Table S3. List of differentially regulated proteins in *yda1* mutant seedlings as identified by shot gun differential proteomic analysis. Only proteins with statistically significant change in abundance with ANOVA $p \leq 0.05$ are presented in the table.

Accession	**Description**	**Score**	**Unique**	***yda1*:Ler_Ratio**	**Rel Profile SD**
	Upregulated proteins				
NP_001119183.1	glutamate dehydrogenase 2	2082.5	*yda1*		
NP_973900.2	spermidine synthase 1	288.19	*yda1*		
NP_194091.1	cystine lyase	4223.5	*yda1*		
NP_177837.1	alcohol dehydrogenase 1	951.67	*yda1*		
NP_173173.3	alanine aminotransferase	740.49	*yda1*		
NP_197069.1	reversibly glycosylated polypeptide 2	234.04	*yda1*		
NP_001031073.1	catalase 3	11833	*yda1*		
NP_850759.1	fructose bisphosphate aldolase 4	3220.2	*yda1*		
NP_195500.1	phosphoenolpyruvate carboxykinase ATP	654.2	*yda1*		
NP_190016.1	nitrilase 2	2456.9	*yda1*		
NP_001078234.1	nitrilase 1	552.03		3.706	0.12
NP_564647.1	GDSL esterase lipase	283.49		3.456	0.14
NP_190481.1	peroxidase 34	1976.3		3.254	0.07
NP_196982.1	formate dehydrogenase	1719.9		3.034	0.08
NP_001078275.1	pyruvate kinase	377.32		2.915	0.24
NP_192839.1	nucleoside diphosphate kinase 3	1001.7		2.509	0.16
NP_973873.1	catalase 3	4378.3		2.460	0.05
NP_180873.1	3 ketoacyl CoA thiolase 2	700.54		2.411	0.13
NP_197972.2	myrosinase 1	946.28		2.363	0.1
NP_173732.1	putative phosphoglucomutase	694.05		2.363	0.21
NP_001118421.1	aspartate aminotransferase	518.6		2.316	0.16
NP_001190885.1	aspartate aminotransferase	574.66		2.293	0.16
NP_200227.1	caffeic acid 5 hydroxyferulic acid O methyltransferase	712.34		2.293	0.17

NP_190468.1	4 coumarate CoA ligase like 10	353.65	2.248	0.31
NP_174810.1	annexin 1	5169.2	2.203	0.07
NP_195146.1	D 3 phosphoglycerate dehydrogenase	802.62	2.203	0.14
NP_192202.1	putative elongation factor Tu	413.45	2.138	0.29
NP_175802.1	GDSL esterase lipase	748.11	2.138	0.15
NP_179997.1	aminopeptidase family protein	431.4	2.138	0.14
NP_564571.1	Formate tetrahydrofolate ligase	232.11	2.117	0.19
NP_171936.1	malate dehydrogenase	10056	2.096	0.05
NP_191703.1	cysteine synthase C1	2883.5	2.096	0.09
NP_001077901.1	cyclophilin ROC3	4284.4	2.096	0.08
NP_172801.1	glyceraldehyde 3 phosphate dehydrogenase	32745	2.054	0.04
NP_195288.1	phosphoserine aminotransferase	910.89	2.014	0.17
NP_001031879.1	isopropylmalate dehydrogenase 1	1329.7	1.994	0.1
NP_180644.1	glutathione S transferase PHI 10	1487.5	1.994	0.02
NP_849696.1	protein disulfide isomerase like 1 1	1128.8	1.974	0.02
NP_181192.1	bifunctional enolase 2 transcriptional activator	5373.4	1.954	0.15
NP_193361.4	putative beta 1 3 endoglucanase that interacts with the 30C02 cyst nematode effector May play a rol	373.73	1.954	0.15
NP_849841.1	Monodehydroascorbate reductase	2132.2	1.954	0.1
NP_196521.1	mitochondrial HSO70 2	1687.1	1.954	0.12
NP_178634.2	aconitate hydratase 3	777.99	1.935	0.04
NP_568098.1	ABA modulated tyrosine phosphorylated protein	1232.1	1.935	0.24
NP_190336.1	malate dehydrogenase	1840.6	1.935	0.1
NP_186858.1	probable mitochondrial processing peptidase subunit beta	1077.8	1.916	0.11
NP_195504.2	heat shock protein 70 1	562.3	1.916	0.1
NP_177958.1	glutathione S transferase TAU 20	1706.6	1.896	0.22
NP_190856.1	monodehydroascorbate reductase NADH	1304.8	1.878	0.17
NP_001190274.1	40S ribosomal protein S6 2	3742.5	1.878	0.11
NP_175314.1	40S ribosomal protein S7 1	716.01	1.840	0.17
NP_191104.1	triosephosphate isomerase	15871	1.822	0.11

NP_566840.1	AIG2 like protein	716.88	1.822	0.11
NP_186777.1	voltage dependent anion channel 1	2042	1.804	0.15
NP_199017.2	Luminal binding protein 2	6538.6	1.804	0.14
NP_192161.1	glutathione S transferase F2	28650	1.786	0.29
NP_197960.1	NADP dependent malic enzyme 3	728.76	1.786	0.06
NP_198206.1	Luminal binding protein 1	6829.5	1.786	0.25
NP_193129.1	serine hydroxymethyltransferase 4	2569.6	1.751	0.15
NP_191008.1	aspartyl protease family protein	952.42	1.733	0.05
NP_199207.1	alcohol dehydrogenase class 3	536.08	1.716	0.04
NP_849818.1	elongation factor EF 2	2610.9	1.716	0.18
NP_001189665.1	heat shock protein 60 2	811.64	1.699	0.05
NP_181187.1	fructose bisphosphate aldolase 6	4544.4	1.682	0.08
NP_189041.1	heat shock protein 60	1432.6	1.682	0.12
NP_200288.1	thiazole biosynthetic enzyme	224.58	1.682	0.14
NP_190861.1	fructose bisphosphate aldolase	8781.3	1.649	0.07
NP_565178.1	glutathione S transferase TAU 19	1937	1.649	0.12
NP_195308.1	aconitate hydratase 1	441.72	1.632	0.06
NP_199898.1	pyruvate dehydrogenase E1 beta	2295.7	1.632	0.08
NP_850018.1	mitochondrial F1F0 ATP synthase subunit Fad	2937.4	1.632	0.17
NP_177875.1	protein disulfide isomerase 2	644.67	1.616	0.05
NP_201145.1	adenylate kinase 1	2030.4	1.616	0.11
NP_568204.1	ATP synthase subunit beta 2	10919	1.616	0.15
NP_179393.1	ribosomal protein L2 family protein	2406.6	1.616	0.12
NP_851137.1	60S ribosomal protein L11 2	4557	1.600	0.15
NP_178788.1	ATPase F1 complex alpha subunit protein	3743	1.600	0.16
NP_195870.1	heat shock cognate protein 70 1	17394	1.600	0.17
NP_564625.1	malate dehydrogenase 1	14860	1.600	0.18
NP_001119156.1	heat shock cognate protein 70 1	16376	1.600	0.07
NP_001031628.1	adenosylhomocysteinase	7423.1	1.584	0.14
NP_197294.1	5 methyltetrahydropteroyltriglutamate homocysteine	12835	1.584	0.13

	methyltransferase			
NP_849932.1	Chaperone protein htpG family protein	1602.2	1.584	0.09
NP_176768.1	isocitrate dehydrogenase	12799	1.584	0.03
NP_085571.2	ATPase subunit 1	3635.5	1.584	0.09
NP_001030663.1	60S ribosomal protein L4 1	1244.8	1.568	0.03
NP_001030698.1	protein DJ 1 like A	2418	1.568	0.11
NP_974269.1	adenosine kinase 1	6013.3	1.568	0.04
NP_187555.1	heat shock protein 70 3	11268	1.568	0.1
NP_565191.1	curculin like mannose binding lectin like protein	501.86	1.553	0.11
NP_564418.1	60S ribosomal protein L9 1	5030.3	1.553	0.06
NP_001189847.1	heat shock protein 70 3	11268	1.553	0.06
NP_198403.1	40S ribosomal protein S3 3	2957.4	1.553	0.13
NP_567763.2	aconitase 2	244.94	1.553	0.12
NP_178011.1	V type proton ATPase catalytic subunit A	1514.8	1.553	0.11
NP_187864.1	heat shock protein 70 4	9733.6	1.553	0.05
NP_565527.1	PLAT plant stress domain containing protein	1318.8	1.537	0.15
NP_001189621.1	60S acidic ribosomal protein P2 2	14196	1.537	0.11
NP_051110.1	photosystem I subunit VII	20097	1.522	0.05
NP_850490.1	carbonic anhydrase 1	35526	1.522	0.2
NP_567818.2	photosystem I reaction center subunit E	25606	1.522	0.19
NP_173459.1	DNA damage resistance protein DRT112	21968	1.522	0.08
	Downregulated proteins			
NP_051044.1	ATP synthase CF1 alpha subunit	21797	0.657	0.03
NP_001031969.1	glutamine synthetase	14743	0.657	0.05
NP_174996.1	glyceraldehyde 3 phosphate dehydrogenase B	16356	0.644	0.03
NP_190651.1	oxygen evolving enhancer protein 1 2	21452	0.631	0.04
NP_565913.1	ribulose bisphosphate carboxylase oxygenase activase	63984	0.613	0.02
NP_198659.1	ribulose bisphosphate carboxylase small chain 1B	56854	0.607	0.02
NP_850321.1	ribulose bisphosphate carboxylase oxygenase activase	61872	0.607	0.03

NP_192703.1	F type H transporting ATPase subunit delta	1374		0.600	0.18
NP_001190778.1	plasma membrane associated cation binding protein 1	5168.7		0.589	0.17
NP_849295.1	cytochrome b6 f complex iron sulfur subunit	16620		0.589	0.09
NP_001117239.1	photosystem II subunit P 1	22825		0.583	0.05
NP_172405.1	chloroplast stem loop binding protein	9518.9		0.583	0.09
NP_974782.1	carbonic anhydrase 2	28632		0.571	0.06
NP_193860.1	oxygen evolving complex of photosystem II subunit PsbQ	23096		0.566	0.04
NP_171812.1	photosystem I reaction center subunit D 2	18836		0.533	0.06
NP_565786.1	photosystem II light harvesting complex protein B1B2	15484		0.517	0.07
NP_051110.1	photosystem I subunit VII	20097		0.482	0.12
NP_850490.1	carbonic anhydrase 1	35526		0.482	0.04
NP_567818.2	photosystem I reaction center subunit E	25606		0.458	0.08
NP_173459.1	DNA damage resistance protein DRT112	21968		0.353	0.09
NP_001189913.1	JA responsive protein 1	2256.9	Ler		
NP_178073.1	phosphoglycerate kinase	9757.4	Ler		
NP_173386.1	Glutathione S transferase like protein	1129.2	Ler		
NP_568437.1	tubulin beta 8 chain	1187	Ler		
NP_196598.1	40S ribosomal protein S6 2	3833.6	Ler		
NP_565265.1	MLP like protein 329	13142	Ler		
NP_197563.1	germin like protein subfamily 3 member 3	903.35	Ler		