Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:16:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716195.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_SRR9716195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:16:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,535,394
Mapped reads	3,264,747 / 71.98%
Unmapped reads	1,270,647 / 28.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	87,943 / 1.94%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	150,278 / 3.31%
Duplication rate	3.25%
Clipped reads	3,348,232 / 73.82%

2.2. ACGT Content

Number/percentage of A's	62,839,198 / 25.77%
Number/percentage of C's	48,694,843 / 19.97%
Number/percentage of T's	74,283,352 / 30.46%
Number/percentage of G's	57,997,855 / 23.78%
Number/percentage of N's	29,933 / 0.01%
GC Percentage	43.75%

2.3. Coverage

Mean	0.0788

Standard Deviation	0.5645

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

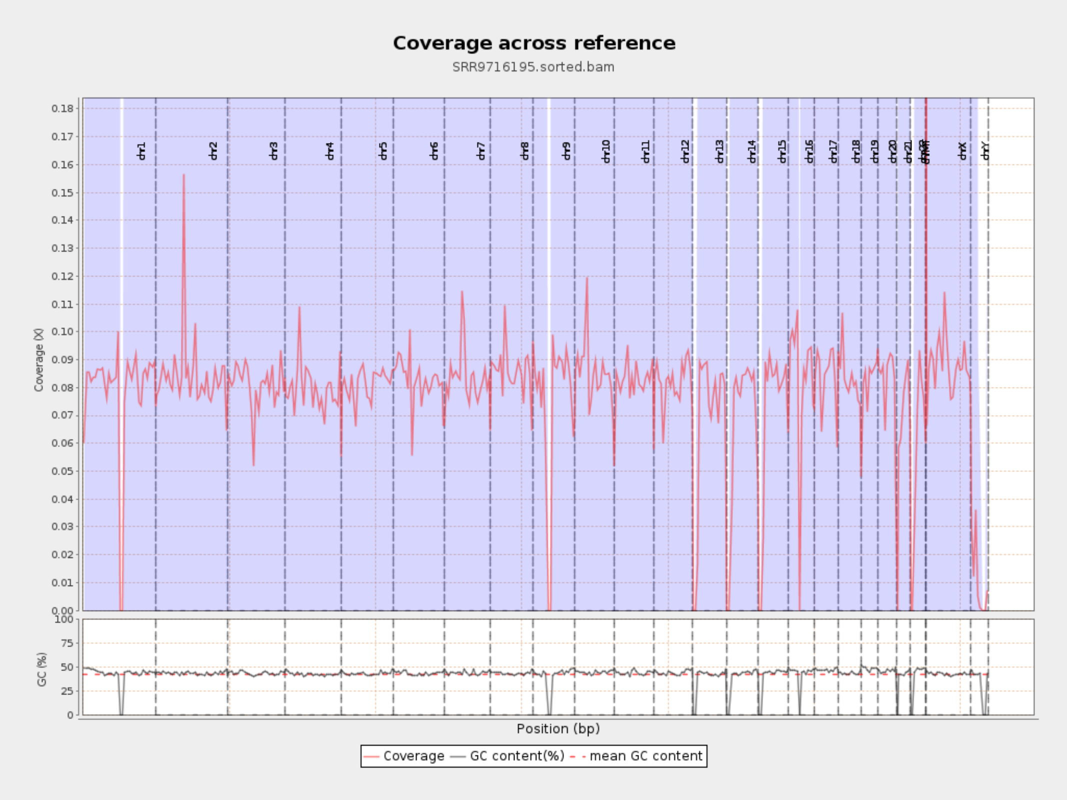
General error rate	0.75%
Mismatches	1,785,681
Insertions	20,236
Mapped reads with at least one insertion	0.61%
Deletions	47,819
Mapped reads with at least one deletion	1.45%
Homopolymer indels	40.7%

