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Disruption of thrombocyte and T lymphocyte development by a mutation in *ARPC1B*

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Supplementary Figure 1. Differential *VDJ* **gene usage relative to the number of unique sequences in the patients'** *TRB***,** *TRG* **and** *IGH* **repertoires.** The frequencies of gene usages based on unique sequences for the patients for *TRBV* and *TRBJ* genes (A), *TRGV* and *TRGJ* genes (B) and *IGHV*, *IGHD* and *IGHJ* genes (C), are compared to the frequencies (average \pm SEM) of gene usage of two controls in *TRB* repertoire and four controls in *TRG* and *IGH* repertoires.

Supplementary Figure 2. WISH analysis of *arpc1b* **and** *arpc1a* **expression in zebrafish hematopoietic system.**

A, Amino acid sequence alignments of human, mouse and zebrafish *arpc1b*. * beneath the sequences indicates identity. *B,* Syntenic relationship between zebrafish *arpc1b* (on Dre.3) and human *ARPC1B* (on Hsa.7). Red arrows indicate that the *arpc1b* gene in zebrafish and the *ARPC1B* gene in humans are flanked by other syntenic orthologs. *C-D,* WISH analysis on 26hpf zebrafish embryo for *arpc1b* **(C)** and *arpc1a* **(D)**. Lateral view with head to the left. Insets depict the blood cells in yolk (black arrows), AGM and PBI regions (bold black arrows). *Aprc1a* WISH exhibits staining in head and trunk areas but unlike that of *arpc1b,* it does not stain hematopoietic cells.

Supplementary Figure 3. Validation of *arpc1b* **knockdown in zebrafish embryo.**

A. Genomic structure of zebrafish *arpc1b* locus*.* Red lines mark the targeting sites of translationblocking or splicing site MO. *B.* RT-PCR examination of endogenous *arpc1b* expression in control and *arpc1b* splice site MO injected embryos. *β-actin* serves as the internal loading control. *C.* EGFP reporter assay for functional validation of *arpc1b* ATG (translation-blocking) MO. *D.* Thrombocyte development was disrupted after *arpc1b* knockdown in 3.5dpf *Tg(cd41:EGFP)* transgenic embryos (red rectangles and white arrows). The embryos were photographed by lateral views. The numbers on the images refer to the fraction of embryos with the depicted phenotype. CHT: caudal hematopoietic tissue. *E.* The presence of the intact and mutant human *ARPC1B* mRNA employed to rescue development was verified by RT-PCR analysis at 3.5dpf.

Supplementary Table 1. Summary of the *V(D)J* **gene usages in the total and unique sequences of TCR and BCR repertoires from patients and controls.**

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The gene usages frequencies of the patients, and mean and two Standard Errors (SE) below or above the mean of the gene frequencies for the healthy controls (Mean \pm 2 x SE) are summarized and compared for the total and unique sequences of the T and B cell receptor repertoires. For each gene that are utilized either more or less than two SE above the mean of the controls were noted with either "+" or "-" sign, respectively. The gene names (on the far right column) was colored in: green for genes that are higher in both patients; red for the genes that are higher in patient 1; and orange for the genes that are higher in patient 2.