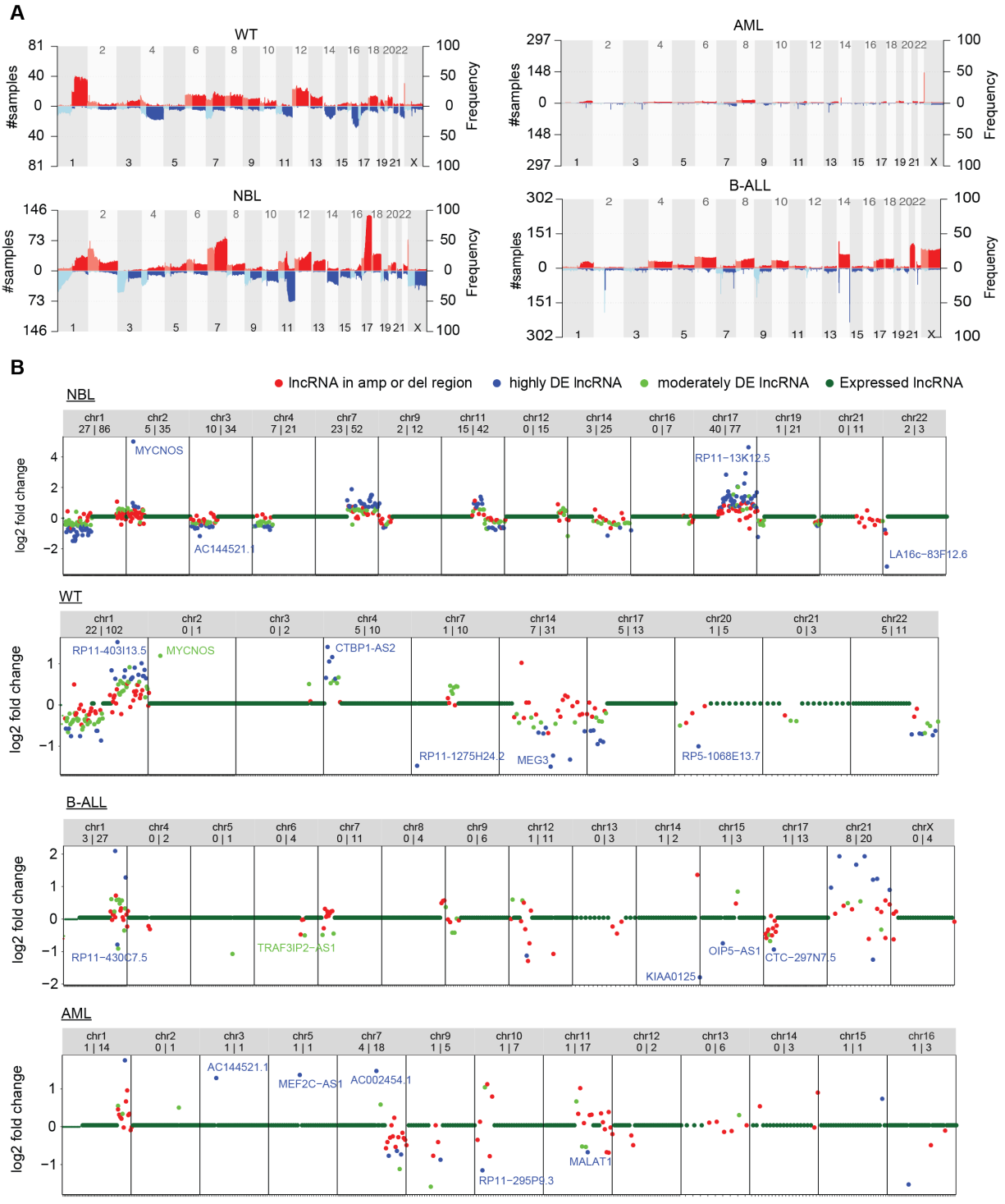

Supplementary Fig. S3: Regions of somatic copy number aberration across cancers and genes dysregulated due to copy number. (A) Plots of the frequency of copy number gain and loss across the genome for four pediatric cancer cohorts in this study. **(B)** lncRNA loci on chromosomes with copy number alterations across the pediatric cancers: NBL, WT, B-ALL, and AML. lncRNAs were evaluated to have differential expression due to copy number using the Wilcoxon rank sum test: highly differential: p-value < 0.05 and log |fold change| > 1.5 and moderately differential: p-value < 0.1 and log |fold change| > 1.0. Points are colored based on loci in an amplified or deleted region of the chromosome and if the lncRNA is highly or moderately differentially expressed.