



S5. Histone modification expression signatures

Using the Human March 2006 hg18, assembly (NCBI Build 36.1), high-resolution maps for the genome-wide distribution have been generated (Barski et al., 2007; Wang et al., 2008). Adding each of 17 histone modification tracks found to be associated with expression to the UCSC browser we were able to show that in T-lymphocytes, for genes we find to be expressed in PBL, almost all of the gene promoters are associated with the signature (<http://dir.nhlbi.nih.gov/papers/lmi/epigenomes/hgtcell.html>). The signature was not present at promoters of genes which were not expressed. The examples of (i) *SNRPN*; an expressed gene, and (ii) the two *MEST* isoforms are shown. Each *MEST* isoform originates from a separate promoter, one of which is active in blood, the other not.