Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:06:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716686.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_SRR9716686 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716686.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:06:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716686.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,056,926
Mapped reads	927,463 / 87.75%
Unmapped reads	129,463 / 12.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,607 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,634 / 1.67%
Duplication rate	1.32%
Clipped reads	929,112 / 87.91%

2.2. ACGT Content

Number/percentage of A's	12,926,248 / 24.5%
Number/percentage of C's	10,208,949 / 19.35%
Number/percentage of T's	16,683,325 / 31.62%
Number/percentage of G's	12,935,836 / 24.52%
Number/percentage of N's	396 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.017

Standard Deviation	0.1673

2.4. Mapping Quality

Mean Mapping Quality	42.28

2.5. Mismatches and indels

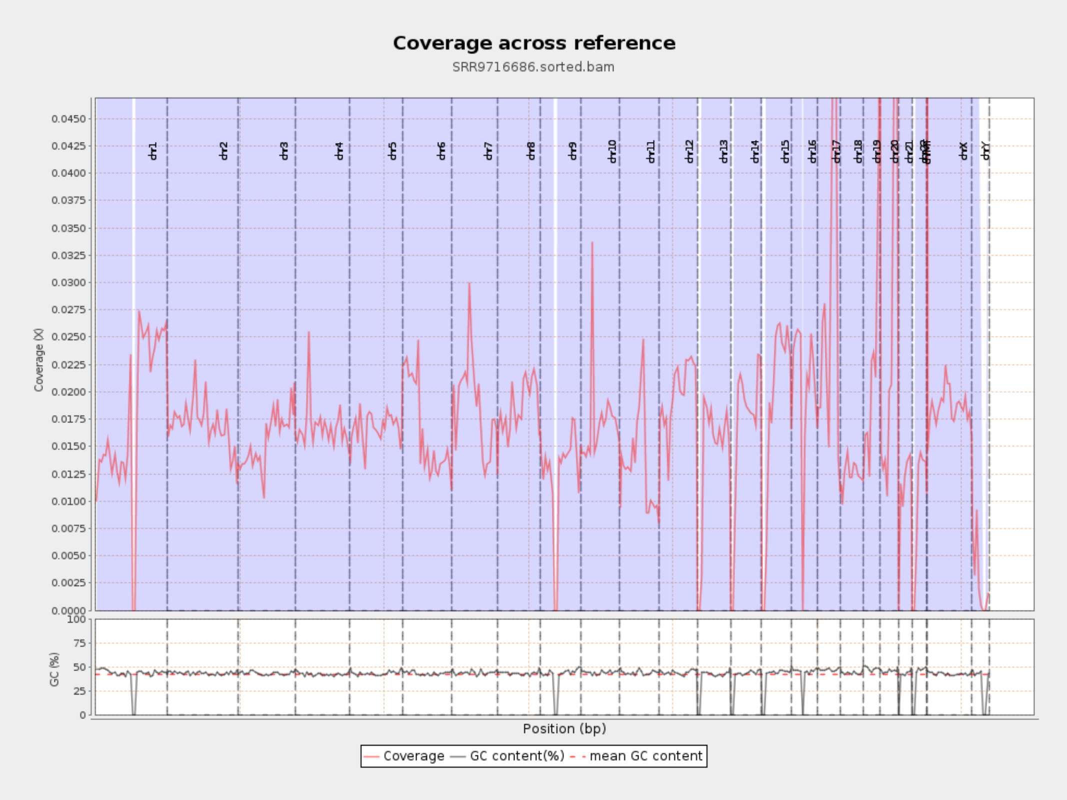
General error rate	0.53%
Mismatches	271,680
Insertions	3,753
Mapped reads with at least one insertion	0.4%
Deletions	10,060
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.92%

2.6. Chromosome stats

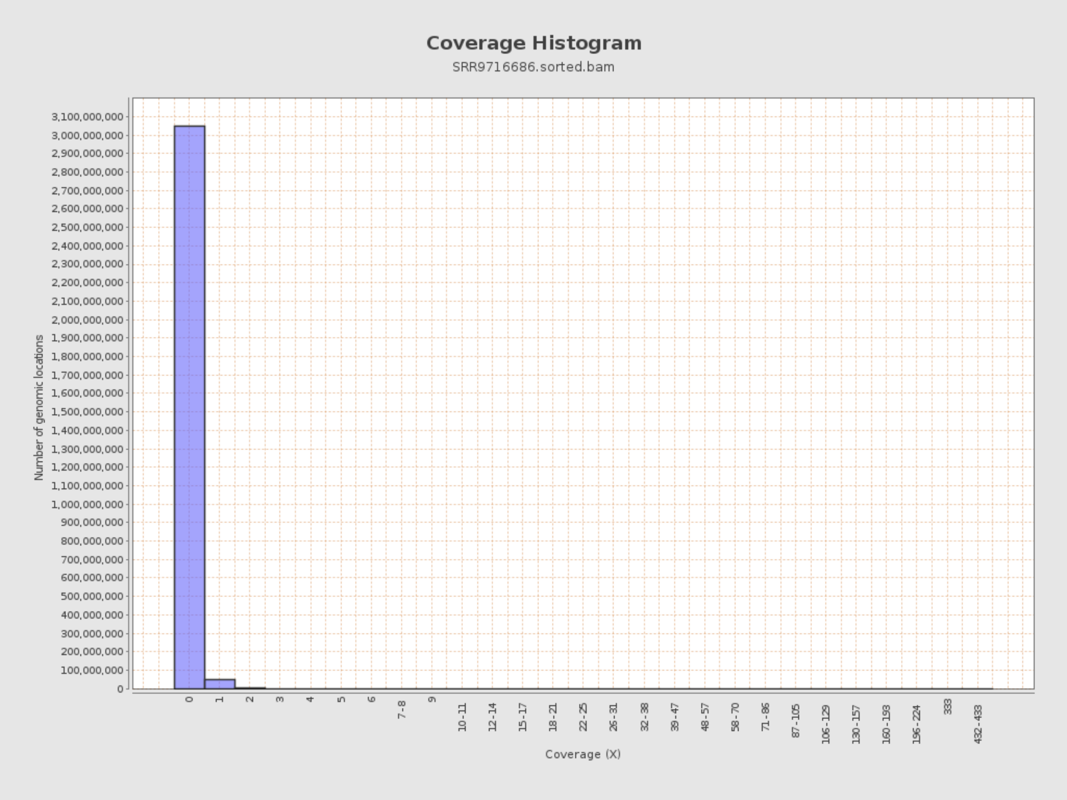
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4432028	0.0178	0.2069
chr2	243199373	4150279	0.0171	0.2258
chr3	198022430	3080304	0.0156	0.1329
chr4	191154276	3218820	0.0168	0.1441
chr5	180915260	3044978	0.0168	0.1358
chr6	171115067	2841729	0.0166	0.1519
chr7	159138663	3004603	0.0189	0.2238

chr8	146364022	2741269	0.0187	0.1697
chr9	141213431	1753484	0.0124	0.1301
chr10	135534747	2346091	0.0173	0.2003
chr11	135006516	1851279	0.0137	0.1404
chr12	133851895	2649225	0.0198	0.1482
chr13	115169878	1621236	0.0141	0.1246
chr14	107349540	1785959	0.0166	0.1393
chr15	102531392	1908882	0.0186	0.1453
chr16	90354753	1825106	0.0202	0.1553
chr17	81195210	2358147	0.029	0.1859
chr18	78077248	971786	0.0124	0.1826
chr19	59128983	1393126	0.0236	0.2025
chr20	63025520	1700358	0.027	0.1782
chr21	48129895	534500	0.0111	0.118
chr22	51304566	492290	0.0096	0.1028
chrMT	16571	3203	0.1933	0.4584
chrX	155270560	2897015	0.0187	0.1496
chrY	59373566	165140	0.0028	0.0853

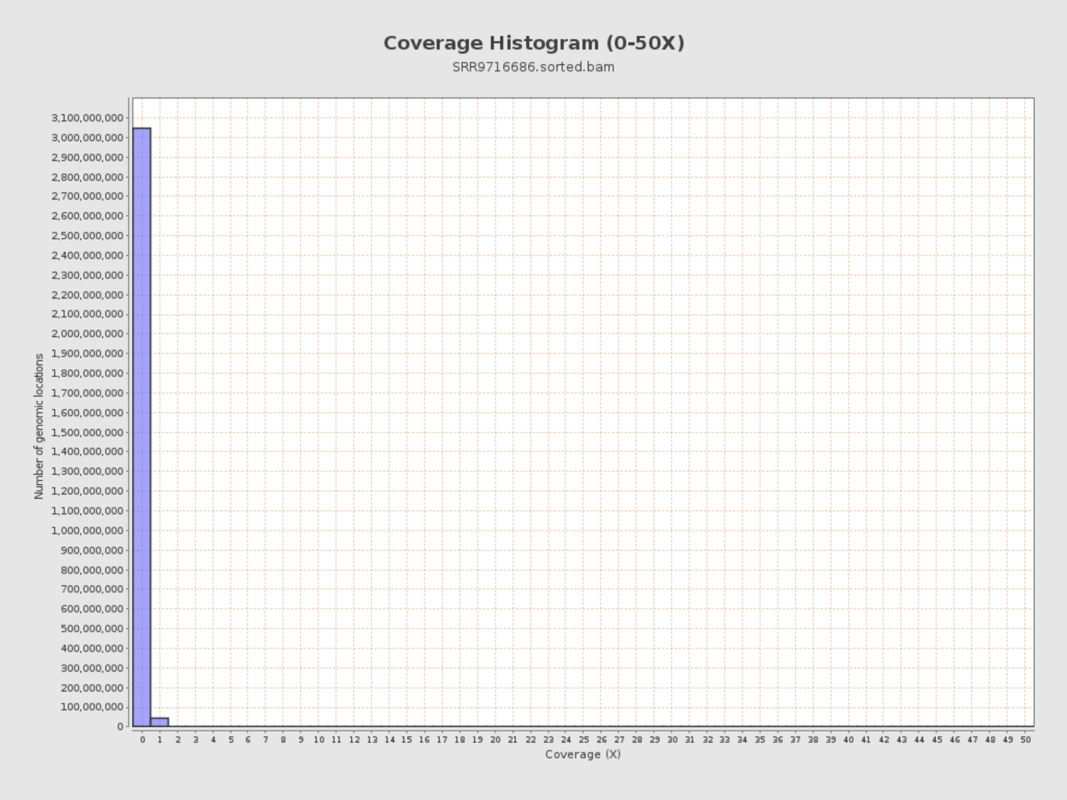
3. Results : Coverage across reference



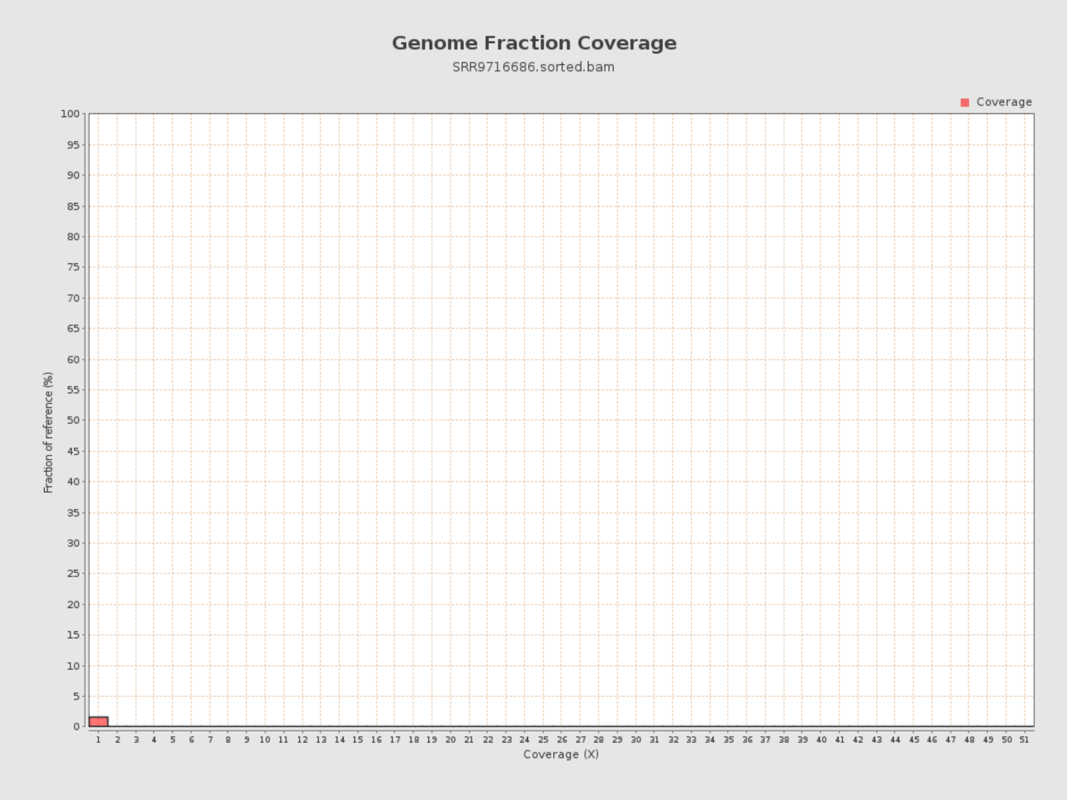
4. Results : Coverage Histogram



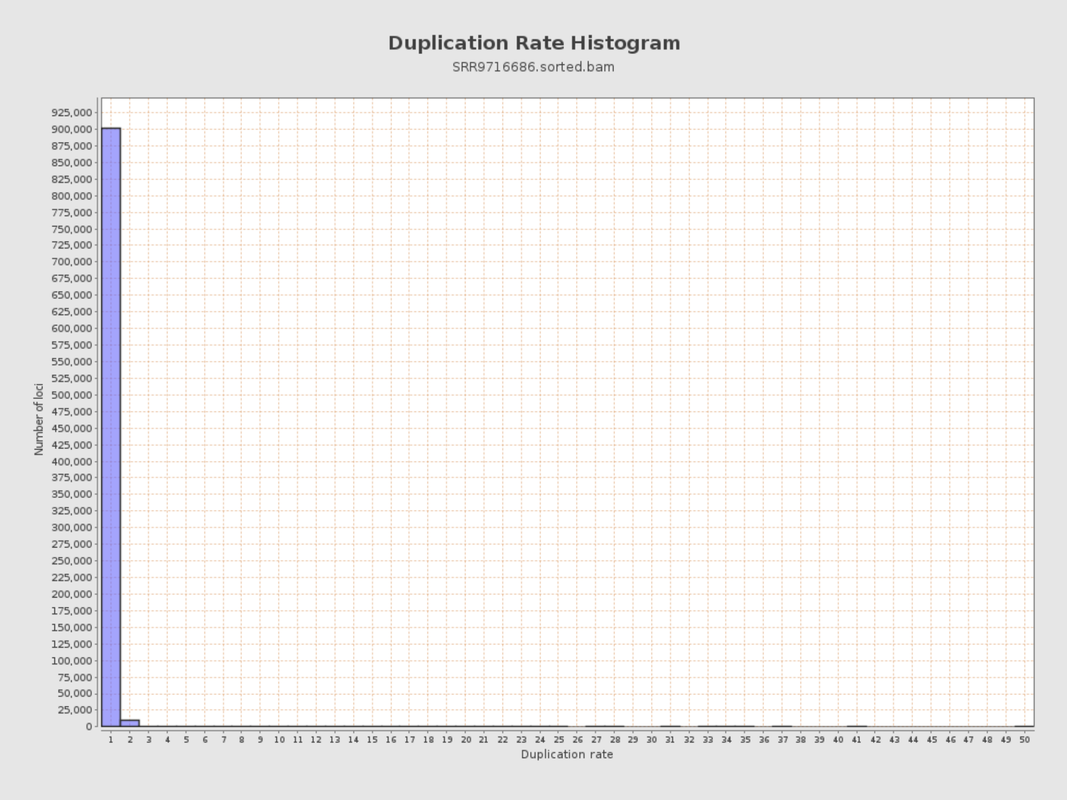
5. Results : Coverage Histogram (0-50X)



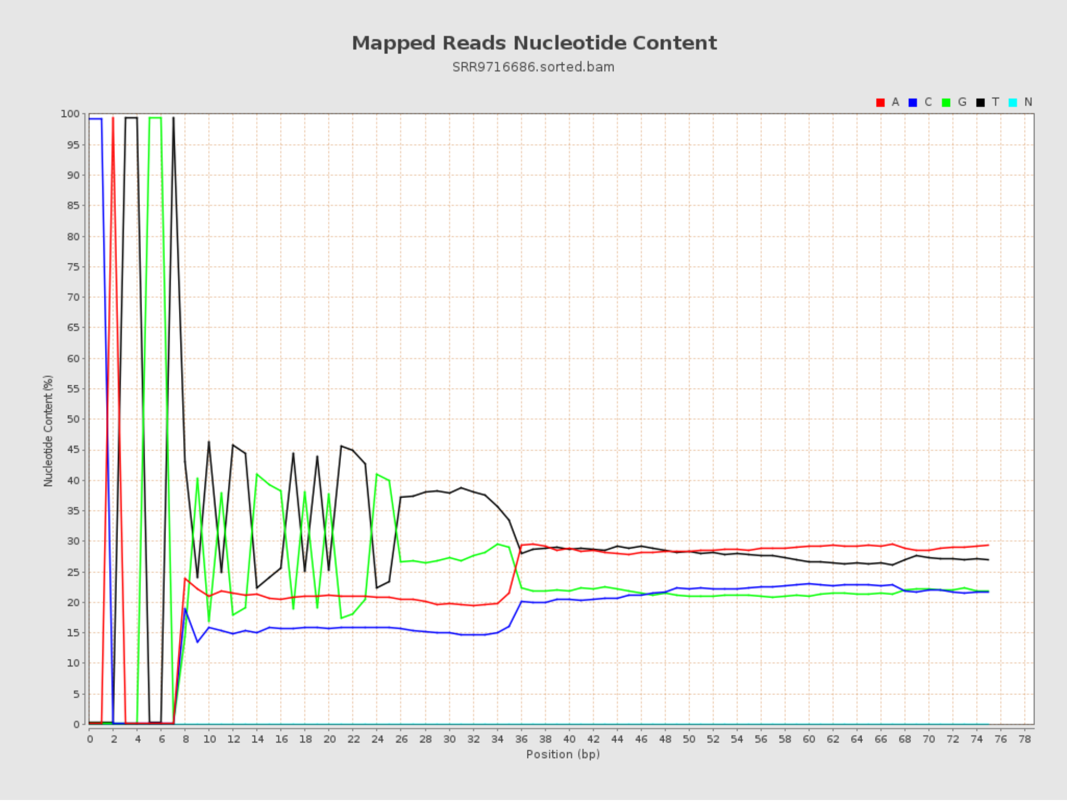
6. Results : Genome Fraction Coverage



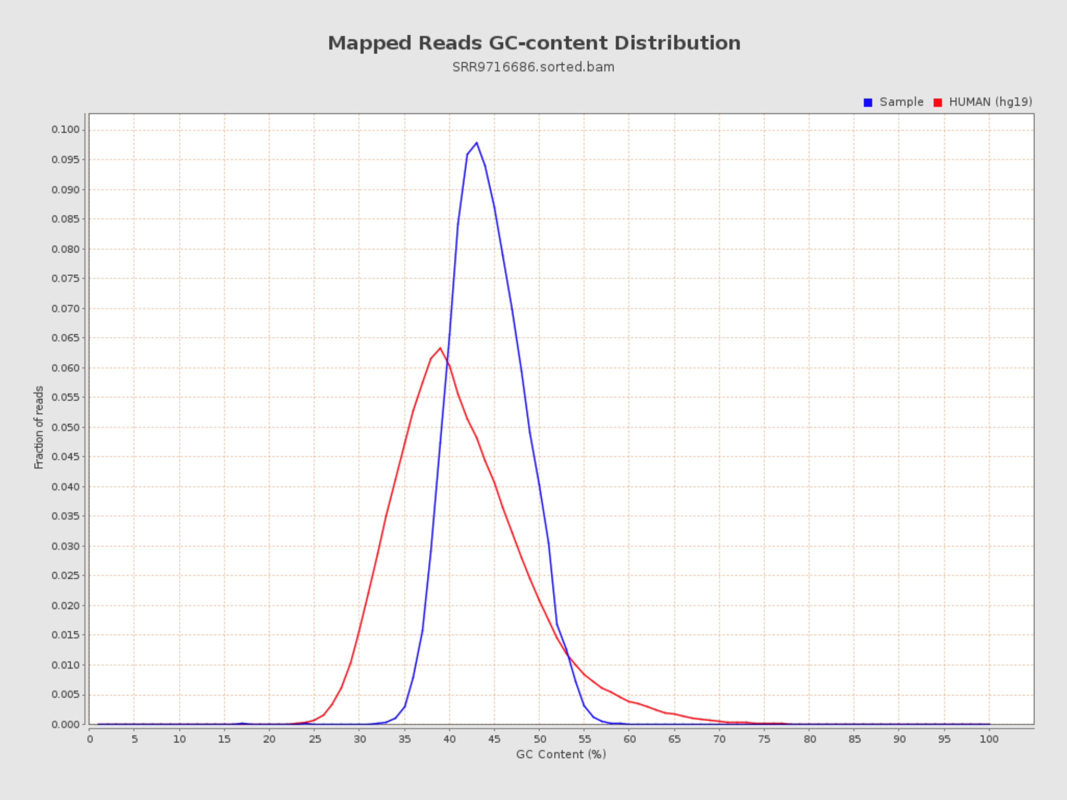
7. Results : Duplication Rate Histogram



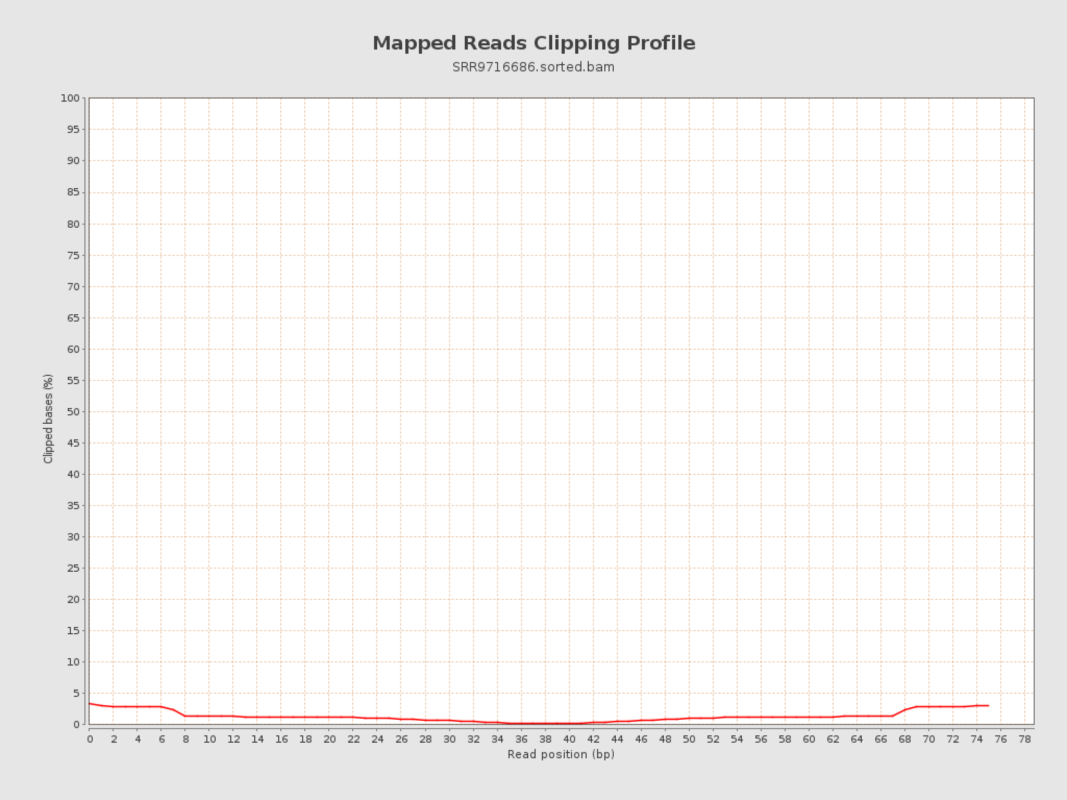
8. Results : Mapped Reads Nucleotide Content



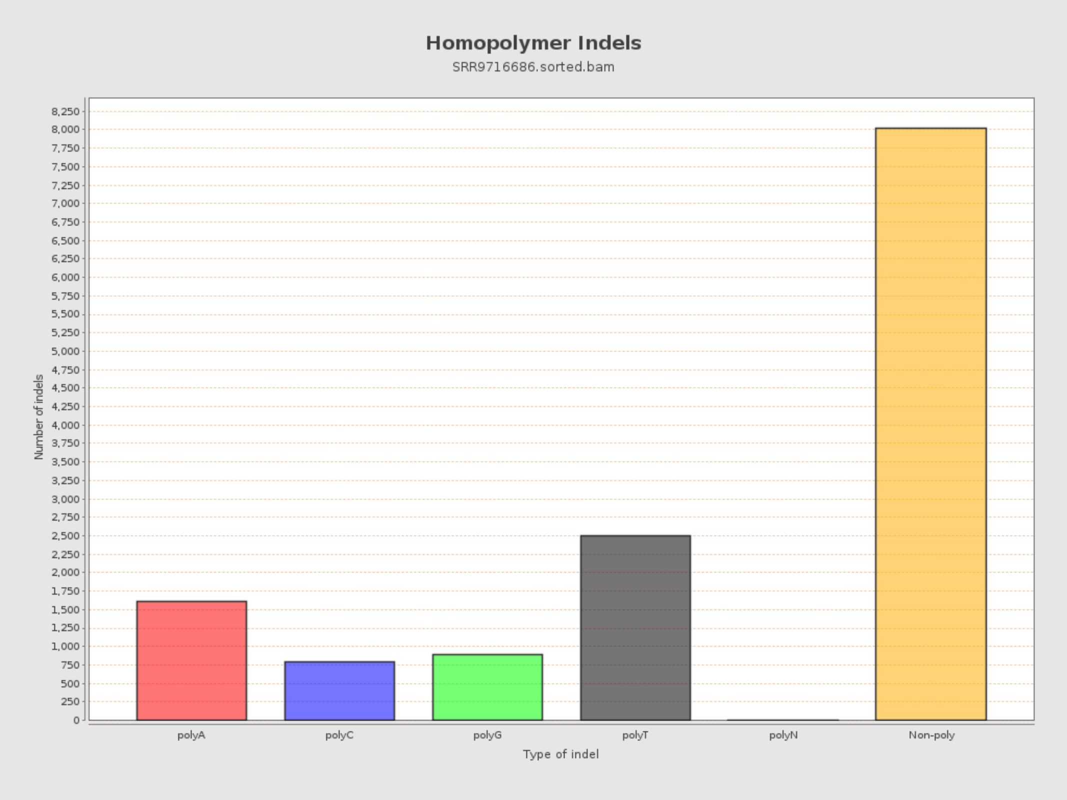
9. Results : Mapped Reads GC-content Distribution



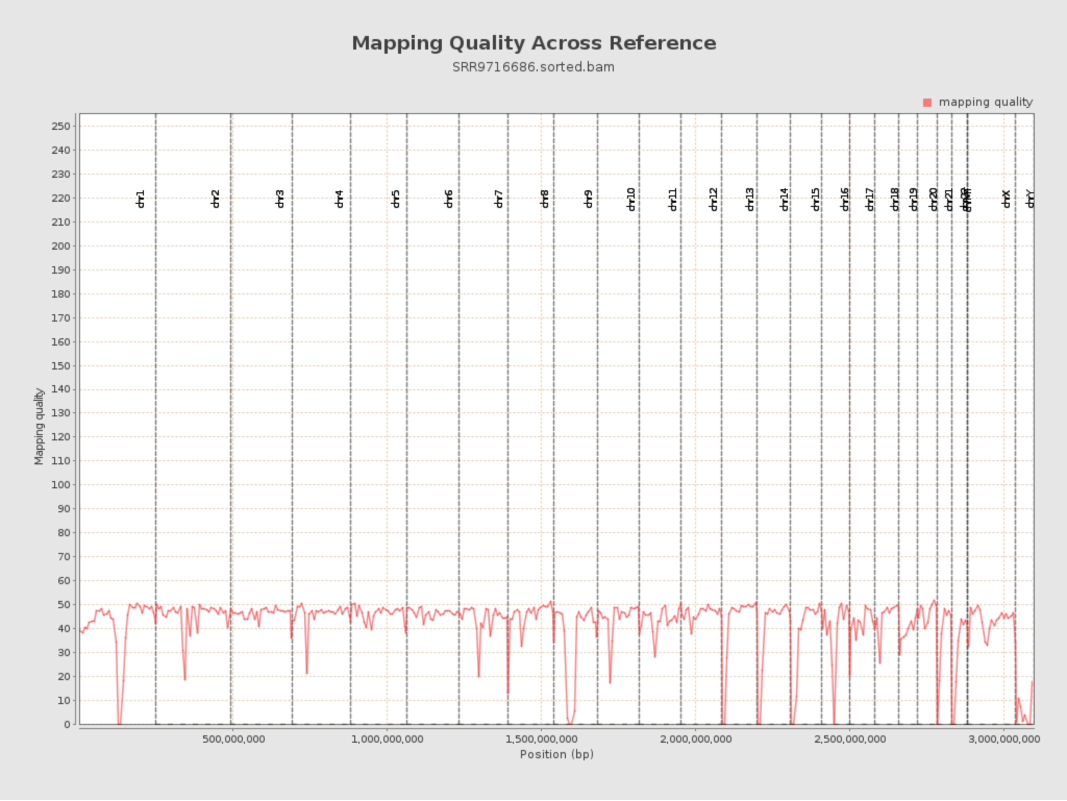
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram