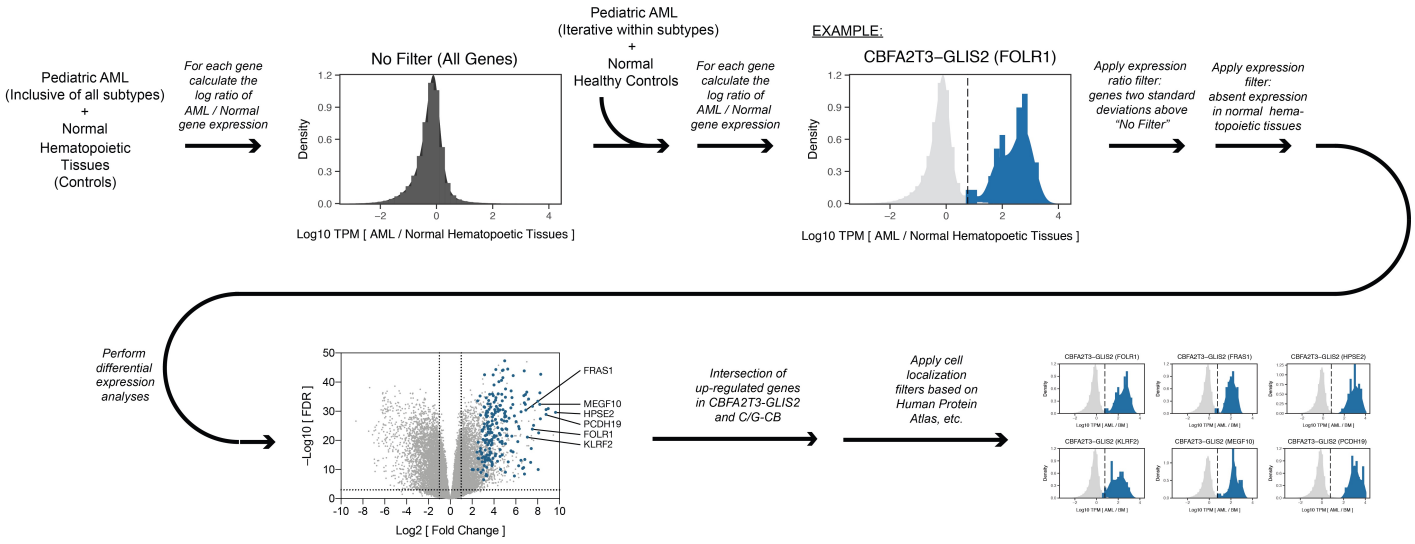

Extended Data Figure 7. Identification of C/G fusion-specific CAR targets. (Related to Fig. 3a) Flow diagram of AML-restricted gene and CAR-T target identification. The procedure involves three main steps: 1) Determine the ratio of expression for AML primary samples versus healthy normal hematopoietic tissue samples (bulk marrows and CD34+ peripheral blood) from log10 transformed normalized gene expression. The ratio is calculated per gene from mean AML expression and mean normal hematopoietic tissue expression, where normal tissue values are the divisor, which acts as a measure of over or under expression. A normal curve is fit to the ratios and this procedure is completed for all heterogenous AML samples as a group, and iteratively within fusion and mutation subtypes; genes with ratios greater than +2 standard deviations and with absent expression in normal hematopoietic tissues were retained (N=607) for further analysis. 2) The AML restricted genes were further selected if found to be significantly overexpressed in fusion positive patient samples compared to healthy marrows and were likewise overexpressed in C/G-CB at weeks 6 and 12 in EC co-culture with absent expression in GFP-CB controls, providing several candidate (N=42) targets. 3) Optimal CAR-T targets were selected by the identification of candidate genes with cell surface localization potential, and those with an absence of expression in healthy tissue controls as noted in step 1, but expression in > 75% of C/G patient samples, and with moderate to high expression levels (N=6).