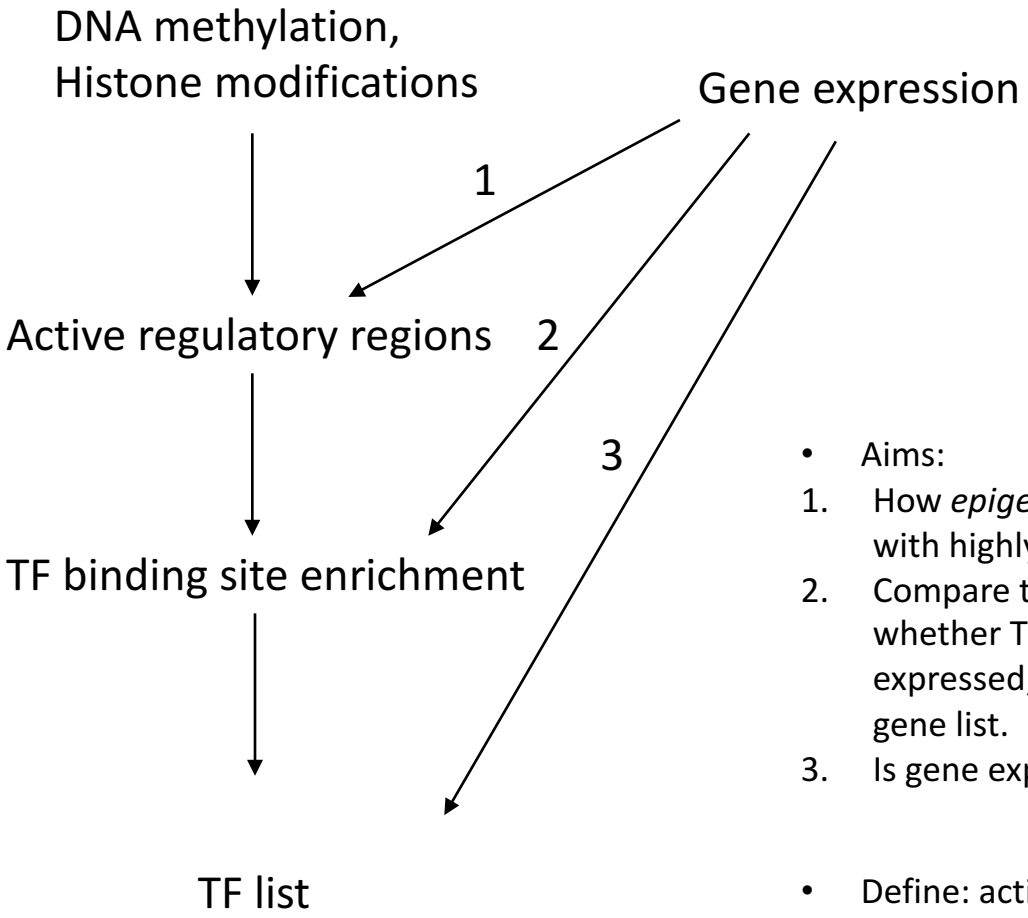
Hypothesis: hematopoietic differentiation and lineage-specific gene expression are driven by developmental stage-dependent transcriptional factors.

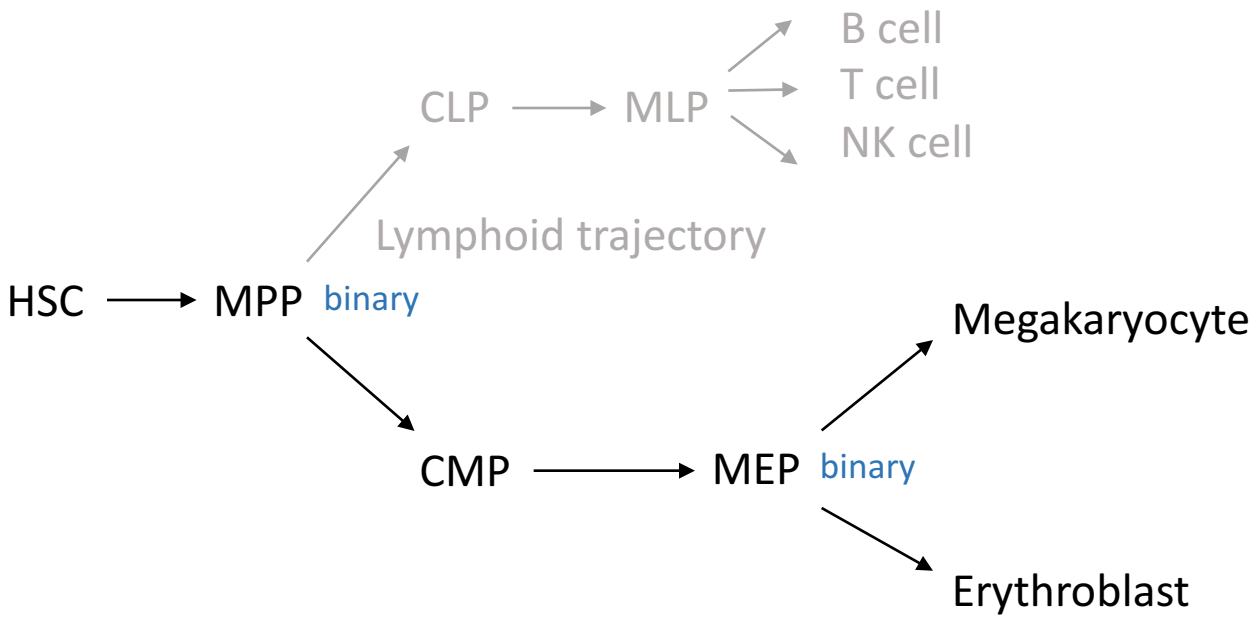


- Aims:

1. How *epigenetic* active region-associated genes are correlated with highly *expressed* genes.
2. Compare this TF list with TF among highly expressed gene list: whether TFs recognized by TFBS enrichment are also highly expressed; combine the TFs with TFs in the highly expressed gene list.
3. Is gene expression signature driven by TFs identified in aim-2?

- Define: active regions, highly expressed gene/signature genes

Selected samples:
Hematopoietic cell populations in the ME trajectory:



Progenitors:

HSC (hematopoietic stem cell)

MPP (multipotent progenitor)

CLP (common lymphoid progenitor)

MLP (multilymphoid progenitor)

CMP (common myeloid progenitor)

MEP (megakaryocyte-erythroid progenitor)

Erythroblast

Mature cells:

B cell

T cell

NK cell

Megakaryocyte

The Mega-erythroid trajectory of HSC differentiation is chosen because the RNA/DNA data are available for all of cell types shown in black, including linear cell development and binary cell fate determination.

For the lymphoid trajectory, most of the intermediate precursors is unavailable to configure the complete picture for lineage commitment, so this is only used as a backup for the project in case of incomplete datasets in the ME trajectory.