Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:16:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818972.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_SRR1818972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:16:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,271,896
Mapped reads	2,241,508 / 98.66%
Unmapped reads	30,388 / 1.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,646 / 1.61%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	1,115,483 / 49.1%
Duplication rate	42.06%
Clipped reads	2,256,374 / 99.32%

2.2. ACGT Content

Number/percentage of A's	60,429,006 / 29.15%
Number/percentage of C's	43,730,029 / 21.1%
Number/percentage of T's	57,519,217 / 27.75%
Number/percentage of G's	45,585,253 / 21.99%
Number/percentage of N's	9,982 / 0%
GC Percentage	43.09%

2.3. Coverage

Mean	0.067

Standard Deviation	0.7804

2.4. Mapping Quality

Mean Mapping Quality	49.1

2.5. Mismatches and indels

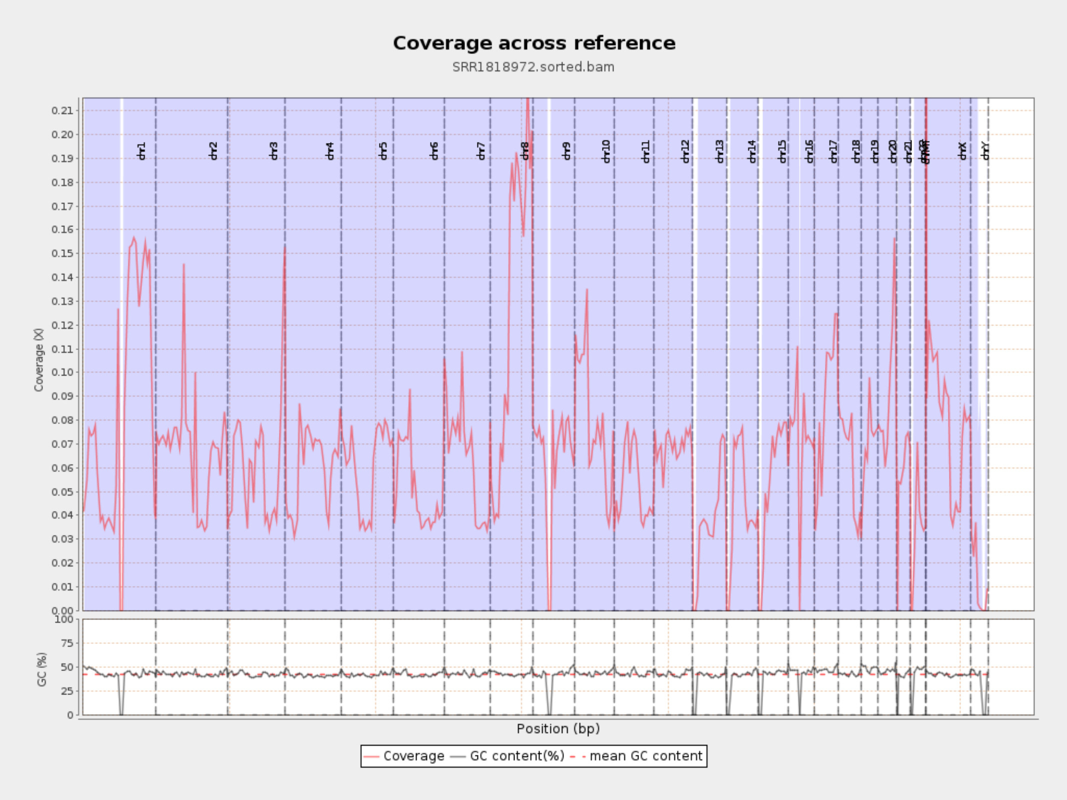
General error rate	0.66%
Mismatches	1,285,500
Insertions	35,920
Mapped reads with at least one insertion	1.56%
Deletions	67,667
Mapped reads with at least one deletion	2.95%
Homopolymer indels	39.72%

2.6. Chromosome stats

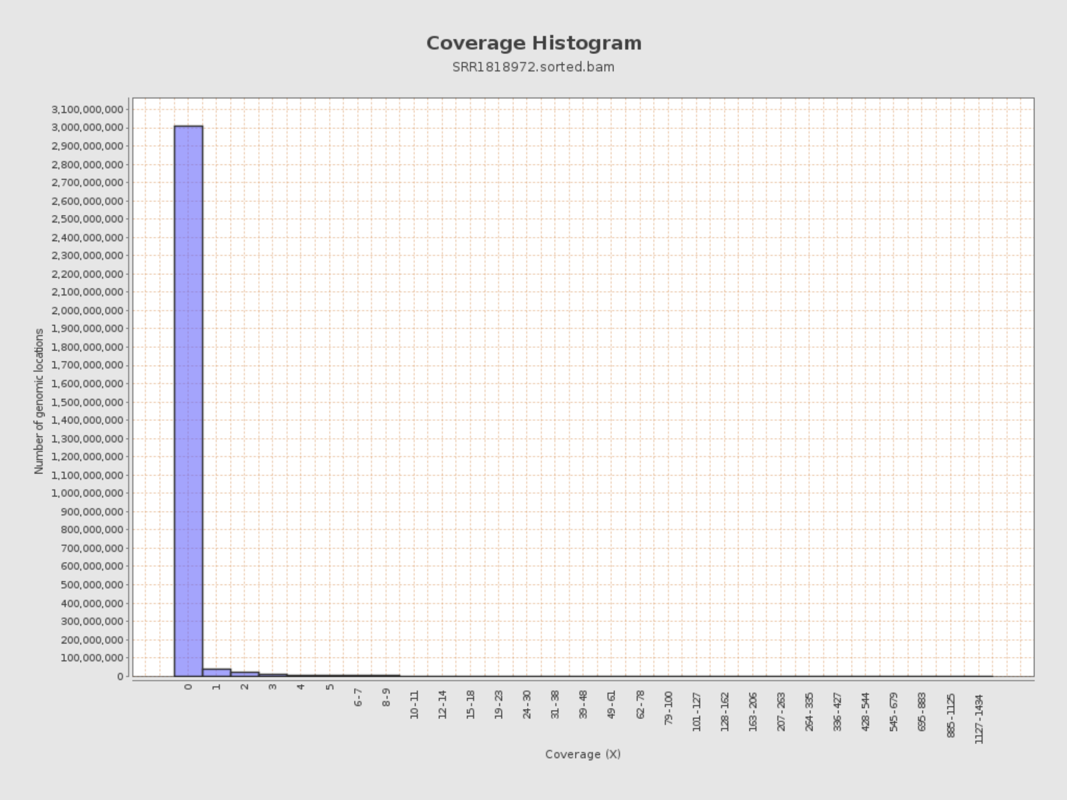
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21040501	0.0844	1.3573
chr2	243199373	16607244	0.0683	1.104
chr3	198022430	12103639	0.0611	0.4851
chr4	191154276	11565289	0.0605	0.5434
chr5	180915260	11030565	0.061	0.5006
chr6	171115067	8696295	0.0508	0.5259
chr7	159138663	10111002	0.0635	0.8971

chr8	146364022	19254627	0.1316	0.8008
chr9	141213431	8979442	0.0636	0.723
chr10	135534747	10763564	0.0794	0.9101
chr11	135006516	7061524	0.0523	0.5244
chr12	133851895	9308670	0.0695	0.5338
chr13	115169878	4382239	0.0381	0.3801
chr14	107349540	4803208	0.0447	0.4407
chr15	102531392	5485626	0.0535	0.4681
chr16	90354753	6389087	0.0707	0.9035
chr17	81195210	7068773	0.0871	0.6518
chr18	78077248	4934754	0.0632	0.8373
chr19	59128983	4167651	0.0705	1.2276
chr20	63025520	5947776	0.0944	0.6553
chr21	48129895	2784720	0.0579	0.5121
chr22	51304566	1656919	0.0323	0.3906
chrMT	16571	22561	1.3615	2.0245
chrX	155270560	12502289	0.0805	0.6167
chrY	59373566	731529	0.0123	0.7207

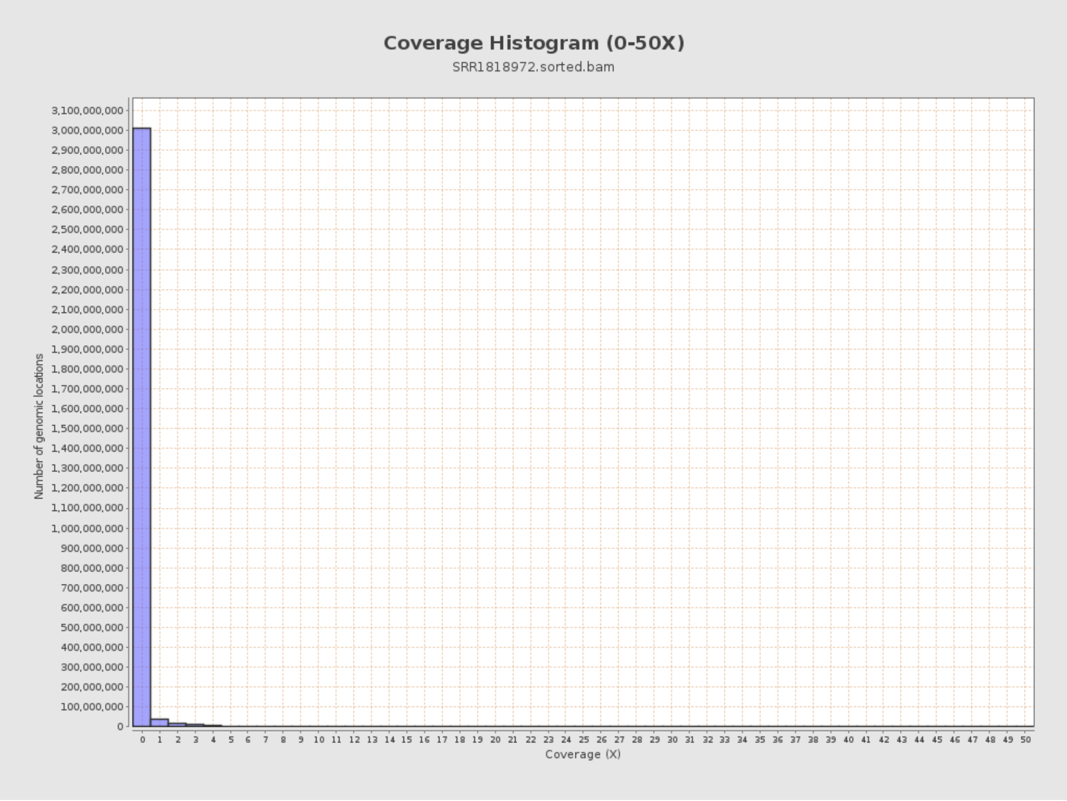
3. Results : Coverage across reference



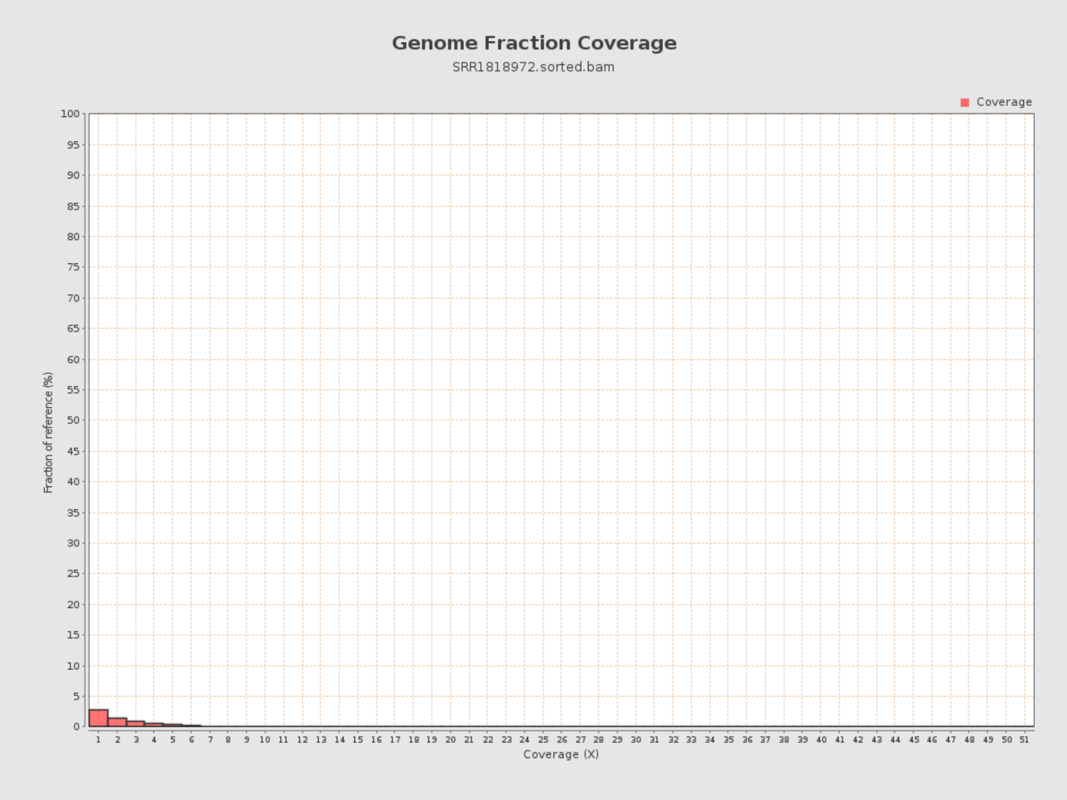
4. Results : Coverage Histogram



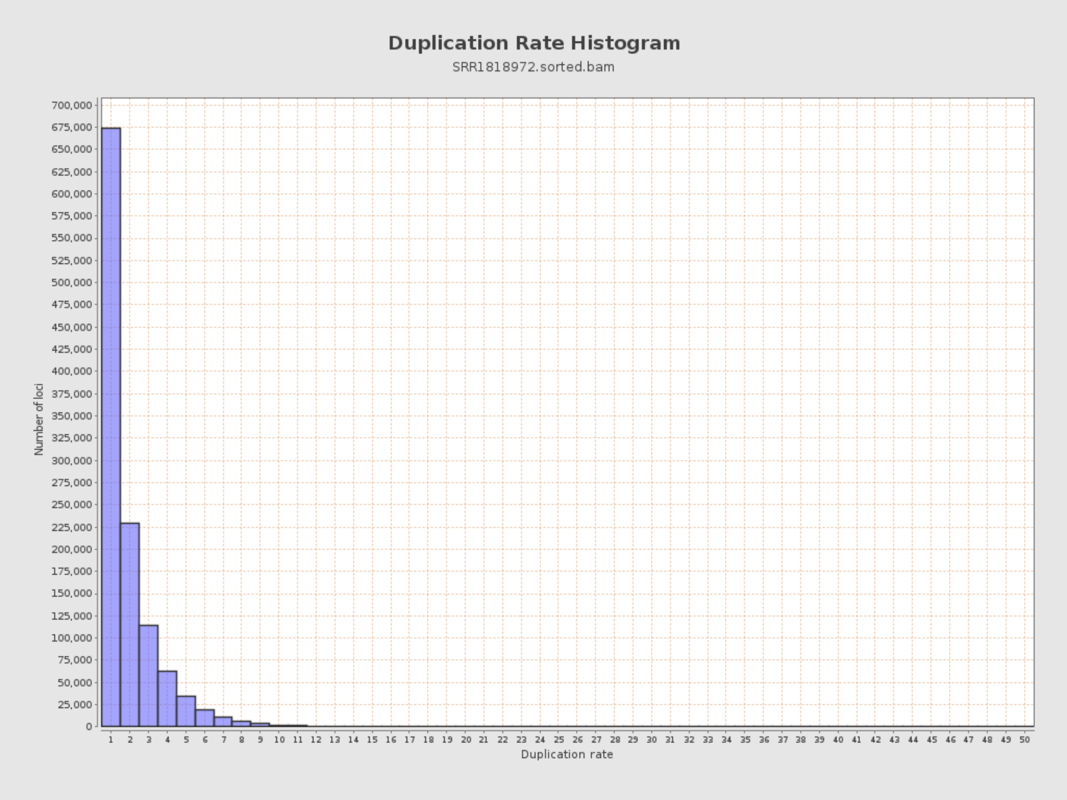
5. Results : Coverage Histogram (0-50X)



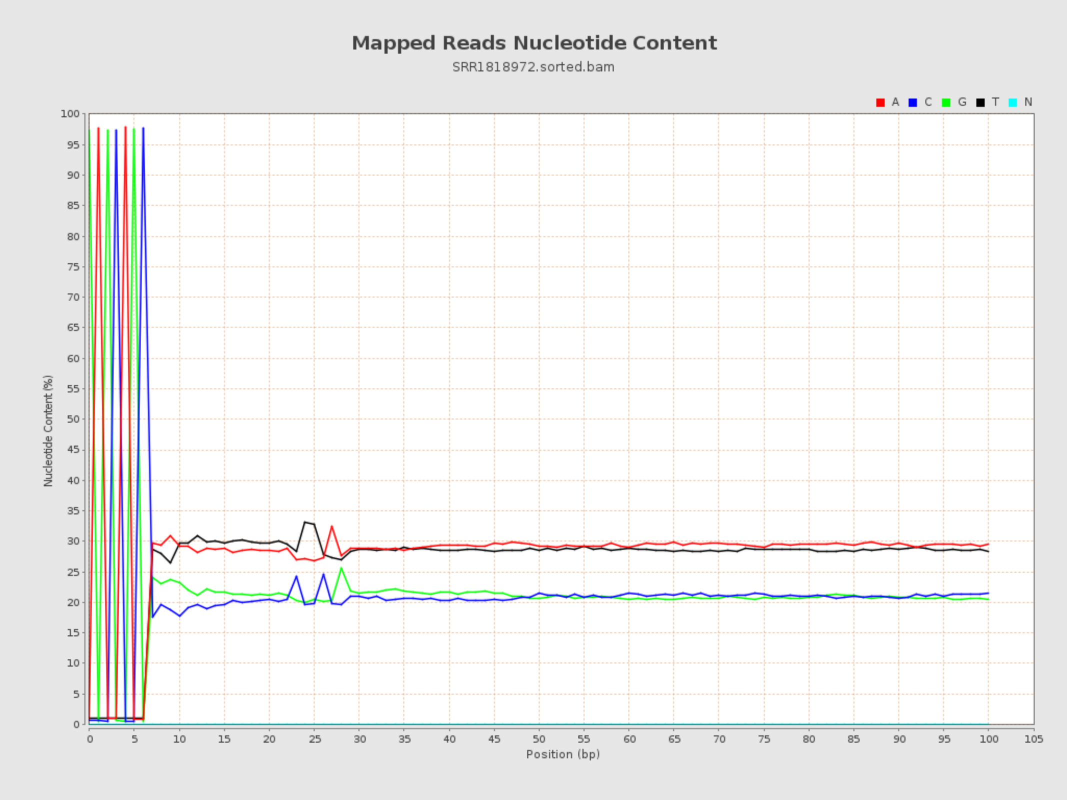
6. Results : Genome Fraction Coverage



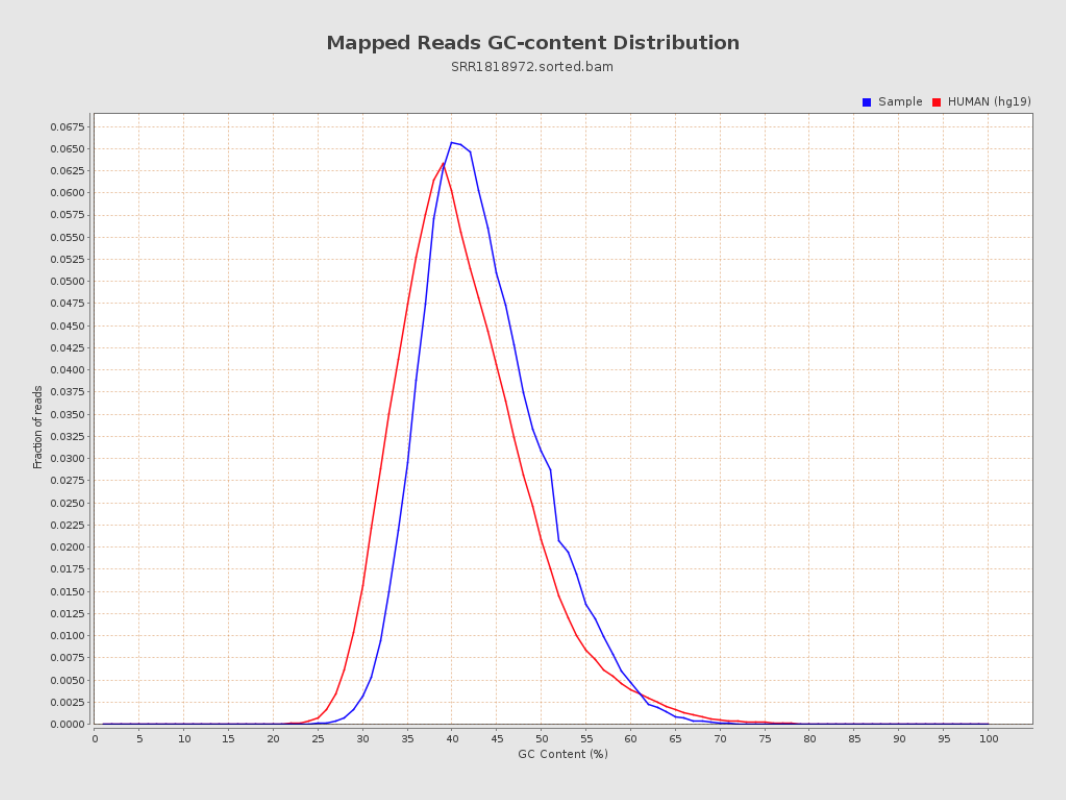
7. Results : Duplication Rate Histogram



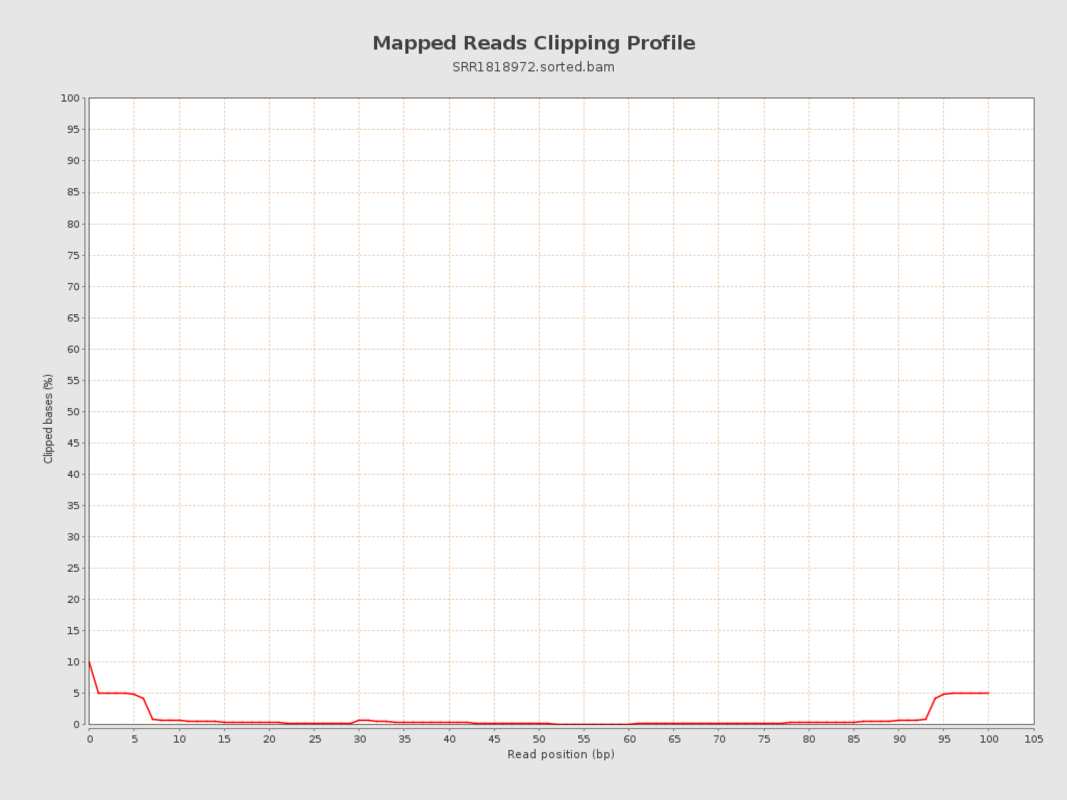
8. Results : Mapped Reads Nucleotide Content



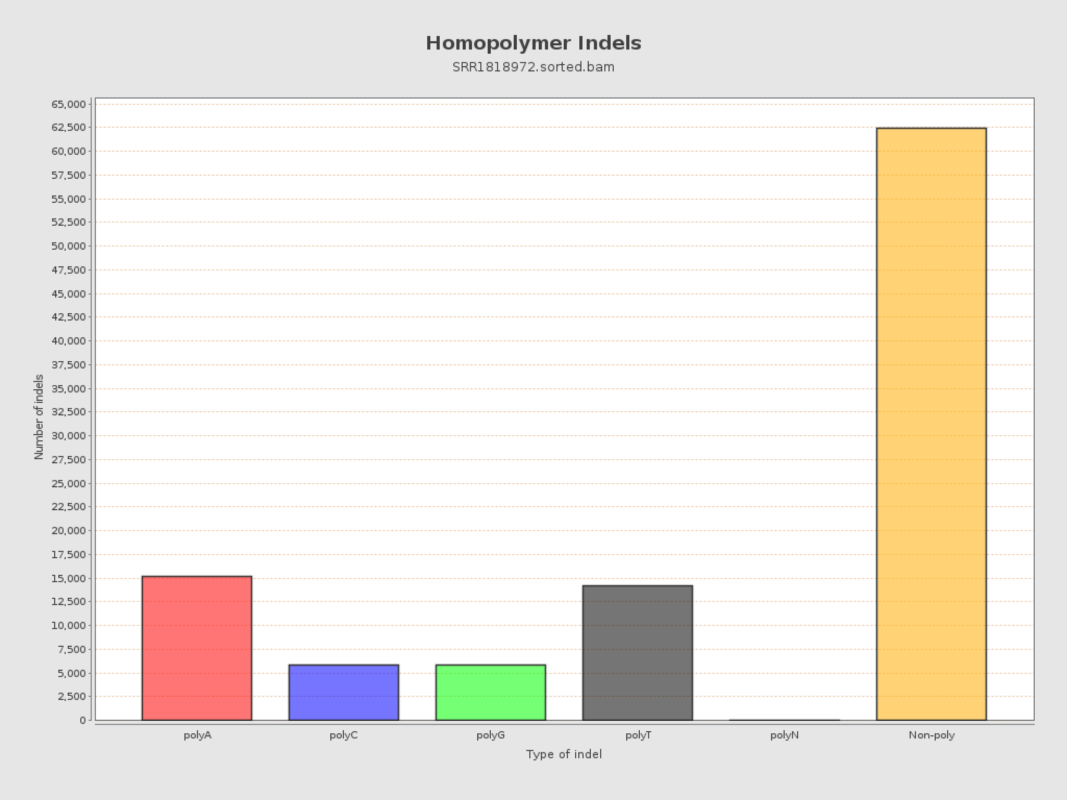
9. Results : Mapped Reads GC-content Distribution



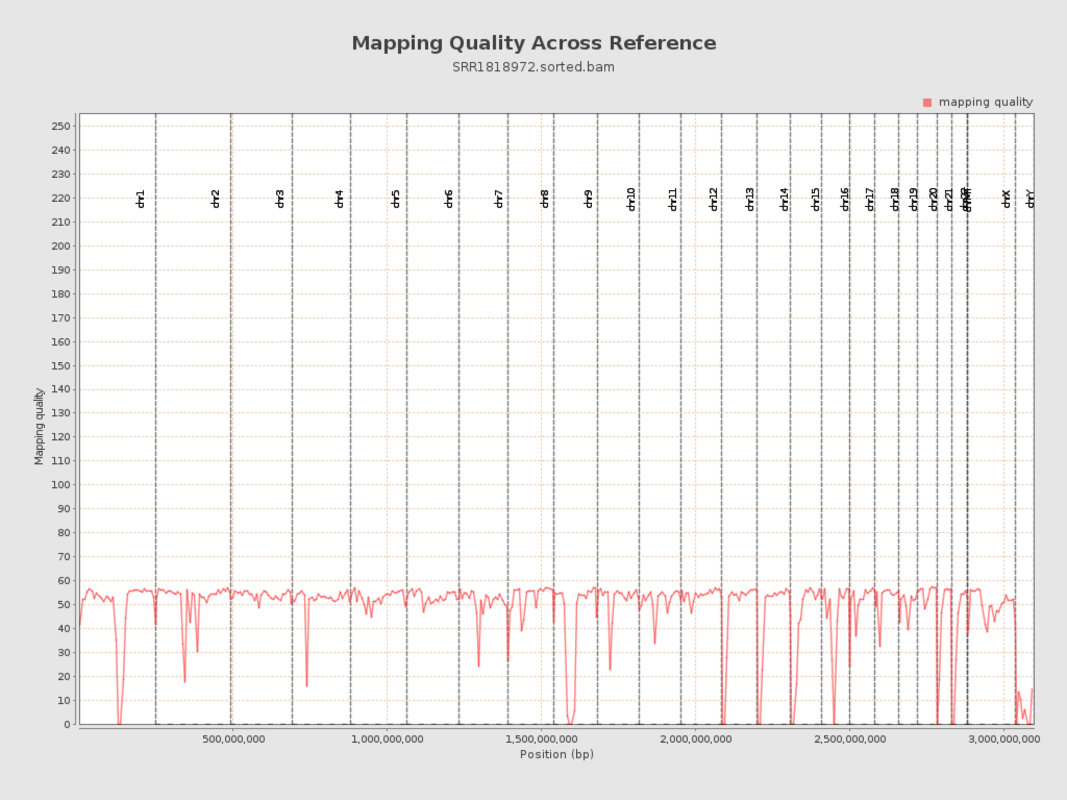
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram