SUPPLEMENTAL MATERIAL

Supplemental figure 1. Rate of glutamine hydrolysis as a function of the concentration of glutamine. PDX1.1 (10 μM) was incubated with an equimolar concentration of either, full length PDX2 (filled circles), or a C-terminally truncated version of PDX2, PDX2ΔC30, (open circles) while systematically varying the concentration of glutamine (0-20 mM). The rate of glutamine hydrolysis was measured employing a coupled assay as described under methods. The data shown is the average of three independent experiments fitted according to the Michaelis-Menten equation ($f(x)=a.x/b+c$).

Supplemental figure 2. Sequence analysis of PDX proteins. *A,* Alignment of PDX2 amino acid sequences from *Arabidopsis thaliana* (At), *Nicotiana tabacum* (Nc), *Oryza sativa* (Os), *Bacillus subtilis* (Bs), *Saccharomyces cerevisiae* (Sc) and *Plasmodium falciparum* (Pf). The blue box highlights the C-terminal extension of the plant PDX2 sequences. *B,* Comparison of the PDX1 N-termini from *Arabidopsis thaliana*.

Supplemental figure 3. Absolute transcript abundance of *PDX2* (black bars) compared to *PDX1.1* (light gray bars) and *PDX1.3* (dark gray bars). The examples shown are roots and rosette leaves of seedlings 2 weeks after germination under the conditions described for figure 2, and seedlings grown in continuous dark (DD) for 5 days after imbibition. For absolute amounts of mRNA, standard curves were generated using known concentrations of plasmids carrying the *PDX* genes (*PDX2, PDX1.1, PDX1.3*, respectively). Plasmid DNA was diluted to 1 ng μl^{-1} followed by 10-fold serial dilutions to 1 fg μl^{-1}.

Supplemental figure 4. *Gene Correlator* analysis of the expression of *PDX2* in relation to *PDX1* (Zimmermann et al., 2004). The plots display *PDX2* and each of the *PDX1* genes (*PDX1.1, PDX1.2* and *PDX1.3*) on the X and Y axes, respectively. Each spot represents one individual GeneChip; red indicates when both *PDX1* and *PDX2* have a detectable level of expression (p-values < 0.05); green indicates when expression of both *PDX1* and *PDX2* is not detected (p-values ≥ 0.05); dark blue, indicates that only *PDX2* (X axis) is present; and light blue, indicates when *PDX1* (Y axis) is present but *PDX2* is absent.