

**Supplementary**  
**Leaf proteome analysis of wheat-rye translocation lines**

**Supplementary Table 1.** List of identified proteins in leaf of wheat-rye translocation line, and differentially expressed proteins between leaf of non 2RL-Coker797 and 2RL-NIL using MALDI-TOF-TOF MS (SN spot number, Mr mass range, pI iso-electric point, MS mowse score, PM peptide matches, SC sequence coverage).

SN	Accession No.	Protein name	Mr (kDa)/pI	MS	PM	E. value	SC (%)	Source	Possible function
1	gi 34922469	Lipoxygenase 2.1, chloroplast precursor	105.79/5.72	99	18	6.00E-05	18	MS	Lipid metabolic process
				161	4	3.90E-11	6	MS/MS	
2	gi 34922469	Lipoxygenase 2.1, chloroplast precursor	105.79/5.72	79	17	6.30E-03	17	MS	Lipid metabolic process
				171	4	3.90E-12	4	MS/MS	
5	gi 125571778	Hypothetical protein OsJ_003118	111.65/6.5	83	15	7.20E-04	22	MS	Cellular amino acid metabolic process
6	gi 42416979	Glycine dehydrogenase P protein	96.88/6.03	69	11	1.80E-02	19	MS	Cellular amino acid metabolic process
7	gi 125553376	Hypothetical protein OsI_020318	36.18/6.27	65	7	4.00E-02	32	MS	Unknown
9	gi 120564759	Dehydration-induced protein	71.84/7.55	59	11	5.00E-03	22	MS	Stress responsive
10	gi 38347158	Hypothetical protein OSJNBa0039C07.4	98.43/5.79	107	16	2.70E-06	21	MS	Protein metabolic process
11	gi 38347158	Hypothetical protein OSJNBa0039C07.4	98.43/5.79	171	21	1.10E-12	28	MS	Protein metabolic process
				75	3	6.70E-08	5	MS/MS	
16	gi 9082278	Alpha 1,4-glucan phosphorylase; cytosolic starch phosphorylase	93.55/7.27	85	10	1.20E-05	18	MS	Carbohydrate metabolic process
				54	3	1.50E-02	5	MS/MS	
20	gi 168037791	Predicted protein	74.04/6.12	71	7	3.90E-02	14	MS	Transcription
24	gi 115489652	Hypothetical protein Os12g0623900	84.53/5.93	85	14	4.00E-04	25	MS	Cellular amino acid metabolic process
25	gi 50897038	Methionine synthase	84.45/5.68	215	4	1.50E-16	9	MS/MS	Cellular amino acid metabolic process
				39	6	6.70E+01	13	MS	
26	gi 115452177	Hypothetical protein Os03g0271200	87.63/8.5	106	14	3.40E-06	20	MS	Protein transport
				93	4	3.40E-08	7	MS/MS	
42	gi 133872536	Bp2A protein	25.71/5.86	37	5	7.60E-01	28	MS	Carbohydrate metabolic process
				100	4	3.80E-07	22	MS/MS	
44	gi 18076790	Phosphoglucomutase	62.75/5.66	40	7	4.10E-01	16	MS	Carbohydrate metabolic process
				64	3	1.60E-03	7	MS/MS	
46	gi 623204	Nitrite reductase	63.09/6.05	79	3	6.10E-03	6	MS/MS	Transport

51	gi 1430900	ATP A	55.27/5.7	42	8	2.80E+01	11	MS	Transport
				84	14	1.40E-05	32	MS	
				243	4	1.90E-21	8	MS/MS	
52	gi 90990912	Beta-glucosidase	64.46/6.55	56	13	9.50E-03	23	MS	Carbohydrate metabolic process
				84	4	1.60E-05	7	MS/MS	
53	gi 17371040	ATP synthase F1 subunit alpha (ATPase subunit alpha)	55.26/6.11	64	13	1.30E-03	31	MS	Transport
