Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:59:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716804.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_SRR9716804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:59:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	486,532
Mapped reads	372,459 / 76.55%
Unmapped reads	114,073 / 23.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,595 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	6,150 / 1.26%
Duplication rate	1.29%
Clipped reads	373,114 / 76.69%

2.2. ACGT Content

Number/percentage of A's	5,466,863 / 25.49%
Number/percentage of C's	4,097,948 / 19.11%
Number/percentage of T's	6,816,598 / 31.78%
Number/percentage of G's	5,067,682 / 23.63%
Number/percentage of N's	307 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0069

Standard Deviation	0.0972

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

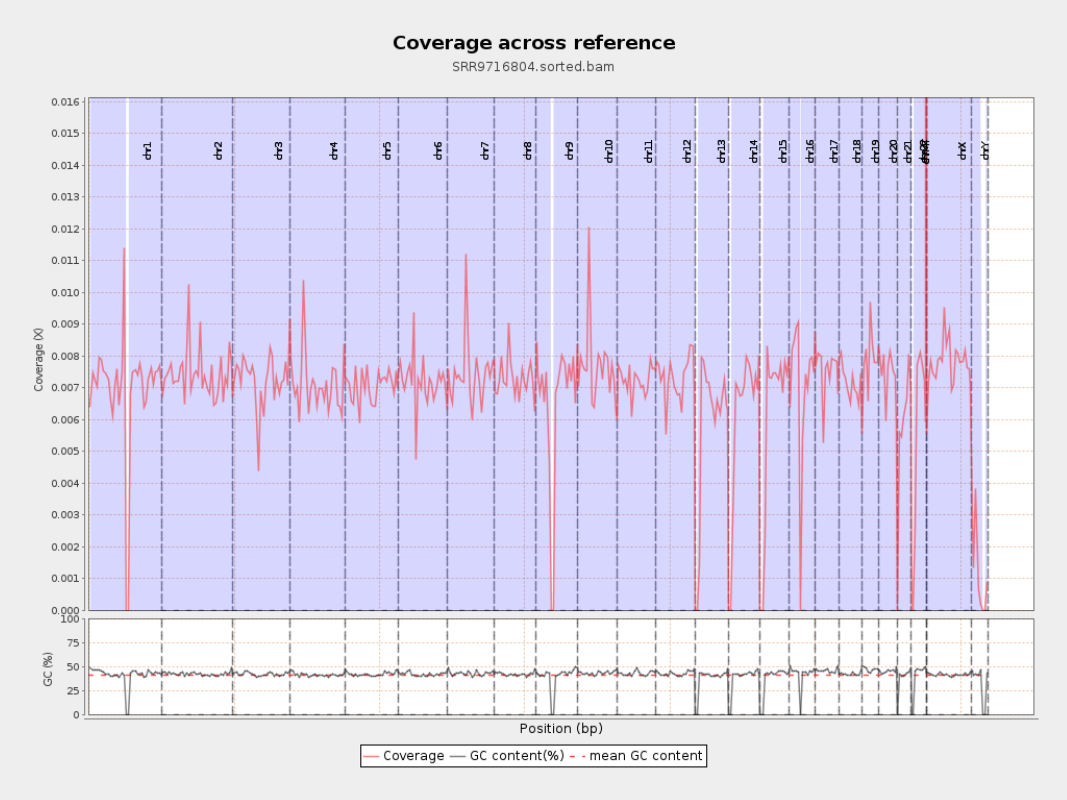
General error rate	0.52%
Mismatches	107,676
Insertions	1,575
Mapped reads with at least one insertion	0.42%
Deletions	3,909
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.72%

2.6. Chromosome stats

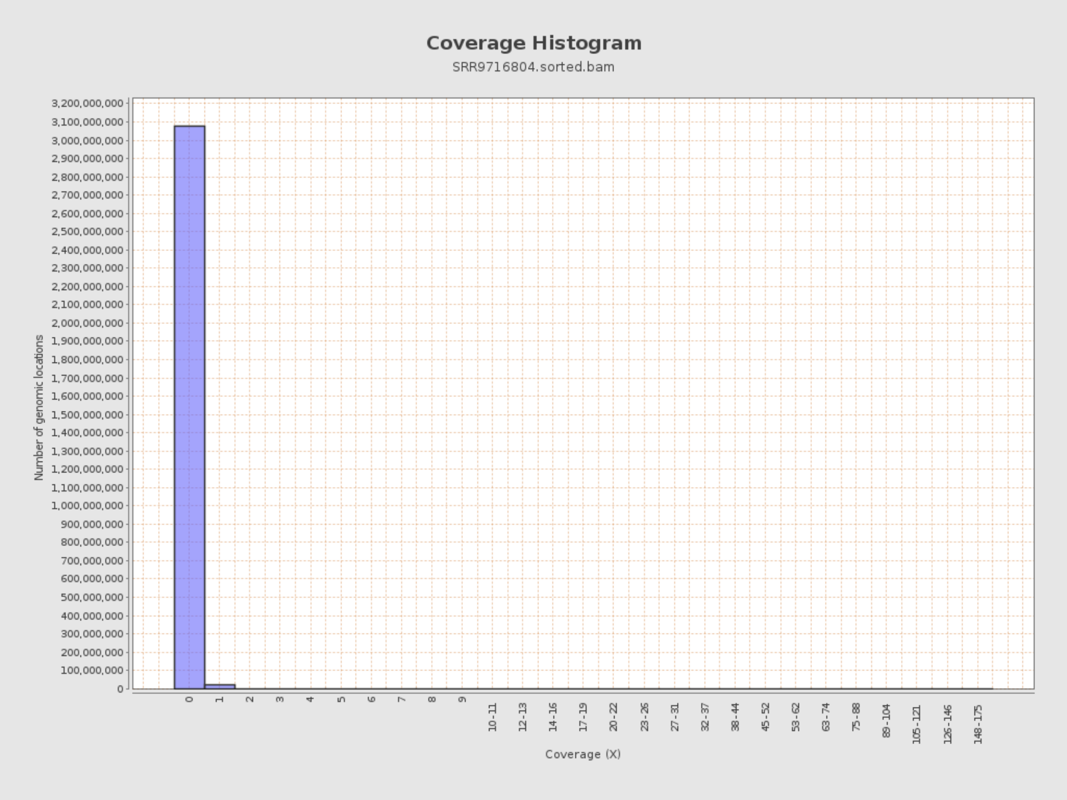
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1722722	0.0069	0.1388
chr2	243199373	1807452	0.0074	0.1153
chr3	198022430	1428264	0.0072	0.0874
chr4	191154276	1352262	0.0071	0.0883
chr5	180915260	1274339	0.007	0.0863
chr6	171115067	1232693	0.0072	0.0917
chr7	159138663	1183660	0.0074	0.1088

chr8	146364022	1066249	0.0073	0.0938
chr9	141213431	899305	0.0064	0.0883
chr10	135534747	1039335	0.0077	0.0976
chr11	135006516	975873	0.0072	0.0926
chr12	133851895	980653	0.0073	0.0883
chr13	115169878	660911	0.0057	0.0781
chr14	107349540	639345	0.006	0.0804
chr15	102531392	621248	0.0061	0.0808
chr16	90354753	636532	0.007	0.0877
chr17	81195210	609157	0.0075	0.09
chr18	78077248	560582	0.0072	0.1079
chr19	59128983	468476	0.0079	0.1146
chr20	63025520	467116	0.0074	0.0887
chr21	48129895	280601	0.0058	0.0797
chr22	51304566	269807	0.0053	0.0748
chrMT	16571	3018	0.1821	0.4518
chrX	155270560	1207647	0.0078	0.0931
chrY	59373566	68275	0.0011	0.0437

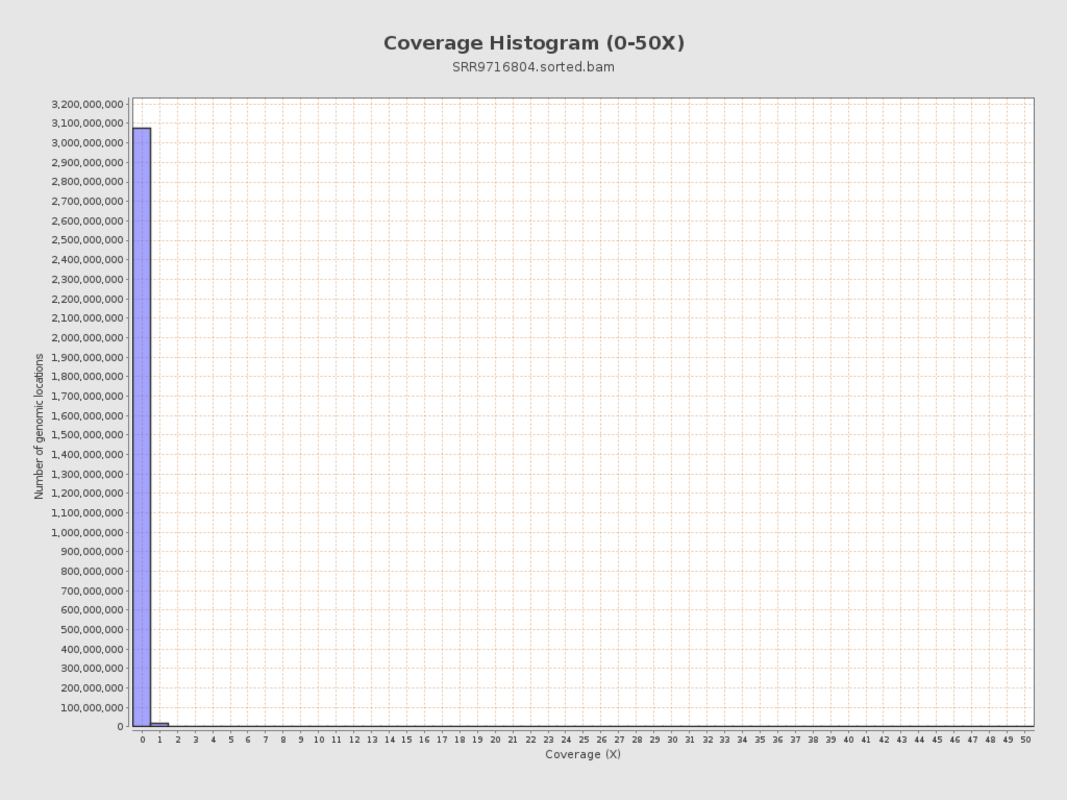
3. Results : Coverage across reference



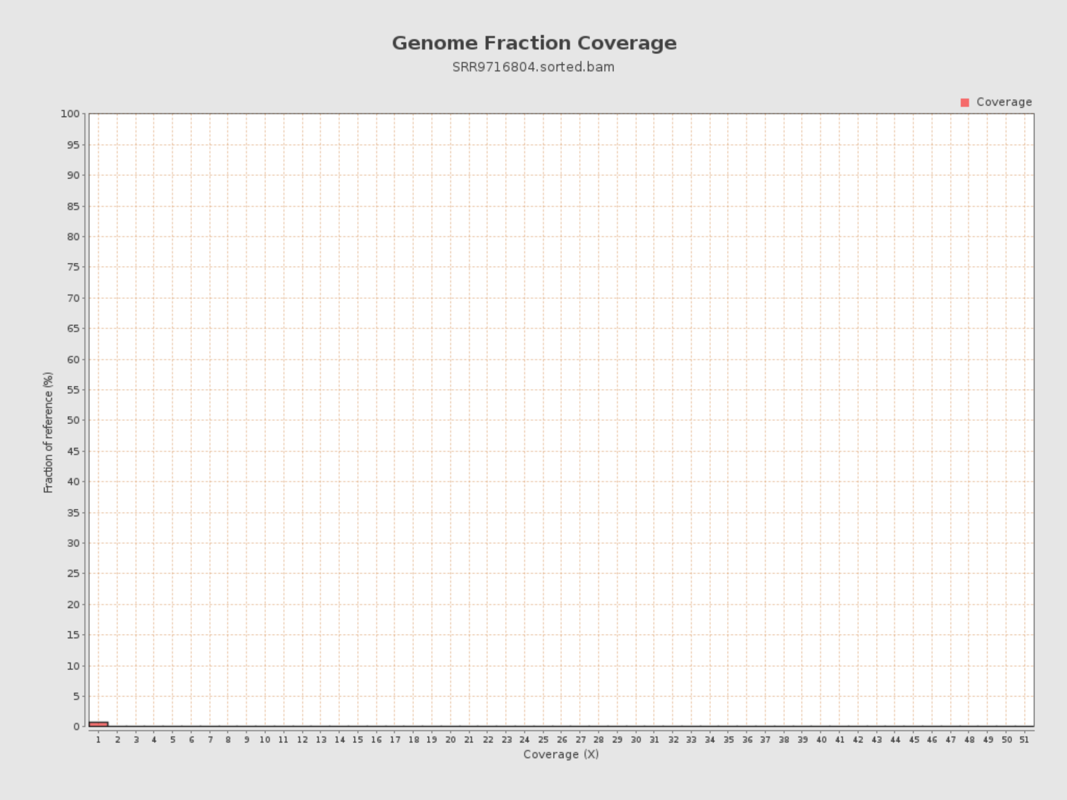
