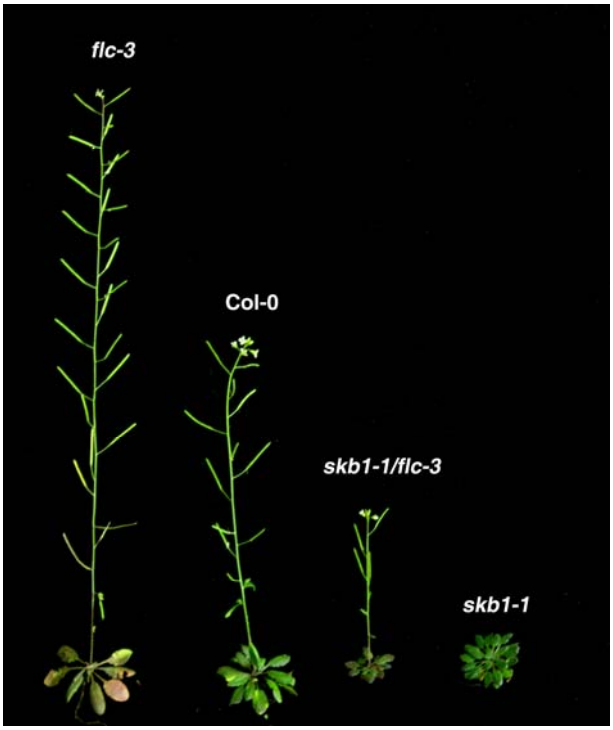
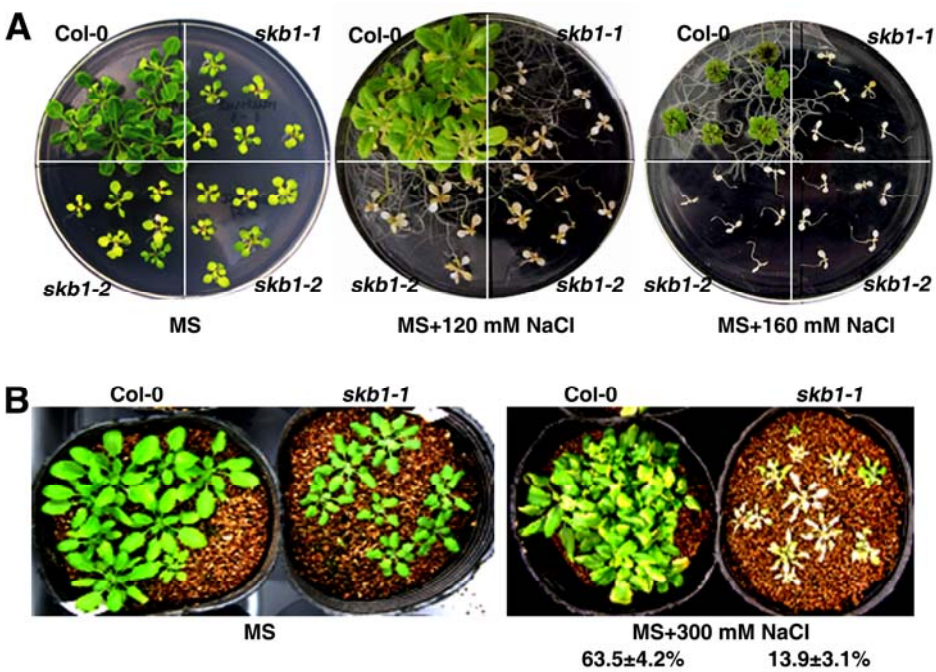
Supplemental Figure 1. The phenotypes of *flc-3*, wild type (Col-0), *skb1-1 flc-3* and *skb1-1* grown in soil for 35 days under long day

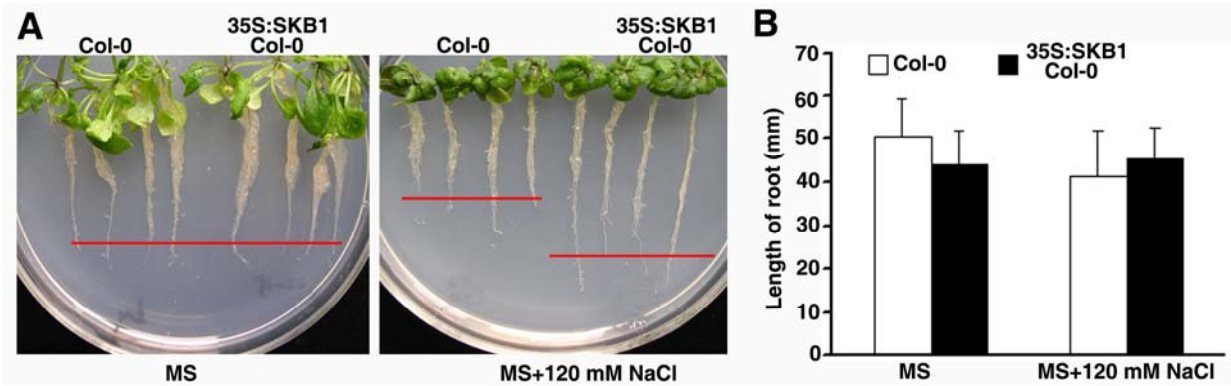


Supplemental Figure 2. The *skb1* mutants are hypersensitive to salt stress



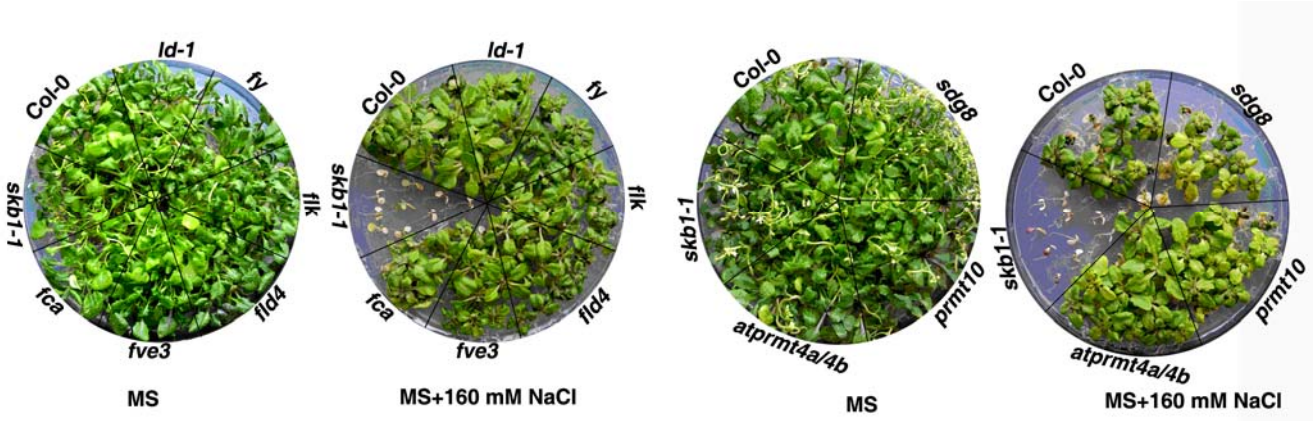
Supplemental Figure 2. The sensitivity of the wild type (Col-0) and *skb1* mutants to salt stress. (A) *skb1-1* and *skb1-2* mutants were all hypersensitive to salt stress. Four-day-old seedlings were transferred from MS medium alone to MS medium with 0, 120 or 160 mM NaCl. Photographs were taken at 20 days (MS) or 40 days (120 and 160 mM NaCl) after seedling transfer to the treatment medium. (B) Three-week-old Col-0 and *skb1-1* plants were grown in soil without NaCl (left) or with 300 mM NaCl every three days for two additional weeks (right). The survival rate (bottom) was measured at the end of NaCl treatment and is the means ± SE of two independent experimental results (n=40).

Supplemental Figure 3. Overexpression of SKB1 slightly increases the tolerance to salt stress



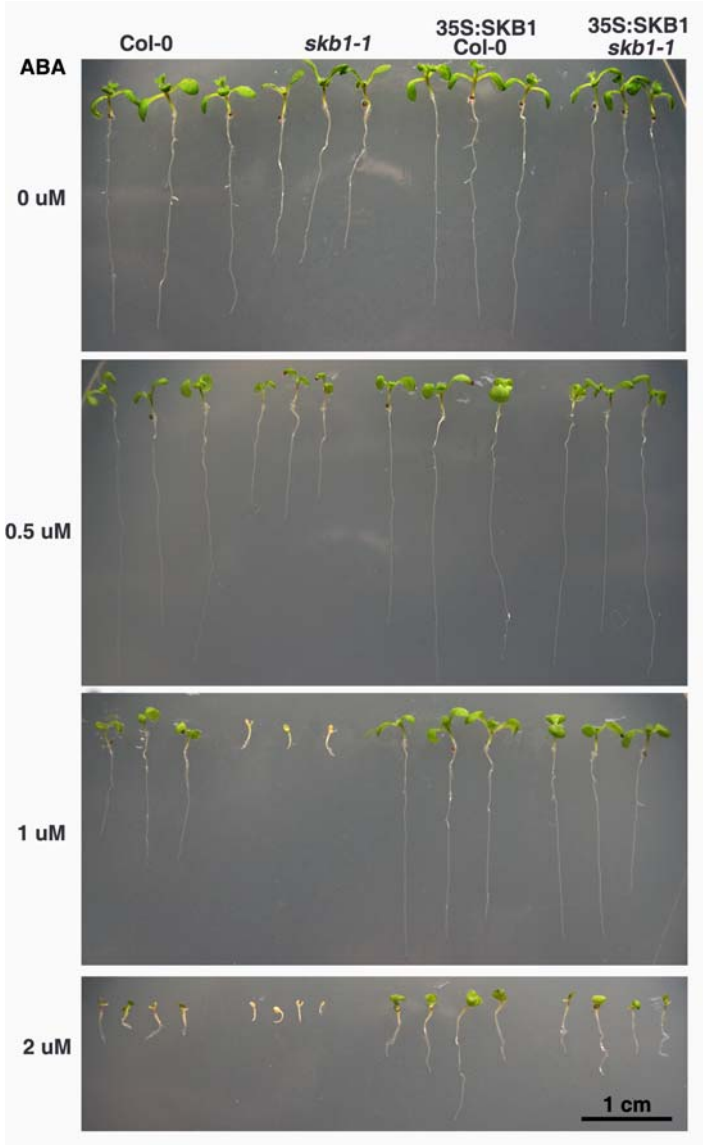
Supplemental Figure 3. Overexpression of SKB1 in a Col-0 background slightly increases tolerance to salt stress. (A)Four-day-old seedlings were transferred from MS medium to MS medium with 0 or 120 mM NaCl and grown horizontally for 30 days. Representative plants were selected for photographs and laid vertically to observe root length. The red line indicate the root length of Col-0 and 35S:SKB1 Col-0. (B) More than 20 roots were measured to score the root length shown in A. The quantitative results represent the mean ± SE of two independent experiment results.

Supplemental Figure 4. The phenotypes of flowering time-controlling gene mutants grown on medium with salt.



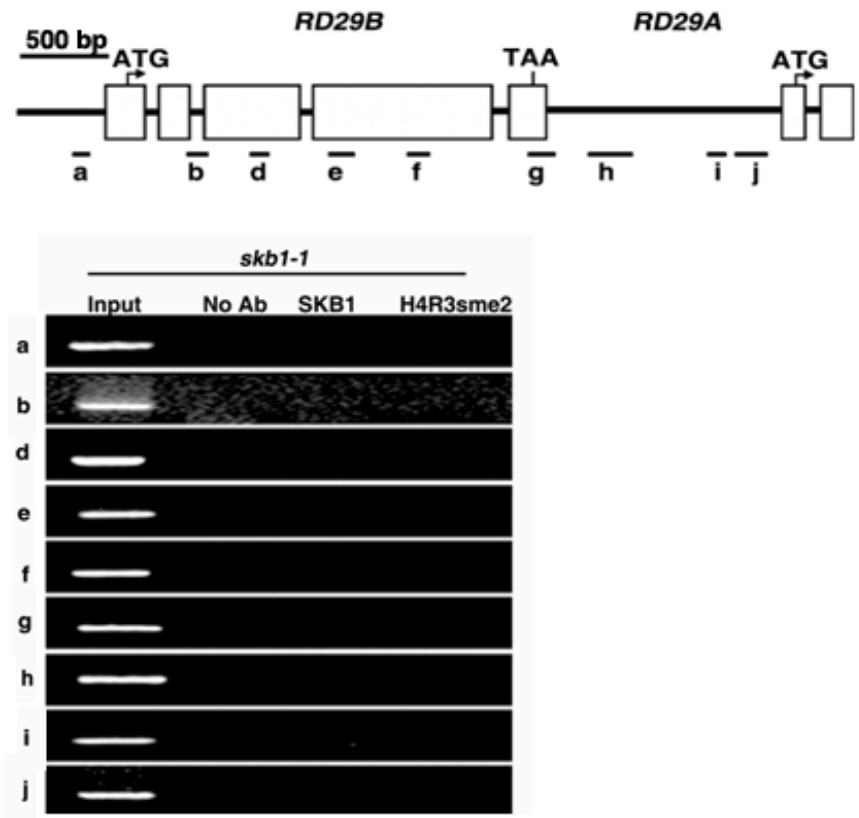
Supplemental Figure 4. The phenotypes of flowering time-controlling gene mutants, including *skb1-1*, *fca*, *fve*, *fld4*, *flk*, *fy*, *ld-1*, *prmt4a prmt4b*, *prmt10* and *sdg8*, grown on MS medium with salt. Four-day-old seedlings were transferred from MS medium to MS medium with 0 or 160 mM NaCl. Photographs were taken 30 days after seedling transfer to the treatment medium.

Supplemental Figure 5. Growth of plants on MS medium containing different concentrations of ABA.



Supplemental Figure 5. Growth of Col-0, *skb1-1*, 35S:SKB1 Col-0 and 35S:SKB1 *skb1-1* on MS medium containing 0, 0.5, 1 or 2 μM ABA. Seeds were germinated for 9 days on MS medium with or without ABA, and representative plants are shown.

Supplemental Figure 6. Anti-SKB1 and -H4R3sme2 antibodies could not pull down chromatin DNA in *skb1-1* mutant.

