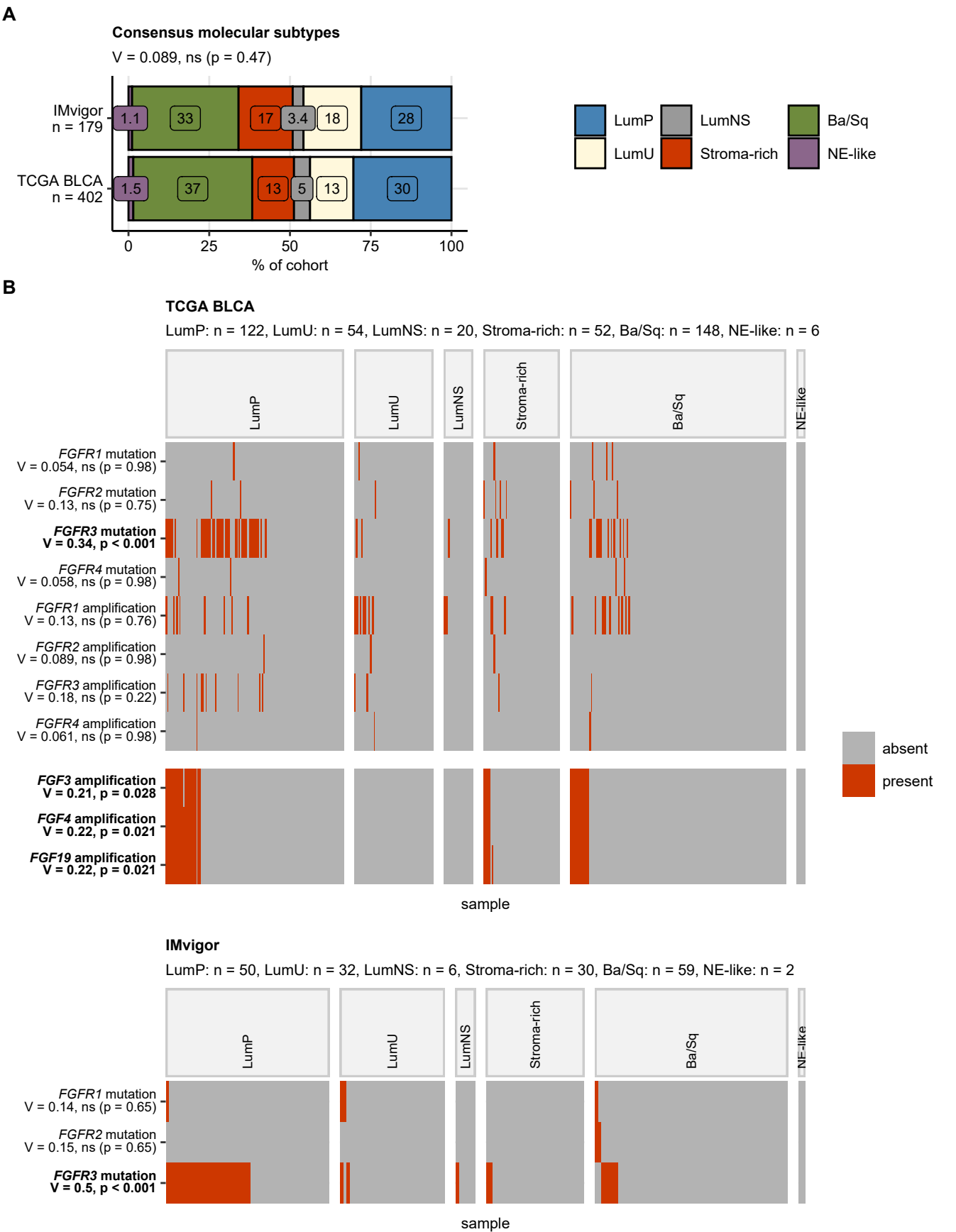
A
Consensus molecular subtypes
V = 0.089, ns (p = 0.47)
IMvigor
n = 179
TCGA BLCA
n = 402
1.1
33
17
3.4
18
28
1.5
37
13
5
13
30
0
25
50
75
100
% of cohort
LumP
LumNS
Ba/Sq
LumU
Stroma-rich
NE-like
B
TCGA BLCA
LumP: n = 122, LumU: n = 54, LumNS: n = 20, Stroma-rich: n = 52, Ba/Sq: n = 148, NE-like: n = 6
FGFR1 mutation
V = 0.054, ns (p = 0.98)
FGFR2 mutation
V = 0.13, ns (p = 0.75)
FGFR3 mutation
V = 0.34, p < 0.001
FGFR4 mutation
V = 0.058, ns (p = 0.98)
FGFR1 amplification
V = 0.13, ns (p = 0.76)
FGFR2 amplification
V = 0.089, ns (p = 0.98)
FGFR3 amplification
V = 0.18, ns (p = 0.22)
FGFR4 amplification
V = 0.061, ns (p = 0.98)
FGF3 amplification
V = 0.21, p = 0.028
FGF4 amplification
V = 0.22, p = 0.021
FGF19 amplification
V = 0.22, p = 0.021
absent
present
sample
IMvigor
LumP: n = 50, LumU: n = 32, LumNS: n = 6, Stroma-rich: n = 30, Ba/Sq: n = 59, NE-like: n = 2
FGFR1 mutation
V = 0.14, ns (p = 0.65)
FGFR2 mutation
V = 0.15, ns (p = 0.65)
FGFR3 mutation
V = 0.5, p < 0.001
sample