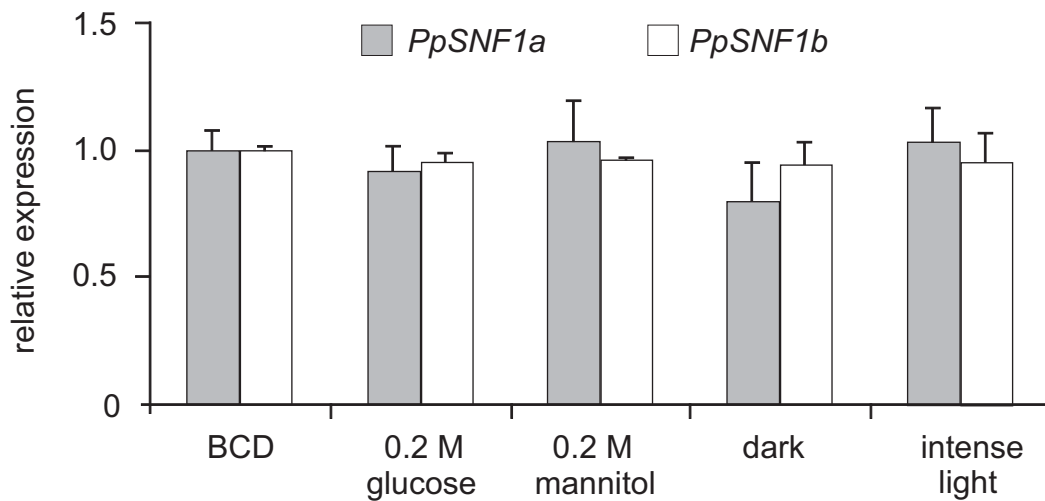
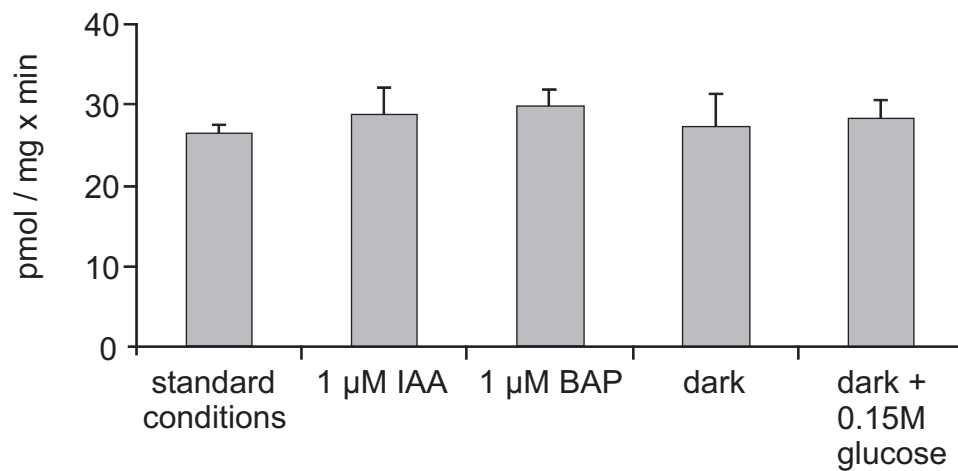


Supplementary Figure 1. Low stringency Southern blots. Genomic *Physcomitrella* DNA was digested with either *EcoRI* (E), *BglII* (B) or *HindIII* (H), none of which cut within the probes, blotted to nylon filters and hybridized to *PpSNF1a* (left) or *PpSNF1b* (right) specific probes. In each case, the most strongly hybridizing bands correspond to the gene from which the probe was derived, and the weaker band to the other gene.



Supplementary Figure 3. Expression of the *PpSNF1a* and *PpSNF1b* mRNAs under different conditions. Young protonemal tissue was exposed to various treatments for 24 hours, after which the cells were harvested and RNA was isolated. Relative expression levels are shown as the ratio between the transcript dependent RT-PCR product and an internal standard product (Siebert and Larrick, 1992). Untreated tissue grown under standard conditions (BCD) was assigned a value of 1. The error bars show standard deviations of three independent samples.



Supplementary Figure 4. Comparison of SAMS phosphorylating activities in extracts from wild type colonies subjected to different treatments. Tissue was pregrown on BCD media under standard conditions and was then exposed for 20 hours to different conditions as shown in the figure. The enzyme activity is expressed as pmol phosphate incorporated into SAMS peptide per minute and mg of protein. The numbers shown are averages \pm standard deviations for three samples. For each sample, the activity without added peptide was subtracted from the activity with added peptide.