LETTER TO THE EDITOR

Depletion of the RNA binding protein QKI and circular RNA dysregulation in T-cell acute lymphoblastic leukemia

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Supplementary Results

Figure S1. a. Unsupervised principal component analysis of T-ALL patients (n=25) according to expression profiles of the circRNA linear counterpart (overlapping mRNAs in circRNA-expressing genes; Samples are colored according to a gradient of *QKI* expression levels); b. Scatter plot of expression log Fold Change of circRNAs and their linear counterpart when comparing QKI_low with QKI_normal T-ALL; c) CircRNAs importance plot in the Random Forest classification model of QKI_low and QKI_normal T-ALL samples (Gini index and Accuracy measure were used to rank the most discriminating circRNAs; Dots are colored according to Adj. p-value significance; Names are reported for the top 6 circRNAs); d) Boxplot of circRNA isoforms expressed from the same host gene and with opposite behavior upon QKI KD in Jurkat cells.

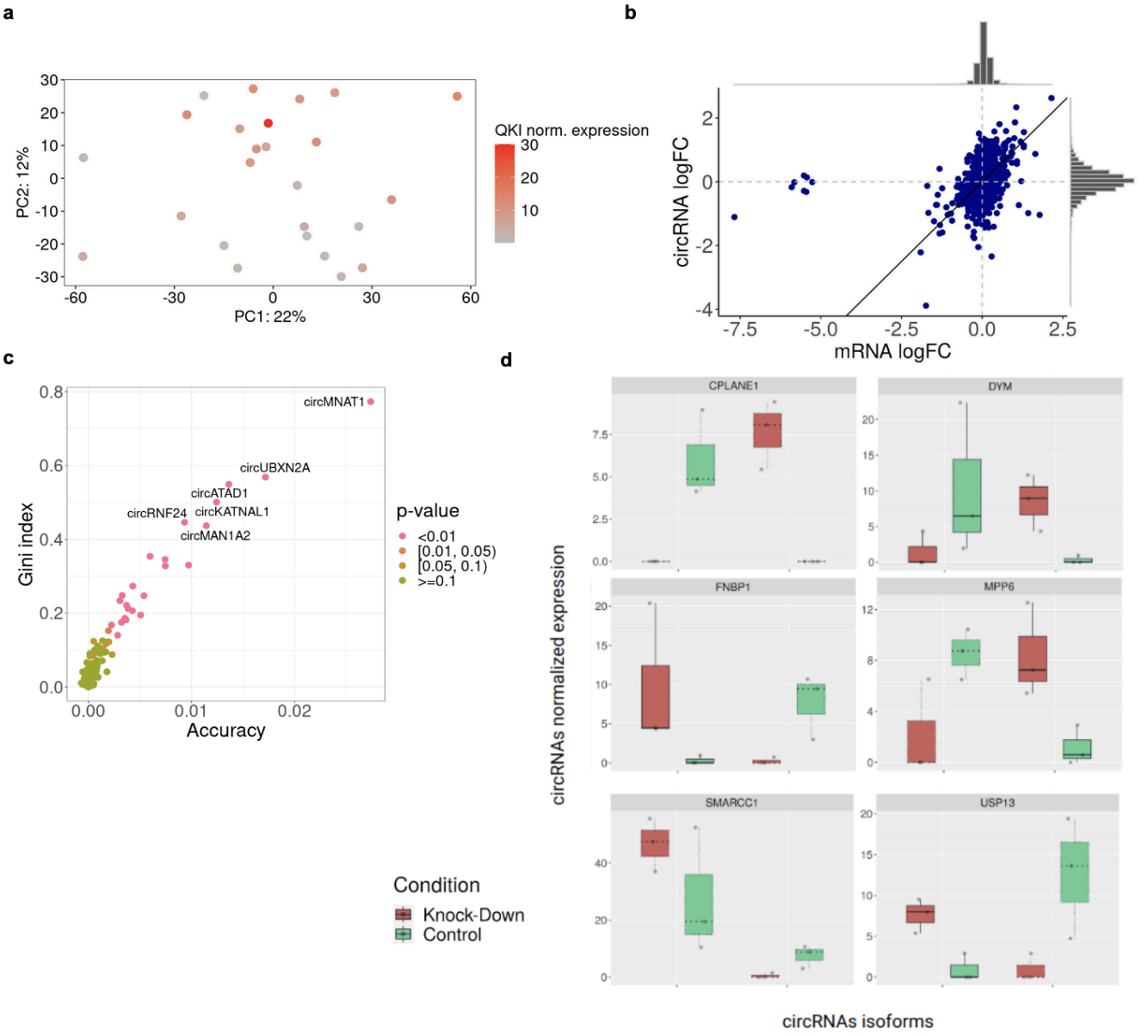

Table S1. Table of 3 376 circRNAs used to compare T-ALL patients with low QKI and with normal expression level (QKI_low vs QKI_normal). For each circRNAs are reported the host gene info; absolute (.EXP) and relative (.CLP) average expression; statistical test and p-value of the QKI-subgroups comparison for absolute and relative expression, respectively.

(see file .xls)

Table S2. QKI response elements coordinates from PAR-CLIP experiment or predicted by using regular expression within 1000 nt upstream or downstream of the circRNAs backsplice sites detected in QKI Knock-Down experiment in Jurkat cells. The distance from the backsplice junction and the position (Upstream/Downstream) relative to the backsplice are also reported. For predicted QRE the string is reported in the last column.

(see file .xls)