ESM Fig. 8 Histogram of enhancer widths for H3K4me1-predicted (black) and PDX1-, NEUROD1-, MAFA- and FOXA2-bound (PMNF) enhancers (red). Verticle dashed lines indicate the lower and upper thresholds selected to filter the H3K4me1-predicted (black) and PMNF (red) enhancers in order to discriminate loci with flanking nucleosome spacing characteristic of real enhancers. Note that the relatively high abundance of H3K4me1 flanked loci with nucleosome spacing below 250 bp as compared to in the PMNF data, which neccessitated the use of a much more stringent nucleosome spacing threshold for this data, in order to minimize false regions. This resulted in the identification of a number of regions using the PMNF data, that although were flanked by H3K4me1 enriched nuclesomes, were not identified in our H3K4me1 nucleosome based predictions