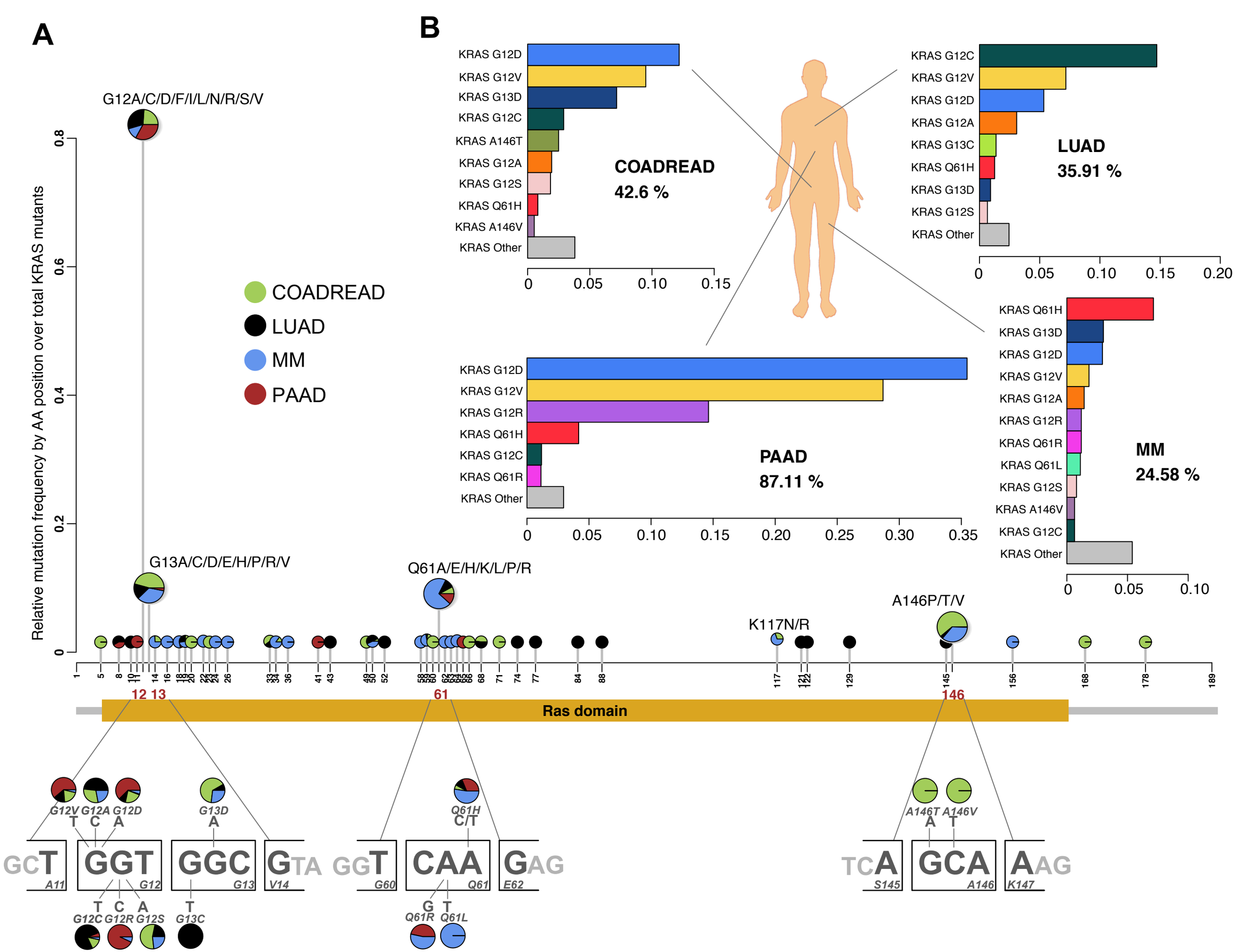
A
B
G12A/C/D/F/I/L/N/R/S/V
G13A/C/D/E/H/P/R/V
Q61A/E/H/K/L/P/R
K117N/R
A146P/T/V
Relative mutation frequency by AA position over total KRAS mutants
COADREAD
LUAD
MM
PAAD
COADREAD
42.6 %
LUAD
35.91 %
PAAD
87.11 %
MM
24.58 %
Ras domain
12 13
61
146
G12V G12A G12D
G13D
Q61H
A146T A146V
GCT
GGT
GGC
GTA
GGT
CAA
GAG
TCA
GCA
AAG
A11
G12
G13
V14
G60
Q61
E62
S145
A146
K147
G12C G12R G12S
G13C
Q61R Q61L