

## ***LIN28B* Upregulation is Associated with Cancer Stemness and Chemotherapy Resistance in Favorable Histology Wilms Tumor.**

Andrew M. Fleming, MD<sup>1,2</sup>, Karissa M. Dieseldorff Jones, PhD<sup>3</sup>, Changde Cheng, PhD<sup>3</sup>, Christopher L. Morton BS, MBA<sup>2</sup>, Mary A Woolard, BS<sup>2</sup>, Carolyn Jablonowski, PhD<sup>2</sup>, Prahalathan Pichavaram, PhD<sup>2</sup>, Sivaraman Natarajan, PhD<sup>3</sup>, John Easton, PhD<sup>3</sup>, Emilia M. Pinto, PhD<sup>4</sup>, Jerold E. Rehg, DVM<sup>4</sup>, Laura Janke, DVM<sup>4</sup>, PhD, Teresa Santiago, MD<sup>4</sup>, Gerard P. Zambetti, PhD<sup>4</sup>, Andrew M. Davidoff, MD<sup>1,2</sup>, Jun Yang, MD, PhD<sup>2</sup>, Xiang Chen, PhD<sup>3</sup>, Andrew J. Murphy, MD<sup>1,2</sup>

<sup>1</sup>The University of Tennessee Health Science Center, Department of Surgery

<sup>2</sup>St. Jude Children's Research Hospital, Department of Surgery

<sup>3</sup>St. Jude Children's Research Hospital, Department of Computational Biology

<sup>4</sup>St. Jude Children's Research Hospital, Department of Pathology

### **Abstract**

#### **Background**

Developing chemotherapy resistance in the favorable-histology Wilms tumor (WT) patient-derived xenograft (PDX) KT-47 revealed blastemal enrichment and early, robust upregulation of the *Let-7* microRNA (miRNA) regulator *LIN28B*. We interrogated *LIN28B* in the original patient (PT-47) after relapse, quantified *Let-7* miRNAs in KT-47, and investigated potential underlying mechanisms of *LIN28B* enrichment.

#### **Methods**

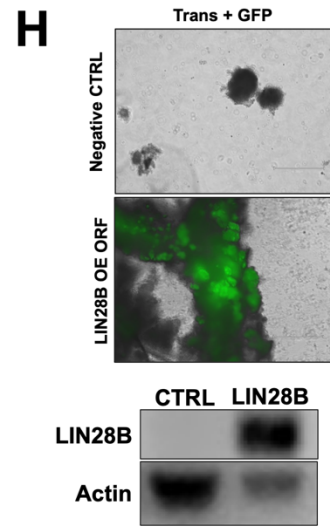
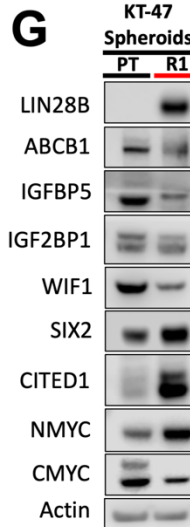
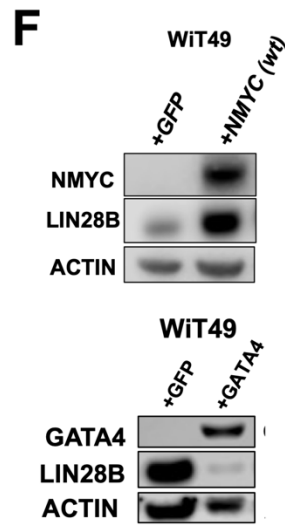
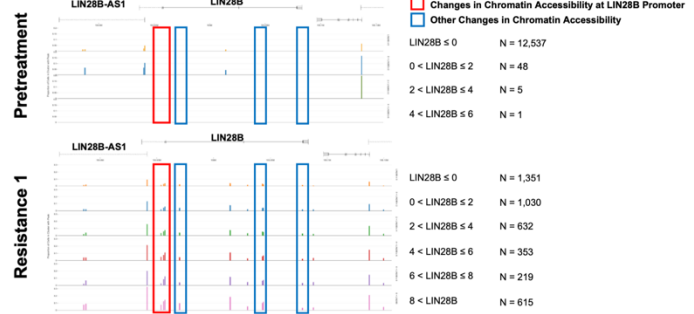
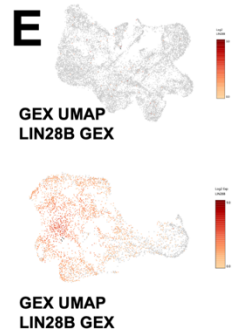
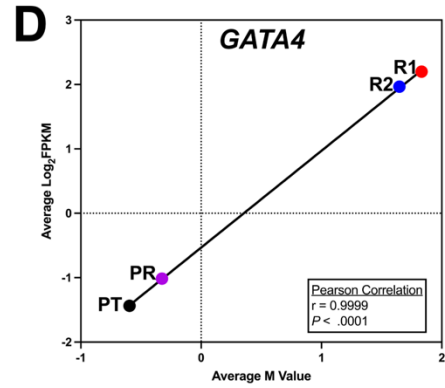
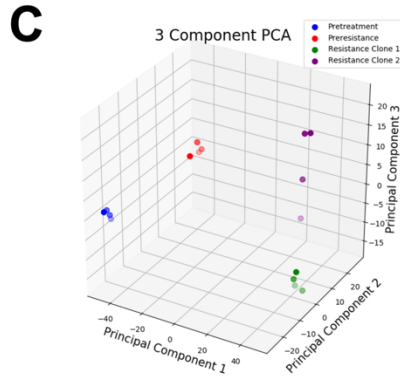
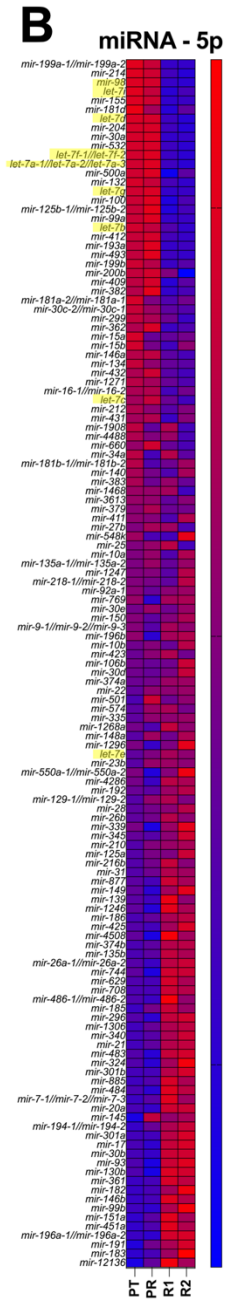
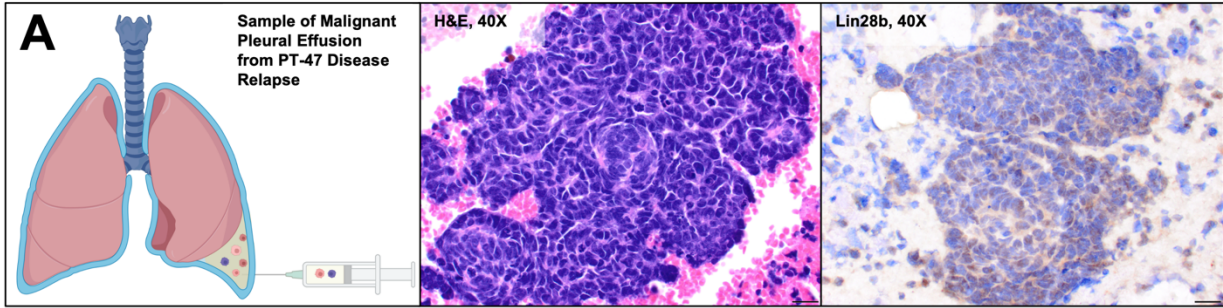
Pleural effusion samples were obtained from PT-47 after relapse. Immunohistochemistry (IHC) was performed for *LIN28B*. In KT-47, miRNA sequencing, whole exome sequencing (WES), 850K MethylationEPIC BeadChip analysis, and single nuclear multiomic transcriptomic/epigenomic profiling were performed. Pearson correlations for *Let-7* levels and validated *Let-7* targets were performed. Relevant genes were overexpressed in a WT cell line and KT-47 spheroids via lentiviral transduction.

#### **Results**

Relapsed PT-47 WT cells were positive for *LIN28B* (Figure 1A). In KT-47, *Let-7* miRNAs were downregulated with chemotherapy resistance (all  $P < .05$ ) (Figure 1B). Reduced *Let-7a* correlated with enriched stemness mediators *HMG2* ( $R^2=0.8665$ ,  $P<.0001$ ) and *TRIM71* ( $R^2=.7381$ ,  $P=.0003$ ). WES demonstrated no copy number alterations, single nucleotide variants, or insertions/deletions for *LIN28B*, nor was *LIN28B* differentially methylated. Differential methylation correlated with enrichment of embryonic transcription factor *GATA4* (Figure 1D) and stemness-associated multidrug resistance protein *ABCB1* (both  $r>0.999$ ,  $P<.001$ ). Chemotherapy-resistant nuclei demonstrated enhanced chromatin accessibility throughout the *LIN28B* locus (Figure 1E). Nuclei expressing *LIN28B* demonstrated motif enrichment for *GATA4* ( $P<.001$ ), *MYC* ( $P<.0001$ ), and *MYCN* ( $P<.05$ ). Overexpression of *NMYC* *in vitro* yielded increased protein levels of *LIN28B*, while overexpression of *GATA4* decreased *LIN28B* (Figure 1F). KT-47 spheroids recapitulated protein profiles of KT-47 WTPDX (Figure 1G). *LIN28B* was successfully overexpressed in KT-47 pretreatment spheroids (Figure 1H).

**Conclusions**

*LIN28B* enrichment was confirmed in PT-47 relapse and correlated with a cancer stemness phenotype in KT-47. Enhanced chromatin accessibility and NMYC motif enrichment may drive *LIN28B* transcription. Further *in vitro* and *in vivo* experiments will determine the importance of *LIN28B* in chemotherapy resistance.



**Figure 1. (A)** Schematic of pleural effusion sampling from PT-47 with representative images demonstrating hematoxylin-and-eosin-staining of relapsed tumor cells and LIN28B immunohistochemistry. **(B)** Heat map of Z-scores demonstrating differential expression of miRNAs with the development of chemotherapy resistance. *Let-7* family members are highlighted in yellow. **(C)** 3 component principal component analysis demonstrating clustering of treatment phenotypes by global DNA methylation status. **(D)** Correlation of DNA methylation with *GATA4* enrichment during the development of chemotherapy resistance in KT-47. **(E)** Gene expression UMAPs demonstrating an increased number of nuclei expressing *LIN28B* at the Resistance 1 phenotype / timepoint compared to the pretreatment timepoint. The *LIN28B* locus in Resistance 1 nuclei demonstrated chromatic accessibility peaks absent in the Pretreatment nuclei. **(F)** Western blots of whole cell lysate from Wilms tumor cell line WiT49 demonstrating upregulation of LIN28B with *NMYC* over-expression and downregulation of LIN28B with *GATA4* overexpression. **(G)** Western blot comparing the protein profiles of KT-47 Pretreatment and Resistance 1 spheroid cultures. **(H)** Light microscopy demonstrating successful lentiviral transduction of KT-47 pretreatment spheroids via human *LIN28B* open reading frame, with protein-level expression confirmed on Western blot. “PT-47” = patient whose tumor contributed to the KT-47 model; “H&E” = hematoxylin-and-eosin; “miRNA-5p” = 5-prime microRNA; “PT” = pretreatment; “PR” = Preresistance; “R1” = resistance clone 1; “R2” = resistance clone 2; “PCA” = principal component analysis; “FPKM” = fragments per kilobase million; “GEX” = gene expression; “UMAP” = uniform manifold approximation and projection; “GFP” = green fluorescent protein; “wt” = wild type; “OE” = overexpression; “ORF” = open reading frame; “CTRL” = control.