auricles at the leaf sheath / leaf blade boundary.

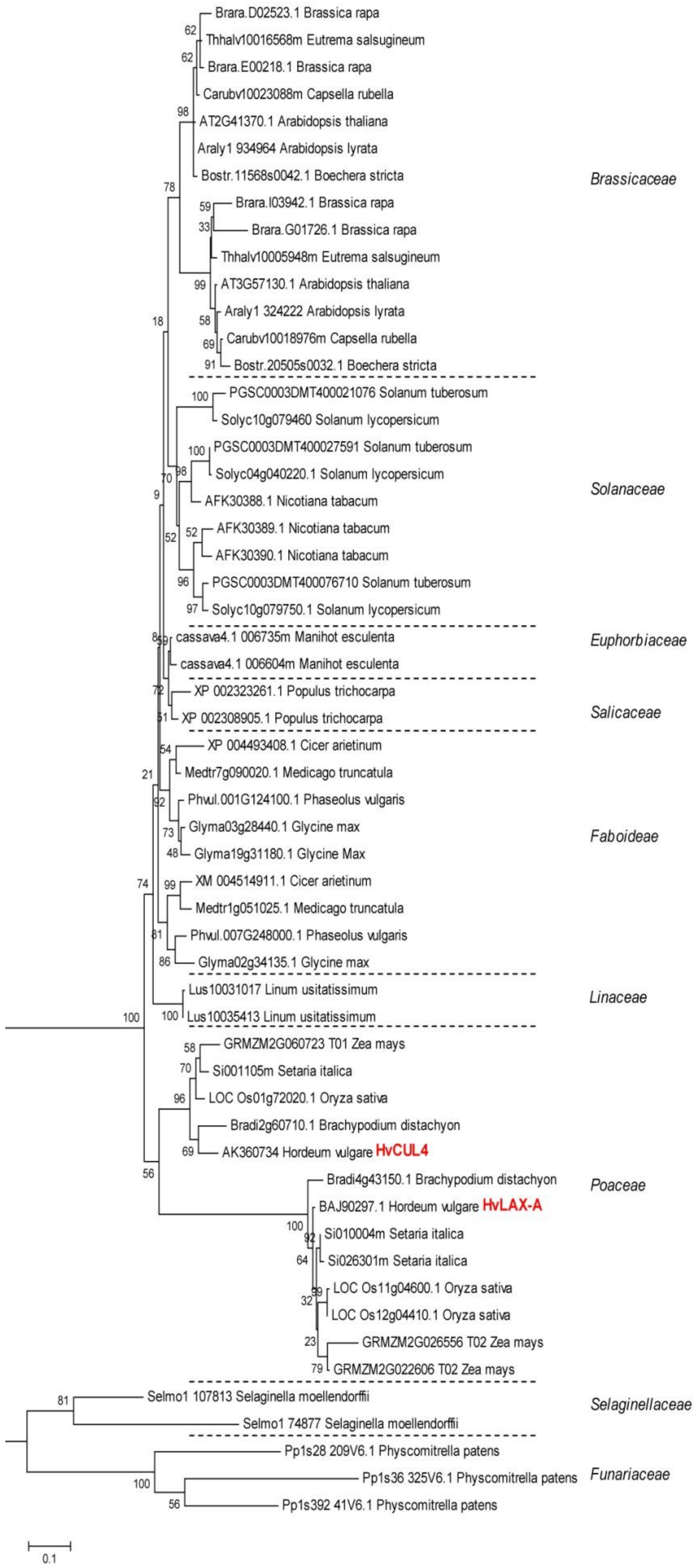

Figure S8: Phylogenetic analysis of BOP-like genes in the plant kingdom

A maximum likelihood phylogenetic tree was constructed based on protein sequences of BOP-like genes within the plant kingdom. All genes separated in clades according to their respective plant families (indicated by dashed lines). Each protein was labeled by the protein ID as well the plant species.

Table S1: Statistics of target enrichment sequencing

Sample	Index sequence	Total number of reads	Mapped reads[1]	Properly paired reads	Properly paired reads after duplicate removal
lax1	CGATGT	67,592,236	53,732,601	37,281,384	33,754,256
lax2	TGACCA	60,720,904	48,809,894	34,525,624	32,025,587
lax3	GCCAAT	74,331,140	59,242,078	41,465,344	37,510,881
lax4	CAGATC	106,034,474	83,848,875	61,404,722	55,777,226
lax5	CTTGTA	81,812,718	65,155,410	47,083,348	42,338,700

[1] mapped against Bowman WGS sequence assembly (IBSC, 2012)

Table S2: Filter for cosegregating targets with expected SNP frequency within captured pools

Bowman WGS_contig[1]	pos	ref	alt	ratio_lax_1	ratio_lax_2	ratio_lax_3	ratio_lax_4	ratio_lax_5	depth_lax_1	depth_lax_2	depth_lax_3	depth_lax_4	depth_lax_5	cM[1]	MB[1]	FPcontig[1]
contig_221364	6495	C	G	0.57	0	1	0.95	0.59	7	19	5	19	17	44.23	203.9	contig_2862
contig_859419	2590	C	G	0.55	0	1	0.96	0.57	11	8	9	23	7	44.23	206.6	contig_38549
contig_13430	1449	C	T	0.43	0	1	1	0.42	7	8	17	11	19	44.23	219.9	no_fpc
contig_879642	2867	T	C	0.53	0	0.86	0.94	0.47	17	17	14	32	17	44.23	255	contig_46895
contig_1998524	3326	T	G	0.55	0.17	1	0.93	0.58	11	12	6	15	12	59.58	402.6	contig_48749
contig_108294	2503	A	G	0.6	0	1	0.94	0.45	10	12	8	18	11	/	/	/
contig_108294	2512	T	C	0.55	0	1	1	0.5	11	11	9	18	8	/	/	/
contig_166251	562	T	C	0.61	0.13	0.95	0.97	0.62	18	23	19	35	39	/	/	/
contig_1989744	1326	C	G	0.57	0	1	0.97	0.41	14	13	19	31	17	/	/	/
contig_230144	457	C	A	0.67	0	1	1	0.5	6	7	4	10	8	/	/	/
contig_245492	475	C	T	0.6	0	1	1	0.36	10	8	12	14	14	/	/	/
contig_366956	1131	G	T	0.55	0.05	0.95	0.98	0.49	55	60	60	104	67	/	/	/
contig_366956	1132	C	G	0.54	0.03	0.93	0.94	0.49	56	61	61	108	67	/	/	/
contig_582766	131	G	A	0.5	0	1	1	0.67	4	1	2	6	3	/	/	/
contig_871803	1453	T	C	0.4	0	1	1	0.36	10	11	12	11	14	/	/	/
contig_876951	1295	C	G	0.5	0	1	0.98	0.59	20	19	15	41	27	/	/	/
contig_876951	1995	C	T	0.57	0.12	0.83	1	0.46	7	17	6	13	13	/	/	/
contig_876951	1996	A	G	0.57	0.12	1	1	0.54	7	17	6	13	13	/	/	/
contig_921063	560	A	G	0.57	0	1	0.83	0.5	14	8	10	6	8	/	/	/

ratio = number of reads with alter/tive base (mutant allele)

depth = read coverage at SNP position

[1] (IBSC, 2012)

Table S3: Filtered candidate targets of read coverage analysis within captured pools

Bowman WGS_contig[1]	Contig_length	Start	End	Length	lax_1	lax_2	lax_3	lax_4	lax_5	cM[1]	MB[1]	FPcontig[1]
contig_1387056	882	412	526	115	5.49	8.07	6.00	10.88	7.50	/	/	/
contig_1387056	882	626	692	67	2.45	1.62	2.12	1.30	7	/	/	/
contig_1387056	882	779	842	64	7.04	6.19	1.79	0.96	5.30	/	/	/
contig_1498435	470	354	421	68	5.65	6.97	1.83	1.38	5.41	/	/	/
contig_1532510	797	337	445	109	6.46	6.60	0.35	1.96	6.57	/	/	/
contig_1532510	797	456	520	65	6.37	2.73	1.85	3.78	3.46	/	/	/
contig_1532510	797	593	670	78	1.53	1.77	2.89	6.23	0.57	/	/	/
contig_1534971	630	550	617	68	5.89	5.79	0.79	1.68	5.02	/	/	/
contig_1764579	240	160	227	68	5.47	5.26	1.58	1.94	5.20	/	/	/
contig_212370	1415	827	903	77	0.34	5.55	1.48	6.71	0.57	/	/	/
contig_212370	1415	1283	1399	117	5.20	5.16	1.92	1.84	6.41	/	/	/
contig_335772	224	41	118	78	5.01	6.22	1.79	1.72	7.25	/	/	/
contig_350085	316	135	237	103	5.33	6.32	1.11	1.11	6.18	/	/	/
contig_380230	686	88	198	111	5.69	5.98	0.55	0.94	6.86	/	/	/
contig_380230	686	316	391	76	5.04	3.30	3.53	4.86	6.13	/	/	/
contig_380230	686	415	676	262	7.26	4.32	5.62	6.49	5.83	/	/	/
contig_523676	220	31	127	97	6.13	6.05	1.89	1.41	7.95	/	/	/
contig_68343	10094	112	203	92	0.23	1.83	0.65	5.86	1.86	/	/	/
contig_68343	10094	3410	3506	97	0.37	5.80	0	0	1.69	/	/	/
contig_68343	10094	3523	3942	420	4.39	14.03	0.38	0.64	7.76	/	/	/
contig_68343	10094	3968	4033	66	0.46	6.13	0	1	0	/	/	/
contig_68343	10094	5216	5285	70	0.85	5.57	1.56	0	2.62	/	/	/
contig_68343	10094	5286	6083	798	2.79	10.35	0.65	0.40	5.13	/	/	/
contig_68343	10094	6103	6714	612	9.53	17.21	0.06	1.63	11.38	/	/	/
contig_872010	5225	4	66	63	7.69	6.61	1.91	0.91	5.61	/	/	/

[1] (IBSC, 2012)

Table S4: Exome capture targets with SNPs which cosegregate with *HvLAX-A* phenotype

Capture targets mapped to WGS contigs of Bowman		Gene information for WGS contigs		
WGS_contig[1]	length	HC_genes[1]	LC_genes[1]	Brachypodium[2]
contig_166251	1241bp	/	MLOC_31793.1	/
contig_230144	763 bp	/	/	/
contig_245492	677 bp	/	/	/
contig_582766	205 bp	/	/	/
contig_876951	4598 bp	/	/	/
contig_859419	3668 bp	/	MLOC_37094.1	/
contig_921063	2228 bp	/	/	/
contig_13430	9835 bp	MLOC_20538.1	/	Bradi4g43300.1
		AK368065	/	Bradi4g43290.1
contig_108294	3369 bp	MLOC_27594.1	MLOC_31684.1	/
contig_221364	13089 bp	MLOC_69804.2	/	Bradi4g43130.1
contig_366956	4997 bp	MLOC_34262.1	MLOC_34261.1	Bradi4g43090.1
contig_871803	3230 bp	AK248835.1	/	Bradi4g43230.1
contig_879642	4375 bp	MLOC_18639.1	/	Bradi4g43237.1
contig_1989744	3111 bp	MLOC_44739.1	/	Bradi4g42290.1
contig_1998524	4042 bp	MLOC_75706.1	MLOC_75707.1	/

[1](IBSC, 2012), [2]Homologous Brachypodium gene models (v1.2) predicted by BLAST

Table S5: Targets with low coverage in captured pools with mutant phenotype

Capture targets mapped to WGS contigs of Bowman		Gene information for WGS contigs		
WGS_contig[1]	length	HC_genes[1]	LC_genes[1]	Brachypodium[2]
contig_1387056	882 bp	/	/	/
contig_1498435	470 bp	/	/	/
contig_1532510	797 bp	/	/	/
contig_1534971	630 bp	/	/	/
contig_1764579	240 bp	/	/	/
contig_212370	1415 bp	/	/	/
contig_335772	224 bp	/	/	/
contig_350085	316 bp	/	/	/
contig_380230	686 bp	/	/	/
contig_523676	220 bp	/	/	/
contig_872010	5225 bp	/	/	/
contig_68343	10094 bp	MLOC_61451.6	/	Bradi4g43150.1

[1](IBSC, 2012), [2]Homologous Brachypodium gene models (v.1.2) predicted by BLAST

Table S6: Sequenced BACs

FPC_2862: HVVMRXALLmA0117O22
HVVMRXALLmA0114D14
HVVMRXALLeA0185O05
HVVMRXALLrA0187L16
HVVMRXALLeA0324B05
HVVMRXALLmA0029K21
HVVMRXALLeA0046E04-2
HVVMRXALLmA0255O17
HVVMRXALLmA0033O13
HVVMRXALLhA0071F16
HVVMRXALLrA0261G02
HVVMRXALLeA0171I14
HVVMRXALLeA0137L10
HVVMRXALLmA0433B15
HVVMRX83KHA0024J08
HVVMRXALLmA0012H10
HVVMRXALLmA0072A18
HVVMRXALLmA0014N12
HVVMRXALLeA0258L22
HVVMRXALLmA0201L14
HVVMRX83KHA0157G10

Table S7: Genes on sequenced BACs of FPC_2862

BAC_clone	**HC_genes**[1]	**LC_genes**[1]
HVVMRXALLmA0117O22	/	/
HVVMRXALLmA0114D14	/	/
HVVMRXALLeA0185O05	/	MLOC_8443.1
HVVMRXALLrA0187L16	/	/
HVVMRXALLeA0324B05	/	/
HVVMRXALLmA0029K21	MLOC_61451.6	/
HVVMRXALLeA0046E04	MLOC_61451.6	/
HVVMRXALLmA0255O17	/	/
HVVMRXALLmA0033O13	/	/
HVVMRXALLhA0071F16	/	/
HVVMRXALLrA0261G02	/	/
HVVMRXALLeA0171I14	/	/
HVVMRXALLeA0137L10	AK373675	/
HVVMRXALLmA0433B15	MLOC_69804.2	MLOC_20145.1
HVVMRX83KHA0024J08	MLOC_69804.2	MLOC_20145.1
HVVMRXALLmA0012H10	/	/
HVVMRXALLmA0072A18	/	/
HVVMRXALLmA0014N12	/	/
HVVMRXALLeA0258L22	/	/
HVVMRXALLmA0201L14	MLOC_10658.1	/
HVVMRX83KHA0157G10	MLOC_10658.1	/
HVVMRXALLhB0169O19	/	MLOC_34165.1

[1] (IBSC, 2012)

Table S8: Identified TILLING mutants within *HvLAX-A*

Plant	SNP	Status M3[1]	effect	phenotype
6574_1	C28T	HOM	L10=	/
4164_1	A73C	HOM	S25R	wild-type
14134_1	G89A	HET	S30N	wild-type
10389_1	G94A	HET	E32K	wild-type
8476_1	C127T	HET	L43F	mutant
2905_1	G152A	HET	R51K	wild-type
3105_1	C202T	HET	L68F	wild-type
10899_1	C228T	HOM	G76=	/
4782_1	G256A	HET	G86S	wild-type
14423_1	C309T	HET	I103=	/
12687_1	G378A	HET	K126=	/
9017_1	G387A	HOM	P129=	/
12029_1	G436A	HET	A146T	wild-type
9605_1	G439A	HOM	V147I	wild-type
4125_1	C453A	HET	L151=	/
9122_1	C465T	HOM	A155=	/
4607_1	G1636T	HET	S237=	/
3374_1	C1697T	HOM	P258S	wild-type
16023_1	G1714A	HET	P263=	/
10074_1	G1741A	HET	K272=	/
3428_1	C1744T	HET	I273=	/
11801_1	C1750T	HET	R275=	/
9346_1	C1773T	HOM	A283V	wild-type
6661_1	C1813T	HOM	G296=	/
6201_1	C1832T	HET	L303F	wild-type
11039_1	C1906T	HET	D327=	/
2573_1	C1916T	HET	R331C	wild-type
10884_1	G1936A	HOM	K337=	/
12210_1	G1936A	HOM	K337=	/
7969_1	G1960A	HET	E345=	/
10241_1	C1991T	HET	L356F	wild-type
4094_1	A1998T	HET	H358L	wild-type
6835_1	G2056A	HOM	R377=	/
10920_1	C2107T	HET	H394=	/
15189_1	C2110T	HET	I395=	/
11578_1	C2114T	HET	P397S	wild-type
3265_1	T2206A	HET	A427=	/
3265_1	G2207T	HET	G428W	wild-type
3859_1	G2238A	HOM	G438D	wild-type

[1] HOM = homozygote, HET = heterozygote

Table S9: Identified TILLING mutants for *HvCul4*

Plant	SNP	Status M3[1]	Effect	Phenotype
10131_1	G4A	HOM	D2N	wild-type
7902_1	G4A	HET	D2N	wild-type
14598_1	C117T	HOM	C39=	/
9985_1	C147T	HET	R49=	/
14030_1	C217T	HET	L73F	wild-type
8853_1	C217T	HET	L73F	wild-type
15147_1	T241A	HOM	S81T	wild-type
4515_1	G250A	HET	G84S	wild-type
9673_2	C300T	HET	S100=	/
3511_1	G301A	HET	A101T	wild-type
9741_1	G319A	HET	G107R	wild-type
10441_1	C364T	HET	L122=	/
11076_1	A385T	HET	S129C	wild-type
14628_1	A410G	HOM	Q137R	wild-type
7366_1	G411A	HET	Q137=	/
14645_1	G414A	HET	K138=	/
4128_1	G417A	HOM	G139=	/
9425_1	G453A	HET	W151*	mutant
11239_1	C462T	HOM	H154=	/
11494_1	C481T	HET	L161=	/
10561_1	C495T	HET	T165=	/
13391_1	G547A	HET	Splice Junction	mutant
3616_1	C1814T	HET	D244=	/
14799_1	C1847T	HOM	S255=	/
3208_1	G1868A	HET	Q262=	/
6800_1	G1949A	HET	R289=	/
7393_1	G1952A	HOM	M290I	wild-type
3667_1	C1970T	HOM	S296=	/
4419_1	G2007A	HET	E309K	wild-type
13286_1	G2036A	HOM	A318=	/
10095_1	C2037T	HET	L319=	/
14188_1	G2054A	HET	E324=	/
6525_1	G2065A	HET	R328Q	wild-type
15334_1	G2069A	HOM	E329=	/
4087_1	T2071A	HET	V330E	wild-type
6869_1	G2122A	HET	G347E	wild-type
13142_1	C2169T	HOM	P363S	wild-type
14634_1	G2172A	HET	D364N	wild-type
10496_1	T2242A	HOM	L387H	wild-type
10893_1	C2259T	HET	L393F	wild-type
10916_1	C2266T	HET	S395F	wild-type
14600_1	C2274T	HET	L398F	wild-type
11976_1	G2296A	HOM	G405E	wild-type
9922_1	C2417T	HET	H445=	/
4652_1	C2421T	HOM	P447S	wild-type
3387_1	C2480T	HOM	N466=	/

[1] HOM = homozygote, HET = heterozygote

Table S10: Information of plant material used to identify sequence haplotypes of *HvLAX-A* and *HvCUL4*

→ Accessions sorted according *HvCUL4* haplotypes

Accession[1]	Material	Region[2]	Country	*HvCUL4*	*HvLAX-A*
FT011	*Hordeum spontaneum*	WANA	ISR	Hap_1	Hap_2
FT031	*Hordeum spontaneum*	WANA	ISR	Hap_1	Hap_2
FT067	*Hordeum spontaneum*	WANA	ISR	Hap_2	Hap_2
FT144	*Hordeum spontaneum*	WANA	ISR	Hap_2	Hap_2
FT248	*Hordeum spontaneum*	WANA	IRN	Hap_2	Hap_4
FT276	*Hordeum spontaneum*	WANA	JOR	Hap_2	Hap_4
FT361	*Hordeum spontaneum*	WANA	GRC	Hap_2	Hap_2
FT64	*Hordeum spontaneum*	WANA	ISR	Hap_2	Hap_10
FT643	*Hordeum spontaneum*	WANA	ISR	Hap_2	Hap_2
BCC524	cultivar	EA	IND	Hap_2	Hap_2
BCC526	breeding / research material	EA	IND	Hap_2	Hap_2
BCC533	cultivar	EA	IND	Hap_2	Hap_4
BCC538	cultivar	EA	IND	Hap_2	Hap_2
BCC577	cultivar	EA	IND	Hap_2	Hap_2
BCC579	cultivar	EA	IND	Hap_2	Hap_2
BCC581	cultivar	EA	IND	Hap_2	Hap_2
BCC732	landrace	EA	NPL	Hap_2	Hap_2
BCC745	cultivar	EA	NPL	Hap_2	Hap_2
BCC761	landrace	EA	NPL	Hap_2	Hap_2
BCC766	landrace	EA	NPL	Hap_2	Hap_2
BCC768	landrace	EA	NPL	Hap_2	Hap_2
HOR11403	landrace	EA	IND	Hap_2	Hap_4
FT218	*Hordeum spontaneum*	WANA	ISR	Hap_3	Hap_2
FT340	*Hordeum spontaneum*	WANA	ISR	Hap_3	Hap_8
FT569	*Hordeum spontaneum*	WANA	IRN	Hap_3	Hap_2
FT037	*Hordeum spontaneum*	WANA	ISR	Hap_4	Hap_2
FT147	*Hordeum spontaneum*	WANA	ISR	Hap_4	Hap_2
FT219	/	/	/	Hap_4	Hap_2
BCC003	landrace	WANA	AFG	Hap_4	Hap_2
BCC093	/	/	/	Hap_4	Hap_2
BCC1367	cultivar	EU	DEU	Hap_4	Hap_2
BCC1372	cultivar	EU	POL	Hap_4	Hap_2
BCC1376	cultivar	EU	DNK	Hap_4	Hap_2
BCC1377	cultivar	EU	FRA	Hap_4	Hap_2
BCC1378	cultivar	EU	GBR	Hap_4	Hap_2
BCC1381	cultivar	EU	GBR	Hap_4	Hap_2
BCC1382	cultivar	EU	GBR	Hap_4	Hap_2
BCC1384	cultivar	EU	DEU	Hap_4	Hap_2
BCC1386	cultivar	EU	DEU	Hap_4	Hap_2
BCC1387	cultivar	EU	NLD	Hap_4	Hap_2
BCC1388	/	/	/	Hap_4	Hap_2

BCC1389	cultivar	EU	IRL	Hap_4	Hap_2
BCC1392	cultivar	EU	DNK	Hap_4	Hap_2
BCC1394	cultivar	EU	NLD	Hap_4	Hap_2
BCC1395	cultivar	EU	NLD	Hap_4	Hap_2
BCC1396	cultivar	EU	SWE	Hap_4	Hap_2
BCC1397	landrace	EU	HUN	Hap_4	Hap_2
BCC1398	breeding / research material	EU	HUN	Hap_4	Hap_2
BCC1399	cultivar	EU	SWE	Hap_4	Hap_2
BCC1400	cultivar	EU	FRA	Hap_4	Hap_2
BCC1401	cultivar	EU	DEU	Hap_4	Hap_2
BCC1402	cultivar	EU	SWE	Hap_4	Hap_2
BCC1404	cultivar	EU	GBR	Hap_4	Hap_2
BCC1405	cultivar	EU	GBR	Hap_4	Hap_2
BCC1407	cultivar	EU	AUT	Hap_4	Hap_2
BCC1408	cultivar	EU	GBR	Hap_4	Hap_2
BCC1409	cultivar	EU	AUT	Hap_4	Hap_2
BCC1410	cultivar	EU	SWE	Hap_4	Hap_2
BCC1412	cultivar	EU	SWE	Hap_4	Hap_2
BCC1415	cultivar	EU	GBR	Hap_4	Hap_2
BCC1418	cultivar	EU	DNK	Hap_4	Hap_2
BCC1419	cultivar	EU	DEU	Hap_4	Hap_2
BCC1422	cultivar	EU	NLD	Hap_4	Hap_2
BCC1425	cultivar	EU	DEU	Hap_4	Hap_2
BCC1428	cultivar	EU	GBR	Hap_4	Hap_2
BCC1439	cultivar	EU	CZE	Hap_4	Hap_2
BCC1444	cultivar	EU	CZE	Hap_4	Hap_2
BCC1453	cultivar	EU	FIN	Hap_4	Hap_2
BCC1456	cultivar	EU	RUS	Hap_4	Hap_2
BCC1458	cultivar	EU	RUS	Hap_4	Hap_2
BCC1465	cultivar	EU	UKR	Hap_4	Hap_2
BCC1466	cultivar	EU	UKR	Hap_4	Hap_2
BCC1467	cultivar	EU	BLR	Hap_4	Hap_2
BCC1472	cultivar	EU	LTU	Hap_4	Hap_2
BCC1479	landrace	EU	RUS	Hap_4	Hap_2
BCC1482	cultivar	EU	RUS	Hap_4	Hap_2
BCC1484	landrace	EU	RUS	Hap_4	Hap_2
BCC1485	cultivar	EU	RUS	Hap_4	Hap_2
BCC1491	landrace	EU	RUS	Hap_4	Hap_2
BCC1494	landrace	WANA	KAZ	Hap_4	Hap_2
BCC1498	landrace	WANA	UZB	Hap_4	Hap_2
BCC1505	cultivar	EU	UKR	Hap_4	Hap_2
BCC1524	cultivar	EU	DEU	Hap_4	Hap_2
BCC1529	cultivar	EU	AUT	Hap_4	Hap_2
BCC1541	cultivar	EU	YUG	Hap_4	Hap_2
BCC1565	landrace	EU	ALB	Hap_4	Hap_2
BCC161	landrace	WANA	MAR	Hap_4	Hap_2