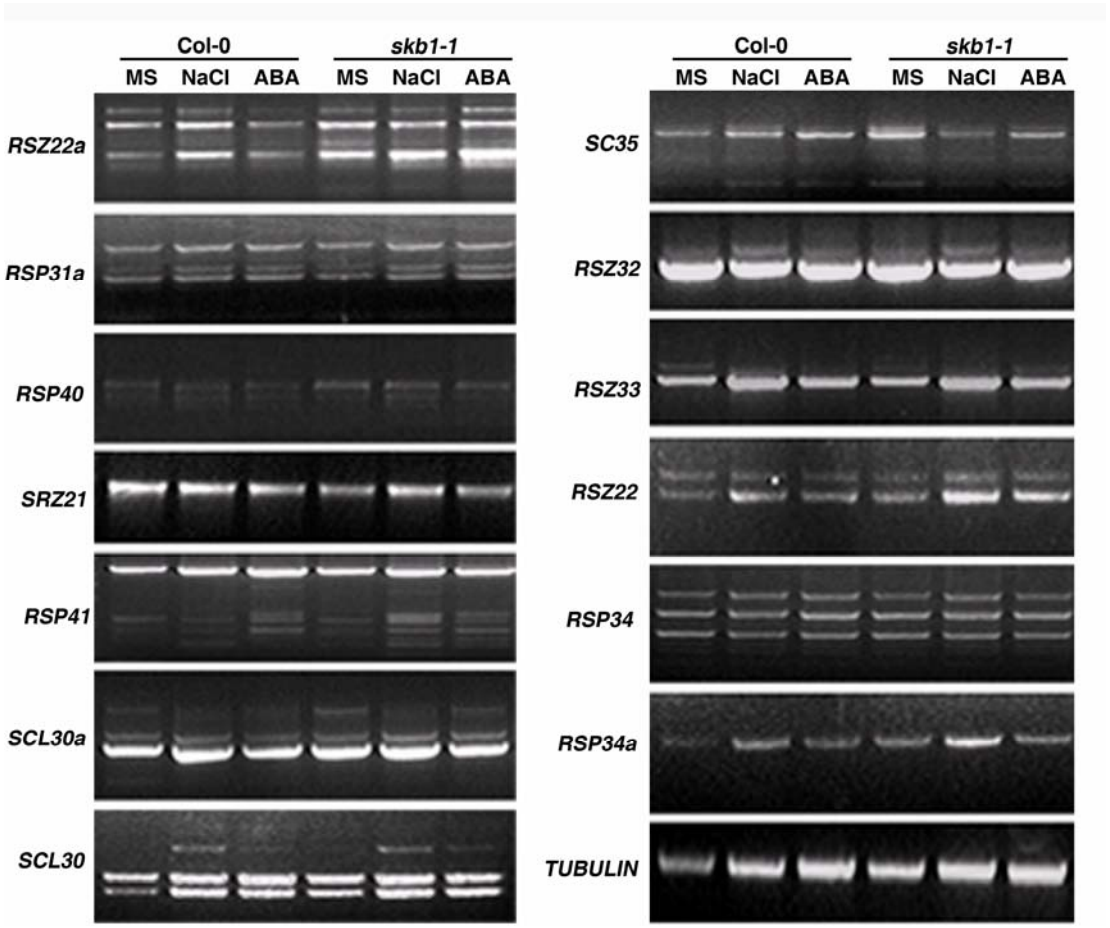


Supplemental Figure 6. Anti-SKB1 and -H4R3sme2 antibodies could not pull down chromatin DNA in *skb1-1* mutant. In the upper *RD29B* and *RD29A* genes structure, white boxes represent exons or 5` or 3` untranslated regins, and black lines reprent introns.

Supplemental Figure 7. Sequence alignment of LSM4 homologs in Arabidopsis, human, mouse, and yeast.

Supplemental Figure 7. Sequence alignment of LSM4 homologs in *Arabidopsis*, human, mouse, and yeast. Sequence alignment of LSM4 homologs in Arabidopsis (AtLSM4: NP_NP_198124.1), human (hLSM4: NP_036453.1), mouse (mLSM4: NP_056631.1) and yeast (SpLSM4: NP_596279.1).

Supplemental Figure 8. RT-PCR analysis of the splice variants of serine/arginine rich proteins encoding genes.



Supplemental Figure 8. RT-PCR analysis of the splice variants serine/arginine rich proteins encoding genes. Template RNA isolated from 11-day-old seedlings grown on MS medium was treated with 200 mM NaCl for 6 h or 100 μM ABA for 3 h. The experiment was performed independently three times with similar results. *TUBULIN* was the loading control.

Table SI: Primers for real-time quantitative, quantitative RT-PCR, gene cloning and verification of SALK T-DNA insertion mutants.

Quantitative RT-PCR primers		
Gene names	Forward primer	Reverse primer
RD29A	CGGTGGGAGATCAAACTCAA	AACTTCGTCGTCACGGCAGA
RD29B	GAAACATCGGACTGGGAAGC	CACAGGAGTGTTCAATGGCTCT
RD24	TGGCGTCGCAGTCCACA	CCAACGTAAATCGGTCTTCC
COR47	AAGTGAAACCTCAAGAGACAACGA	CAGCTAACTCCGGTTCAGAGATC
DREB2A	TCAGAGGAGTTAGGCAAAGGATT	TCAGCCGCCGCCTTTT
ABF3	GAATTCCGCAGAGGCAACA	CCAGCCCTGACCAAAAACTC
ABI1	TGGCAAGGAAGCGGATTCT	CGCGAGCAACGATGCAT
HAB1	CTTGGTTTGCTCATCACATATAGTAG	TGGCTTCTTTGCCACGGAA
MRK1	CGATACTTCAGGGCAGATAC	AGGACGCTGCTAGTAGAG
MEK1	CTTATGCCCTAATCCCATCTGT	ACAGAGACACGGTCTGGAT
MEKK1	CTTACCATCCGTGGGTTCA	TGTGTCGAAGAATCATGTCTCGT
At1G17170	AGTATGTTTGGGATGAGGACAAG	CATCTCGAGGAGCAAGGAG
At5G17460	ATGTTCGCGCGAAGACTCTC	CACTTGCATAAAATCGAGTTGCTTG
ChIP quantitative PCR primers		
Primer names	Forward primer	Reverse primer
RD29-a	ccaataaacgtggaccgact	ctctctacgtggctatgcga
RD29-b	GCGCACCAGgttaatttctc	TCACGGCAGAGGATTCATAC
RD29-d	CCGACTCATTATCCTCTCGG	CACGTCCTCTGTTGCTGAAA
RD29-e	AAGACAAGGACGCGAAGAAG	TCACATCACCTCTTGTCGGA
RD29-f	ACTGCTTACGGGCAGAAAGT	TTCACTCCACTTCCACCTCC
RD29-g	GGGAACTGAagatttggggt	aatgggccgctaaaagagtt
RD29-h	tgtgacatttagaccttatcggaa	tcctccatcaaatcatgcgt
RD29-i	ttcgttcttgacatcattcaattt	aaacggcacatccttctcat
RD29-j	gccaatagacatggaCCGAC	TTGCTCTCTACGCGTGTCTG
FLC-1	ggcacagctccgagtgtta	atggagccacacaaacatttc
FLC-2	ttgccatatgtgtggacatt	cactcgcctacgtcatcaaa
HAB1-1	ggctgtcgtcttccatcttt	tcagtgtttaatggaatcgtctt
HAB1-2	aaaaaggaaagagaaagaaatcaa	ttttaaggtcgcttcaggca
HAB1-3	ttttcaatcggaagatttttgc	agaacatgggtttccttggat
HAB1-4	AGAAGCGGGTCTTCCAATGT	ATAATCGCGGTTGCAAGAAC
HAB1-5	AGCAGGTGCAGTGGGATAAAG	TACGGTCTCAGACGCAACAG
HAB1-6	AGGTCCATCGgtaagcattg	gaggaggaaagaaaccggag

Gene cloning primers		
Gene names	Forward primer	Reverse primer
At1g65700 (*LSM8*)	GGAATTCATGGCGGCAACTACTGGACTTG	CCCTCGAGTCAATGCACTACGGGTTTCAACG
At3g11500 (*SMG-B*)	GGAATTCATGAGTCGATCAGGTCAGCCTC	CCCTCGAGCTAAGATCTTCCAACTGGTTCG
AT2g43810 (*LSM6-B*)	GGAATTCATGAGTGGAGTTGGAGAGAAAGC	CCCTCGAGCTATGCTCCATCTGACAATGTCC
AT2g03870 (*LSM7*)	GGAATTCATGTCTGGAAGAAAAGAAACGG	CCCTCGAGTTAGACAGCCTCTGCAGTAAC
At2g18740 (*SME-B*)	GGAATTCATGGCGAGCACCAAAGTTCAAAG	CCCTCGAGTCACTTTCCCGTGTTCATCATCAG
At4g30330 (*SME-A*)	GGAATTCATGGCGAGCACCAAAGTTC	CCCTCGAGTCACTTGCCCGCGTTCATCATG
At5g27720 (*LSM4*)	GGAATTCATGCTTCCTCTATCGCTGCTTAAAACTG	CCCTCGAGTCAACCACGGCCGCGAC
At5g27720 (*LSM4*-d1)	GGAATTCATGCTTCCTCTATCGCTGCTTAAAACTG	CCCTCGAGTCTGTTGCCACCCATCTTCC
At5g27720 (*LSM4*-d2)	GGAATTCATGCTTCCTCTATCGCTGCTTAAAACTG	CCCTCGAGTCCTCCATCATCCACACCAC
At5g27720 (*LSM4*-d3)	GGAATTCATGCTTCCTCTATCGCTGCTTAAAACTG	CCCTCGAGTCCAACACCTGGTGGTTTTCTATC
quantitative RT-PCR primers		
Gene names	Forward primer	Reverse primer
SKB1	TGGTTAAGATGGAAGGATGGGAAGACG	GGTGTTGCTGTTGTAGGCTCGATCC
RD22	ATGGCGATTCGTCTTCCTCTGATCT	CTAGTAGCTGAACCACACAACATGAG
SRP34	ATGAGCAGTCGTTCGAGTAG	TTACCTCGATGGACTCCTAG
SRP34A	ATGAGTGGGCGATTTTCTCGG	TCACACACTGCCTTCGCG
RSP31A	AGCAAGTTCGGGAGAGTGAA	GCCCAACAACATCTTCAACC
RSP40	ACTACGCCTGCCAAAATCAT	CACCATCATACCCACCATCA
RSP41	GAGAGCCTCGAAGAAAGCAA	GCGATTTCGAATGGAGTCAT
RSZ21	TGCAACATGACGAGGGTTTA	AAAAGGCGCCACAGAGTAGA
RSZ22a	AAGAGCCAAAGCCGTTTCTT	TGCATAGGTTTTTAGCAGAGCTT
FLC	CCCCATATGGGAAGAAAAAAACTAG	CCCGGATCCCTAATTAAGTAGTGGGAG
RSZ32	GTATCATCCGCGGTTCACTT	TGTCCTCCACGCTTTTCTCT
RSZ33	GCAGTGCTCTCCTTCAATCC	ACATGCTACAATGCCTGCAA
SC35	CCTTCCGTACGACTGCTGAT	TCAACATGGTTGTGCCATCT
RSZ22	CCCTTGAGTGCTTTCAGCTC	GAAACGCTTAGGCATTTAGCA

SCL30	CTCCTCGACGTGGATATGGT	ACCTTCATAGCCAGGGGAGT
SCL30a	TTCCCCTGTGTTTTTCTTCG	CTTTGGCTCCTTGCTTGTTC
AT1G13350	AAGCGGCACAAGTCCCGTC	CCCTCTCTCTACTACTATACCTGG
TUBULIN	TTTGGAGCCTGGGACTATGGAT	ACGGGGGAATGGGATGAGAT
HAB1	CTTGGTTTGCTCATCACATATAGTAG	CACATCAATATCCGTCTCCTTGC
FIP1	CATAGAGGACATGAAGACTTCTCTG	TGTATCTCATCACCAGAGGATGC
AT1G15940	TCCTCTTGTCGAAGCGACTGA	AAGCACCAGTTGAGGATGATCC
AT1G28060	ATCGTGATCGAGATTCGAGTCC	AGCCACATCCTCAAACCTGCT
AT1G24160	GCATATCTCTATGAATCTGGATCCAC	GAGCTTTTCGATACGGTCCGC
AT1G69250	ATCTGCCATTGAATGCAATGCCG	TTACACGAAGCTTACGGTCTGC
AT1G42440	CTGCTTGGATTGTGGATGAAACAG	CTTCGTCATCAGCATATGCCTC
CDPK13	GAGTTGAAAGCCGGACTTCG	GAGATGCTCATCGTTTGCTACC
CBL1	GTGAGTGAGGTTGAAGCATTATTTGAG	CCGAAATCGATGACTCCTTTTCG
AT1G18160	TGAGCTACAGCTTGAAAGCAACC	ACTGGCAGAGTAGACAGAATCATC
At1g45249	TGTTACGCCATTGTCATCAGAAGG	TGCTTTCGTTGTAACTCGTCATTCTC
At1g17550	GTGTATATGATGGCCACGGAG	ACCTGGACATGGCAAGAACG
AT1G72050	GCAGCATATGCAGAGTCATTCG	AGCTAGCAGCACAATCATCCAC
AT1G49670	GTTGGACTAATTGCAGCAGTGG	TGCAGTTAATCCCGAGGTAAGC
CDKP2	GTTGGACTAATTGCAGCAGTGG	CTCATCATTGCTGTAAACTCCGAG
CIPK3	GTTGGACTAATTGCAGCAGTGG	AGAACCCTCAGAGACTTGAGC
AT1G49670	GTTGGACTAATTGCAGCAGTGG	AGCCTTATCCAACTGAGCTGC
RLP4	GTTGGACTAATTGCAGCAGTGG	GGTAGGAAACCTTTCAGACCTTG
SALK T-DNA insertion mutants verification primers		
SALK number	Forward primer	Reverse primer
SALK_057540	AAGTGGAGGCTGTCAGACATG	TTCATCCCGCATGAGATAGAC
SALK_007750	CGAGAATCTTTATTCGAGCCC	GAATCTCTCTCTTTCTCCGCC
SALK_150861	AAAAGCTGCTGGAAAGAGTCC	GCTACTGCTTGAGTTTGGTGC
SALK_065480	CCTTCATCGCAATCGTAAATC	TTTTGCGCTAAACTAGTTGGG

Table S2. Alternative Splicing changes in wild type and *sbh1-1* mutant

Gene locus*	Splicing event	Alternative Splicing regions	Splicing position
At2g43410	IR	18028320-18028448	intron 4
At4g23260	A3'S	12168162-12168399; 12167917-12168070; 12167917-12168017	exon 6
At5g24270	A5'S	8239181-8239261; 8239381-8239433; 8239352-8239433	exon 6
At3g16800	A3'S	5721105-5721154; 5721256-5721542; 5721274-5721542	exon 2
At4g24740	IR	12755783-12755931; 12756047-12756144	intron 5,6
At3g20270	A3'S	7067772-7068038; 7068130-7068281; 7068124-7068281	exon 3
At3g25840	A5'S	9451861-9452032; 9452135-9452183; 9452110-9452183	exon 14
At3g01150	IR	51915-52154	intron 1
At1g54360	A5'S	20291458-20291595; 20291302-20291378; 20291302-20291357	exon 5
At5g57630	IR	23342391-23342488	intron 3
At2g15530	A5'S	6774084-6775826; 6773917-6773964; 6773917-6773983	exon 2
At1g53650	A3'S	20029591-20029659; 20030962-20031447; 20029405-20029466; 20030554-20030667; 20029405-20029462;20030554-20030665	exon 9 exon 2
At4g38510	A5'S	18014735-18014796; 18014903-18014975; 18014884-18014975;1679826-1679886; 1679826-1679909	exon 2
At2g04790	A3'S	1679516-1679719; 1679521-1679719; 1679528-1679719 1679805-1679886; 1679805-1679909; 1679805-1679886	exon 2
At5g18620	A3'S	6197403-6197461; 6197152-6197317; 6197152-6197297	exon 21
At2g39730	A3'S	16571180-16571472; 16570746-16571066; 16570746-16571060	exon 7
At1g72650	A3'S	27351194-27351246; 27350924-27351246	exon 4
At3g12250	A5'S	3906244-3906525;3906451-3906525;3906244-3906416;3906451-3906416	exon 3
At3g23900	A3'S	8634745-8635182; 8634109-8634616; 8634109-8634305	exon 3
At3g29160	A3'S	11129883-11129966; 11131004-11131188; 11129659-11129799; 11130727-11130909; 11129659-11129794; 11130727-11130893	exon 9 exon 4
At2g33480	IR / A3'S / A5'S	14181790-14181878; 14181536-14181789; 14181879-14182402; 14181908-14182402	intron 2 exons 2, 3
At3g62190	IR	23022260-23022334	intron 4
At4g31720	IR	15355516-15355611	intron 2
At1g60850	A3'S	22400285-22400362; 22400021-22400178; 22400021-22400167	exon 2
At3g12570	ES / IR	3988714-3988823; 3989180-3989266; 3989386-3991079; 3989267-3989385; 3989267-3989356	exon 2 intron 2
At4g12790	ES/A3'S/ A5'S	7518643-7518751;7518848-7518955;7519326-7519422; 7518848-7518926;7519326-7519396;7518848-7518924; 7519326-7519397;7519173-7519422; 7518848-7519081	exon 2 exons 2, 1

Note: * A comparison of our RNA deep sequence results and data in the Sanchez, *et. al*.(Sanchez et al., 2010) paper (Supplementary Table 4). Splicing defects of Genes shown here exist in both datasets.
IR: intron retention; A5'S: alternative 5' splicing; A3'S: alternative 3' splicing; ES: exon skipping.