

## Proteomic analysis of phytase transgenic and non-transgenic maize seeds

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### Supporting Information File:

Supplementary Figure S1: The original 2-DE gels for maize seeds.

Supplementary Table S1: MS/MS identification information of DEPs obtained by 2-DE.

Supplementary Table S2: Identification information of DEPs obtained by iTRAQ.

Supplementary Table S3: GO numbers of 148 identified proteins.

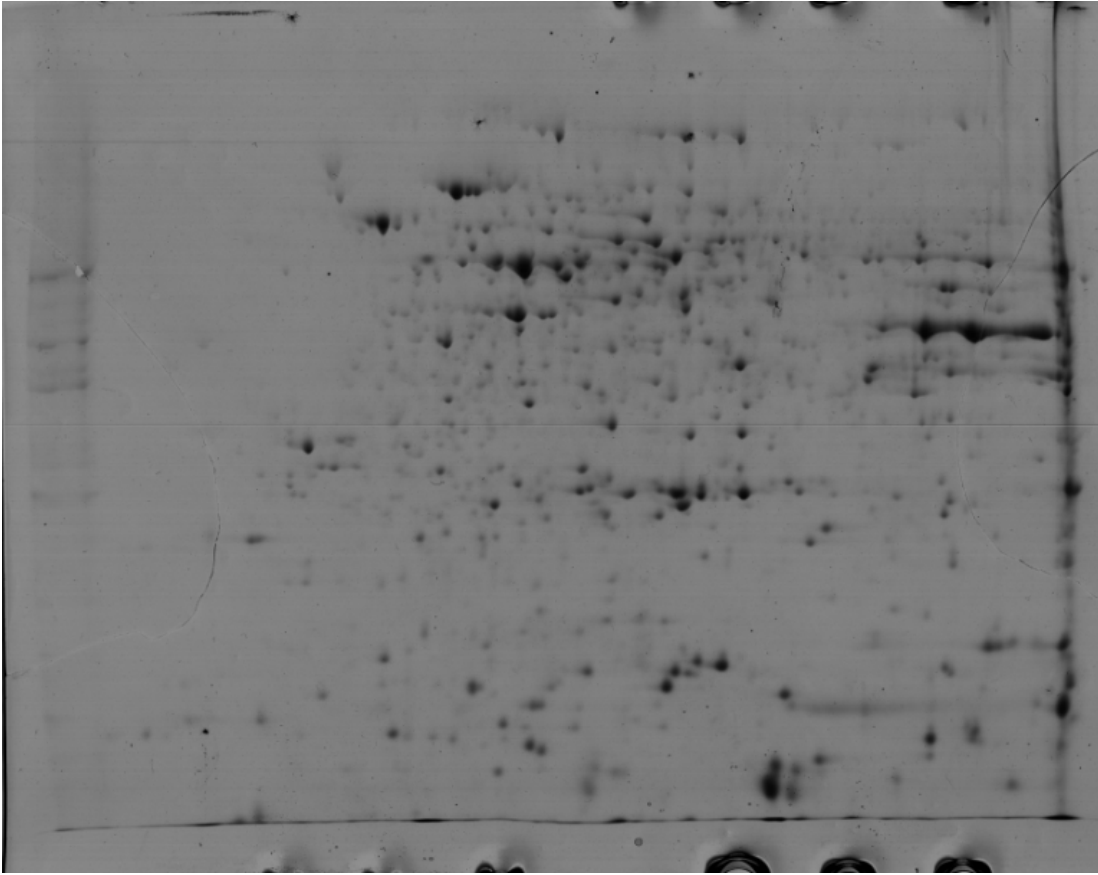
Supplementary Table S4: Classification of COG of 148 identified DEPs.

Supplementary Table S5: KEGG pathway enrichment of identified DEPs.

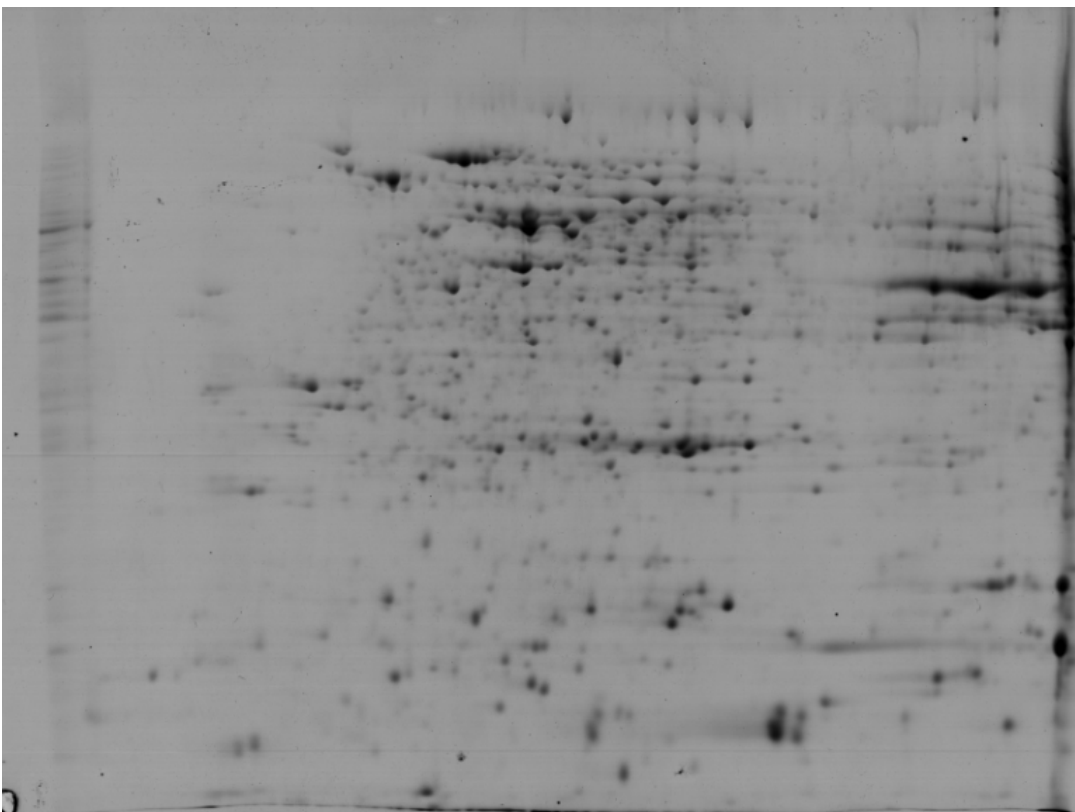
Supplementary Table S6: Primers used in qRT-PCR

