

## Single cell chromatin accessibility data

#### Metadata: Sample ID

## Metadata: Cell type

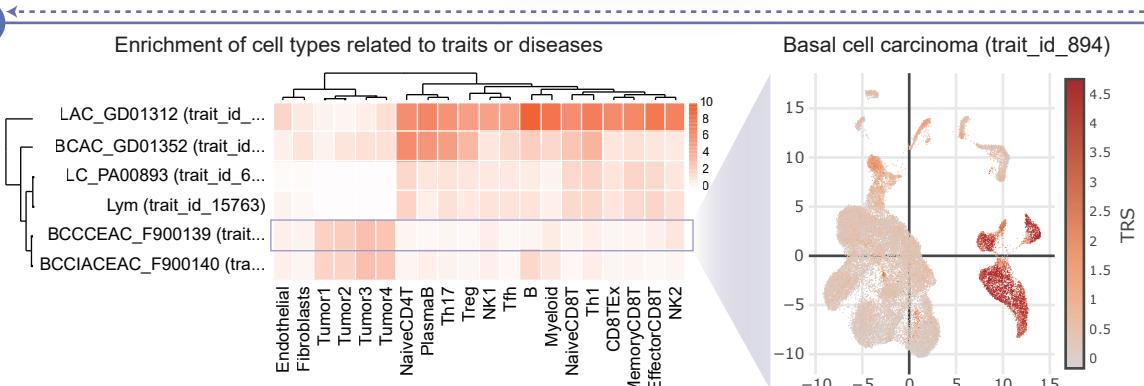
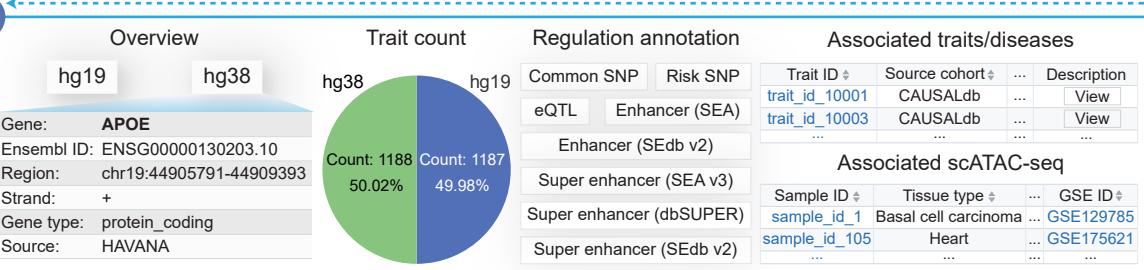
### Trait or disease data

Tissue type	Sample ID	Tissue type	Health type Description	Cell count	GSE ID	PMID
Heart	sample_id_1	Basal cell carcinoma	Tumor Microenvironment (TME)	36721	GSE129785	31375813
...	sample_id_2	PBMC	Healthy blood development	28774	GSE139369	31792411,37597510
Health type	sample_id_3	PBMC	Healthy blood development	32457	GSE139369	31792411,37597510
Disease	107					

Tissue type	Trait ID	Source cohort	Type	Trait abbreviation	Trait Description	VC	PP sum
Category	trait_id_1	BBJ	disease	AD	Atopic dermatitis	1409	19.666316
Subcategory	trait_id_2	BBJ	disease	AFib	Atrial fibrillation	1568	38.500634
Source cohort	trait_id_3	BBJ	indicator	AG	Albumin/Globulin ratio	4573	81.803071
	...	...	...	...	...	...	...

- Q Search information by category or source cohort
- Q Search information by tissue type or cell type
- Q Search information by gene
- Q Search information by TF
- Q Search information by SNP

- [Analyze variant-to-function mapping](#) >
- [Analyze variant-to-function mapping with genes](#) >
- [Analyze variant-to-function mapping with TFs](#) >



≡ Statistics of fine-mapping results

### Statistics of scATAC-seq data

### ≡ Statistics of trait/disease-relevant cell score (TRS) data

### ≡ Statistics of annotation data

- Download trait/disease-relevant cell score (TRS) data
- Download fine-mapping result data
- Download other data