

Table 1. Suppl. Characters and annotations of down-regulated proteins identified by MALDI-TOF-MS in SL anthers.

Spot	GI	Acc Version	Protein Name	Species	Scores	Annotation
550	gi 974605	AAA75104.1	single-stranded nucleic acid binding protein	<i>Triticum aestivum</i>	101	RNA/double&single-stranded DNA binding; alternative mRNA splicing, via spliceosome; response to cold/abscisic acid/salt stress/zinc ion
1125	gi 41688709	Q8MAI9.1	DNA-directed RNA polymerase subunit alpha	<i>Leymus californicus</i>	143	DNA-directed RNA polymerase activity; transcription, DNA-dependent ; protein dimerization activity
1943	gi 109716224	ABG43094.1	histone acetyltransferase HAT1	<i>Triticum aestivum</i>	177	histone acetyltransferase activity; covalent chromatin modification response to UV-B/DNA repair
2371	gi 109716226	ABG43095.1	histone acetyltransferase HAT2	<i>Triticum aestivum</i>	225	cell proliferation/organ growth/regulation of leaf formation regulation of auxin mediated signaling pathway protein kinase regulator activity/phosphorylase kinase regulator activity transcriptional attenuation/transcription antitermination DNA-directed RNA polymerase II, holoenzyme
550	gi 28611029	CAD62367.1	succinate dehydrogenase	<i>Triticum aestivum</i>	101	mitochondrial respiratory chain complex II mitochondrial electron transport, succinate to ubiquinone oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor
794	gi 74129314	AAZ99790.1	type RGA	<i>Triticum aestivum</i>	76	defense response/apoptotic process cytoplasmic membrane-bounded vesicle ADP/ATP binding
1240	gi 75136950	Q70KG5.1	Protein RAFTIN 1A	<i>Triticum aestivum</i>	222	exine; pollen development

2171	gi 115589736	ABJ15727.1	serine hydroxymethyltransferase	<i>Triticum monococcum</i>	351	photosynthesis, light reaction/mitochondrial respiratory chain complex I L-serine metabolic process glycine hydroxymethyltransferase activity/methyltransferase activity plant-type hypersensitive response/circadian rhythm tetrahydrofolate interconversion
1035/1465	gi 226316441	ACO44684.1	fructose-bisphosphate aldolase	<i>Triticum aestivum</i>	351/137	Glycolysis; fructose-bisphosphate aldolase activity response to karrikin/cadmium ion/salt stress
1386	gi 300681519	CBH32613.1	fructose-bisphosphate aldolase, chloroplast precursor, expressed	<i>Triticum aestivum</i>	97	mitochondrion/chloroplast stroma/chloroplast thylakoid/plastoglobule response to oxidative stress/cadmium ion
1438	gi 119388723	ABL74258.1	alcohol dehydrogenase ADH1A	<i>Triticum aestivum</i>	189	response to hypoxia/salt stress/cadmium ion alcohol dehydrogenase (NAD) activity oxidation-reduction process
1658	gi 119388733	ABL74263.1	alcohol dehydrogenase ADH1A	<i>Triticum dicoccoides</i>	108	response to salt stress/hypoxia oxidation-reduction process alcohol dehydrogenase (NAD) activity
2703	gi 144583299	ABP01352.1	4-amino-4-deoxychoris mate synthase	<i>Triticum aestivum</i>	155	anthranilate synthase activity folic acid-containing compound metabolic process/biosynthetic process pteridine-containing compound metabolic process/biosynthetic process
2497	gi 148840392	ABR14627.1	ZTL	<i>Triticum aestivum</i>	90	proteasomal protein catabolic process/SCF ubiquitin ligase complex flower development circadian rhythm/regulation of circadian rhythm

2483	gi 162957175	ABY25986.1	NADP-dependent malic enzyme 1	<i>Triticum aestivum</i>	82	malate metabolic process/malate dehydrogenase oxidation-reduction process protein homodimerization activity
1050	gi 226427702	ACO55040.1	RGA2	<i>Triticum aestivum</i>	98	defense response ADP binding cytoplasmic membrane-bounded vesicle
2057	gi 283806359	BAI66421.1	alanine-glyoxylate aminotransferase	<i>Triticum aestivum</i>	121	alanine-glyoxylate transaminase activity arginine catabolic process to glutamate vacuolar membrane/response to cadmium ion
829	gi 291061974	ADD73514.1	putative pyruvate dehydrogenase E1 component alpha subunit	<i>Triticum aestivum</i>	84	pyruvate dehydrogenase (acetyl-transferring) activity zinc ion/cobalt ion binding response to salt stress
1501	gi 305419320	ADM52965.1	nudix hydrolase	<i>Triticum aestivum</i>	217	chloroplast/peroxisome NAD catabolic/NADP catabolic process NADH pyrophosphatase activity
879	gi 326494092	BAJ85508.1	predicted protein	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	184	proteasome complex/cytosol plasma membrane
551/801	gi 340842127	AEK78081.1	26S proteasome non-ATPase regulatory subunit	<i>Triticum aestivum</i>	239/146	proteasome complex
879	gi 32400818	AF475120_1	26S proteasome ATPase subunit	<i>Triticum aestivum</i>	95	response to salt stress/yeast proteasome complex
544	gi 380447728	AFD54042.1	hypersensitive induced reaction protein 1	<i>Triticum aestivum</i>	207	plasma membrane vacuole/vacuolar membrane/Golgi apparatus/plasmodesma/chloroplast protein histidine kinase binding

Table 2. Characters and annotations of up-regulated proteins identified by MALDI-TOF-MS in SL anthers.

Spot	GI	Acc Version	Protein Name	Species	Scores	Anotation
53	gi 136644	P16577.1	Ubiquitin-conjugating enzyme E2-23 kDa	<i>Triticum aestivum</i>	97	ubiquitin-protein ligase activity ubiquitin-dependent protein catabolic process
61	gi 14017596	NP_114282.1	ATP-dependent Clp protease proteolytic subunit	<i>Triticum aestivum</i>	147	proteolysis/serine-type endopeptidase activity regulation of timing of transition from vegetative to reproductive phase chloroplastic endopeptidase Clp complex
41	gi 75246527	Q8LRM8.1	Translationally-controlled tumor protein homolog	<i>Triticum aestivum</i>	80	regulation of cell growth/mitotic cell cycle embryo/post-embryonic development/auxin homeostasis positive regulation of microtubule depolymerization root/lateral root development/root hair cell tip growth
164	gi 29409366	AAM29179.1	prohibitin protein Wph	<i>Triticum aestivum</i>	188	negative regulation of transcription from RNA polymerase II promoter negative regulation of cell proliferation/programmed cell death protein deacetylation/deacylation microtubule associated complex/lipid particle
185	gi 558652	CAA57646.1	Voltage dependent anion channel	<i>Triticum aestivum</i>	195	voltage-gated anion channel activity organelle outer membrane/integral to mitochondrial membrane vacuole/chloroplast
20	gi 4138871	AAD03605.1	small heat shock protein Hsp23.6	<i>Triticum aestivum</i>	112	response to heat/osmotic stress

49	gi 11990897	BAB19812.1	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	<i>Triticum aestivum</i>	111	ribulose-bisphosphate carboxylase activity photorespiration/chloroplast oxidation-reduction process
28	gi 23504745	CAD29478.1	glutathione transferase F5	<i>Triticum aestivum</i>	81	glutathione transferase activity protein homodimerization activity toxin metabolic/catabolic process
33	gi 40641599	CAE54279.1	putative alanine aminotransferase	<i>Triticum aestivum</i>	219	L-alanine catabolic process, by transamination pyruvate family amino acid catabolic process response to hypoxia/oxygen levels/decreased oxygen levels/cadmium ion
1560	gi 109450934	CAJ15412.1	unnamed protein product	<i>Triticum aestivum</i>	95	polyketide biosynthetic process sporopollenin biosynthetic process pollen exine formation
1126	gi 109940109	Q95H43.2	NAD(P)H-quinone oxidoreductase subunit 1, chloroplastic	<i>Triticum aestivum</i>	151	NADH dehydrogenase (ubiquinone) activity photosynthesis, light reaction/electron transport chain chloroplast thylakoid membrane
56	gi 210061129	ACJ05645.1	ferritin 1A	<i>Triticum aestivum</i>	138	flower development/leaf development response to reactive oxygen species/iron ion oxidoreductase activity, oxidizing metal ions, oxygen as acceptor
79/98/99/154	gi 226897533	ACO90196.1	ascorbate peroxidase	<i>Triticum aestivum</i>	114/150/oxidation-reduction process 176/175	seed trichome elongation response to hydrogen peroxide/ethylene stimulus
47	gi 231274771	CAX36917.1	MPBQ methyltransferase	<i>Triticum aestivum</i>	135	vitamin E biosynthetic process

