

Figure S1. Multiple sequence alignments of eight GST sequences from *Lolium* species, identified by BLAST search using as a query either of the *LpGSTU* sequences. Five sequences are from *Lolium perenne* (accession numbers: XP_051177894.1; AMY26593.1, XP_051177895.1; AMY26592.1; XP_051177900.1), one from *Lolium multiflorum* (accession number KAK1643535.1), and two from *Lolium rigidum* (accession numbers: XP_047090606.1; XP_047090605.1). The sequences with accession numbers AMY26592, AMY26593.1, XP_051177894 corresponds to *LpGSTU25*, *LpGSTU2*, *LpGSTU5* of the present study, respectively. Sequences were aligned with CLUSTAL Omega [33] and displayed using ESPrpt 3 [34]. Conserved areas are shown shaded. A column is framed, if more than 70% of its residues are similar according to physico-chemical properties.

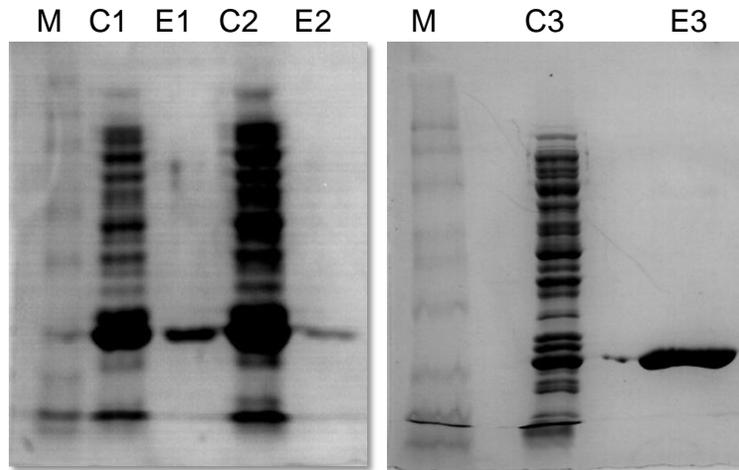


Figure S2. SDS-PAGE analysis of purified *LpGSTU25*, *LpGSTU2*, *LpGSTU5*. Elution was carried out using GSH (10 mM). M protein markers. Lane C1, C2, C3: recombinant *E. coli* BL21(DE3) crude extracts, expressing *LpGSTU25*, *LpGSTU2*, *LpGSTU5*, respectively. Lanes E1-E3 purified *LpGSTU25*, *LpGSTU2*, *LpGSTU5*, respectively.