Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716643.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_SRR9716643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:56:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,407,992
Mapped reads	1,251,087 / 88.86%
Unmapped reads	156,905 / 11.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,273 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	30,475 / 2.16%
Duplication rate	1.81%
Clipped reads	1,252,840 / 88.98%

2.2. ACGT Content

Number/percentage of A's	16,567,351 / 23.41%
Number/percentage of C's	14,178,539 / 20.03%
Number/percentage of T's	22,819,992 / 32.24%
Number/percentage of G's	17,208,434 / 24.31%
Number/percentage of N's	1,604 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.199

2.4. Mapping Quality

Mean Mapping Quality	43.19

2.5. Mismatches and indels

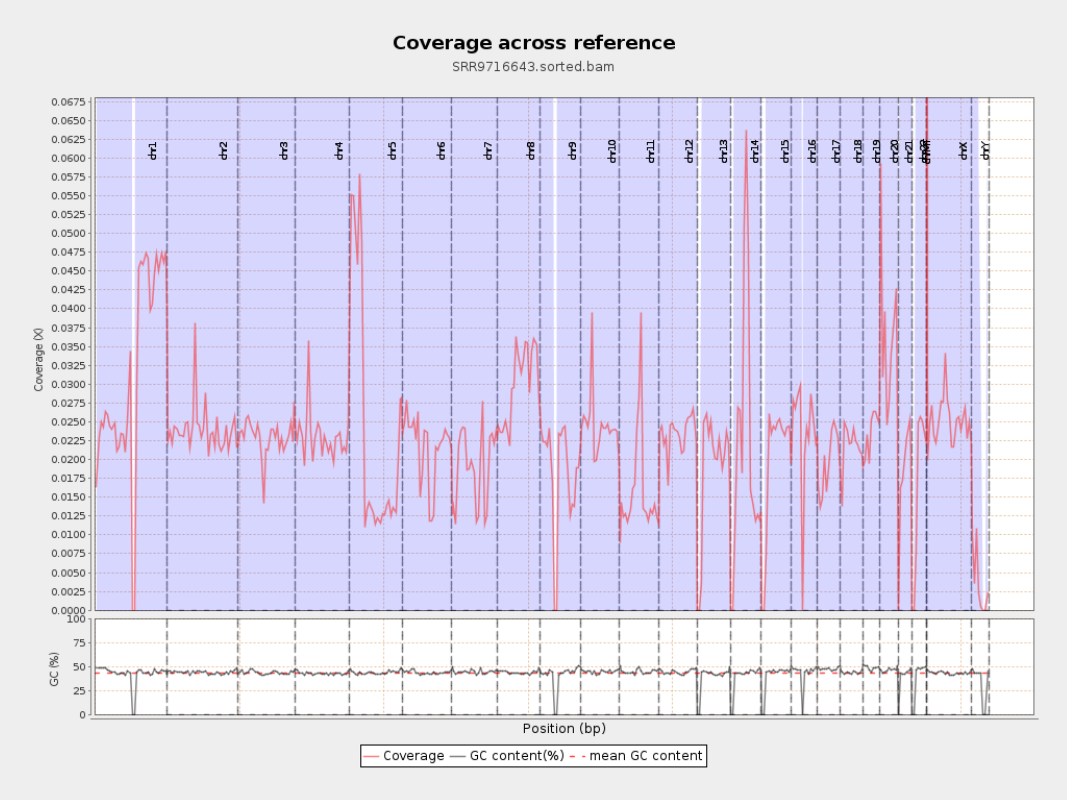
General error rate	0.51%
Mismatches	350,883
Insertions	4,419
Mapped reads with at least one insertion	0.35%
Deletions	11,229
Mapped reads with at least one deletion	0.89%
Homopolymer indels	42.02%

2.6. Chromosome stats

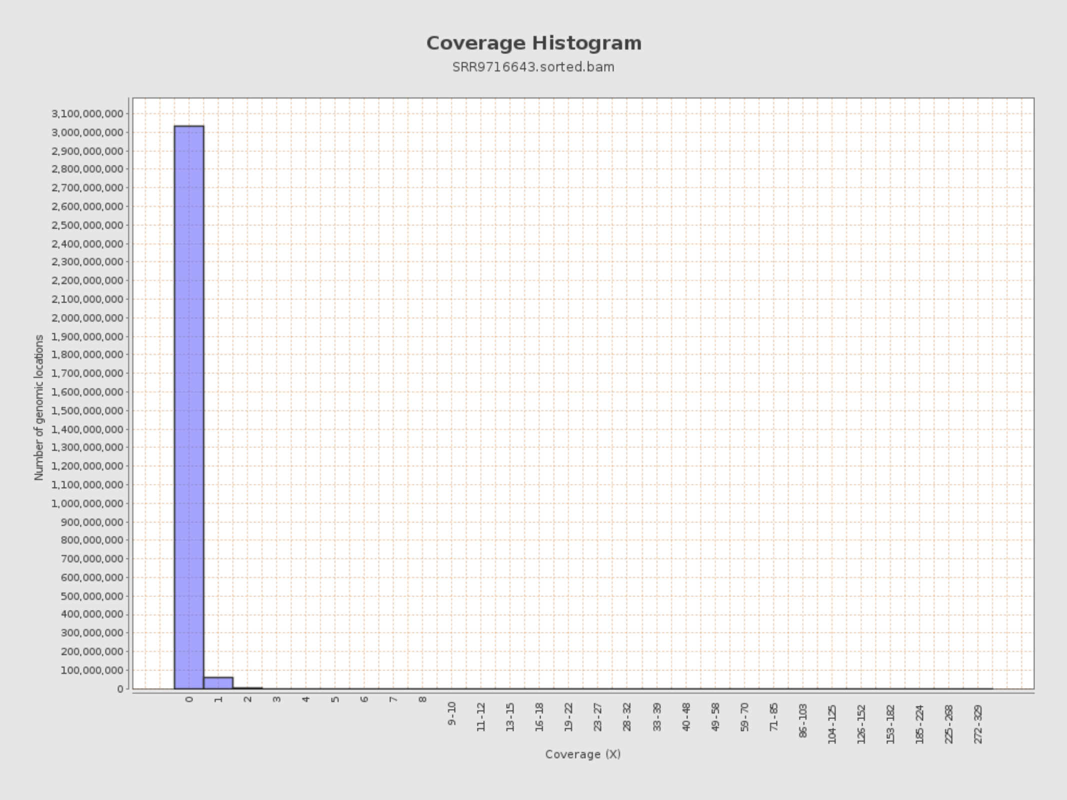
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7836045	0.0314	0.3083
chr2	243199373	5833801	0.024	0.2218
chr3	198022430	4530481	0.0229	0.1637
chr4	191154276	4409277	0.0231	0.1728
chr5	180915260	4392995	0.0243	0.1703
chr6	171115067	3680335	0.0215	0.1676
chr7	159138663	3026638	0.019	0.1669

chr8	146364022	4389533	0.03	0.2066
chr9	141213431	2546037	0.018	0.1934
chr10	135534747	3328584	0.0246	0.2125
chr11	135006516	2204732	0.0163	0.1694
chr12	133851895	3133747	0.0234	0.1661
chr13	115169878	2147662	0.0186	0.1454
chr14	107349540	2414526	0.0225	0.172
chr15	102531392	2014852	0.0197	0.1501
chr16	90354753	2090923	0.0231	0.1759
chr17	81195210	1594804	0.0196	0.1535
chr18	78077248	1680485	0.0215	0.3469
chr19	59128983	1393362	0.0236	0.2379
chr20	63025520	2264878	0.0359	0.2088
chr21	48129895	891142	0.0185	0.1577
chr22	51304566	867344	0.0169	0.1391
chrMT	16571	6232	0.3761	0.6675
chrX	155270560	3912505	0.0252	0.1869
chrY	59373566	203746	0.0034	0.0819

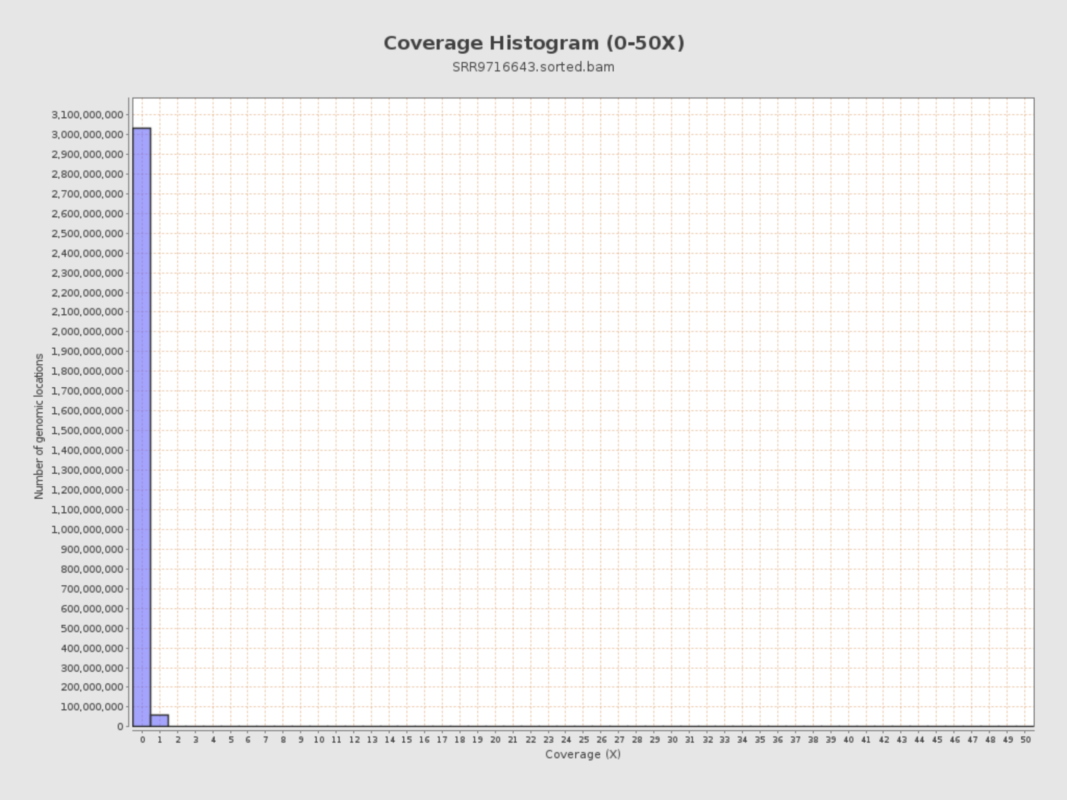
3. Results : Coverage across reference



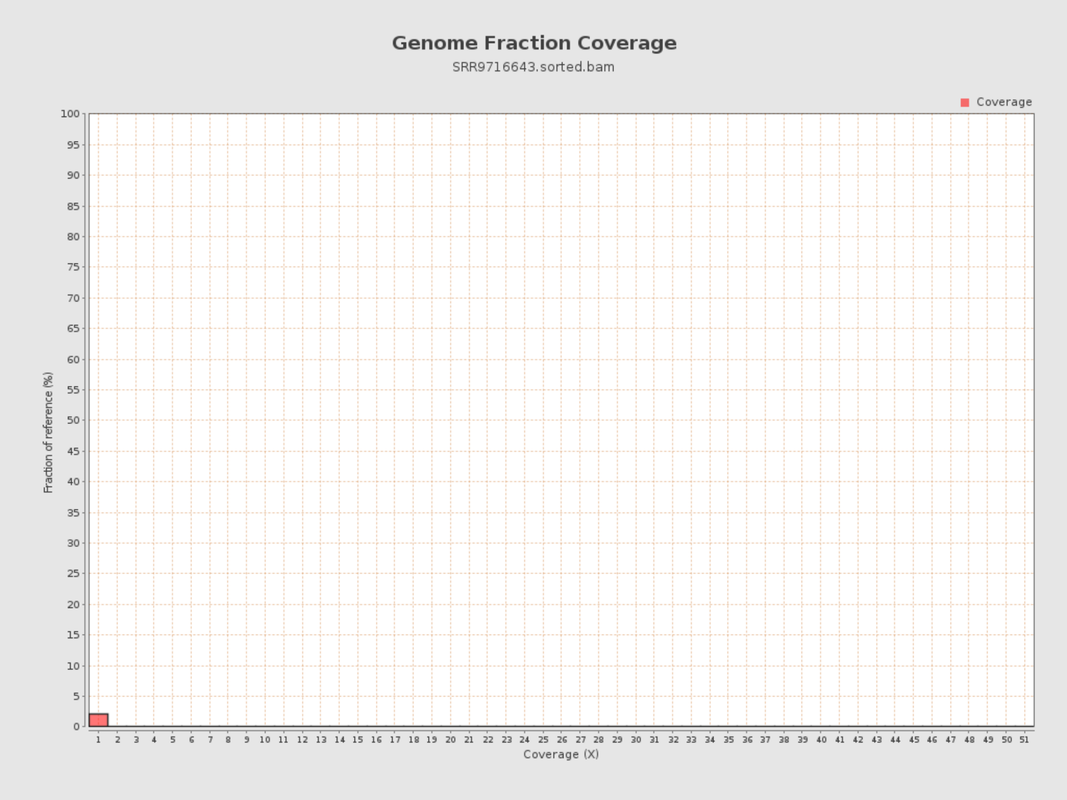
4. Results : Coverage Histogram



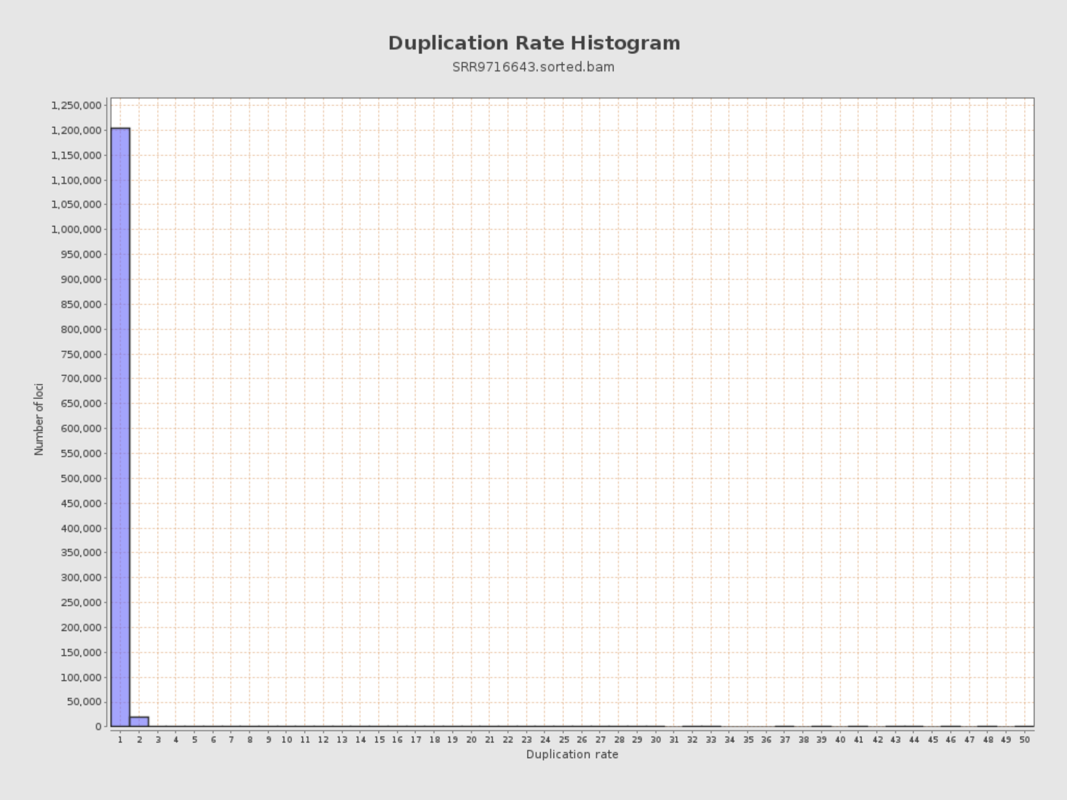
5. Results : Coverage Histogram (0-50X)



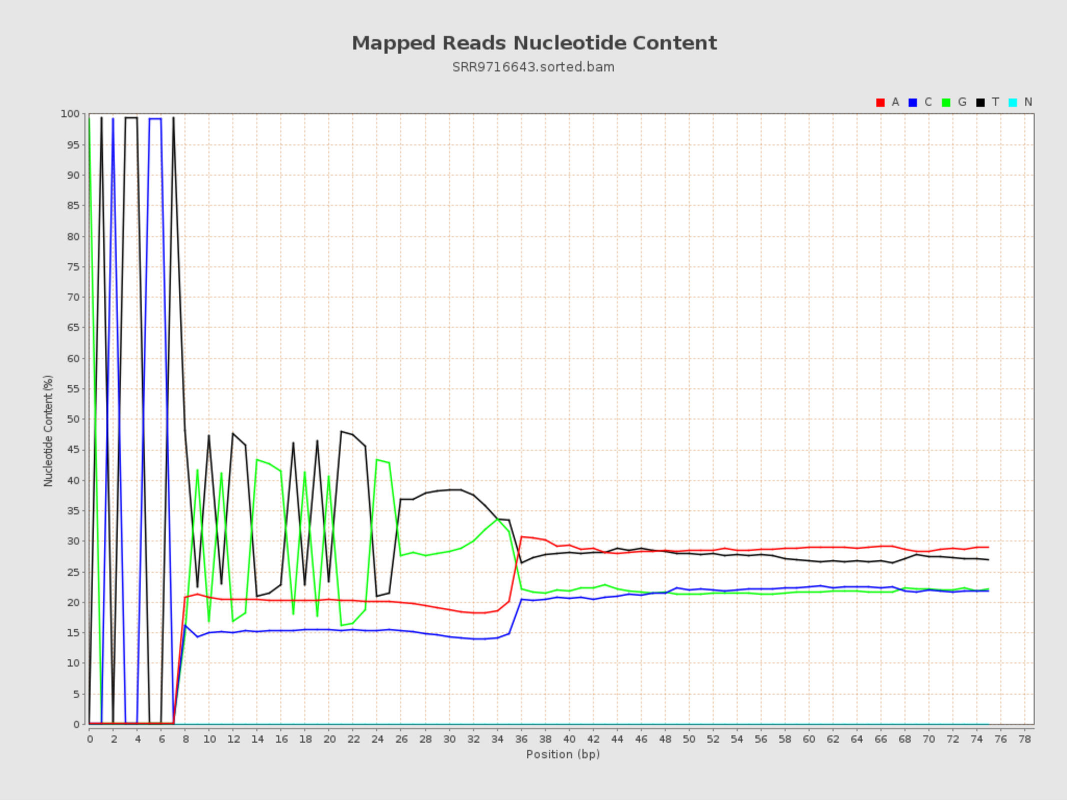
6. Results : Genome Fraction Coverage



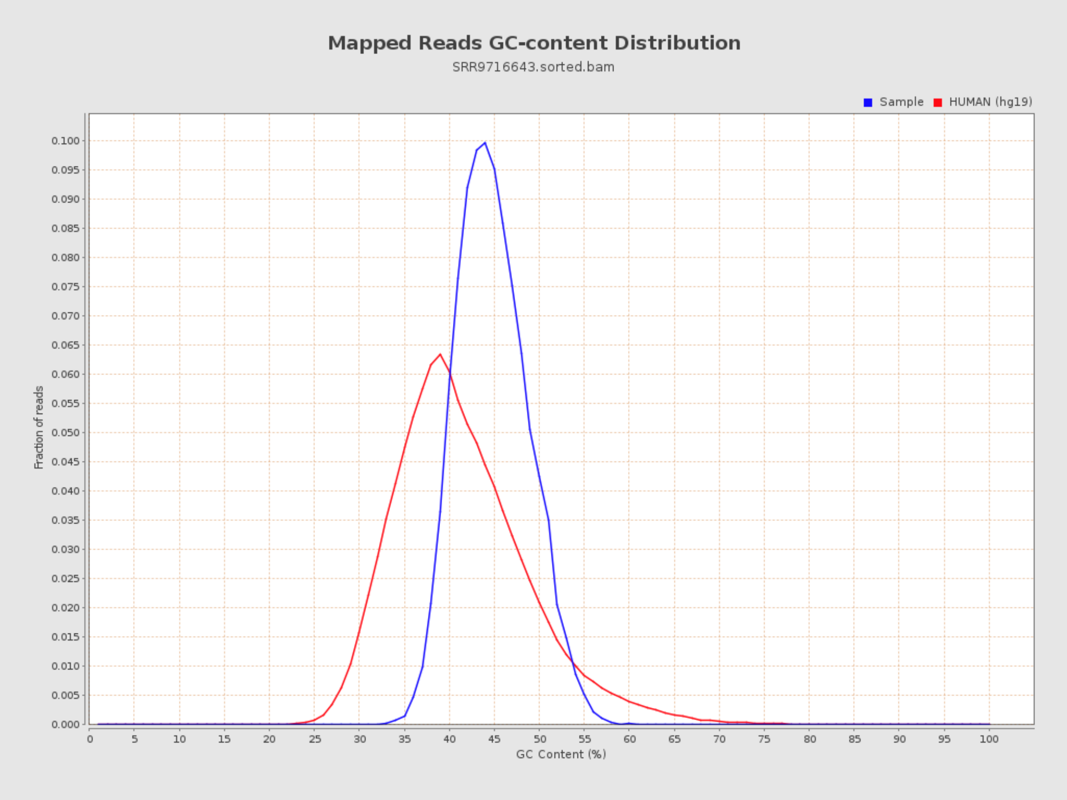
7. Results : Duplication Rate Histogram



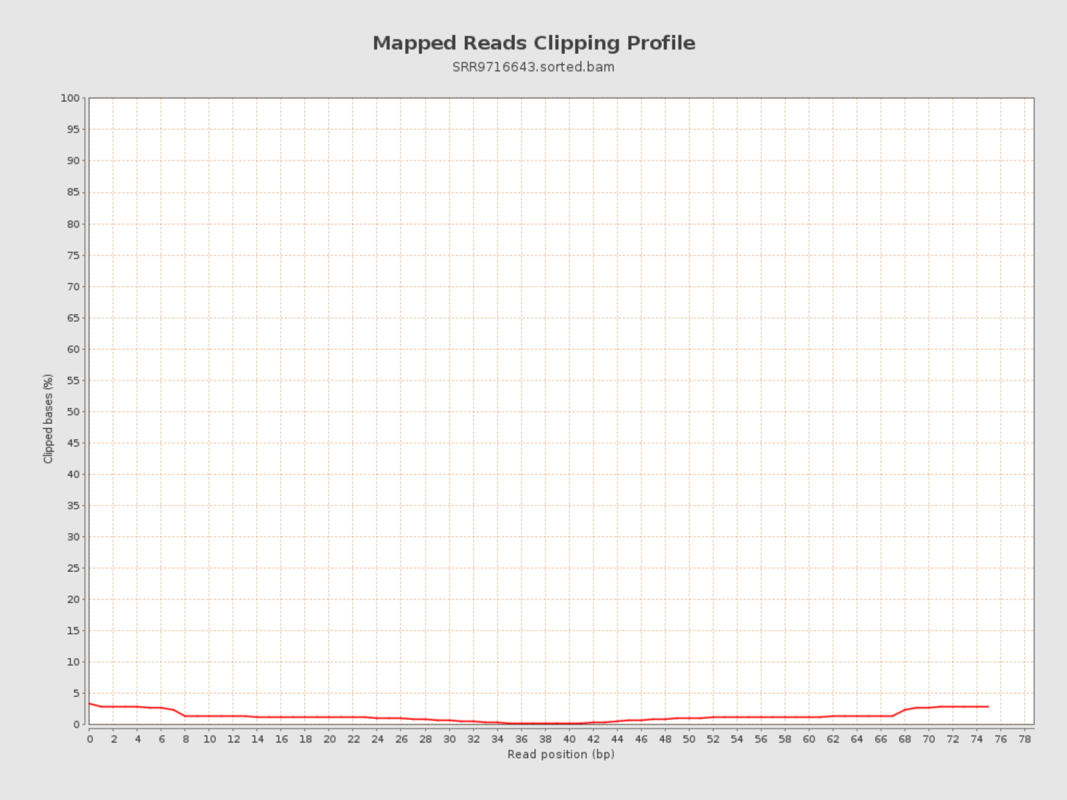
8. Results : Mapped Reads Nucleotide Content



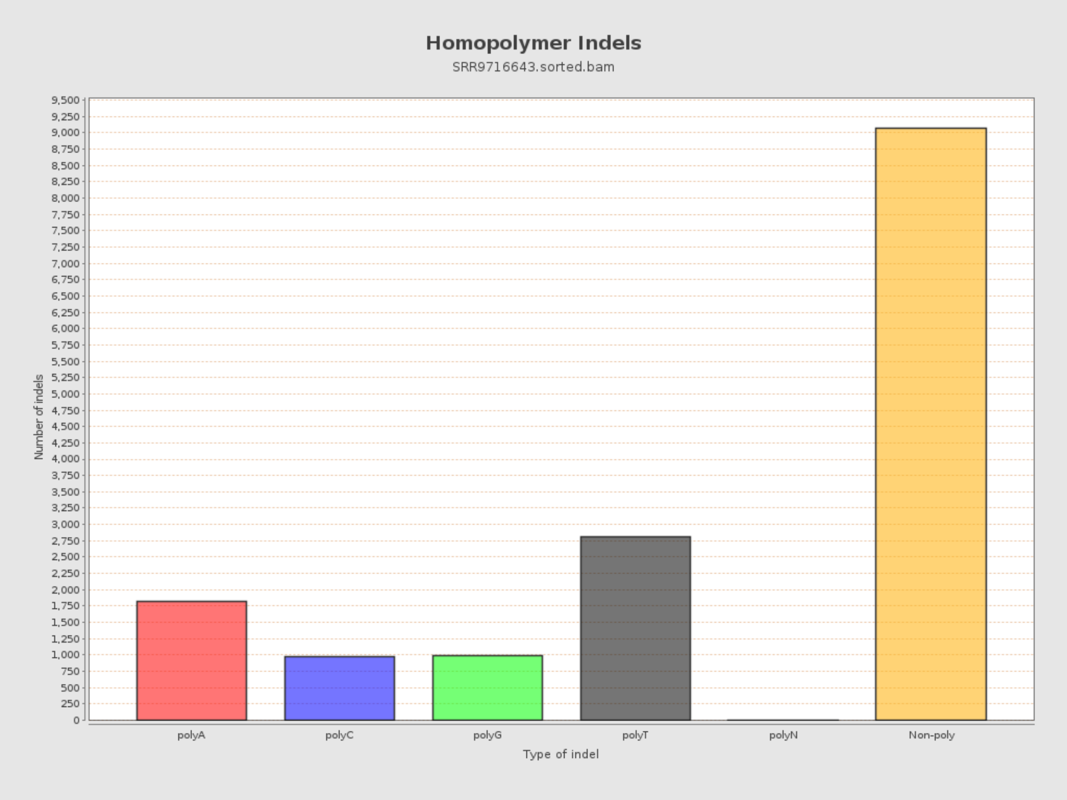
9. Results : Mapped Reads GC-content Distribution



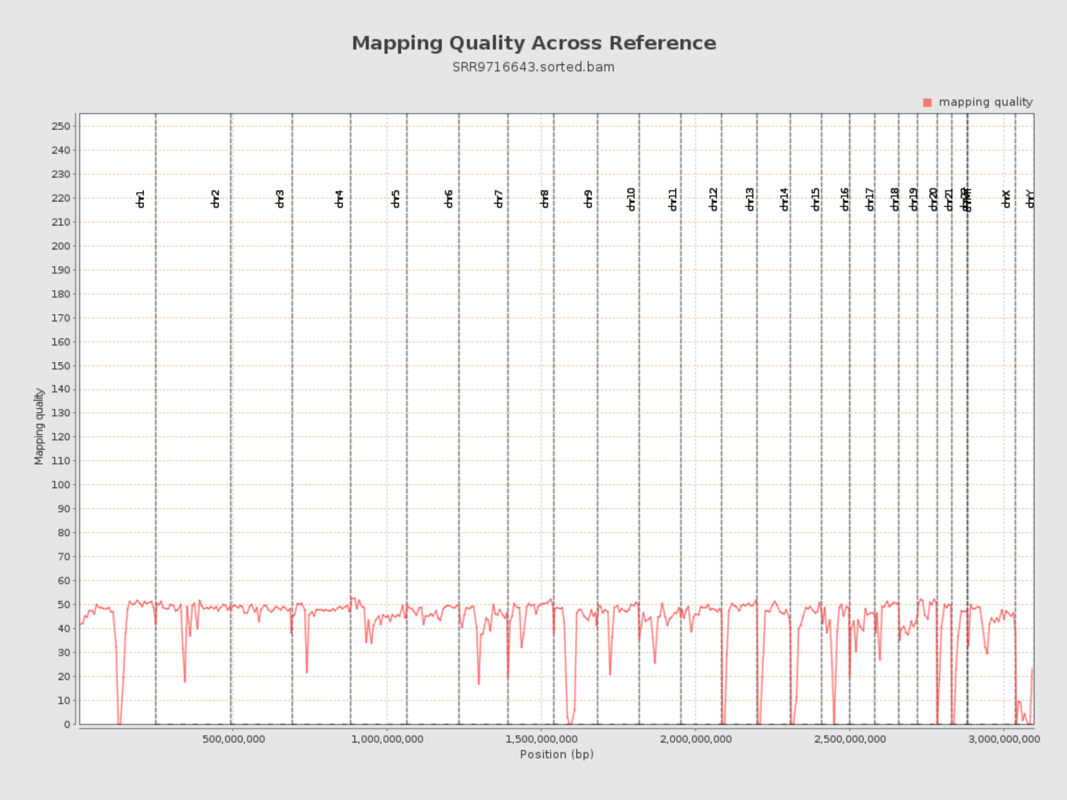
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram