BS-Seq report (2x100bp):

```
Input file:                             '129_Cast_bismark_bt2_pe.bam'
Writing allele-flagged output file to:  '129_Cast_bismark_bt2_pe.allele_flagged.bam'
```

Allele-tagging report
`=====================`
```
Processed 162441396 read alignments in total
Reads were unaligned and hence skipped: 0 (0.00%)
109109113 reads were unassignable (67.17%)
30267901 reads were specific for genome 1 (18.63%)
22697499 reads were specific for genome 2 (13.97%)
15807753 reads did not contain one of the expected bases at known SNP positions (9.73%)
366883 contained conflicting allele-specific SNPs (0.23%)
```

SNP coverage report
`==================`
```
SNP annotation file:  ../all_Cast_SNPs_129S1_reference.mgp.v4.txt.gz
N-containing reads:    68984287
non-N:                 93301360
total:                 162441396
Reads had a deletion of the N-masked position (and were thus dropped):    155749 (0.10%)
Of which had multiple deletions of N-masked positions within the same read:        65

Of valid N containing reads,
N was present in the list of known SNPs:      119119643 (99.99%)
Positions were skipped since they involved C>T SNPs: 38464451
N was not present in the list of SNPs:              7517 (0.01%)

Input file:                             129_Cast_bismark_bt2_pe.allele_flagged.bam'
Writing unassigned reads to:            129_Cast_bismark_bt2_pe.unassigned.bam'
Writing genome 1-specific reads to:     129_Cast_bismark_bt2_pe.genome1.bam'
Writing genome 2-specific reads to:     129_Cast_bismark_bt2_pe.genome2.bam'
```

Allele-specific paired-end sorting report
`=======================================`
```
Read pairs/singletons processed in total:       81220698
       thereof were read pairs:                 81220698
       thereof were singletons:                 0
Reads were unassignable (not overlapping SNPs):         40420625 (49.77%)
       thereof were read pairs:    40420625
       thereof were singletons:    0
Reads were specific for genome 1:               23037433 (28.36%)
       thereof were read pairs:    23037433
       thereof were singletons:    0
Reads were specific for genome 2:               17303663 (21.30%)
       thereof were read pairs:    17303663
       thereof were singletons:    0
Reads contained conflicting SNP information:    458977 (0.57%)
       thereof were read pairs:    458977
       thereof were singletons:    0
```