

# **B-lineage acute lymphoblastic leukemia causes cell-autonomous defects in long-term hematopoietic stem cell function**

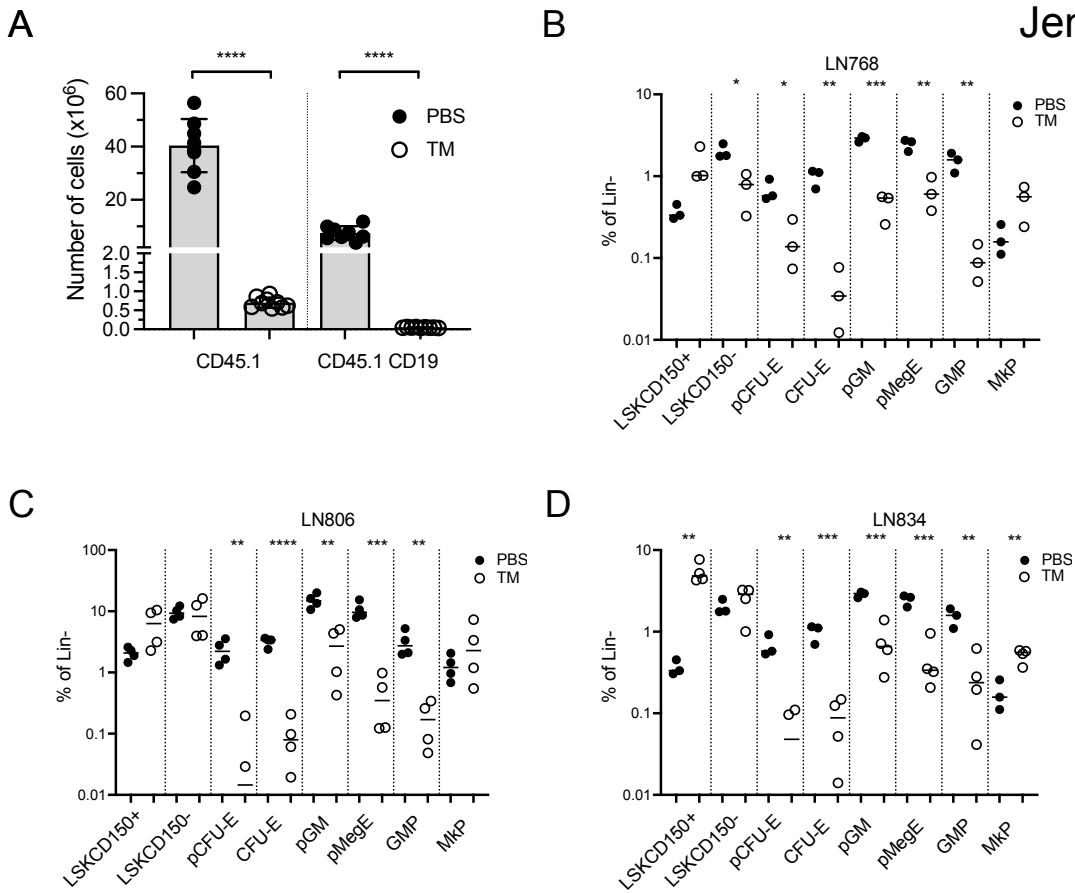
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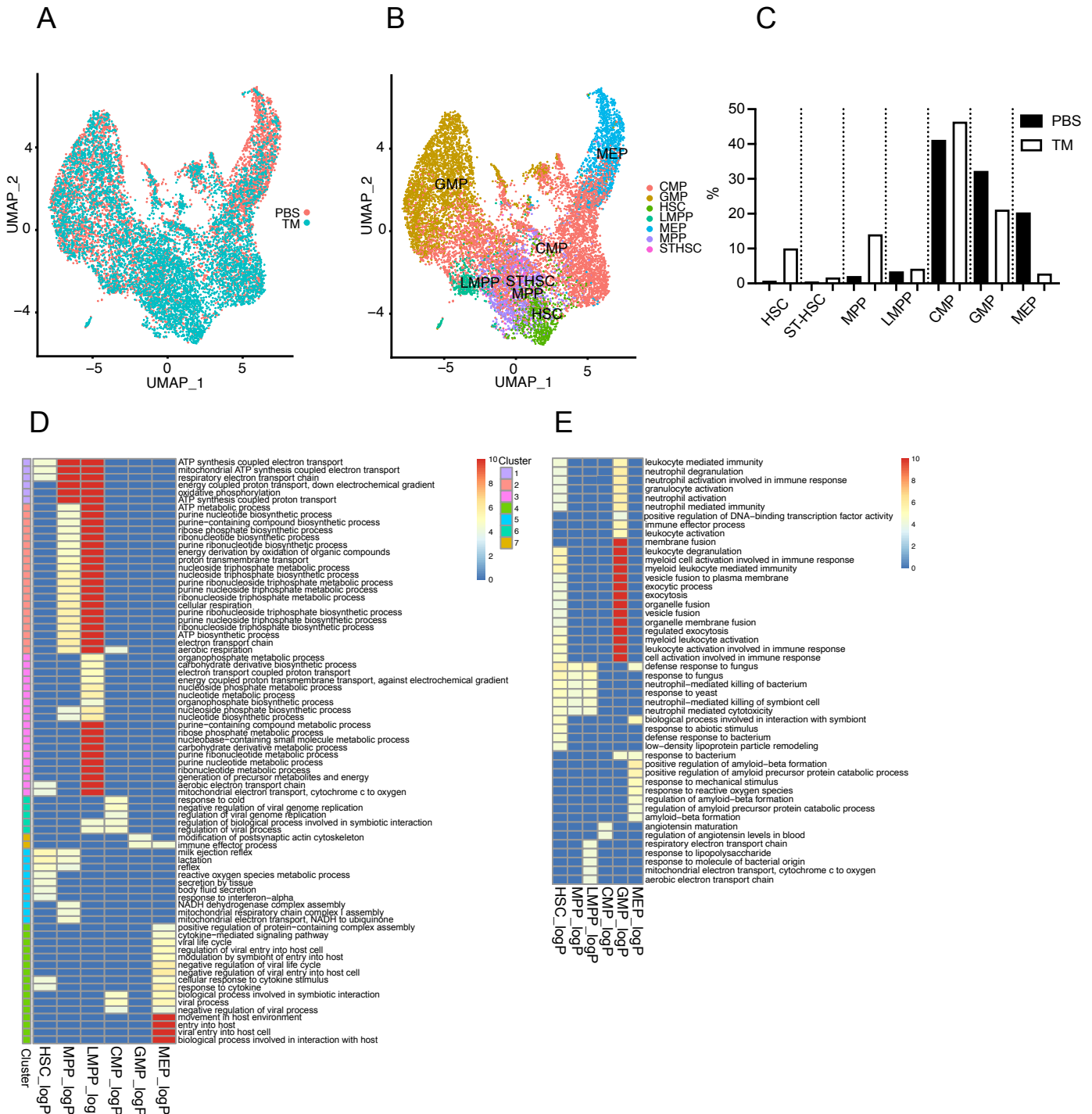
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<https://doi.org/10.3324/haematol.2022.282430>



**Figure S1: Leukemia causes a selective depletion of lineage restricted progenitors with a preserved HSC compartment.**

(A) The graph shows the total endogenous cell contribution (CD45.1<sup>+</sup> and CD45.1<sup>+</sup>CD19<sup>+</sup>) to the BM at 22 days in PBS or tumor transplanted (TM) CD45.1 mice. \*\*\*\*  $p < 0.0001$  (Student's t test), from a total of 8 PBS and 9 TM samples per condition from 2 independent experiments. The graphs display the percentage of BM progenitors of Lin<sup>-</sup> cells in PBS or tumor transplanted CD45.1 mice where the tumor engraftment exceed 60% of the BM in TM samples (B) LN768, (C) LN806 and (D) LN834. \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ , \*\*\*\*  $p < 0.0001$  (Student's t test), from a total of 4 PBS (control for LN806) and 4 LN806 samples and 3 PBS (the same controls for LN768 and LN834 as done in the same experiment), 3 LN768 and 4 LN834 samples. In panels C and D, two TM mice showed undetectable numbers of pCFU-E cells.



**Figure S2 : Leukemia exposure impacts gene expression patterns in non-transformed progenitor compartments in the BM.**

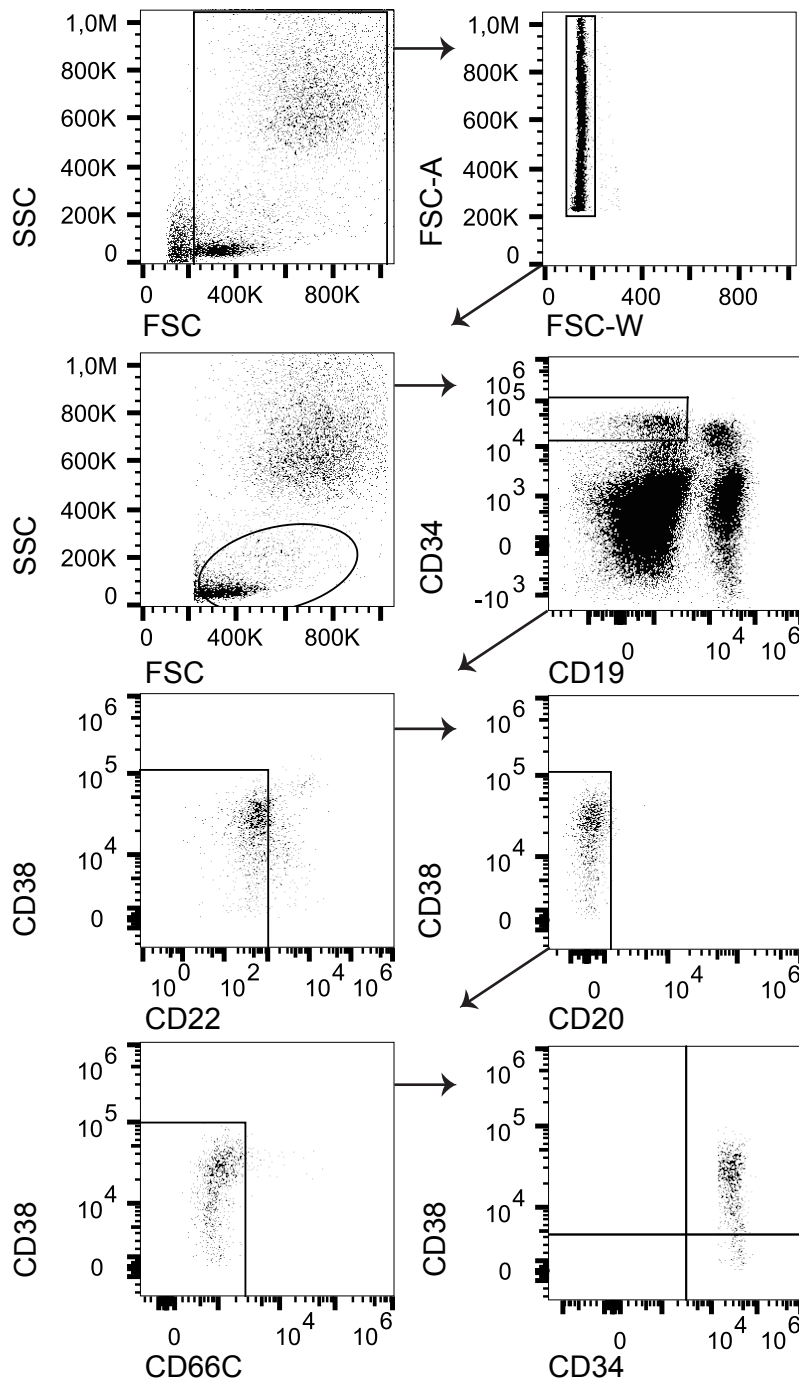
(A) UMAP with single cell RNA sequencing data of 11,764 KIT +Lin-CD45.2-CD45.1+ BM cells merged from PBS and TM injected mice.

(B) Shows a UMAP indicating specific progenitor populations according to Nesterowa et al.

(C) The frequencies of each population in leukemic and control BM.

(D) A heatmap showing enriched ontologies from differentially expressed upregulated genes in TM over PBS cells within an assigned cell type.

(E) A heatmap showing enriched ontologies from differentially expressed downregulated genes in TM over PBS cells within an assigned cell type.



**Figure S3: Reanalysis of patient data allows for the identification of endogenous progenitor cell compartments in leukemia.**

Flow cytometry profiles showing the gating strategy for analyzing HSC and progenitors in patient BM applied in Figure1 and 2.