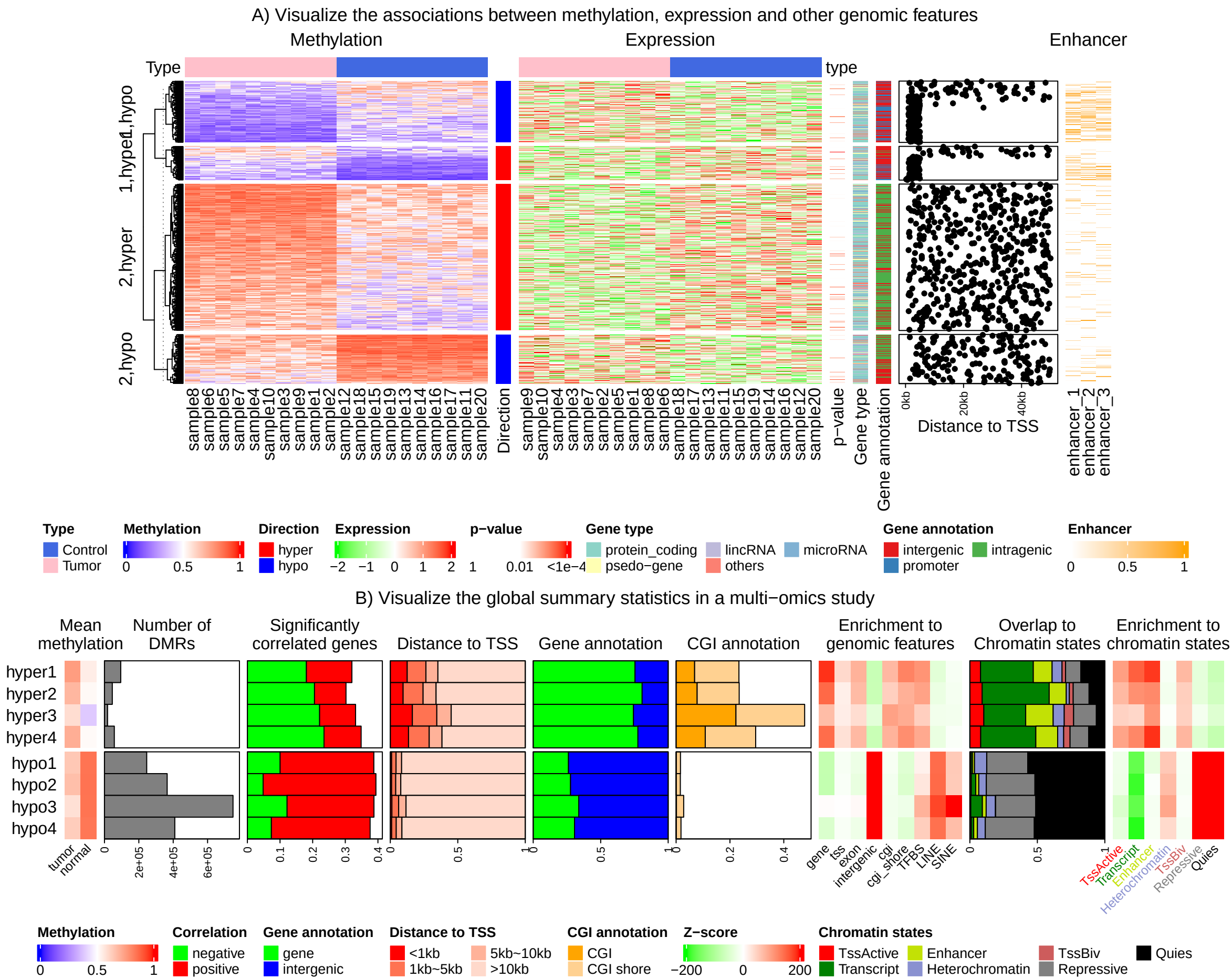
A) Visualize the associations between methylation, expression and other genomic features
Methylation
Expression
Enhancer
Type
type
1,hypo
1,hyper
2,hyper
2,hypo
sample8 sample6 sample5 sample7 sample4 sample10 sample3 sample9 sample1 sample2 sample12 sample18 sample15 sample19 sample13 sample14 sample16 sample17 sample11 sample20
Direction
sample9 sample10 sample4 sample3 sample7 sample2 sample5 sample1 sample8 sample6 sample18 sample17 sample13 sample11 sample15 sample19 sample14 sample16 sample12 sample20
p−value
Gene type
Gene annotation
0kb
20kb
40kb
Distance to TSS
enhancer_1
enhancer_2
enhancer_3
Type
Control
Tumor
Methylation
0 0.5 1
Direction
hyper
hypo
Expression
−2 −1 0 1 2
p−value
1 0.01 <1e−4
Gene type
protein_coding
psedo−gene
lincRNA
others
microRNA
Gene annotation
intergenic
promoter
intragenic
Enhancer
0 0.5 1
B) Visualize the global summary statistics in a multi−omics study
Mean methylation
Number of DMRs
Significantly correlated genes
Distance to TSS
Gene annotation
CGI annotation
Enrichment to genomic features
Overlap to Chromatin states
Enrichment to chromatin states
hyper1
hyper2
hyper3
hyper4
hypo1
hypo2
hypo3
hypo4
tumor
normal
0 2e+05 4e+05 6e+05
0 0.1 0.2 0.3 0.4
0 0.5 1
0 0.5 1
0 0.2 0.4
gene tss exon intergenic cgi cgi_shore TFBS LINE SINE
0 0.5 1
TssActive Transcript Enhancer Heterochromatin TssBiv Repressive Quies
Methylation
0 0.5 1
Correlation
negative
positive
Gene annotation
gene
intergenic
Distance to TSS
<1kb
1kb~5kb
5kb~10kb
>10kb
CGI annotation
CGI
CGI shore
Z−score
−200 0 200
Chromatin states
TssActive
Transcript
Enhancer
Heterochromatin
TssBiv
Repressive
Quies