Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:49:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524449.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_SRR10524449 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524449.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524449.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,324,787
Mapped reads	4,941,764 / 92.81%
Unmapped reads	383,023 / 7.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,075 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	470,637 / 8.84%
Duplication rate	6.95%
Clipped reads	4,939,469 / 92.76%

2.2. ACGT Content

Number/percentage of A's	69,678,621 / 24.06%
Number/percentage of C's	51,774,040 / 17.88%
Number/percentage of T's	94,743,677 / 32.72%
Number/percentage of G's	73,392,508 / 25.34%
Number/percentage of N's	5,766 / 0%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0936

Standard Deviation	0.7233

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

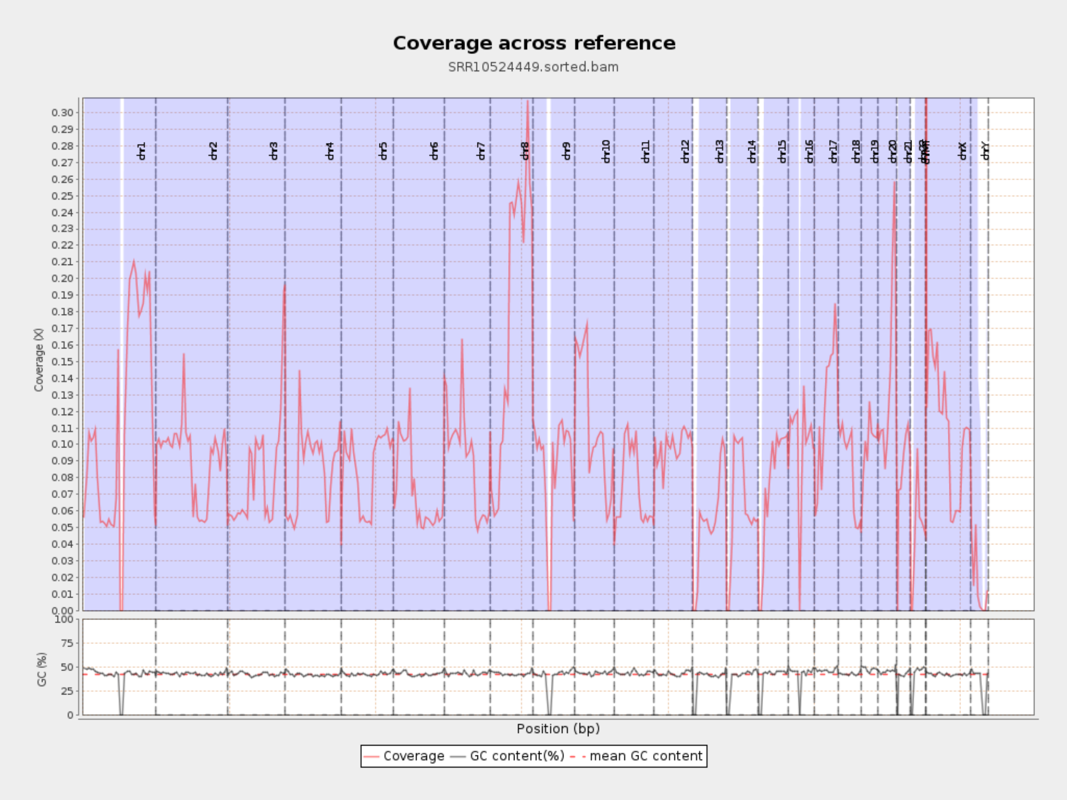
General error rate	0.47%
Mismatches	1,320,983
Insertions	18,612
Mapped reads with at least one insertion	0.37%
Deletions	51,300
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.12%

2.6. Chromosome stats

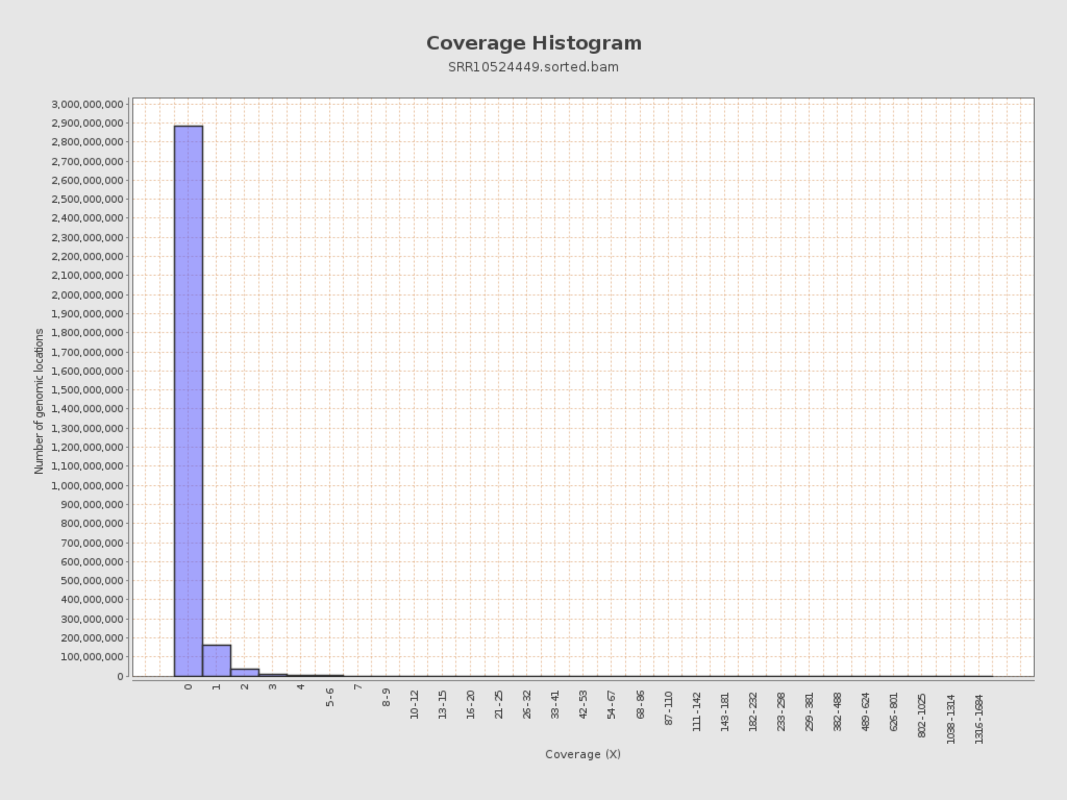
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28271809	0.1134	1.3669
chr2	243199373	22486795	0.0925	0.8271
chr3	198022430	15972311	0.0807	0.3785
chr4	191154276	16352428	0.0855	0.5085
chr5	180915260	15664939	0.0866	0.3922
chr6	171115067	12441236	0.0727	0.5472
chr7	159138663	14603189	0.0918	1.077

chr8	146364022	26699756	0.1824	0.7358
chr9	141213431	12159595	0.0861	0.6187
chr10	135534747	15185438	0.112	0.7513
chr11	135006516	9955543	0.0737	0.7111
chr12	133851895	13305916	0.0994	0.4184
chr13	115169878	6339082	0.055	0.3197
chr14	107349540	6929936	0.0646	0.3547
chr15	102531392	7555789	0.0737	0.3961
chr16	90354753	8902385	0.0985	0.4684
chr17	81195210	10030574	0.1235	0.5129
chr18	78077248	6750425	0.0865	1.1995
chr19	59128983	5915133	0.1	0.9342
chr20	63025520	9130017	0.1449	0.53
chr21	48129895	4040080	0.0839	0.4427
chr22	51304566	2332031	0.0455	0.2775
chrMT	16571	341282	20.5951	12.8717
chrX	155270560	17387082	0.112	0.5483
chrY	59373566	930444	0.0157	0.3662

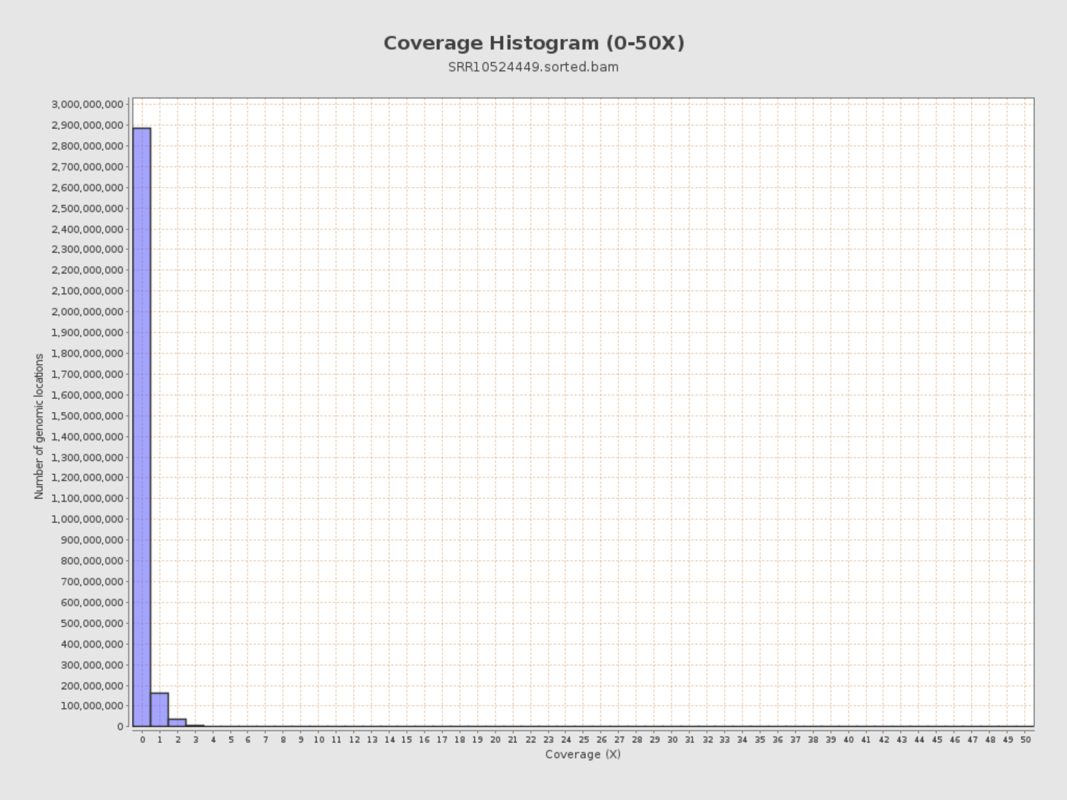
3. Results : Coverage across reference



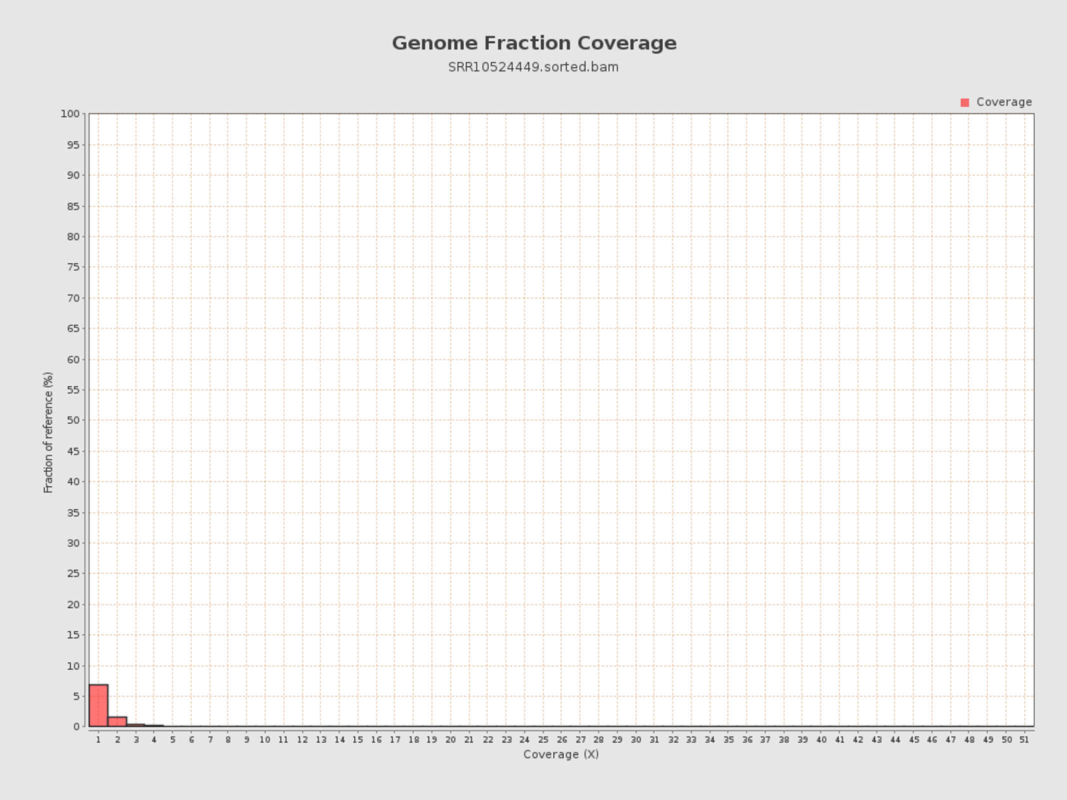
4. Results : Coverage Histogram



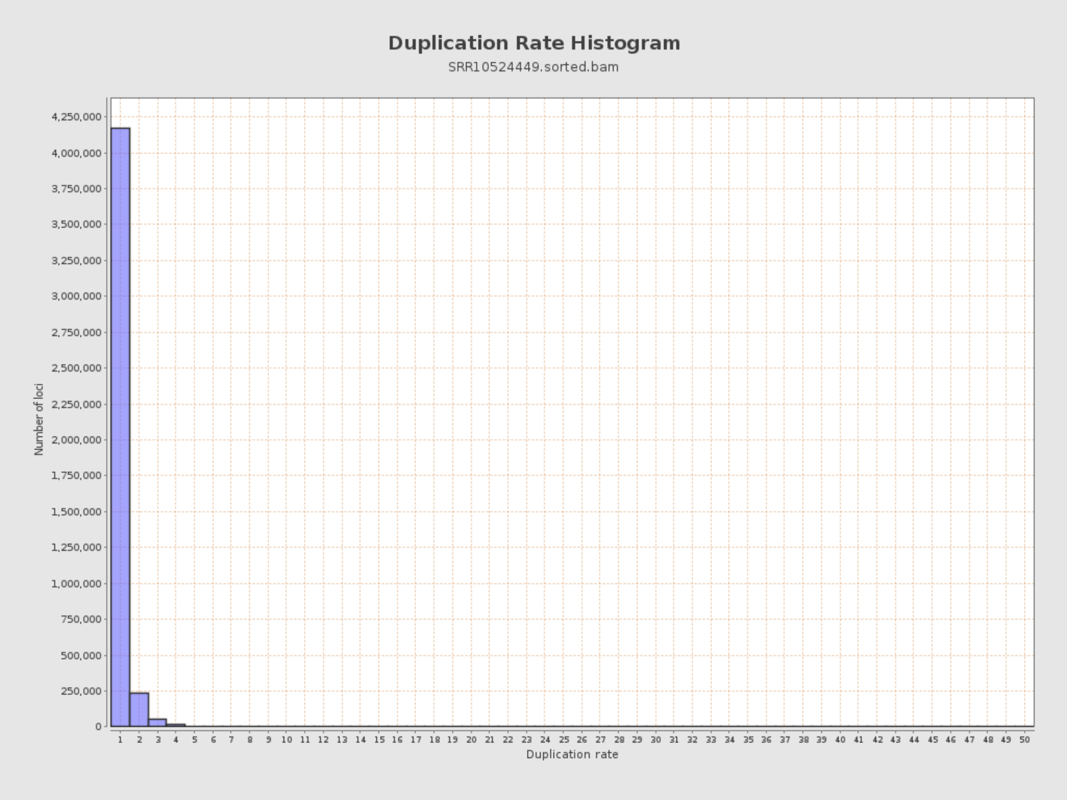
5. Results : Coverage Histogram (0-50X)



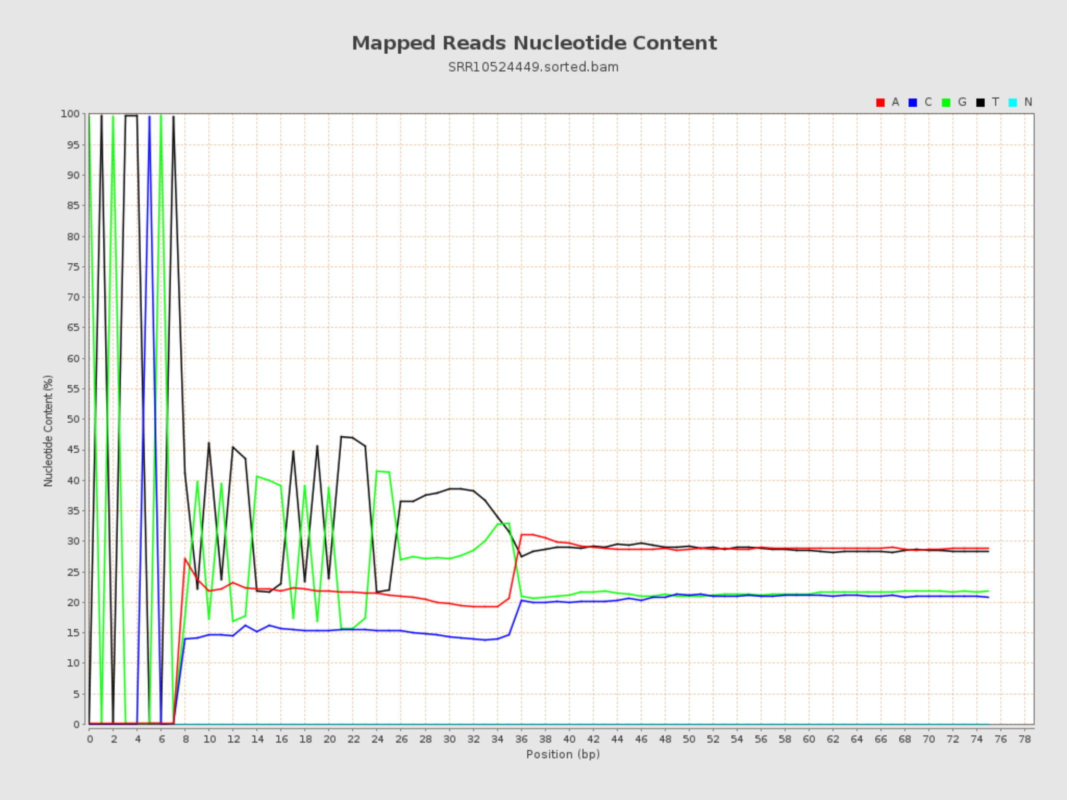
6. Results : Genome Fraction Coverage



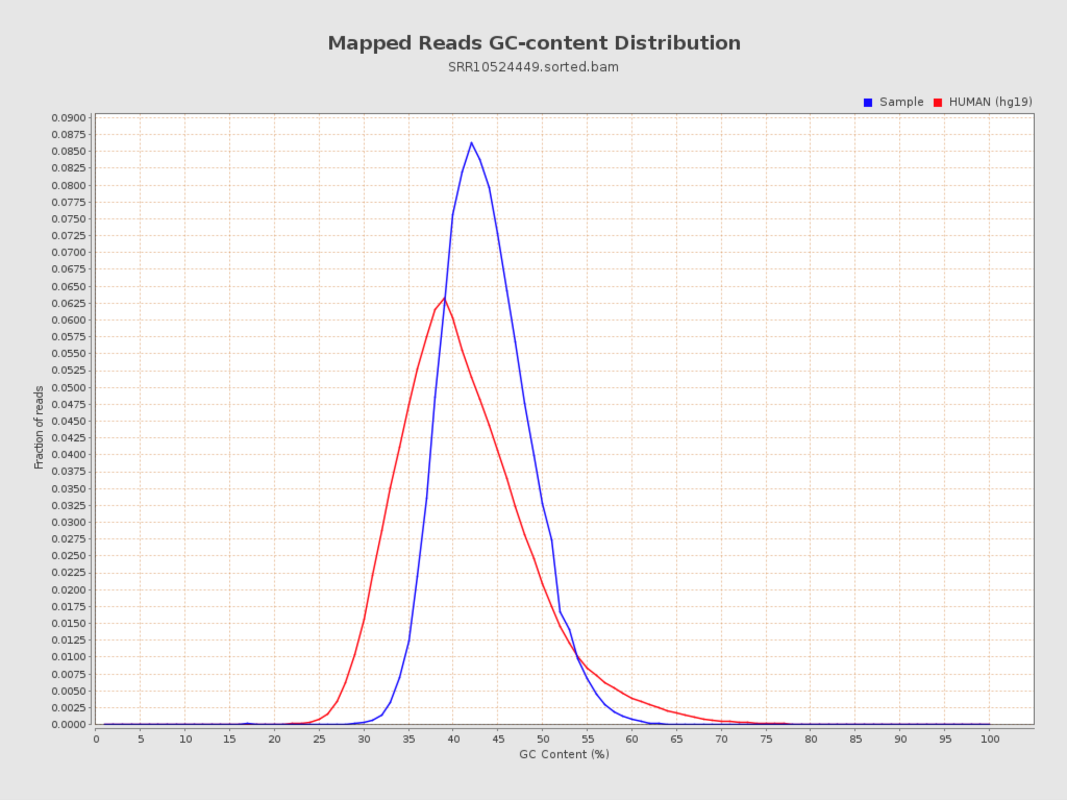
7. Results : Duplication Rate Histogram



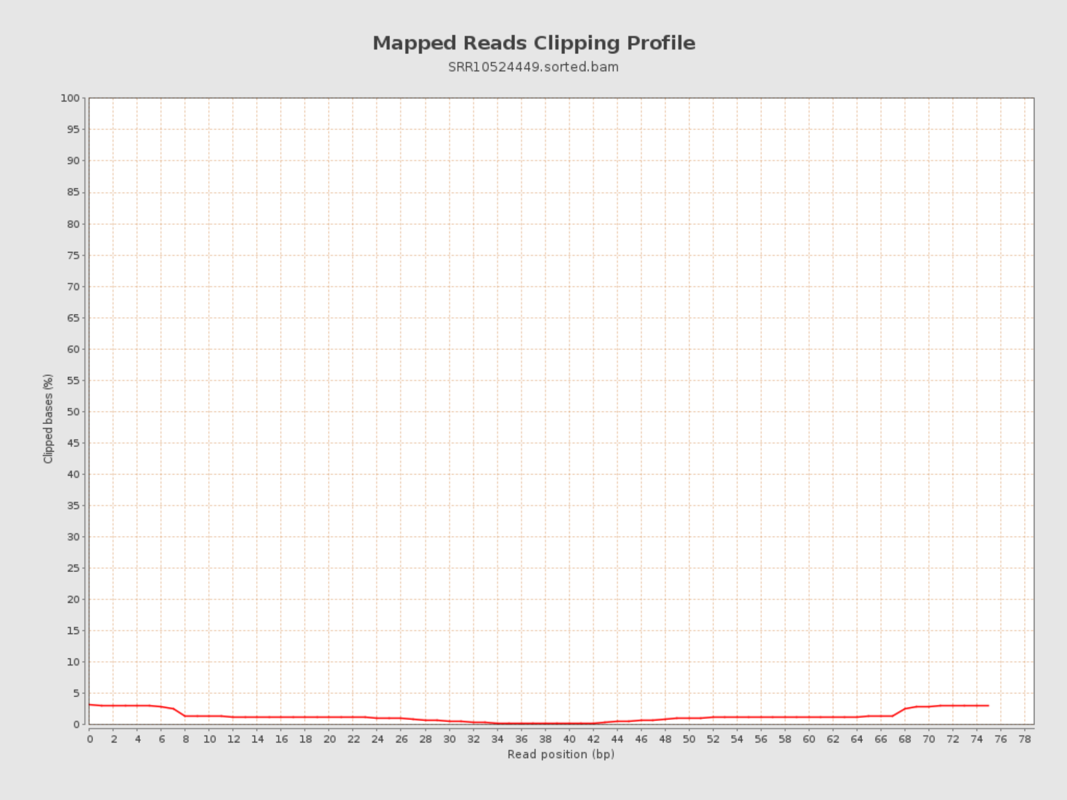
8. Results : Mapped Reads Nucleotide Content



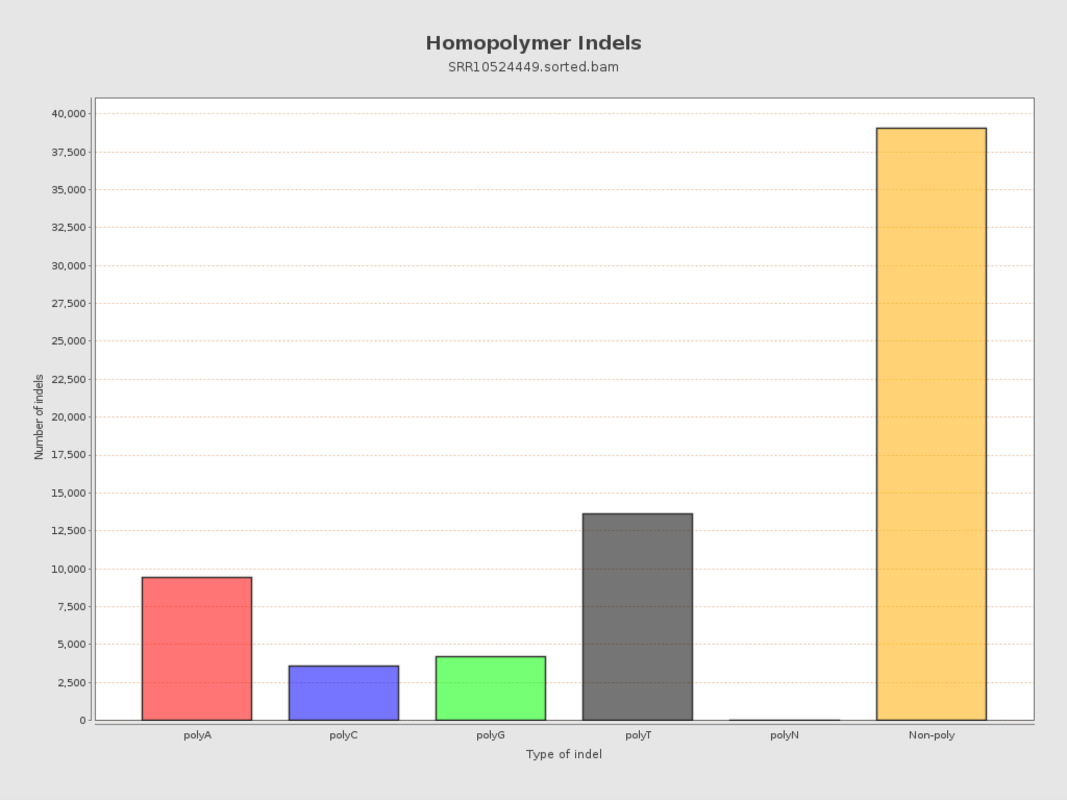
9. Results : Mapped Reads GC-content Distribution



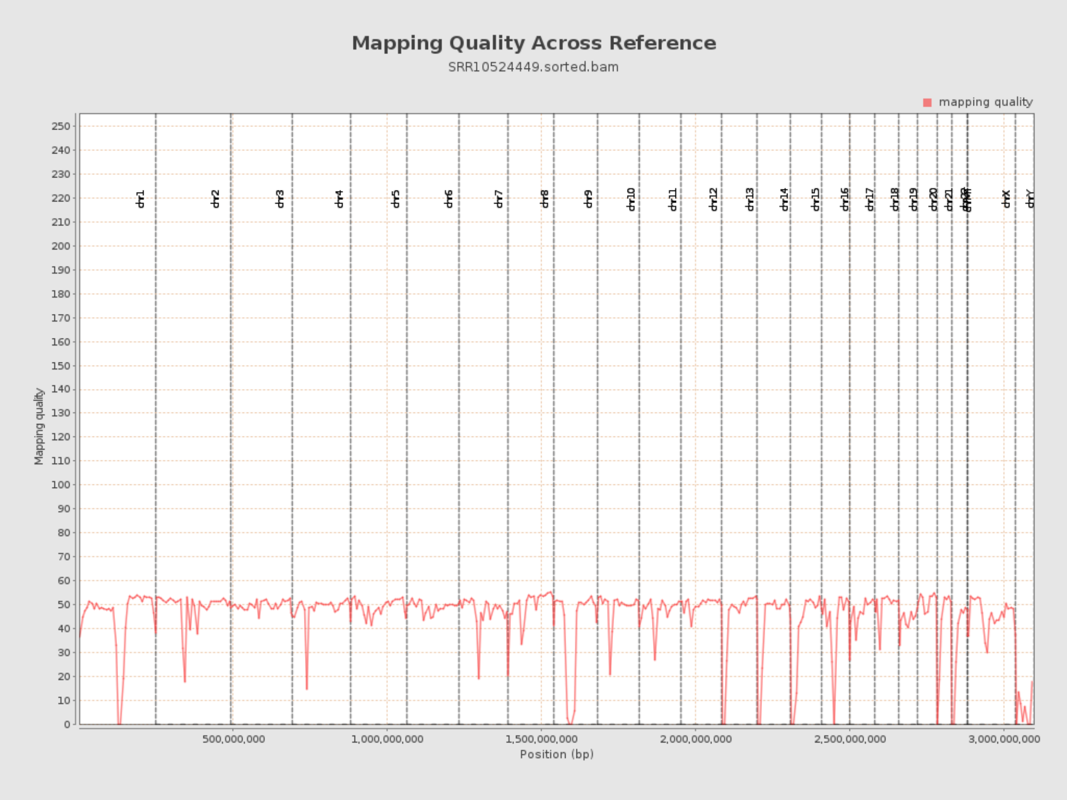
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram