Supplementary Figures.

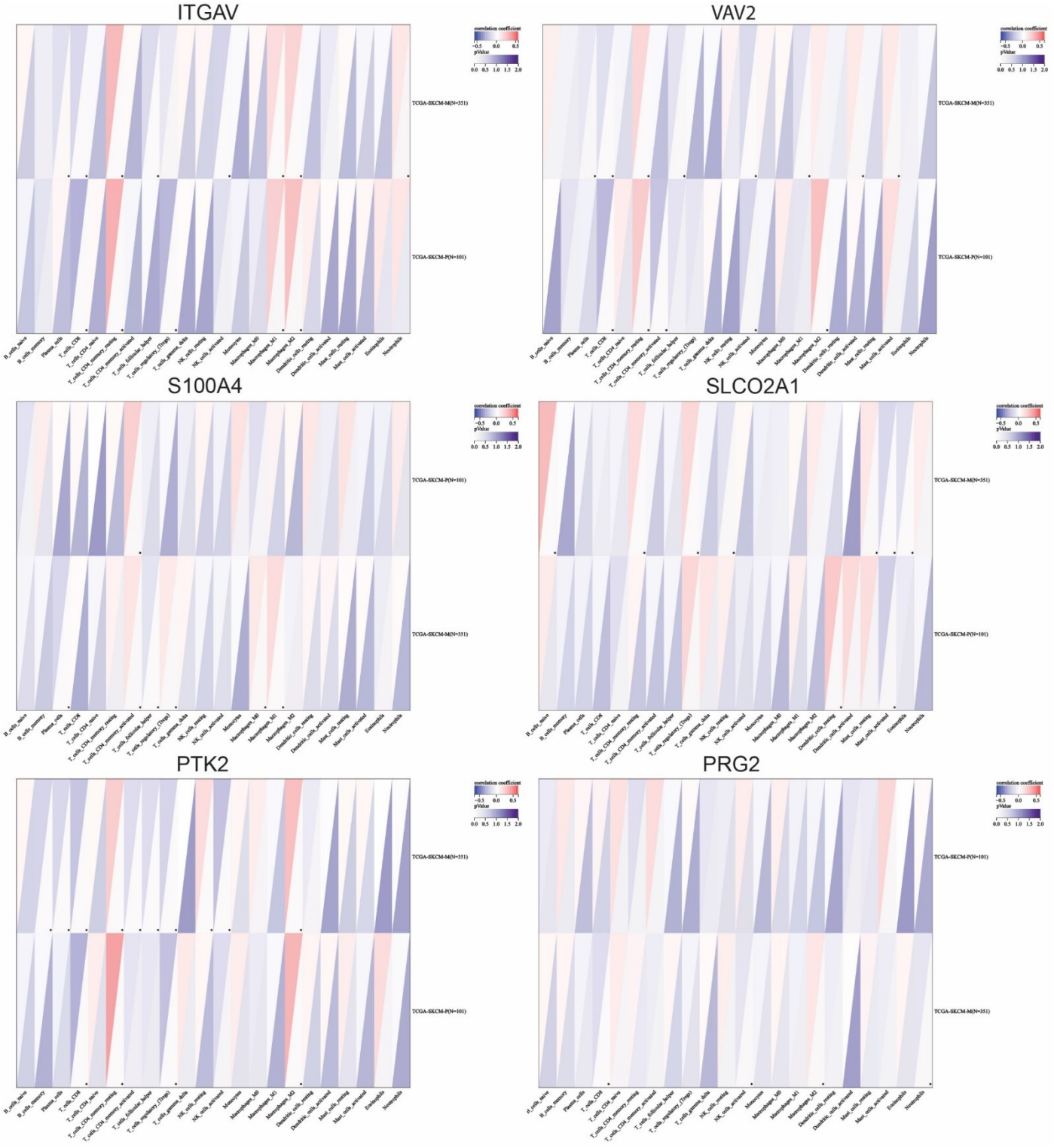


Figure S1 Spearman's correlations between the expression of *ITGAV, VAV2, S100A4, SLCO2A1, PTK2,* and *PRG2,* and the infiltration in different immune cells in primary and metastatic skin melanoma, using CIBERSORT. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

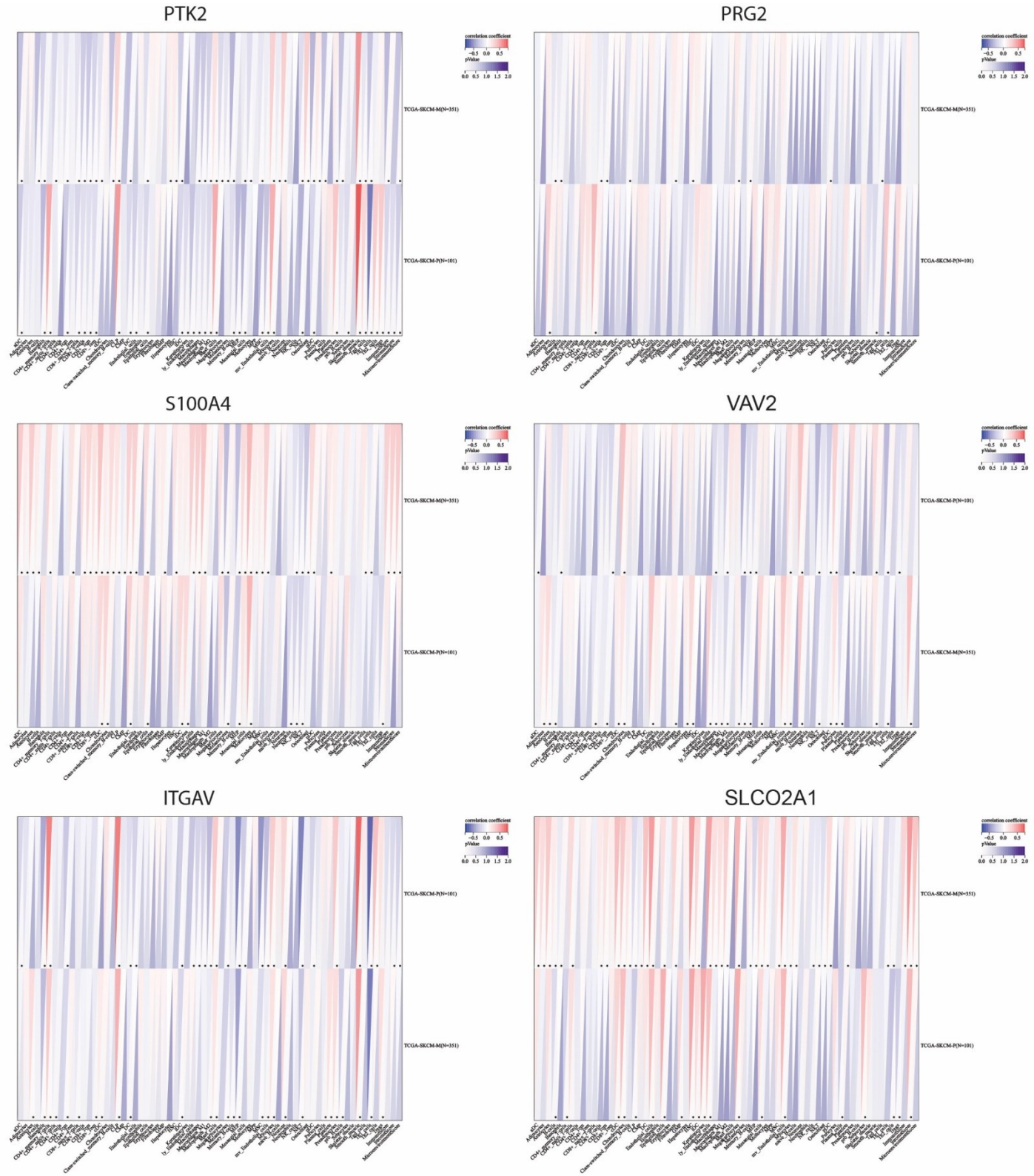
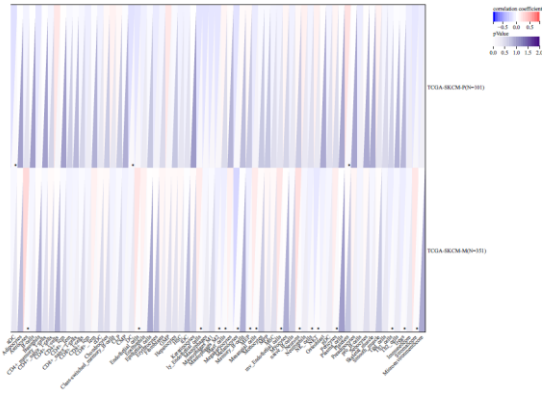


Figure S2. Spearman's correlations between the expression of *PTK2, PRG2, S100A4, VAV2, ITGAV* and *SLCO2A1,* and the infiltration in different immune cells in primary and metastatic skin melanoma, using xCELL. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

APOH



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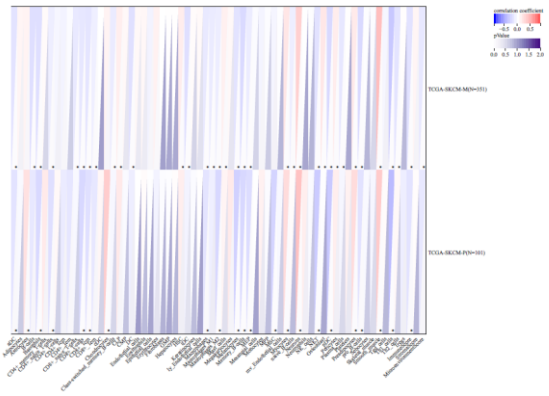

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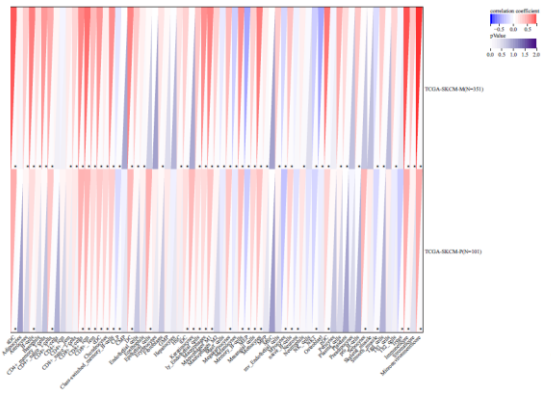

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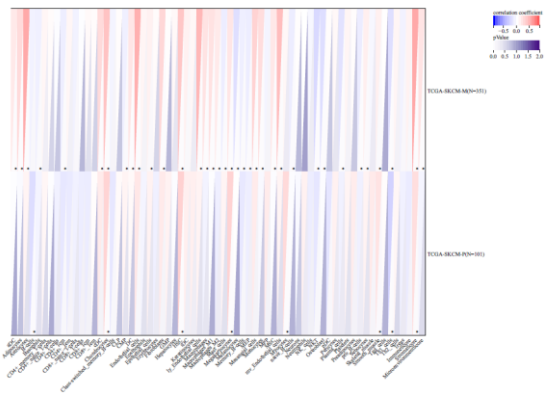

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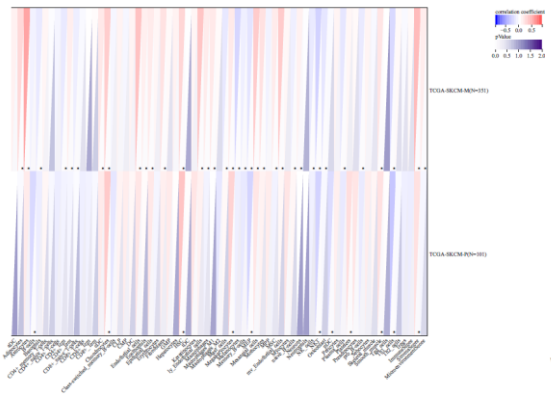

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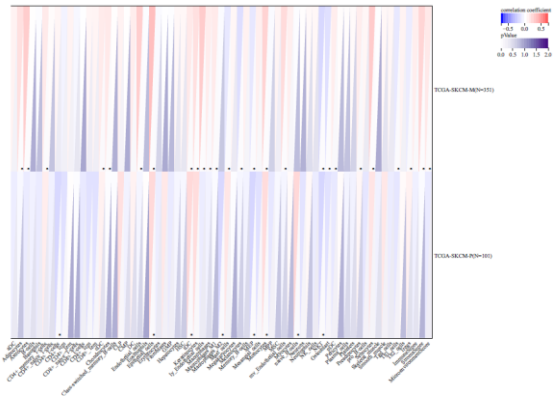

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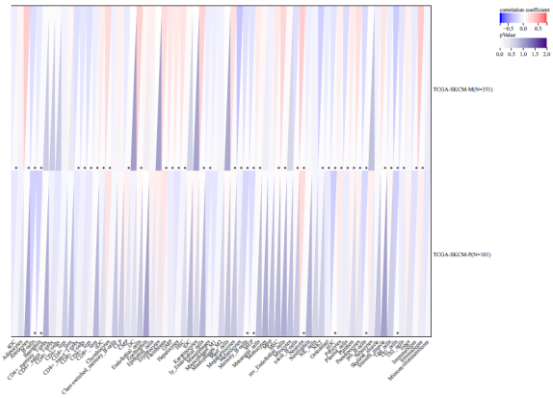

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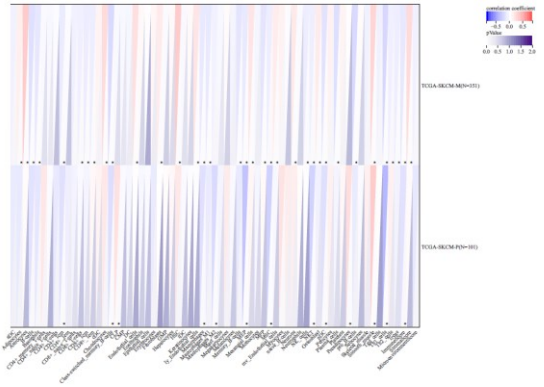

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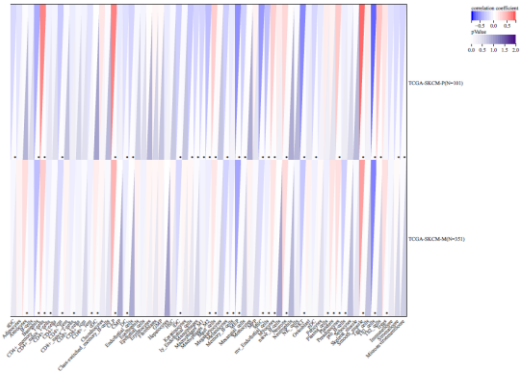

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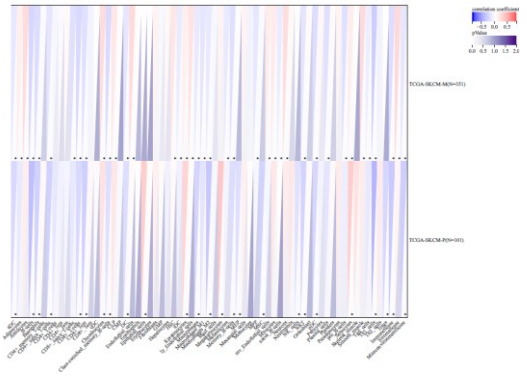

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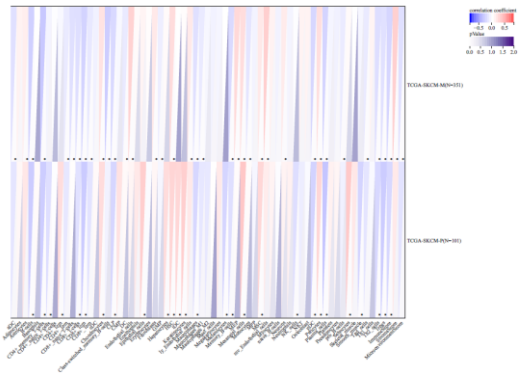

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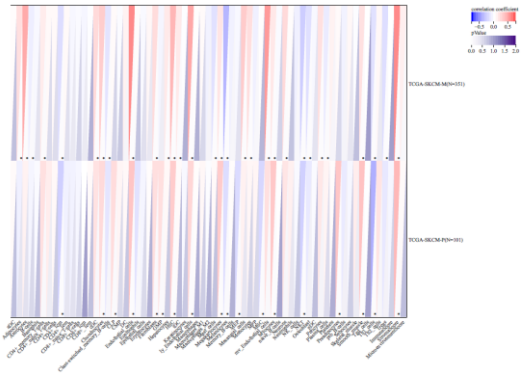

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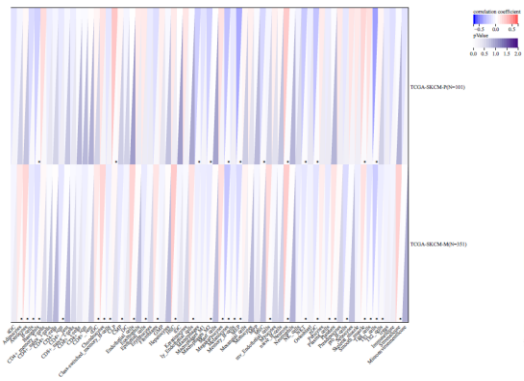

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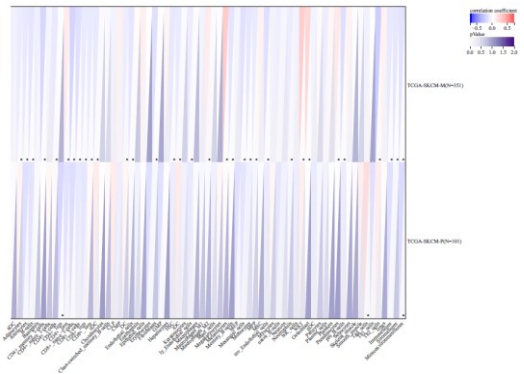

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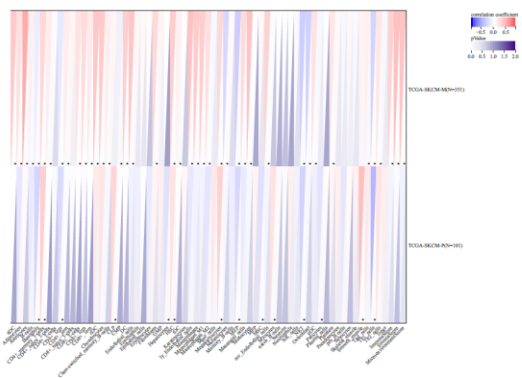

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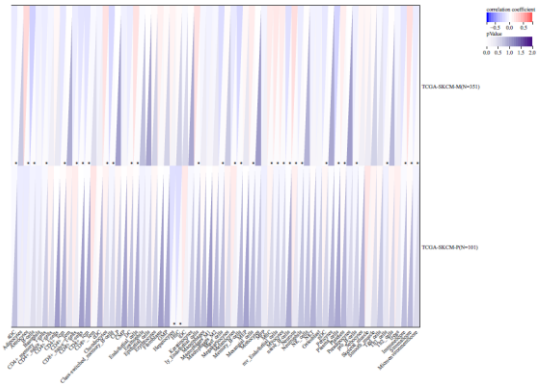

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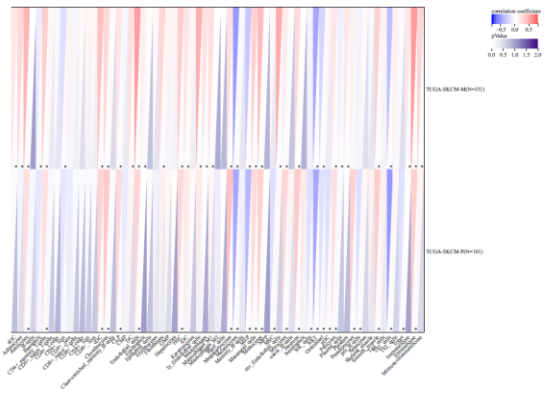

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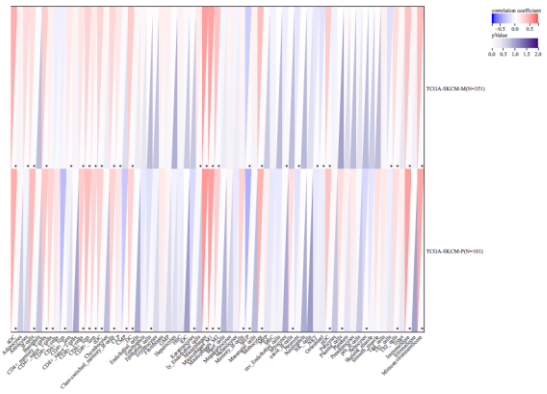

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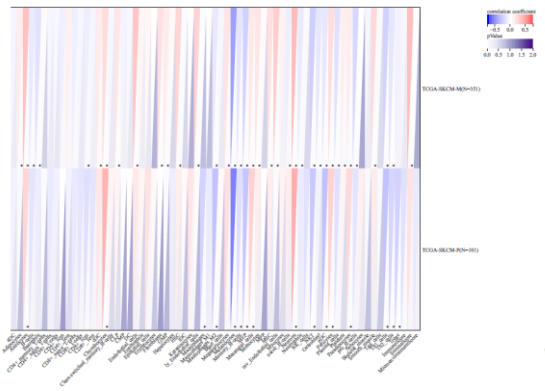

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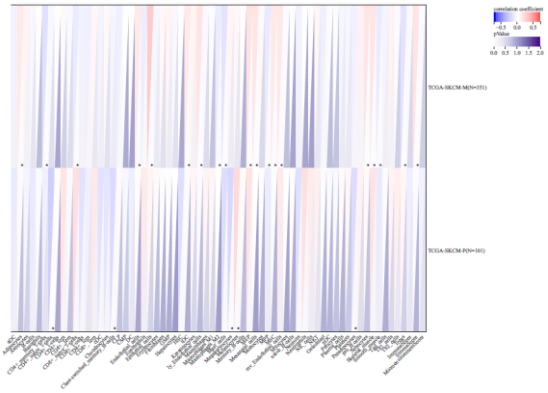

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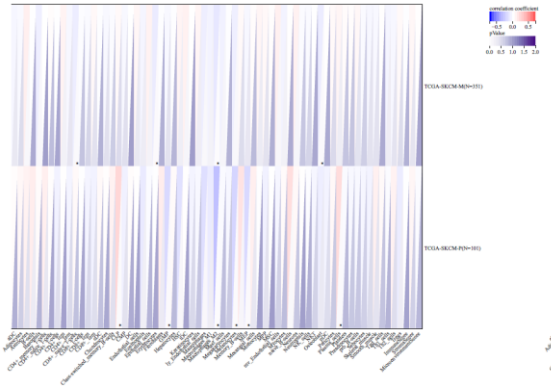

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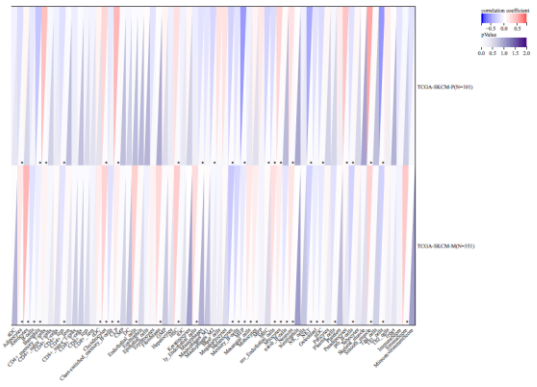

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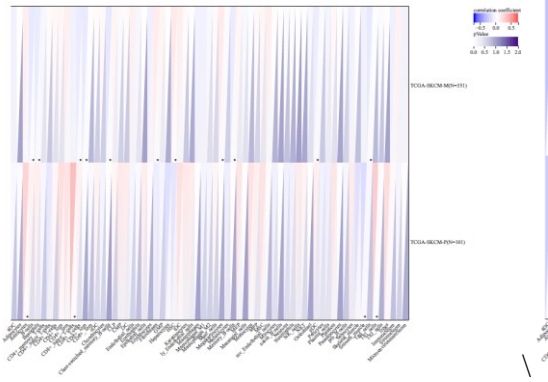

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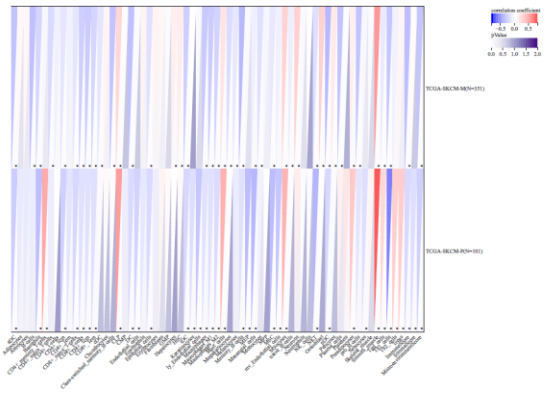

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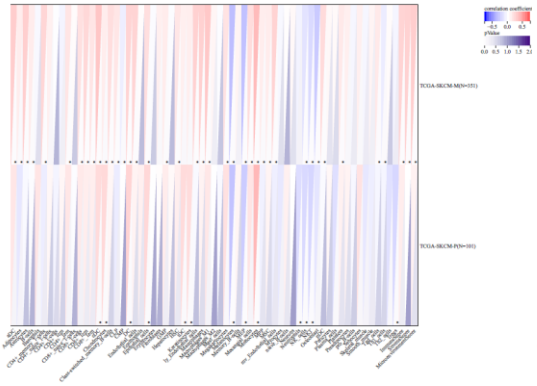

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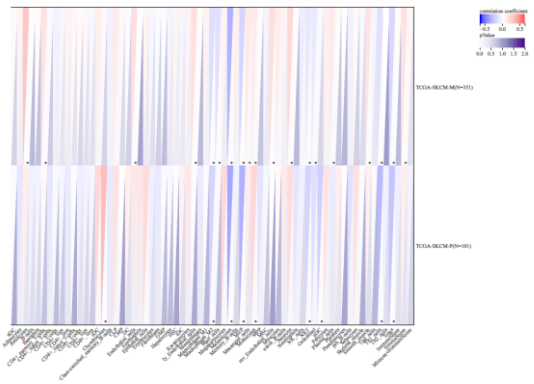

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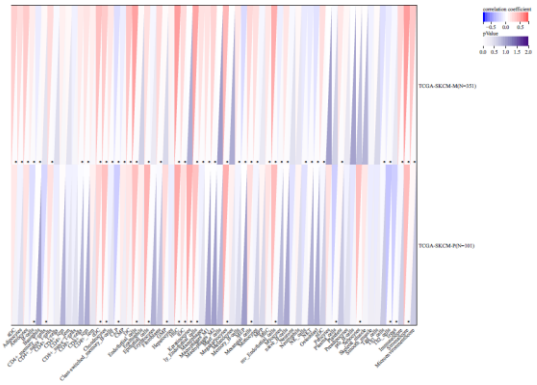

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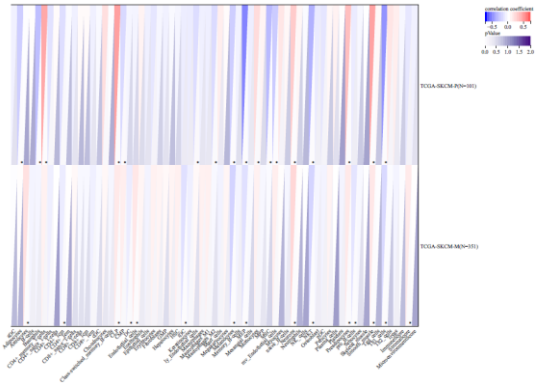

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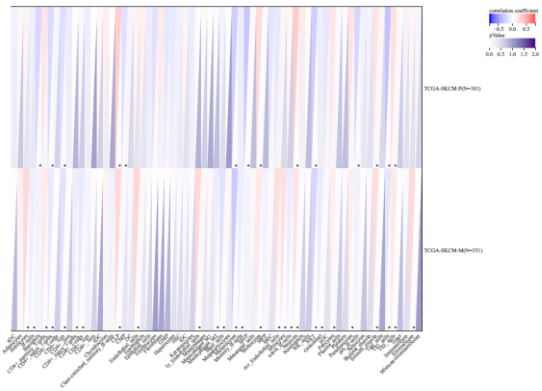

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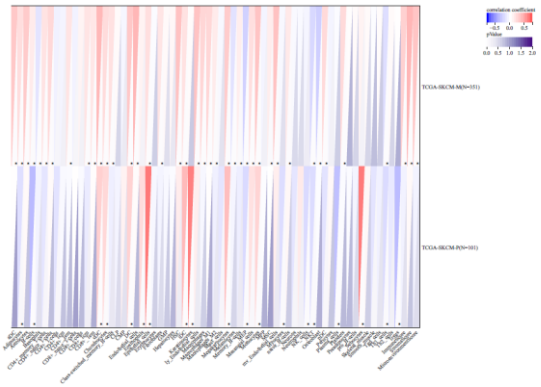

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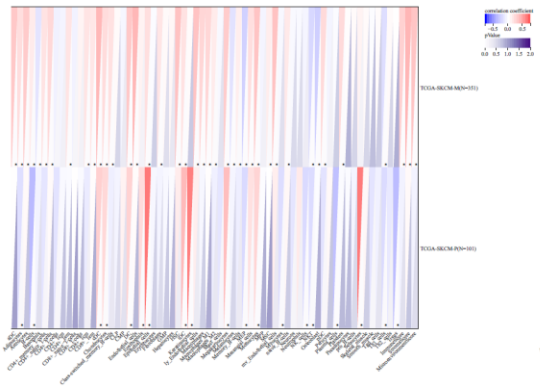

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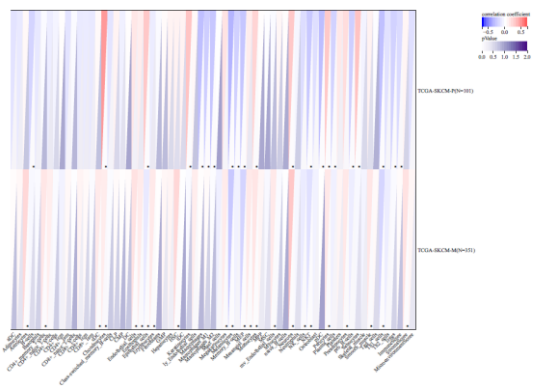

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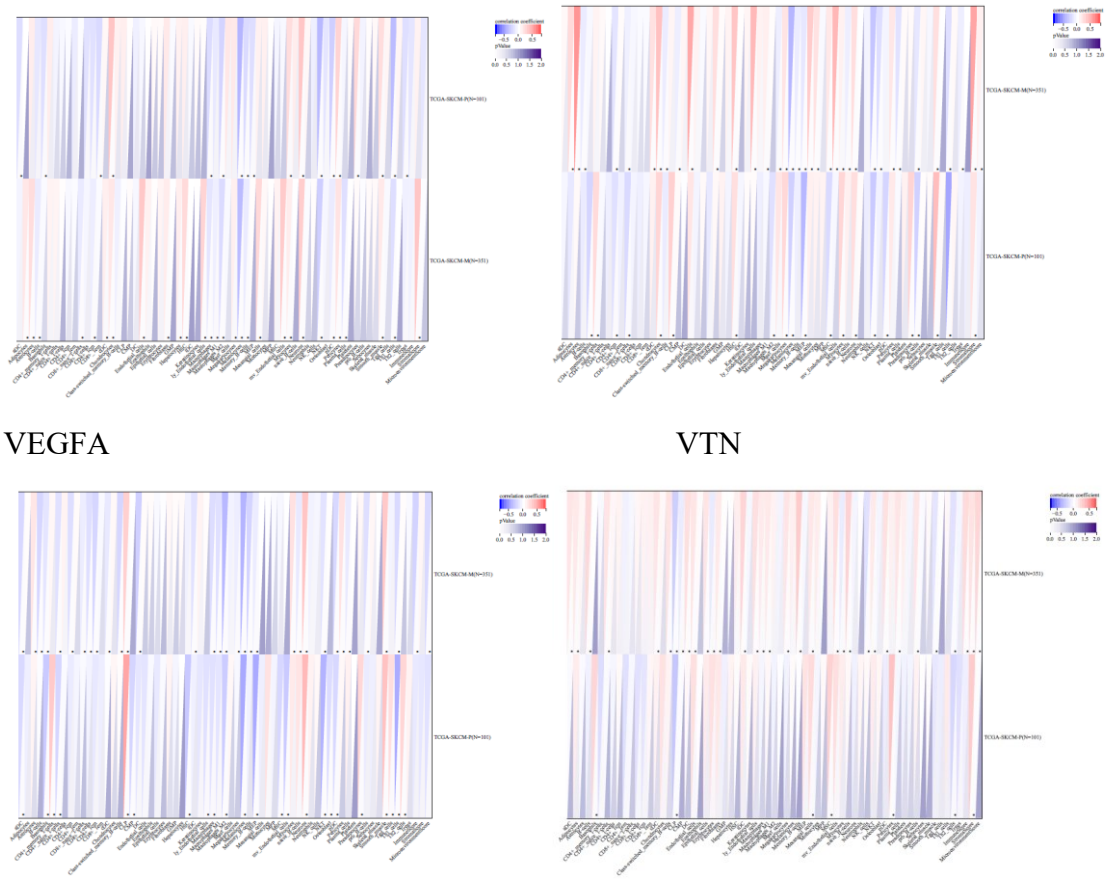


Figure S3. Spearman's correlations between the expression of ARGs and the infiltration in different immune cells in primary and metastatic skin melanoma, using xCELL. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

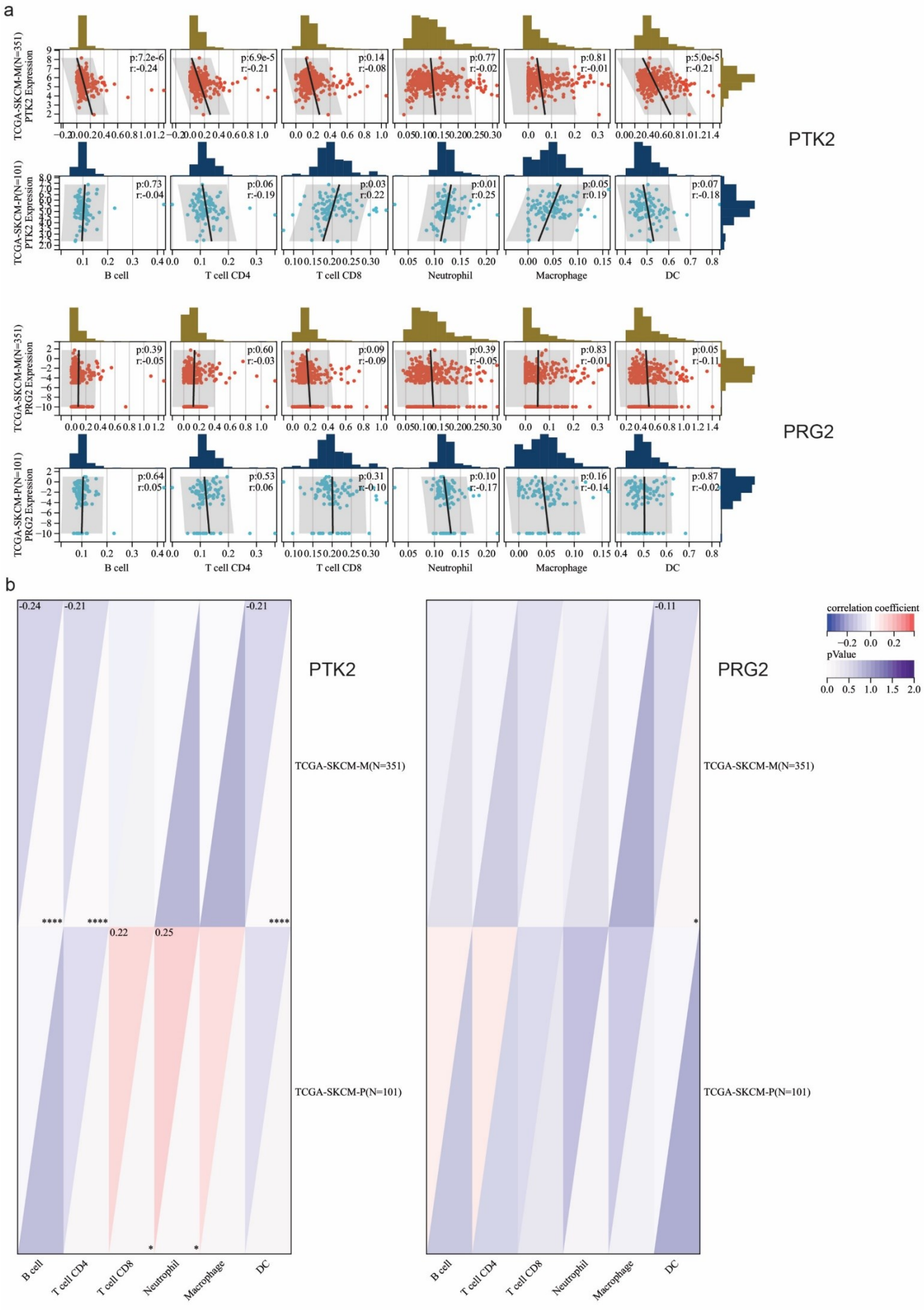
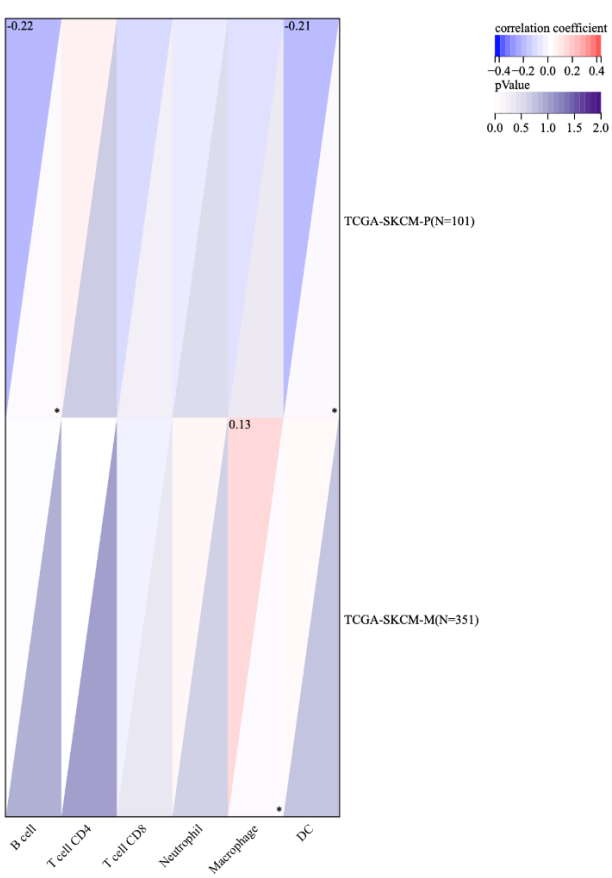

a
TCGA-SKCM-M(N=351)
PTK2 Expression
p:7.2e-6
r:-0.24
p:6.9e-5
r:-0.21
p:0.14
r:-0.08
p:0.77
r:-0.02
p:0.81
r:-0.01
p:5.0e-5
r:-0.21
PTK2
TCGA-SKCM-P(N=101)
PTK2 Expression
p:0.73
r:-0.04
p:0.06
r:-0.19
p:0.03
r:0.22
p:0.01
r:0.25
p:0.05
r:0.19
p:0.07
r:-0.18
B cell
T cell CD4
T cell CD8
Neutrophil
Macrophage
DC
TCGA-SKCM-M(N=351)
PRG2 Expression
p:0.39
r:-0.05
p:0.60
r:-0.03
p:0.09
r:-0.09
p:0.39
r:-0.05
p:0.83
r:-0.01
p:0.05
r:-0.11
PRG2
TCGA-SKCM-P(N=101)
PRG2 Expression
p:0.64
r:0.05
p:0.53
r:0.06
p:0.31
r:-0.10
p:0.10
r:-0.17
p:0.16
r:-0.14
p:0.87
r:-0.02
B cell
T cell CD4
T cell CD8
Neutrophil
Macrophage
DC
b
-0.24
-0.21
-0.21
PTK2
TCGA-SKCM-M(N=351)
****
****
****
0.22
0.25
TCGA-SKCM-P(N=101)
*
*
B cell
T cell CD4
T cell CD8
Neutrophil
Macrophage
DC
-0.11
PRG2
TCGA-SKCM-M(N=351)
*
TCGA-SKCM-P(N=101)
B cell
T cell CD4
T cell CD8
Neutrophil
Macrophage
DC
correlation coefficient
−0.2 0.0 0.2
pValue
0.0 0.5 1.0 1.5 2.0

Figure S4. Spearman's correlation analysis depicted in the form of scatterplots (**a**) and heatmaps (**b**) between the expression of *PTK2* (or *PRG2*) and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using TIMER. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

APOH



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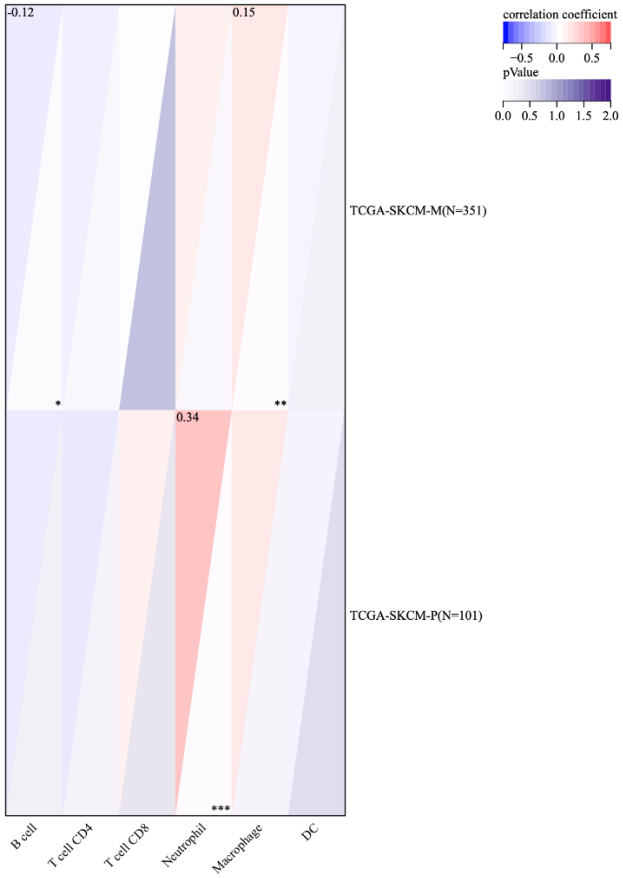

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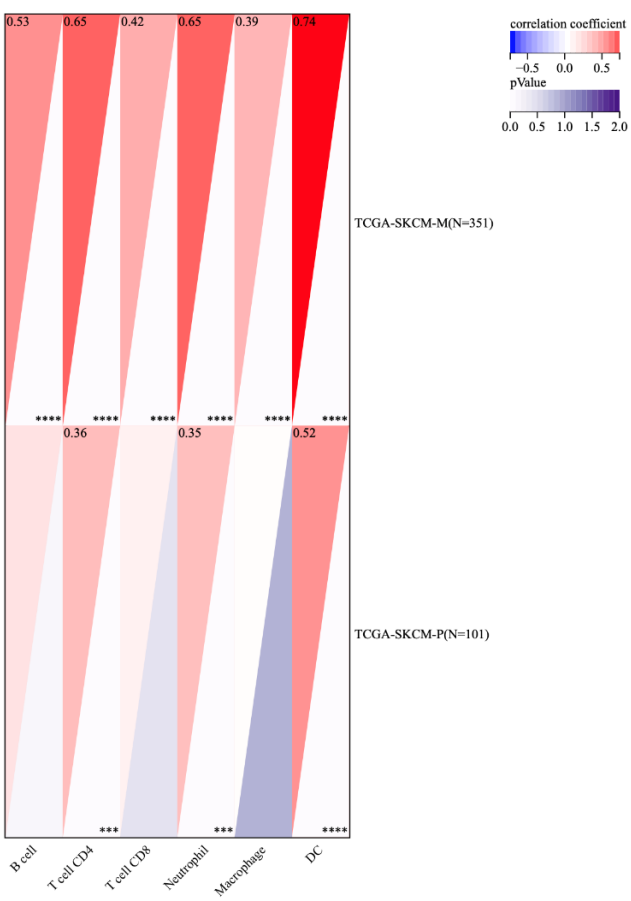

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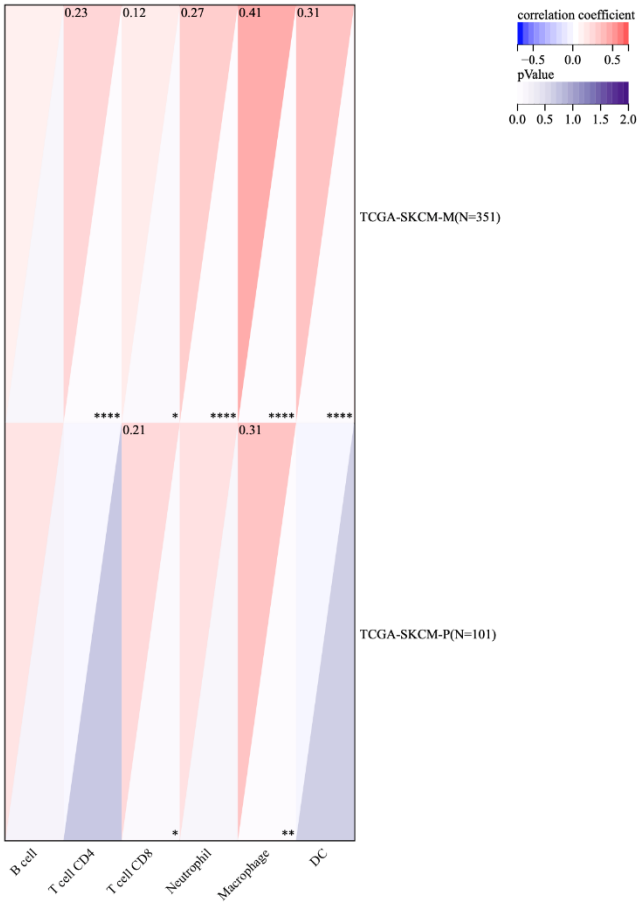

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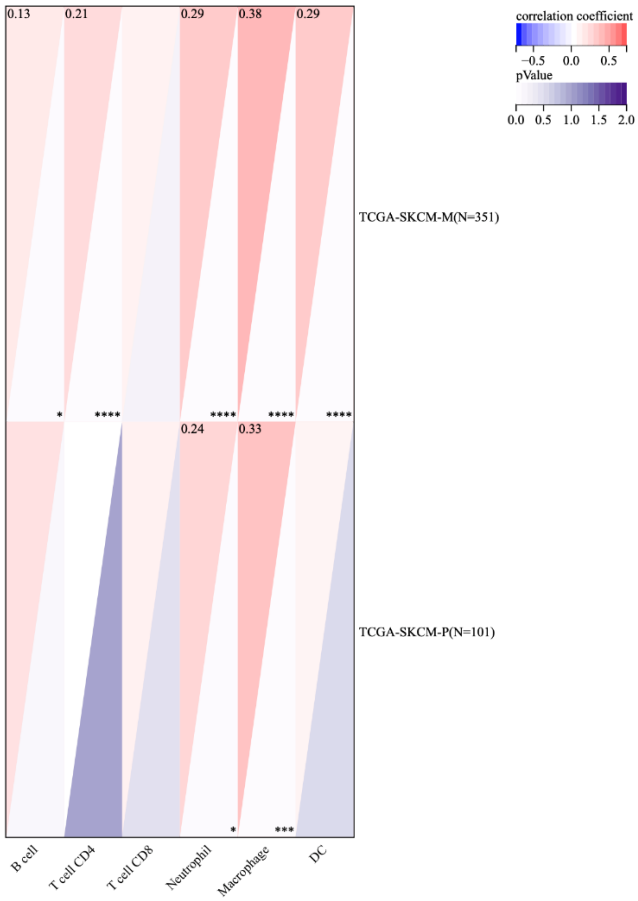

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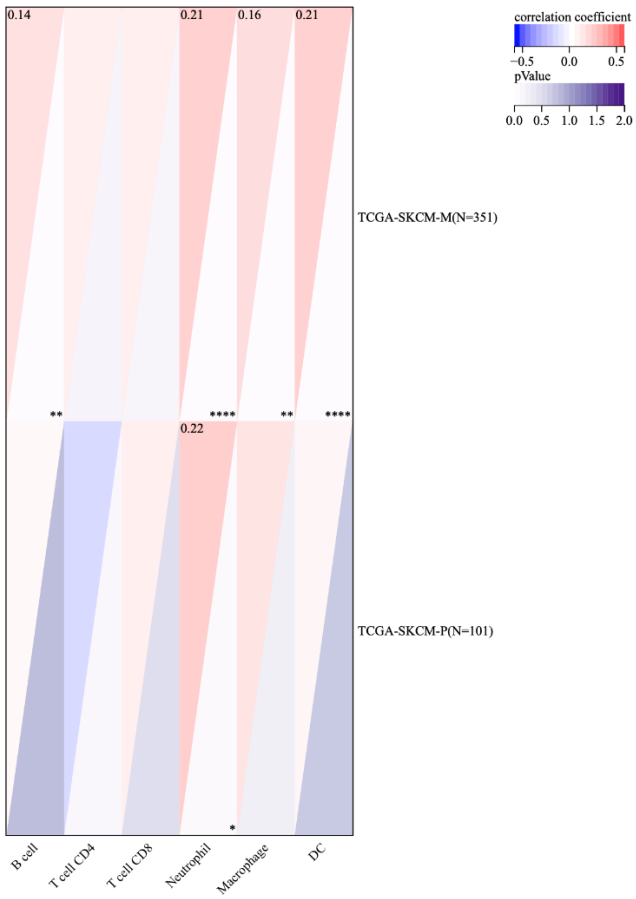

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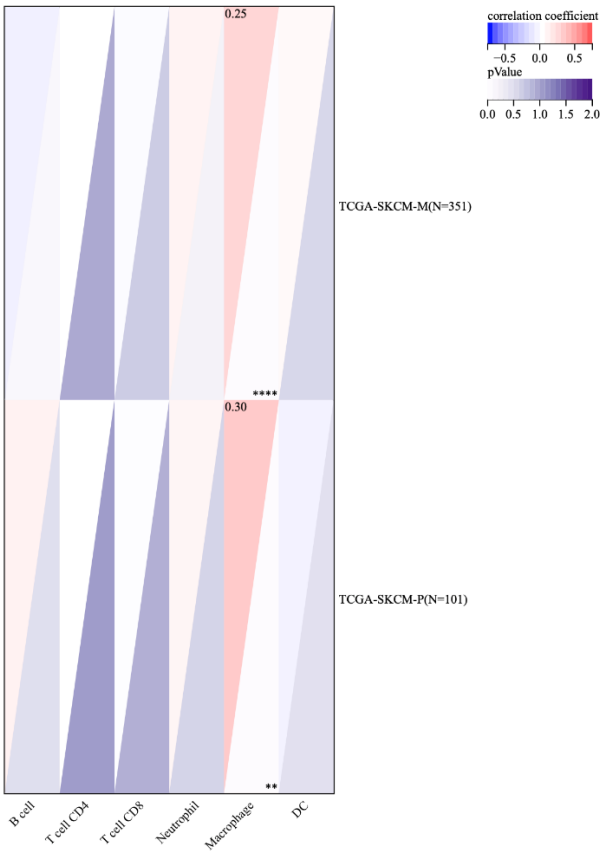

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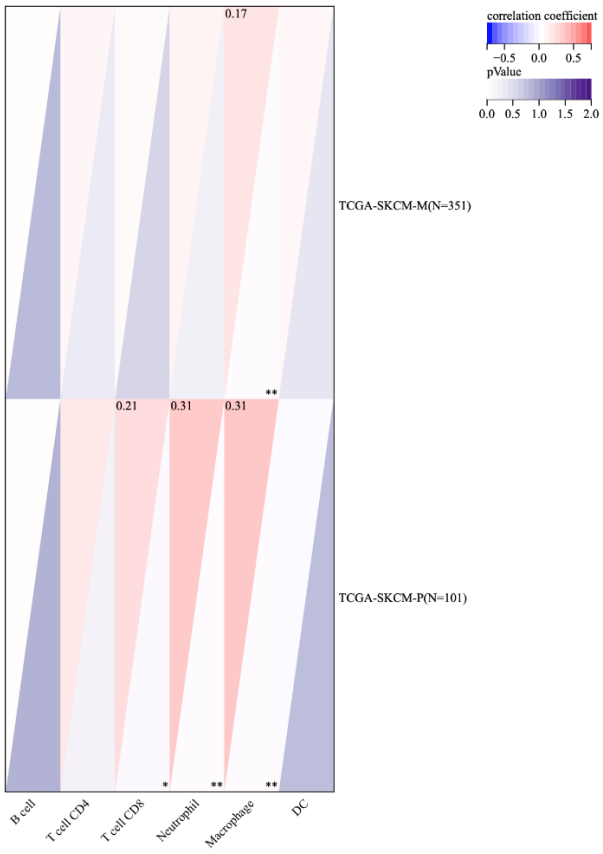

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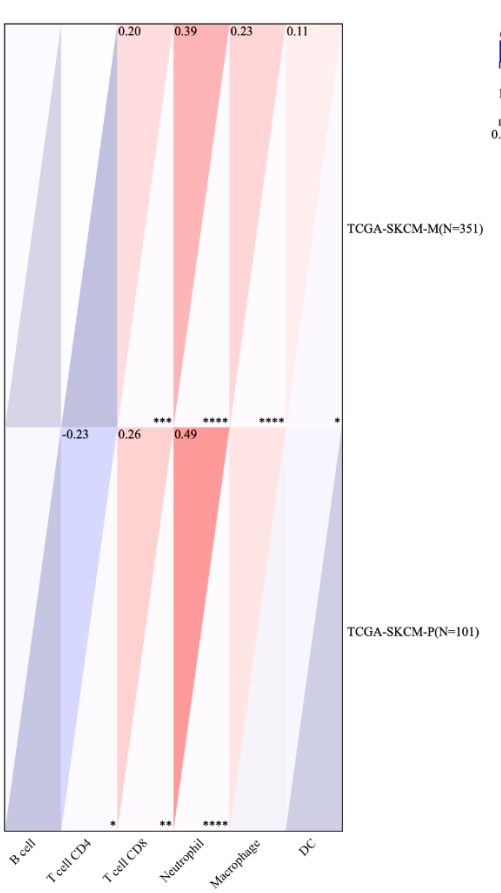

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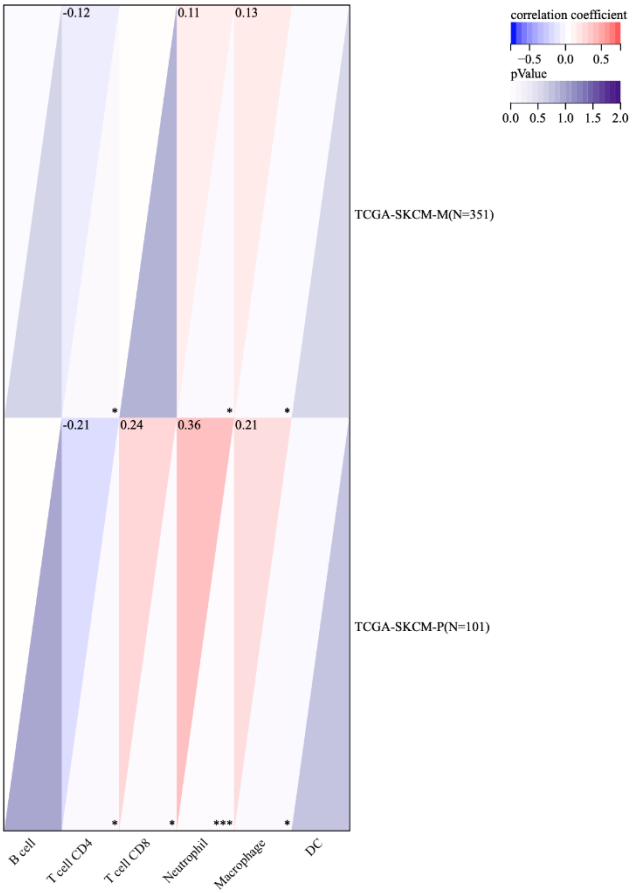

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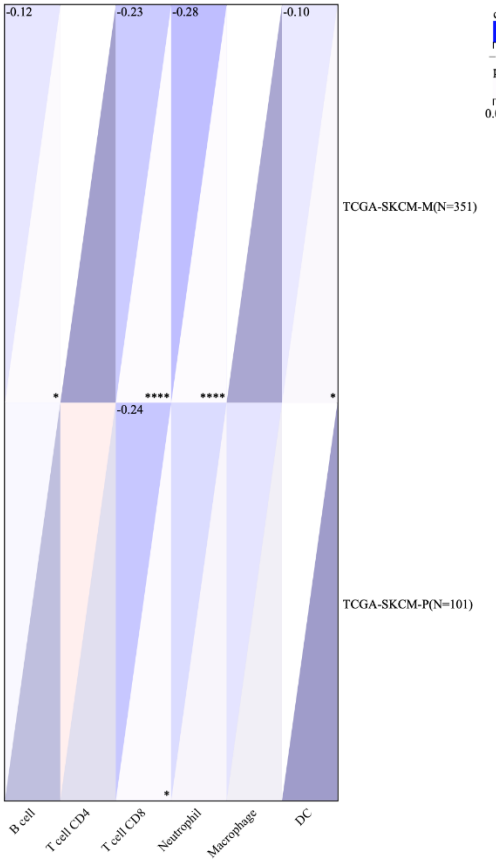

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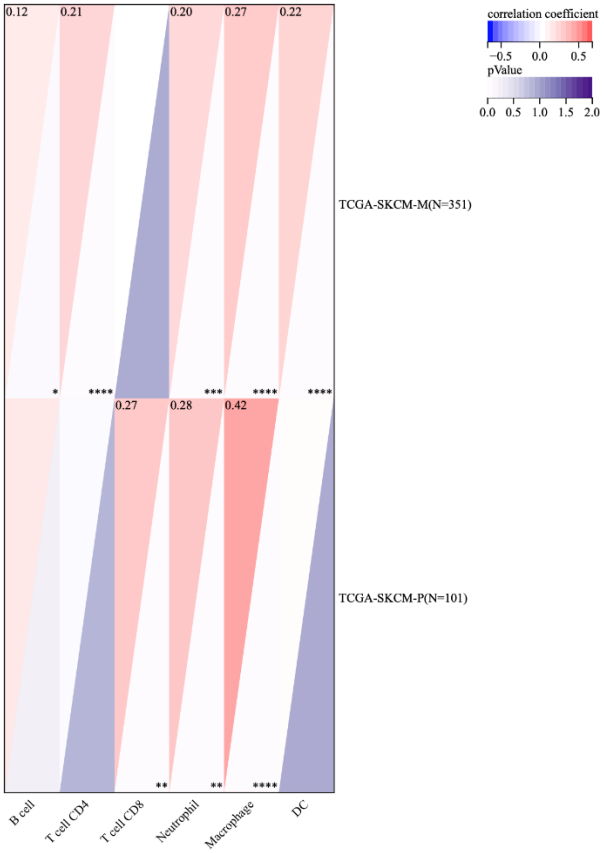

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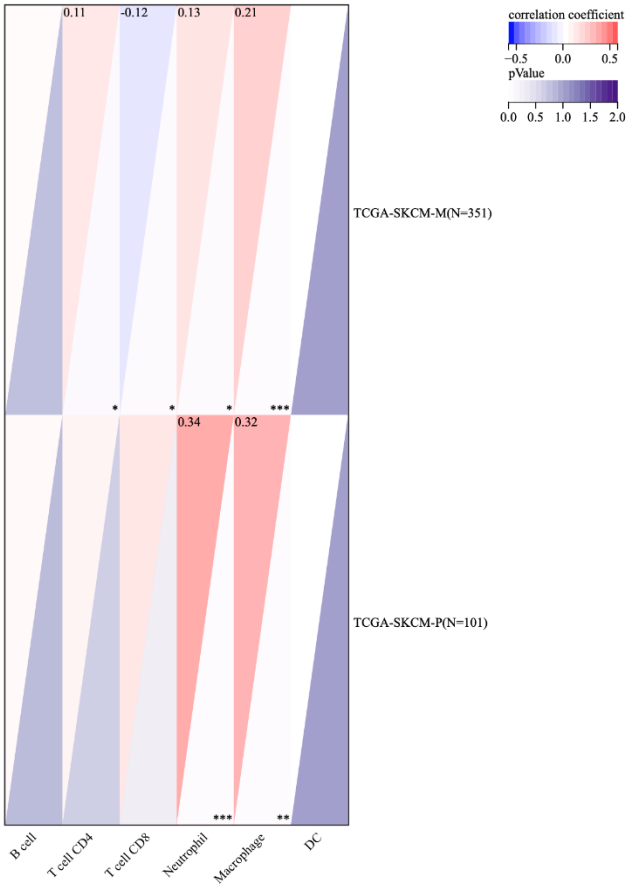

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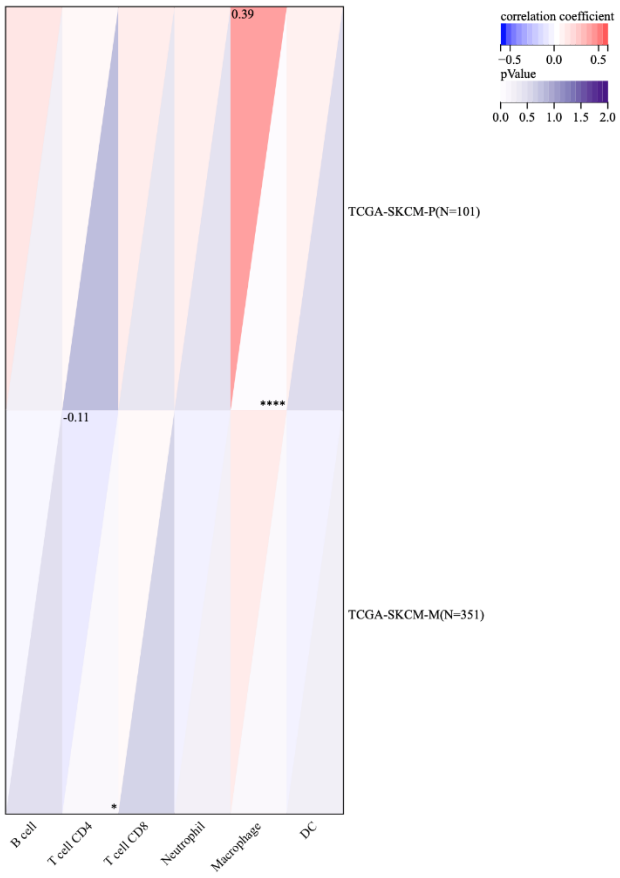

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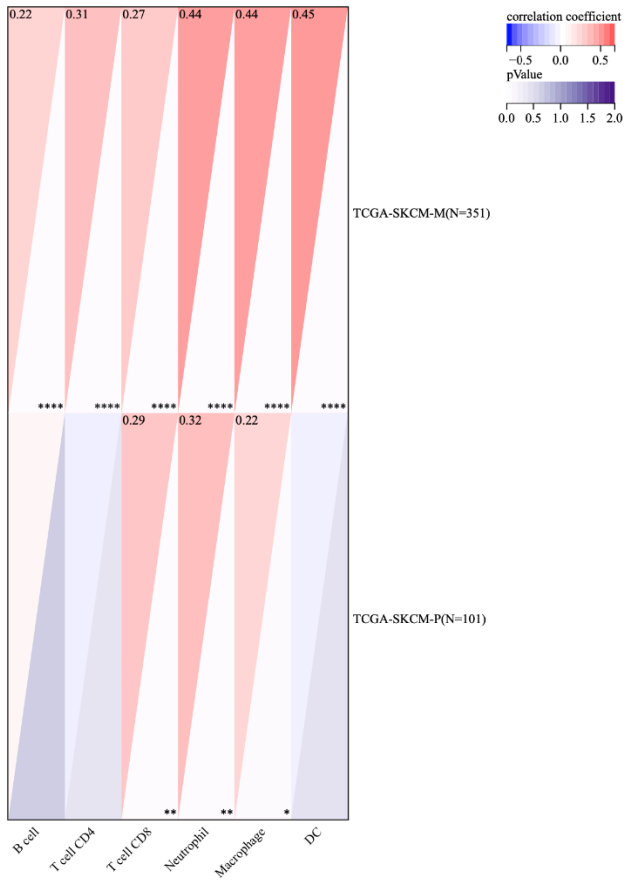

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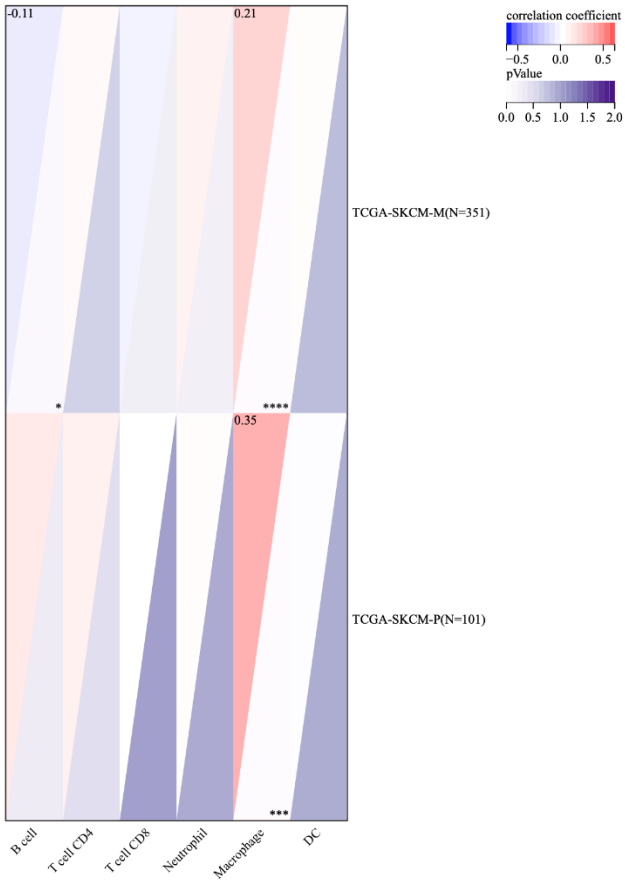

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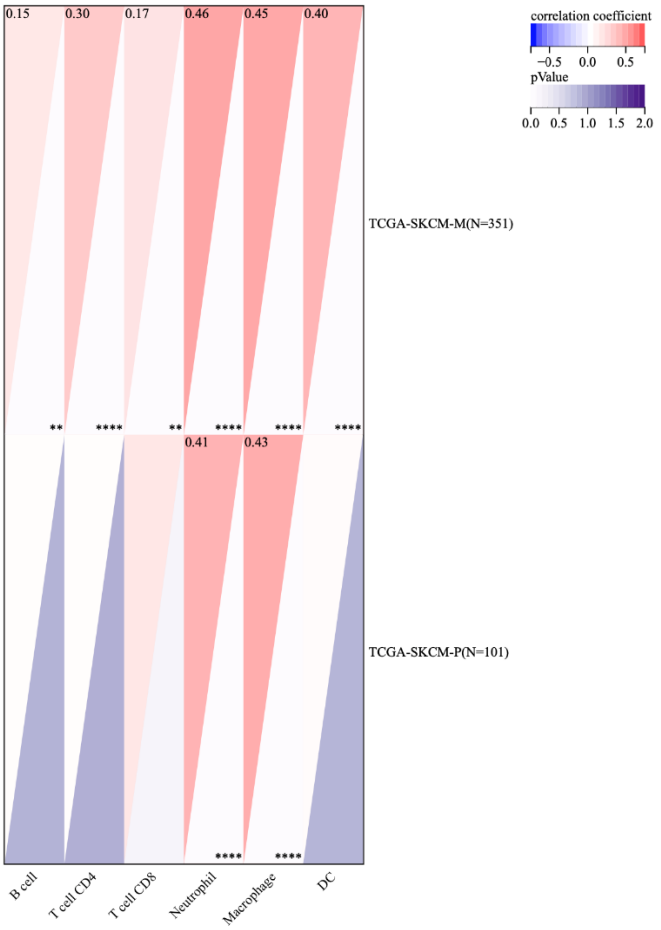

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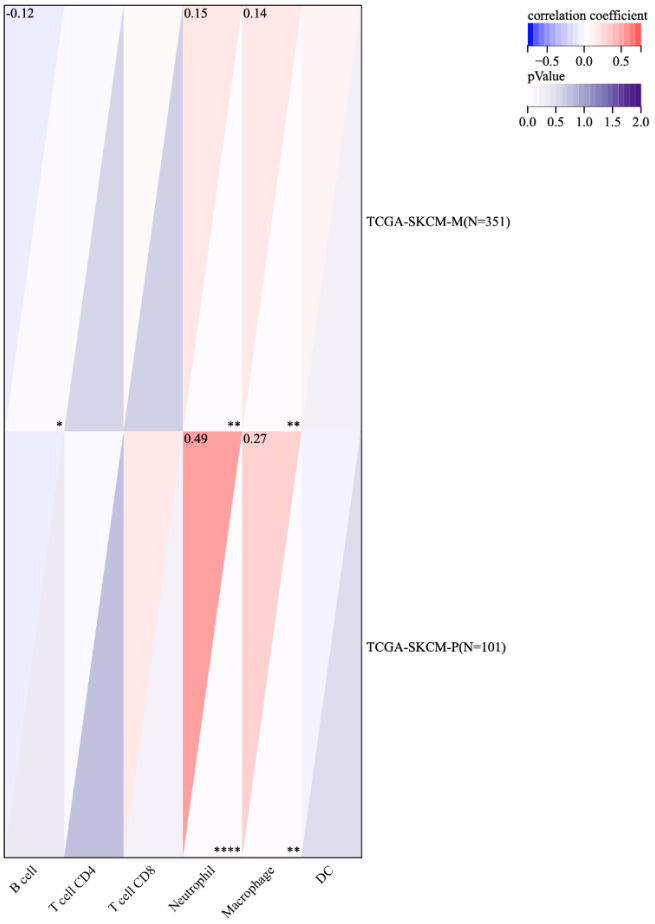

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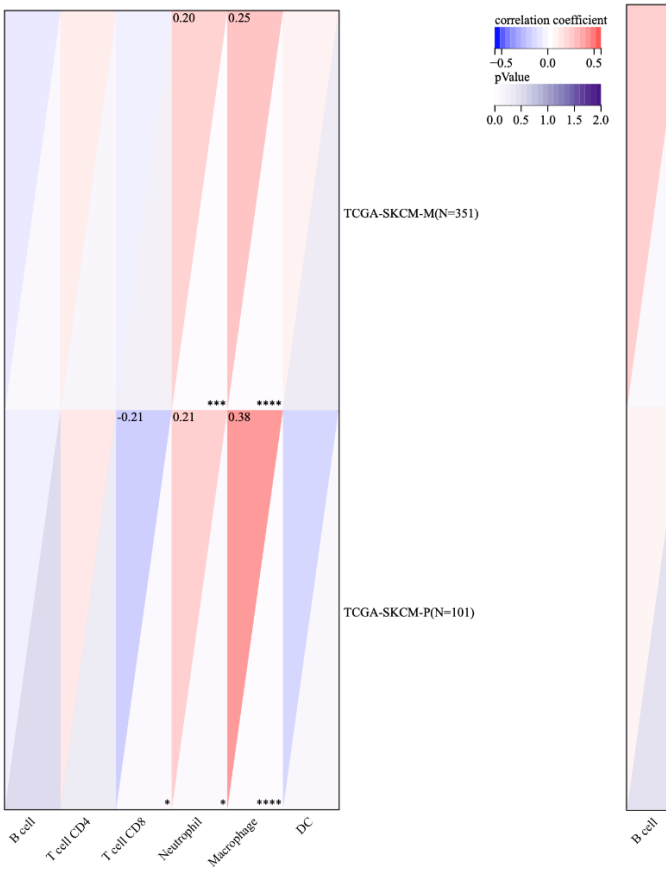

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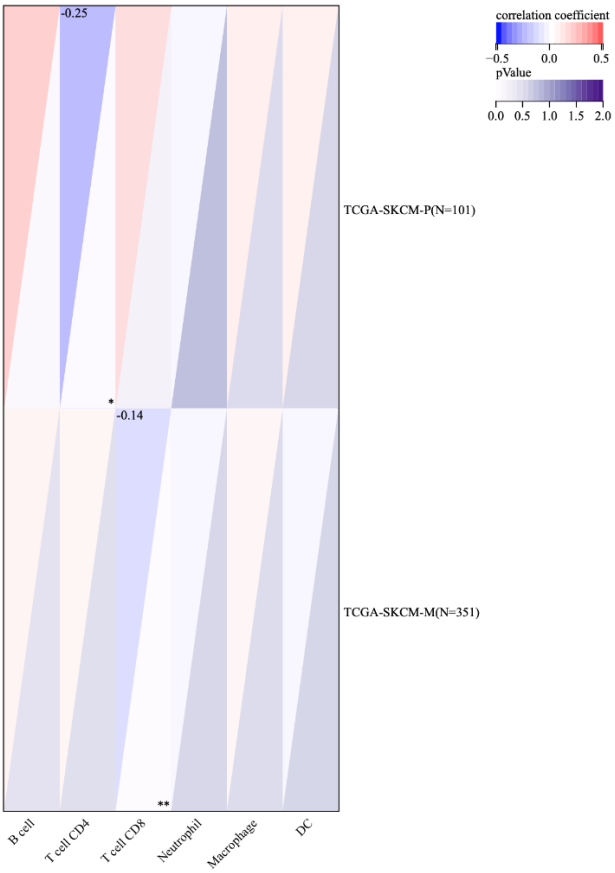

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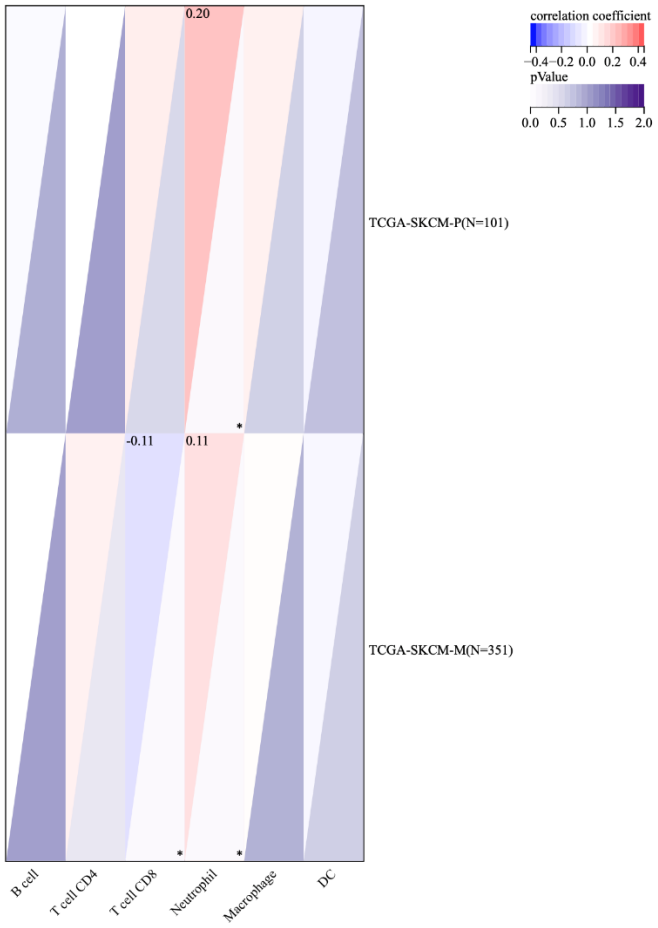

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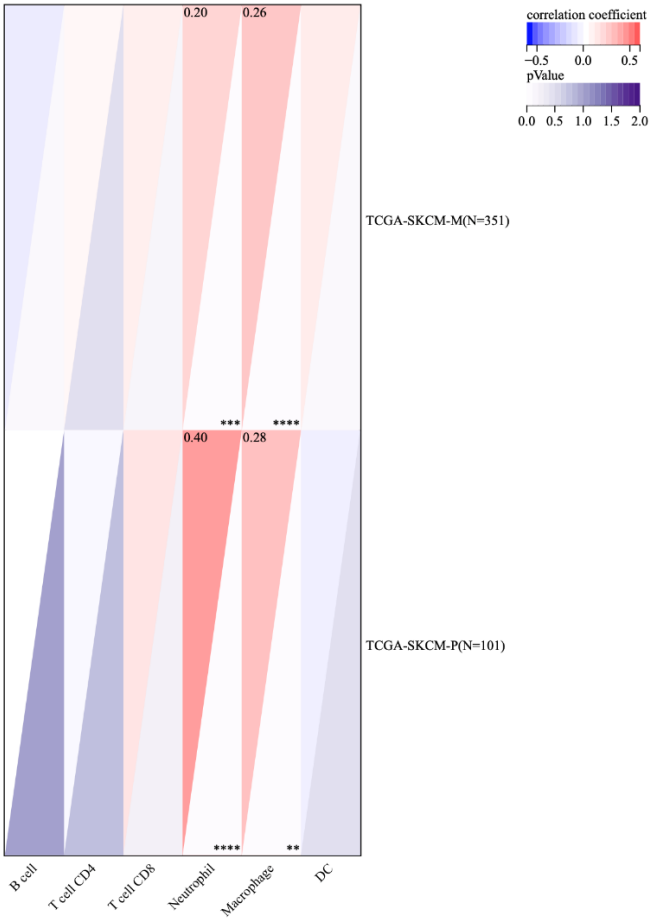

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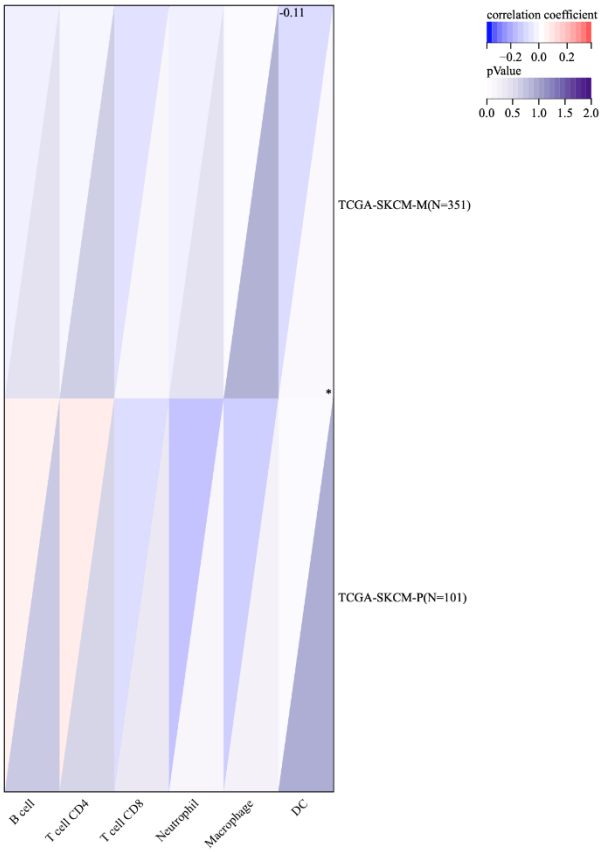

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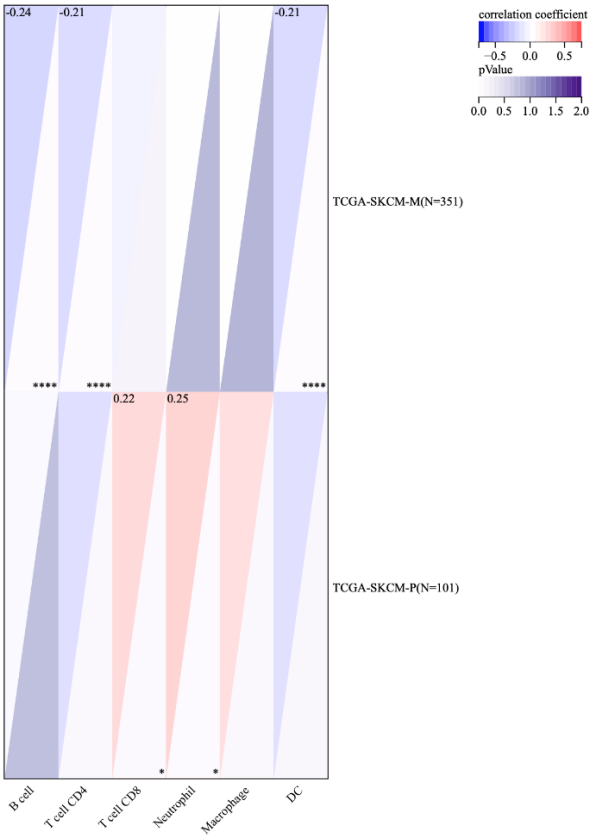

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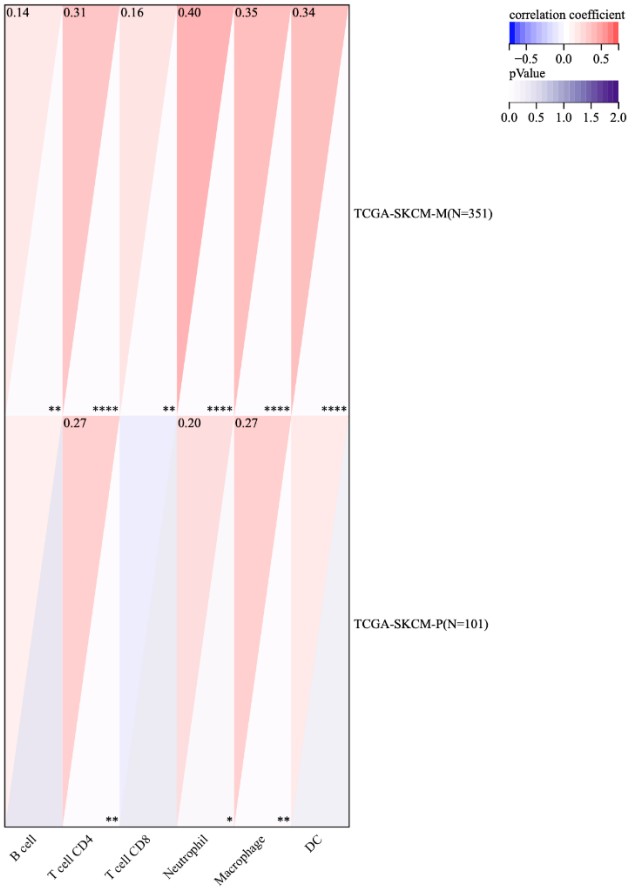

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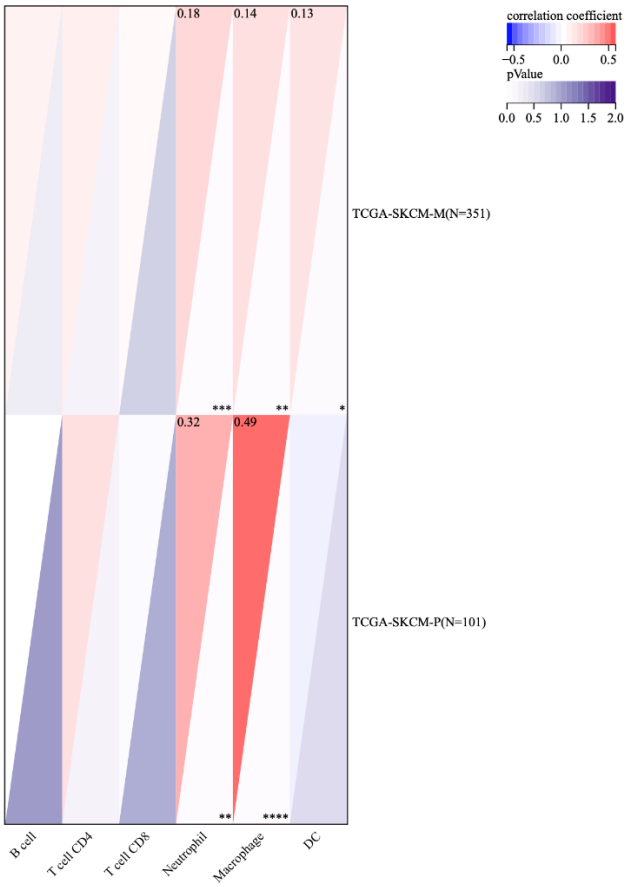

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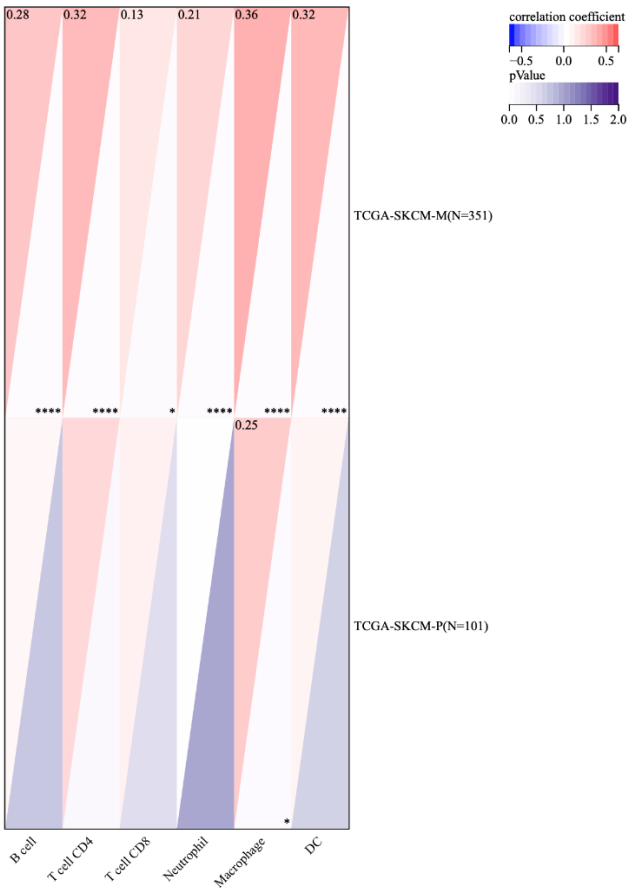

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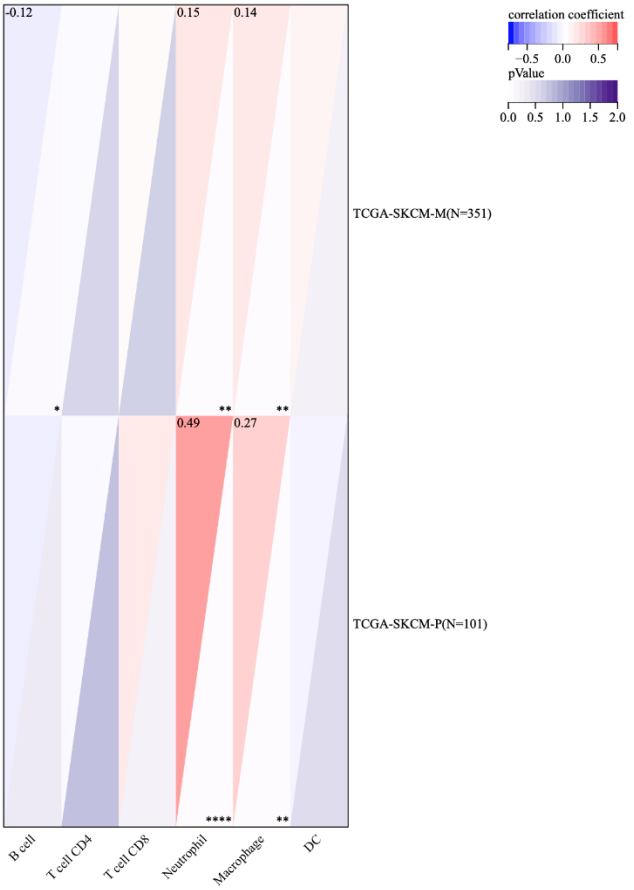

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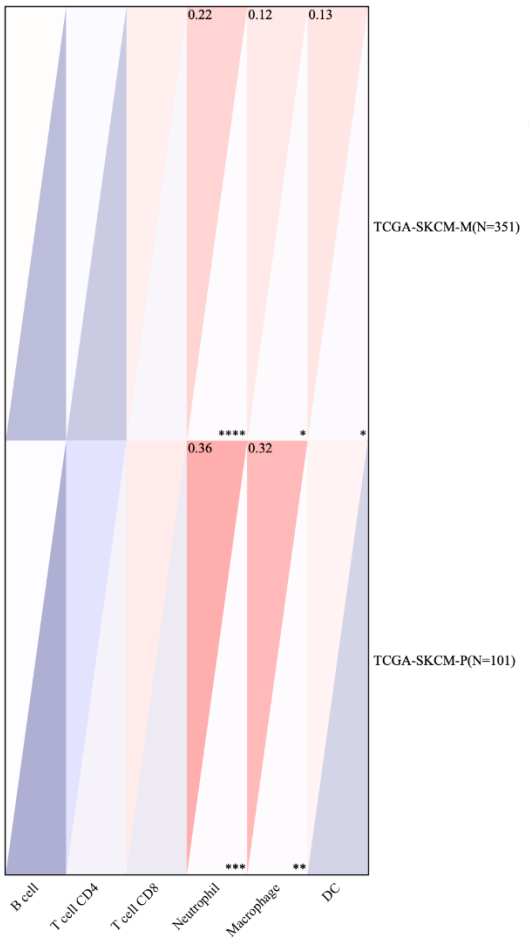

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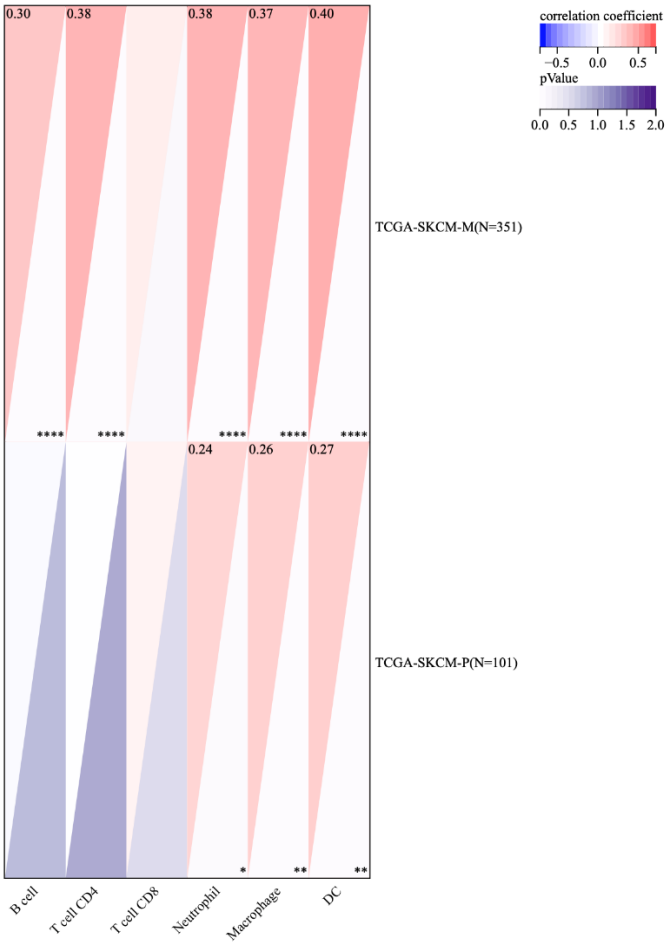

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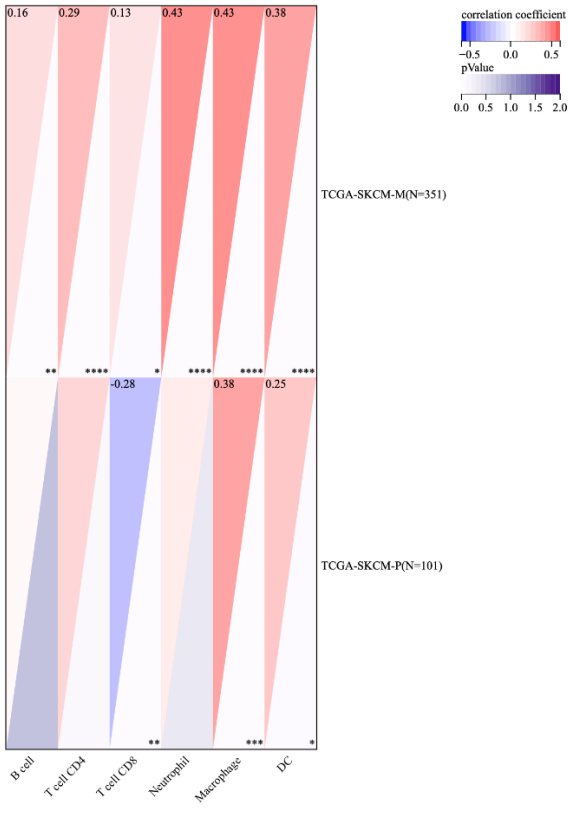

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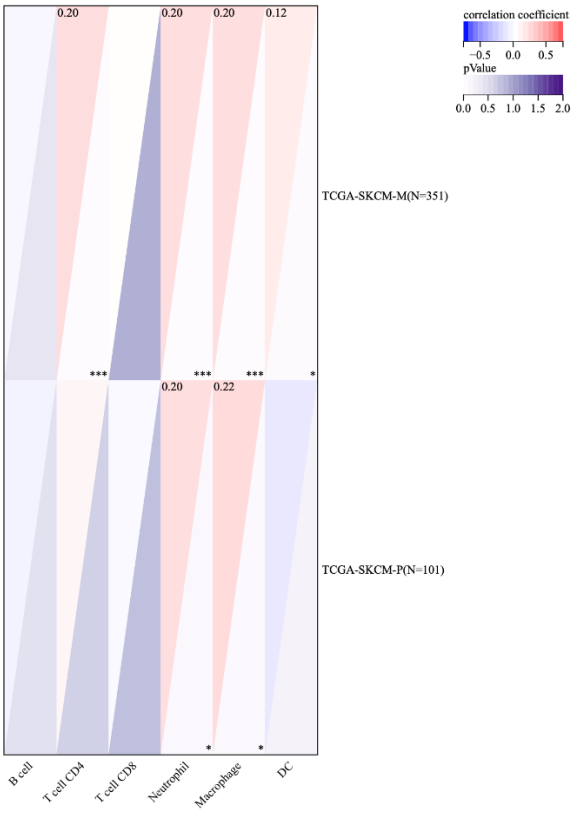

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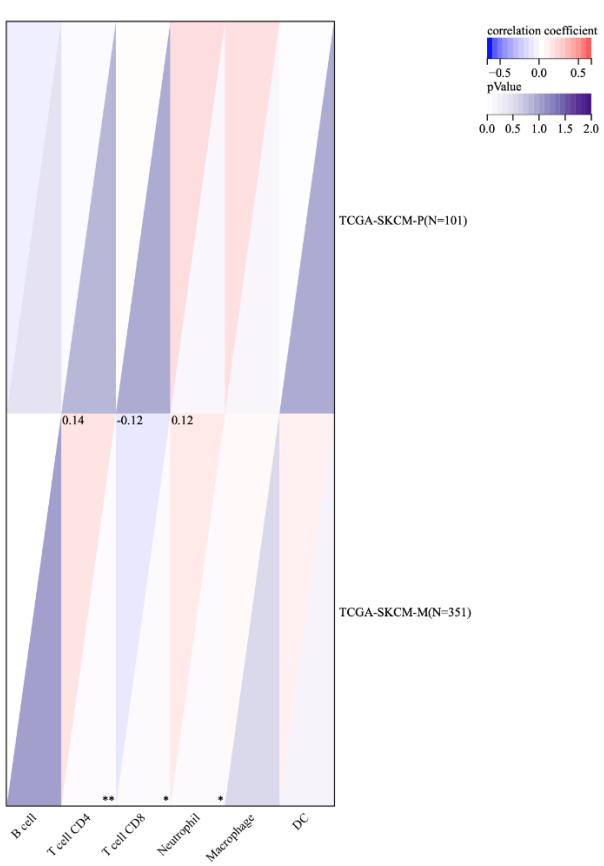

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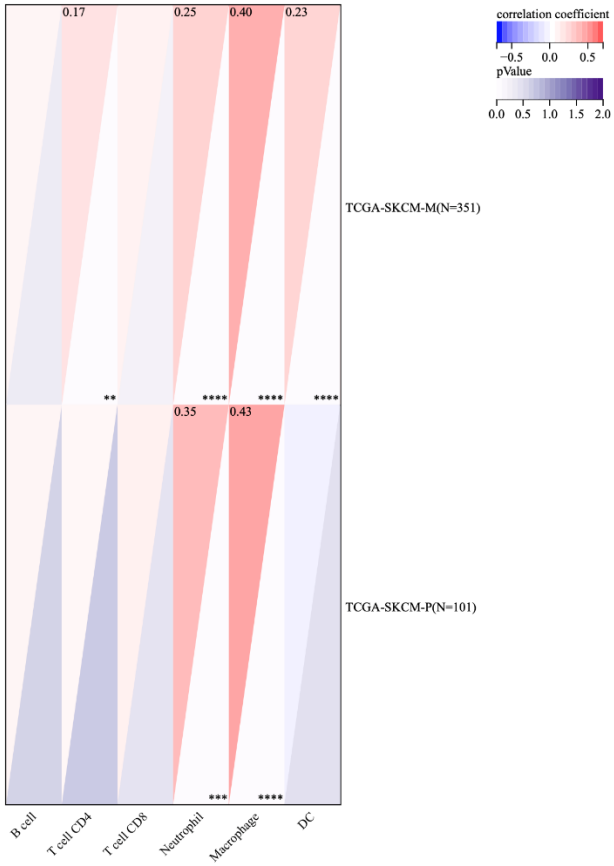

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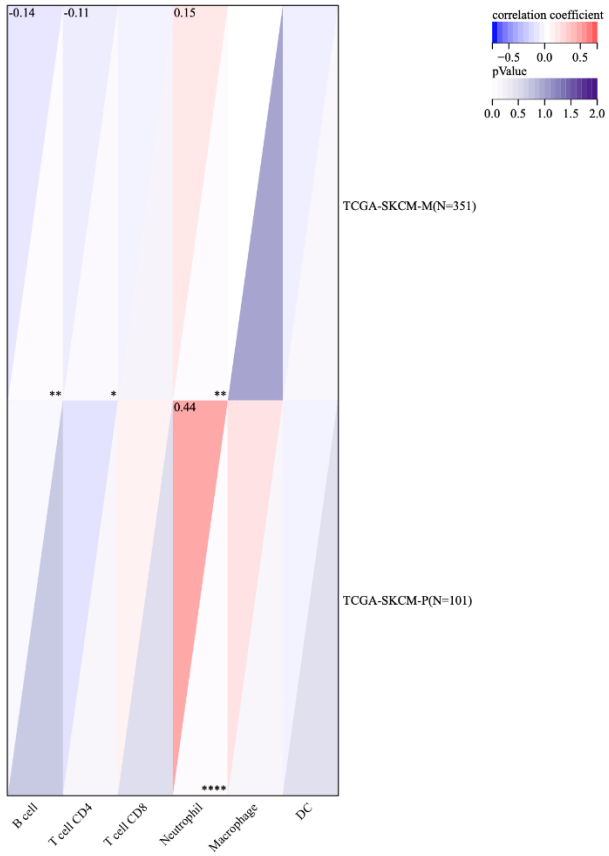

Figure S5. Spearman's correlation analysis depicted in the form of scatterplots (**a**) and heatmaps (**b**) between the expression of ARGs and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using TIMER. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

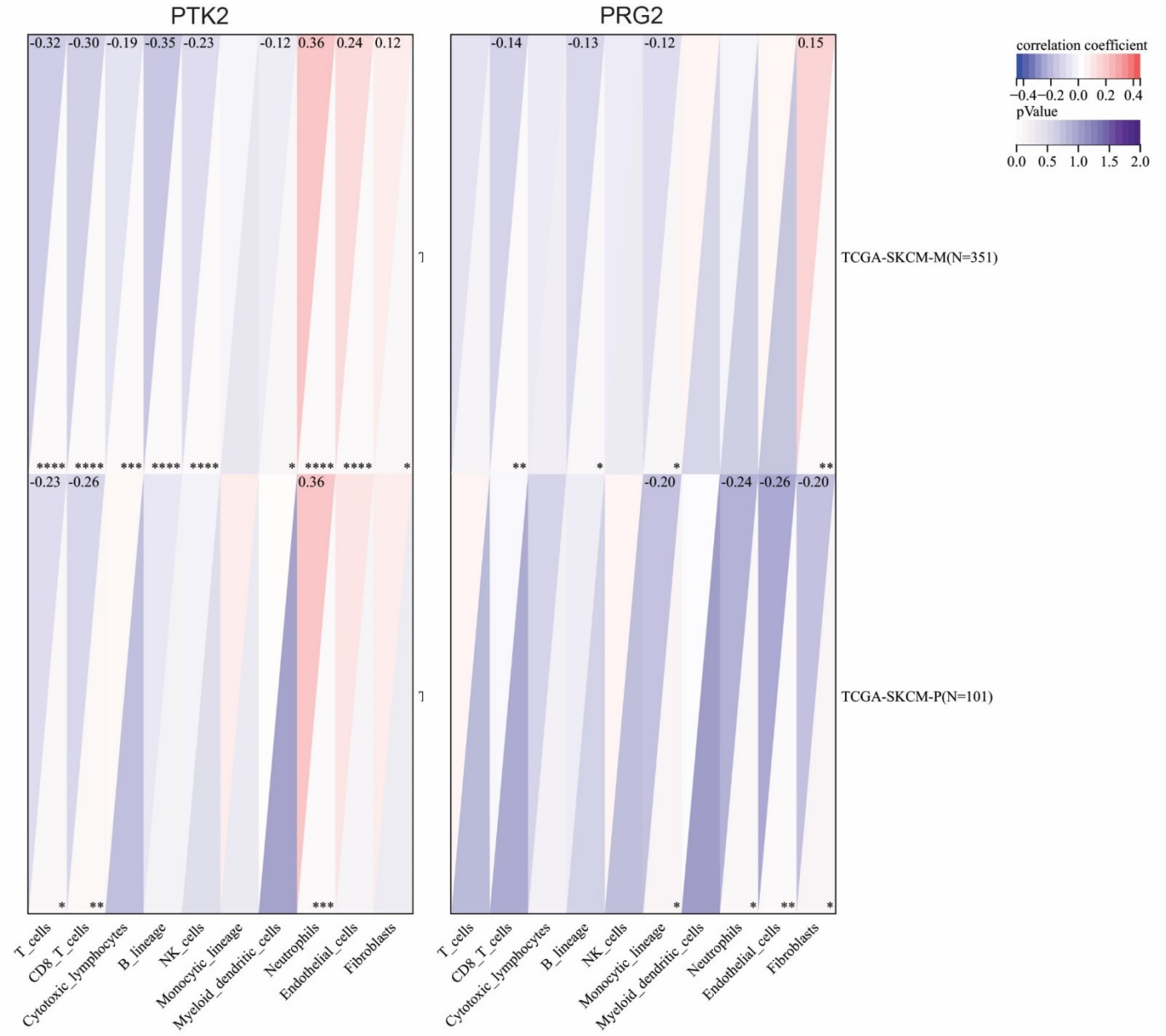

Figure S6. Spearman's correlation analysis between the expression of *PTK2* (or *PRG2*) and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using MCPCounter. Asterisks denote statistical significance: *, p<0.05; **, p<0.01; ***, p<0.005; ****, p<0.001.

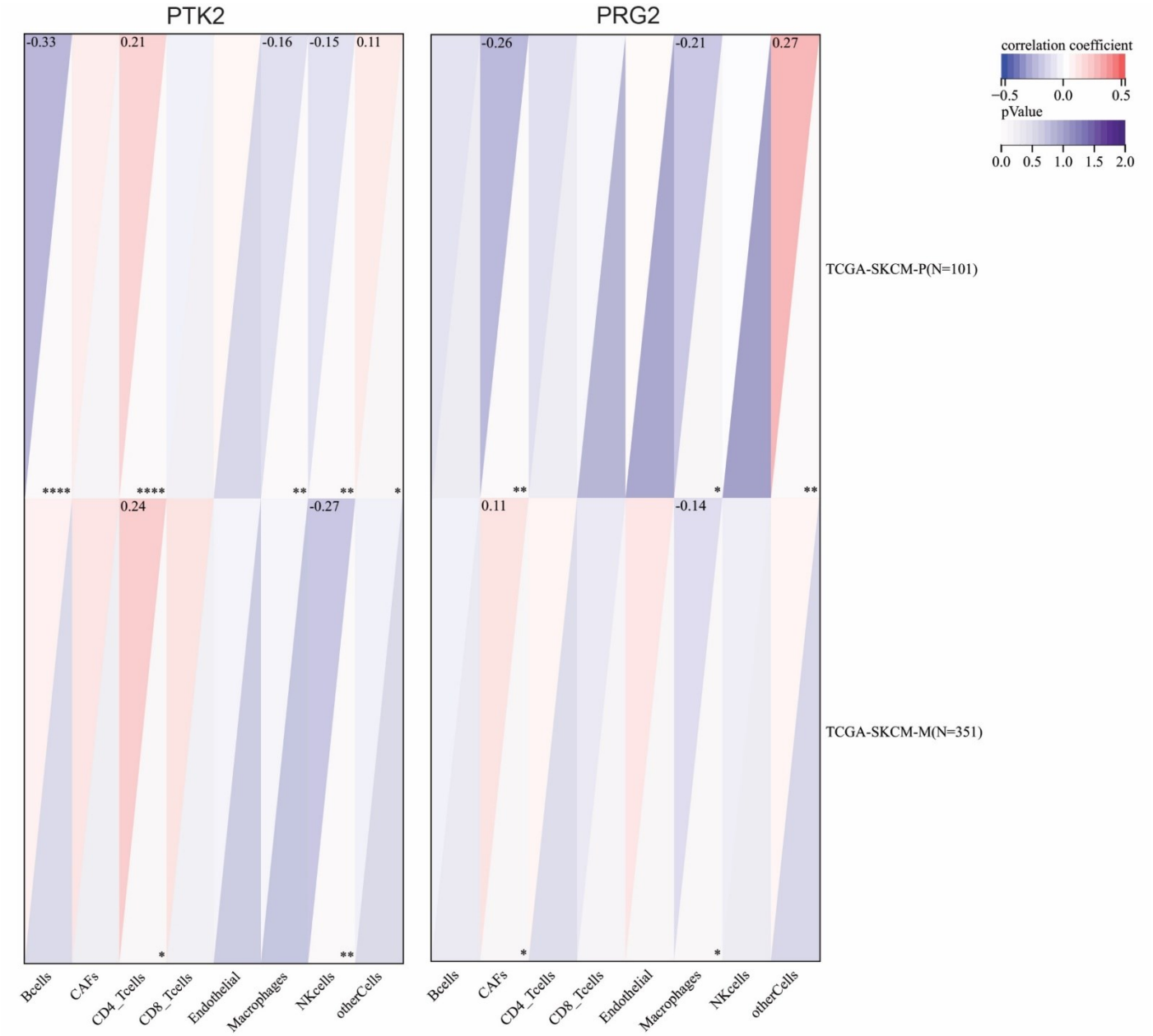

Figure S7. Spearman's correlation analysis between the expression of *PTK2* (or *PRG2*) and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using EPIC. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

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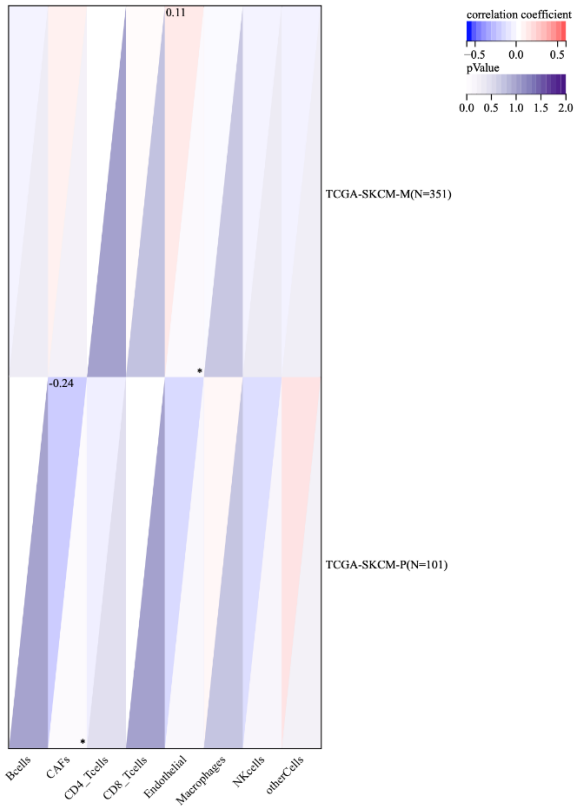

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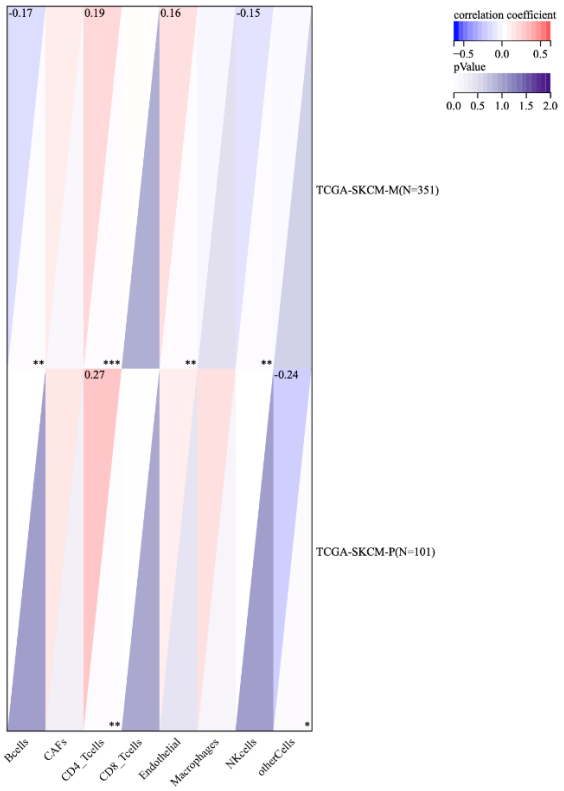

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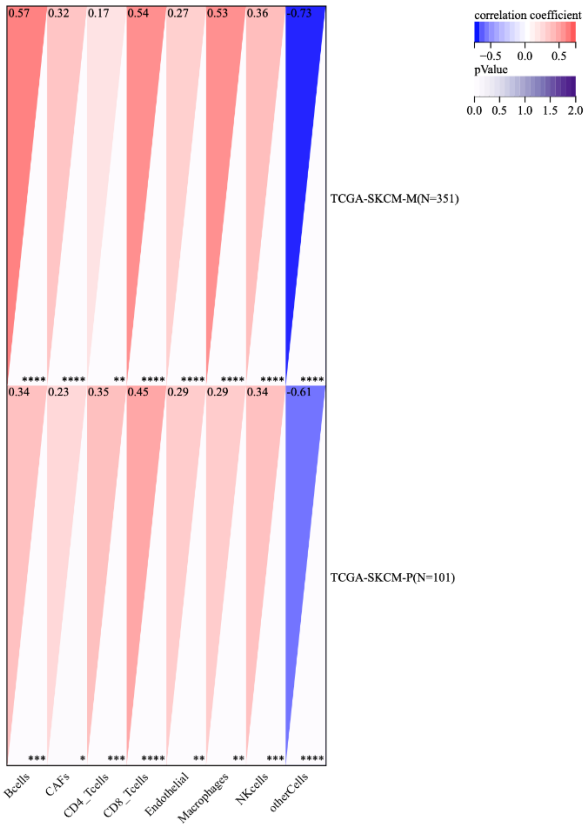

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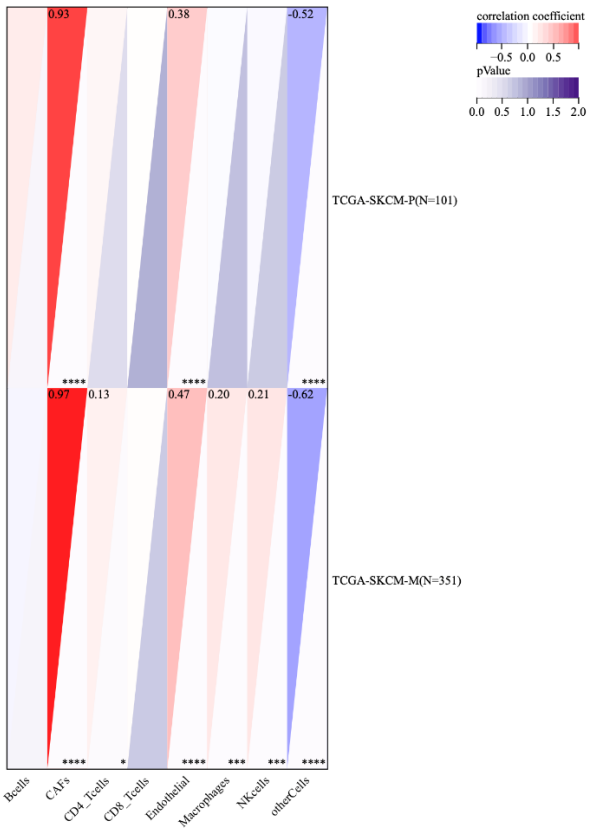

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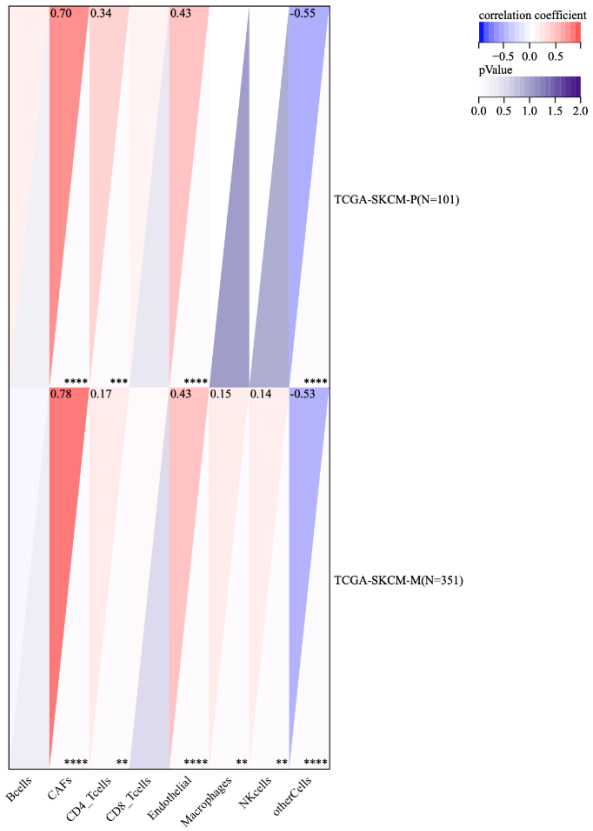

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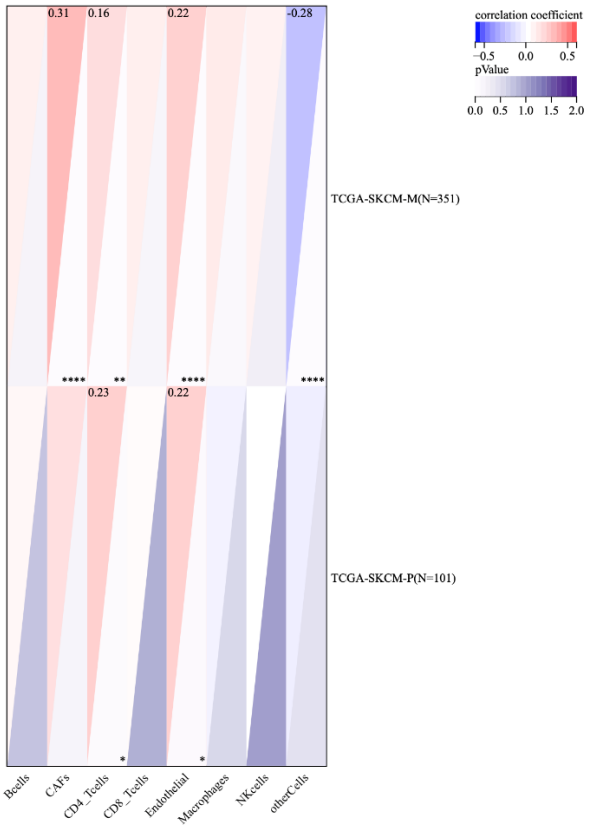

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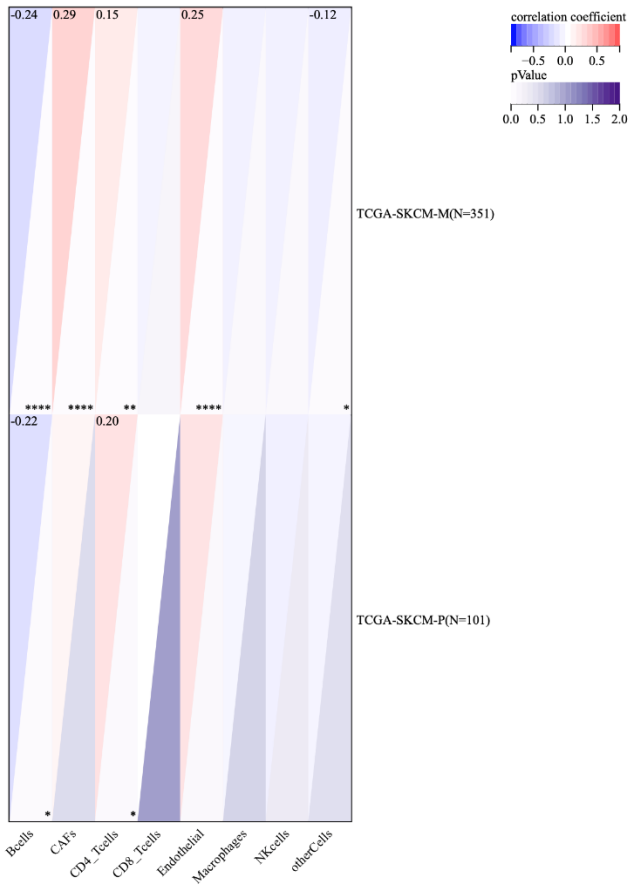

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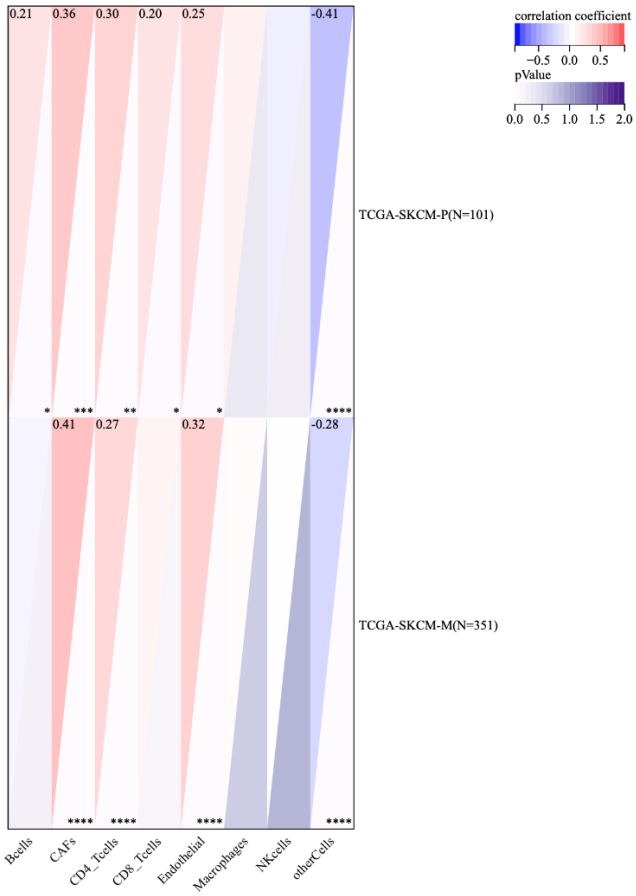

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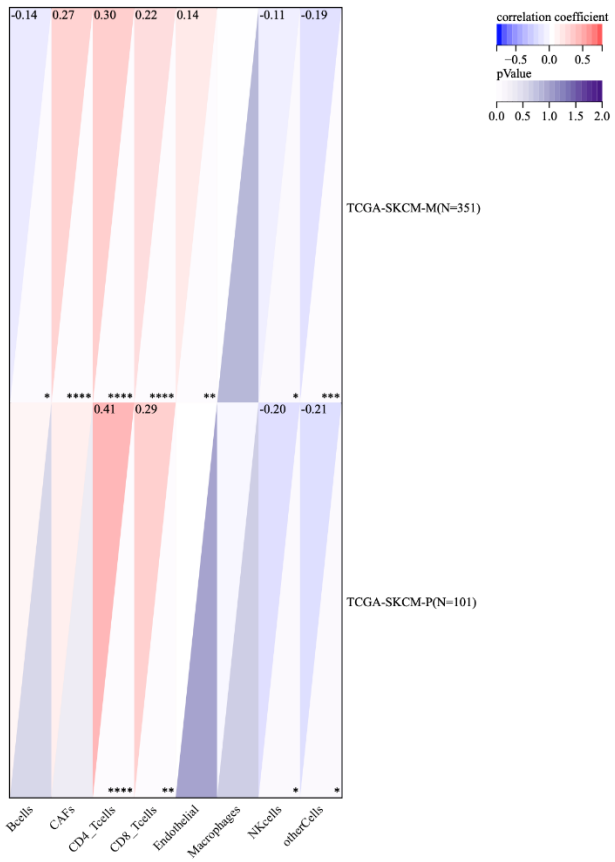

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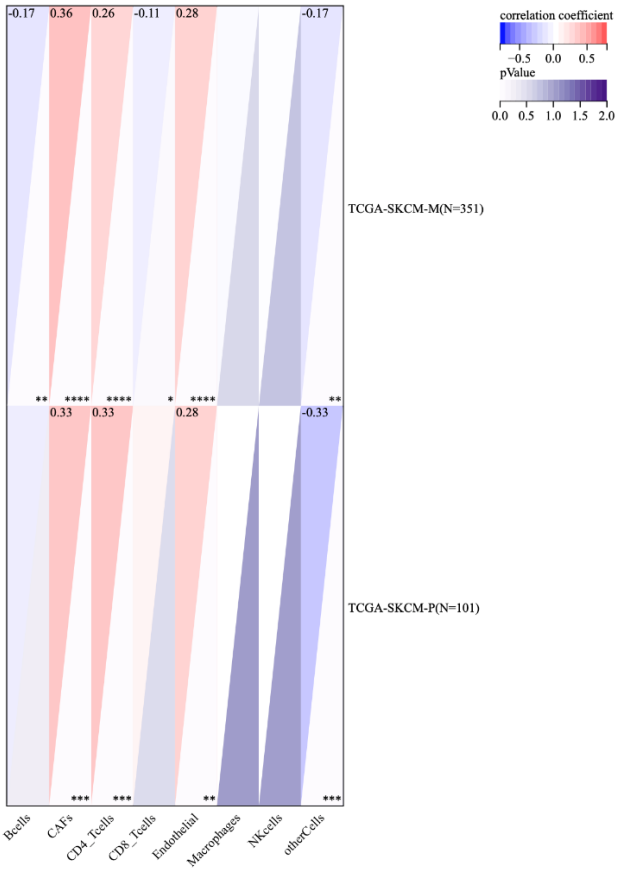

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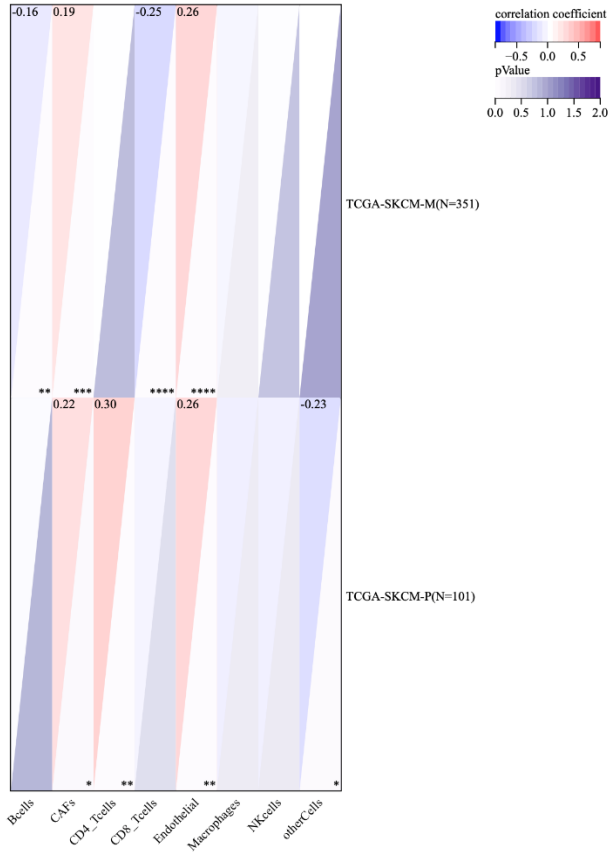

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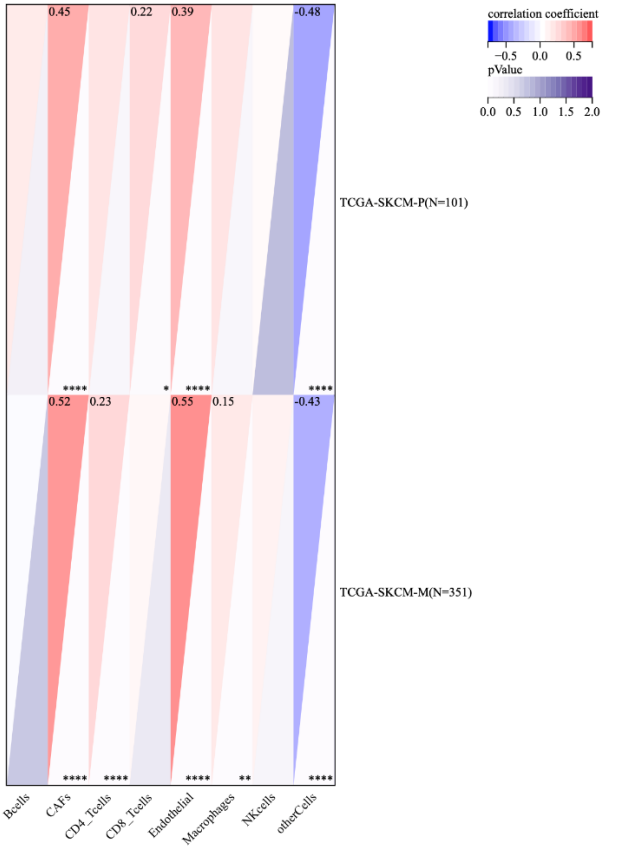

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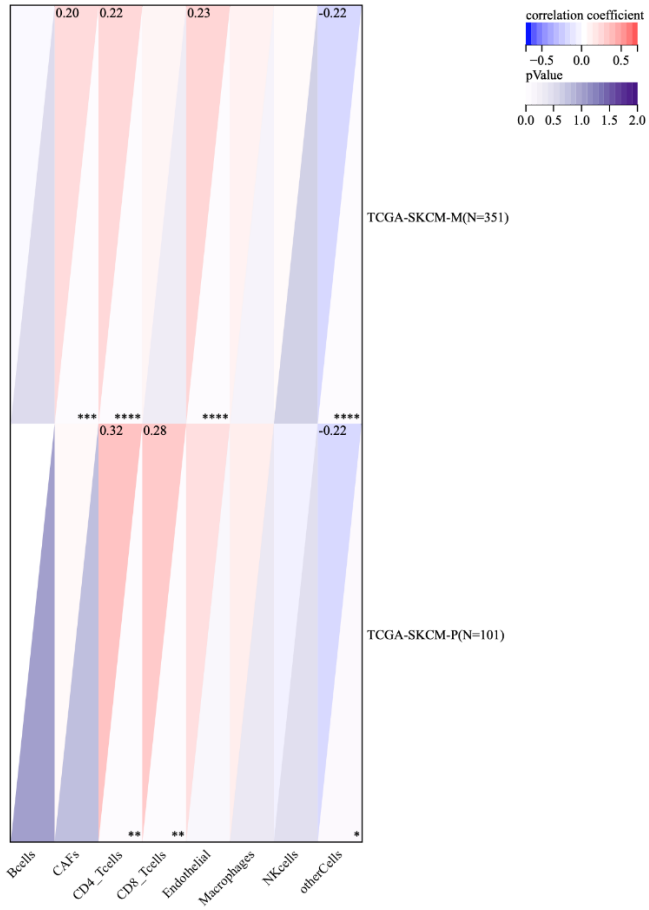

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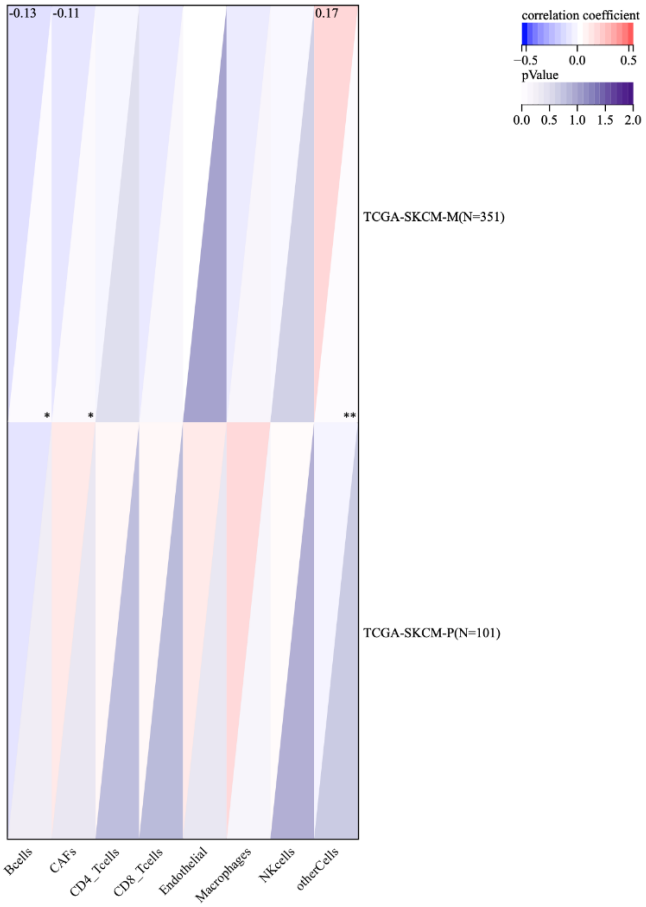

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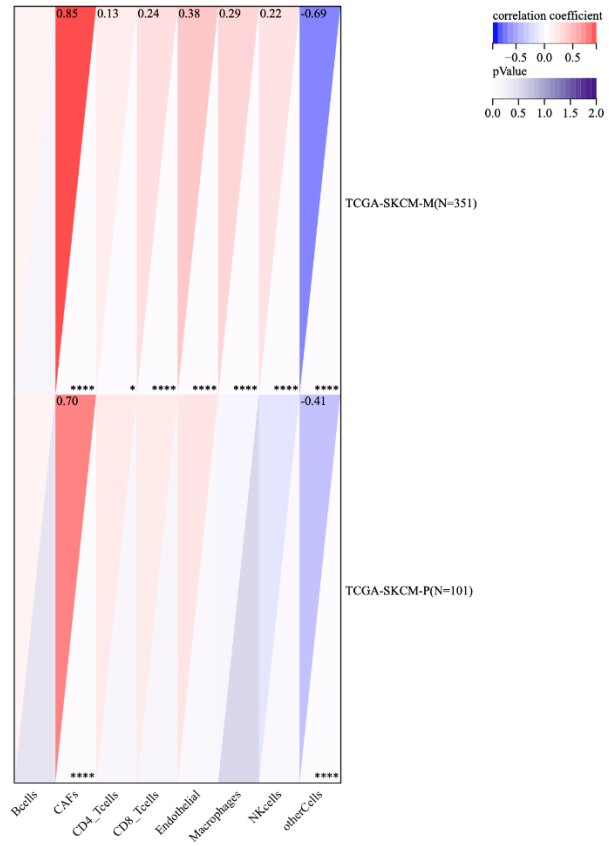

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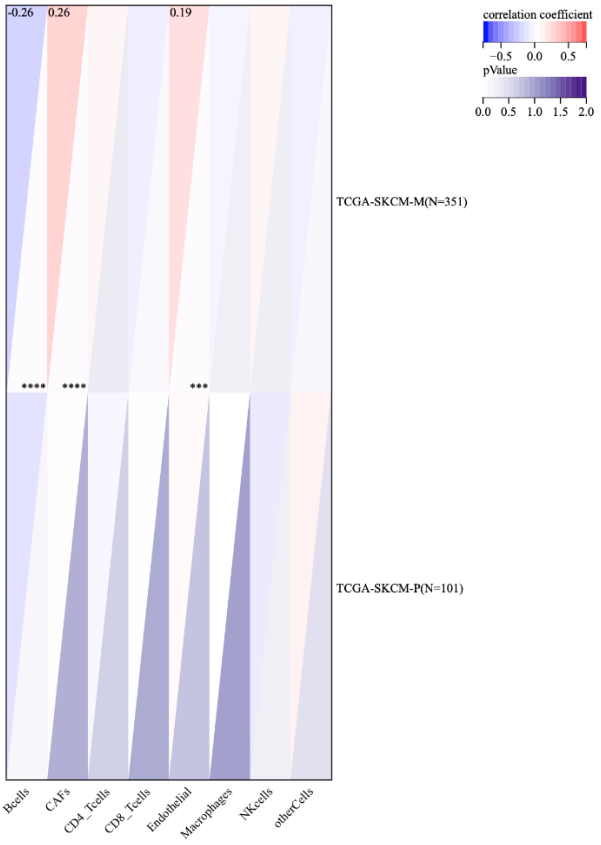

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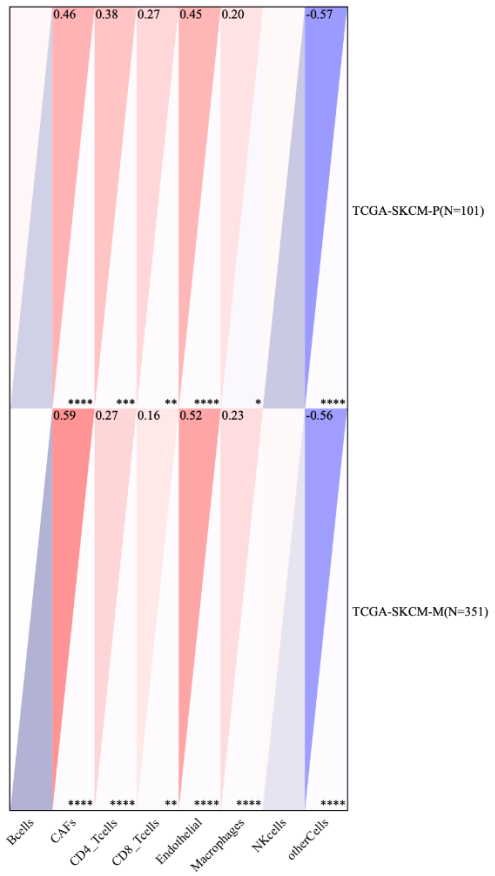

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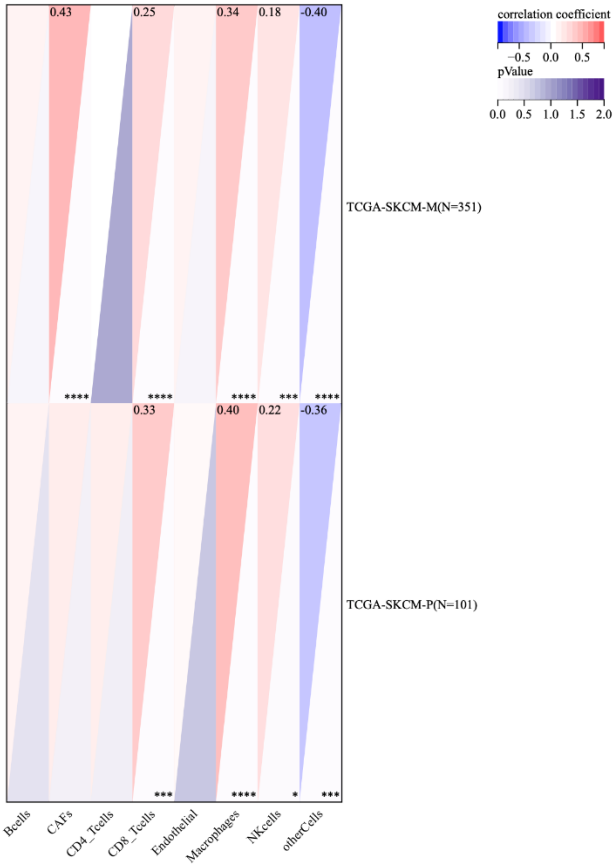

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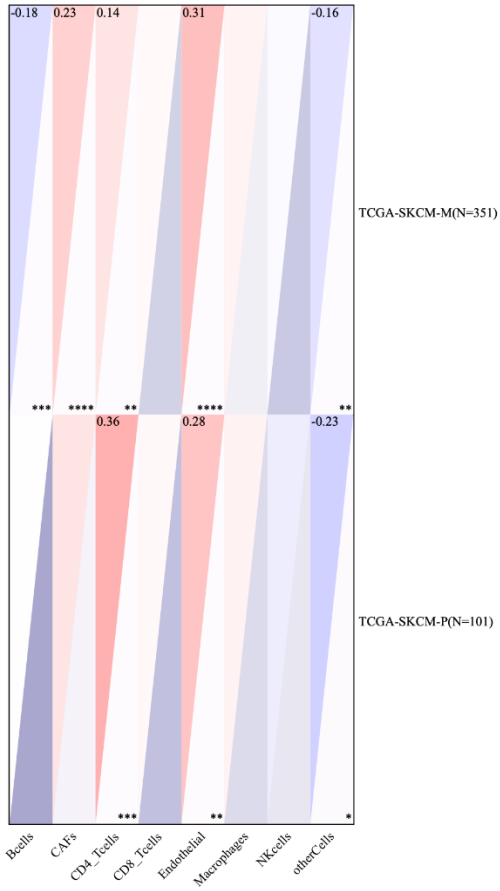

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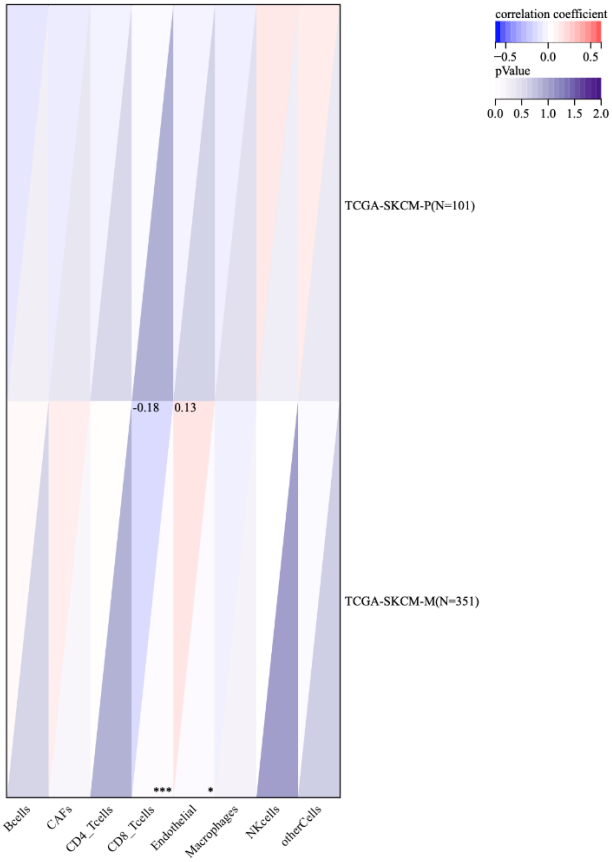

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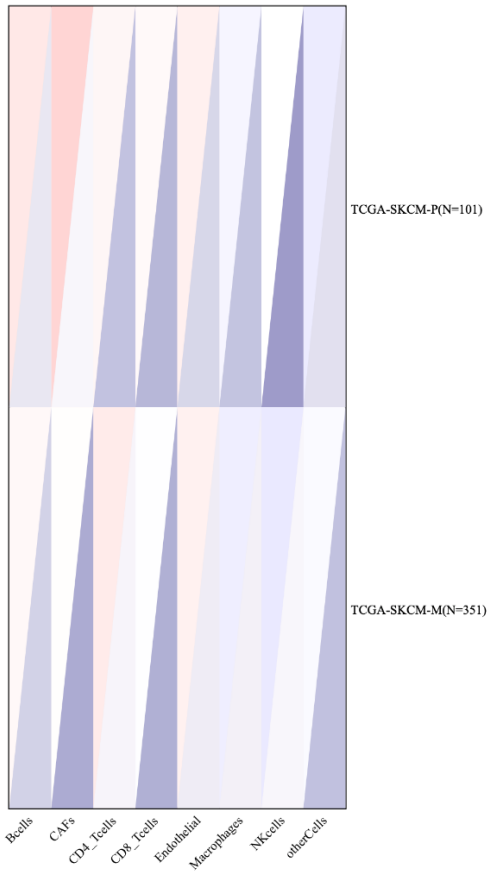

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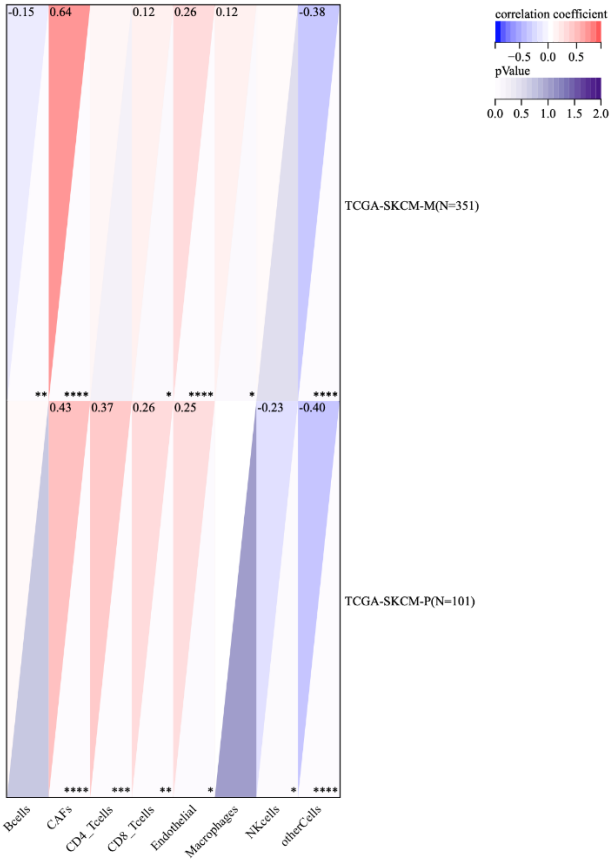

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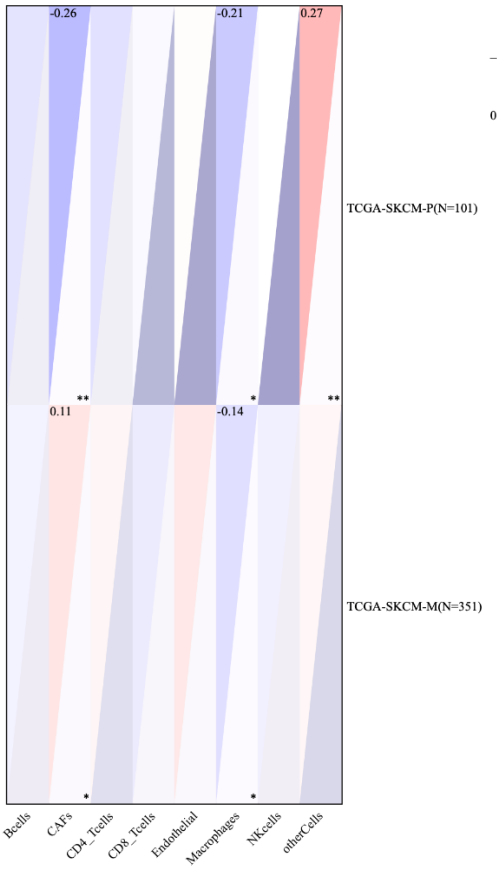

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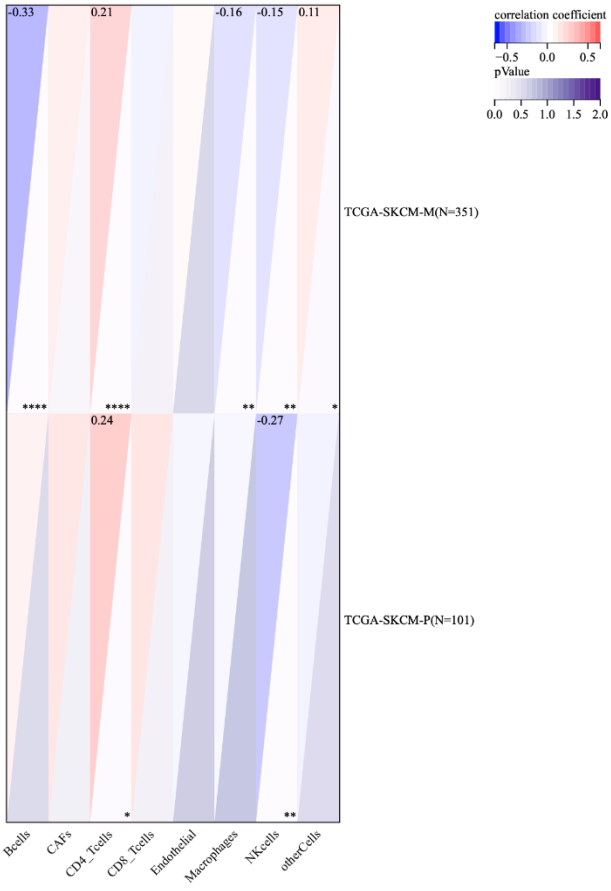

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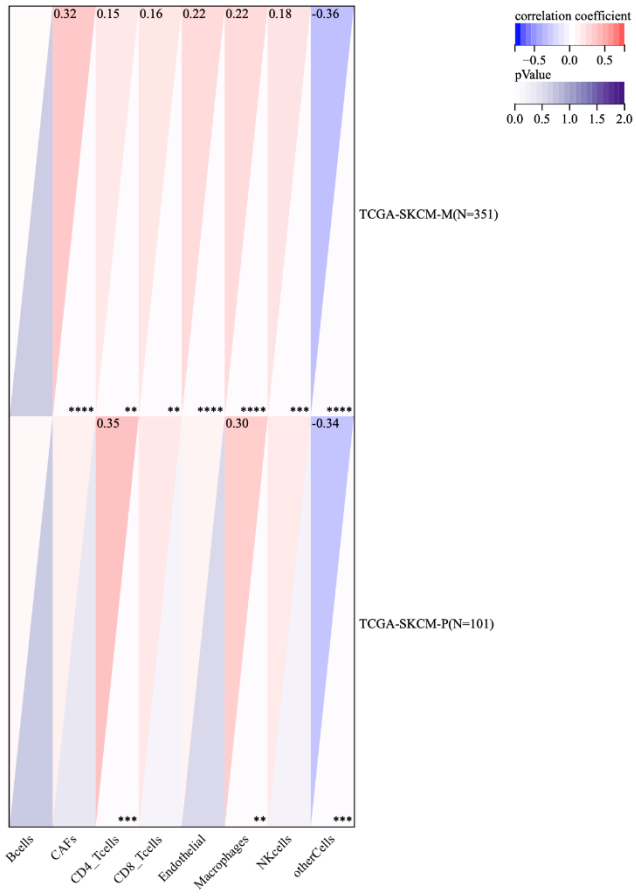

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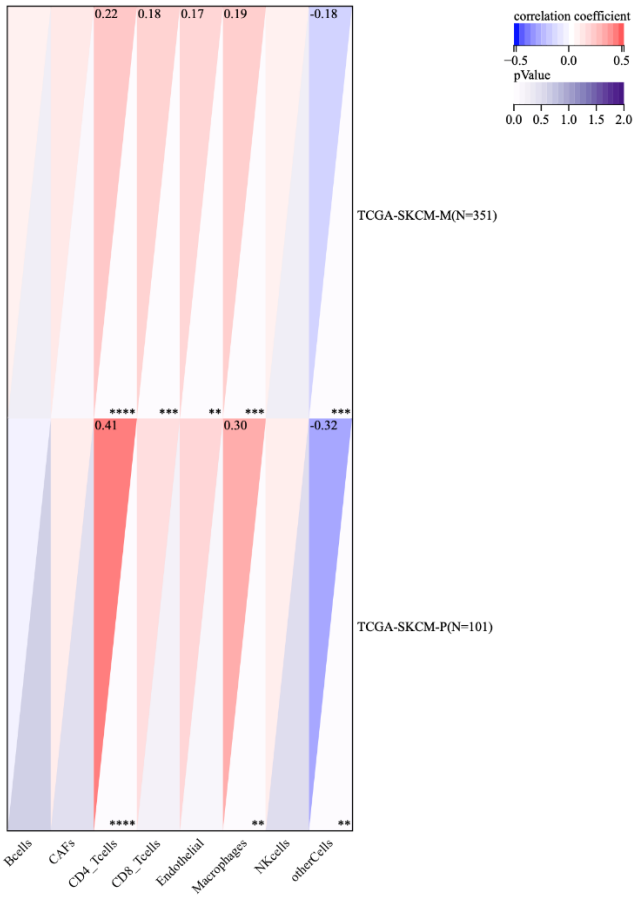

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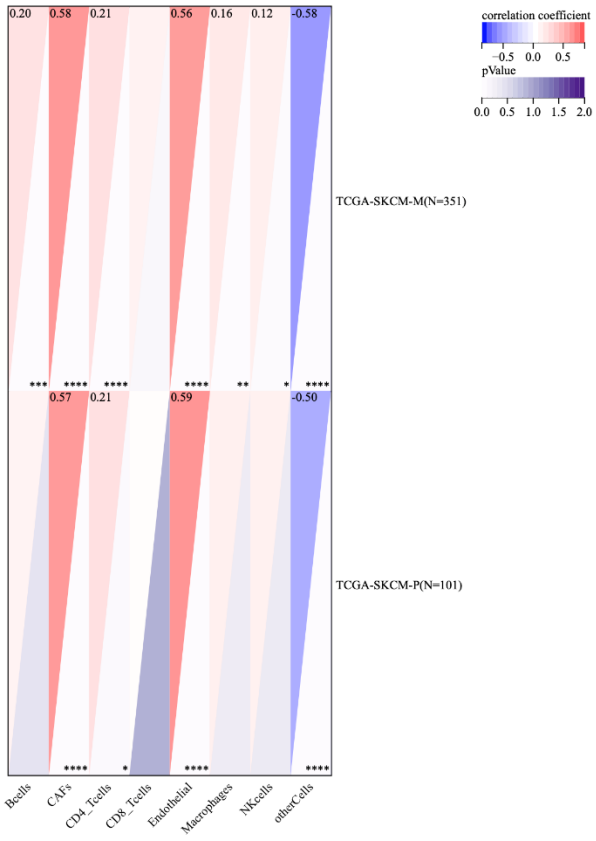

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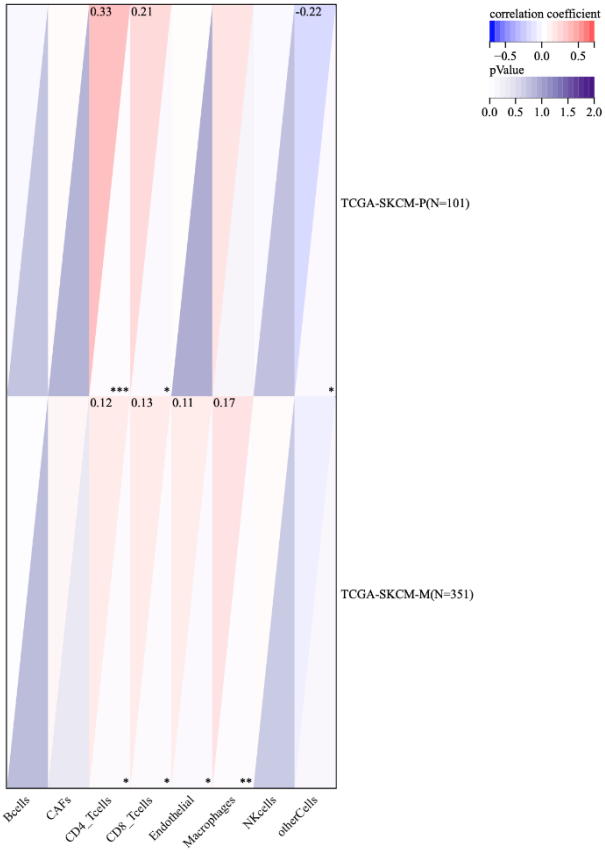

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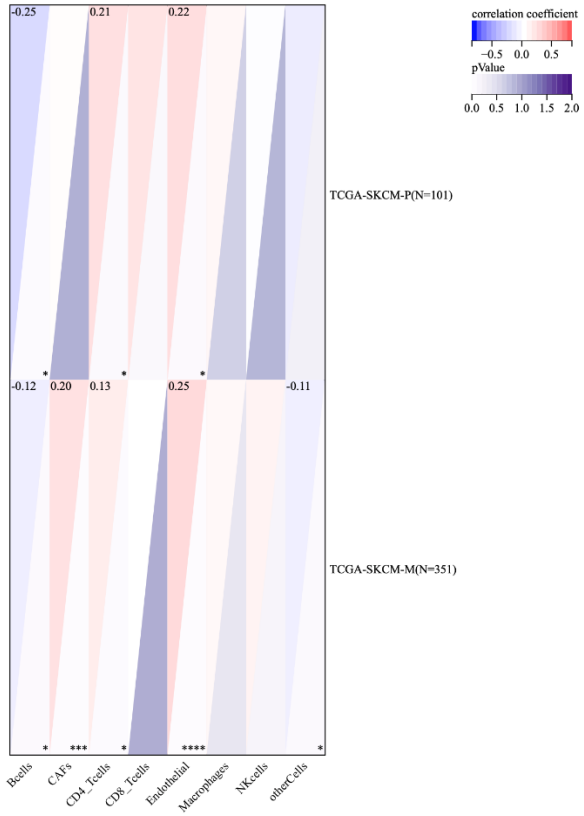

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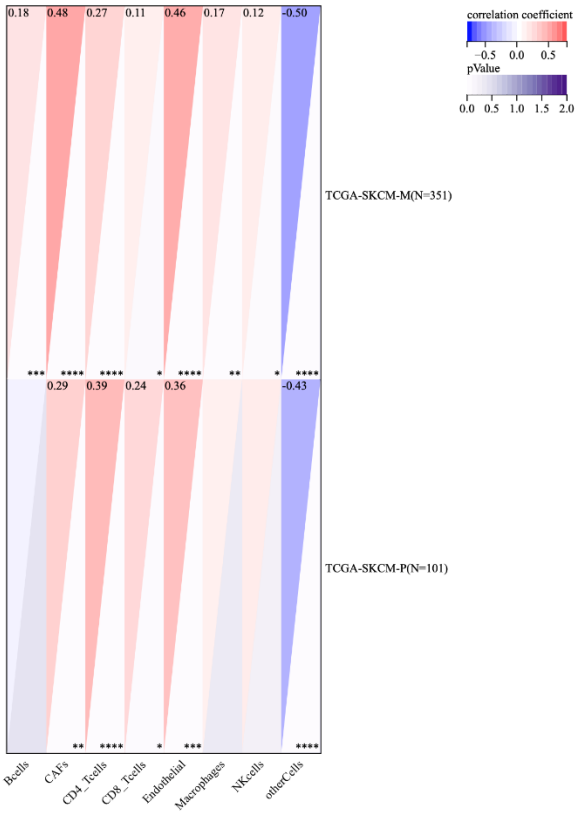

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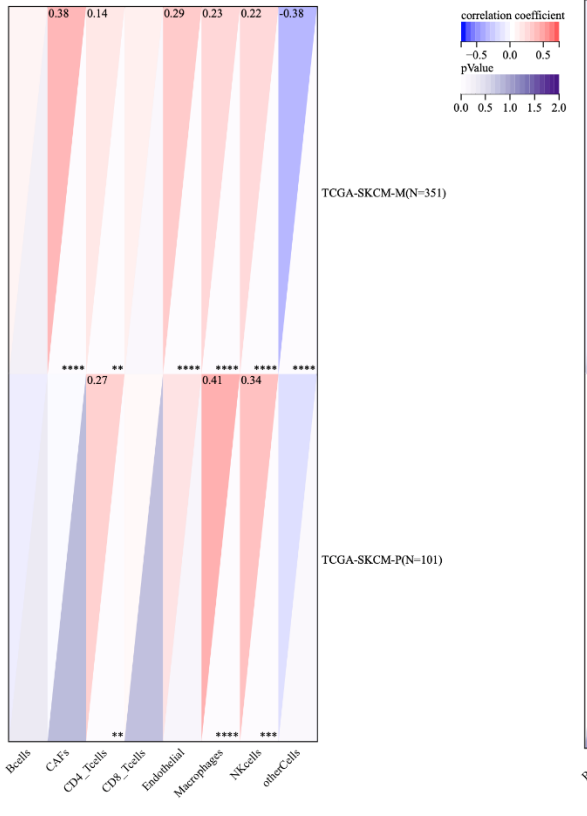

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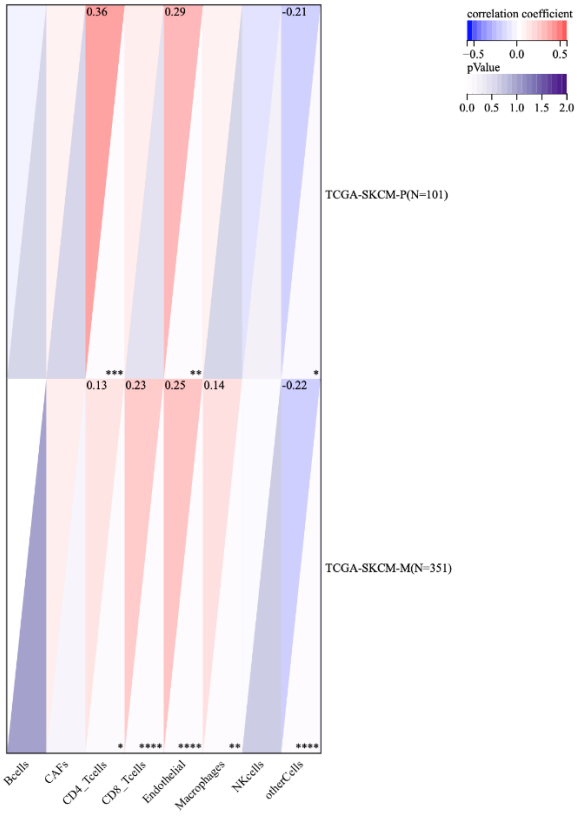

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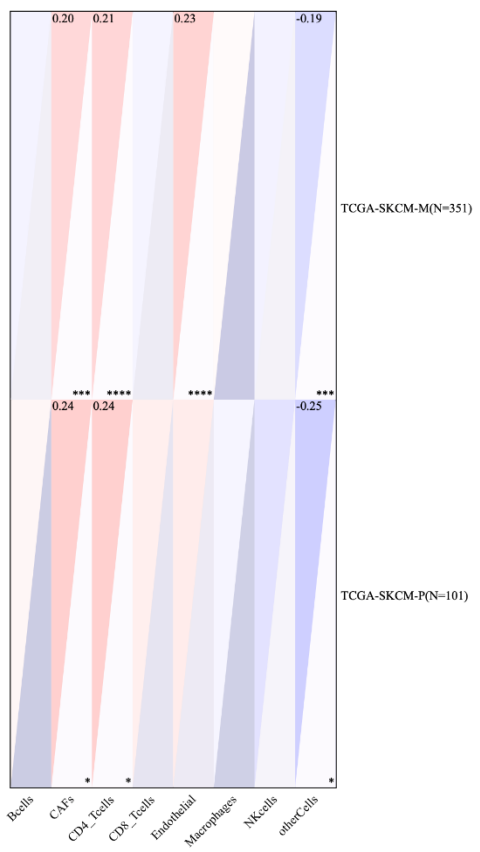

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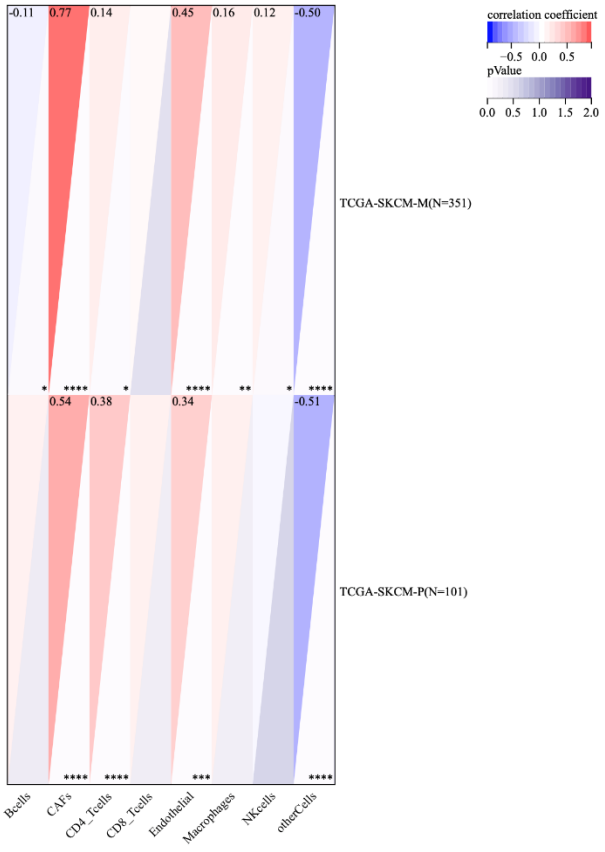

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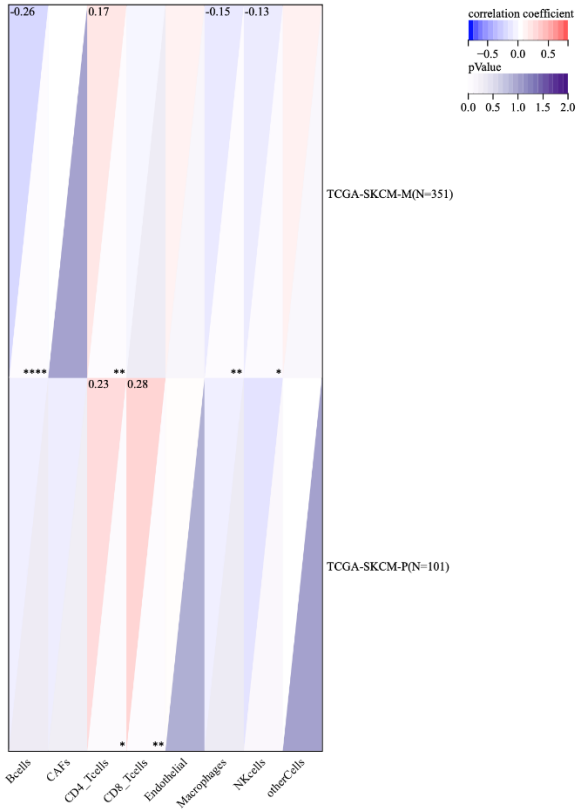

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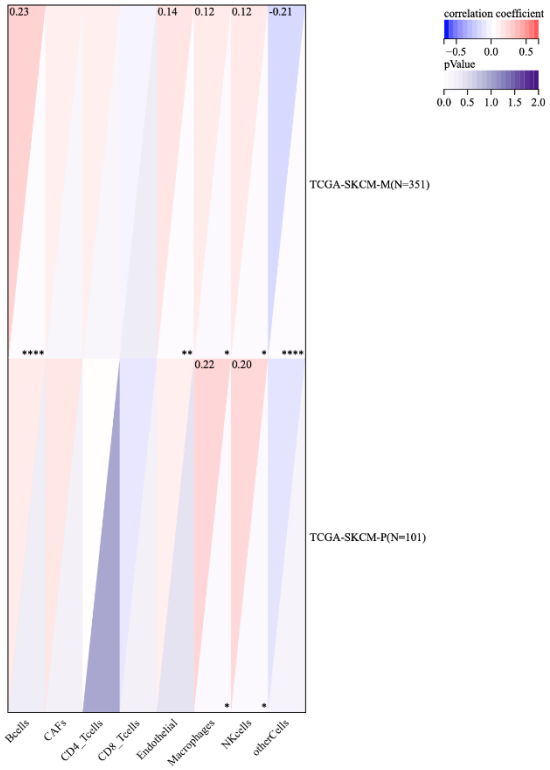


Figure S8. Spearman's correlations between the expression of ARGs and the infiltration in different immune cells in primary and metastatic skin melanoma, using EPIC. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

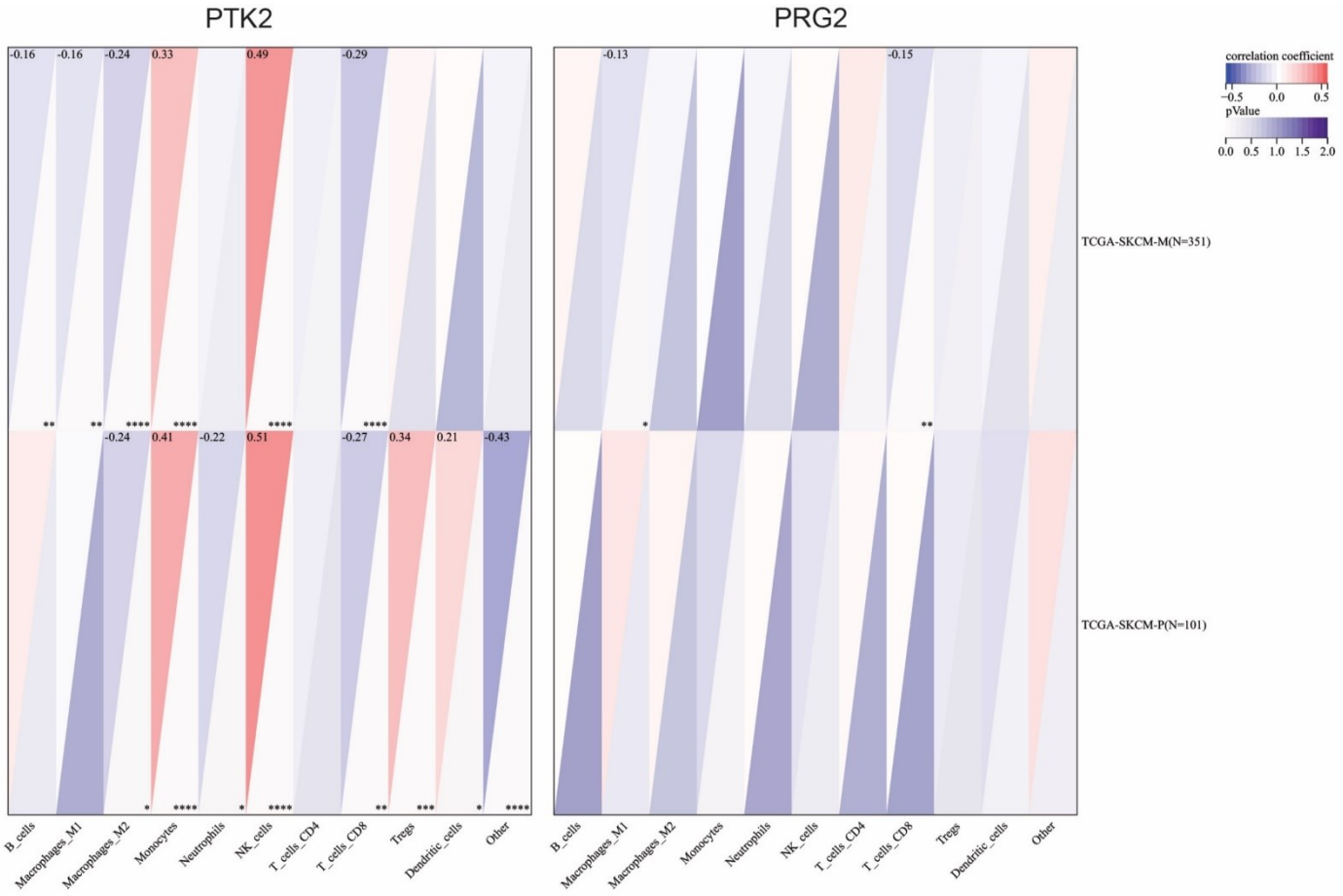
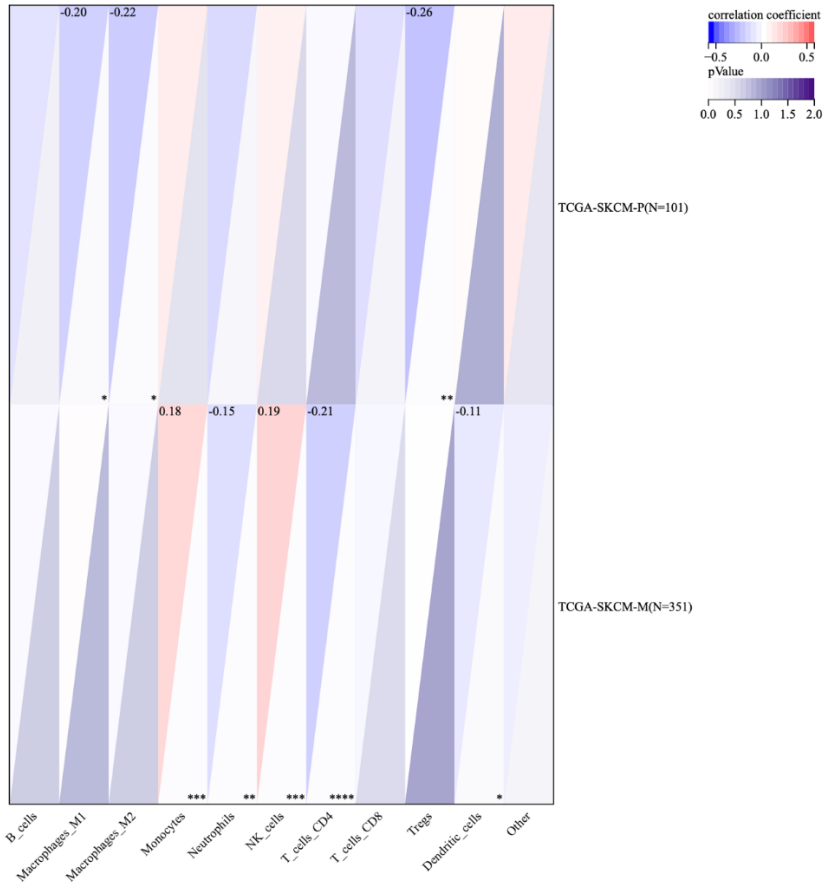


Figure S9 Spearman's correlation analysis between the expression of *PTK2* (or *PRG2*) and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using QUANTISEC. Asterisks denote statistical significance: *, $p<0.05$; **, $p<0.01$; ***, $p<0.005$; ****, $p<0.001$.

APOH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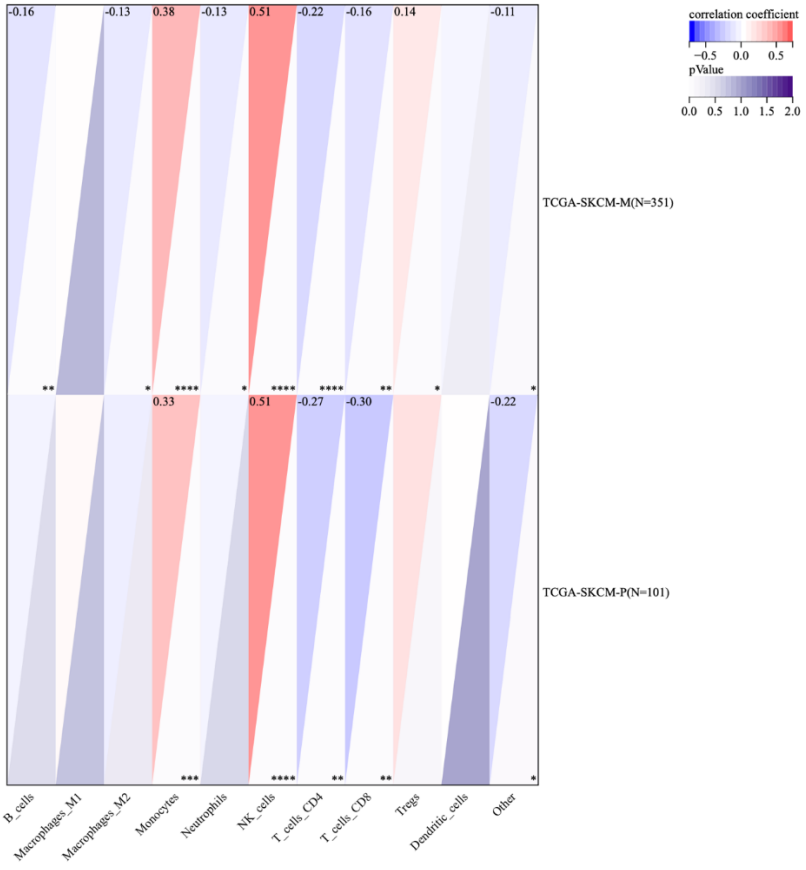
pValue
0.0 0.5 1.0 1.5 2.0
-0.20 -0.22 -0.26
0.18 -0.15 0.19 -0.21 -0.11
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

APP


correlation coefficient
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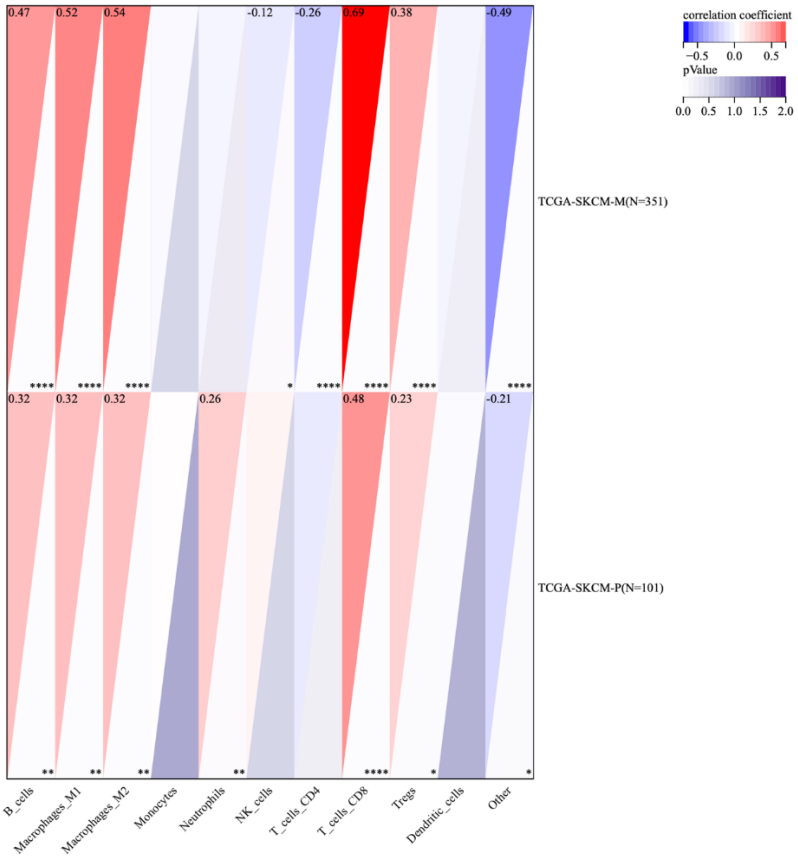
pValue
0.0 0.5 1.0 1.5 2.0
-0.16 -0.13 0.38 -0.13 0.51 -0.22 -0.16 0.14 -0.11
0.33 0.51 -0.27 -0.30 -0.22
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

CCND2



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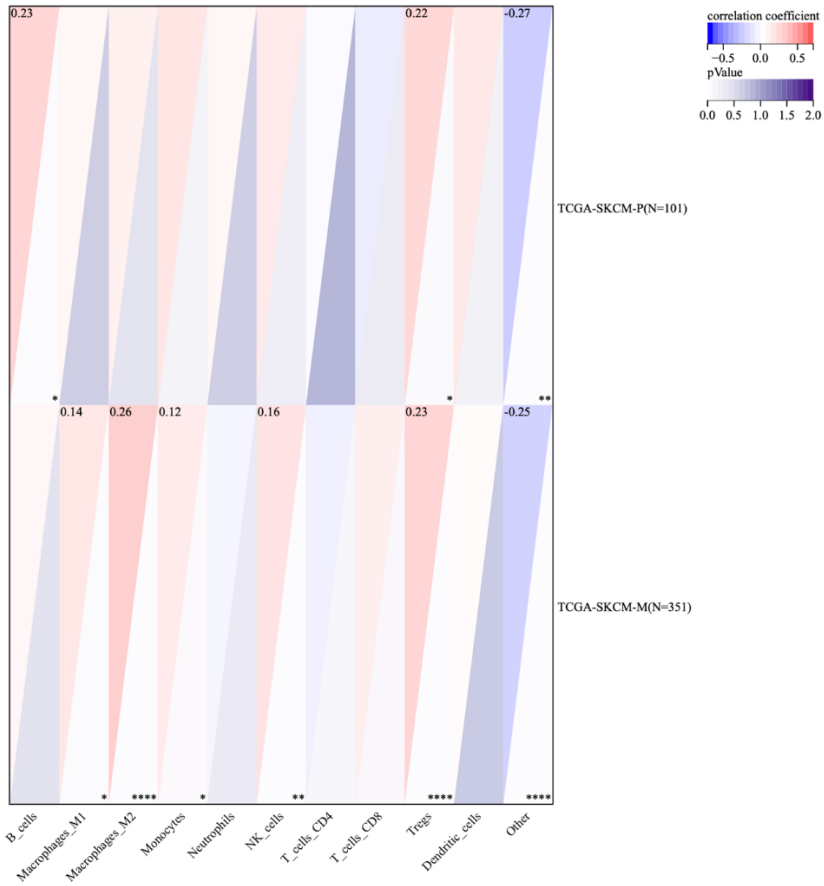

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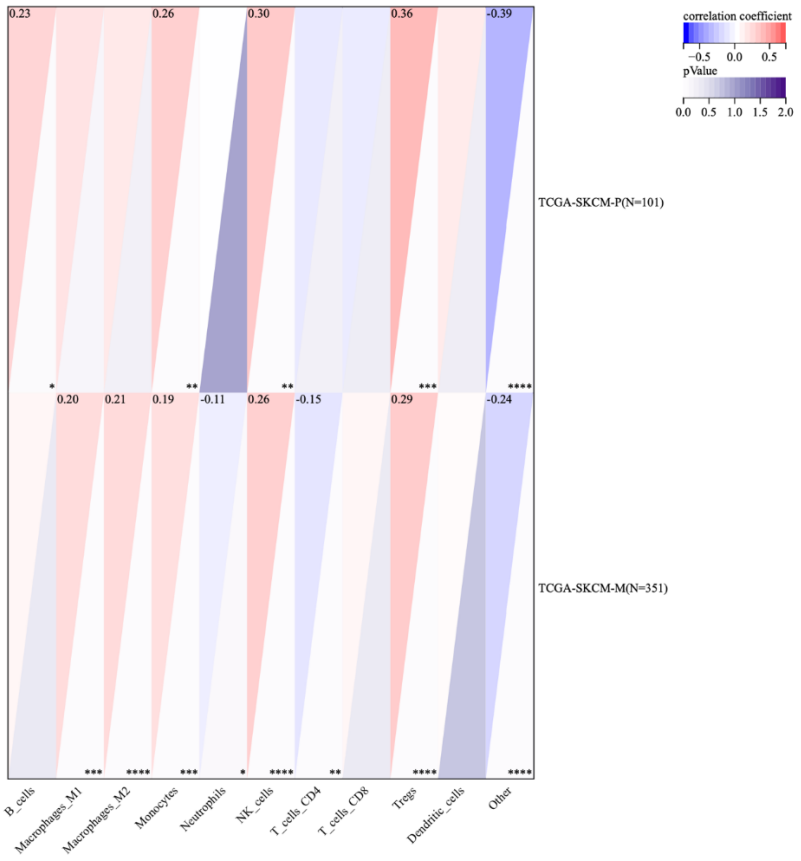

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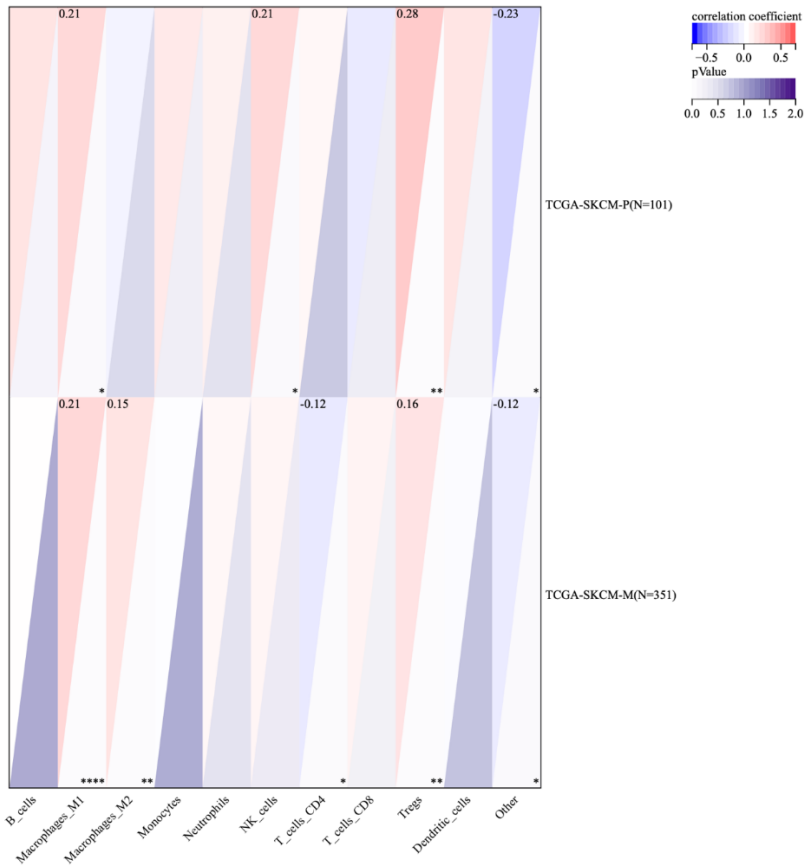

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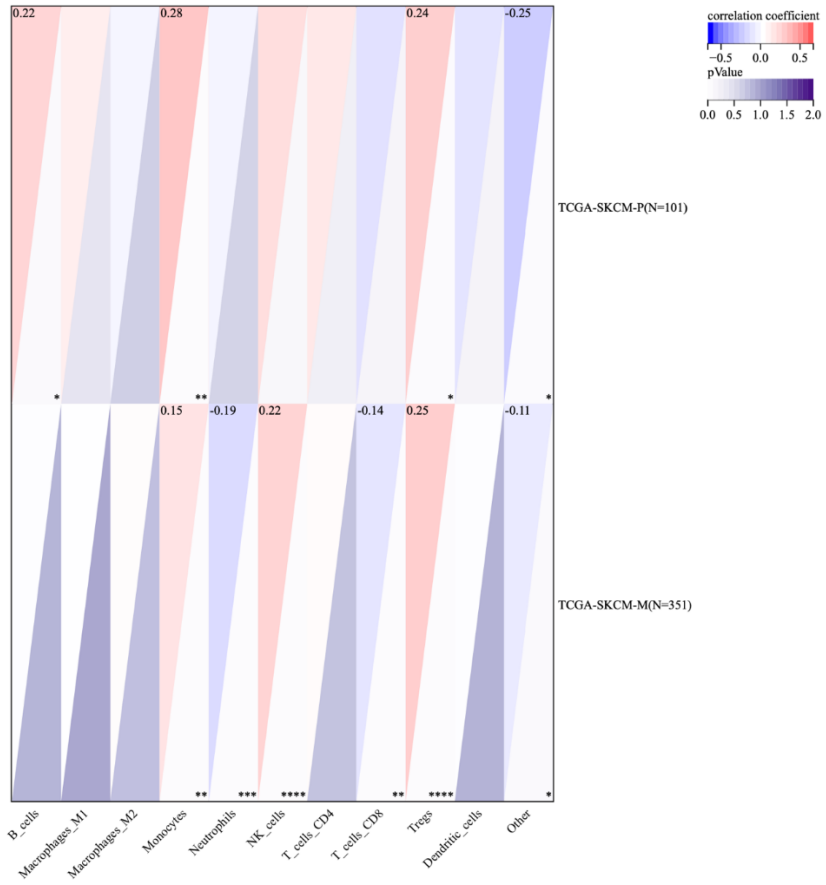
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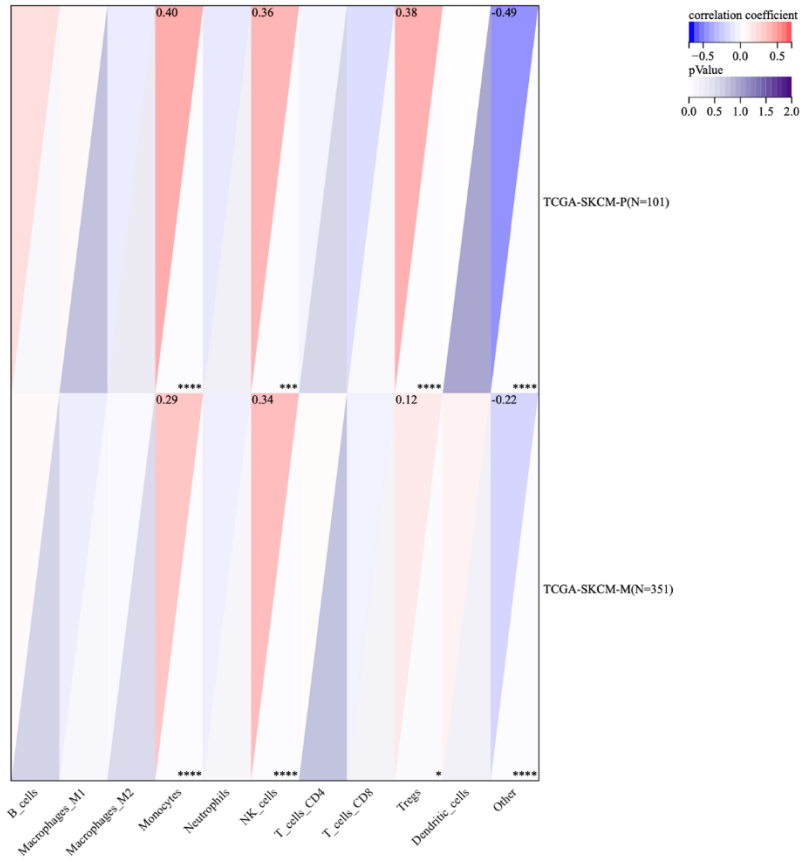
pValue
0.0 0.5 1.0 1.5 2.0
0.22
0.28
0.24
-0.25
TCGA-SKCM-P(N=101)
0.15
-0.19
0.22
-0.14
0.25
-0.11
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

FSTL1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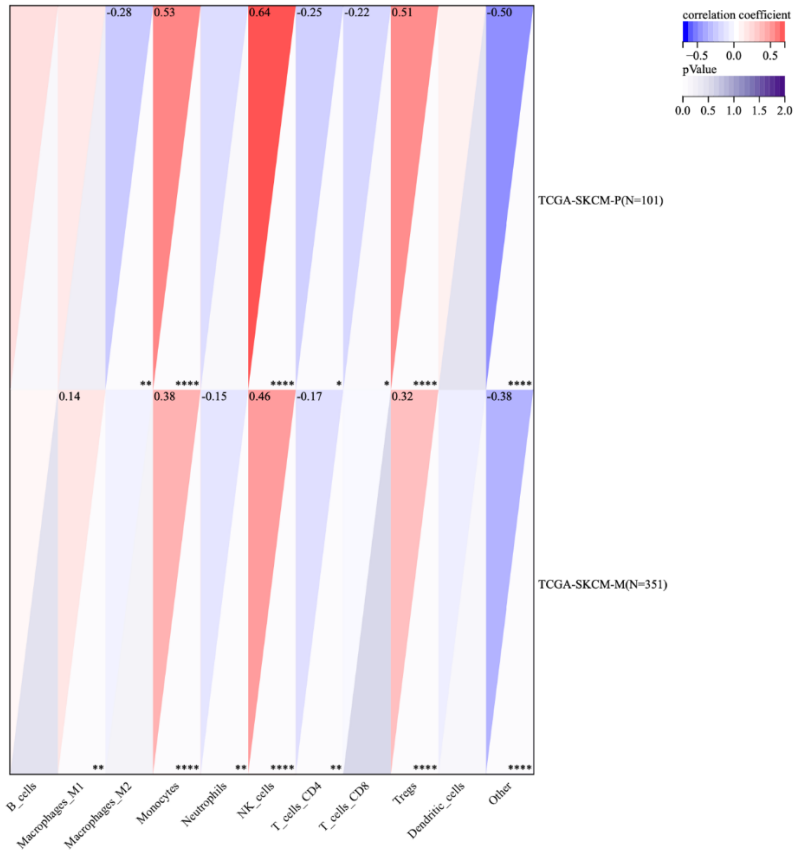
pValue
0.0 0.5 1.0 1.5 2.0
0.40
0.36
0.38
-0.49
TCGA-SKCM-P(N=101)
0.29
0.34
0.12
-0.22
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

ITGAV


correlation coefficient
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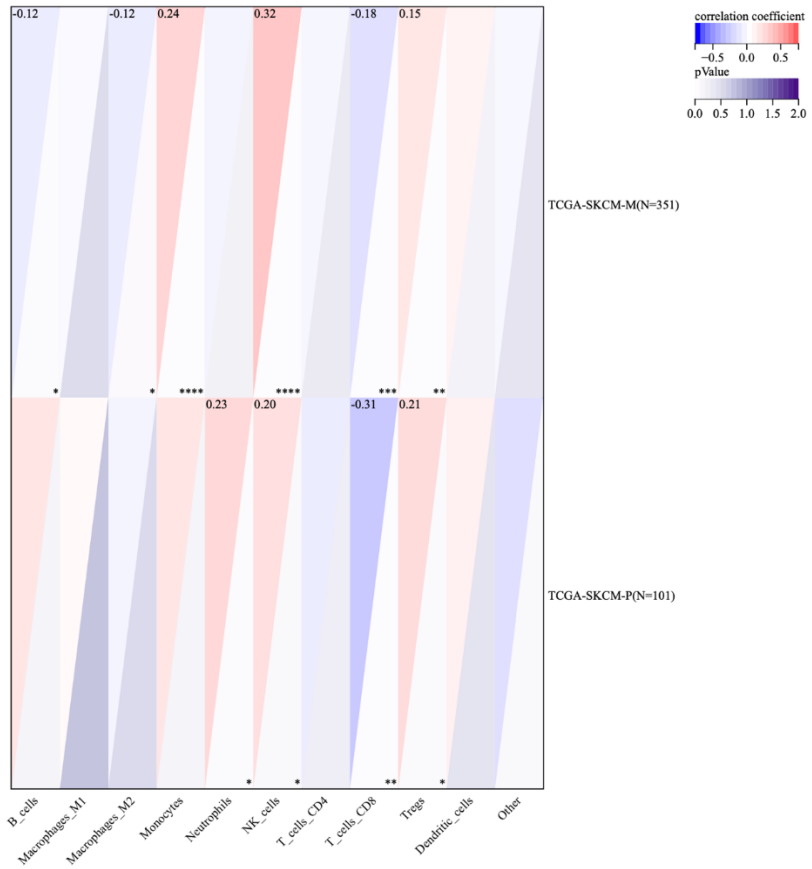
pValue
0.0 0.5 1.0 1.5 2.0
-0.28 0.53 0.64 -0.25 -0.22 0.51 -0.50
0.14 0.38 -0.15 0.46 -0.17 0.32 -0.38
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

JAG1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pValue
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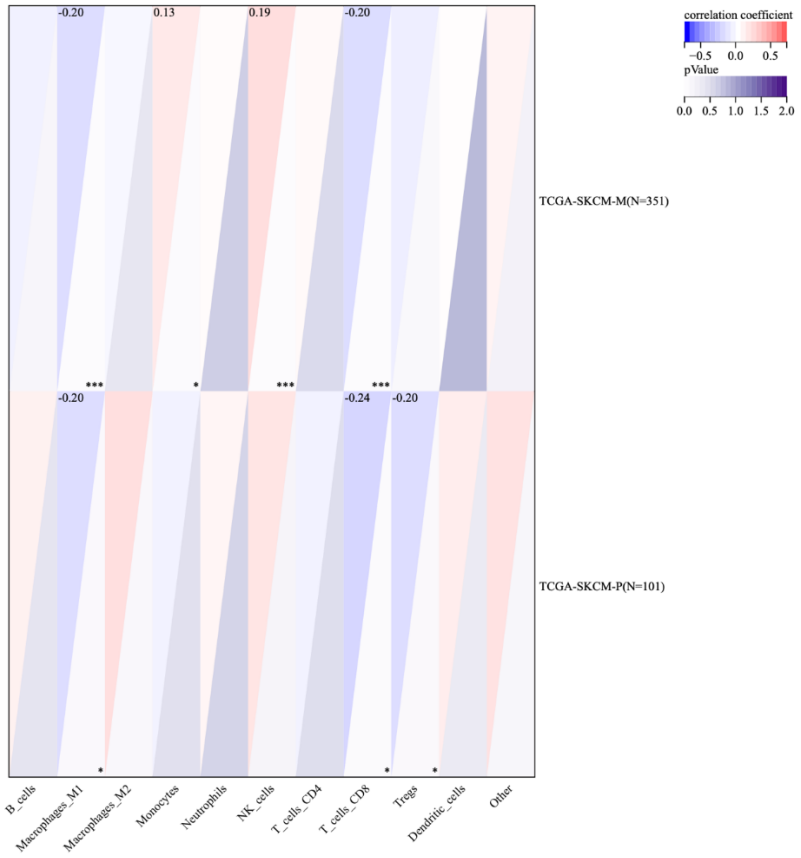
-0.12 -0.12 0.24 0.32 -0.18 0.15
0.23 0.20 -0.31 0.21
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

JAG2


correlation coefficient
−0.5 0.0 0.5
pValue
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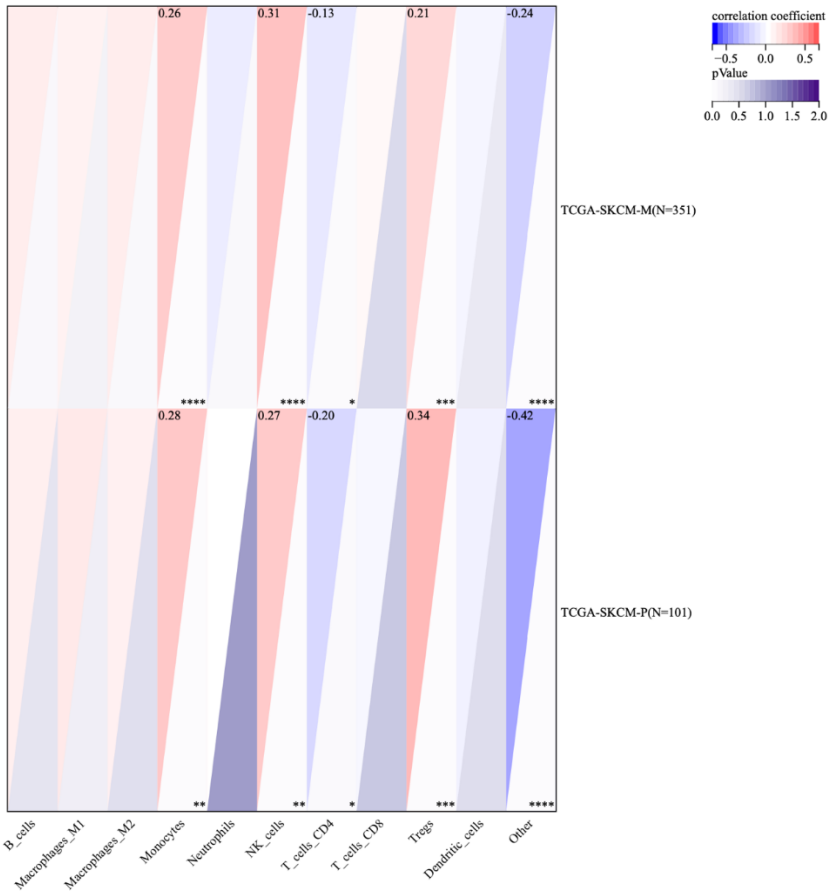
-0.20 0.13 0.19 -0.20
*** * *** ***
-0.20 -0.24 -0.20
* * *
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

KCNJ8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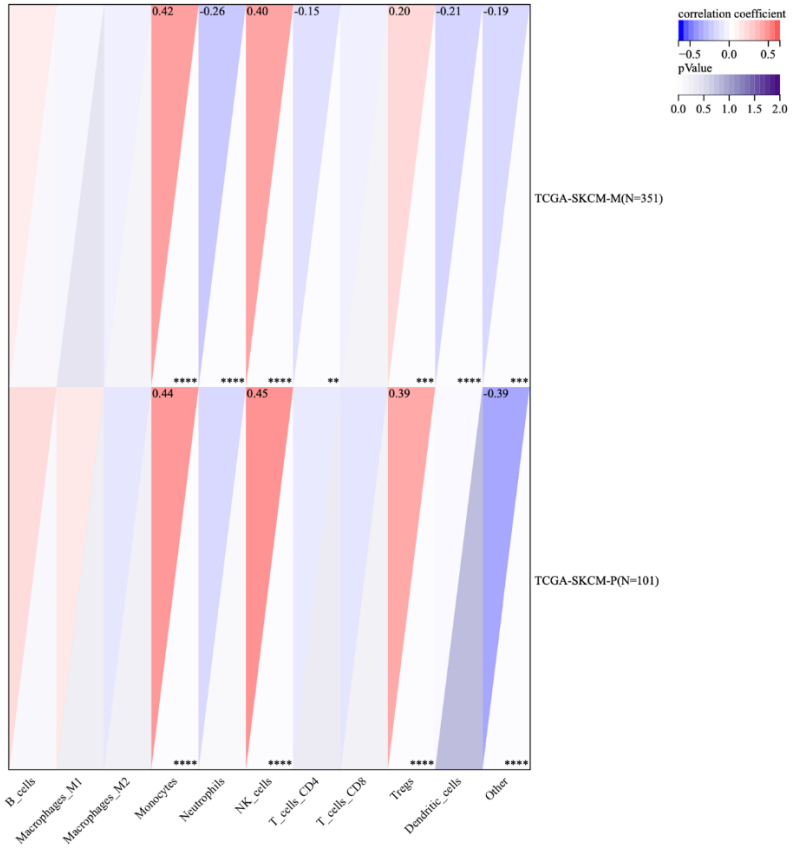
pValue
0.0 0.5 1.0 1.5 2.0
0.26 0.31 -0.13 0.21 -0.24
**** **** * *** ****
0.28 0.27 -0.20 0.34 -0.42
** ** * *** ****
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

LPL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pValue
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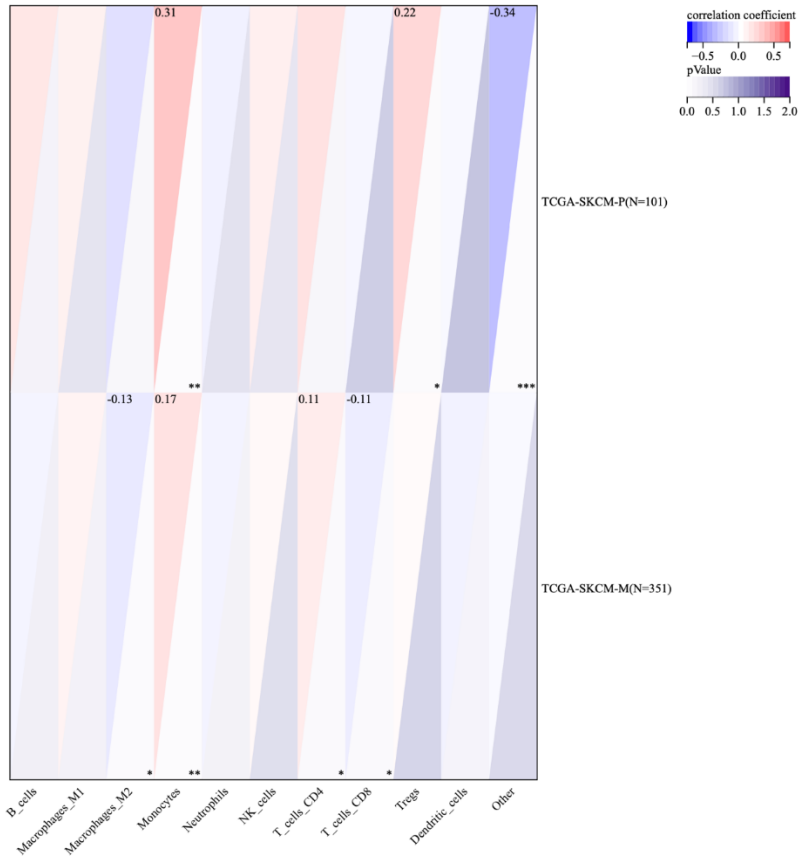
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

LRPAP1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pValue
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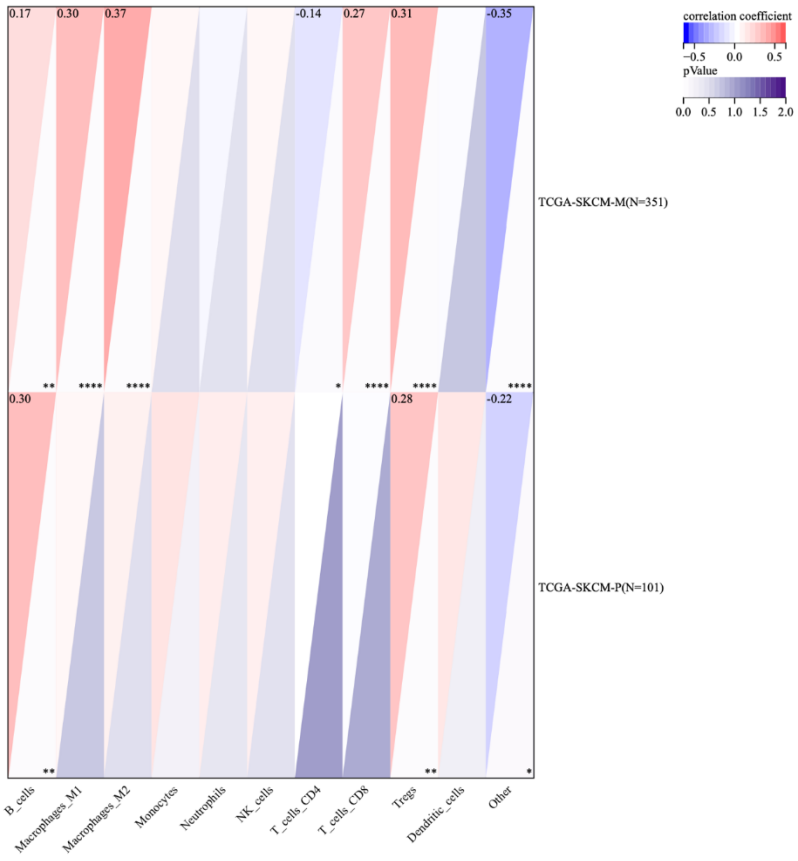
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

LUM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pValue
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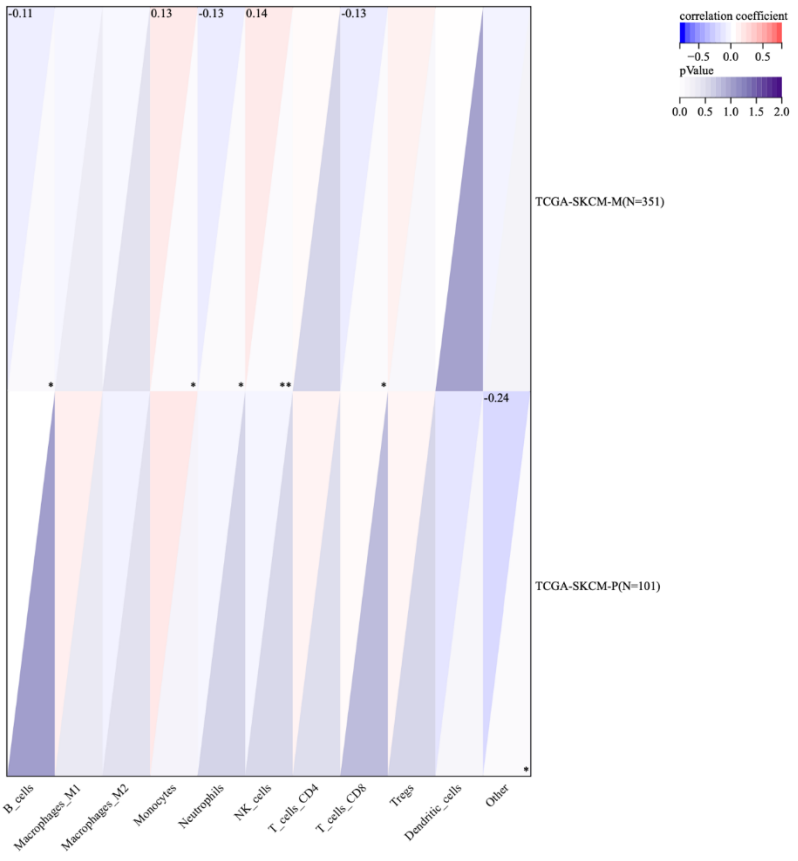
TCGA-SKCM-M(N=351)
0.30 0.28 -0.22
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

MSX1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pValue
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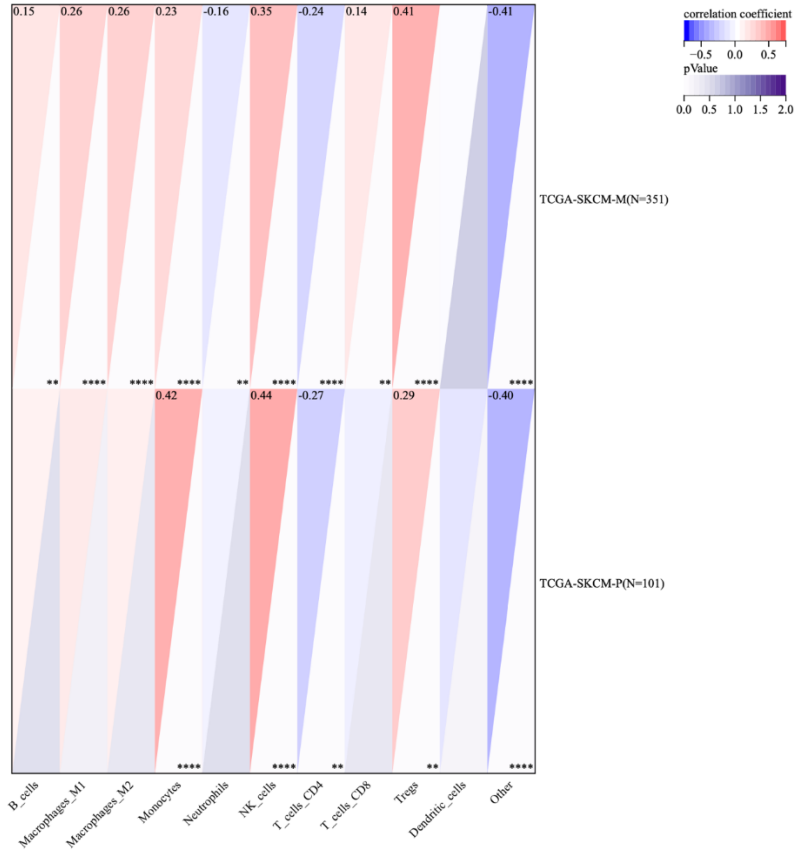
TCGA-SKCM-M(N=351)
-0.24
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

NRP1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pValue
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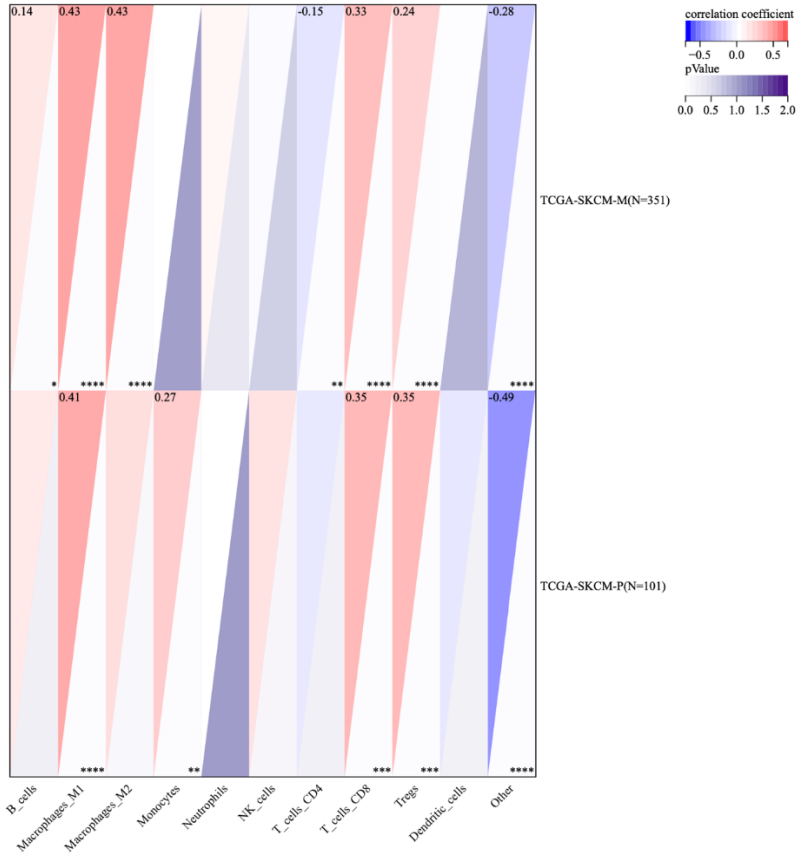
0.15 0.26 0.26 0.23 -0.16 0.35 -0.24 0.14 0.41 -0.41
0.42 0.44 -0.27 0.29 -0.40
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

OLR1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pValue
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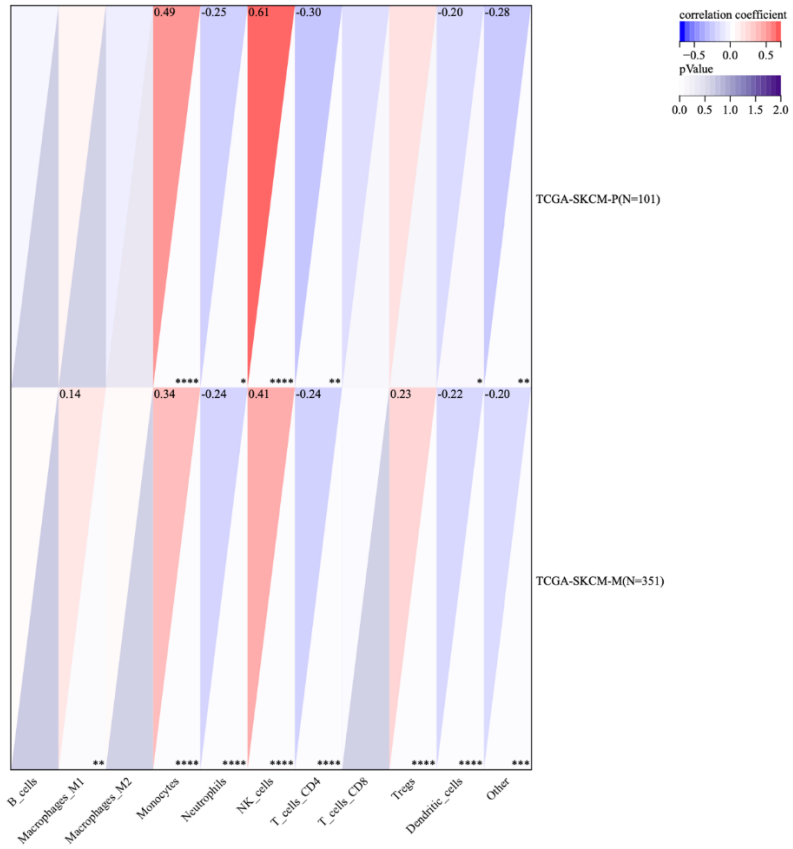
0.14 0.43 0.43 -0.15 0.33 0.24 -0.28
0.41 0.27 0.35 0.35 -0.49
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

PDGFA


correlation coefficient
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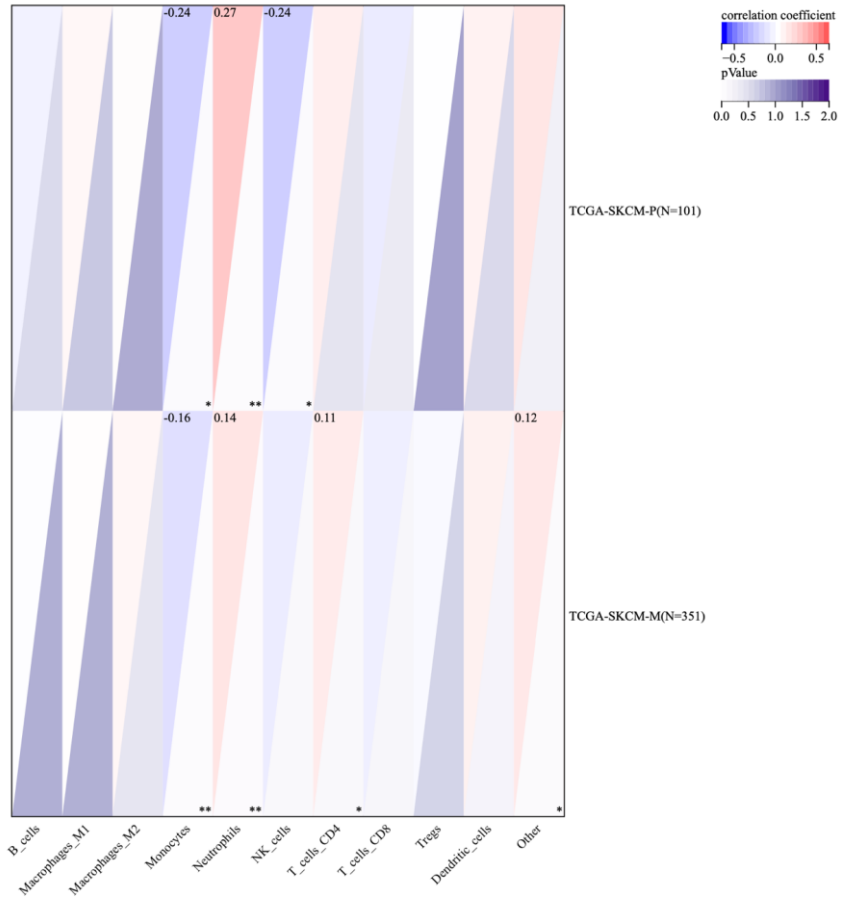
pValue
0.0 0.5 1.0 1.5 2.0
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

PF4


correlation coefficient
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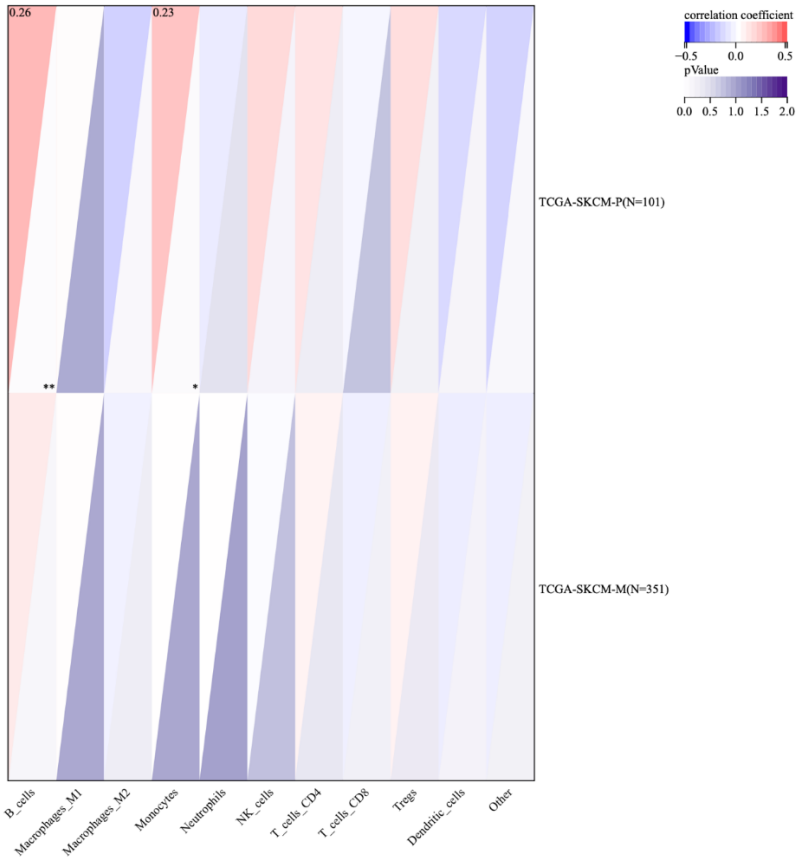
pValue
0.0 0.5 1.0 1.5 2.0
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

PGLYRP1



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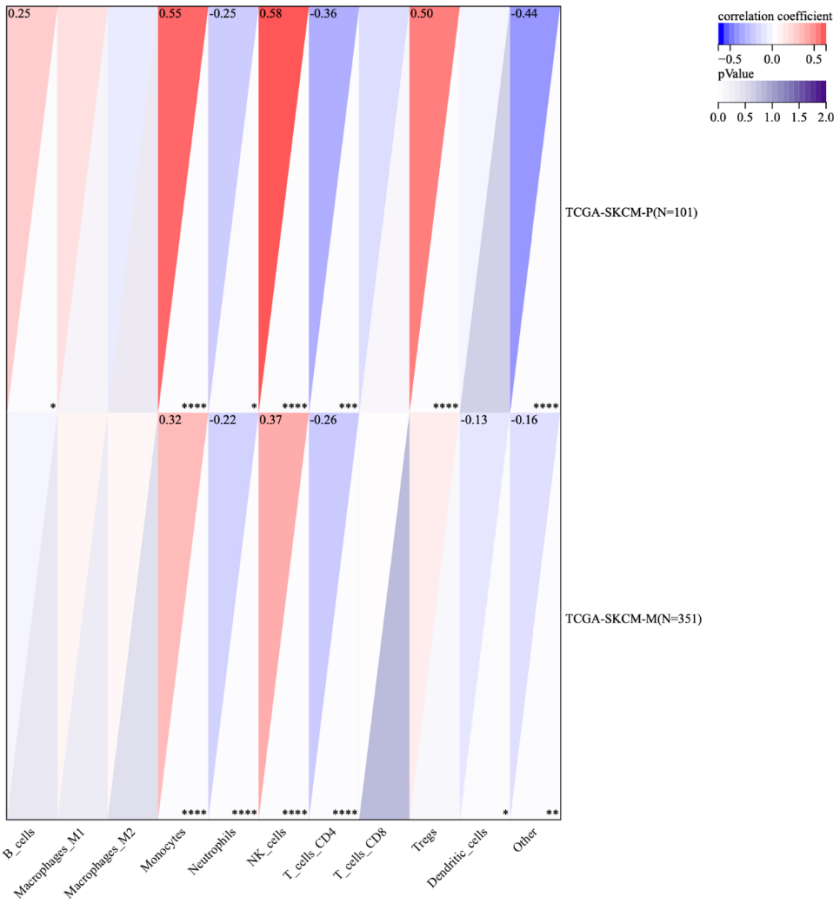
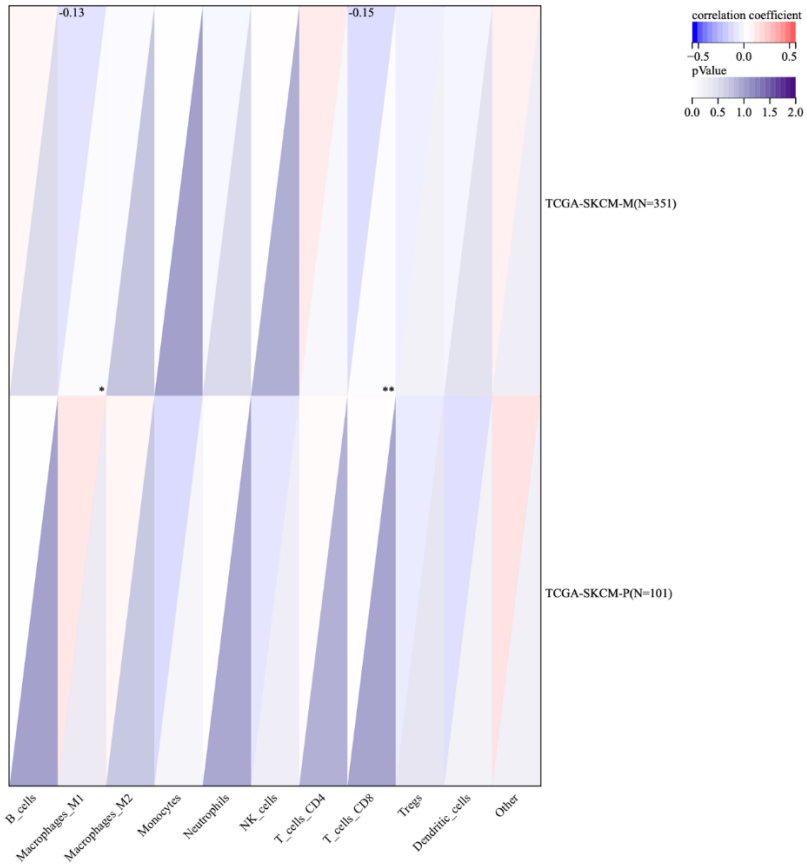


PRG2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pValue
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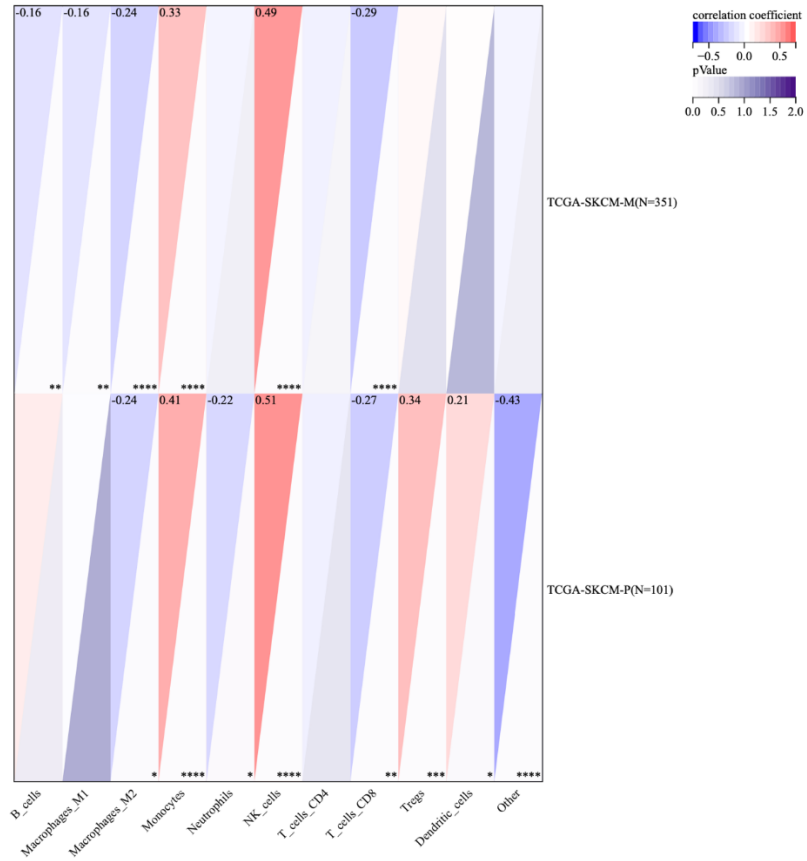
-0.13
-0.15
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

PTK2


correlation coefficient
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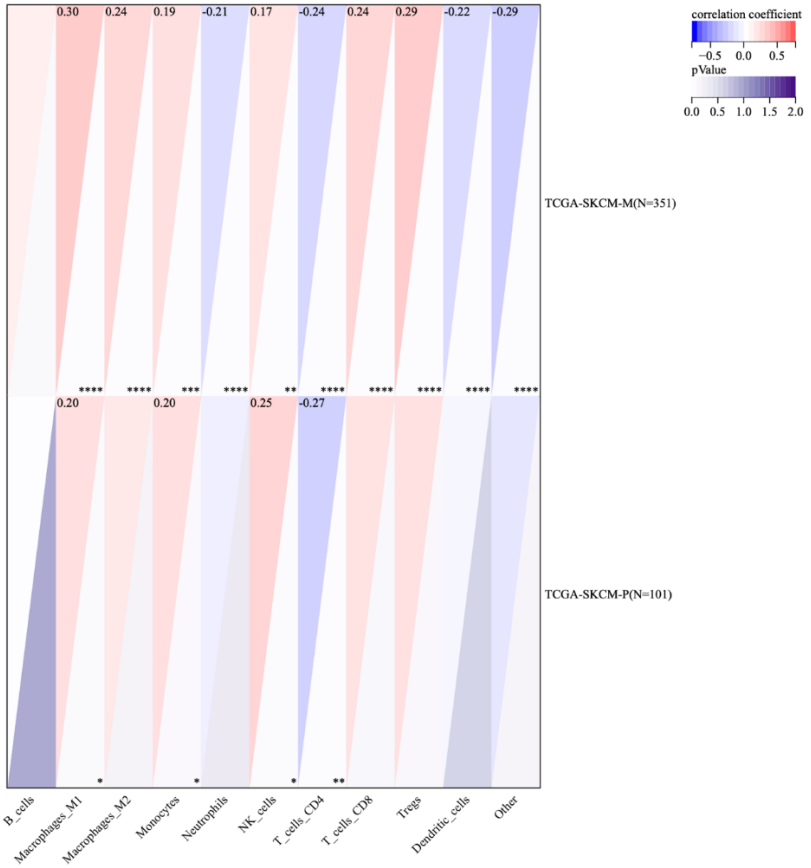
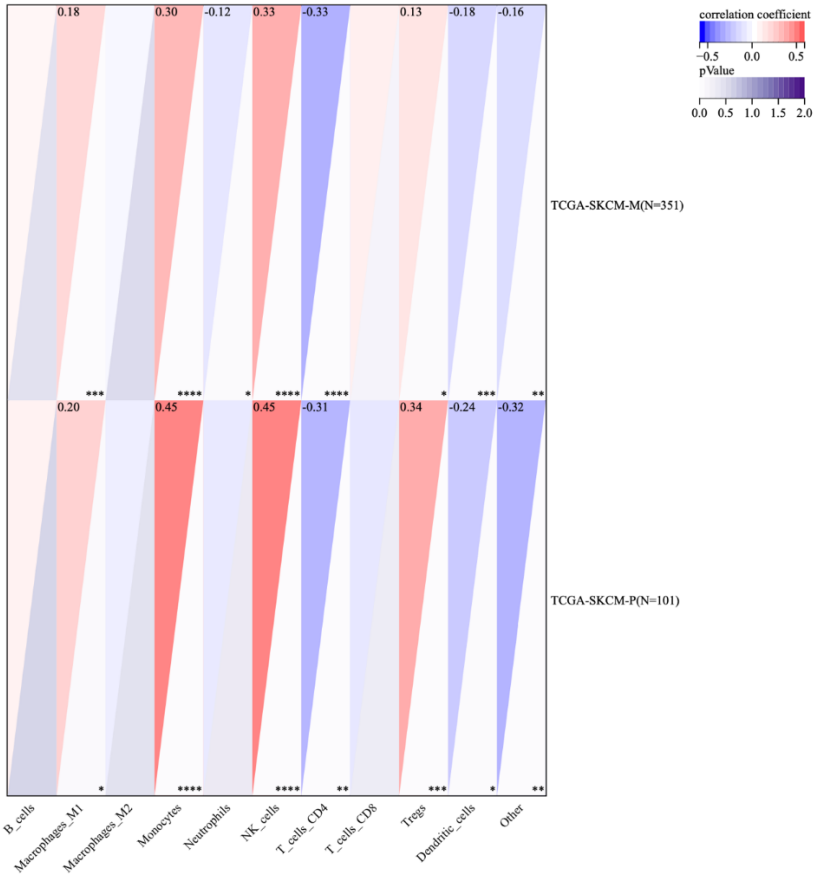
pValue
0.0 0.5 1.0 1.5 2.0
-0.16 -0.16 -0.24 0.33 0.49 -0.29
-0.24 0.41 -0.22 0.51 -0.27 0.34 0.21 -0.43
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

S100A4



SERPINA5



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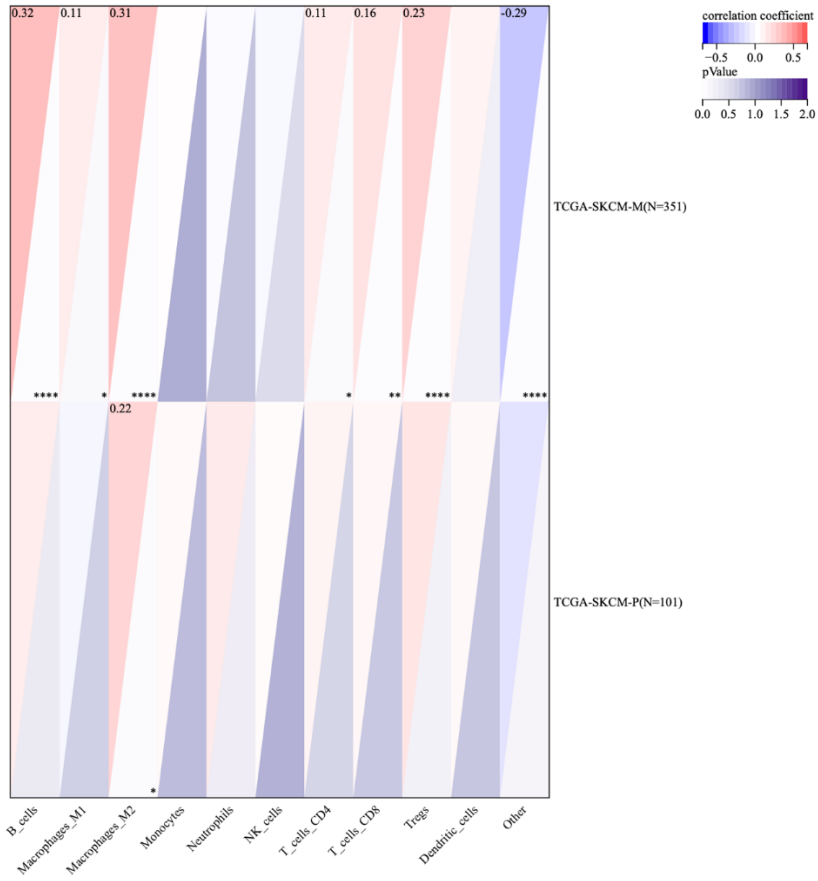
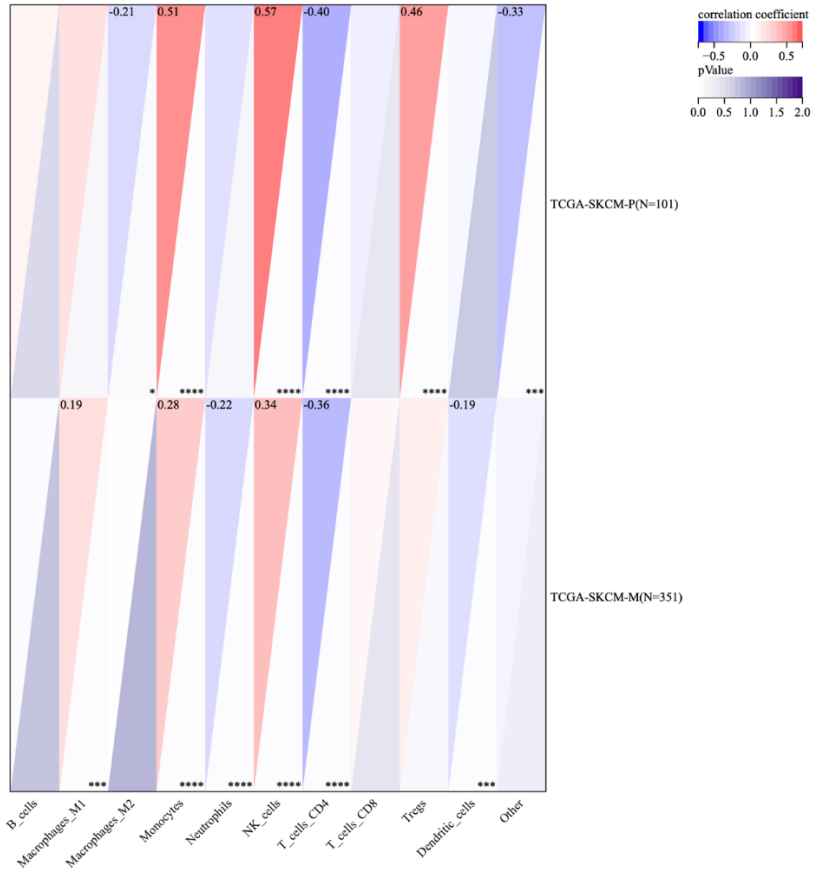
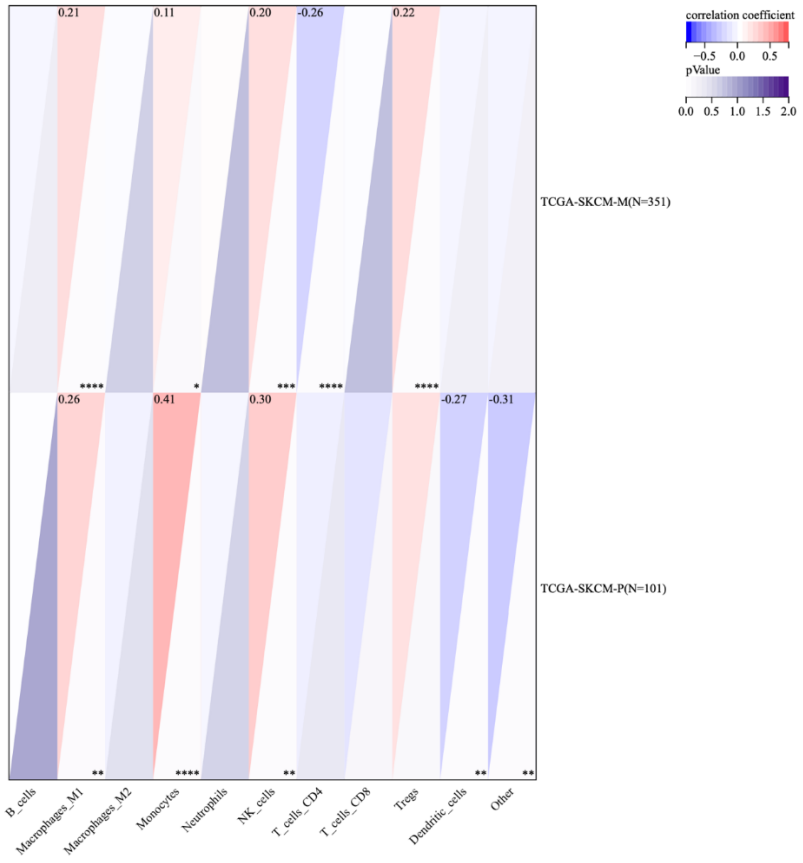


SPP1



STC1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pValue
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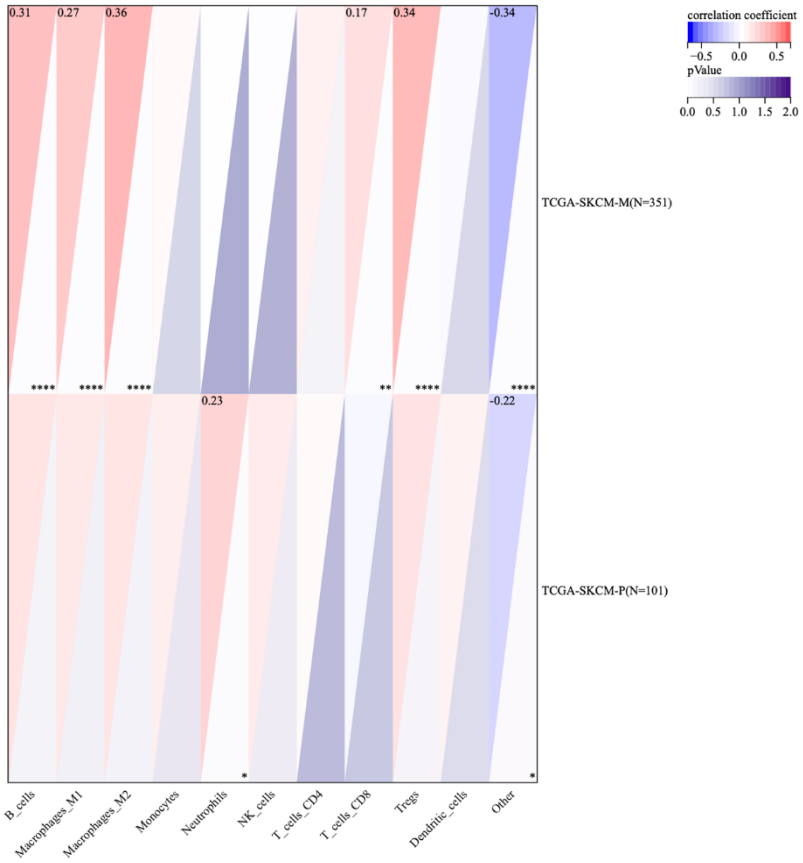
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

THBD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pValue
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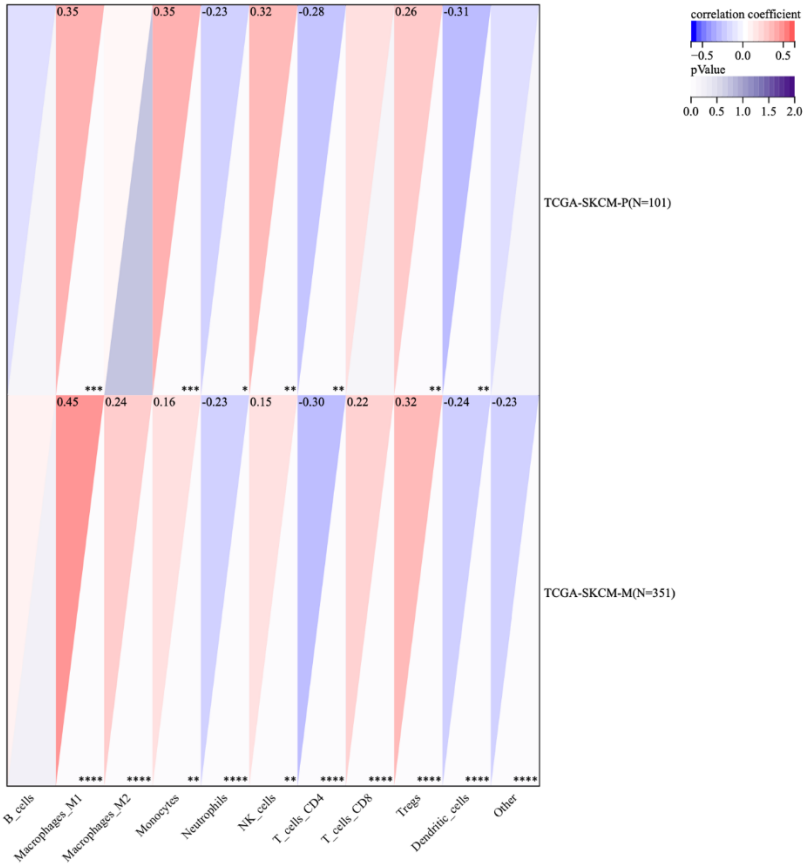
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

TIMP1



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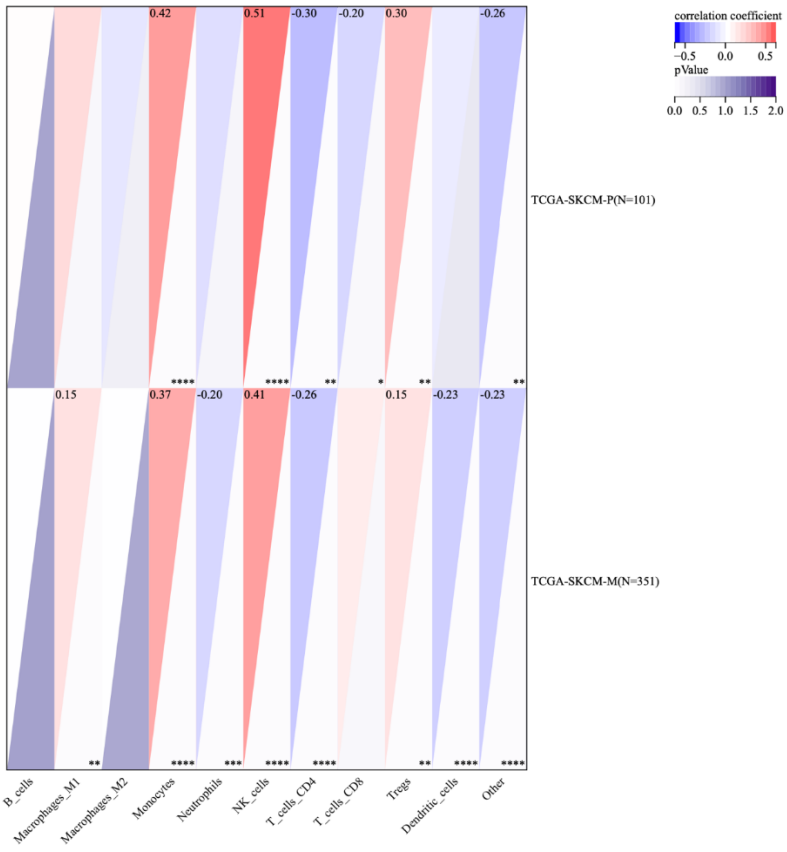
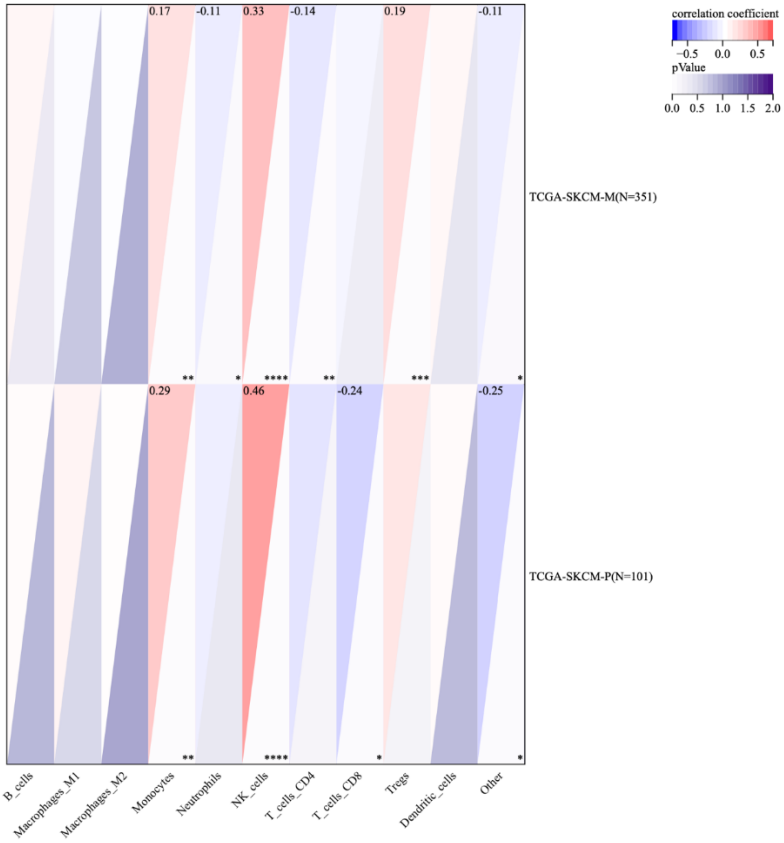


VAV2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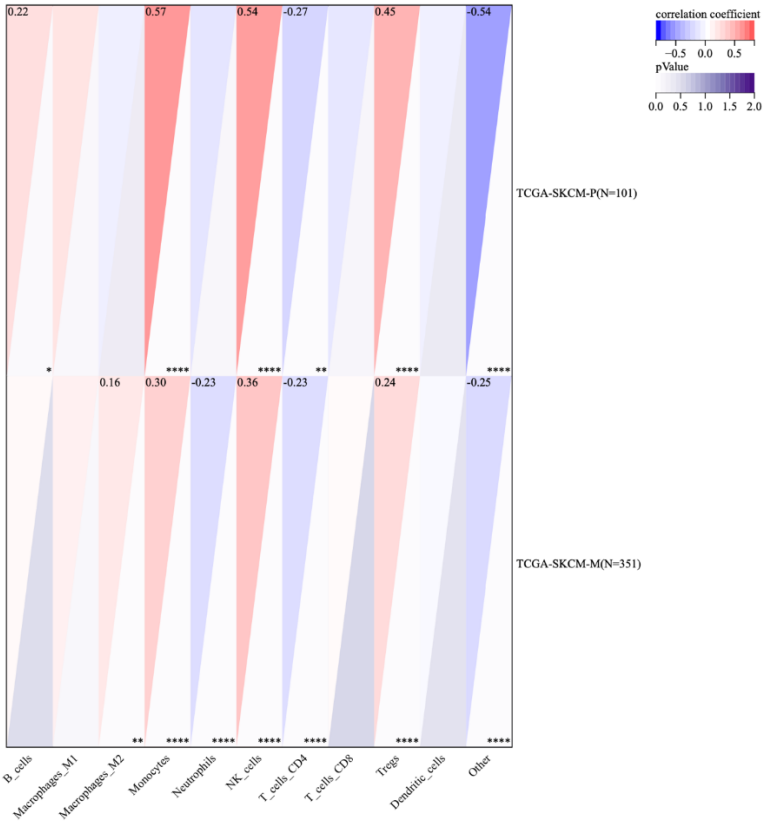
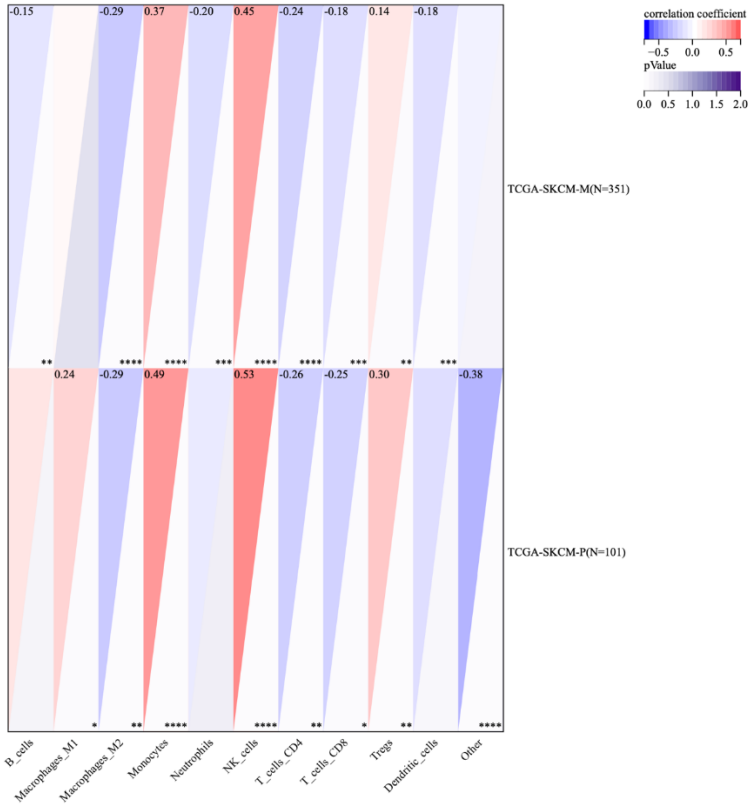
−0.5 0.0 0.5
pValue
0.0 0.5 1.0 1.5 2.0
0.17 -0.11 0.33 -0.14 0.19 -0.11
0.29 0.46 -0.24 -0.25
TCGA-SKCM-M(N=351)
TCGA-SKCM-P(N=101)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

VCAN


correlation coefficient
−0.5 0.0 0.5
pValue
0.0 0.5 1.0 1.5 2.0
0.22 0.57 0.54 -0.27 0.45 -0.54
0.16 0.30 -0.23 0.36 -0.23 0.24 -0.25
TCGA-SKCM-P(N=101)
TCGA-SKCM-M(N=351)
B_cells
Macrophages_M1
Macrophages_M2
Monocytes
Neutrophils
NK_cells
T_cells_CD4
T_cells_CD8
Tregs
Dendritic_cells
Other

VEGFA



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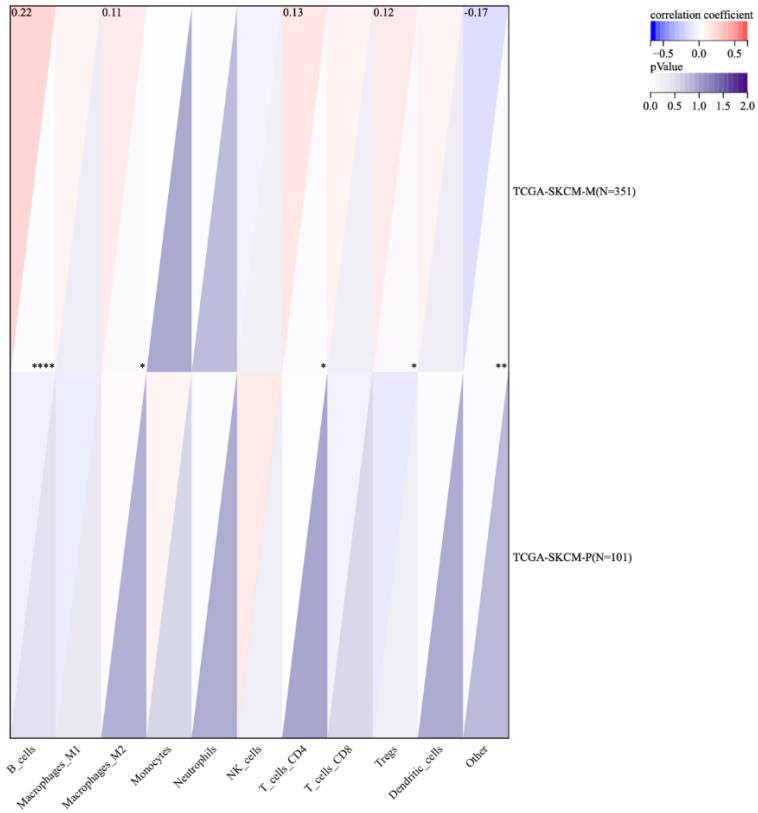


Figure S10. Spearman's correlations between the expression of ARGs and the infiltration in different immune cells in primary and metastatic skin melanoma, using QUANTISEQ.

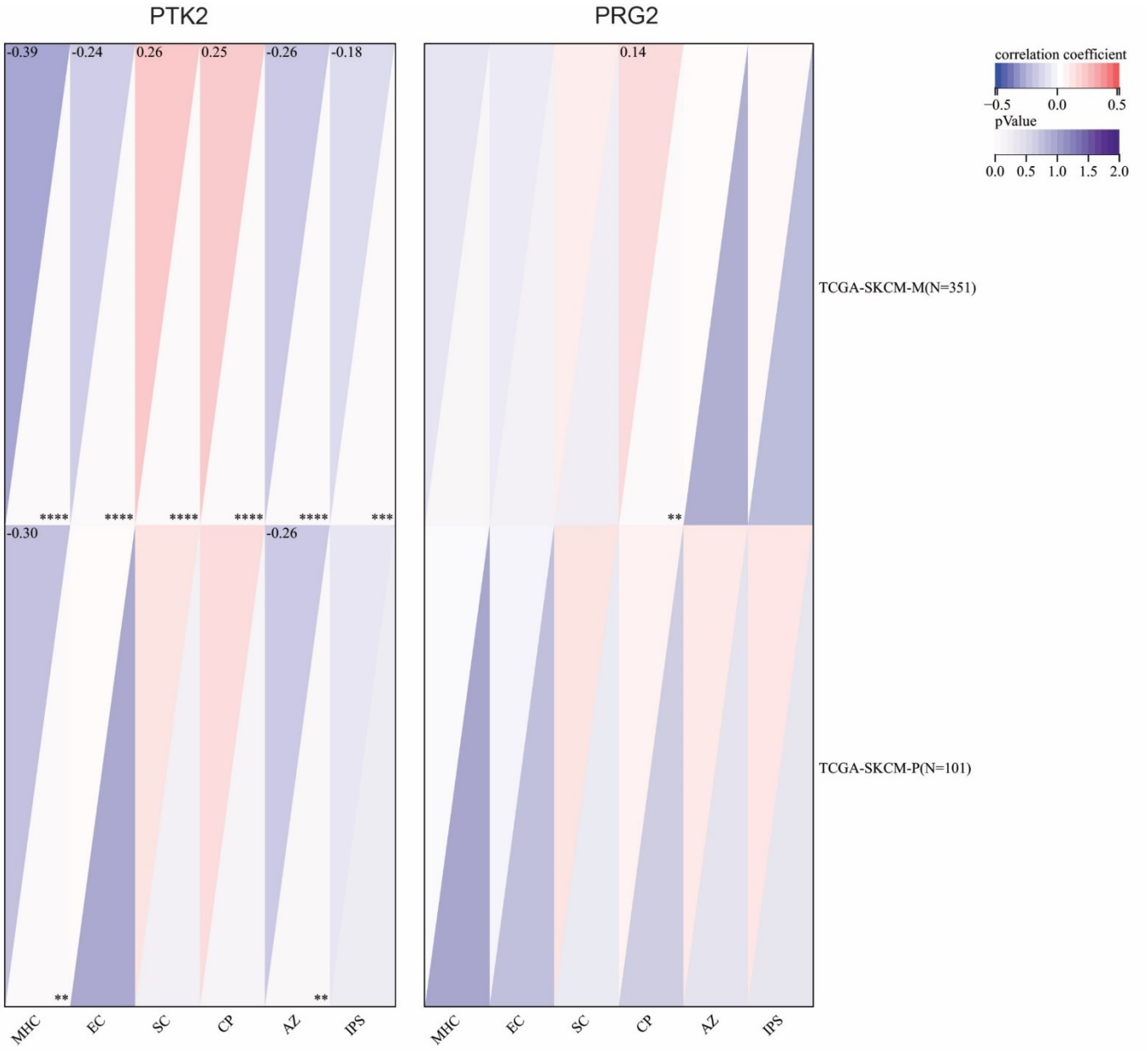
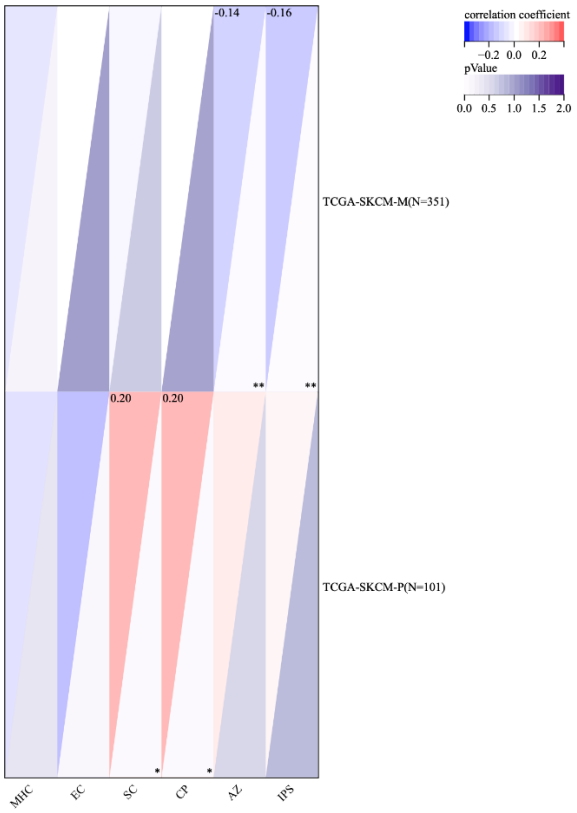
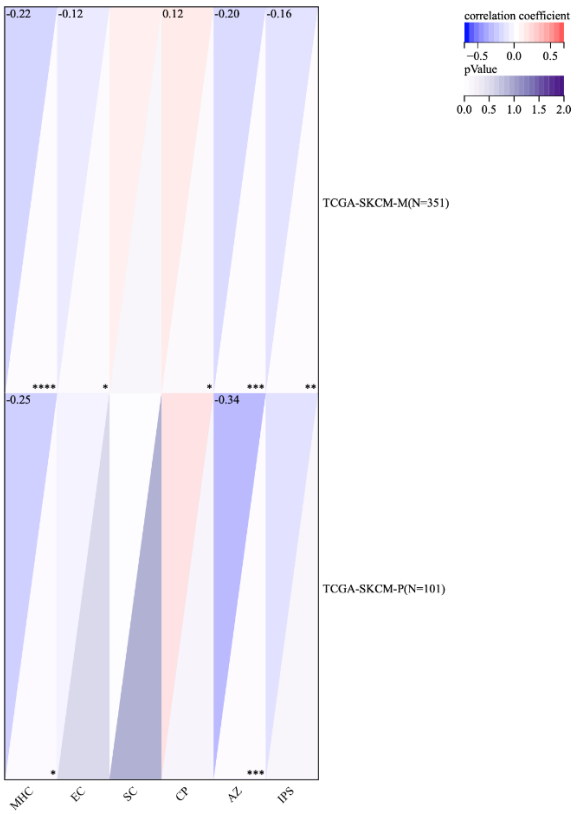


Figure S11 Spearman's correlation analysis between the expression of *PTK2* (or *PRG2*) and immune cell populations in primary (TCGA-SCKM-P) and metastatic skin melanoma (TCGA-SCKM-M), respectively, using Immune cell profiling (IPS). Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.

APOH



APP



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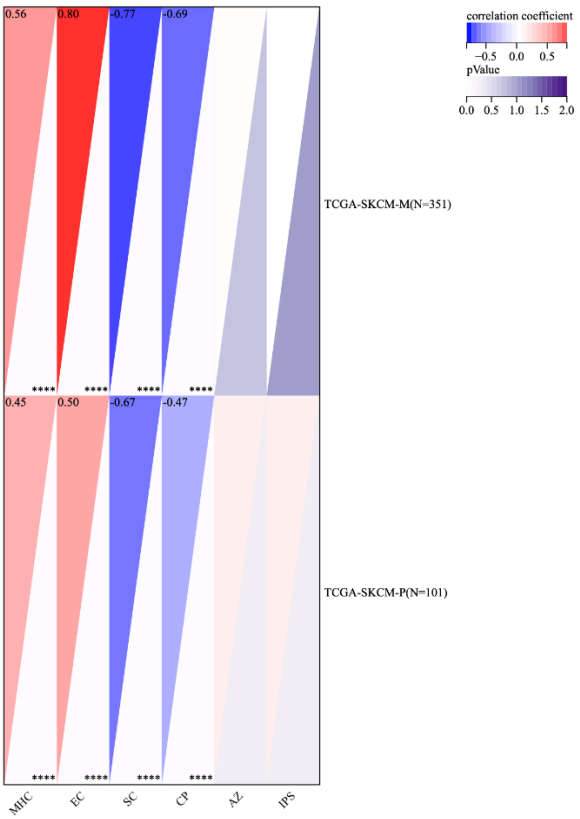

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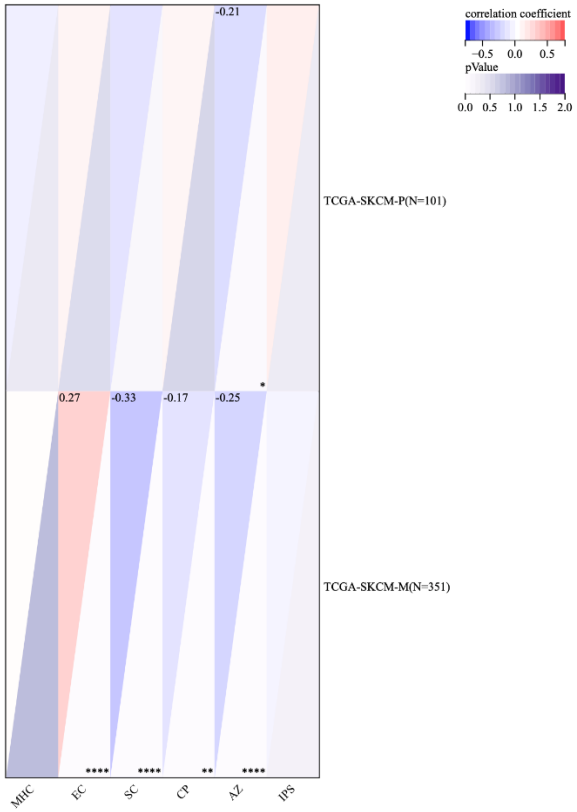

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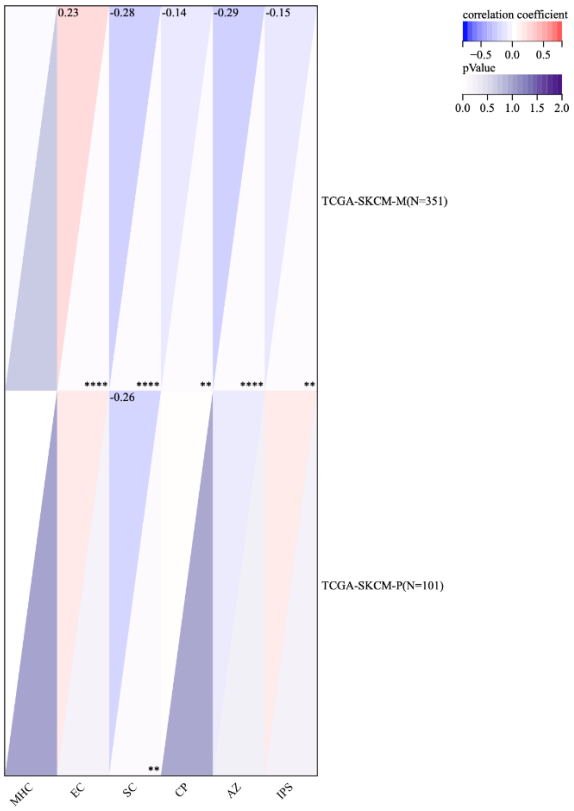

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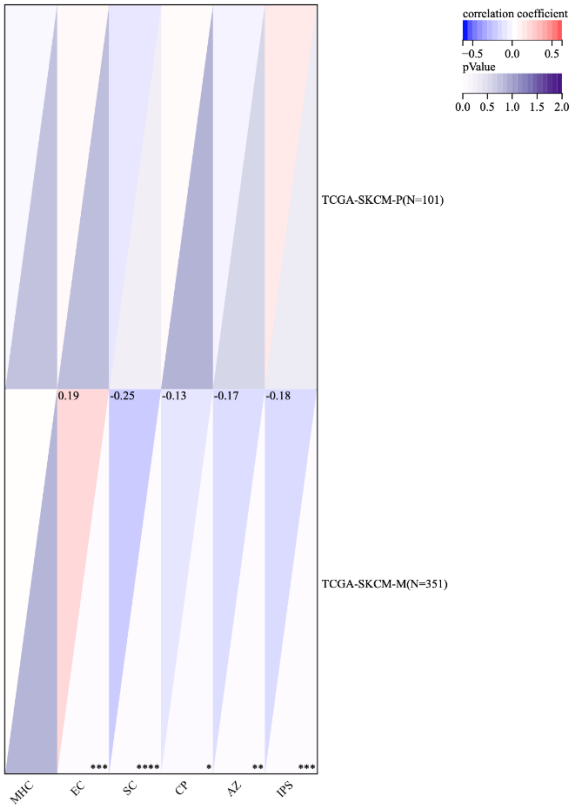

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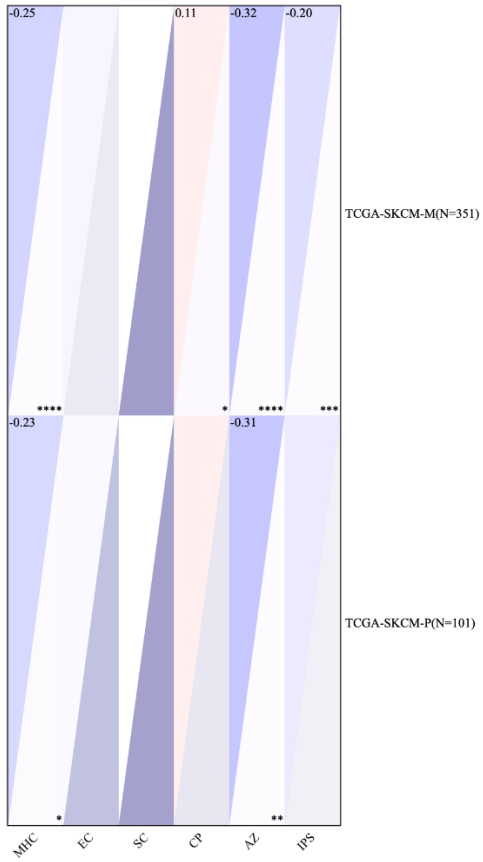

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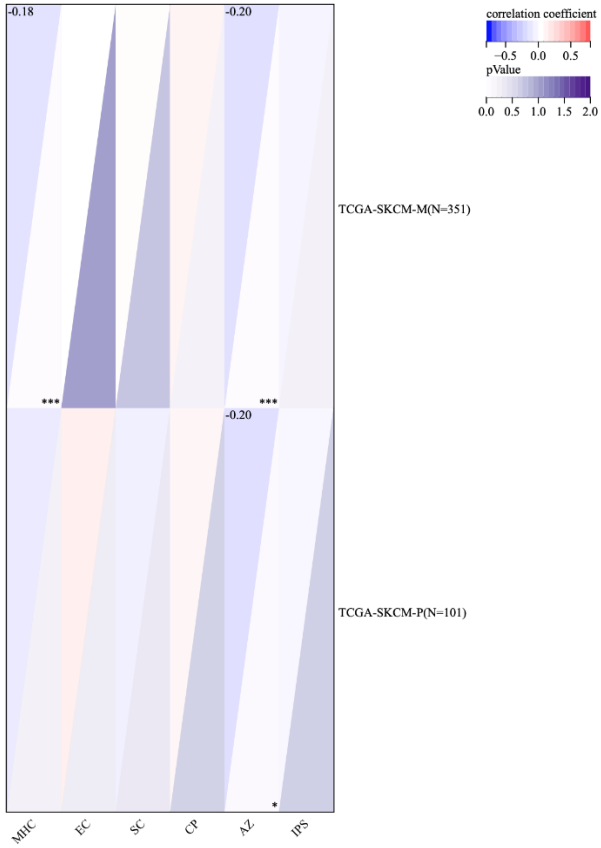

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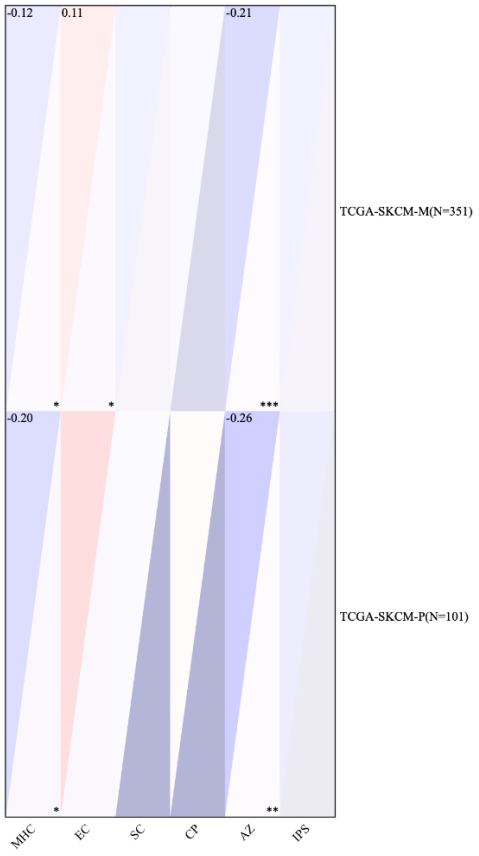

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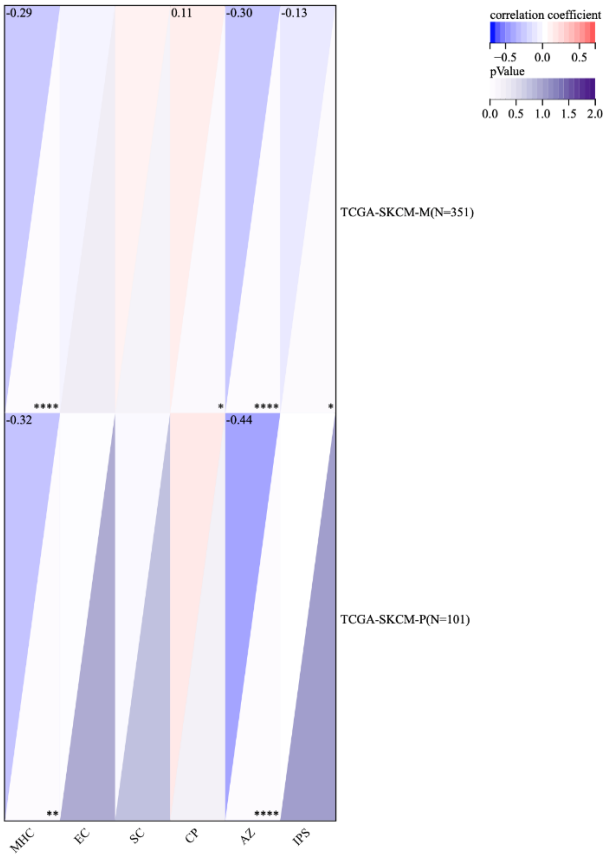

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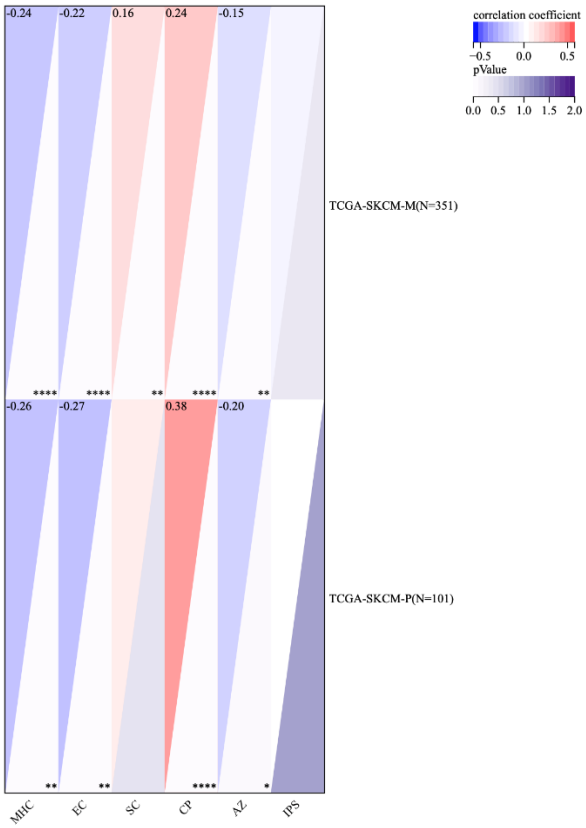

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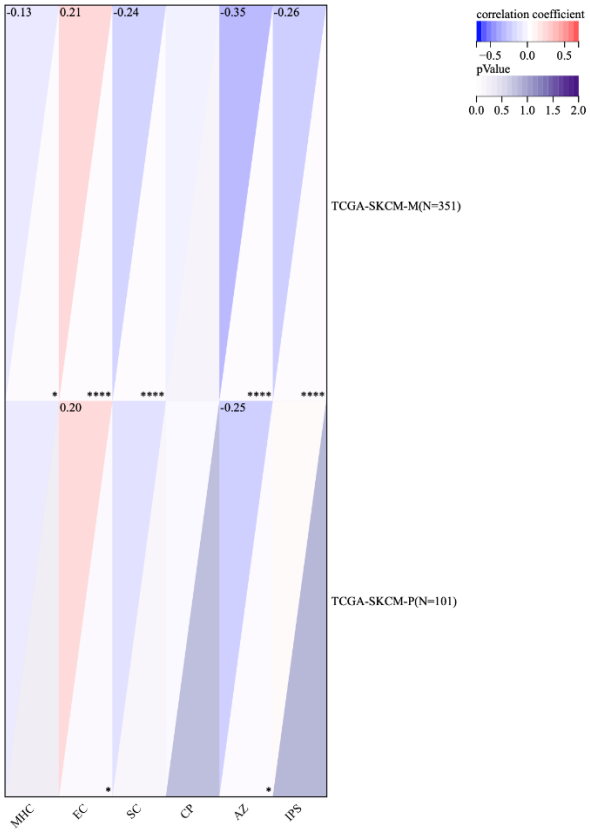

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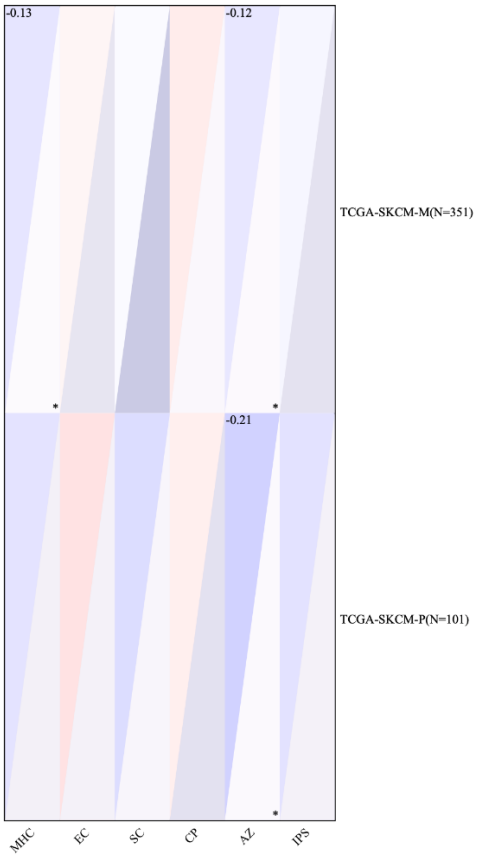

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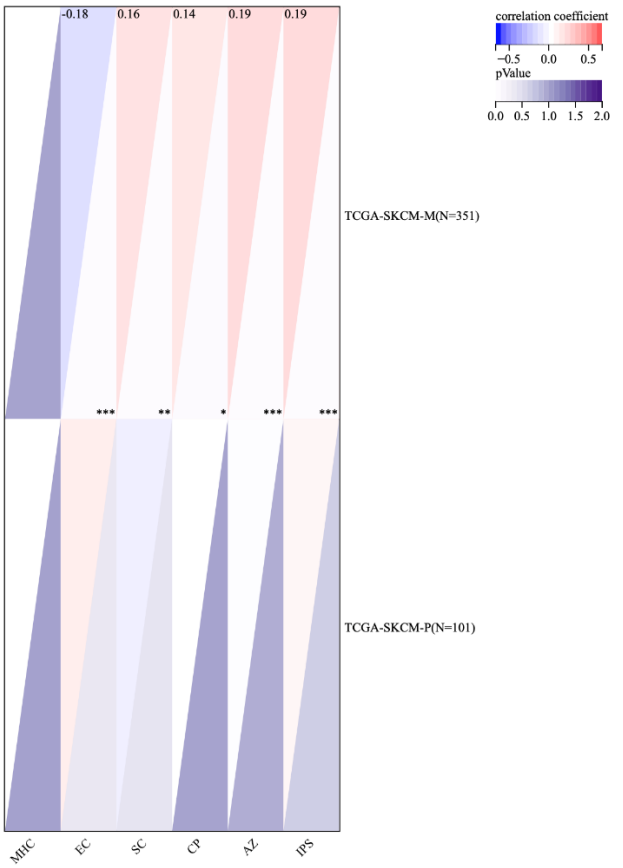

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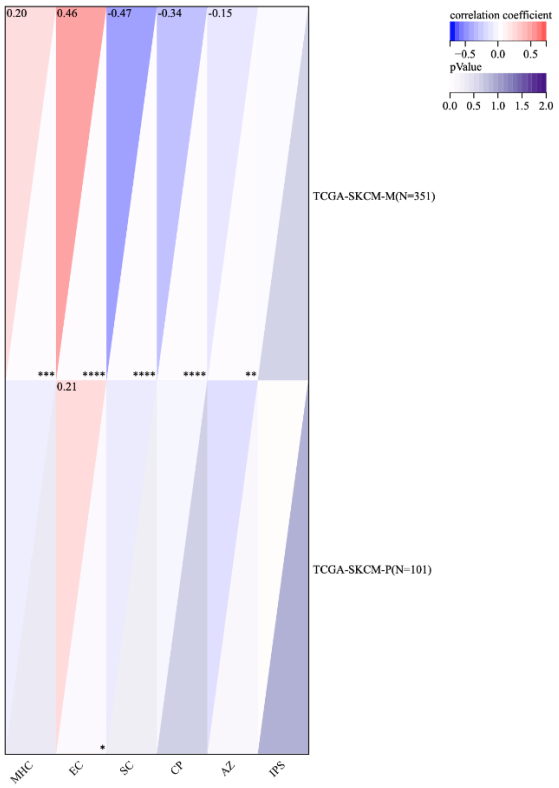

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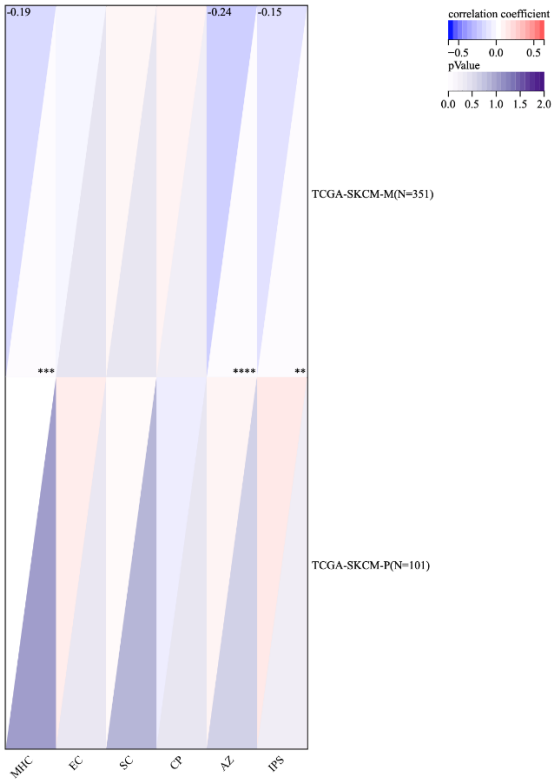

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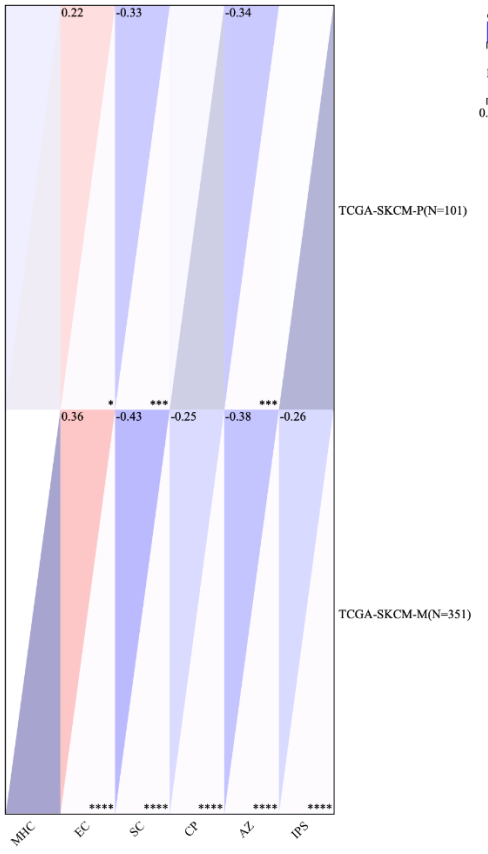

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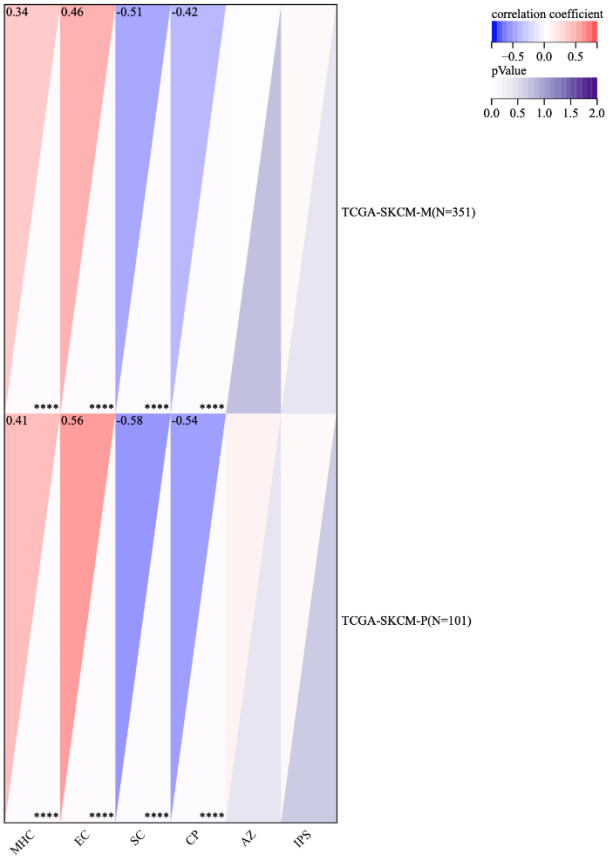

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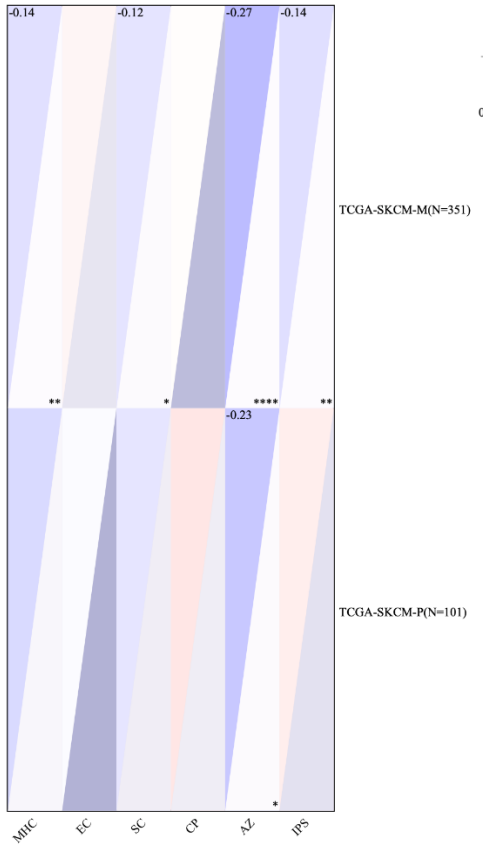

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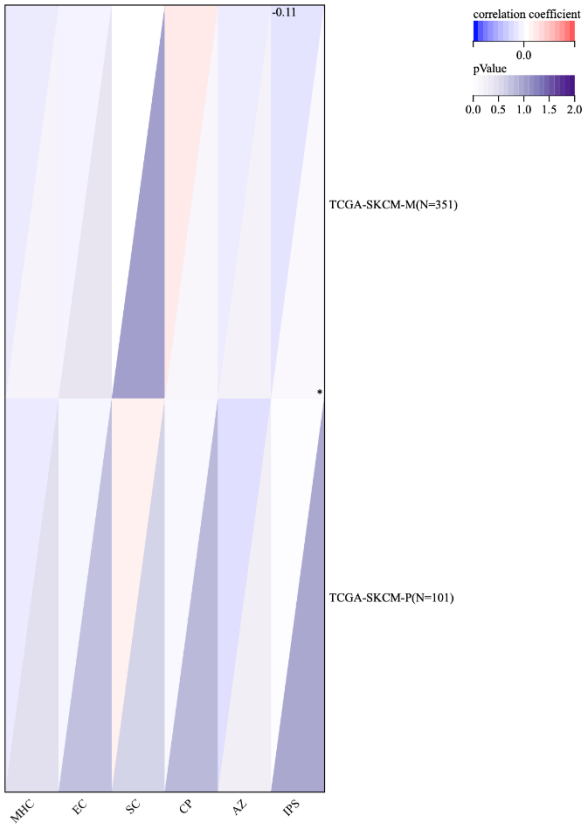

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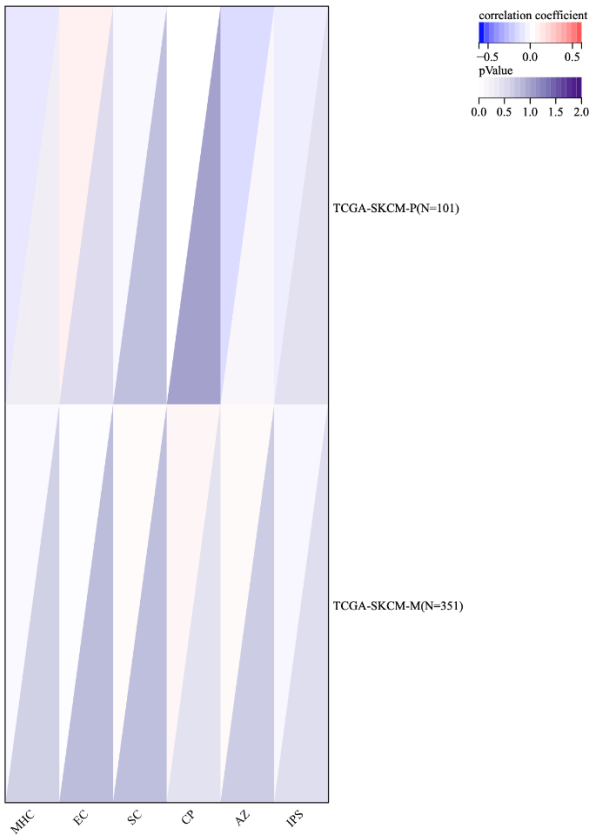

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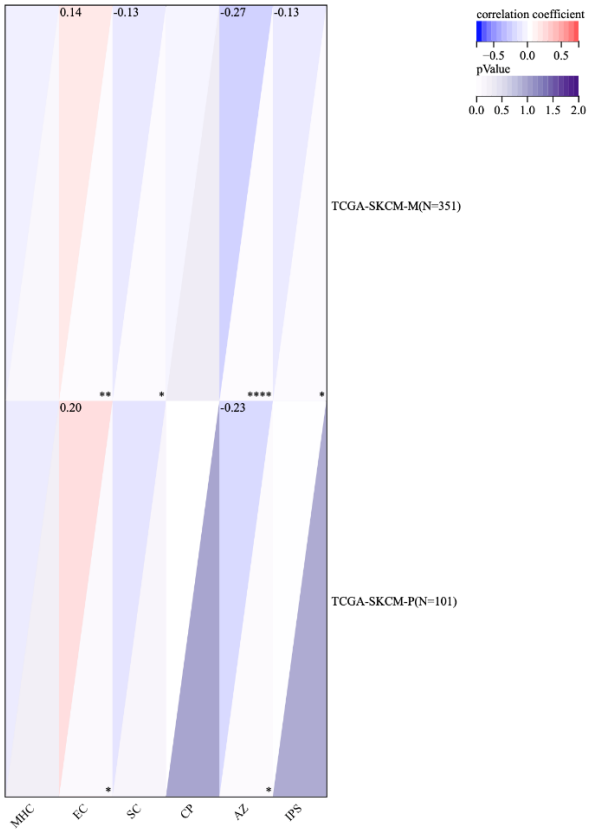

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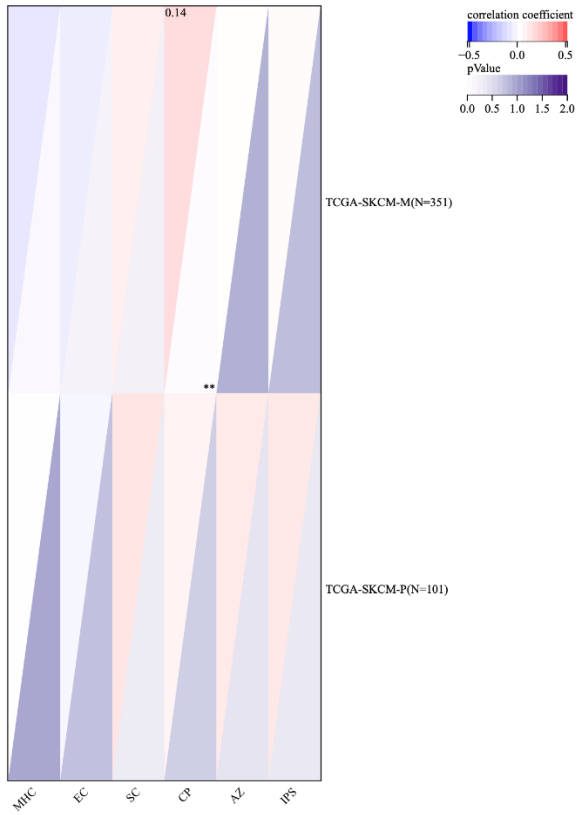

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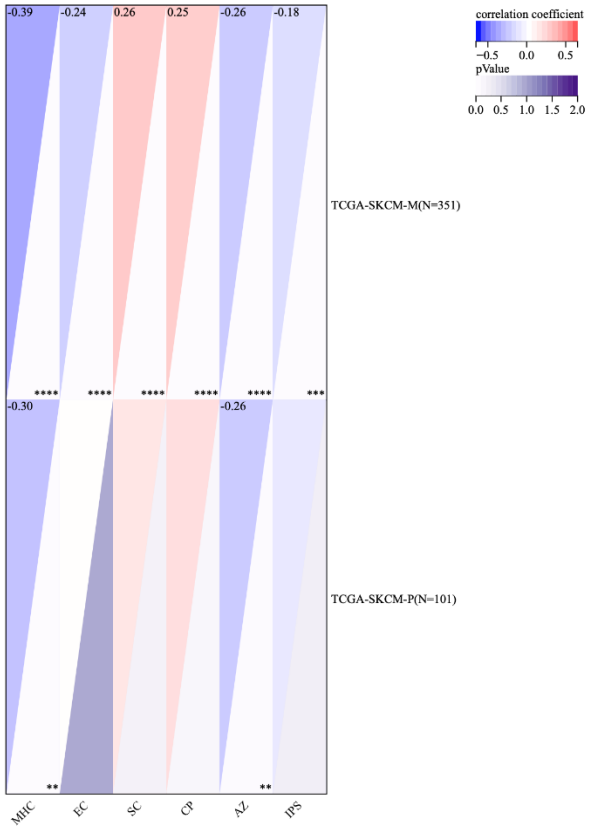

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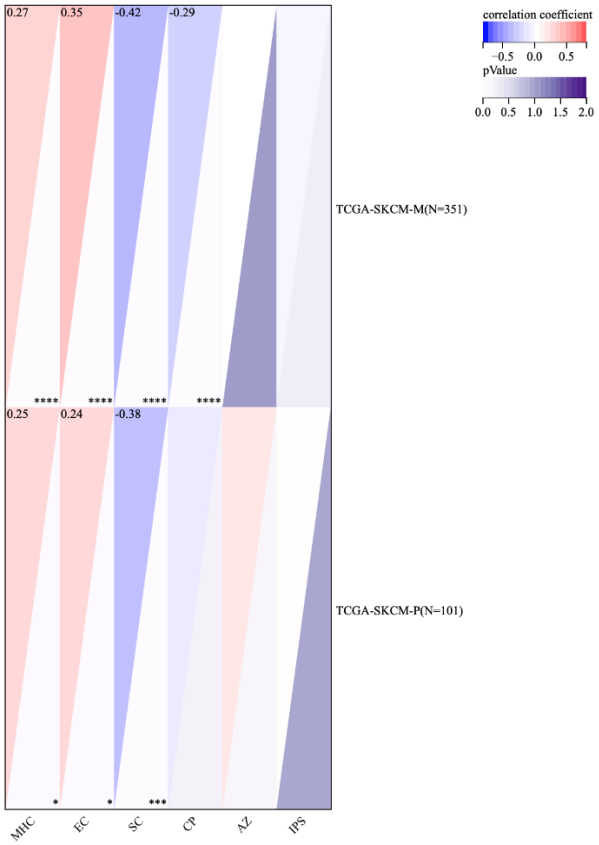

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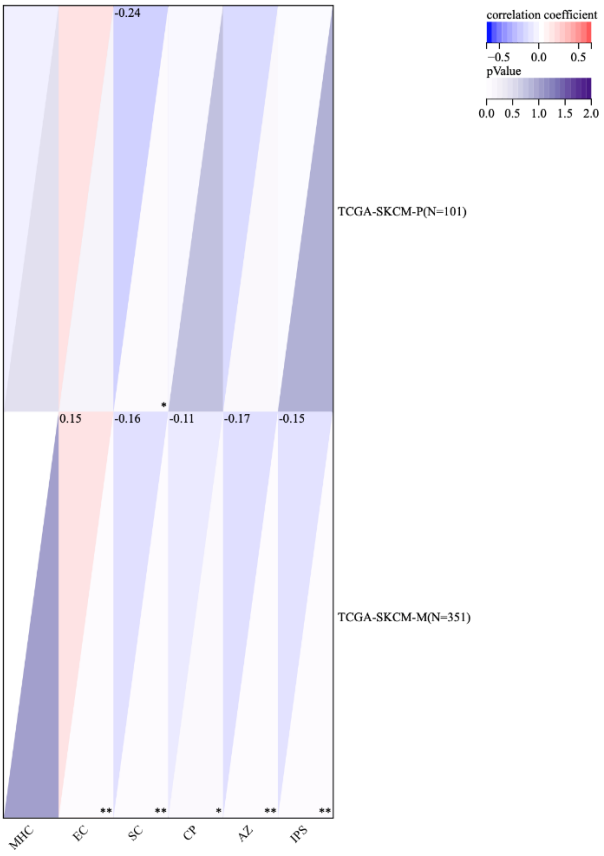

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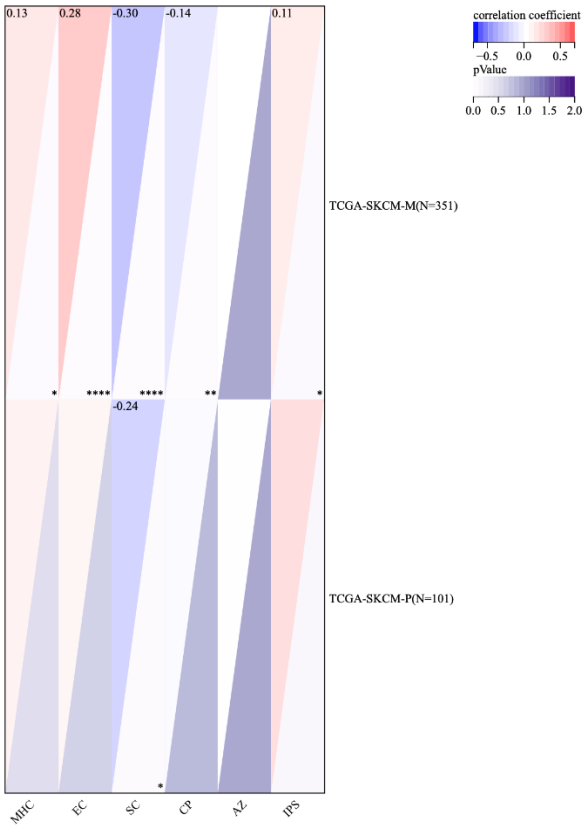

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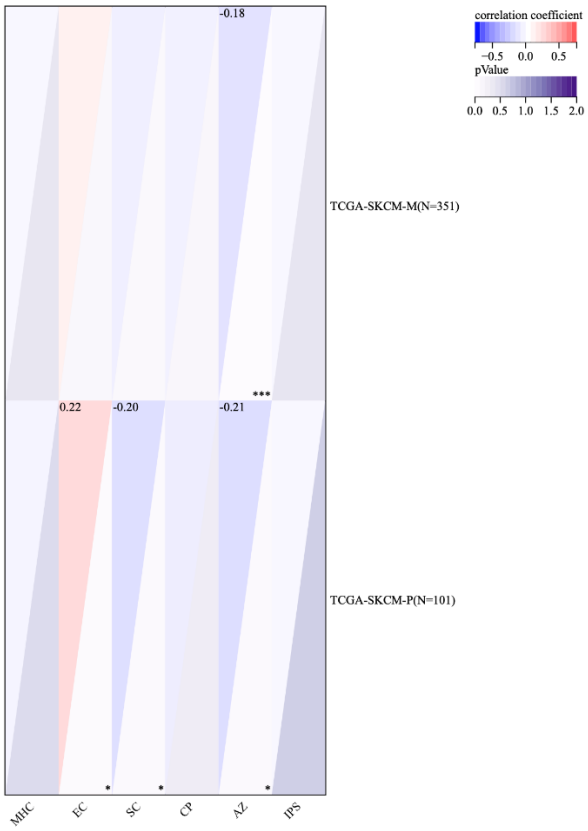

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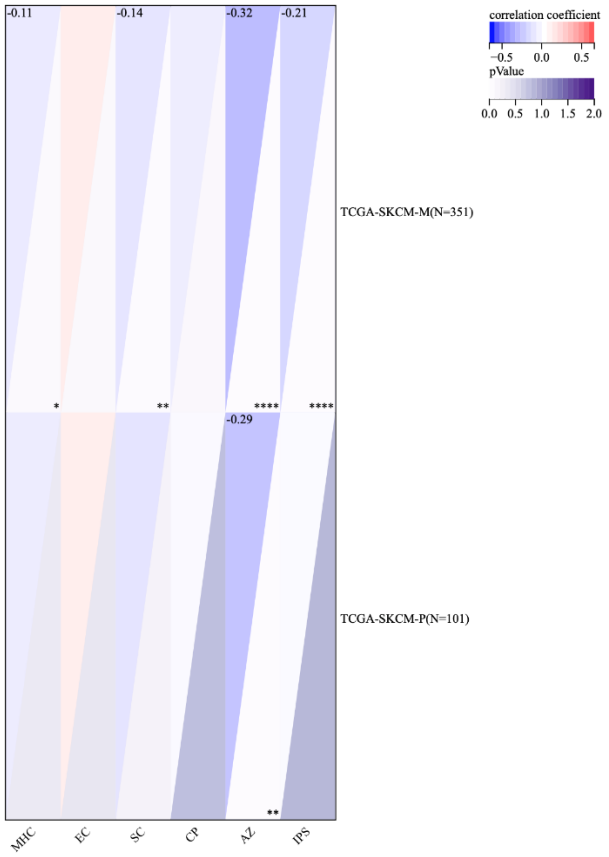

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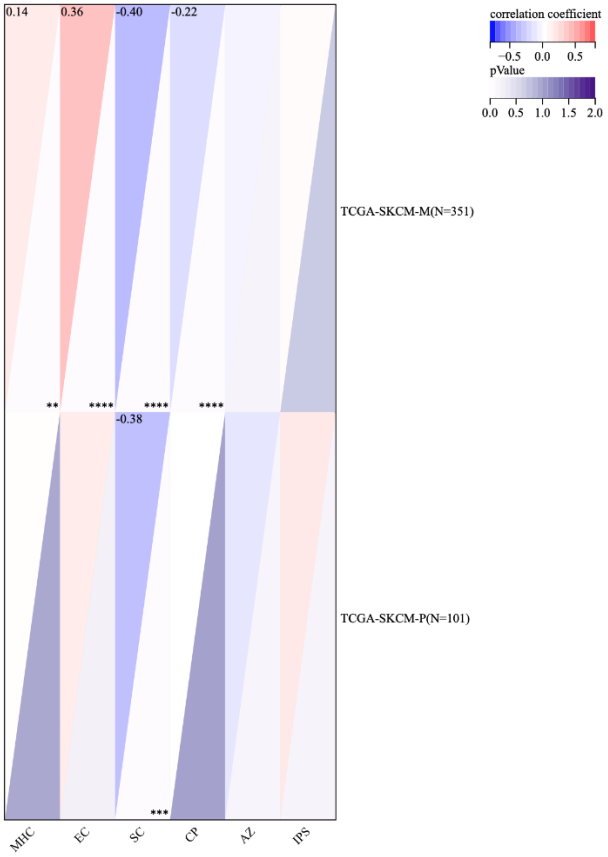

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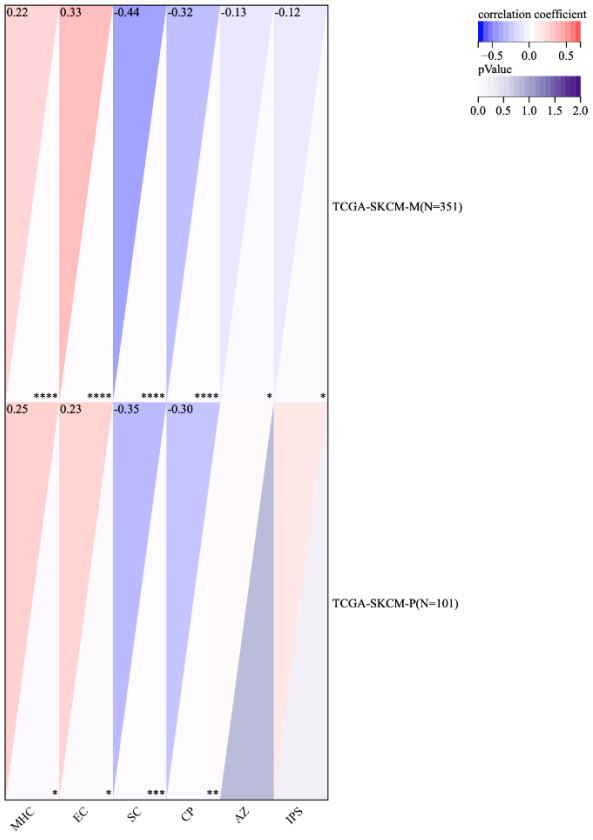

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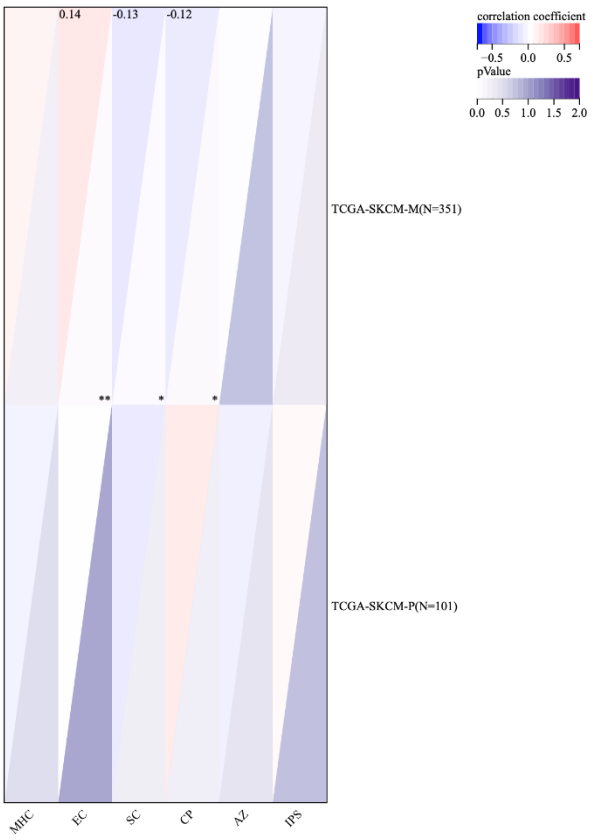

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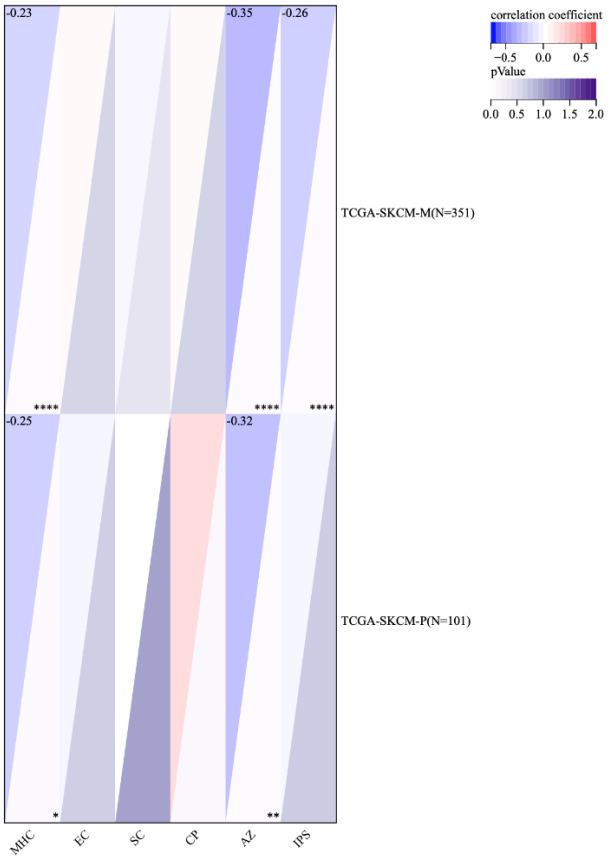

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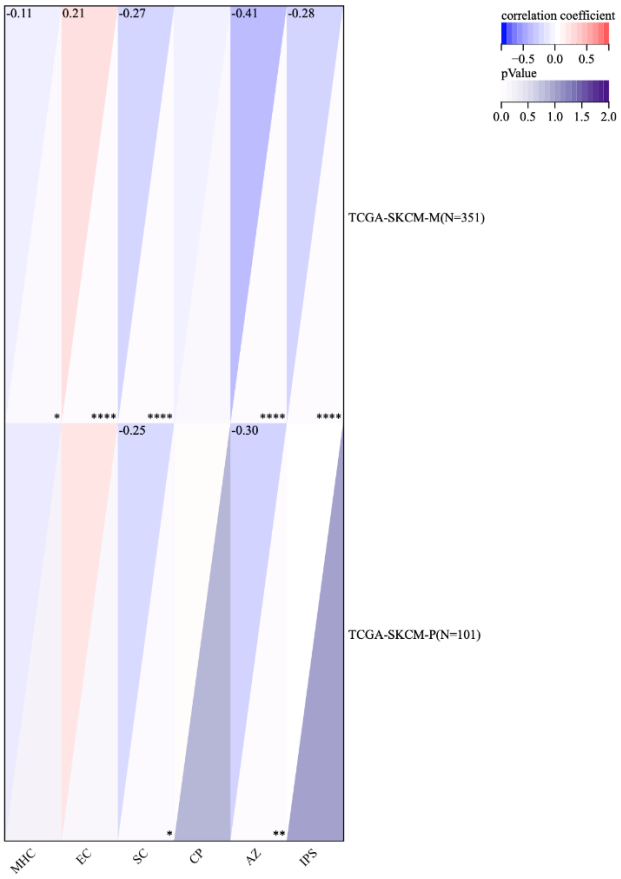

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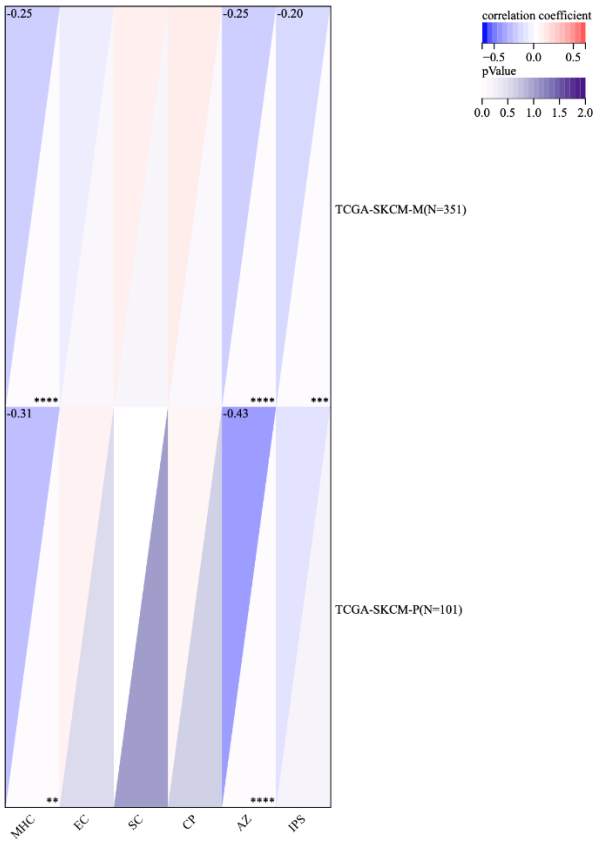

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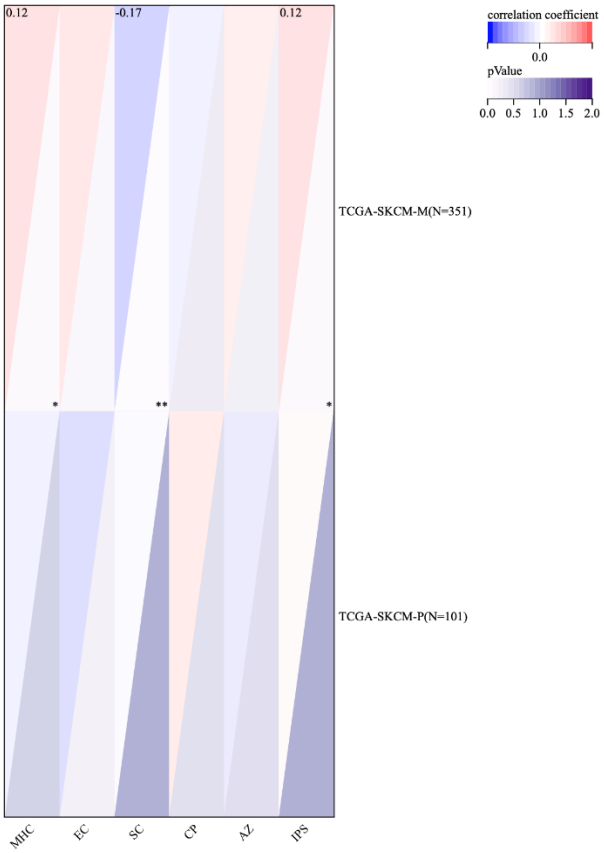

Figure S12. Spearman's correlations between the expression of ARGs and the infiltration in different immune cells in primary and metastatic skin melanoma, using IPS. Asterisks denote statistical significance: *, $p<0.05$; ****, $p<0.001$.