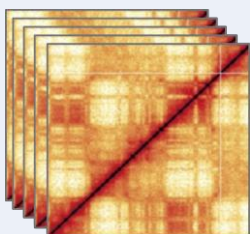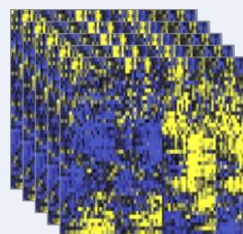**Chromatin Structure**

**HiC**

Chromosome Territories, Compartments, TADs, Enhancer and Promoter Annotation, and more, …
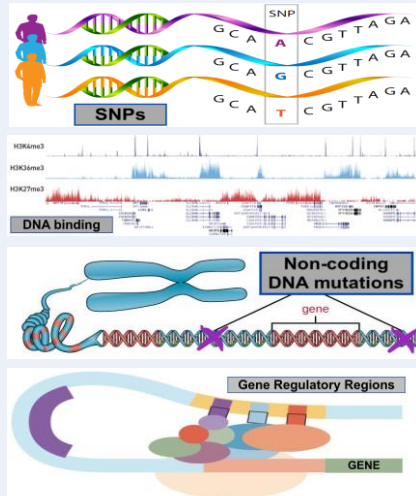
**Gene Expression**

**GE**

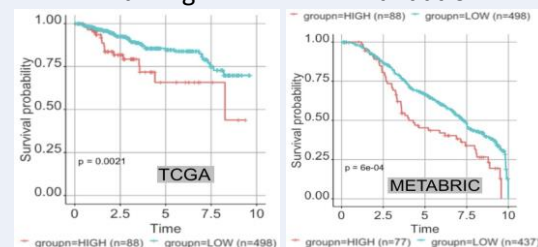Expression Levels, Gene-pair Correlations, Epigenomic Context, and more …

**Genomic Context**

SNPs

H3K4me3
H3K36me3
H3K27me3

DNA binding

Non-coding DNA mutations

gene

Gene Regulatory Regions

GENE

SNPs, Non-Coding Mutations, TFBS, DNA-binding, and more …

**Phenotype Analysis**

Training | Validation

groupn=HIGH (n=88) | groupn=LOW (n=498)

Survival probability

TCGA

groupn=HIGH (n=88) | groupn=LOW (n=498)

METABRIC

groupn=HIGH (n=77) | groupn=LOW (n=437)
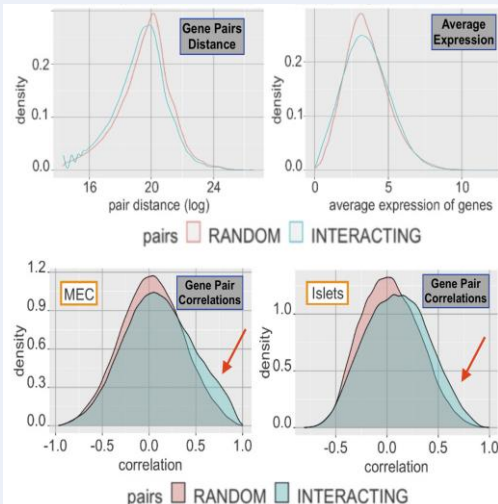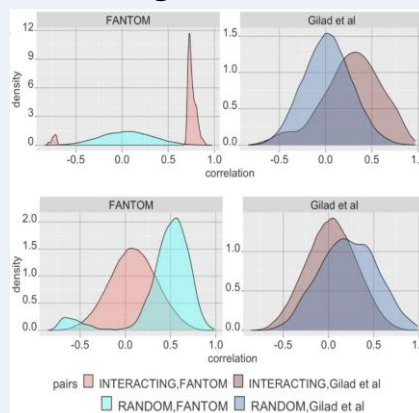
Patients with tumor displaying larger dysregulation showed shorter survival in training and testing cohorts

**HiC/GEP Integration**

Gene Pairs Distance

Average Expression

density

pair distance (log)

average expression of genes

pairs ☐ RANDOM ☐ INTERACTING

MEC | Gene Pair Correlations

Islets | Gene Pair Correlations
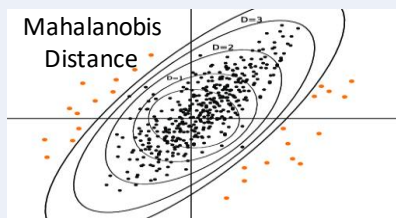
density

correlation

pairs ☐ RANDOM ☐ INTERACTING

Expression for gene pairs involved in true chromatin interactions are more correlated than chance

**Regulatory Modules Ranking and Selection**

FANTOM | Gilad et al

density

correlation

FANTOM | Gilad et al

density

correlation

pairs ☐ INTERACTING,FANTOM ☐ INTERACTING,Gilad et al
☐ RANDOM,FANTOM ☐ RANDOM,Gilad et al

• Absolute Correlation > 0.5
• 10 genes or more
• At least 1 lncRNA, etc …

**Patient Outliers Detection**

Mahalanobis Distance

**Dysregulated Modules**

Candidate Gene Regulatory Module

Chr17

legend: coding_mRNA, lncRNA_divergent, lncRNA_intergenic, lncRNA_sense_intronic