



Figure S6. Sliding window analysis employed to estimate selective pressures on 35 pairs of duplicated Hsf genes in *G. max*. For sliding window analysis, nucleotide sequences of *G. max* Hsf genes are used. Window size is 150 bp, and step size is 9 bp. The gray blocks, from dark to light, indicate the positions of the DBD domain, HR-A/B region, NLS, NES and AHA motifs, respectively.