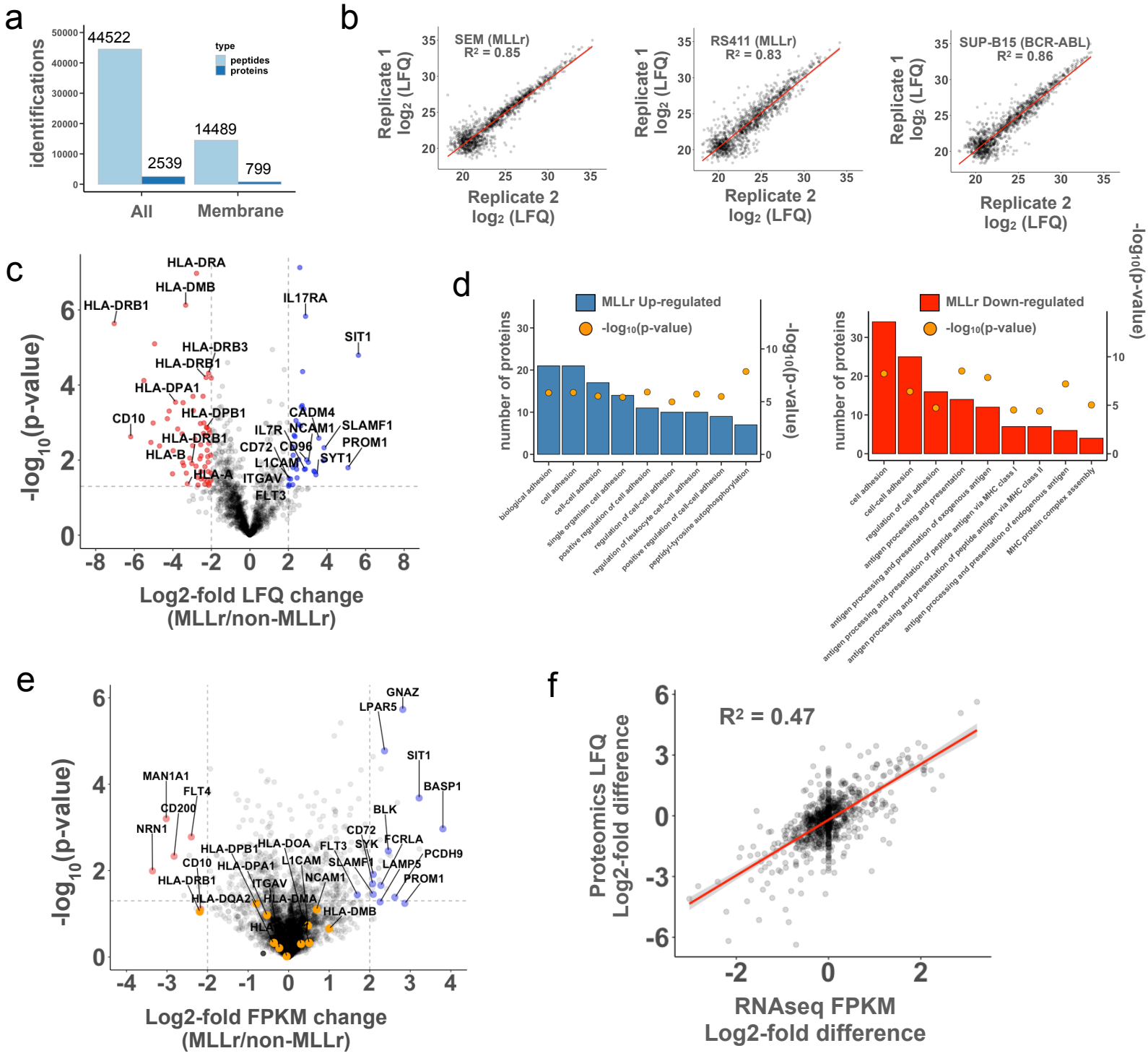
Supplementary Figure S1



Supplementary Figure S1: Identification of upregulated cell surface proteins in MLLr vs non-MLLr leukemia

(**a**) Proteomic results summary showing number of identifications for all proteins, and membrane proteins after bioinformatic filtering. (**b**) Correlation plots comparing replicates for cell surface proteomics experiments for select cell lines. Axes are log2 transformed label-free quantification values (LFQ). Correlation coefficients are shown. (**c**) Volcano plot displaying differentially abundant cell surface proteins. The log2-fold change comparing the LFQ values of MLLr versus non-MLLr cell lines is shown on the *x*-axis, while the -log10(*p*-value) is shown on the *y*-axis. Proteins with log2-fold change > 2 or < -2, and -log10(*p*-value) > 1.3 were considered significantly upregulated (colored blue) or downregulated (colored red), with select membrane proteins labeled. Significance cut-offs are shown by dotted lines. Statistical analysis was conducted using a two-sided Welch's T-test. (**d**) Results of a DAVID gene ontology analysis of upregulated (blue bars and downregulated (red bars) cell surface proteins. Bar height (left *y*-axis) displays the number of proteins associated with each GO term (*x*-axis) while the yellow dots (right *y*-axis) shows the -log10(*p*-value) of a modified Fisher Exact test for each GO term enrichment. (**e**) Volcano plot displaying differentially abundant transcripts of cell surface proteins from RNAseq analysis comparing MLLr to non-MLLr B-ALL cell lines. Upregulated genes (blue circles) and down regulated genes (red circles) are labeled. Genes identified as up or down regulated by proteomics, but not by transcriptomics, are colored orange and labeled. (**f**) Correlation plot comparing the log2-fold transcript change (RNAseq, x-axis) to protein change (proteomics, y-axis) of MLLr vs non-MLLr B-ALL cell lines.