

## SUPPLEMENTARY DATA

FIG. S1 Alignment of maize putative ZmCNGT protein with *Arabidopsis* and maize CNGTs. Protein sequences were aligned using a clustal align algorithm. Protein names are labelled with the genus abbreviation followed by GI number and trivial abbreviation. Putative kernel-specific cytokinin *N*-glucosyltransferase is labeled as ZmCNGT. Exact matches and conservative substitutions are boxed and colour-coded. \* indicates positions that have a single, fully conserved residue; ‘:’ indicates that one of the ‘strong’ groups of amino acids is fully conserved; ‘.’ indicates one of the ‘weaker’ groups is fully conserved; ‘-’ indicates a gap. Bar graphs below the sequences represent the percentage of similarity between the sequences compared. The amino acid site number is indicated below the aligned sequences at every ten residues.

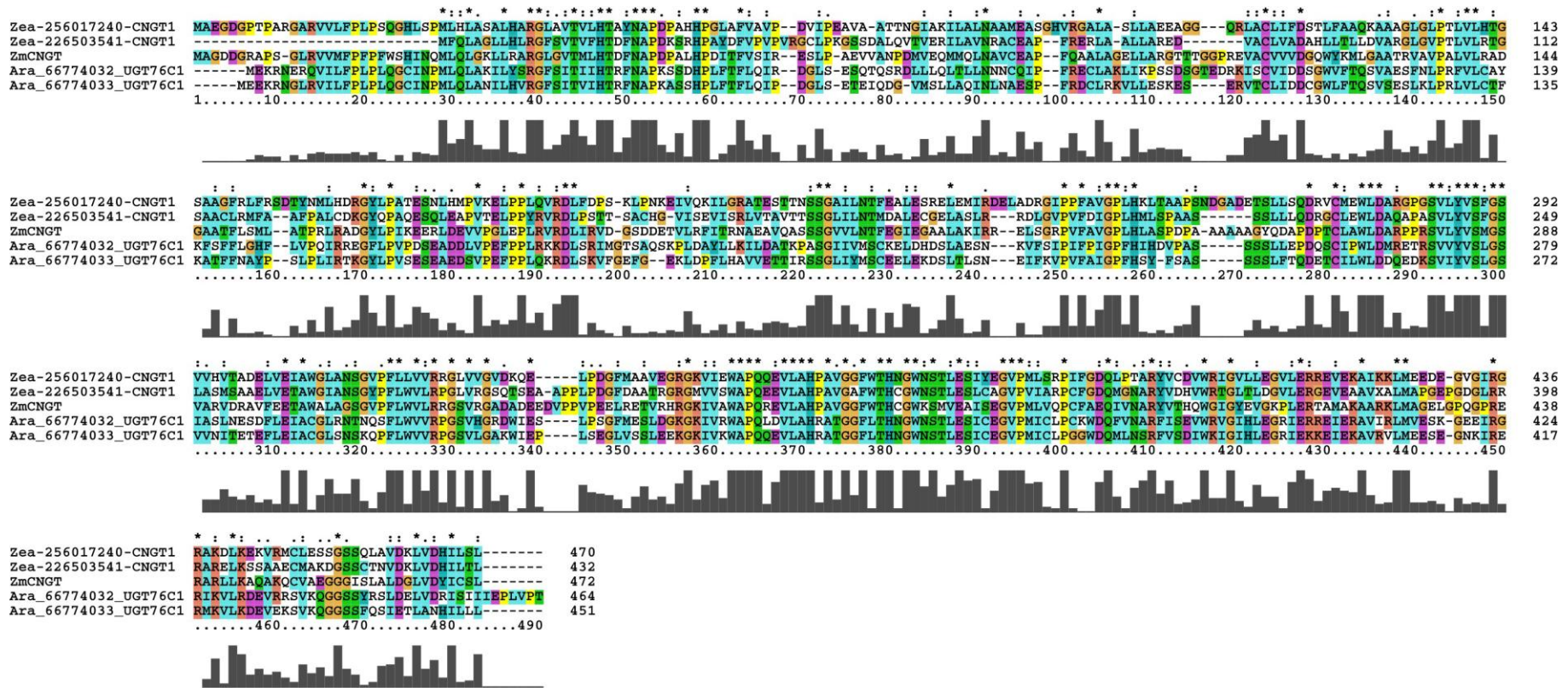


FIG. S2. Phylogenetic tree calculated using *Arabidopsis* (Ara), *Phaseolus* (Pha) and *Zea mays* (Zm) full-length N-glucosyl transferase proteins. Protein names are labelled with the genus abbreviation followed by GI number. Protein function is labelled for the individual protein or group of proteins. The results indicate that ZmCNGT clusters together with two maize putative cytokinin glucosyltransferases (i.e. GI: 226503541 and GI: 256017240) and two *Arabidopsis* cytokinin glucosyltransferases (i.e. GI: 42567677 and GI: 42567678). Glucosyl transferases that catalyse the conversion of other substrates and cytokinin O-glucosyl transferases are positioned elsewhere on the phylogenetic tree. Scale bar = 0.1 amino acid substitutions per site.

