

Table S1:

Putative Cis-regulatory elements found in promoter regions of *StYAB* genes.

Gene Id	Start-Seq	End-seq	Cis-Elements	Function
<i>StYAB1</i>	447	438	I-box	Part of light responsive element
<i>StYAB1</i>	682	675	MRE	MYB binding site involved in light responsive elements
<i>StYAB1</i>	449	439	GATA-motif	Part of light responsive element
<i>StYAB1</i>	89	95	MYC	Activates expression of proliferative genes
<i>StYAB1</i>	853	848	STRE	Stress related function
<i>StYAB2</i>	42	37	STRE	Stress related function
<i>StYAB2</i>	78	84	MYC	Activates expression of proliferative genes
<i>StYAB2</i>	173	179	GT1-motif	light responsive element
<i>StYAB2</i>	791	797	ABRE3a	Positive regulator of abiotic stress and ABA signaling
<i>StYAB2</i>	899	893	ARE	cis-acting regulatory element essential for the anaerobic induction
<i>StYAB2</i>	663	672	I-box	Part of light responsive element
<i>StYAB2</i>	680	674	MYB	Plant Development
<i>StYAB2</i>	461	470	WUN-motif	A defense and stress responsive element
<i>StYAB2</i>	234	244	AT-rich element	Binding site of AT-rich DNA binding protein (ATBP-1)
<i>StYAB2</i>	226	232	Box 4	Part of a conserved DNA module involved in light responsiveness
<i>StYAB2</i>	792	797	ABRE	Cis-acting element involved in the abscisic acid responsiveness
<i>StYAB2</i>	791	785	ABRE 4	Mediate ABA-dependent stress responses.
<i>StYAB2</i>	674	667	MRE	MYB binding site involved in light responsive elements
<i>StYAB3</i>	521	528	AAGAA-motif	cis-acting regulatory element
<i>StYAB3</i>	583	589	ARE	cis-acting regulatory element essential for the anaerobic

				induction
<i>StYAB3</i>	835	829	Box 4	part of a conserved DNA module involved in light responsiveness
<i>StYAB3</i>	763	753	CAG-motif	part of a light response element
<i>StYAB3</i>	640	646	GT1-motif	light responsive element
<i>StYAB3</i>	199	193	LTR	cis-acting element involved in low-temperature responsiveness
<i>StYAB3</i>	799	805	MYB	Plant Development
<i>StYAB3</i>	899	905	MYC	Activates expression of proliferative genes
<i>StYAB3</i>	727	721	TGA-Element	Auxin-responsive element
<i>StYAB3</i>	176	185	Circadian	cis-acting regulatory element involved in circadian control
<i>StYAB4</i>	565	572	AAGAA-motif	cis-acting regulatory element
<i>StYAB4</i>	531	537	ABRE	Cis-acting element involved in the abscisic acid responsiveness
<i>StYAB4</i>	953	961	AE-box	part of a module for light response
<i>StYAB4</i>	410	416	ARE	cis-acting regulatory element essential for the anaerobic induction
<i>StYAB4</i>	768	758	GATA-motif	Part of light responsive element
<i>StYAB4</i>	1100	1107	GCN4-motif	cis-regulatory element involved in endosperm expression
<i>StYAB4</i>	221	211	I-box	Part of light responsive element
<i>StYAB4</i>	576	582	MYB	Plant Development
<i>StYAB4</i>	1024	1018	MYC	Activates expression of proliferative genes
<i>StYAB4</i>	445	436	WUN-motif	A defense and stress responsive element
<i>StYAB5</i>	111	117	Box 4	Part of conserved DNA module involved in light responsiveness
<i>StYAB5</i>	895	887	GA-motif	Part of light responsive element

<i>StYAB5</i>	676	682	MYB	Plant Development
<i>StYAB5</i>	69	78	TCA element	cis-acting element involved in salicylic acid responsiveness
<i>StYAB5</i>	341	347	TGA-Element	Auxin-responsive element
<i>StYAB5</i>	481	486	TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness
<i>StYAB6</i>	1	7	Box 4	Part of conserved DNA module involved in light responsiveness
<i>StYAB6</i>	343	338	CGTCA-motif	cis-acting regulatory element involved in the MeJA-responsiveness
<i>StYAB6</i>	766	760	G-box	light responsive element
<i>StYAB6</i>	520	511	I-box	light responsive element
<i>StYAB6</i>	376	370	MYC	Activates expression of proliferative genes
<i>StYAB6</i>	51	59	O2-site	cis-acting regulatory element involved in zein metabolism regulation
<i>StYAB6</i>	257	266	TCA	Salicylic acid responsiveness
<i>StYAB6</i>	739	745	TCT-motif	light responsive element
<i>StYAB6</i>	343	348	TGACG-motif	cis-acting regulatory element involved in MeJA-responsiveness
<i>StYAB7</i>	982	988	ARE	Anaerobic induction
<i>StYAB7</i>	807	801	Box 4	light responsive element
<i>StYAB7</i>	734	728	MYC	Activates expression of proliferative genes
<i>StYAB7</i>	474	463	O2-site	cis-acting regulatory element involved in zein metabolism regulation
<i>StYAB7</i>	164	169	STRE	Stress related function
<i>StYAB7</i>	863	853	TCA	Salicylic acid responsiveness
<i>StYAB7</i>	398	389	TCA element	Salicylic acid responsiveness
<i>StYAB7</i>	679	685	TGA-Element	Auxin-responsive element

<i>StYAB7</i>	375	384	Circadian	cis-acting regulatory element involved in circadian control
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Table S2

StYAB genes distribution among groups based on phylogenetic analysis.

Group s	Potato	Arabidopsis		Tomato		Cultivated Squash		Cucumber		
	NO. of YABB Y genes	Gene- id	NO. of YABBY genes	Gene- id	NO. of YABBY genes	Gene-id	NO. of YABBY genes	Gene-id	NO. of YABBY genes	Gene-id
INO	1	StYAB 2.	1	AtINO	1	SlYABBY 2	2	CmYABBY9, CmYABBY10	2	CsYABBY 4, CsYABBY 8
YAB2	2	StYAB 7, StYAB 5.	1	AtYAB 2	2	SlYABBY 6, SlYABBY 4	2	CmYABBY13, CmYABBY6	1	CsYABBY 1
AFO / YAB3	2	StYAB 4, StYAB 3.	2	AtAF O, AtYAB 3	2	SlYABBY 5, SlYABBY 7	3	CmYABBY1, CmYABBY2, CmYABBY3	2	CsYABBY 6, CsYABBY 7
YAB5	2	StYAB 1, StYAB 6.	1	AtYAB 5	2	SlYABBy1 , SlYABBY 9	3	CmYABBY4, CmYABBY5, CmYABBY8	2	CsYABBY 2, CsYABBY 5
CRC	0		1	AtCRC	2	SlYABBY 3, SlYABBY 8	3	CmYABBY7, CmYABBY11, CmYABBY12	1	CsYABBY 3

Table S3:

Ka/Ks ratio duplicated gene pairs in potato.

Gene Id	Ka	Ks	Ka/Ks	T(MYA)
StYAB1-StYAB6	0.140981	0.443162	0.318126	8.52235E-05
StYAB3-StYAB4	0.19983	1.431631	0.139582	0.000275314
StYAB5-StYAB7	0.168917	0.612267	0.275888	0.000117744

Table S4:

miRNA targets prediction of *StYAB* genes. The miRNA data was downloaded from psRNATarget (Online Web tool).

miRNA	Target Gene	E-value	Length	Target-start'	Target-end'	miRNA-sequence
stu-miR390-3p	<i>StYAB7</i>	4	21	485	505	CGCUAUCCAUCUUGAGUUUUA
stu-miR5303g	<i>StYAB4</i>	4	24	185	209	AUAUUUUUGAAGAGUC- UGAGCAAC
stu-miR5303i	<i>StYAB4</i>	4	24	185	209	AUAUUUUUGAAGAGUC- UGAGCAAC
stu-miR172d-5p	<i>StYAB3</i>	4.5	21	343	362	GGAGCAUCAUCAAGAUUCACA
stu-miR5303h	<i>StYAB4</i>	4.5	24	186	210	AACAUUUUUUGAAGAGUC- UGAGCAA
stu-miR1886g-5p	<i>StYAB7</i>	5	24	448	471	GAGAUGAGAUCAAUGUUUGGACAU
stu-miR1886g-5p	<i>StYAB4</i>	5	24	681	703	GAGAUGAGAUCAAUGUUUGGACAU

stu-miR5303j	<i>StYAB4</i>	5	24	186	210	AAUAUUUUUGAAGAGUC- UGAGCAA
stu-miR7992-5p	<i>StYAB6</i>	5	24	540	563	UUUGACAAUGCACAUUAGACACU
stu-miR8037	<i>StYAB5</i>	5	22	280	301	AUAAUUUGGAGGAUAGGAACC

Figure S1:

The sequence logos are based on alignments of *StYAB* gnese. *YABBY* domain is highly conserved across all *StYAB* genes while C2-C2 domain is highly conserved in only six *YABBY* proteins (*StYAB1*, *StYAB3*, *StYAB4*, *StYAB5*, *StYAB6*, *StYAB7*). Black bars representing start and end point of C2-C2 type domain & *YABBY* domain. Single alphabet on the respective number representing the highly conserve nature of that respective amino acid in s all *StYAB* genes sequence.

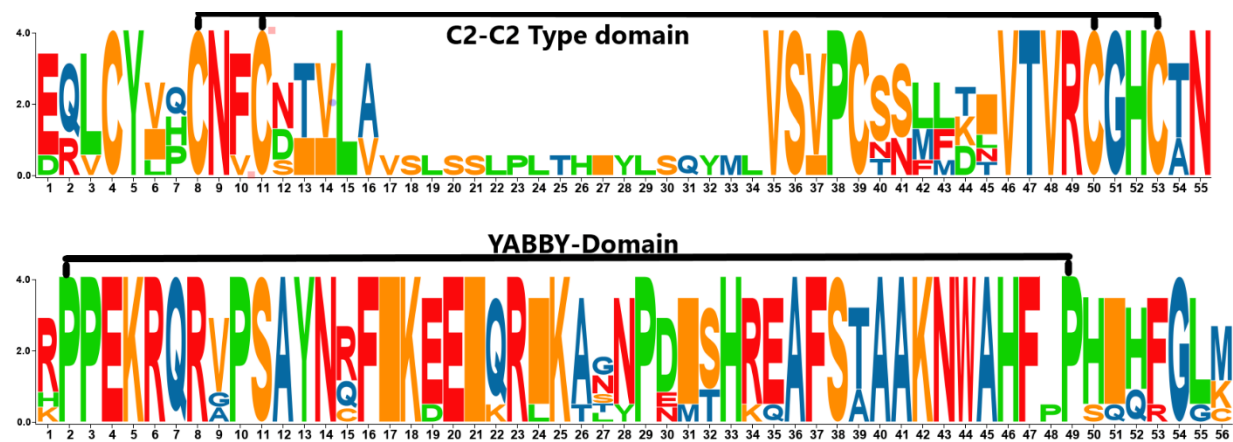


Figure S2:

Heat Map representing sub-cellular localization of all seven *StYAB* genes. Grey color represents absence of respective genes in that cell region. White and Red color represents minimum and maximum value of gene in that region.

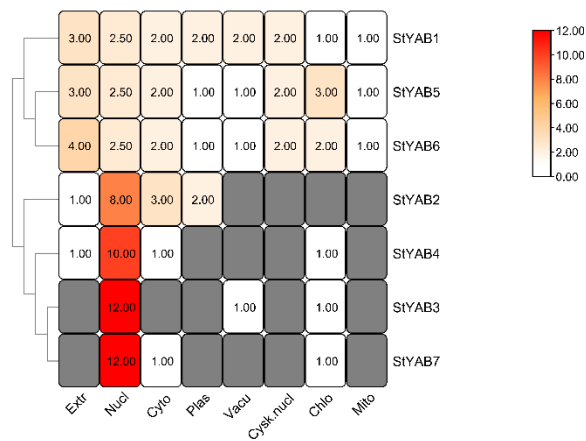


Figure S3:

YABBY genes distribution chart representing, total number of *YABBY* genes from different species in 5 sub-groups based on phylogenetic analysis.

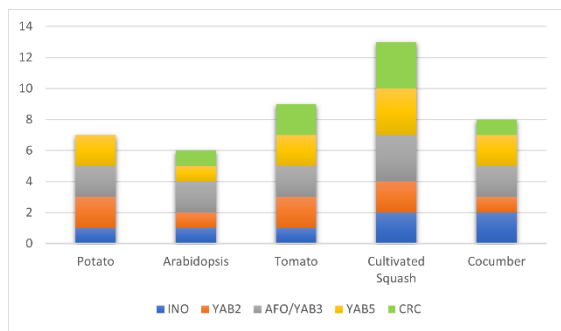


Figure S4:

Distribution of *StYAB* genes on potato chromosomes, lines predicting the possible gene duplication on different chromosomes.

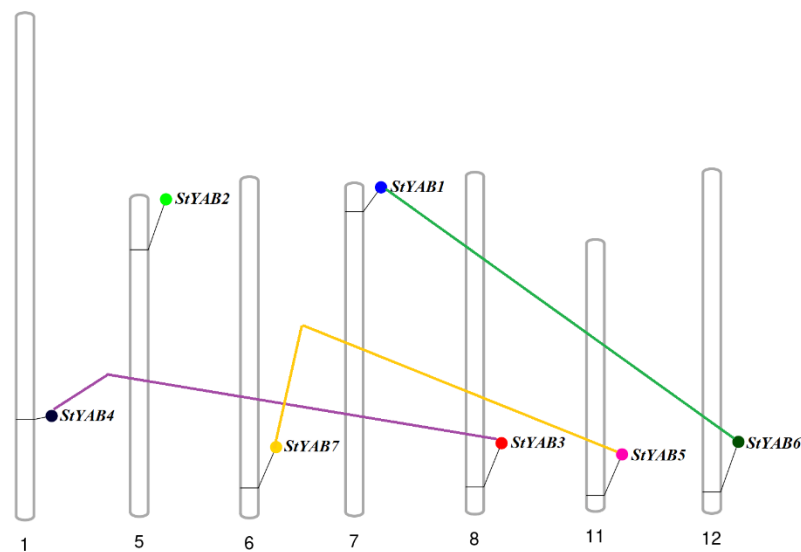
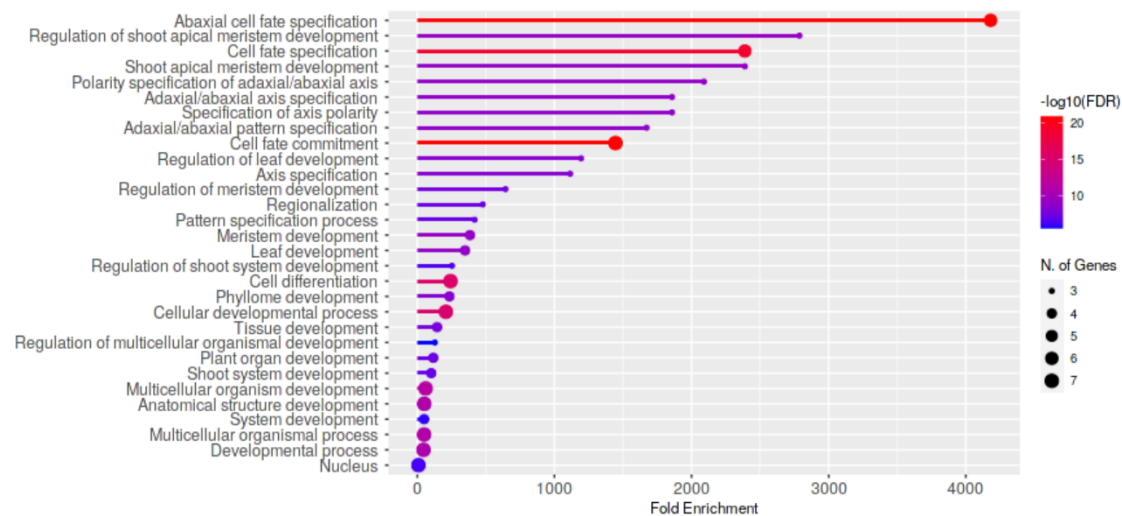
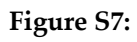


Figure S5:

Fold Enrichment chart representing the overlapping *StYAB* genes functions. Bigger lollipop tip size represents the more no. of genes involved in that process and vice versa for small tip size.



Heat map shows the expression profile of the *StYAB* genes in leaves and Roots of potato cultivar under different levels of Cadmium stress i.e., Control= 0mg per kg, T1= 1mg per kg and T2= 5mg per kg).



Heatmap showing the expression of SIYAB3, SIYAB6, SIYAB5, and SIYAB7 across eight conditions. The color scale ranges from 0.00 (green) to 14.00 (red). SIYAB3 and SIYAB6 show low expression (green) across all conditions. SIYAB5 shows moderate expression (pink) across all conditions. SIYAB7 shows high expression (red) in the first four conditions (Dormant 1-4) and moderate expression (pink) in the last four conditions (Non-Dormant 1-4).

Figure S8:

Heat map shows the expression profile of the *StYAB* genes in leaves of four different potato cultivars under drought stress.

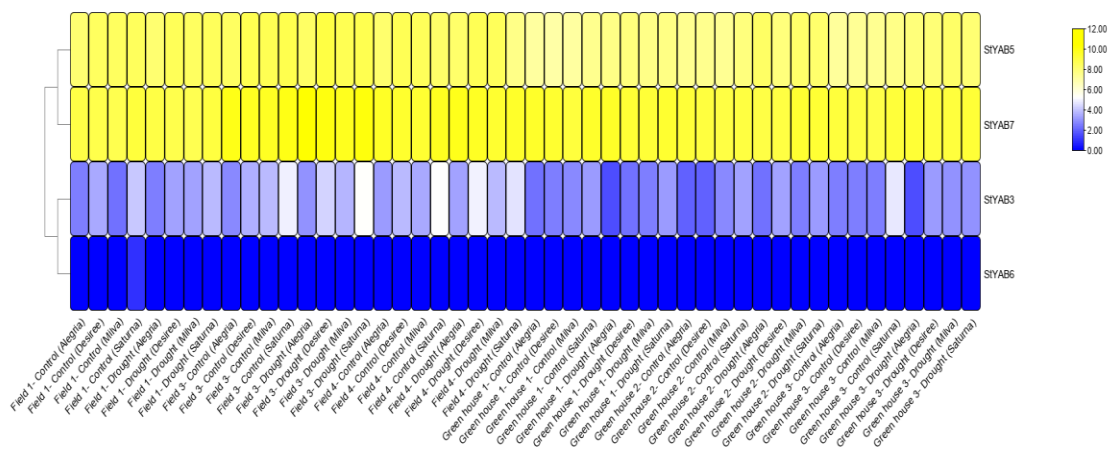
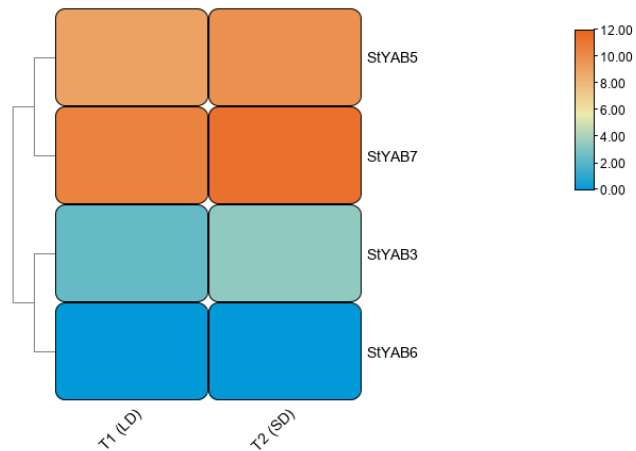
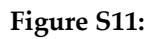


Figure S9:

Heat map shows the expression profile of the *StYAB* genes in petiole of potato cultivars under different photoperiod.



Heat map shows the expression profile of the *StYAB* genes in phloem associated cells of petiole and lower stem of potato cultivar.

[illegible]