						plastoquinone biosynthetic process
151	gi 269854690	ACZ51371.1	plasma membrane intrinsic protein	<i>Triticum aestivum</i>	196	plasma membrane
26	gi 283806365	BAI66424.1	UDP-D-glucuronate decarboxylase	<i>Triticum aestivum</i>	169	endoplasmic reticulum protein binding/protein complex Golgi apparatus/trans-Golgi network/endosome D-xylose metabolic process UDP-glucuronate decarboxylase activity
1510	gi 322367792	ADW95819.1	glutamate dehydrogenase	<i>Triticum aestivum</i>	191	glutamate dehydrogenase [NAD(P)+] activity response to absence of light/salt stress/cadmium ion regulation of nitrogen compound metabolic process
2199	gi 326527331	BAK04607.1	predicted protein	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	143	lyase activity/choline dehydrogenase activity
2478	gi 327241210	AEA40449.1	phytochrome A type 3	<i>Triticum aestivum</i>	90	alcohol metabolic/oxidation-reduction process cytoplasmic membrane-bounded vesicle negative regulation of translation
100	gi 7381271	AF139816_1	plasma membrane intrinsic protein 3	<i>Triticum aestivum</i>	113	red light/far-red light signaling pathway gravitropism/photomorphogenesis plasma membrane/protein complex endoplasmic reticulum
65/67/80	gi 16903082	AF433653_1	small Ras-related GTP-binding protein	<i>Triticum aestivum</i>	142/110/100	Golgi apparatus/plasmodesma/cell wall/apoplast response to salt stress/cadmium ion
142	gi 32400847	AF479036_1	formate dehydrogenase, partial	<i>Triticum aestivum</i>	157	response to cadmium ion/wounding formate dehydrogenase (NAD+) activity oxidation-reduction process

43	gi 32400855	AF479040_1	dynamamin like Pr6(ADL6), partial	<i>Triticum aestivum</i>	359	Golgi apparatus/Golgi to vacuole transport vacuole/plasmodesma; clathrin-mediated endocytosis
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Table 3 Suppl. Primers used in the real time quantitative PCR assay. Up, Lw ??

Gene Name	Primer
<i>GAPDH</i>	Up TGACTGCAACCCAGAAGACTGTT
	Lw CCCTCAGACTCCTCCTTGATAGC
<i>26SPA</i>	Up TGGGCAAGTCAAAGGTTCTAGTG
	Lw GGTGGGCAATTCCGAGAC
<i>Hsp23.6</i>	Up TGGACAAGATCAAGGCCGAGAT
	Lw CGGCCAACTTCACCTACTCGAT
<i>26SPN</i>	Up ATTCATGGGCTCAATAGACACT
	Lw GGTCTGAACTATGTTsGACGAC
<i>CLP</i>	Up CACCAAGCGTATAGCATTCC
	Lw ATTTTCGCGAACTTTGTGTAACTC
<i>HAT1</i>	Up TAAAGTGGGAACACCGGAGCGTC
	Lw GCAGCGTGCTCAAGATGTCGTC
<i>HAT2</i>	Up CATTCGAGCAGATGGTCTAAAG
	Lw AAGCAAGCTCACGCAGGTTAC
<i>RFTIN</i>	Up CGCCGACTCCGTCCCGTTCA
	Lw CGAGGTCGCGCAGAACTTGGACTC
<i>SSBP</i>	Up AGATCATCAACGACCGCGAGAC
	Lw GTCGAGCTCCTTGCCGTTTCAT
<i>TTTP</i>	Up GTCGATGACCAGGCCGTGAAG
	Lw ATCATGCATGCTCTCGCCAACA