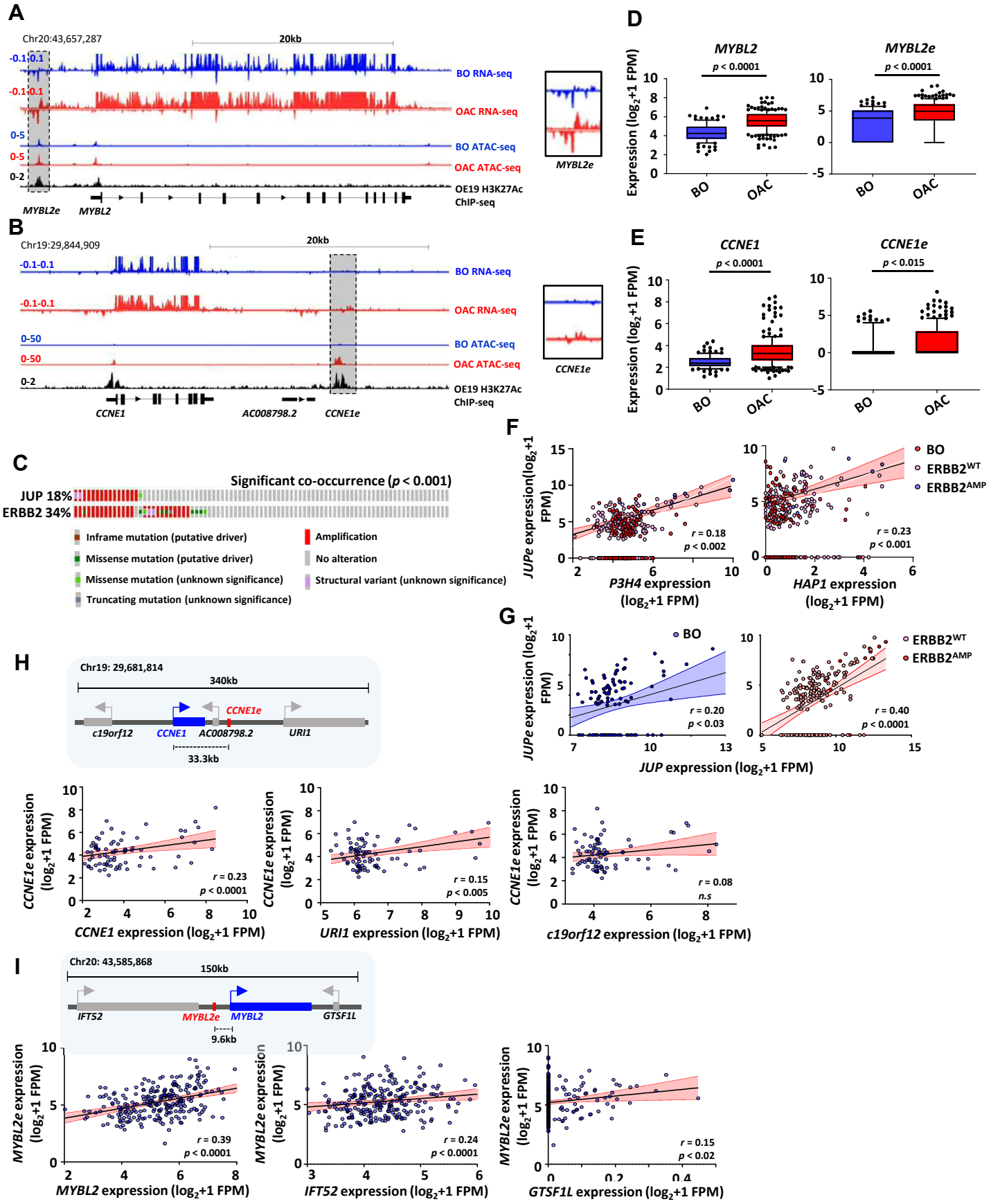
A
Chr20:43,657,287
20kb
BO RNA-seq
OAC RNA-seq
BO ATAC-seq
OAC ATAC-seq
OE19 H3K27Ac ChIP-seq
MYBL2e
MYBL2
B
Chr19:29,844,909
20kb
CCNE1
AC008798.2
CCNE1e
C
Significant co-occurrence (p < 0.001)
JUP 18%
ERBB2 34%
Inframe mutation (putative driver)
Missense mutation (putative driver)
Missense mutation (unknown significance)
Truncating mutation (unknown significance)
Amplification
No alteration
Structural variant (unknown significance)
D
MYBL2
MYBL2e
p < 0.0001
Expression (log2+1 FPM)
BO
OAC
E
CCNE1
CCNE1e
p < 0.0001
p < 0.015
F
JUPe expression(log2+1 FPM)
P3H4 expression (log2+1 FPM)
HAP1 expression (log2+1 FPM)
r = 0.18
p < 0.002
r = 0.23
p < 0.001
BO
ERBB2WT
ERBB2AMP
G
JUPe expression (log2+1 FPM)
JUP expression (log2+1 FPM)
r = 0.20
p < 0.03
r = 0.40
p < 0.0001
H
Chr19: 29,681,814
340kb
c19orf12
CCNE1
AC008798.2
CCNE1e
URI1
33.3kb
CCNE1e expression (log2+1 FPM)
CCNE1 expression (log2+1 FPM)
URI1 expression (log2+1 FPM)
c19orf12 expression (log2+1 FPM)
r = 0.23
p < 0.0001
r = 0.15
p < 0.005
r = 0.08
n.s
I
Chr20: 43,585,868
150kb
IFT52
MYBL2e
MYBL2
GTSF1L
9.6kb
MYBL2e expression (log2+1 FPM)
MYBL2 expression (log2+1 FPM)
IFT52 expression (log2+1 FPM)
GTSF1L expression (log2+1 FPM)
r = 0.39
p < 0.0001
r = 0.24
p < 0.0001
r = 0.15
p < 0.02