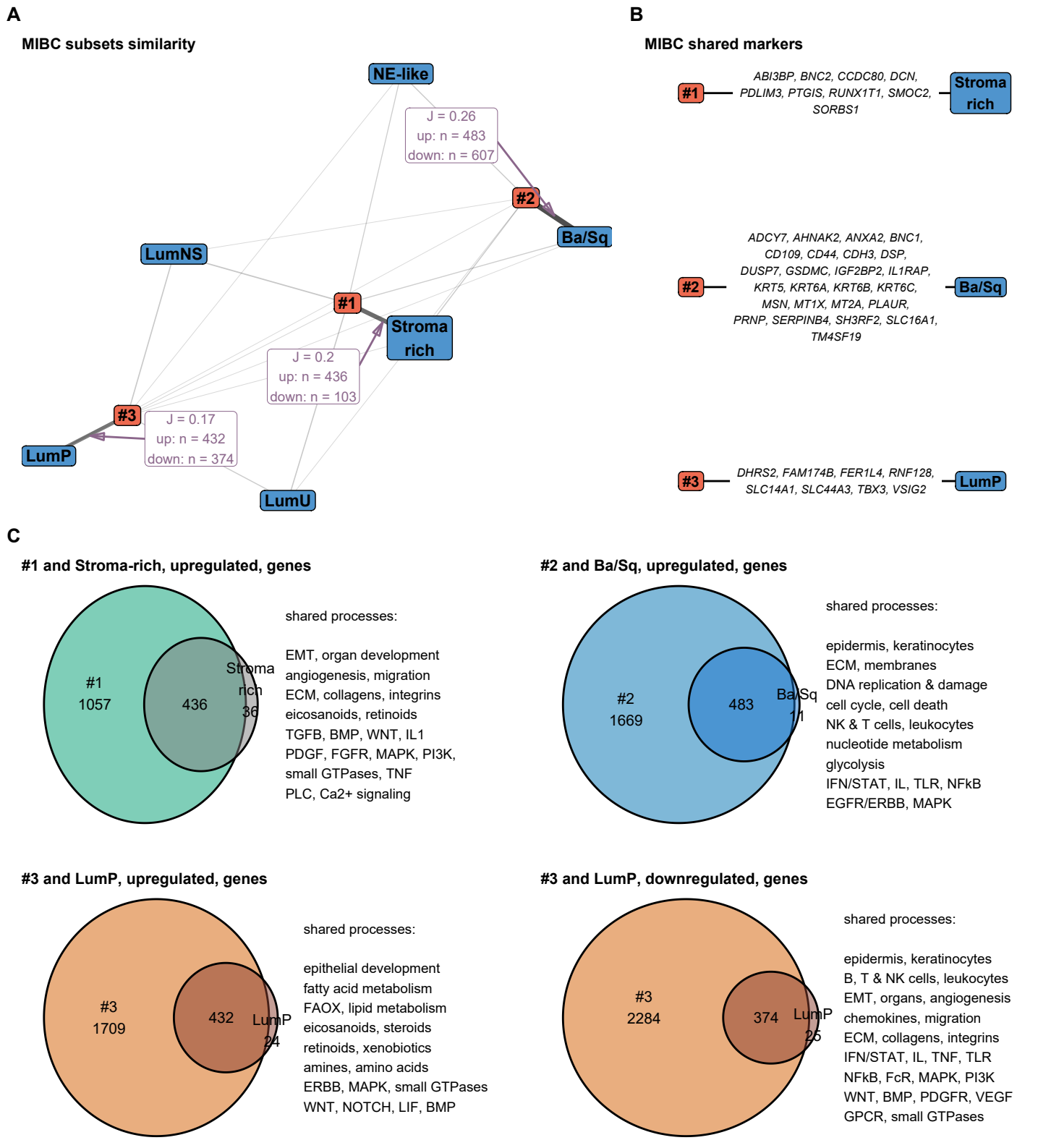
A
MIBC subsets similarity
NE-like
J = 0.26
up: n = 483
down: n = 607
#2
Ba/Sq
LumNS
#1
Stroma rich
J = 0.2
up: n = 436
down: n = 103
#3
J = 0.17
up: n = 432
down: n = 374
LumP
LumU
B
MIBC shared markers
#1
ABI3BP, BNC2, CCDC80, DCN, PDLIM3, PTGIS, RUNX1T1, SMOC2, SORBS1
Stroma rich
#2
ADCY7, AHNAK2, ANXA2, BNC1, CD109, CD44, CDH3, DSP, DUSP7, GSDMC, IGF2BP2, IL1RAP, KRT5, KRT6A, KRT6B, KRT6C, MSN, MT1X, MT2A, PLAUR, PRNP, SERPINB4, SH3RF2, SLC16A1, TM4SF19
Ba/Sq
#3
DHRS2, FAM174B, FER1L4, RNF128, SLC14A1, SLC44A3, TBX3, VSIG2
LumP
C
#1 and Stroma-rich, upregulated, genes
#1
1057
436
Stroma rich
36
shared processes:
EMT, organ development
angiogenesis, migration
ECM, collagens, integrins
eicosanoids, retinoids
TGFB, BMP, WNT, IL1
PDGF, FGFR, MAPK, PI3K,
small GTPases, TNF
PLC, Ca2+ signaling
#2 and Ba/Sq, upregulated, genes
#2
1669
483
Ba/Sq
11
shared processes:
epidermis, keratinocytes
ECM, membranes
DNA replication & damage
cell cycle, cell death
NK & T cells, leukocytes
nucleotide metabolism
glycolysis
IFN/STAT, IL, TLR, NFkB
EGFR/ERBB, MAPK
#3 and LumP, upregulated, genes
#3
1709
432
LumP
24
shared processes:
epithelial development
fatty acid metabolism
FAOX, lipid metabolism
eicosanoids, steroids
retinoids, xenobiotics
amines, amino acids
ERBB, MAPK, small GTPases
WNT, NOTCH, LIF, BMP
#3 and LumP, downregulated, genes
#3
2284
374
LumP
25
shared processes:
epidermis, keratinocytes
B, T & NK cells, leukocytes
EMT, organs, angiogenesis
chemokines, migration
ECM, collagens, integrins
IFN/STAT, IL, TNF, TLR
NFkB, FcR, MAPK, PI3K
WNT, BMP, PDGFR, VEGF
GPCR, small GTPases