

Genetic disarray follows mutant KLF1-E325K expression in a congenital dyserythropoietic anemia patient

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Supplemental information for:

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Supplemental Figure 1

Figure S1. Analysis of patient RNA. (A) RT-qPCR analysis of γ - and β -globin RNA expressed in the proliferation/differentiation CDA series (P d11, P d15, D d5) and presented as $\gamma/(\gamma+\beta)$. (B) cDNA sequence chromatograms confirming transcription of both alleles (WT codon GAG (glu: E) and mutant codon AAG (lys: K)) in the CDA cells in the proliferation/differentiation series (P d11, P d15, Diff d5); WT only expresses codon GAG (glu: E).

Supplemental Figure 2

Figure S2. Expression levels of megakaryocyte genes. Relative FPKM expression values of selected megakaryocyte genes⁶¹ from the proliferation/differentiation series, grouped together and color coded as in Figure 2.

Supplemental Table 1

FPKM values of all six samples (CDA d11, d15, diff d5, and WT d11, d15, diff d5) for all genes.

Supplemental Table 2

Genes exclusively expressed within selected subsets (relevant to Figure 4).

Supplemental FIGURE S1

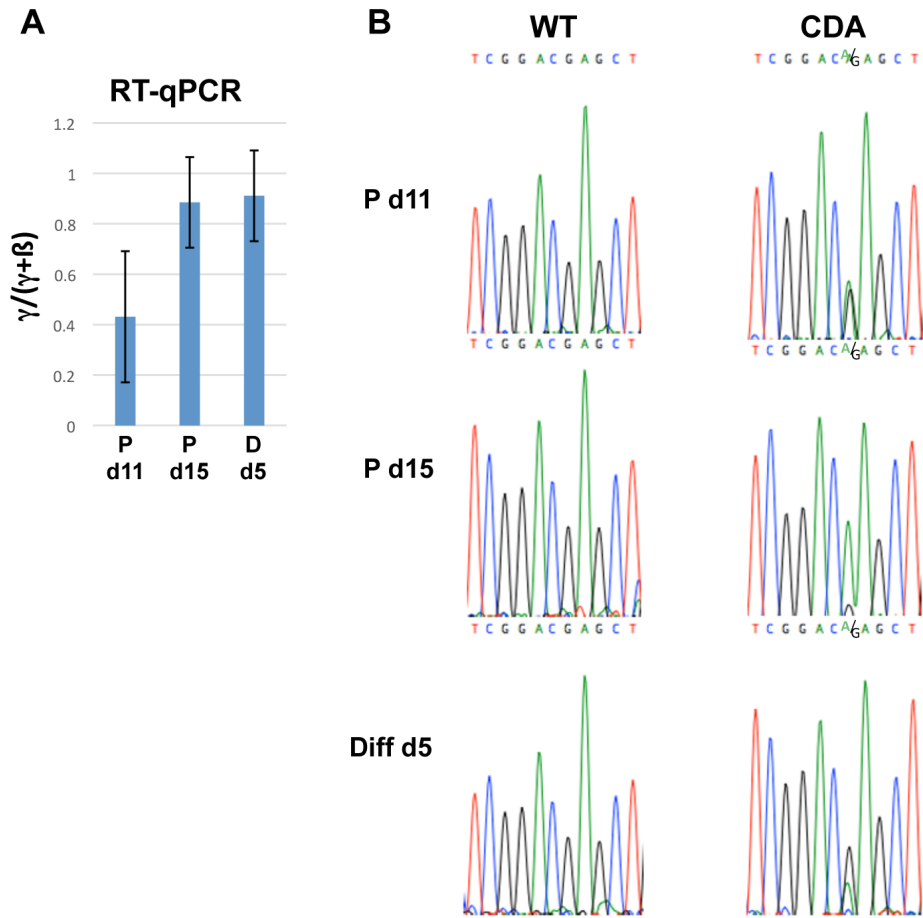


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Supplemental FIGURE S2

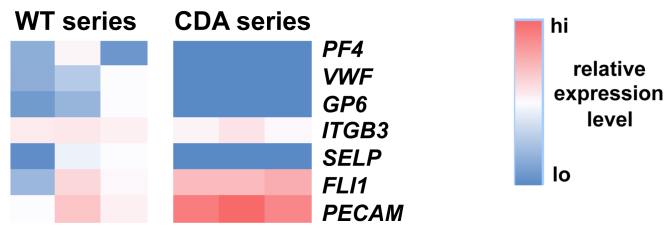


Figure S2. Expression levels of megakaryocyte genes. Relative FPKM expression values of selected megakaryocyte genes (ref 61) from the proliferation/differentiation series, grouped together and color coded as in Figure 2.