



Supplemental Figure S1. Phylogenetic tree of β -amylases.

The β -amylases from Arabidopsis, rice and barley were aligned and used to generate a maximum-likelihood tree displayed using DNASTar software. Phylogram showing that plant β -amylase proteins fall into four sub-families (Fulton et al., 2008). Barley putative β -amylases are shown in bolt, proved chloroplast-localized β -amylases of Arabidopsis are shown in bolt and green, predicted chloroplast-targeted proteins are shown in green, predicted proteins with signal peptides are shown in red.

The Genbank accession numbers are as follow: *AtBAM1* (At3g23920), *AtBAM2* (At4g00490), *AtBAM3* (At4g17090), *AtBAM4* (At5g55700), *AtBAM5* (At4g15210), *AtBAM6* (At2g32290), *AtBAM7* (At2g45880), *AtBAM8* (At5g45300), *AtBAM9* (At5g18670), *OsBAM1* (Os10g0565200), *OsBAM2* (Os07g0543300), *OsBAM3* (Os07g0543100), *OsBAM4* (Os07g0667100), *OsBAM5* (Os10g0465700), *OsBAM6* (Os09g0569200), *OsBAM7* (Os03g0141200), *OsBAM8* (Os01g0236800), *OsBAM9* (Os02g0129600), *OsBAM10* (Os03g0351300).