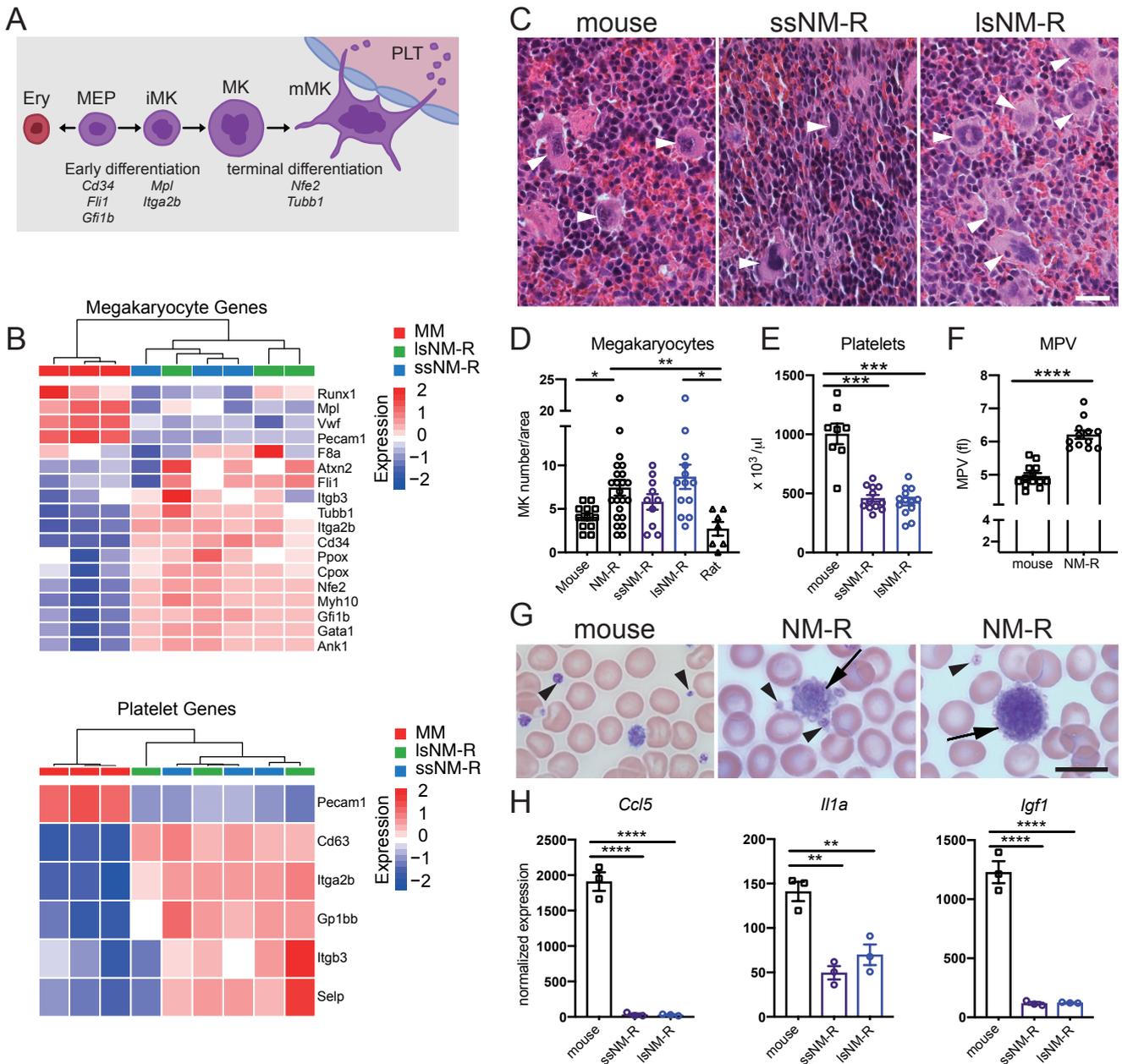


Fig. S8



**Fig. S8: Extramedullary megakaryopoiesis does not contribute to the hyperplastic spleen of IsNM-Rs.**

**(A)** Schematic representation of megakaryocytic differentiation. Ery: erythrocyte, MEP: megakaryocyte-erythroid progenitor, iMK: immature MK, mMK: mature MK, PLT: platelets. **(B)** Heatmap of genes associated with megakaryopoiesis (top) and platelets (bottom) in mouse and NM-R spleen. Samples are hierarchically clustered based on Pearson correlation. **(C)** H&E staining of megakaryocytes (white arrowheads) in the spleen of mouse, ssNM-R and IsNM-R. **(D)** Quantification of megakaryocytes (MK) found in mice ( $n = 12$ ), NM-R (combined ssNM-R and IsNM-R,  $n = 23$ ), ssNM-R ( $n = 10$ ), IsNM-R ( $n = 13$ ) and rat ( $n = 7$ ). **(E)** Platelet count in the PB of mice ( $n = 8$ ), ssNM-R ( $n = 12$ ) and IsNM-R ( $n = 13$ ). **(F)** Mean platelet volume (MPV) in PB of mice ( $n = 13$ ) and NM-Rs ( $n = 12$ ). **(G)** Representative May-Grünwald staining of platelets found in PB smears of mouse and NM-R: mature platelets (arrowhead); immature platelets (arrow). **(H)** Normalized RNA expression levels of 3 regulatory genes of MK terminal differentiation. Unpaired t test in D-F and one-way ANOVA with Tukey's post-hoc test for multiple comparisons in H: p value  $* < 0.05$ ,  $** < 0.01$ ,  $*** < 0.001$  and  $**** < 0.0001$ . Transcriptomic data is based on RNAseq, MM: mouse (*Mus musculus*). Data represent mean  $\pm$  s.e.m, scale bars = 20  $\mu\text{m}$  (C) and 10  $\mu\text{m}$  (G).