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Functional Plant Biology

Supplementary Material

Integrated analysis of transcriptomic and proteomic data reveals novel regulators of soybean (*Glycine max*) hypocotyl development

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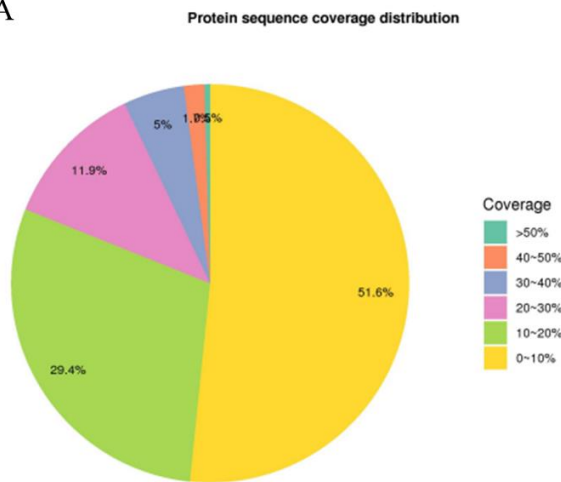
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A



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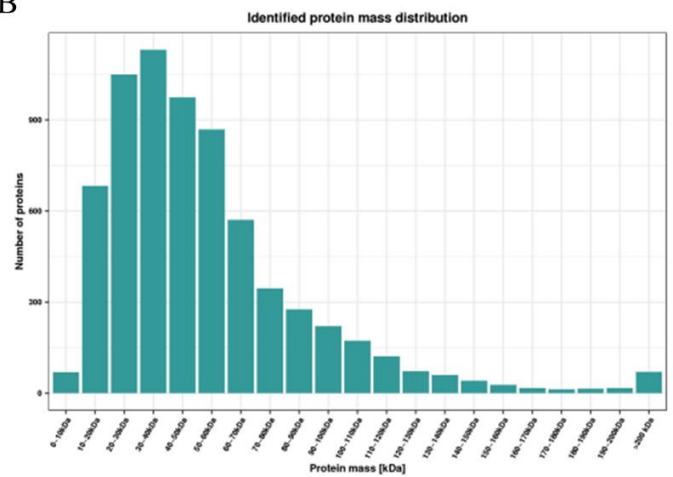


Fig. S1. Summary of proteome data of soybean hypocotyls. (A) Pie plot illustrating the distribution of sequence coverage of proteins identified. (B) Histogram illustrating the mass distribution of proteins identified.

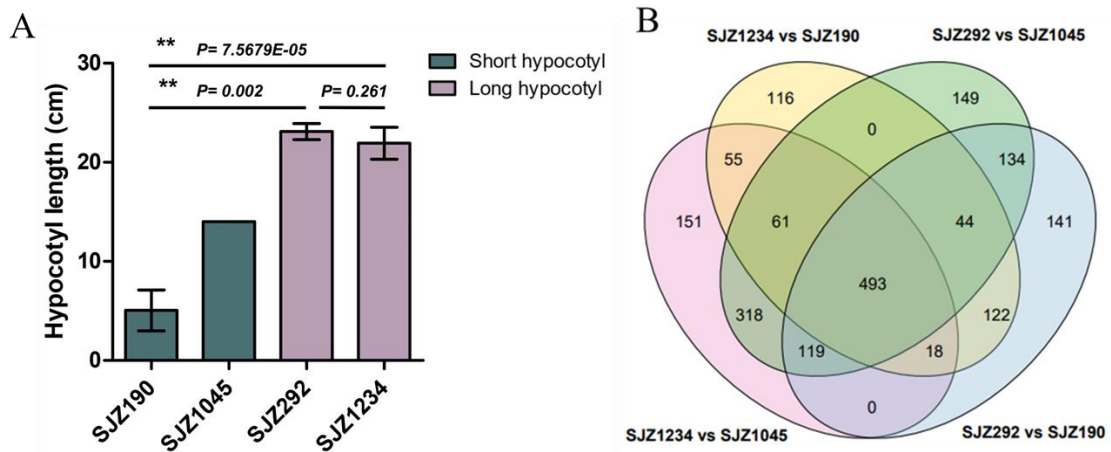


Fig. S2. Soybean cultivars used in this study. (A) Hypocotyl length of 5-d-old dark-grown seedlings of different soybean cultivars. Note that hypocotyls of SJZ292 and SJZ1234 are constantly longer than SJZ190 and SJZ1045. Data are presented as mean \pm SD ($n \geq 5$). * $P < 0.05$ relative to SJZ190. (B) Venn diagram showing shared and unique DEPs in 4-d-old dark-grown hypocotyls of SJZ1045, SJZ190 (with shorter hypocotyls) and SJZ1234, SJZ292 (with longer hypocotyls).

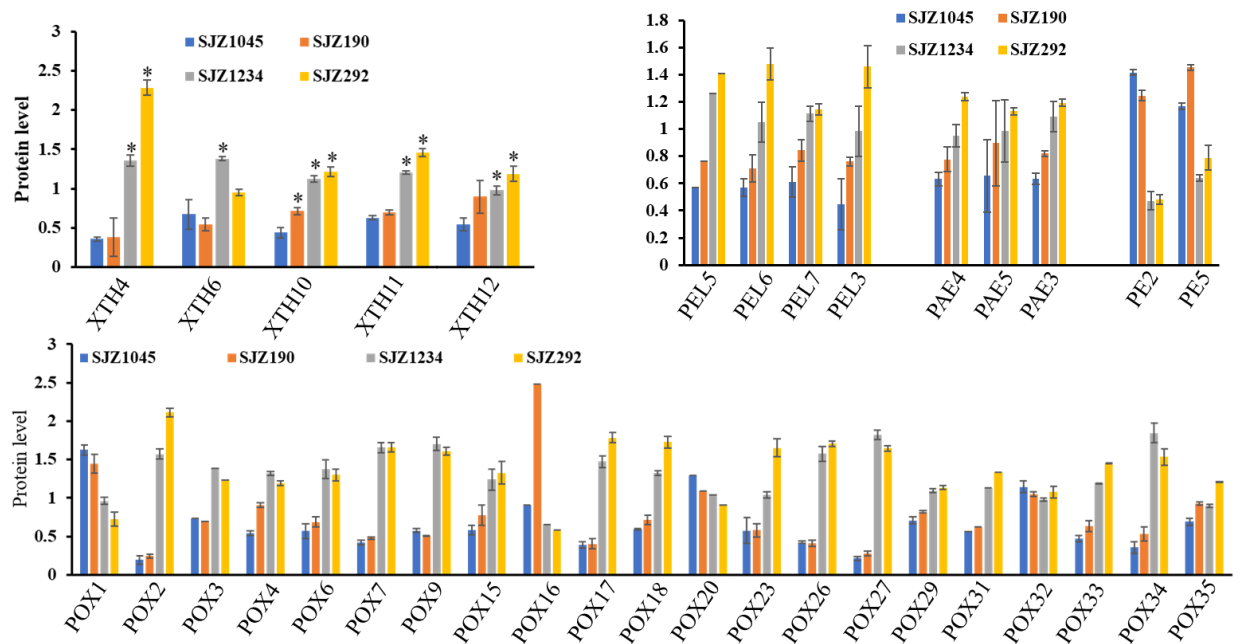


Fig. S3. Protein abundance of target genes in soybean cultivars with long and short hypocotyls. Protein expression of 4 XTHs (A), 4 PELs, 3 PAEs and 2 PEs (B) and 22 peroxidases (C) in 4-d-old dark-grown hypocotyls of different soybean cultivars, including SJZ1045, SJZ190 (with shorter hypocotyls) and SJZ1234, SJZ292 (with longer hypocotyls). Data are from Label-free quantitative proteomic data and presented as mean \pm SD (n = 3). * $P < 0.05$ relative to SJZ1045. The protein/gene names corresponding to the abbreviations could be found in table S2.

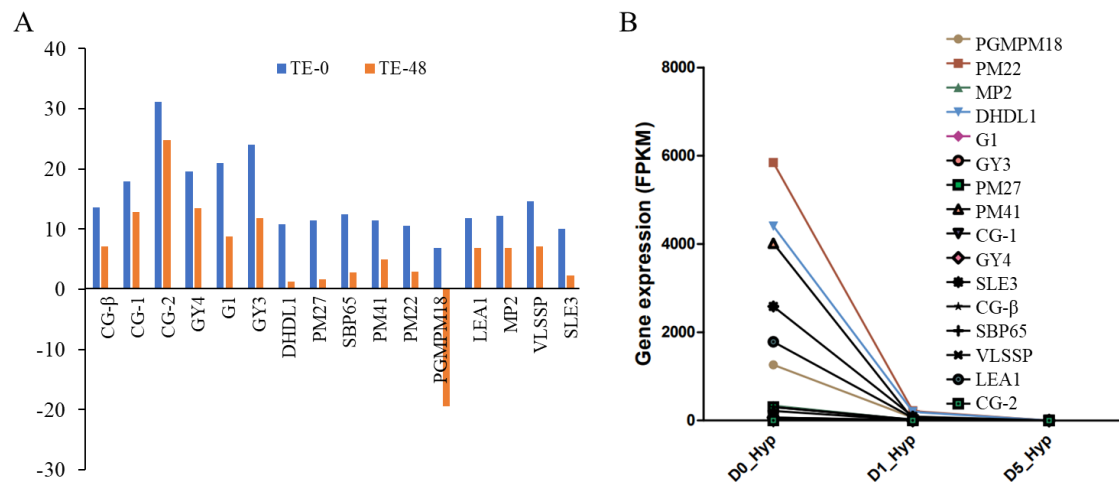


Fig. S4. Change of TE values (A) and mRNA levels (B) of multiple seed storage proteins and seed maturation proteins during hypocotyl development. The protein/gene names corresponding to the abbreviations could be found in table S3.

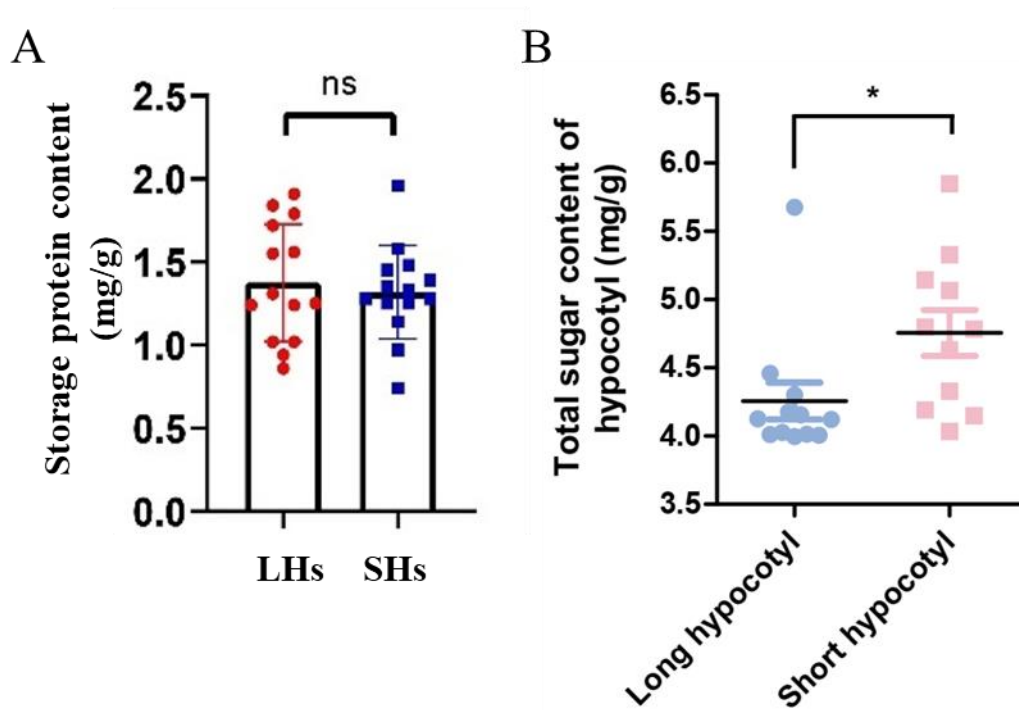


Fig. S5 (A) Total storage protein content (mg/g) in undeveloped hypocotyls of cultivars with longer hypocotyls (LH) and shorter hypocotyls (SH). (B) Total sugar content (mg/g) in 4-d-old hypocotyls of LH and SH cultivars. Data are presented as mean \pm SD ($n \geq 5$). * $P < 0.05$.

