

Metabolic step	Introgression line					
	IL4-4	IL7-3	IL7-5	IL2-6	IL12-4	IL1-4
phloem unloading						
1		0.316		-0.409	0.167	
1	-0.307	0.375	0.616	-0.071	0.184	-0.273
1				0.329	0.066	
2	0.3394					0.103
2	0.7357		-0.054	1.163	-0.366	0.169
3				0.096		
3	1.4384	2.263	0.370	0.008	0.754	1.460
soluble carbohydrate metabolism						
4						
5	1.187	0.406	-1.253	0.222	0.337	-0.300
5	0.911	0.431	-0.858	0.161	0.005	-0.146
5	0.423			-0.274	0.247	-0.078
6	-0.138	-0.129		-0.201	-1.305	-0.321
6			-0.221	0.594	-0.001	0.187
6		-0.299	-0.521	-0.163	-0.252	-0.160
7	0.184	0.117	-0.281	-0.063	0.116	0.119
8	0.806	0.049	-0.322	-0.384	0.206	-0.405
8		-0.018		-0.261	0.019	
9						
Glycolysis						
10	0.576		0.921		0.050	0.135
10	0.707	0.005	0.086	-0.248	0.250	-0.078
11		0.028		-0.105	0.248	
12	0.336	0.266		-0.163	-0.201	0.039
12		0.132		-0.325	-0.057	0.210
13		-0.077		-0.347	-0.241	0.042
14	-0.518	-0.388		-0.142	-0.076	-0.293
14	0.326	0.134	-0.117	-0.251	-0.055	0.004
14	0.057	0.076	-0.720	-0.267	-0.009	-0.258
15	0.383	0.078	-0.121	-0.076	0.273	-0.072
16	0.566	0.319	-0.372	-0.054	-0.041	
16	0.690	0.423	-1.223	-0.679	-0.012	-0.118
16	0.785	0.513	-0.881	-0.384	-0.174	0.100
16	0.457	0.520	-0.155	-0.533	-0.014	-0.045
17	0.659	0.388	-0.148	-0.295	-0.033	0.047
18						
19	0.877	0.115	-0.230	-0.153	0.117	0.233
19	0.629	0.251	-0.252	-0.265	0.175	0.076
20	0.369	0.084	0.146	0.205	0.135	0.234
20		-0.310	-0.890	-0.255	-0.065	-0.265
20	0.143	-0.072		0.113	-0.193	-0.209
20	-0.277		-0.534	0.269	-0.053	-0.237
21	0.306	-0.052	-0.128	0.087	-0.008	-0.126
21	0.085	0.405	-0.079	0.025	-0.156	-0.139
22	0.762	0.487	0.462	0.564	0.101	0.065

Metabolic step	Introgression line						
	IL4-4	IL7-3	IL7-5	IL2-6	IL12-4	IL1-4	
Starch metabolism							
23	ADPGpyrophosphorylase LSU	0.034	0.367		-0.554	-0.086	-0.308
24	ADPGpyrophosphorylase SSU	-0.347	-0.086		-0.527	-0.069	-0.669
25	glucosyl transferase, jasmonate-induced		0.374		-0.157	0.095	0.228
25	glucosyltransferase IS5a (EC 2.4.1.-), salicylate-induced	0.282	0.227		0.062	-0.128	-0.003
26	starch phosphorylase						
27	starch synthase-isoform 3		-0.698		-0.240	-0.036	
27	starch synthase-isoform 4				0.035	0.159	
27	starch synthase-isoform 5					-0.863	
28	starch-branching enzyme		-0.492		-0.005	-0.019	
29	beta-amylase	-0.094	-0.425		0.123	-0.211	0.034
Oxidative pentose phosphate pathway							
30	Glucose 6 phosphate dehydrogenase-cytoplasmic isoform	0.451	-0.254		0.076	-0.089	0.164
31	lactonase		0.074	0.817	0.110	-0.123	
32	6-phosphogluconate dehydrogenase	0.100	0.479	-0.151	0.169	0.049	0.005
33	pentose phosphate isomerase						
33	pentose phosphate epimerase						
34	transketolase 1	0.691	0.407		-0.226	0.010	-0.209
35	transaldolase	0.378	-0.002	-0.094	-0.124	-0.119	0.028
35	transaldolase 2						0.002
Tricarboxylic acid cycle							
36	pyruvate dehydrogenase E1 alpha subunit	0.341	0.448	-0.241	-0.088	-0.096	-0.142
36	pyruvate dehydrogenase E1 beta subunit isoform 1	0.186	0.229	0.679	-0.151	-0.040	-0.332
36	pyruvate dehydrogenase E1 beta subunit isoform 2		0.146		-0.207	0.037	
37	citrate synthase	0.328	0.026	0.850	-0.138	-0.009	0.169
38	aconitase	0.404	-0.040	0.113	0.338	-0.196	0.071
39	NAD-dependent isocitrate dehydrogenase		0.462		-0.009	0.029	0.220
40	2-oxoglutarate dehydrogenase					-0.321	0.055
41	succinyl coa-ligase		0.488		-0.153	0.208	0.259
42	succinate dehydrogenase, iron-sulphur subunit	0.487	0.195	-0.161	-0.159	0.110	-0.018
42	succinate dehydrogenase flavoprotein alpha subunit	0.235	-0.064	-0.015	0.065	0.057	-0.055
43	fumarase						0.388
44	malate dehydrogenase 2, cytosolic	0.631	0.437	-0.209	-0.056	0.031	-0.234
44	malate dehydrogenase mitochondrial	0.554	0.064		-0.182	-0.161	0.129
44	malate dehydrogenase cytosolic	0.557	-0.824	-0.680	0.044	-0.108	0.186
45	cytosolic NADP-malic enzyme	0.620	0.071	-0.487	0.146	-0.086	-0.062
Amino acid metabolism							
	glutamate synthase (ferredoxin)	0.505				0.348	-0.033
	glutamate synthase (NADH-dependent)	0.240	0.154	0.119	0.250	0.128	
	glutamine synthase	-0.239	0.475	-0.624		-0.440	-0.011
	Glutamate dehydrogenase A		0.032		0.024	-0.271	
	aspartate kinase						-0.029
	aspartate aminotransferase	-0.769	-0.501	-0.530	0.200	-0.134	-0.063
	glycerate dehydrogenase	-0.464	-0.185	-0.216	0.159	-0.350	-0.153
	serine acetyltransferase	0.722	0.243		-0.334	-0.034	
	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase		0.153		-0.337	-0.093	0.241
	shikimate kinase	0.012	-0.044	0.213	-0.188	-0.133	0.025