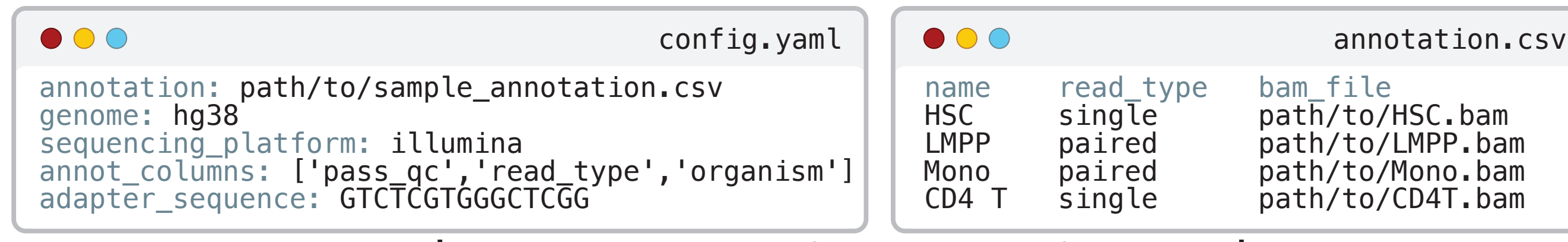




# MrBiomics: Composable modules and recipes for automated multi-omics data analysis

# MrBiomics

Best practices as modular, executable, reproducible & scalable workflows



## Modules

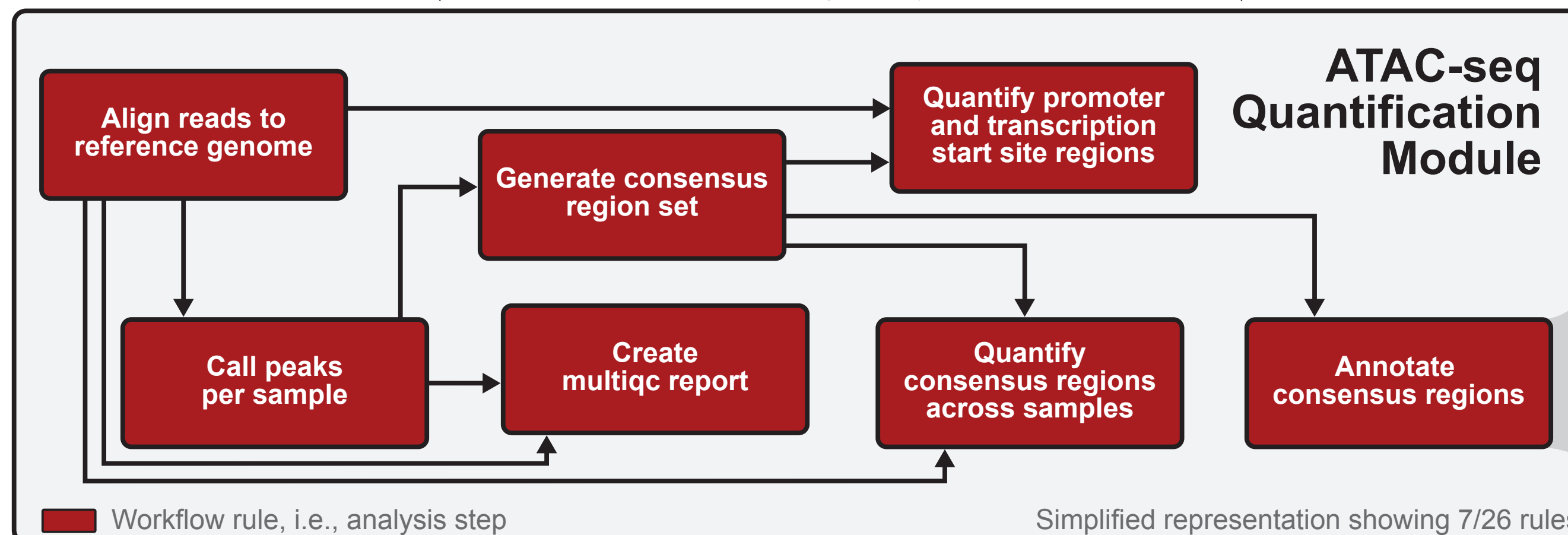
11 composable Snakemake workflows.

## Recipes

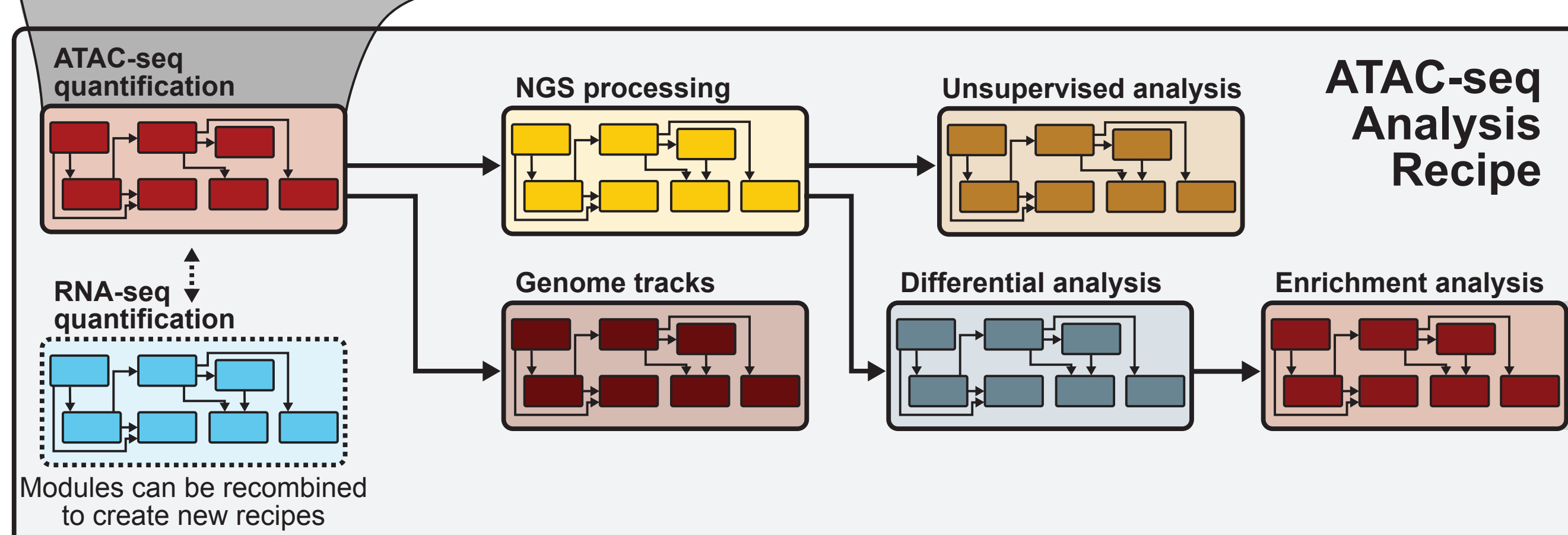
5 data-type specific recipes for common omics assays from raw data to figure-ready results.

## Projects

Case study: A multi-omics analysis of human hematopoiesis. Cell-type-specific signatures, reconstructed lineage tree, key differences of transcriptomic vs epigenomic state. Validate key regulator with high-content CRISPR screen data.

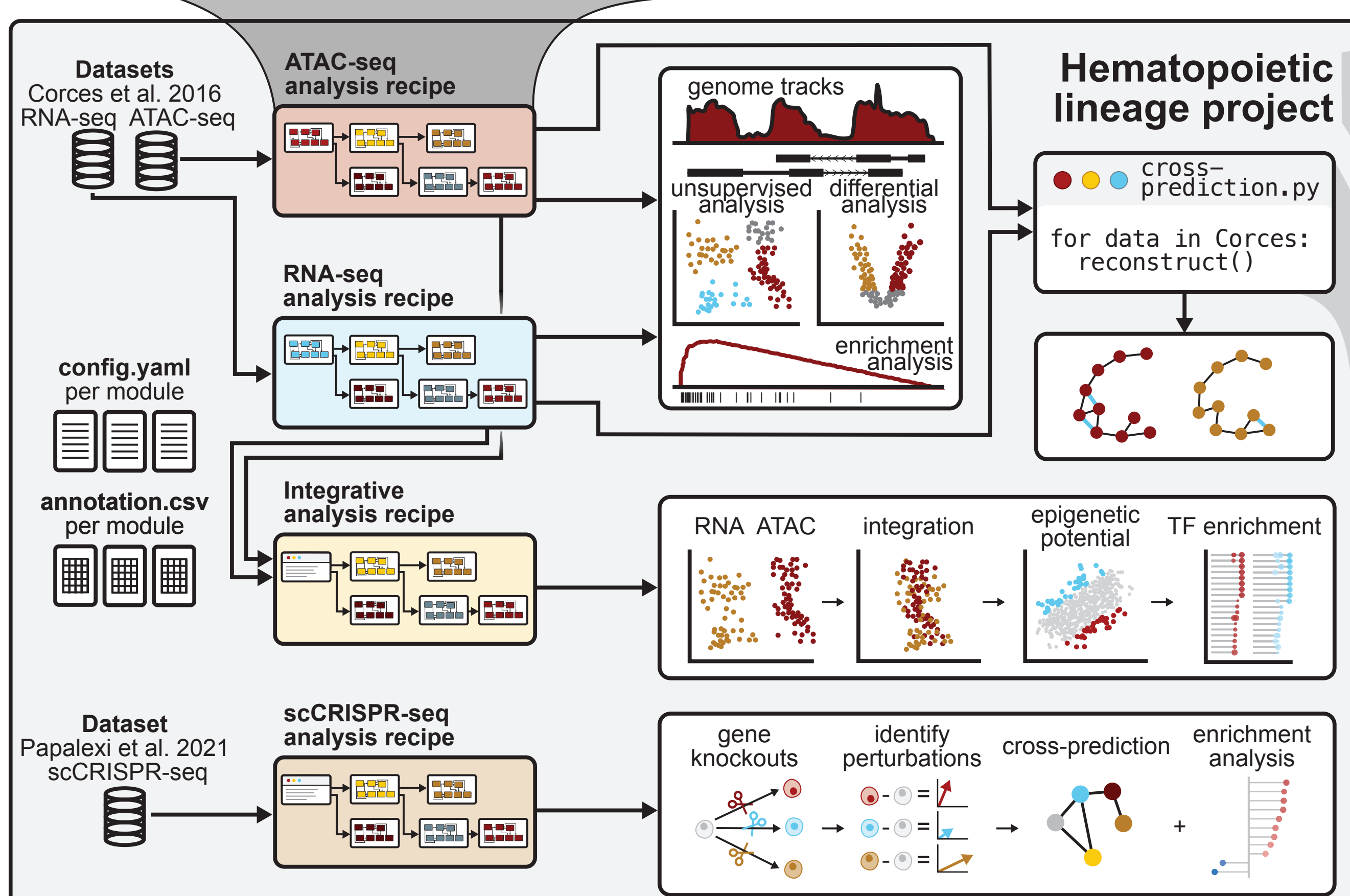


```
ATACseq_module.smk
rule annotate_consensus_regions:
  input:
    regions = path/to/regions.csv
    annot_db = path/to/database
  output:
    annotated = path/to/results
  params:
    genome = hg38
  conda:
    path/to/env.yaml
  resources:
    mem_mb = 32000
  script:
    path/to/script.py
```



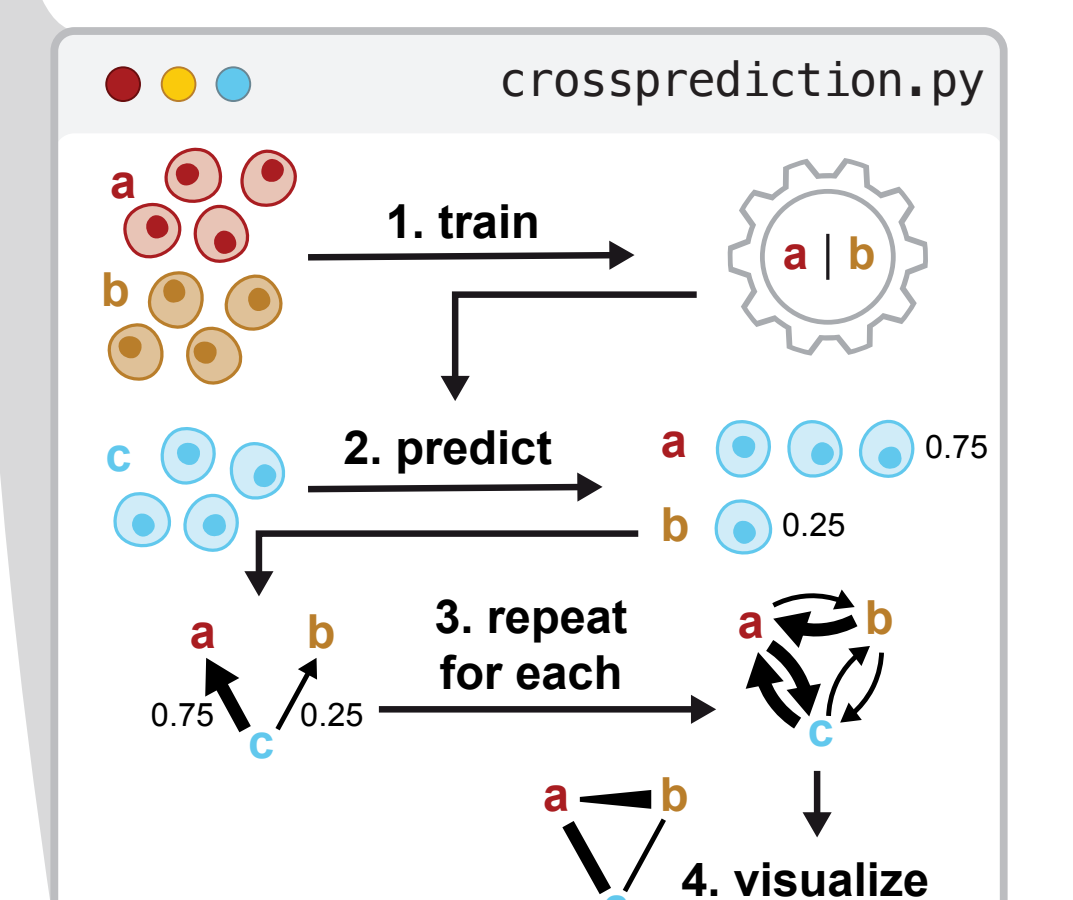
```
ATACseq_recipe.smk
# load module
module ATAC_enrichment_analysis:
  snakefile:
    github(enrichment, v3.0.2)
  config:
    config_dict

# add module rules to recipe
use rule * from \
  ATAC_enrichment_analysis \
  as ATAC_enrichment_analysis_*
```

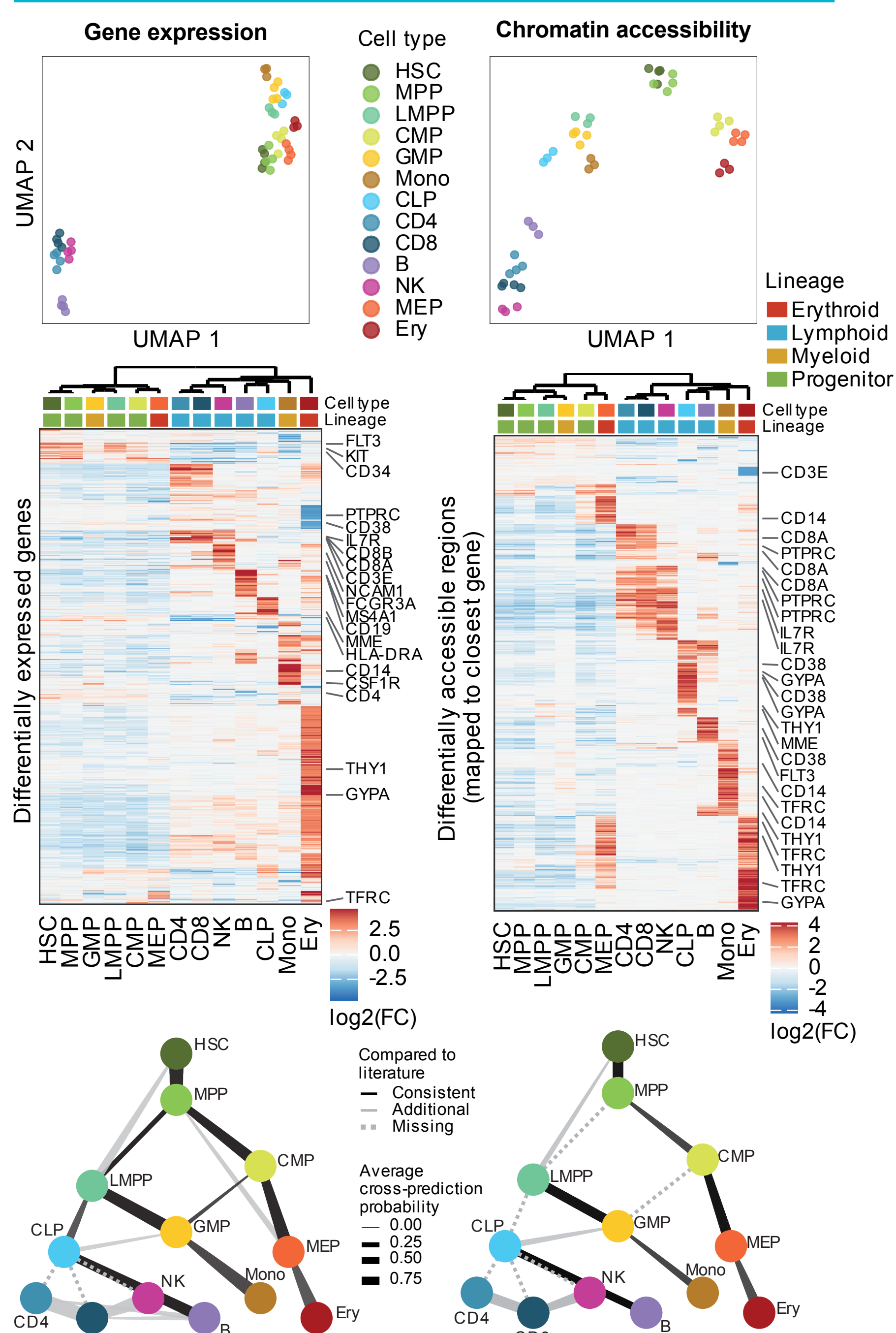


```
hematopoiesis_project.smk
# load recipes into project
include: ATACseq_recipe.smk
include: RNAseq_recipe.smk
include: Integrative_recipe.smk
include: scCRISPRseq_recipe.smk

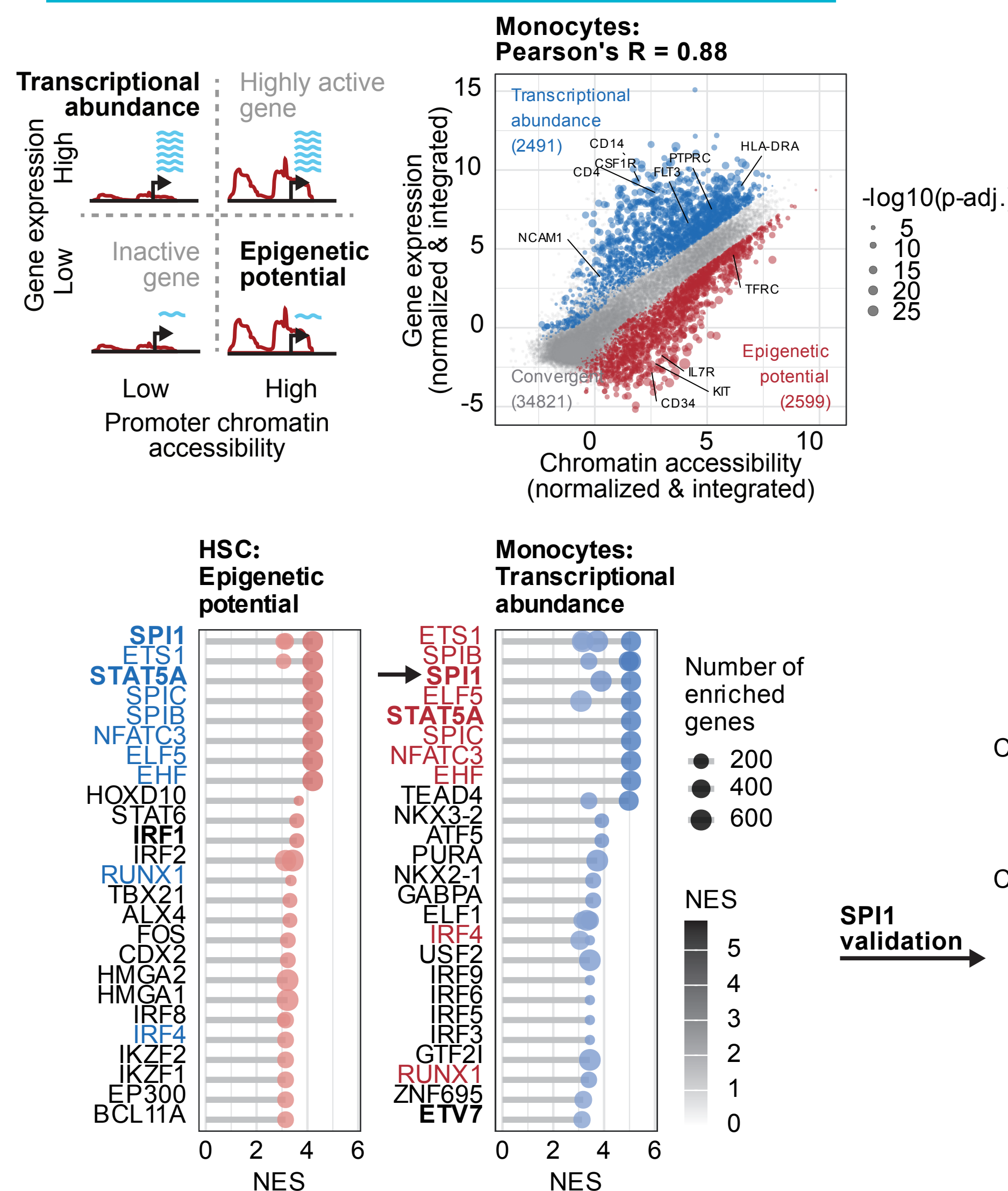
# add custom scripts
rule reconstruct_lineage:
  input:
    RNAseq_recipe_results/
    ATACseq_recipe_results/
  output:
    lineage_reconstruction.png
  script:
    path/to/crossprediction.py
```



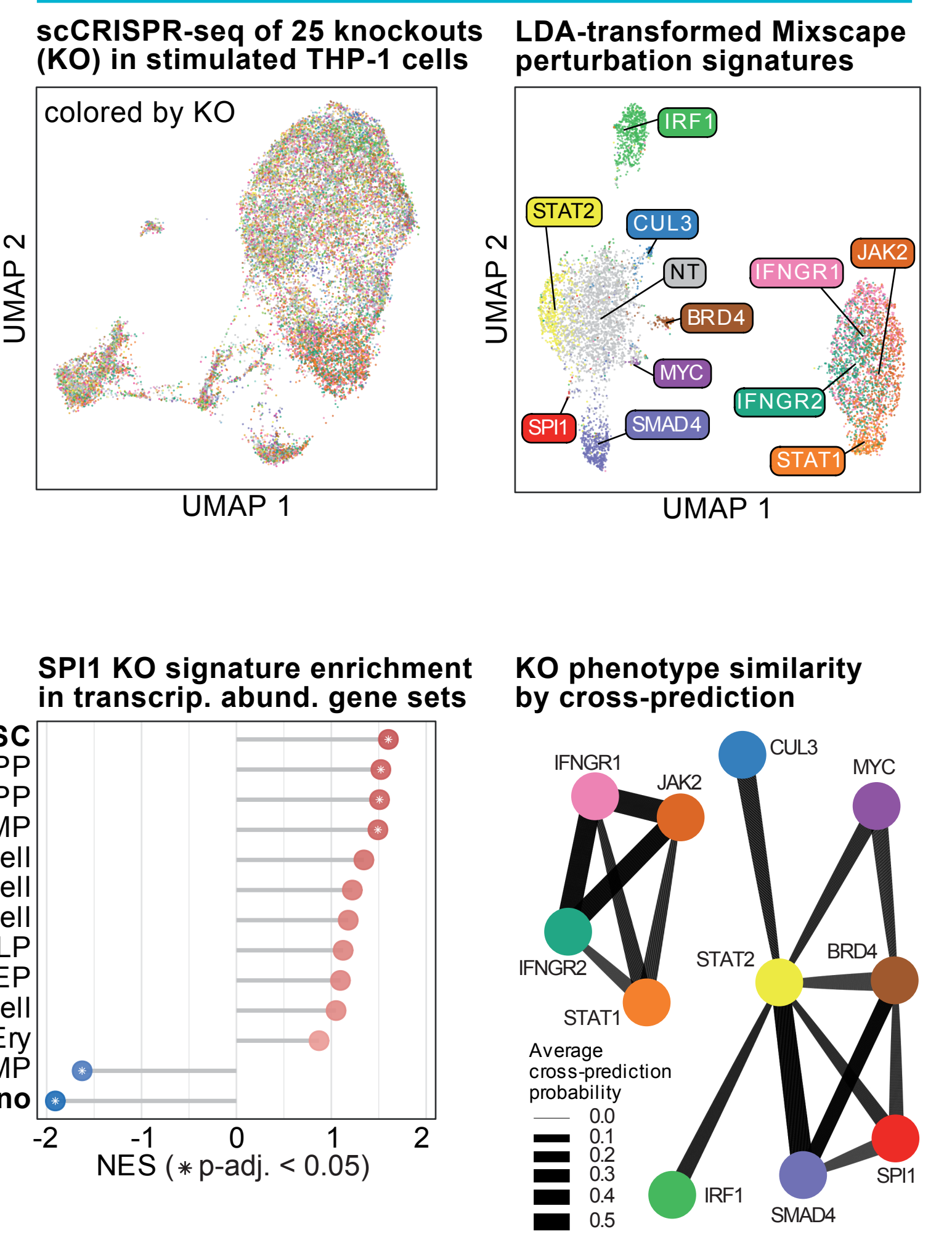
## Gene expression and chromatin accessibility profiles of human hematopoiesis



## Integrative analysis reveals epigenetic potential and transcriptional abundance



## Perturbation analysis validates regulator of transcriptional abundance



MrBiomics is a human- and agent-configurable analysis engine for accelerated molecular discovery