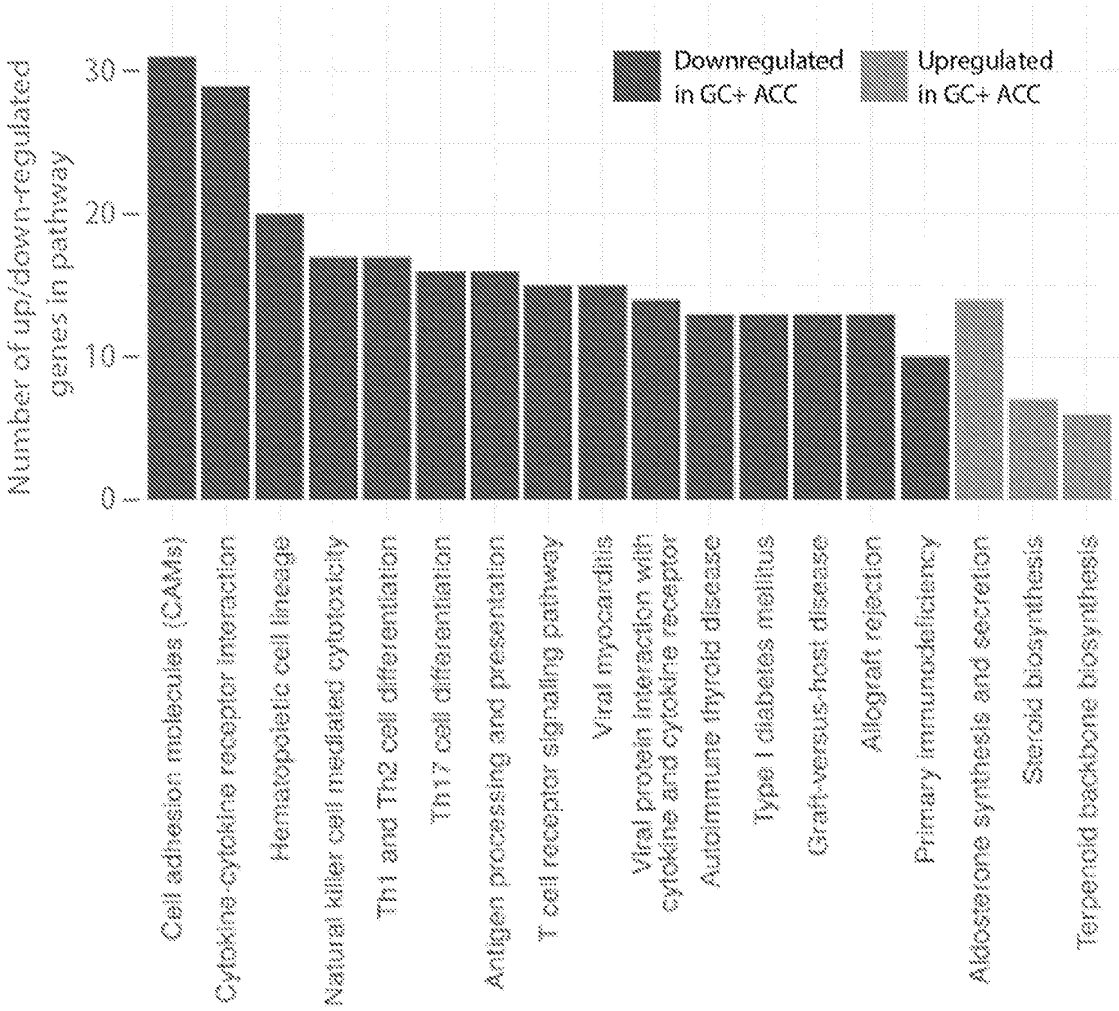

Number of up/down-regulated genes in pathway
0
10
20
30
Downregulated in GC+ ACC
Upregulated in GC+ ACC
Cell adhesion molecules (CAMs)
Cytokine-cytokine receptor interaction
Hematopoietic cell lineage
Natural killer cell mediated cytotoxicity
Th1 and Th2 cell differentiation
Th17 cell differentiation
Antigen processing and presentation
T cell receptor signaling pathway
Viral myocarditis
Viral protein interaction with cytokine and cytokine receptor
Autoimmune thyroid disease
Type I diabetes mellitus
Graft-versus-host disease
Allograft rejection
Primary immunodeficiency
Aldosterone synthesis and secretion
Steroid biosynthesis
Terpenoid backbone biosynthesis

Fig. 1

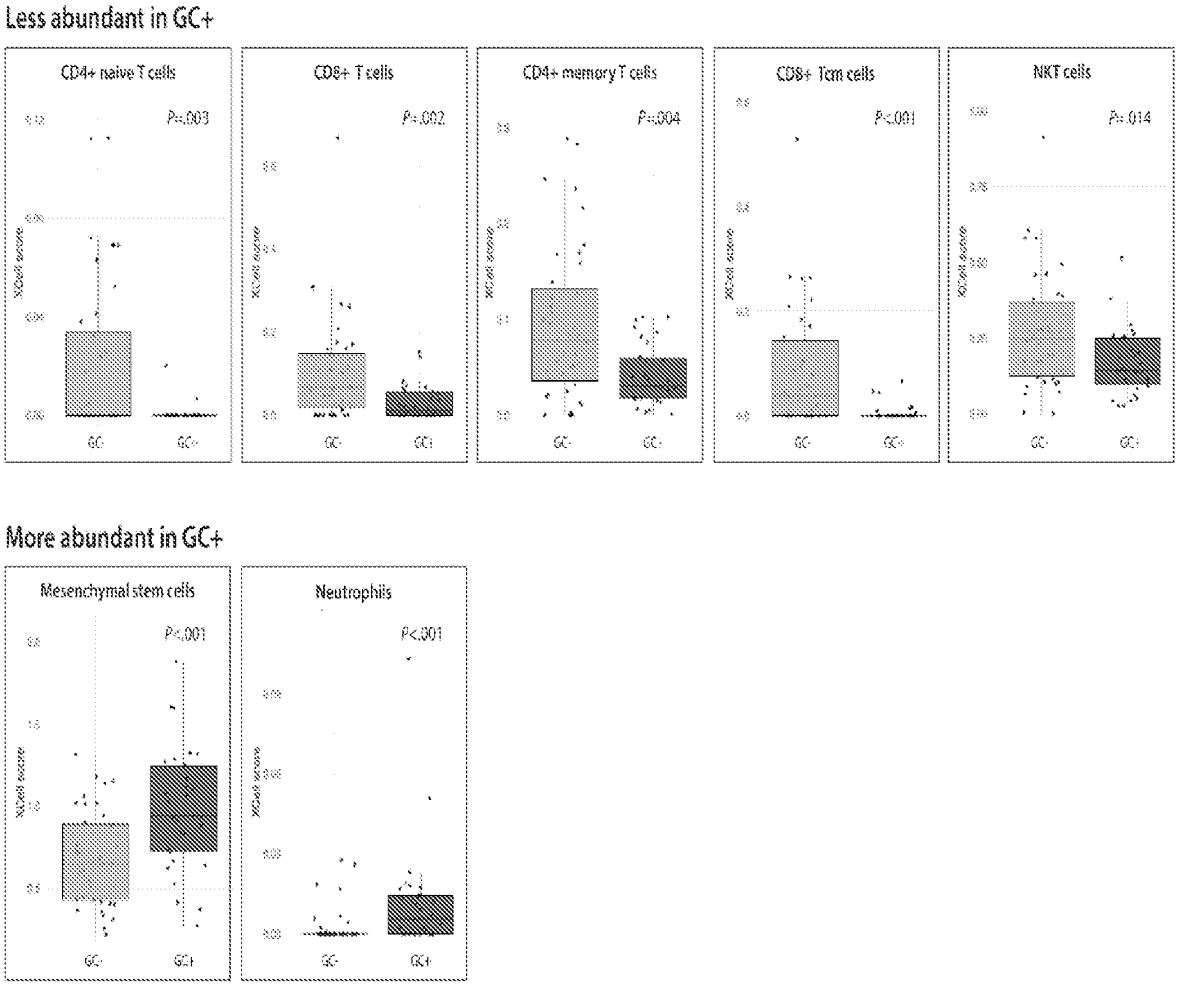

Less abundant in GC+
CD4+ naive T cells
P=.003
CD8+ T cells
P=.002
CD4+ memory T cells
P=.004
CD8+ Tem cells
P<.001
NKT cells
P=.014
More abundant in GC+
Mesenchymal stem cells
P<.001
Neutrophils
P<.001

Fig. 2

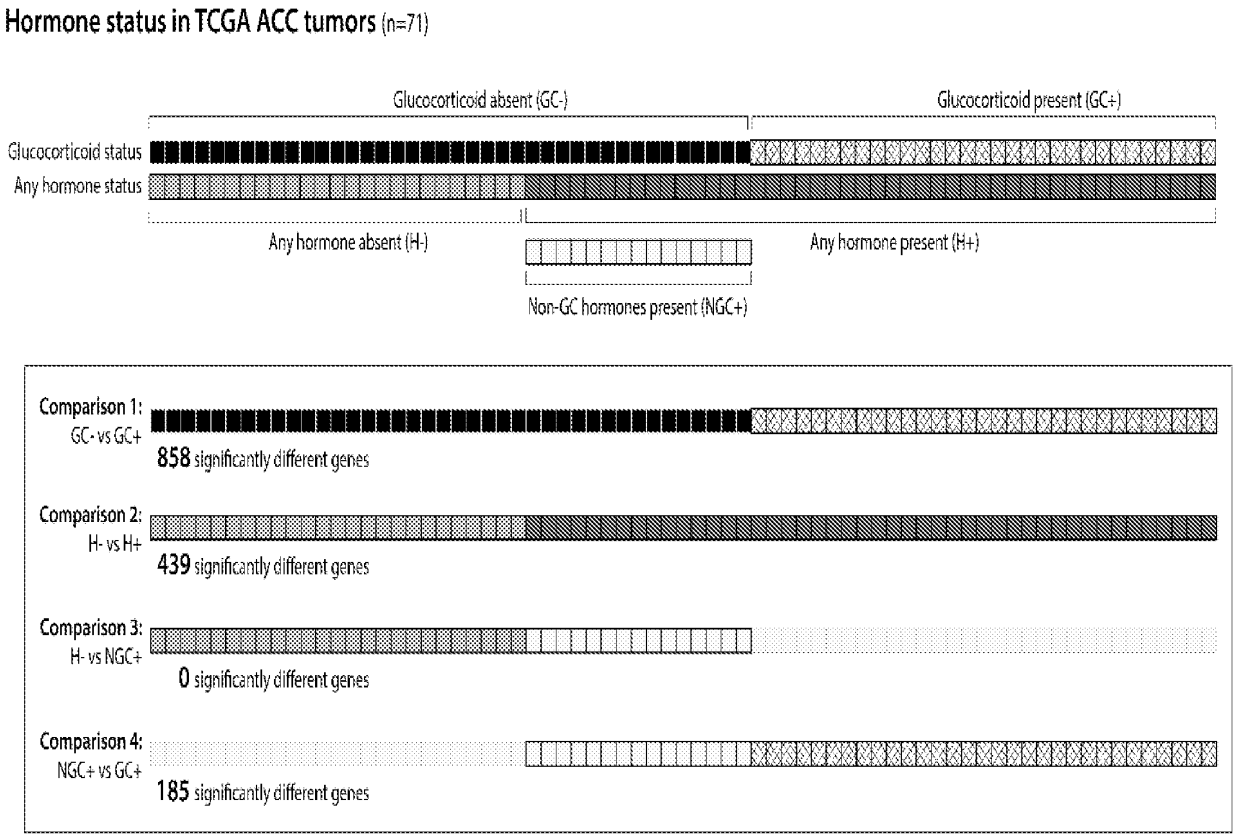

Hormone status in TCGA ACC tumors (n=71)
Glucocorticoid absent (GC-)
Glucocorticoid present (GC+)
Glucocorticoid status
Any hormone status
Any hormone absent (H-)
Any hormone present (H+)
Non-GC hormones present (NGC+)
Comparison 1:
GC- vs GC+
858 significantly different genes
Comparison 2:
H- vs H+
439 significantly different genes
Comparison 3:
H- vs NGC+
0 significantly different genes
Comparison 4:
NGC+ vs GC+
185 significantly different genes

Fig. 3A

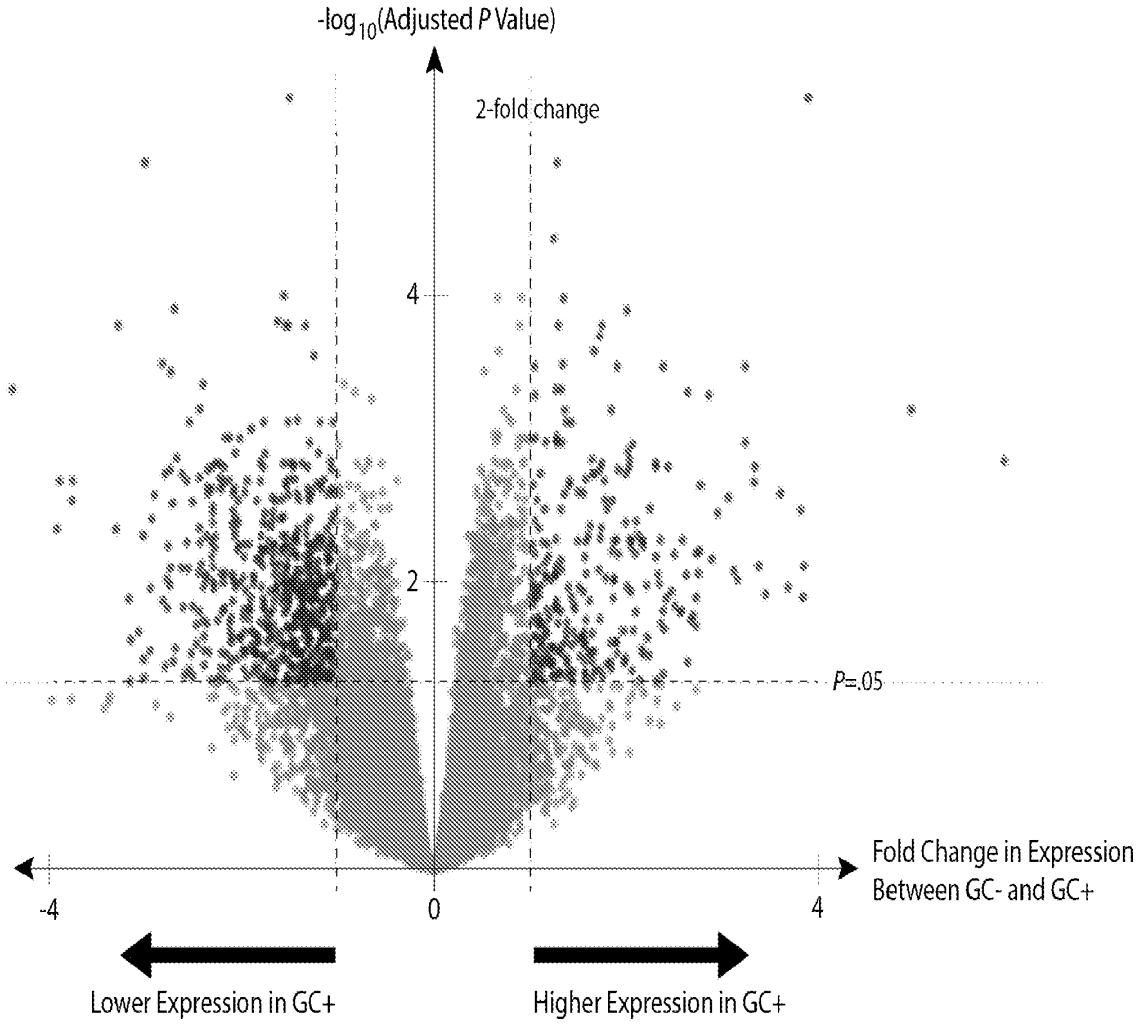

-log10(Adjusted P Value)
2-fold change
4
2
P=.05
-4
0
4
Fold Change in Expression
Between GC- and GC+
Lower Expression in GC+
Higher Expression in GC+

Fig. 3B

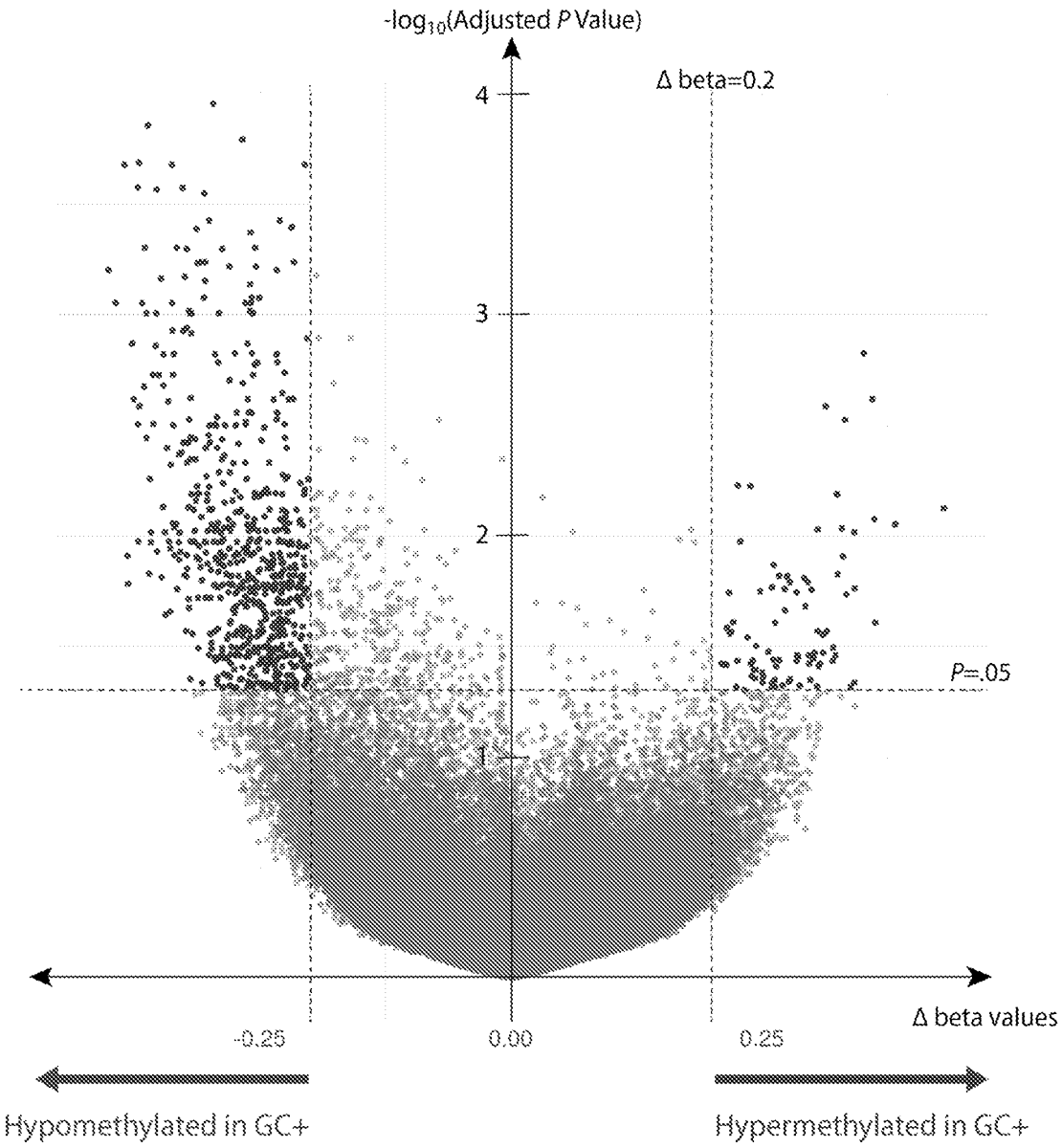

-log10(Adjusted P Value)
Δ beta=0.2
4
3
2
1
P=.05
Δ beta values
-0.25
0.00
0.25
Hypomethylated in GC+
Hypermethylated in GC+

Fig. 4

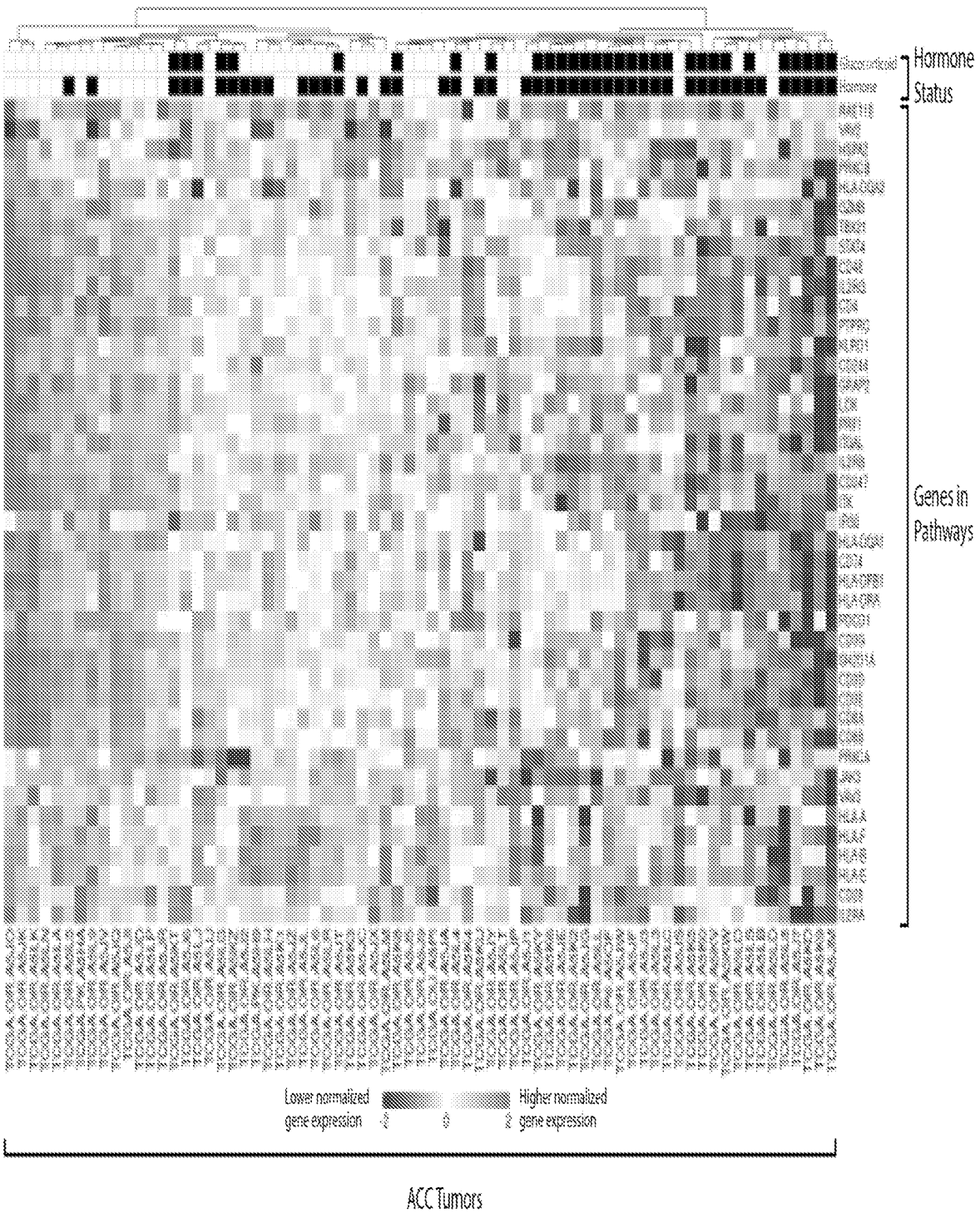

Hormone Status
Genes in Pathways
Lower normalized gene expression
Higher normalized gene expression
ACC Tumors

Fig. 5

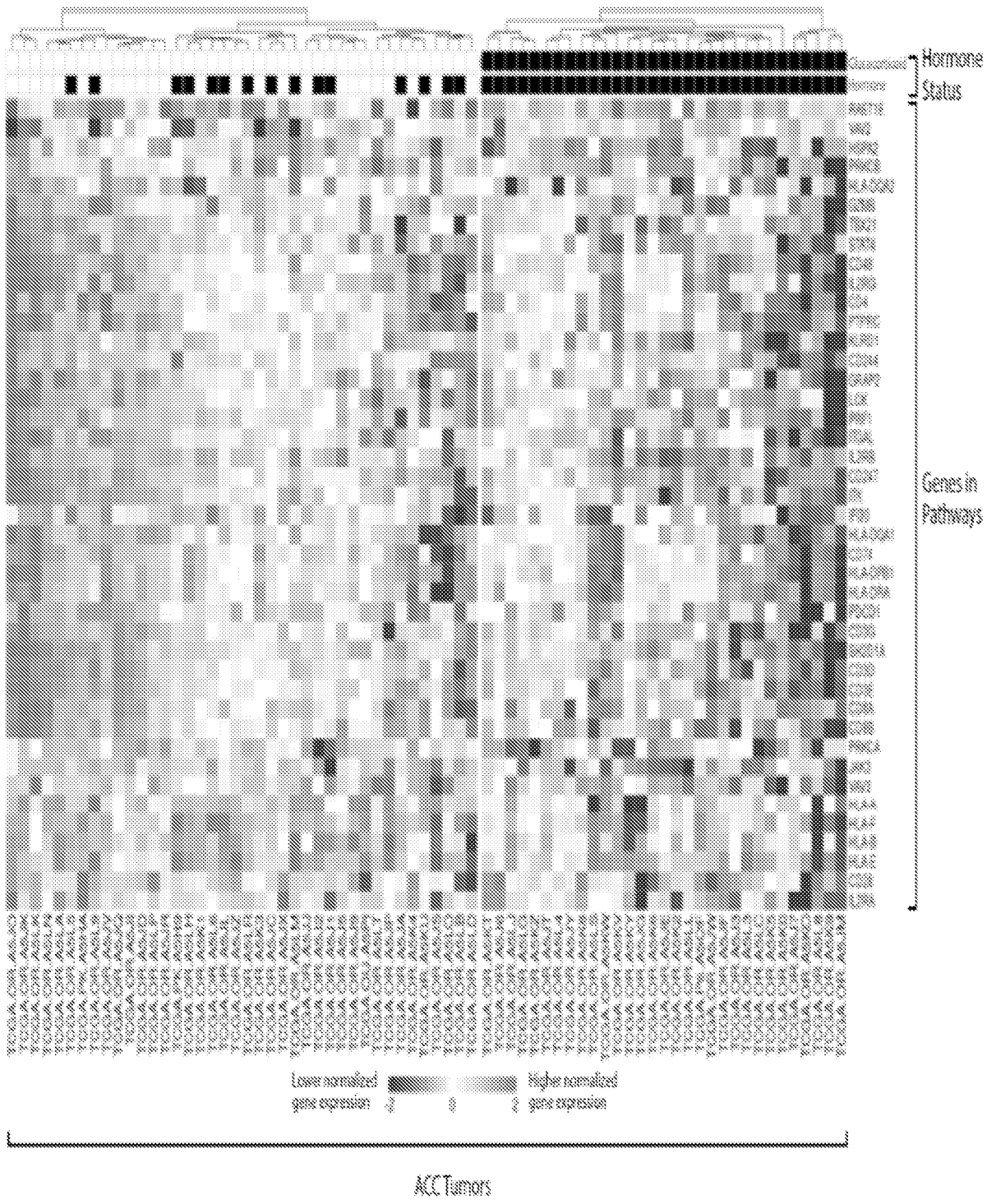

Hormone Status
Genes in Pathways
Lower normalized gene expression
Higher normalized gene expression
ACC Tumors

Fig. 6

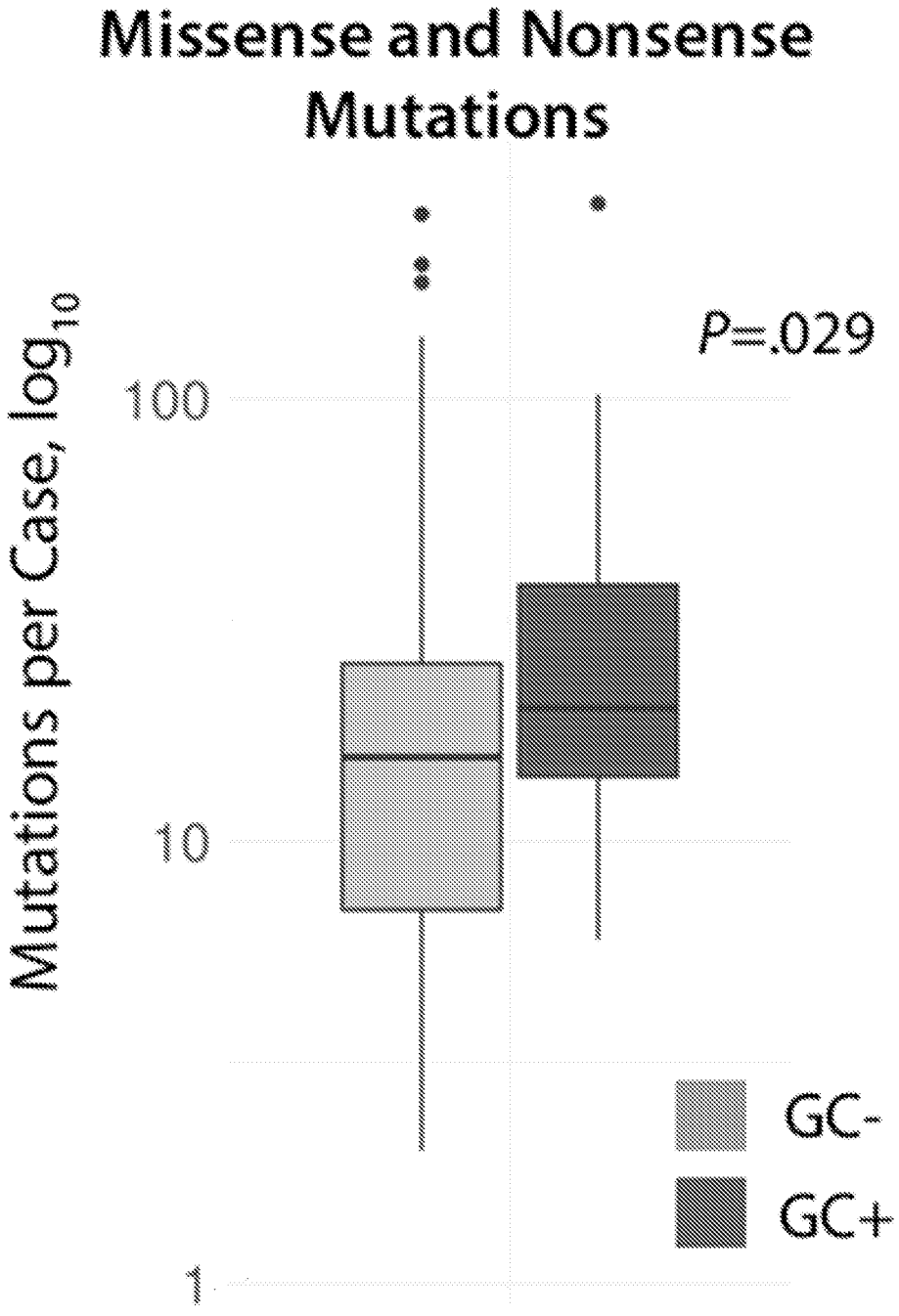

Missense and Nonsense Mutations
Mutations per Case, log10
100
10
1
P=.029
GC-
GC+

Fig. 7

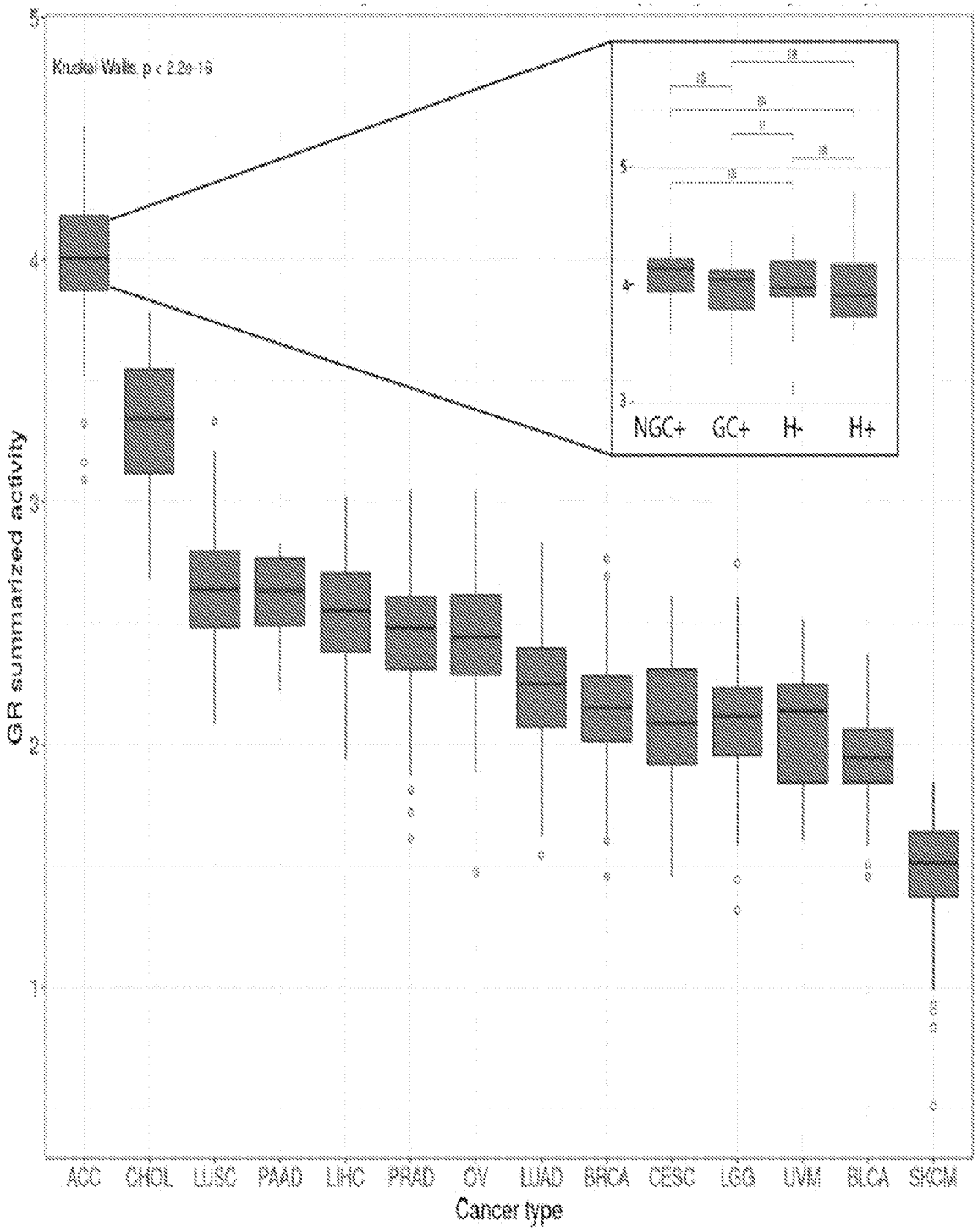

Kruskal Wallis, p < 2.2e-16
NGC+
GC+
H-
H+
GR summarized activity
Cancer type
ACC
CHOL
LUSC
PAAD
LIHC
PRAD
OV
LUAD
BRCA
CESC
LGG
UVM
BLCA
SKCM

Fig. 8

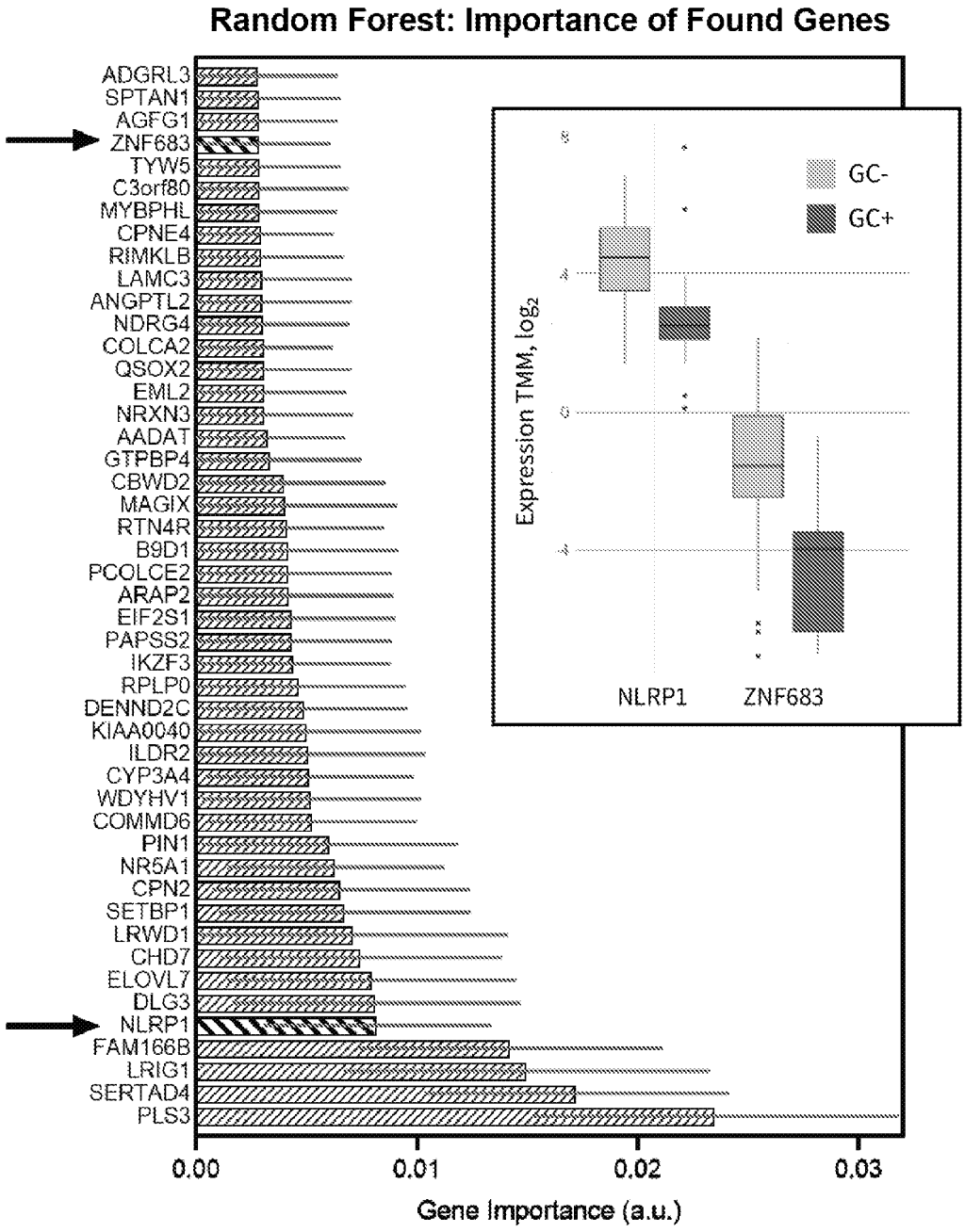

Random Forest: Importance of Found Genes
ADGRL3
SPTAN1
AGFG1
ZNF683
TYW5
C3orf80
MYBPHL
CPNE4
RIMKLB
LAMC3
ANGPTL2
NDRG4
COLCA2
QSOX2
EML2
NRXN3
AADAT
GTPBP4
CBWD2
MAGIX
RTN4R
B9D1
PCOLCE2
ARAP2
EIF2S1
PAPSS2
IKZF3
RPLP0
DENND2C
KIAA0040
ILDR2
CYP3A4
WDYHV1
COMMD6
PIN1
NR5A1
CPN2
SETBP1
LRWD1
CHD7
ELOVL7
DLG3
NLRP1
FAM166B
LRIG1
SERTAD4
PLS3
0.00
0.01
0.02
0.03
Gene Importance (a.u.)
GC-
GC+
Expression TMM, log2
NLRP1
ZNF683

Fig. 9

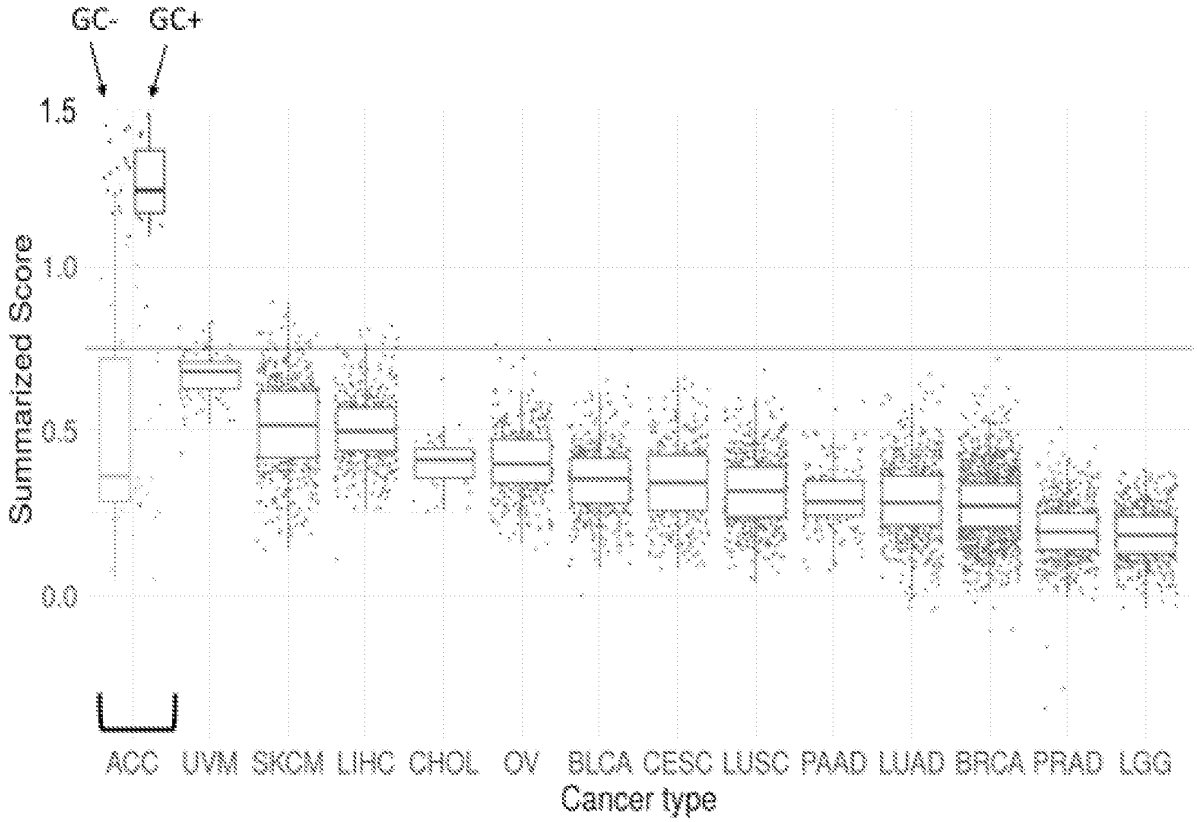

GC-
GC+
1.5
1.0
0.5
0.0
Summarized Score
ACC
UVM
SKCM
LIHC
CHOL
OV
BLCA
CESC
LUSC
PAAD
LUAD
BRCA
PRAD
LGG
Cancer type

Fig. 10A

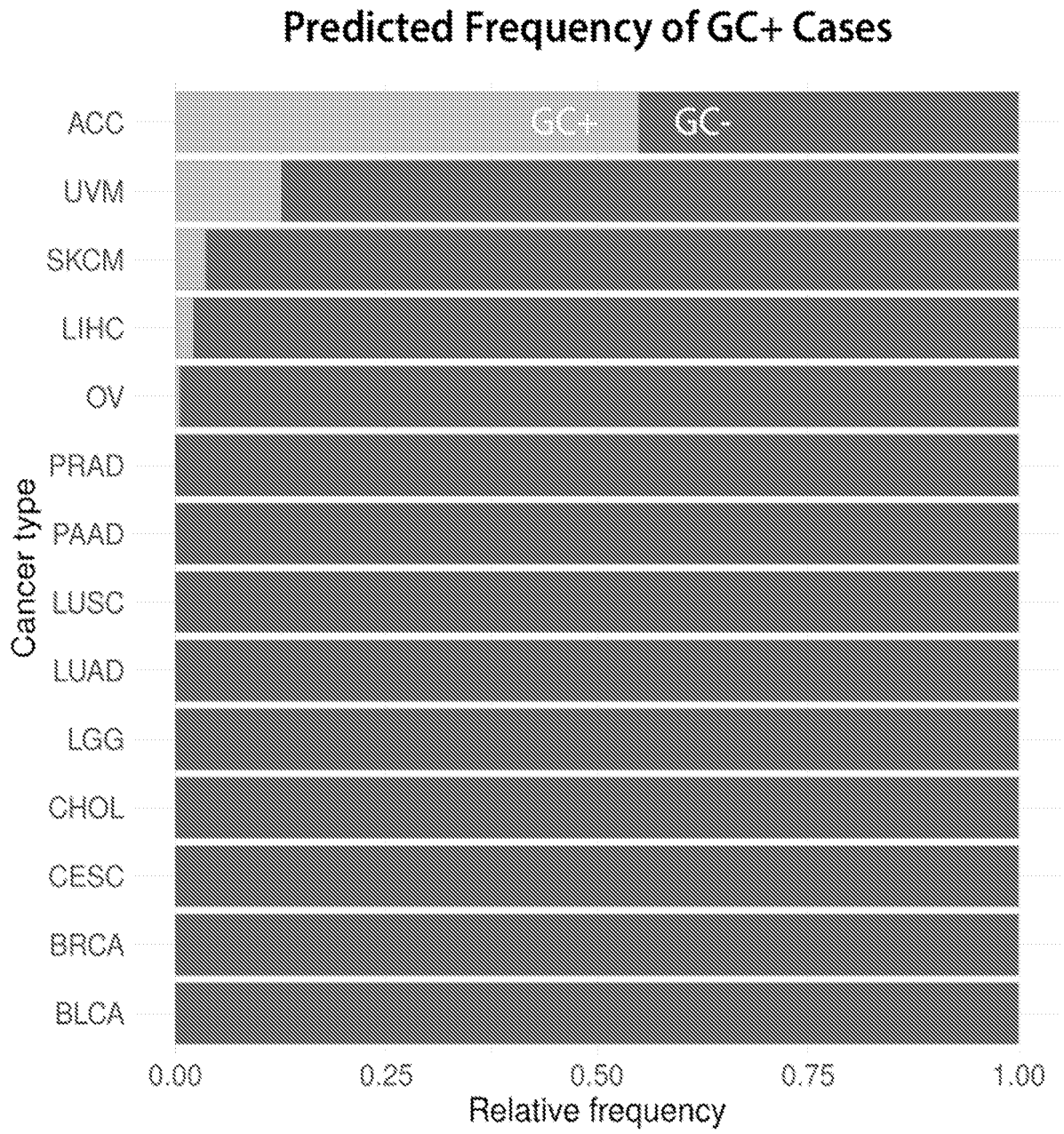

Predicted Frequency of GC+ Cases
GC+
GC-
ACC
UVM
SKCM
LIHC
OV
PRAD
PAAD
LUSC
LUAD
LGG
CHOL
CESC
BRCA
BLCA
Cancer type
0.00
0.25
0.50
0.75
1.00
Relative frequency

Fig. 10B

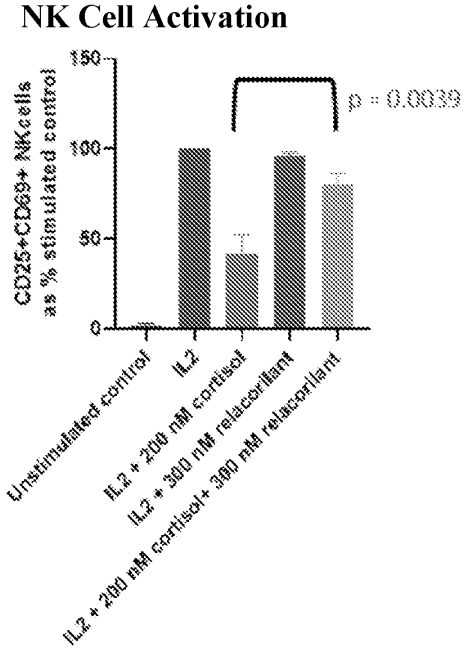


Fig. 11A

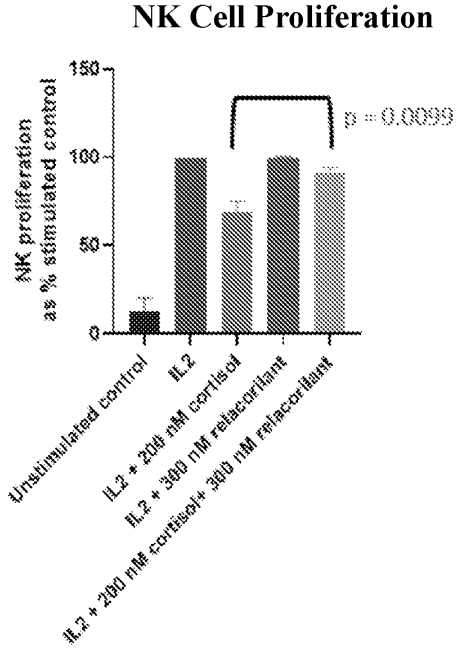


Fig. 11B

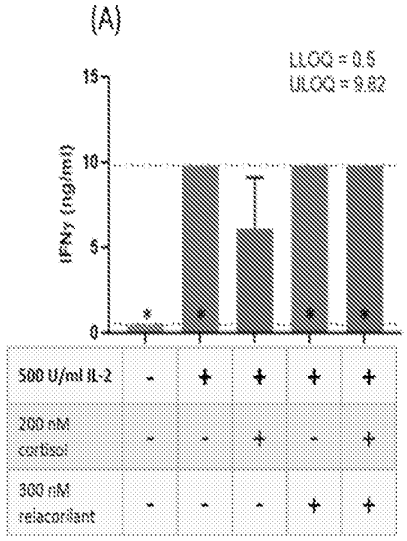


Fig. 12A

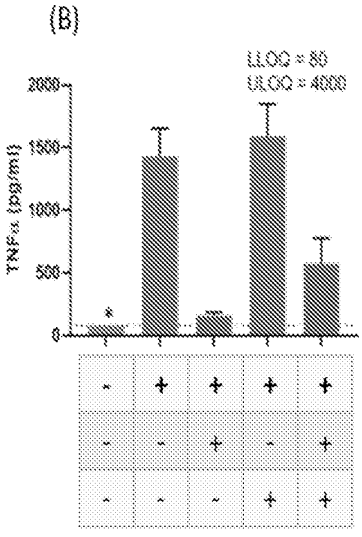


Fig. 12B

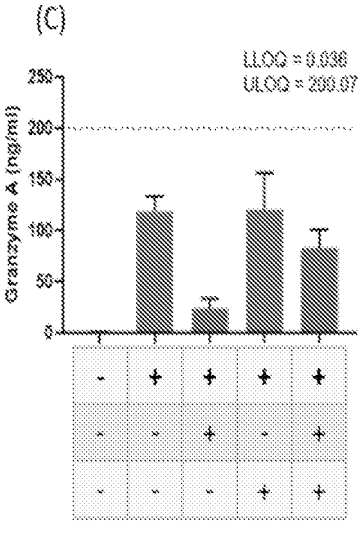
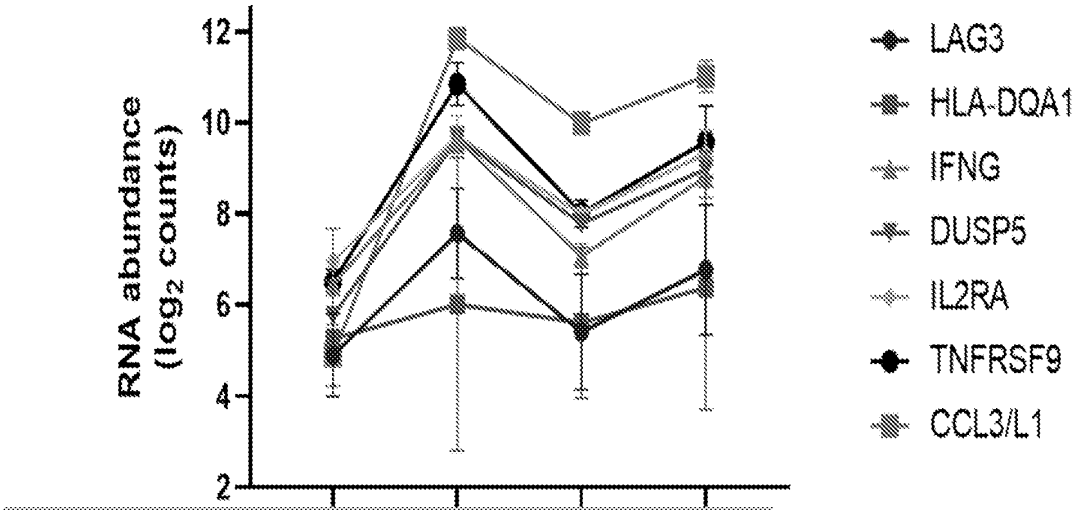


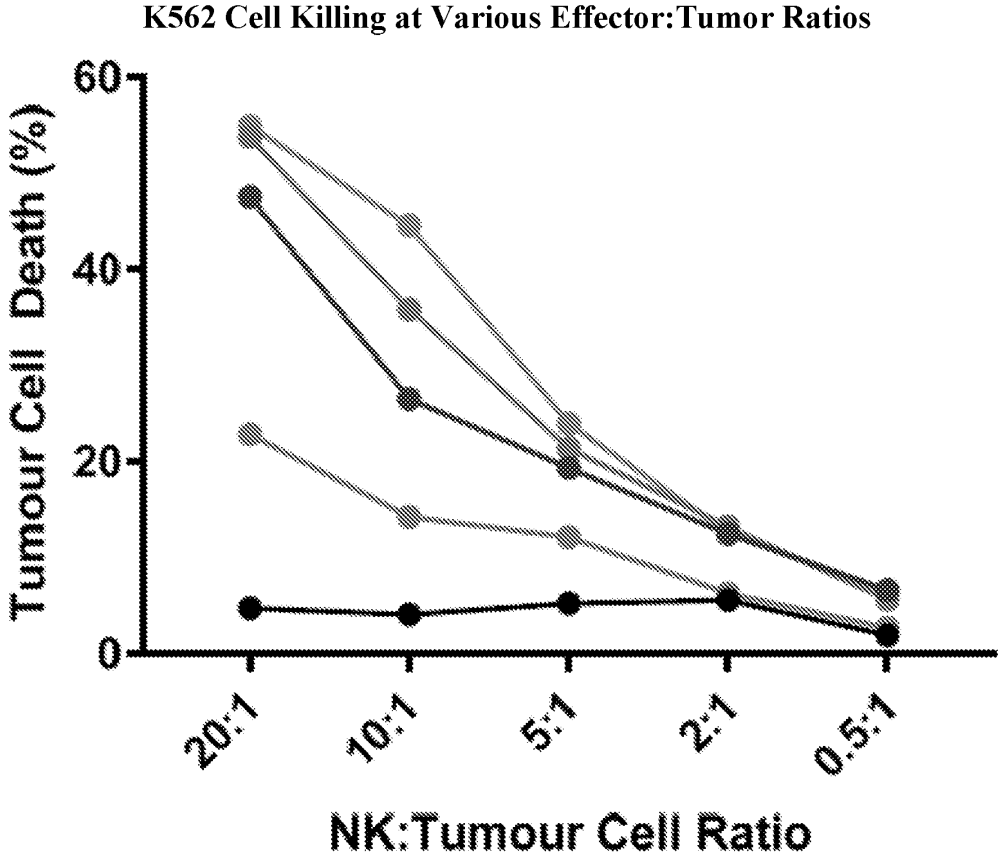
Fig. 12C

NK Cells



500 U/ml IL-2	-	+	+	+
200 nM cortisol	-	-	+	+
300 nM relacorilant	-	-	-	+

Fig. 12D



500 U/ml IL-2	-	+	+	+	+
200 nM cortisol	-	-	+	-	+
300 nM relacorilant	-	-	-	+	+

Fig. 13A

K562 Cell Killing (5:1 Ratio)

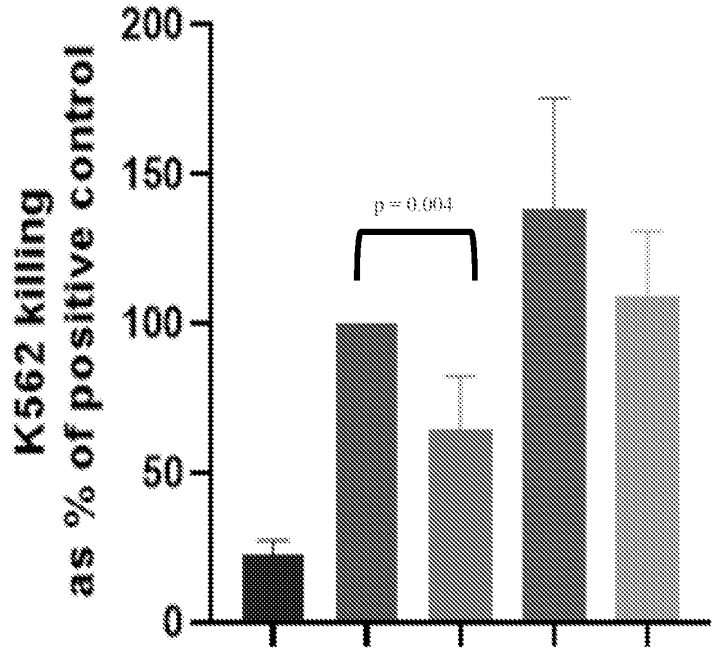


Fig. 13B