Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:01:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819070.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_SRR1819070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:01:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,284,362
Mapped reads	1,172,726 / 91.31%
Unmapped reads	111,636 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,684 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,754 / 2.94%
Duplication rate	2.6%
Clipped reads	1,174,157 / 91.42%

2.2. ACGT Content

Number/percentage of A's	17,529,959 / 25.96%
Number/percentage of C's	12,873,920 / 19.07%
Number/percentage of T's	20,316,448 / 30.09%
Number/percentage of G's	16,793,485 / 24.87%
Number/percentage of N's	1,579 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.1916

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

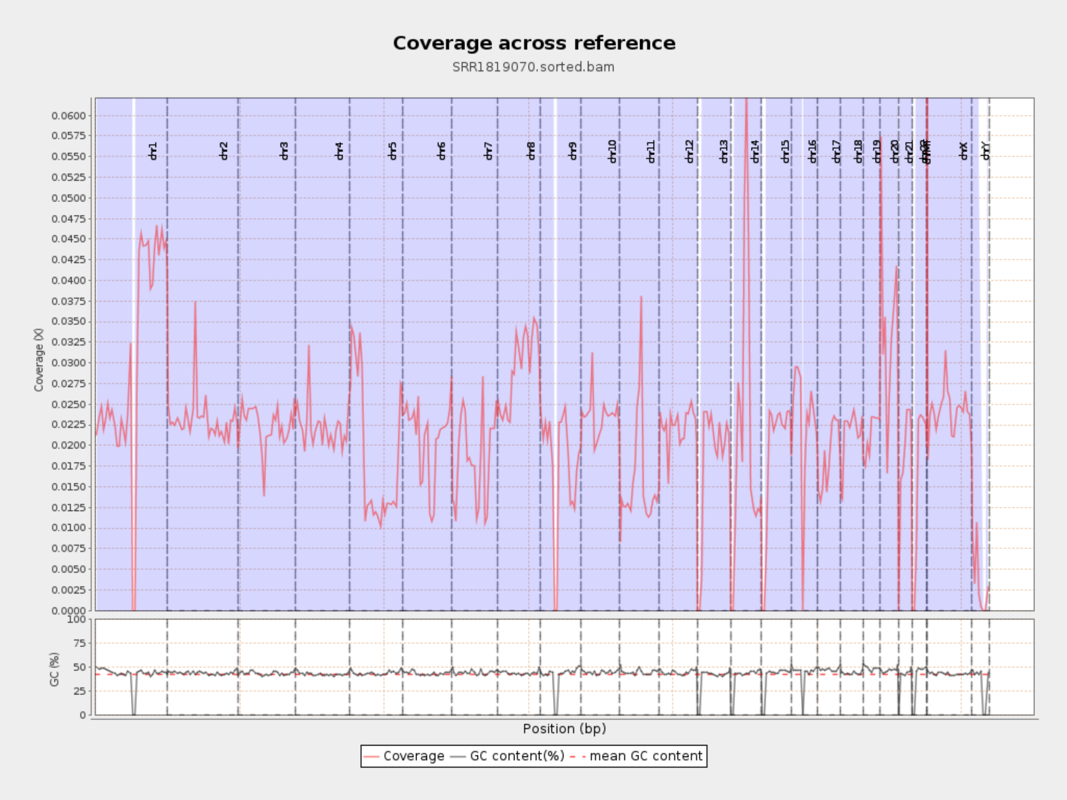
General error rate	0.5%
Mismatches	327,702
Insertions	4,624
Mapped reads with at least one insertion	0.39%
Deletions	10,455
Mapped reads with at least one deletion	0.89%
Homopolymer indels	40.84%

2.6. Chromosome stats

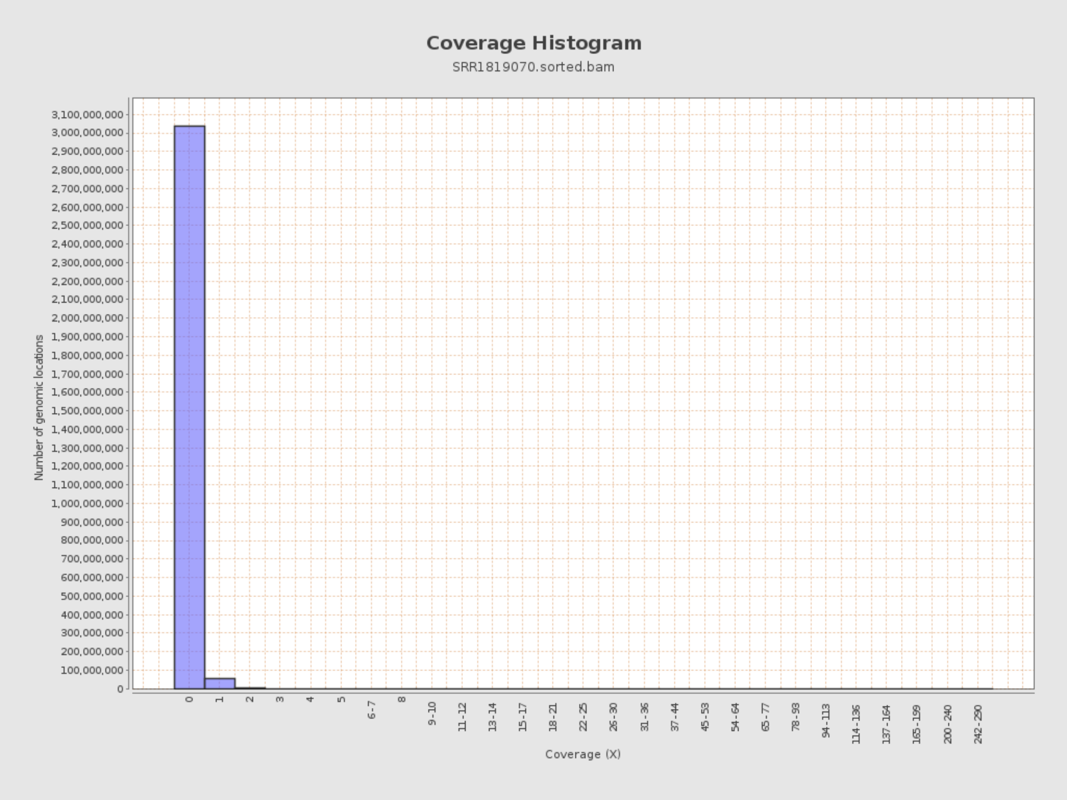
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7564707	0.0303	0.2888
chr2	243199373	5645050	0.0232	0.2122
chr3	198022430	4422439	0.0223	0.1608
chr4	191154276	4258091	0.0223	0.1707
chr5	180915260	3348373	0.0185	0.1482
chr6	171115067	3557770	0.0208	0.163
chr7	159138663	2951814	0.0185	0.1742

chr8	146364022	4304056	0.0294	0.2144
chr9	141213431	2480352	0.0176	0.1954
chr10	135534747	3202053	0.0236	0.1893
chr11	135006516	2164549	0.016	0.1747
chr12	133851895	2992871	0.0224	0.1631
chr13	115169878	2077474	0.018	0.145
chr14	107349540	2340773	0.0218	0.1654
chr15	102531392	1927139	0.0188	0.1476
chr16	90354753	2033150	0.0225	0.1675
chr17	81195210	1511349	0.0186	0.1515
chr18	78077248	1665626	0.0213	0.3208
chr19	59128983	1261739	0.0213	0.2174
chr20	63025520	2145010	0.034	0.2031
chr21	48129895	891580	0.0185	0.1563
chr22	51304566	816566	0.0159	0.1361
chrMT	16571	2253	0.136	0.3656
chrX	155270560	3772912	0.0243	0.183
chrY	59373566	195731	0.0033	0.0811

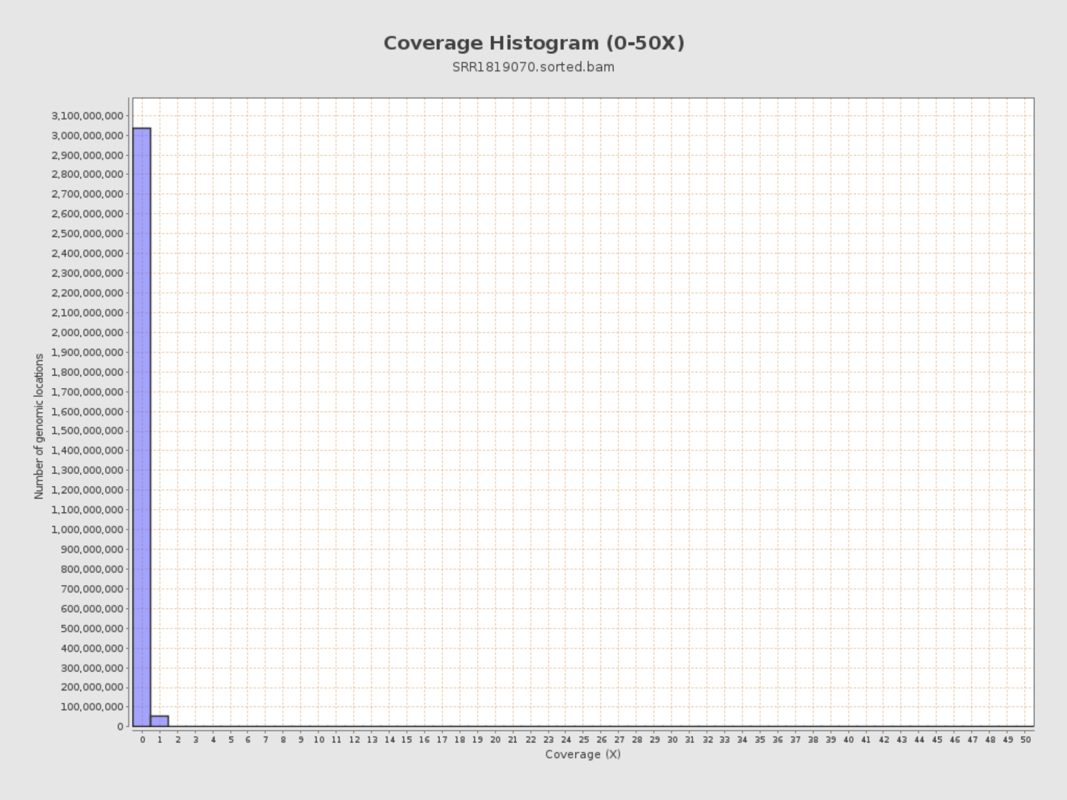
3. Results : Coverage across reference



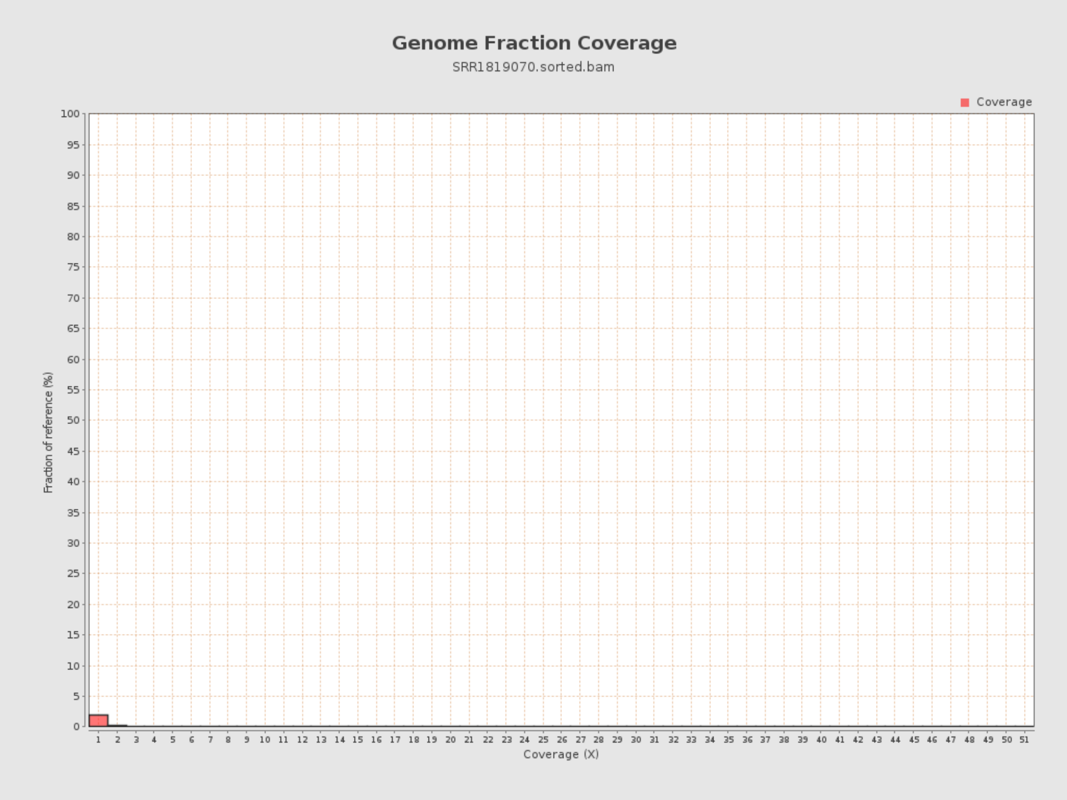
4. Results : Coverage Histogram



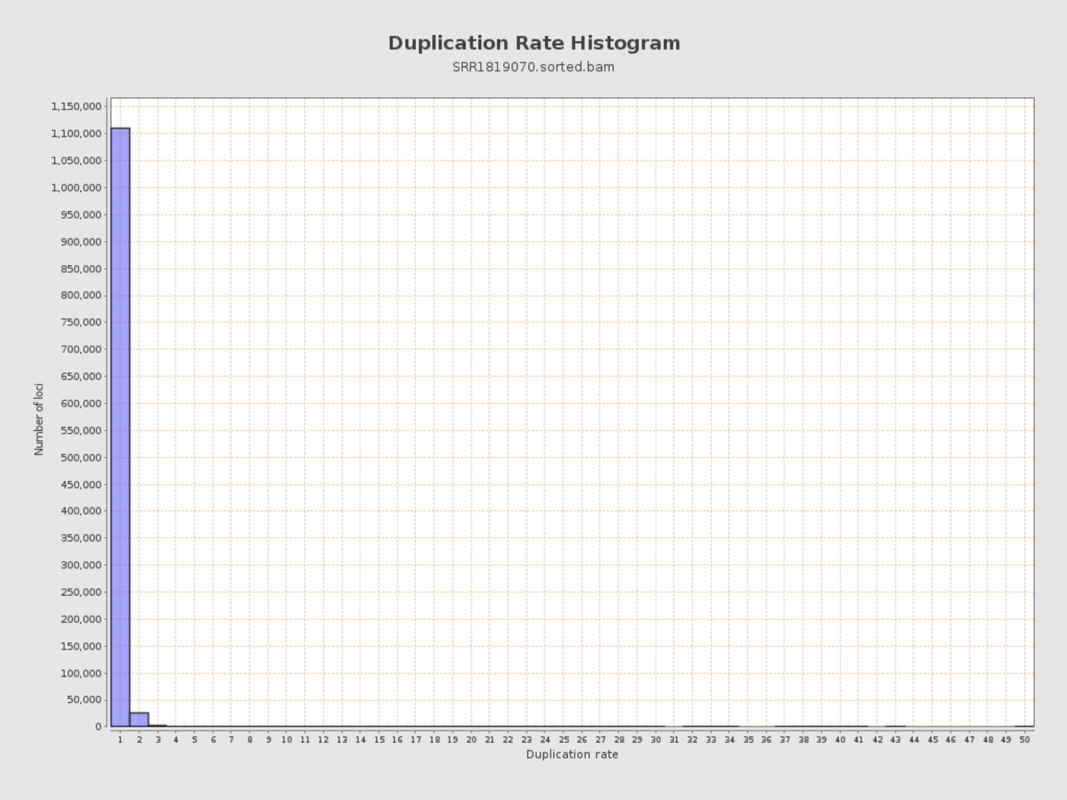
5. Results : Coverage Histogram (0-50X)



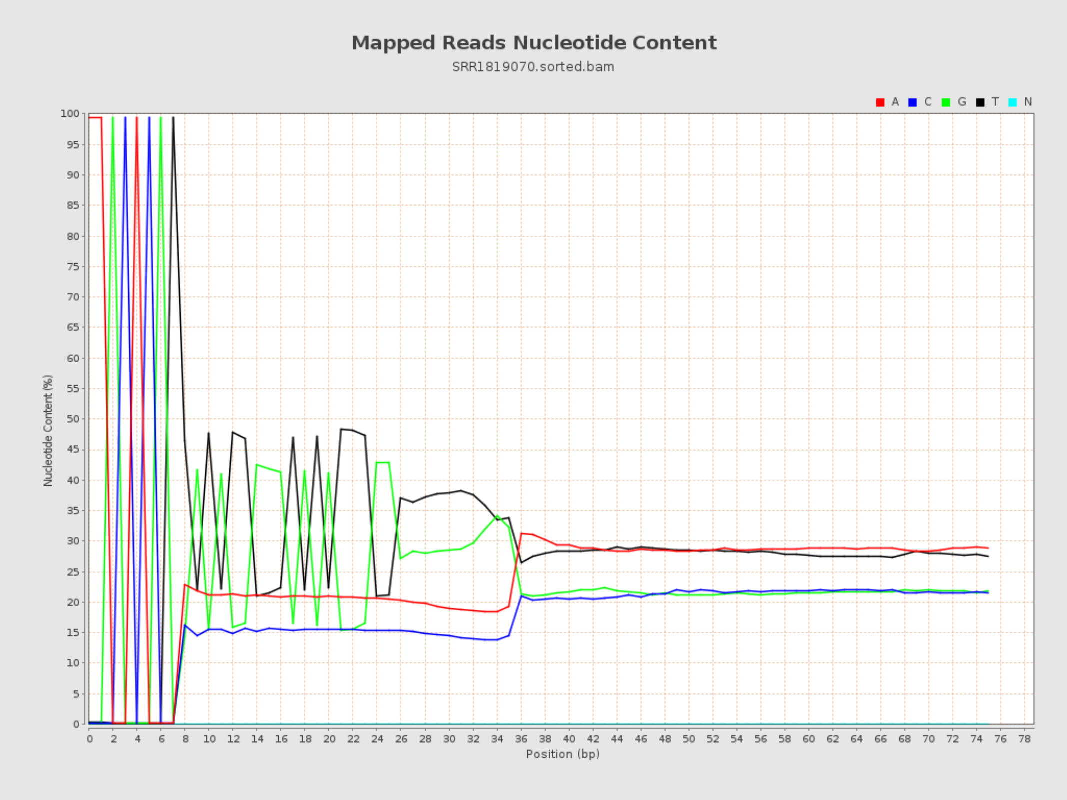
6. Results : Genome Fraction Coverage



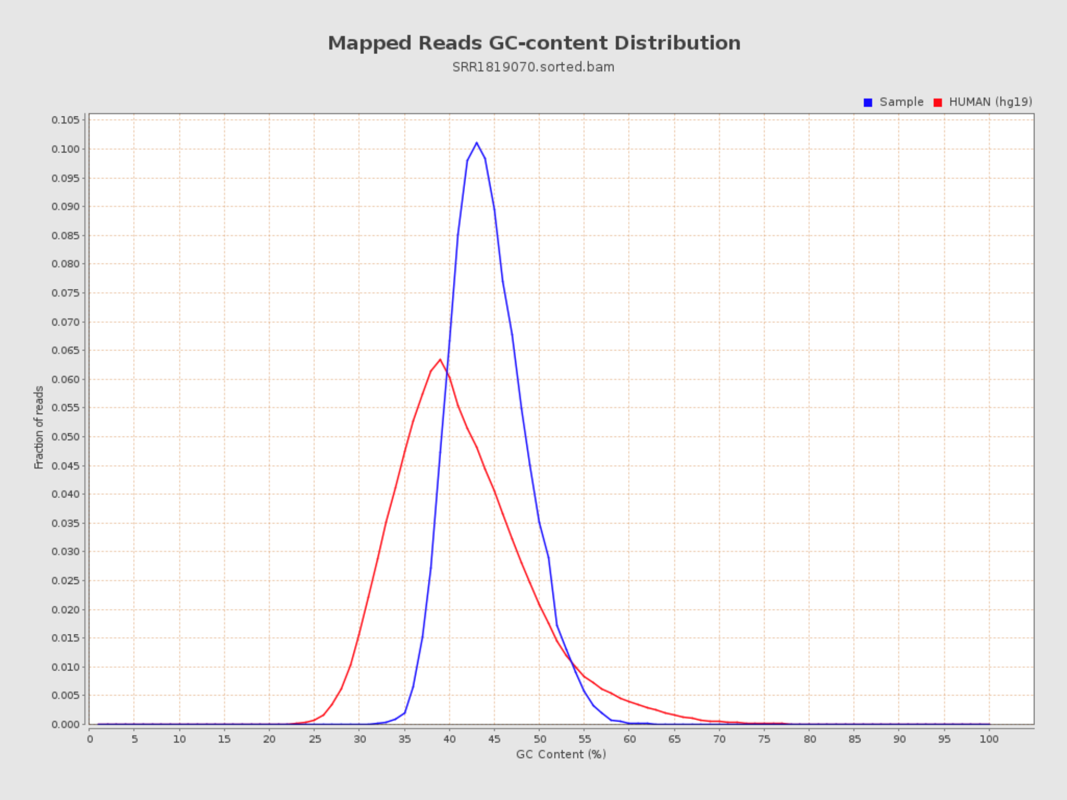
