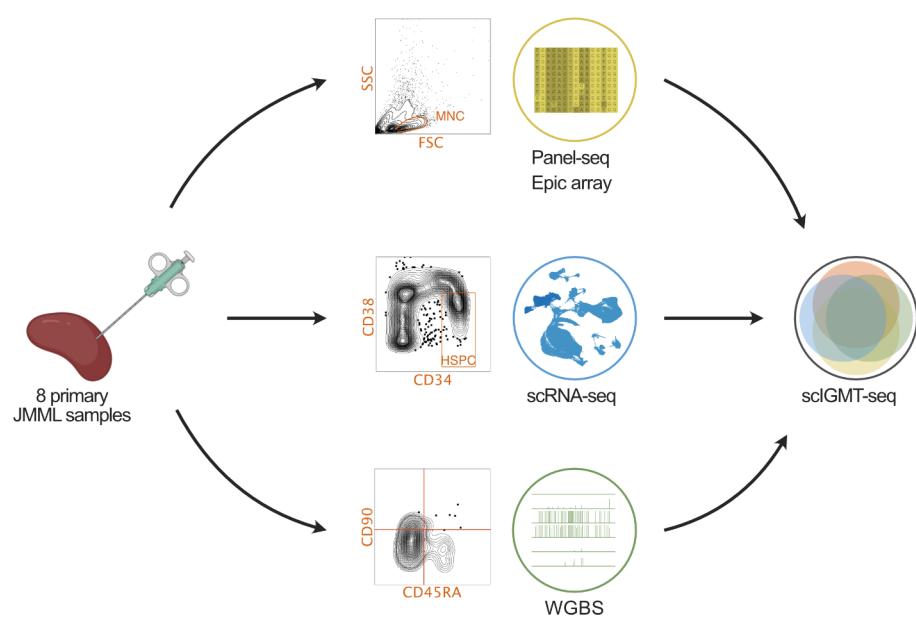
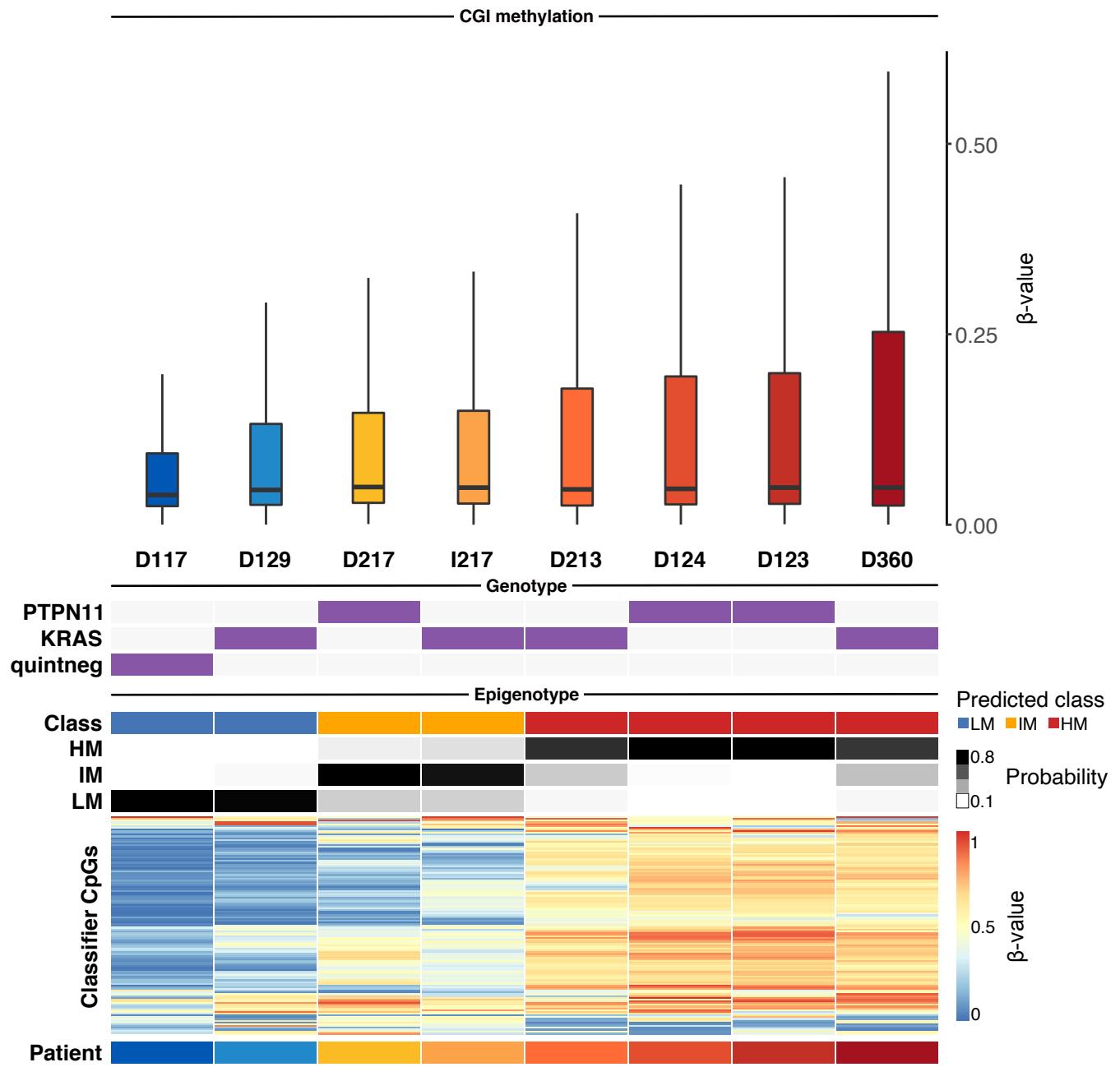


Aspect 1: Multi-modal analysis of epigenetic subgroups (risk groups) in JMML