2.6. Chromosome stats

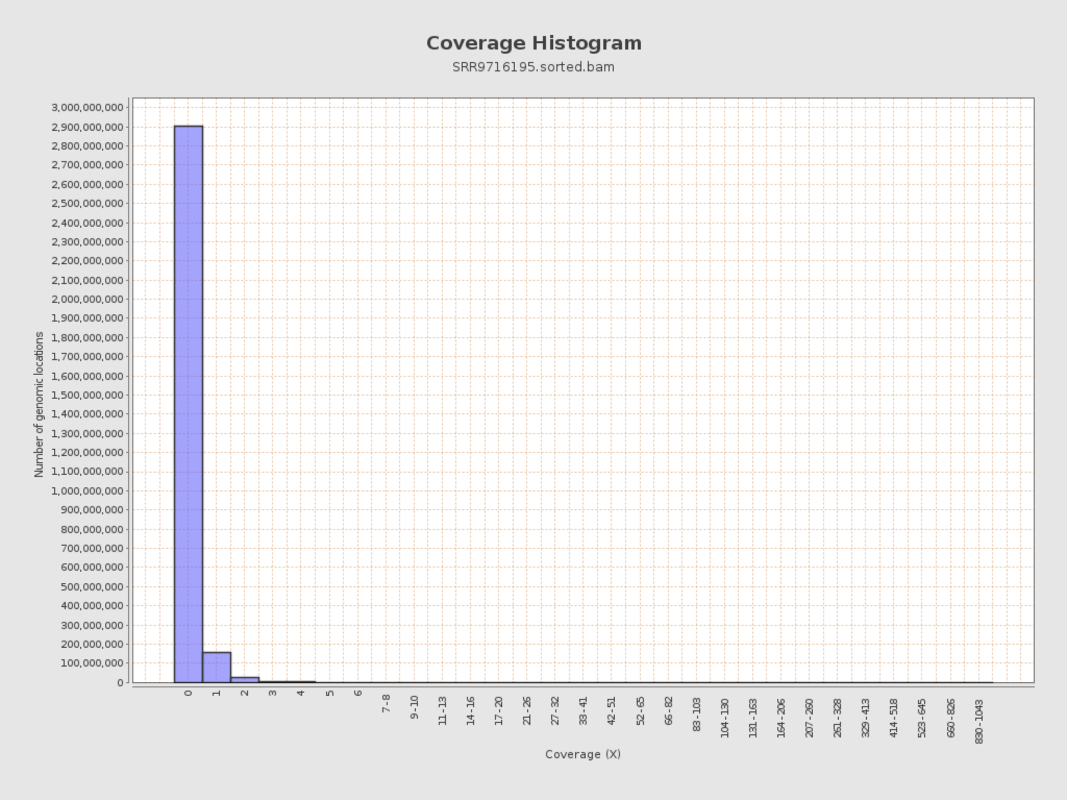
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19571644	0.0785	0.6218
chr2	243199373	20646184	0.0849	0.8844
chr3	198022430	16006833	0.0808	0.3453
chr4	191154276	15322784	0.0802	0.3954
chr5	180915260	14718428	0.0814	0.3525
chr6	171115067	14150753	0.0827	0.424
chr7	159138663	13346993	0.0839	0.7149

chr8	146364022	12524645	0.0856	0.7649
chr9	141213431	10487105	0.0743	0.622
chr10	135534747	11620500	0.0857	0.5558
chr11	135006516	11145069	0.0826	0.6316
chr12	133851895	11047302	0.0825	0.3623
chr13	115169878	7767624	0.0674	0.3162
chr14	107349540	7283257	0.0678	0.4117
chr15	102531392	7009513	0.0684	0.3205
chr16	90354753	7316836	0.081	0.4047
chr17	81195210	6874833	0.0847	0.4108
chr18	78077248	6563076	0.0841	1.1766
chr19	59128983	4876245	0.0825	0.5932
chr20	63025520	5226509	0.0829	0.3805
chr21	48129895	3221847	0.0669	0.3597
chr22	51304566	2847233	0.0555	0.2906
chrMT	16571	10642	0.6422	1.0875
chrX	155270560	13713915	0.0883	0.4774
chrY	59373566	628673	0.0106	0.2973

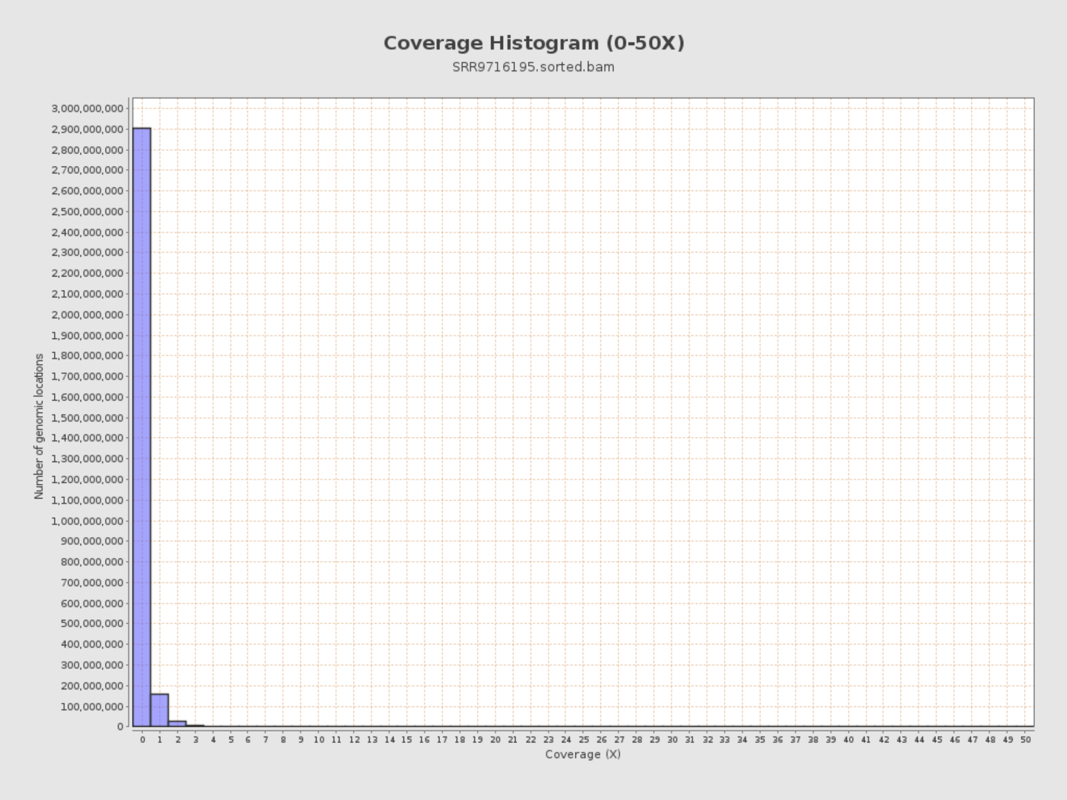
3. Results : Coverage across reference



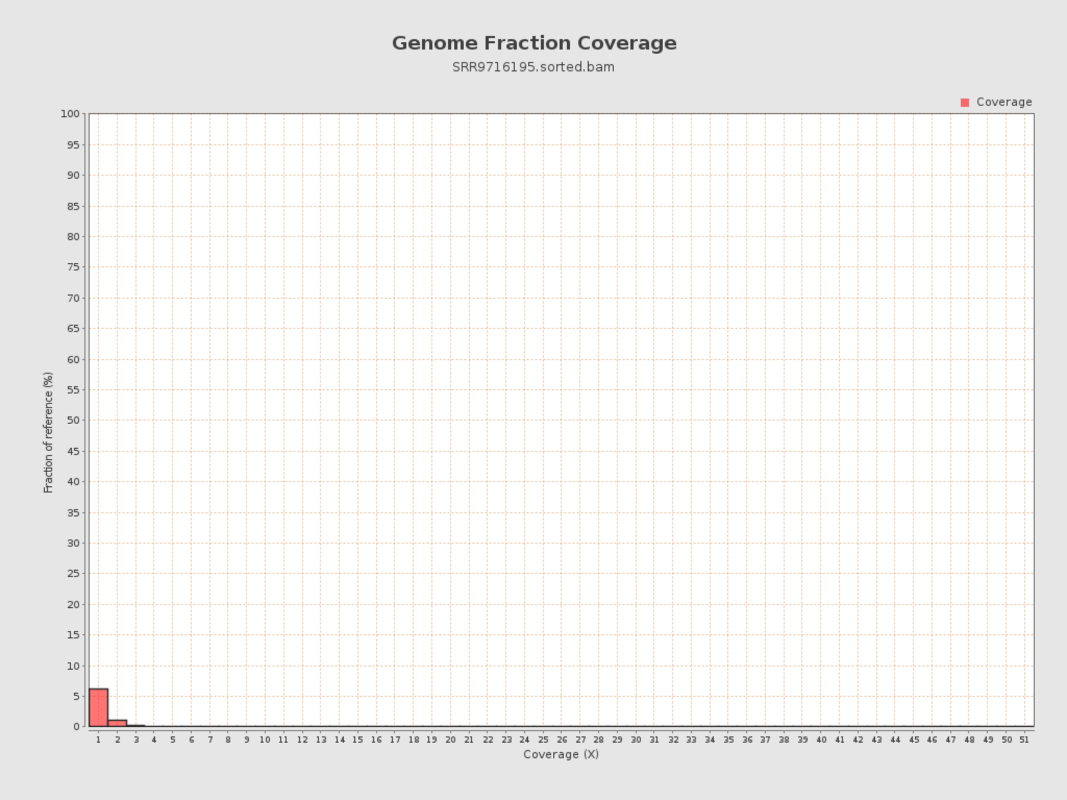
4. Results : Coverage Histogram



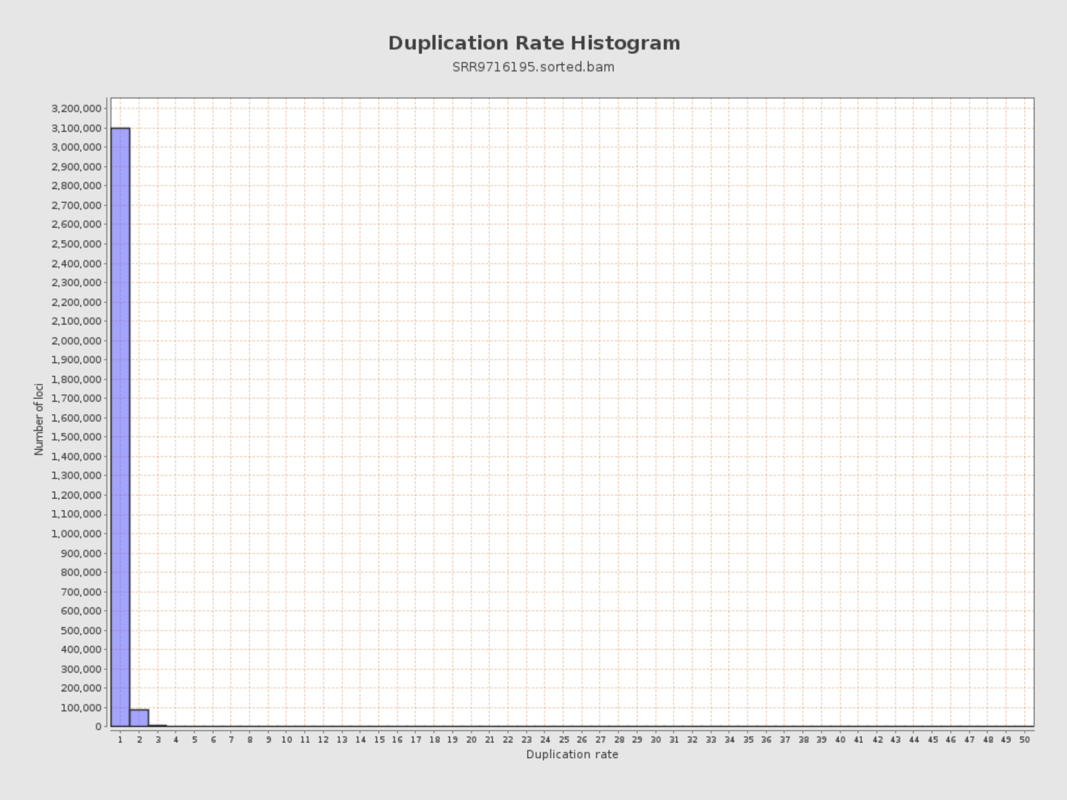
5. Results : Coverage Histogram (0-50X)



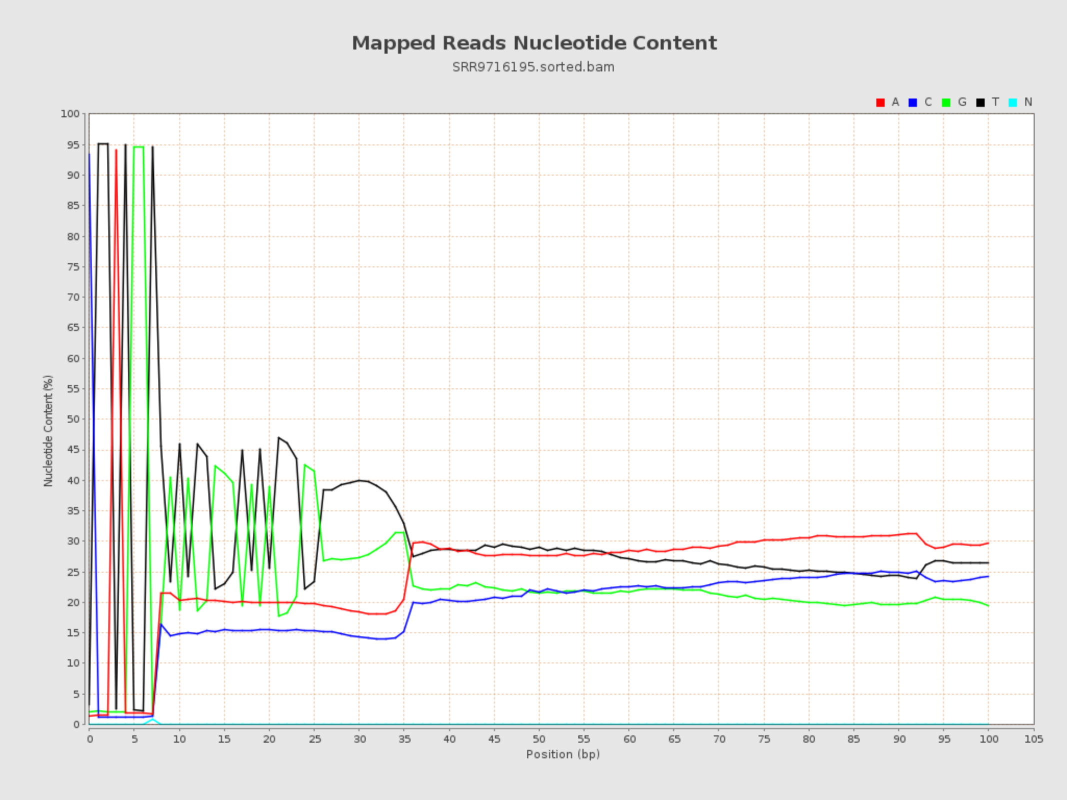
6. Results : Genome Fraction Coverage



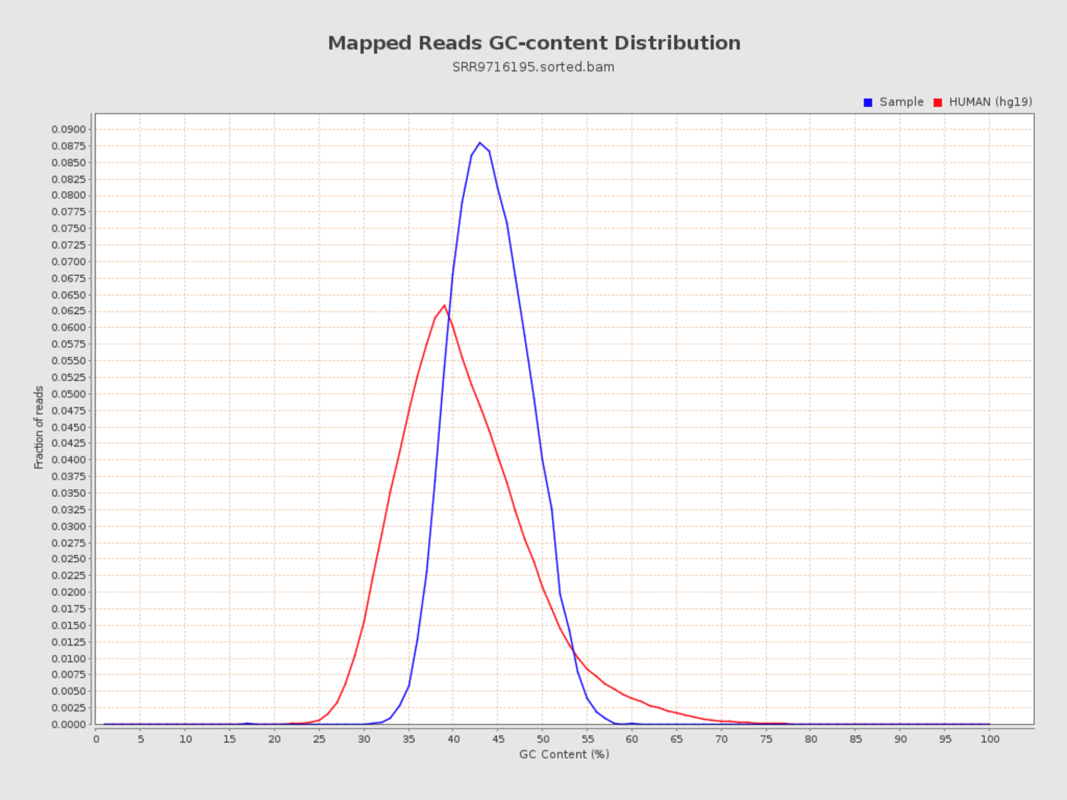
7. Results : Duplication Rate Histogram



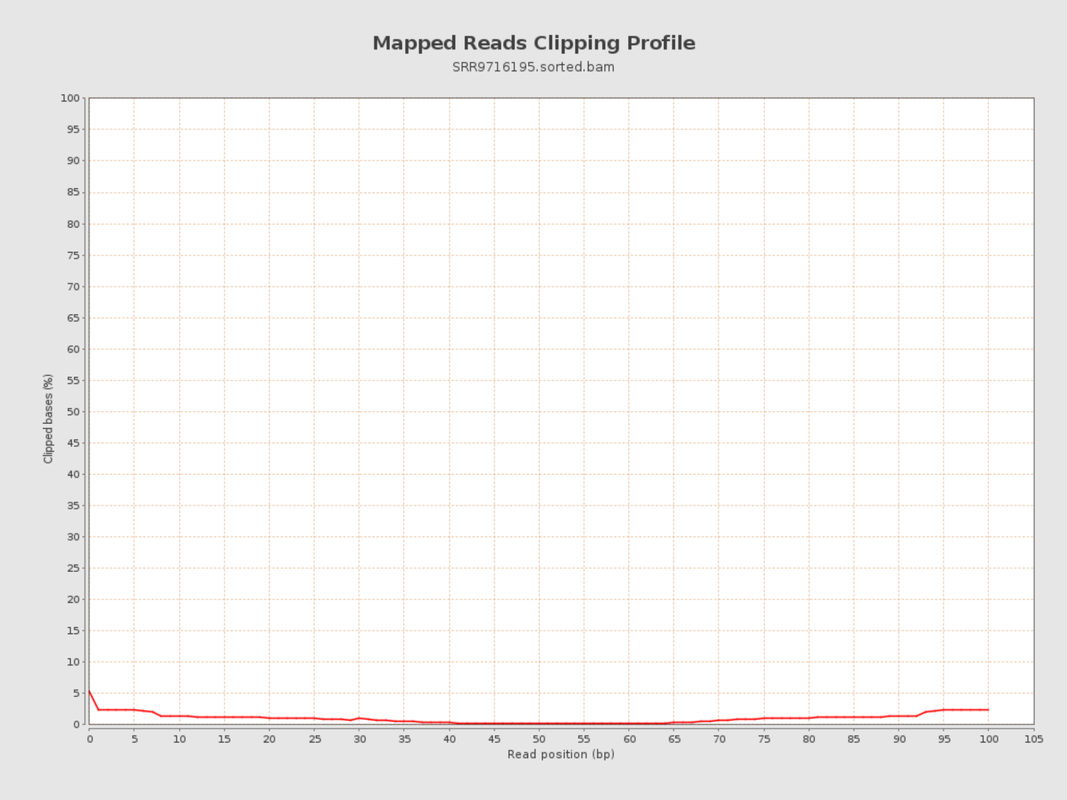
8. Results : Mapped Reads Nucleotide Content



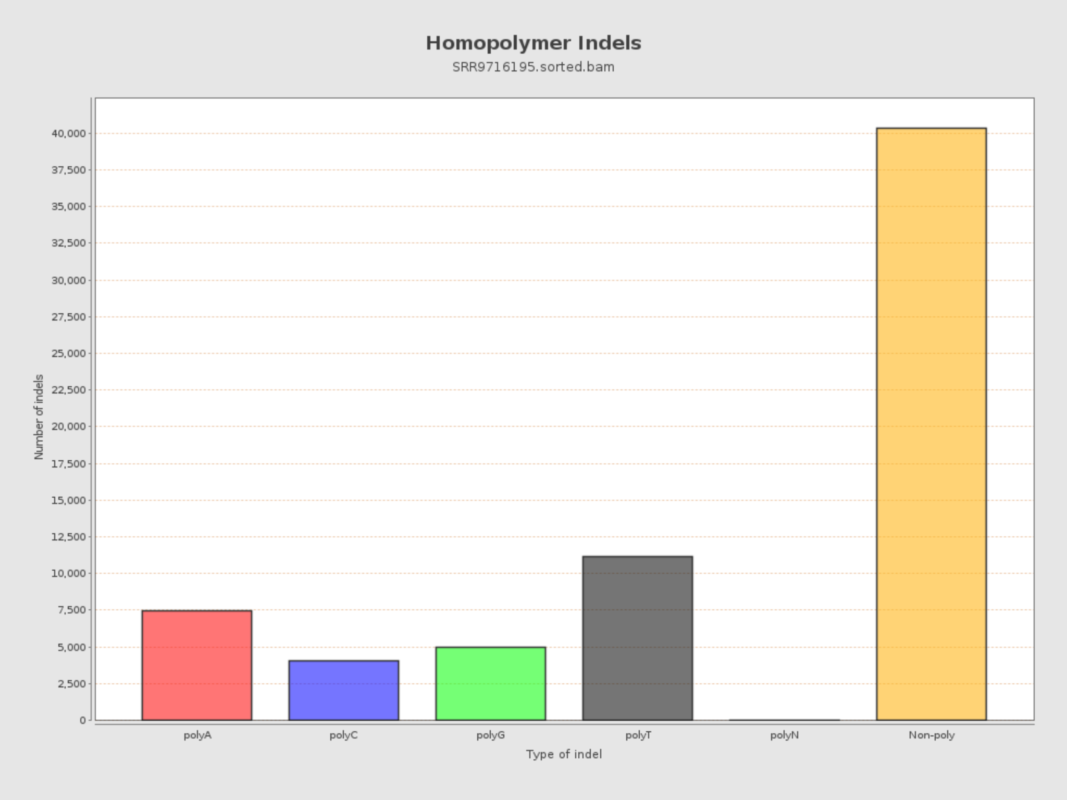
9. Results : Mapped Reads GC-content Distribution



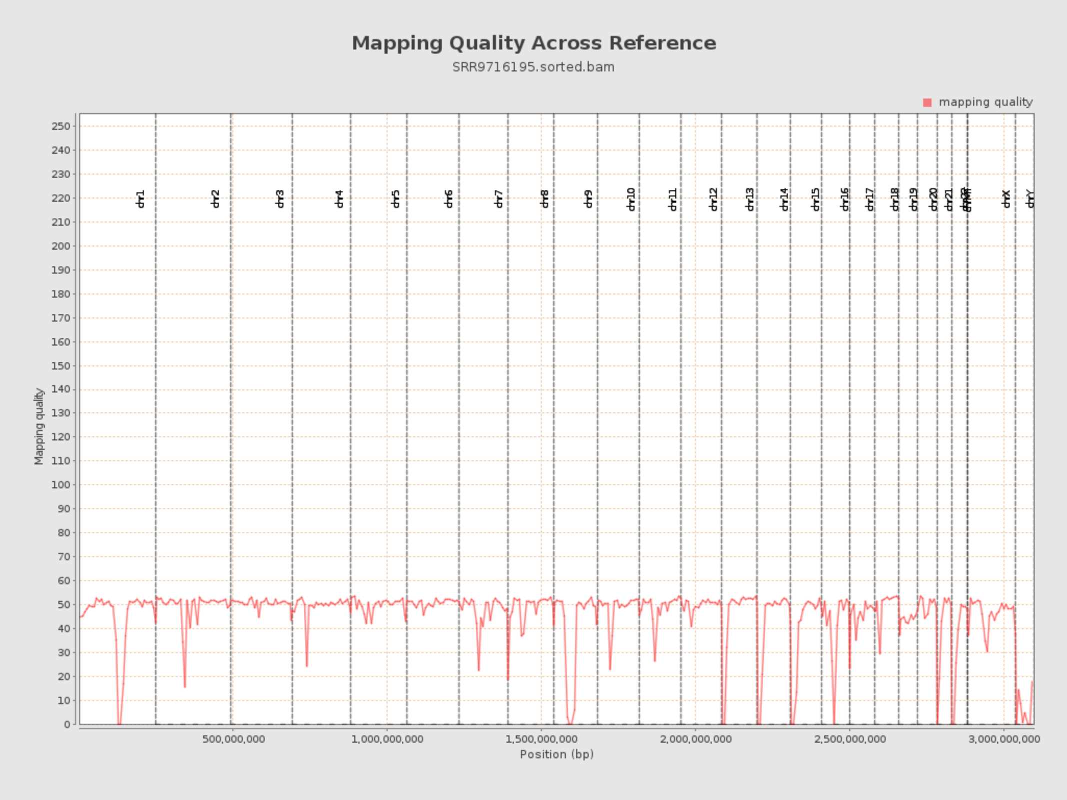
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram