Supplementary Figure 1

A

Control

B

OTM
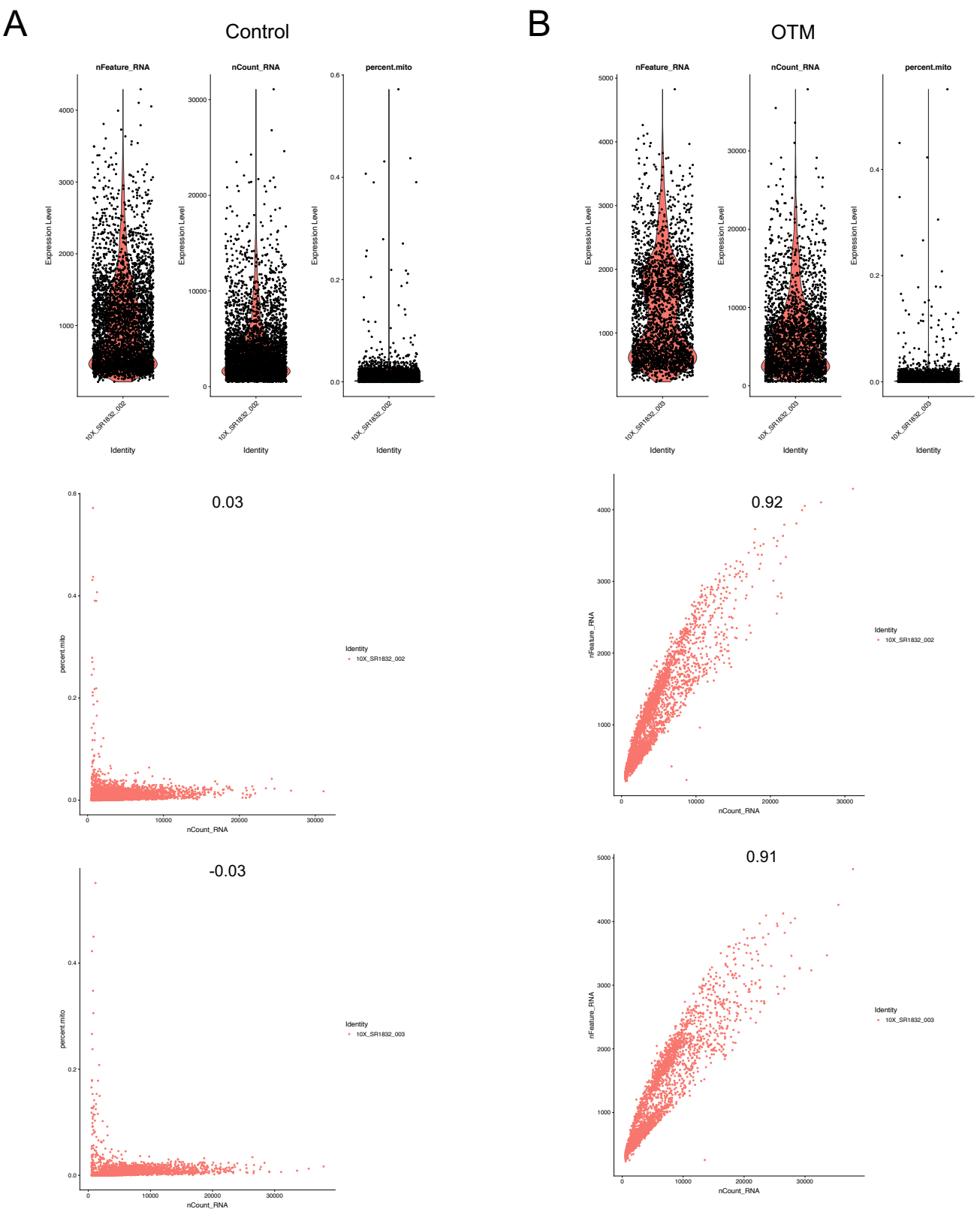
Supplementary Fig. 1 Quality control of the alveolar bone tissue scRNA-seq data.
(A, C) The violin plots showed the distribution of feature RNA, count RNA and mitochondrial RNA proportions in control and OTM group.
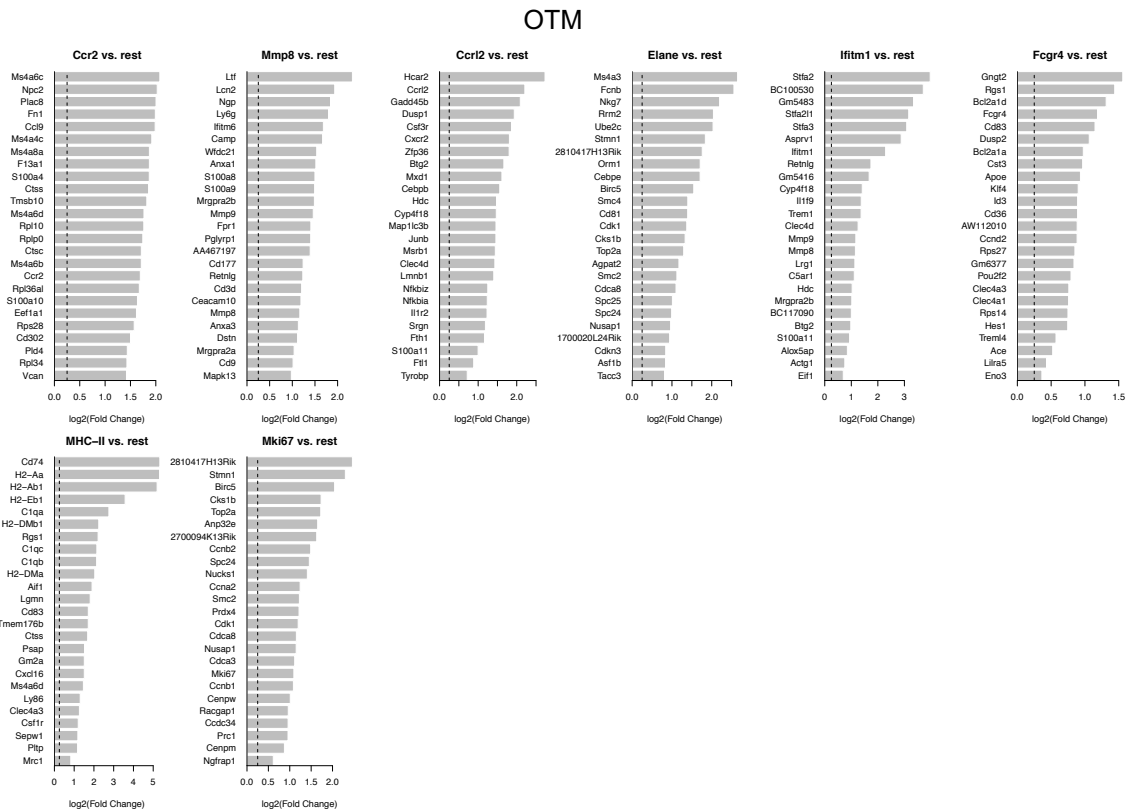(B, D) FeatureScatter plot exhibited the relationship between Feature RNA and count RNA, as well as mitochondrial RNA and count RNA in two groups.
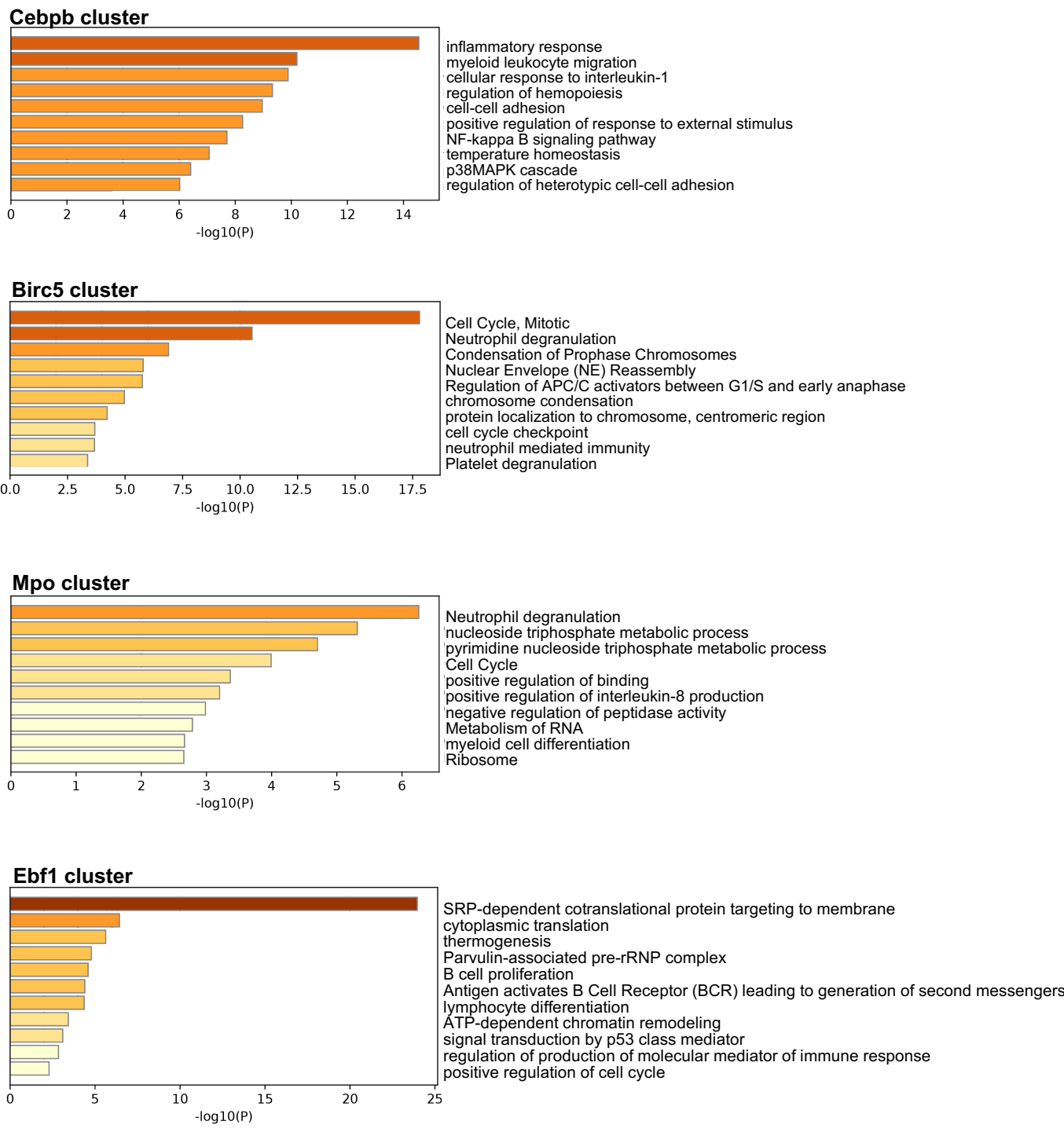
Supplementary Figure 2

A
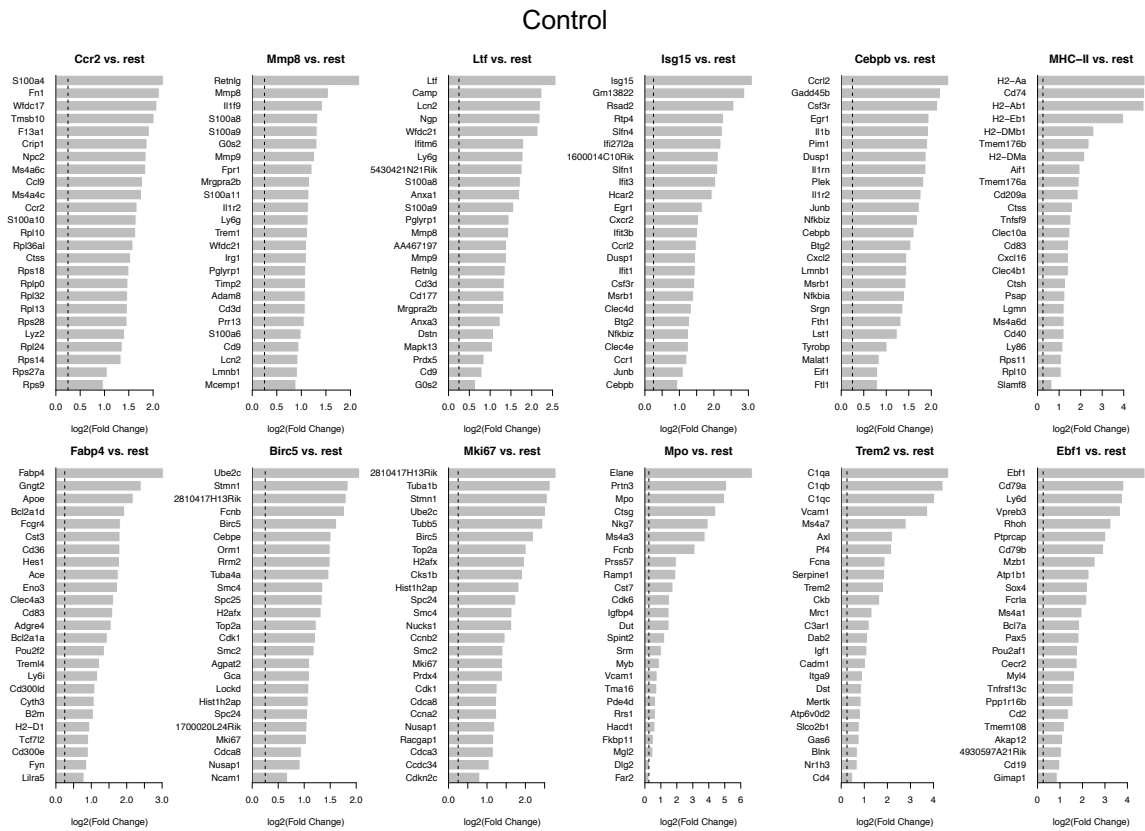
B

Supplementary Fig. 2 Barplot of top 25 differential expressed genes in control and OTM group.

Supplementary Figure 3

A

Cebpb cluster

inflammatory response
myeloid leukocyte migration
cellular response to interleukin-1
regulation of hemopoiesis
cell-cell adhesion
positive regulation of response to external stimulus
NF-kappa B signaling pathway
temperature homeostasis
p38MAPK cascade
regulation of heterotypic cell-cell adhesion

-log10(P)

Birc5 cluster

Cell Cycle, Mitotic
Neutrophil degranulation
Condensation of Prophase Chromosomes
Nuclear Envelope (NE) Reassembly
Regulation of APC/C activators between G1/S and early anaphase
chromosome condensation
protein localization to chromosome, centromeric region
cell cycle checkpoint
neutrophil mediated immunity
Platelet degranulation

-log10(P)

Mpo cluster

Neutrophil degranulation
nucleoside triphosphate metabolic process
pyrimidine nucleoside triphosphate metabolic process
Cell Cycle
positive regulation of binding
positive regulation of interleukin-8 production
negative regulation of peptidase activity
Metabolism of RNA
myeloid cell differentiation
Ribosome

-log10(P)

Ebf1 cluster

SRP-dependent cotranslational protein targeting to membrane
cytoplasmic translation
thermogenesis
Parvulin-associated pre-rRNP complex
B cell proliferation
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers
lymphocyte differentiation
ATP-dependent chromatin remodeling
signal transduction by p53 class mediator
regulation of production of molecular mediator of immune response
positive regulation of cell cycle

-log10(P)

Supplementary Fig. 3 Functional enrichment analysis for the remaining clusters in the steady state.
(A)The top 60-65 markers (adj. p-value < 0.05) per cluster were used to identify the functional enrichment categories using Metascape. Pathway enrichment is expressed as the -log10(P) adjusted for multiple comparison.
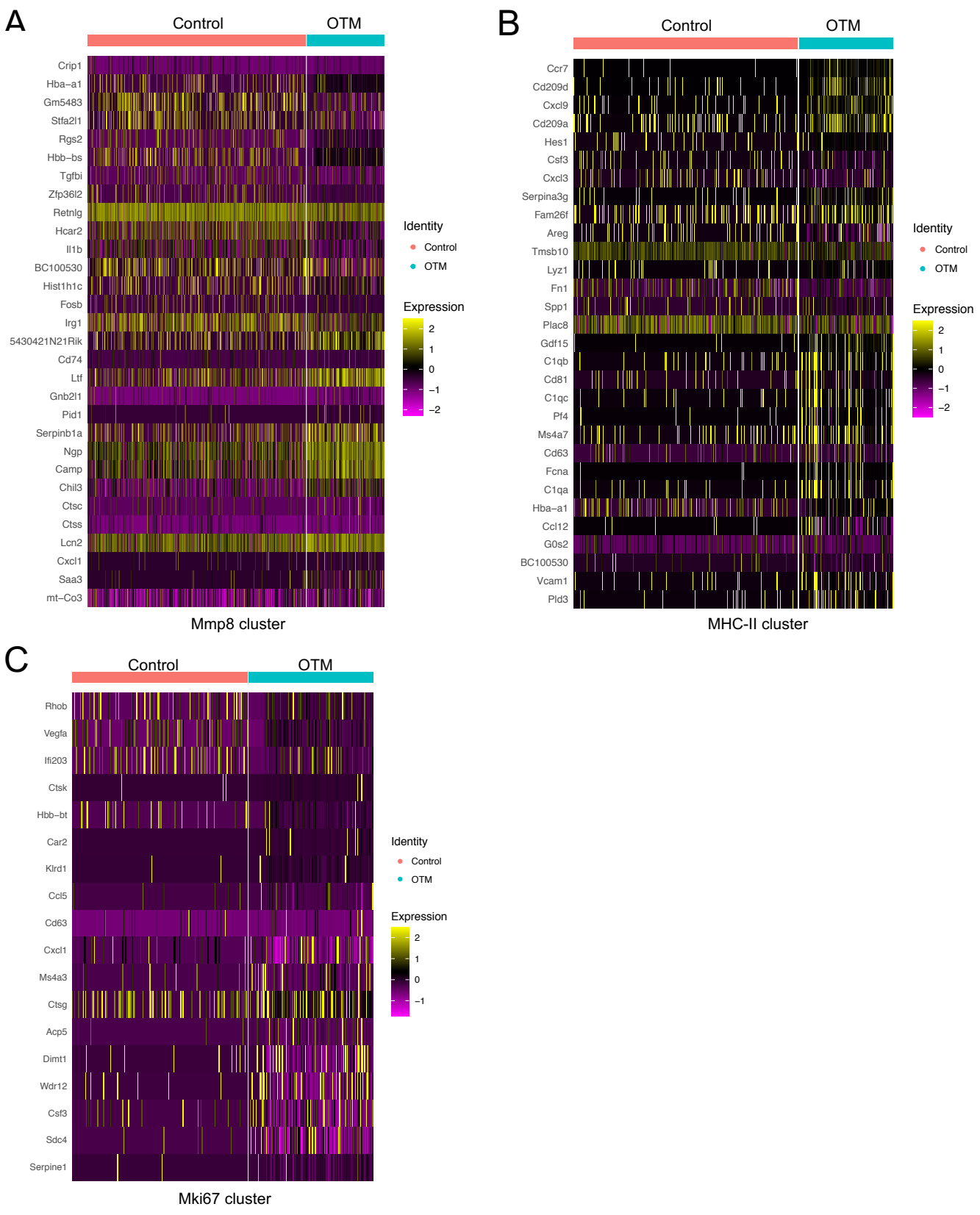
Supplementary Figure 4

A
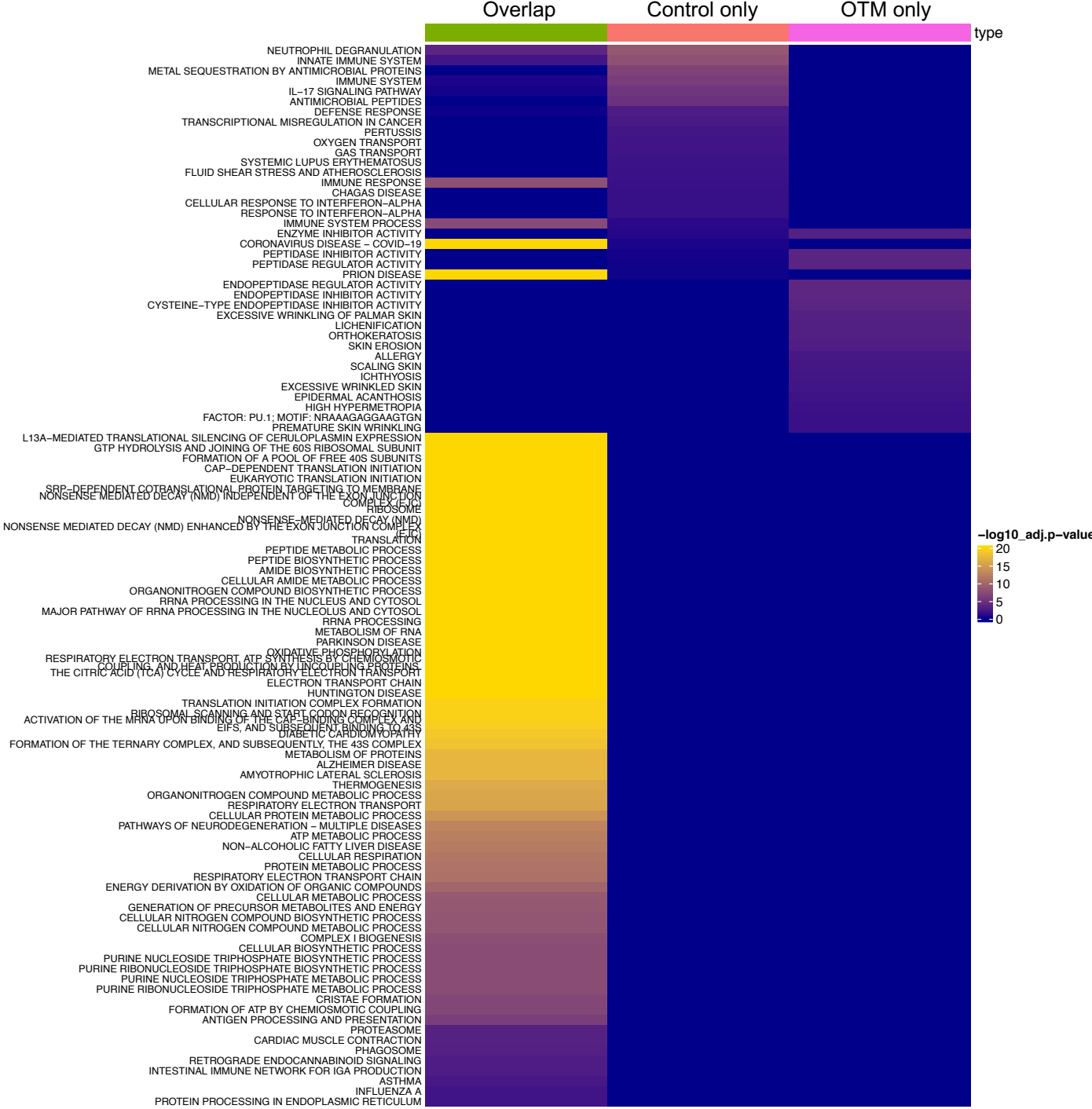
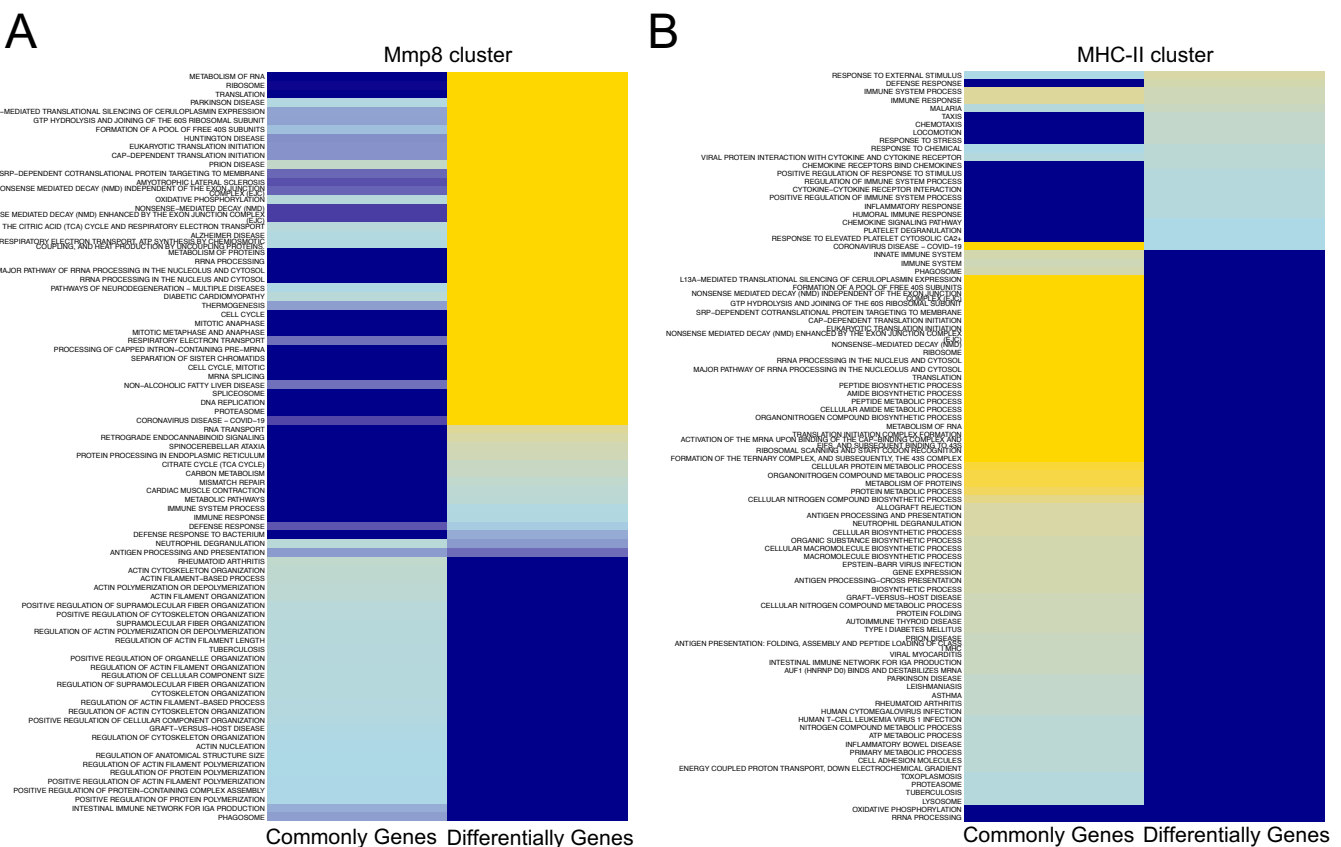**Supplementary Fig. 4 Heatmap of pathway analysis.**
(A) Heatmap of pathway analysis (gProfiler) of differentially expressed genes in control only, OTM only, and overlapping populations.

Supplementary Figure 5

Supplementary Fig. 5 Heatmap of gene differentially expressed genes in common clusters between two groups.
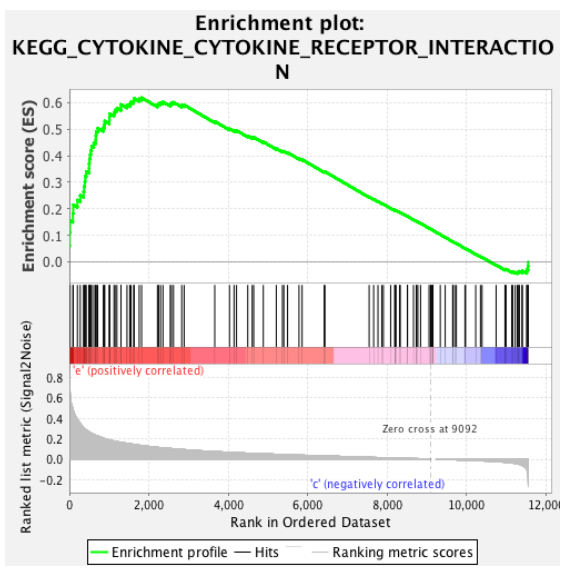(A-C) Differentially expressed genes in *Mmp8*, *MHC-II*, *Mki67* cluster between control and OTM.
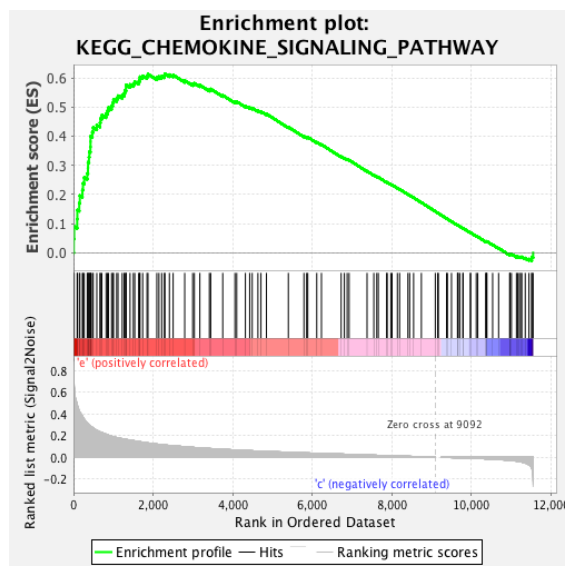
Supplementary Figure 6

Supplementary Fig. 6 Heatmap of Pathway analysis in common clusters
(A-C) Pathway analysis (gProfiler) of commonly and differentially expressed genes in *Mmp8*, *MHC-II*, *Mki67* cluster.
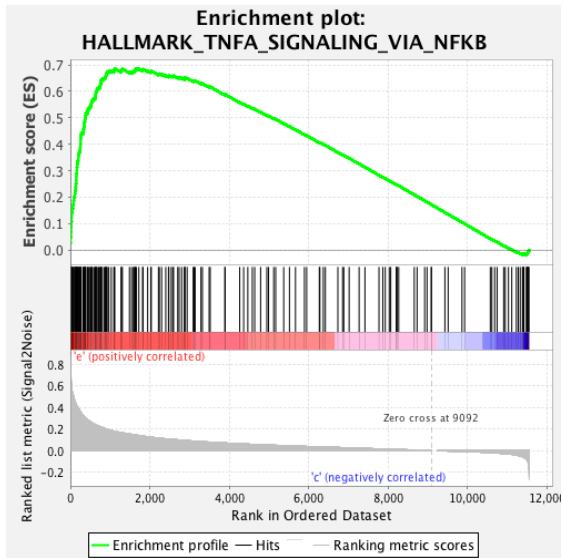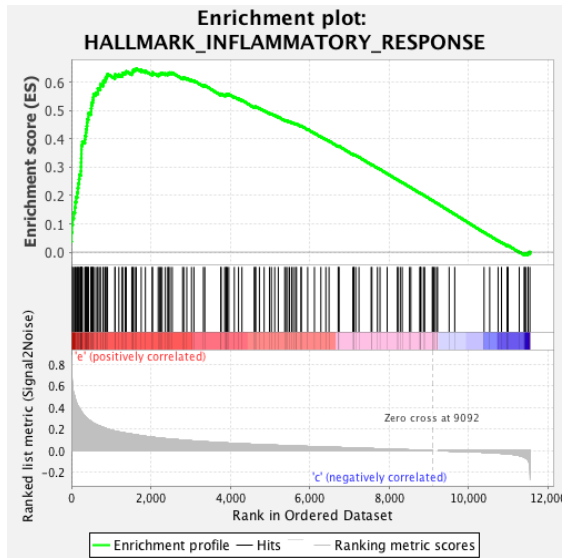
Supplementary Figure 7

A

B

C

D

Supplementary Fig. 7 GSEA (gene set enrichment analysis) in *Ccr2* clusters between control and OTM.
(A-D) GSEA enrichment plots for representative signaling pathways upregulated in *Ccr2* cluster during OTM compared to normal state.