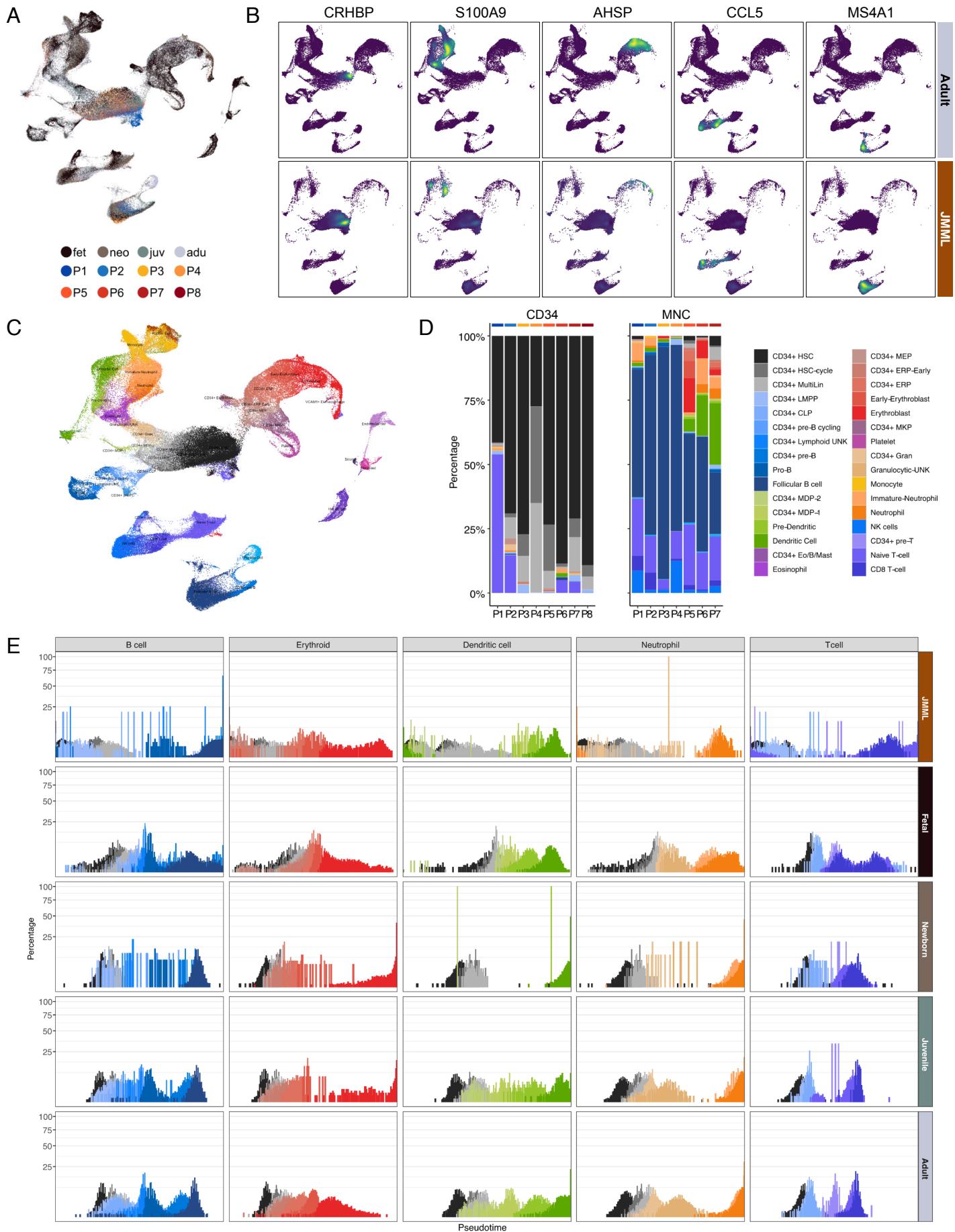
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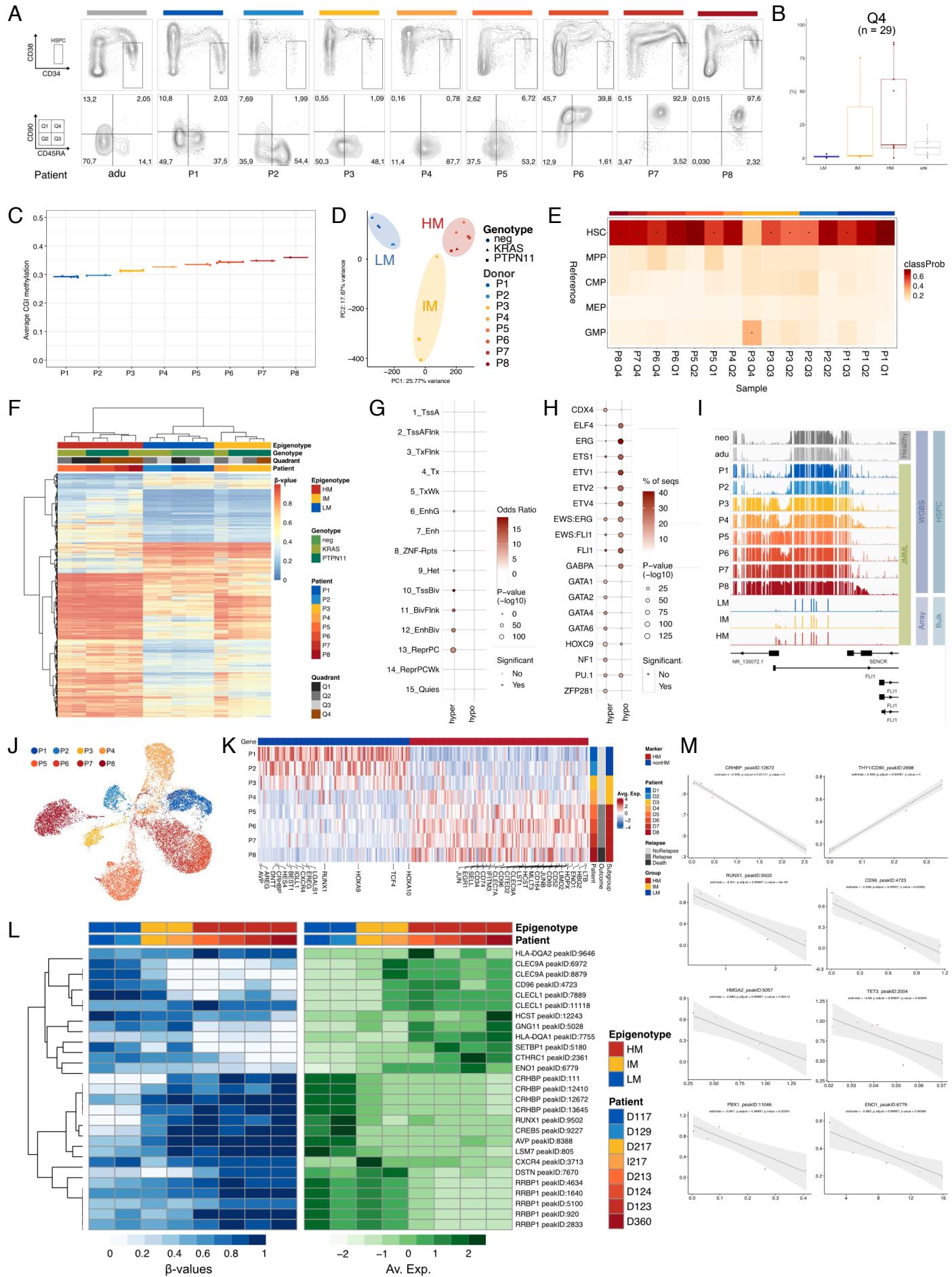
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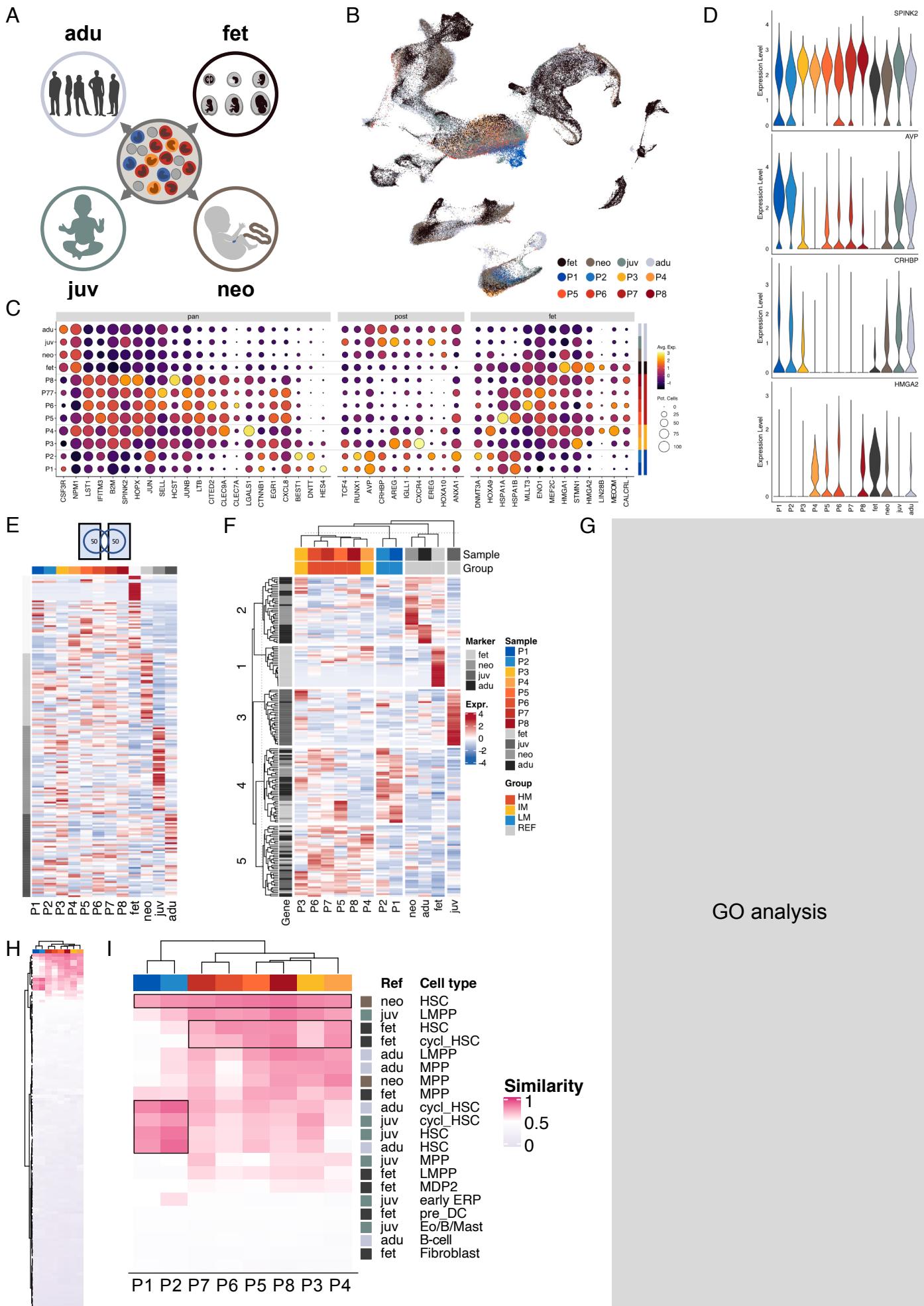
Aspect 2: JMML-related aberrations affect total hematopoiesis starting from HSPCs



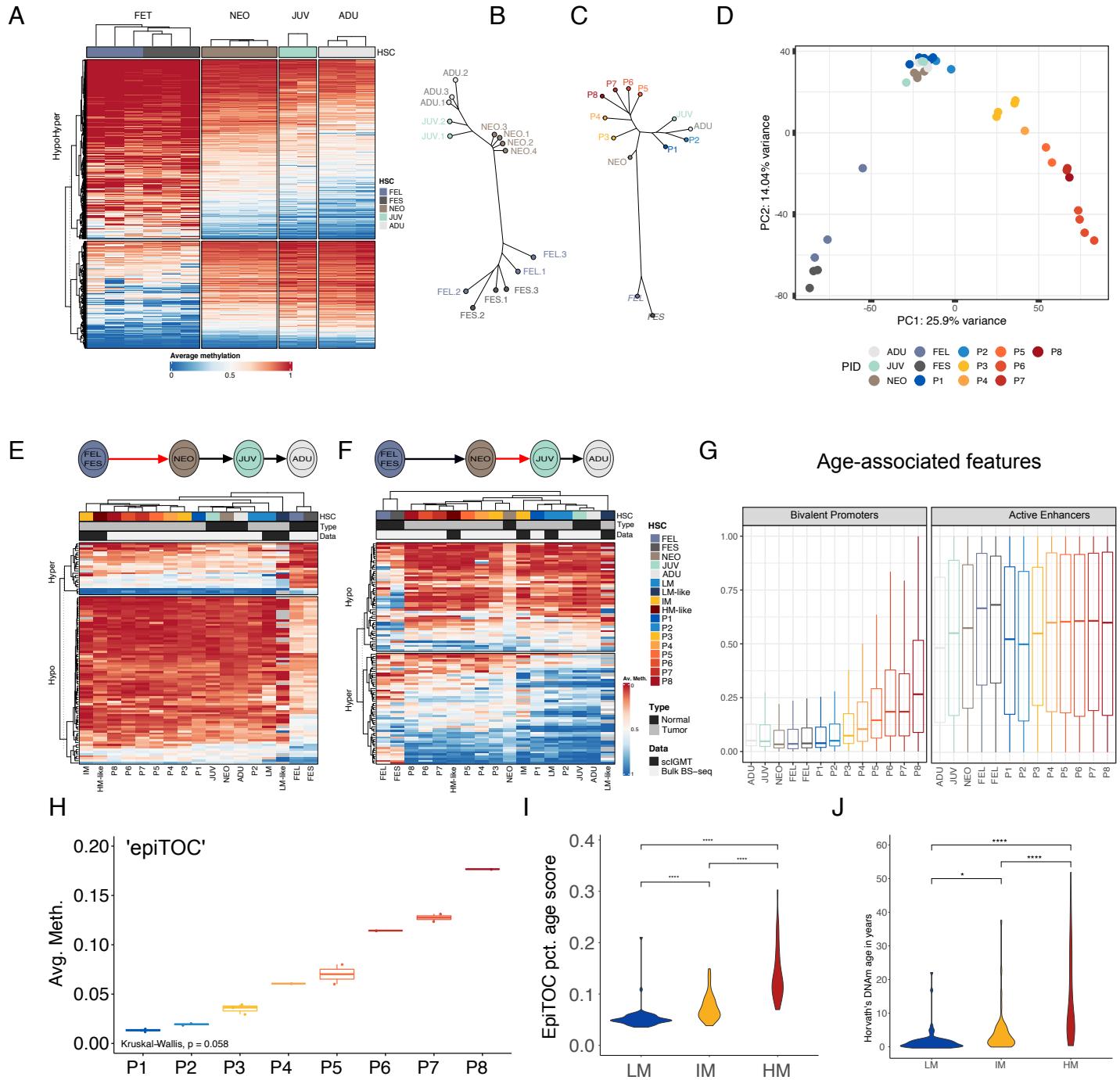
Aspect 3: Subgroup-specific heterogeneity reveals HSPCs as the compartment of origin in JMM



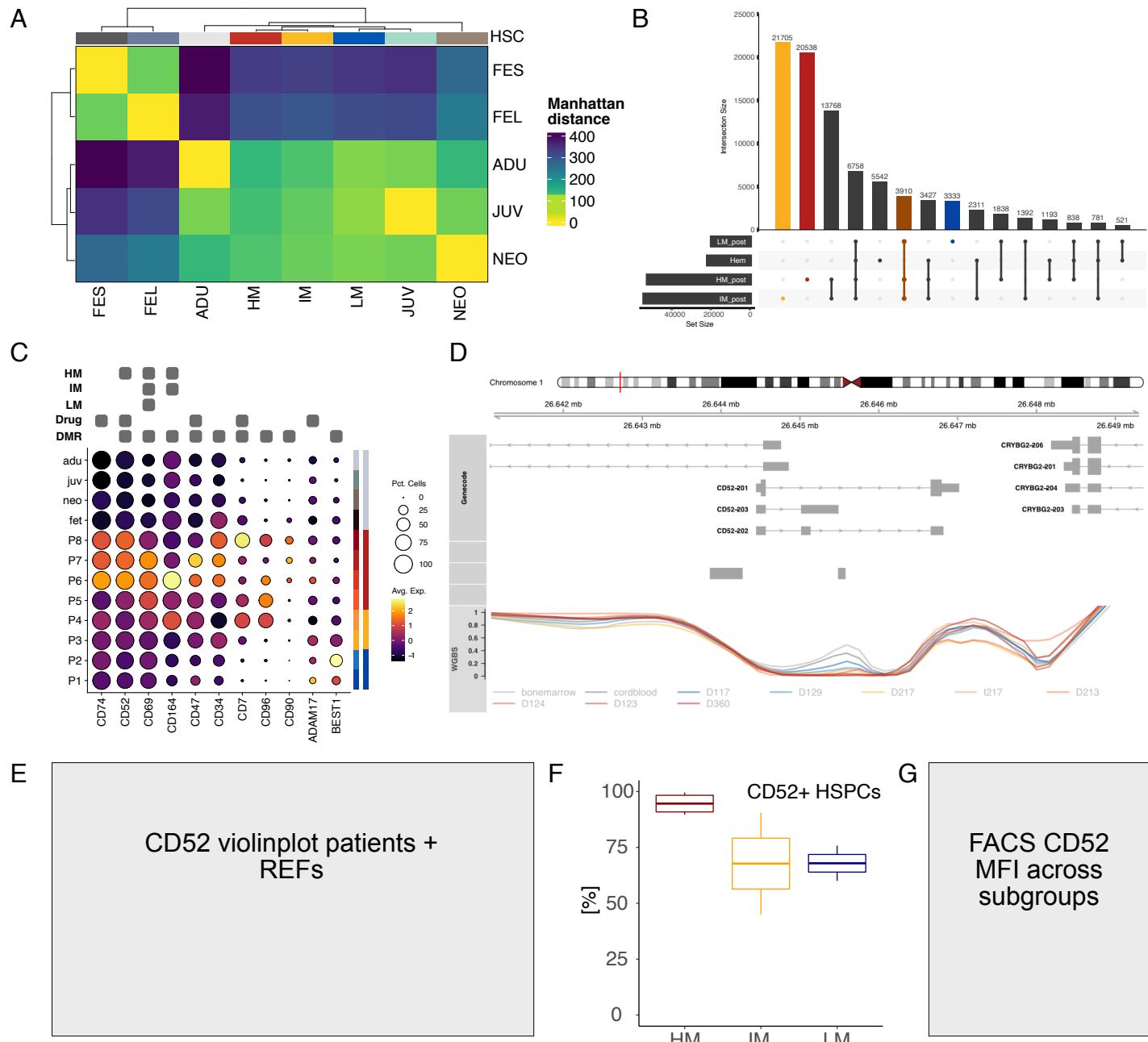
Aspect 4: Distinct developmental programs in HSPCs across JMML subgroups



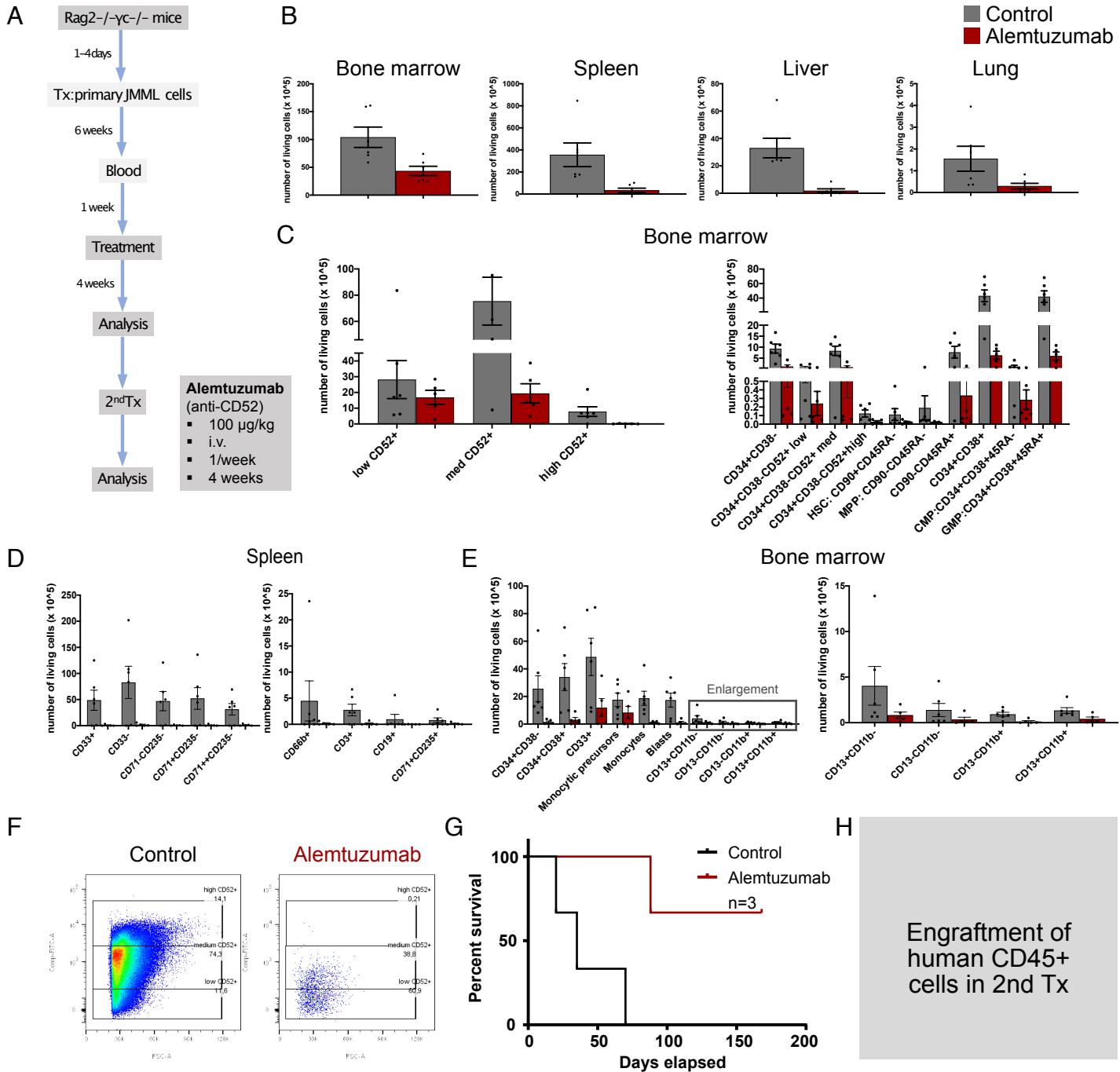
Aspect 5: Progressive epigenomic reprogramming of high-risk HSPCs results in accelerated aging and onco-fetal signatures



Aspect 6: Subgroup-specific aberrations reveal CD52 as a prognostic biomarker for high-risk HSPCs.



Aspect 7: An anti-CD52 treatment efficiently depletes HM LSCs and improves survival in a JMML PDX model



Aspect 8: A native single-cell multi-omics analysis reveals CD52 as a marker of high-risk leukemia stem cells

