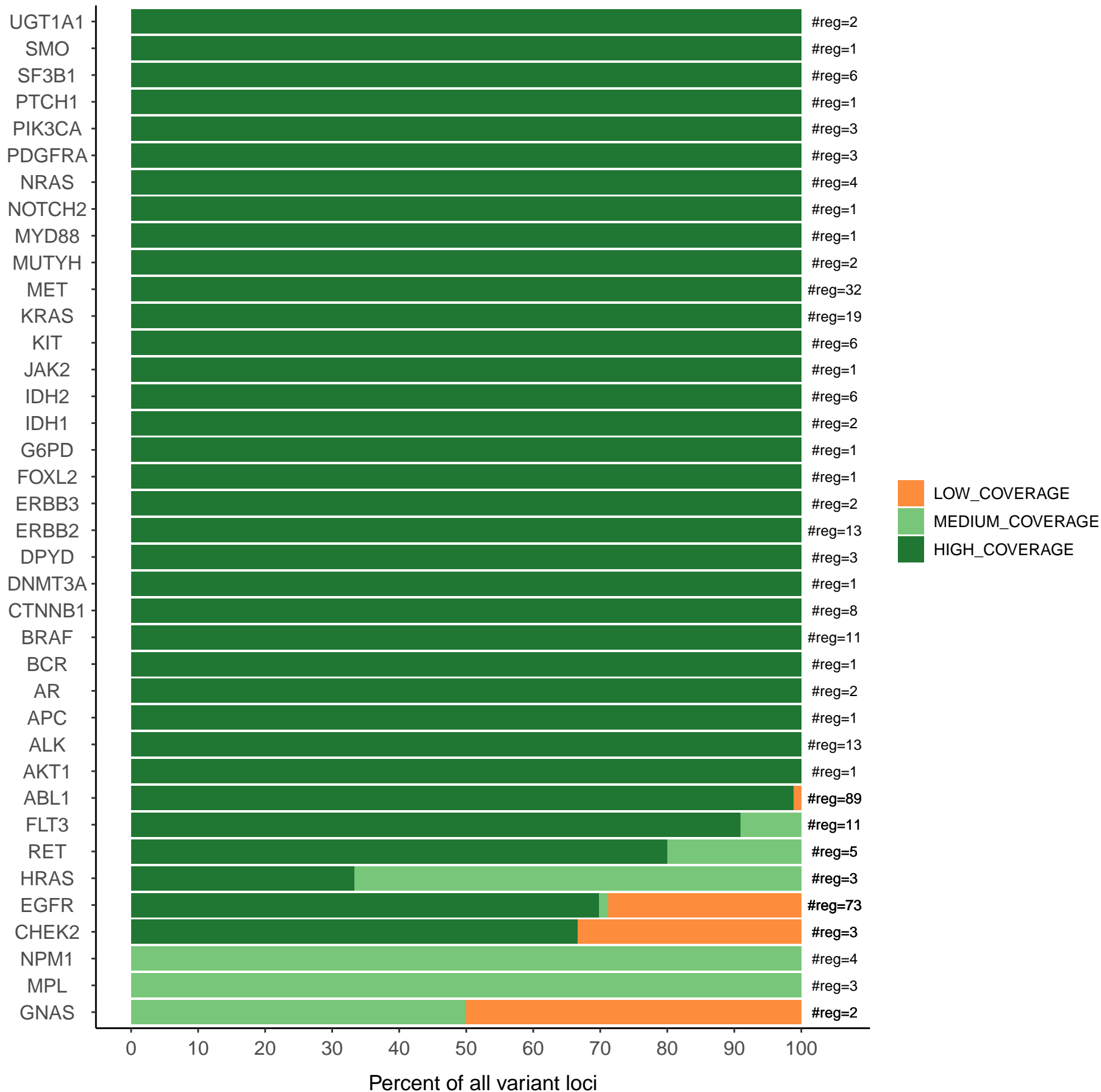
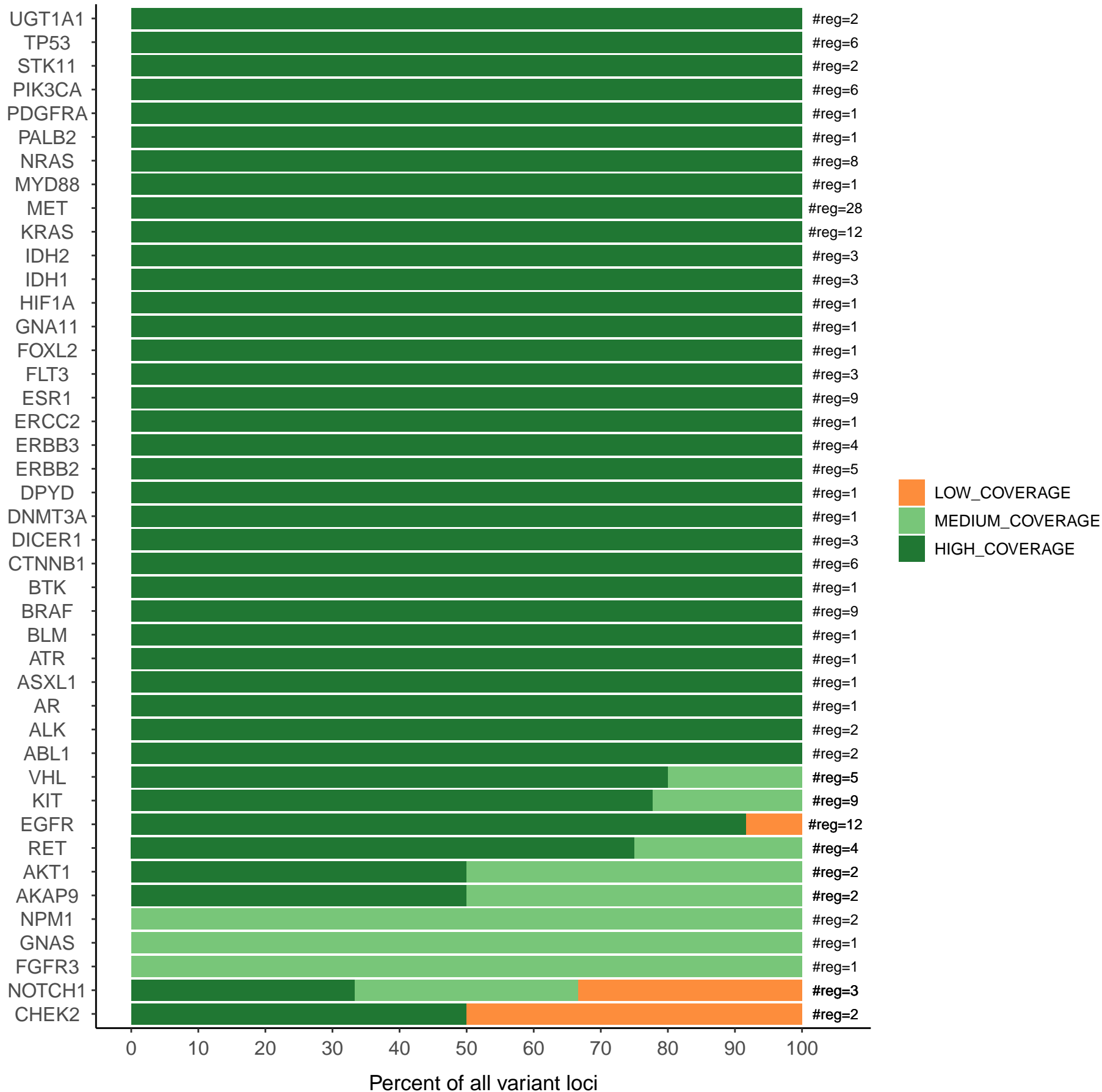


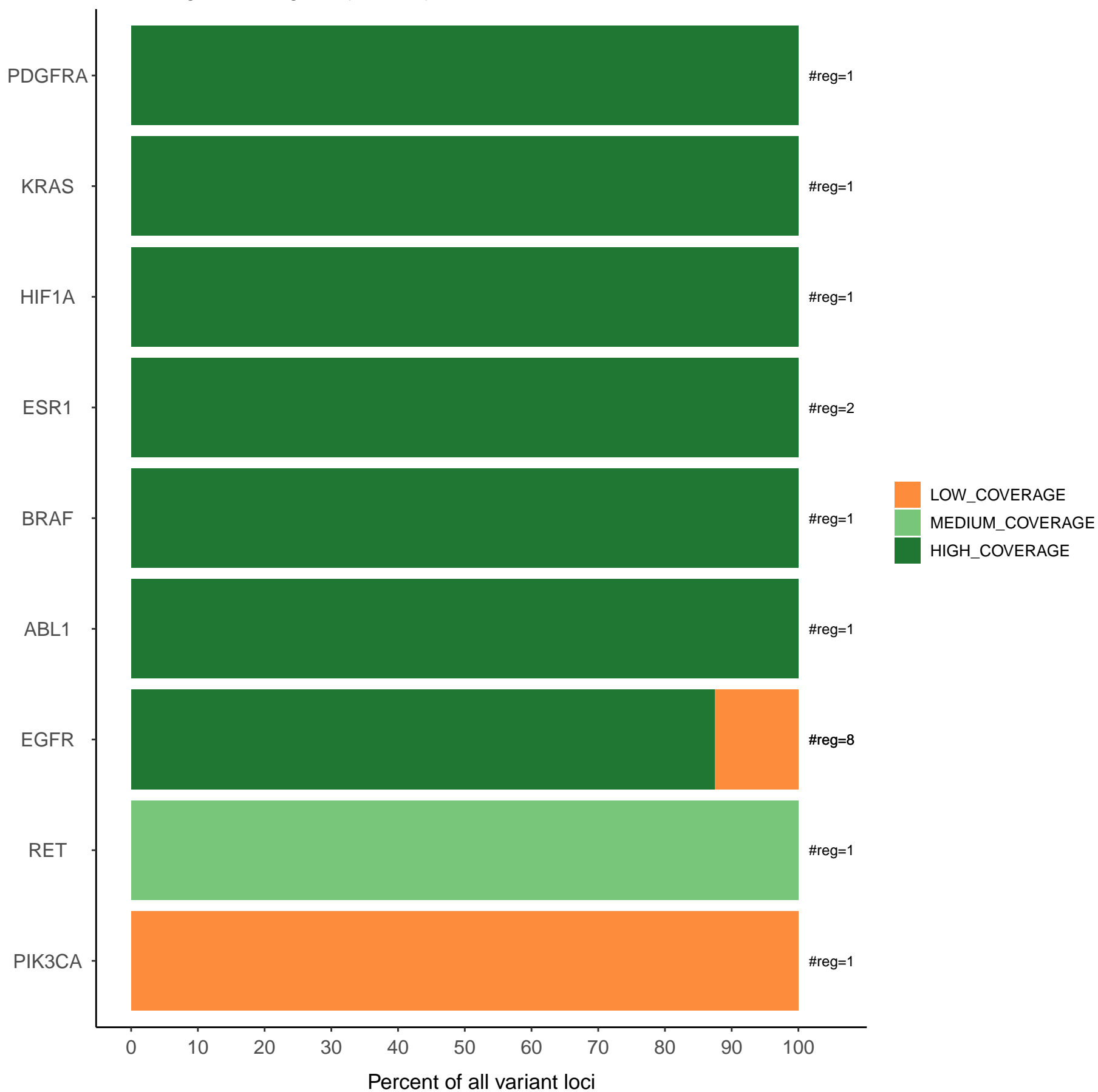
Clinical significant regions (level A)



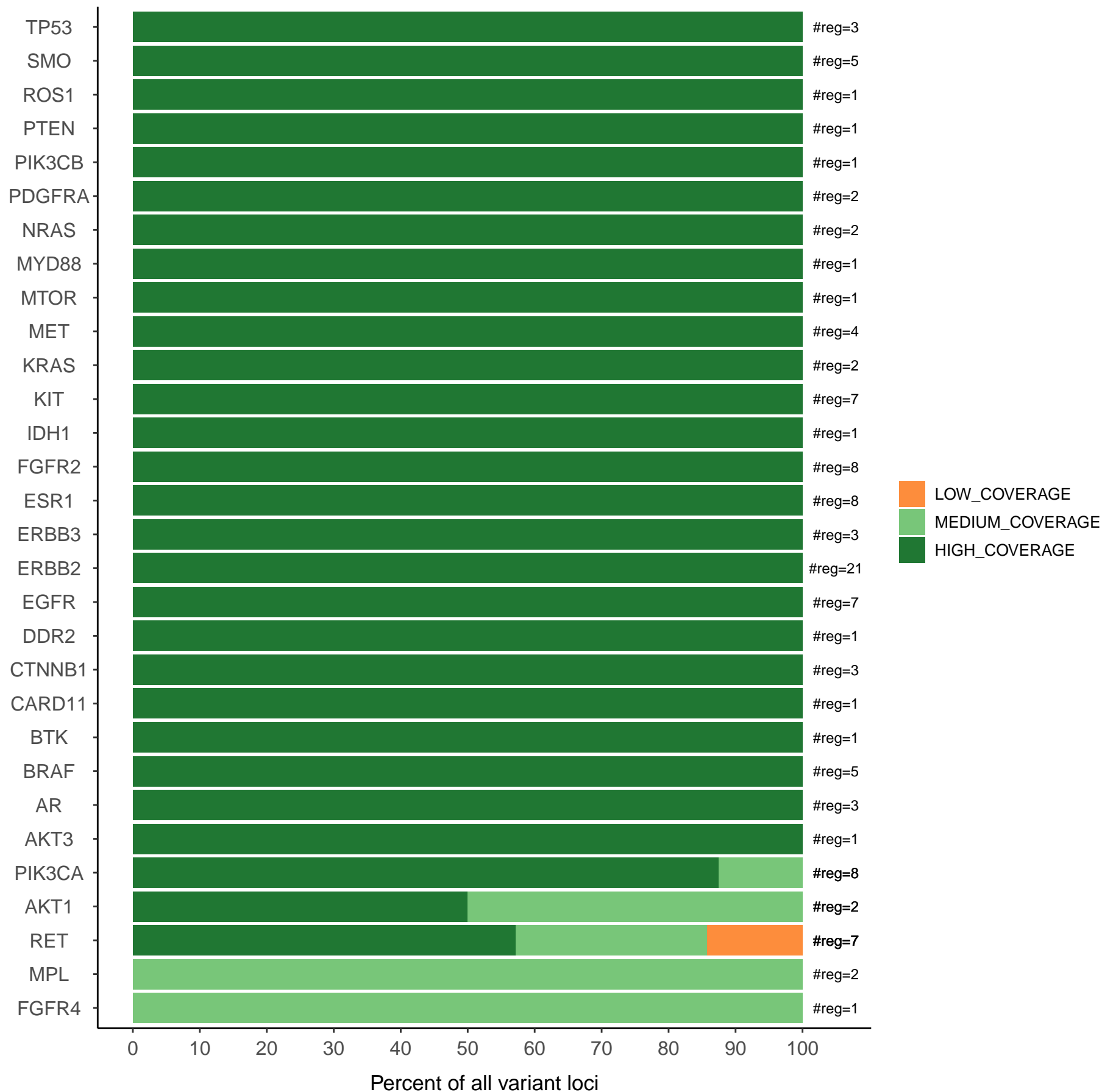
Clinical significant regions (level B)



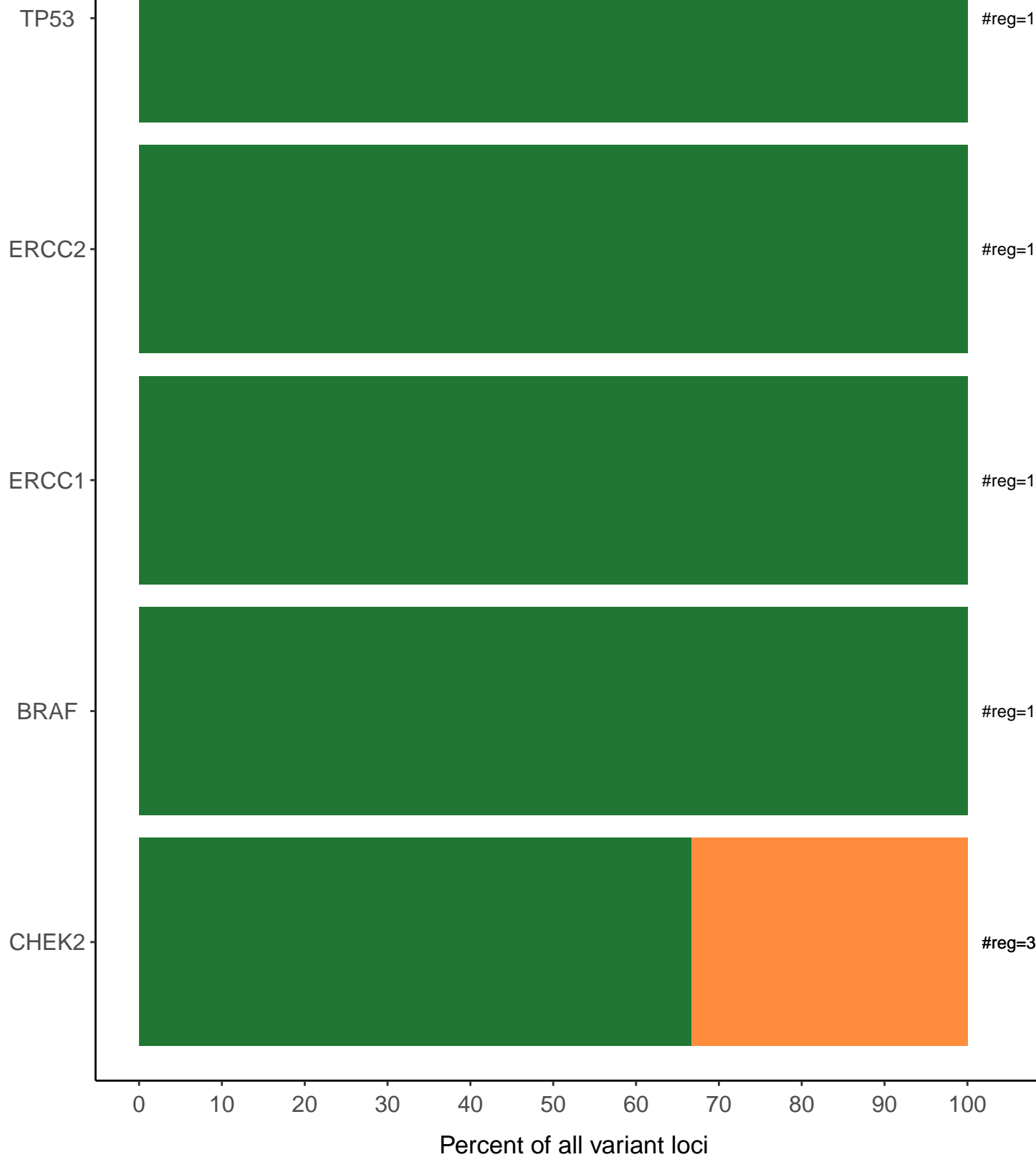
Clinical significant regions (level B1)



Clinical significant regions (level B2)



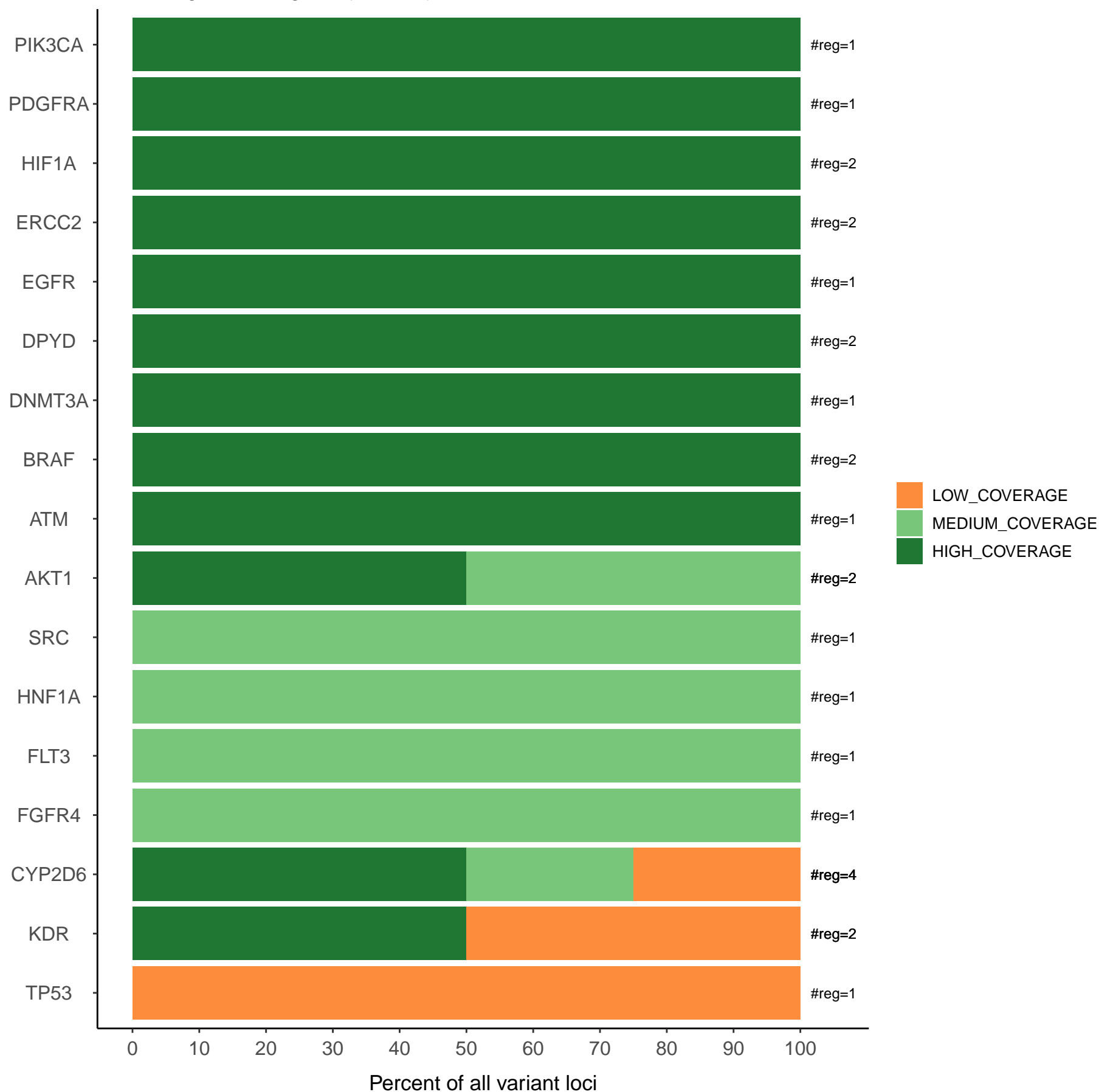
Clinical significant regions (level B3)



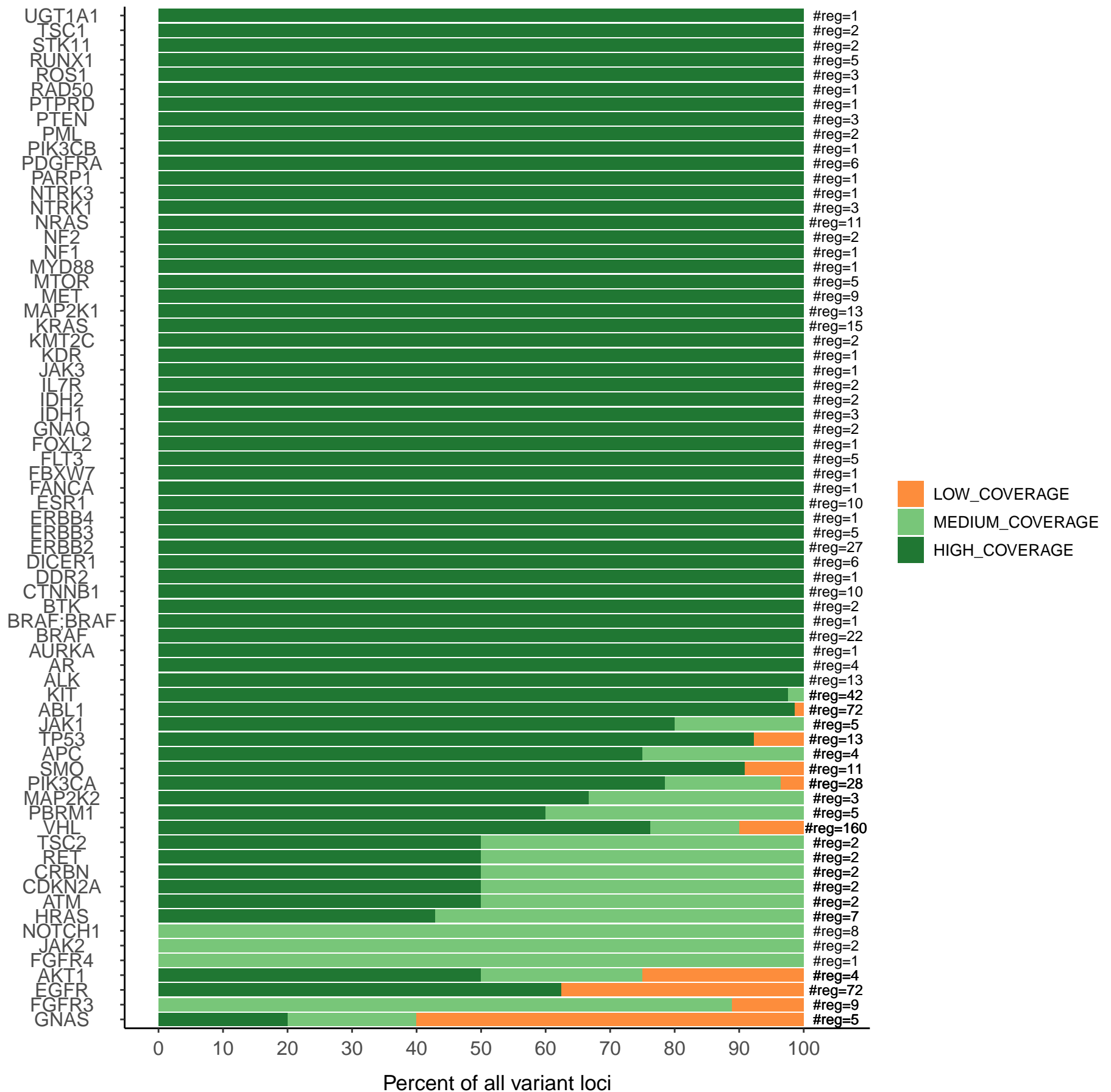
LOW_COVERAGE

HIGH_COVERAGE

Clinical significant regions (level B4)



Clinical significant regions (level C)



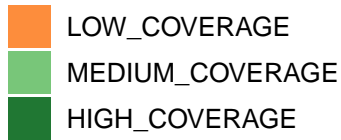
Clinical significant regions (level A), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=341



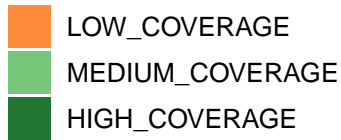
Clinical significant regions (level B), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=170



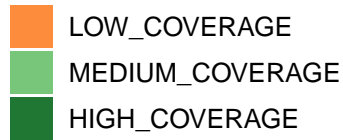
Clinical significant regions (level B1), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=17



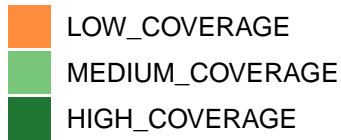
Clinical significant regions (level B2), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=113



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
HIGH_COVERAGE



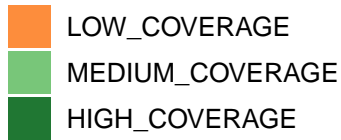
Clinical significant regions (level B4), all gene summary

CALLABILITY

0 10 20 30 40 50 60 70 80 90 100

Percent of all variant loci

#reg=26



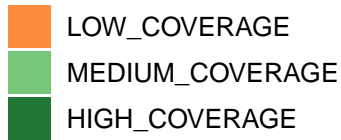
Clinical significant regions (level C), all gene summary

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

