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Supplementary data

In-silico prediction of an uncharacterized protein generated from heat responsive SSH library in wheat (*Triticum aestivum* L.)

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Supplementary Table: Representative ESTs of forward 37^{o}C heat stress SSH library from wheat. ESTs 1-19 are contigs and ESTs 20-78 are singlets. EST-39 represents the uncharacterized protein under study.

EST No.	Locus ID	E-value	Identity Percentage (%)	Best match in TIGR database
EST-1	LOC_Os01g71670.1	6.70E-30	62.00%	Glycosyl hydrolases family 17
EST-2	LOC_Os03g39370.1	0.994	48.15%	Expressed protein
EST-3	LOC_Os02g44470.1	1.90E-18	80.00%	Actin-depolymerizing factor
EST-4	LOC_Os01g31690.1	7.40E-63	87.14%	Oxygen-evolving enhancer protein 1, chloroplast precursor
EST-5	LOC_Os09g36220.1	0.00065	26.09%	Response regulator receiver domain containing protein
EST-6	LOC_Os12g06100.2	3.80E-43	50.83%	TLD family protein
EST-7	LOC_Os01g67220.2	1.00E-58	66.67%	Os1bglu4 - beta-glucosidase-like protein without signal sequence
EST-8	LOC_Os01g53610.1	1.20E-25	34.64%	Selenium-binding protein, related
EST-9	LOC_Os07g43810.1	4.90E-18	71.67%	RNA recognition motif containing protein
EST-10	LOC_Os06g16380.1	2.00E-14	100.00%	Expressed protein
EST-11	LOC_Os04g38520.1	8.30E-31	60.17%	CPuORF18 - conserved peptide uORF-containing transcript
EST-12	LOC_Os03g34300.1	2.40E-32	66.34%	TMS membrane protein/tumour differentially expressed protein
EST-13	LOC_Os01g53520.1	7.60E-38	67.86%	Reticulon domain containing protein

EST-14	LOC_Os02g44704.2	9.30E-08	64.71%	LYR motif containing protein
EST-15	LOC_Os03g01530.1	3.90E-73	97.89%	Tubulin/FtsZ domain containing protein
EST-16	LOC_Os03g05730.1	4.30E-36	93.90%	Cell division control protein 48 homolog E
EST-17	LOC_Os03g24220.1	3.60E-24	67.95%	Villin protein
EST-18	LOC_Os07g49360.1	2.80E-22	54.35%	Peroxidase precursor
EST-19	LOC_Os05g27510.1	0.24	41.38%	Expressed protein
EST-20	LOC_Os01g67220.2	5.60E-49	63.97%	Os1bglu4 - beta-glucosidase-like protein without signal sequence
EST-21	LOC_Os05g45420.3	4.50E-47	91.43%	CAMK_KIN1/SNF1/Nim1_like_AMPKh.3 - CAMK includes calcium/calmodulin depedent protein kinases
EST-22	LOC_Os06g40640.3	0.66	65.38%	Fructose-bisphospate aldolase isozyme
EST-23	LOC_Os11g06720.1	4.20E-05	58.62%	Abscisic stress-ripening
EST-24	LOC_Os11g47970.1	5.00E-41	96.51%	AAA-type ATPase family protein
EST-25	LOC_Os07g36450.1	1.10E-27	69.51%	PPR repeat domain containing protein
EST-26	LOC_Os01g59150.1	2.60E-28	96.61%	Tubulin/FtsZ domain containing protein
EST-27	LOC_Os11g06720.1	2.70E-26	65.85%	Abscisic stress-ripening
EST-28	LOC_Os01g57410.1	9.60E-08	47.37%	Pentatricopeptide repeat domain containing protein
EST-29	LOC_Os11g15000.1	0.032	50.00%	Expressed protein
EST-30	LOC_Os05g45550.1	7.20E-06	36.67%	Retrotransposon protein, putative, unclassified
EST-31	LOC_Os04g57810.1	3.50E-24	82.46%	GA18008-PA
EST-32	LOC_Os10g21190.1	1.40E-13	94.87%	Expressed protein
EST-33	LOC_Os09g33810.5	2.30E-59	74.52%	Ankyrin repeat domain containing protein
EST-34	LOC_Os06g27970.1	3.20E-07	47.27%	FKBP12-interacting protein of 37 kDa
EST-35	LOC_Os01g58000.1	4.90E-50	97.12%	ATP synthase epsilon chain
EST-36	LOC_Os06g43044.1	1.80E-45	61.81%	GDSL-like lipase/acylhydrolase
EST-37	LOC_Os09g39670.1	2.40E-57	71.34%	Oxidoreductase, short chain dehydrogenase/reductase family domain containing family
EST-38	LOC_Os03g09840.1	0.00026	36.36%	C2 domain containing protein
EST-39	LOC_Os04g57430.1	5.80E-16	58.90%	Uncharacterized protein At4g06744 precursor
EST-40	LOC_Os11g03430.1	9.10E-33	81.61%	CDC45B - Putative DNA replication initiation protein
EST-41	LOC_Os08g03670.1	9.50E-47	71.93%	Galactosyltransferase family protein
EST-42	LOC_Os07g12510.1	2.40E-13	46.53%	AP2 domain containing protein
EST-43	LOC_Os02g47200.1	2.80E-24	92.73%	Transposon protein, putative, unclassified
EST-44	LOC_Os02g01150.3	2.30E-13	80.49%	Erythronate-4-phosphate dehydrogenase domain containing protein
EST-45	LOC_Os12g15420.1	9.90E-12	37.50%	Nucampholin
EST-46	LOC_Os01g65902.1	1.50E-13	90.48%	Apocytochrome f precursor
EST-47	LOC_Os01g04730.1	5.20E-30	84.21%	Ribosomal protein L24
EST-48	LOC_Os08g09690.2	0.55	35.71%	Nuclear transcription factor Y subunit
EST-49	LOC_Os08g10020.2	4.80E-27	72.37%	Photosystem II 10 kDa polypeptide, chloroplast precursor

EST-50	LOC_Os01g74280.1	1.70E-20	77.78%	TGD2
EST-51	LOC_Os06g04020.1	1.40E-11	50.00%	Histone H1
EST-52	LOC_Os04g58640.1	1.50E-55	89.19%	Cleavage and polyadenylation specificity factor subunit 5
EST-53	LOC_Os05g39110.2	4.00E-09	52.54%	selT-like protein precursor
EST-54	LOC_Os03g27310.1	9.90E-36	100.00%	Histone H3
EST-55	LOC_Os07g16750.1	2.20E-26	45.52%	Retrotransposon protein, putative, unclassified
EST-56	LOC_Os12g42420.1	5.50E-35	62.28%	DNA binding protein
EST-57	LOC_Os11g47970.1	1.00E-58	84.92%	AAA-type ATPase family protein
EST-58	LOC_Os11g06870.1	8.50E-13	57.89%	Glyoxal oxidase-related
EST-59	LOC_Os06g42670.1	4.30E-05	38.46%	Transposon protein, putative, CACTA, En/Spm sub-class
EST-60	LOC_Os02g40260.1	1.70E-20	46.30%	Uncharacterized protein At4g06744 precursor
EST-61	LOC_Os10g21268.1	5.60E-33	92.96%	Ribulose bisphosphate carboxylase large chain precursor
EST-62	LOC_Os01g62820.1	5.40E-20	46.25%	Transcription initiation factor TFIID subunit A containing protein
EST-63	LOC_Os01g03680.1	1.50E-07	45.83%	BBTI8 - Bowman-Birk type bran trypsin inhibitor precursor
EST-64	LOC_Os09g26810.1	4.50E-56	80.00%	Chlorophyll A-B binding protein
EST-65	LOC_Os04g09550.1	0.53	72.73%	Expressed protein
EST-66	LOC_Os06g21790.1	0.99	36.36%	Retrotransposon protein, putative, unclassified
EST-67	LOC_Os08g38460.1	8.30E-16	65.31%	Zinc finger, C3HC4 type domain containing protein
EST-68	LOC_Os01g18630.2	6.10E-20	70.49%	Aspartic proteinase oryzasin-1 precursor
EST-69	LOC_Os02g05470.2	2.10E-10	76.00%	CCT motif family protein
EST-70	LOC_Os12g25670.1	0.82	52.00%	Retrotransposon, putative, centromere-specific
EST-71	LOC_Os06g01260.2	7.70E-08	38.89%	Glutathione gamma-glutamylcysteinyltransferase 1
EST-72	LOC_Os12g17900.1	1.30E-67	68.69%	Armadillo/beta-catenin repeat family protein
EST-73	LOC_Os01g61320.2	3.20E-30	77.92%	Thioredoxin
EST-74	LOC_Os02g48560.3	1.10E-15	55.26%	Fatty acid desaturase
EST-75	LOC_Os12g39610.1	0.29	34.62%	Retrotransposon protein, putative, Ty3-gypsy subclass
EST-76	LOC_Os06g41030.1	0.36	36.76%	DUF1680 domain containing protein
EST-77	LOC_Os01g70780.1	3.70E-25	69.74%	WD40-like domain containing protein
EST-78	LOC_Os01g14860.4	1.90E-12	81.58%	CGMC_GSK.1 - CGMC includes CDA, MAPK, GSK3, and CLKC kinases