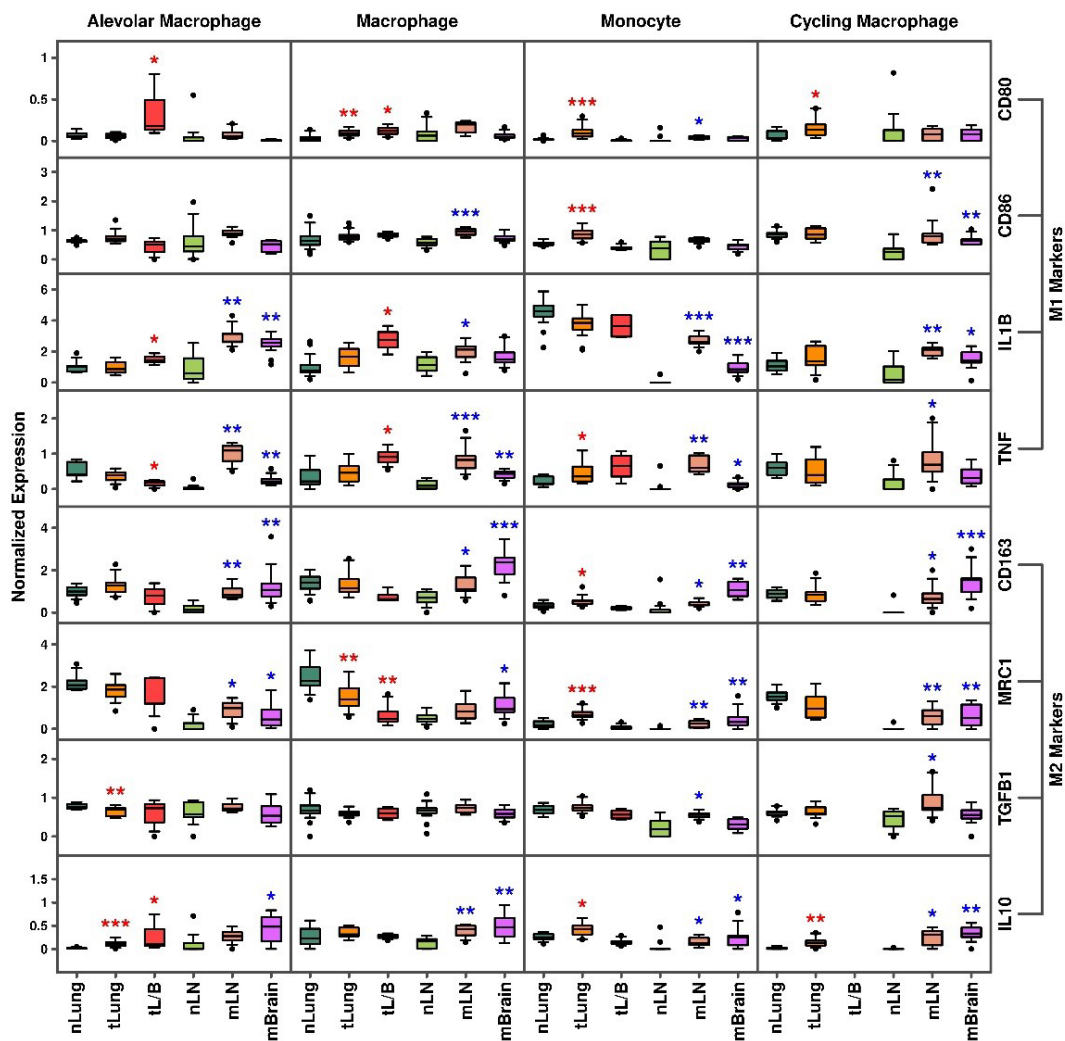


**Figure S1** Cell type characteristics of each sample type. From left to right: UMAP plot showing the distribution patterns of all cell subgroups, bar plot showing the number of cells in each cell subgroup, UMAP plot showing the sample sources of all cell profiles, and bar plot showing the ratios of sample origins in each cell subgroup. (A) nLung: paracancer normal lung samples. (B) tLung: early-stage lung cancer samples. (C) tL/B: advanced-stage lung cancer samples. (D) nLN: normal lymph node samples. (E) mLN: metastatic lymph node samples. (F) mBrain: metastatic brain samples. UMAP, Uniform Manifold Approximation and Projection; T/NK, T and natural killer cells; MAST, Mast cells; NA, not applied.



**Figure S2** Boxplots showing the relative expression levels of M1 and M2 markers across different sample types. One-way ANOVA was performed in the comparison, and a “Bonferroni” method was used in the correction. \*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001. nLung, paracancer normal lung samples; tLung, early-stage lung cancer samples; mBrain, metastatic brain samples; mLN, metastatic lymph node samples; tL/B, advanced-stage lung cancer samples; nLN, normal lymph node samples.

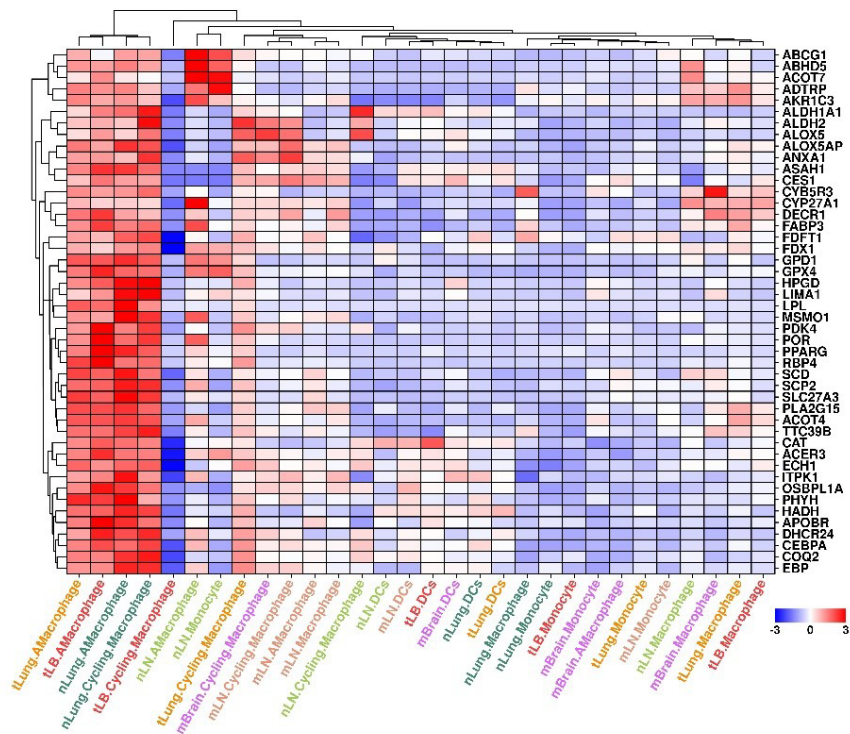


Figure S3 Heatmap representing the expression levels of metabolic related genes across different subgroups.

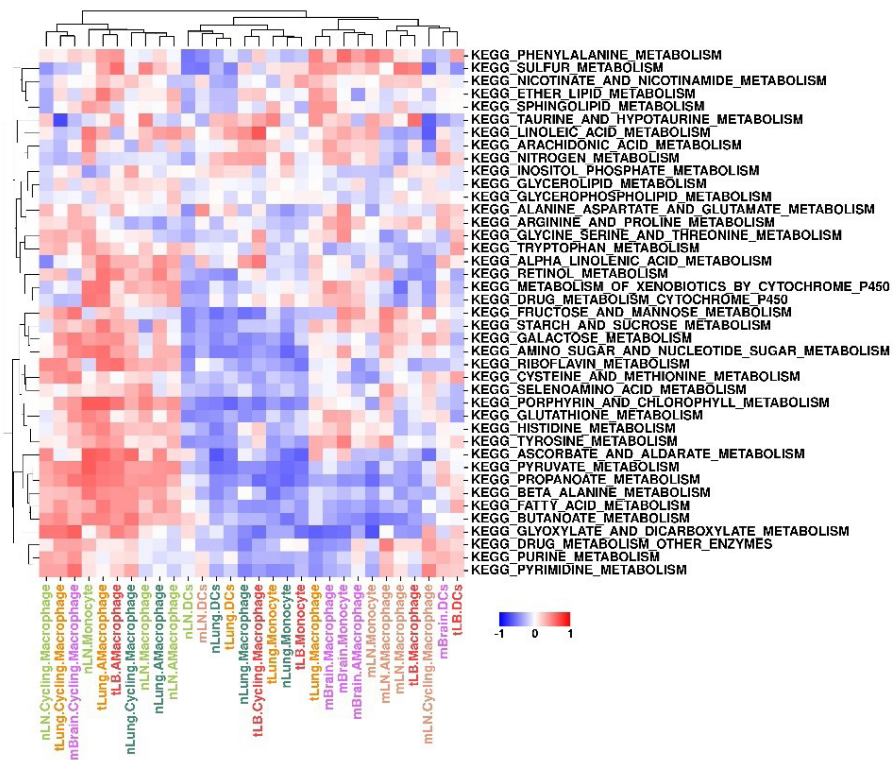


Figure S4 Heatmap representing the GSEA scores of metabolism related KEGG items across different subgroups.