Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 12:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006000.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_SRR1006000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006000_1.fastq.gz SRR1006000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 12:30:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,309,920
Mapped reads	11,908,794 / 83.22%
Unmapped reads	2,401,126 / 16.78%
Mapped paired reads	11,908,794 / 83.22%
Mapped reads, first in pair	6,025,098 / 42.1%
Mapped reads, second in pair	5,883,696 / 41.12%
Mapped reads, both in pair	10,867,376 / 75.94%
Mapped reads, singletons	1,041,418 / 7.28%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	691,282 / 4.83%
Duplication rate	4.95%
Clipped reads	871,388 / 6.09%

2.2. ACGT Content

Number/percentage of A's	130,475,144 / 28.35%
Number/percentage of C's	98,536,509 / 21.41%
Number/percentage of T's	131,152,247 / 28.5%
Number/percentage of G's	99,861,482 / 21.7%
Number/percentage of N's	141,197 / 0.03%
GC Percentage	43.11%

2.3. Coverage

Mean	0.1487
Standard Deviation	0.9955

2.4. Mapping Quality

Mean Mapping Quality	46.52

2.5. Insert size

Mean	60,950.37
Standard Deviation	2,382,612.92
P25/Median/P75	60 / 85 / 120

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	2,283,899
Insertions	14,093
Mapped reads with at least one insertion	0.12%
Deletions	39,607
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.9%

