

**Table S1.** Final germination percentage during germination under water stress of *Solanum paniculatum* L. seeds submitted to osmopriming and control treatments.

Osmotic Potential of the Germinative Conditions (MPa)	Osmotic Potential of Osmopriming Solutions (MPa)				
	NC	−0.4	−0.8	−1.0	−1.2
0.0	99 a	100 a	97 a	94 a	100 a
−0.2	97 ab	97 ab	95 ab	93 ab	100 a
−0.4	26 b	68 a	62 ab	69 a	86 a
−0.6	10 a	26 a	44 a	11 a	17 a
−0.8	0 a	1 a	0 a	0 a	0 a
−1.0	0 a	0 a	0 a	0 a	0 a

\*Means followed by same letters do not differ in Tukey's test (0.05), capital letter are compared in the columns and lower letter are compared in the lines. Data were transformed by  $\sqrt{x} + 1$ .

**Table S2.** Normal seedling percentage during germination under water stress of *Solanum paniculatum* L. seeds submitted to osmopriming and control treatments.

Osmotic Potential of the Germinative Conditions (MPa)	Osmotic Potential of Osmopriming Solutions (MPa)				
	NC	−0.4	−0.8	−1.0	−1.2
0.0	91a	100a	95a	94a	98a
−0.2	95a	94a	95a	91a	97a
−0.4	20d	66ab	51bcd	55abc	85a
−0.6	0 a	7 a	6 a	4 a	8 a
−0.8	0 a	0 a	0 a	0 a	0 a
−1.0	0 a	0 a	0 a	0 a	0 a

\*Means followed by same letters do not differ in Tukey's test (0.05), capital letter are compared in the columns and lower letter are compared in the lines. Data were transformed by  $\sqrt{x} + 1$ .

**Table S3.** Transcripts differentially expressed in primed and unprimed *Solanum paniculatum* L. seeds. Fold change was calculated using Baggerley's test considering  $p < 0.05$ .

Gene ID	Fold Change	Annotation
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10229	836.832.956	dep domain-containing protein 1a isoform x1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10230	824.242.174	dna repair protein rhp42
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10417	343.636.882	heat shock cognate 70 kda protein 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1042	443.005.992	vicilin-like antimicrobial peptides 2-2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10492	298.200.969	chd3-type chromatin-remodeling factor pickle-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1054	127.721.938	glutathione peroxidase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10558	455.587.874	poly [ADP-ribose] polymerase 3-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1056	885.308.266	poly [ADP-ribose] polymerase 3-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10620	1.051.406.015	chalcone isomerase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10653	393.423.663	transcriptional regulator
PASMA_ACAGTG_L001_R1_001_trimmed_contig_11327	2.403.475.001	multidrug transporter
PASMA_ACAGTG_L001_R1_001_trimmed_contig_11727	7.239.372.597	iron transporter
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1181	6.348.179.601	polyprotein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1185	18.845.495.977	transcription factor ap-2-delta
PASMA_ACAGTG_L001_R1_001_trimmed_contig_119	2.477.484.801	PREDICTED: uncharacterized protein LOC101259110
PASMA_ACAGTG_L001_R1_001_trimmed_contig_12008	7.520.745.843	low quality protein:piezo-type mechanosensitive ion channel component 1

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_12252	2.281.654.388	beta-glucosidase 44-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13008	5.245.362.441	glucomannan 4-beta-mannosyltransferase 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1311	2.562.908.145	PREDICTED: uncharacterized protein LOC102598803
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13194	9.167.227.705	ribosomal protein l2
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13312	5.006.397.414	abc transporter permease
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1334	2.380.308.101	inner centromere protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13630	4.446.842.595	aspartate-semialdehyde dehydrogenase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13671	5.228.761.086	bidirectional sugar transporter sweet1-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13713	3.838.366.452	ga4 desaturase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14046	6.606.626.136	---NA---
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14161	8.311.059.741	rho gtpase-activating protein 24 isoform x1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14206	7.419.015.896	activin receptor type-1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1421	1.613.150.255	maturase partial
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1426	3.075.501.223	2s sulfur-rich seed storage protein 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_144	1.866.351.943	thiamine biosynthesis protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_145	1.840.886.345	polyadenylate-binding protein 8-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_146	2.759.956.924	high affinity camp phosphodiesterase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14734	18.908.311.774	ribulose biphosphate carboxylase small chloro- plastic-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14796	31.527.702.705	exonuclease v subunit beta

