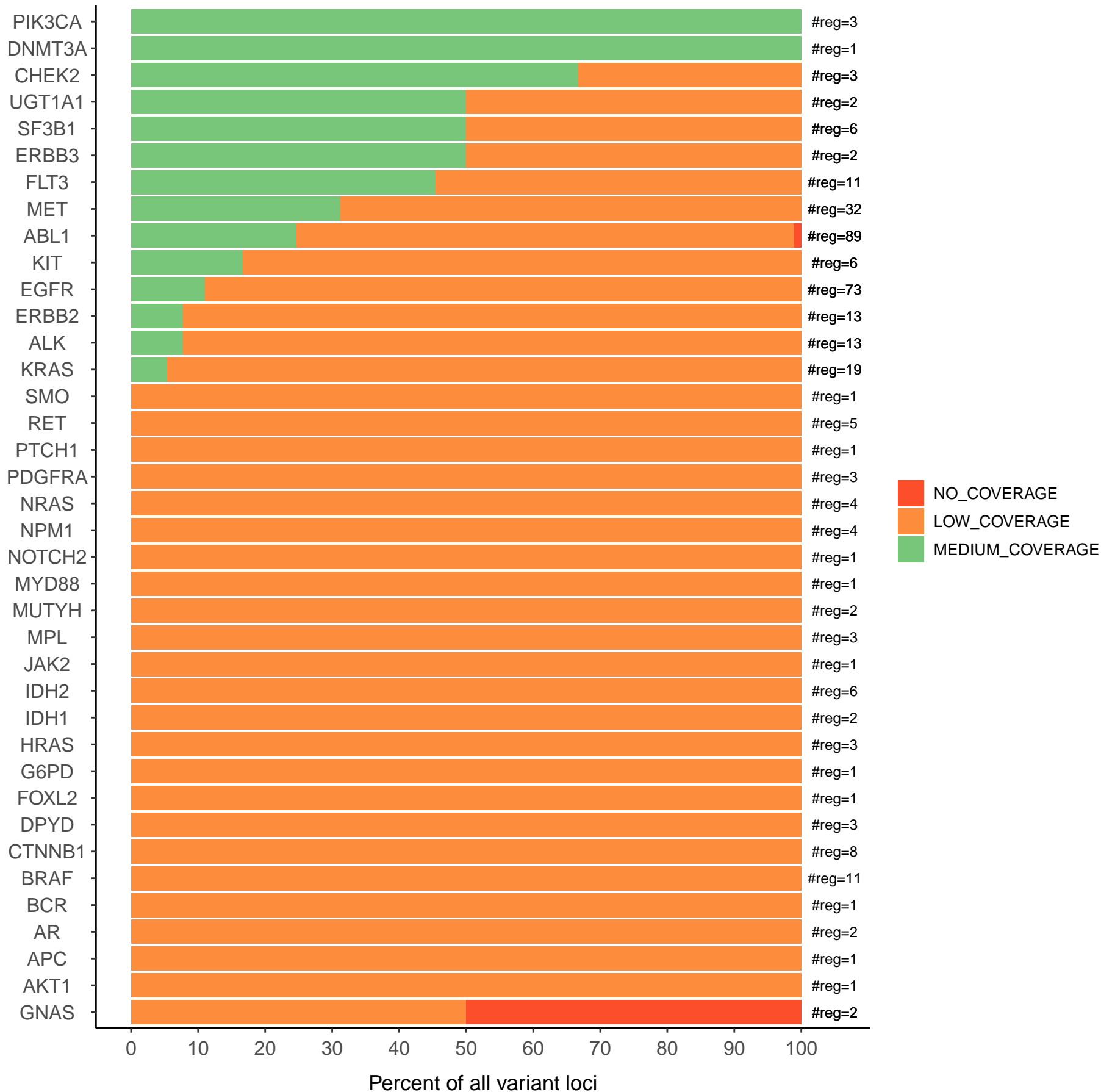
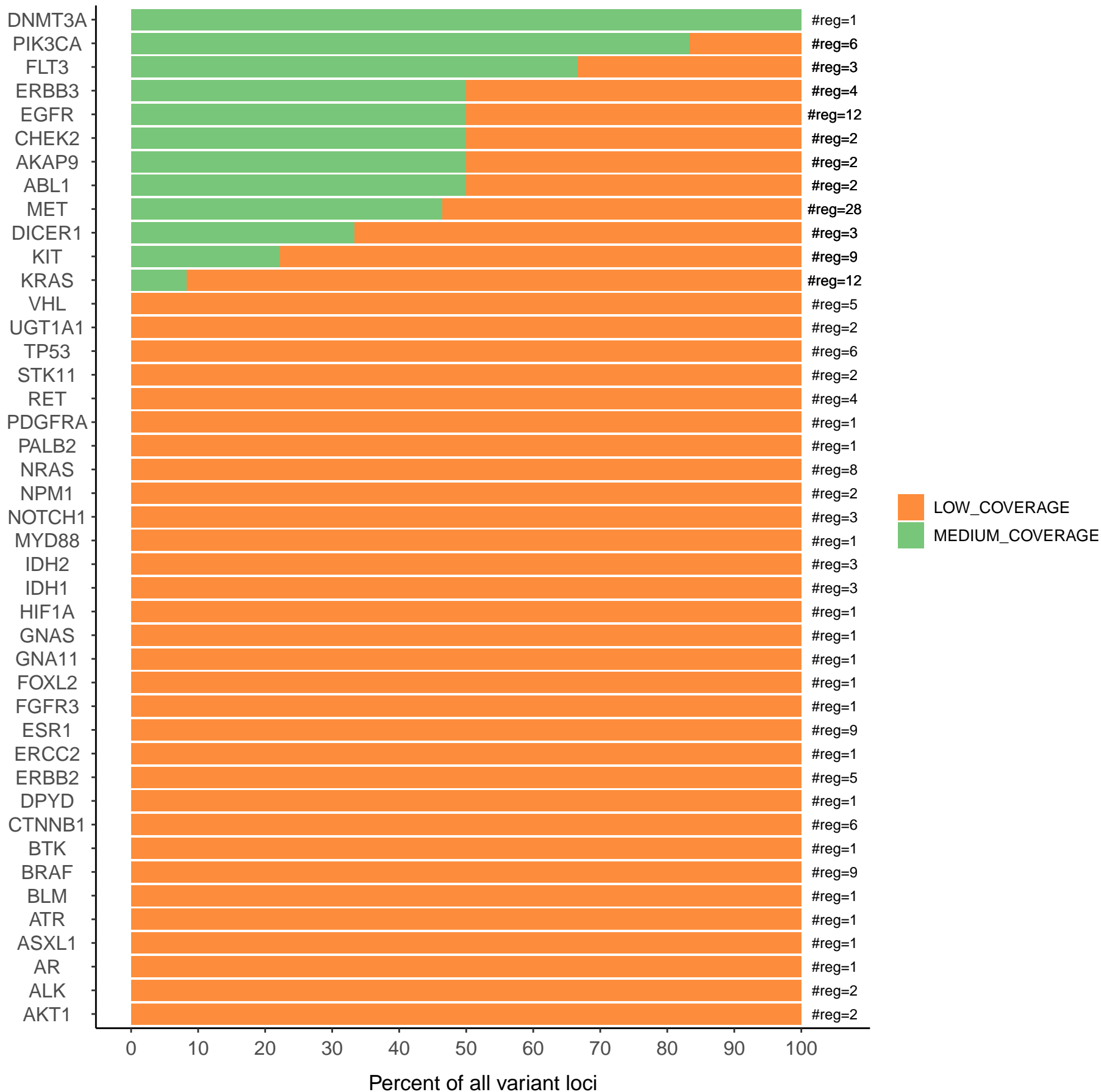


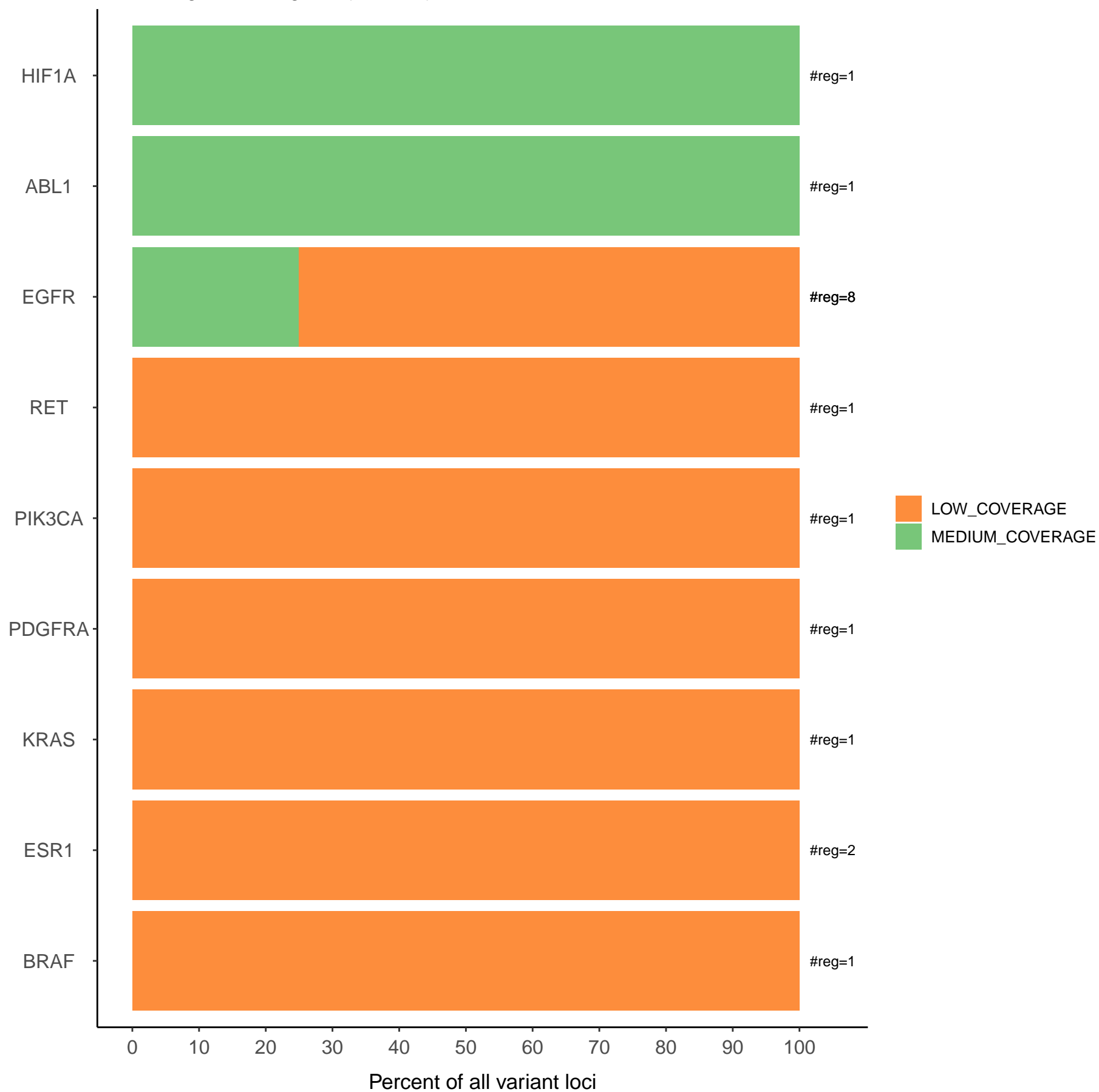
Clinical significant regions (level A)



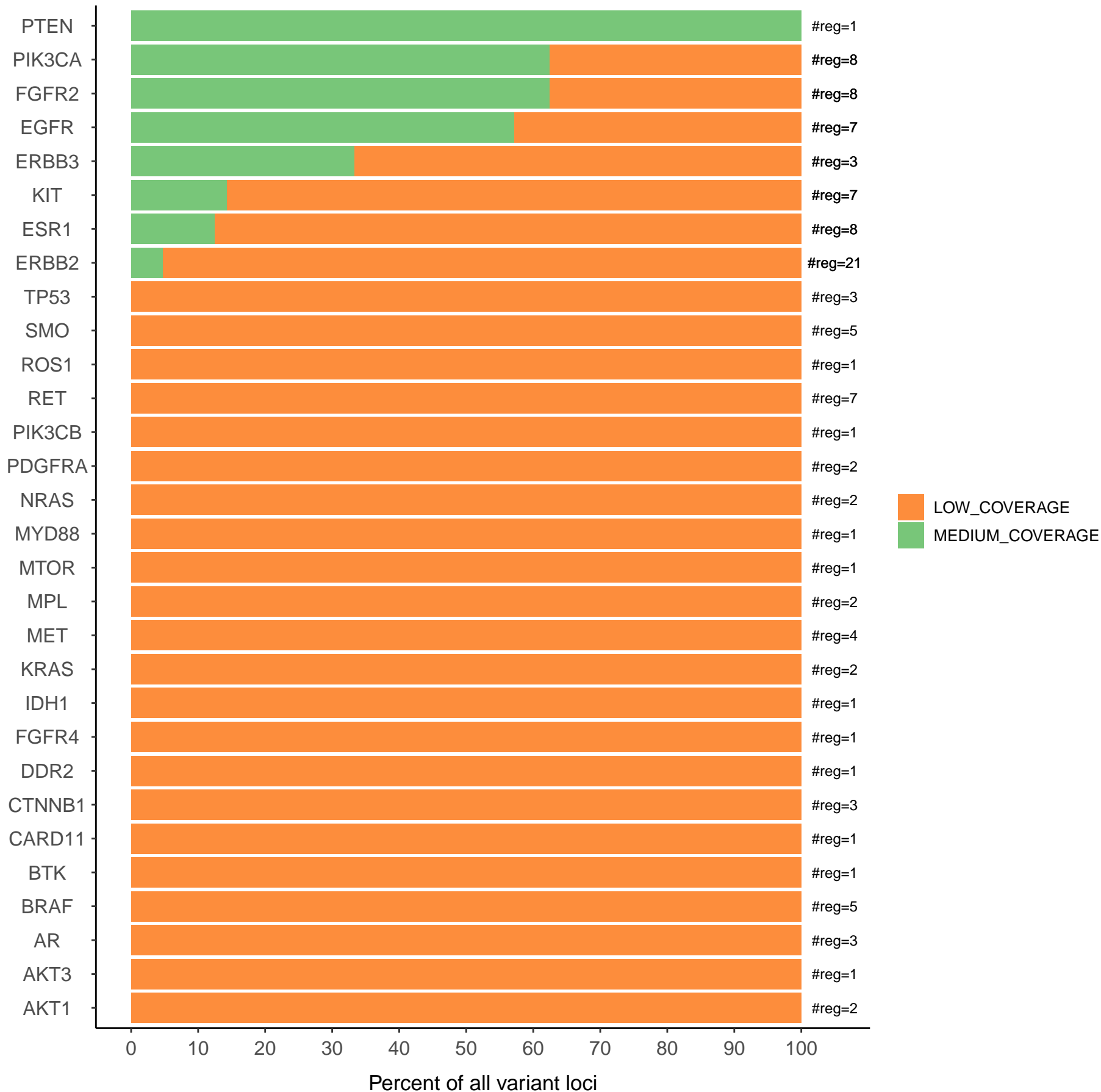
Clinical significant regions (level B)



Clinical significant regions (level B1)



Clinical significant regions (level B2)



Clinical significant regions (level B3)

CHEK2



#reg=3

TP53



#reg=1

ERCC2



#reg=1

ERCC1

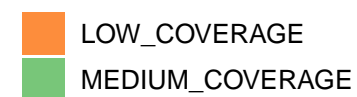


#reg=1

BRAF



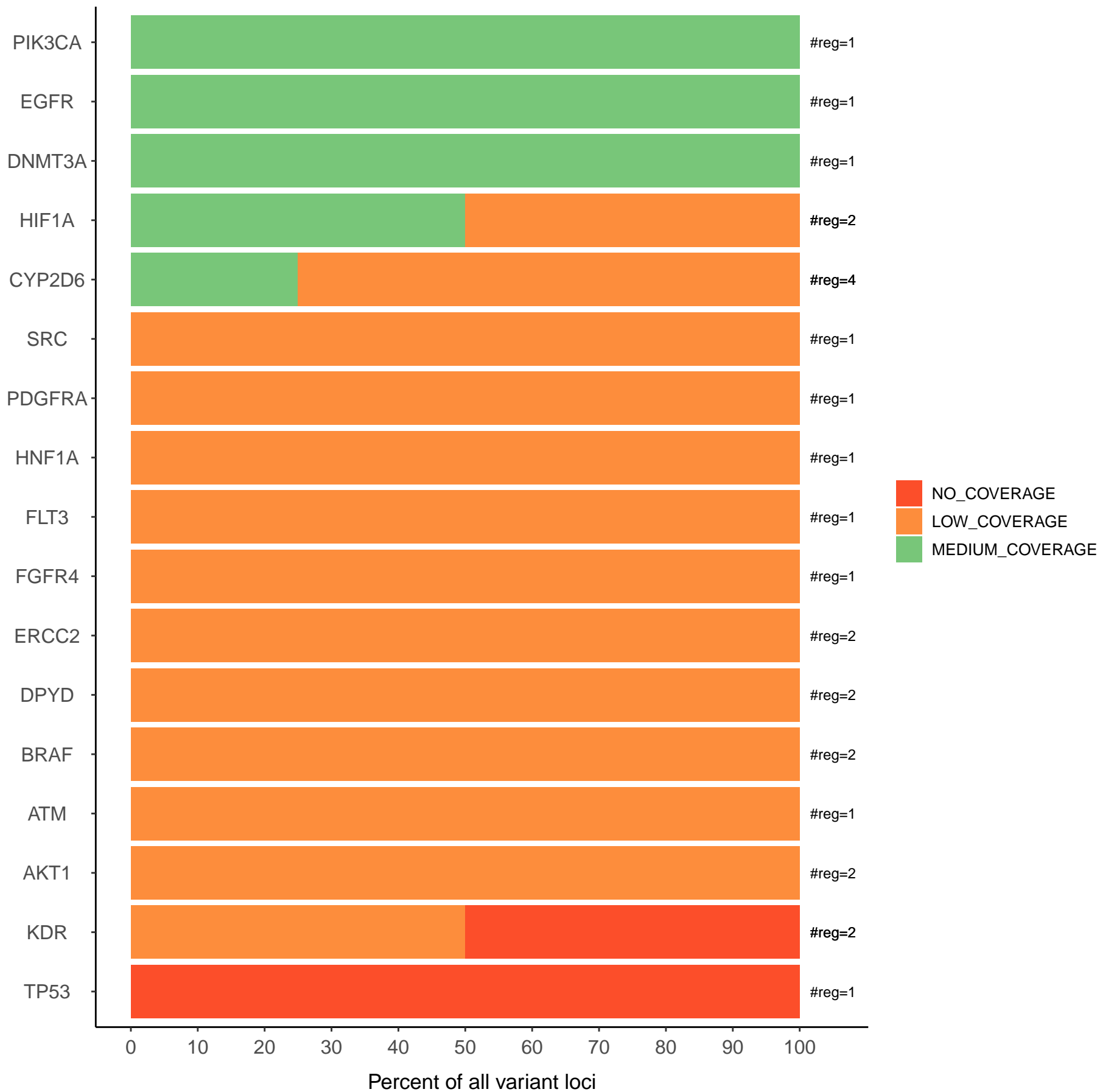
#reg=1



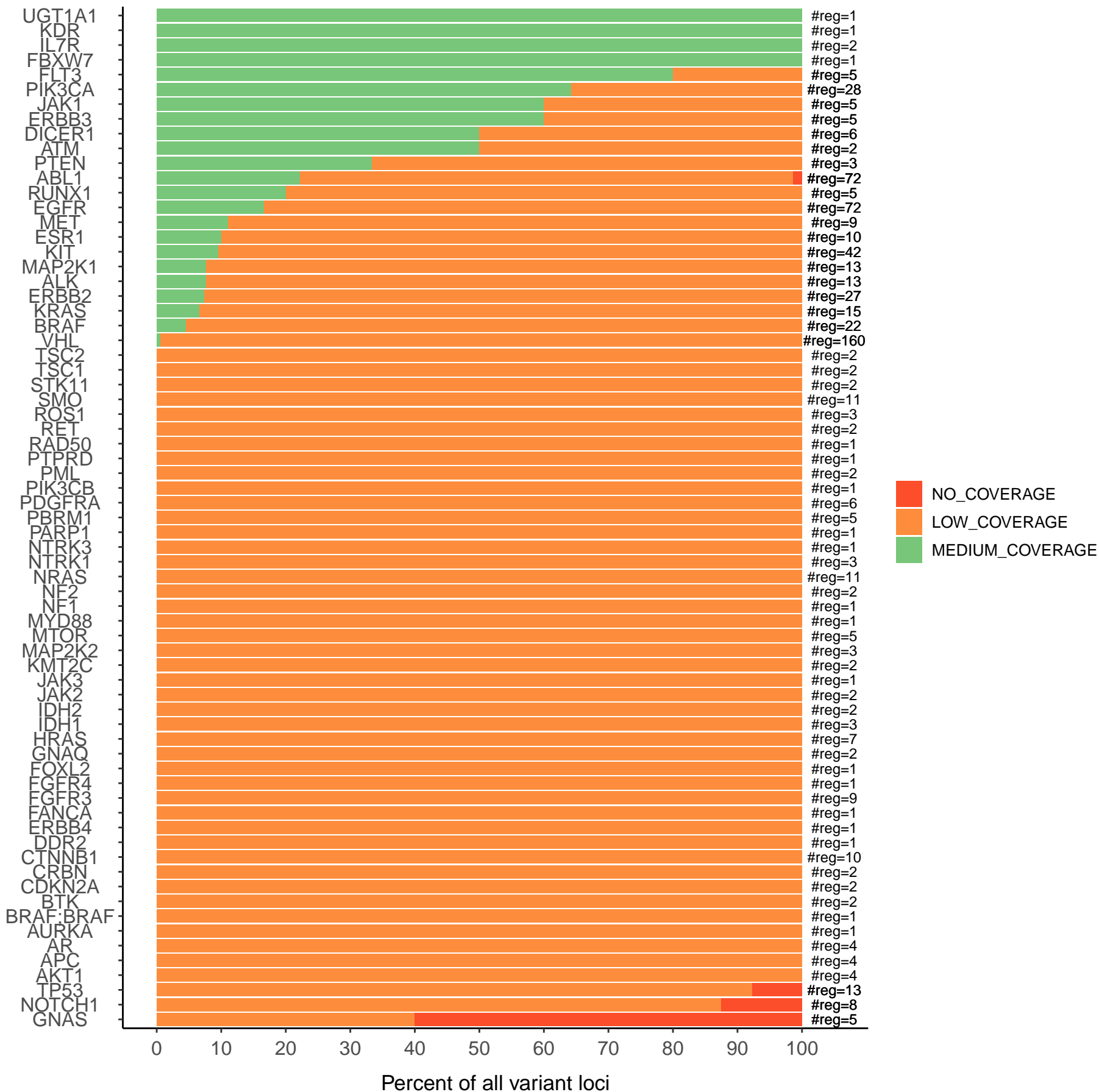
0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

Clinical significant regions (level B4)



Clinical significant regions (level C)



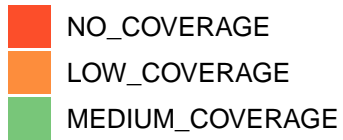
Clinical significant regions (level A), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=341



Clinical significant regions (level B), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=170

LOW_COVERAGE
MEDIUM_COVERAGE



Clinical significant regions (level B1), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=17

LOW_COVERAGE
MEDIUM_COVERAGE



Clinical significant regions (level B2), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=113

LOW_COVERAGE
MEDIUM_COVERAGE



Clinical significant regions (level B3), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=7

LOW_COVERAGE
MEDIUM_COVERAGE



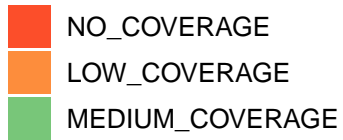
Clinical significant regions (level B4), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=26



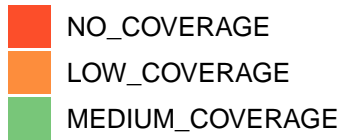
Clinical significant regions (level C), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=672



Clinical significant regions (level D), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=980

