

**Table S2. The DAPs and functional classification identified in the Yangmai 5-Haynaldia villosa 6VS/6AL translocation line by MALDI-TOF/TOF-MS**

Spot ID	Accession No.	Protein Name	Specis	KOG number	Protein MW/PI	Protein Score	p-value	Subcellular location prediction
<b>Stress/defense</b>								
2	EMT27039	Non-specific lipid-transfer protein	<i>A. tauschii</i>	NA	12.35/8.23	122	0.018	Extr
7	AAP80655	Formate dehydrogenase	<i>T. aestivum</i>	KOG0069	28.67/8.72	198	0.021	Cyto*
11	AAD22629	Heat shock protein 101	<i>T. aestivum</i>	KOG1051	101.23/5.75	738	0.032	Cyto
13	EMS47713	Basic endochitinase C	<i>T. urartu</i>	KOG4742	28.56/8.78	129	0.031	Vacu
14	EMS55427	ATP-dependent zinc metalloprotease FTSH 2	<i>T. urartu</i>	KOG0731	71.68/5.76	154	0.013	Chlo
15	I6QF63	Small heat shock protein	<i>T. aestivum</i>	KOG0710	18.34/5.76	143	0.014	Cyto
16	AAD22629	Heat shock protein 101	<i>T. aestivum</i>	KOG1051	101.23/5.57	921	0.042	Cyto
22	AAX83263	class II chitinase	<i>T. aestivum</i>	KOG4742	28.15/8.45	136	0.013	Vacu
23	EMT15199	Isocitrate dehydrogenase	<i>A. tauschii</i>	KOG1526	46.23/5.78	325	0.042	Chlo*
28	EMT10403	Betaine aldehyde dehydrogenase 1	<i>A. tauschii</i>	KOG2450	55.13/5.76	114	0.012	Chlo
29	P93692	Serpin-Z2B	<i>T. aestivum</i>	KOG2392	42.77/5.45	145	0.032	Mito
30	ACN59483	Serpin 1	<i>T. aestivum</i>	KOG2392	43.23/5.65	478	0.015	Mito
35	EMS46550	Putative NADP-dependent oxidoreductase P1	<i>T. urartu</i>	KOG1196	38.23-8/5.64	197	0.026	Cyto
36	ADJ67792	Peroxidase 1	<i>T. aestivum</i>	NA	38.43/8.78	335	0.031	Extr
37	AAM34280	Translationally controlled tumor protein	<i>T. aestivum</i>	KOG1727	18.76/4.83	267	0.024	Cyto*
38	EMS46317	Alanine aminotransferase 2	<i>T. urartu</i>	KOG0258	57.43/6.86	312	0.037	Chlo
41	W5AEN0	Proteasome subunit alpha type	<i>T. aestivum</i>	KOG0183	27.22/6.65	109	0.015	Cyto
42	AAM15877	Thaumatococcus-like protein	<i>T. aestivum</i>	NA	24.77/7.45	334	0.017	Chlo
43	AAD56395	Glutathione S-transferase	<i>T. aestivum</i>	KOG0867	23.56/5.54	205	0.035	Cyto
44	ABO70341	Pm3b-like disease resistance protein 15Q1	<i>T. aestivum</i>	KOG4658	59.12/6.34	148	0.045	Cyto
47	ADJ67792	Peroxidase 1	<i>T. aestivum</i>	NA	39.44/8.21	335	0.037	Extr
52	EMT23015	Alanine aminotransferase 2	<i>A. tauschii</i>	KOG0258	56.56/6.32	745	0.016	Cyto
54	EMT23015	Alanine aminotransferase 2	<i>A. tauschii</i>	KOG0258	56.33/6.21	253	0.041	Cyto
57	AAX83263	Class II chitinase	<i>T. aestivum</i>	KOG4742	28.34/8.54	136	0.027	Vacu
58	CAD19440	Chymotrypsin inhibitor WCI	<i>T. aestivum</i>	NA	12.78/7.34	126	0.024	ER

60	AAL05264	Betaine-aldehyde dehydrogenase	<i>T. aestivum</i>	KOG2450	54.56/5.74	437	0.013	Chlo*
62	I6QF63	Small heat shock protein	<i>T. aestivum</i>	KOG0710	16.76/6.15	184	0.043	Cyto
64	BAC41494	Cold regulated protein	<i>T. aestivum</i>	NA	17.67/4.75	212	0.015	Cyto
69	EMT14862	Stromal 70 kDa heat shock-related protein	<i>A. tauschii</i>	KOG0102	73.16/5.35	212	0.042	Cyto
70	A0A1D5UM70	Isocitrate dehydrogenase	<i>T.aestivum</i>	KOG1526	48.23/6.54	478	0.022	Chlo
72	ABO70341	Pm3b-like disease resistance protein 15Q1	<i>T. aestivum</i>	KOG4658	59.34/6.56	267	0.013	Cyto
73	AAV39517	0.19 dimeric alpha-amylase inhibitor	<i>T. aestivum</i>	NA	13.32/5.77	784	0.032	Chlo
75	Q4U0C9	Stress responsive protein	<i>T. aestivum</i>	NA	39.21/6.32	294	0.012	Cyto
76	EMS46390	Serpin-Z2B	<i>T. urartu</i>	KOG2392	45.25/6.12	389	0.023	Chlo
78	P42755	Em protein H5	<i>T. aestivum</i>	NA	10.45/5.98	178	0.047	Nucl
79	Q4U0C9	Stress responsive protein	<i>T. aestivum</i>	NA	42.23/6.42	548	0.013	Cyto
80	AAR10959	Alpha amylase inhibitor protein	<i>T. aestivum</i>	NA	18.33/7.53	286	0.045	Chlo*
82	ADJ67792	Peroxidase 1	<i>T. aestivum</i>	NA	39.31/8.35	226	0.026	Extr
88	CBM38934	Small heat shock protein	<i>T. aestivum</i>	KOG0710	27.42/5.76	638	0.031	Cyto
90	CAA60505	Peptidylprolyl isomerase	<i>T.aestivum</i>	KOG0543	62.33/5.36	175	0.011	Memb
100	A0A0H4TIG5	chitinase	<i>T. aestivum</i>	KOG4742	33.12/7.42	114	0.012	Vacu
103	R7W001	1-Cys peroxiredoxin PER1	<i>A. tauschii</i>	KOG0854	24.09/6.23	568	0.013	Cyto
104	M8AI06	Disease resistance protein RPP8	<i>T. urartu</i>	KOG4658	78.25/8.67	146	0.011	Cyto
106	N1QR17	Aldose reductase	<i>A. tauschii</i>	KOG1577	35.13/6.44	434	0.022	Cyto

### Energy metabolism

1	EMT22217	Dihydrolipoyl dehydrogenase 1	<i>A. tauschii</i>	KOG1335	58.35/7.57	792	0.036	Mito
17	EMT25675	Pyrophosphate--fructose 6-phosphate 1-Phosphotransferase subunit beta	<i>A. tauschii</i>	KOG2440	60.75/5.87	225	0.035	Mito
21	A0A1D5TTT2	Glyceraldehyde 3-phosphate dehydrogenase	<i>T.aestivum</i>	KOG0657	18.22/6.43	278	0.013	Mito
27	EMT22217	Dihydrolipoyl dehydrogenase 1	<i>A. tauschii</i>	KOG1335	58.75/7.31	792	0.035	Mito
46	P26517	Glyceraldehyde-3-phosphate dehydrogenase 1	<i>T.aestivum</i>	KOG0657	39.35/6.66	976	0.017	Cyto
53	AGH20063	Enolase	<i>T. aestivum</i>	KOG2670	48.12/5.44	368	0.015	Cyto
71	ABQ81648	Glyceraldehyde-3-phosphate dehydrogenase	<i>T. aestivum</i>	KOG0657	36.55/7.24	195	0.032	Cyto
74	CAA52636	ATP synthase beta subunit	<i>T. aestivum</i>	KOG1350	59.54/5.75	547	0.028	Mito
84	EMS58841	Fructose-bisphosphate aldolase cytoplasmic	<i>T. urartu</i>	KOG1557	38.24/6.64	315	0.017	Cyto

94	Q7XYD2	Phosphoglycerate mutase	<i>T. aestivum</i>	KOG4513	129.77/5.21	276	0.015	Cyto
96	Q8VWM9	Putative fructose 1-,6-biphosphate aldolase	<i>T. aestivum</i>	KOG1557	29.86/8.56	146	0.025	Chlo
107	Q8VX48	Phosphoglucomutase	<i>T. aestivum</i>	KOG0625	62.86/5.57	478	0.027	Cyto
<b>Carbon metabolism</b>								
18	CBH32516	Alpha-1,4 glucan phosphorylase	<i>T. aestivum</i>	KOG2099	93.67 /7.54	612	0.043	Cyto
34	CAZ76054	Glyceraldehyde-3-phosphate dehydrogenase	<i>T. aestivum</i>	KOG0657	36.57/7.47	273	0.031	Cyto
77	AAM13693	Endoglucanase	<i>T. aestivum</i>	NA	35.43/8.22	244	0.018	Wall
<b>Starch metabolism</b>								
3	EMS65561	Sucrose synthase 2	<i>T. urartu</i>	KOG0853	93.54/6.12	437	0.015	Cyto
6	ABG88200	ADP-glucose pyrophosphorylase large subunit	<i>T. aestivum</i>	KOG1322	57.67/6.33	758	0.037	Chlo
93	Q7XJA9	ADP-glucose pyrophosphorylase large subunit	<i>T. aestivum</i>	KOG1322	58.24/5.66	479	0.047	Chlo
<b>Nitrogen metabolism</b>								
9	CBM36829	Pyruvate decarboxylase isozyme 2	<i>T. urartu</i>	KOG1184	65.26/5.53	268	0.027	Cyto
24	EMT31101	5-methyltetrahydropteroyltriglutamate--	<i>A. tauschii</i>	KOG2263	84.43/5.77	1213	0.024	Cyto
26	M7YTL8	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	<i>T. aestivum</i>	KOG2263	84.11/6.21	325	0.033	Chlo
45	CBM36829	Pyruvate decarboxylase isozyme 2	<i>T. urartu</i>	KOG1184	65.77/5.53	179	0.013	Cyto
49	EMT07372	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	<i>A. tauschii</i>	KOG2263	84.79/5.82	1215	0.042	Cyto
50	CBM36829	Pyruvate decarboxylase isozyme 2	<i>T. urartu</i>	KOG1184	65.47/5.43	317	0.025	Cyto
59	CBD28063	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	<i>T.aestivum</i>	KOG2263	84.22/5.78	466	0.027	Chlo
<b>Protein metabolism/Folding</b>								
8	I6QF63	Small heat shock protein	<i>T. aestivum</i>	KOG0710	17.53/6.23	225	0.013	Cyto
10	CBM37261	26S protease regulatory subunit 6B-like protein	<i>A. tauschii</i>	KOG0727	46.69/5.77	178	0.017	Cyto
40	EMT08036	Lactoylglutathione lyase	<i>A. tauschii</i>	KOG2943	32.67/5.33	385	0.016	Cyto
87	EMS63121	2-isopropylmalate synthase A	<i>T. urartu</i>	KOG2367	56.46/5.55	259	0.027	Chlo
<b>Storage protein</b>								
4	ACJ65514	Globulin 3	<i>T. aestivum</i>	NA	66.43/7.68	482	0.015	Vacu
12	ACJ65513	Globulin 3C	<i>T. aestivum</i>	NA	38.33/9.12	215	0.024	Vacu

20	ACJ03482	Gamma-gliadin	<i>T. aestivum</i>	NA	33.22/8.54	134	0.036	Extr
25	EMS66832	Globulin-1 S allele	<i>T. urartu</i>	NA	57.24/9.22	436	0.032	Vacu
31	EMT26971	12S seed storage globulin 1	<i>A. tauschii</i>	NA	62.56/6.35	821	0.024	Nucl
32	CAJ32654	Avenin-like a1	<i>T. aestivum</i>	NA	19.34/8.53	158	0.016	Extr
33	ACJ03423	Gamma-gliadin	<i>A. tauschii</i>	NA	16.11/8.79	138	0.013	Vacu
39	AFM30909	Globulin-3A	<i>T. aestivum</i>	NA	66.53/8.65	537	0.044	Vacu
51	AFM30909	Globulin-3A	<i>T. aestivum</i>	NA	66.42/8.25	759	0.042	Vacu
55	EMS62417	Globulin-1 S allele	<i>T. urartu</i>	NA	55.24/7.79	217	0.028	Vacu
56	CAJ32654	Avenin-like a1	<i>T. aestivum</i>	NA	18.22/8.35	109	0.018	Vacu
61	EMS62417	Globulin-1 S allele	<i>T. urartu</i>	NA	55.23/7.57	417	0.032	Vacu
63	EMS66832	Globulin-1 S allele	<i>T. urartu</i>	NA	56.78/9.23	538	0.017	Vacu
67	ACJ65513	Globulin 3C	<i>T. aestivum</i>	NA	38.57/9.23	147	0.014	Vacu
81	AFM30909	Globulin-3A	<i>T. aestivum</i>	NA	66.43/8.58	538	0.016	Vacu
83	EMS62417	Globulin-1 S allele	<i>T. urartu</i>	NA	55.24/7.57	766	0.014	Vacu
86	ACJ65514	Globulin 3	<i>T. aestivum</i>	NA	66.24/7.84	128	0.043	Vacu
89	EMS66832	Globulin-1 S allele	<i>T. urartu</i>	NA	57.64/9.22	357	0.024	Vacu
91	M8A380	Globulin-1 S allele	<i>T. urartu</i>	NA	57.21/9.56	356	0.016	Vacu
92	B6UKQ8	Gamma-gliadin	<i>T. aestivum</i>	NA	33.25/8.67	128	0.014	Extr
95	M8BY97	Small ubiquitin-related modifier	<i>A. tauschii</i>	KOG1769	12.64/5.78	147	0.036	Mito
101	B7U6L3	Globulin 3C	<i>T. aestivum</i>	NA	38.23/9.21	215	0.024	Vacu
102	M8A380	Globulin-1 S allele	<i>T. urartu</i>	NA	57.32/9.54	357	0.032	Vacu
105	M7YTL8	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	<i>T. urartu</i>	KOG2263	81.76/6.44	837	0.045	Chlo
<b>Photosynthesis</b>								
48	BAB19812	Ribulose biphosphate carboxylase small chain	<i>T. aestivum</i>	NA	19.32/8.67	288	0.017	Chlo
<b>Nucleic acid metabolism</b>								
65	A0A3B6SPW8	Replication factor C subunit 1	<i>T. aestivum</i>	KOG1968	22.24/8.87	238	0.032	Nucl
66	EMT24359	Uridine 5'-monophosphate synthase	<i>A. tauschii</i>	KOG1377	45.45/7.17	187	0.026	Chlo
<b>Others</b>								
5	CBD23646	Unnamed protein product	<i>T. aestivum</i>	KOG2240	18.55/8.87	187	0.015	Nucl

19	EMS66582	Hypothetical protein	<i>T. urartu</i>	NA	22.77/8.12	123	0.034	Nucl
68	EMT29398	Hypothetical protein	<i>A. tauschii</i>	NA	15.54/5.87	166	0.017	Cyto
85	EMS50737	Hypothetical protein	<i>T. urartu</i>	NA	126.56/8.21	142	0.014	Mito
97	D9ZLW0	outer membrane channel protein OEP16-2	<i>T. aestivum</i>	NA	17.65/6.67	169	0.025	Nucl
98	Q4W1F9	5a2 protein	<i>T. aestivum</i>	NA	10.32/8.12	138	0.037	Golg
99	A0A1D5XF07	Predicted protein	<i>T. aestivum</i>	NA	39.52/6.43	217	0.025	Chlo

\*Verified by subcellular localization experiments