Supplementary Material

# Supplementary Figures



**Figure S1** PCA of RNA-seq data prior to batch effect correction. The dot colors represent different macrophage phenotypes and lipid-loaded macrophages, as illustrated in the figure.

图表

描述已自动生成

**Figure S2** Preliminary WGCNA results using lipid-loaded and polarized samples. Heatmap showing the associations between module eigengenes, and all identified co-expression modules.

图表

描述已自动生成

**Figure S3** The eigengene network's heatmap shows correlations between various modules; those with strong connections are grouped together.

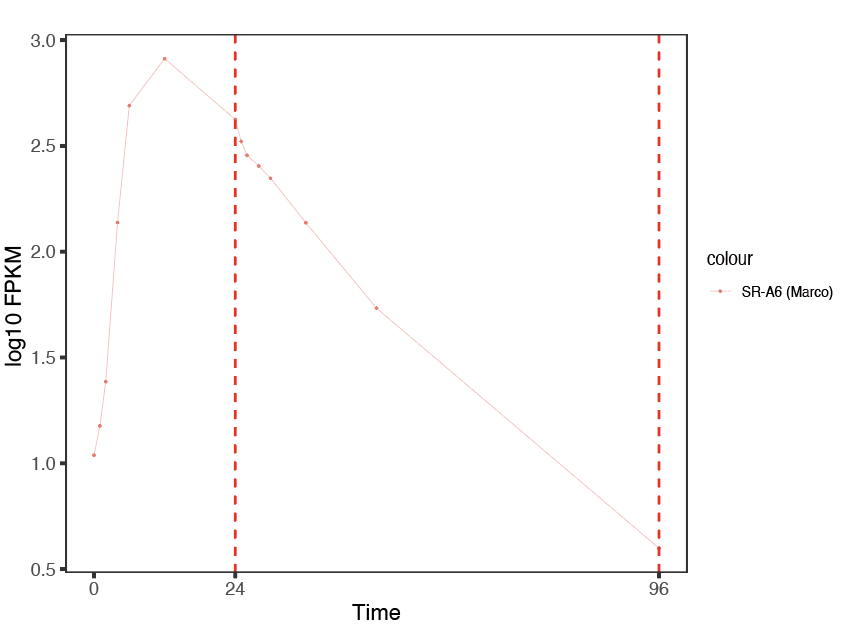
 **Figure S4** The gene expression levels of hysteresis genes in the MEblue across macrophage polarization data.

 **Figure S5** The gene expression levels of hysteresis genes in the MEbrown across macrophage polarization data.

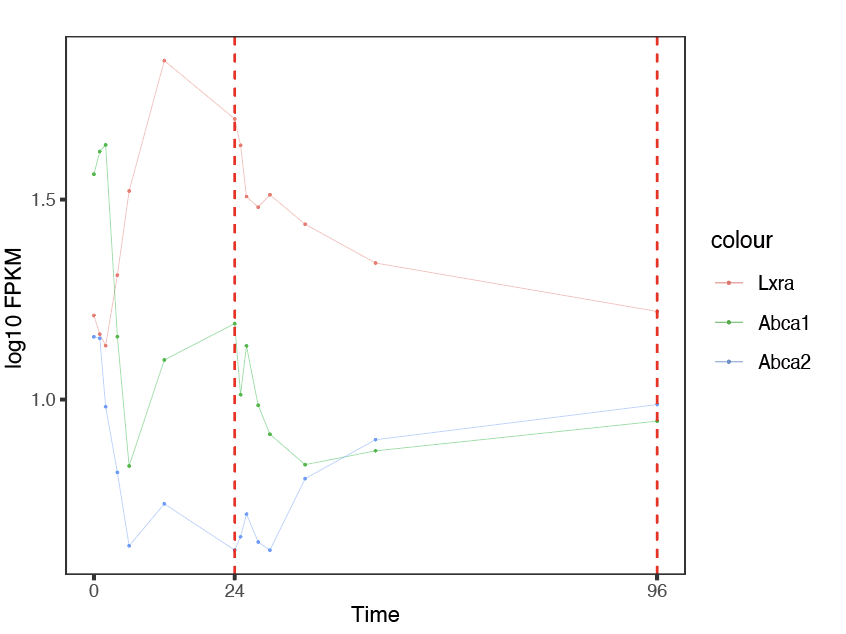
图表, 折线图

描述已自动生成

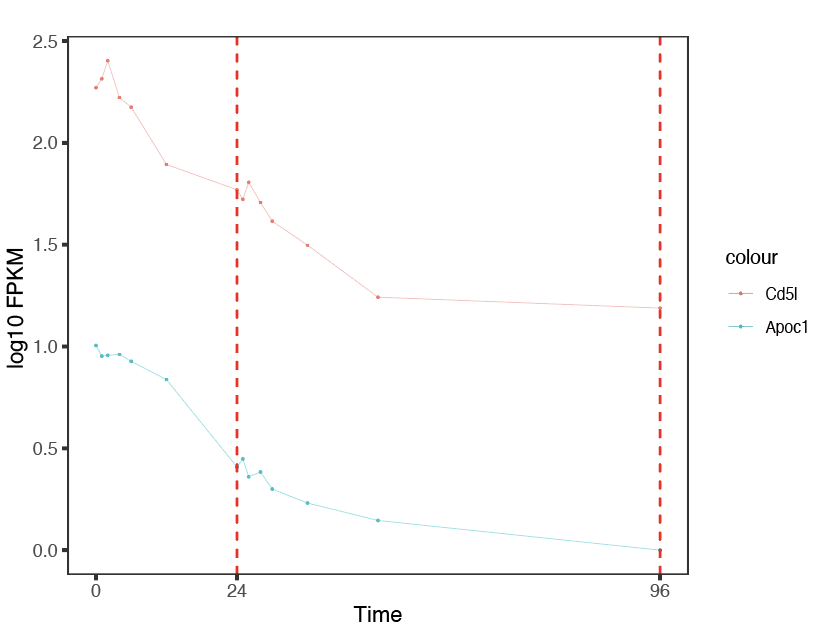
**Figure S6** Gene expression levels of Lox-1, Cd68, SR-A1, Cd36 under M0->M1->M2 between 0 to 96 hours.



**Figure S7** Gene expression levels of Marco under M0->M1->M2 between 0 to 96 hours.



**Figure S8** Gene expression levels of Lxra, Abca1, Abca2 under M0->M1->M2 between 0 to 96 hours.



**Figure S9** Gene expression levels of Cd5l, Apoc1under M0->M1->M2 between 0 to 96 hours.