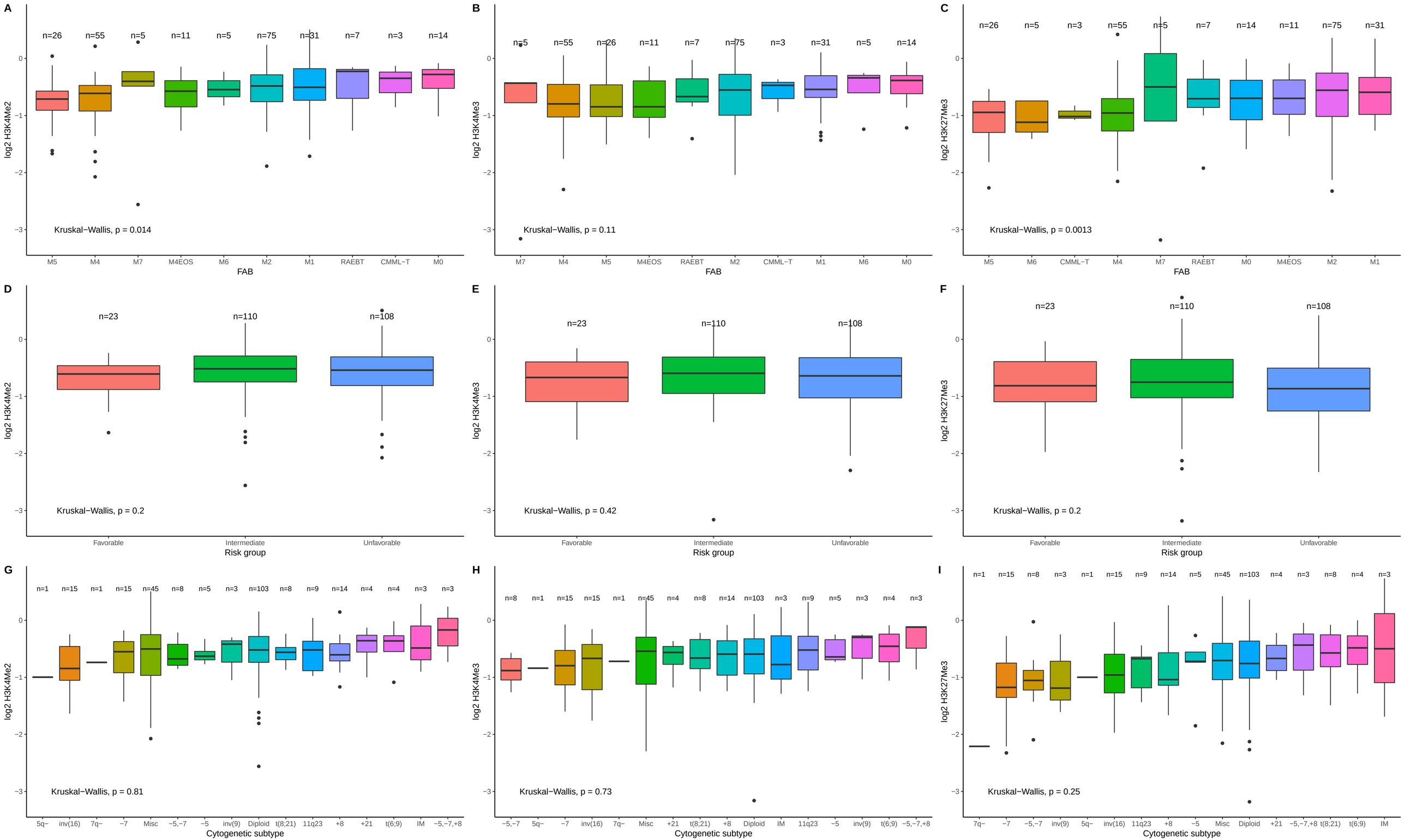
A
log2 H3K4Me2
n=26 n=55 n=5 n=11 n=5 n=75 n=31 n=7 n=3 n=14
Kruskal−Wallis, p = 0.014
M5 M4 M7 M4EOS M6 M2 M1 RAEBT CMML−T M0
FAB
B
log2 H3K4Me3
n=5 n=55 n=26 n=11 n=7 n=75 n=3 n=31 n=5 n=14
Kruskal−Wallis, p = 0.11
M7 M4 M5 M4EOS RAEBT M2 CMML−T M1 M6 M0
FAB
C
log2 H3K27Me3
n=26 n=5 n=3 n=55 n=5 n=7 n=14 n=11 n=75 n=31
Kruskal−Wallis, p = 0.0013
M5 M6 CMML−T M4 M7 RAEBT M0 M4EOS M2 M1
FAB
D
log2 H3K4Me2
n=23 n=110 n=108
Kruskal−Wallis, p = 0.2
Favorable Intermediate Unfavorable
Risk group
E
log2 H3K4Me3
n=23 n=110 n=108
Kruskal−Wallis, p = 0.42
Favorable Intermediate Unfavorable
Risk group
F
log2 H3K27Me3
n=23 n=110 n=108
Kruskal−Wallis, p = 0.2
Favorable Intermediate Unfavorable
Risk group
G
log2 H3K4Me2
n=1 n=15 n=1 n=15 n=45 n=8 n=5 n=3 n=103 n=8 n=9 n=14 n=4 n=4 n=3 n=3
Kruskal−Wallis, p = 0.81
5q− inv(16) 7q− −7 Misc −5,−7 −5 inv(9) Diploid t(8;21) 11q23 +8 +21 t(6;9) IM −5,−7,+8
Cytogenetic subtype
H
log2 H3K4Me3
n=8 n=1 n=15 n=15 n=1 n=45 n=4 n=8 n=14 n=103 n=3 n=9 n=5 n=3 n=4 n=3
Kruskal−Wallis, p = 0.73
−5,−7 5q− −7 inv(16) 7q− Misc +21 t(8;21) +8 Diploid IM 11q23 −5 inv(9) t(6;9) −5,−7,+8
Cytogenetic subtype
I
log2 H3K27Me3
n=1 n=15 n=8 n=3 n=1 n=15 n=9 n=14 n=5 n=45 n=103 n=4 n=3 n=8 n=4 n=3
Kruskal−Wallis, p = 0.25
7q− −7 −5,−7 inv(9) 5q− inv(16) 11q23 +8 −5 Misc Diploid +21 −5,−7,+8 t(8;21) t(6;9) IM
Cytogenetic subtype