a
RPN1
PML
risk score
StromalScore
ImmuneScore
ESTIMATEScore
TumorPurity
r
0.1
0.0
−0.1
−0.2
b
T_cells_CD8
Monocyte
T cell CD8+
Class−switched memory B cell
Common myeloid progenitor
Endothelial cell
Hematopoietic stem cell
Macrophage M2
Myeloid dendritic cell activated
T cell CD4+ naive
T cell CD8+
T cell CD8+ effector memory
T cell NK
microenvironment score
Cancer associated fibroblast
NK cell
Cancer associated fibroblast
Macrophage M1
Neutrophil
Common lymphoid progenitor
T cell CD4+ Th2
RPN1
Negative correlation
Positive correlation
c
B cells naive
uncharacterized cell
Monocyte
T cell CD4+ (non−regulatory)
B cell plasma
Endothelial cell
Hematopoietic stem cell
Mast cell
Macrophages M0
Macrophages_M0
Cancer associated fibroblast
NK cell
Cancer associated fibroblast
Macrophage M1
Neutrophil
Myeloid dendritic cell
Neutrophil
T cell CD4+
Plasmacytoid dendritic cell
T cell CD4+ effector memory
PML
Negative correlation
Positive correlation
* p < 0.05
** p < 0.01
*** p < 0.001
Correlation
1.0
0.5
0.0
−0.5
−1.0
d
Software
CIBERSORT
CIBERSORT−ABS
EPIC
MCPCOUNTER
QUANTISEQ
TIMER
XCELL
−0.2
−0.1
0.0
0.1
Correlation Coefficient
e
XENOBIOTIC_METABOLISM
WNT_BETA_CATENIN_SIGNALING
UV_RESPONSE_UP
UV_RESPONSE_DN
UNFOLDED_PROTEIN_RESPONSE
TNFA_SIGNALING_VIA_NFKB
TGF_BETA_SIGNALING
SPERMATOGENESIS
REACTIVE_OXYGEN_SPECIES_PATHWAY
PROTEIN_SECRETION
PI3K_AKT_MTOR_SIGNALING
PEROXISOME
PANCREAS_BETA_CELLS
P53_PATHWAY
OXIDATIVE_PHOSPHORYLATION
NOTCH_SIGNALING
MYOGENESIS
MYC_TARGETS_V2
HMYC_TARGETS_V1
MTORC1_SIGNALING
MITOTIC_SPINDLE
KRAS_SIGNALING_UP
KRAS_SIGNALING_DN
INTERFERON_GAMMA_RESPONSE
INTERFERON_ALPHA_RESPONSE
INFLAMMATORY_RESPONSE
IL6_JAK_STAT3_SIGNALING
IL2_STAT5_SIGNALING
HYPOXIA
HEME_METABOLISM
HEDGEHOG_SIGNALING
GLYCOLYSIS
G2M_CHECKPOINT
FATTY_ACID_METABOLISM
ESTROGEN_RESPONSE_LATE
ESTROGEN_RESPONSE_EARLY
EPITHELIAL_MESENCHYMAL_TRANSITION
E2F_TARGETS
DNA_REPAIR
COMPLEMENT
COAGULATION
CHOLESTEROL_HOMEOSTASIS
BILE_ACID_METABOLISM
APOPTOSIS
APICAL_SURFACE
APICAL_JUNCTION
ANGIOGENESIS
ANDROGEN_RESPONSE
ALLOGRAFT_REJECTION
ADIPOGENESIS
RPN1
PML
risk score
f
RPN1-Macrophage M1_QUANTISEQ
Purity
Macrophage M1_QUANTISEQ
Rho = −0.02
p = 7.96e−01
Rho = 0.31
p = 3.67e−05
PAAD
RPN1 Expression Level (log2 TPM)
Purity
Infiltration Level
PML-Macrophage M1_QUANTISEQ
Rho = −0.061
p = 4.26e−01
Rho = 0.363
p = 1.07e−06
PML Expression Level (log2 TPM)
PML-Macrophage M0_CIBERSORT−ABS
Macrophage M0_CIBERSORT−ABS
Rho = −0.061
p = 4.26e−01
Rho = 0.306
p = 4.59e−05
PML-Macrophage M2_TIDE
Macrophage M2_TIDE
Rho = −0.061
p = 4.26e−01
Rho = −0.458
p = 2.87e−10