



Supplementary Figure 2: Transcription factor binding sites at the *c-fms* promoter and FIRE are partially occupied in *Pax5*^{-/-} progenitor cells. *In vivo* DMS footprinting analysis with freshly purified pro-B cells. From left to right, DMS-treated naked DNA (G), freshly purified primary pro-B cells and bone marrow-derived macrophages from *Pax5*^{-/-} and *RAG2*^{-/-} mice respectively. Transcription factor binding sites are indicated as a line. Black circles indicate hypermethylated G residues, open circles are hypomethylated G residues compared with DMS-treated naked DNA (G). Grey circles indicate weak footprints seen in *Pax5*^{-/-} progenitor cells. An enlarged view of each factor-binding site is shown to the right.