Supplemental Figures

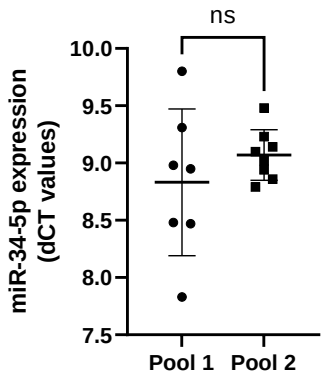

Figure S1. miR-34a-5p expression levels in B-lymphocytes CD19+ pools. The expression level of miR34a-5p was measured by RT-qPCR in pools 1 and 2 of B-Lymphocytes CD19+. dCT value was calculated using the CT value of miR-34a-5p and the CT value of U6 (dCT = CT miR-34a-5p – CT U6). Each point represents an individual measurement, and lines represents the mean ± SEM; T-test p = 0.339, ns = not significant.

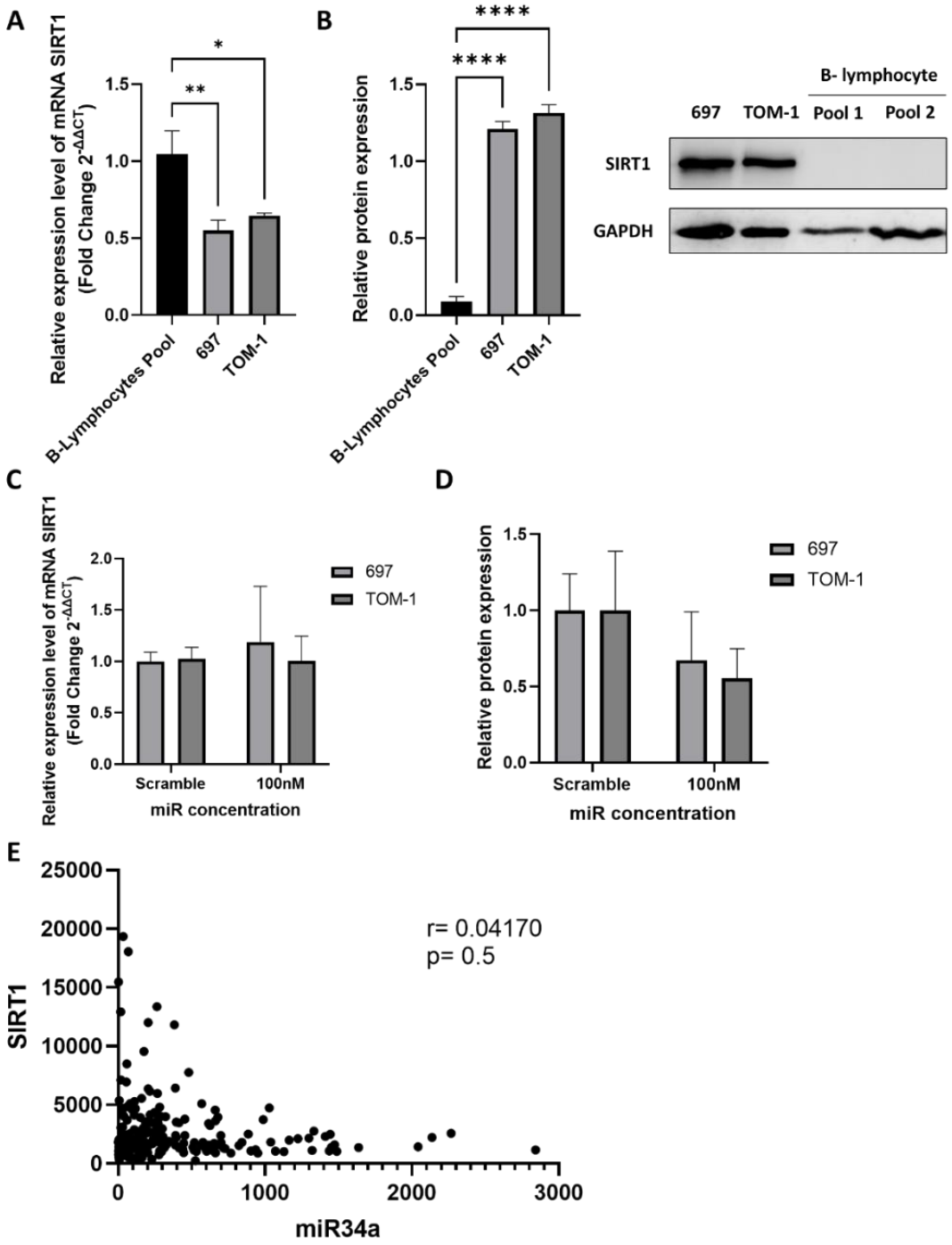

Figure S2. SIRT1 expression levels in B-ALL cells. (A) SIRT1 mRNA expression was measured by RT-qPCR in 697 and TOM-1 cell lines, as well as a pool of CD19+ B lymphocytes from healthy individuals (n=8). The $2^{-\Delta\Delta Ct}$ method was used to calculate SIRT1 expression, normalized to GAPDH expression level. Data was plotted as the mean ± SEM of the $2^{-\Delta\Delta Ct}$ value; n = 3 biological replicates; One-way ANOVA *p < 0.05; **p < 0.01 (B) SIRT1 protein expression in B-ALL cells and a pool of CD19+ B lymphocytes was examined by Western blot (left). Densitometric analysis was calculated using the SIRT1/GAPDH ratio in Imaje J (right).

Data were plotted as the mean ± SEM of relative protein level from 3 biological replicates; One way ANOVA; ****p < 0.0001. (C) SIRT1 mRNA expression level was measured by RT-qPCR in 697 and TOM-1 cell lines transfected with 100nM of miR-34a-5p or a miRNA scramble used as control. The $2^{-\Delta\Delta Ct}$ method was used to calculate SIRT1 expression, normalized to GAPDH expression level. Data was plotted as the mean ± SEM of the $2^{-\Delta\Delta Ct}$ value; n = 3 biological replicates; One-way ANOVA, ns = not significant. (D) Densitometric analysis of SIRT1 protein levels in B-ALL cells transfected with 100nM of miR-34a-5p or a miRNA scramble used as control. Data were plotted as the mean ± SEM of relative protein level from 3 biological replicates; One-way ANOVA, ns = not significant. (E) miR-34a-5p and SIRT1 expression values from B-ALL patients obtained from the TCGA Pediatric ALL TARGET II Project (n = 181) were used for a linear regression analysis; r = Spearman's correlation coefficient; p = level of significance (not significant).

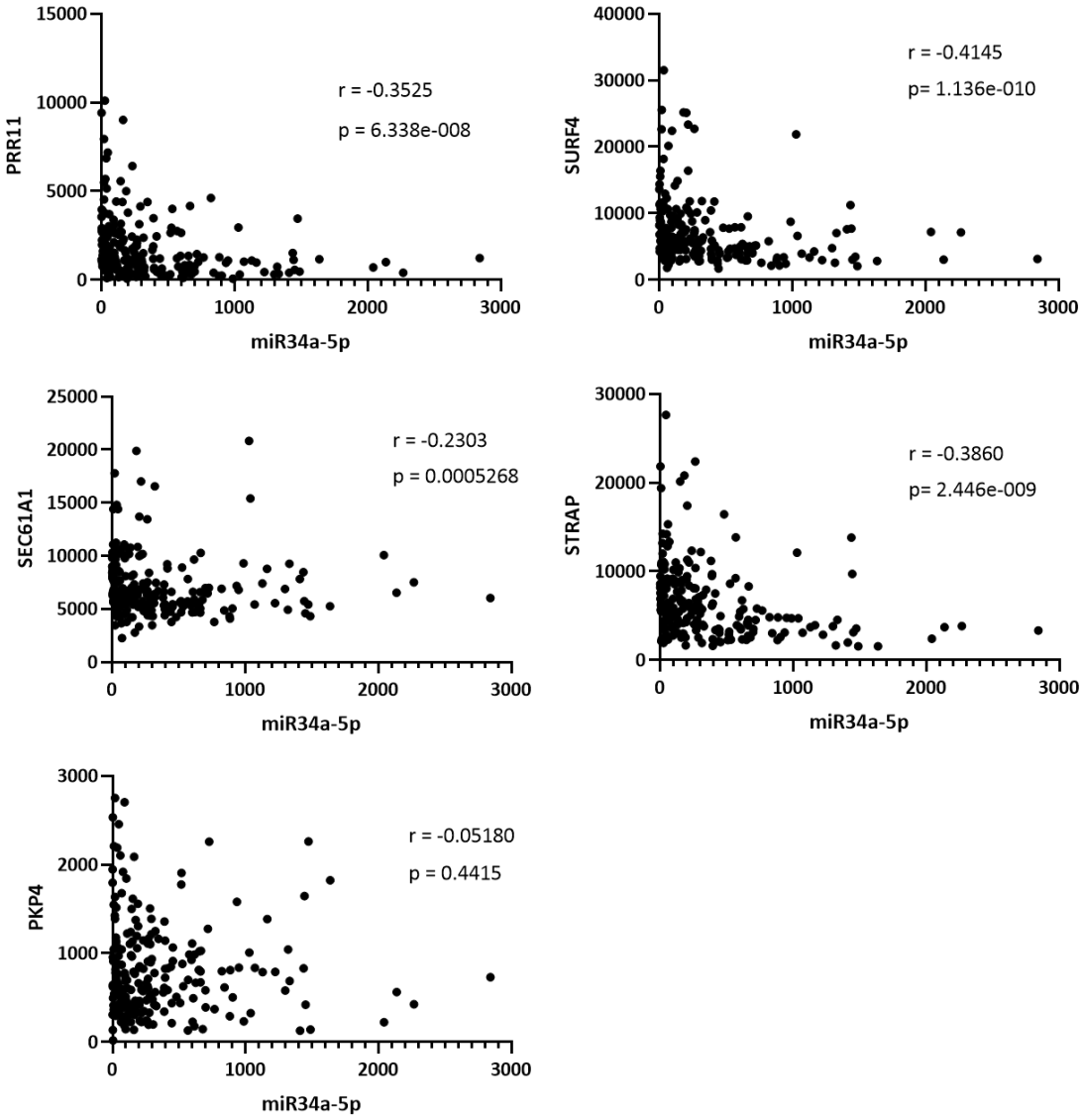

Figure S3. Linear regression analysis between the expression of the previously selected genes (PRR11, SEC61A1, STRAP and SURF4) and miR-34a-5p in B-ALL patients. miR-34a-5p PRR11, SEC61A1, STRAP and SURF4 expression values from B-ALL patients were obtained from the TCGA Pediatric ALL TARGET II Project (n = 181) to carry out a linear regression analysis; r = Spearman's correlation coefficient; p = level of significance.

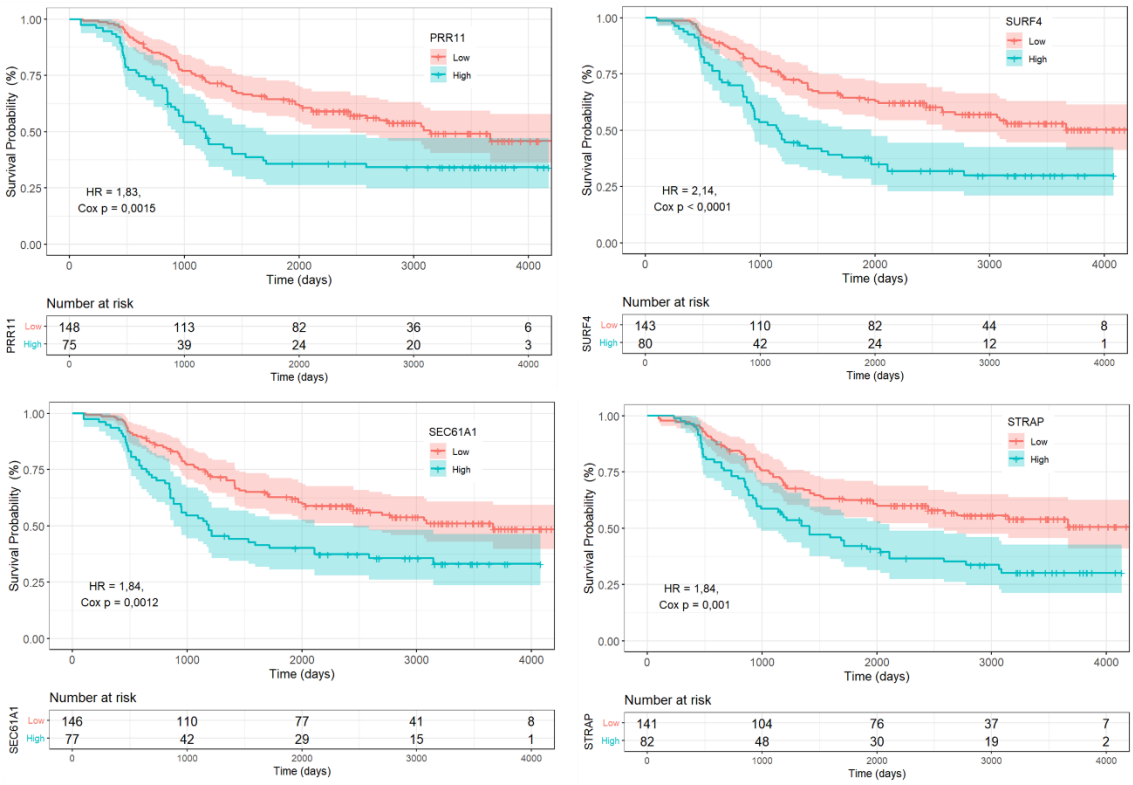

Figure S4. Overall survival analysis of PRR11, SEC61A1, STRAP and SURF4 expression in samples of B-ALL patients. Kaplan-Meier curve using data extracted from the TCGA database for overall survival (OS) of B-ALL patients segregated based on the expression of PRR11 (upper left), SURF4 (upper right), SEC61A1 (lower left) and STRAP (lower right). In all cases patients with low expression (blue line) were considered as the reference group. HR = Hazard ratio. Cox p = p value from the Cox proportional hazards model. Statistical significance was set at Cox $p < 0.05$.