BCC167	landrace	WANA	OMN	Hap_4	Hap_2
BCC427	breeding / research material	EA	CHN	Hap_4	Hap_2
BCC432	breeding / research material	EA	CHN	Hap_4	Hap_2
BCC666	cultivar	EA	KOR	Hap_4	Hap_2
BCC667	cultivar	EA	KOR	Hap_4	Hap_2
BCC675	cultivar	EA	KOR	Hap_4	Hap_2
BCC807	cultivar	AM	URY	Hap_4	Hap_2
BCC814	breeding / research material	AM	USA	Hap_4	Hap_2
BCC817	cultivar	AM	USA	Hap_4	Hap_2
BCC818	cultivar	AM	USA	Hap_4	Hap_2
BCC847	cultivar	AM	USA	Hap_4	Hap_2
BCC852	cultivar	AM	CAN	Hap_4	Hap_2
BCC860	breeding / research material	AM	URY	Hap_4	Hap_2
BCC861	breeding / research material	AM	URY	Hap_4	Hap_2
BCC929	cultivar	AM	CAN	Hap_4	Hap_2
BCC942	cultivar	AM	USA	Hap_4	Hap_2
HOR11374	breeding / research material	WANA	ISR	Hap_4	Hap_2
HOR1962	landrace	/	/	Hap_4	Hap_2
HOR4727	landrace	WANA	TUR	Hap_4	Hap_2
HOR7985	landrace	WANA	TUR	Hap_4	Hap_2
HOR8006	landrace	WANA	TUR	Hap_4	Hap_2
HOR930	landrace	WANA	TUR	Hap_4	Hap_2
FT222	*Hordeum spontaneum*	WANA	ISR	Hap_5	Hap_2
FT232	*Hordeum spontaneum*	WANA	IRQ	Hap_6	Hap_2
FT268	*Hordeum spontaneum*	WANA	SYR	Hap_6	Hap_5
FT278	*Hordeum spontaneum*	WANA	AFG	Hap_6	Hap_5
FT279	*Hordeum spontaneum*	WANA	AFG	Hap_6	Hap_5
FT376	*Hordeum spontaneum*	WANA	TKM	Hap_6	Hap_5
FT469	*Hordeum spontaneum*	WANA	TUR	Hap_6	Hap_5
BCC190	landrace	WANA	SYR	Hap_6	Hap_2
FT237	*Hordeum spontaneum*	WANA	IRN	Hap_7	Hap_5
FT252	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_5
FT462	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_2
FT507	*Hordeum spontaneum*	WANA	IRQ	Hap_7	Hap_5
FT578	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_5
FT581	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_5
FT582	*Hordeum spontaneum*	WANA	SYR	Hap_7	Hap_5
FT660	*Hordeum spontaneum*	WANA	IRN	Hap_7	Hap_5
FT661	*Hordeum spontaneum*	WANA	IRN	Hap_7	Hap_2
FT730	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_2
FT731	*Hordeum spontaneum*	WANA	TUR	Hap_7	Hap_5
FT878	*Hordeum spontaneum*	WANA	IRN	Hap_7	Hap_5
BCC1442	cultivar	EU	GBR	Hap_7	Hap_2

FT272	*Hordeum spontaneum*	WANA	JOR	Hap_8	Hap_6
FT333	*Hordeum spontaneum*	WANA	IRN	Hap_8	Hap_2
FT589	*Hordeum spontaneum*	WANA	SYR	Hap_8	Hap_2
FT604	*Hordeum spontaneum*	WANA	IRQ	Hap_8	Hap_5
FT875	*Hordeum spontaneum*	WANA	UZB	Hap_8	Hap_5
FT879	*Hordeum spontaneum*	WANA	IRN	Hap_8	Hap_2
FT885	*Hordeum spontaneum*	WANA	TJK	Hap_8	Hap_5
FT286	*Hordeum spontaneum*	WANA	IRN	Hap_9	Hap_7
FT332	*Hordeum spontaneum*	WANA	IRN	Hap_10	Hap_5
FT379	*Hordeum spontaneum*	WANA	EGY	Hap_10	Hap_5
FT613	*Hordeum spontaneum*	WANA	IRN	Hap_10	Hap_4
FT747	*Hordeum spontaneum*	WANA	TUR	Hap_10	Hap_2
FT880	*Hordeum spontaneum*	WANA	IRN	Hap_10	Hap_5
FT262	*Hordeum spontaneum*	WANA	TUR	Hap_11	Hap_2
FT338	*Hordeum spontaneum*	WANA	ISR	Hap_11	Hap_2
FT473	*Hordeum spontaneum*	WANA	TUR	Hap_11	Hap_2
FT566	*Hordeum spontaneum*	WANA	TKM	Hap_11	Hap_4
FT567	*Hordeum spontaneum*	WANA	TKM	Hap_11	Hap_4
FT568	*Hordeum spontaneum*	WANA	AFG	Hap_11	Hap_4
FT572	*Hordeum spontaneum*	WANA	JOR	Hap_11	Hap_2
FT627	*Hordeum spontaneum*	WANA	JOR	Hap_11	Hap_2
FT658	*Hordeum spontaneum*	WANA	IRQ	Hap_11	Hap_9
BCC131	landrace	WANA	MAR	Hap_11	Hap_2
BCC195	landrace	WANA	SYR	Hap_11	Hap_2
BCC197	landrace	WANA	SYR	Hap_11	Hap_2
BCC527	breeding / research material	EA	IND	Hap_11	Hap_2
BCC535	cultivar	EA	IND	Hap_11	Hap_2
BCC695	cultivar	EA	KOR	Hap_11	Hap_4
HOR12830	landrace	WANA	SYR	Hap_11	Hap_2
FT357	*Hordeum spontaneum*	WANA	LBY	Hap_12	Hap_2
FT590	*Hordeum spontaneum*	WANA	SYR	Hap_13	Hap_2
FT595	*Hordeum spontaneum*	WANA	IRQ	Hap_14	Hap_5
FT670	*Hordeum spontaneum*	WANA	TUR	Hap_14	Hap_2
FT735	*Hordeum spontaneum*	WANA	TUR	Hap_14	Hap_2
FT748	*Hordeum spontaneum*	WANA	TUR	Hap_14	Hap_2
FT363	*Hordeum spontaneum*	WANA	CYP	Hap_15	Hap_2
FT380	*Hordeum spontaneum*	WANA	EGY	Hap_15	Hap_2
FT616	*Hordeum spontaneum*	WANA	IRN	Hap_15	Hap_2
FT734	*Hordeum spontaneum*	WANA	TUR	Hap_15	Hap_2
HOR2828	landrace	WANA	IRN	Hap_15	Hap_2
FT470	*Hordeum spontaneum*	WANA	TUR	Hap_16	Hap_5
FT630	*Hordeum spontaneum*	WANA	LBN	Hap_16	Hap_2
FT671	*Hordeum spontaneum*	WANA	LBN	Hap_16	Hap_2
FT754	*Hordeum spontaneum*	WANA	TUR	Hap_16	Hap_5
FT741	*Hordeum spontaneum*	WANA	TUR	Hap_17	Hap_5

FT042	*Hordeum spontaneum*	WANA	ISR	Hap_18	Hap_7
FT359	*Hordeum spontaneum*	WANA	MAR	Hap_19	Hap_2
FT365	*Hordeum spontaneum*	WANA	CHN	Hap_19	Hap_2
FT873	*Hordeum spontaneum*	WANA	UZB	Hap_19	Hap_5
FT886	*Hordeum spontaneum*	WANA	TJK	Hap_19	Hap_5
BCC118	landrace	WANA	LBY	Hap_19	Hap_2
BCC126	landrace	WANA	MAR	Hap_19	Hap_2
BCC129	landrace	WANA	MAR	Hap_19	Hap_2
BCC1368	cultivar	EU	NLD	Hap_19	Hap_2
BCC139196				Hap_19	Hap_2
BCC1455	cultivar	EU	RUS	Hap_19	Hap_2
BCC1457	cultivar	EU	RUS	Hap_19	Hap_2
BCC1474	cultivar	EU	UKR	Hap_19	Hap_2
BCC1476	cultivar	WANA	UZB	Hap_19	Hap_2
BCC149	landrace	WANA	MAR	Hap_19	Hap_2
BCC1493	cultivar	EU	UKR	Hap_19	Hap_2
BCC1503	landrace	WANA	TKM	Hap_19	Hap_2
BCC1504	cultivar	EU	RUS	Hap_19	Hap_2
BCC1548	cultivar	EU	CYP (GRC)	Hap_19	Hap_2
BCC173	landrace	WANA	PAK	Hap_19	Hap_4
BCC182	landrace	WANA	PAK	Hap_19	Hap_2
BCC218	landrace	WANA	TJK	Hap_19	Hap_4
BCC421	cultivar	EA	CHN	Hap_19	Hap_2
BCC423	cultivar	EA	CHN	Hap_19	Hap_2
BCC434	breeding / research material	EA	CHN	Hap_19	Hap_2
BCC438	cultivar	EA	CHN	Hap_19	Hap_2
BCC439	cultivar	EA	CHN	Hap_19	Hap_2
BCC502	cultivar	EA	CHN	Hap_19	Hap_2
BCC532	cultivar	EA	IND	Hap_19	Hap_2
BCC551	cultivar	EA	IND	Hap_19	Hap_5
BCC625	cultivar	EA	JPN	Hap_19	Hap_2
BCC642	cultivar	EA	JPN	Hap_19	Hap_4
BCC719	cultivar	EA	KOR	Hap_19	Hap_2
BCC729	cultivar	EA	KOR	Hap_19	Hap_2
BCC759	cultivar	EA	NPL	Hap_19	Hap_2
BCC801	landrace	EA	NPL	Hap_19	Hap_2
BCC806	cultivar	AM	MEX	Hap_19	Hap_2
BCC844	cultivar	AM	COL	Hap_19	Hap_2
BCC846	breeding / research material	AM	USA	Hap_19	Hap_2
BCC868	breeding / research material	AM	MEX	Hap_19	Hap_2
BCC869	cultivar	AM	MEX	Hap_19	Hap_2
BCC875	cultivar	AM	USA	Hap_19	Hap_2
BCC888	cultivar	AM	CAN	Hap_19	Hap_2
BCC892	cultivar	AM	BOL	Hap_19	Hap_2

BCC893	cultivar	AM	USA	Hap_19	Hap_2
BCC899	cultivar	AM	CHL	Hap_19	Hap_2
BCC900	cultivar	AM	MEX	Hap_19	Hap_2
BCC903	cultivar	AM	CAN	Hap_19	Hap_2
BCC907	cultivar	AM	USA	Hap_19	Hap_2
BCC921	cultivar	AM	COL	Hap_19	Hap_2
HOR1804	landrace	WANA	AFG	Hap_19	Hap_4
HOR1842	landrace	WANA	AFG	Hap_19	Hap_4
FT584	*Hordeum spontaneum*	WANA	SYR	Hap_20	Hap_5
FT746	*Hordeum spontaneum*	WANA	TUR	Hap_21	Hap_2
BCC1447	cultivar	EU	FRA	Hap_21	Hap_2
BCC1500	landrace	WANA	TJK	Hap_21	Hap_2
BCC219	landrace	WANA	TJK	Hap_21	Hap_2
FT18	*Hordeum spontaneum*	WANA	ISR	Hap_22	Hap_2
FT56	*Hordeum spontaneum*	WANA	ISR	Hap_23	Hap_4
FT75	*Hordeum spontaneum*	WANA	ISR	Hap_24	Hap_2
FT592	*Hordeum spontaneum*	WANA	SYR	Hap_25	Hap_5
FT628	*Hordeum spontaneum*	WANA	SYR	Hap_26	Hap_2
BCC192	landrace	WANA	SYR	Hap_27	Hap_2
HOR2800	landrace	WANA	IRN	Hap_27	Hap_2
BCC1452	cultivar	EU	NLD	Hap_28	Hap_2
BCC1461	cultivar	EU	RUS	Hap_28	Hap_2
BCC1468	cultivar	WANA	KAZ	Hap_28	Hap_2
BCC1469	cultivar	WANA	KAZ	Hap_28	Hap_2
BCC1490	breeding / research material	EU	RUS	Hap_28	Hap_2
BCC1561	landrace	EU	BGR	Hap_28	Hap_2
BCC436	cultivar	EA	CHN	Hap_28	Hap_2
BCC445	cultivar	EA	CHN	Hap_28	Hap_2
BCC446	cultivar	EA	CHN	Hap_28	Hap_2
BCC447	cultivar	EA	CHN	Hap_28	Hap_2
BCC718	cultivar	EA	KOR	Hap_28	Hap_2
BCC881	cultivar	AM	CAN	Hap_28	Hap_2
BCC1370	cultivar	EU	FRA	Hap_29	Hap_2
BCC1371	cultivar	EU	FRA	Hap_29	Hap_2
BCC1373	cultivar	EU	GBR	Hap_29	Hap_2
BCC1374	cultivar	EU	NLD	Hap_29	Hap_2
BCC1379	cultivar	EU	CZE	Hap_29	Hap_2
BCC1380	cultivar	EU	FRA	Hap_29	Hap_2
BCC1383	cultivar	EU	GBR	Hap_29	Hap_2
BCC1385	cultivar	EU	POL	Hap_29	Hap_2
BCC1390	cultivar	EU	SWE	Hap_29	Hap_2
BCC1391	cultivar	EU	DEU	Hap_29	Hap_2
BCC1403	cultivar	EU	DEU	Hap_29	Hap_2
BCC1411	cultivar	EU	DEU	Hap_29	Hap_2
BCC1413	cultivar	EU	DEU	Hap_29	Hap_2

BCC1414	cultivar	EU	CZE	Hap_29	Hap_2
BCC1416	cultivar	EU	SWE	Hap_29	Hap_2
BCC1417	cultivar	EU	DEU	Hap_29	Hap_2
BCC1420	cultivar	EU	NLD	Hap_29	Hap_2
BCC1421	cultivar	EU	CZE	Hap_29	Hap_2
BCC1423	cultivar	EU	FRA	Hap_29	Hap_2
BCC1424	cultivar	EU	DEU	Hap_29	Hap_2
BCC1430	cultivar	EU	FRA	Hap_29	Hap_2
BCC1431	cultivar	EU	AUT	Hap_29	Hap_2
BCC1432	cultivar	EU	CZE	Hap_29	Hap_2
BCC1433	cultivar	EU	DEU	Hap_29	Hap_2
BCC1440	cultivar	EU	AUT	Hap_29	Hap_2
BCC1441	cultivar	EU	DEU	Hap_29	Hap_2
BCC1443	cultivar	EU	DEU	Hap_29	Hap_2
BCC1445	breeding / research material	EU	FRA	Hap_29	Hap_2
BCC1450	cultivar	EU	FIN	Hap_29	Hap_2
BCC1459	cultivar	EU	RUS	Hap_29	Hap_2
BCC1463	cultivar	EU	RUS	Hap_29	Hap_2
BCC1470	cultivar	WANA	UZB	Hap_29	Hap_2
BCC1471	cultivar	EU	ARM	Hap_29	Hap_2
BCC1480	landrace	EU	RUS	Hap_29	Hap_2
BCC1481	landrace	EU	RUS	Hap_29	Hap_2
BCC1483	landrace	EU	RUS	Hap_29	Hap_2
BCC1487	landrace	EU	RUS	Hap_29	Hap_2
BCC1497	landrace	WANA	KGZ	Hap_29	Hap_2
BCC1506	cultivar	EU	UKR	Hap_29	Hap_2
BCC1566	landrace	EU	GRC	Hap_29	Hap_2
BCC1589	landrace	EU	ITA	Hap_29	Hap_2
BCC8050	cultivar	AM	CAN	Hap_29	Hap_2
BCC812	cultivar	AM	MEX	Hap_29	Hap_2
BCC857	cultivar	AM	MEX	Hap_29	Hap_2
BCC913	cultivar	AM	USA	Hap_29	Hap_2
HOR11370	breeding / research material	WANA	ISR	Hap_29	Hap_2
HOR11371	breeding / research material	WANA	ISR	Hap_29	Hap_2
HOR11373	breeding / research material	WANA	ISR	Hap_29	Hap_2
HOR2829	landrace	WANA	IRN	Hap_29	Hap_2
HOR2835	landrace	WANA	IRN	Hap_29	Hap_2
HOR8113	landrace	WANA	TUR	Hap_29	Hap_2
BCC1448	cultivar	EU	FIN	Hap_30	Hap_2
BCC927	cultivar	AM	PER	Hap_30	Hap_2
HOR8160	landrace	WANA	TUR	Hap_31	Hap_2

[1] Accessions starting with BCC taken from: (Haseneyer et al., 2010)

[2] Europe (EU); East Asia (EA); West Asia and North Africa (WANA); America (AM)

Table S11: Oligonucleotides of *HvLAX-A*

Name	forward sequence (5' - 3')	reverse sequence (5' - 3')
HvLAX_Ex1	ACCCCTCCCACTTTTACCAC	TGGCAGGCCTAACTACCATC
HvLAX_Ex2	ACTGATCCAGACCCCAACAG	GGATCGAGAGCGAGATATGC
HvLAX_1	GCTGGTGTTGCAGTTCCTCT	GAAGCGACAGACACAAACGA
HvLAX_2	GGTGCAGTGTGTACTGAACGA	CATGACCATGAGCTTGACGA
HvLAX_3	CCACTACCTGCCAATCAACA	CATGTCCAACGATGATGCAG
HvLAX_4	CCCTAACCTTTCCGTCTTCC	CGACTGGAGATCGAGTTAGC
HvLAX_5	ATGCATTGCTGTGCGGTA	AGGAGGACGGACACCATATC
HvLAX_6	AGCTCGTCAAGCTCATGGTC	CGATACAGCACCGTCGTATG
HvLAX_7	AGTGCACTGGACTGTACACCAC	GAAGCGACAGACACAAACGA
HvLAX_8	(additional sequencing primer for HvLAX_7)	ATGGATGGGAAGACATGGAA
HvLAX_9	CTACGAGGTGCTGGTGCTG	AGCTTGACGAGCTCGATGT
HvLAX_10	TCGTTTGTGTCTGTCGCTTC	TGGGGAAGTACAAGGTGGAG
HvLAX_11	CACCACTACCTGCCAATCAA	ATTCATTCGATTCCACGCTTAG
contig_71318	CCGTCAGCCTCAGTTTTTGT	AGCAGAGTAAAAGGGCGACA
contig_129575	GGATCCCCTAGATGCAAGGA	GGGAGATGGAGGGGTATATG

Table S12: Marker information of genetic mapping

Marker[1]	**Type**	**forward sequence (5' - 3')**	**reverse sequence (5' - 3')**	**Enzyme**
1_0974[2]	CAPS	TTGCTGGTTGGGATCTCTTC	ACACTGGCTGACACATGGAA	*Sau3A I*
1_0580	CAPS	CATACCGAAAGTACAGAGCACA	TCACCGAACAGACTCTCAAGG	*Aci I*
1_1198	CAPS	AACCTCCCAGCTGACCTCAT	ACACAATCAGCAGCAACACC	*Fau I*
1_0157	CAPS	ACACCAAAGATGACCTCAAGC	CCTGAAAAGATGCACGGAAT	*HpyCH4 III*
1_0481	CAPS	AGGCTAGACGGCAACGATACT	GACTCCAACAACATCGCAGAG	*Aci I*
2_0524	CAPS	TTCTCTGCCGCATCAACAG	CCGCATGGATACTCACTTCCT	*Taq I*
1_1469[2]	CAPS	GTGGTGTTCTGGGCAACTTT	ACGGTCATGTGACCCTATCA	*HpyCH4 IV*
2_1148	seq[3]	ACTACATGTCCGGCTTCCAC	CCTACGTACGACTAGCAAAGCA	/
2_0306	seq[3]	GCTTCTGCACTTGCCAATTC	GCACAAAGCAAACAGTGCTC	/
2_0713	CAPS	AGCACTCCTAGTGTCCGTGAG	CGGCTCCGCTTCTTATCTTT	*HpyCH4 IV*
HvBradi4g43680	CAPS	GAGACAGGACAGAGGCTTGC	ATCCTTCCTTTCCACCCTTG	*BfuA1*
1_1260[2]	seq[3]	CTCGGAGCGCCACTTCTTAG	CTGGGTAGATGGCATCCATTG	/
2_0239[2]	CAPS	TGTAGTCGGGGTGTTGTGTG	AGTGGGTTCTGAGGAAAGCA	*Sau96 I*

[1] (Close et al., 2009)

[2] not the Illumina SNP but located on the same unigene

[3] genotyping by sanger sequencing of recombinant plants

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Table S13: SNaPshot genotyping assays

Pool	Marker	Oligo type	Sequence
1	1_0580	*forward*	TGAGCAAGTTATGCATGTGCT
		reverse	CAGTGACCGGTTAATTTCACG
		extension	d(T)$_{7}$GATGGTCAGATTTGCTCTCCTAC
1	1_1198	*forward*	TTGACCTCGACGACGATATG
		reverse	AGGTGGAAGATCGCAAACAC
		extension	d(T)$_{17}$ CGATATCGACATGGACAGCAG
1	1_0157[1]	*forward*	ACCACGCCCGAGAAAATAGT
		reverse	GCAGATCAAGGATGGGTTTG
		extension	d(T)$_{26}$ CCAATGTCCTTGAGCGCATT
1	2_0713	*forward*	CGTGAATCAAGGATGTCTGC
		reverse	ACTCATTCTTGGGCACCAGT
		extension	d(T)$_{33}$ATAGATGCCGCTGATTCAAGG
2	1_0481	*forward*	CCTCTTGCCTCACATTGTTC
		reverse	GGCTGATGAGATGGAGCATT
		extension	d(T)$_{37}$TCTGAGTTGAGACTCTTGAGTA
2	2_1148	*forward*	GCCTGCTCGACTCAAGAGAA
		reverse	CGATCTCGAGCAAGGAAAAC
		extension	d(T)$_{44}$GGCAAGTGAAGAGGAGAGGC
2	2_0524	*forward*	GGCGGAGCAGTATCAGAAGA
		reverse	GCAGCTCCAGGGAACAAATA
		extension	d(T)$_{47}$TTGCTTTGGAAGTGAGGCCTTC
2	1_1469	*forward*	CGATTCGGTGAGAACTGGAT
		reverse	CCGCCTACAAACATGAACCT
		extension	d(T)$_{51}$CCACCTTTTTATATATTCTGTTC

[1] not the SNP from (Close et al., 2009) map but located on the same EST

Table S14: SNP marker used for F1 test

Contig[1]	Length	SNP position	Parent	Genotype
Bowman_contig_71318	7031 bp	C5024T	BW458	C
HVVMRXALLeA0185O05[2]			BW457	T
~350 kb[3]			8476_1_1	/
Bowman_contig_129575	6517 bp	G3377A	BW458	G
HVVMRX83KHA0157G10 [2]			8476	G
~2275 kb[3]			BW457	A
		T3735G	BW457	T
			BW458	G
			8476	G

[1] (IBSC, 2012), [2] Corresponding BAC, [3] position within the FPcontig_2862

Table S15: Oligonucleotides of *HvCUL4*

Name	Forward sequence (5' - 3')	Reverse sequence (5' - 3')
HvCUL4_Ex1	GATTGGAGGGCAACAACAAG	TCGACGACATACTGCGCTAC
HvCUL4_Ex2	CGGTCTCTCCATGCCATATT	CATTCTCGTCGACCGATCTC
HvCUL4_1	GCTCTAGCTCGATCTGATTCATCC	CCATCTTGATCCCCACAATC
HvCUL4_2	CCTCTAGTAAGCTCTCTCGGTCTC	ATGTCCGGGCAGACCATCT
HvCUL4_3	CTCGACGACCACAACAAGAT	CAGCCCAAAAGGATCATCTG

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