

Legends for all supplementary data

Supplemental Data 1: Baseline characteristics table of patients included for single nuclei RNA-sequencing.

Supplemental Data 2: Clinical characteristics of patients included for single nuclei RNA-sequencing.

Supplemental Data 3: Marker genes for all global cell types identified with single nuclei RNA-sequencing. Area under the receiver operating characteristic curve is calculated comparing nuclei-level expression between cell types. Log fold-change estimates and two-sided p-values are calculated using the limma-voom differential expression analysis between cell types and corrected for multiple testing with the Benjamini-Hochberg procedure.

Supplemental Data 4: Differentially expressed genes between AF and CTRL samples, by global cell type calculated using the limma-voom differential expression analysis. Two-sided p-values were calculated for each gene and corrected for multiple testing using the Benjamini-Hochberg correction.

Supplemental Data 5: Differential expression analysis comparing *ATRNL1* siRNA-1 versus control scramble siRNA treatment. Two-sided p-values were calculated using DEseq2 for each gene and corrected for multiple testing using the Benjamini-Hochberg correction.

Supplemental Data 6: Differential expression analysis comparing *ATRNL1* siRNA-2 versus control scramble siRNA treatment. Two-sided p-values were calculated using DEseq2 for each gene and corrected for multiple testing using the Benjamini-Hochberg correction.

Supplemental Data 7: Differential expression analysis comparing *ATRNL1-OE* versus control lentivirus treatment. Two-sided p-values were calculated using DEseq2 for each gene and corrected for multiple testing using the Benjamini-Hochberg correction.

Supplemental Data 8: Comparison of significant differentially expressed genes identified from *ATRNL1* siRNA-1 and *ATRNL1* siRNA-2. All values obtained from Supplemental Table 5 and Supplemental Table 6. Adjusted P-value < 0.05 and Log2 fold change > 0.5.

Supplemental Data 9: Comparison of significant differentially expressed genes identified from *ATRNL1* siRNA-2 and *ATRNL1-OE*. All values obtained from Supplemental Table 6 and Supplemental Table 7. Adjusted P-value < 0.05 and Log2 fold change > 0.5.

Supplemental Data 10: Target gene prediction network of miRNAs with significant binding scores to *circATRNL1*, as identified using ScanMiR.

Supplemental Data 11: Venn diagram results from the intersection of TargetScan and miRTarBase with the combined differentially expressed genes from *ATRNL1* siRNA-2 and *ATRNL1*-OE treatments.

Supplemental Data 12: Sample quality control metrics for snRNA-seq.