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_15075	5.668.217.038	family transcriptional regulator
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15174	18.821.312.239	replication protein a 70 kda dna-binding subunit b-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15325	19.510.548.770	replication protein a 70 kda dna-binding subunit b-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15916	12.772.096.432	radical sam protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1638	6.219.127.628	11s seed storage globulin
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1695	4.198.733.300	androgen receptor
PASMA_ACAGTG_L001_R1_001_trimmed_contig_16971	2.923.650.738	2-methylcitrate dehydratase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1710	2.994.866.378	PREDICTED: uncharacterized protein LOC102578250
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1719	3.515.092.540	non-specific lipid-transfer protein 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1736	12.401.097.728	sh2 domain containing protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1774	2.464.410.290	snf1-related protein kinase regulatory subunit gamma-like pv42a-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_17947	11.116.804.902	dna-directed rna polymerase i subunit rpa1-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1801	4.975.597.707	kda class i heat shock protein 3
PASMA_ACAGTG_L001_R1_001_trimmed_contig_18192	26.831.948.132	teichoic acid biosynthesis protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1923	1.761.960.007	minor structural protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1938	3.126.243.422	leucine-rich repeat-containing protein 16a-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_194	1.932.976.851	methionyl-trna formyltransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_1956	9.128.201.757	phenylalanine ammonia-lyase-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_19832	13.849.702.420	poly [ADP-ribose] polymerase 3-like

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_19839	10.818.052.779	ribonuclease h
PASMA_ACAGTG_L001_R1_001_trimmed_contig_19886	5.133.015.238	integrase core domain containing protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2004	1.515.285.207	elongation factor 1-
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2005	5.313.090.529	duf21 domain-containing protein at4g14240-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2018	3.609.418.227	ec protein homolog 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_20743	4.398.382.668	nad-glutamate dehydrogenase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_20781	13.580.395.100	transcriptional activator
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2136	3.320.480.855	probable aquaporin tip3-2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_21837	26.018.065.344	9-divinyl ether synthase-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_221	1.736.988.382	elongation factor 1-alpha
PASMA_ACAGTG_L001_R1_001_trimmed_contig_222	2.227.589.218	translation elongation factor 1- partial
PASMA_ACAGTG_L001_R1_001_trimmed_contig_22593	8.087.975.366	chalcone isomerase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23	2.798.285.917	abc-2 type transporter
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23208	3.043.727.720	tellurium resistance protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_239	7.495.581.120	kelch repeat protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_24085	4.658.024.932	maleylacetoacetate isomerase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2441	5.205.380.718	evolutionarily conserved c-terminal region 2 iso- form 1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_254	3.116.297.551	oleosin 1-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2645	2.682.734.698	translocator protein homolog

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_26597	16.625.319.737	exonuclease v subunit beta
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2688	2.473.415.257	aspartic proteinase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_26882	52.287.519.064	hypothetical protein PHAVU_011G058900g
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2711	3.363.229.194	elongation factor g
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2730	2.233.549.418	reticulon-like protein b13-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2733	3.550.761.336	wd repeat protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2828	3.499.836.634	1-hydroxy-2-methyl-2- -butenyl 4-diphosphate synthase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2884	3.731.276.497	hmg1 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2915	2.822.775.540	adenine dna phage-associated
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2973	5.255.162.523	ribosomal biogenesis gtpase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2977	2.315.471.216	probable aquaporin tip3-2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_306	1.528.388.975	non-specific lipid-transfer protein a-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3102	2.633.437.115	hypothetical protein TPHA_0H03010
PASMA_ACAGTG_L001_R1_001_trimmed_contig_31366	14.047.171.155	beige beach domain containing protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3233	3.334.089.026	homeobox protein dbx2
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3284	9.985.104.723	glutamate synthase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_33325	41.602.687.084	alpha- -mannosyltransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_334	1.763.386.152	nucleocapsid protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_339	1.660.837.895	malate glyoxysomal-like

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_3405	1.643.314.511	polyubiquitin containing 7 ubiquitin monomers
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3417	16.143.622.963	gdsl esterase lipase at5g03820-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3459	6.327.211.939	transposon mudra-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3485	2.173.200.672	peroxidase 12-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_35	1.833.792.772	eukaryotic translation initiation factor 3 subunit a
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3565	5.463.143.348	tubulin beta-1 chain
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3594	3.978.078.221	glycoside hydrolase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3683	3.004.004.885	cullin associated nedd8 dissociated protein 1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3684	4.681.627.018	50s ribosomal protein l15
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3929	2.597.506.807	dnaj protein homolog 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3949	4.589.697.669	ndp-sugar dehydrogenase like udp-glucose dehydrogenase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_397	1.873.813.777	membrane protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4082	2.255.207.958	cold shock protein cs66-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4244	4.772.017.845	cell envelope biogenesis protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4403	1.792.963.843	late embryogenesis abundant protein group 8
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4435	3.184.169.538	glycosyltransferase family 2 protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_452	4.451.642.652	thyroid hormone receptor-associated protein 3-like iso- form x1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4524	4.682.518.045	membrane protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_470	2.128.271.744	cell death abnormality protein partial

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_4776	2.995.038.757	sepiapterin reductase a
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4808	3.273.675.253	histidine-rich glyco
PASMA_ACAGTG_L001_R1_001_trimmed_contig_488	-26.626.873.804	nad(p)h dehydrogenase (quinone) fqr1-like 1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5032	8.078.838.491	glycosyl hydrolase family 35
PASMA_ACAGTG_L001_R1_001_trimmed_contig_52	2.520.354.433	cysteine protease cp8
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5231	5.850.916.714	protein scribble-like partial
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5245	4.914.594.340	protein creg1-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_527	2.512.757.430	transcription accessory protein (s1 rna-binding domain)
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5291	2.034.738.089	low-temperature-induced 65 kda protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_531	4.064.996.368	burp domain-containing protein 3-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5352	8.294.031.629	replication protein a 70 kda dna-binding subunit b-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5501	6.526.189.698	ribosomal subunit interface protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5519	3.404.236.619	glutathione gamma-glutamylcysteinyltransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5548	-53.082.952.951	small heat shock protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5756	2.131.231.050	vacuolar-processing enzyme-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5914	7.526.268.102	thiazole synthase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5927	3.803.126.296	nuclear polyadenylated rna-binding protein 4-like iso-form x1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_599	5.454.159.471	homoserine dehydrogenase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6228	3.397.603.039	protein dehydration-induced 19 homolog 3-like



---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_625	1.413.612.154	late embryogenesis abundant protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_626	2.241.694.741	dead-box atp-dependent rna helicase 7-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_636	3.413.585.546	general transcription factor 3c polypeptide 5-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6404	2.871.272.701	methyl-accepting chemotaxis sensory transducer with cache sensor
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6434	8.431.214.734	protamine p1
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6440	7.787.390.449	peptidase m16
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6508	2.488.828.271	alginate o-acetyltransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6576	7.244.611.783	heat shock factor protein hsf30-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6590	3.518.266.039	aspartate aminotransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6783	5.493.236.059	rho guanine nucleotide exchange factor 10-like protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7056	3.725.513.127	ornithine carbamoyltransferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7089	3.807.393.513	sugar transferase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7098	5.321.197.489	thiamine thiazole synthase chloroplastic-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7206	2.799.525.960	glycine-rich protein a3-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7288	2.871.351.219	ppgpp synthetase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_736	2.843.012.198	sec14 cytosolic factor family protein
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7442	3.283.333.013	coproporphyrinogen dehydrogenase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7600	5.480.029.331	gdsl esterase lipase at1g71250-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7666	5.981.989.751	transposase

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_7667	4.732.269.993	complex i intermediate-associated protein mitochondrial
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7845	5.047.352.389	n-acetylglucosamine-6-sulfatase-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8235	2.478.170.188	heat shock cognate 70 kda protein 2-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_853	2.911.422.448	sensor histidine kinase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8608	10.918.548.032	leucyl-trna synthetase
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8610	4.175.746.110	probable polygalacturonase at3g15720-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8645	3.250.758.049	histone h1 subtype 5
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9026	16.970.789.221	protein spinster homolog 2 isoform 2
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9117	3.919.826.731	sugar transporter
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9183	2.029.298.834	elongation factor 1-alpha
PASMA_ACAGTG_L001_R1_001_trimmed_contig_925	2.360.008.289	sodium hydrogen exchanger 10
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9460	4.315.269.824	citrate glyoxysomal-like
PASMA_ACAGTG_L001_R1_001_trimmed_contig_99	-3.616.913.314	26s ribosomal rna
PASMA_ACAGTG_L001_R1_001_trimmed_contig_10540	2.237.109.091	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_11775	6.469.633.567	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_11873	3.484.475.906	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_11950	4.048.948.214	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_12235	56.020.446.967	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_12480	3.979.389.874	Potential non coding transcript

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_12572	9.070.122.058	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_12710	11.918.313.178	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_12825	5.275.213.933	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13205	8.034.092.301	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_13468	2.225.153.917	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_140	2.021.857.712	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14314	13.479.470.016	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14349	5.470.934.289	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_14458	5.866.741.765	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15162	10.174.575.111	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15167	9.813.223.429	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15329	16.383.953.208	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_15913	20.320.013.026	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_16223	9.630.381.492	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_16755	11.399.704.922	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_16841	20.970.553.555	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_18365	7.050.559.681	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_18798	7.900.646.301	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_19019	8.456.127.568	Potential non coding transcript

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_19565	5.544.440.124	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2078	1.863.795.852	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_20919	31.653.712.708	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_21009	55.687.730.900	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_21024	5.992.048.175	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_21588	23.506.593.253	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2242	3.711.618.326	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_22827	3.959.005.179	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23041	6.534.589.869	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23080	4.585.461.415	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23289	14.319.905.961	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_23701	3.696.293.416	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_24043	16.520.475.593	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_24383	14.081.369.764	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_24436	10.348.250.027	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_25030	22.720.572.816	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_25613	19.118.149.199	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_2913	11.554.569.389	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_29187	6.120.144.592	Potential non coding transcript

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_30089	44.243.512.100	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3081	5.297.002.300	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_31691	49.107.898.241	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_32081	51.790.111.158	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3283	2.826.577.318	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_341	5.200.750.995	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_3550	3.196.020.520	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_409	22.214.426.724	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4318	2.868.746.353	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_4613	2.197.650.388	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_55	1.269.854.226	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_5989	2.411.633.448	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6330	2.571.334.550	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6644	3.450.602.680	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_6828	6.120.247.422	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7185	6.220.378.174	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_7376	7.151.975.139	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_806	3.802.375.701	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8101	3.067.231.716	Potential non coding transcript

---

PASMA_ACAGTG_L001_R1_001_trimmed_contig_824	90.090.250.563	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8245	4.254.573.953	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8325	3.128.048.025	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8423	3.795.398.057	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8531	4.473.062.054	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_8973	3.520.901.115	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_914	2.563.114.982	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9578	2.546.909.869	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9738	2.757.571.212	Potential non coding transcript
PASMA_ACAGTG_L001_R1_001_trimmed_contig_9843	2.802.980.534	Potential non coding transcript

---

**Table S4.** Transcripts differentially expressed associated with *Solanum paniculatum* osmoprimed (−1.0 MPa) seeds.

Contig	Annotation	Fold Change	Type of Stress
10620	CHALCONE ISOMERASE	1.051.406.015	drought and oxidativestresses
1056	POLY [ADP-RIBOSE] POLYMERASE 3-LIKE	88.530.826.654	drought and oxidativestresses
14206	GALACTINOL SYNTHASE	7.419.015.896	drought stress
15325	REPLICATION PROTEIN A 70 KDA DNA-BINDING SUBUNIT B-LIKE	1.951.054.877	heat stress
1719	NON-SPECIFIC LIPID-TRANSFER PROTEIN 2-LIKE	351.509.254	drought stress
1801	KDA CLASS I HEAT SHOCK PROTEIN 3	4.975.597.707	heat stress
20743	NAD-GLUTAMATE DEHYDROGENASE	4.398.382.668	drought stress
2645	TRANSLOCATOR PROTEIN HOMOLOG	2.682.734.698	salt stress
2884	HMG1 2-LIKE	3.731.276.497	salt and drought stresses
2688	ASPARTIC PROTEINASE	2.473.415.257	drought stress
3485	PEROXIDASE 12-LIKE	2.173.200.672	drought and oxidativestresses
3929	DNAJ PROTEIN HOMOLOG 2-LIKE	2.597.506.807	heat stress
4082	COLD SHOCK PROTEIN CS66-LIKE	2.255.207.958	heat stress
5291	LOW-TEMPERATURE-INDUCED 65 KDA PROTEIN	2.034.738.089	heat stress
5927	NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN 4-LIKE ISOFORM 1	3.803.126.296	oxidative, salt and drought stresses
6440	PHENYLANINE AMMONIA-LYASE 1-LIKE	7.787.390.449	oxidative stress
6576	HEAT SHOCK FACTOR PROTEIN HSF30-LIKE	7.244.611.783	heat stress
6590	ASPARTATE AMINOTRANSFERASE	3.518.266.039	drought stress
7098	THIAMINE THIAZOLE SYNTHASE CHLOROPLASTIC-LIKE	5.321.197.489	drought stress
7206	GLYCINE-RICH PROTEIN A3-LIKE	279.952.596	salt stress
7288	PPGPP SYNTHETASE	2.871.351.219	salt stress
8235	HEAT SHOCK COGNATE 70 KDA PROTEIN 2-LIKE	2.478.170.188	heat stress
853	SENSOR HISTIDINE KINASE	2.911.422.448	salt stress and drought stress
9460	CITRATE GLYOXYSOMAL-LIKE	4.315.269.824	drought stress and oxidative stress
448	NAD(P)H DEHYDROGENASE (QUINONE) FQR1-LIKE 1	−26.626.873.804	Metabolism
5548	SMALL HEAT SHOCK PROTEIN	−53.082.952.951	Longevity
99	26S RIBOSOMAL RNA	−3.616.913.314	Translation