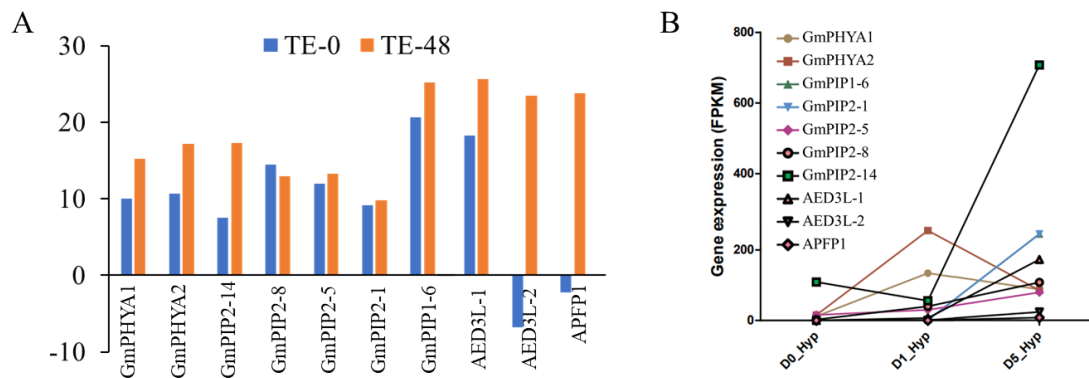


Fig. S6. Change of (A) TE values and mRNA levels (B) of GmPHYAs, GmPIPs and aspartic proteases during hypocotyl development. The protein/gene names corresponding to the abbreviations could be found in table S4.

Protein family	Protein name	Gene name	TE value
	A0A0R0H569	GLYMA_13G347600	18.05
	I1M596	GLYMA_13G347500	20.44
Lipoxygenase	K7L7J7	GLYMA_08G189600	22.85
	I1KUQ3	GLYMA_08G189500	25.81
	I1KUQ0	GLYMA_08G189200	29.62
	I1JYA9	GLYMA_04G221300	17.61
Superoxide dismutase	I1LCI3	GLYMA_10G193500	17.69
	I1L7P6	GLYMA_10G012700	20.65
	I1JBG1	GLYMA_02G012300	24.19
	P11827	GLYMA_10G246300	17.95
	I1KSR6	GLYMA_08G127600	19.58
Seed storage protein	P02858	GLYMA_10G037100	19.65
	A0A0R0KK84	GLYMA_03G163500	21.04
	A0A0R0GMV1	GLYMA_13G123500	23.70
	F7J077	GLYMA_20G148200	23.79

Supplemental table S1 Proteins with highest TE in undeveloped hypocotyl.

Protein family	Protein name	Gene name	TE value
	I1JPQ7	GLYMA_03G184500 (XTH1)	23.86
	C6TJL7	GLYMA_11G193600 (XTH2)	23.33
glucan endotransglucosylase/h ydrolase (XTH) Xylo	I1M403	GLYMA_13G304400 (XTH3)	23.33
	I1MH66	GLYMA_15G169100 (XTH4)	23.26
	A0A0R0FLF0	GLYMA_16G045000 (XTH5)	24.32
	C6TMX0	GLYMA_16G045100	25.32

		(XTH6)	
	A0A0R0FQV9	GLYMA_16G150300	24.78
		(XTH7)	
	K7MRZ1	GLYMA_18G137500	23.75
		(XTH8)	
	I1N842	GLYMA_19G106700	25.50
		(XTH9)	
	I1NGA4	GLYMA_20G141800	24.11
		(XTH10)	
	A0A0R0KYU7	GLYMA_02G068900	-
		(XTH11)	
	I1LZ59	GLYMA_13G141200	-
		(XTH12)	
	I1MYL5	GLYMA_18G012200	24.04
		(PEL1)	
	K7LAU1	GLYMA_08G356800	20.28
		(PEL2)	
Pectate lyase	I1N2D3	GLYMA_18G175300	19.99
		(PEL3)	
	I1JQX5	GLYMA_03G224600	23.29
		(PEL4)	
	I1LAJ4	GLYMA_10G125000	-

		(PEL5)	
	A0A0R0E8X8	GLYMA_20G077300	-
		(PEL6)	
	I1NFF3	GLYMA_20G112600	-
		(PEL7)	
	I1LAY1	GLYMA_10G142100	22.95
		(PAE1)	
	K7LZ56	GLYMA_13G117000	24.93
		(PAE2)	
Pectin acetylsterase	I1JQY5	GLYMA_03G225400	22.02
		(PAE3)	
	I1MS08	GLYMA_17G042900	-
		(PAE4)	
	K7MT28	GLYMA_18G179800	-
		(PAE5)	
	I1J7T0	GLYMA_01G137700 (PE1)	24.47
	I1L1X0	GLYMA_09G077100 (PE2)	23.60
	K7MZI8	GLYMA_19G212600 (PE3)	22.34
Pectin esterase	I1JAV9	GLYMA_01G240300 (PE4)	21.30
	A0A0R0JNR4	GLYMA_06G314200 (PE5)	22.16
	I1MK76	GLYMA_16G014100 (PE6)	24.11
Polygalacturonase	A0A0R0KR00	GLYMA_02G015600	23.58

	I1KPE5	GLYMA_08G017300	21.35
	A0A0R0I3J8	GLYMA_09G041000	23.07
	K7MF03	GLYMA_16G033000	23.42
	I1JY99	GLYMA_04G220600	20.60
		(POX1)	
	I1LI46	GLYMA_11G080300	20.82
		(POX2)	
	I1MC15	GLYMA_14G221400	20.93
		(POX3)	
	I1MBI9	GLYMA_14G201700	21.05
		(POX4)	
	I1KPE5	GLYMA_08G017300	21.35
Peroxidase		(POX5)	
	I1MZT0	GLYMA_18G055300	21.36
		(POX6)	
	A0A0R0KSM2	GLYMA_02G052700	21.39
		(POX7)	
	A0A0R4J539	GLYMA_13G346100	21.43
		(POX8)	
	C6TEG1	GLYMA_18G055400	21.73
		(POX9)	
	A0A0R4J2T7	GLYMA_03G039800	21.76

	(POX10)	
I1JK63	GLYMA_03G007700	21.78
	(POX12)	
A0A0R0KM06	GLYMA_03G208200	22.13
	(POX13)	
I1J9D2	GLYMA_01G192500	22.17
	(POX14)	
A0A0R4J4U7	GLYMA_12G195500	22.19
	(POX15)	
A0A0R4J5A2	GLYMA_15G128700	22.36
	(POX16)	
A0A0R0INP8	GLYMA_08G179600	22.42
	(POX17)	
A0A0R0I1Y7	GLYMA_10G222500	22.71
	(POX18)	
A0A0R0I3J8	GLYMA_09G041000	23.07
	(POX19)	
A0A0R4J594	GLYMA_15G052700	23.18
	(POX20)	
I1L7Z5	GLYMA_10G022500	23.20
	(POX21)	
A0A0R0KR00	GLYMA_02G015600	23.58

	(POX22)	
I1KEL7	GLYMA_06G275900	23.69
	(POX23)	
O22443	GLYMA_09G022300	24.28
	(POX24)	
A0A0R0HPI8	GLYMA_10G050800	24.50
	(POX25)	
I1LHW6	GLYMA_11G072000	24.53
	(POX26)	
A0A0R4J3J1	GLYMA_06G302600	24.94
	(POX27)	
A0A0R0GXD9	GLYMA_13G307000	25.07
	(POX28)	
C6TL64	GLYMA_11G049600	25.28
	(POX29)	
I1JHK1	GLYMA_02G234000	25.53
	(POX30)	
I1MVN5	GLYMA_17G163200	25.57
	(POX31)	
A0A0R0I2M6	GLYMA_09G022400	26.02
	(POX32)	
A0A0R0JYS9	GLYMA_05G103600	26.43

(POX33)		
I1LU76	GLYMA_12G195600	26.52
(POX34)		
C6TCA1	GLYMA_16G164400	29.01
(POX35)		

Supplemental table S2 Proteins with highest TE in developing hypocotyl.

Protein family	Protein name	Gene name	Gene description	Gene symbol
Seed storage protein	A0A0R0HYM3	GLYMA_10G246500	beta-conglycinin, beta chain-like	CG-β
	P11827	GLYMA_10G246300	beta-conglycinin alpha prime subunit	CG-1
	P0DO15	GLYMA_20G148400	Beta-conglycinin alpha subunit 2	CG-2

	P02858	GLYMA_10G037100	glycinin G4	GY4
	P04776	GLYMA_03G163500	Glycinin G1	G1
	P11828	GLYMA_19G164900	Glycinin G3	GY3
Seed	K7LEQ5	GLYMA_09G185500	dehydrin-like	DHDL1
maturation			protein	
protein	I1LNN8	GLYMA_12G001600	seed maturation	PM27
			protein PM27	
	A0A0R0JWF4	GLYMA_06G283900	seed	SBP65
			biotin-containing	
			protein SBP65	
	Q9SWB2	GLYMA_08G160800	seed maturation	PM41
			protein PM41	
	Q9XER5	GLYMA_16G031300	seed maturation	PM22
			protein PM22	
	Q9ZTY1	GLYMA_03G189200	35 kDa seed	PGMPM18
			maturation protein	
	I1L957	GLYMA_10G064400	late	LEA1
			embryogenesis	
			abundant protein	
			At3g53040	
	Q39871	GLYMA_13G149000	maturation	MP2
			polypeptide	

Protein family	Protein name	Gene name	Gene description	Gene symbol
	K7K4G2	GLYMA_01G177000	vicilin-like seed storage protein At2g18540	VLSSP
	C6T0L2	GLYMA_01G119600	protein SLE3	SLE3
Stachyose synthase	I1NBD9	GLYMA_19G217700	stachyose synthase	STS

Supplemental table S3 Proteins with significantly decreased TE along with hypocotyl development.

Phytochrome	B5U9F5	GLYMA_10G141400	phytochrome A	GmPHYA1
	B4YB07	GLYMA_20G090000	phytochrome A	GmPHYA2
PIP	A0A0R0ED38	GLYMA_20G179700	aquaporin PIP2-14	GmPIP2-14
	A0A0R0EPA1	GLYMA_19G181300	aquaporin PIP2-8	GmPIP2-8
	K7LVG8	GLYMA_12G172500	aquaporin PIP2-5	GmPIP2-5
	A0A0R0K972	GLYMA_04G003200	aquaporin PIP2-1	GmPIP2-1
	A0A0R0IM08	GLYMA_08G015300	aquaporin PIP1-6	GmPIP1-6
	A0A0R0JZ42	GLYMA_05G208700	aquaporin PIP1-5	GmPIP1-5
Aspartic protease	A0A0R0K666	GLYMA_04G091800	aspartyl protease AED3	AED3L-1
	A0A0R0JPL6	GLYMA_06G093600	aspartyl protease AED3	AED3L-2
	K7MQS3	GLYMA_18G090900	aspartyl protease family protein At5g10770	APFP1
Glycosyltransferase	A0A0R0F150	GLYMA_19G187400	UDP-glucosyltransferase family protein	LOC100527132
	I1KWD8	GLYMA_08G244700	UDP-glycosyltransferase 83A1	LOC100816177
glutathione	I1JPH6	GLYMA_03G176300	glutathione S-transferase	GSTL1
S-transferase	Q9FQE6	GLYMA_06G193500	glutathione S-transferase GST 12	LOC547581
Stress/disease	I1MUM7	GLYMA_17G128000	malate synthase	MS
responsive proteins	I1K5C5	GLYMA_05G245800	thaumatin-like protein	LOC100777800

I1KQK1	GLYMA_08G053600	thaumatin-like protein	LOC100784636
K7MYX6	GLYMA_19G176700	protein MODIFIER OF SNC1 11	LOC100791970
C6SVW2	GLYMA_13G244800	uncharacterized	LOC100499725 LOC100499725
A0A0R0H9B4	GLYMA_13G318600	stress-responsive A/B barrel domain-containing protein	LOC100306664

Supplemental table S4 Proteins with significantly increased TE along with hypocotyl development.