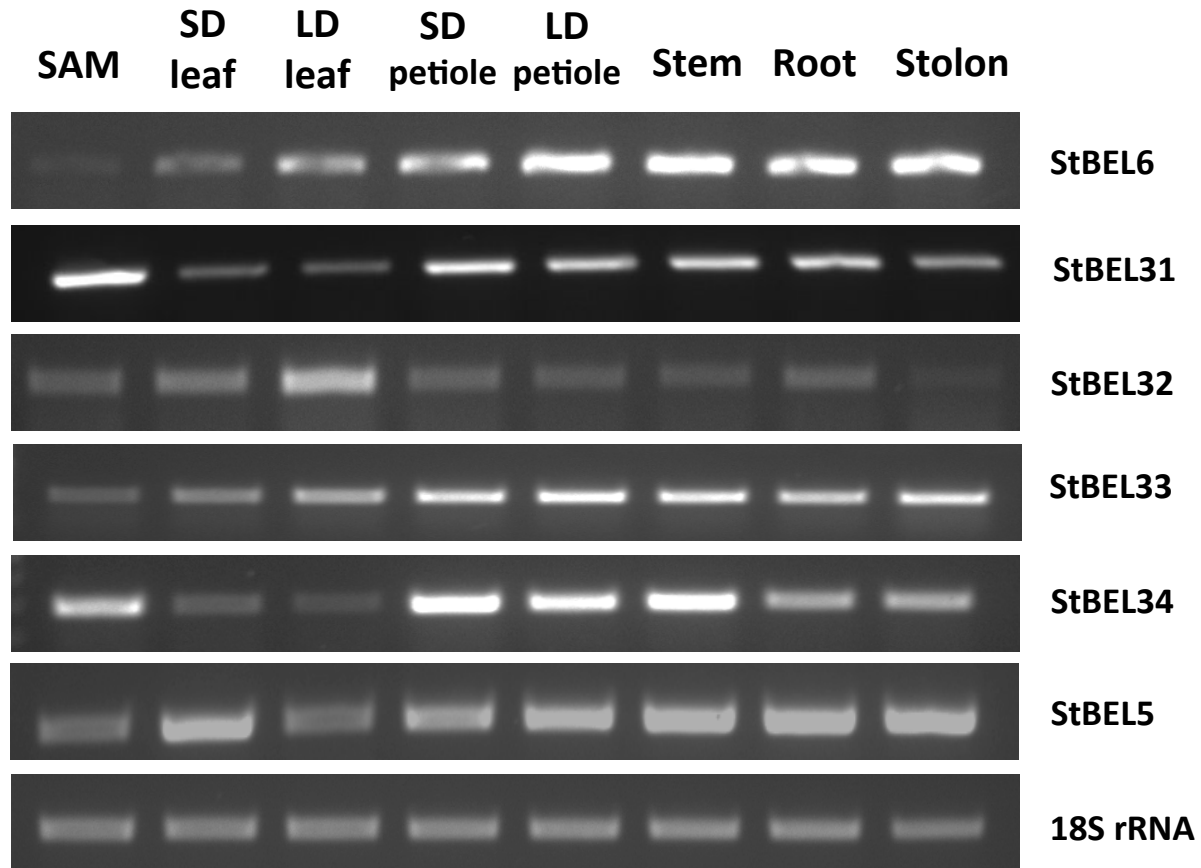
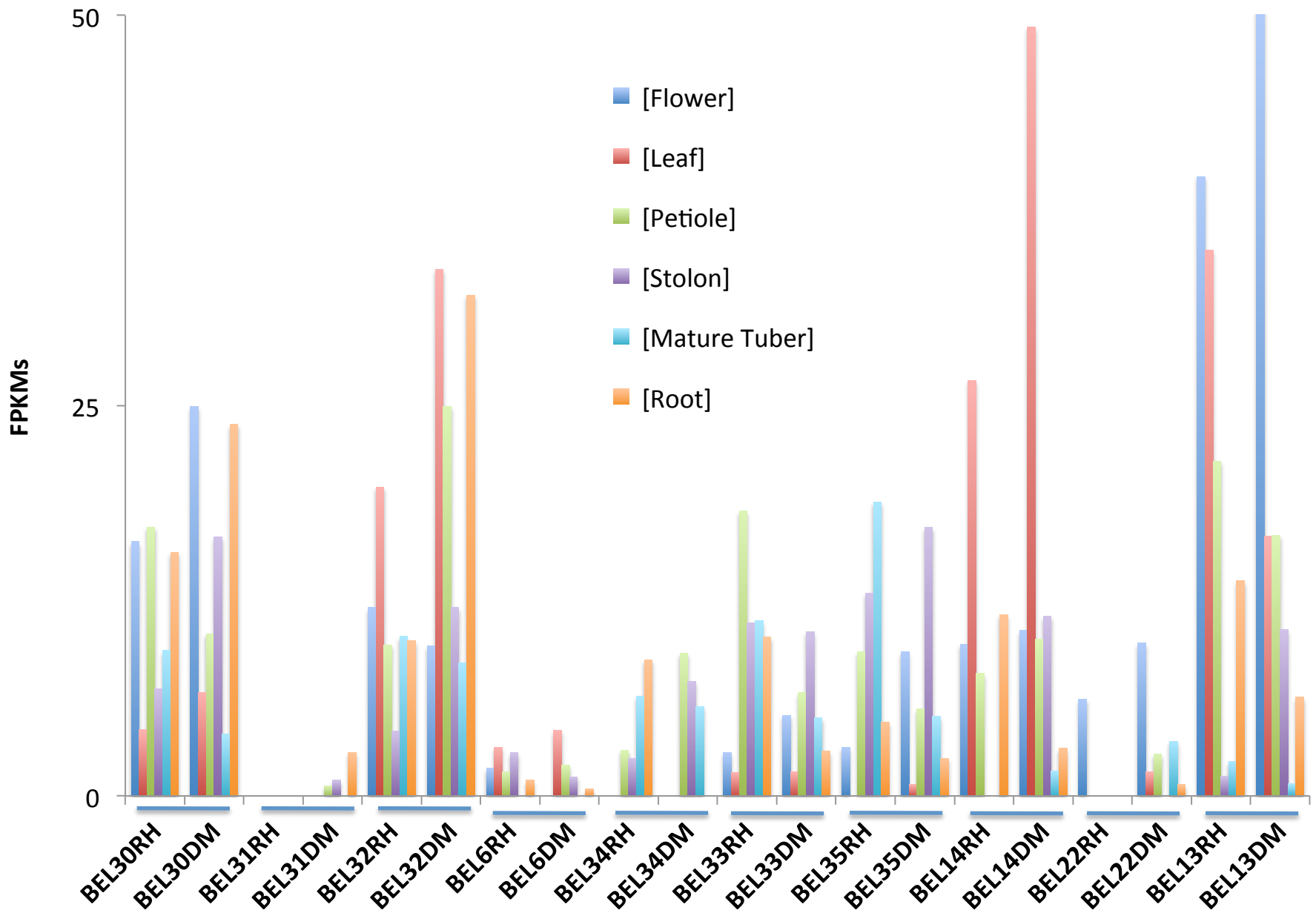


**Figure S1.** Protein structure of StBELs. All StBELs contain a SKY box, a BELL domain and a homeodomain made up of three helices. A conserved three aa loop extension (TALE), proline-tyrosine-proline (PYP), is located between the first and second helices. The VSLTLGL motif is conserved but its function is unknown.





**Fig. S3.** RT-PCR with gene-specific primers for *StBEL5*, *-6*, *-31*, *-32*, *-33* and *-34* using total RNA extracted from the shoot apical meristem (SAM), leaf (SD and LD), petiole (SD and LD), stem, root and stolon of soil-grown potato plants, *Solanum tuberosum* ssp. *andigena*. RT-PCR product for 18S rRNA was used as an internal control.



**Figure S4.** Expression profile for StBEL family members mined using the RNA-seq data from the publicly available Potato Genome Database from both the RH and DM genotypes (Xu *et al.*, 2011). Six organs and ten StBELs are presented and abundance values are shown in FPKMs (fragments per kb per million mapped reads).

**Table S1.** Primers and oligonucleotides

For qRT-PCR of BELs LD/SD

BEL5-F: AGGGATACTCTTATATTGTGTGAGG  
BEL5-R: GTCTCCACTTCTTTTCTCCTATG  
BEL6-F: GGATGCAGAGAAGCAATTGCTGG  
BEL6-R: TGGTTTCCATAGACGAACTCGAG  
BEL31-F: CTCCATCCATATCCAAATGACTC  
BEL31-R: CGTTAATAAACCAGTTGGAAACCTGA  
BEL32-F: TGCTGTTTCAGTCCTTCGTGCTT  
BEL32-R: AACCTGTTTGCCTCGCCAGCATGAT  
BEL33-F: CTTCTGAACGTGCTGTCCTGTA  
BEL33-R: CATTACTTTATCGCTGTCCGTGG  
BEL34-F: GCACATGTTGGCTTCTCAAAC  
BEL34-R: CATCCGATTTTCTTGTGTTGATCTC  
BEL35-F: GACTGGTCTTTCAAGGAATCAG  
BEL35-R: GTGTATTTCTTCAACCATAGGC  
Actin-F: GGAAAAGCTTGCCTATGTGG  
Actin-R: CTGCTCCTGGCAGTTTCAA

For cloning Y2H constructs

StBEL6fw: CATGCCATGGAGATGGCAGAGCCTCATCGG  
StBEL6rev: TCCCCCGGGTCACTTCATTGTAAATAAATG

StBEL31fw: GAATTCGAATGGTTTCAAAGACTCACCCC  
StBEL31rev: CTCGAGTCATTCTTCTGCAGAATCAGTAACAC

StBEL32fw: CATGCCATGGAGATGTCTGCTTACTATTCAAATTTG  
StBEL32rev: TCCCCCGGGTTACTACTACAAAATCGGATAG

StBEL33fw: CATGCCATGGAGATGGCTGAAGGATTTGAAC  
StBEL33rev: TCCCCCGGGTCAACCACCAAATCATGC

StBEL34fw: CGGGATCCGAATGGTGGCTTTTTTGGCGATG  
StBEL34rev: CCGCTCGAGTCAATCAACAAAGTCATG

StBEL35fw: GAATTCGAATGGCTGCAGAAGGATTTGAA  
StBEL35rev: CTCGAGTCAACCAACAAAATCATGCAAC

GSPs for BEL6, -14, -22, and -34 of Fig. 8

BEL6Fw: GTATGCTGAGATGAATAGAAG  
BEL6Rv: GGCATAGCATACAACATGG

BEL34Fw: CGGATGTGAATAAGCTCGTG  
BEL34Rv: CAGCTCCGATATTACCTCC

18SFw: GGATGTTGCTTTTAGGACTC  
81SRv: CATCACAGACCTGTTATTGC

BEL22Fw: ATTGTCGCAATGAATACACATTA  
BEL22Rv: TTATGTAGCAGTGTTTGAATACAC

BEL14Fw: TATGGAAGCCAATGGTGGAAAG  
BEL14Rv: ATGATCCACCACTTCCACCAT

Oligos for EMSA DNA bait 6, 22, and 34 for Fig. 9

BEL6S: TGCTTGCCTTTTGACAGTCACTATTGTATG  
BEL6A: CATACAATAGTGACTGTCAAAAGGCAAGCA

BEL22S: TATGTCCGTTGCATAATTAGTCACAATTGACATGCTCCTATTAGATATAA  
BEL22A: TTATATCTAATAGGAGCATGTCAATTGTGACTAATTATGCAACGGACATA

BEL34S: CCTTTCAATAAGATTATTGACGGTGACAATACTCGCCGTCAAA  
BEL34A: TTTGACGGCGAGTATTGTCACCGTCAATAATCTTATTGAAAGG

**Table S2**

<b>Chr no.</b>	<b>Size of chr</b>	<b>BEL gene location</b>	
chr01	81.48 Mbp	(BEL29) 3.678 kbp from chr01, positions 2,458,978 to 2,462,655	(BEL30)5.85 kbp from chr01, positions 79,264,769 to 79,270,618
chr02	47.07 Mbp	(BEL13)7.139 kbp from chr02, positions 43,219,985 to 43,227,123	(BEL22)5.199 kbp from chr02, positions 23,380,997 to 23,386,195
chr03	47.88 Mbp	none	
chr04	64.34 Mbp	(BEL31)2.258 kbp from chr04, positions 62,325,726 to 62,327,983	(BEL32)4.917 kbp from chr04, positions 62,330,004 to 62,334,920 bel31 and 32 are 2.021 kbp apart, tandemly duplicated genes?
chr05	47.05 Mbp	none	
chr06	54.98 Mbp	(BEL5)4.015 kbp from chr06, positions 49,229,263 to 49,233,277	
chr07	53.43 Mbp	none	
chr08	43.65 Mbp	(BEL14)4.946 kbp from chr08, positions 43,062,646 to 43,067,591	(BEL6)2.659 kbp from chr08, positions 24,072,529 to 24,075,187
chr09	53.64 Mbp	(BEL33)5.086 kbp from chr09, positions 5,515,256 to 5,520,341	
chr10	52.31 Mbp	(BEL35)4.593 kbp from chr10, positions 50,859,636 to 50,864,228	

chr11	42.25 Mbp	(BEL34)4.122 kbp from chr11, positions 38,532,179 to 38,536,300	(BEL11)6.483 kbp from chr11, positions 37,602,233 to 37,608,715	<b>BEL34 and 11 are 0.923 Mbp apart</b>
chr12	59.1 Mbp	none		



BEL	Gene	Flower	Tuber Sprout	Leaf	Petiole	Shoot Apex	Stem	Stolon	Young Tuber	Mature Tuber	Root
31	PGSC0003DMG400003750	0	2.5	0	0	2.7	0	0	0	0	0
32	PGSC0003DMG400003751	12	10.3	19.8	9.7	8.8	16.6	4.2	5.5	10.2	9.9
<b>5</b>	<b>PGSC0003DMG400005930</b>	<b>35</b>	<b>60</b>	<b>39</b>	<b>170.3</b>	<b>25</b>	<b>76.7</b>	<b>24</b>	<b>55.4</b>	<b>76.4</b>	<b>41.6</b>
34	PGSC0003DMG400008057	0	15.1	0	2.9	2.5	7.8	2.4	4.1	6.4	8.7
13	PGSC0003DMG400010086	<b>39.7</b>	4.1	<b>34</b>	21.4	<b>45</b>	14.2	1.3	1	2.2	13.8
14	PGSC0003DMG400012329	9.7	2.7	<b>26.6</b>	7.8	2.51	3.6	0	0	0	11.6
35	PGSC0003DMG400019142	3.1	20.8	0	9.2	4.7	17.7	<b>12</b>	13.9	<b>18.8</b>	4.7
<b>11</b>	<b>PGSC0003DMG400019635</b>	15.5	<b>46.4</b>	4.9	<b>120.6</b>	3.8	17	4.7	11.6	13.4	<b>43</b>
<b>29</b>	<b>PGSC0003DMG400021323</b>	<b>66.8</b>	<b>61.5</b>	21.4	<b>153</b>	<b>22.7</b>	<b>51.5</b>	<b>23</b>	<b>22.2</b>	<b>38.4</b>	<b>188.4</b>
22	PGSC0003DMG400022011	6.2	0	0	0	3.7	0	0	0	0	0
33	PGSC0003DMG400024267	2.8	20.6	1.5	18.2	8.7	14	11.1	<b>25.4</b>	11.2	10.2
6	PGSC0003DMG400029946	1.8	1.9	3.1	1.5	21.6	2.6	2.8	1.1	0	1
30	PGSC0003DMG400030961	16.3	14.9	4.2	17.2	9.8	<b>17.8</b>	6.8	8.2	9.3	15.6

**Table S3.** RNA-seq data for thirteen *StBEL* genes from the RH potato genotype (Xu *et al.*, 2011). *BEL1*-like protein coding genes were identified, and the FPKM value of each is shown for several organs. Bold numbers represent the top three values in each category. *StBEL5* is the most abundant RNA in 6 of 10 organs. *BEL29* is most abundant in three others. *BEL5* and *BEL29* are top two most RNAs abundant in nine of the organs.

**Table S4.** Interaction of select tobacco KNOX proteins with potato BELs verified with  $\beta$ -galactosidase assays in the yeast two-hybrid system. The plus sign indicates strong  $\beta$ -gal induction; the negative sign, no induction. The NTH Knox genes 1, 15, 20, and 22 are from *Nicotiana tabacum*. POTH1 and the class II-Knox are from potato.

<b>Knox type</b>	<b>BEL5</b>	<b>BEL11</b>	<b>BEL13</b>	<b>BEL14</b>	<b>BEL22</b>	<b>BEL29</b>	<b>BEL30</b>
<b>class II-Knox</b>	–	–	–	–	–	–	+
<b>POTH1</b>	+	+	+	+	+	+	+
<b>NTH1</b>	+	+	+	+	+	+	+
<b>NTH15</b>	+	+	+	+	+	+	+
<b>NTH20</b>	+	+	+	+	+	+	+
<b>NTH22</b>	+	+	+	+	+	+	+