

Cutaneous leishmaniasis (CL)

is the most common form and causes skin lesions, mainly ulcers, on exposed parts of the body. These can leave life-long scars and cause serious disability or stigma.



Step 1: Read Mapping & Quality Control

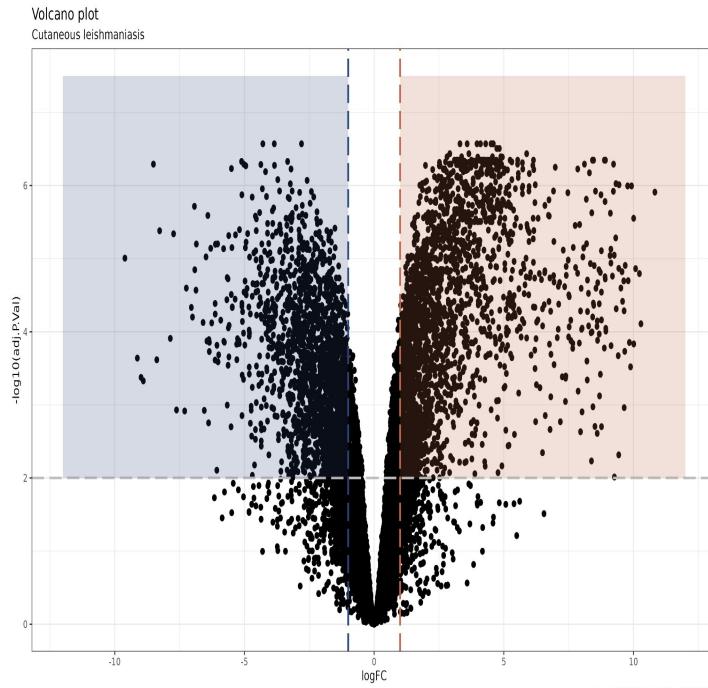
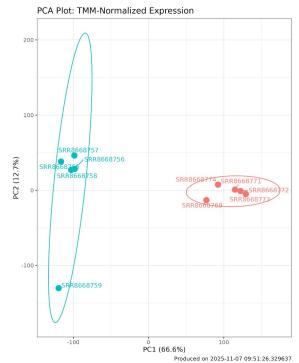
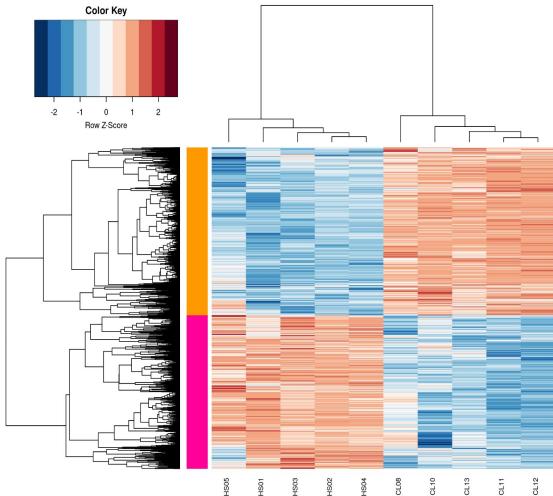
Create Conda env and run these tool in on the fastq files

- **FastQC** -> Quality assessment using
- **fastp**-> Adapter trimming and quality filtering with
- **Kallisto**-> Transcript quantification using



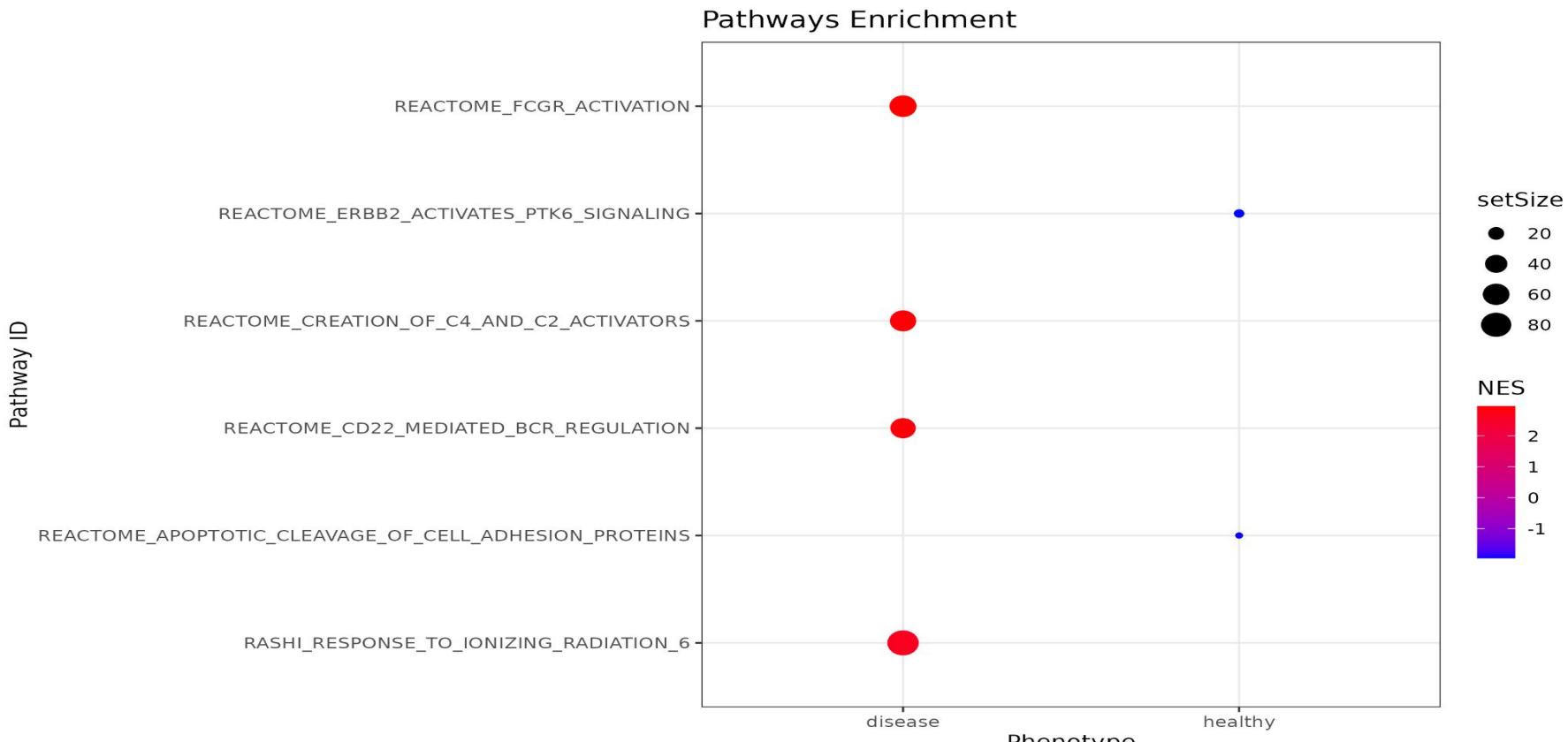
Step 2: Differential Expression Analysis

- **Data Preprocessing:**
CPM calculation, filtration, and TMM normalization
 - **Differential Expression:**
Identified ~16,000 DEGs using limma
 - Clear separation between diseased and healthy samples

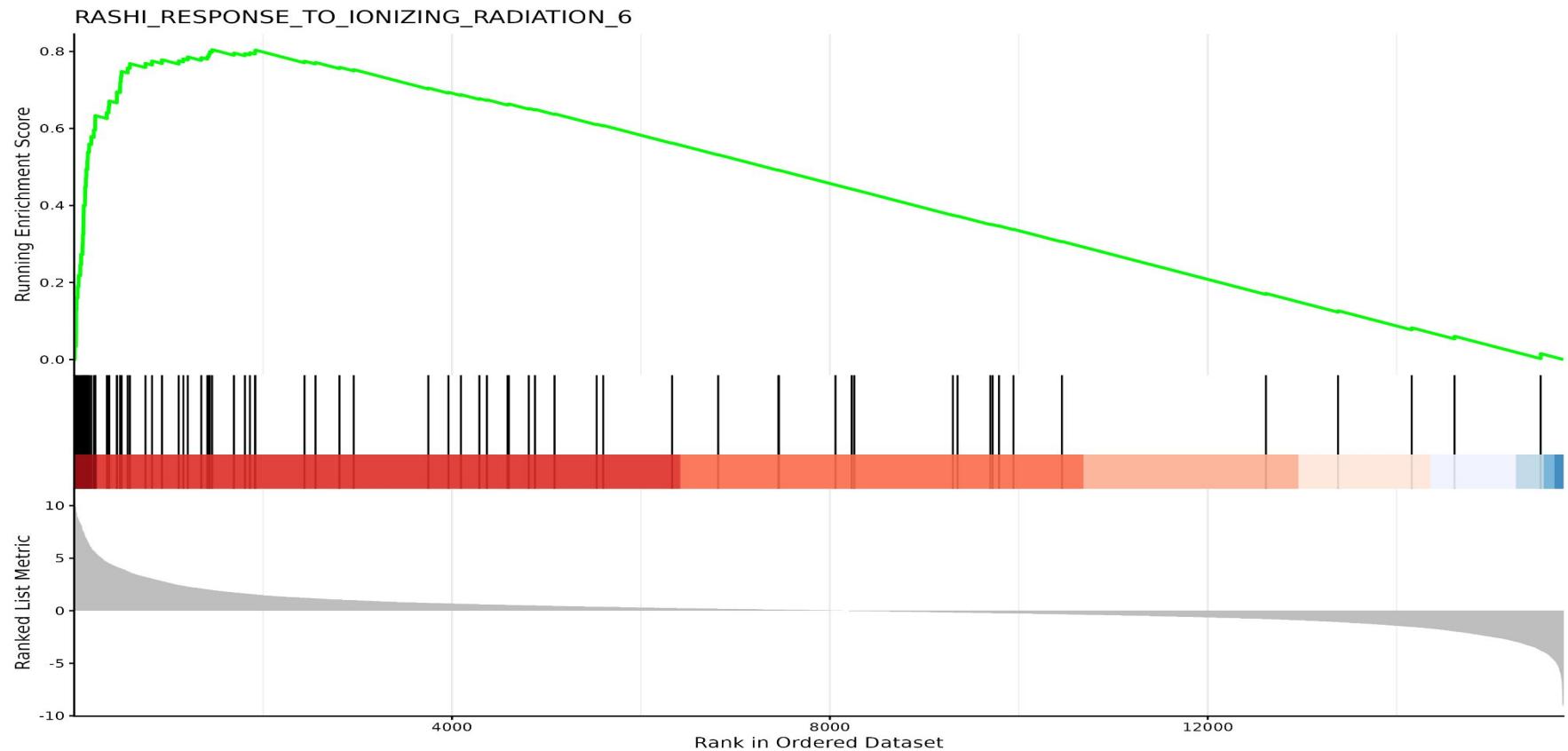


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Step 3: Gene Set Enrichment Analysis (GSEA)



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Pathway Dysregulation in Cutaneous Leishmaniasis:

● Upregulated in Disease:

- **REACTOME_FCGR_ACTIVATION**: Fc gamma receptor activation
- **REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS**: Complement system activation
- **REACTOME_CD22_MEDIATED_BCR_REGULATION**: B cell receptor signaling

→ Chronic immune hyperactivation with elevated antibody response (IGH, IGK, IGL genes)

● Downregulated in Disease:

- **REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION_PROTEINS**: Reduced apoptosis
- **REACTOME_ERBB2_ACTIVATES_PTK6_SIGNALING**: Altered growth regulation

→ Impaired cell death mechanisms allowing abnormal cell survival

Step 3: Gene Set Enrichment Analysis (GSEA)

Biological Insight: Diseased samples show excessive inflammation with chronic B cell activation, while apoptotic pathways are suppressed.

suggesting prolonged survival of infected/abnormal cells and sustained tissue damage.