Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:03:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819051.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_SRR1819051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:03:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	926,268
Mapped reads	824,180 / 88.98%
Unmapped reads	102,088 / 11.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,526 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	16,506 / 1.78%
Duplication rate	1.53%
Clipped reads	825,707 / 89.14%

2.2. ACGT Content

Number/percentage of A's	11,732,811 / 25.11%
Number/percentage of C's	8,901,105 / 19.05%
Number/percentage of T's	14,790,712 / 31.66%
Number/percentage of G's	11,296,196 / 24.18%
Number/percentage of N's	1,025 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1485

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

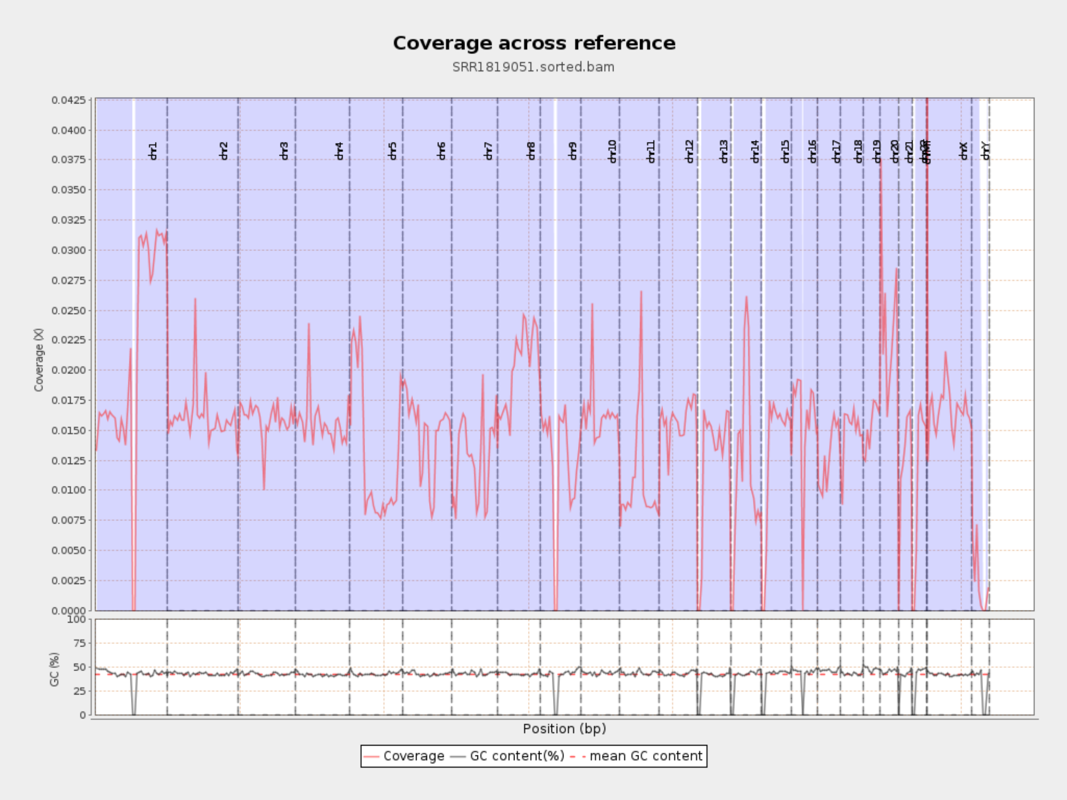
General error rate	0.5%
Mismatches	228,621
Insertions	3,323
Mapped reads with at least one insertion	0.4%
Deletions	7,159
Mapped reads with at least one deletion	0.86%
Homopolymer indels	40.71%

2.6. Chromosome stats

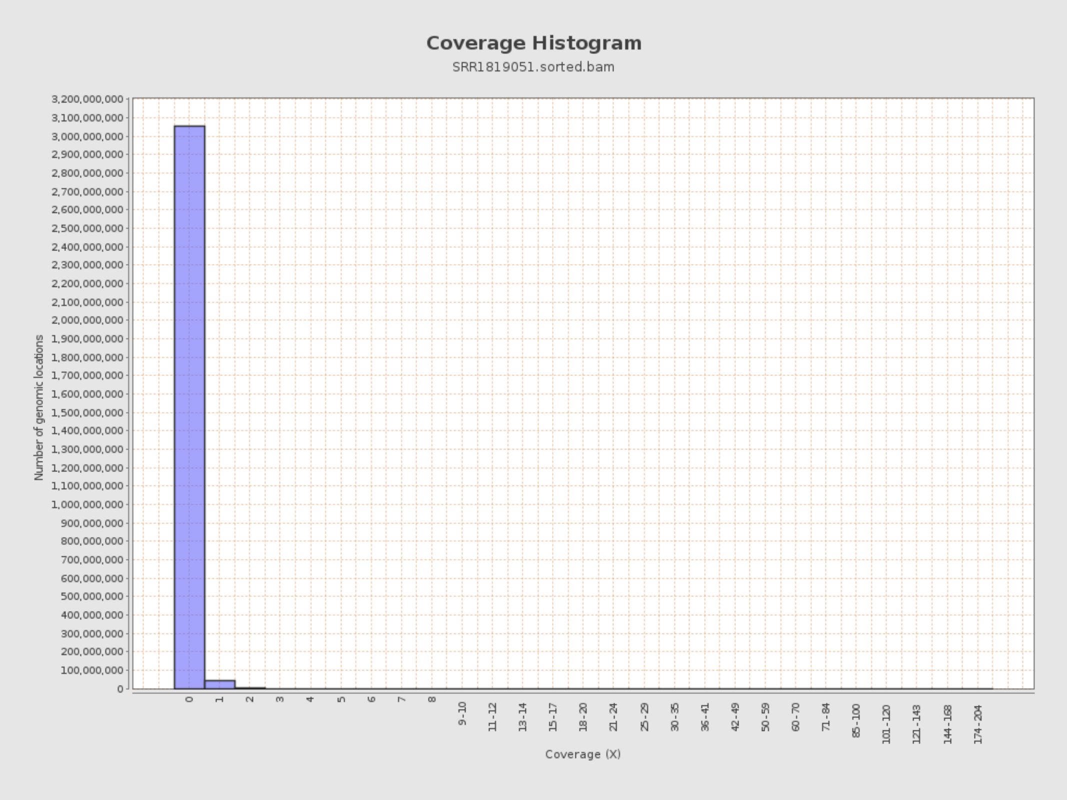
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5240157	0.021	0.2113
chr2	243199373	3930022	0.0162	0.1665
chr3	198022430	3146916	0.0159	0.1325
chr4	191154276	2994973	0.0157	0.1369
chr5	180915260	2364636	0.0131	0.1207
chr6	171115067	2537779	0.0148	0.1332
chr7	159138663	2046135	0.0129	0.1328

chr8	146364022	2961522	0.0202	0.1632
chr9	141213431	1727227	0.0122	0.1451
chr10	135534747	2215761	0.0163	0.1606
chr11	135006516	1483805	0.011	0.1317
chr12	133851895	2122817	0.0159	0.1329
chr13	115169878	1436876	0.0125	0.1164
chr14	107349540	1274511	0.0119	0.1201
chr15	102531392	1348729	0.0132	0.1213
chr16	90354753	1398584	0.0155	0.1374
chr17	81195210	1039293	0.0128	0.1205
chr18	78077248	1152112	0.0148	0.2264
chr19	59128983	909370	0.0154	0.1641
chr20	63025520	1492154	0.0237	0.1644
chr21	48129895	606141	0.0126	0.1254
chr22	51304566	564049	0.011	0.1103
chrMT	16571	1805	0.1089	0.3488
chrX	155270560	2603215	0.0168	0.145
chrY	59373566	135374	0.0023	0.0654

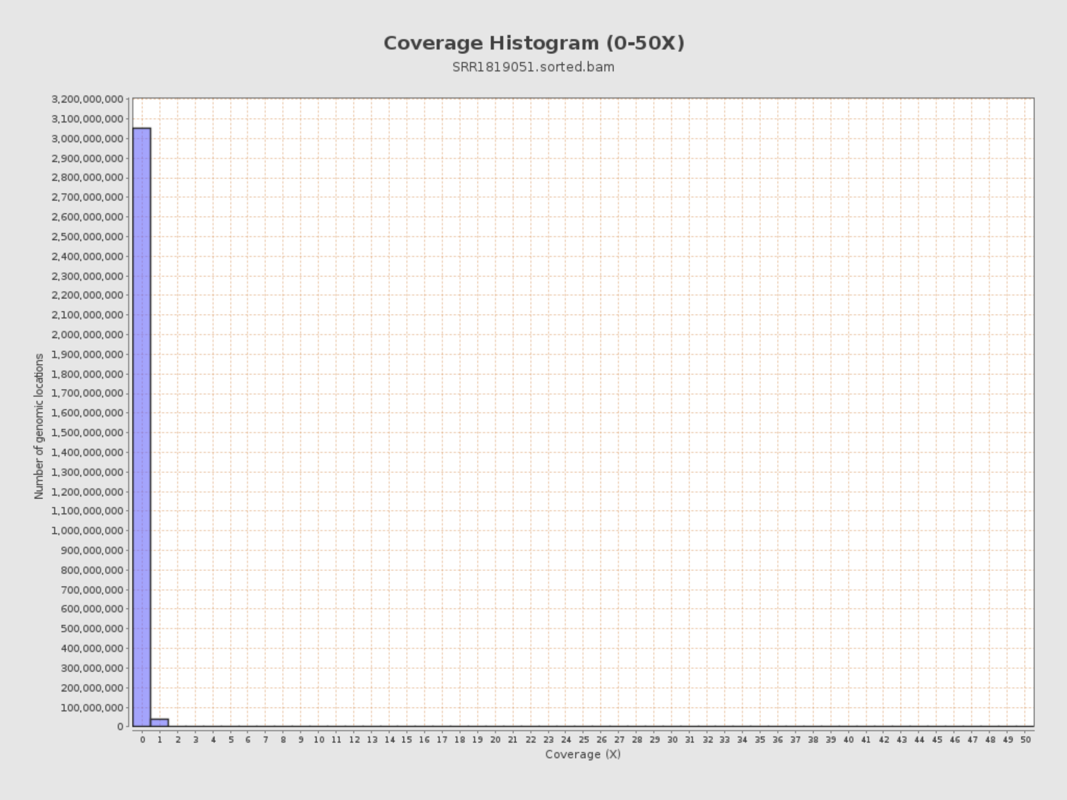
3. Results : Coverage across reference



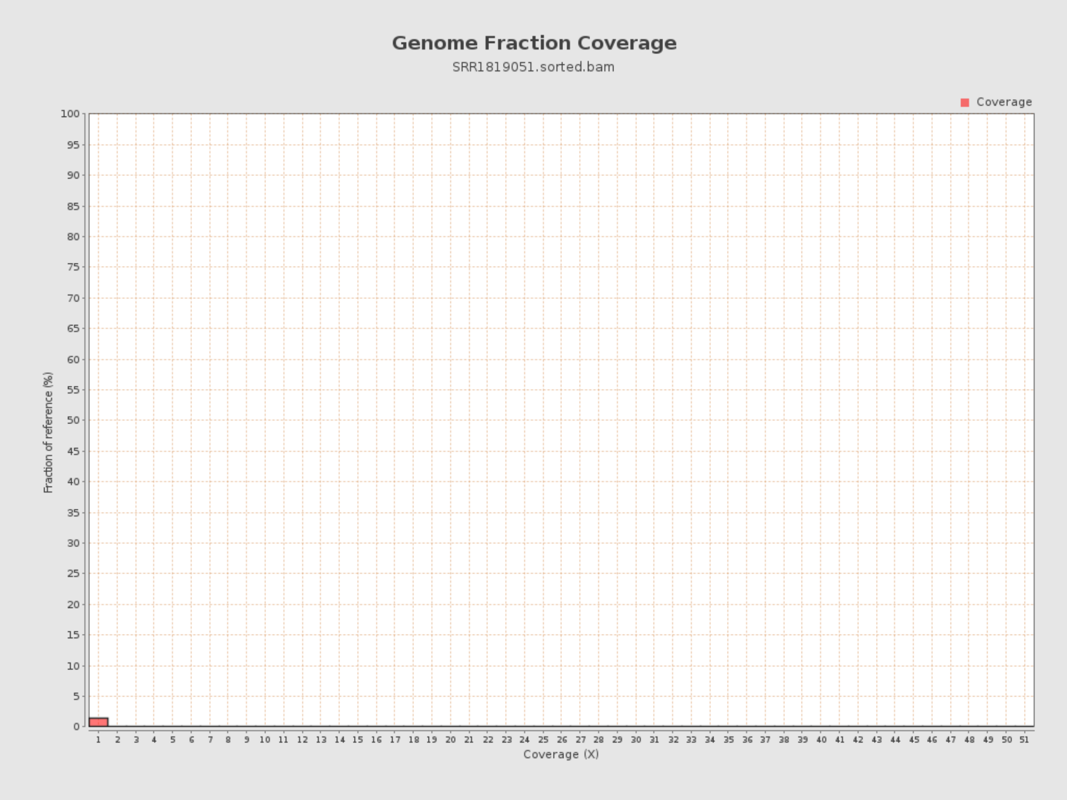
4. Results : Coverage Histogram



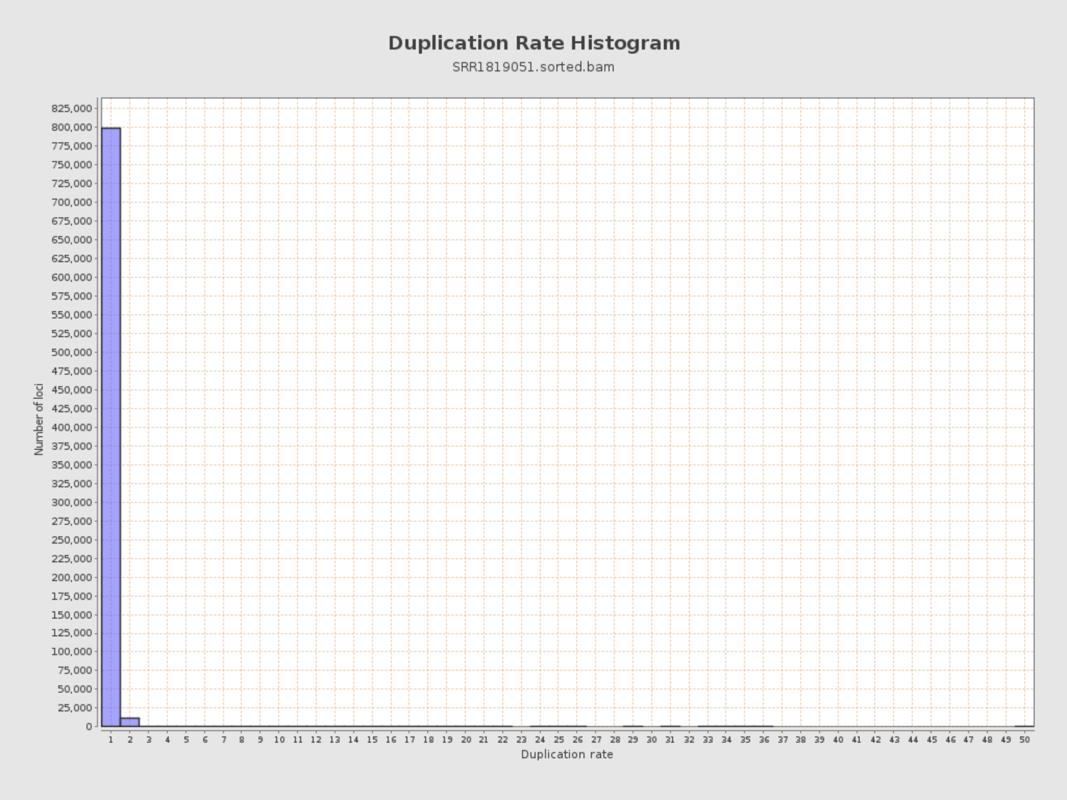
5. Results : Coverage Histogram (0-50X)



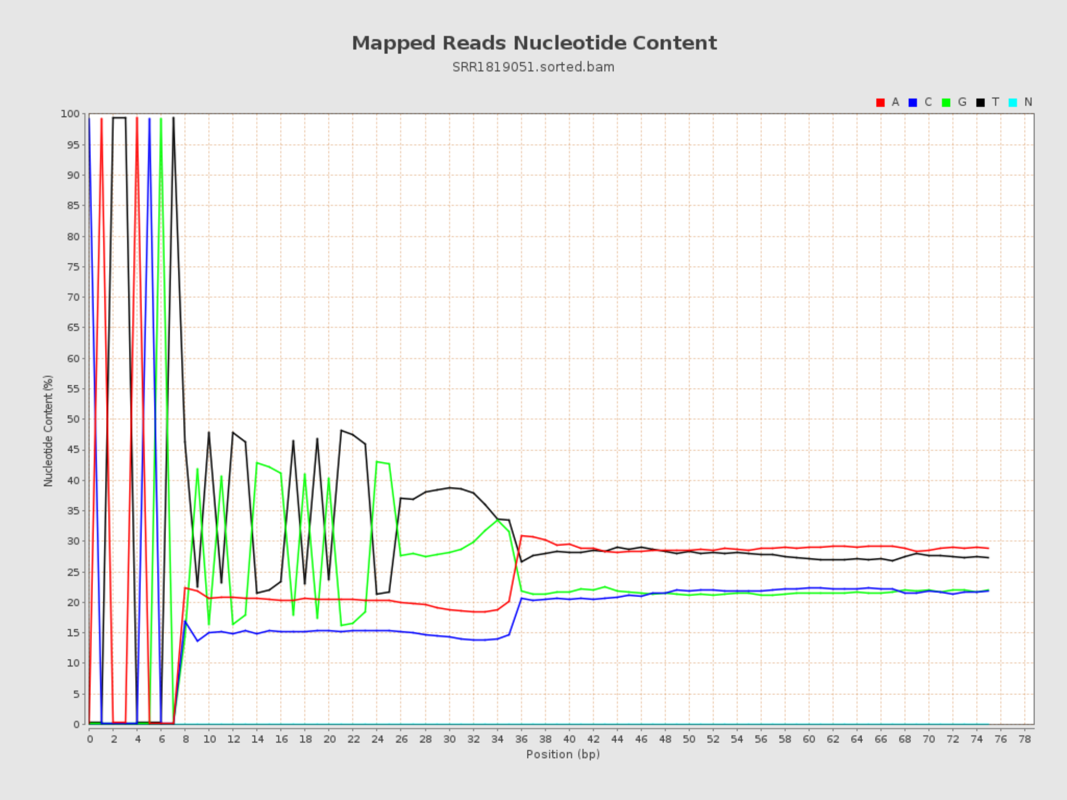
6. Results : Genome Fraction Coverage



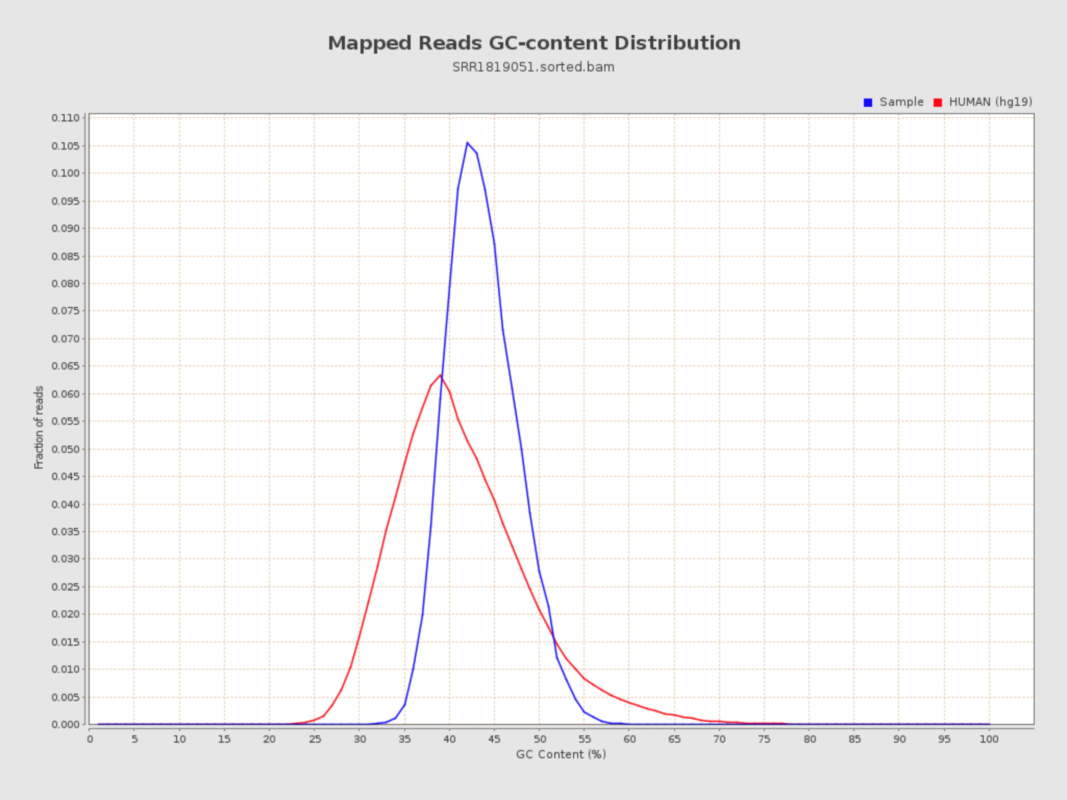
7. Results : Duplication Rate Histogram



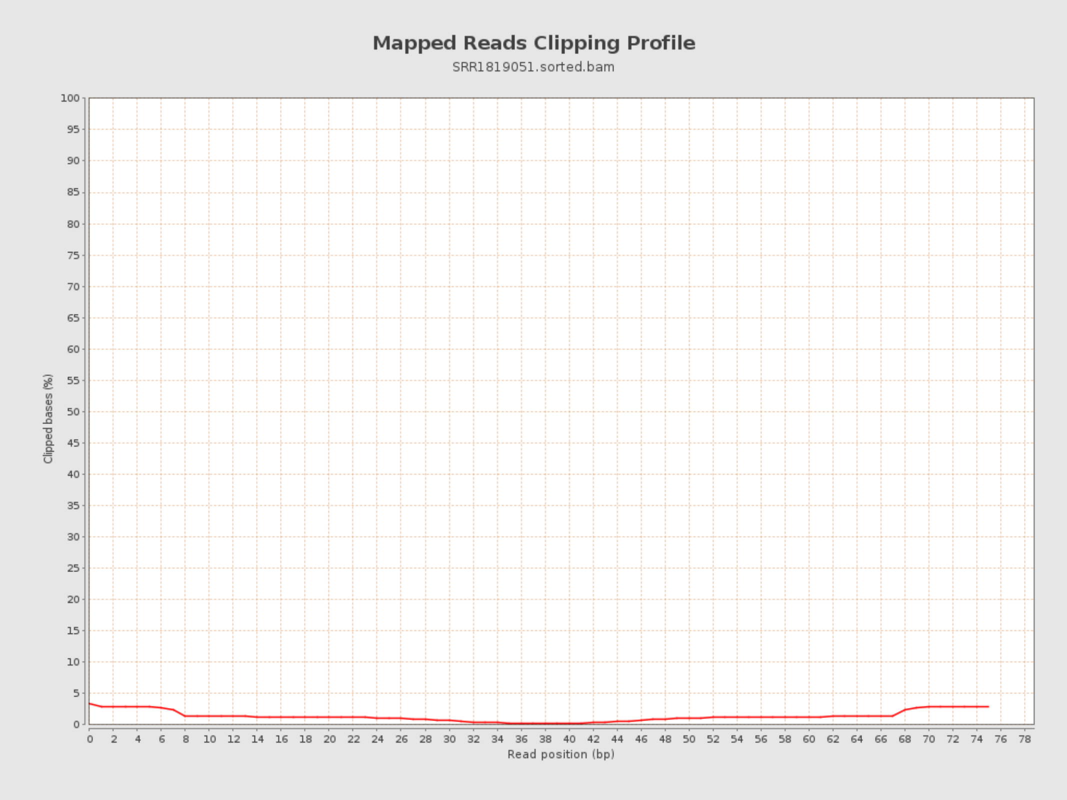
8. Results : Mapped Reads Nucleotide Content



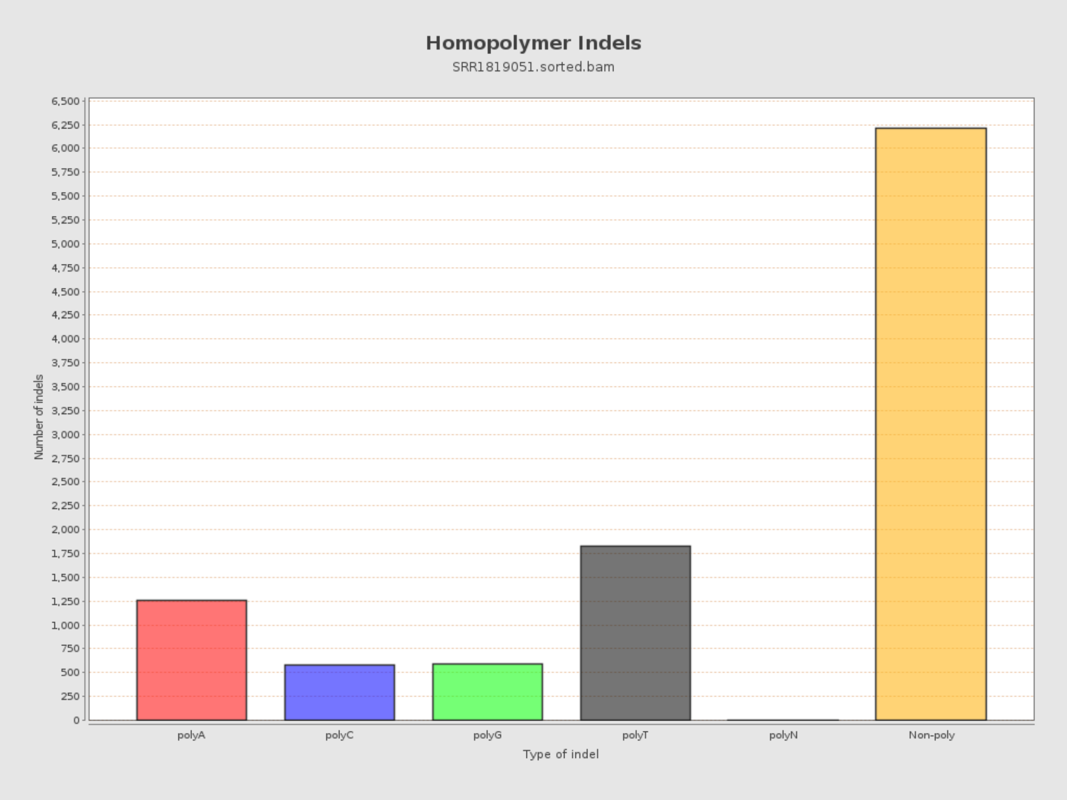
9. Results : Mapped Reads GC-content Distribution



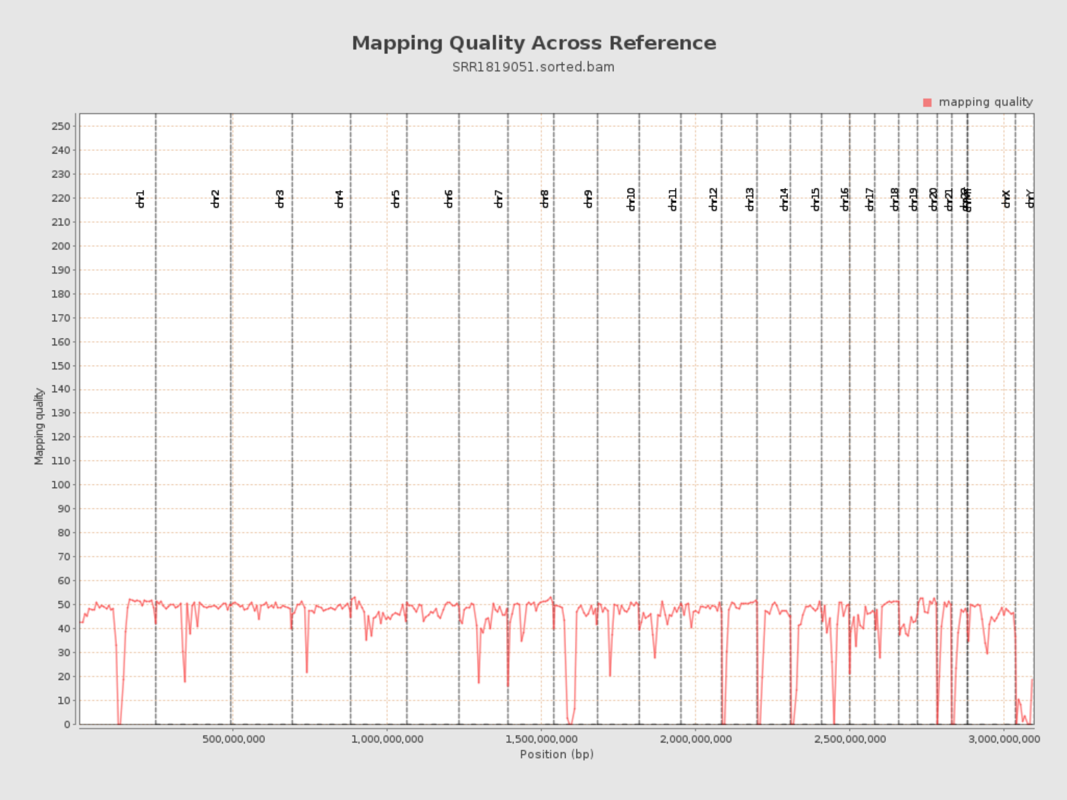
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram