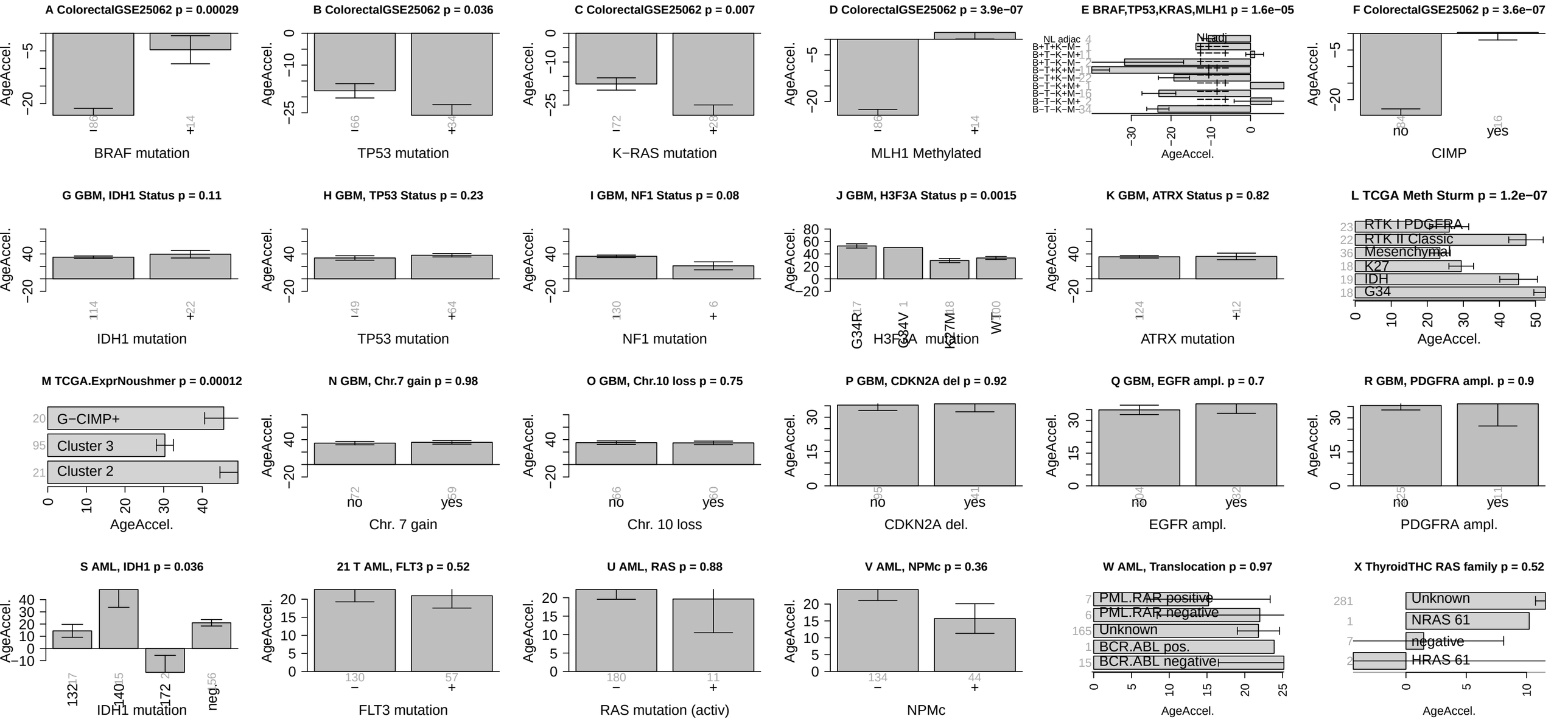
A ColorectalGSE25062 p = 0.00029
AgeAccel.
BRAF mutation
B ColorectalGSE25062 p = 0.036
TP53 mutation
C ColorectalGSE25062 p = 0.007
K−RAS mutation
D ColorectalGSE25062 p = 3.9e−07
MLH1 Methylated
E BRAF,TP53,KRAS,MLH1 p = 1.6e−05
NL adjac
B+T+K−M−
B+T−K−M+
B+T−K−M−
B−T+K+M−
B−T+K−M−
B−T−K+M+
B−T−K+M−
B−T−K−M+
B−T−K−M−
F ColorectalGSE25062 p = 3.6e−07
no
yes
CIMP
G GBM, IDH1 Status p = 0.11
IDH1 mutation
H GBM, TP53 Status p = 0.23
TP53 mutation
I GBM, NF1 Status p = 0.08
NF1 mutation
J GBM, H3F3A Status p = 0.0015
G34R
G34V
K27M
WT
H3F3A mutation
K GBM, ATRX Status p = 0.82
ATRX mutation
L TCGA Meth Sturm p = 1.2e−07
RTK I PDGFRA
RTK II Classic
Mesenchymal
K27
IDH
G34
M TCGA.ExprNoushmer p = 0.00012
G−CIMP+
Cluster 3
Cluster 2
N GBM, Chr.7 gain p = 0.98
Chr. 7 gain
O GBM, Chr.10 loss p = 0.75
Chr. 10 loss
P GBM, CDKN2A del p = 0.92
CDKN2A del.
Q GBM, EGFR ampl. p = 0.7
EGFR ampl.
R GBM, PDGFRA ampl. p = 0.9
PDGFRA ampl.
S AML, IDH1 p = 0.036
IDH1 mutation
21 T AML, FLT3 p = 0.52
FLT3 mutation
U AML, RAS p = 0.88
RAS mutation (activ)
V AML, NPMc p = 0.36
NPMc
W AML, Translocation p = 0.97
PML.RAR positive
PML.RAR negative
Unknown
BCR.ABL pos.
BCR.ABL negative
X ThyroidTHC RAS family p = 0.52
Unknown
NRAS 61
negative
HRAS 61