Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:45:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819044.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_SRR1819044 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819044.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:45:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819044.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,736,185
Mapped reads	1,551,611 / 89.37%
Unmapped reads	184,574 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,274 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	38,675 / 2.23%
Duplication rate	1.85%
Clipped reads	1,557,021 / 89.68%

2.2. ACGT Content

Number/percentage of A's	21,969,603 / 24.72%
Number/percentage of C's	17,246,129 / 19.41%
Number/percentage of T's	26,335,862 / 29.64%
Number/percentage of G's	23,307,807 / 26.23%
Number/percentage of N's	1,823 / 0%
GC Percentage	45.64%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2286

2.4. Mapping Quality

Mean Mapping Quality	43.95

2.5. Mismatches and indels

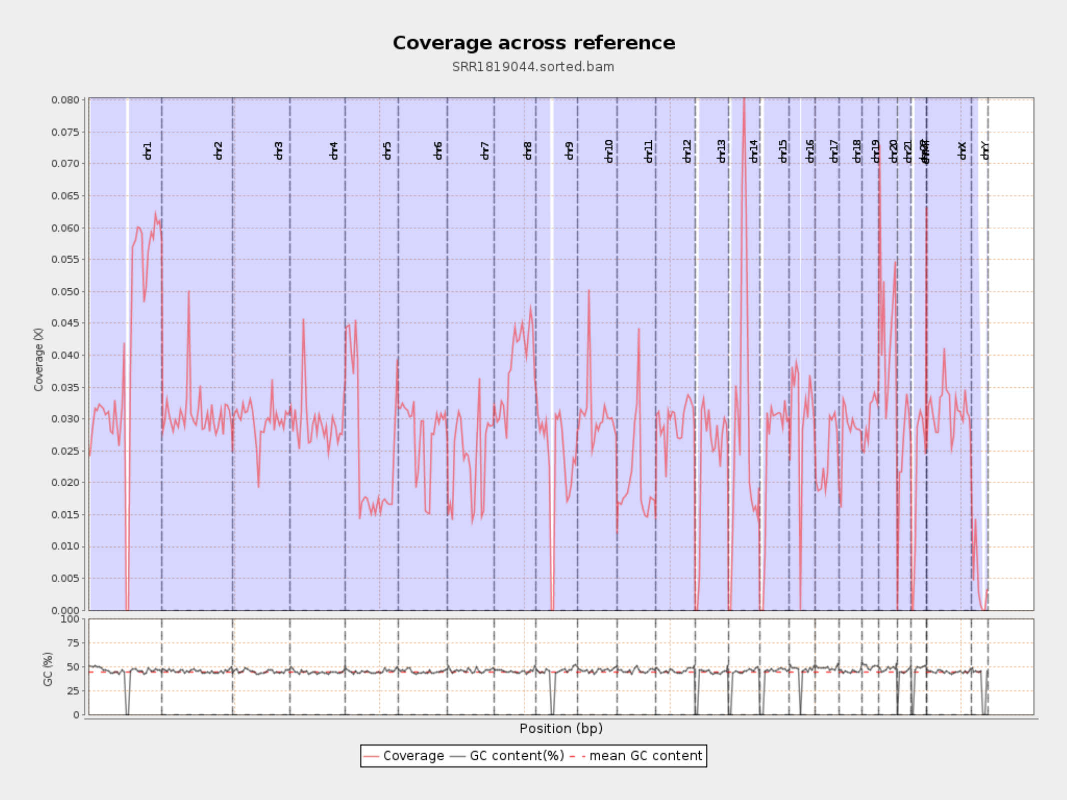
General error rate	0.52%
Mismatches	452,594
Insertions	4,856
Mapped reads with at least one insertion	0.31%
Deletions	14,068
Mapped reads with at least one deletion	0.9%
Homopolymer indels	43.82%

