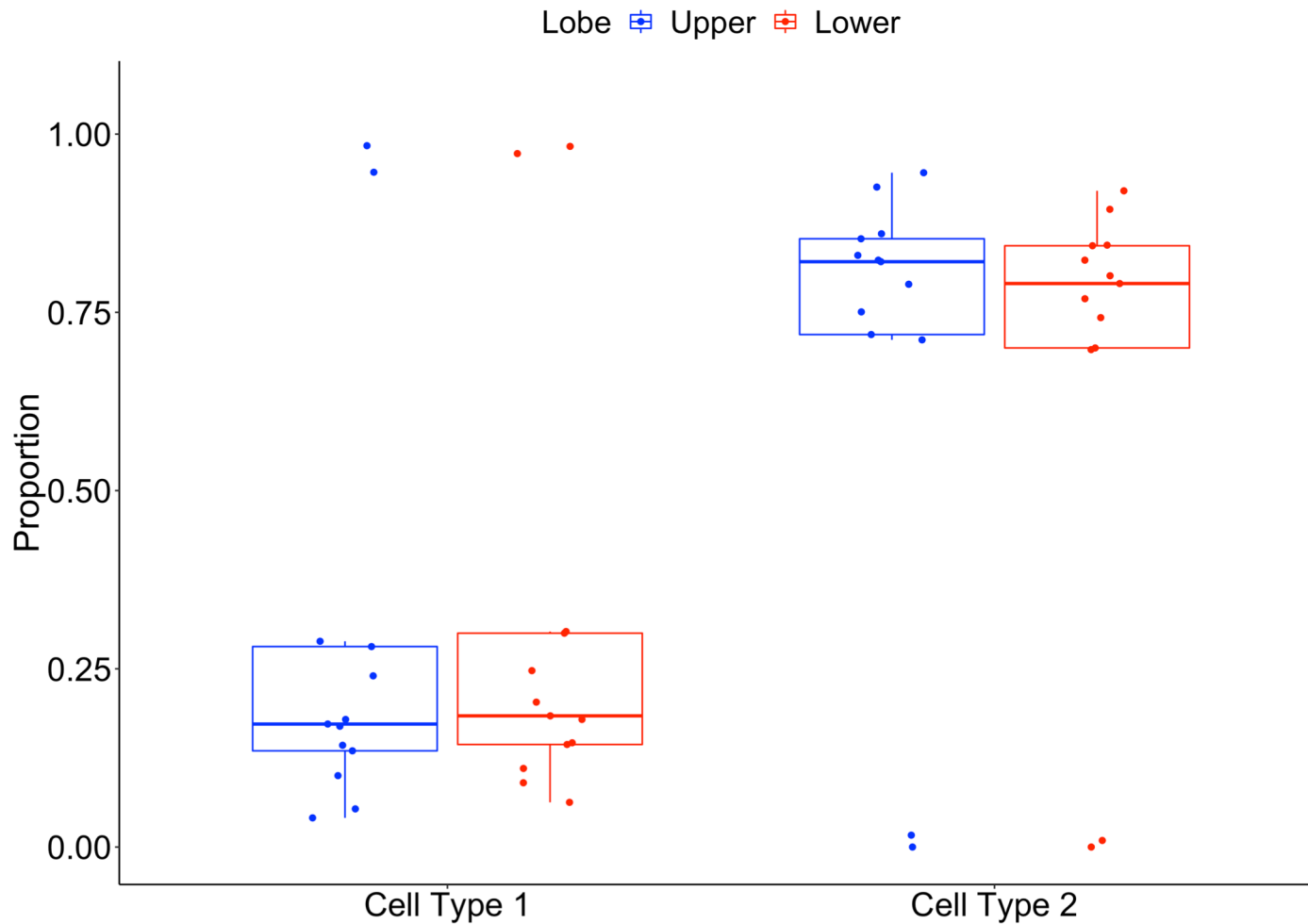


# Supplemental Figure 1.



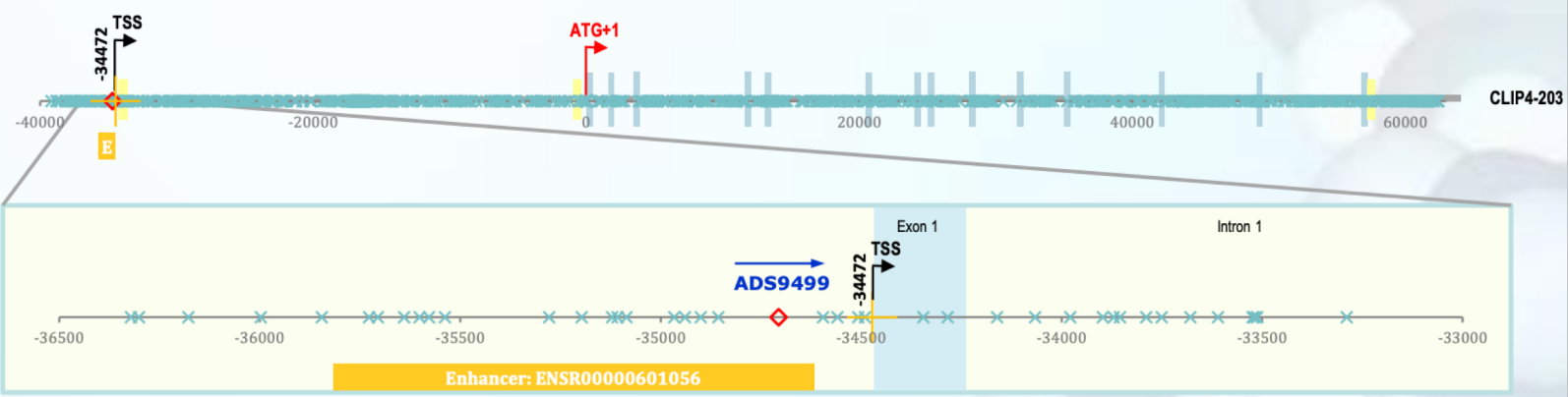
## Supplemental Figure 1. Reference-free deconvolution of putative cell types.

RefFreeEWAS algorithm (R package v.2.1, Linux R version 3.5) was applied to 10,000 of the most variable CpGs with 500 bootstraps, 10 iterations, and 9 presumptive cell types (K=2 to 10) to determine putative cell type composition. A K=2 was chosen as this value reduced the column variance of the deviance matrix (n=13 subjects). Upper: right upper lobe BAL cells. Lower: right lower lobe BAL cells.

# Supplemental Figure 2

## Human CLIP4 Gene Ensembl Gene ID: ENSG00000115295

Transcript ID: ENST00000401617.6    Transcript Length: 2162 bp, 571aa  
 Location: Chromosome 2: 29,097,728-29,189,643 forward strand



Assay ID	Assay Location	From ATG	From TSS	GRCh38 (+)	# of CpG
ADS9499	5-Upstream	-34706	-234	Chr2:29097494	1

**Keys**

- TSS : Transcriptional Start Site
- ATG : Translational Start Codon
- ◊ : CpG site analyzed
- \* : CpG site not analyzed
- : Exon coding region
- : 5' or 3' (UTR)
- : *In silico* Design
- E : Enhancer

**Supplemental Figure 2. Targeted Next-Gen Bisulfite Sequencing Assay for CLIP4.**  
 Illustration of tNGBS assay design for CAP-Gly Domain-Containing Linker Protein Family Member 4 (CLIP4), located at position Chr2:29097494, -234 bases upstream from the CLIP4 transcription start site.