Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:08:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716687.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_SRR9716687 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716687.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:08:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716687.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,261,760
Mapped reads	1,086,121 / 86.08%
Unmapped reads	175,639 / 13.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,644 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	22,824 / 1.81%
Duplication rate	1.44%
Clipped reads	1,087,739 / 86.21%

2.2. ACGT Content

Number/percentage of A's	14,855,395 / 24.06%
Number/percentage of C's	12,440,902 / 20.15%
Number/percentage of T's	19,074,778 / 30.9%
Number/percentage of G's	15,360,457 / 24.88%
Number/percentage of N's	459 / 0%
GC Percentage	45.04%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.1891

2.4. Mapping Quality

Mean Mapping Quality	41.9

2.5. Mismatches and indels

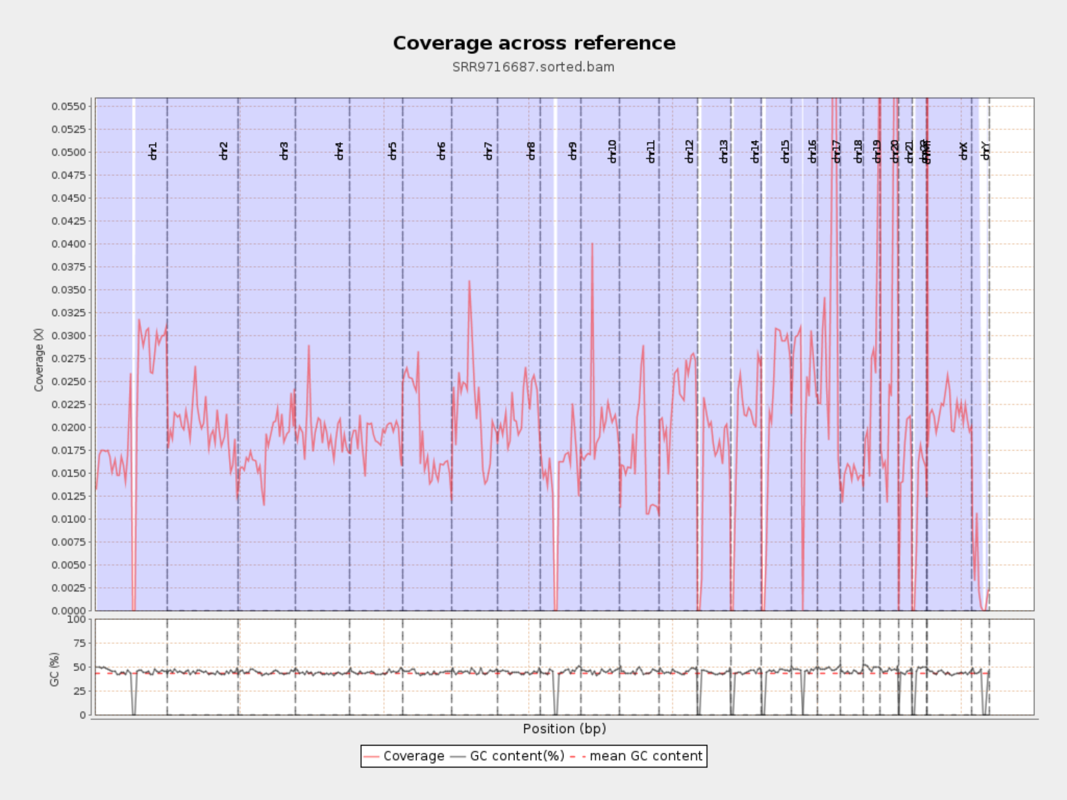
General error rate	0.54%
Mismatches	323,605
Insertions	4,098
Mapped reads with at least one insertion	0.38%
Deletions	12,061
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.32%

2.6. Chromosome stats

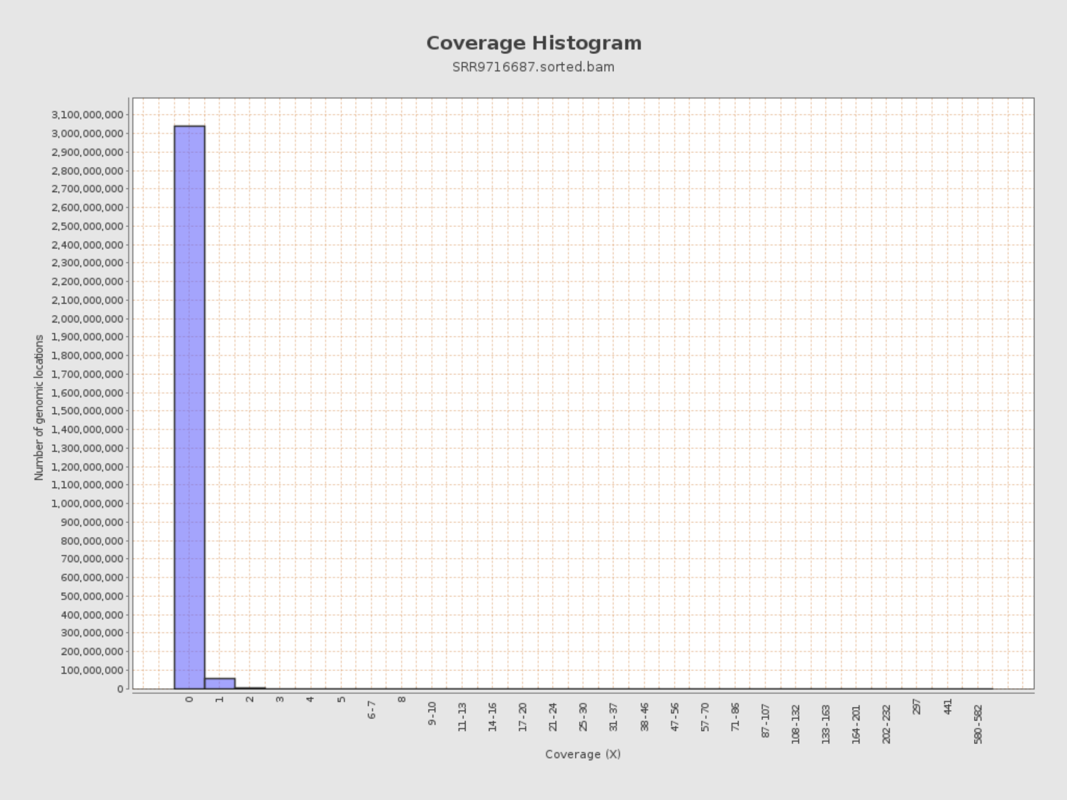
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5233398	0.021	0.2305
chr2	243199373	4832444	0.0199	0.2748
chr3	198022430	3533925	0.0178	0.1437
chr4	191154276	3720848	0.0195	0.1556
chr5	180915260	3466904	0.0192	0.1459
chr6	171115067	3271761	0.0191	0.1696
chr7	159138663	3520195	0.0221	0.2642

chr8	146364022	3174957	0.0217	0.1847
chr9	141213431	2047501	0.0145	0.1424
chr10	135534747	2751215	0.0203	0.2292
chr11	135006516	2190163	0.0162	0.1619
chr12	133851895	3115767	0.0233	0.1629
chr13	115169878	1837417	0.016	0.1336
chr14	107349540	2078510	0.0194	0.1502
chr15	102531392	2266677	0.0221	0.1614
chr16	90354753	2184736	0.0242	0.1734
chr17	81195210	2785064	0.0343	0.2033
chr18	78077248	1147972	0.0147	0.1996
chr19	59128983	1687640	0.0285	0.2362
chr20	63025520	2003549	0.0318	0.1963
chr21	48129895	768279	0.016	0.1398
chr22	51304566	589284	0.0115	0.1146
chrMT	16571	7393	0.4461	0.7564
chrX	155270560	3345316	0.0215	0.1634
chrY	59373566	190348	0.0032	0.0917

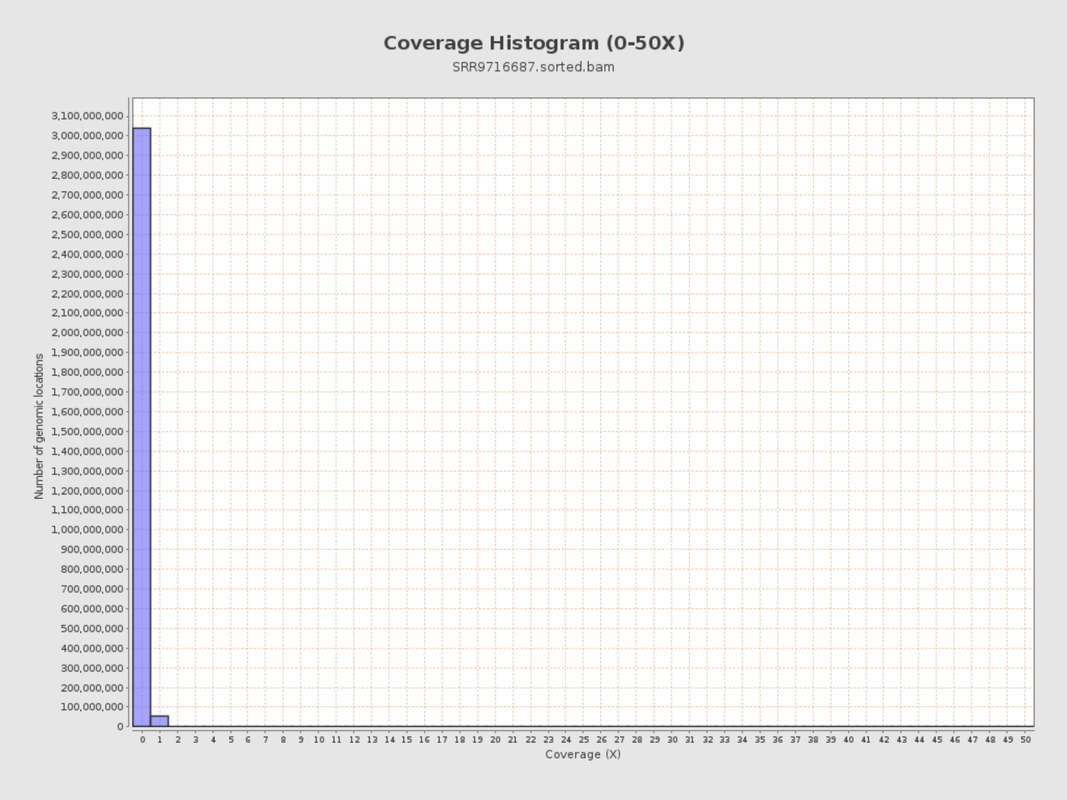
3. Results : Coverage across reference



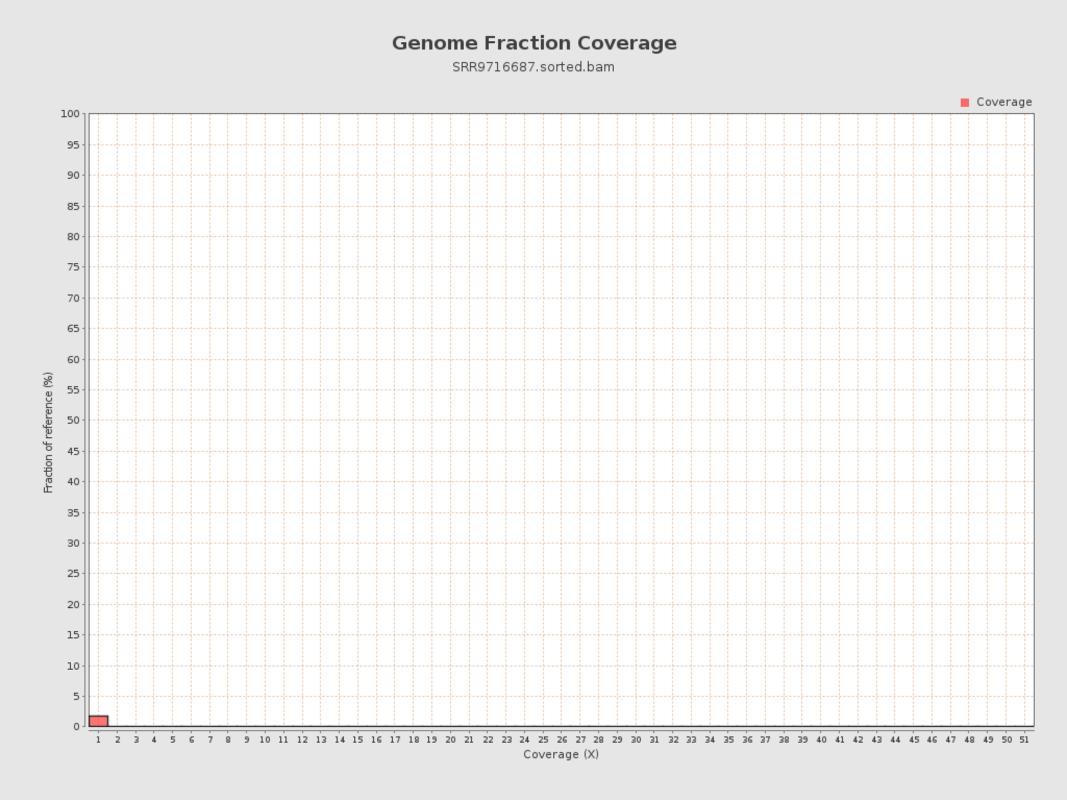
4. Results : Coverage Histogram



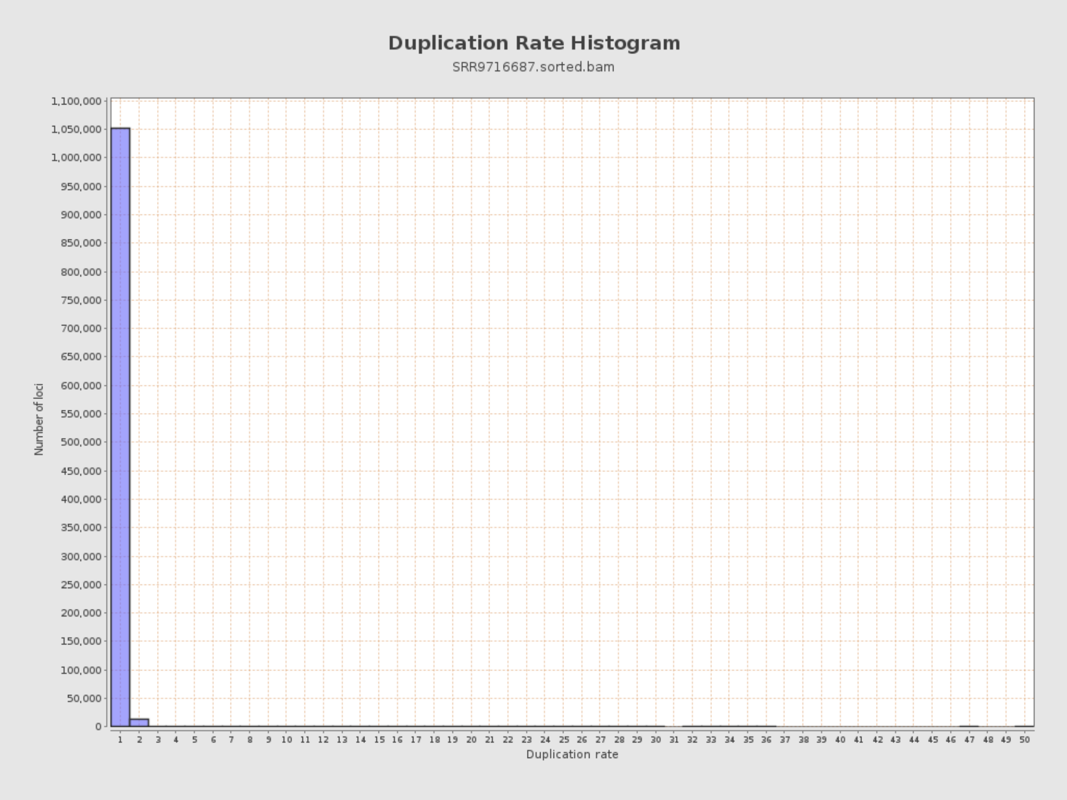
5. Results : Coverage Histogram (0-50X)



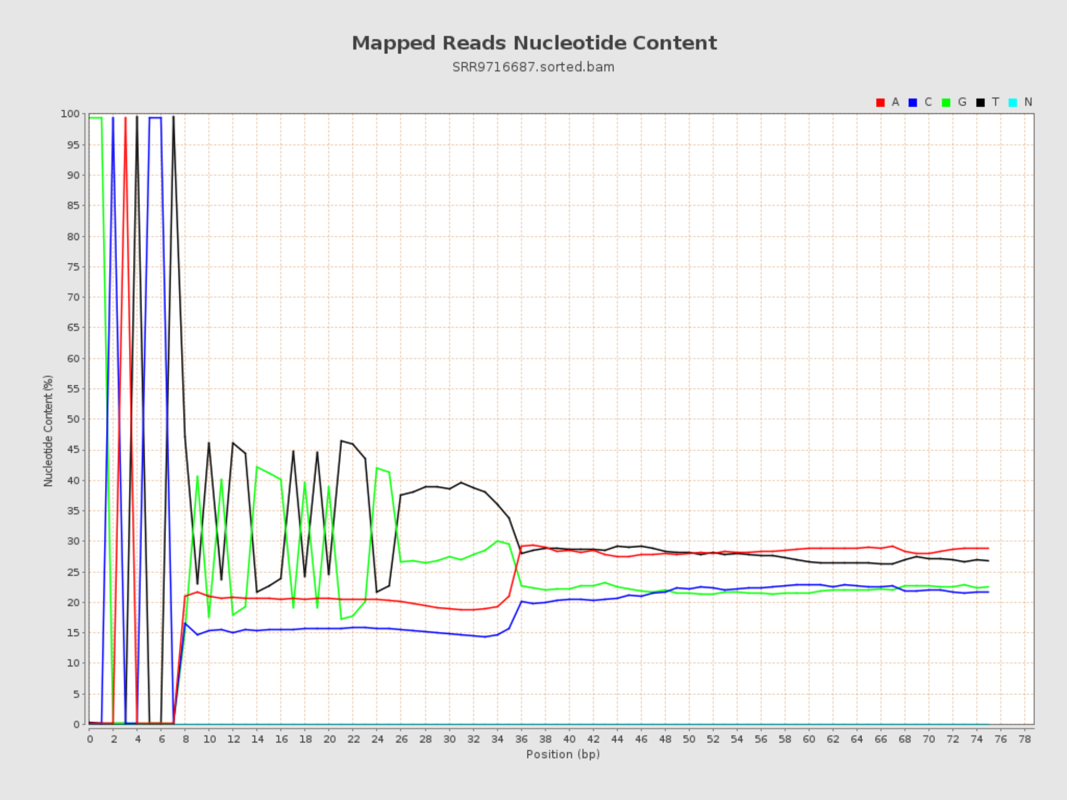
6. Results : Genome Fraction Coverage



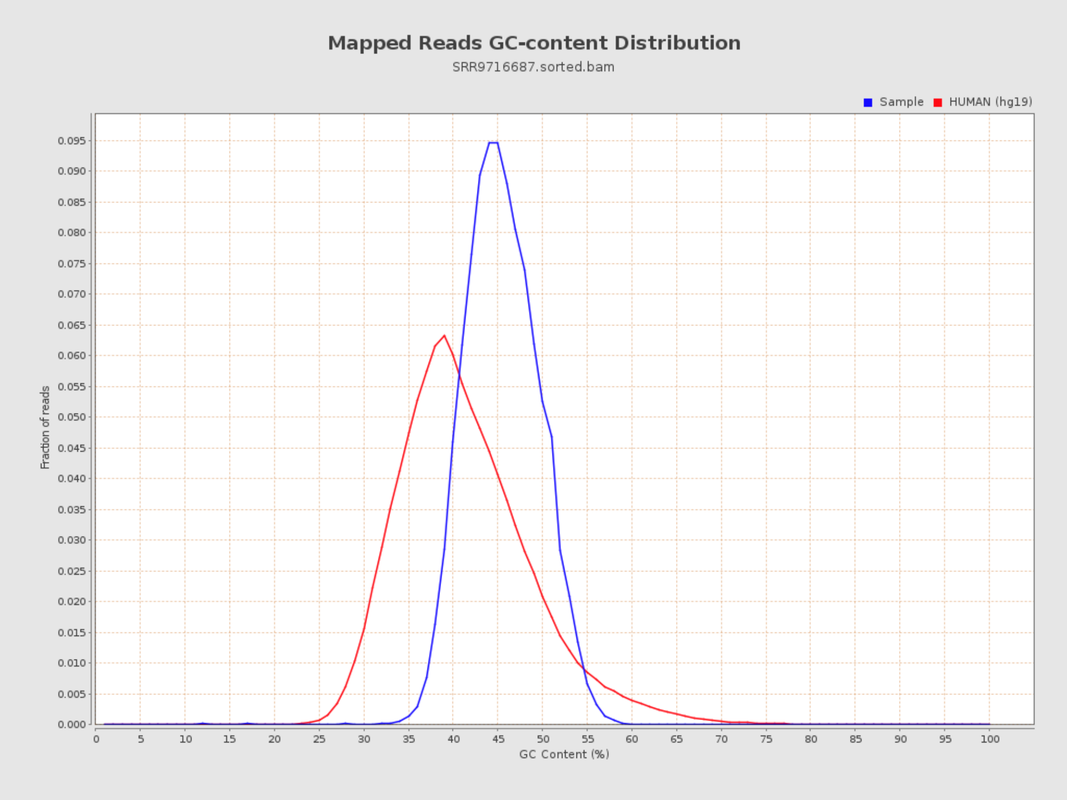
7. Results : Duplication Rate Histogram



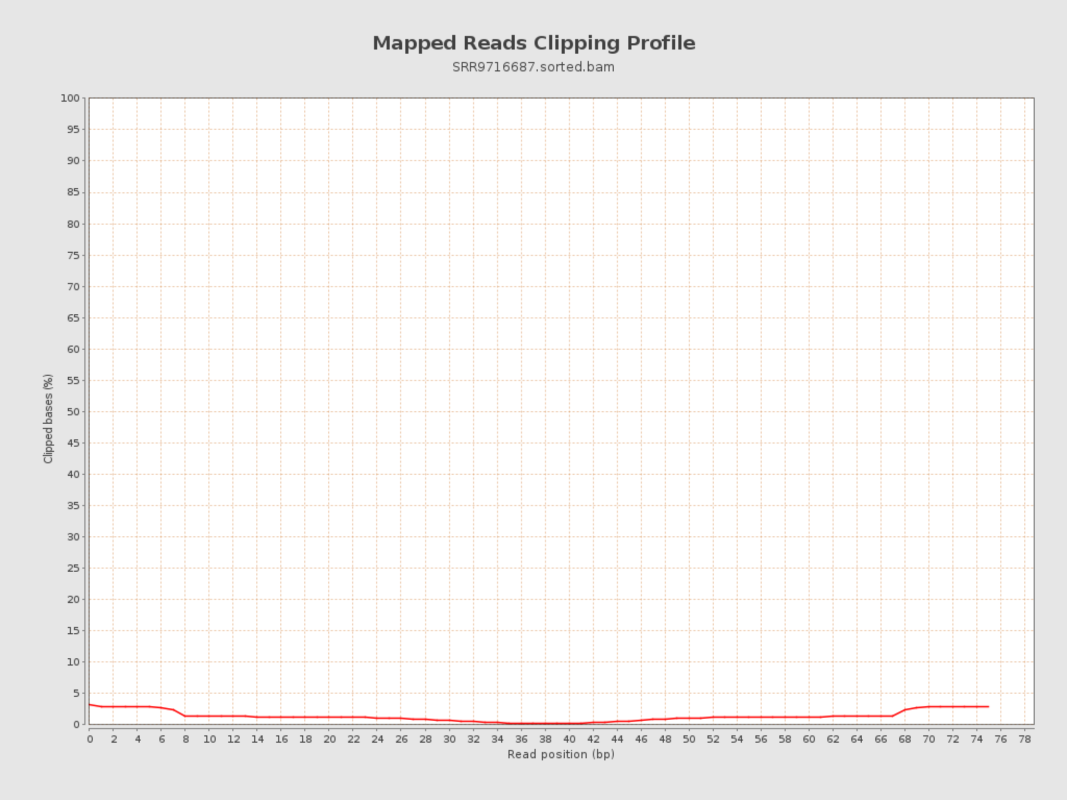
8. Results : Mapped Reads Nucleotide Content



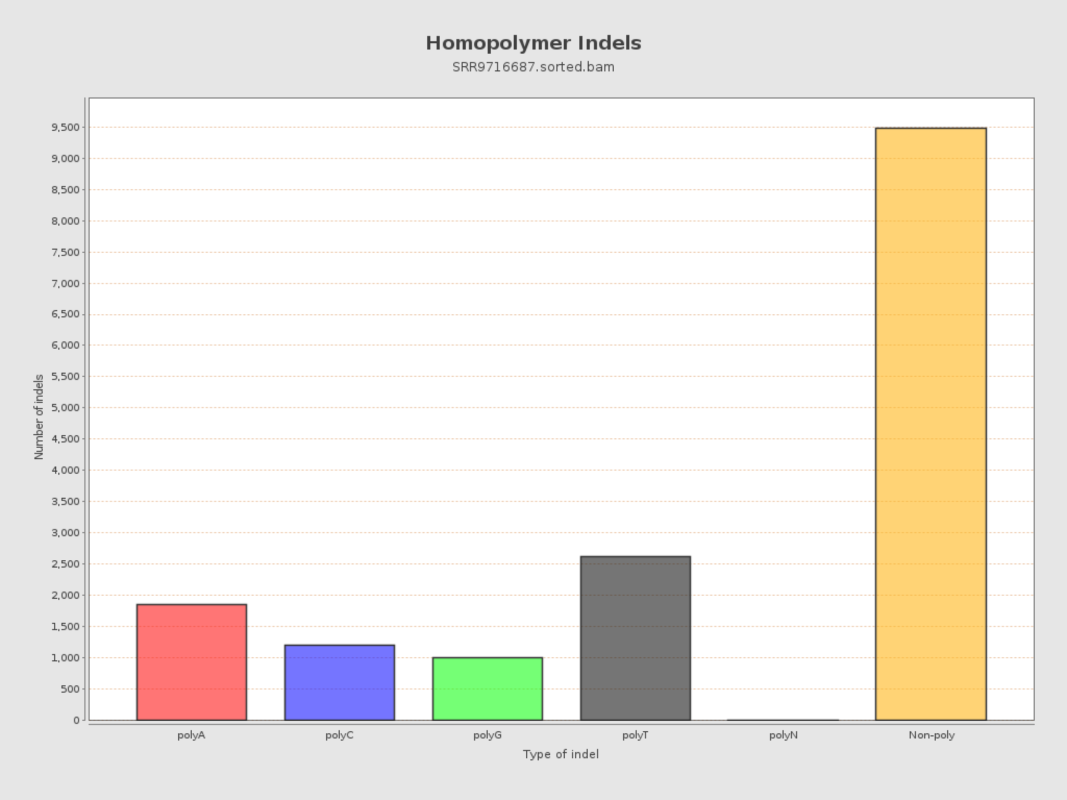
9. Results : Mapped Reads GC-content Distribution



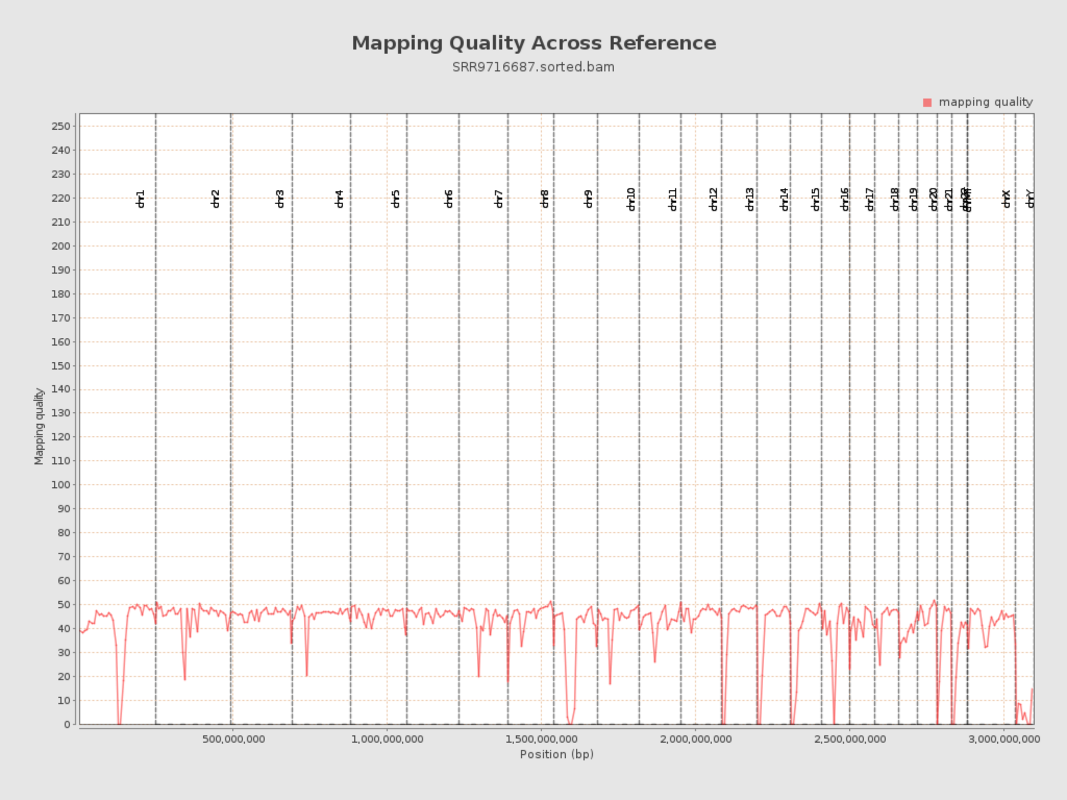
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram