Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:45:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818766.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_SRR1818766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818766.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:45:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	833,308
Mapped reads	486,275 / 58.35%
Unmapped reads	347,033 / 41.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,621 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	58,525 / 7.02%
Duplication rate	10.08%
Clipped reads	488,271 / 58.59%

2.2. ACGT Content

Number/percentage of A's	9,084,507 / 27.55%
Number/percentage of C's	6,750,985 / 20.47%
Number/percentage of T's	9,616,798 / 29.16%
Number/percentage of G's	7,521,454 / 22.81%
Number/percentage of N's	2,016 / 0.01%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1806

2.4. Mapping Quality

Mean Mapping Quality	47.14

2.5. Mismatches and indels

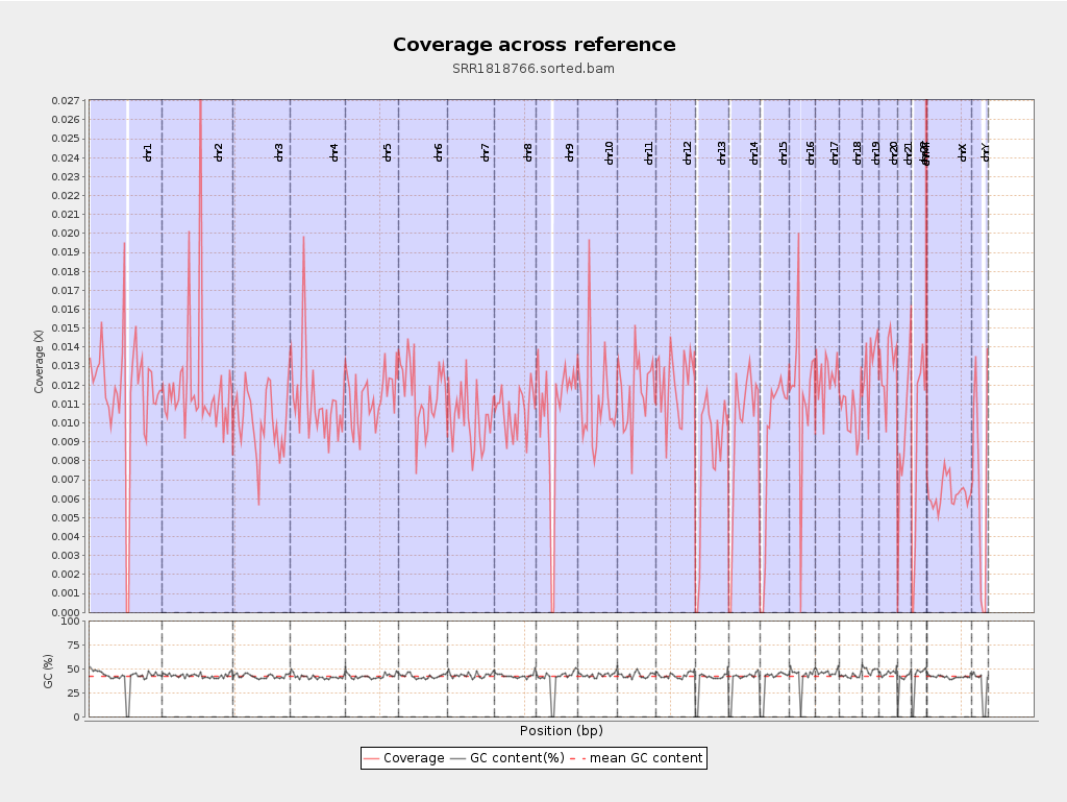
General error rate	0.55%
Mismatches	170,683
Insertions	4,013
Mapped reads with at least one insertion	0.8%
Deletions	9,275
Mapped reads with at least one deletion	1.88%
Homopolymer indels	41.31%

