

1 Supplementary data.

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3 Supplementary figure 1. Phylogenetic tree of the AtYUCCA and StYUCCA genes used in this study.  
4 AtYUCCAs are identified as “NCBI gene name (TAIR gene number)” and StYUCCAs are identified with  
5 “NCBI gene name(v4.1 transcript id)”. The alignment was performed using UGENE v.36.0, multiple  
6 sequence alignments with ClustalW default settings. The phylogenetic tree was built using MrBayes tree  
7 building methods with default settings.

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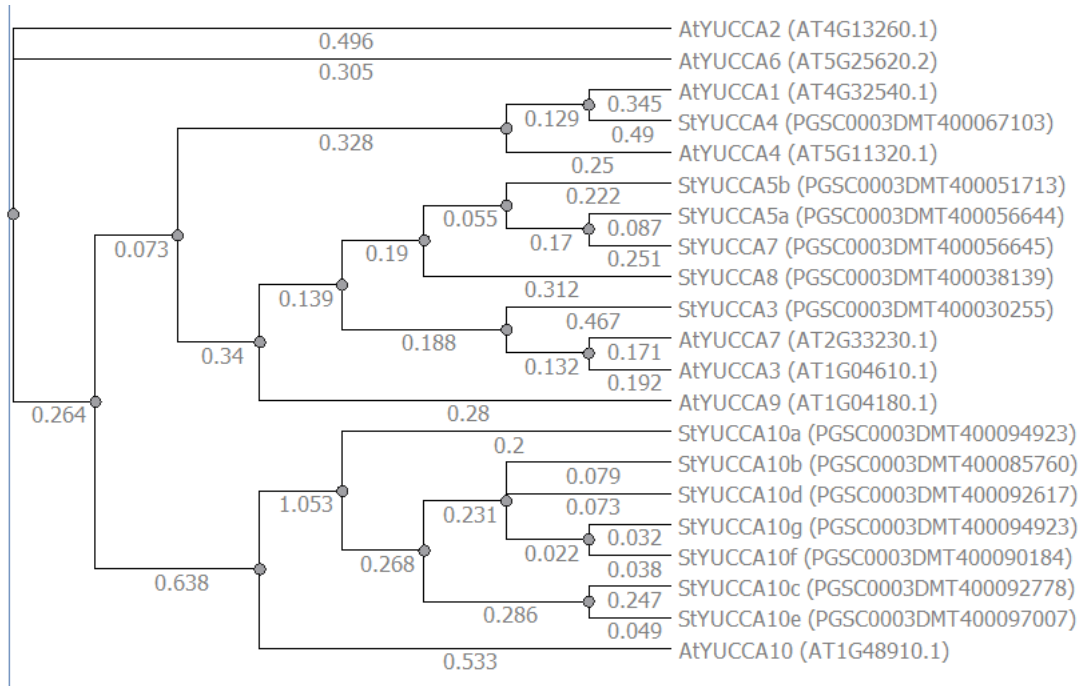
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10 Supplementary figure 2. Heat map of expression of the *StYUCCA* predicted genes in the corresponding  
11 tissues according to the RNA-seq data of the potato diploid genotype RH. Expression levels in the  
12 various tissues are indicated by shades of red, where white indicates no expression detected. Numbers  
13 in the cells correspond to the RFPK values of each gene (third column from left) for the corresponding  
14 sample (top line). All *YUCCA* genes that were annotated in the NCBI library are included. In red font  
15 colour are the *YUCCA-like* genes that exhibited low RPKM values in only one sample and were not  
16 included in our study. Transcript\_id(v4.1) numbers correspond to the BLAST results of the  
17 corresponding *StYUCCA-like* gene against PGSC\_DM\_v3.4\_transcript-update.fa using the  
18 <http://solanaceae.plantbiology.msu.edu> blast tool. Accession n. (v6.1) correspond to the BLAST results  
19 against DM\_1-3\_516\_R44\_potato.v6.1.hc\_gene\_models.cdna.fa using the  
20 <http://solanaceae.plantbiology.msu.edu> blast tool.

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22 Supplementary figure 3. Primers for qRT PCR used in this study.

23 Supplementary figure 1.



25 Supplementary figure 2.

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Accession number (NCBI)	transcript_id (v4.1)	Accession n. (v6.1)	Gene name	Flower	Leaf	Petiole	Shoot Apex	Stem	Stolon	Young Tuber	Mature Tuber	Root
XM_006364488.2	PGSC0003D MT400038139	Soltu.DM.06 G002120.1	StYUCCA8	0	0,17571	1,44056	0,39238	0,56307	0,44525	2,72323	0	0
XM_006350223.2	PGSC0003D MT400056645	Soltu.DM.09 G018710.1	StYUCCA7	13,632	1,73727	1,76987	0,82641	4,48427	1,75053	1,0768	0,82219	2,16117
XM_006350224.2	PGSC0003D MT400056644	Soltu.DM.09 G018700.1	StYUCCA5a	3,35006	0,25761	0,35201	0,12784	0,61915	0,23211	0,86175	0,12719	0,56416
XM_006353587.2	PGSC0003D MT400067103	Soltu.DM.06 G019760.1	StYUCCA4	0,23432	0	0	0,96603	0,23105	1,75395	1,61836	1,20137	0
XM_006340840.2	PGSC0003D MT400030255	Soltu.DM.09 G027910.1	StYUCCA3	0,56674	0,13079	0,13404	0,29207	0	0,39771	1,25817	0,29057	0,07161
XM_006352661.2	PGSC0003D MT400051713	Soltu.DM.06 G034100.1	StYUCCA5b	0	0,33115	0	0	0	0	0	0	
XM_015306949.1	PGSC0003D MT400094923	Soltu.DM.09 G028780.1	StYUCCA10 a	0,06644	0	0	0	0	0	0	0	0
XM_015306950.1	PGSC0003D MT400085760	Soltu.DM.07 G009370.1	StYUCCA10 b	0	0	0	0	0	0	0	0	0
XM_015310803.1	PGSC0003D MT400092778	Soltu.DM.07 G008090.1	StYUCCA10 c	0	0	0,445	0	0	0	0	0	0
XM_015312506.1	PGSC0003D MT400092617	Soltu.DM.09 G013380.1	StYUCCA10 d	0	0	0	0	0	0	0	0	0
XM_015313553.1	PGSC0003D MT400097007	Soltu.DM.10 G014520.1	StYUCCA10 e	0	0	0	0	0	0	0	0	0
XM_015314778.1	PGSC0003D MT400090184	Soltu.DM.09 G028780.1	StYUCCA10 f	0,12774	0	0	0	0	0	0	0	0
XM_015314779.1	PGSC0003D MT400094923	Soltu.DM.09 G028790.1	StYUCCA10 g	0,06644	0	0	0	0	0	0	0	0

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Supplementary figure 3.

<b>Primer Name</b>	<b>sequence ( in 5'----&gt; 3' order)</b>
<i>eIF3e F</i>	GGAGCACAGGAGGAAGATGAAGGA G
<i>eIF3e R</i>	CGTTGGTGAATGCGGCAGGAAGGA G
<i>StYUCCA8 F</i>	TGTTTTGGACATTGGTGCAT
<i>StYUCCA8 R</i>	AACGGTGCCACATGAAAAC