

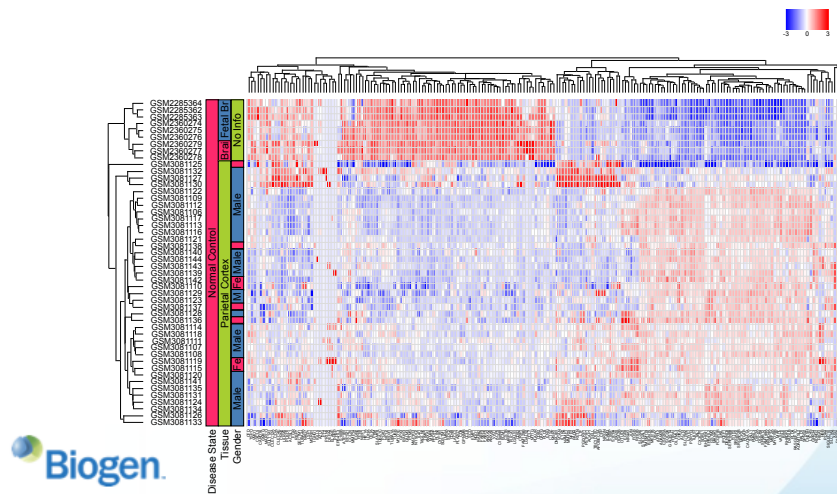
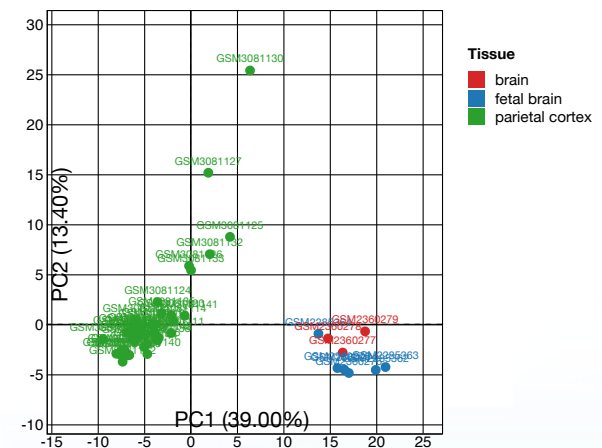
Heterogeneity in microglial samples from different GEO studies

There are stark differences between gene expression profiles of microglia that originate from different studies. These differences might not reflect true biology and they make it difficult to find the right reference dataset to which in-house generated iPSC-derived microglia can be compared.

I selected 48 samples from 3 studies (GSE85839, GSE89189, GSE99074) to compare the gene expression profiles of a subset of genes. These genes were derived from the Chris Glass dataset of isolated microglia and monocytes by cell type deconvolution with CellDistinguisher. These are the distinguisher genes that differentiate isolated microglia (ex vivo) from isolated monocytes and cultured microglia.

Based on the heatmap, there seem to be approximately three types of cells dominating these samples corresponding to freshly isolated microglia, monocytes and cultured microglia.

PCA plots showing the grouping of the samples



Newberg LA, Chen X, Kodira CD, Zavodszky MI. Computational de novo discovery of distinguishing genes for biological processes and cell types in complex tissues. *PLoS One*. 2018. PMID: 29494600