**Supplementary Figure S1: The typical original 2-DE gels for maize seeds.**

**NT- Repeat 1**



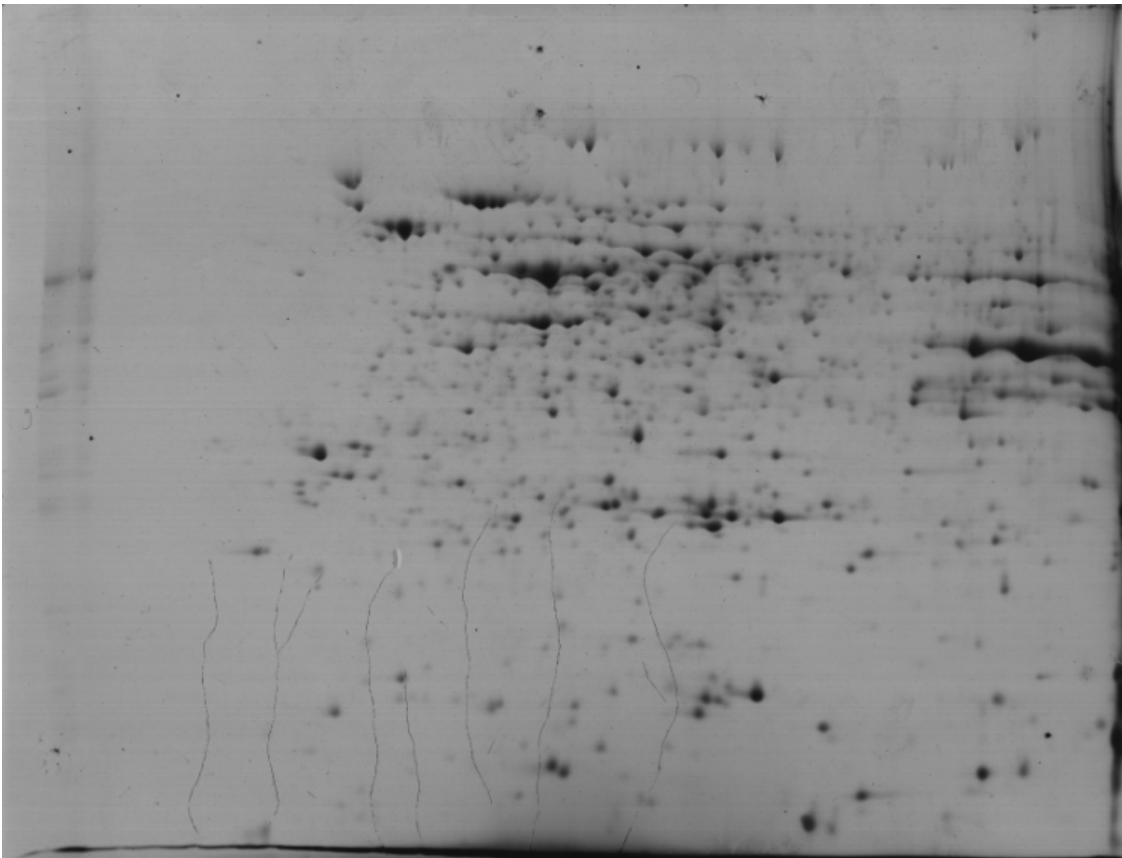
**PT-Repeat 1**



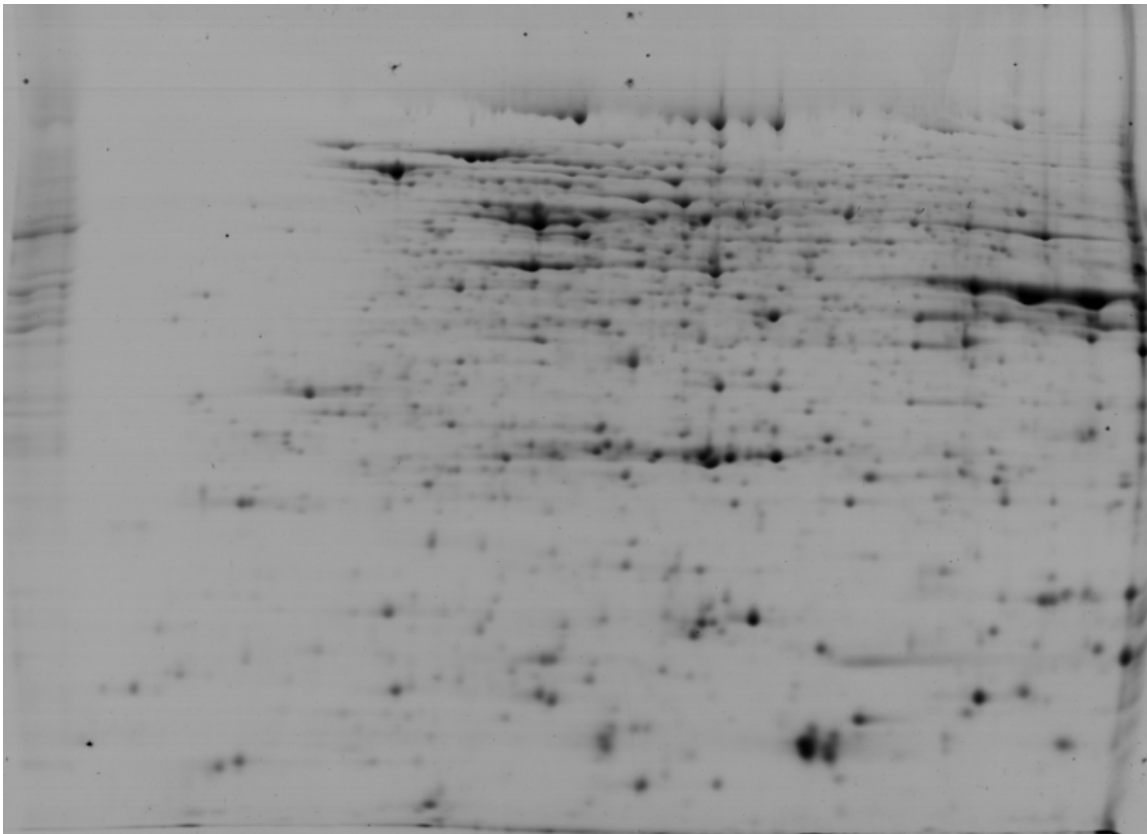
**NT- Repeat 2**



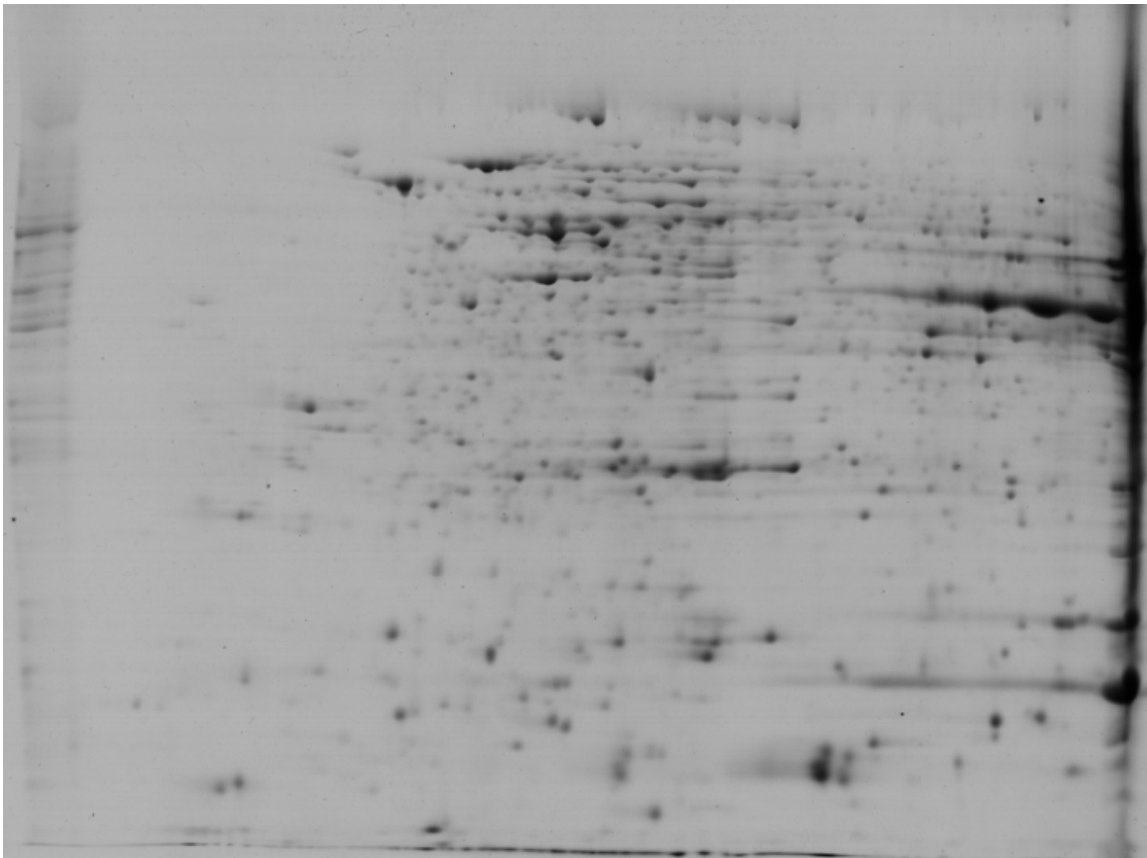
**PT- Repeat 2**



**NT- Repeat 3**



**PT- Repeat 3**



**Supplementary Table S1: MS/MS identification information of DEPs obtained by 2-DE.**

Spots No	Ac. No	Thero. PI/kDad	MP	Protein Score	Fold change	p value	Protein Description
1	gi 293336560	5.47/60.42	5	591	1.56	1.5E-17	phosphoglycerate mutase1
2	gi 223974403	6.55/50.18	2	102	1.67	0.018	unknown
	gi 226533244	6.55/50.14	2	102		0.018	transaminase/ transferase, transferring nitrogenous groups
3	gi 308080934	5.45/46.82	3	137	1.89	3.0E-04	cytosolic monodehydroascorbate reductase
4	gi 226493582	5.33/38.69	5	198	1.51	8.3E-02	uncharacterized protein LOC100285670
	gi 226508732	5.38//39.01	3	124		0.075	activator of 90 kDa heat shock protein ATPase
	gi 413921986	5.95/49.32	3	124		0.083	activator of heat shock protein ATPase
5	gi 413918083	4.83/39.35	3	214	1.81	2.E-08	eukaryotic translation initiation factor 3 subunit 3
	gi 226493027	4.83/39.42	3	214		2.E-08	uncharacterized protein LOC100280503
	gi 413918085	4.83/38.59	3	214		2.E-08	hypothetical protein ZEAMMB73_519156
	gi 670442963	4.83/39.23	3	214		2.E-08	PREDICTED: LOC100280503 isoform X1
6	gi 162461501	6.41/36.63	5	520	2.04	5.5E-10	glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic
	gi 194700850	6.40/32.08	5	520		5.5E-10	unknown
	gi 413941770	6.67/37.27	5	520		5.5E-10	glyceraldehyde-3-phosphate dehydrogenase2
	gi 413921389	6.45/32.03	3	240		1.20E-08	glyceraldehyde-3-phosphate dehydrogenase1 isoform 1
7	gi 413916077	6.89/21.80	3	278	1.94	9.0E-11	hypothetical protein ZEAMMB73_718489
	gi 308080598	5.86/25.67	3	278		9.0E-11	uncharacterized protein LOC100502283
8	gi 226532150	5.04/26.68	2	90	1.73	0.05	isoamyl acetate-hydrolyzing esterase
9	gi 195605636	5.53/27.28	2	157	1.57	8.90E-06	triosephosphate isomerase, cytosolic
	gi 670440305	6.31/71.39	3	382		5.00E-11	PREDICTED: globulin-1 S allele-like
10	gi 226498252	5.14/19.56	4	392	1.55	1.6E-11	adenine phosphoribosyltransferase 1
	gi 414877870	8.93/24.14	4	392		1.6E-11	TPA: adenine phosphoribosyltransferase 1
	gi 194701624	5.14/19.51	4	392		1.6E-11	unknown
11	gi 413944599	5.38/18.20	3	180	1.61	1.3E-05	USP family protein
	gi 212721114	5.63/18.30	3	180		1.3E-05	uncharacterized protein LOC100194018
12	gi 413949326	6.04/103.78	4	84	0.66	0.34	pyruvate, phosphate dikinase 1, Precursor
13	gi 413949326	6.04/103.78	11	487	0.53	2.2E-05	pyruvate, phosphate dikinase 1, Precursor
14	gi 413949326	5.81/64.69	2	198	0.53	1.0E-09	ruBisCO large subunit-binding protein subunit beta
	gi 226493641	5.81/64.52	2	198		1.0E-09	ruBisCO large subunit-binding protein subunit beta
	gi 413926905	5.81/64.62	2	198		1.0E-09	putative TCP-1/cpn60 chaperonin family protein isoform 1
15	gi 189027076	6.16/57.89	7	740	0.52	1.9E-12	glucose-1-phosphate adenyltransferase large subunit 1
16	gi 217330650	5.29/42.16	3	233	0.66	7.2E-08	actin related protein 1
17	gi 169245755	5.25/39.57	2	186	0.64	9.1E-09	glutamine synthetase
	gi 162463755	5.34/39.57	2	186		9.1E-09	glutamine synthetase root isozyme 3
18	gi 194703858	5.50/39.20	4	157	0.59	0.0035	gibberellin 20 oxidase 2

