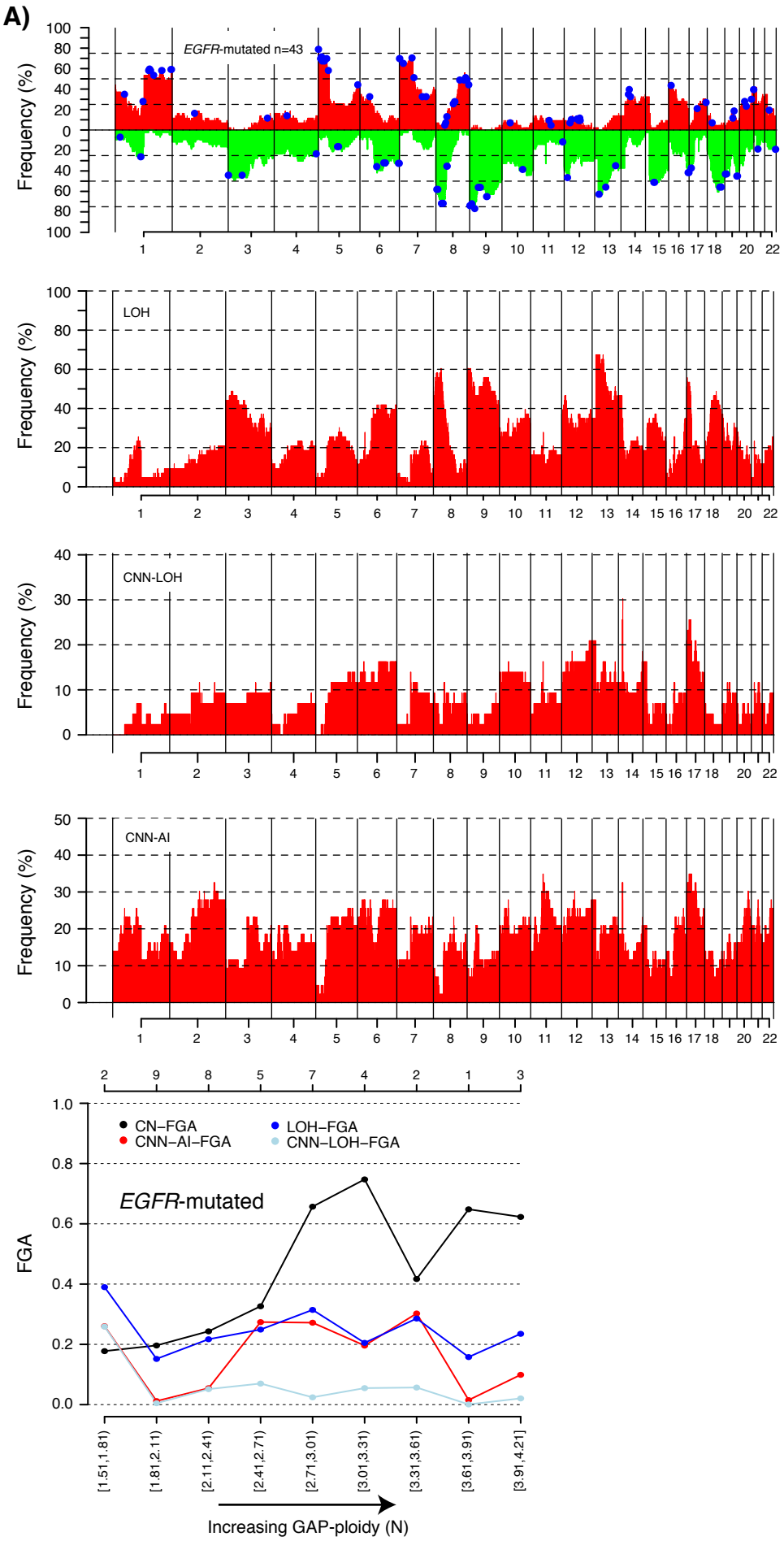
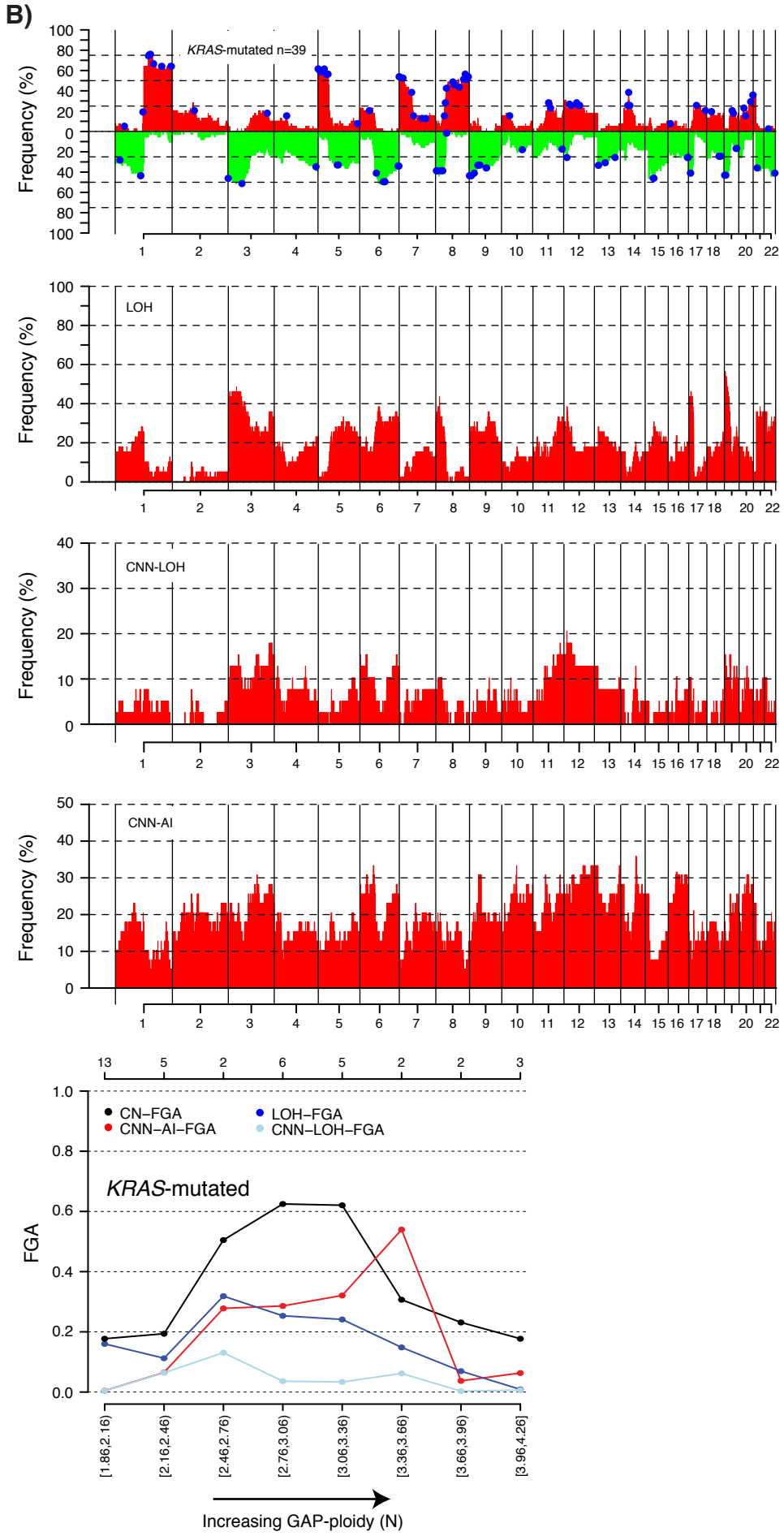
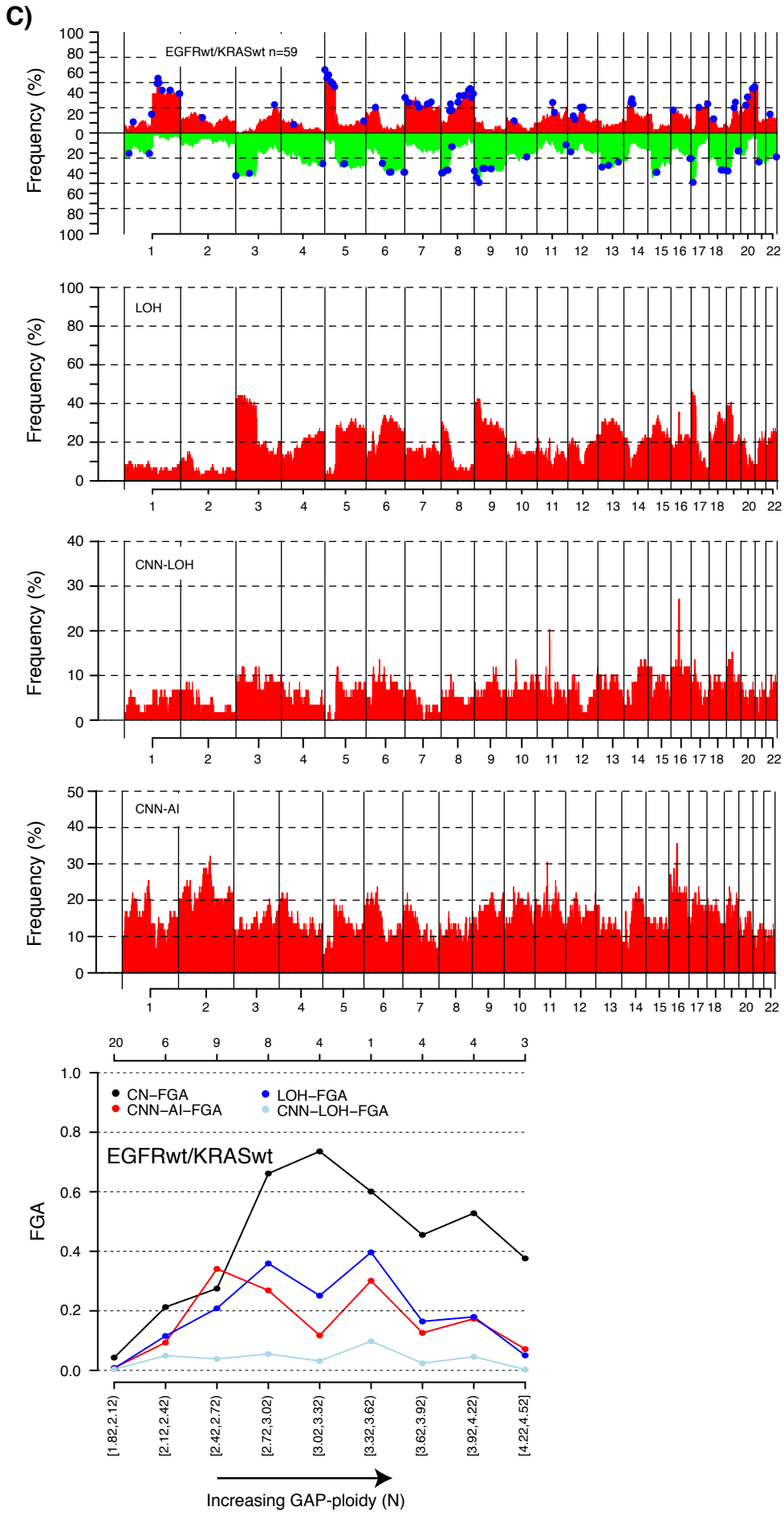

A)
EGFR-mutated n=43
Frequency (%)
LOH
CNN-LOH
CNN-AI
CN–FGA
LOH–FGA
CNN–AI–FGA
CNN–LOH–FGA
EGFR-mutated
FGA
[1.51,1.81)
[1.81,2.11)
[2.11,2.41)
[2.41,2.71)
[2.71,3.01)
[3.01,3.31)
[3.31,3.61)
[3.61,3.91)
[3.91,4.21]
Increasing GAP-ploidy (N)


B)
KRAS-mutated n=39
Frequency (%)
LOH
CNN-LOH
CNN-AI
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 20 22
13 5 2 6 5 2 2 3
CN–FGA
CNN–AI–FGA
LOH–FGA
CNN–LOH–FGA
KRAS-mutated
FGA
[1.86,2.16)
[2.16,2.46)
[2.46,2.76)
[2.76,3.06)
[3.06,3.36)
[3.36,3.66)
[3.66,3.96)
[3.96,4.26]
Increasing GAP-ploidy (N)


C)
EGFRwt/KRASwt n=59
Frequency (%)
LOH
CNN-LOH
CNN-AI
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 20 22
20 6 9 8 4 1 4 4 3
CN–FGA
LOH–FGA
CNN–AI–FGA
CNN–LOH–FGA
EGFRwt/KRASwt
FGA
[1.82,2.12)
[2.12,2.42)
[2.42,2.72)
[2.72,3.02)
[3.02,3.32)
[3.32,3.62)
[3.62,3.92)
[3.92,4.22)
[4.22,4.52]
Increasing GAP-ploidy (N)