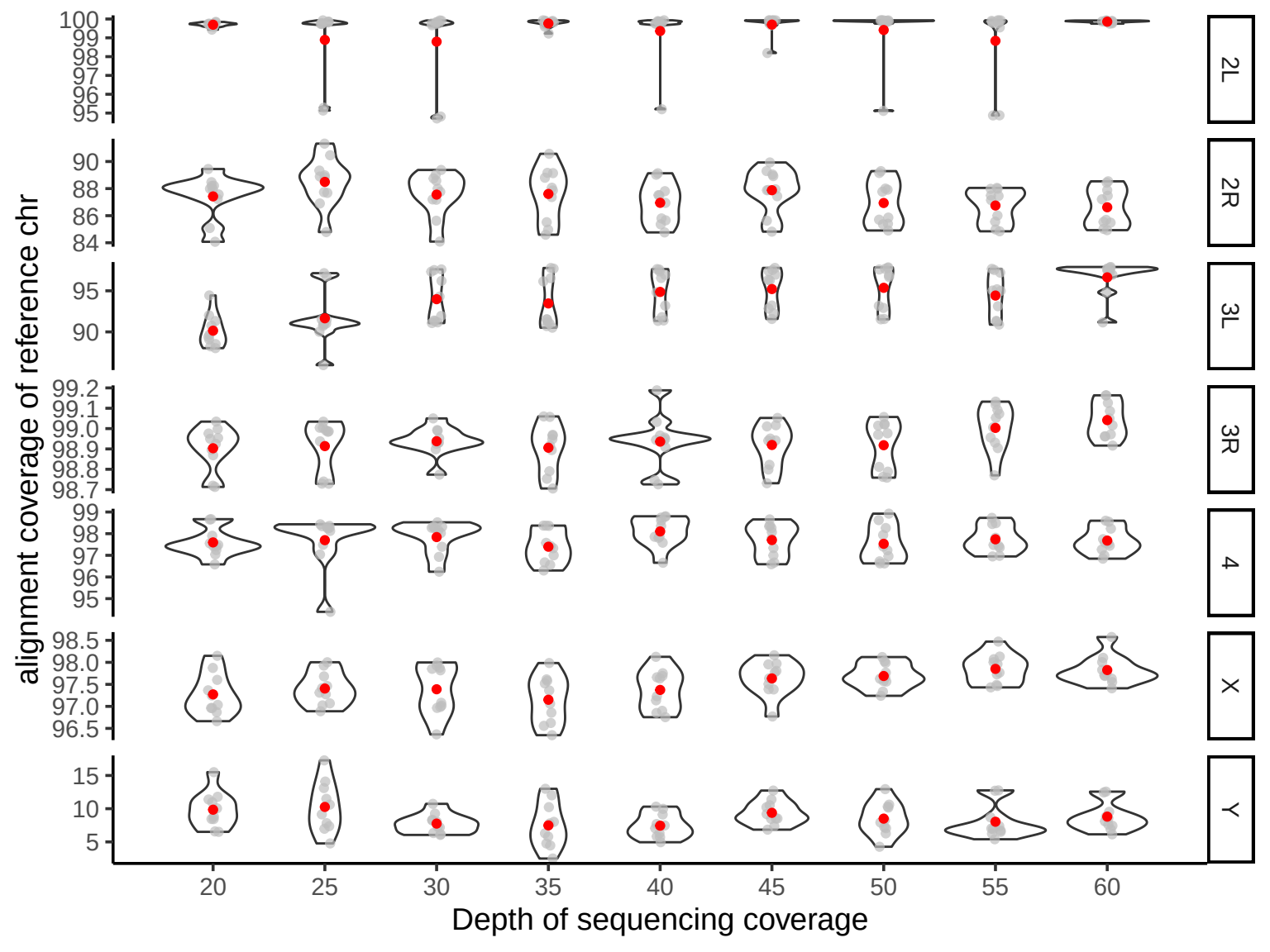
alignment coverage of reference chr
Depth of sequencing coverage
2L
2R
3L
3R
4
X
Y
20
25
30
35
40
45
50
55
60