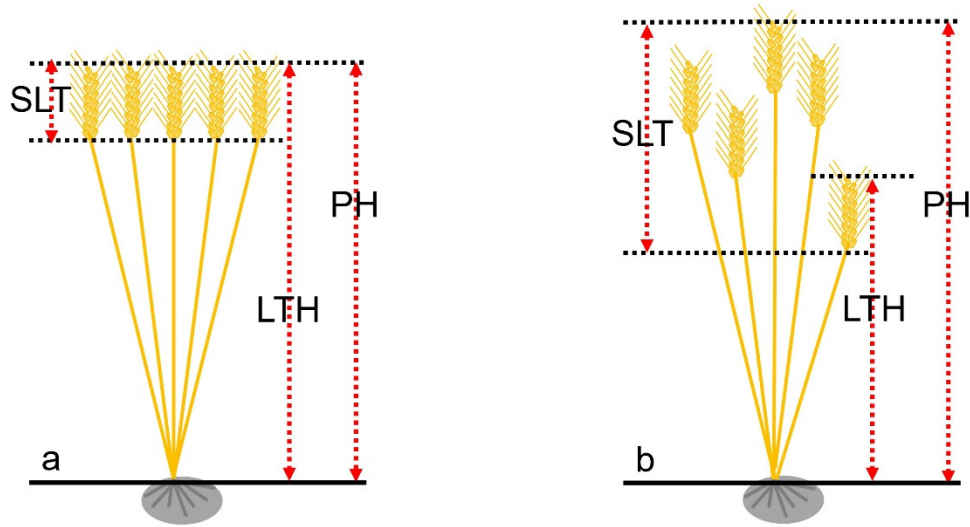


Supplementary Figure S1 Heat map of in silico gene expression analysis for predicted genes in the interval of *Qslu.sicau-2B-2*. The RNA-seq expression data of these predicted genes are from the wheat expression browser (<http://www.wheat-expression.com/>).



Supplementary Figure S2 The intuitional visualization of the phenotype was investigated in this study. Spike-layer thickness (SLT) was calculated as $PH - LTH + SL$. Each line's spike-layer uniformity (SLU) was calculated as $SL / (PH - LTH + SL)$. **(a)** The plant sample shows that the most consistent spikes are distributed in the vertical space (SLU=1). All tillers have the same height, indicating that LTH equals PH. **(b)** The plant sample shows inconsistent spikes are distributed in the vertical space ($0 < SLU < 1$). Note: LTH, lowest tiller height; PH, plant height, SL, spike length.