				157	5	7.40E-13	17	MS/MS	
54	gi 17371040	ATP synthase F1 subunit alpha (ATPase subunit alpha)	55.26/6.11	162	22	2.30E-13	42	MS	Transport
				149	4	4.70E-12	11	MS/MS	
55	gi 17371040	ATP synthase F1 subunit alpha (ATPase subunit alpha)	55.26/6.11	101	18	3.00E-07	36	MS	Transport
				140	5	3.70E-11	16	MS/MS	
63	gi 13928213	RuBisCO large subunit	52.81/6.22	91	15	2.80E-06	31	MS	Photosynthesis
				105	3	1.20E-07	7	MS/MS	
66	gi 1170509	Eukaryotic initiation factor 4A (eIF-4A)	46.89/5.31	54	10	1.50E-02	29	MS	Translation
				102	4	2.30E-07	15	MS/MS	
67	gi 125570164	Hypothetical protein OsJ_001504	41.20/5.97	80	9	1.30E-03	37	MS	Metabolism
68	gi 125570164	Hypothetical protein OsJ_001504	41.20/5.97	72	10	7.90E-03	39	MS	Metabolism
74	gi 2832528	R2R3-MYB transcription factor	5.34/9.52	73	4	2.40E-02	71	MS	Transcription
78	gi 37783283	Ribulose-1,5-bisphosphate carboxylase activase	22.32/4.98	65	2	1.10E-03	17	MS/MS	Photosynthesis
				33	6	1.90E+00	36	MS	
80	gi 46806576	Putative ent-kaurene synthase	89.60/5.1	70	11	1.40E-02	19	MS	Response to stimulus
84	gi 13928213	RuBisCO large subunit	52.81/6.22	97	16	7.40E-07	32	MS	Photosynthesis
				55	9	1.30E-02	54	MS	
91	gi 37783283	Ribulose-1,5-bisphosphate carboxylase activase	22.32/4.98	81	3	3.10E-05	21	MS/MS	Photosynthesis
				52	7	2.60E-02	48	MS	
92	gi 37783283	Ribulose-1,5-bisphosphate carboxylase activase	22.32/4.98	55	8	1.10E-02	51	MS	Photosynthesis
94	gi 37783283	Ribulose-1,5-bisphosphate carboxylase activase	22.32/4.98	55	8	1.10E-02	51	MS	Photosynthesis
98	gi 13928213	RuBisCO large subunit	52.81/6.22	95	17	1.20E-06	29	MS	Photosynthesis
				203	5	1.90E-17	8	MS/MS	
100	gi 21811	Heat shock protein 26.6B	26.57/9.4	54	8	1.40E-02	35	MS	Response to stimulus
102	gi 32966580	Ribulose-1,5-bisphosphate carboxylase/oxygenase large	52.75/6.22	54	12	1.70E-02	22	MS	Photosynthesis
108	gi 148508784	Glyceraldehyde-3-phosphate dehydrogenase	36.62/7.08	67	11	7.60E-04	31	MS	Carbohydrate metabolic process
113	gi 123559	Small heat shock protein (Hsp 26.6), chloroplast precursor	26.57/9.64	63	8	2.00E-03	42	MS	Response to stimulus
115	gi 115447073	Hypothetical protein Os01g0501800	55.71/9.13	68	9	2.20E-02	28	MS	Photosynthesis
124	gi 125562856	Hypothetical protein OsI_029468	111.36/6.55	64	14	5.30E-02	15	MS	Protein biosynthesis
128	gi 115484441	Hypothetical protein Os11g0176000	57.31/5.77	72	11	8.30E-03	24	MS	Signal transduction
134	gi 115436780	Hypothetical protein Os01g0501800	34.84/6.1	68	9	2.20E-02	36	MS	Photosynthesis
141	gi 13928217	Cytochrome f	35.31/7.66	50	7	3.80E-02	34	MS	Photosynthesis
146	gi 3915029	Acyl-[acyl-carrier-protein] desaturase, chloroplast	44.45/6.53	64	10	5.70E-02	18	MS	Lipid metabolic process
148	gi 168002894	Hexokinase protein HXK7	56.96/6.84	74	12	1.70E-02	32	MS	Carbohydrate metabolic process
152	gi 3915029	Acyl-[acyl-carrier-protein] desatu rase, chloroplast precursor	44.45/6.53	75	10	4.40E-03	21	MS	Lipid metabolic process
				42	7	2.10E-01	23	MS	
156	gi 1174745	Triosephosphate isomerase, chloroplast precursor (TIM)	31.61/6	76	2	9.50E-05	7	MS/MS	Photosynthesis
				47	9	7.10E-02	36	MS	
166	gi 1657859	Chlorophyll a/b-binding protein WCAB precursor	28.20/5.3	188	2	5.90E-16	9	MS/MS	Photosynthesis
				70	4	4.90E-02	20	MS	
169	gi 168041144	Predicted protein	29.43/10.51	70	4	4.90E-02	20	MS	Translation
170	gi 21837	23kDa oxygen evolving protein of photosystem II	27.25/8.84	240	4	3.70E-21	14	MS/MS	Photosynthesis

				34	7	1.30E+00	25	MS	
171	gi 1658313	Hypothetical protein osr40g2	38.63/7.28	68	8	2.40E-02	25	MS	Unknown
172	gi 86439747	POZ domain protein	30.15/9.87	49	9	4.50E-02	29	MS	Protein modification
174	gi 20067415	Glutathione transferase	24.98/6.35	72	9	2.20E-04	39	MS	Other
				47	2	7.80E-02	9	MS/MS	
175	gi 23237821	Hypothetical protein	6.00/5	65	9	4.00E-02	34	MS	Unknown
178	gi 37719728	Histidine-containing phosphor transfer protein	16.19/4.94	53	6	1.70E-02	35	MS	Response to stimulus
181	gi 125589744	Hypothetical protein OsJ_013577	12.29/9.43	70	6	1.40E-02	41	MS	Unknown
186	gi 25989332	Chitin-inducible gibberellin- responsive protein	64.38/6.22	65	7	4.60E-02	14	MS	Transcription
187	gi 68566191	Cytochrome b6-f complex iron- sulfursubunit, chloroplast	23.71/8.47	42	6	2.30E-01	35	MS	Photosynthesis
				121	3	3.00E-09	14	MS/MS	
189	gi 115481406	Hypothetical protein Os10g0198600	63.87/9.48	64	12	5.50E-02	23	MS	Endonuclease activity
193	gi 32400800	Oxygen-evolving complex precursor	20.10/9.98	290	3	3.70E-26	23	MS/MS	Photosynthesis
				25	4	1.10E+01	23	MS	
195	gi 4038689	Ribulose-1,5-bisphosphate carboxylase/oxygenase small	18.57/8.83	60	9	3.70E-03	50	MS	Photosynthesis
				143	3	1.90E-11	16	MS/MS	
198	gi 11990901	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	19.44/8.81	64	11	1.50E-03	58	MS	Photosynthesis
				100	3	3.70E-07	15	MS/MS	
199	gi 4038719	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	18.51/8.83	85	12	1.10E-05	65	MS	Photosynthesis
				258	4	5.90E-23	21	MS/MS	
201	gi 4038719	Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit	18.51/8.83	40	7	3.60E-01	44	MS	Photosynthesis
				67	2	6.80E-04	11	MS/MS	
202	gi 56201800	Hypothetical protein	8.31/11.66	67	5	2.50E-02	50	MS	Unknown
205	gi 125595298	Hypothetical protein OsJ_018840	55.89/5.46	61	7	1.20E-01	13	MS	Unknown
				65	4	5.10E-05	7	MS/MS	
210	gi 115469444	Hypothetical protein Os06g0669400	65.43/5.16	102	15	8.50E-06	36	MS	Protein metabolic process
				160	4	2.10E-14	11	MS/MS	
<b>Group A: Up-regulated proteins in NIL</b>									
40	gi 75114857	Cell division protease ftsH homolog 2, chloroplast	72.49/5.54	83	14	6.10E-04	23	MS	Protein metabolic process
				207	4	5.30E-20	9	MS/MS	
47	gi 116310837	Hypothetical protein OSIGBa0140J09.5	159.71/9.32	77	9	2.60E-03	10	MS	DNA replication
176	gi 77550794	Transposon protein, putative, CACTA, En/Spm sub-class	74.69/5.39	70	11	1.30E-02	19	MS	Unknown
191	gi 86439747	POZ domain protein	30.15/9.87	51	6	2.70E-02	34	MS	Protein modification
<b>Group B: Down-regulated proteins in NIL</b>									
28	gi 37538489	FtsH-like protein precursor	75.96/5.78	62	10	2.70E-01	16	MS	Protein metabolic process
				176	3	1.20E-12	6	MS/MS	
41	gi 75114857	Cell division protease ftsH homolog 2, chloroplast	72.49/5.54	134	20	5.30E-09	33	MS	Protein metabolic process
				377	4	6.70E-37	10	MS/MS	
48	gi 116000583	RNA recognition motif (ISS)	31.94/5.32	70	6	5.50E-02	31	MS	RNA processing
59	gi 13928213	RuBisCO large subunit	52.81/6.22	53	11	1.90E-02	23	MS	Photosynthesis
89	gi 72256525	Geranylgeranyl hydrogenase	50.51/9.26	69	14	4.80E-04	29	MS	Photosynthesis
110	gi 108708252	Hypothetical protein LOC_Os03g24290	12.49/11.41	73	6	7.20E-03	31	MS	Unknown
112	gi 473690	ATP synthase beta subunit	53.82/5.06	103	15	1.90E-07	39	MS	Photosynthesis
179	gi 115484679	Hypothetical protein Os11g0210200	29.52/9.53	68	10	2.20E-02	40	MS	Unknown
196	gi 62176930	Putative rubisco small subunit	19.03/8.59	95	9	1.60E-04	57	MS	Photosynthesis
<b>Group C: Exclusive proteins in NIL</b>									

12	gi 50251595	Hypothetical protein	12.44/8.8	69	7	1.80E-02	52	MS	Unknown
13	gi 50251595	Hypothetical protein	12.44/8.8	68	5	2.40E-02	52	MS	Unknown
17	gi 116310785	Hypothetical protein H0315A08.7	77.10/8.69	70	8	1.50E-02	17	MS	Protein modification process
39	gi 115449023	Hypothetical protein Os02g0777700	163.49/9.21	69	10	1.80E-02	11	MS	Transport
43	gi 9837589	Beta-glucosidase	64.17/5.84	203	25	1.90E-17	48	MS	Carbohydrate metabolic process
				348	5	5.90E-32	12	MS/MS	
118	gi 13928213	RuBisCO large subunit	52.81/6.22	91	16	3.00E-06	33	MS	Photosynthesis
135	gi 77552045	Retrotransposon protein, putative, unclassified	81.62/6.29	71	13	1.00E-02	18	MS	DNA integration
151	gi 16903082	Small Ras-related GTP-binding protein	25.11/6.66	160	3	3.70E-13	14	MS/MS	Transport
				29	5	4.40E+00	27	MS	
153	gi 125575076	Hypothetical protein OsJ_030569	57.93/6.92	68	16	1.90E-02	24	MS	Carbohydrate metabolic process
<b>Group D: Proteins disappeared in NIL</b>									
213	gi 32966580	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	52.75/6.22	101	16	3.00E-07	42	MS	Photosynthesis
				143	4	1.90E-11	9	MS/MS	
216	gi 3915029	Acyl-[acyl-carrier-protein] desaturase, chloroplast precursor	44.45/6.53	76	7	3.40E-03	14	MS	Lipid metabolism