



Supplementary Figure 2. Nucleotide sequence alignments of PvGmGSTUG with the first 12 sequences identified following BLASTP search (Clustal Omega; Sievers et al., 2011). The figure was created using Geneious v9.1.2 software (Kearse et al., 2012). Conserved areas are shown shaded: ■ 100% identity, ■ 80-100% identity, ■ 60-80% identity, <60% identity. The accession numbers of the sequences that were used were: *MtGST1*, (*Medicago truncatula*, XM_003623148.2); *CaGST1*,

(*Cicer arietinum*, XM_004492319.2); *MtGST2*, (*Medicago truncatula*, XM_003623126.2); *MtGST3*, (*Medicago truncatula*, XM_003623120.2); *CaGST2*, (*Cicer arietinum*: KT336759.1); *CaGST3*, (*Cicer arietinum*, XM_012713550.1); *MtGST4*, (*Medicago truncatula*, XM_003623159.1); *MtGST5*, (*Medicago truncatula*, XM_003623156.2); *MtPr1*, (*Medicago truncatula*: BT053471.1); *AiGST1* (*Arachis ipaensis*: XM_016342954.2); *AiGST2* (*Arachis ipaensis*: XM_016333558.2).