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Supplemental Material to:

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Variable maternal methylation overlapping the nc886/vtRNA2-1 locus is locked between hypermethylated repeats and is frequently altered in cancer

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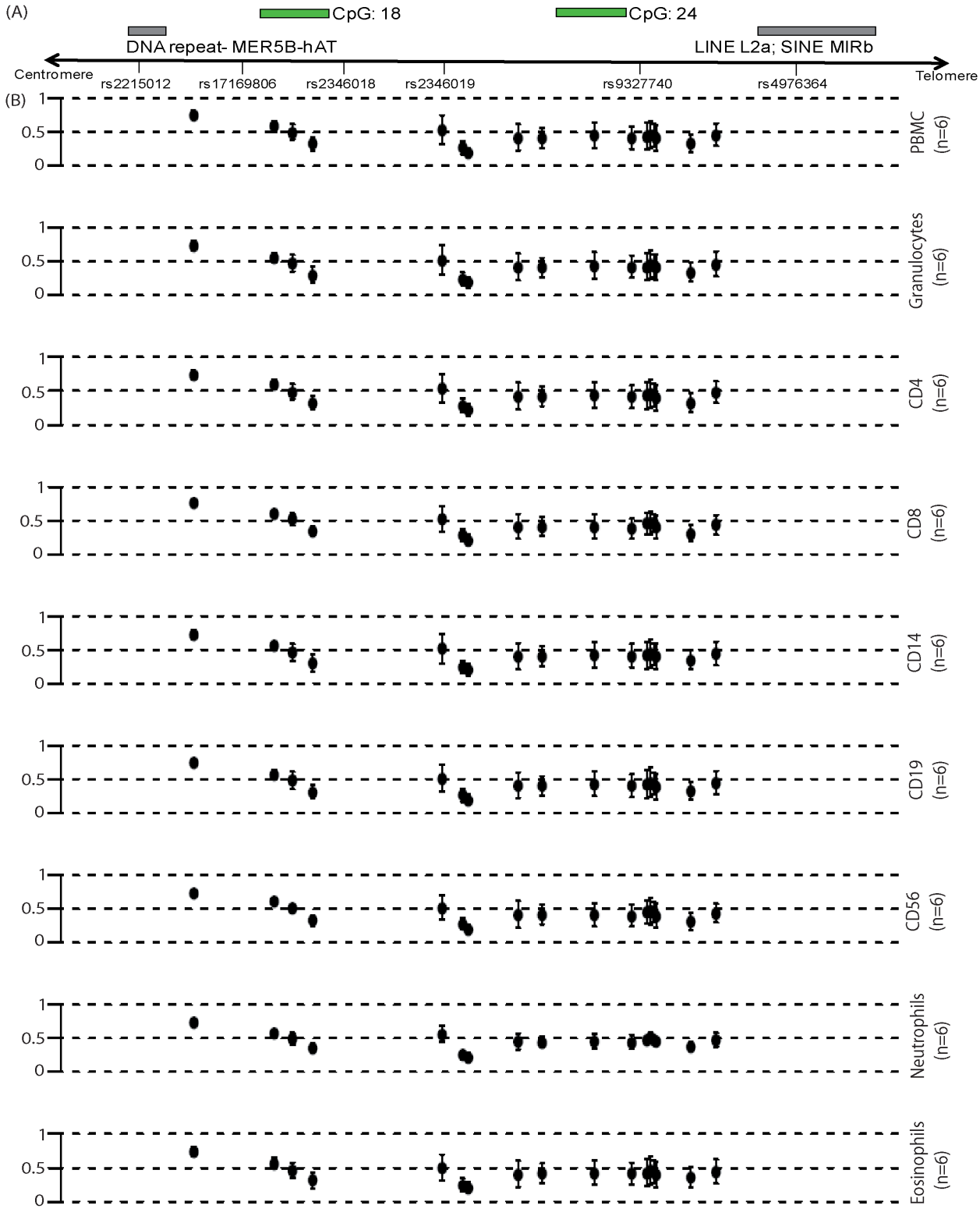

Supplementary Figure 1. Confirming the allelic methylation profile in immuno-selected blood lineages. (A) Map of the *nc886* locus and (B) Detailed methylation profile of peripheral blood mononucleated cells (PBMCs), granulocytes, CD4, CD8, CS14, CD19, CD14, CD56, neutrophils and eosinophil cells as determined by Infinium HumanMethylation450 beadChip arrays. The data points represent the average of 6 individual cell enrichments and the bars give the range of methylation.