Supplementary Figures

A comprehensive, cell specific microRNA catalogue of human peripheral blood

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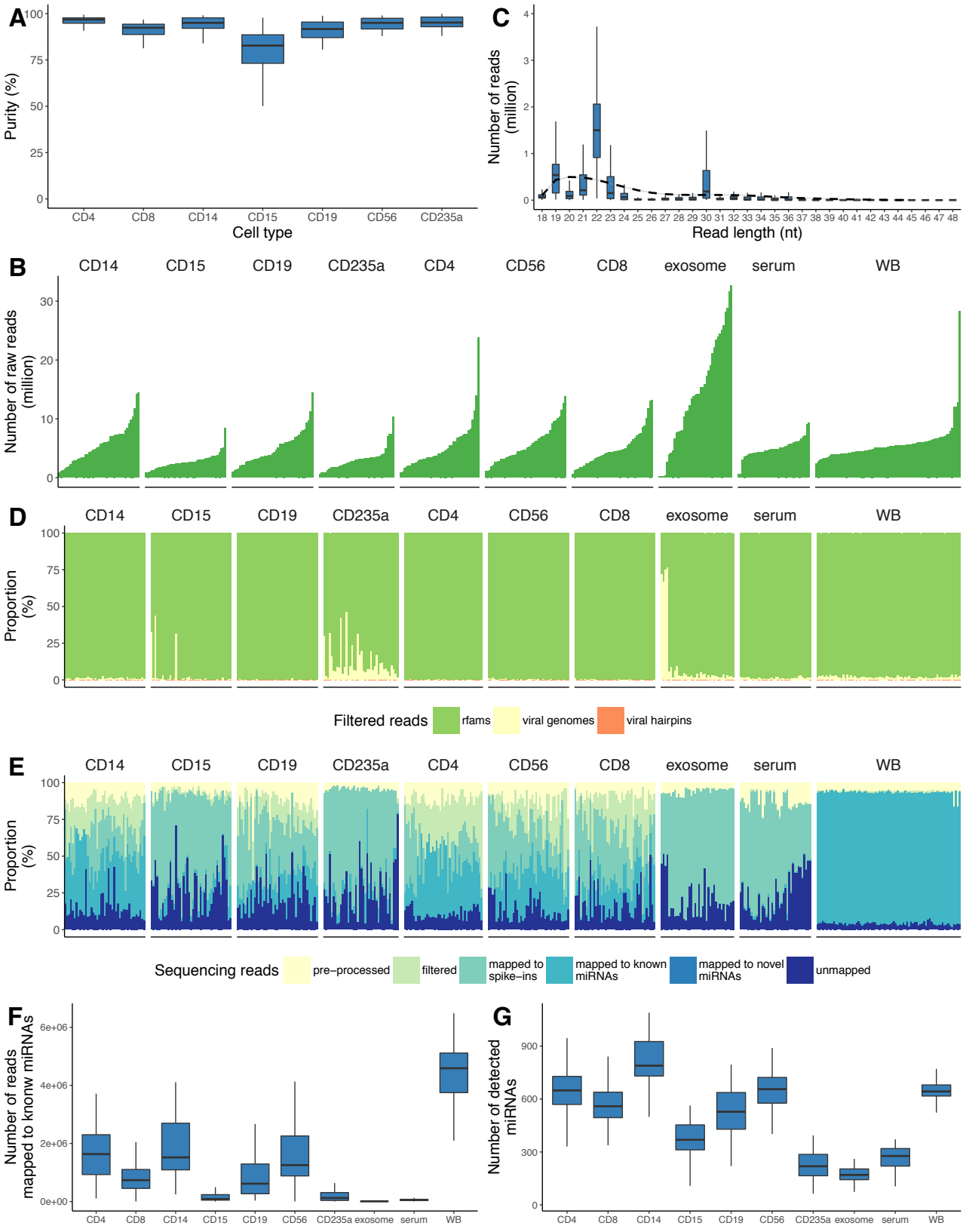
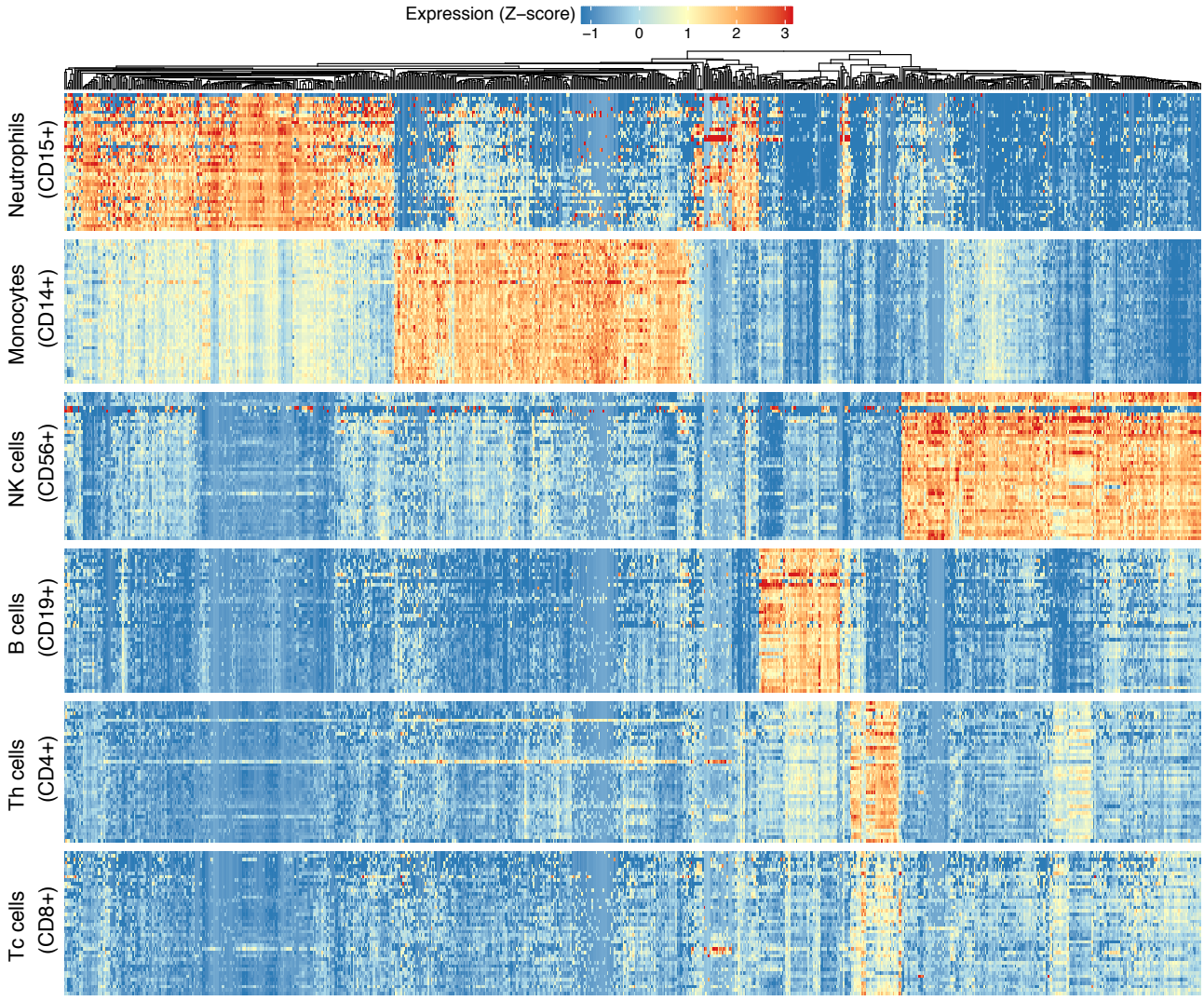
Supplementary Figures



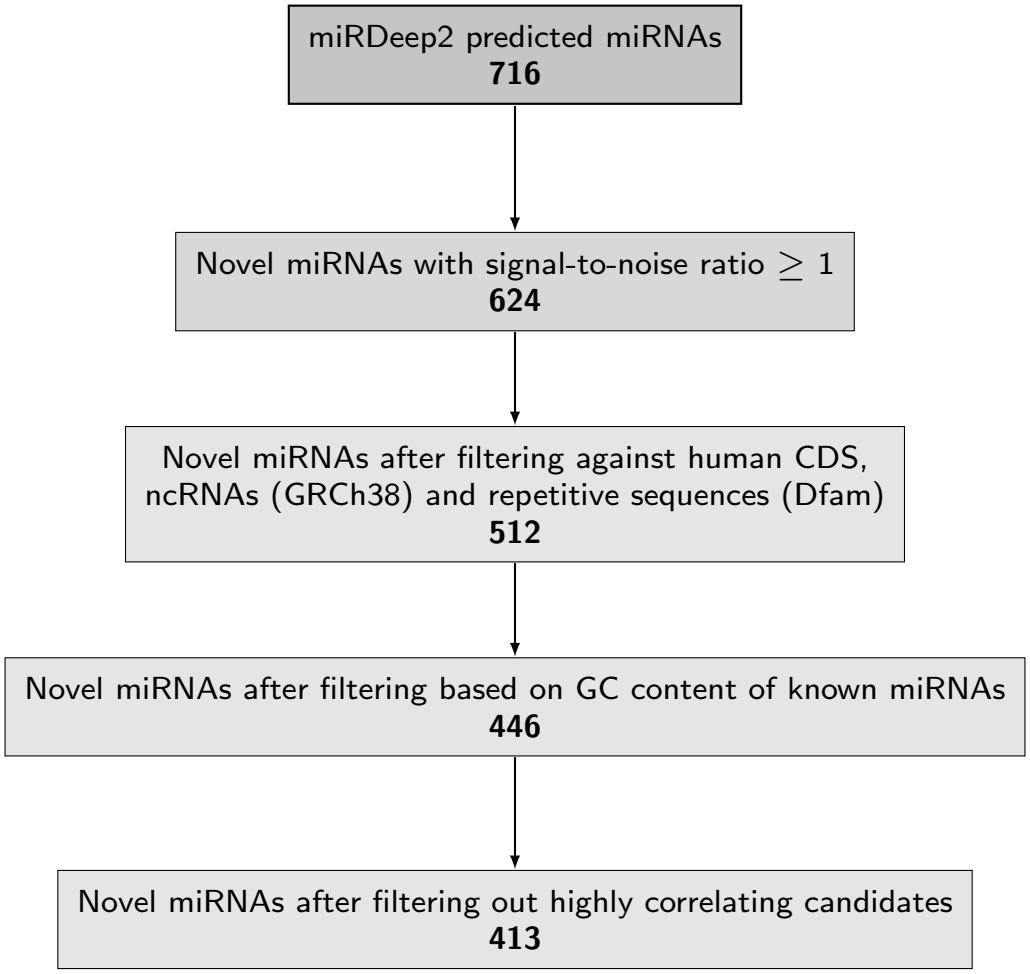
Supplementary Figure S1: Overview of the small RNA transcriptome data. **A)** The purity of blood cell populations after sorting by MACS; **B)** Raw reads per sample within different blood compounds; **C)** Read length distribution of pre-filtered sequencing reads; **D)** Composition of filtered reads within different blood compounds. The reads were filtered against non-miRNA small RNAs from Rfam (green), viral genomes from RefSeq (yellow) and viral precursors from miRBase (orange); **E)** Overall composition of the initial reads per sample in distinct blood compounds. Due to a small fraction of novel miRNAs, their proportions within most of the samples are not visible in graphs; **F)** Number of reads mapped to known miRNAs per distinct blood compound; **G)** Number of mature miRNAs detected per individual blood compound. **Note:** Samples in graphs B, D and E are aligned in the same order.

Supplementary Figures



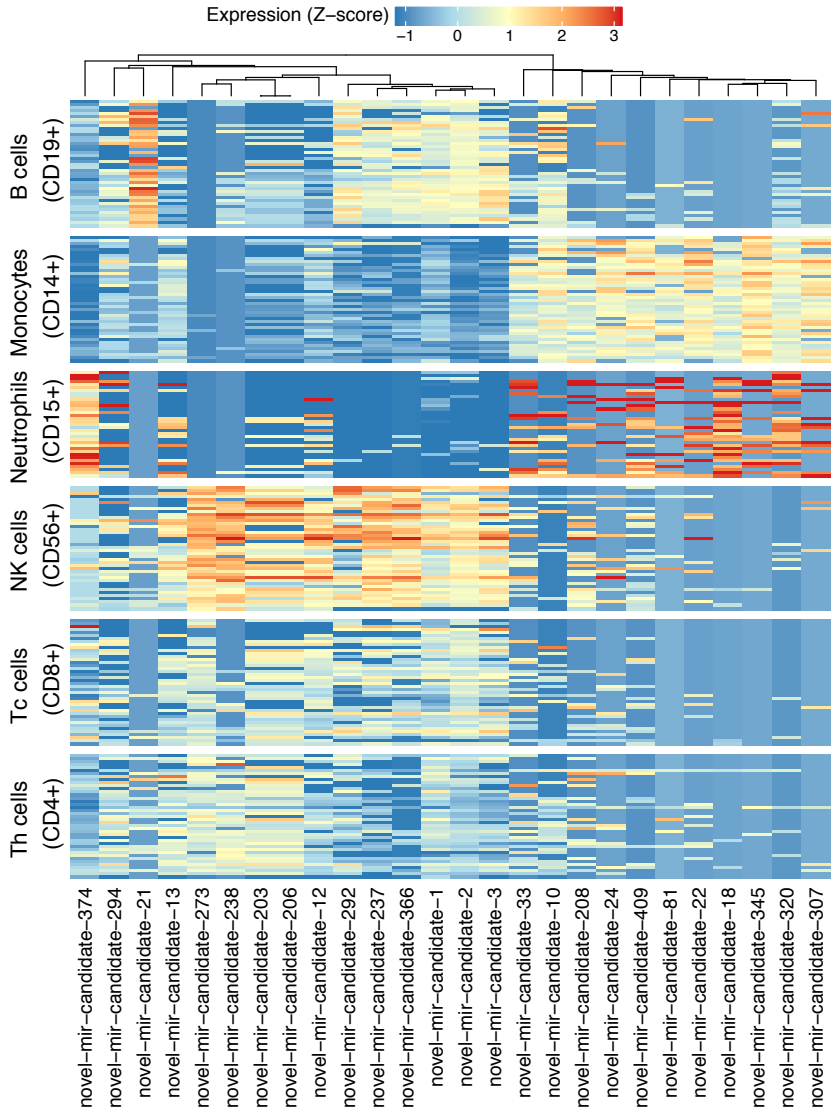
Supplementary Figure S2: Heatmap representing the expression levels of blood cell lineage-specific isomiRs. Each row of the heatmap corresponds to the one of the samples per blood cell types, and each column corresponds to an isomiR. All molecules were significantly up-regulated (FDR p-value$<$0.001; $|$log2FC$|>$1) exclusively in one of the cell types. The unsupervised hierarchical clustering of isomiRs was performed using Spearman's correlation distance as metric and average linkage clustering as linkage criterion.

Supplementary Figures



Supplementary Figure S3: Filtering pipeline of novel miRNA candidates.

Supplementary Figures



Supplementary Figure S4: Expression of blood cell specific novel miRNA candidates in different blood cells. In the heatmap, rows represent samples and columns represent novel miRNA candidate transcripts which are exclusively significantly up-regulated (FDR p-value$<$0.001; $|$log2FC$|>$1) in one of the cell types. The Z-score represents standardized normalized expression values. The unsupervised hierarchical clustering was performed using Spearman's correlation distance as metric and average linkage clustering as linkage criterion.