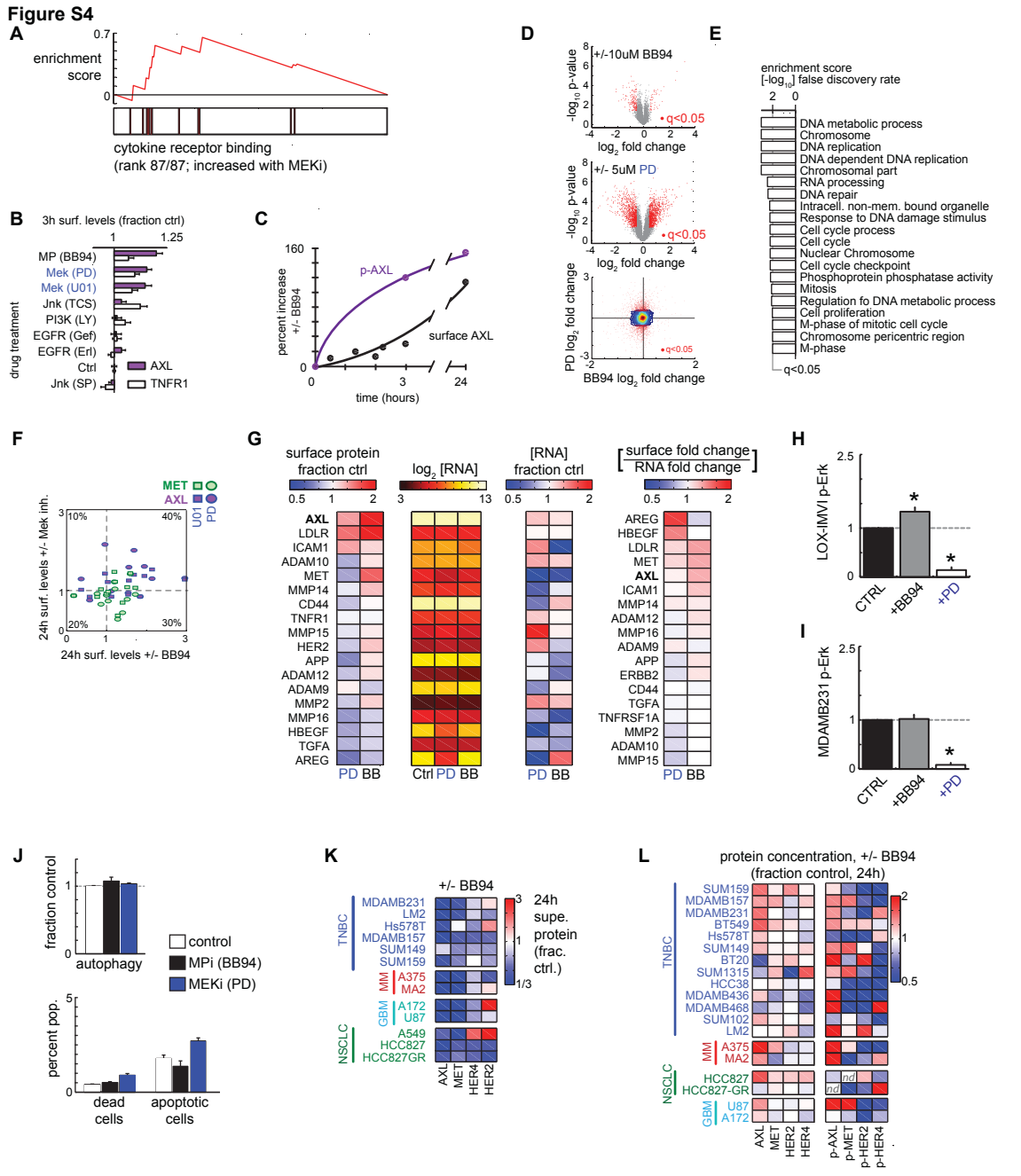
Figure S4


A
enrichment score
0.7
0
cytokine receptor binding
(rank 87/87; increased with MEKi)
B
3h surf. levels (fraction ctrl)
1
1.25
drug treatment
MP (BB94)
Mek (PD)
Mek (U01)
Jnk (TCS)
PI3K (LY)
EGFR (Gef)
EGFR (Erl)
Ctrl
Jnk (SP)
AXL
TNFR1
C
160
0
percent increase +/- BB94
p-AXL
surface AXL
0
3
24
time (hours)
D
+/-10uM BB94
-log10 p-value
q<0.05
log2 fold change
+/- 5uM PD
-log10 p-value
q<0.05
log2 fold change
PD log2 fold change
q<0.05
BB94 log2 fold change
E
enrichment score
[-log10] false discovery rate
2
0
DNA metabolic process
Chromosome
DNA replication
DNA dependent DNA replication
Chromosomal part
RNA processing
DNA repair
Intracell. non-mem. bound organelle
Response to DNA damage stimulus
Cell cycle process
Cell cycle
Nuclear Chromosome
Cell cycle checkpoint
Phosphoprotein phosphatase activity
Mitosis
Regulation fo DNA metabolic process
Cell proliferation
M-phase of mitotic cell cycle
Chromosome pericentric region
M-phase
q<0.05
F
MET
AXL
U01
PD
24h surf. levels +/- Mek inh.
10%
40%
20%
30%
24h surf. levels +/- BB94
G
surface protein fraction ctrl
0.5
1
2
AXL
LDLR
ICAM1
ADAM10
MET
MMP14
CD44
TNFR1
MMP15
HER2
APP
ADAM12
ADAM9
MMP2
MMP16
HBEGF
TGFA
AREG
PD BB
log2 [RNA]
3
13
Ctrl PD BB
[RNA] fraction ctrl
0.5
1
2
PD BB
[surface fold change / RNA fold change]
0.5
1
2
AREG
HBEGF
LDLR
MET
AXL
ICAM1
MMP14
ADAM12
MMP16
ADAM9
APP
ERBB2
CD44
TGFA
TNFRSF1A
MMP2
ADAM10
MMP15
PD BB
H
LOX-IMVI p-Erk
2.5
1
0
CTRL
+BB94
+PD
I
MDAMB231 p-Erk
2.5
1
0
CTRL
+BB94
+PD
J
fraction control
1
0
autophagy
control
MPi (BB94)
MEKi (PD)
percent pop.
5
0
dead cells
apoptotic cells
K
+/- BB94
TNBC
MDAMB231
LM2
Hs578T
MDAMB157
SUM149
SUM159
MM
A375
MA2
GBM
A172
U87
NSCLC
A549
HCC827
HCC827GR
AXL
MET
HER4
HER2
3
1
1/3
24h supe. protein (frac. ctrl.)
L
protein concentration, +/- BB94
(fraction control, 24h)
TNBC
SUM159
MDAMB157
MDAMB231
BT549
Hs578T
SUM149
BT20
SUM1315
HCC38
MDAMB436
MDAMB468
SUM102
LM2
MM
A375
MA2
NSCLC
HCC827
HCC827-GR
nd
GBM
U87
A172
AXL
MET
HER2
HER4
p-AXL
p-MET
p-HER2
p-HER4
2
1
0.5