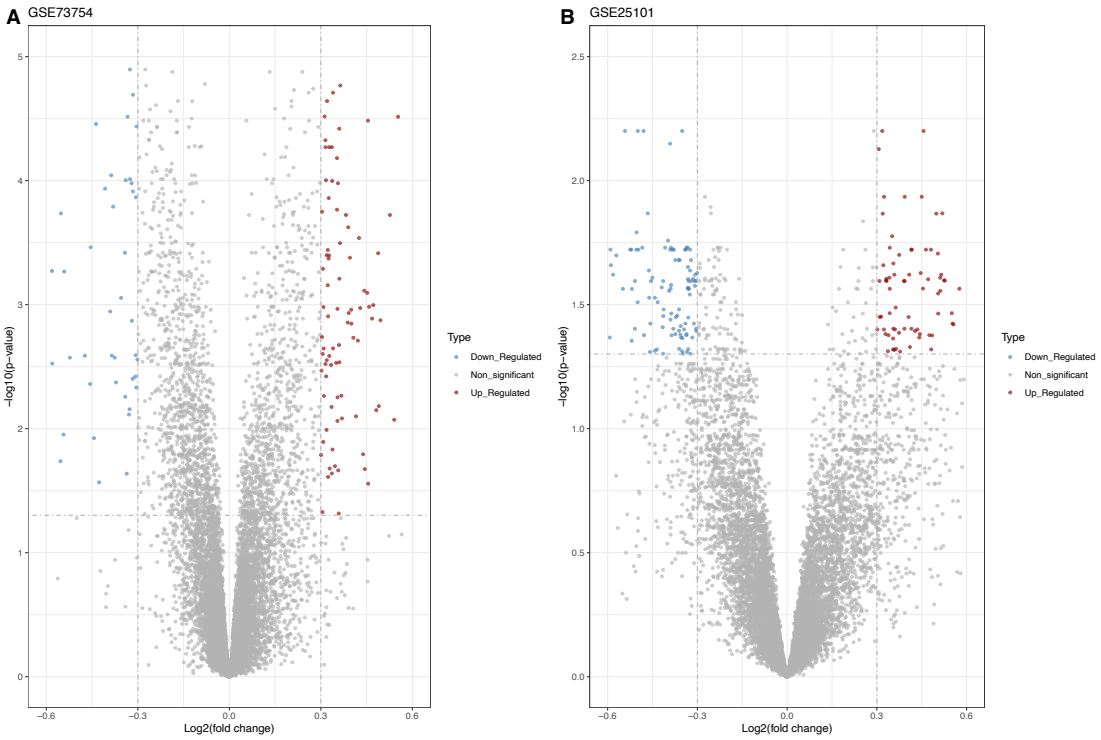
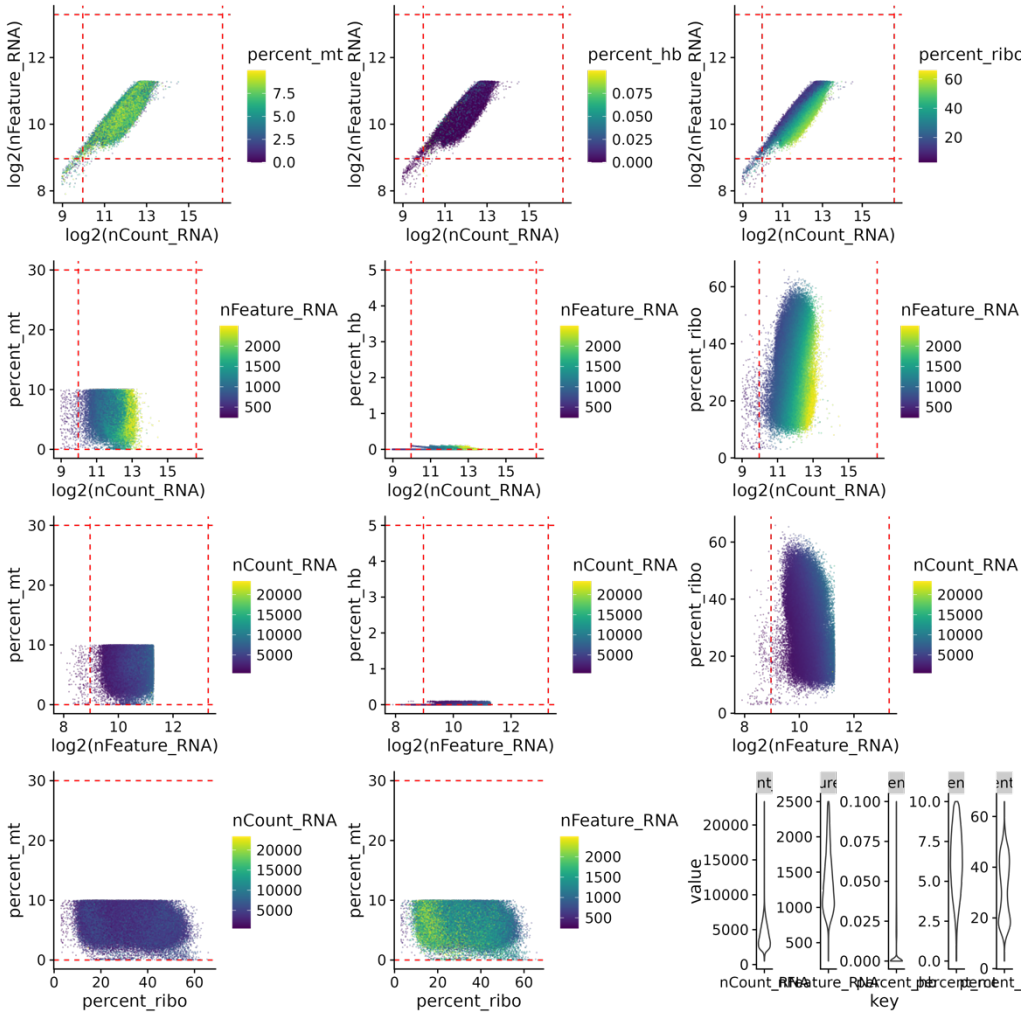
Sup_Table 1. The primer sequences for the genes

Genes	Primer sequences	Product length
IL2RB-F	5'-GGTGGAACCAAACCTGTGAGCT-3'	110 bp
IL2RB-R	5'-GGTGACGATGTCAACTGTGGTC-3'	
CD247-F	5'-GCCAGAACCAGCTCTATAACG-3'	75 bp
CD247-R	5'-GGCCACGTCTCTTGTCCAA-3'	
PLEKHF1-F	5' – GGTGTGGACTCGAGGGCT – 3'	203 bp
PLEKHF1-R	5' – CTTCTTGCGGCACTCTTTGG – 3'	
EOMES-F	5' – CGGCCTCTGTGGCTCAAA – 3'	76 bp
EOMES-R	5' – AAGGAAACATGCGCCTGC – 3'	
S1PR5-F	5' – AGGGCGCAGACCTTGG – 3'	104 bp
S1PR5-R	5' – GGAGCTTGCCGGTGTAGTT – 3'	
FGFBP2-F	5' – TGGGAACATTGTTGGAAACC – 3'	112 bp
FGFBP2-R	5' – GGTTGTCTGTCAGGGAGAGG – 3'	
GAPDH-F	5' – TCCTCTGACTTCAACAGCGACA – 3'	72 bp
GAPDH-R	5' – GTGGTCGTTGAGGGCAATG – 3'	

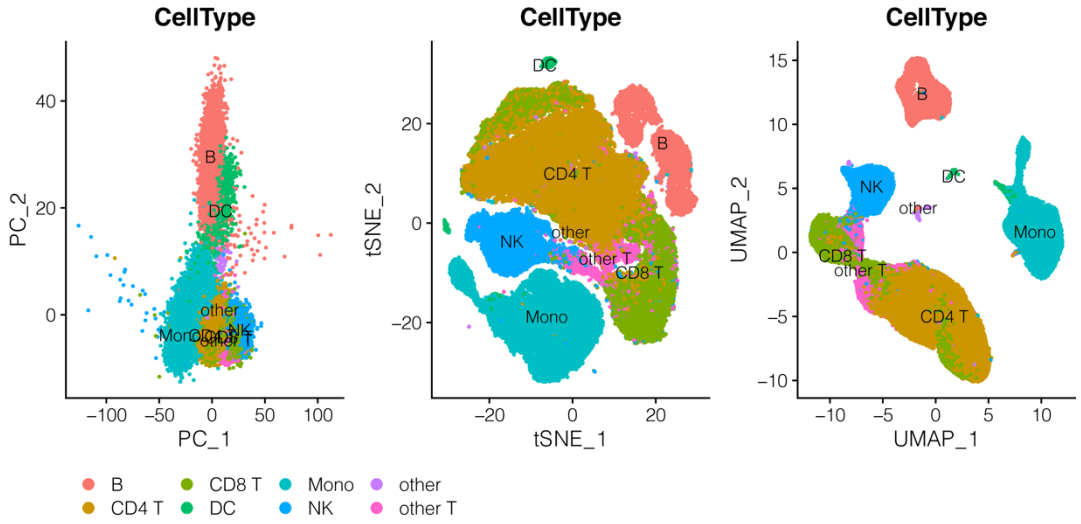


Sup_Figure 1. Volcano map of GSE73754 (1A) and GSE25101 (1B).

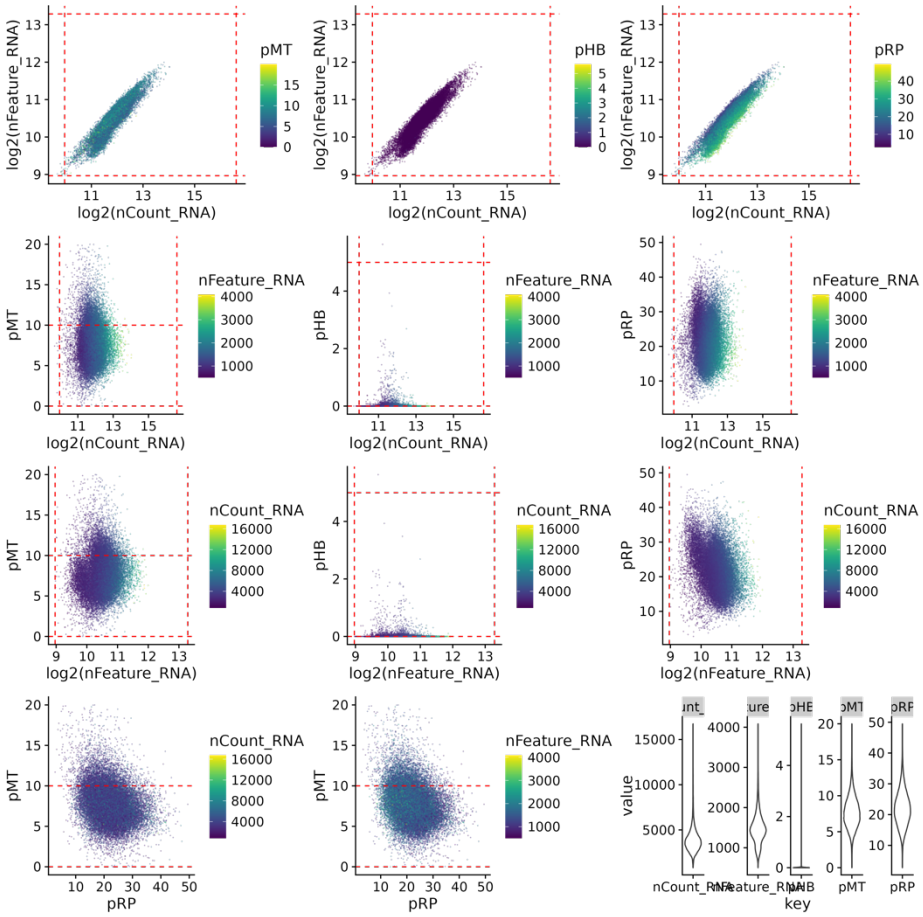
Volcano plots are shown for differentially expressed genes (DEGs) between AS and healthy patients in GSE73754(1A) and GSE25101 (1B). Absolute logFC ≥0.3 and adj.P.Val >0.05 are set as cutoff point.



Sup_Figure 2. The data from GSE194315 used standard Seurat pipeline to filter out low-quality cells based on (1) genes expressed < 200 or > 2500; (2) mitochondrial-associated genes expressed > 10%.



Sup_Figure 3. Different cell populations of PBMC was analyzed by PCA, tSNE and UMAP method; All cells were divided into 8 cell subpopulations, including B cells, CD8 T cells, monocyte cells, CD4 T cells, DC cells, NK cells, other T cells and other cells.



Sup_Figure 4. Another data using the standard Seurat pipeline filtered out low quality cells based on (1) gene expression <200 or >2500; and (2) mitochondria-related gene expression >10%.