

Table S2. Genes in glycolysis and tricarboxylic acid cycle pathways in response to Al at 24 h in the roots of KF (T) and GF (S).

Genes	T-24h(FC)	S-24h(FC)	description
Fructose-6-P to Fructose-1,6-bis-P1			
Glyma.07g263800	0.98	0.35	Phosphofructokinase
Glyma.18g145500	0.91	0.36	Phosphofructokinase
Glyma.08g280700	2.41	0.71	Phosphofructokinase
PEP to Pyruvate			
Glyma.16g173100	0.86	0.23	Pyruvate kinase
Glyma.20g024800	0.98	0.35	Pyruvate kinase
PEP to Oxaloacetate (OAA)			
Glyma.06g229900	0.69	0.18	PEPC
Glyma.06g277500	1.02	0.22	PEPC
Glyma.13g270400	0.85	0.15	PEPC
Isocitrate to 2-oxoglutarate			
Glyma.08g160500	0.82	0.22	Isocitrate dehydrogenase
Glyma.16g118900	0.94	0.45	Isocitrate dehydrogenase
Succinate to Fumarate			
Glyma.02g057400	0.58	0.17	Succinate dehydrogenase
Glyma.12g099000	0.66	0.25	Succinate dehydrogenase
Fumarate to Malate			
Glyma.02g015700	0.67	0.39	Fumarate lyase

FC: Fold change

Fructose-6-P: fructose-6-phosphate;

Fructose-1,6-bis-P1: fructose-1,6-bisphosphatase;

PEP: phosphoenolpyruvate;

PEPC: Phosphoenolpyruvate Carboxylase;

OAA: Oxaloacetate.