2.6. Chromosome stats

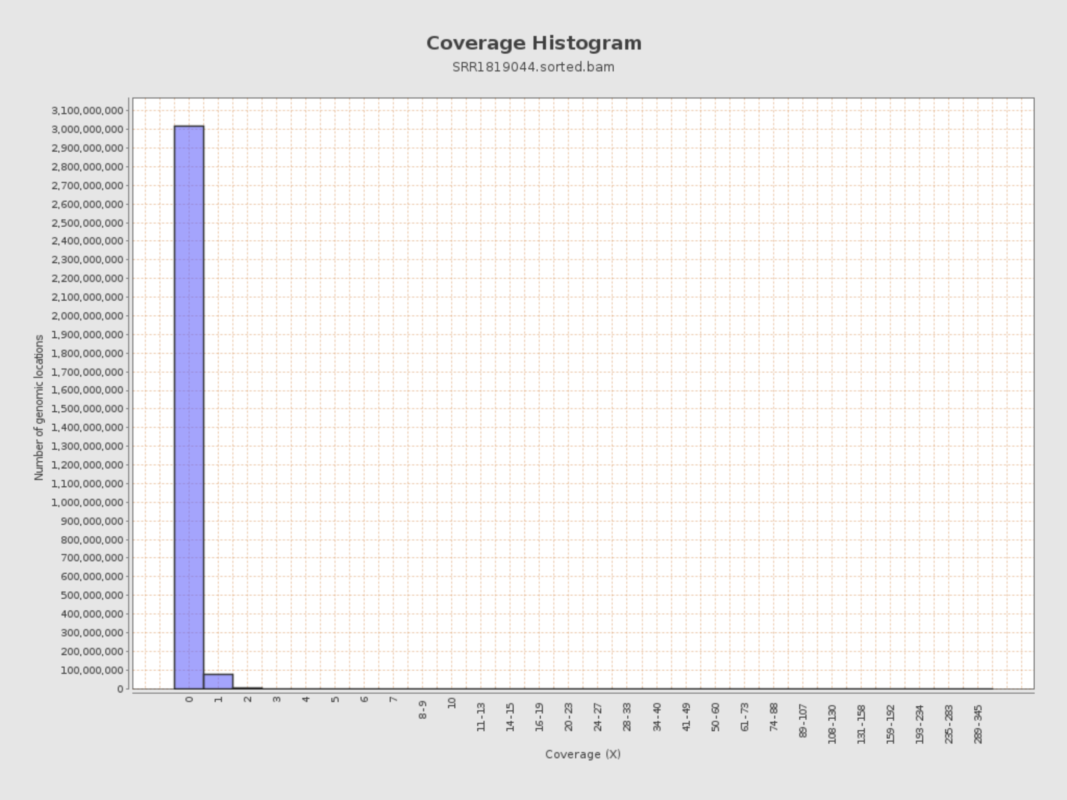
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9998890	0.0401	0.3319
chr2	243199373	7497845	0.0308	0.2599
chr3	198022430	5891549	0.0298	0.1874
chr4	191154276	5614743	0.0294	0.2006
chr5	180915260	4438577	0.0245	0.1717
chr6	171115067	4708026	0.0275	0.1901
chr7	159138663	3767188	0.0237	0.2037

chr8	146364022	5604202	0.0383	0.2393
chr9	141213431	3247990	0.023	0.2278
chr10	135534747	4153418	0.0306	0.2604
chr11	135006516	2759765	0.0204	0.1956
chr12	133851895	3984255	0.0298	0.1893
chr13	115169878	2728056	0.0237	0.1659
chr14	107349540	3098616	0.0289	0.1951
chr15	102531392	2513381	0.0245	0.1688
chr16	90354753	2768446	0.0306	0.2067
chr17	81195210	1950897	0.024	0.1719
chr18	78077248	2175529	0.0279	0.4449
chr19	59128983	1780929	0.0301	0.263
chr20	63025520	2846938	0.0452	0.2359
chr21	48129895	1181433	0.0245	0.1899
chr22	51304566	1029671	0.0201	0.1533
chrMT	16571	1047	0.0632	0.2475
chrX	155270560	4884857	0.0315	0.2126
chrY	59373566	259119	0.0044	0.1049

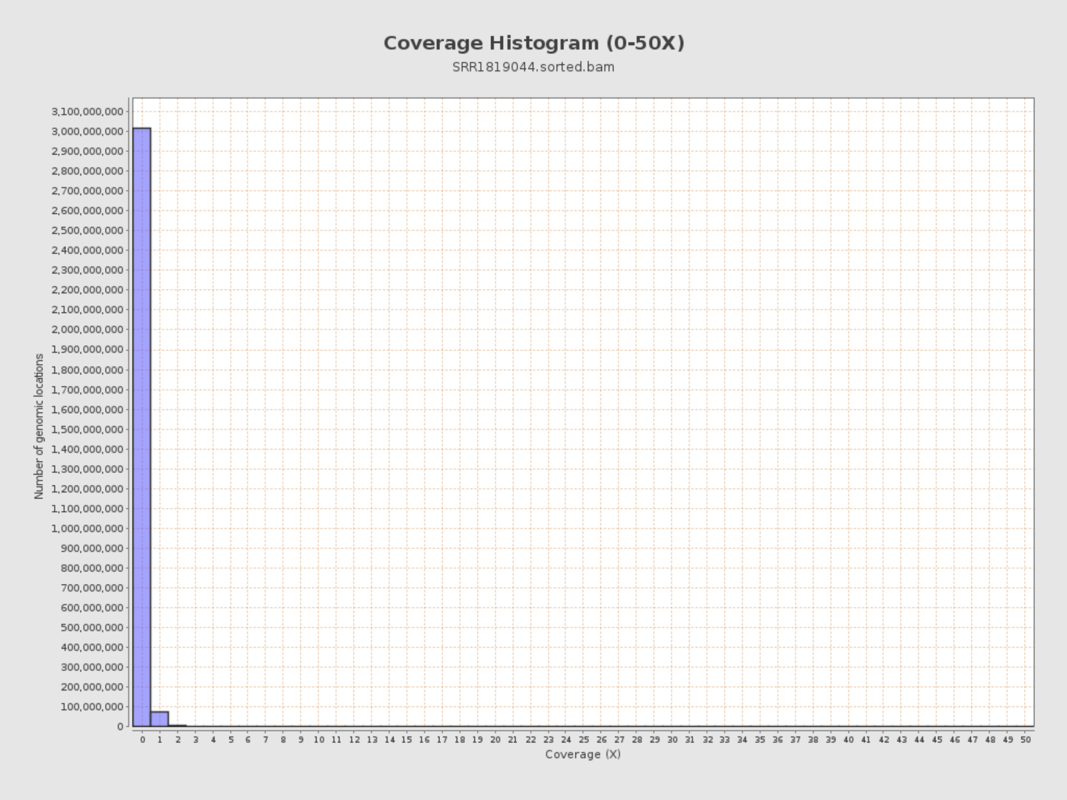
3. Results : Coverage across reference



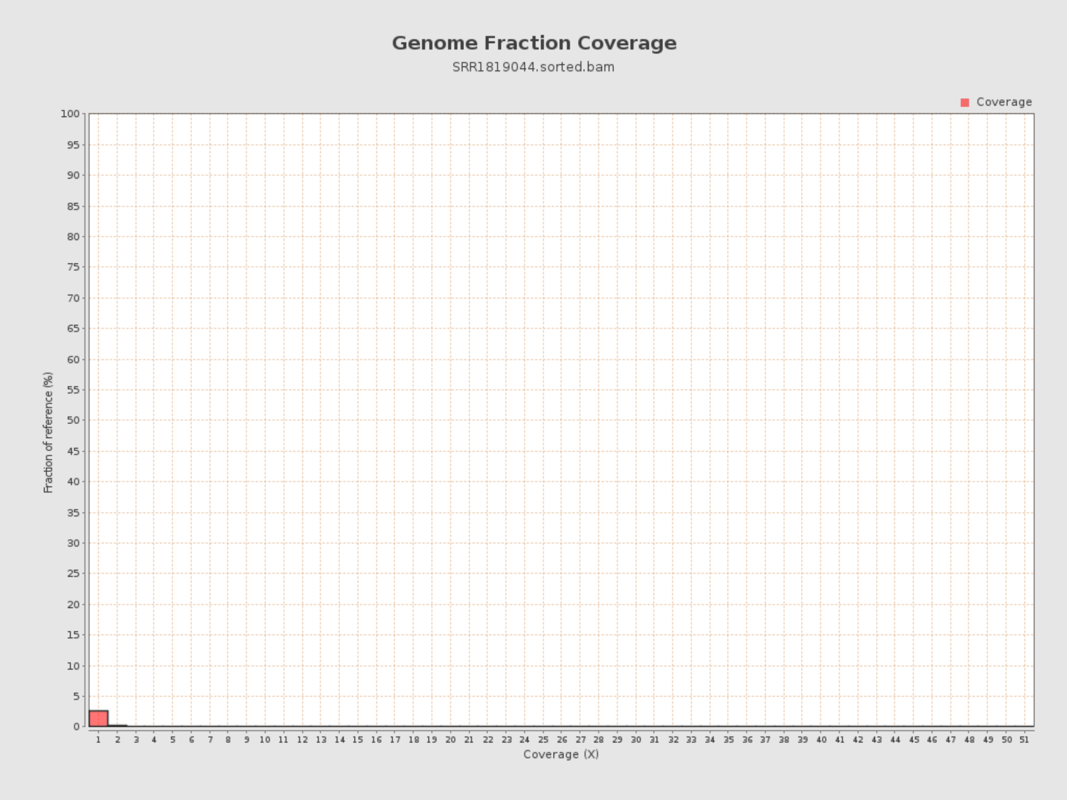
4. Results : Coverage Histogram



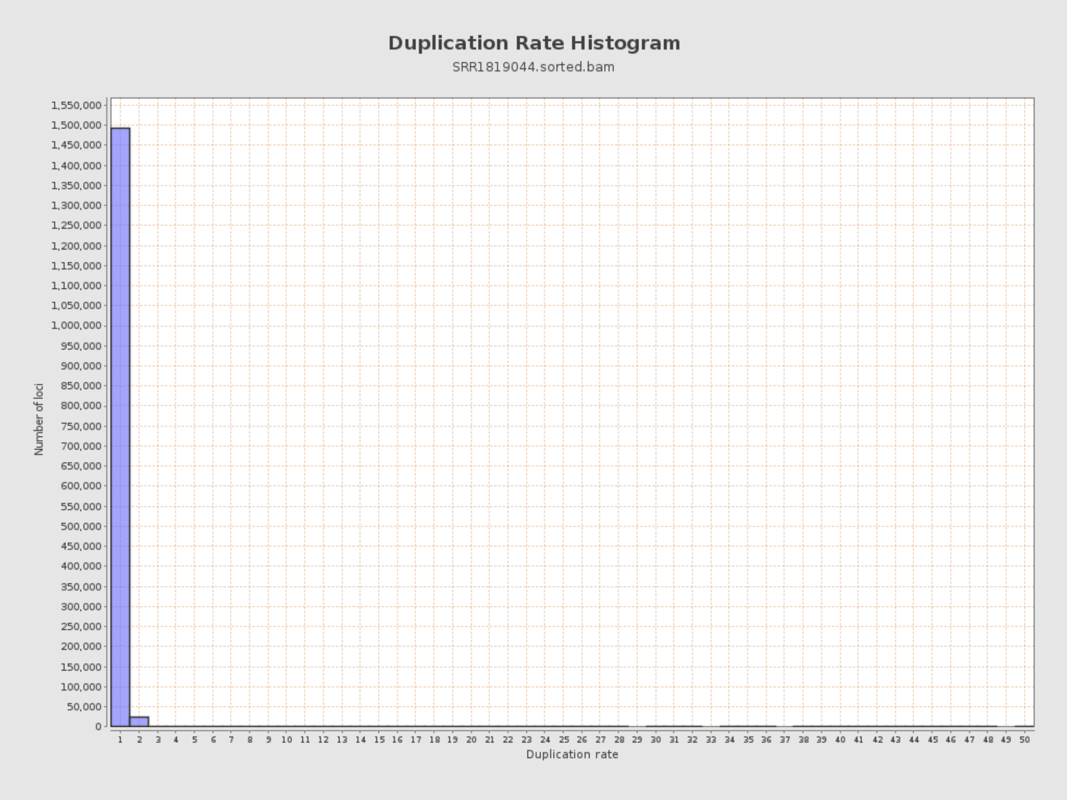
5. Results : Coverage Histogram (0-50X)



