Fig. S1

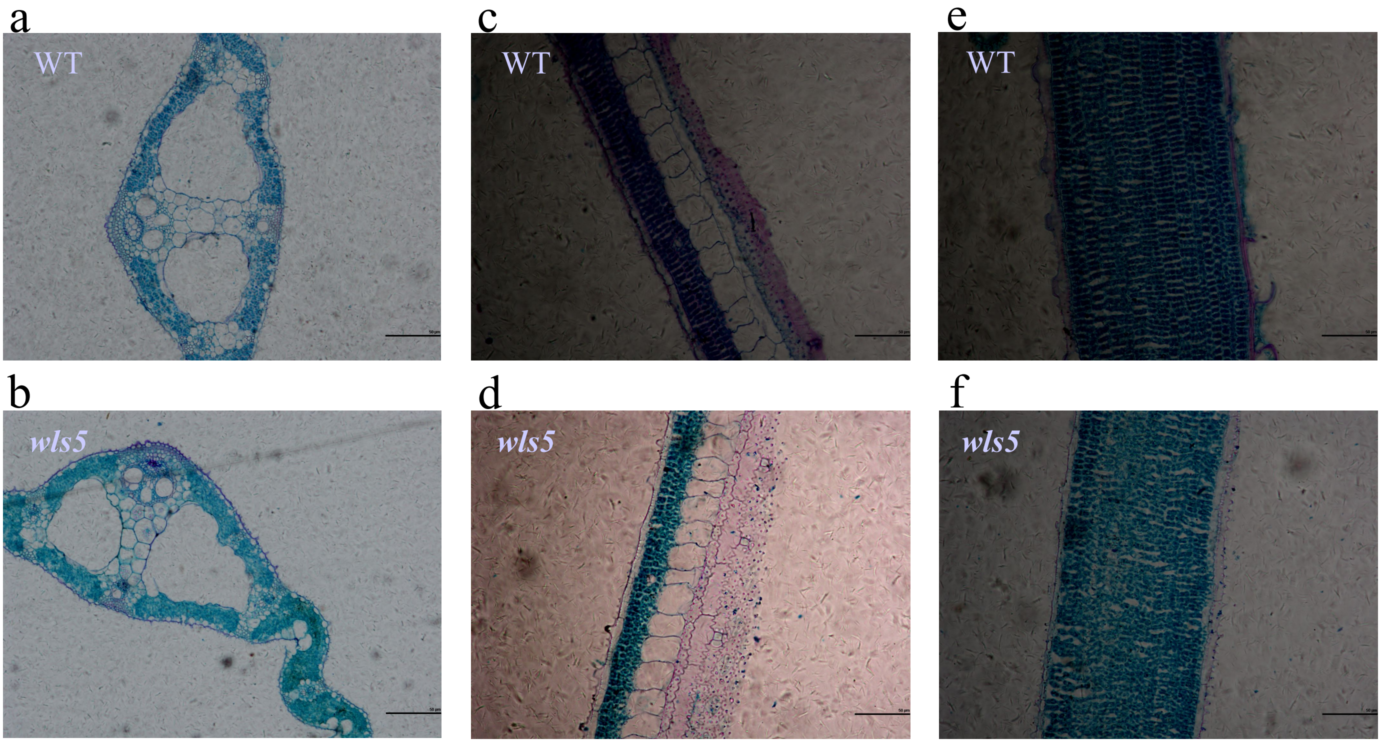

Fig. S1 Histological characterization of leaves in wild-type and *wls5* plants. **a**, **b** Cross sections of leaves of wild-type (‘93-11’) and *wls5*. **c-f** Longitudinal sections of leaves of wild-type and *wls5* plants. Scale bar = 50 μm.

Fig. S2

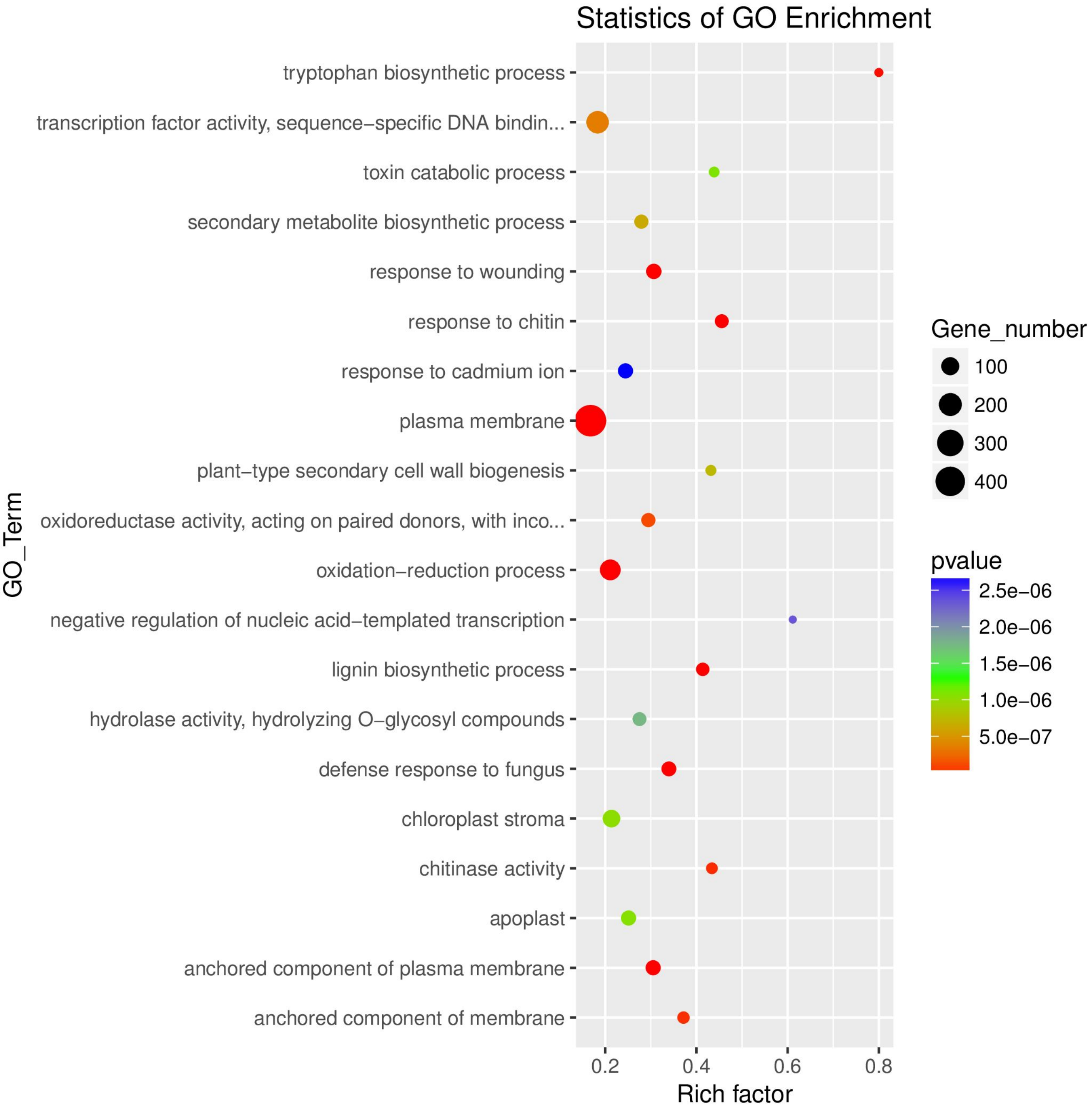

Fig. S2 Statistics of GO enrichment analysis of differential expression genes between wild-type (WT) and *wls5* plants. mRNA was purified from total RNA isolated from tillering-stage plants of WT (‘93-11’) and *wls5*.

Fig. S3

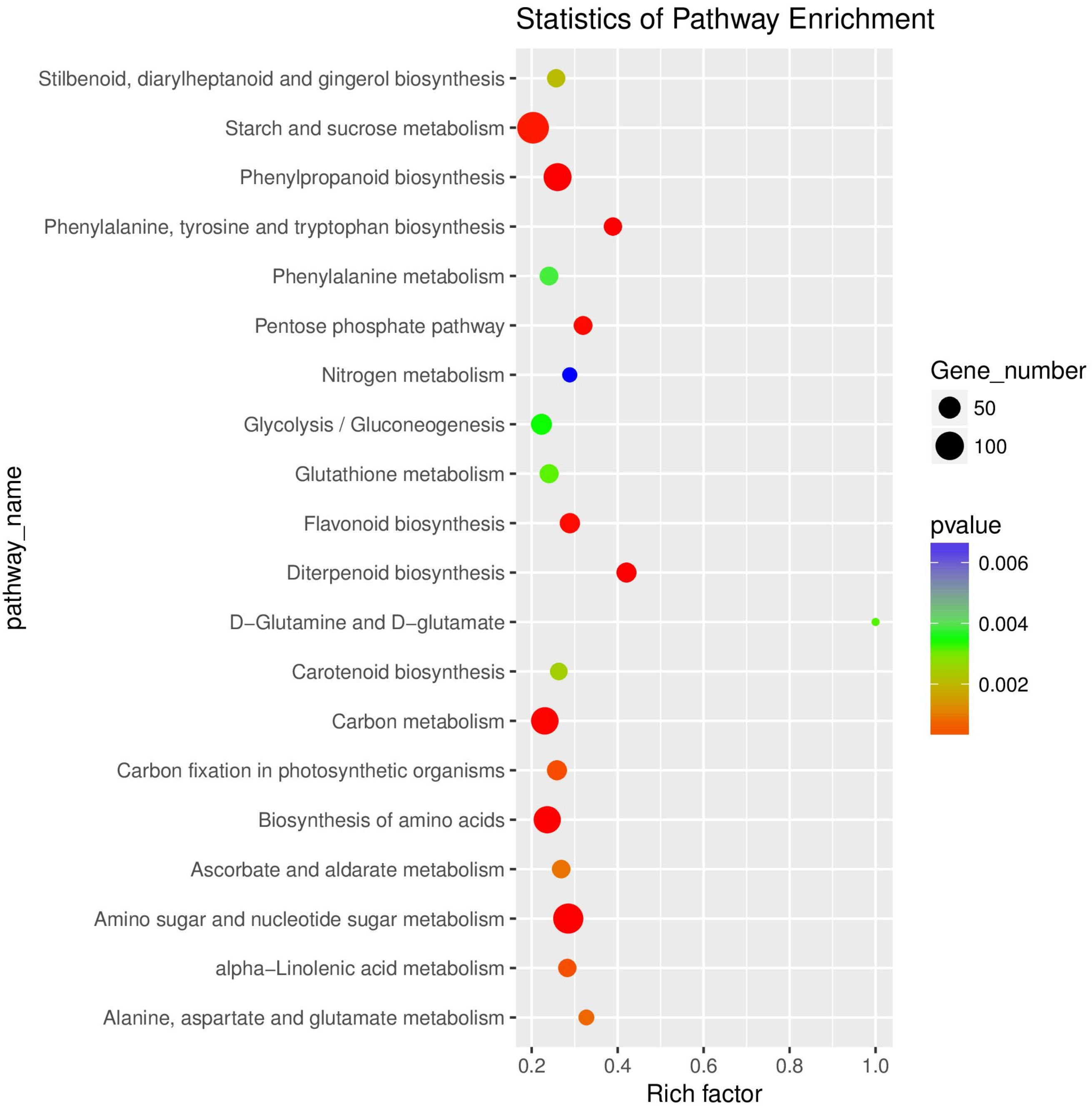

Fig. S3 Statistics of pathway enrichment analysis of differential expression genes between wild-type (WT) and *wls5* plants. mRNA was purified from total RNA isolated from tillering-stage plants of WT (‘93-11’) and *wls5*.

Fig. S4

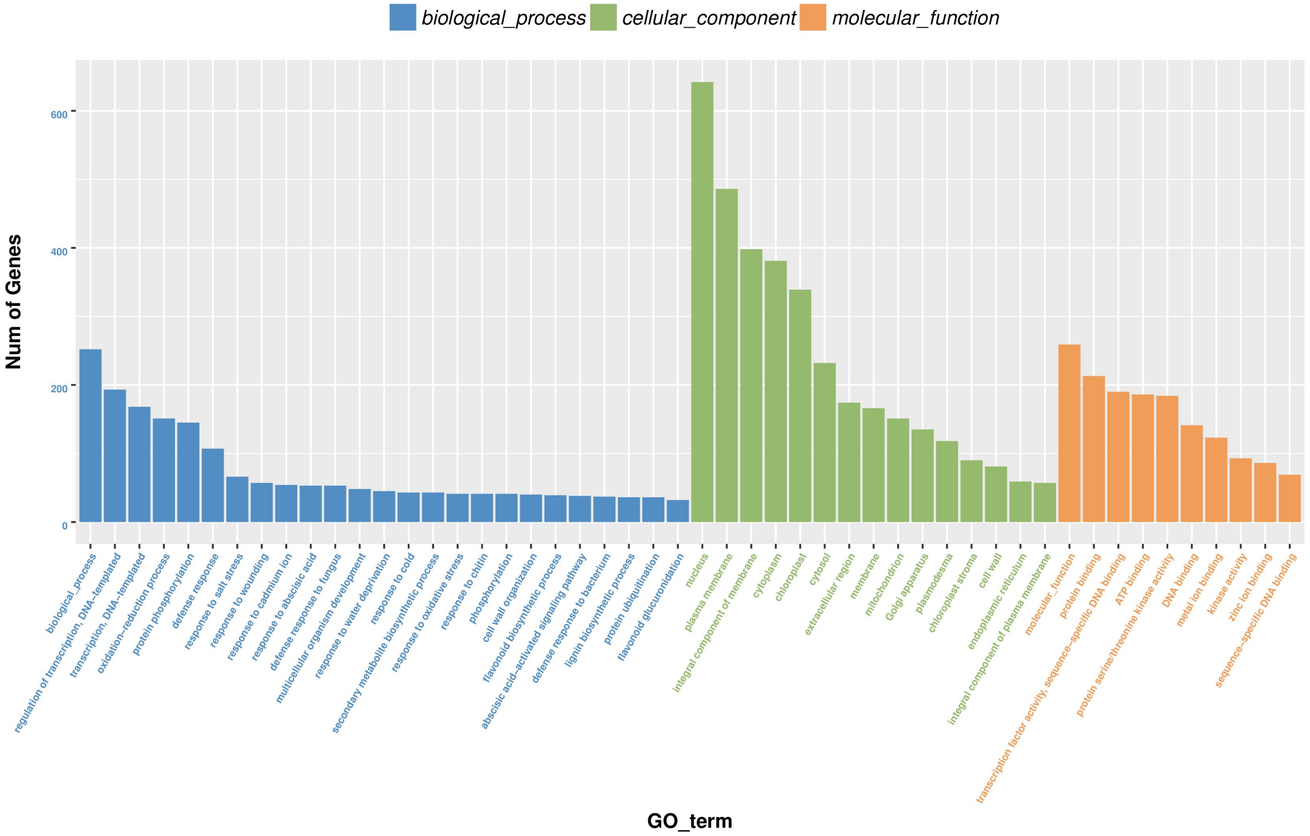

Fig. S4 The number of differential expression genes involved in different biological processes, cellular components and molecular functions. mRNA was purified from total RNA isolated from tillering-stage plants of WT (‘93-11’) and *wls5*.