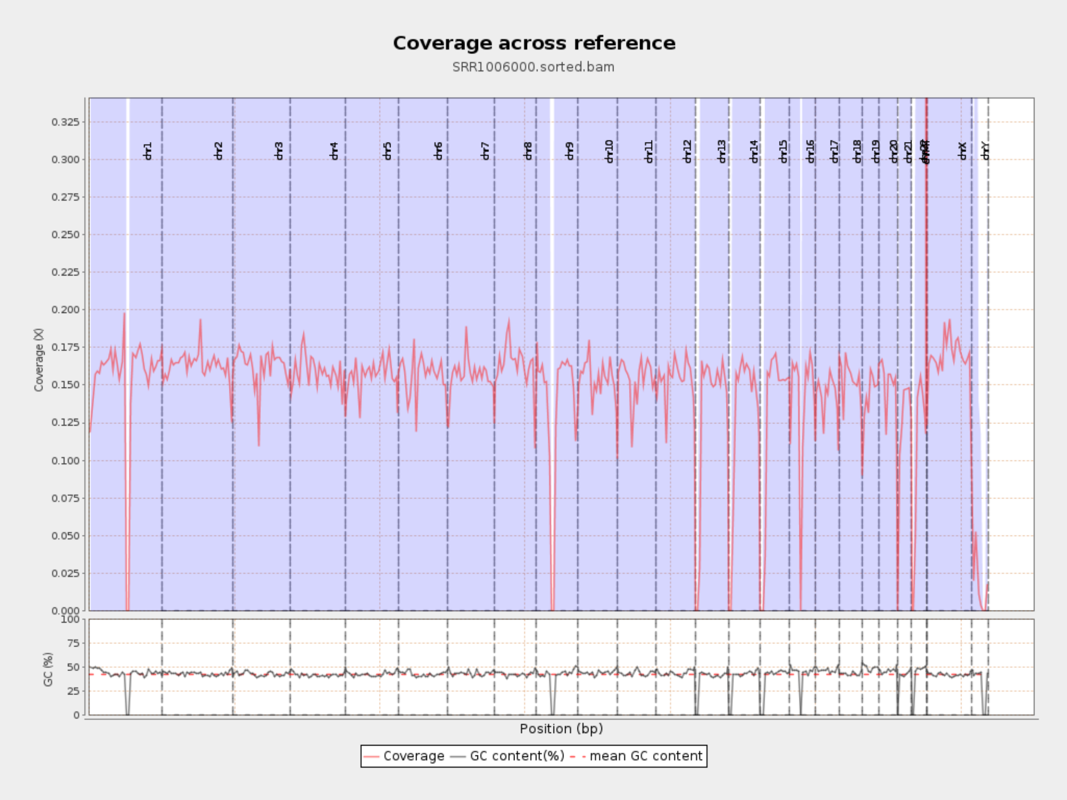
2.7. Chromosome stats

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

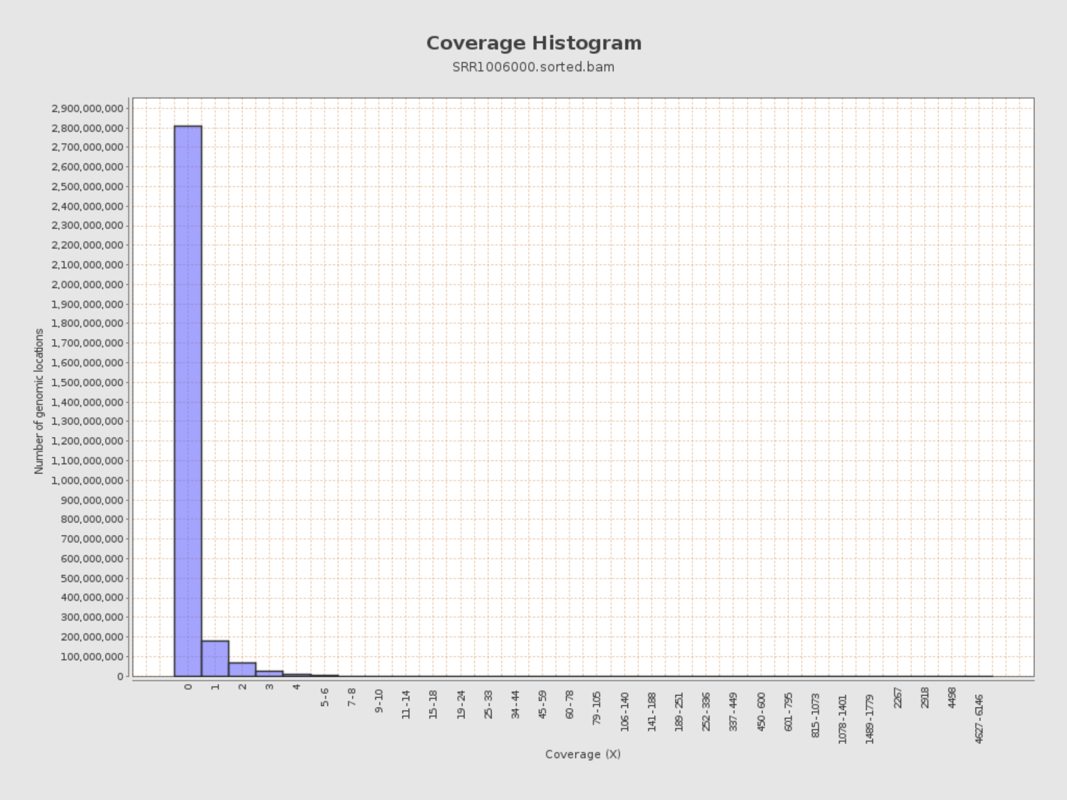
chr1	249250621	37986989	0.1524	1.3706
chr2	243199373	39715835	0.1633	0.7321
chr3	198022430	32216315	0.1627	0.5873
chr4	191154276	30348307	0.1588	0.6118
chr5	180915260	28431884	0.1572	0.5773
chr6	171115067	26823199	0.1568	0.6798
chr7	159138663	25112513	0.1578	1.0334
chr8	146364022	23891589	0.1632	3.0473
chr9	141213431	19001611	0.1346	0.6328
chr10	135534747	21039515	0.1552	0.7031
chr11	135006516	20735470	0.1536	0.6705
chr12	133851895	20634307	0.1542	0.5782
chr13	115169878	14979373	0.1301	0.5243
chr14	107349540	13840778	0.1289	0.5592
chr15	102531392	13028840	0.1271	0.5218
chr16	90354753	12551151	0.1389	0.5805
chr17	81195210	11605501	0.1429	0.5804
chr18	78077248	12027653	0.154	0.9633
chr19	59128983	8498756	0.1437	1.1859
chr20	63025520	9495906	0.1507	0.5949
chr21	48129895	5805762	0.1206	0.5548
chr22	51304566	5043369	0.0983	0.5284
chrMT	16571	51338	3.0981	2.7007
chrX	155270560	26251599	0.1691	0.651

chrY	59373566	1099881	0.0185	0.3209

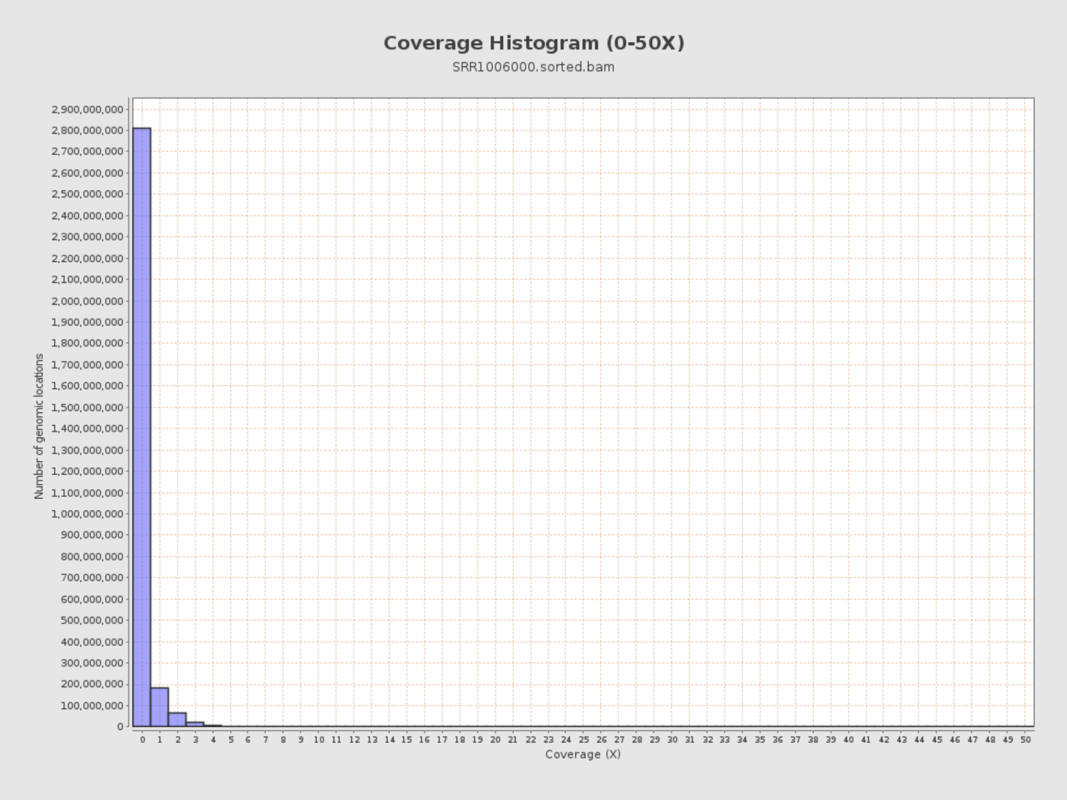
3. Results : Coverage across reference



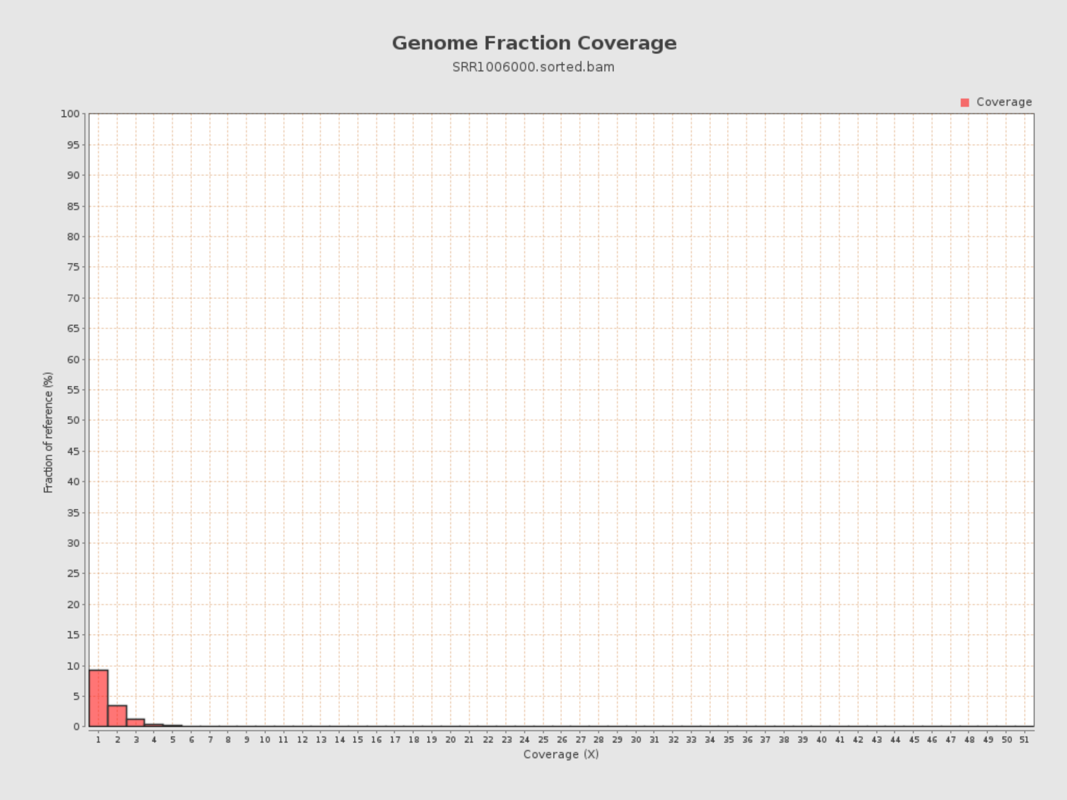
4. Results : Coverage Histogram



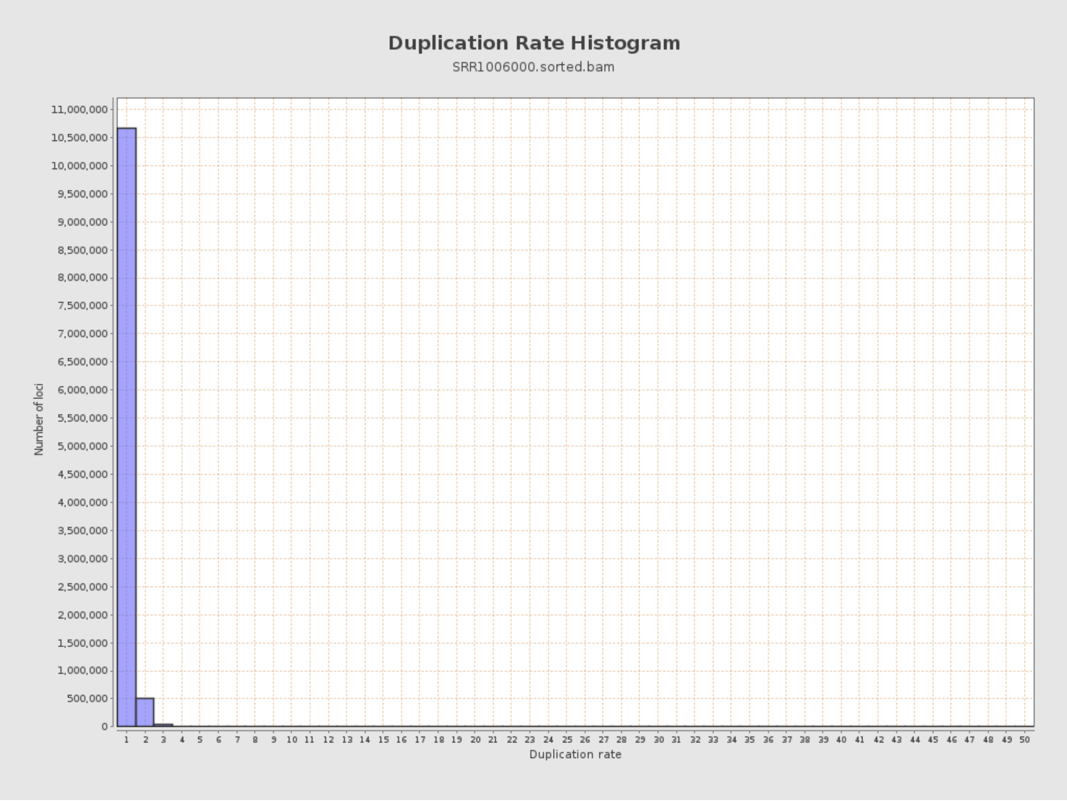
5. Results : Coverage Histogram (0-50X)



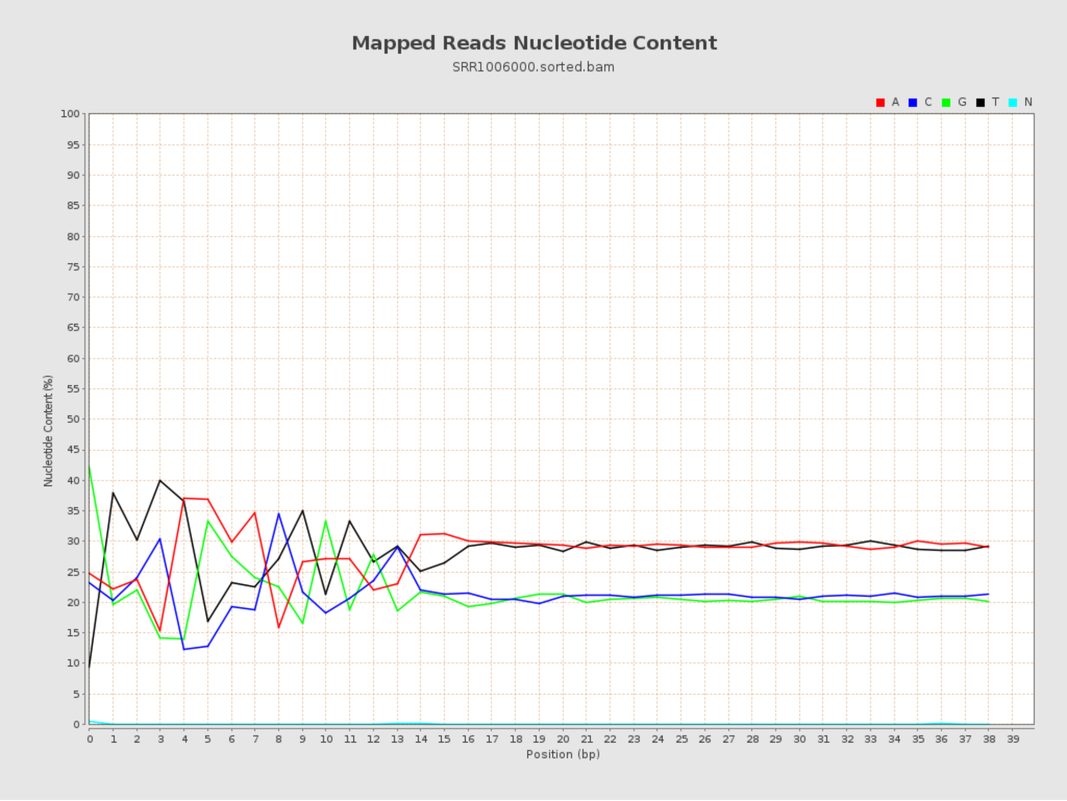
6. Results : Genome Fraction Coverage



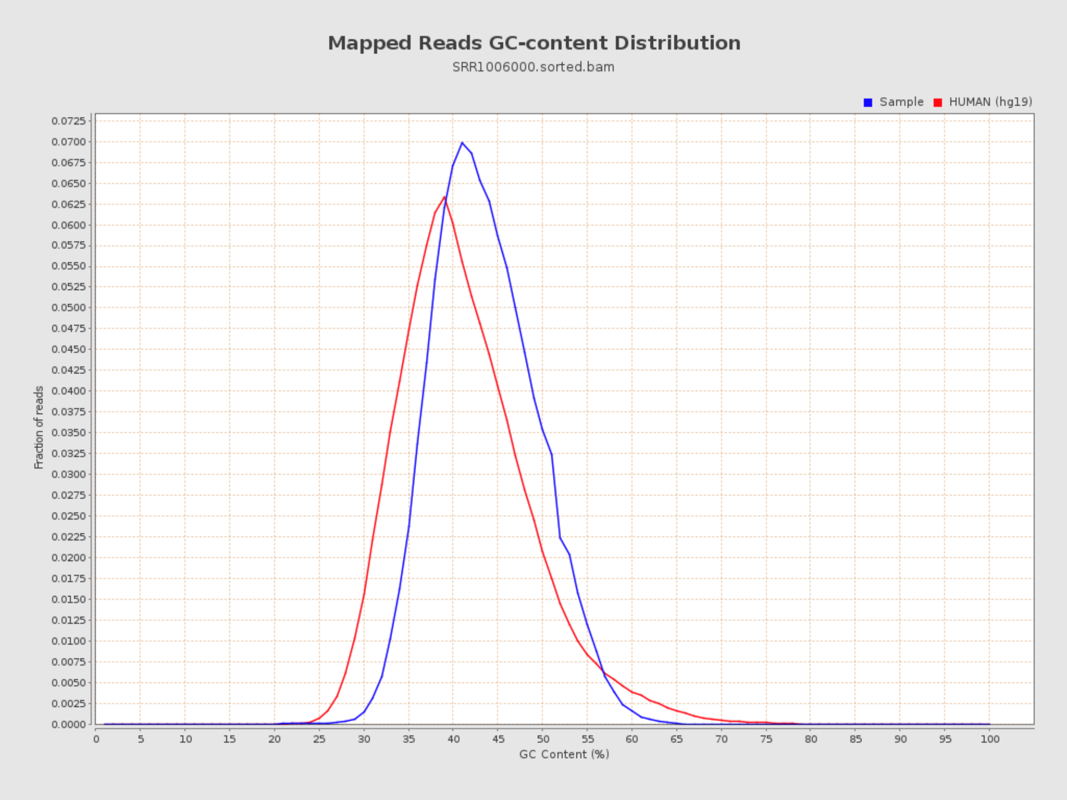
7. Results : Duplication Rate Histogram



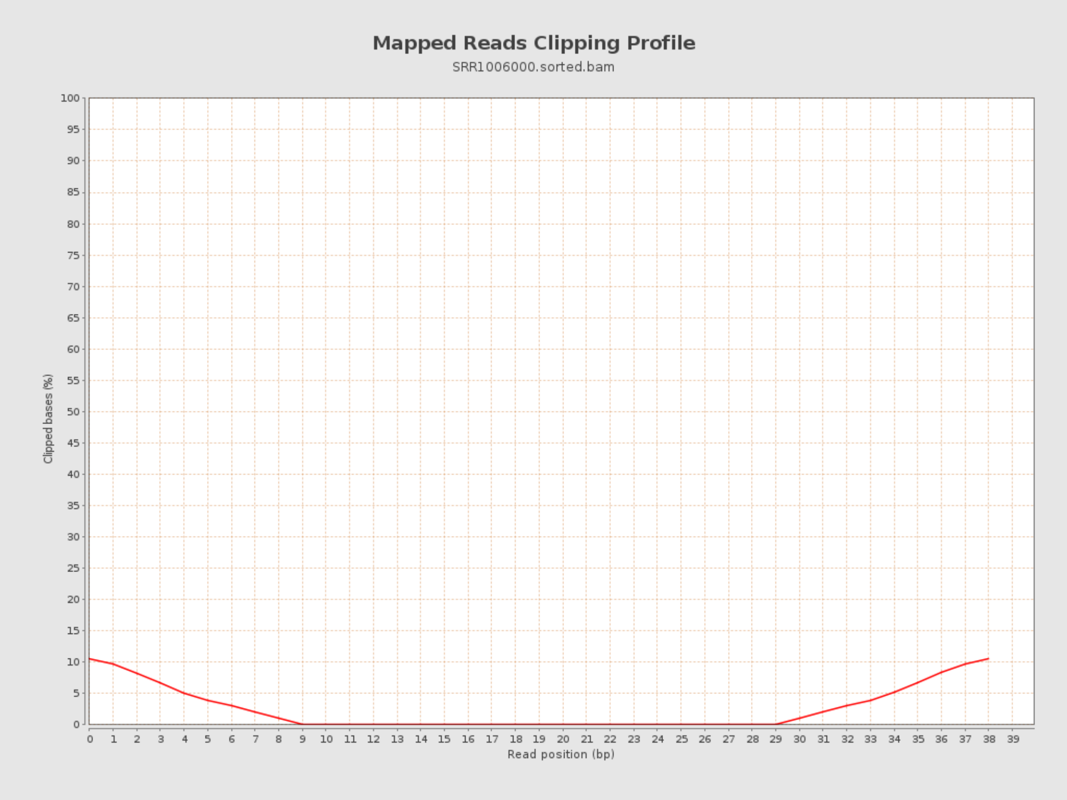
8. Results : Mapped Reads Nucleotide Content



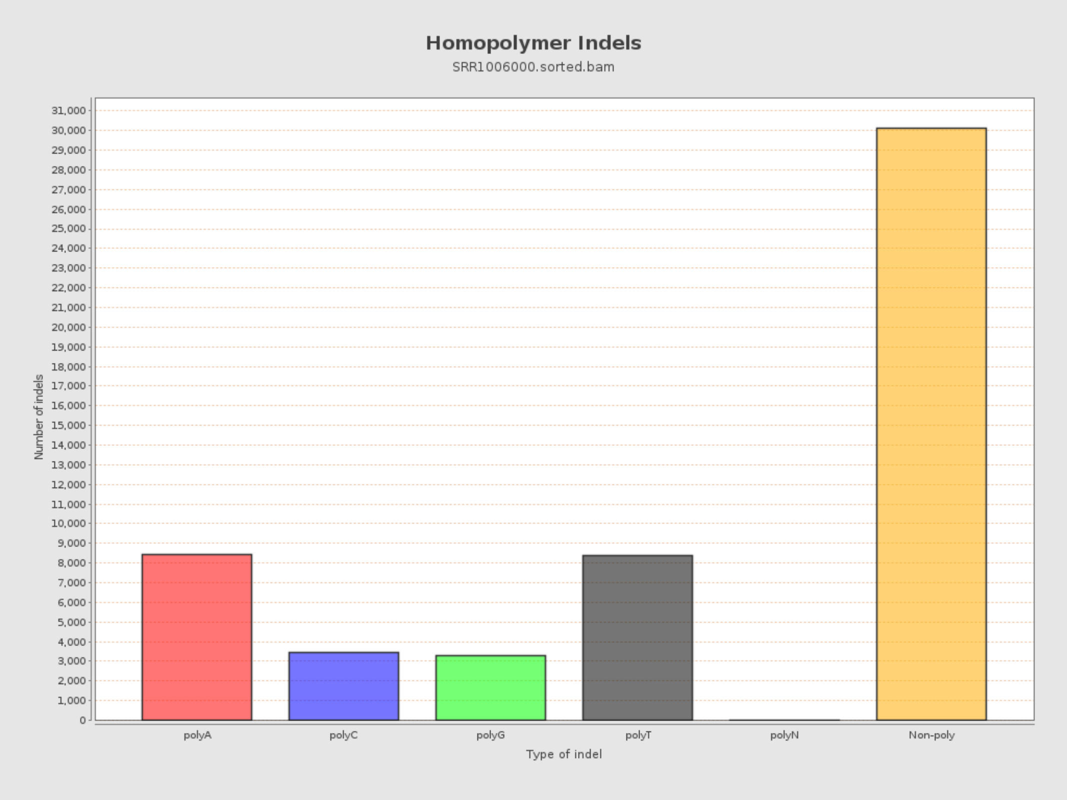
9. Results : Mapped Reads GC-content Distribution



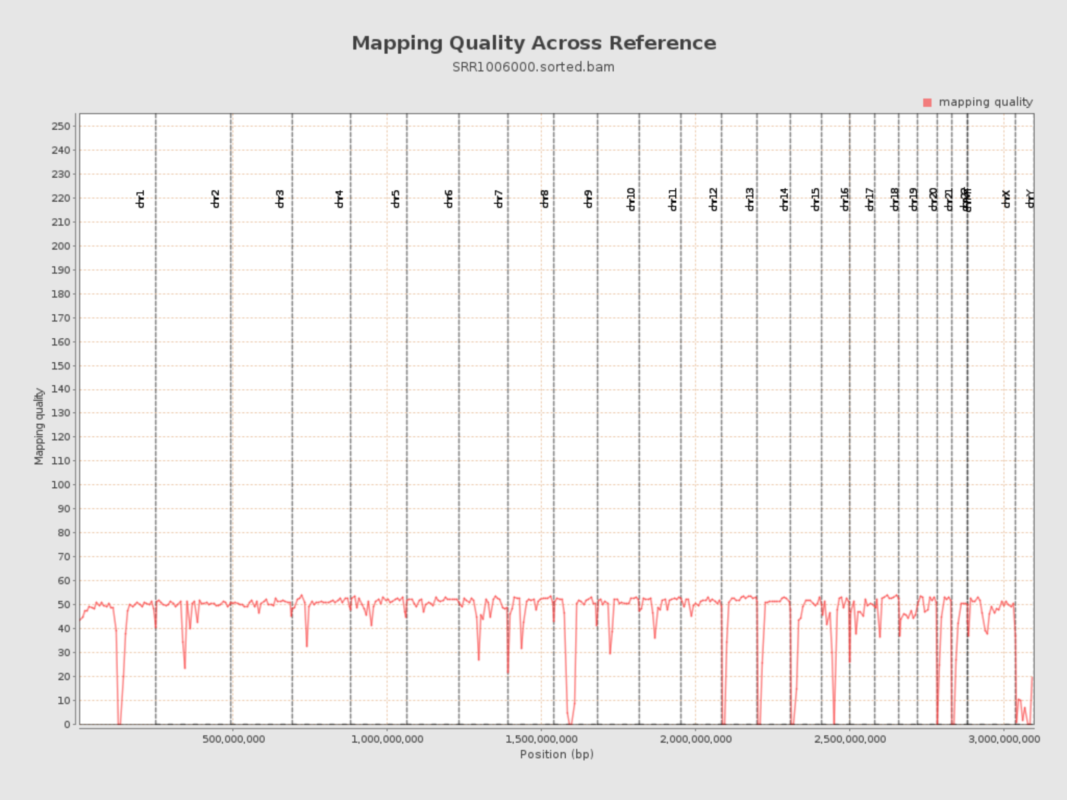
10. Results : Mapped Reads Clipping Profile



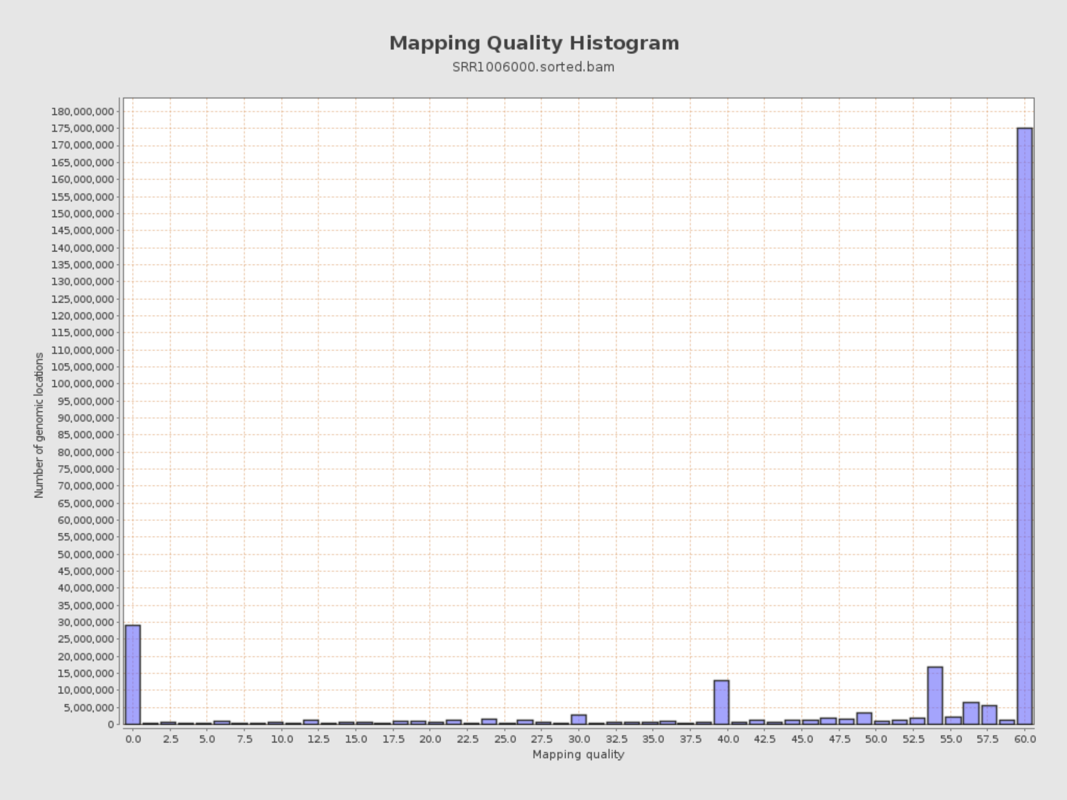
11. Results : Homopolymer Indels



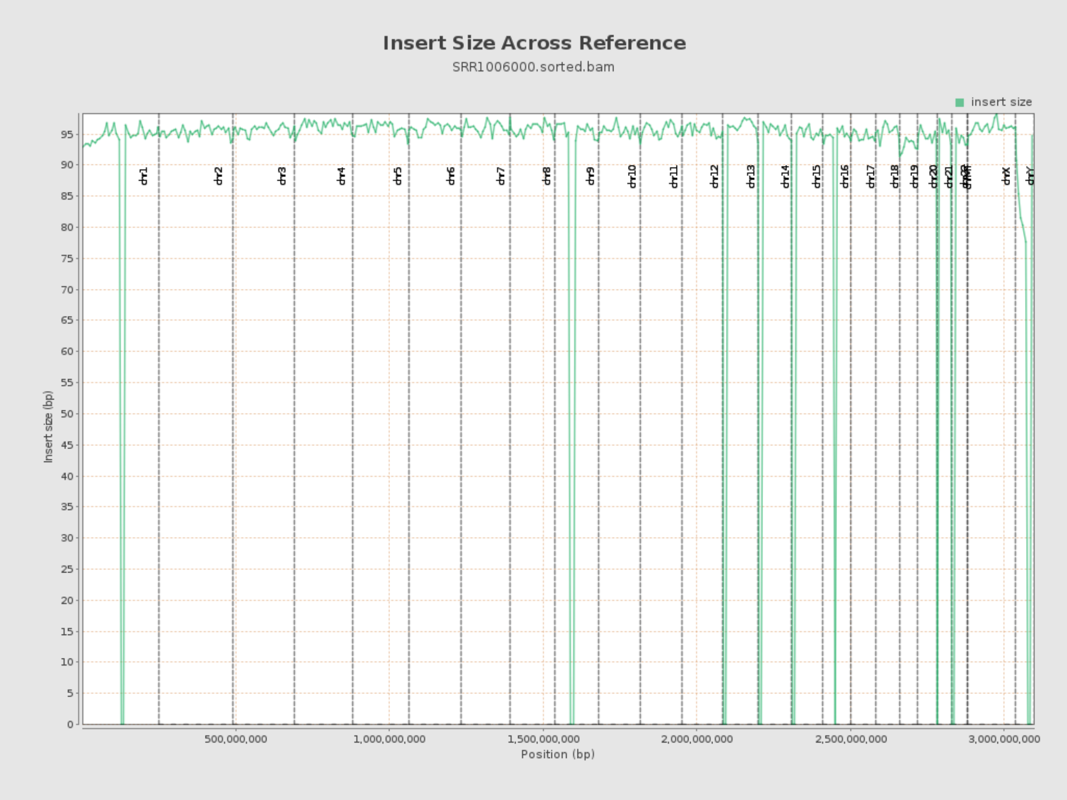
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram