

Supplementary 1

Figure S1

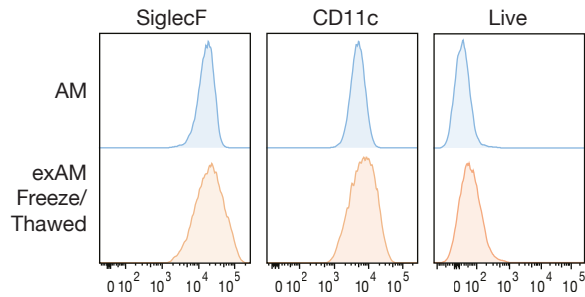


Figure S1. Flow cytometric comparison of classical AM cell-surface markers SiglecF and CD11c and viability dye (Zombie NIR) on freshly isolated AM and Freeze-thawed exAM. Frozen exAM (2mo expanded, 2y5mo frozen) were thawed and expanded for 1 month before evaluation. Data shown are representative of 2 independent experiments.

Figure S2

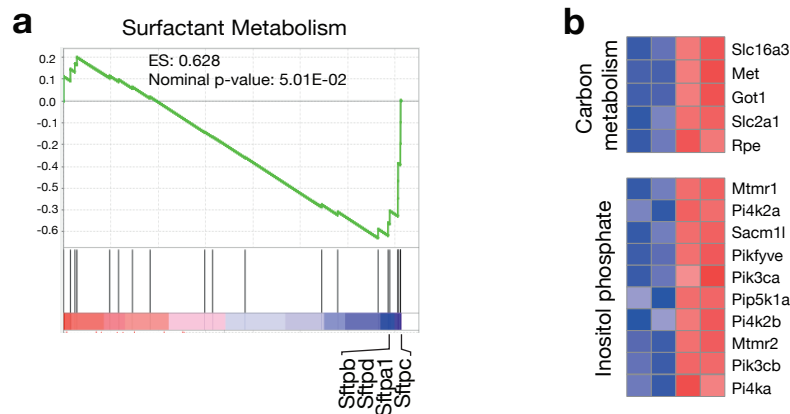


Figure S2. Analysis from AM versus exAM RNAseq analysis (Fig.3)
a) Gene set enrichment analysis (GSEA) for Reactome: Surfactant metabolism (R-HAS-9006936) in host AM vs exAM. Leading edge surfactant related genes highlighted below.
b) Heatmaps of gene expression showing key genes on recurring, complementary GO terms, Carbon metabolism and Inositol phosphate signalling from analysis shown in Figure3F.

Supplementary 2

Figure S3

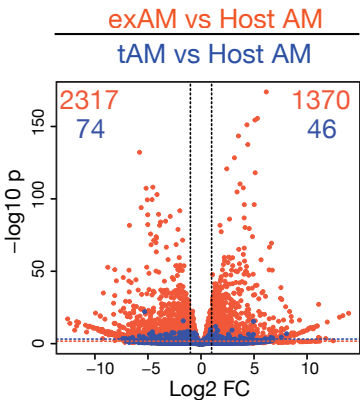


Figure S3. Overlaid volcano plot showing DEGs in exAM (red) or tAM (blue) compared to Host AM. (2FC, <0.05 FDR)

Figure S4

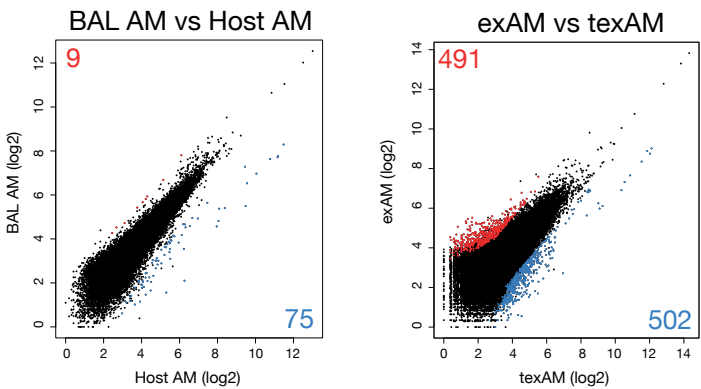


Figure S4. Scatter plot analysis of ATAC-seq peaks differentially open or closed. BAL AM vs Host AM and exAM vs texAM in log₂ scale. Data generated pooled from 3 independent experiments with 2-3 biological

Figure S5

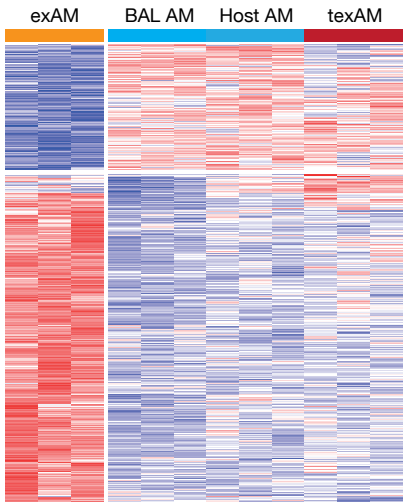


Figure S5. Heatmap of unsupervised clustering differential ATAC-seq peaks across all conditions.

Supplementary 3

Figure S6

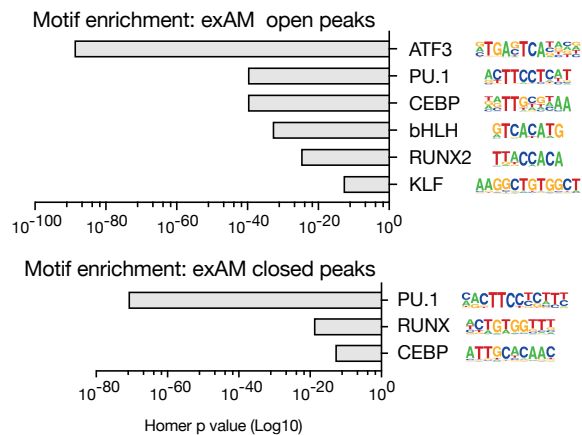


Figure S6. Motif enrichment analysis (MEA) for transcription factor (TF) binding sites on OCRs gained in exAM (top panel) or in host AM (bottom panel).

Figure S7

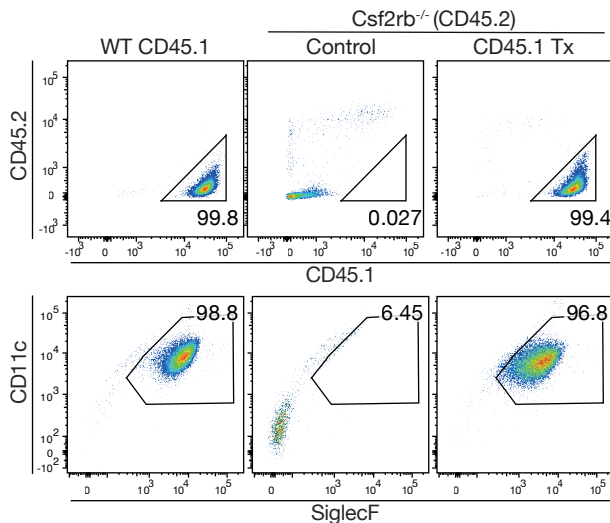


Figure S7. Flow cytometric analysis of exAM contribution to the *csf2rb*^{-/-} lungs at 3 months post exAM transplantation. FACS plots showing engrafted texAM (top panel) and maintenance of typical AM surface markers SiglecF and CD11c (bottom panel). Quantifications shown in Figure 6E-H.