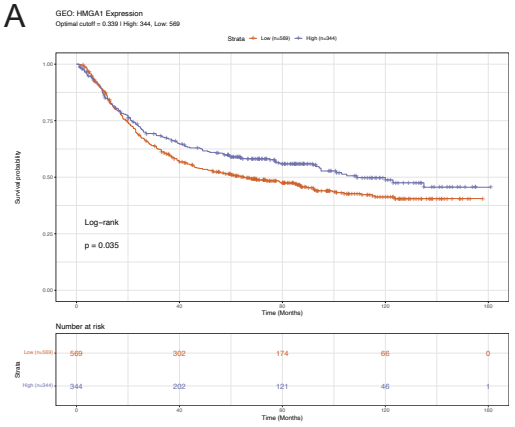
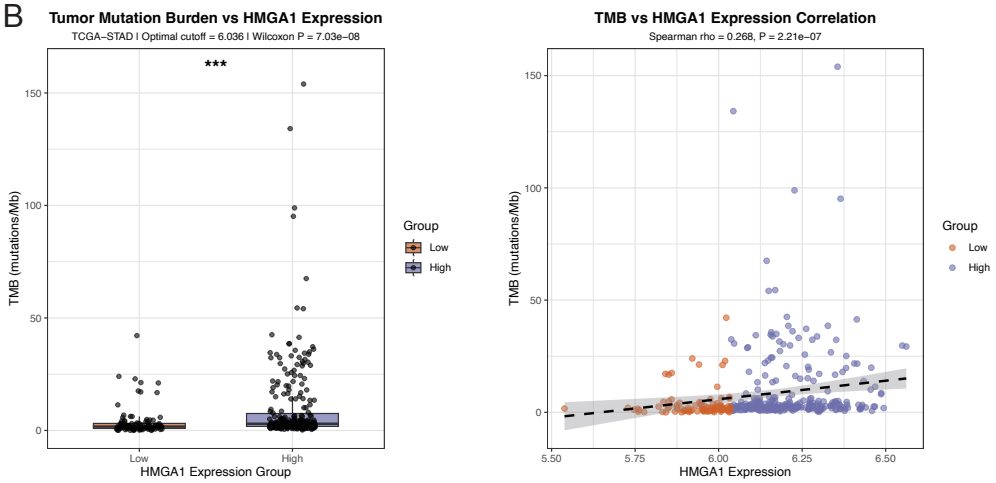
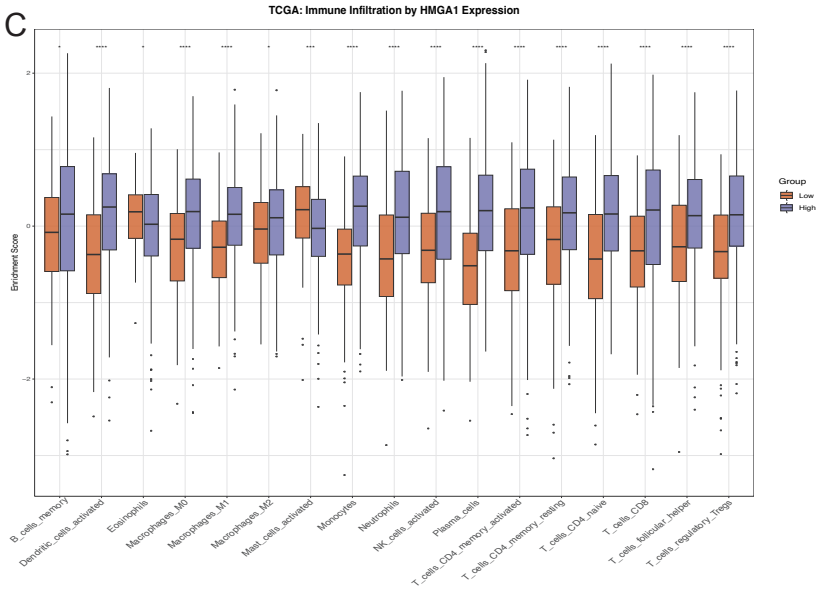
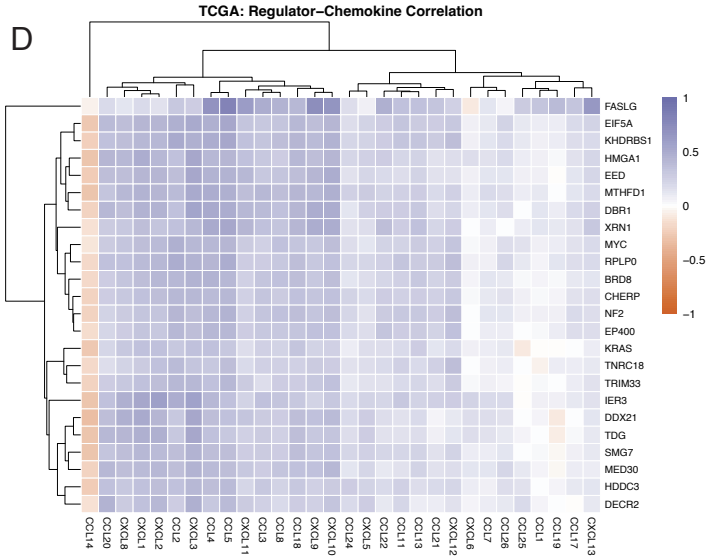
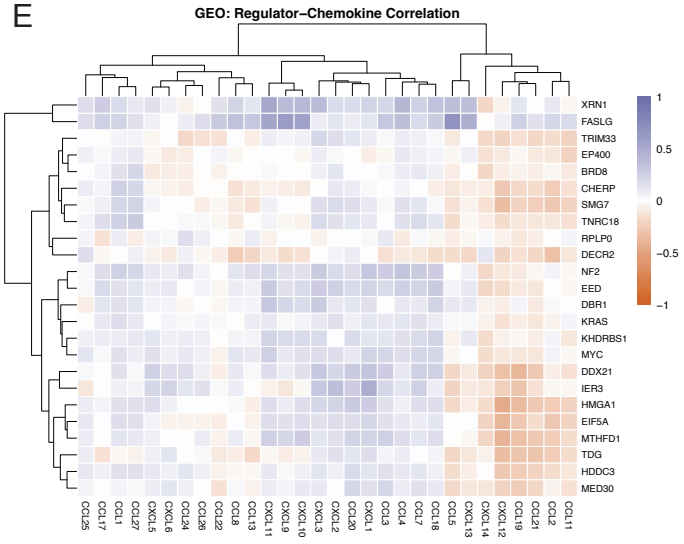
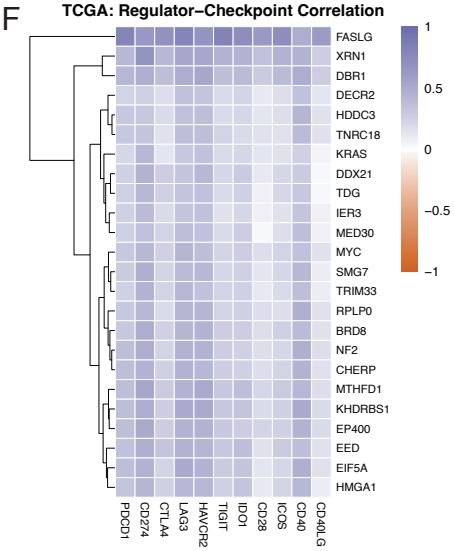

A
GEO: HMGA1 Expression
Optimal cutoff = 0.339 | High: 344, Low: 569
Strata Low (n=569) High (n=344)
Survival probability
Log−rank
p = 0.035
Time (Months)
Number at risk
Low (n=569) 569 302 174 66 0
High (n=344) 344 202 121 46 1
Time (Months)

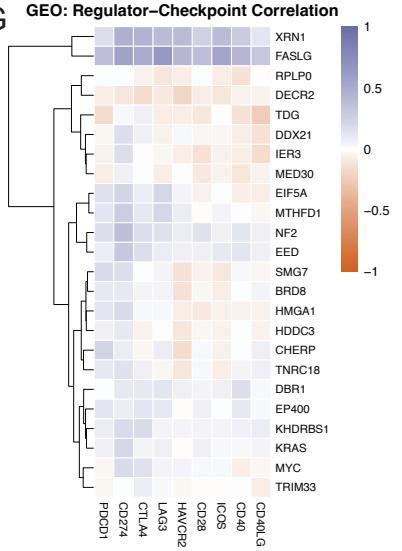

B
Tumor Mutation Burden vs HMGA1 Expression
TCGA−STAD | Optimal cutoff = 6.036 | Wilcoxon P = 7.03e−08
***
TMB (mutations/Mb)
Low
High
HMGA1 Expression Group
Group
Low
High
TMB vs HMGA1 Expression Correlation
Spearman rho = 0.268, P = 2.21e−07
TMB (mutations/Mb)
HMGA1 Expression
Group
Low
High


C
TCGA: Immune Infiltration by HMGA1 Expression
Enrichment Score
Group
Low
High
B_cells_memory
Dendritic_cells_activated
Eosinophils
Macrophages_M0
Macrophages_M1
Macrophages_M2
Mast_cells_activated
Monocytes
Neutrophils
NK_cells_activated
Plasma_cells
T_cells_CD4_memory_activated
T_cells_CD4_memory_resting
T_cells_CD4_naive
T_cells_CD8
T_cells_follicular_helper
T_cells_regulatory_Tregs


D
TCGA: Regulator−Chemokine Correlation
FASLG
EIF5A
KHDRBS1
HMGA1
EED
MTHFD1
DBR1
XRN1
MYC
RPLP0
BRD8
CHERP
NF2
EP400
KRAS
TNRC18
TRIM33
IER3
DDX21
TDG
SMG7
MED30
HDDC3
DECR2
CCL14 CCL20 CXCL8 CXCL1 CXCL2 CCL2 CXCL3 CCL4 CCL5 CXCL11 CCL3 CCL8 CCL18 CXCL9 CXCL10 CCL24 CXCL5 CCL22 CCL11 CCL13 CCL21 CXCL12 CXCL6 CCL7 CCL26 CCL25 CCL1 CCL19 CCL17 CXCL13


E
GEO: Regulator−Chemokine Correlation
XRN1
FASLG
TRIM33
EP400
BRD8
CHERP
SMG7
TNRC18
RPLP0
DECR2
NF2
EED
DBR1
KRAS
KHDRBS1
MYC
DDX21
IER3
HMGA1
EIF5A
MTHFD1
TDG
HDDC3
MED30
CCL25 CCL17 CCL1 CCL27 CXCL5 CXCL6 CCL24 CCL26 CCL22 CCL8 CCL13 CXCL11 CXCL9 CXCL10 CXCL3 CXCL2 CCL20 CXCL1 CCL3 CCL4 CCL7 CCL18 CCL5 CXCL13 CXCL14 CXCL12 CCL19 CCL21 CCL2 CCL11


F
TCGA: Regulator−Checkpoint Correlation
FASLG
XRN1
DBR1
DECR2
HDDC3
TNRC18
KRAS
DDX21
TDG
IER3
MED30
MYC
SMG7
TRIM33
RPLP0
BRD8
NF2
CHERP
MTHFD1
KHDRBS1
EP400
EED
EIF5A
HMGA1
PDCD1 CD274 CTLA4 LAG3 HAVCR2 TIGIT IDO1 CD28 ICOS CD40 CD40LG


G
GEO: Regulator−Checkpoint Correlation
XRN1
FASLG
RPLP0
DECR2
TDG
DDX21
IER3
MED30
EIF5A
MTHFD1
NF2
EED
SMG7
BRD8
HMGA1
HDDC3
CHERP
TNRC18
DBR1
EP400
KHDRBS1
KRAS
MYC
TRIM33
PDCD1 CD274 CTLA4 LAG3 HAVCR2 CD28 ICOS CD40 CD40LG