Mutant KLF1 in Adult Anemic *Nan* Mice Leads to Profound Transcriptome Changes and Disordered Erythropoiesis

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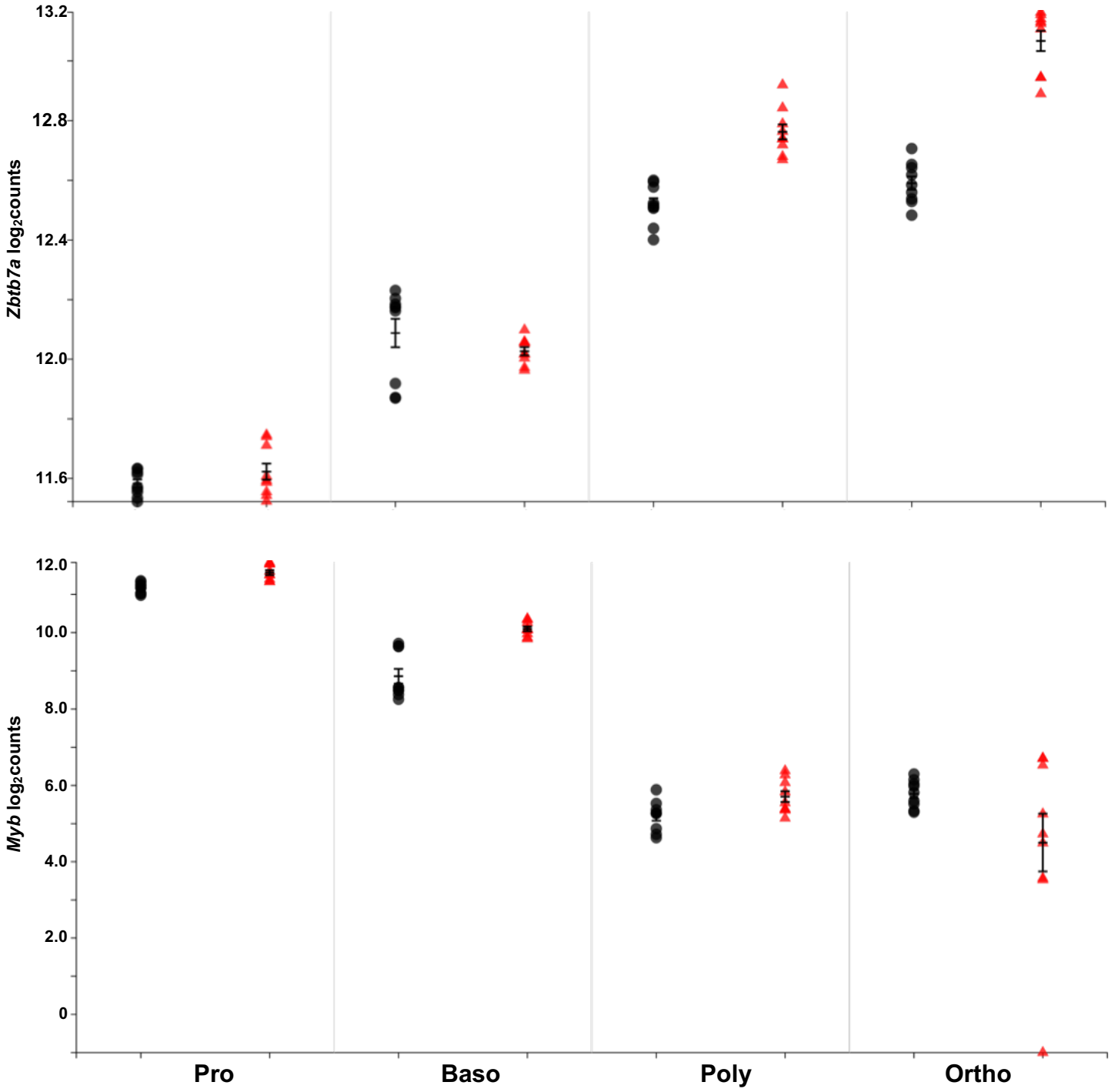
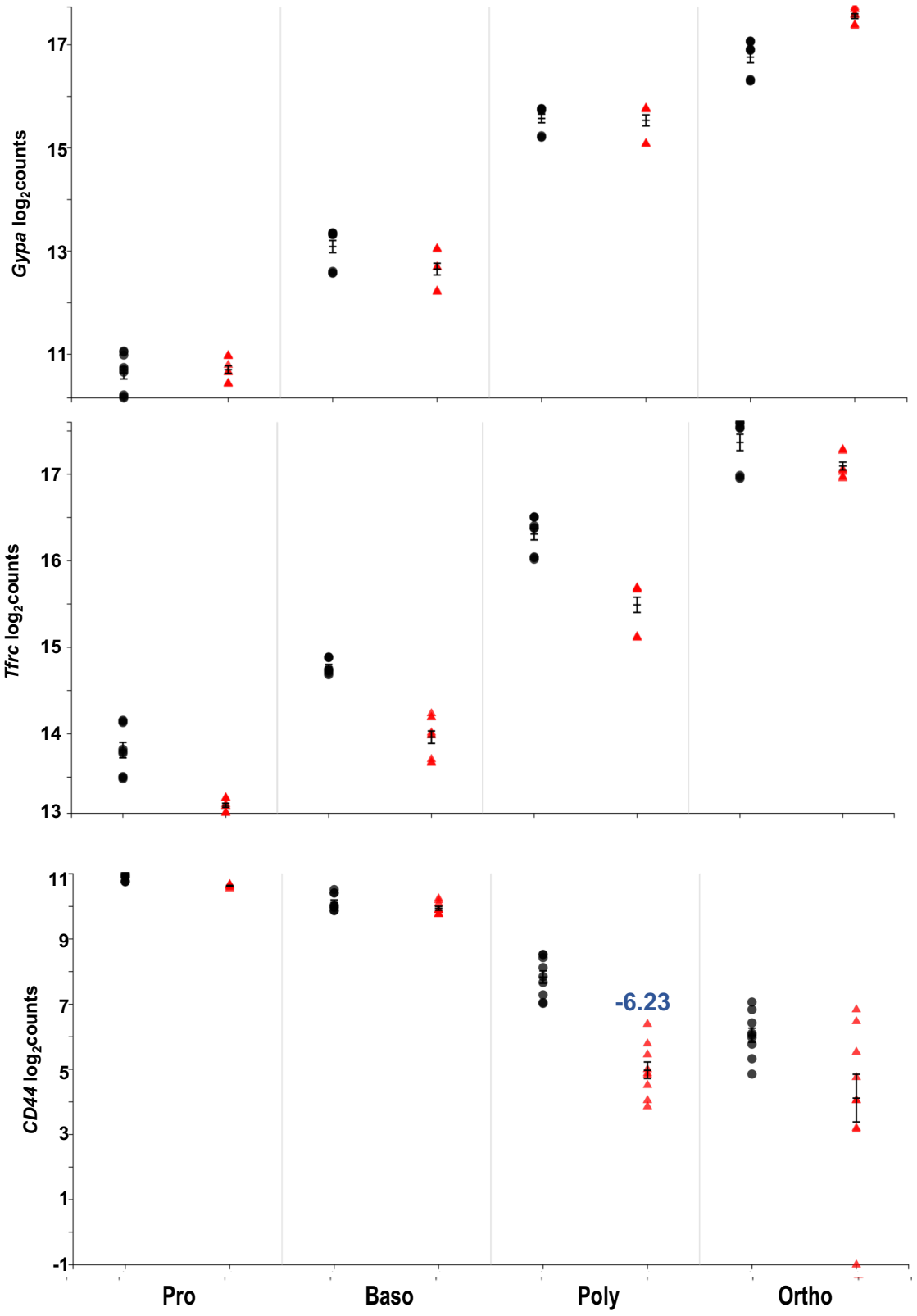
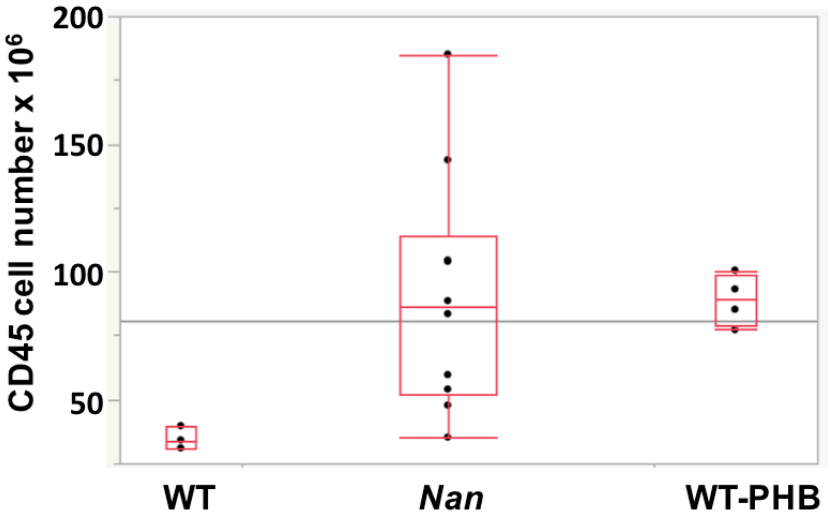


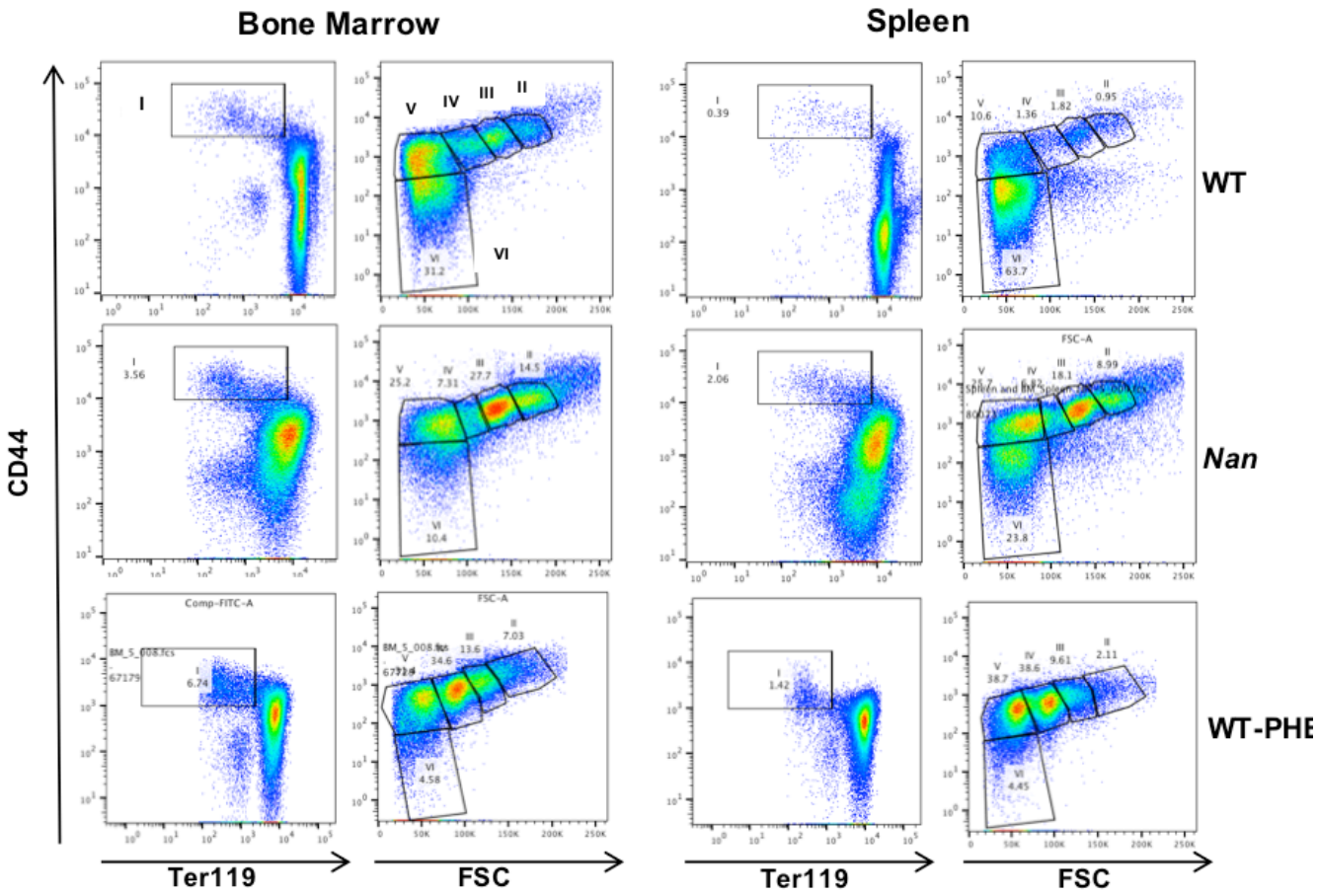
Supplemental figure 1. Expression of *Zbtb7a* and *Myb* in *Nan* and WT-PHB spleen erythroid precursors (RNAseq).



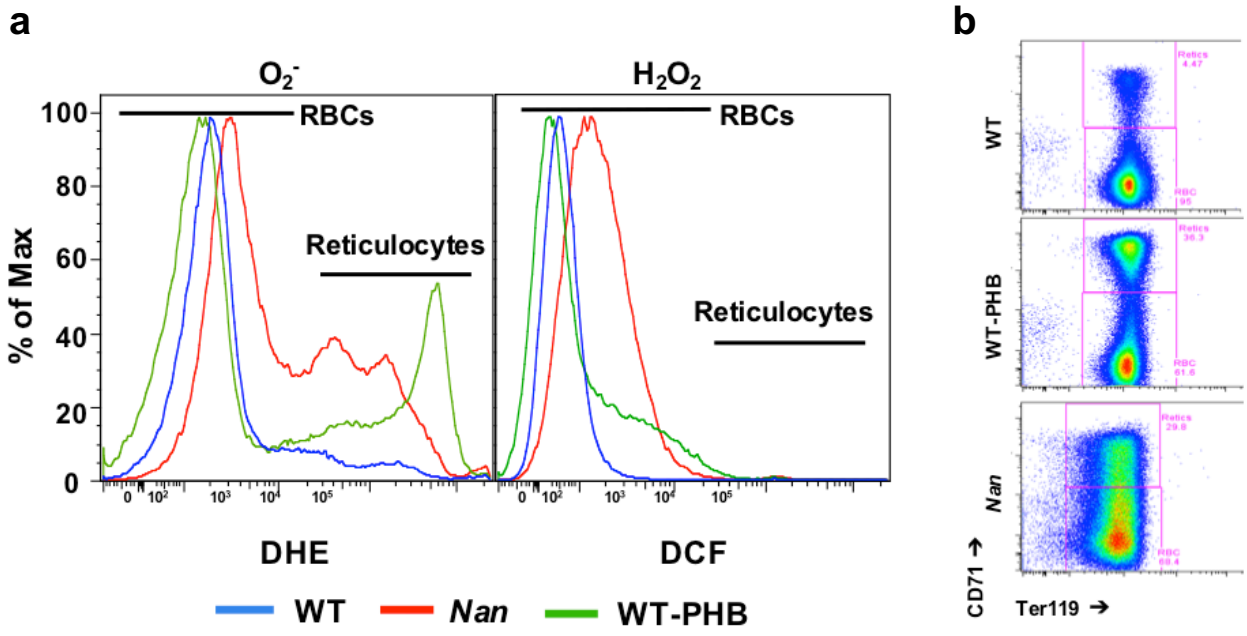
Supplemental figure 2. Surface markers for flow-cytometric analysis of erythropoiesis. With the exception of CD44 in polychromatophilic erythroblasts, which is downregulated in *Nan* (6.23 fold), no significant differential expression is seen in *Nan* vs. WT-PHB precursors (see also supplemental Tables 3-6). *Gypa* encodes mouse Ter119; *Tfrc* encodes surface marker CD71 (transferrin receptor).



Supplemental figure 3. Boxplots illustrating range of values for erythroid cell counts in WT, *Nan* and WT-PHB spleen.



Supplemental figure 4. Flow cytograms showing gating of cell populations in bone marrow and spleen. I, pro-; II, baso-; III, Poly-; IV, orthochromatophilic erythroblasts; V, reticulocytes; VI, mature red cells



Supplemental figure 5. (a) Representative flow cytometric analysis of WT, WT-PHB, and *Nan* whole blood incubated with superoxide-sensitive dye DHE and peroxide-sensitive H2DCFDA (DCF). Mature red cells are the major peak while reticulocytes, which produce higher ROS levels, are in the tail. **(b)** Separation of reticulocyte and RBCs populations in whole blood using CD71 and Ter119.