Paired-end report (2x50bp):

```
Input file:                                 'FVBNJ_Cast.bam'
Writing allele-flagged output file to:      'FVBNJ_Cast.allele_flagged.bam'


Allele-tagging report
=====================
Processed 194564995 read alignments in total
149380724 reads were unassignable (76.78%)
35143075 reads were specific for genome 1 (18.06%)
9860248 reads were specific for genome 2 (5.07%)
118662 reads did not contain one of the expected bases at known SNP positions (0.06%)
180948 contained conflicting allele-specific SNPs (0.09%)


SNP coverage report
===================
N-containing reads:   45276050
non-N:                149262062
total:                194564995
Reads had a deletion of the N-masked position (and were thus dropped):     26883 (0.01%)
Of which had multiple deletions of N-masked positions within the same read:       30

Of valid N containing reads,
N was present in the list of known SNPs:            61087551 (99.99%)
N was not present in the list of SNPs:              4773 (0.01%)

Input file:                                         'FVBNJ_Cast.allele_flagged.bam'
Writing unassigned reads to:                        'FVBNJ_Cast.unassigned.bam'
Writing genome 1-specific reads to:                 'FVBNJ_Cast.genome1.bam'
Writing genome 2-specific reads to:                 'FVBNJ_Cast.genome2.bam'


Allele-specific paired-end sorting report
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Read pairs/singletons processed in total:           98215744
       thereof were read pairs:                     96349251
       thereof were singletons:                     1866493
Reads were unassignable (not overlapping SNPs):     61174812 (62.29%)
       thereof were read pairs:      59662537
       thereof were singletons:      1512275
Reads were specific for genome 1:                   28657857 (29.18%)
       thereof were read pairs:      28446094
       thereof were singletons:      211763
Reads were specific for genome 2:                   8122687 (8.27%)
       thereof were read pairs:      7985424
       thereof were singletons:      137263
Reads contained conflicting SNP information:        260388 (0.27%)
       thereof were read pairs:      255196
       thereof were singletons:      5192
```