4. Results : Coverage Histogram



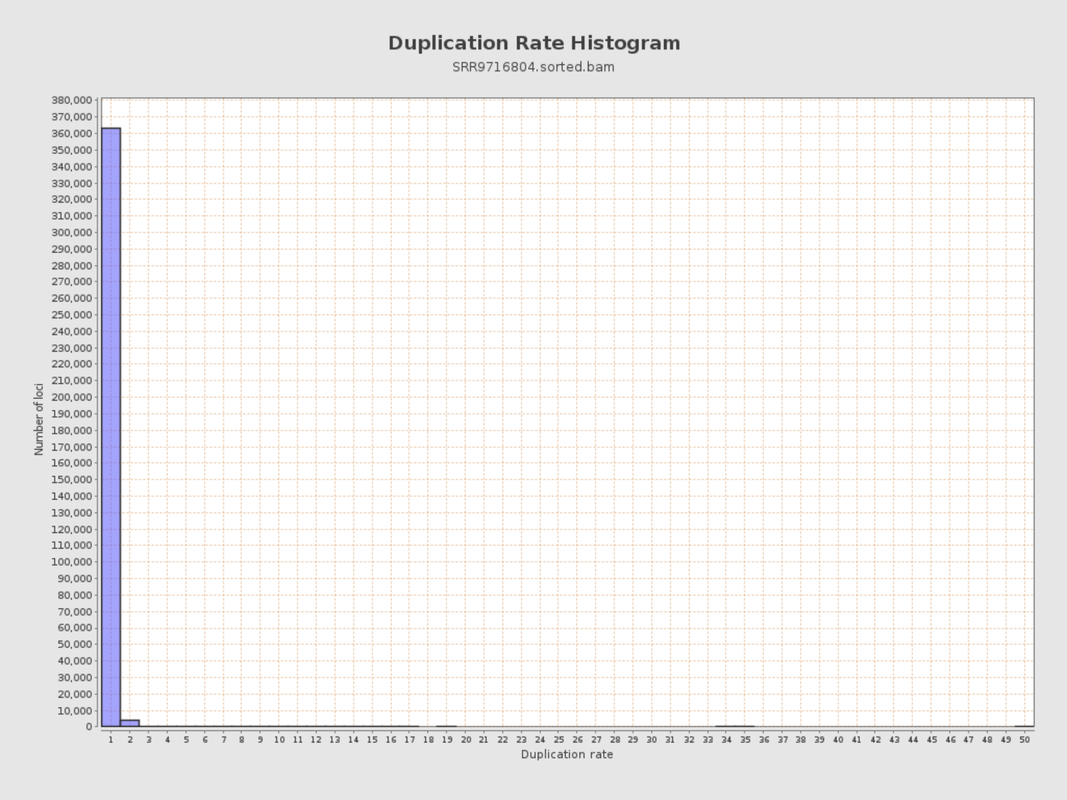
5. Results : Coverage Histogram (0-50X)



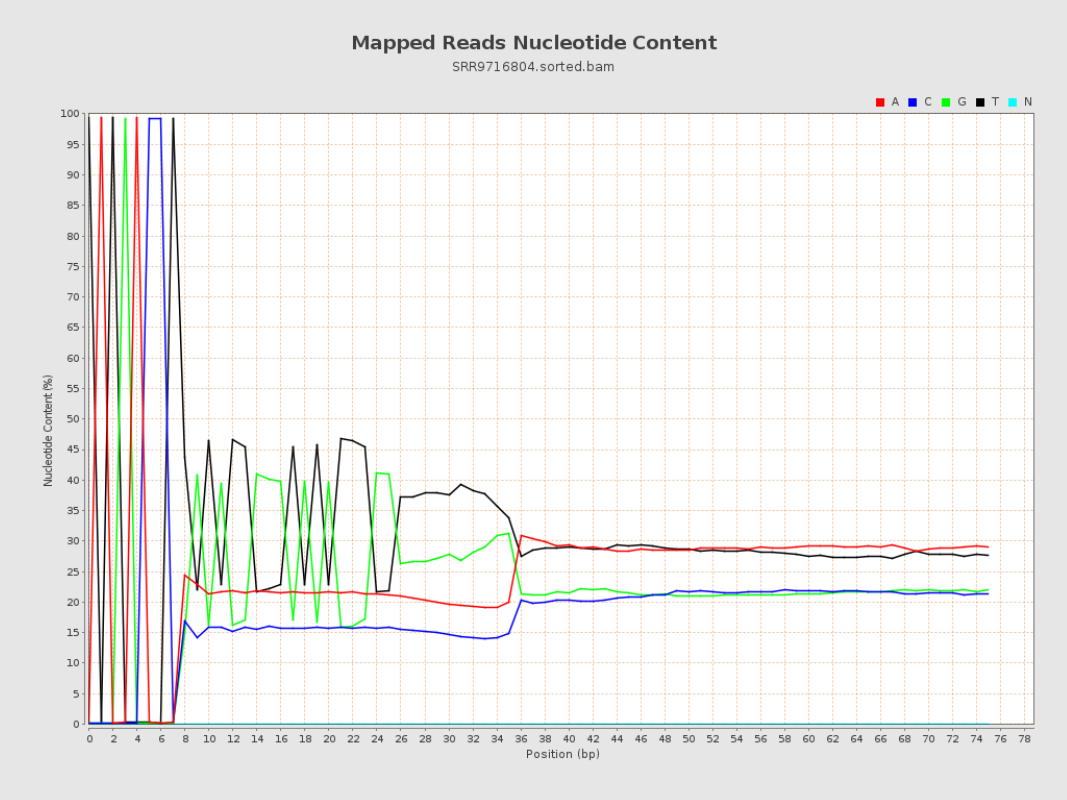
6. Results : Genome Fraction Coverage



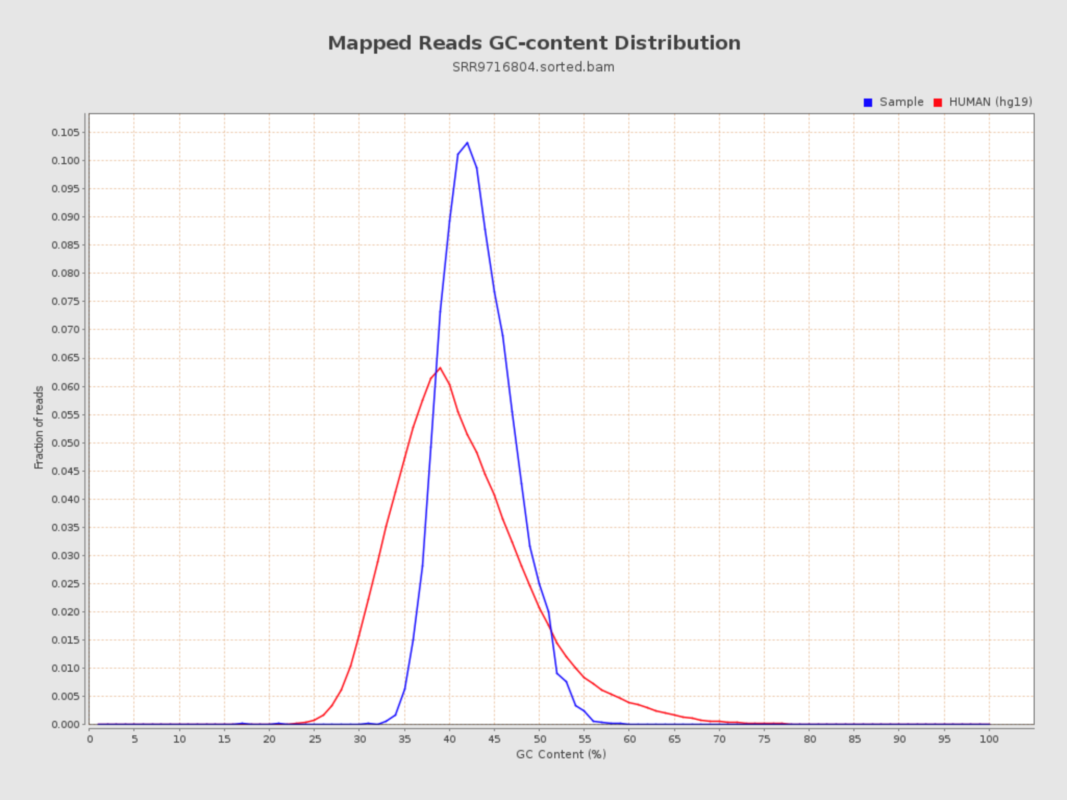
7. Results : Duplication Rate Histogram



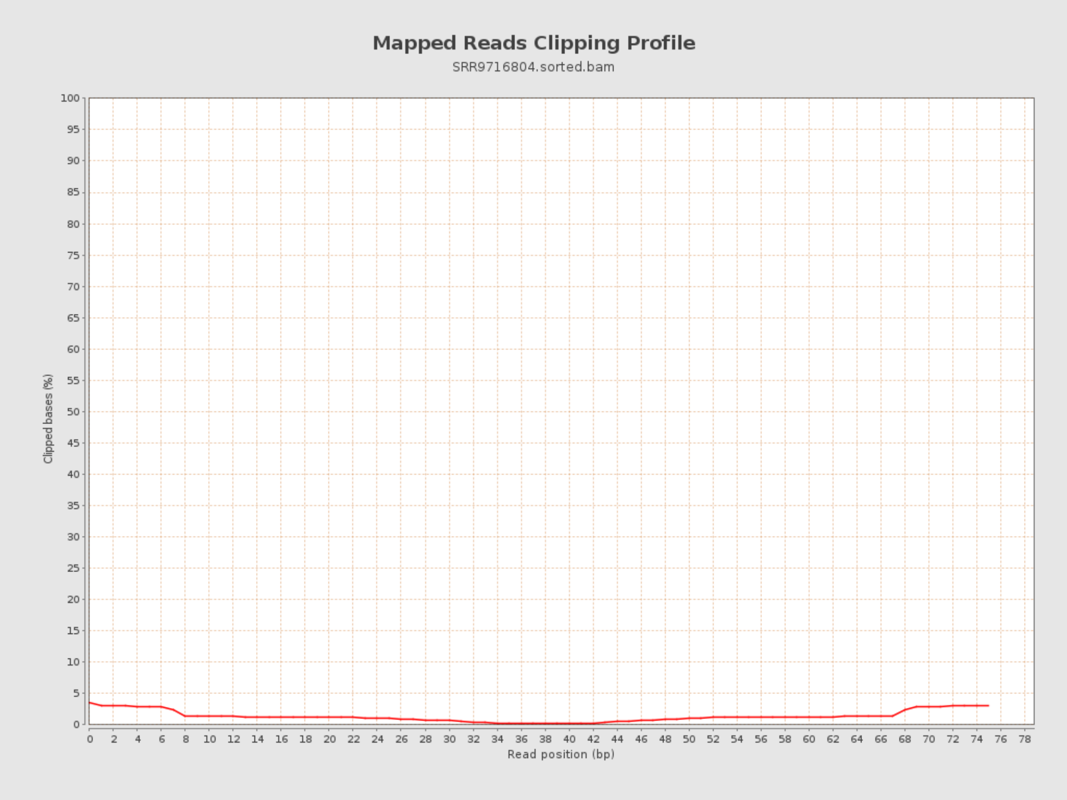
8. Results : Mapped Reads Nucleotide Content



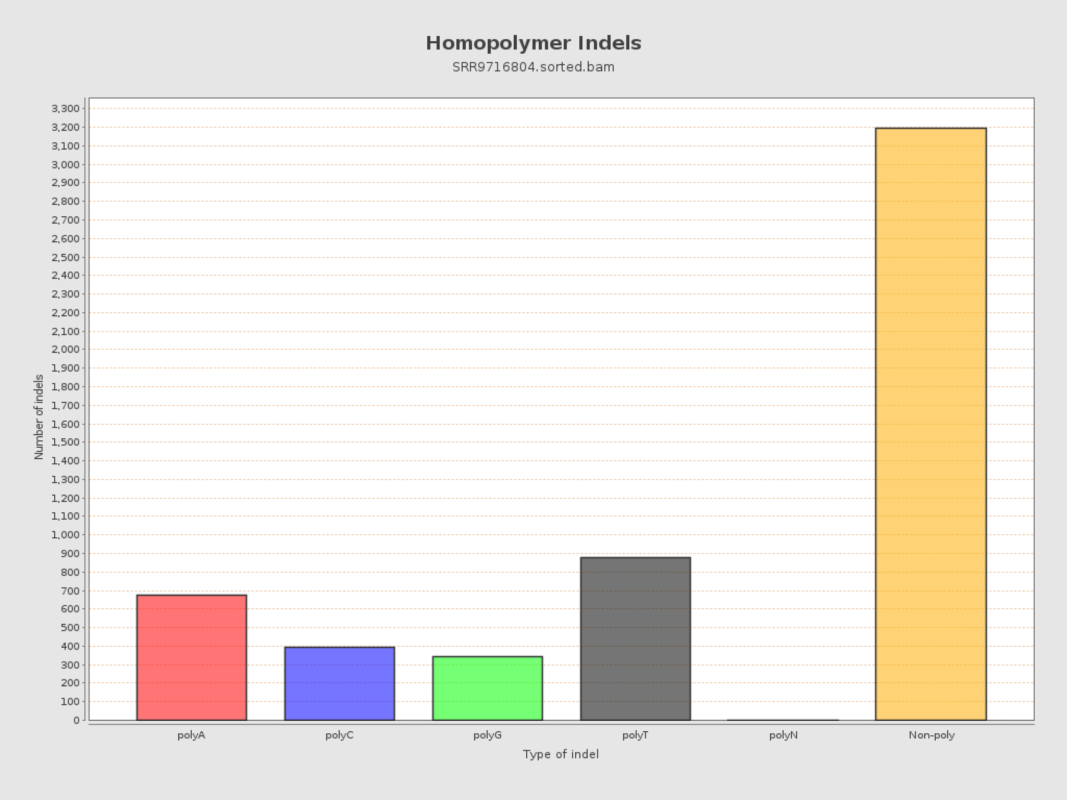
9. Results : Mapped Reads GC-content Distribution



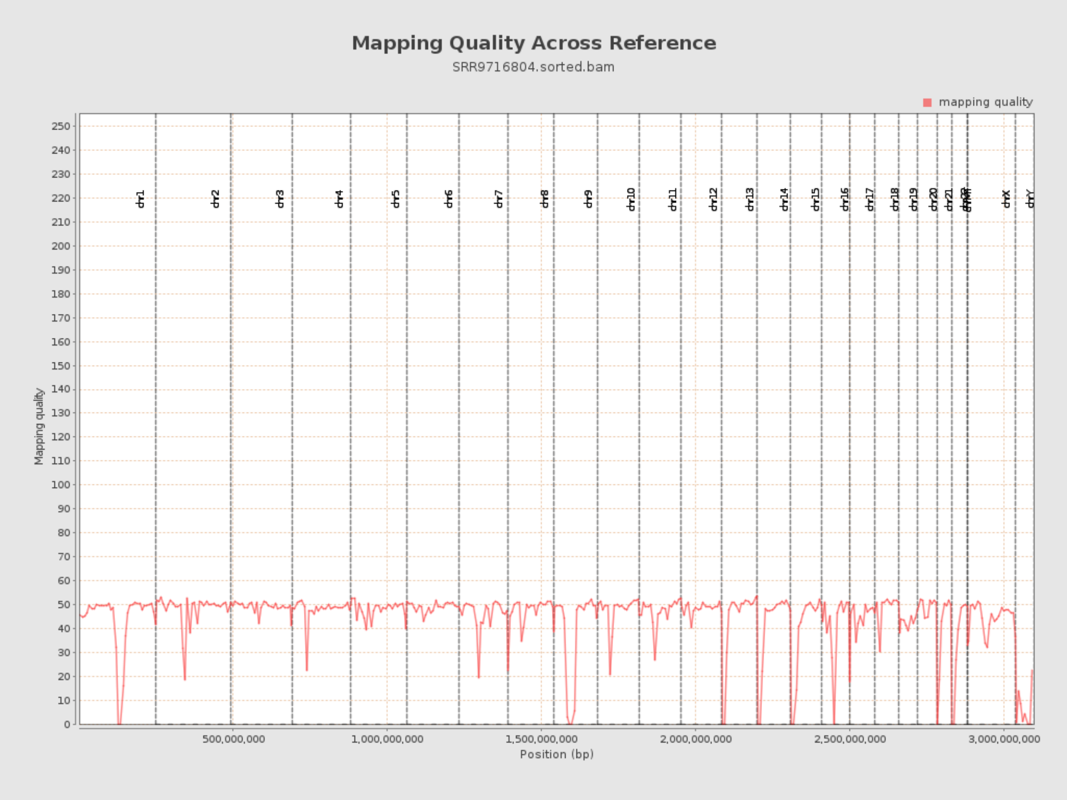
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram