**Hi-C data**

*ask Yuanlong*

**TAD data**

- description: size, number => full data

- description: size, number => retained data

**RNAseq data**

- number of genes

**Significance vs.**

- mean variance

- number of genes

- comparison types (norm vs. mut, etc.)

**AUC FCC and AUC coexprdist**

- ranking

- vs. variance

- by comparison types