Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:27:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716632.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_SRR9716632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716632.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:27:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,682,439
Mapped reads	1,845,015 / 68.78%
Unmapped reads	837,424 / 31.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,669 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	100,492 / 3.75%
Duplication rate	4.28%
Clipped reads	1,850,569 / 68.99%

2.2. ACGT Content

Number/percentage of A's	26,371,767 / 25%
Number/percentage of C's	18,618,301 / 17.65%
Number/percentage of T's	33,307,758 / 31.57%
Number/percentage of G's	27,200,987 / 25.78%
Number/percentage of N's	1,608 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0341

Standard Deviation	0.3093

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

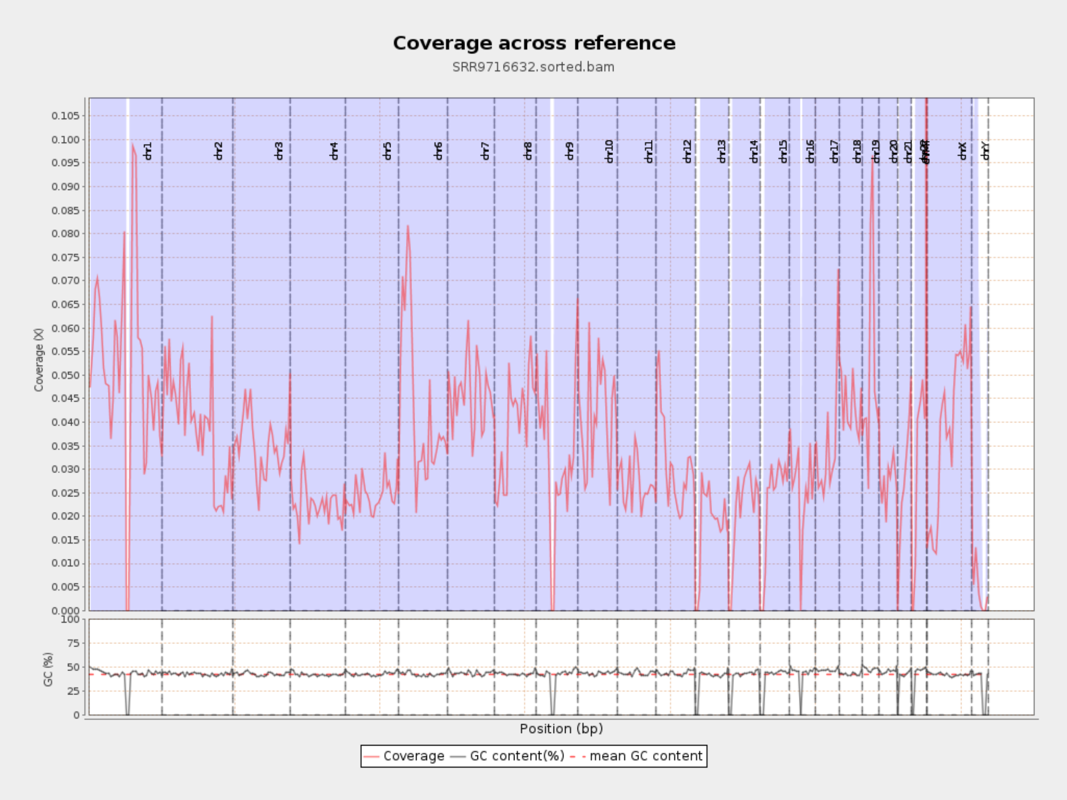
General error rate	0.51%
Mismatches	527,053
Insertions	7,079
Mapped reads with at least one insertion	0.38%
Deletions	17,797
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.6%

2.6. Chromosome stats

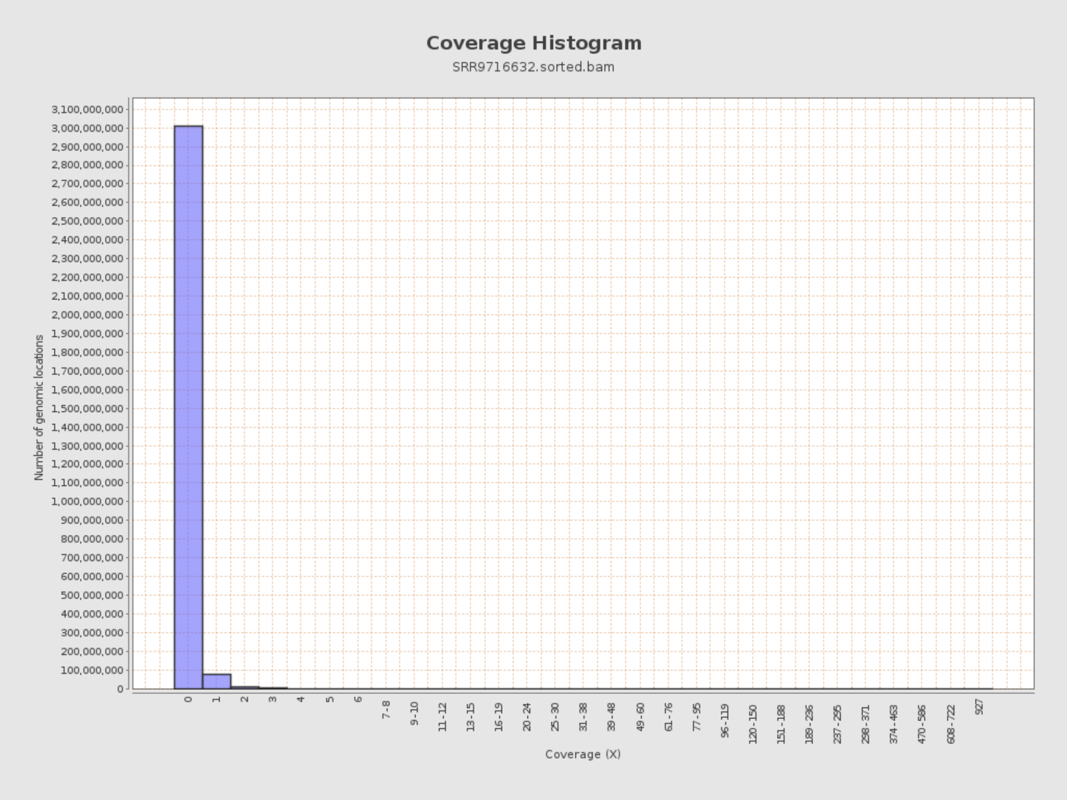
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12809801	0.0514	0.5785
chr2	243199373	9590699	0.0394	0.4446
chr3	198022430	6934044	0.035	0.2219
chr4	191154276	4315768	0.0226	0.1919
chr5	180915260	4428368	0.0245	0.1837
chr6	171115067	7286150	0.0426	0.2657
chr7	159138663	7294642	0.0458	0.3892

chr8	146364022	5794033	0.0396	0.2633
chr9	141213431	4334519	0.0307	0.2532
chr10	135534747	5603271	0.0413	0.315
chr11	135006516	3621525	0.0268	0.2551
chr12	133851895	4190555	0.0313	0.2091
chr13	115169878	2096965	0.0182	0.1563
chr14	107349540	2301342	0.0214	0.1812
chr15	102531392	2357771	0.023	0.1816
chr16	90354753	2332407	0.0258	0.2032
chr17	81195210	2853325	0.0351	0.2296
chr18	78077248	3417672	0.0438	0.398
chr19	59128983	3092581	0.0523	0.4115
chr20	63025520	1725848	0.0274	0.1954
chr21	48129895	1307298	0.0272	0.2024
chr22	51304566	1513743	0.0295	0.2027
chrMT	16571	62200	3.7535	2.7803
chrX	155270560	6013095	0.0387	0.2584
chrY	59373566	250367	0.0042	0.1045

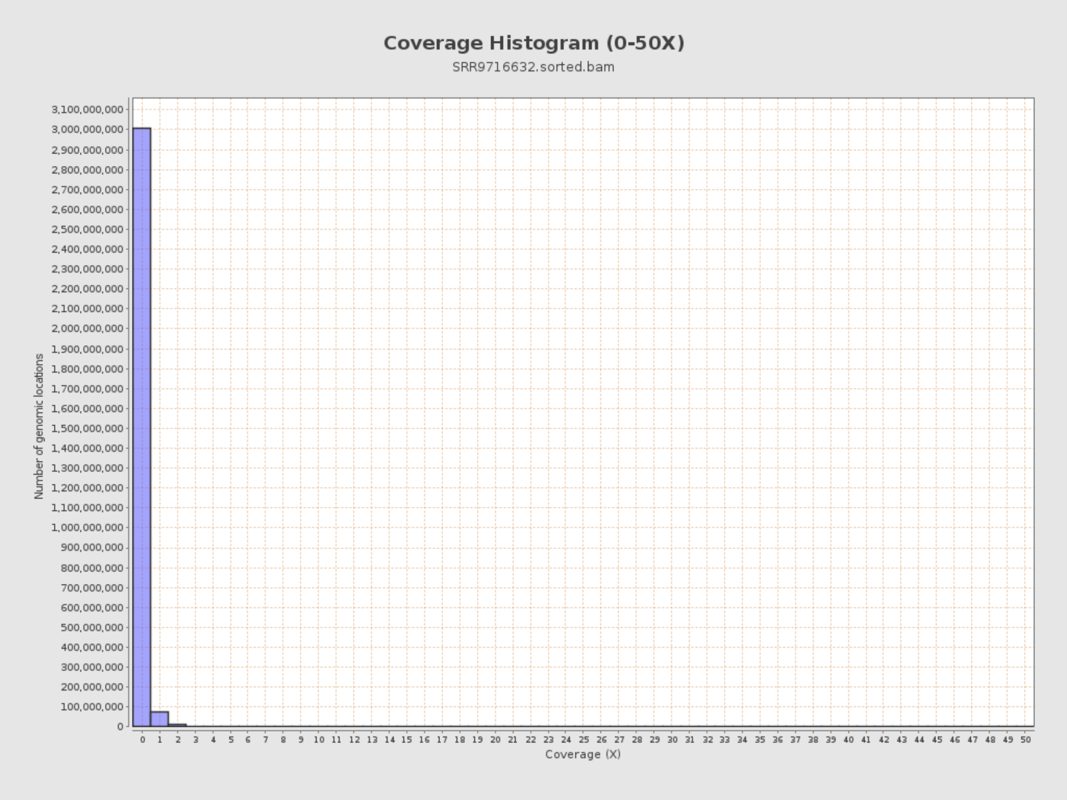
3. Results : Coverage across reference



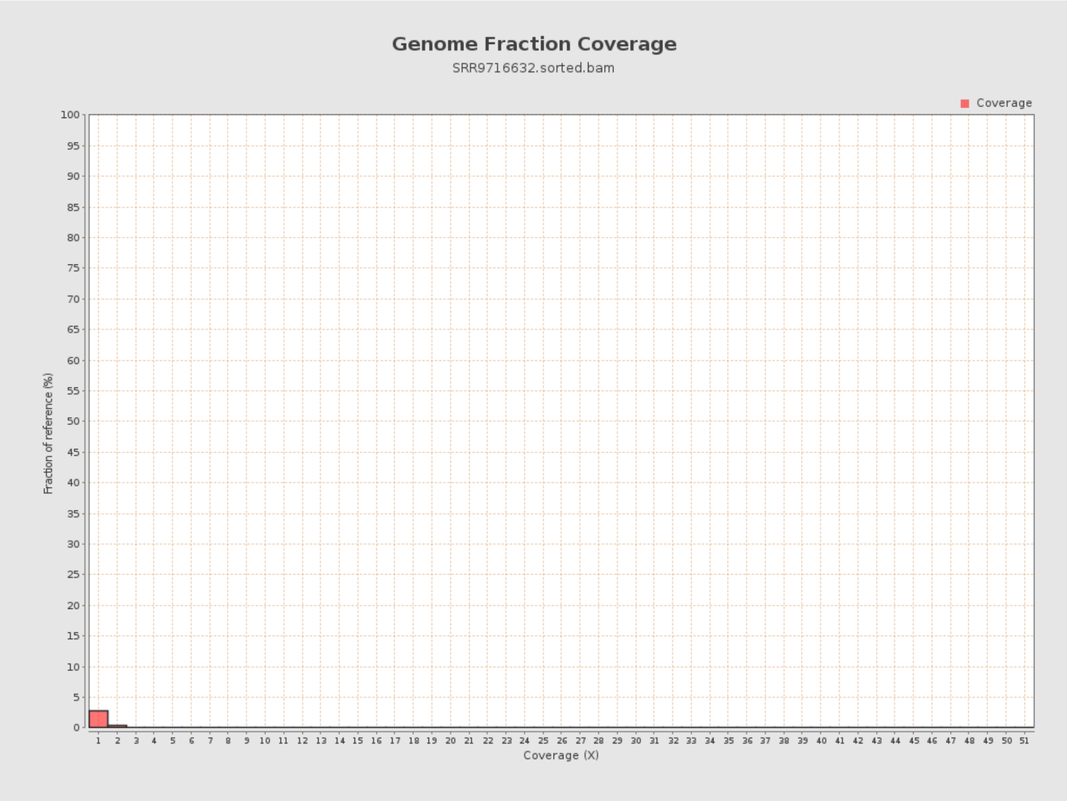
4. Results : Coverage Histogram



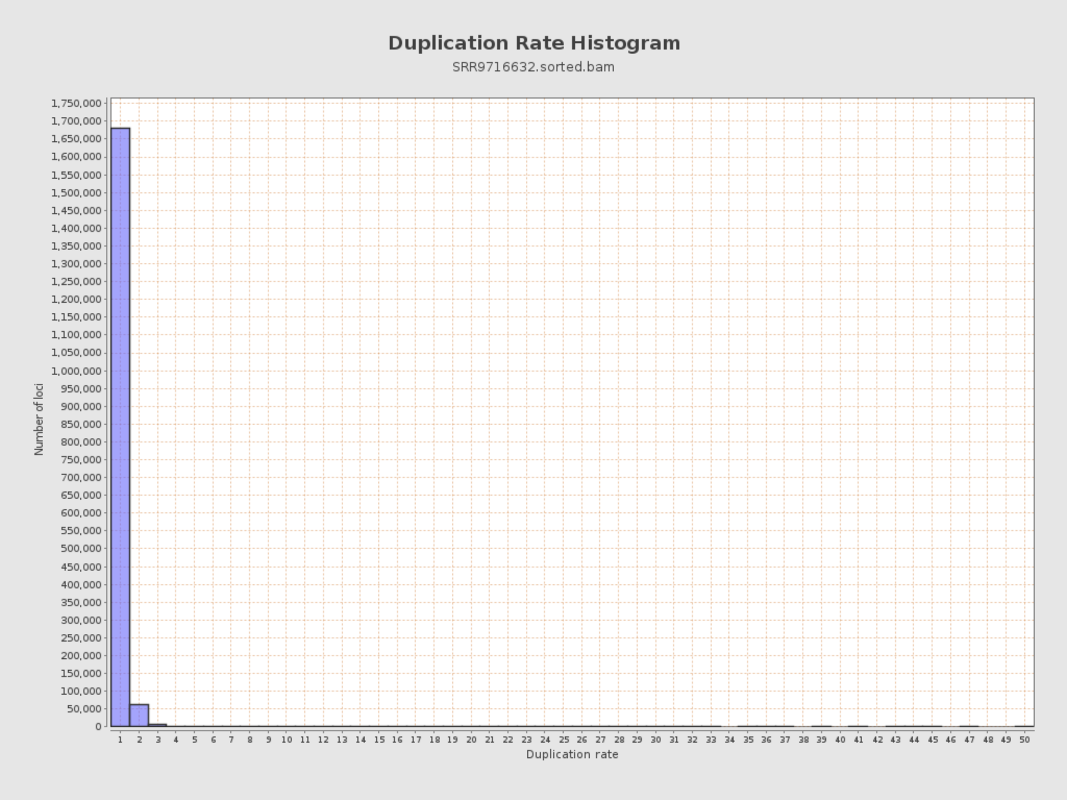
5. Results : Coverage Histogram (0-50X)



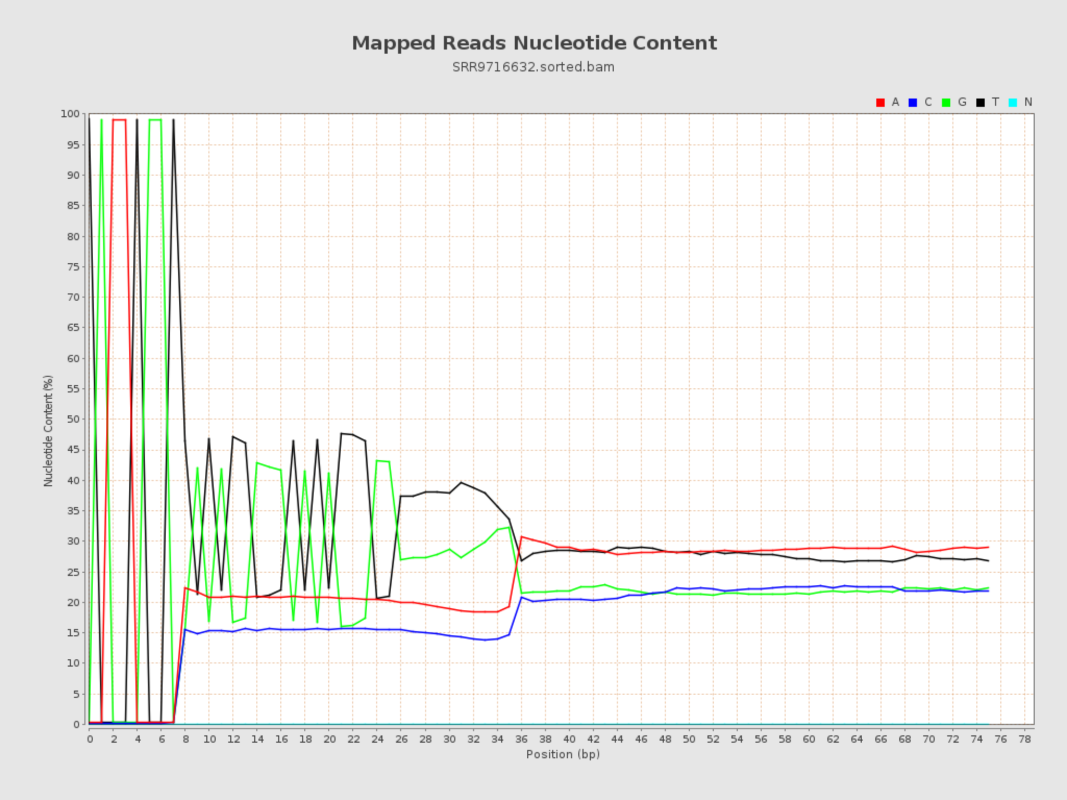
6. Results : Genome Fraction Coverage



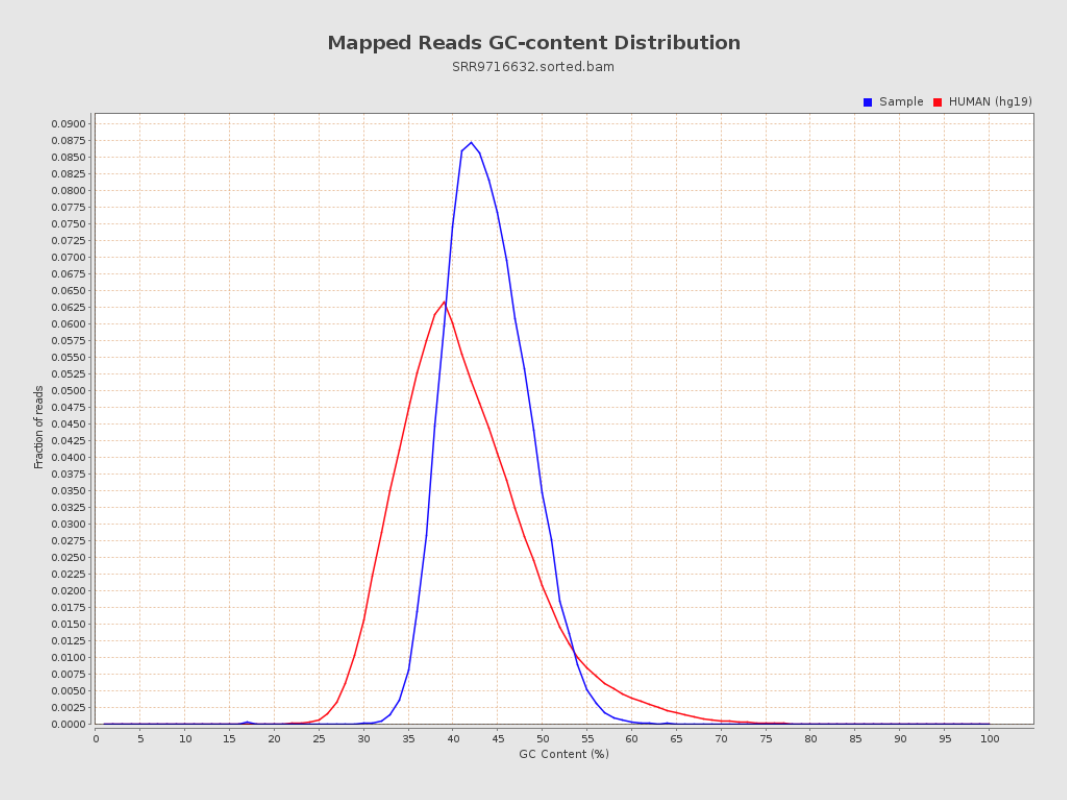
7. Results : Duplication Rate Histogram



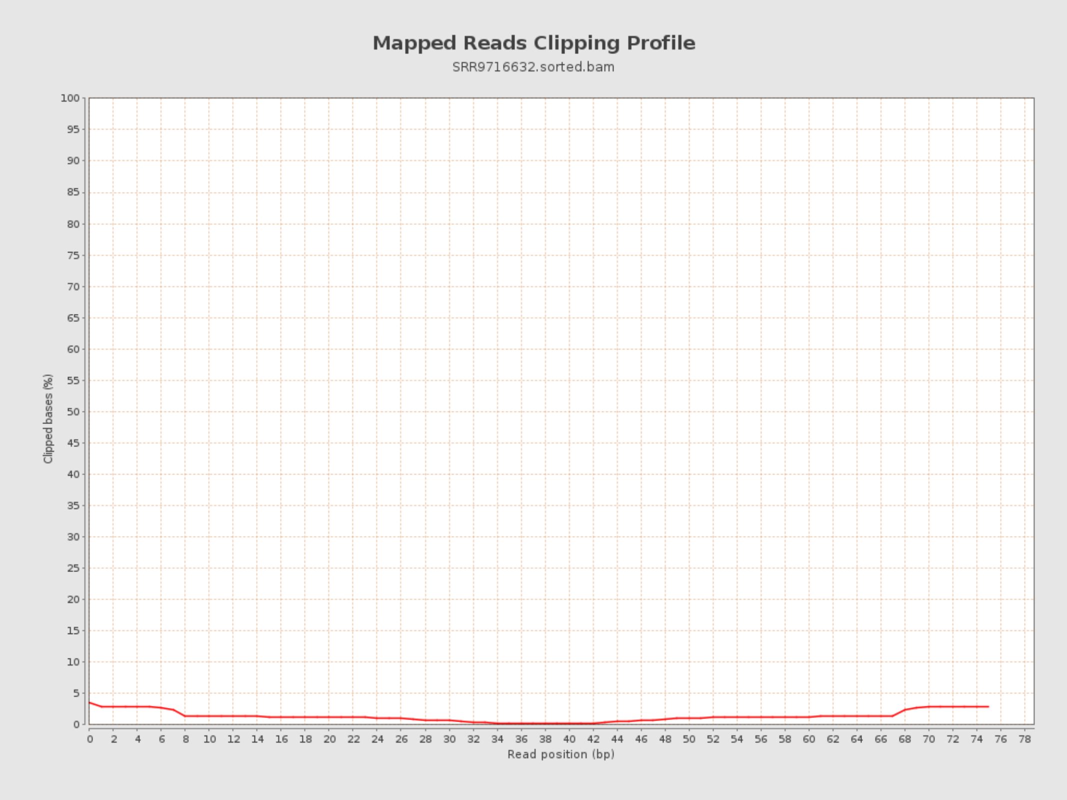
8. Results : Mapped Reads Nucleotide Content



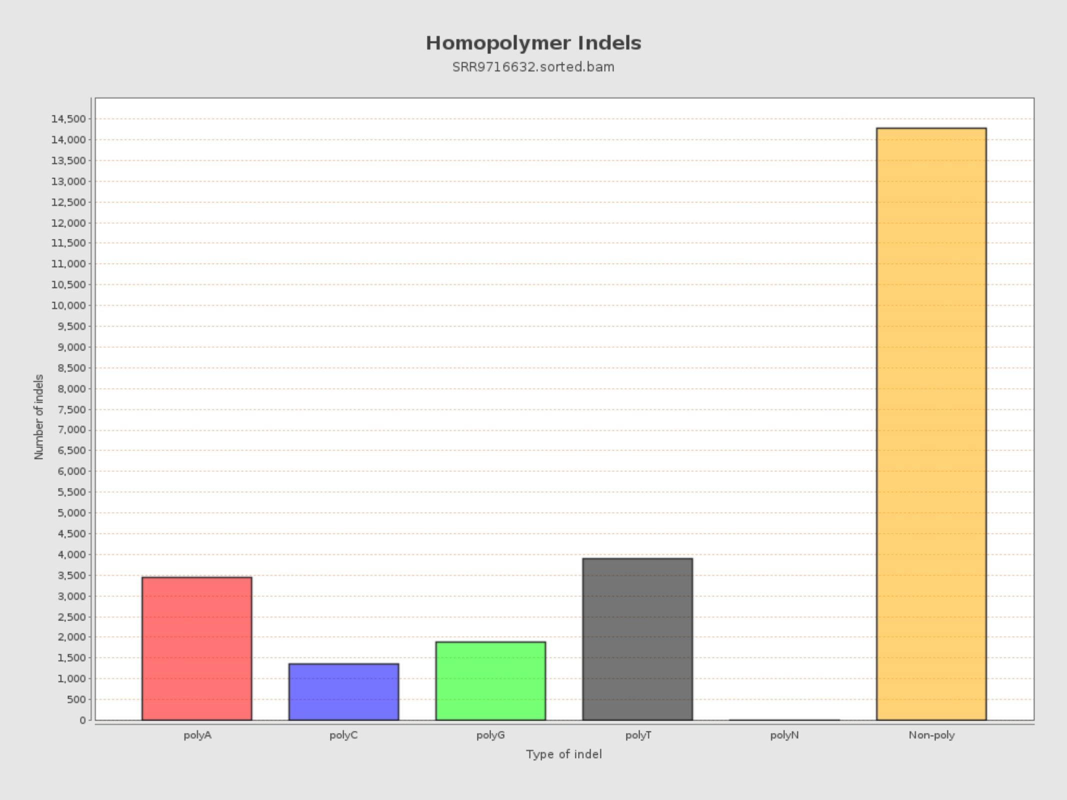
9. Results : Mapped Reads GC-content Distribution



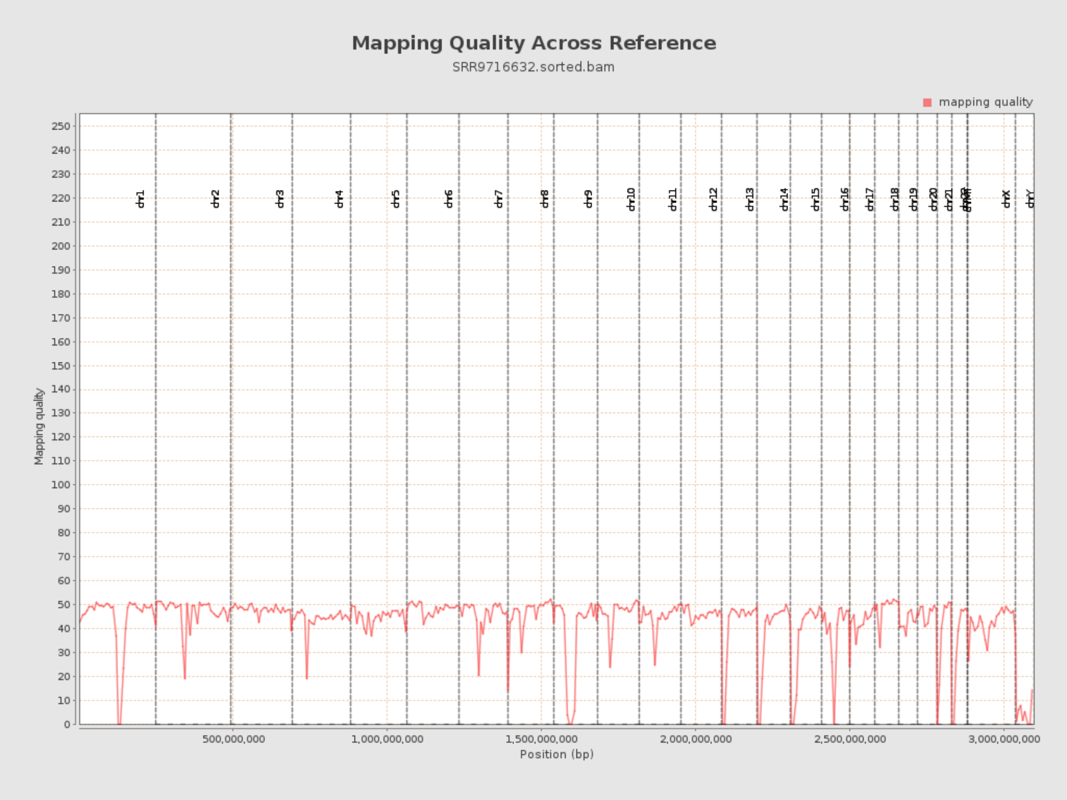
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram