分析报告

# M1 and M2

为了分析C，Y和W组的表型跟倾向于M1还是M2，我们到Gene Expression Omnibus（GEO）数据库上寻找M1和M2巨噬细胞的测序数据，我们发现Schmidt等人的测序数据符合我们的要求1。因此，我们将其下载下来，然后使用下面的公式分别将我们自己的测序数据和Schmidt等人的测序数据标准化。

其中表示比对到基因g的reads数，D表示测序深度，表示基因g的长度（bp）。

数据标准化后分别计算C，Y和W与M1和M2的spearman相关系数。结果显示C，Y和W的表型都更倾向于M2，但是C组的表型更接近于M2表型，W组的表型与M2的相似度最小。

In order to analyze whether the phenotype of C, Y, and W groups tends towards M1 or M2, we searched for sequencing data of M1 and M2 macrophages in the Gene Expression Omnibus (GEO) database. We found that the sequencing data of Schmidt et al. met our requirements1. Therefore, we downloaded it and standardized our own sequencing data and Schmidt et al.’s sequencing data using the following formula.

Among them, represents the number of reads aligned to gene g, D represents sequencing depth, and represents the length (bp) of gene g.

Calculate the Spearman correlation coefficients of C, Y, and W with M1 and M2 after data standardization. The results showed that the phenotypes of C, Y, and W were more inclined towards M2, but the phenotypes of Group C were closer to M2, while the phenotypes of Group W had the smallest similarity to M2.

# fatty acid biosysnthesis

为了研究C，Y和W三组哪个的脂肪合成代谢最为旺盛，我们首先从KEGG数据库中下载了fatty acid biosysnthesis和Biosynthesis of unsaturated fatty acids两个与脂肪合成相关代谢通路中的基因，然后分析了这些基因在C，Y和W三组中的表达水平。结果显示W组的脂肪合成代谢最为旺盛，尤其是ACSL4基因，在W组的表达水平非常高，其主要参与长链脂肪酸的合成。

In order to investigate which group C, Y, and W had the most vigorous fat synthesis metabolism, we first downloaded the genes related to fat acid biosynthesis and Biosynthesis of Unsaturated fat acids from the KEGG database, and then analyzed the expression levels of these genes in the C, Y, and W groups. The results showed that the fat synthesis metabolism in group W was the most vigorous, especially the ACSL4 gene, which had a very high expression level in group W and was mainly involved in the synthesis of long-chain fatty acids.

# 参考文献

1. Schmidt, S. V. *et al.* The transcriptional regulator network of human inflammatory macrophages is defined by open chromatin. *Cell Res.* **26**, 151–170 (2016).