

Description of Additional Supplementary Files

Supplementary Data 1. Quality control metrics for bulk RNA-seq data analysis.

Salmon⁵ and FastQC quality control metrics after processing and mapping of raw sequencing reads. Provided are two sheets for resting and inflammatory analysis, and two sheets for the lineage analysis, separated by species, respectively.

Supplementary Data 2. List of studies included in the analysis.

One sheet per species. Metadata was retrieved using GEOQuery⁶ and curated manually to obtain consistency.

Supplementary Data 3. Results from Fisher's combined test.

Mean log₂ fold change and results from Fisher's combined test generated in the analysis of inflammation, as outlined in Methods.