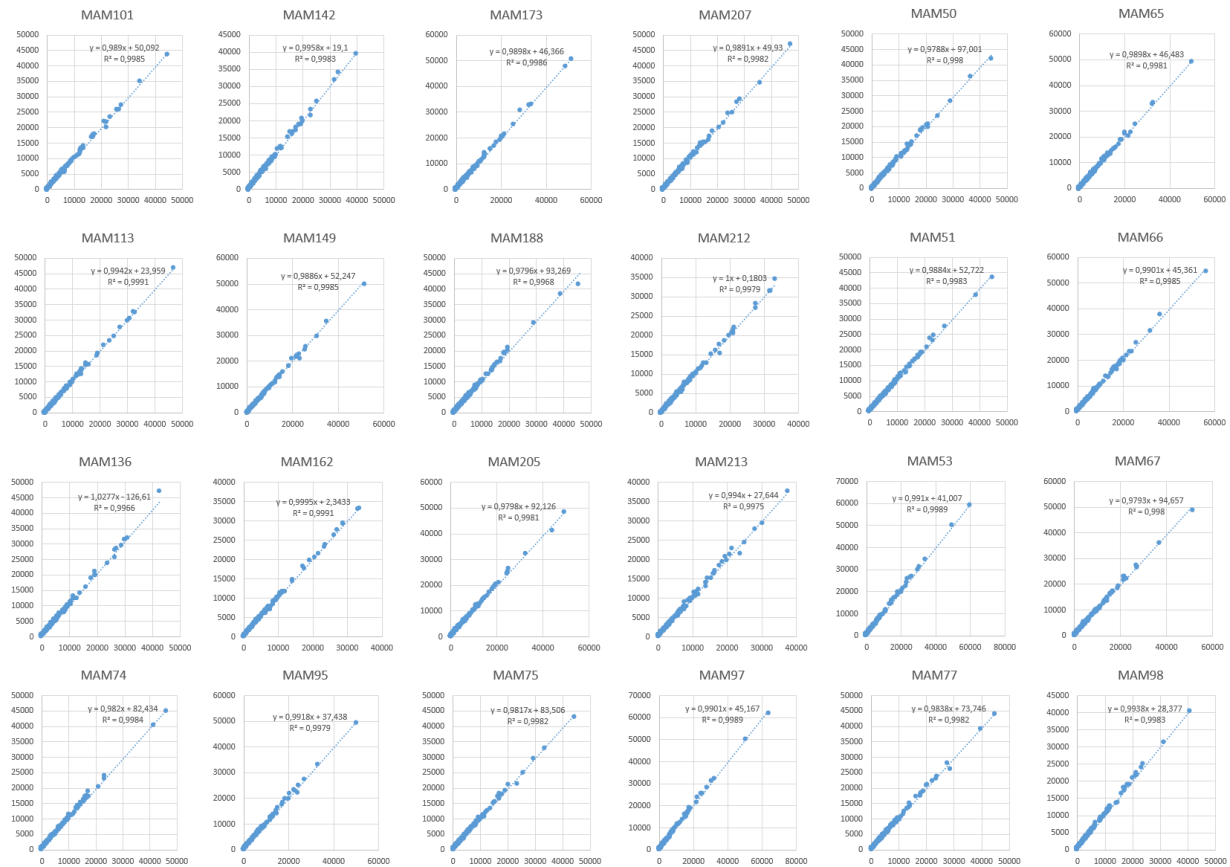


Supplementary Figures

Supplementary Figure S1 Inter-instrument reproducibility of the RNA-targeted sequencing approach. Identical libraries analyzed on either NextSeq or NovaSeq - individual analysis of 24 samples. The x- and y-axes show the expression of particular genes (normalized to million transcripts). Note: Data for the correlations individual sample are available as Supplementary Table S6



Supplementary Figure S2 Inter-run (A.) and Inter-capture (B.) reproducibility of the RNA-targeted sequencing approach. **A.** independently prepared NGS library duplicate (from seven blood RNA samples) using the standard CZECANCA panel protocol; **B.** 17 sample pre-libraries enriched with CZECANCA (226 genes, 0.63 Mb) or HyperExome probes (43 Mb), respectively. The x- and y-axes show the expression of particular genes (normalized to million transcripts). Note: Data for the correlations individual sample are available as Supplementary Tables S7-8.

