



Figure S1: Binding site plots showing predicted Gt binding sites in different enhancers.

Three PWMs were used with the PATSER program to predict Gt binding sites within the enhancer sequences using a p-value of 0.001. All binding site plots have been aligned to the left. The light blue binding site present in the minWT is the gt-2 binding site deleted in the minΔgt-2 enhancer. The binding site with overlapping bars at the right end of the extWT and extΔgt-2 enhancers represents the gt-4 site predicted by the three PWMs in the flanking sequence of the extended enhancer. This binding site has been mutated in the extΔgt-2,Δgt-4 enhancer.