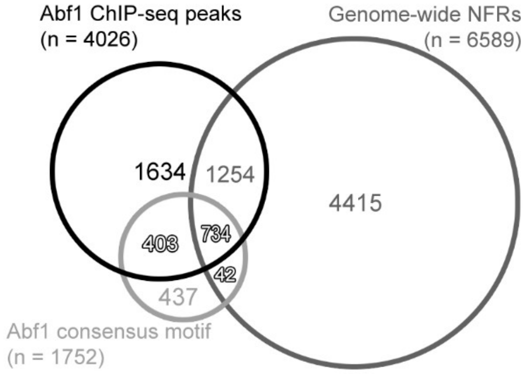

Figure S1 – Identification of GG-NER complex binding sites derived from Abf1 ChIP-seq peaks, genome-wide NFRs and Abf1 consensus sequence sites. The Venn diagram presented here subcatergorises the ChIP-seq Abf1 binding sites into classes based on their localisation to NFRs (n = 6,589) and/or Abf1 consensus motifs (n = 1,752). This Venn is used to identify GCBS's as described in Figure 2A. The numbers indicate precisely overlapping events for each category.