Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:48:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716781.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_SRR9716781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:48:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,683,961
Mapped reads	3,029,874 / 64.69%
Unmapped reads	1,654,087 / 35.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,886 / 1.47%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	133,859 / 2.86%
Duplication rate	3.1%
Clipped reads	3,094,373 / 66.06%

2.2. ACGT Content

Number/percentage of A's	59,617,826 / 26.38%
Number/percentage of C's	45,895,937 / 20.31%
Number/percentage of T's	68,058,369 / 30.11%
Number/percentage of G's	52,423,557 / 23.19%
Number/percentage of N's	27,952 / 0.01%
GC Percentage	43.5%

2.3. Coverage

Mean	0.073

Standard Deviation	0.5458

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

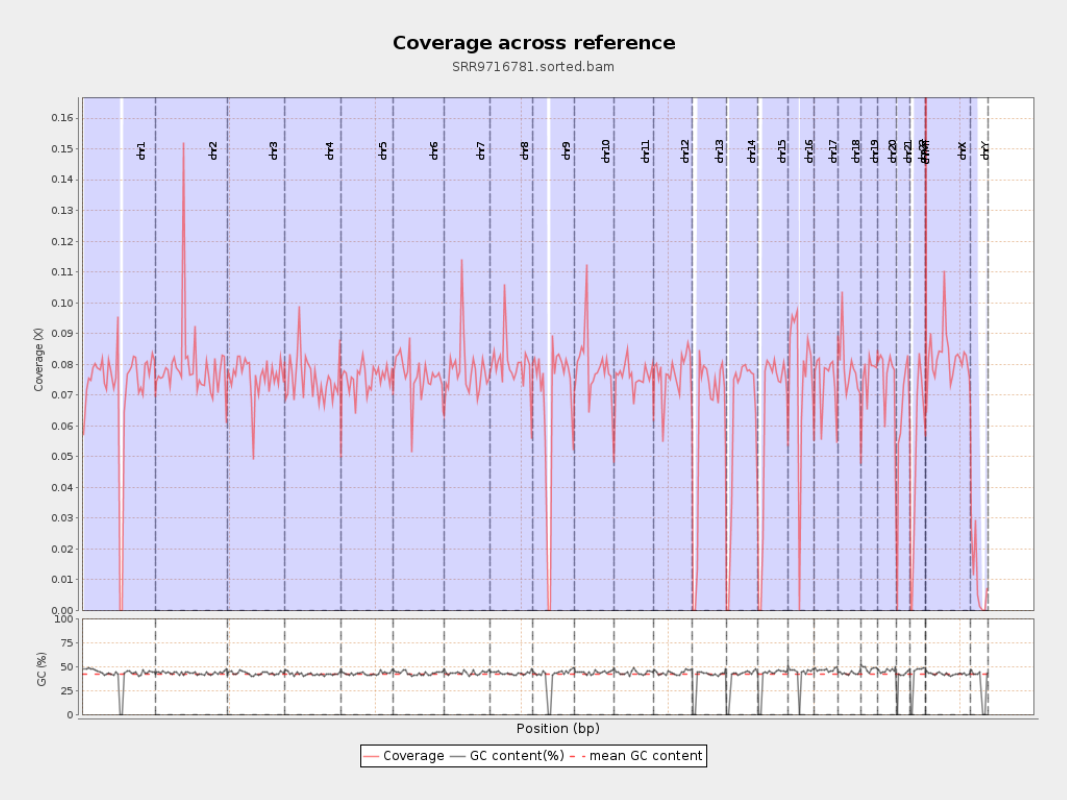
General error rate	0.77%
Mismatches	1,697,589
Insertions	18,429
Mapped reads with at least one insertion	0.6%
Deletions	44,551
Mapped reads with at least one deletion	1.45%
Homopolymer indels	39.62%

2.6. Chromosome stats

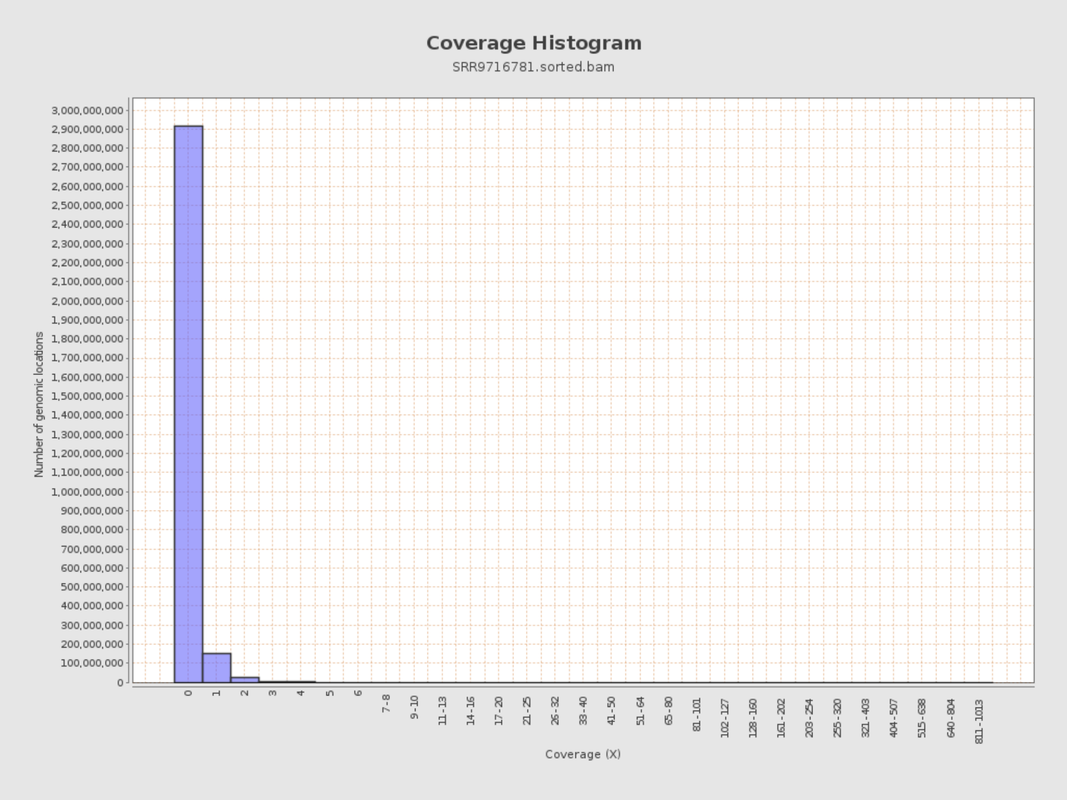
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17952012	0.072	0.6421
chr2	243199373	19331479	0.0795	0.8372
chr3	198022430	15028822	0.0759	0.3303
chr4	191154276	14459180	0.0756	0.3704
chr5	180915260	13662958	0.0755	0.3377
chr6	171115067	13025744	0.0761	0.401
chr7	159138663	12459556	0.0783	0.7246

chr8	146364022	11641895	0.0795	0.7369
chr9	141213431	9600788	0.068	0.5889
chr10	135534747	10718795	0.0791	0.5405
chr11	135006516	10243905	0.0759	0.6
chr12	133851895	10319833	0.0771	0.3434
chr13	115169878	7209038	0.0626	0.3001
chr14	107349540	6765066	0.063	0.3995
chr15	102531392	6424993	0.0627	0.3044
chr16	90354753	6734181	0.0745	0.3831
chr17	81195210	6119250	0.0754	0.3791
chr18	78077248	6197594	0.0794	1.1278
chr19	59128983	4504771	0.0762	0.566
chr20	63025520	4788270	0.076	0.3523
chr21	48129895	2980406	0.0619	0.3405
chr22	51304566	2598744	0.0507	0.2729
chrMT	16571	5845	0.3527	0.6631
chrX	155270560	12769250	0.0822	0.4807
chrY	59373566	558022	0.0094	0.2437

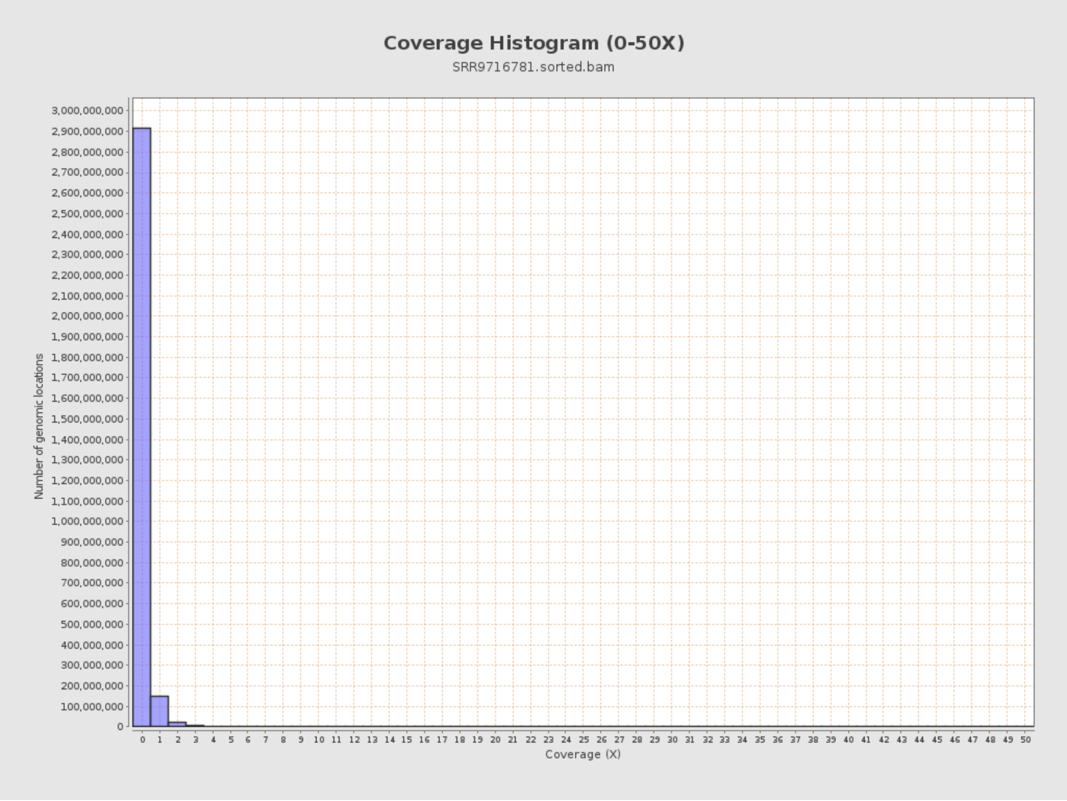
3. Results : Coverage across reference



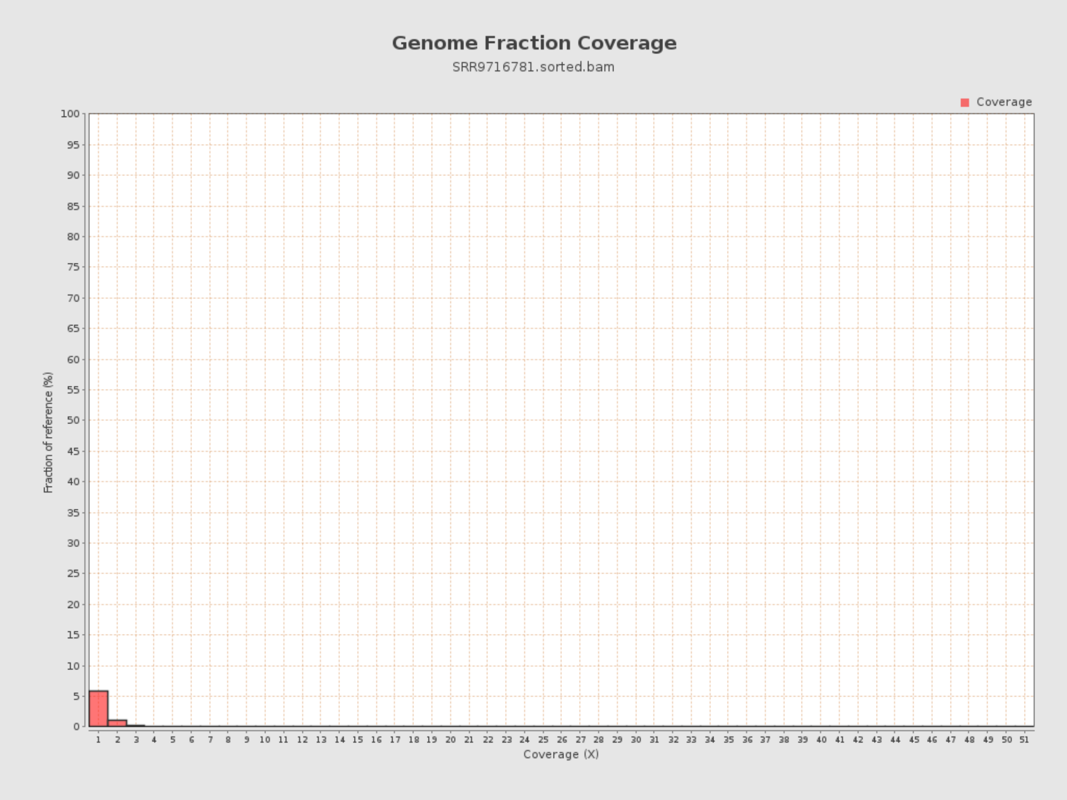
4. Results : Coverage Histogram



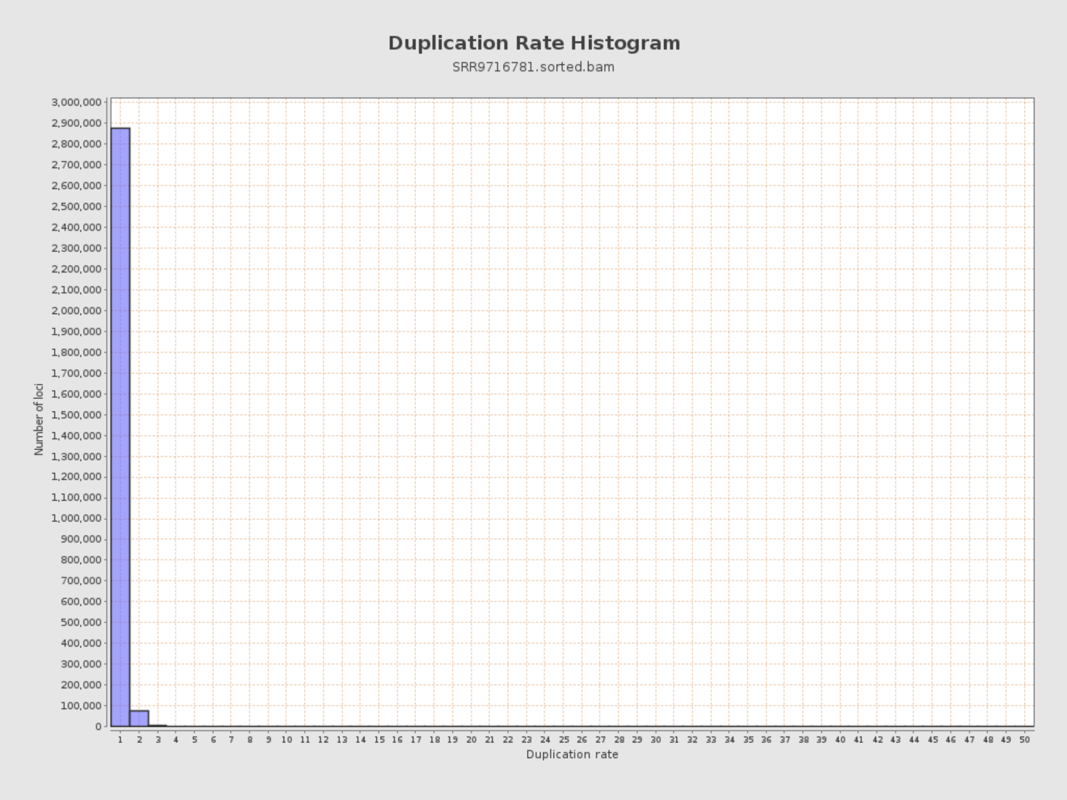
5. Results : Coverage Histogram (0-50X)



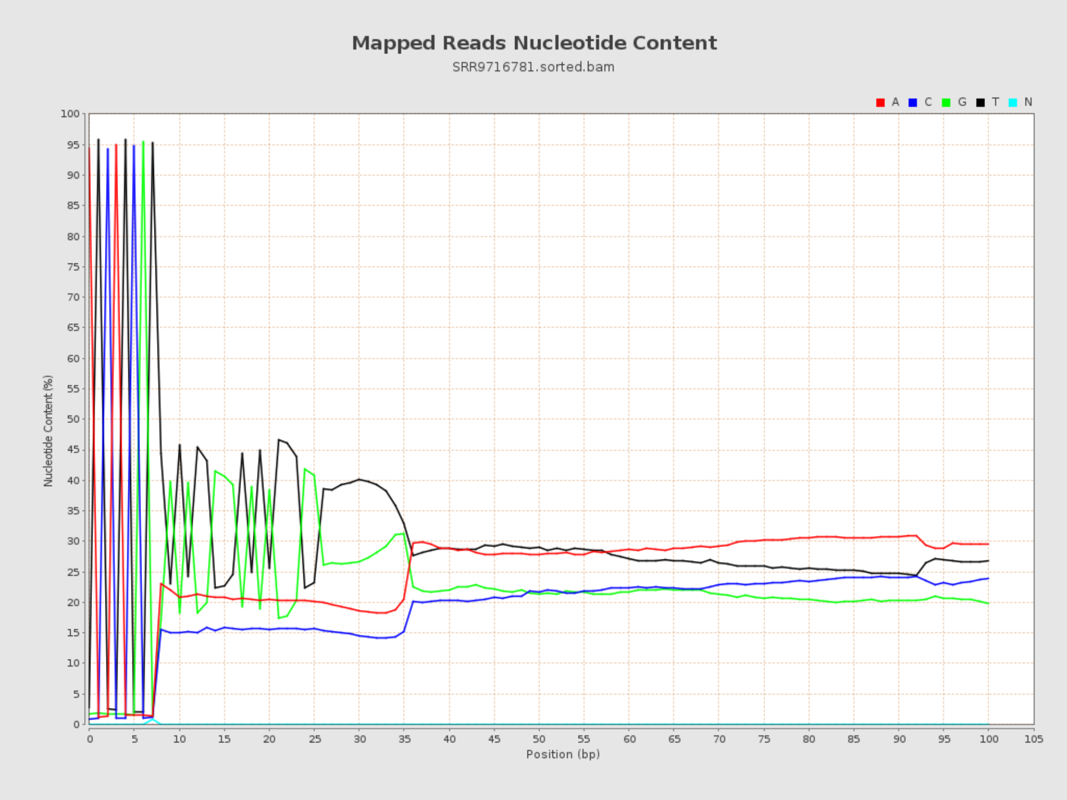
6. Results : Genome Fraction Coverage



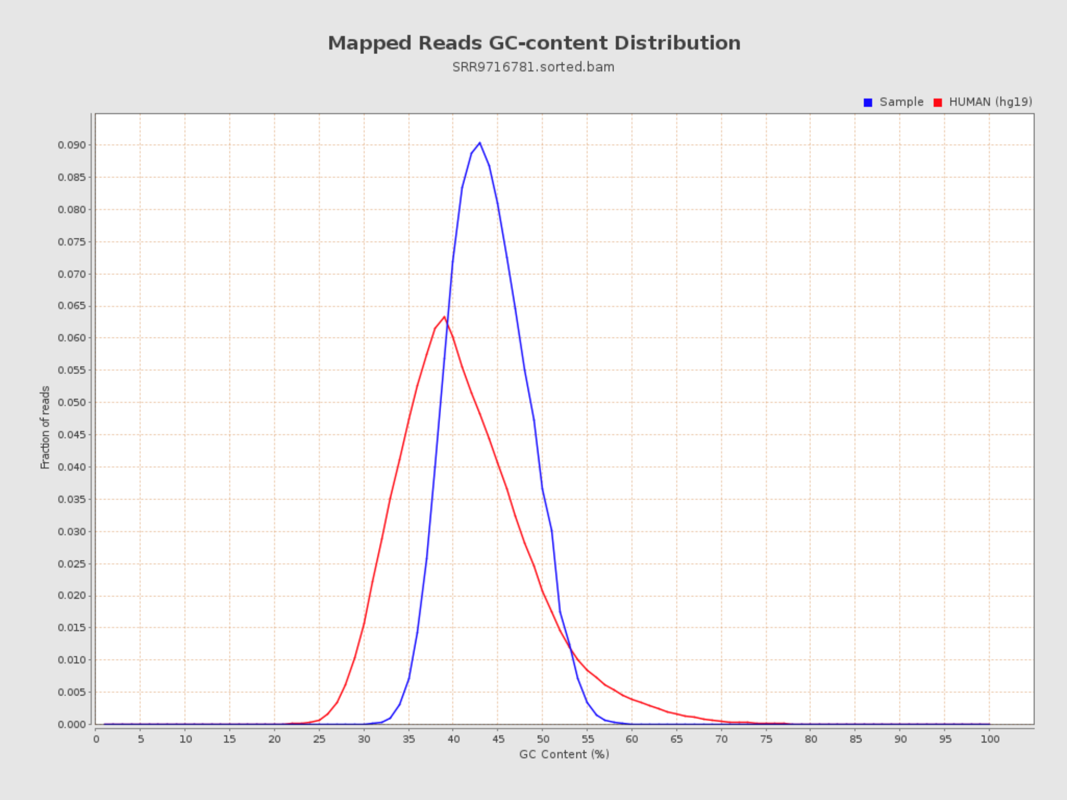
7. Results : Duplication Rate Histogram



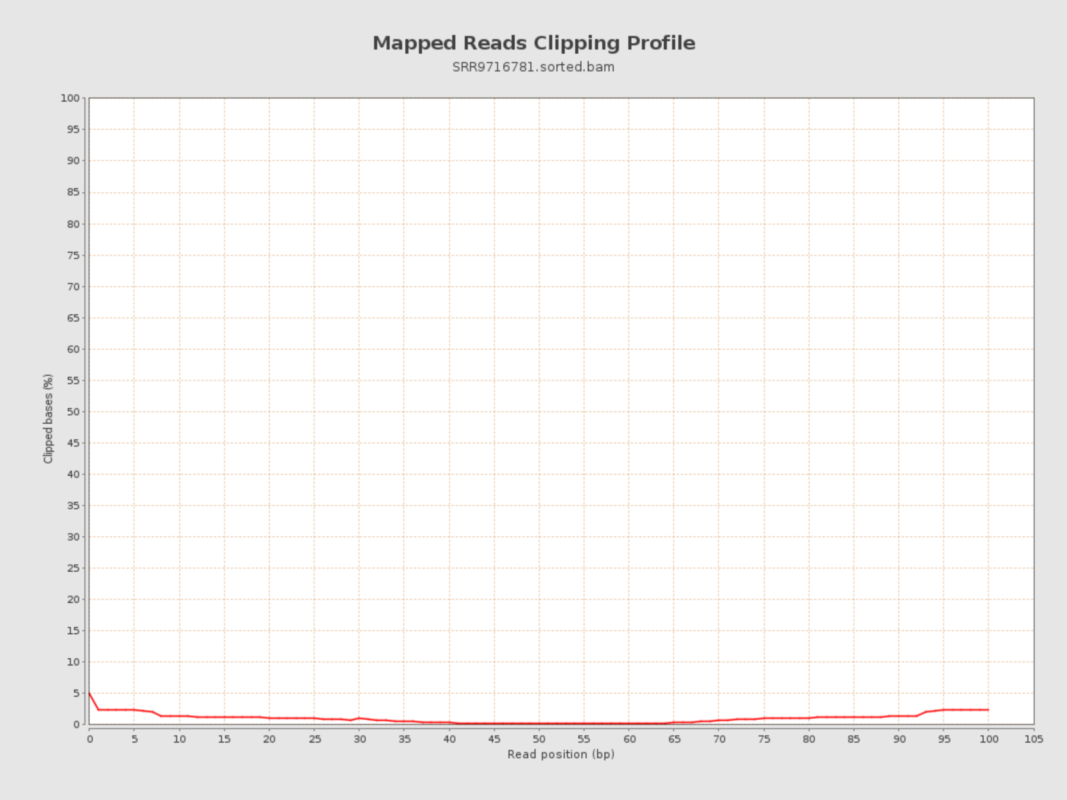
8. Results : Mapped Reads Nucleotide Content



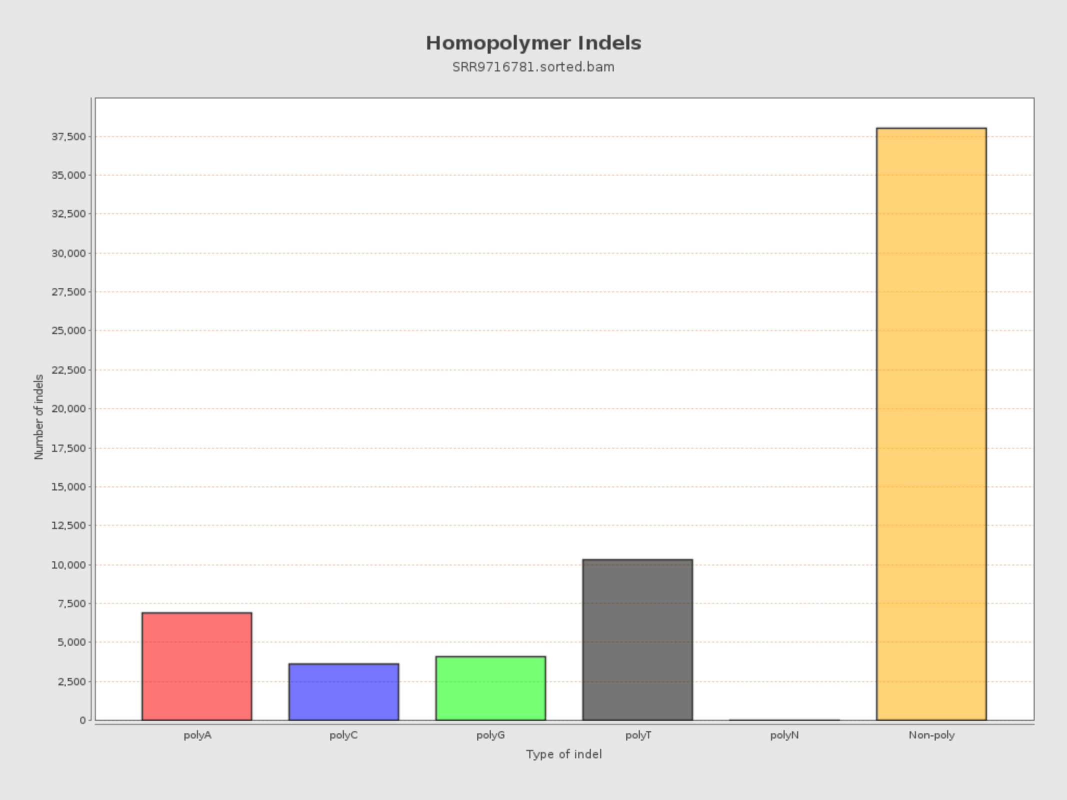
9. Results : Mapped Reads GC-content Distribution



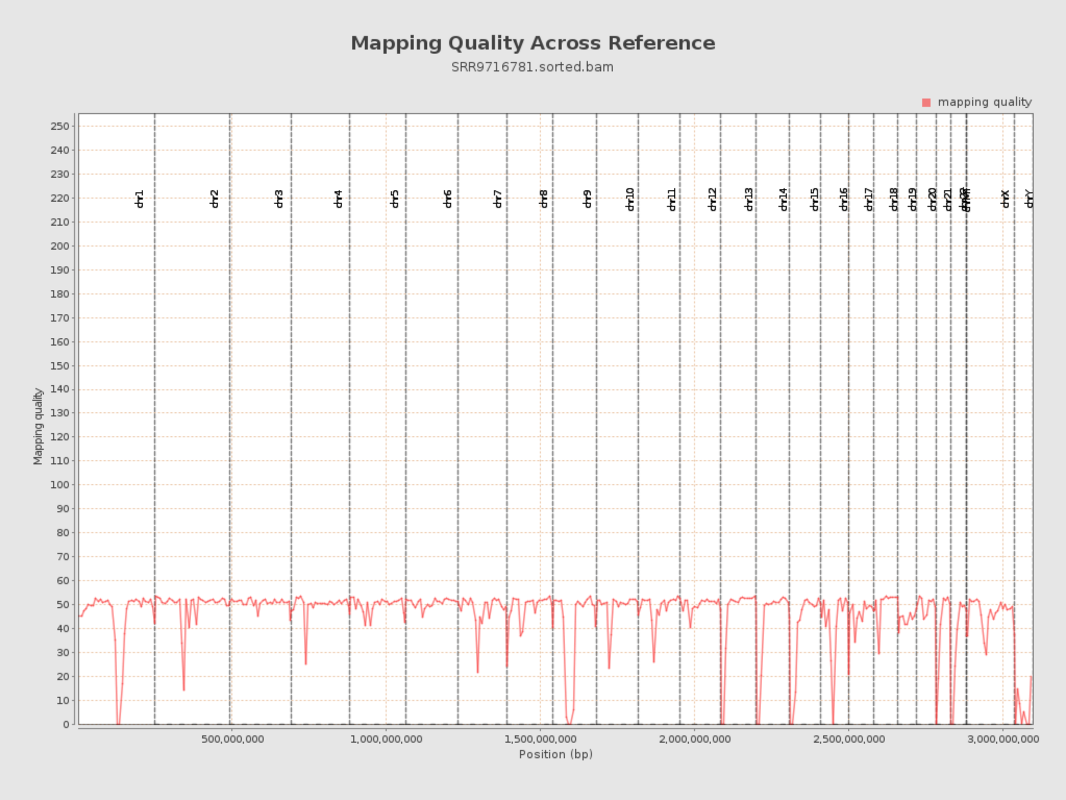
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram