

## Hi-C report (2x100bp):

Input file: Black6\_129S1.bam  
Writing allele-flagged output file to: Black6\_129S1.allele\_flagged.bam

### Allele-tagging report

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Processed 94887256 read alignments in total  
59662038 reads were unassignable (62.88%)  
19851697 reads were specific for genome 1 (20.92%)  
15047281 reads were specific for genome 2 (15.86%)  
47261 reads did not contain one of the expected bases at known SNP positions (0.05%)  
326240 contained conflicting allele-specific SNPs (0.34%)

### SNP coverage report

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N-containing reads: 35231977  
non-N: 59614777  
total: 94887256  
Reads had a deletion of the N-masked position (and were thus dropped): 40502 (0.04%)  
Of which had multiple deletions of N-masked positions within the same read: 59  
  
Of valid N containing reads,  
N was present in the list of known SNPs: 57101748 (99.99%)  
N was not present in the list of SNPs: 4211 (0.01%)

Input file: Black6\_129S1.allele\_flagged.bam'  
Writing unassigned reads to: Black6\_129S1.UA\_UA.bam'  
Writing genome 1-specific reads to: Black6\_129S1.G1\_G1.bam'  
Writing genome 2-specific reads to: Black6\_129S1.G2\_G2.bam'  
Writing G1/UA reads to: Black6\_129S1.G1\_UA.bam'  
Writing G2/UA reads to: Black6\_129S1.G2\_UA.bam'  
Writing G1/G2 reads to: Black6\_129S1.G1\_G2.bam'

### Allele-specific paired-end sorting report

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Read pairs processed in total: 47443628  
Read pairs were unassignable (UA/UA): 18862725 (39.76%)  
Read pairs were specific for genome 1 (G1/G1): 3533932 (7.45%)  
Read pairs were specific for genome 2 (G2/G2): 2592040 (5.46%)  
Read pairs were a mix of G1 and UA: 12306421 (25.94%). Of these,  
    were G1/UA: 6018598  
    were UA/G1: 6287823  
Read pairs were a mix of G2 and UA: 9430675 (19.88%). Of these,  
    were G2/UA: 4603429  
    were UA/G2: 4827246  
Read pairs were a mix of G1 and G2: 395296 (0.83%). Of these,  
    were G1/G2: 198330  
    were G2/G1: 196966  
Read pairs contained conflicting SNP information: 322539 (0.68%)