Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:48:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006185.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1006185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006185_1.fastq.gz SRR1006185_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:48:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,859,340
Mapped reads	1,665,196 / 89.56%
Unmapped reads	194,144 / 10.44%
Mapped paired reads	1,665,196 / 89.56%
Mapped reads, first in pair	833,748 / 44.84%
Mapped reads, second in pair	831,448 / 44.72%
Mapped reads, both in pair	1,551,680 / 83.45%
Mapped reads, singletons	113,516 / 6.11%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	30,962 / 1.67%
Duplication rate	1.62%
Clipped reads	86,410 / 4.65%

2.2. ACGT Content

Number/percentage of A's	17,826,086 / 27.64%
Number/percentage of C's	14,050,689 / 21.79%
Number/percentage of T's	18,163,016 / 28.17%
Number/percentage of G's	14,441,522 / 22.4%
Number/percentage of N's	2,494 / 0%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0208
Standard Deviation	0.1722

2.4. Mapping Quality

Mean Mapping Quality	48.25

2.5. Insert size

Mean	66,529.09
Standard Deviation	2,435,057.19
P25/Median/P75	89 / 120 / 164

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	184,179
Insertions	1,864
Mapped reads with at least one insertion	0.11%
Deletions	6,236
Mapped reads with at least one deletion	0.37%
Homopolymer indels	43.68%

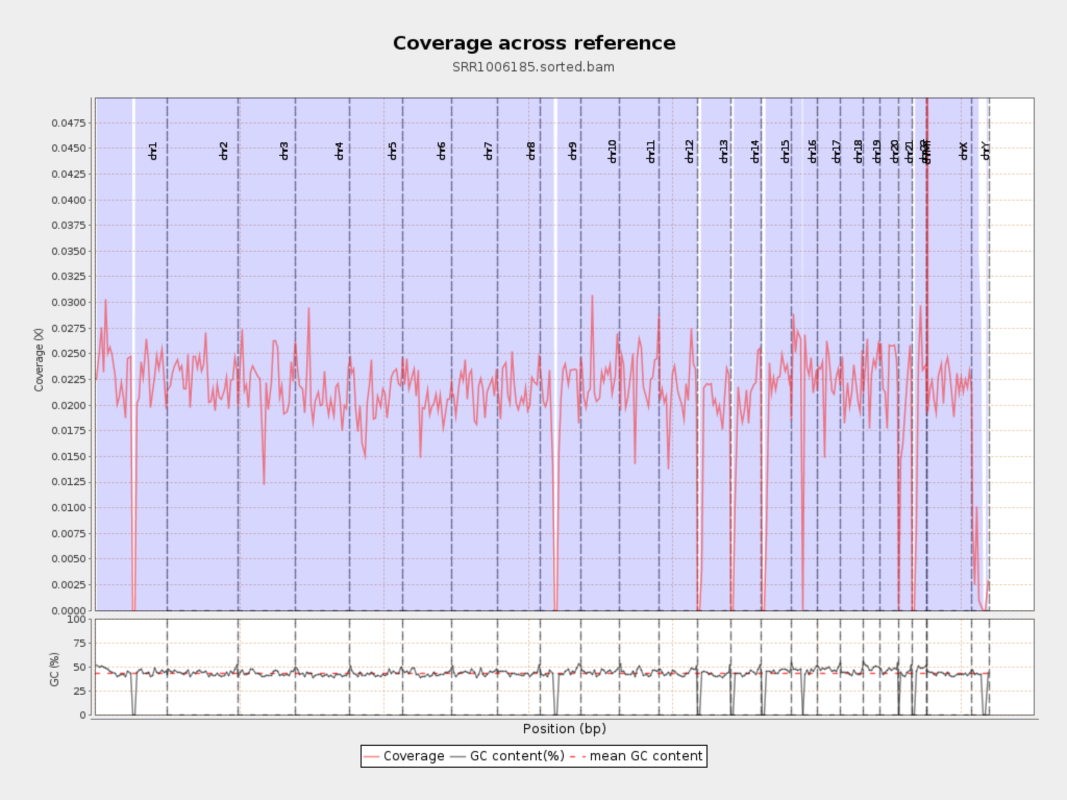
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

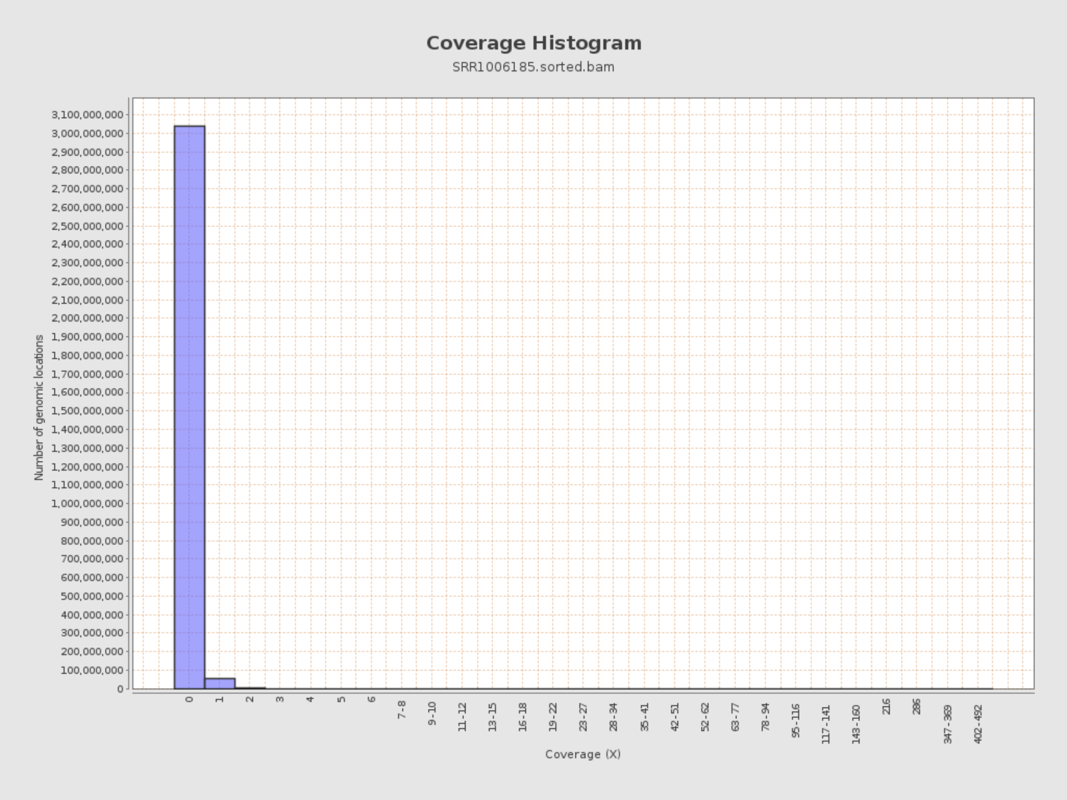
chr1	249250621	5436146	0.0218	0.1983
chr2	243199373	5500169	0.0226	0.1697
chr3	198022430	4358530	0.022	0.1577
chr4	191154276	4060805	0.0212	0.1602
chr5	180915260	3744961	0.0207	0.153
chr6	171115067	3557541	0.0208	0.1575
chr7	159138663	3421864	0.0215	0.1844
chr8	146364022	3150542	0.0215	0.2857
chr9	141213431	2667788	0.0189	0.1498
chr10	135534747	3090257	0.0228	0.184
chr11	135006516	3051206	0.0226	0.1668
chr12	133851895	2844343	0.0212	0.1551
chr13	115169878	2024791	0.0176	0.1411
chr14	107349540	1924519	0.0179	0.1484
chr15	102531392	1898579	0.0185	0.1444
chr16	90354753	2035327	0.0225	0.1726
chr17	81195210	1832391	0.0226	0.1619
chr18	78077248	1694884	0.0217	0.1886
chr19	59128983	1389802	0.0235	0.1803
chr20	63025520	1473379	0.0234	0.1639
chr21	48129895	870358	0.0181	0.1485
chr22	51304566	884915	0.0172	0.1416
chrMT	16571	4179	0.2522	0.5021
chrX	155270560	3401062	0.0219	0.1604

chrY	59373566	173920	0.0029	0.0924

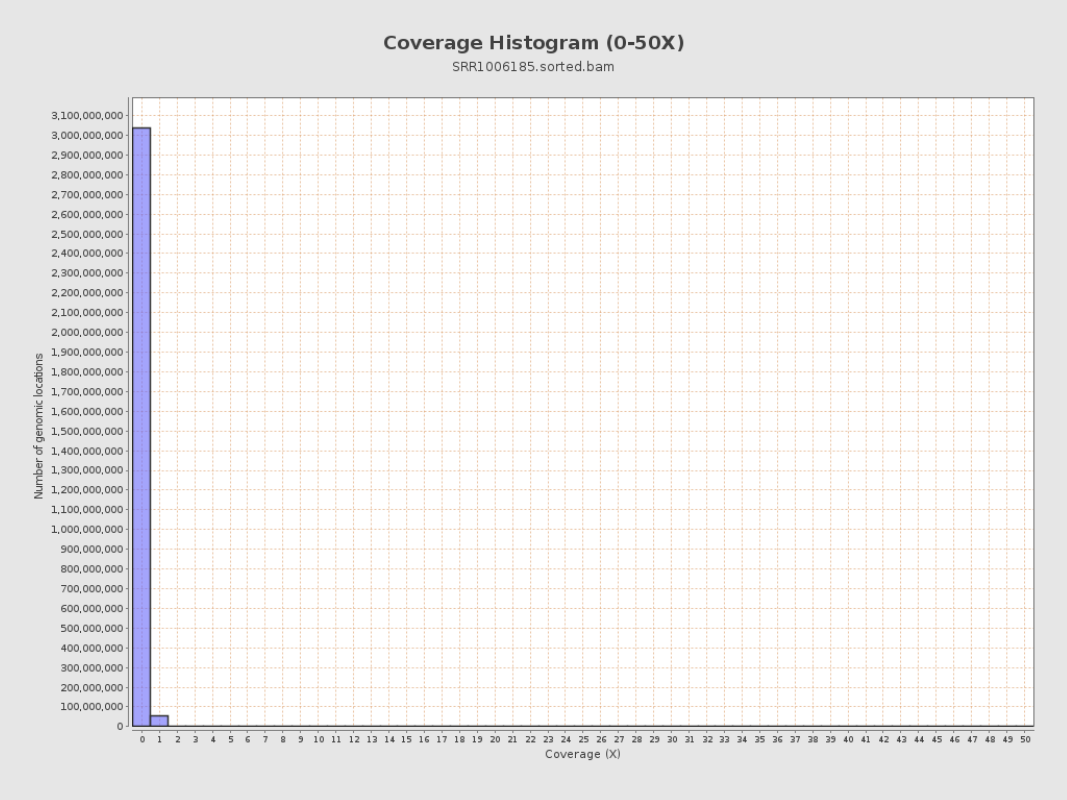
3. Results : Coverage across reference



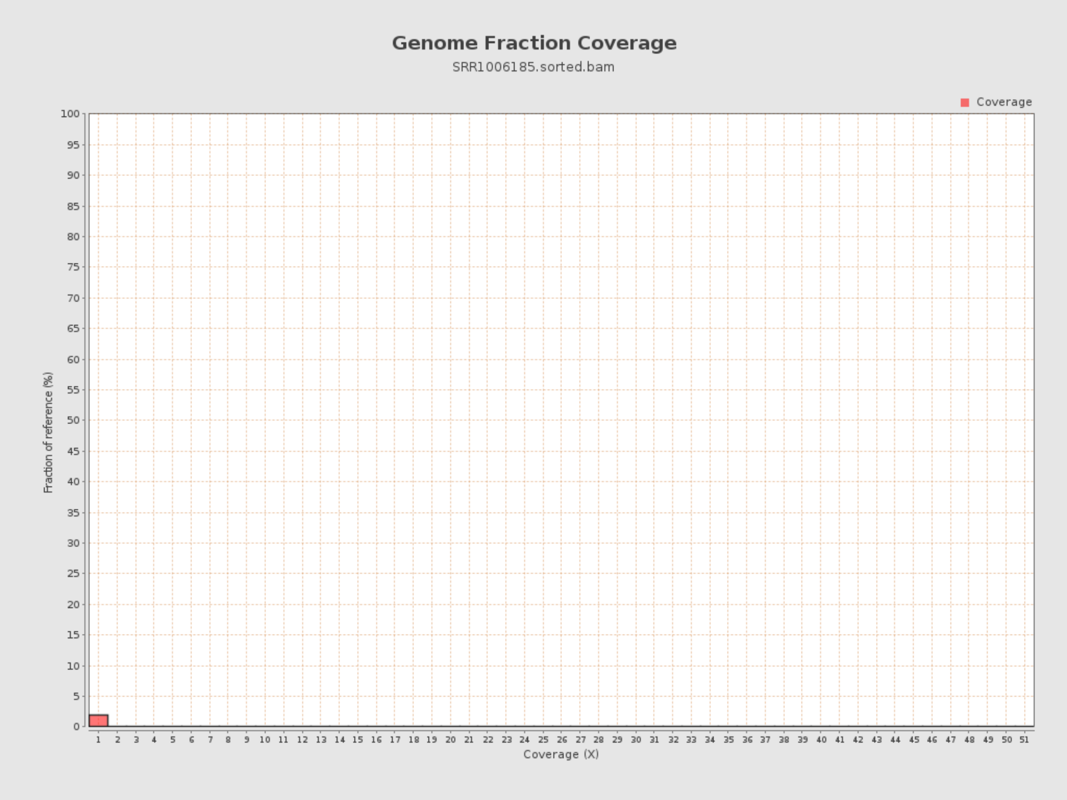
4. Results : Coverage Histogram



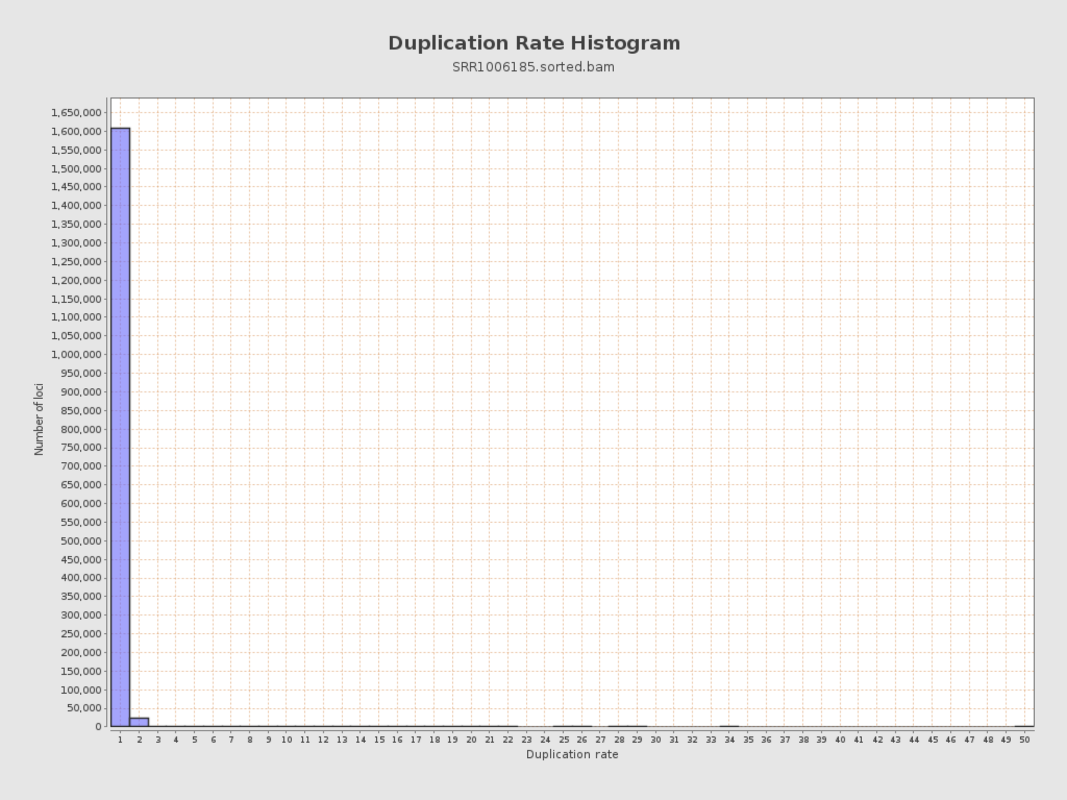
5. Results : Coverage Histogram (0-50X)



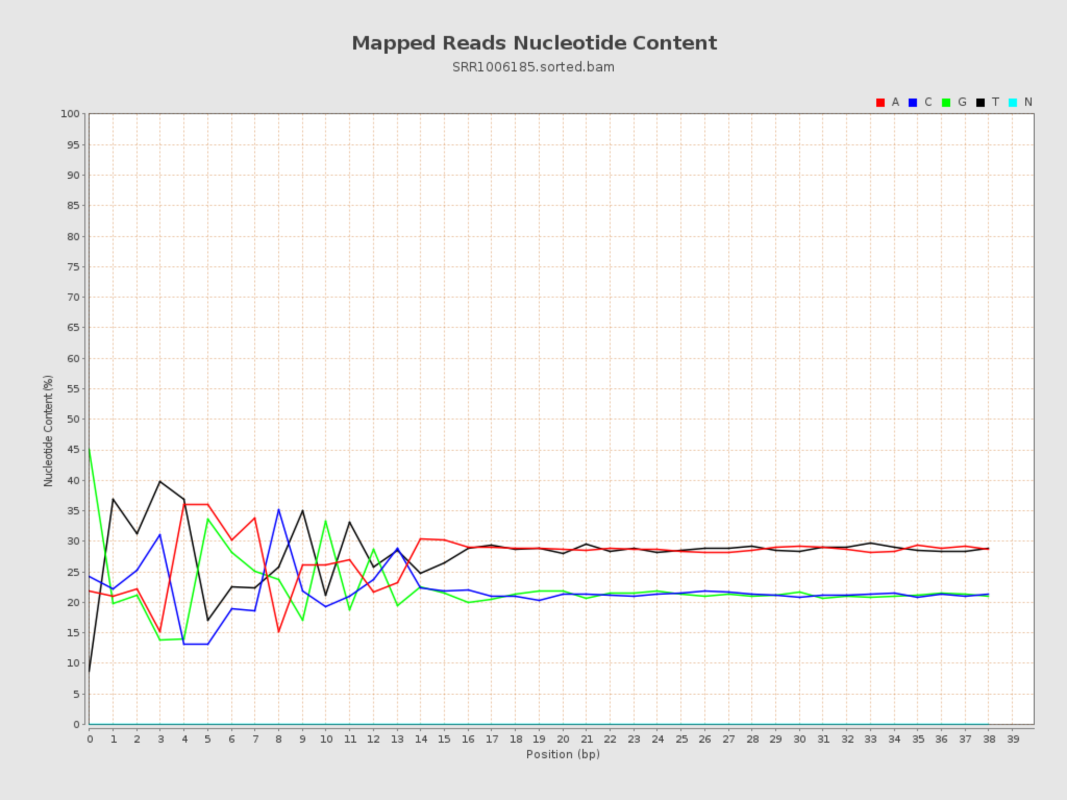
6. Results : Genome Fraction Coverage



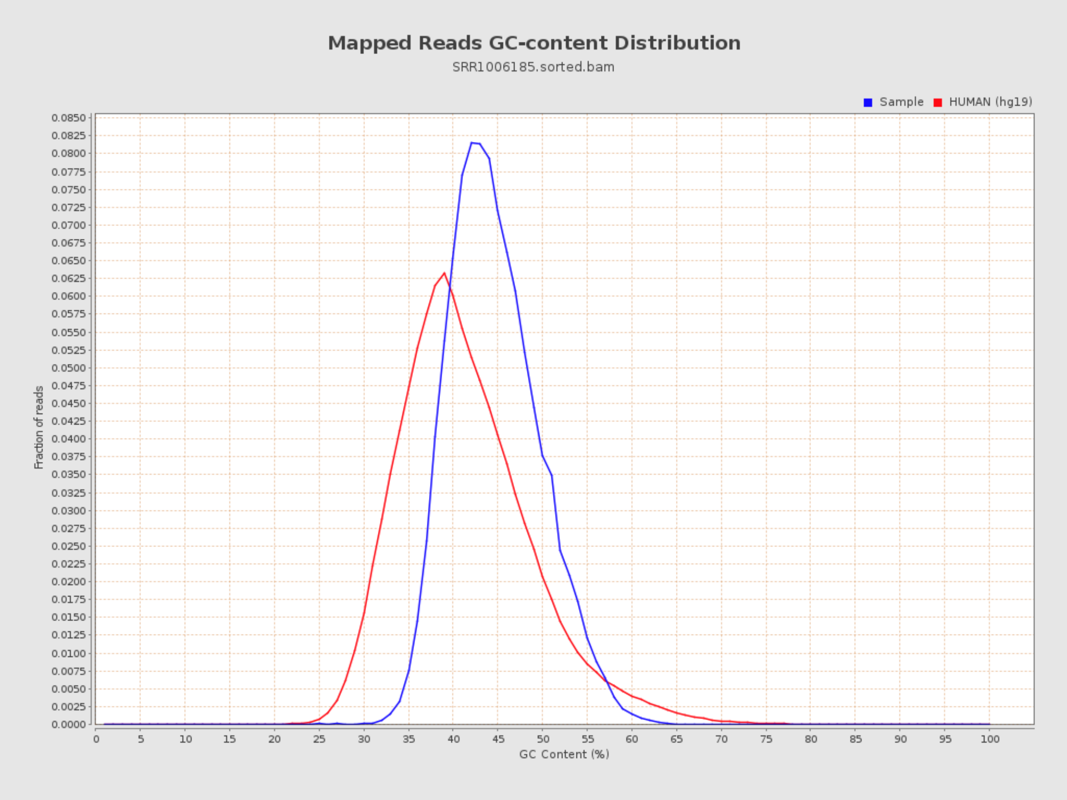
7. Results : Duplication Rate Histogram



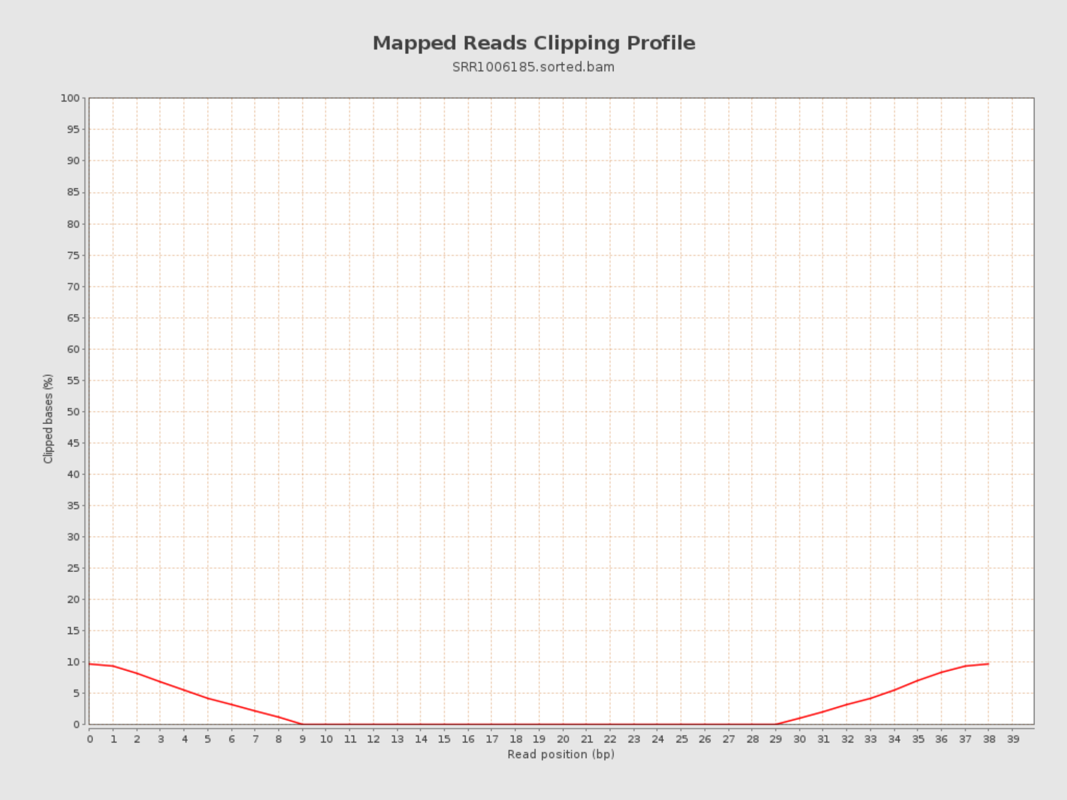
8. Results : Mapped Reads Nucleotide Content



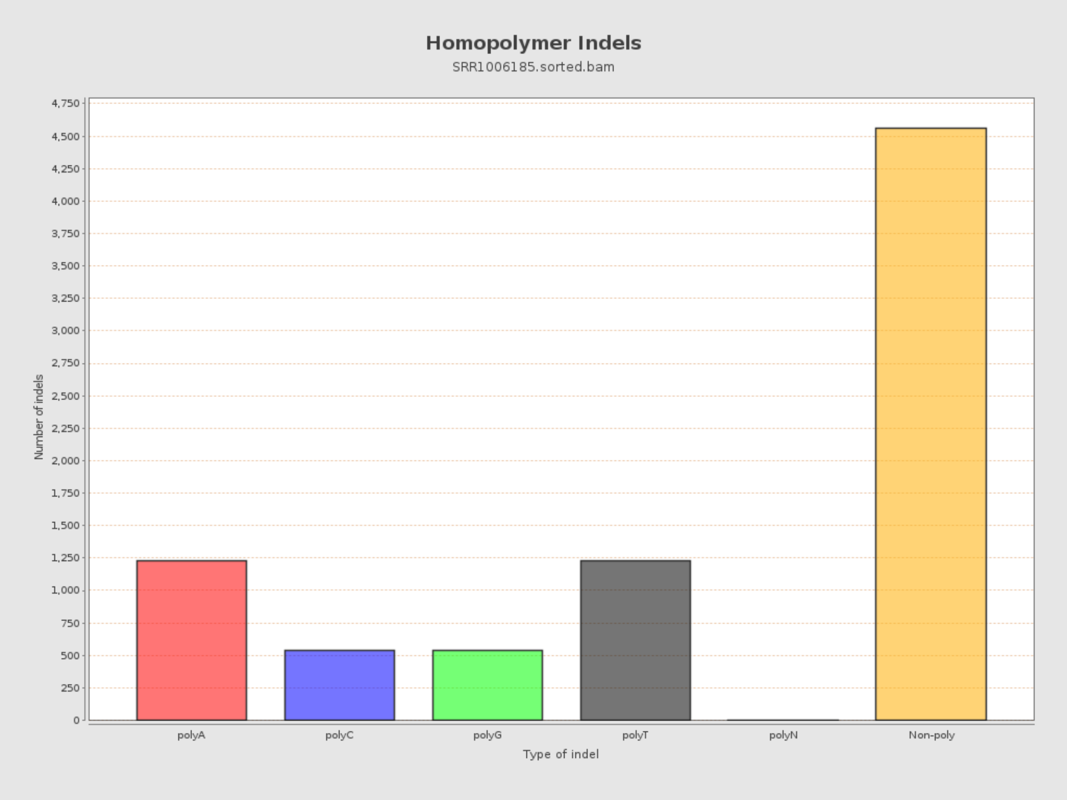
9. Results : Mapped Reads GC-content Distribution



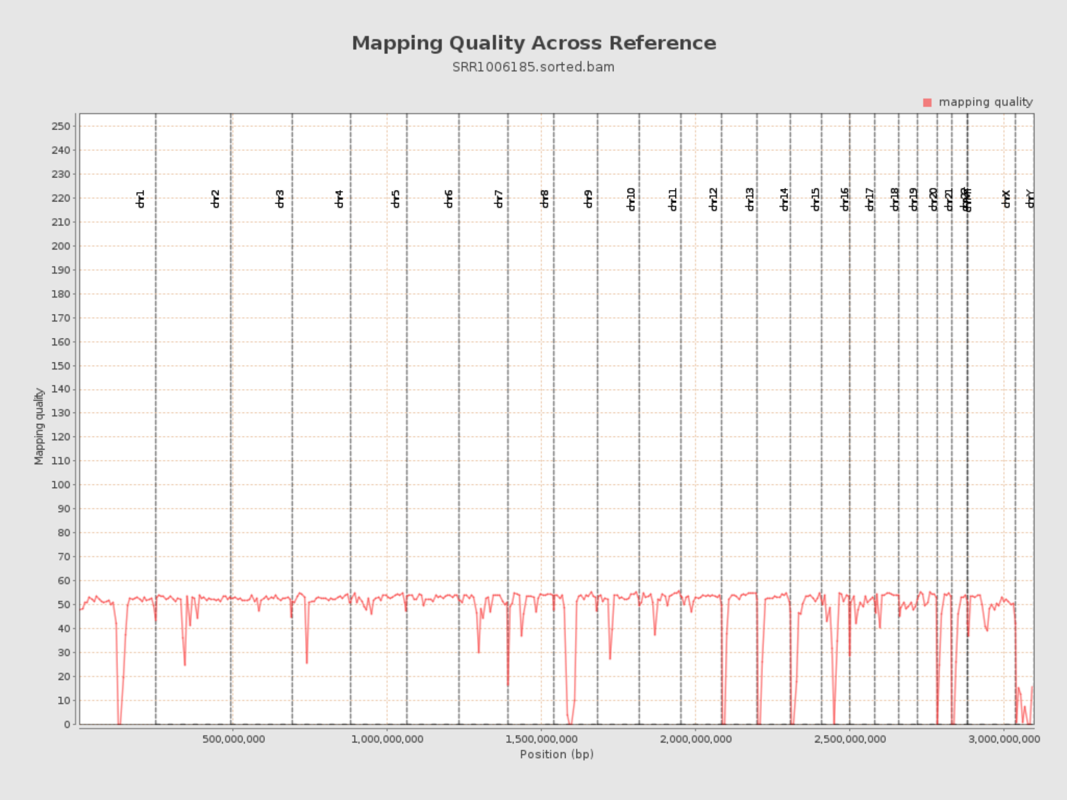
10. Results : Mapped Reads Clipping Profile



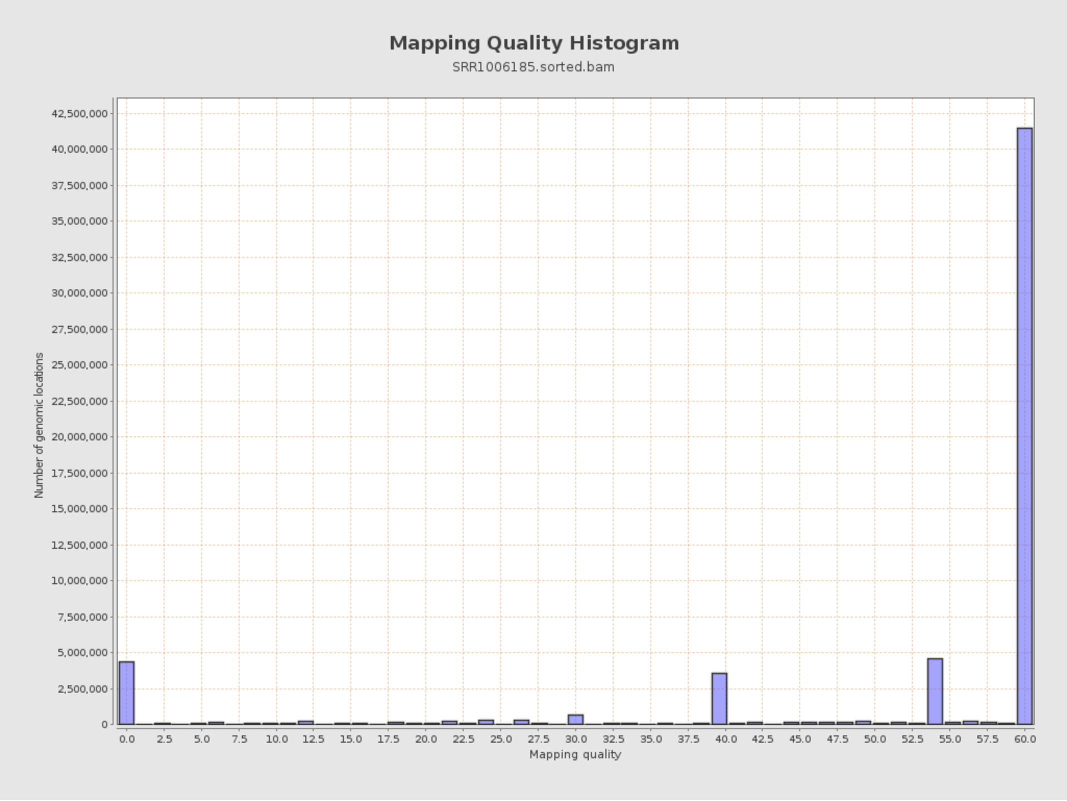
11. Results : Homopolymer Indels



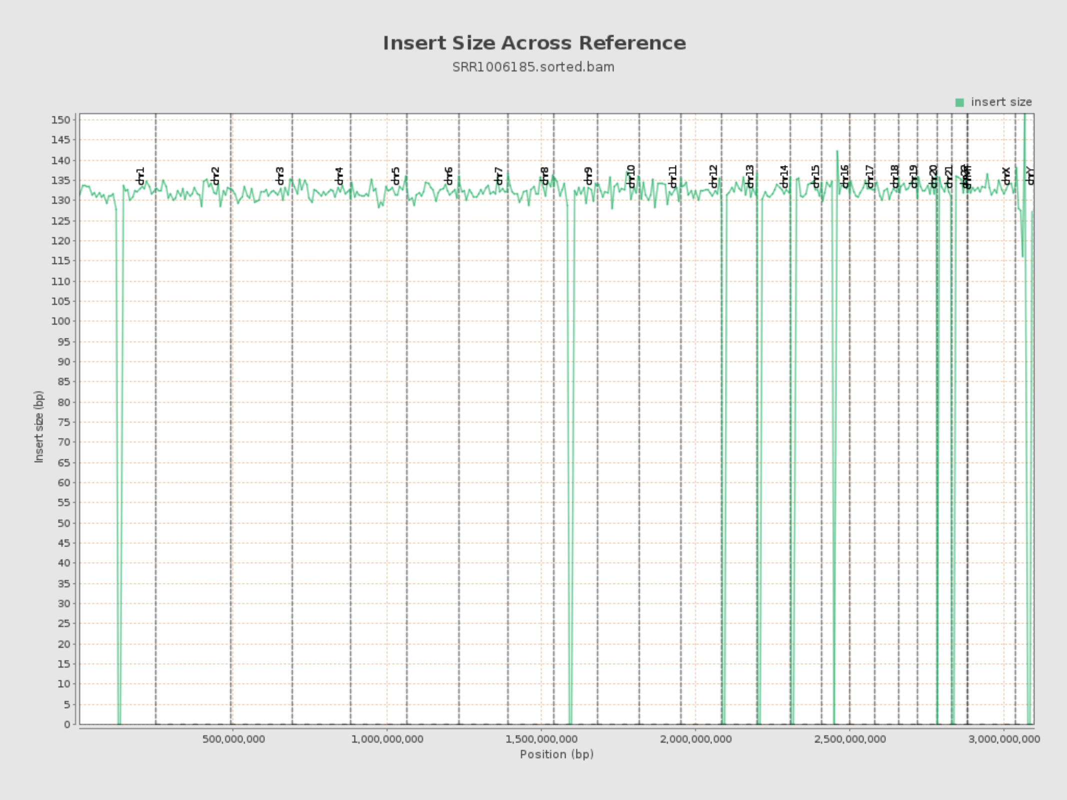
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram