Supplemental Figure 4. Chromatin state of varying deleted regions. There is a greater variability in terms of chromatin composition of the lost regions in comparision to the region of gain. The D1 region had identical an A-compartment percentage (56%) across all samples and reflected loss of significant subtelomeric region, including *TNFRSF4*. The D2 region was consistent across all samples (range 96-100% A-compartment) with the exception of KMS11 (47%), however this switch to a B-compartment occurred in a gene-sparse region. The D3 region encompasses the tumour suppressor genes *CDKN2C* and *FAF1* and had similar active chromatin profiles (range 44-77%) except in RPMI8226 (0%). The D4 and D5 regions lie completely (100%) and near completely (>87%) in inactive compartments. Interestingly, the small A-compartments in D5 across U266 and RPMI8226 correspond to the tumour suppressor *FUBP1*. The D6 region showed conserved A-compartment across the samples specifically at the *RPL5* and *MTF2* loci while *EVI5* and *GFI1* showed switching from B-A across the differentiation stages. The D7 region, focused on *TENT5C* lies within an A-compartment across all samples except for KMS11, NBC=Naïve B-cell, MBC=Memory B-cell, GCBC=Germinal Center B-cell, PC=plasma cell.