7. Results : Duplication Rate Histogram



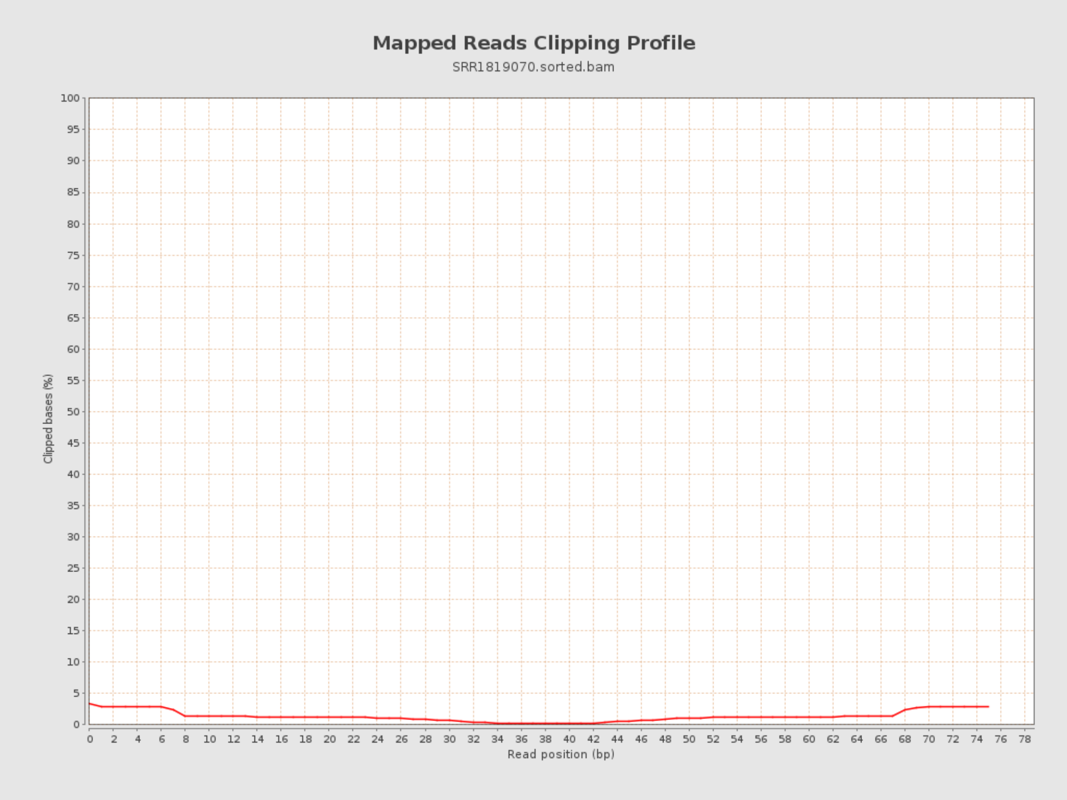
8. Results : Mapped Reads Nucleotide Content



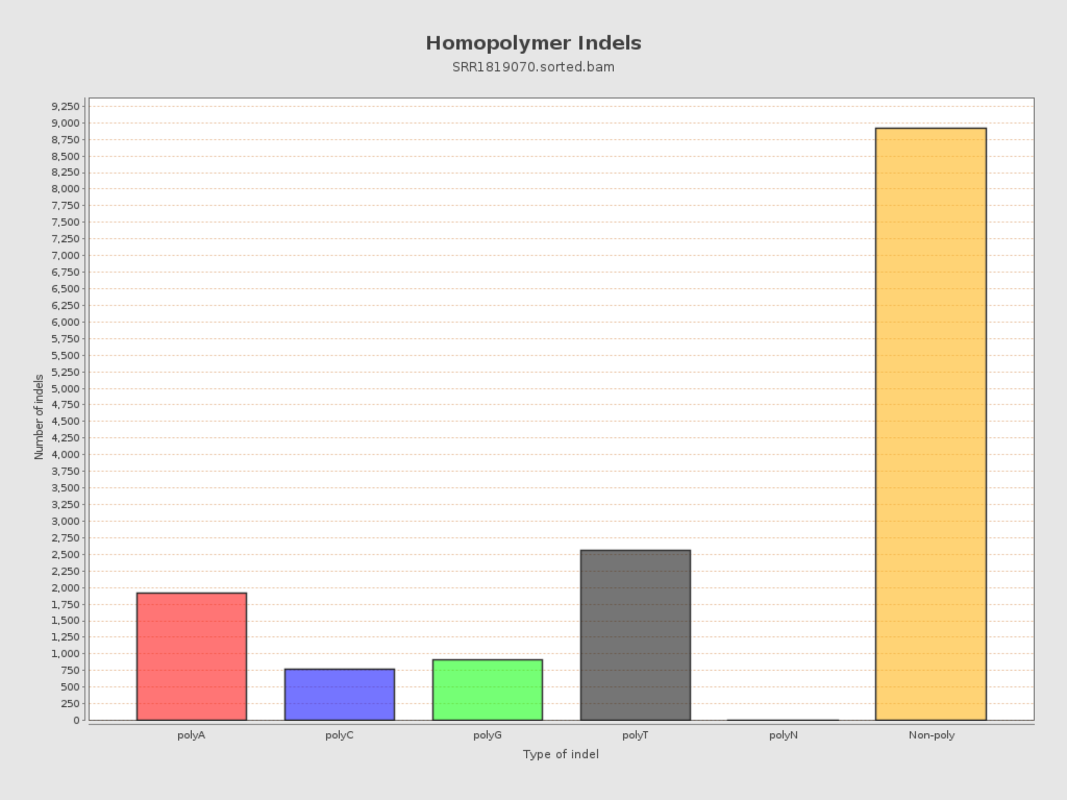
9. Results : Mapped Reads GC-content Distribution



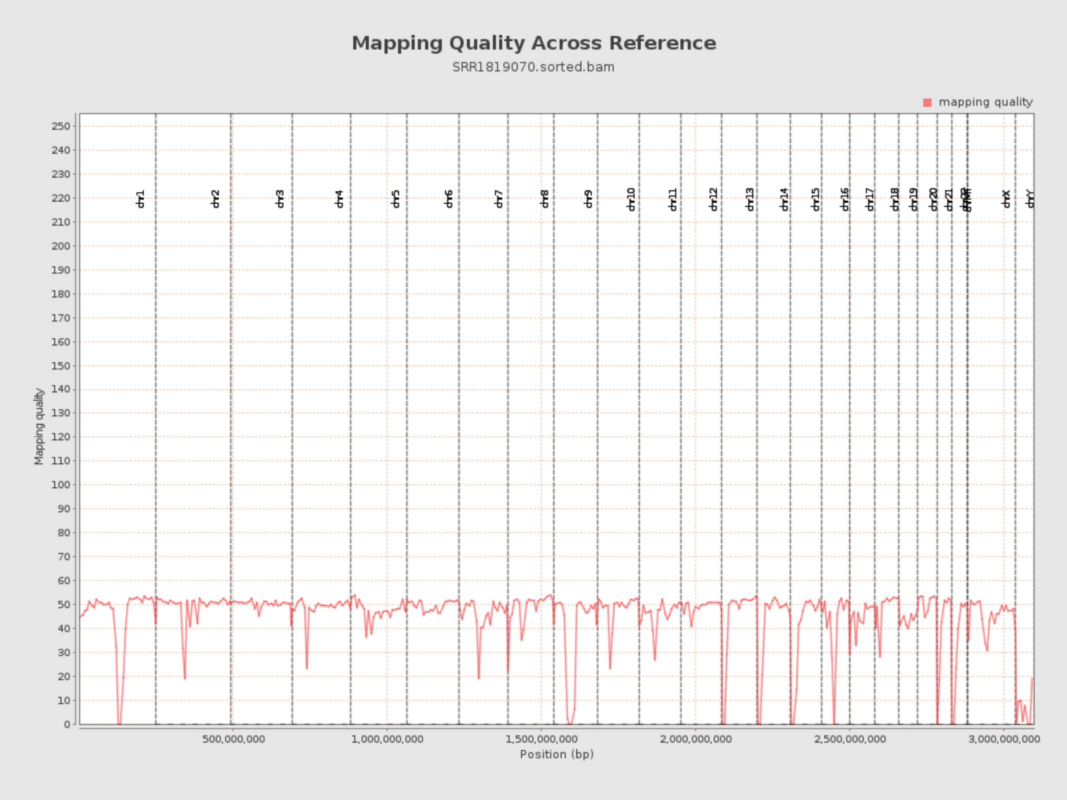
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram