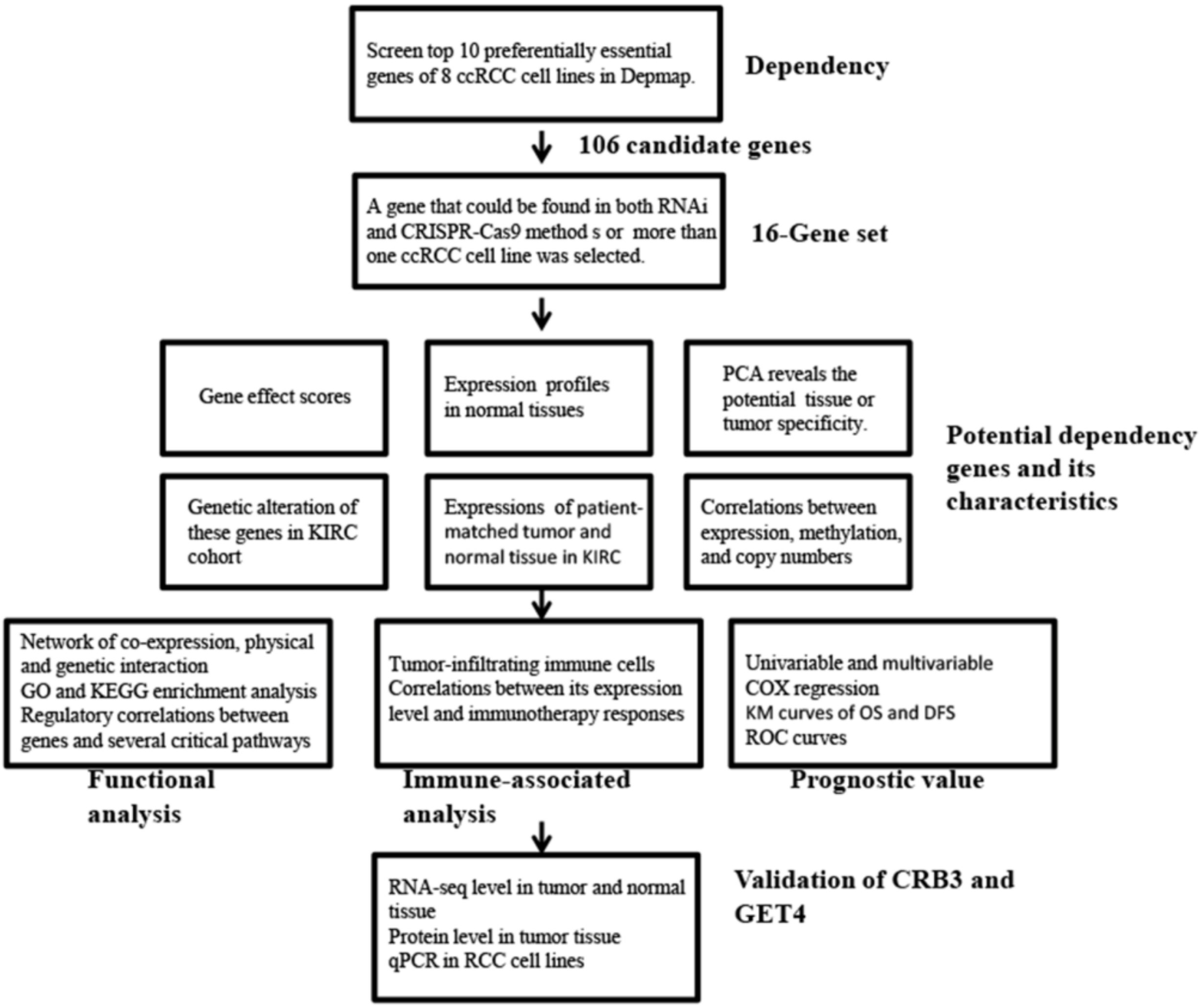
Supplementary Table 1. Correlation between expression, relative copy number and methylation of selected genes

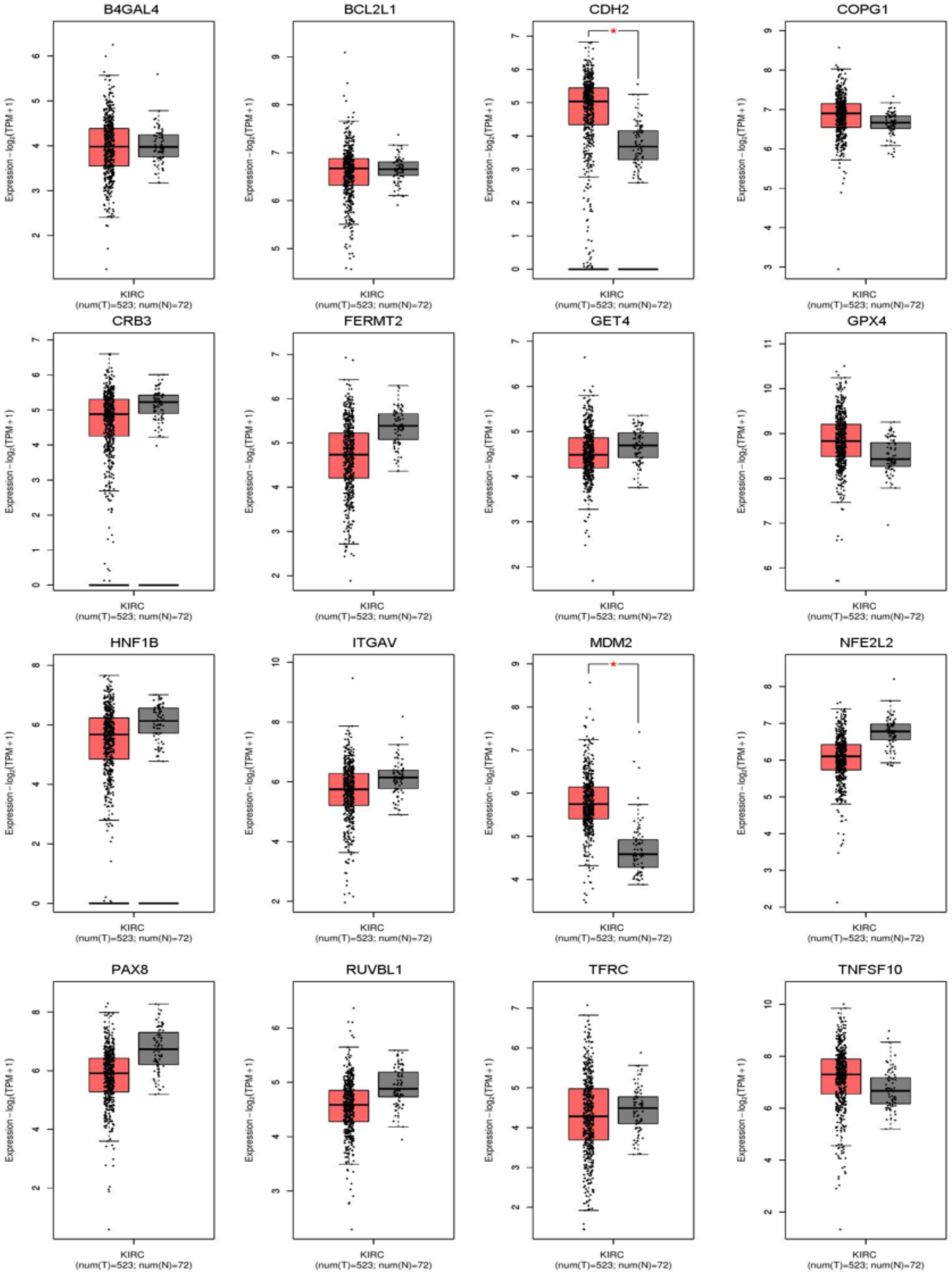
Gene	Correlation between expression and relative copy number (Spearman coefficient)	Correlation between expression and methylation (Spearman coefficient)
B4GALT4	0.42	-0.28
BCL2L1	0.17	-0.18
CDH2	0.25	-0.37
COPG1	0.51	NA
CRB3	0.13	-0.47
FERMT2	0.42	-0.38
GET4	0.34	NA
GPX4	0.24	-0.28
HNF1B	0.15	-0.16
ITGAV	0.14	-0.27
MDM2	0.14	-0.13
NFE2L2	0.19	-0.09
PAX8	0.14	-0.27
RUVBL1	0.39	-0.34
TFRC	0.21	-0.01
TNFSF10	0.10	-0.43

NA, not available

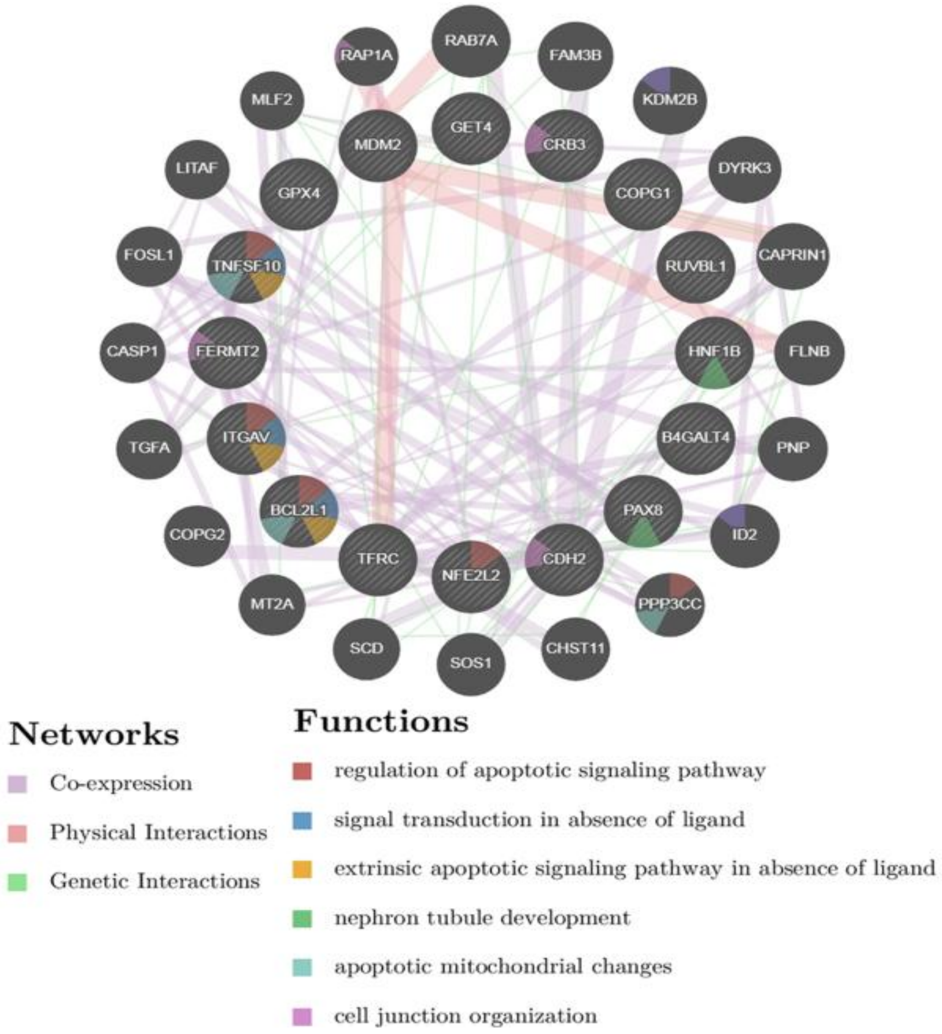
Supplementary Figure 1 Flow diagram of data acquisition and analysis



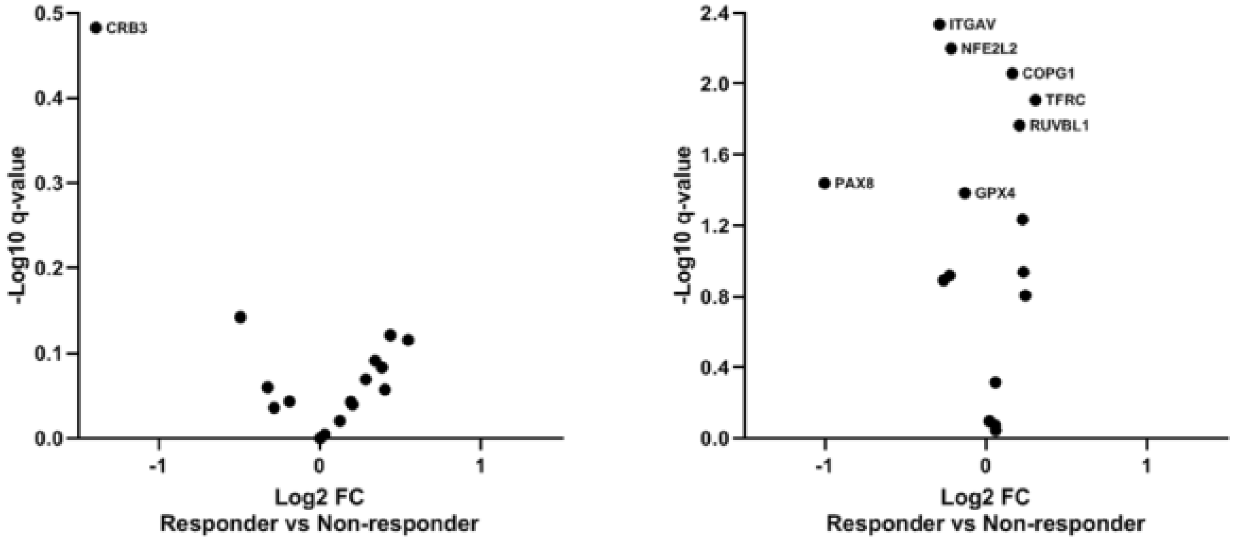
Supplementary Figure 2. Expression of genes in tumor and unpaired adjacent normal tissue in the KIRC cohort



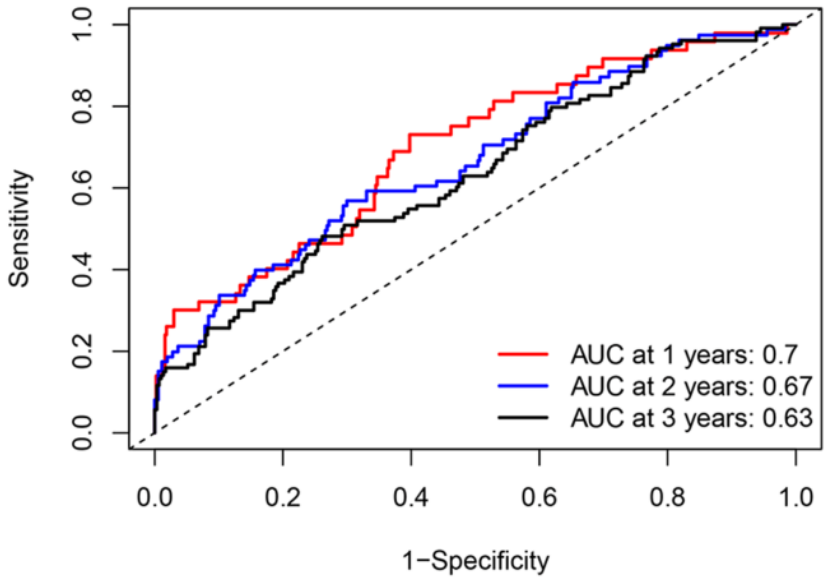
Supplementary Figure 3. Functional analysis



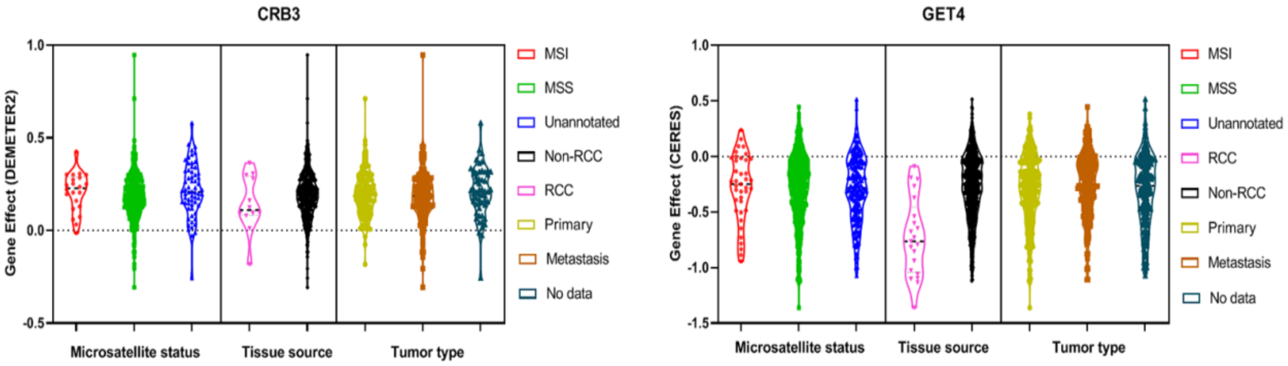
Supplementary Figure 4. Differential expression between responders and non-responders from two datasets



Supplementary Figure 5. ROC curves



Supplementary Figure 6. Gene effect scores of GET4 and CRB3 between different lineages, microsatellite status, and tumor types of cell lines



Supplementary Figure 7. Expression levels of CRB3 and GET4 in cell lines (qPCR)