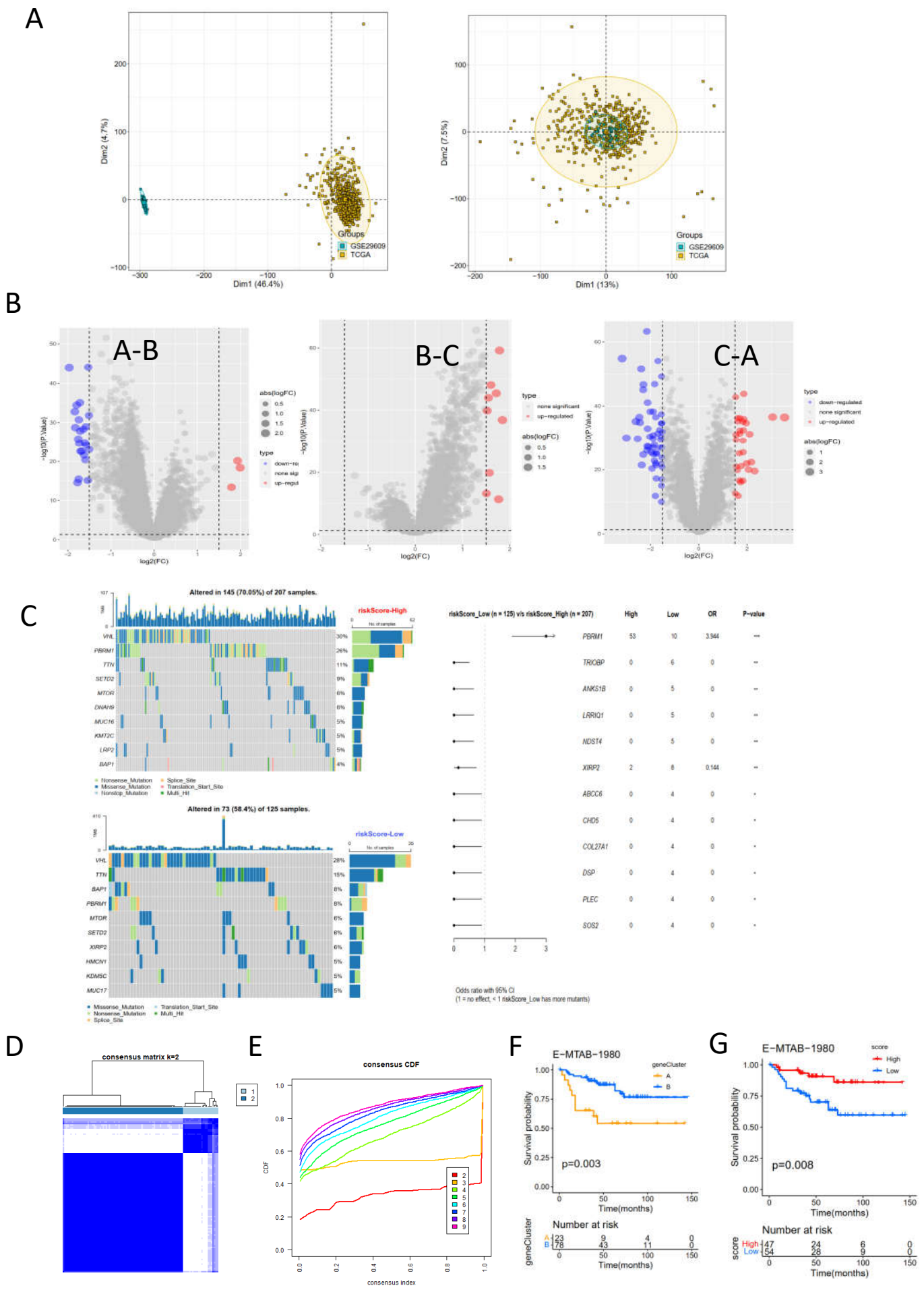
Figure S1


A
Dim1 (46.4%)
Dim2 (4.7%)
Groups
GSE29609
TCGA
Dim1 (13%)
Dim2 (7.5%)
B
A-B
B-C
C-A
log2(FC)
-log10(P.Value)
abs(logFC)
type
none significant
up-regulated
down-regulated
C
Altered in 145 (70.05%) of 207 samples.
riskScore-High
Altered in 73 (58.4%) of 125 samples.
riskScore-Low
VHL
PBRM1
TTN
SETD2
MTOR
DNAH9
MUC16
KMT2C
LRP2
BAP1
HMCN1
KDM5C
MUC17
Nonsense_Mutation
Missense_Mutation
Nonstop_Mutation
Splice_Site
Translation_Start_Site
Multi_Hit
riskScore_Low (n = 125) v/s riskScore_High (n = 207)
High
Low
OR
P-value
TRIOBP
ANKS1B
LRRIQ1
NDST4
XIRP2
ABCC6
CHD5
COL27A1
DSP
PLEC
SOS2
Odds ratio with 95% CI
(1 = no effect, < 1 riskScore_Low has more mutants)
D
consensus matrix k=2
E
consensus CDF
CDF
consensus index
F
E-MTAB-1980
geneCluster
Survival probability
p=0.003
Time(months)
Number at risk
G
E-MTAB-1980
score
High
Low
p=0.008
Time(months)
Number at risk