**Figure S1.** PkpC clusters phylogenetically apart from PkpA and PkpB. **A.** Phylogenetic tree of the protein sequences from the 3 pyruvate dehydrogenases of *Aspergillus spp*, *Trichoderma spp*., *Neurospora crassa*, *Penicillium chrysogenum* and the two pyruvate dehydrogenase protein sequences of *Fusarium oxysporum*, *Candida albicans*, *Candida glabrata*, *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Branch values are based on the aLRT (approximate Likelihood Ratio Test) statistical test of branch support. **B.** Alignment of PkpA, PkpB and PkpC [blue box = branched chain alpha-ketoacid dehydrogenase kinase (BCDHK) domain; red box = ATP-binding domain; \* = fully conserved residue; : = conservation between groups of similar properties > 0.5 in the Gonnet PAM (Point Accepted Mutation) 250 matrix; . = conservation between groups of weakly similar properties =< 0.5 Gonnet PAM 250 matrix].

**Figure S2.** PDHK gene expression and growth of the deletion strains in the presence of glucose. **A.** Expression of *pkpA*, *pkpB* and *pkpC*, as determined by RT-qPCR, when the wild-type strain was grown for 24 h in casamino acid (CA)-rich medium and after transfer to glucose-rich medium for 1 h, 8 h and 16 h; or to cellulose-rich medium for 2 h, 8 h, 24 h and 48 h. Error bars represent the standard deviation between biological triplicates (\*P-value < 0.05; \*\*P-value < 0.005; \*\*\*P-value < 0.0005 as determined by a one-tailed, paired student t-test). **B.** Growth of the wild-type and PDHK deletion strains in the presence of 0.25% (w/v) acetate at different pH. **C.** Deletion of *pkpA* and *pkpC* severely delays growth in the presence of glucose.Growth, as determined by microscopy, of the wild-type (TN02a3) and the pyruvate dehydrogenase kinase deletion strains in minimal medium supplemented with 1% w/v glucose for 7 h at 37°C (left panel) and 16 h at 30°C (right panel). Nuclei were stained with Hoechst33342 and viewed under the DAPI filter (DIC = differential interference contrast). Graphs show the percentage of spores with an emerged germ tube or the number of hyphae with more than 5 nuclei. Error bars indicate standard deviations between three biological replicates (\*P-value < 0.05; \*\*P-value < 0.005; \*\*\*P-value < 0.0005 as determined by a one-tailed, paired student t-test) and 50 hyphal germlings were counted for each replicate.

**Figure S3.** The Δ*pkpA* and Δ*pkpC* strains do not have a glucose sensing defect. Spore swelling and germ tube emergence as assessed by microscopy in the wild-type, Δ*pkpA*, Δ*pkpB* and Δ*pkpC* strains when grown in minimal medium supplemented with glucose for 8 h at 37°C, 160 rpm.

**File S4.** Putative PkpC protein interaction partners after 24 h growth in minimal medium supplemented with casamino acids or after 10, 30 and 60 min exposure to acetate.All proteins were identified after immunoprecipitation and mass spectrophotometry and functionally classified according to MIPS. Identified proteins involved in cell signalling (kinases), RNA metabolism and carbon source-related metabolism are listed separately.

**Figure S5.** Carbon catabolite repression is defective in the Δ*pkpA* and Δ*pkpC* strains. **A.** Cellular localisation, as determined by microscopy, of CreA::GFP in different strains when grown for 16 h at 25°C in minimal medium supplemented with 1% w/v glucose. Nuclei were stained with Hoechst33342 and viewed under the DAPI filter (DIC = differential interference contrast, GFP = green fluorescent protein). Scale bars represent 10 μm. The graph shows the percentage of CreA::GFP nuclear localisation in all strains. Error bars indicate standard deviations between three biological replicates (\*P-value < 0.05; \*\*P-value < 0.005; \*\*\*P-value < 0.0005 as determined by a one-tailed, paired student t-test) and 50 hyphal germlings were counted for each replicate. **B.** Growth of the wild-type and the protein kinase deletion strains in the presence of 1% w/v milk and glucose.

**Table S1.** Strains used in this study.

**Table S2.** Primers used in this study.

**File S1.** Putative PkpC protein interaction partners after 24 h growth in casamino acid-rich medium and subsequent exposure to glucose for 10, 30 and 60 min.All proteins were identified after immunoprecipitation and mass spectrophotometry and functionally classified according to MIPS.

**File S2.** Metabolite analysis of the wild-type and the protein kinase deletion strains after 16 h growth in glucose-rich medium. Metabolites were compared between the protein kinase deletion strains and the WT (wild-type strain) with P-values < 0.05 being highlighted (blue = Δ*pkpA*, red = Δ*pkpB* and green = Δ*pkpC*) (HCA= hierarchical cluster analysis).

**File S3.** Metabolite analysis of the wild-type and the protein kinase deletion strains after 48 h growth in cellulose-rich medium. Metabolites were compared between the protein kinase deletion strains and the WT (wild-type strain) with P-values < 0.05 being highlighted (blue = Δ*pkpA*, red = Δ*pkpB* and green = Δ*pkpC*) (HCA= hierarchical cluster analysis).

**File S4.** Putative PkpC protein interaction partners after 24 h growth in minimal medium supplemented with casamino acids or after 10, 30 and 60 min exposure to acetate.All proteins were identified after immunoprecipitation and mass spectrophotometry and functionally classified according to MIPS. Identified proteins involved in cell signalling (kinases), RNA metabolism and carbon source-related metabolism are listed separately.