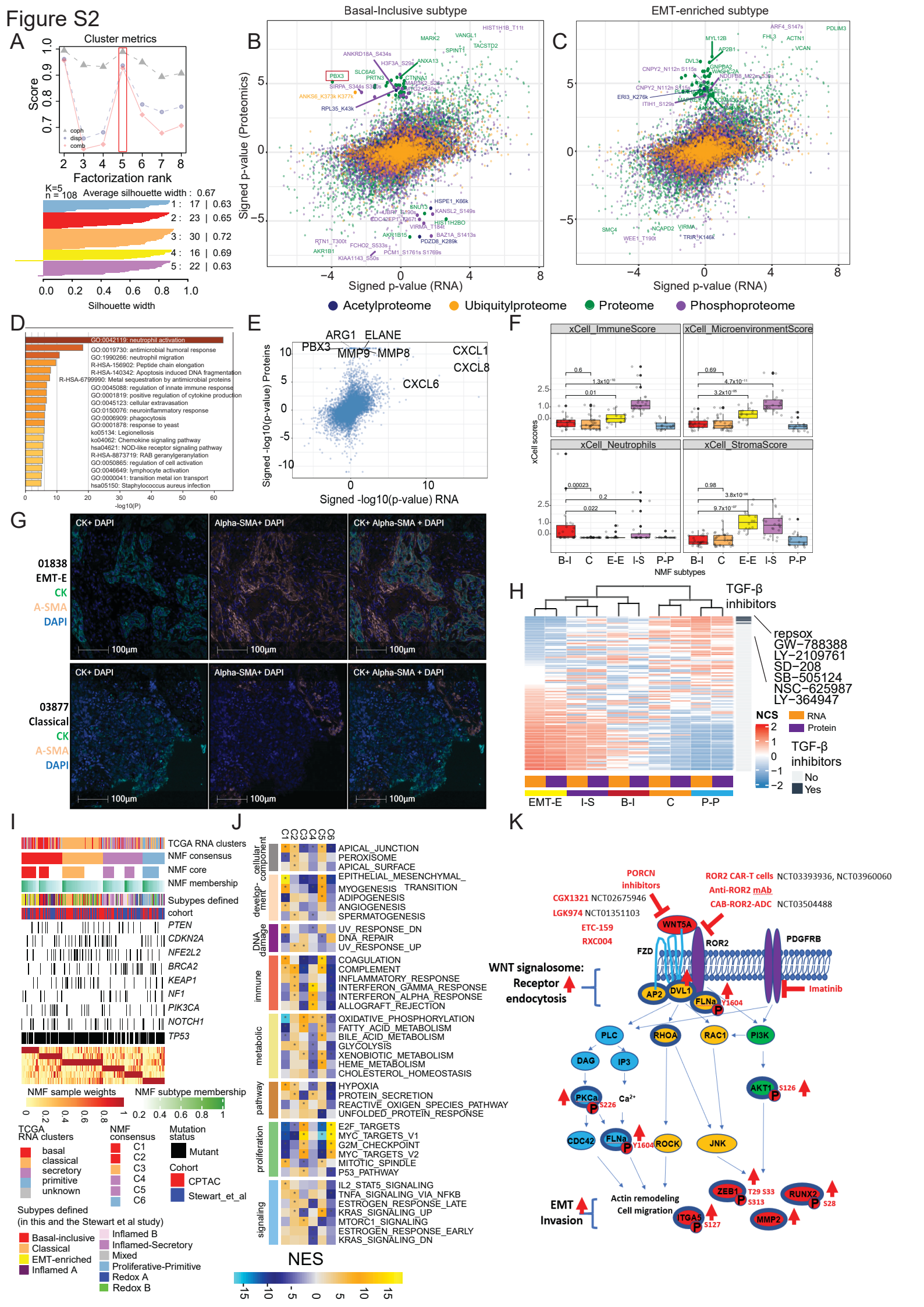
Figure S2


A
Cluster metrics
Score
Factorization rank
coph
disp
comb
K=5
n = 108
Average silhouette width : 0.67
1 : 17 | 0.63
2 : 23 | 0.65
3 : 30 | 0.72
4 : 16 | 0.69
5 : 22 | 0.63
Silhouette width
B
Basal-Inclusive subtype
Signed p-value (Proteomics)
Signed p-value (RNA)
C
EMT-enriched subtype
Signed p-value (RNA)
Acetylproteome
Ubiquitylproteome
Proteome
Phosphoproteome
D
GO:0042119: neutrophil activation
GO:0019730: antimicrobial humoral response
GO:1990266: neutrophil migration
R-HSA-156902: Peptide chain elongation
R-HSA-140342: Apoptosis induced DNA fragmentation
R-HSA-6799990: Metal sequestration by antimicrobial proteins
GO:0045088: regulation of innate immune response
GO:0001819: positive regulation of cytokine production
GO:0045123: cellular extravasation
GO:0150076: neuroinflammatory response
GO:0006909: phagocytosis
GO:0001878: response to yeast
ko05134: Legionellosis
ko04062: Chemokine signaling pathway
hsa04621: NOD-like receptor signaling pathway
R-HSA-8873719: RAB geranylgeranylation
GO:0050865: regulation of cell activation
GO:0046649: lymphocyte activation
GO:0000041: transition metal ion transport
hsa05150: Staphylococcus aureus infection
-log10(P)
E
ARG1
ELANE
PBX3
MMP9
MMP8
CXCL1
CXCL8
CXCL6
Signed -log10(p-value) Proteins
Signed -log10(p-value) RNA
F
xCell_ImmuneScore
xCell_MicroenvironmentScore
xCell_Neutrophils
xCell_StromaScore
xCell scores
B-I
C
E-E
I-S
P-P
NMF subtypes
G
CK+ DAPI
Alpha-SMA+ DAPI
CK+ Alpha-SMA + DAPI
01838
EMT-E
CK
A-SMA
DAPI
03877
Classical
100μm
H
TGF-β inhibitors
repsox
GW−788388
LY−2109761
SD−208
SB−505124
NSC−625987
LY−364947
NCS
RNA
Protein
No
Yes
EMT-E
I-S
B-I
C
P-P
I
TCGA RNA clusters
NMF consensus
NMF core
NMF membership
Subypes defined
cohort
PTEN
CDKN2A
NFE2L2
BRCA2
KEAP1
NF1
PIK3CA
NOTCH1
TP53
NMF sample weights
NMF subtype membership
TCGA RNA clusters
basal
classical
secretory
primitive
unknown
NMF consensus
C1
C2
C3
C4
C5
C6
Mutation status
Mutant
Cohort
CPTAC
Stewart_et_al
Subypes defined
(in this and the Stewart et al study)
Basal-inclusive
Classical
EMT-enriched
Inflamed A
Inflamed B
Inflamed-Secretory
Mixed
Proliferative-Primitive
Redox A
Redox B
J
cellular component
develop-ment
DNA damage
immune
metabolic
pathway
proliferation
signaling
APICAL_JUNCTION
PEROXISOME
APICAL_SURFACE
EPITHELIAL_MESENCHYMAL_TRANSITION
MYOGENESIS
ADIPOGENESIS
ANGIOGENESIS
SPERMATOGENESIS
UV_RESPONSE_DN
DNA_REPAIR
UV_RESPONSE_UP
COAGULATION
COMPLEMENT
INFLAMMATORY_RESPONSE
INTERFERON_GAMMA_RESPONSE
INTERFERON_ALPHA_RESPONSE
ALLOGRAFT_REJECTION
OXIDATIVE_PHOSPHORYLATION
FATTY_ACID_METABOLISM
BILE_ACID_METABOLISM
GLYCOLYSIS
XENOBIOTIC_METABOLISM
HEME_METABOLISM
CHOLESTEROL_HOMEOSTASIS
HYPOXIA
PROTEIN_SECRETION
REACTIVE_OXIGEN_SPECIES_PATHWAY
UNFOLDED_PROTEIN_RESPONSE
E2F_TARGETS
MYC_TARGETS_V1
G2M_CHECKPOINT
MYC_TARGETS_V2
MITOTIC_SPINDLE
P53_PATHWAY
IL2_STAT5_SIGNALING
TNFA_SIGNALING_VIA_NFKB
ESTROGEN_RESPONSE_LATE
KRAS_SIGNALING_UP
MTORC1_SIGNALING
ESTROGEN_RESPONSE_EARLY
KRAS_SIGNALING_DN
NES
K
PORCN inhibitors
CGX1321 NCT02675946
LGK974 NCT01351103
ETC-159
RXC004
ROR2 CAR-T cells NCT03393936, NCT03960060
Anti-ROR2 mAb
CAB-ROR2-ADC NCT03504488
WNT5A
FZD
ROR2
PDGFRB
Imatinib
WNT signalosome:
Receptor endocytosis
AP2
DVL1
FLNa
Y1604
PLC
RHOA
RAC1
PI3K
DAG
IP3
PKCa
S226
Ca2+
AKT1
S126
CDC42
ROCK
JNK
EMT
Invasion
Actin remodeling
Cell migration
ITGA5
S127
ZEB1
T29 S33
S313
RUNX2
S28
MMP2