19	gi 414586767	5.46/19.71	2	157		7.5E-06	TPA: hypothetical protein ZEAMMB73_925834
	gi 162460084	5.25/34.66	2	157	0.54	7.5E-06	L-galactose dehydrogenase
20	gi 226508112	6.97/41.84	3	194	0.66	8.3E-08	cysteine synthase1
21	gi 219887709	6.77/40.13	5	293	0.62	2.9E-06	unknown
22	gi 195650645	6.16/32.83	4	401	0.49	6.7E-10	carbonyl reductase 1
23	gi 224029461	5.08/28.96	2	184	0.66	4.9E-09	6-phosphogluconolactonase
24	gi 226504576	5.65/27.48	3	173	0.62	1.6E-04	APx1 - Cytosolic Ascorbate Peroxidase
25	gi 224029787	6.10/27.51	4	311	0.47	1.1E-07	proteasome subunit alpha type
26	gi 194704678	5.95/21.60	4	295	0.60	6.2E-07	minor allergen Alt a 7
27	gi 4468794	5.96/23.87	5	408	0.53	2.2E-13	glutathione transferase III(b)
28	gi 195605616	4.53/18.79	5	327	0.54	1.9E-07	translationally-controlled tumor protein
29	gi 195605616	4.54/18.79	3	182	0.33	2.5E-04	translationally-controlled tumor protein
30	gi 226504982	8.34/21.74	2	110	0.66	5.5E-04	eukaryotic translation initiation factor 1A
31	gi 840086919	6.30/16.53	2	153	0.65	1.0E-07	nucleoside diphosphate kinase 1
32	gi 266398	8.07/16.86	3	181	0.47	3.0E-04	trypsin/factor XIIA inhibitor

Note: 1) Spots No is assigned spot numbers as indicated in Figure 2.

2) Best Protein Accession is according to UNIProt.

3) Thero.kDa and Thero. pI are the theoretical values of molecular weight (Mr., kDa) and pI for the identified proteins.

4) MP is the numbers of the matched peptides

5) Percent values of coverage (%) of the matched peptides in the whole protein sequence.

6) p value is the highest score's Expect of the matched peptides.

7) Fold change is the ratio of PT maize seeds compared to NT maize seeds.

**Supplementary Table S2: Identification information of DEPs obtained by iTRAQ.**

<b>Protein No.</b>	<b>Unused Score</b>	<b>Cov. (95%)</b>	<b>Peptides (95%)</b>	<b>Fold (PT/NT)</b>	<b>p value</b>	<b>Accession</b>	<b>Name</b>
33	3.09	44.64	5	0.045000 1	0.043 54	tr A3KLI1 A3KLI1_MA IZE	RAB17 protein
34	16	68.13	16	0.067237 7	0.040 12	tr B6SI37 B6SI37_MAI ZE	Embryonic abundant protein 1
35	74.43	51.92	81	0.094233 9	0.016 67	tr C0PGM3 C0PGM3_ MAIZE	Uncharacterized protein
36	32.89	57.5	25	0.102399 9	0.010 05	tr Q41815 Q41815_MAI ZE	Heat shock protein 26
37	61.65	60.44	118	0.11171 99	0.010	tr Q7M1Z8 Q7M1Z8_M AIZE	Globulin-2
38	30.63	61.66	243	0.145216 6	0.002 3	tr K7VJF3 K7VJF3_MA IZE	Uncharacterized protein
39	10.11	29.07	6	0.152435 9	0.006 73	tr B8QY31 B8QY31_ZE AMP	Zeamatin-like protein
40	17.79	18.83	12	0.190091 17	0.004	tr B6SLF6 B6SLF6_MA IZE	Antimicrobial peptide MBP-1
41	6.17	40.74	12	0.208429 8	0.033 46	tr B6TLK8 B6TLK8_M AIZE	17.4 kDa class I heat shock protein 3
42	12	62.83	9	0.210916 5	0.024 05	tr B6T8E4 B6T8E4_MA IZE	Embryonic abundant protein 1
43	7.11	26.71	4	0.214135 6	0.000 21	tr B6SQM6 B6SQM6_ MAIZE	Pathogenesis protein 10
44	46.84	38.57	57	0.218984 5	0.026 33	tr K7W272 K7W272_M AIZE	Uncharacterized protein
45	3.08	84.6	133	0.219432 5	0.027 21	tr Q4U168 Q4U168_MA IZE	Glucose-1-phosphate adenylyltransferase
46	20.01	21.69	12	0.240035 7	0.039 1	tr A0A096TN72 A0A09 6TN72_MAIZE	Uncharacterized protein
47	17.38	30.03	14	0.245141 4	0.032 6	tr B4FKP4 B4FKP4_M AIZE	Uncharacterized protein
48	75.08	59.21	88	0.250743 5	0.025 44	tr Q9S822 Q9S822_MAI ZE	Heat shock protein 101
49	17.66	35.71	9	0.266474 6	0.016 18	tr B6UGU4 B6UGU4_ MAIZE	Steroleosin
50	7.08	38.98	5	0.301911 7	0.004 68	tr B6UGS5 B6UGS5_M AIZE	Putative uncharacterized protein
51	22.07	50.42	22	0.305629 9	0.010 59	tr B4FFZ9 B4FFZ9_MA IZE	Lipoprotein
52	33.25	46.81	19	0.318147 7	0.024 09	tr Q8S532 Q8S532_MAI ZE	Cytosolic aldehyde dehydrogenase

53	10.02	35.43	11	0.318202	0.034	tr C0P5U8 C0P5U8_MA 9	0.034 93	IZE	Glutathione S-transferase 4
54	36.75	45.21	29	0.324057	0.003	tr B6SK46 B6SK46_MA 84	0.003 84	IZE	Cupin family protein
55	18.9	47.33	23	0.325087	0.017	tr C0P451 C0P451_MAI 3	0.017 58	ZE	Endochitinase B
56	10.22	41.89	35	0.329906	0.010	tr B6TSQ9 B6TSQ9_M 8	0.010 38	AIZE	Aspartic proteinase oryzasin-1
57	0.12	2.448	2	0.330878	0.035	tr B6SSB8 B6SSB8_MA 5	0.035 03	IZE	Transposon protein
58	8	49.21	4	0.331446	0.042	tr K7WCU4 K7WCU4_ 4	0.042 01	MAIZE	Uncharacterized protein
59	28.25	78.17	29	0.334605	0.020	tr B4FFK9 B4FFK9_M 4	0.020 4	AIZE	Uncharacterized protein
60	12.19	59.09	27	0.341679	0.042	tr C0PPC9 C0PPC9_MA 6	0.042 13	IZE	Uncharacterized protein
61	26.79	65.58	21	0.345023	0.025	tr Q19VG6 Q19VG6_M 1	0.025 13	AIZE	Major latex protein 22
62	4.91	7.616	4	0.345319	0.033	tr A0A096RYL4 A0A09 5	0.033 03	6RYL4_MAIZE	Uncharacterized protein
63	7.53	15.96	5	0.351526	0.013	tr K7V5N4 K7V5N4_M 9	0.013 56	AIZE	Uncharacterized protein
64	2.7	60.24	65	0.352958	0.049	tr E9NQE3 E9NQE3_M 9	0.049 9	AIZE	Malate dehydrogenase
65	10.58	39.2	22	0.361260	0.028	tr B6UGN9 B6UGN9_ 6	0.028 39	MAIZE	Oleosin
66	40.12	59.56	24	0.363651	0.010	tr B4F9K0 B4F9K0_MA 8	0.010 22	IZE	Uncharacterized protein
67	6.55	21.17	9	0.364626	0.038	tr B8A3K0 B8A3K0_M 4	0.038 97	AIZE	Uncharacterized protein
68	13.44	73.24	11	0.373108	0.039	tr B4FJM6 B4FJM6_M 3	0.039 43	AIZE	Uncharacterized protein
69	8.26	70	9	0.373772	0.012	tr A0A096RTN1 A0A09 5	0.012 97	6RTN1_MAIZE	Uncharacterized protein
70	13.72	42.24	9	0.379674	0.049	tr B6U9I3 B6U9I3_MAI 38	0.049 38	ZE	Eukaryotic translation initiation factor 3
71	26.06	52.88	19	0.397955	0.033	tr B4G1C2 B4G1C2_M 3	0.033 14	AIZE	Uncharacterized protein
72	6.01	15.74	5	0.399932	0.007	tr B6SGN7 B6SGN7_M 1	0.007 82	AIZE	Embryonic protein
73	14.84	47.13	11	0.416975	0.005	tr B6TTP4 B6TTP4_MA 5	0.005 45	IZE	Stress-inducible membrane pore protein
74	23.87	39.18	16	0.422440	0.022	tr K7UTW6 K7UTW6_ 8	0.022 45	MAIZE	Plasminogen activator inhibitor



75	6	22.88	4	0.430430	0.030	tr B6UDH8 B6UDH8_8	MAIZE	Putative uncharacterized protein
76	50.92	54.88	65	0.432737	0.021	tr Q8S4W8 Q8S4W8_M1	AIZE	Pyruvate decarboxylase
77	48.24	59.84	44	0.444518	0.028	tr B4FAL8 B4FAL8_M1	AIZE	Uncharacterized protein
78	6.38	12.53	4	0.461243	0.019	tr B6TII3 B6TII3_MAIZ3	E	ADP-ribosylation factor GTPase-activating protein 3
79	6	26.32	6	0.461747	0.016	tr B6TKN6 B6TKN6_M9	AIZE	Nonspecific lipid-transfer protein
80	15.89	53.17	34	0.466296	0.036	tr B6TF92 B6TF92_MA61	IZE	Stress responsive protein
81	15.33	23.06	10	0.466692	0.032	tr C0HFV7 C0HFV7_M4	AIZE	Putative apyrase family protein
82	1.87	4.021	3	0.476355	0.025	tr B8A0H4 B8A0H4_M3	AIZE	Uncharacterized protein
83	10.01	36.84	9	0.483058	0.041	tr B4F9E8 B4F9E8_MA7	IZE	Uncharacterized protein
84	0.18	17.13	18	0.492498	0.015	tr A0A096SBR2 A0A096SBR2_MAIZE		Uncharacterized protein
85	1.02	42.53	4	0.500184	0.025	tr K7TQT5 K7TQT5_M7	AIZE	Uncharacterized protein
86	7.14	10.76	7	0.506318	0.005	tr K7V5M7 K7V5M7_4	MAIZE	Uncharacterized protein
87	2	7.659	2	0.508617	0.002	tr A0A096RDK8 A0A096RDK8_MAIZE		Uncharacterized protein
88	41.5	78.22	30	0.519775	0.033	tr C0HFQ1 C0HFQ1_M5	AIZE	Uncharacterized protein
89	14.24	25.87	9	0.519907	0.024	tr A0A096TAP2 A0A096TAP2_MAIZE		Uncharacterized protein
90	87.32	48.67	69	0.524785	0.012	tr K7VD78 K7VD78_M2	AIZE	Putative chaperone clbp family protein
91	10.67	24.93	7	0.527738	0.014	tr B6UHC9 B6UHC9_M7	AIZE	Putative uncharacterized protein
92	18.89	42.91	11	0.544157	0.037	tr B4FRD1 B4FRD1_M6	AIZE	Adaptin ear-binding coat-associated protein 1
93	19.45	46.82	13	0.551989	0.026	tr B6THJ5 B6THJ5_MA1	IZE	Phosphosulfolactate synthase-related protein
94	4.61	18.31	5	0.553265	0.006	tr B6UGM9 B6UGM9_3	MAIZE	Putative uncharacterized protein
95	5.89	12.61	7	0.553520	0.012	tr A0A096TH62 A0A096TH62_MAIZE		Uncharacterized protein
96	5.82	23.1	8	0.555698	0.041	tr C0HI30 C0HI30_MAI6	ZE	Uncharacterized protein

97	4.05	3.289	3	0.558307	0.031	tr A0A096QKY4 A0A096QKY4_MAIZE	Uncharacterized protein
98	2.06	28.02	12	0.561774	0.002	tr B4FL64 B4FL64_MAIZE	Ribosomal protein L19
99	81.97	55.44	61	0.564937	0.029	tr Q9AXG8 Q9AXG8_MAIZE	Lipoxygenase
100	4.09	7.818	2	0.568327	0.004	tr B6TRW7 B6TRW7_MAIZE	Sigma factor sigB regulation protein rsbQ
101	11.01	21.19	9	0.578298	0.000	tr B4G0U5 B4G0U5_MAIZE	Uncharacterized protein
102	3.18	9.502	4	0.580278	0.015	tr B6TA85 B6TA85_MAIZE	Protein binding protein
103	25.61	25.79	20	0.590458	0.014	tr A0A096SXV7 A0A096SXV7_MAIZE	Uncharacterized protein
104	0.29	2.361	2	0.594147	0.039	tr A0A096PME5 A0A096PME5_MAIZE	Uncharacterized protein
105	9.97	25.37	6	0.595445	0.044	tr B7ZZM7 B7ZZM7_MAIZE	Uncharacterized protein
106	37.55	34.18	25	0.597541	0.006	tr A0A096QF11 A0A096QF11_MAIZE	Uncharacterized protein
107	14.11	9.063	8	0.606014	0.000	tr A0A096TMH0 A0A096TMH0_MAIZE	Uncharacterized protein
108	12.26	13.43	13	0.611000	0.007	tr A0A096QBA0 A0A096QBA0_MAIZE	Uncharacterized protein
109	22.26	44.65	16	0.611933	0.029	tr C0PF66 C0PF66_MAIZE	Aminoacylase-1
110	23.53	36.49	14	0.622543	0.047	tr B4FEU5 B4FEU5_MAIZE	Uncharacterized protein
111	17.28	57.35	13	0.625172	0.008	tr B6U8P6 B6U8P6_MAIZE	ABA-responsive protein
112	2.04	24.45	7	0.635782	0.040	tr B4FSU1 B4FSU1_MAIZE	Transmembrane emp24 domain-containing protein 10
113	39.54	39.72	21	0.636687	0.032	tr Q5G1U0 Q5G1U0_MAIZE	Malic enzyme
114	87.46	54.14	87	0.639226	0.035	tr B6SV64 B6SV64_MAIZE	Heat shock 70 kDa protein 4
115	21.81	32.3	24	0.644807	0.035	tr B4G1G1 B4G1G1_MAIZE	Desiccation-related protein
116	12.98	26.63	7	0.645797	0.023	tr B6SMK8 B6SMK8_MAIZE	Inositol-1-monophosphatase
117	4.02	7.2	2	0.656096	0.011	tr A0A096THV6 A0A096THV6_MAIZE	Uncharacterized protein
118	17.23	48.22	11	1.518215	0.006	tr B6T346 B6T346_MAIZE	THO complex subunit 4

119	13.43	14.39	9	1.525494 7	0.032 81	tr K7TNE7 K7TNE7_M AIZE	Uncharacterized protein
120	16.15	48.24	12	1.534568	0.019 38	tr B4G1B0 B4G1B0_M AIZE	Remorin
121	2.04	8.285	4	1.548275 3	0.041 45	tr Q32SG1 Q32SG1_M AIZE	Protein phosphatase 2A regulatory subunit B
122	2	35.19	23	1.553396 9	0.002 37	tr B4FBP3 B4FBP3_MA IZE	Signal recognition particle subunit SRP68
123	31.92	48.31	21	1.561641	0.027 69	tr B4FU39 B4FU39_MA IZE	Uncharacterized protein
124	2	10.64	4	1.567968 4	0.026 55	tr K7UYP8 K7UYP8_M AIZE	Basic endochitinase A
125	2.29	20.33	4	1.568320 7	0.022 47	tr B6SX73 B6SX73_MA IZE	60S ribosomal protein L35
126	26.98	64.46	15	1.576059 2	0.025 78	tr B4F957 B4F957_MAI ZE	Uncharacterized protein
127	52.67	28.18	35	1.582744 3	0.028 44	tr K7U005 K7U005_MA IZE	Uncharacterized protein
128	18.95	42.58	18	1.615043 5	0.039 52	tr B6UHH9 B6UHH9_M AIZE	60S ribosomal protein L23a
129	25.26	42.58	38	1.641585 8	0.036 79	tr B4FSQ4 B4FSQ4_M AIZE	40S ribosomal protein SA
130	1.31	29.25	8	1.646408 1	0.004 03	tr B6TA79 B6TA79_M AIZE	Cell division control protein 2
131	38.98	50.78	34	1.695722 1	0.037 59	tr A0A096QRB1 A0A09 6QRB1_MAIZE	Uncharacterized protein
132	27.05	69.49	271	1.695815 9	0.029 05	tr B7ZZ42 B7ZZ42_MA IZE	Uncharacterized protein
133	60.92	56.5	91	1.720119 1	0.013 06	tr Q6R987 Q6R987_MA IZE	ATP synthase subunit alpha
134	14.15	70.27	8	1.729688 3	0.036 88	tr B6SMY5 B6SMY5_ MAIZE	Putative uncharacterized protein
135	30.84	60.98	27	1.758488 2	0.033 62	tr B4F848 B4F848_MAI ZE	Chaperonin
136	37.4	37.79	21	1.769358 8	0.046 81	tr K7U1M0 K7U1M0_ MAIZE	Uncharacterized protein
137	3.25	9.626	2	1.777826 3	0.040 74	tr B6T6D7 B6T6D7_M AIZE	MIR-interacting saposin-like protein
138	10.02	57.69	9	1.778223 1	0.014 23	tr B6SIF0 B6SIF0_MAI ZE	Glycine-rich RNA-binding protein 2
139	17.09	37.04	11	1.906430 6	0.039 86	tr B6T9E1 B6T9E1_MA IZE	Xyloglucan endotransglucosylase/hydrolase
140	13.97	48.44	8	1.93203	0.009 01	tr B4FTE1 B4FTE1_MA IZE	Signal peptidase complex subunit 2

141	12.11	11.51	9	1.946139	0.000	tr A0A096QQ54 A0A096QQ54_MAIZE	Uncharacterized protein
142	5.11	25.98	5	1.972951	0.030	tr B6SIP0 B6SIP0_MAIZE	NHP2-like protein 1
143	20.56	39.83	15	1.976405	0.049	tr P93852 P93852_MAIZE	Cycloartenol-C-24-methyltransferase 1
144	14.54	32.37	9	1.991969	0.011	tr A0A096RS97 A0A096RS97_MAIZE	Uncharacterized protein
145	14.04	33.21	8	2.033743	0.001	tr K7VTU7 K7VTU7_MAIZE	Uncharacterized protein
146	8.6	45.35	18	2.088233	0.013	tr Q9ZQX9 Q9ZQX9_MAIZE	40S ribosomal protein S27
147	19.26	32.78	15	4.092953	0.012	tr B6UD26 B6UD26_MAIZE	O-methyltransferase ZRP4
148	10	18.22	6	9.260415	0.033	tr C4J5L2 C4J5L2_MAIZE	Uncharacterized protein

**Note:**

- 1) Protein Number is followed the spot numbers as showed in Table S1.
- 2) Best Protein Accession is according to UNIProt.
- 3) MP is the numbers of the matched peptides
- 4) Percent values of coverage (%) of the matched peptides in the whole protein sequence.

**Supplementary Table S3: GO numbers of the 148 identified proteins.**

Q9AXG8	GO:0050832	GO:0002215	GO:0046872	GO:0016702	GO:0031408	
B6T9E1	GO:0048046	GO:0005618	GO:0042546	GO:0071555	GO:0004553	GO:0010411
A0A096SXV7	GO:0004559	GO:0030246	GO:0006013	GO:0008270		
Q6R987	GO:0005524	GO:0015991	GO:0015986	GO:0005739	GO:0046933	GO:0045261
Q5G1U0	GO:0051287	GO:0004471	GO:0006108	GO:0046872		
P93852	GO:0006084	GO:0016132	GO:0042398	GO:0009805	GO:0009793	GO:0005783
C0PF66	GO:0004046	GO:0006520	GO:0005737	GO:0046872	GO:0008237	
Q9ZTQ4	GO:0005975	GO:0004575				
A0A096TAP2	GO:0004185					
E9NQE3	GO:0030060	GO:0005975	GO:0006108	GO:0006099		
B4FSQ4	GO:0022627	GO:0000028	GO:0003735	GO:0006412		
Q9S822	GO:0005524	GO:0019538				
B6U9I3	GO:0016282	GO:0033290	GO:0005852	GO:0001731	GO:0006446	GO:0003743
B4FBP3	GO:0008312	GO:0006614	GO:0030942	GO:0005047	GO:0005786	
B6UGN9	GO:0016021	GO:0012511				
Q9ZQX9	GO:0046872	GO:0005840	GO:0003735	GO:0006412		
Q32SG1	GO:0000159	GO:0008601	GO:0007165			
A0A096QF11	GO:0009738	GO:0005622	GO:0035556	GO:0019243	GO:0010583	GO:0009723
B6TSQ9	GO:0004190	GO:0006629				
B4FSU1	GO:0016021	GO:0006810				
K7VD78	GO:0005524	GO:0005737	GO:0016485	GO:0009408		
B4FL64	GO:0005840					

		GO:0003735	GO:0006412			
B6THJ5	GO:0003824	GO:0019295	GO:0010286	GO:0010608	GO:0006457	GO:0009644
A0A096RS97	GO:0046872	GO:0016491				
B6SSB8	GO:0020037	GO:0005506	GO:0004497	GO:0016705		
K7TNE7	GO:0000911	GO:0000226	GO:0005643	GO:0006611	GO:0009627	
P15590	GO:0045735					
P31927	GO:0005986	GO:0016157	GO:0046524			
M7ZGS7	GO:0016811					
Q94J20						
B6SIP0	GO:0003723	GO:0030529	GO:0005730	GO:0042254		
B6SX73	GO:0005840	GO:0003735	GO:0006412			
B4F922	GO:0010143	GO:0051179	GO:0016747	GO:0010090		
Q19VG6	GO:0006952	GO:0009607				
K7W272	GO:0045735					
B6SQM6	GO:0006952	GO:0009607				
B8A0H4						
B4FU39	GO:0016491	GO:0008270				
B4FRD1	GO:0006897	GO:0016020				
B4F848	GO:0005524	GO:0005737	GO:0006457			
B6TA85						
B4F957						
B6T6D7	GO:0034976	GO:0009627				
B6TA79	GO:0005524	GO:0051301	GO:0004672			
B6SLF6	GO:0050832					
B6TII3	GO:0005096					
B6T8E4						

B6SGN7					
A3KLI1	GO:0006950	GO:0009415			
B4G1C2	GO:0005975	GO:0004553			
B4FGK8	GO:0005850	GO:0003743			
K7UTW6					
C0P5U8	GO:0016740				
B6UHI9	GO:0000166	GO:0005840	GO:0003735	GO:0006412	
Q41815	GO:0010286	GO:0006457			
B6TTP4	GO:0016021				
K7UY8	GO:0005975	GO:0016998	GO:0008061	GO:0006032	GO:0004568
B8A3K0					
K7V5M7					
C0HFV7	GO:0016787				
B4G1G1					
B4FTE1	GO:0016021	GO:0008233	GO:0005787	GO:0006465	
B6SIF0	GO:0003676	GO:0000166			
C0HFQ1					
B6SMK8	GO:0004401	GO:0046854			
K7V5N4	GO:0004190				
Q7M1Z8	GO:0045735				
B6T346	GO:0003676	GO:0000166			
A0A096QKY4					
Q8S4W8	GO:0016831	GO:0000287	GO:0030976		
B4F9E8					
K7VTU7	GO:0005576	GO:0019953			
C0P451	GO:0005975	GO:0016998	GO:0008061	GO:0006032	GO:0004568
B6TRW7	GO:0010223				

GO:1901601

B4G1B0

B6SI37

Q8S532 GO:0016620

K7WCU4

K7U1M0 GO:0003885 GO:0050660 GO:0016020

B6TF92

B6SJE9

B6UGU4 GO:0016491

M8CBN1 GO:0007010 GO:0005829 GO:0006094 GO:0010498

A0A059PZ24 GO:0016021

B9RET0 GO:0030127 GO:0006888 GO:0006886 GO:0008270

B6TFC2 GO:0008430

B6UDH8

A0A096RTN1 GO:0006952 GO:0009607

B6SV64 GO:0005524

A0A096QRB1 GO:0005524 GO:0005737 GO:0016787 GO:0030163

B6STY9 GO:0009269

B6TLK8

B6T871 GO:0016829

B6UGS5 GO:0006950 GO:0009415

A0A096QQ54 GO:0046872 GO:0004222

C4J004 GO:0010223 GO:1901601

B6TXL1

B6TKN6

Q7XZQ2 GO:0003978 GO:0006012

A0A096TN72

B6SMY5

B6UHC9 GO:0016491



B6U8P6						
Q41886	GO:0045735					
B6SK46	GO:0045735					
C4J5L2	GO:0016758					
B6TXJ8	GO:0005975	GO:0071555	GO:0005576	GO:0004650		
A0A096PME5						
B6UD26	GO:0008171					
A0A096TH62						
Q4U168	GO:0008878	GO:0005978				
A0A0A7LS12						
X4Z319	GO:0005524					
B8QY31						
C6F1K2	GO:0005524					
Q10EF5						
B8A306	GO:0005737	GO:0006007	GO:0030145	GO:0004619		
B6TIG6	GO:0010285	GO:0009089	GO:0030170			
Q9XFZ3	GO:0050660	GO:0016656				
B4FNW7	GO:0001671	GO:0006950				
P01088	GO:0005576	GO:0004867				
B4FS87	GO:0051287	GO:0050661	GO:0006006	GO:0016620		
C4J9Y2						
B6THH7						
B6SIG5	GO:0006096	GO:0004807				
B6T920	GO:0003999	GO:0006168	GO:0005737	GO:0009116		
A0A096TB53	GO:0006950					
P55241	GO:0005524	GO:0009501	GO:0009507	GO:0008878	GO:0005978	GO:0019252
Q9XFZ3	GO:0050660	GO:0016656				
B6THN2	GO:0005524	GO:0005737	GO:0042026			
K7TNP5	GO:0016282	GO:0033290	GO:0005852	GO:0001731	GO:0003743	
X1X262	GO:0005524					
B9TSW1	GO:0005524	GO:0004356	GO:0006542			
B6TF99	GO:0005506	GO:0016491				
Q1PBI2						

B8A367	GO:0006535	GO:0004124	GO:0016740		
B8A230					
B6U607					
B6UAK0	GO:0017057	GO:0005975	GO:0006098		
B6UB73	GO:0020037	GO:0004601	GO:0006979		
C0PFK3	GO:0005737	GO:0005634	GO:0019773	GO:0004298	GO:0006511
B4FWD0	GO:0010181	GO:0045892	GO:0016491		
Q9SM20	GO:0004364				
B6SIF5					
B6SIF5					
B6T9H2	GO:0016021	GO:0003743			
B4FK49	GO:0005524	GO:0006241	GO:0006183	GO:0006228	GO:0004550
K7VVI6	GO:0005524	GO:0016301	GO:0046872	GO:0006090	GO:0050242

**Supplementary Table S4: Classification of COG of 148 identified DEPs.**

<b>Protein No</b>	<b>Accession</b>	<b>Protein Name</b>	<b>Species</b>
<b>RNA processing and modification(A)</b>			
86	B6T346_MAIZE	THO complex subunit 4	MAIZE
110	B6SIP0_MAIZE	NHP2-like protein 1	MAIZE
<b>Energy production and conversion(C)</b>			
20	Q8S532_MAIZE	Cytosolic aldehyde dehydrogenase RF2C	MAIZE
32	E9NQE3_MAIZE	Malate dehydrogenase	MAIZE
53	B6TXL1_MAIZE	Mitochondrial NADH ubiquinone oxidoreductase 13kD-like subunit	MAIZE
55	M7ZGS7_TRIUA	Formamidase	Triticum urartu
81	Q5G1U0_MAIZE	Malic enzyme	MAIZE
101	Q6R987_MAIZE	ATP synthase subunit alpha	MAIZE
104	K7U1M0_MAIZE	L-gulonolactone oxidase	MAIZE
116	C4J5L2_MAIZE	Glycosyltransferase	MAIZE
128	K7VVI6_MAIZE	pyruvate, phosphate dikinase 1, Precursor	MAIZE
129	K7VVI6_MAIZE	pyruvate, phosphate dikinase 1, Precursor	MAIZE
135	Q1PBI2_MAIZE	L-galactose dehydrogenase	MAIZE
140	B6UB73_MAIZE	APx1 - Cytosolic Ascorbate Peroxidase	MAIZE
<b>Amino acid transport and metabolism(E)</b>			
44	Q8S4W8_MAIZE	Pyruvate decarboxylase	MAIZE
67	Q9AXG8_MAIZE	Lipoxygenase	MAIZE
77	C0PF66_MAIZE	Aminoacylase-1	MAIZE
118	B6TIG6_MAIZE	transaminase/ transferase, transferring nitrogenous groups	MAIZE
133	B9TSW1_MAIZE	glutamine synthetase	MAIZE
136	B8A367_MAIZE	cysteine synthase1	MAIZE
<b>Nucleotide transport and metabolism(F)</b>			
49	C0HFV7_MAIZE	Putative apyrase family protein	MAIZE
126	B6T920_MAIZE	adenine phosphoribosyltransferase 1	MAIZE
147	B4FK49_MAIZE	nucleoside diphosphate kinase 1	MAIZE
<b>Carbohydrate transport and metabolism(G)</b>			
5	Q7M1Z8_MAIZE	Globulin-2	MAIZE
23	C0P451_MAIZE	Endochitinase B	MAIZE
30	Q9ZTQ4_MAIZE	Cell wall invertase	MAIZE

36	B6T871_MAIZE	Lactoylglutathione lyase	MAIZE
71	A0A096SXV7_MAIZE	alpha-mannosidase	MAIZE
84	B6SMK8_MAIZE	Inositol-1-monophosphatase	MAIZE
107	B6T9E1_MAIZE	Xyloglucan endotransglucosylase/hydrolase	MAIZE
113	K7VTU7_MAIZE	Uncharacterized protein	MAIZE
117	B8A306_MAIZE	phosphoglycerate mutase1	MAIZE
122	B4FS87_MAIZE	glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic	MAIZE
125	B6SIG5_MAIZE	triosephosphate isomerase, cytosolic	MAIZE
139	B6UAK0_MAIZE	6-phosphogluconolactonase	MAIZE

#### **Lipid transport and metabolism (I)**

111	P93852_MAIZE	Cycloartenol-C-24-methyltransferase 1	MAIZE
124	B6THH7_MAIZE	isoamyl acetate-hydrolyzing esterase	MAIZE

#### **Translation, ribosomal structure and biogenesis (J)**

66	B4FL64_MAIZE	Ribosomal protein L19	MAIZE
73	B4FGK8_MAIZE	Eukaryotic translation initiation factor 2 alpha subunit	MAIZE
93	B6SX73_MAIZE	60S ribosomal protein L35	MAIZE
96	B6UHJ9_MAIZE	60S ribosomal protein L23a	MAIZE
97	B4FSQ4_MAIZE	40S ribosomal protein SA	MAIZE
114	Q9ZQX9_MAIZE	40S ribosomal protein S27	MAIZE
121	K7TNP5_MAIZE	eukaryotic translation initiation factor 3 subunit 3	MAIZE
146	B6T9H2_MAIZE	eukaryotic translation initiation factor 1A	MAIZE
34	B6STY9_MAIZE	Salt tolerance protein	MAIZE
38	B6U9I3_MAIZE	Eukaryotic translation initiation factor 3 subunit J	MAIZE
42	K7UTW6_MAIZE	Plasminogen activator inhibitor 1 RNA-binding protein	MAIZE

#### **Transcription (K)**

54	K7V5M7_MAIZE	Uncharacterized protein	MAIZE
106	B6SIF0_MAIZE	Glycine-rich RNA-binding protein 2	MAIZE

#### **Transcription, Replication, recombination and repair (L)**

72	A0A096PME5_MAIZE	Uncharacterized protein	MAIZE
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#### **Cell wall/membrane/envelope biogenesis (M)**

13	Q4U168_MAIZE	Glucose-1-phosphate adenylyltransferase	MAIZE
39	B4G1C2_MAIZE	Uncharacterized protein	MAIZE
52	SPSA_MAIZE	Sucrose-phosphate synthase	MAIZE
64	Q7XZQ2_MAIZE	UDP-glucose-4-epimerase	MAIZE

69	B6TXJ8_MAIZE	glycoside hydrolase, family 28	MAIZE
98	B6TA79_MAIZE	Cell division control protein 2	MAIZE
115	B6UD26_MAIZE	O-methyltransferase ZRP4	MAIZE
131	GLGL1_MAIZE	glucose-1-phosphate adenylyltransferase large subunit 1	MAIZE
144	B6SIF5_MAIZE	translationally-controlled tumor protein	MAIZE
145	B6SIF5_MAIZE	translationally-controlled tumor protein	MAIZE

**Posttranslational modification, protein turnover, chaperones (O)**

4	Q41815_MAIZE	Heat shock protein 26	MAIZE
6	C6F1K2_ORYSJ	Heat shock protein 70	Oryza sativa subsp. japonica
9	B6TLK8_MAIZE	17.4 kDa class I heat shock protein 3	MAIZE
16	Q9S822_MAIZE	Heat shock protein 101	MAIZE
21	C0P5U8_MAIZE	Glutathione S-transferase	MAIZE
24	B6TSQ9_MAIZE	Aspartic proteinase oryzasin-1	MAIZE
28	B6SJE9_MAIZE	17.5 kDa class II heat shock protein	MAIZE
31	K7V5N4_MAIZE	PREDICTED: aspartic proteinase nepenthesin-1-like	MAIZE
35	B8A3K0_MAIZE	GST6 protein	MAIZE
51	B4F9E8_MAIZE	class II heat shock protein	MAIZE
57	A0A096TAP2_MAIZE	Uncharacterized protein	MAIZE
58	K7VD78_MAIZE	Putative chaperone clbp family protein	MAIZE
60	B4FRD1_MAIZE	Adaptin ear-binding coat-associated protein 1	MAIZE
61	B6THJ5_MAIZE	Phosphosulfolactate synthase-related protein	MAIZE
62	Q41886_MAIZE	27kDa storage protein, zein	MAIZE
82	B6SV64_MAIZE	Heat shock 70 kDa protein 4	MAIZE
99	A0A096QRB1_MAIZE	26S protease regulatory subunit 4 homolog	MAIZE
100	X4Z319_9POAL	Hsp70	Saccharum hybrid cultivar
103	B4F848_MAIZE	Chaperonin	MAIZE
109	A0A096QQ54_MAIZE	Uncharacterized protein	MAIZE
120	B4FNW7_MAIZE	activator of 90 kDa heat shock protein ATPase	MAIZE
130	B6THN2_MAIZE	ruBisCO large subunit-binding protein subunit beta	MAIZE
141	C0PFK3_MAIZE	proteasome subunit alpha type	MAIZE
143	Q9SM20_MAIZE	glutathione transferase III(b)	MAIZE

**Inorganic ion transport and metabolism (P)**

45	B6TFC2_MAIZE	Selenium-binding protein	MAIZE
119	Q9XFZ3_ORYSJ	cytosolic monodehydroascorbate reductase	Oryza sativa subsp. japonica (Rice)

**Secondary metabolites biosynthesis, transport, and catabolism (Q)**

17	B6UGU4_MAIZE	Steroleosin	MAIZE
25	B6SSB8_MAIZE	Transposon protein	MAIZE
59	B6UHC9_MAIZE	Putative uncharacterized protein	MAIZE
91	B4FU39_MAIZE	Uncharacterized protein	MAIZE
112	A0A096RS97_MAIZE	Uncharacterized protein	MAIZE
134	B6TF99_MAIZE	gibberellin 20 oxidase 2	MAIZE
138	B6U607_MAIZE	carbonyl reductase 1	MAIZE

**General function prediction only (R)**

68	B6TRW7_MAIZE	Sigma factor sigB regulation protein rsbQ	MAIZE
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**Signal transduction mechanisms(T)**

46	B6TII3_MAIZE	ADP-ribosylation factor GTPase-activating protein 3	MAIZE
70	B6TA85_MAIZE	Protein binding protein	MAIZE
89	Q32SG1_MAIZE	Protein phosphatase 2A regulatory subunit B'	MAIZE
92	K7UYP8_MAIZE	Basic endochitinase A	MAIZE
127	A0A096TB53_MAIZE	USP family protein	MAIZE

**Intracellular trafficking, secretion, and vesicular transport (U)**

33	B6UGN9_MAIZE	Oleosin	MAIZE
41	B6TTP4_MAIZE	Stress-inducible membrane pore protein	MAIZE
47	B6TKN6_MAIZE	Nonspecific lipid-transfer protein	MAIZE
74	A0A096QF11_MAIZE	Uncharacterized protein	MAIZE
75	M8CBN1_AEGTA	Importin-4	Aegilops tauschii
76	Q10EF5_ORYSJ	HEAT repeat family protein, expressed	Oryza sativa subsp. Japonica
80	B4FSU1_MAIZE	Transmembrane emp24 domain-containing protein 10	MAIZE
87	K7TNE7_MAIZE	Uncharacterized protein	MAIZE
90	B4FBP3_MAIZE	Signal recognition particle subunit SRP68	MAIZE
95	B9RET0_RICCO	Protein transport protein Sec24C	Sorghum bicolor
108	B4FTE1_MAIZE	Signal peptidase complex subunit 2	MAIZE

**Nuclear structure (Y)**

142	B4FWD0_MAIZE	minor allergen Alt a 7	MAIZE
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**Cytoskeleton (Z)**

132	X1X262_ACYPI	actin related protein 1	Acyrtosiphon pisum
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**Function unknown (S)**

1	A3KLI1_MAIZE	RAB17 protein	MAIZE
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2	B6SI37_MAIZE	Embryonic abundant protein	MAIZE
3	GLB1_MAIZE	Globulin-1 S allele	MAIZE
7	B8QY31_ZEAMP	Zeamatin-like protein	ZEAMP
8	B6SLF6_MAIZE	Antimicrobial peptide MBP-1	MAIZE
10	B6T8E4_MAIZE	Embryonic abundant protein 1	MAIZE
11	B6SQM6_MAIZE	Pathogenesis protein 10	MAIZE
12	K7W272_MAIZE	PREDICTED: globulin-1 S allele-like	MAIZE
14	A0A096TN72_MAIZE	PREDICTED: embryonic protein DC-8-like	MAIZE
15	A0A059PZ24_9POAL	Caleosin	Saccharum hybrid cultivar R570
18	B6UGS5_MAIZE	Putative uncharacterized protein	MAIZE
19	B4FFZ9_MAIZE	Lipoprotein	MAIZE
22	B6SK46_MAIZE	Cupin family protein	MAIZE
26	K7WCU4_MAIZE	Uncharacterized protein	MAIZE
27	Q94J20_ORYSJ	Lipoprotein-like	Oryza sativa subsp. Japonica
29	Q19VG6_MAIZE	Major latex protein 22	MAIZE
37	A0A096RTN1_MAIZE	PREDICTED: pathogenesis-related protein 1-like	MAIZE
40	B6SGN7_MAIZE	Embryonic protein DC-8	MAIZE
43	B6UDH8_MAIZE	Putative uncharacterized protein	MAIZE
48	B6TF92_MAIZE	Stress responsive protein	MAIZE
50	B8A0H4_MAIZE	Uncharacterized protein	MAIZE
56	C0HFQ1_MAIZE	Uncharacterized protein	MAIZE
63	A0A096TH62_MAIZE	Uncharacterized protein	MAIZE
65	A0A096QKY4_MAIZE	Uncharacterized protein	MAIZE
78	B4F922_MAIZE	Acyltransferase	MAIZE
79	B6U8P6_MAIZE	ABA-responsive protein	MAIZE
83	B4G1G1_MAIZE	Desiccation-related protein PCC13-62	MAIZE
85	A0A0A7LS12_SETIT	Up-frame shift 3 factor	Setaria italica
88	B4G1B0_MAIZE	Remorin	MAIZE
94	B4F957_MAIZE	pro-resilin	MAIZE
102	B6SMY5_MAIZE	Putative uncharacterized protein	MAIZE
105	B6T6D7_MAIZE	MIR-interacting saposin-like protein	MAIZE
123	C4J9Y2_MAIZE	uncharacterized protein LOC100502283	MAIZE
137	B8A230_MAIZE	unknown	MAIZE
148	ITRF_MAIZE	trypsin/factor XIIIa inhibitor	MAIZE

**Supplementary Table S5: KEGG pathway enrichment of identified DEPS.**

Pathway	Seqs in Pathway	Enzyme	Ezyme ID	Seqs of Enzyme	Seqs
Chloroalkane and chloroalkene degradation	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Phenylpropanoid biosynthesis	1	dehydrogenase	ec:1.1.1.19 5	1	tr B4FU39 B4FU39_MAIZE
Glycolysis / Gluconeogenesis	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Arginine and proline metabolism	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Methane metabolism	1	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Fatty acid degradation	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Streptomycin biosynthesis	1	phosphatase	ec:3.1.3.25	1	tr B6SMK8 B6SMK8_MAIZE
Purine metabolism	1	adenylpyrophosphatase	ec:3.6.1.3	1	tr Q6R987 Q6R987_MAIZE
Purine metabolism	1	phosphatase	ec:3.6.1.15	1	tr Q6R987 Q6R987_MAIZE
Steroid biosynthesis	1	24-C-methyltransferase	ec:2.1.1.41	1	tr P93852 P93852_MAIZE
Limonene and pinene degradation	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
T cell receptor signaling pathway	1	phosphatase	ec:3.1.3.16	1	tr K7V5M7 K7V5M7_MAIZE
Tryptophan metabolism	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Arginine biosynthesis	1	acid amidohydrolase	ec:3.5.1.14	1	tr C0PF66 C0PF66_MAIZE
Valine, leucine and isoleucine degradation	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Thiamine metabolism	1	phosphatase	ec:3.6.1.15	1	tr Q6R987 Q6R987_MAIZE
beta-Alanine metabolism	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Glyoxylate and dicarboxylate metabolism	1	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Lysine degradation	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Ascorbate and aldarate metabolism	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Citrate cycle (TCA cycle)	1	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Phosphatidylinositol signaling system	1	phosphatase	ec:3.1.3.25	1	tr B6SMK8 B6SMK8_MAIZE
Inositol phosphate metabolism	1	phosphatase	ec:3.1.3.25	1	tr B6SMK8 B6SMK8_MAIZE
Glycerolipid metabolism	1	dehydrogenase (NAD <sup>+</sup> )	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Cysteine and methionine metabolism	1	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Carbon fixation pathways in prokaryotes	1	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE



Aminobenzoate degradation	2	nitrophenyl phosphatase	ec:3.1.3.41	2	tr B6SMK8 B6SMK8_MAIZE, tr K7V5M7 K7V5M7_MAIZE
Pentose and glucuronate interconversions	2	dehydrogenase (NAD+)	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Pentose and glucuronate interconversions	2	pectin depolymerase	ec:3.2.1.15	1	tr B6TXJ8 B6TXJ8_MAIZE
Carbon fixation in photosynthetic organisms	2	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Carbon fixation in photosynthetic organisms	2	dehydrogenase (decarboxylating)	ec:1.1.1.39	1	tr Q5G1U0 Q5G1U0_MAIZE
Glutathione metabolism	2	transferase	ec:2.5.1.18	2	tr B8A3K0 B8A3K0_MAIZE, tr C0P5U8 C0P5U8_MAIZE
Drug metabolism - cytochrome P450	2	transferase	ec:2.5.1.18	2	tr B8A3K0 B8A3K0_MAIZE, tr C0P5U8 C0P5U8_MAIZE
Histidine metabolism	2	histidinol phosphate phosphatase	ec:3.1.3.15	1	tr B6SMK8 B6SMK8_MAIZE
Histidine metabolism	2	dehydrogenase (NAD+)	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Metabolism of xenobiotics by cytochrome P450	2	transferase	ec:2.5.1.18	2	tr B8A3K0 B8A3K0_MAIZE, tr C0P5U8 C0P5U8_MAIZE
Galactose metabolism	2	4-epimerase	ec:5.1.3.2	1	tr Q7XZQ2 Q7XZQ2_MAIZE
Galactose metabolism	2	invertase	ec:3.2.1.26	1	tr Q9ZTQ4 Q9ZTQ4_MAIZE
Starch and sucrose metabolism	2	invertase	ec:3.2.1.26	1	tr Q9ZTQ4 Q9ZTQ4_MAIZE
Starch and sucrose metabolism	2	alpha-glucosidase	ec:3.2.1.48	1	tr Q9ZTQ4 Q9ZTQ4_MAIZE
Starch and sucrose metabolism	2	pectin depolymerase	ec:3.2.1.15	1	tr B6TXJ8 B6TXJ8_MAIZE
Pyruvate metabolism	3	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Pyruvate metabolism	3	dehydrogenase (decarboxylating)	ec:1.1.1.39	1	tr Q5G1U0 Q5G1U0_MAIZE
Pyruvate metabolism	3	dehydrogenase oxaloacetate-decarboxylating	ec:1.1.1.38	1	tr Q5G1U0 Q5G1U0_MAIZE
Pyruvate metabolism	3	dehydrogenase (NAD+)	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Amino sugar and nucleotide sugar metabolism	4	4-epimerase	ec:5.1.3.2	1	tr Q7XZQ2 Q7XZQ2_MAIZE
Amino sugar and nucleotide sugar metabolism	4	chitodextrinase	ec:3.2.1.14	3	tr B4G1C2 B4G1C2_MAIZE, tr C0P451 C0P451_MAIZE
Biosynthesis of antibiotics	5	dehydrogenase	ec:1.1.1.37	1	tr E9NQE3 E9NQE3_MAIZE
Biosynthesis of antibiotics	5	phosphatase	ec:3.1.3.25	1	tr B6SMK8 B6SMK8_MAIZE
Biosynthesis of antibiotics	5	24-C-methyltransferase	ec:2.1.1.41	1	tr P93852 P93852_MAIZE
Biosynthesis of antibiotics	5	dehydrogenase (NAD+)	ec:1.2.1.3	1	tr Q8S532 Q8S532_MAIZE
Biosynthesis of antibiotics	5	acid amidohydrolase	ec:3.5.1.14	1	tr C0PF66 C0PF66_MAIZE

**Supplementary Table S6: Primers used in qRT-PCR**

<b>Protein No.</b>	<b>Primer pairs (5'--3')</b>
1	F: 5'-ACCAGTACGGCAACCCAGTC-3' R: 5'-TTAAACACGAAACCCACGGA-3'
2	F: 5'-TACAGCGAGATGGGGAAGAA-3' R: 5'-CGTGAAACAGGCTACCAAACACTAC-3'
3	F: 5'-CGTTCGTTCAAGATCGCCTAC-3' R: 5'-CACCTTCTCGTTCCTGTCGG-3'
4	F: 5'-CGCAGGAGAACAGGGACAA-3' R: 5'-GGCGACATCGGGTCAACTA-3'
5	F: 5'-ACAAGAAGCCGACCCATTCC-3' R: 5'-TCCTCGACTTTTGCCCACC-3'
6	F: 5'-GCGAGCGAATCAGAAGAGCA-3' R: 5'-TCAAAGACGGTGTGGTGGG-3'
7	F: 5'-ACTTCTTCGACATCTCCCTCATC-3' R: 5'-TGCTGGTGGCGTCATCCTT-3'
8	F: 5'-GCCATCTCCTCACCCTCGTT-3' R: 5'-CCTTTCCGTACTGCCACTCG-3'
9	F: 5'-GCCAAGAAGCCTGAAGTGAAG-3' R: 5'-AAGTAGACCCAACATACGCAAAG-3'
10	F: 5'-AGGAAAGCAGGGAGGAGCTG-3' R: 5'-GGACTTGGTCCTGAACTTGGA-3'
11	F: 5'-TGCGTCGCCAAGGTCAA-3' R: 5'-CCAATCACAACGTCGGTCT-3'
12	F: 5'-AACTTTGAGCAGGGGAGCAT-3' R: 5'-GCGGTGTCTTGGCAGACTTG-3'
13	F: 5'-GACACGAACTCAGGTCCTCACC-3' R: 5'-CCGCCAAAATGATAGCAGAT-3'
14	F: 5'-CACTAGCGTCGAGCCATTACA-3' R: 5'-TCTCCTGATACGGGACCACAG-3'
15	F: 5'-GACCTCTACGGCTGGATTGC-3' R: 5'-GTTCACTTGGCTTCCATTTTCAT-3'
16	F: 5'-TGAGACGGGGATGAAGTCG-3' R: 5'-ACAAACAGCAGCGTTACAAGAA-3'

17 F: 5'- GCGTCCATCTGGCAAGTGT-3'  
R: 5'- TCCATCCTCAGGGTGTGTA-3'  
F: 5'- CTTGTCTATTGCCCTTCGGAGTT-3'  
86 R: 5'- CCGCCAAGATTGATGCTAAAA-3'  
F: 5'- CCTCACTACAGGGAACAGCG-3'  
87 R: 5'- CTTGAAGATGATGGAAGTATGGG-3'  
F: 5'- ACACCGAGCAGAAAGTGAGAAAC-3'  
88 R: 5'- TGTCAACAACAACGAAAACAACAG-3'  
F: 5'- GCCGCTTCAGCATTTCG-3'  
89 R: 5'- GCCTCTTTATCTCCTTCTCCTTTAT-3'  
F: 5'- GTACAAACGCAAAACAACGC-3'  
90 R: 5'- CAATCATAGGCTCCACTTCG-3'  
F: 5'- CCCCGTTCCATTTCAATTATCC-3'  
91 R: 5'- CGTGACATCGTCGTCTTTAGG-3'  
F: 5'- ATCGGCTACGGGAGCAATCT-3'  
92 R: 5'- TTCAAACCGACGAAGCAACAC-3'  
F: 5'- TCTCGCAGAAGCAGAAGTCG-3'  
93 R: 5'- CAGCAAATGTCCATACAAACCA-3'  
F: 5'- GGCGGACGACTTCGATGAGT-3'  
94 R: 5'- CGAGCACGGGTAGCAGGTTT-3'  
F: 5'- TCTACTGGCGGAAACTTCTTG-3'  
95 R: 5'- CCACCTGTAGTCTGAGGCACAA-3'  
F: 5'- ATCAGCACTACCGGAAGGAAC-3'  
96 R: 5'- GCATCATAGTCGGGAGTCAGC-3'  
F: 5'- CCAGCGTGCTGTCCTCAAGT-3'  
97 R: 5'- AAGGCAATGGTCGGGATGTT-3'  
F: 5'- TGGTCTGTGGGCTGTATCTTTG-3'  
98 R: 5'- TCTTTTGCTTGGCTCGTATCG-3'  
F: 5'- TGTGGCTAACTCAACATCTGCG-3'  
99 R: 5'- CCAACAGCGTCAATCTCATCAATAA-3'  
F: 5'- GTTCAGGGGACAACAAACCTTATG-3'  
100 R: 5'- AACCAGCCTACAGCGGAGAAA-3'  
F: 5'- AATACCGATACCTGTCAGATTCCA-3'  
101 R: 5'- GTGTTCAAGCAGTGCGTCCA-3'

102 F: 5'- GACGAGGCCGAGAAGGAGAT-3'  
R: 5'- TGA CTGACGAAAGGAACTAATACG-3'

103 F: 5'- CTCTGGGAGATAGGGTGCTTGT-3'  
R: 5'- ATTTTCTTGTCCCCGATGGTC-3'

104 F: 5'- CTAGCTGACCAATTCGACACGA-3'  
R: 5'- AGGAGGAGCAAGACGAGGGA-3'

105 F: 5'- CATCTGTAAAACGACCACCCC-3'  
R: 5'- ATGACCTTCCCCTCCCTCTG-3'

106 F: 5'- TCCTTTTCCTTTCATAAACCCC-3'  
R: 5'- TCACCCTCGCTTCAGTAACCT-3'

107 F: 5'- AGCTATCCAGTGGAGACGAAGAT-3'  
R: 5'- CTGCGACGACAGGTAGAAGG-3'

108 F: 5'- AAAGGAAGGAGTTCTTGTGGAGG -3'  
R: 5'- GTTTCTAGGATTCGGACGGATAGT-3'

109 F: 5'- ATTTTATGCCAGCGAGAAGTATCC-3'  
R: 5'- CATCCTCCAGCCATCAGACAAC-3'

110 F: 5'- CATCCTCCAGCCATCAGACAAC-3'  
R: 5'- AGACACCATCACCAGTCCAAGC-3'

111 F: 5'- TTTTAGATGTGGGCTGTGGAATAG-3'  
R: 5'- TCTCCTTGTAGCAACCAACTGGA-3'

112 F: 5'- GTCCTCAACGTCAACCACTACC-3'  
R: 5'- TCAACGCTCTTCAGCAATCC-3'

113 F: 5'- GCCTCCGTTCTCGTCAATG-3'  
R: 5'- TCCAAGCCGTTCCAGTTGC-3'

114 F: 5'- CCAGTCGCCCAACTCCTTCT-3'  
R: 5'- TCAGTGAGCCTTGCCTTTCCT-3'

115 F: 5'-GGGAGTTCAGGGACTTGTTTCG-3'  
R: 5'- GGTGGCAATGATCTTGGGAG-3'

116 F: 5'-TCTTCGCCGAGCAGTTTATC-3'  
R: 5'- TTCGCCACTTGTTCCATAACC-3'

117 F: 5'- GGTGTCCACTCCCGTCTTGA-3'  
R: 5'- TTGAATTTGTAGGGTGCTTCTCC-3'

118 F: 5'- CATCTCGGGACCAACTAACCAA-3'  
R: 5'- ACACCTGTGAACCCAGCGTATT-3'

119 F: 5'- CAAGTTCGGCTCGTACTGGATT-3'  
R: 5'- GAACCTTCACGATGACACGGA-3'

120 F: 5'- CAGGAAGGAAA ACTGATTGCG-3'

R: 5'- AACTGGGTGAGAAACATGGATTG-3'  
121 F: 5'- AGGAGAACATGGCAAGAAAAGC-3'  
R: 5'- TGTCGAAATTCTGACCAGCAAC-3'  
122 F: 5'-GGCTGGTGCTGAGTATGTCGTG-3'  
R: 5'- TGAGGGTCCATCAACAGTCTTCT-3'  
123 F: 5'- CTACGAGAACCCCAAGCACAA-3'  
R: 5'- GCCACTATGTTACACCACCATCC-3'  
124 F: 5'- CTACGAGAACCCCAAGCACAA-3'  
R: 5'- GCCACTATGTTACACCACCATCC-3'  
125 F: 5'- CCTGGGTCATTCTTGGACACTC-3'  
R: 5'- CCAATAGCCCAAACCTGGTTCATA-3'  
126 F: 5'- TCCGTGACACCATCGACCTC-3'  
R: 5'- GGCAACTTCTTCGGCTTCCT-3'  
127 F: 5'- TCAAGGAGCCCGACTACGAG-3'  
R: 5'- CAGGATGTCCAAGGTTTCTATGTC-3'

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