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2 **Description of Additional Supplementary Files**

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4 File Name: Supplementary Data 1

5 Description: **Comparison of HSC transcriptome between endosteal and central BM in WT mice.**

6 Sample information, matrix of raw gene counts, normalized gene counts, differential gene

7 expression analysis (Gene_DE_baseline) and gene set enrichment analysis (GSEA) showing pathways

8 enriched in central (negative NES) or endosteal (positive NES) HSCs. NES, normalized enrichment

9 score. FDR, False Discovery Rate. Kolmogorov Smirnov test.

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11 File Name: Supplementary Data 2

12 Description: **Comparison of HSC transcriptome between endosteal and central BM in Gfra2$_{-/-}$ mice.**

13 Sample information, matrix of raw gene counts, normalized gene counts, differential gene

14 expression analysis (Gene_DE_baseline) and gene set enrichment analysis (GSEA) showing pathways

15 enriched in central (negative NES) or endosteal (positive NES) HSCs. NES, normalized enrichment

16 score. FDR, False Discovery Rate. Kolmogorov Smirnov test.

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18 File Name: Supplementary Data 3

19 Description: **Patient characteristics.** AML, acute myeloid leukemia; MDS, myelodysplastic syndrome;

20 ALL, acute lymphoblastic leukemia; MM, multiple myeloma; NHL, NonHodgkin lymphoma; HL,

21 Hodgkin lymphoma; CLL, chronic lymphocytic leukemia; CMML, chronic myelomonocytic leukemia.

22 File Name: Supplementary Data 4

23 Description: The sequence of oligonucleotides used for quantitative real-time RT-PCR.

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