

Data Set 1. Marker genes defining each neutrophil subcluster.

Each subcluster is annotated with a color corresponding to the UMAP visualization in Figure 2C.

The table includes the following columns:

- **subcluster** – label of the subcluster (0–5).
- **gene** – gene symbol or gene identifier.
- **avg_log2FC** – average log₂ fold change in expression between the subcluster and all other subclusters.
- **pct.1** – percentage of cells in the subcluster expressing the gene.
- **pct.2** – percentage of cells in all other neutrophil subclusters expressing the gene.
- **p_val** – raw p-value for differential expression.
- **p_val_adj** – p-value adjusted for multiple testing.

Data Set 2. Differential gene expression analysis between *HRAS*⁺ and *HRAS*⁻ neutrophils.

The table lists all genes identified as differentially expressed between *HRAS*⁺ and *HRAS*⁻ neutrophils. Columns:

- **gene** – gene symbol or gene identifier.
- **avg_log2FC** – average log₂ fold change in expression between *HRAS*⁺ and *HRAS*⁻ neutrophils (positive values indicate higher expression in *HRAS*⁺ neutrophils, negative values indicate higher expression in *HRAS*⁻ neutrophils).
- **pct.1** – percentage of *HRAS*⁺ neutrophils expressing the gene.
- **pct.2** – percentage of *HRAS*⁻ neutrophils expressing the gene.
- **p_val** – raw p-value for differential expression.
- **p_val_adj** – p-value adjusted for multiple testing.