Supplemental Figure S3

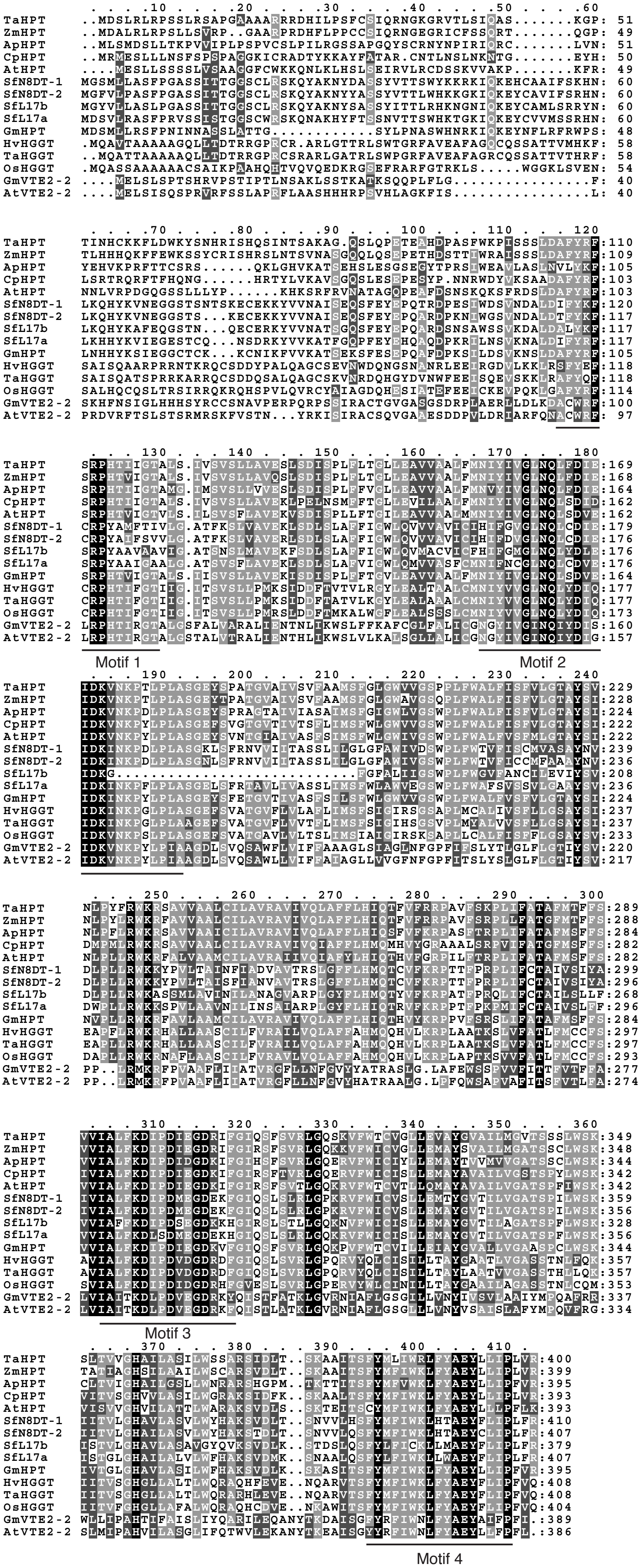

Fig. S3 Multiple alignment of the amino acid sequences among HG substrate prenyltransferases including SfN8DT-1. At, *Arabidopsis thaliana*; Ap, *Allium porrum*; Cp, *Cuphea pulcherrima*; Gm, *Glycine max*; Hv, *Hordeum vulgare*; Os, *Oryza sativa*; Ta, *Triticum aestivum*; Zm, *Zea mays*. Sequences were aligned using the ClustalW program and MacBoxshade. Identical, similar and conserved amino acids are indicated by black, dark grey and light grey shading, respectively, using a 60% consensus threshold. A dot represents a gap. Motiif 1-4 was designated as conserved domain by Venkatesh *et al*. (Planta, 2006, 223, 1134-1144).