

Additional File 1

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Tables S1-S3

Table S1: Sample information for this study

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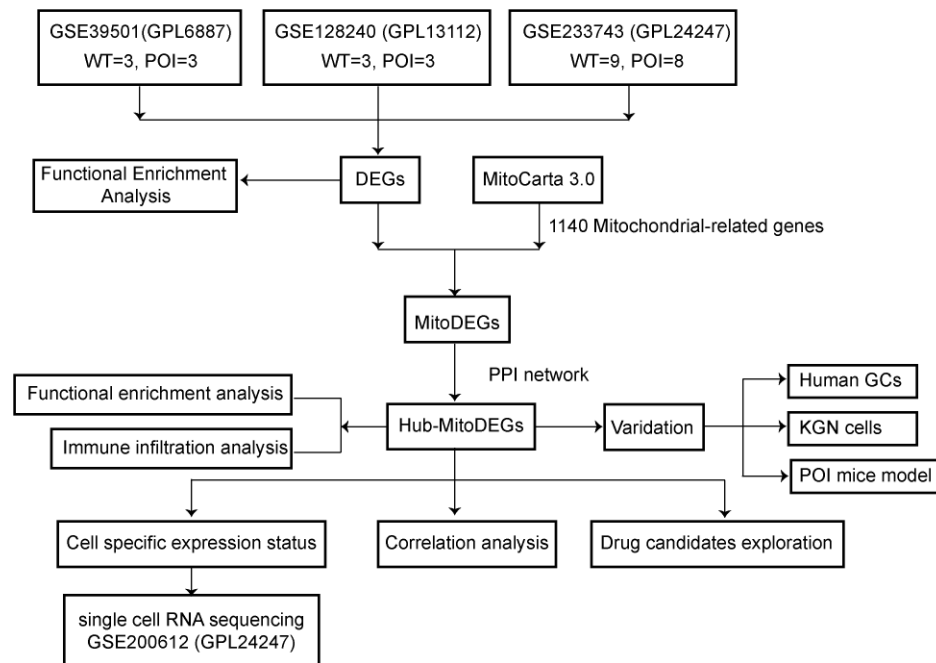


Figure S1 The data processing and flowchart of this study.

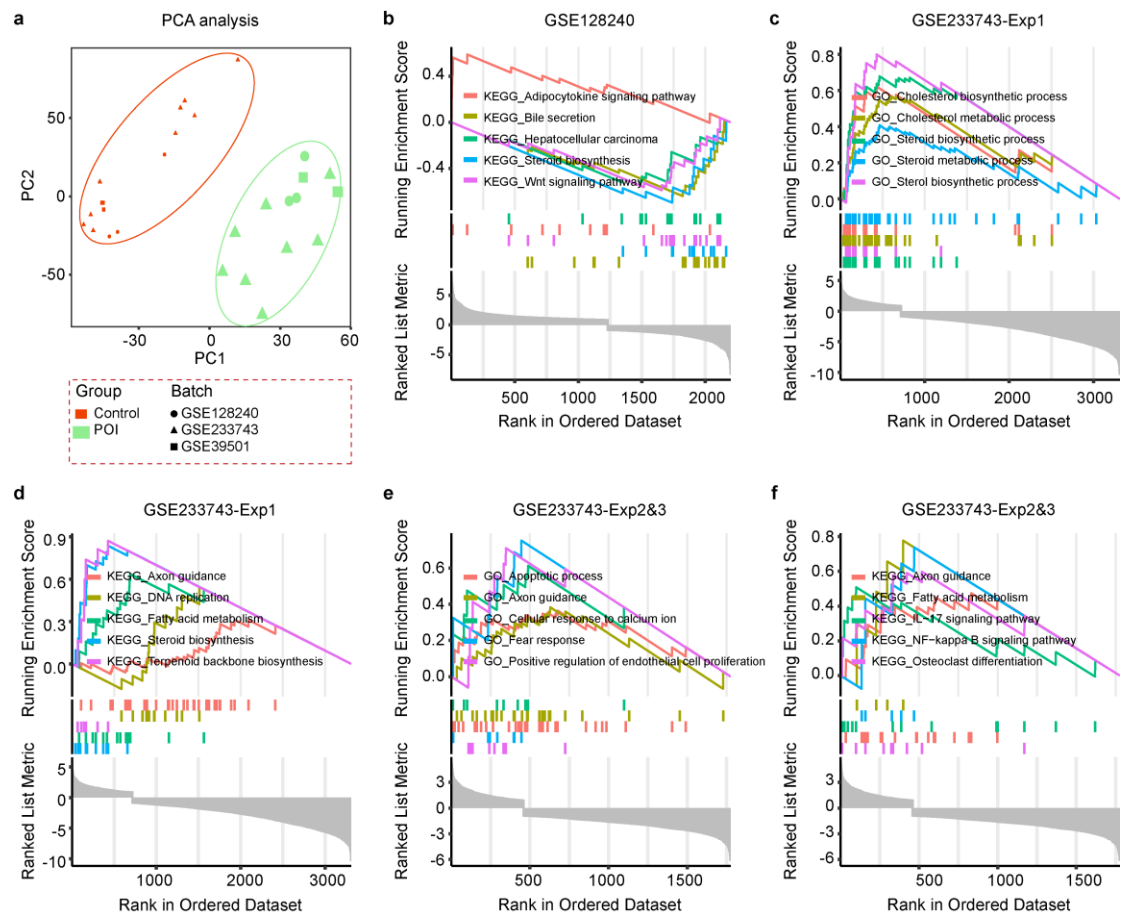


Figure S2 Results of PCA and GSEA analysis.

a Principal component analysis (PCA) plot of control and POI group based on gene expression patterns separated by PC1 and PC2. **b** GSEA analysis for GSE128240, the top 5 KEGG pathways based on the normalized enrichment score (NES) between WT and POI groups. **c-d** GSEA analysis for GSE233743-Exp.1, the top 5 GO terms (**c**) and KEGG pathways (**d**) based on the NES between WT and POI groups. **e-f** GSEA analysis for GSE233743-Exp.2&3, the top 5 GO terms (**e**) and KEGG pathways (**f**) based on the NES between WT and POI groups.

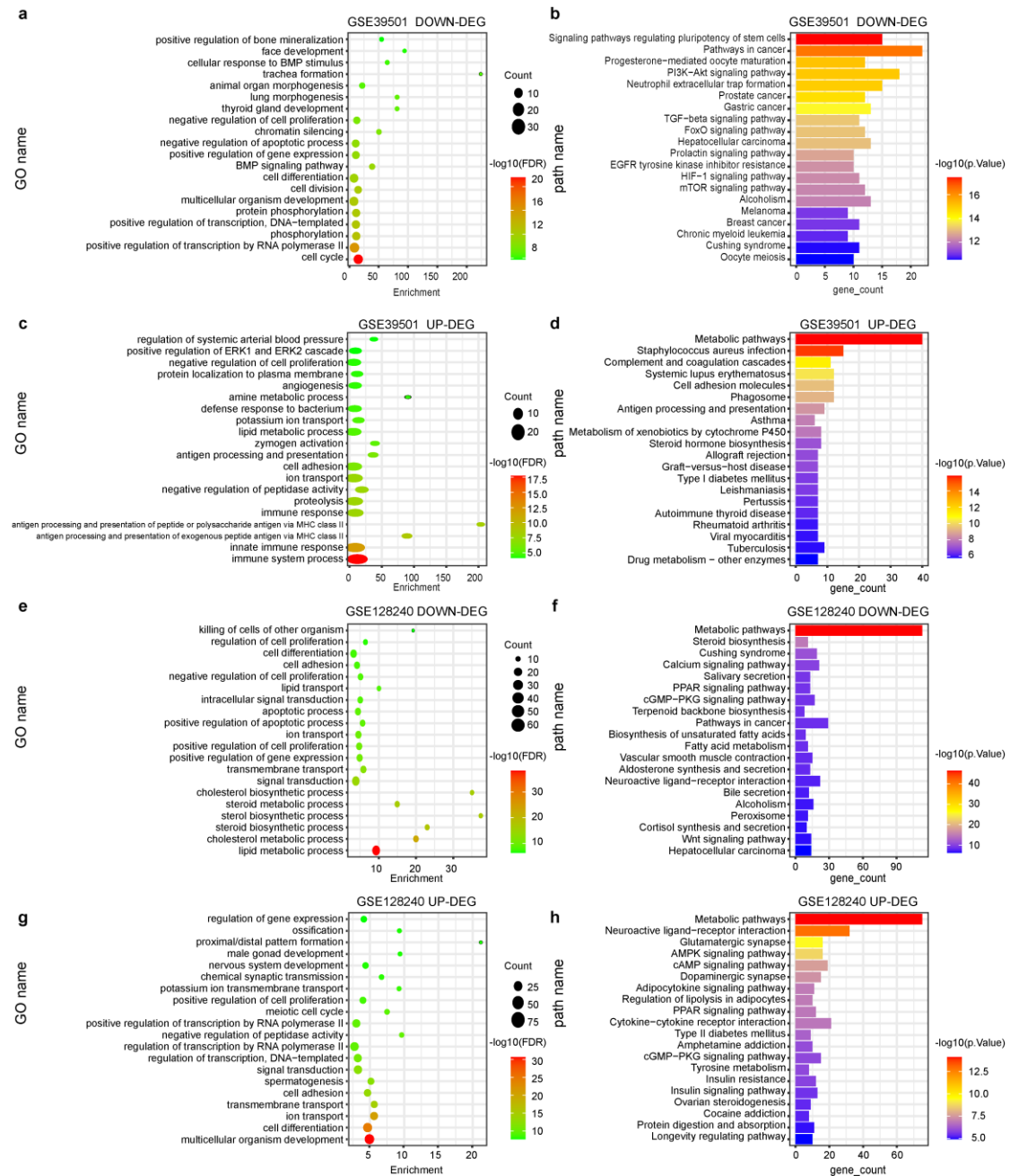


Figure S3 GO and KEGG analysis of GSE39501 and GSE128240.

a-b GO (a) and KEGG pathway (b) enrichment analysis of down-regulated DEGs in GSE39501.

c-d GO (c) and KEGG pathway (d) enrichment analysis of up-regulated DEGs in GSE39501.

e-f GO (e) and KEGG pathway (f) enrichment analysis of down-regulated DEGs in GSE128240.

g-h GO (g) and KEGG pathway (h) enrichment analysis of up-regulated DEGs in GSE128240.

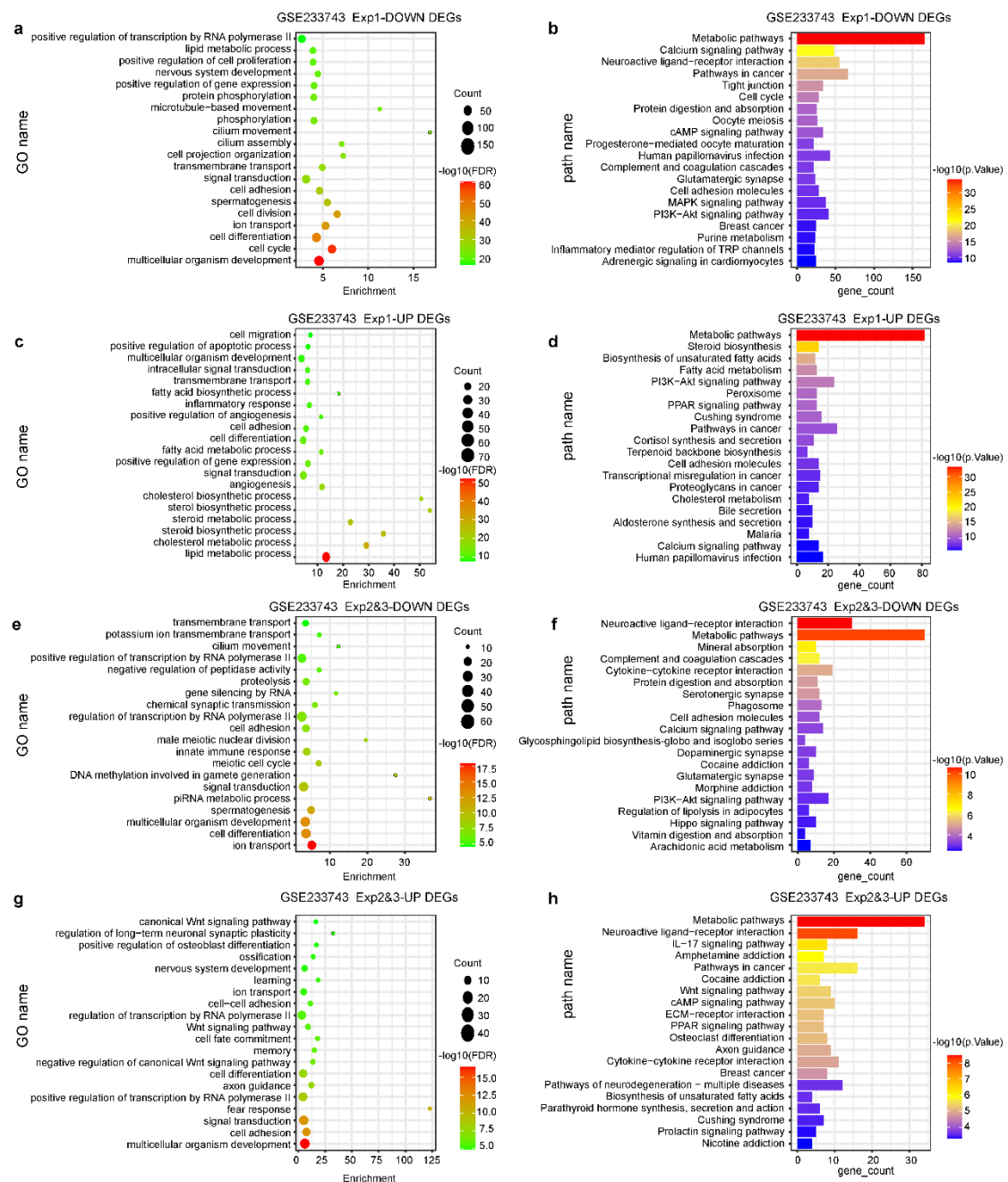


Figure S4 GO and KEGG analysis of GSE233743.

a-b GO (**a**) and KEGG pathway (**b**) enrichment analysis of down-regulated DEGs in GSE233743

Exp1. **c-d** GO (**c**) and KEGG pathway (**d**) enrichment analysis of up-regulated DEGs in

GSE233743 Exp1. **e-f** GO (**e**) and KEGG pathway (**f**) enrichment analysis of down-regulated

DEGs in GSE233743 Exp2&3. **g-h** GO (**g**) and KEGG pathway (**h**) enrichment analysis of up-

regulated DEGs in GSE233743 Exp2&3.

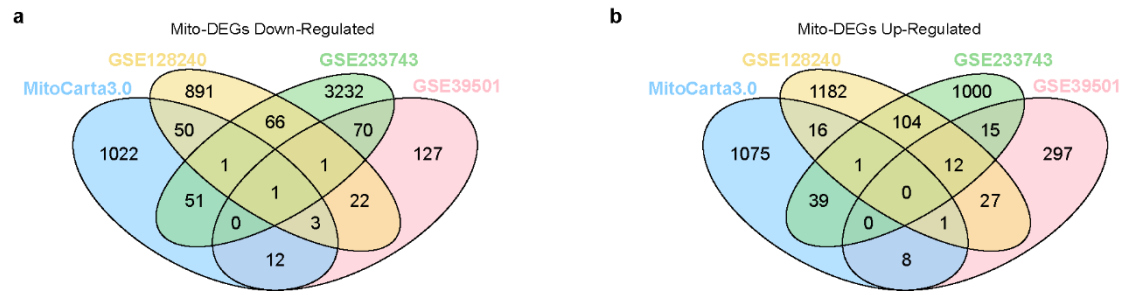


Figure S5 MitoDEGs in POI.

a Venn diagrams showed the number of downregulated DEGs that overlap between GSE128240, GSE233743, GSE39501, MitoCarta3.0. **b** Venn diagrams showed the number of upregulated DEGs that overlap between GSE128240, GSE233743, GSE39501, MitoCarta3.0.

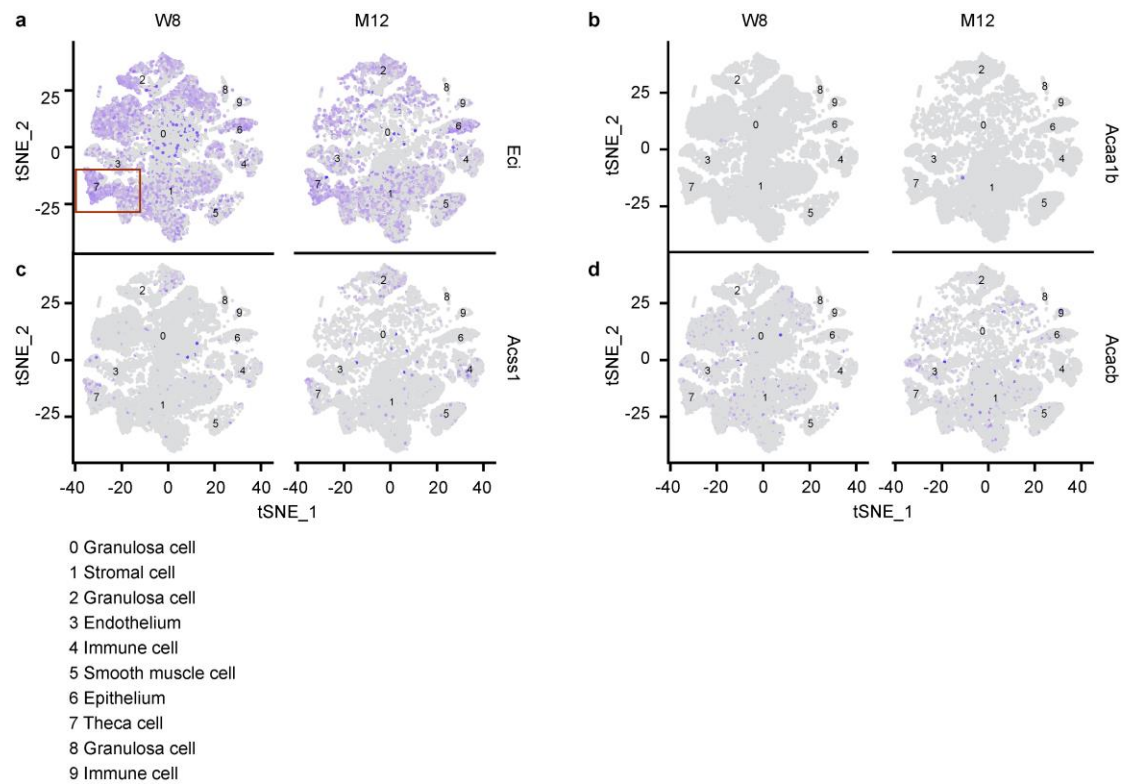


Figure S6 Cell-specific expression of Eci1, Acaa1b, Acss1, Acacb.

a tSNE cluster map showing expression of Eci1. **b** tSNE cluster map showing expression of Acaa1b. **c** tSNE cluster map showing expression of Acss1. **d** tSNE cluster map showing expression of Acacb. Red lines label the main clusters of interest.

MitoDEGs and sulfur metabolism-related genes. **e** Correlation between hub-MitoDEGs and vitamin metabolism-related genes ($****p < 0.0001$, $***p < 0.001$, $**p < 0.01$, $*p < 0.05$).

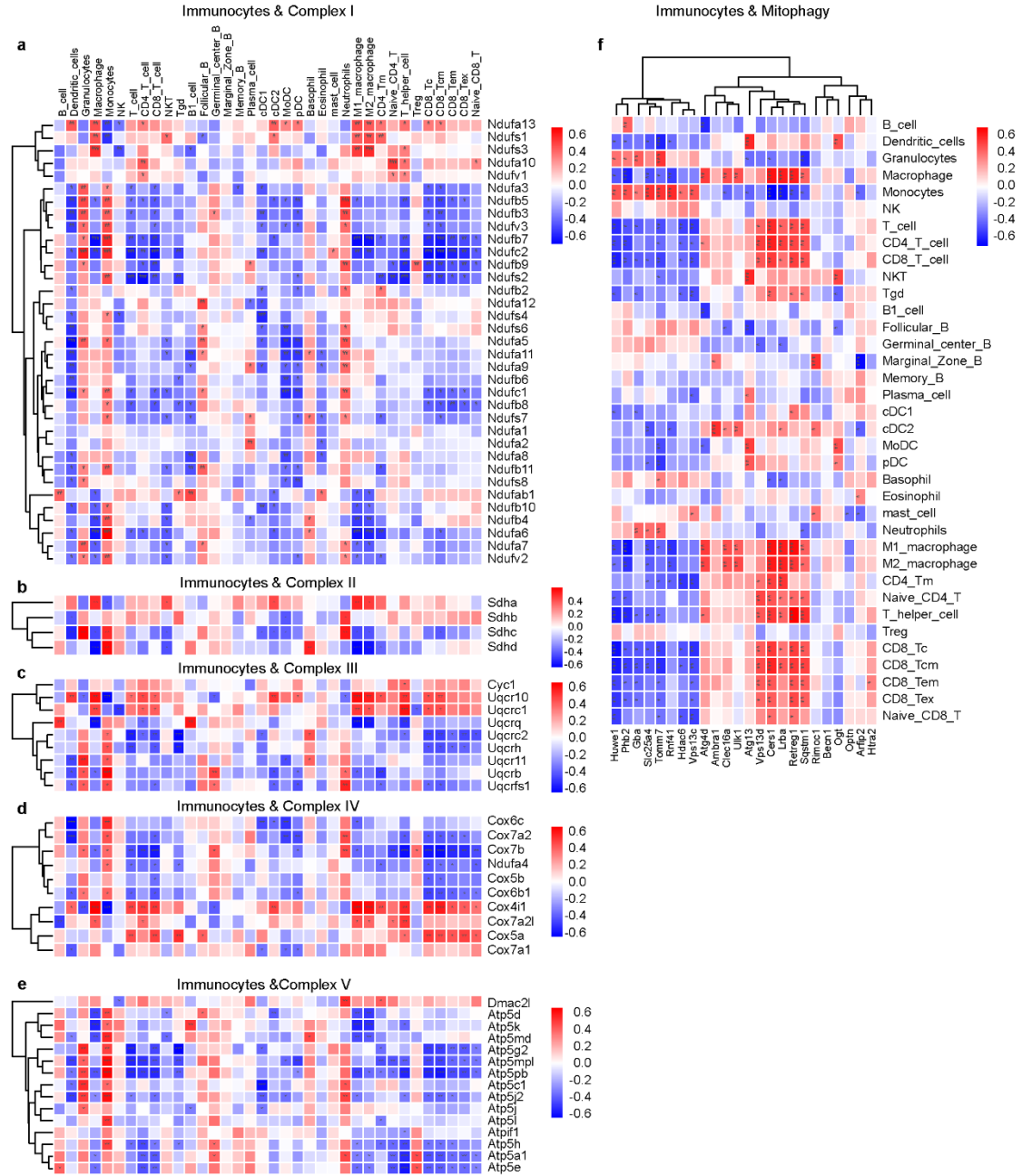


Figure S8 Correlations between mitochondrial related genes and immunocytes.

a-e Correlation between mitochondrial respiratory chain complex genes and immune cells. **f**

Correlation between mitophagy related genes and immune cells. ($****p < 0.0001$, $***p < 0.001$,

$**p < 0.01$, $*p < 0.05$)

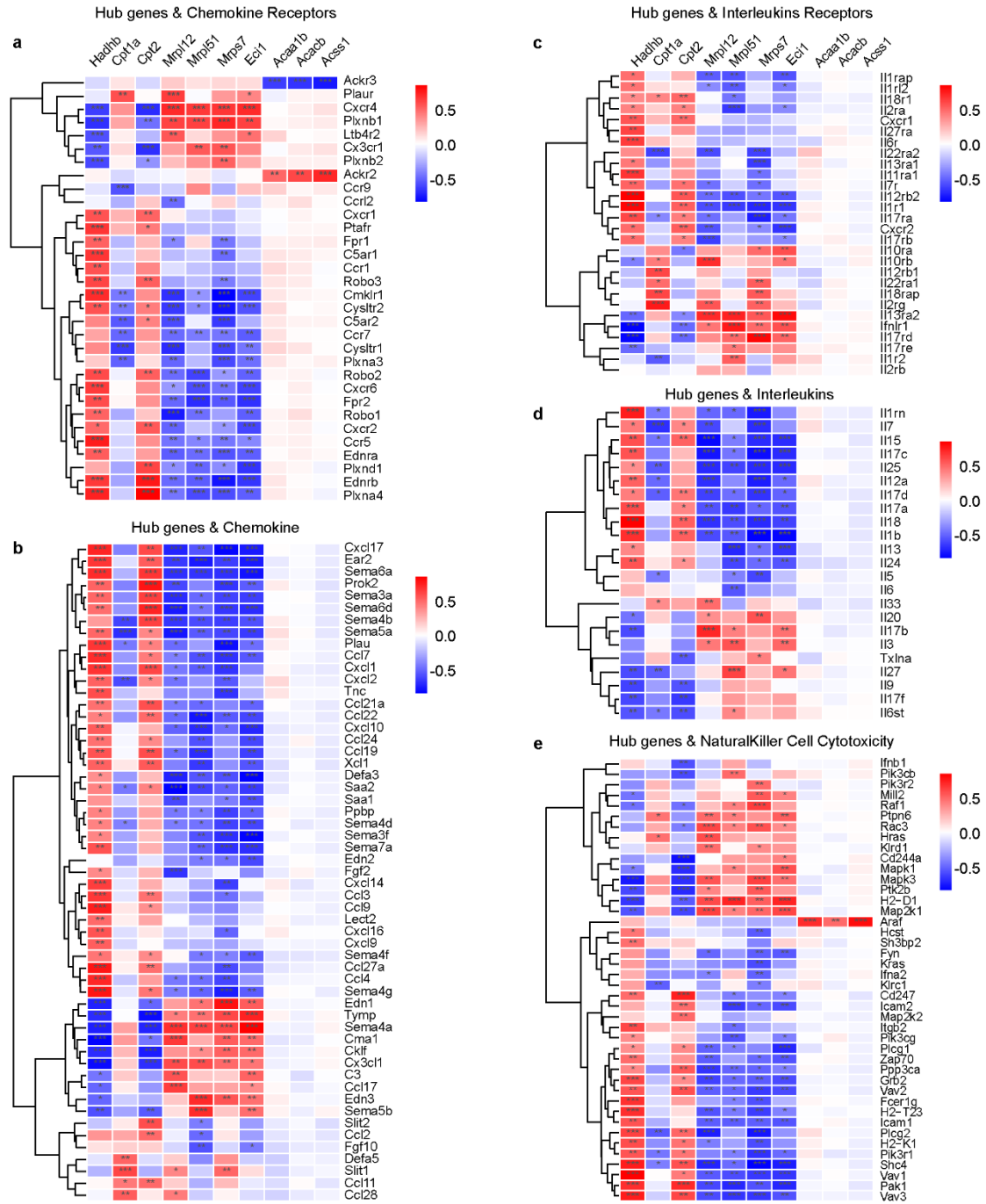


Figure S9 Correlations between hub-MitoDEGs and immune related genes.

a Correlation between hub-MitoDEGs and chemokine receptors related genes. **b** Correlation between hub-MitoDEGs and chemokine related genes. **c** Correlation between hub-MitoDEGs and interleukins receptors related genes. **d** Correlation between hub-MitoDEGs and interleukins related genes. **e** Correlation between hub-MitoDEGs and natural killer cell cytotoxicity related genes. (**** $p < 0.0001$, *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$)

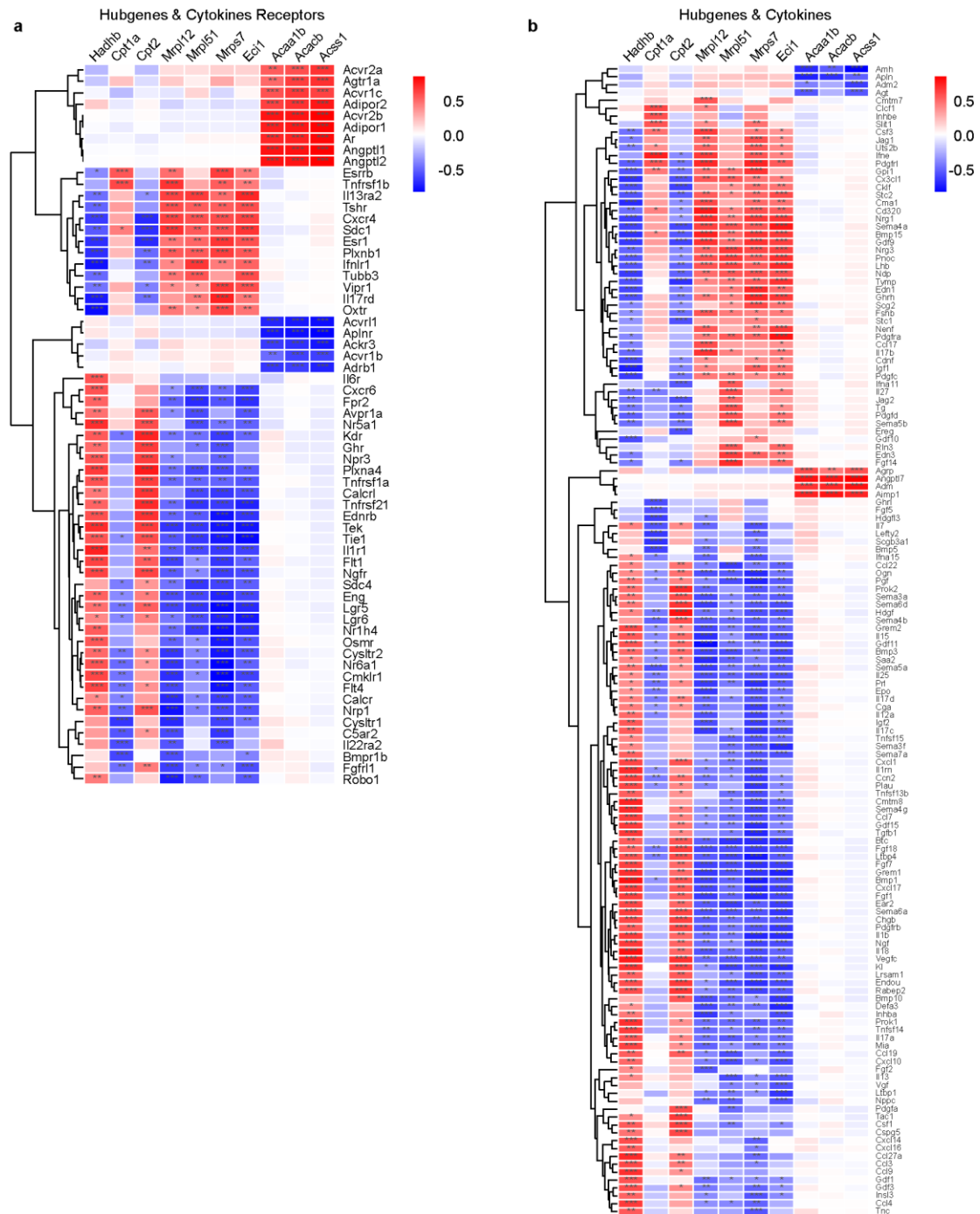


Figure S10 Correlations between hub-MitoDEGs and cytokines receptors- and cytokines-

related genes. a Correlation between hub-MitoDEGs and cytokines receptors related genes. **b**

Correlation between hub-MitoDEGs and cytokines related genes. (**** $p < 0.0001$, *** $p < 0.001$,

** $p < 0.01$, * $p < 0.05$)

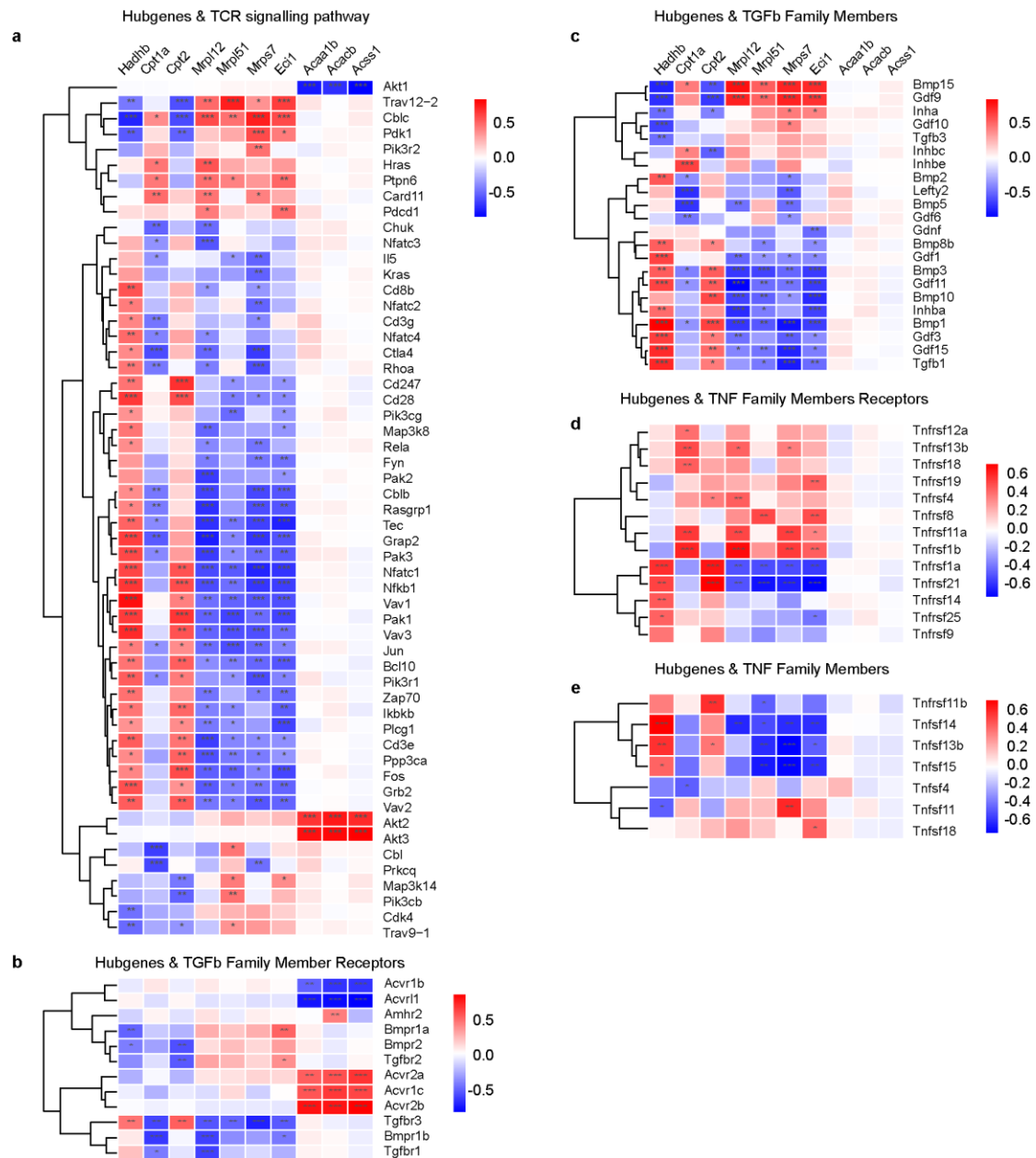


Figure S11 Correlations between hub-MitoDEGs and TCR signalling pathway-, TGFb family member receptors-, TGFb family members -, TNF family member receptors-, and TNF family members- related genes. a Correlation between hub-MitoDEGs and TCR signalling pathway related genes. **b** Correlation between hub-MitoDEGs and TGFb family member receptors related genes. **c** Correlation between hub-MitoDEGs and TGFb family members related genes. **d** Correlation between hub-MitoDEGs and TNF family member receptors related genes. **e**

Correlation between hub-MitoDEGs and TNF family members related genes. (**** $p < 0.0001$,
*** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$).

Table S1: Sample information for this study

GEO name	Sample size	Control group	POI group	Platform	Published	Treatment
RNA-seq data						
GSE128240	6	3	3	GPL13112	1-Jan-20	CTX
GSE233743	17	9	8	GPL24247	30-May-23	CTX+busulfan
Microarray data						
GSE39501	6	3	3	GPL6887	21-Jun-22	/
scRNA-seq						
GSE200612	4	2 (8-week-old)	2 (12-month-old)	GPL24247	31-Dec-22	/

Table S2 Patient information for this study.

Parameters	POI (n=50)	HC (n=50)	<i>p</i> value
Age (years)	32±6	31.5±5.5	0.5139
BMI (kg/m ²)	21.02±4.37	21.1±2.84	0.5823
FSH (IU/L)	31.665±6.585	6.255±3.675	<0.0001
AMH (ng/ml)	0.5±0.48	4.94±3.90	<0.0001
E ₂ (pmol/L)	83.5±64.5	181±91	<0.0001
LH (IU/L)	14.825±6.245	6.575±4.325	<0.0001
AFC (counts)	5±4	12.5±5.5	<0.0001

Table S3 Sequences of the primers used in this study.

Gene	Forward (5'-3')	Reverse (5'-3')
Human:		
HADHB	CTGTCCAGACCAAAACGAAGAA	CGATGCAACAAACCCGTAAGC
CPT1A	ATCAATCGGACTCTGGAACGG	TCAGGGAGTAGCGCATGGT
CPT2	CATACAAGCTACATTTCTGGGACC	AGCCCGGAGTGTCTTCAGAA
MRPS7	TCAAGGGAGGCCGTTTCTAC	TCTTGTGCAAGTCATGCTTCC
MRPL51	AGGGCCATGTTCTGGAGTGTAT	CCCTTTCCAACCTCGAAGCC
MRPL12	ATCCCCATAGCGAAAGAACGG	GGACGAGGTTGATGCCTTGG
ECI1	CTGCGGTTGTACCAGTCCAA	GATGCGGTAGTCACAGGTCA
ACAA1	GCGGTTCTCAAGGACGTGAAT	GTCTCCGGGATGTCACCTCAGA
ACACB	AGAAGACAAGAAGCAGGCAAAC	GTAGACTCACGAGATGAGCCA
ACSS1	CGTCCTTTTTGAGAGCACCC	GCATCACCGTATTTTCAGCAACA
Mouse:		
Hadhb	TCGGGTTTGTTCATCGGA	GGCCAGAAGCTATCAGACCAA
Cpt1a	AGATCAATCGGACCCTAGACAC	CAGCGAGTAGCGCATAGTCA
Cpt2	CCTGCTCGCTCAGGATAAACA	GTGTCTTCAGAAACCGCACTG
Mrps7	TTCTGGCCCGGTCTCTCAT	GGGTTCCGTTCAATGGTGG
Mrpl51	GAGGGCTCTGTTTGGCGTC	TCCAGCCTCGAAGCCATACT
Mrpl12	AGCCACCGAAGGAGTGAAG	GGAGCGTAAGGCTGGCAAT
Eci1	GGGTTGCAGTGATGAAGTTAAGG	CCTCGGATGCTCTTGTCATTTT
Acaa1b	CAGGACGTGAAGCTAAAGCCT	CTCCGAAGTTATCCCCATAGGAA
Acacb	AGGTTCAGATGCTAATGGGT	GCCCAGGATAAAGCTGGTCAT
Acss1	TGCAAGGCTGTTATCACCTTC	TCTTCACTGCTCATGCTCTCA