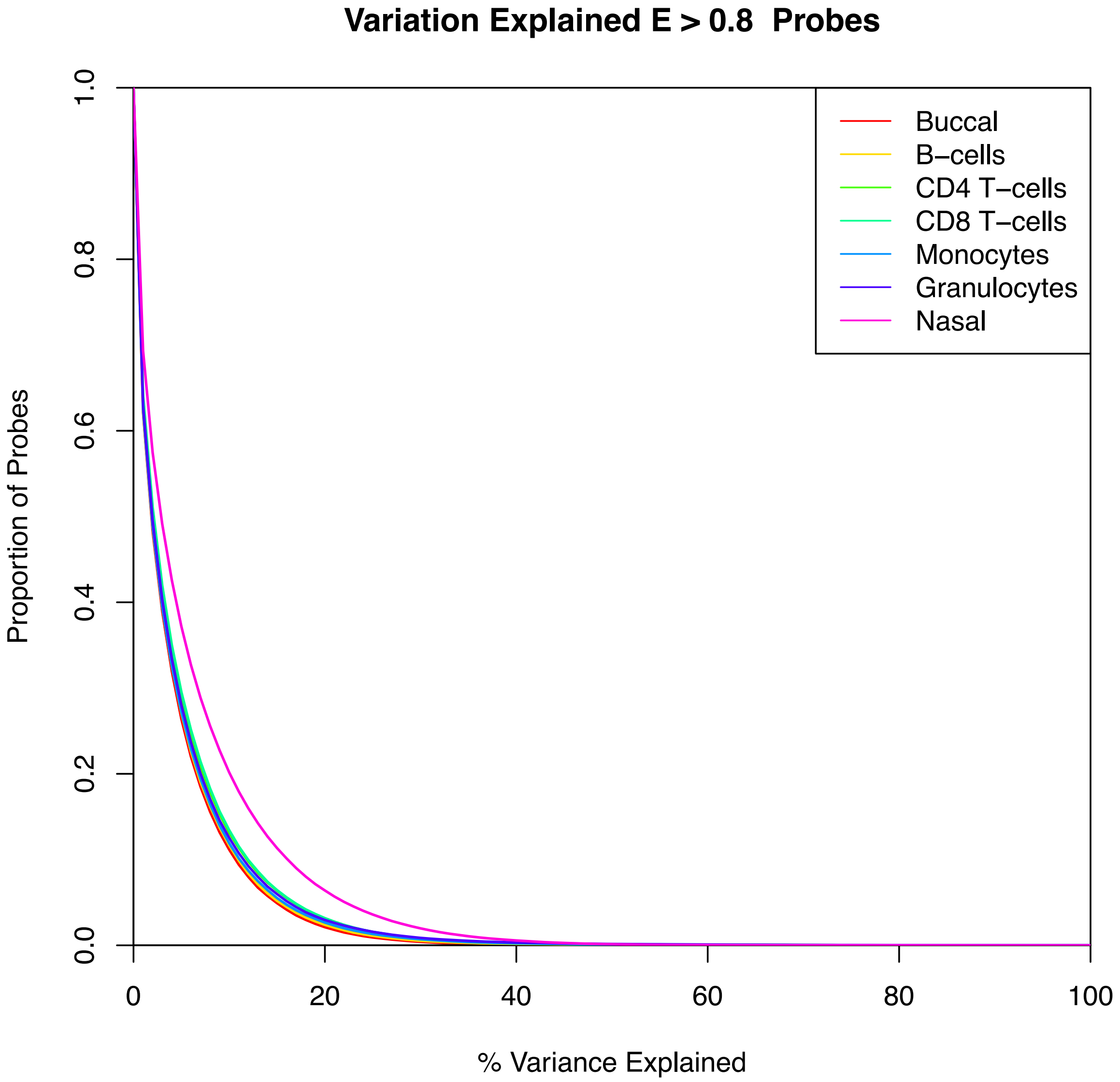
Figure S19. Variation in DNA methylation in whole blood as a predictor of variation in the isolated blood cell types and other peripheral tissues for sites strongly influenced by non-shared environmental factors. Shown for the subset of sites where whole blood DNAm is strongly influenced by non-shared environmental factors (non-shared environmental effects on DNAm > 0.80, n = 143,501 sites) using estimates from Hannon et al[1] is the proportion of sites (y-axis) for which variation in whole blood DNA methylation explains different levels of variance in five blood cell types (monocytes, granulocytes, $CD4^+$ T cells, $CD8^+$ T cells and B cells) isolated from the same individuals.



1. Hannon, E., et al., Characterizing genetic and environmental influences on variable DNA methylation using monozygotic and dizygotic twins. PLoS Genet, 2018. 14(8): p. e1007544.