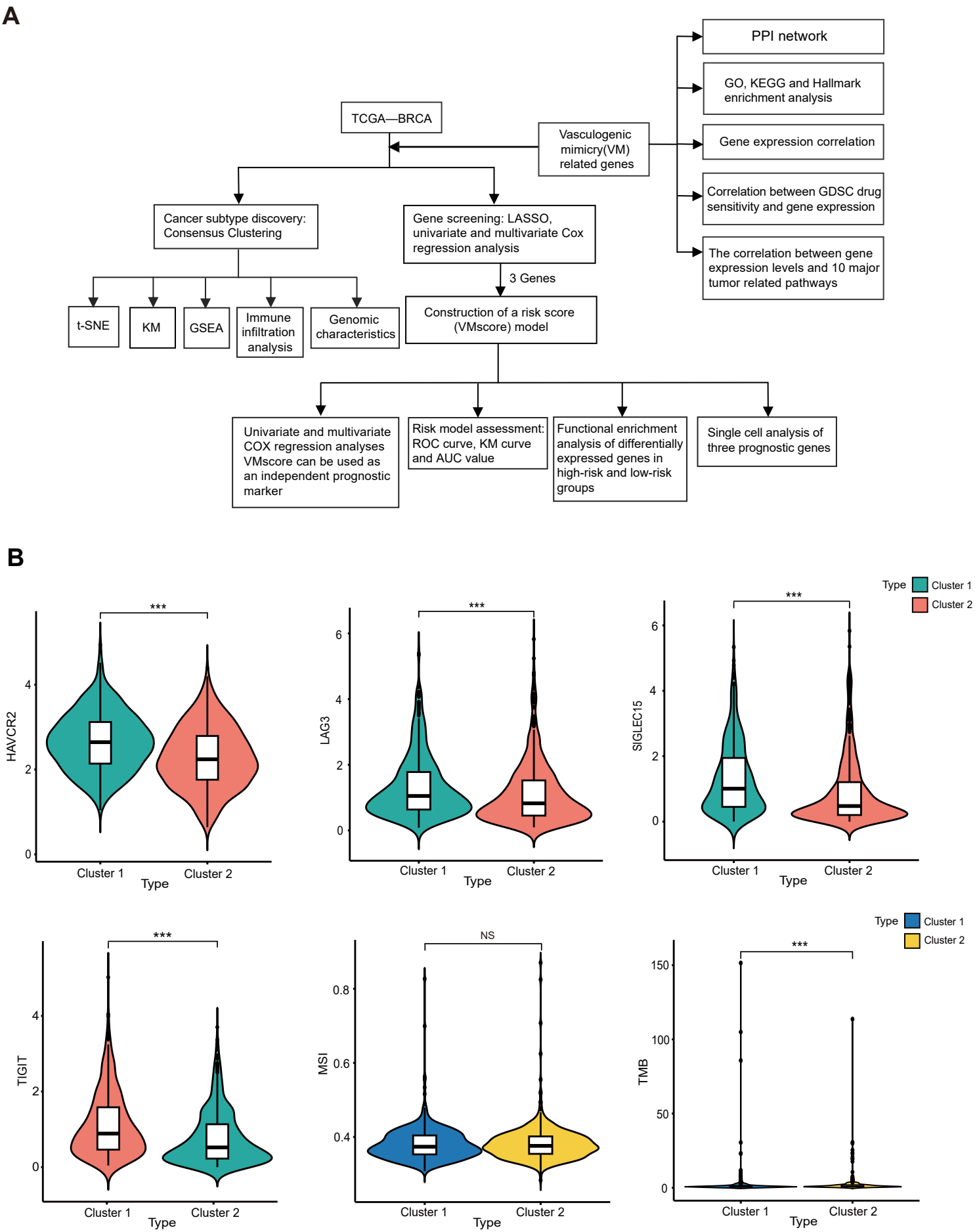
Figure S1


A
PPI network
GO, KEGG and Hallmark enrichment analysis
TCGA—BRCA
Vasculogenic mimicry(VM) related genes
Gene expression correlation
Correlation between GDSC drug sensitivity and gene expression
Cancer subtype discovery: Consensus Clustering
Gene screening: LASSO, univariate and multivariate Cox regression analysis
The correlation between gene expression levels and 10 major tumor related pathways
3 Genes
t-SNE
KM
GSEA
Immune infiltration analysis
Genomic characteristics
Construction of a risk score (VMscore) model
Univariate and multivariate COX regression analyses VMscore can be used as an independent prognostic marker
Risk model assessment: ROC curve, KM curve and AUC value
Functional enrichment analysis of differentially expressed genes in high-risk and low-risk groups
Single cell analysis of three prognostic genes
B
Type
Cluster 1
Cluster 2
HAVCR2
LAG3
SIGLEC15
TIGIT
MSI
TMB
***
NS
Cluster 1
Cluster 2
Type