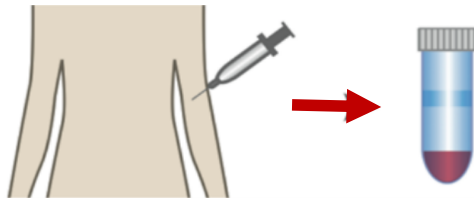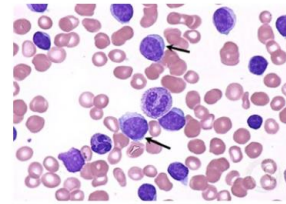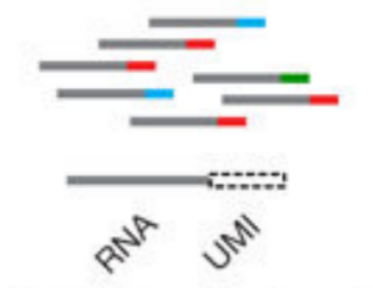# Blood samples

CD19+ selection

RNA sequencing

Data preprocessing, Quality control

Hierachical clustering

Processed mRNA

Exon A   Exon B   Exon C

Mapping to genome

RNA   UMI

PCA

PC1 (7.8%)
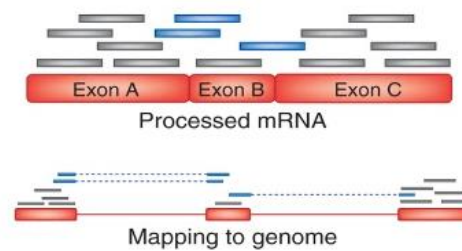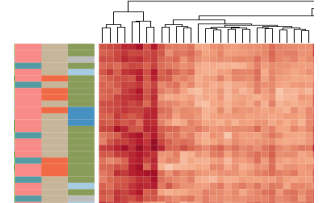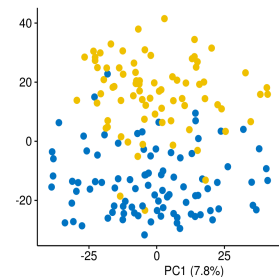
Gene expression signatures, mixed epistasis

Trisomy12

ITGB7

ITGB2