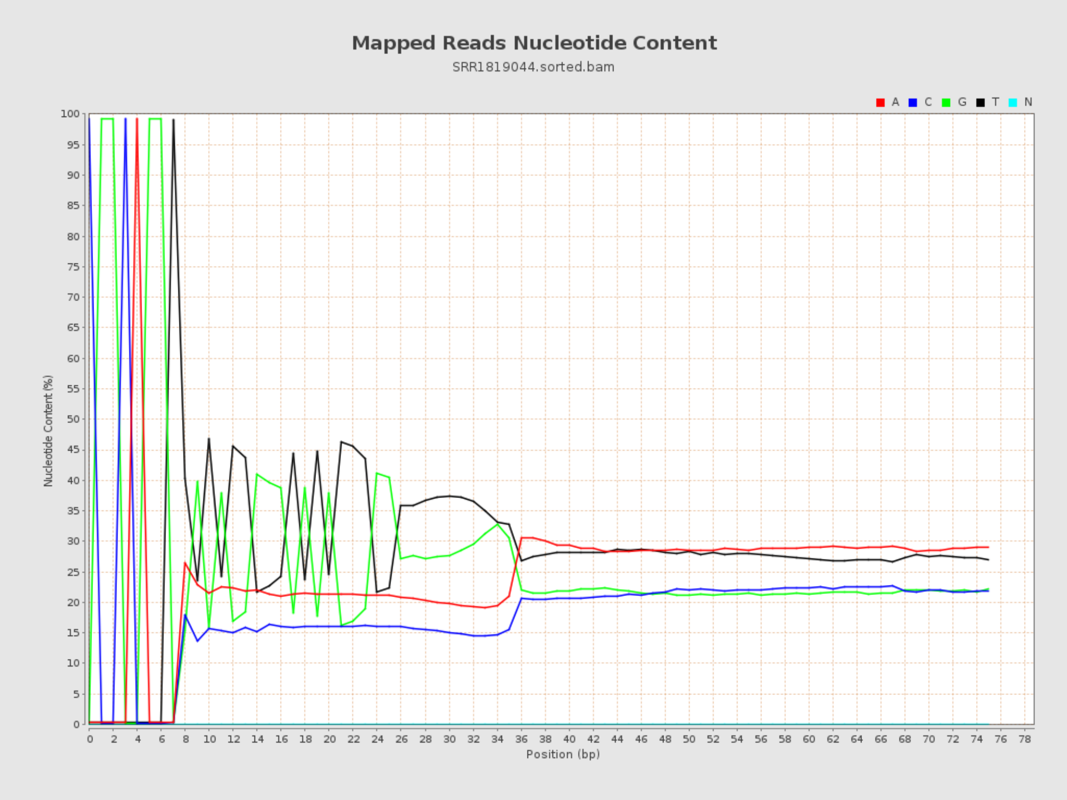
6. Results : Genome Fraction Coverage



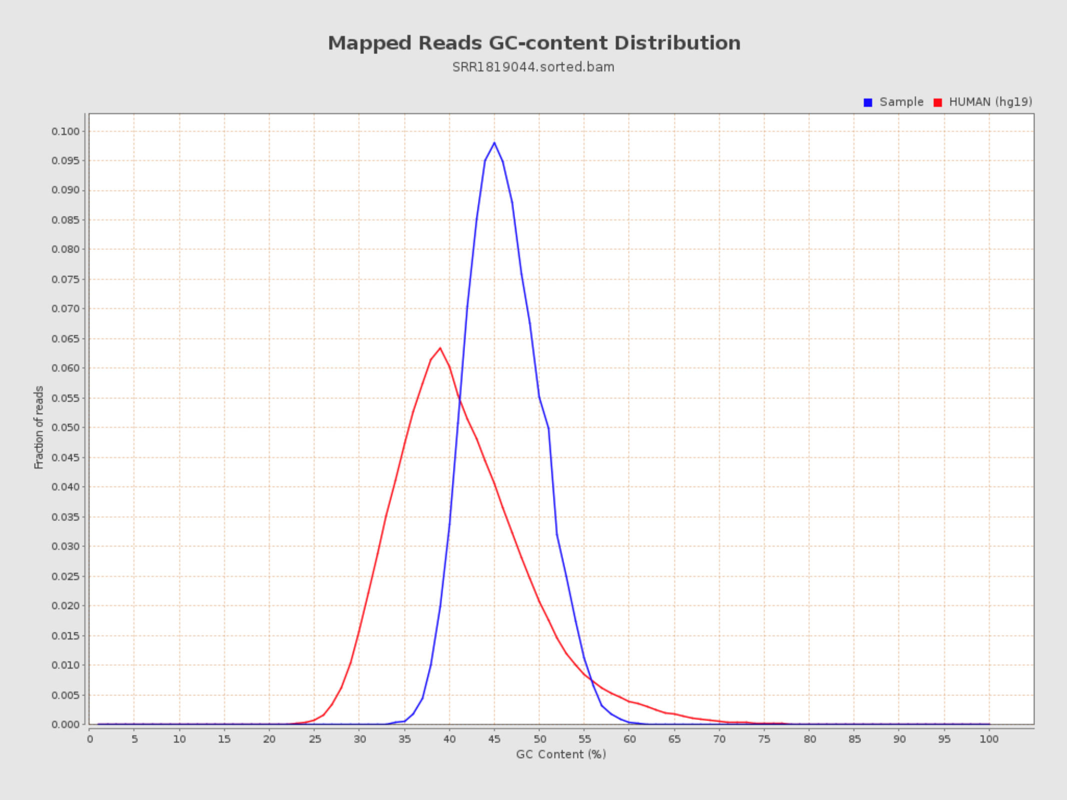
7. Results : Duplication Rate Histogram



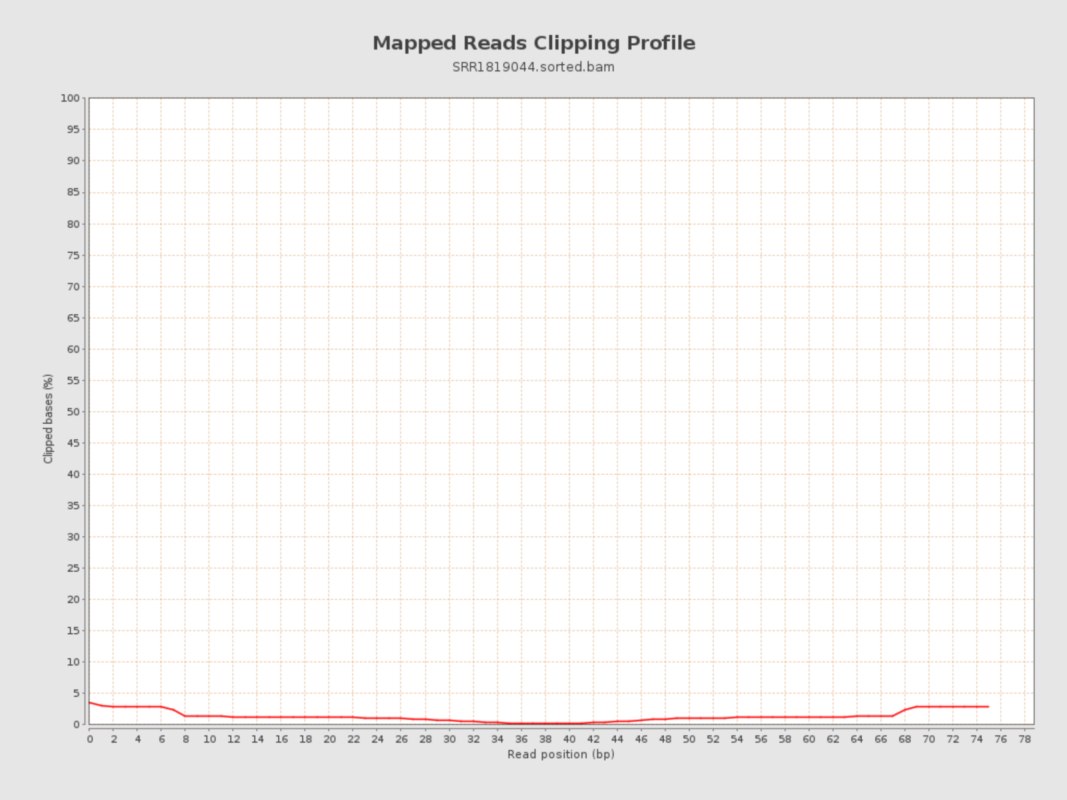
8. Results : Mapped Reads Nucleotide Content



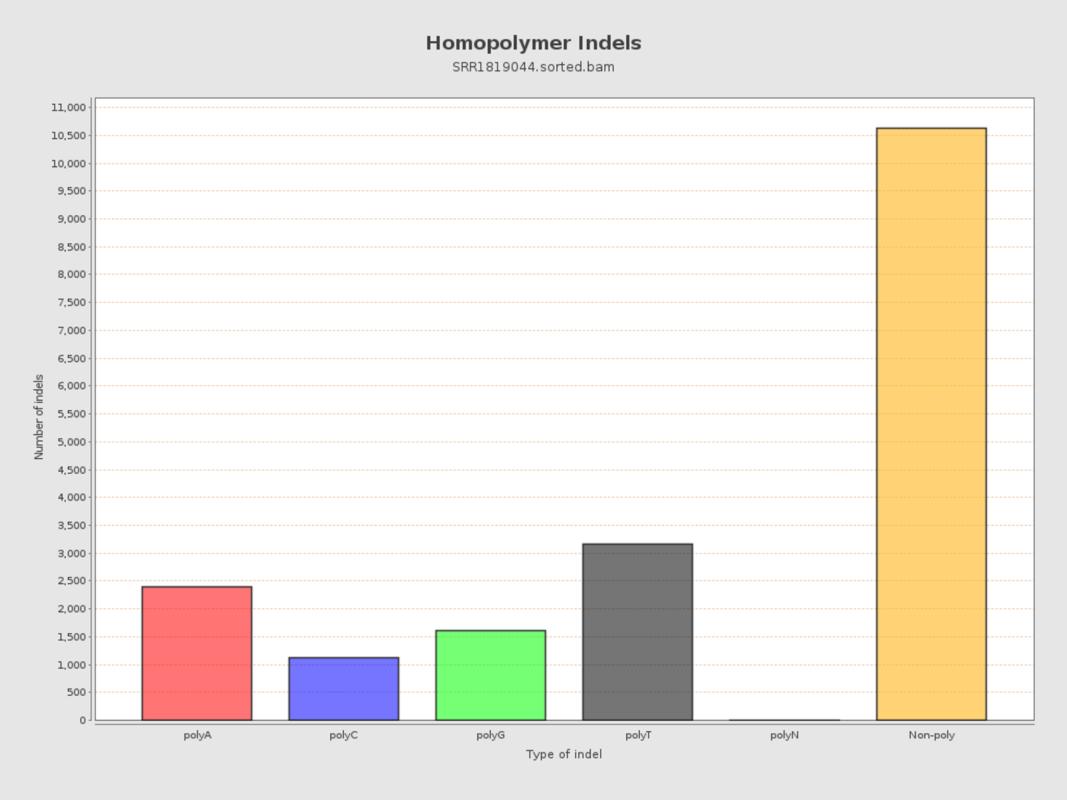
9. Results : Mapped Reads GC-content Distribution



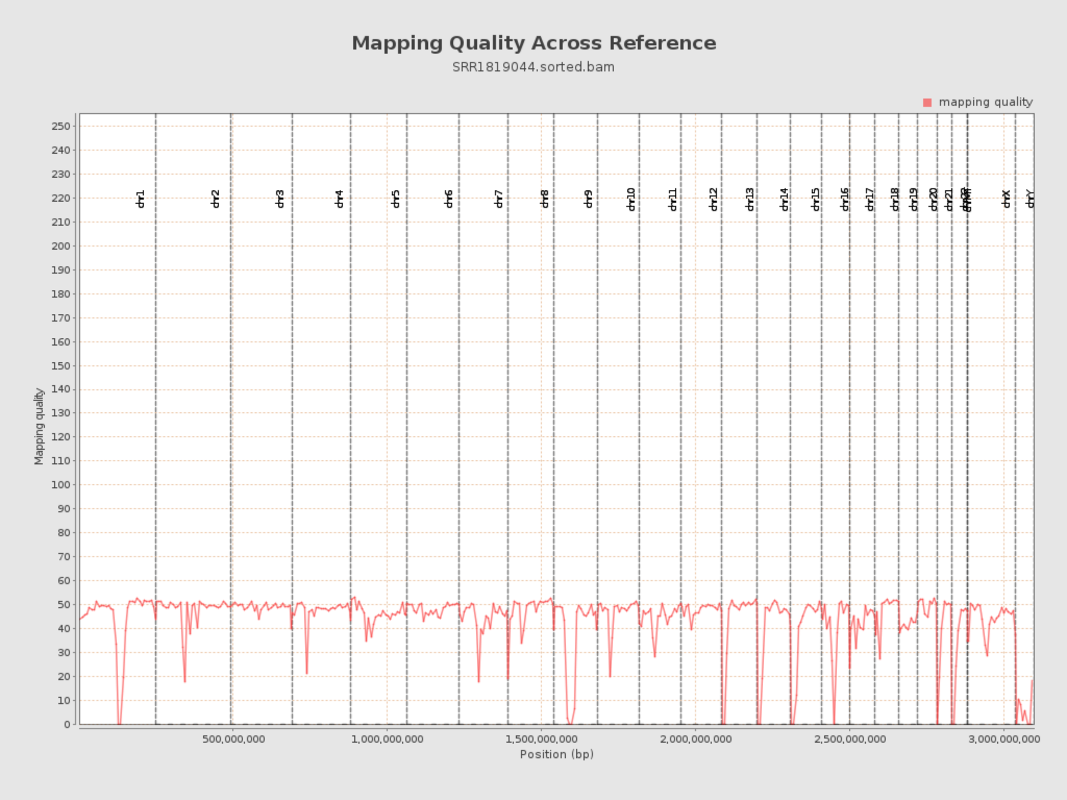
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram