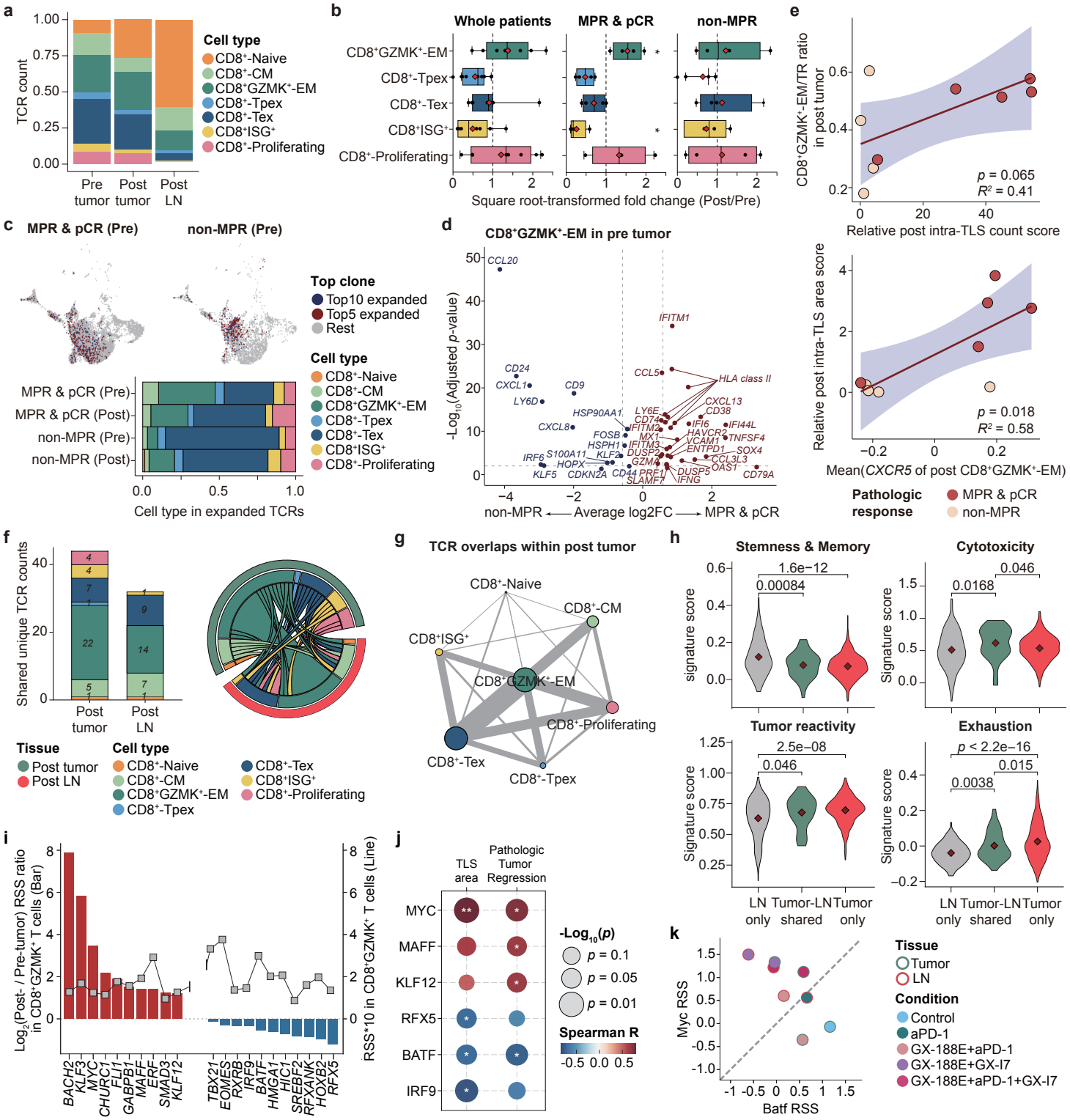

a
TCR count
Pre tumor
Post tumor
Post LN
Cell type
CD8+-Naive
CD8+-CM
CD8+GZMK+-EM
CD8+-Tpex
CD8+-Tex
CD8+ISG+
CD8+-Proliferating
b
Whole patients
MPR & pCR
non-MPR
Square root-transformed fold change (Post/Pre)
e
CD8+GZMK+-EM/TR ratio in post tumor
p = 0.065
R² = 0.41
Relative post intra-TLS count score
Relative post intra-TLS area score
p = 0.018
R² = 0.58
Mean(CXCR5 of post CD8+GZMK+-EM)
Pathologic response
MPR & pCR
non-MPR
c
MPR & pCR (Pre)
non-MPR (Pre)
Top clone
Top10 expanded
Top5 expanded
Rest
MPR & pCR (Pre)
MPR & pCR (Post)
non-MPR (Pre)
non-MPR (Post)
Cell type in expanded TCRs
d
CD8+GZMK+-EM in pre tumor
-Log10(Adjusted p-value)
non-MPR ← Average log2FC → MPR & pCR
f
Shared unique TCR counts
Post tumor
Post LN
Tissue
Post tumor
Post LN
g
TCR overlaps within post tumor
CD8+-Naive
CD8+-CM
CD8+ISG+
CD8+GZMK+-EM
CD8+-Proliferating
CD8+-Tex
CD8+-Tpex
h
Stemness & Memory
Cytotoxicity
Tumor reactivity
Exhaustion
signature score
1.6e−12
0.00084
0.046
0.0168
2.5e−08
0.046
p < 2.2e−16
0.015
0.0038
LN only
Tumor-LN shared
Tumor only
i
Log2(Post- / Pre-tumor) RSS ratio in CD8+GZMK+ T cells (Bar)
RSS*10 in CD8+GZMK+ T cells (Line)
BACH2
KLF3
MYC
CHURC1
FLI1
GABPB1
MAFF
ERF
SMAD3
KLF12
TBX21
EOMES
RXRB
IRF9
BATF
HMGA1
HIC1
SREBF2
RFXANK
HOXB2
RFX5
j
TLS area
Pathologic Tumor Regression
MYC
MAFF
KLF12
RFX5
BATF
IRF9
-Log10(p)
p = 0.1
p = 0.05
p = 0.01
Spearman R
-0.5 0.0 0.5
k
Myc RSS
Batf RSS
Tissue
Tumor
LN
Condition
Control
aPD-1
GX-188E+aPD-1
GX-188E+GX-I7
GX-188E+aPD-1+GX-I7

Figure 5