



Figure S2. Pathway map of carbohydrate metabolism.

The map is based on KEGG database [<http://www.genome.jp/kegg/pathway.html>].

Red, green and black letters and dots represent increased, decreased and unchanged gene expression and carbohydrate levels, respectively, in *TPS1*-transgenic potato leaves compared to the wild-type.

Abbreviations: I, inositol; F, fructose; G, galactose; GI, glucose; M, maltose; Mt, malate;

S, sorbitol; Su, sucrose; FBA, fructose-bisphosphate aldolase;

PDH, pyruvate dehydrogenase; PGK, phosphoglycerate kinase; RBC, RuBisCo;

SUS, sucrose synthase.