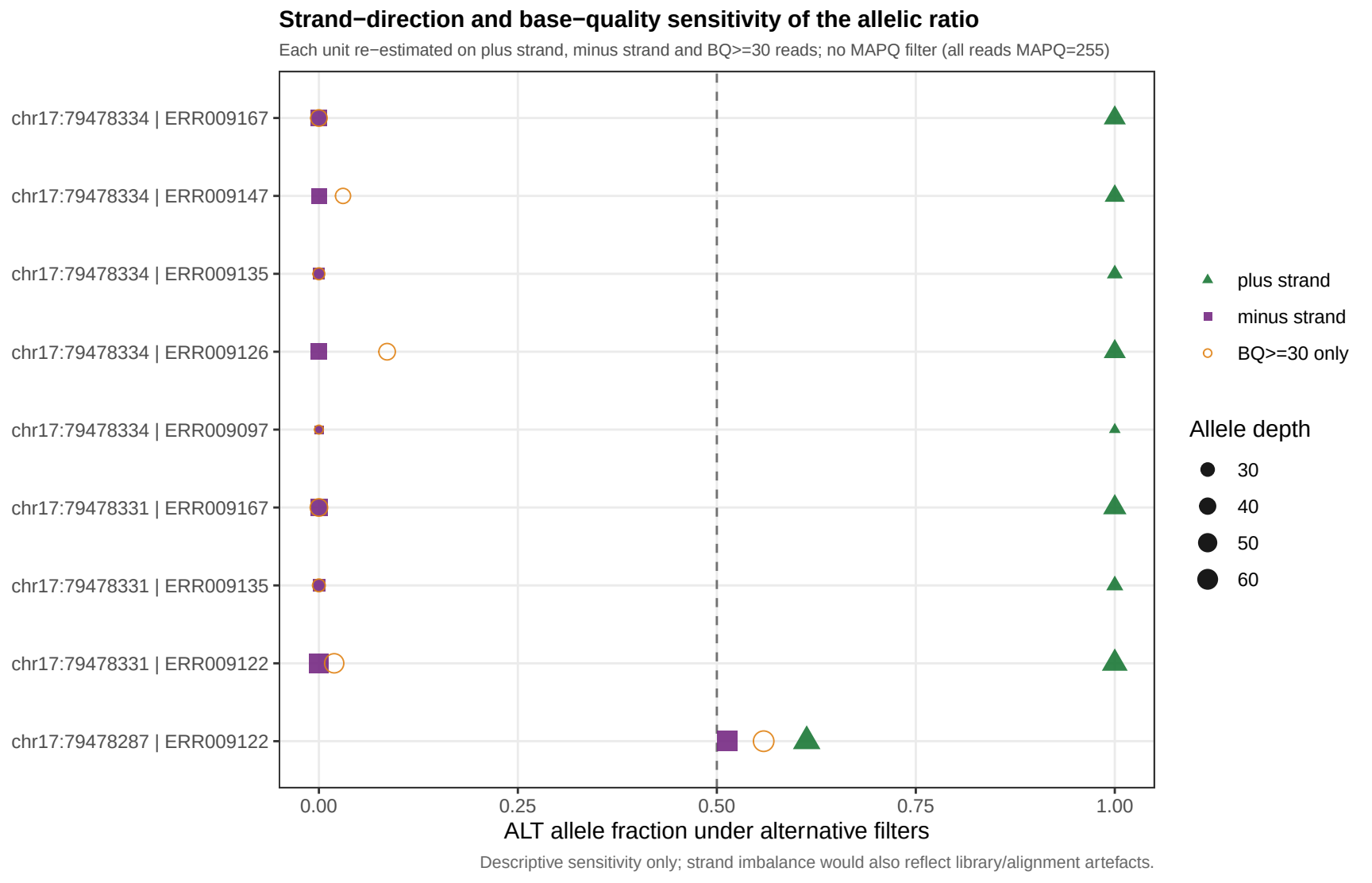

Strand−direction and base−quality sensitivity of the allelic ratio
Each unit re−estimated on plus strand, minus strand and BQ>=30 reads; no MAPQ filter (all reads MAPQ=255)
chr17:79478334 | ERR009167
chr17:79478334 | ERR009147
chr17:79478334 | ERR009135
chr17:79478334 | ERR009126
chr17:79478334 | ERR009097
chr17:79478331 | ERR009167
chr17:79478331 | ERR009135
chr17:79478331 | ERR009122
chr17:79478287 | ERR009122
0.00
0.25
0.50
0.75
1.00
ALT allele fraction under alternative filters
plus strand
minus strand
BQ>=30 only
Allele depth
30
40
50
60
Descriptive sensitivity only; strand imbalance would also reflect library/alignment artefacts.