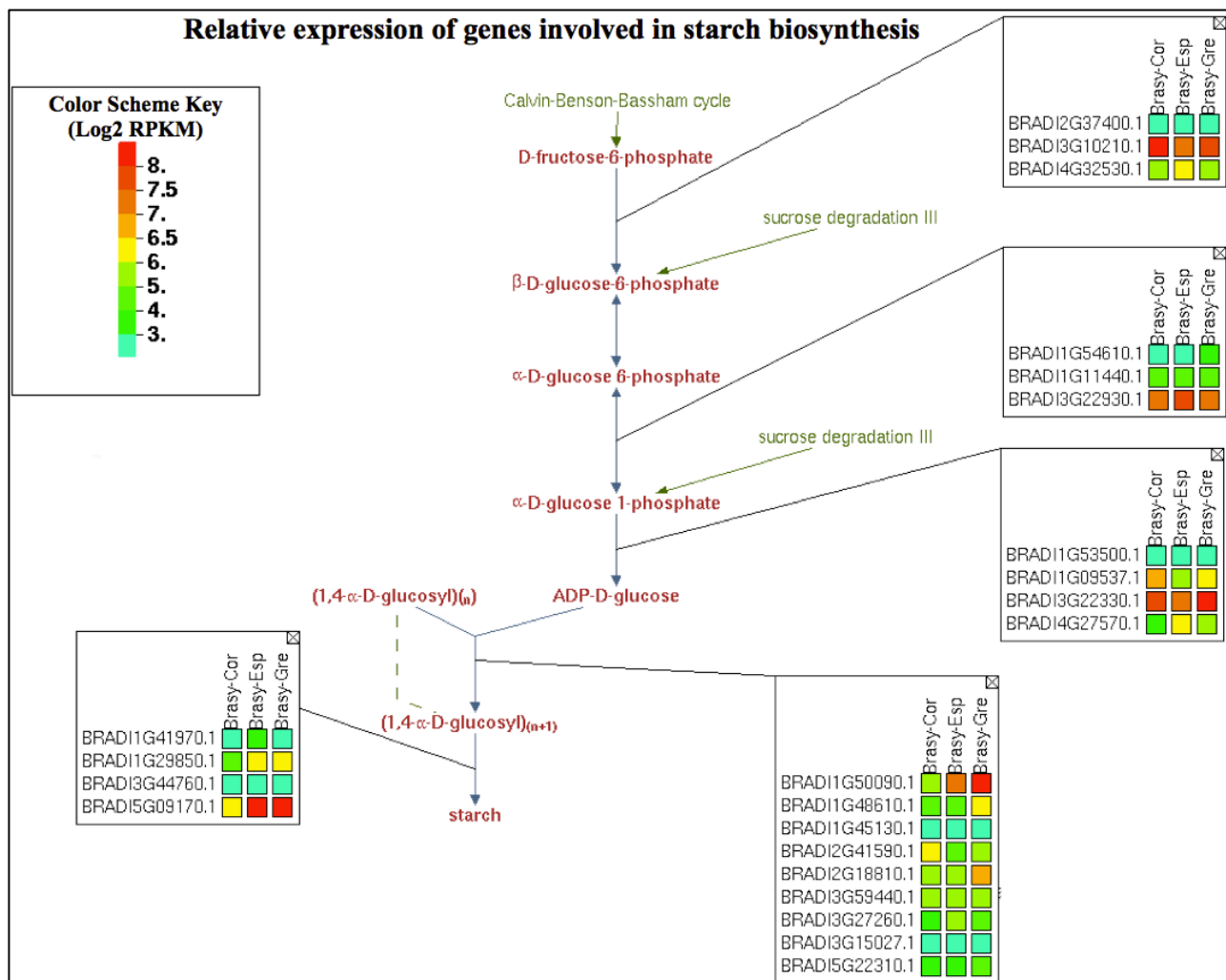


APPENDIX S7. *Brachypodium sylvaticum* RPKM gene expression levels. (A) We mapped the *B. sylvaticum* reads against the *B. distachyon* CDS sequences (v1.2) and calculated the reads per kilobase per million bases. To demonstrate the feasibility of using *B. distachyon* genomic tools for *B. sylvaticum* transcriptome analysis, we visualized the relative expression of genes involved in various metabolic pathways using the BrachyCyc database (<http://mips.helmholtz-muenchen.de/plant/brachypodium/>). Below, we show the relative expression of *B. sylvaticum* orthologs when mapped against the *B. distachyon* starch biosynthesis pathway (log₂ RPKM heat map shown). (B) Overall, we observed similar expression patterns among the three *B. sylvaticum* genotypes, which was not unexpected in that all the sampling was done under similar growth conditions. Pearson correlation coefficients of >0.86 for all three comparisons.

A.



B.