2.6. Chromosome stats

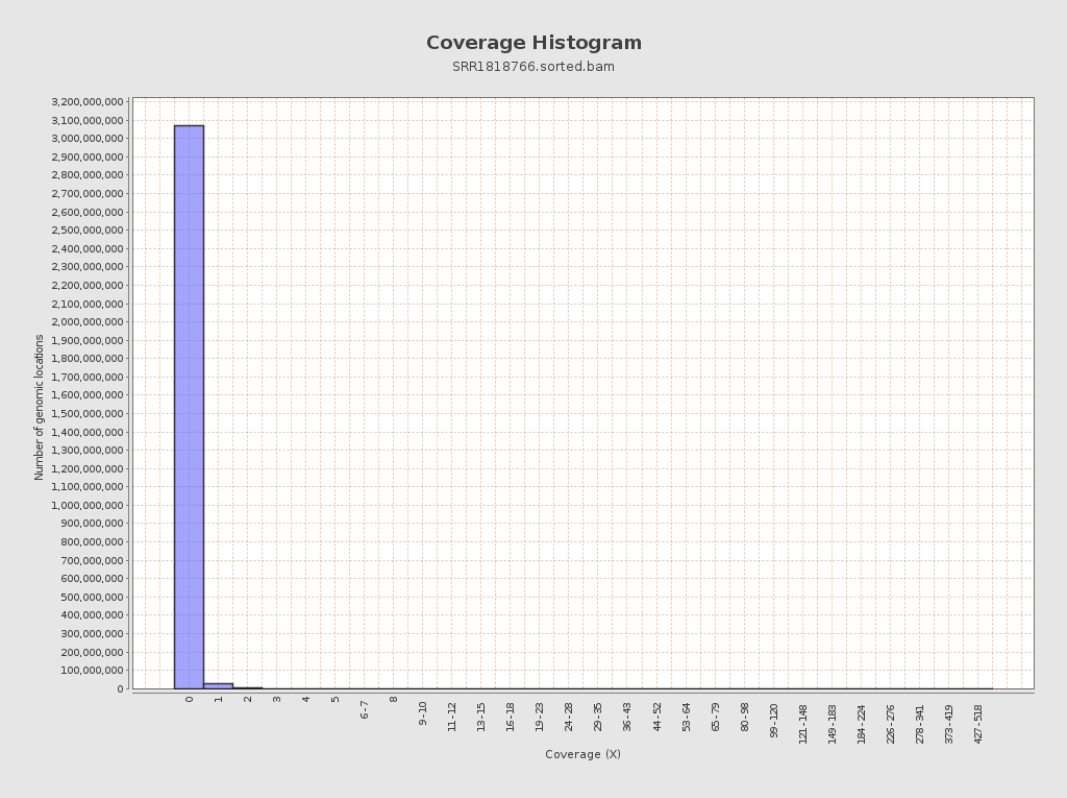
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2883681	0.0116	0.2314
chr2	243199373	2919512	0.012	0.3425
chr3	198022430	1998493	0.0101	0.1151
chr4	191154276	2130185	0.0111	0.163
chr5	180915260	2050844	0.0113	0.1283
chr6	171115067	1988352	0.0116	0.1391
chr7	159138663	1613567	0.0101	0.143

chr8	146364022	1554930	0.0106	0.1292
chr9	141213431	1460290	0.0103	0.1318
chr10	135534747	1488565	0.011	0.2034
chr11	135006516	1578864	0.0117	0.134
chr12	133851895	1624950	0.0121	0.1378
chr13	115169878	945395	0.0082	0.1035
chr14	107349540	1029239	0.0096	0.1297
chr15	102531392	930080	0.0091	0.1094
chr16	90354753	1060149	0.0117	0.2209
chr17	81195210	1013521	0.0125	0.1348
chr18	78077248	821739	0.0105	0.1536
chr19	59128983	772553	0.0131	0.2127
chr20	63025520	819835	0.013	0.1415
chr21	48129895	457760	0.0095	0.1248
chr22	51304566	445881	0.0087	0.1163
chrMT	16571	35099	2.1181	2.2384
chrX	155270560	977152	0.0063	0.1059
chrY	59373566	391491	0.0066	0.3471

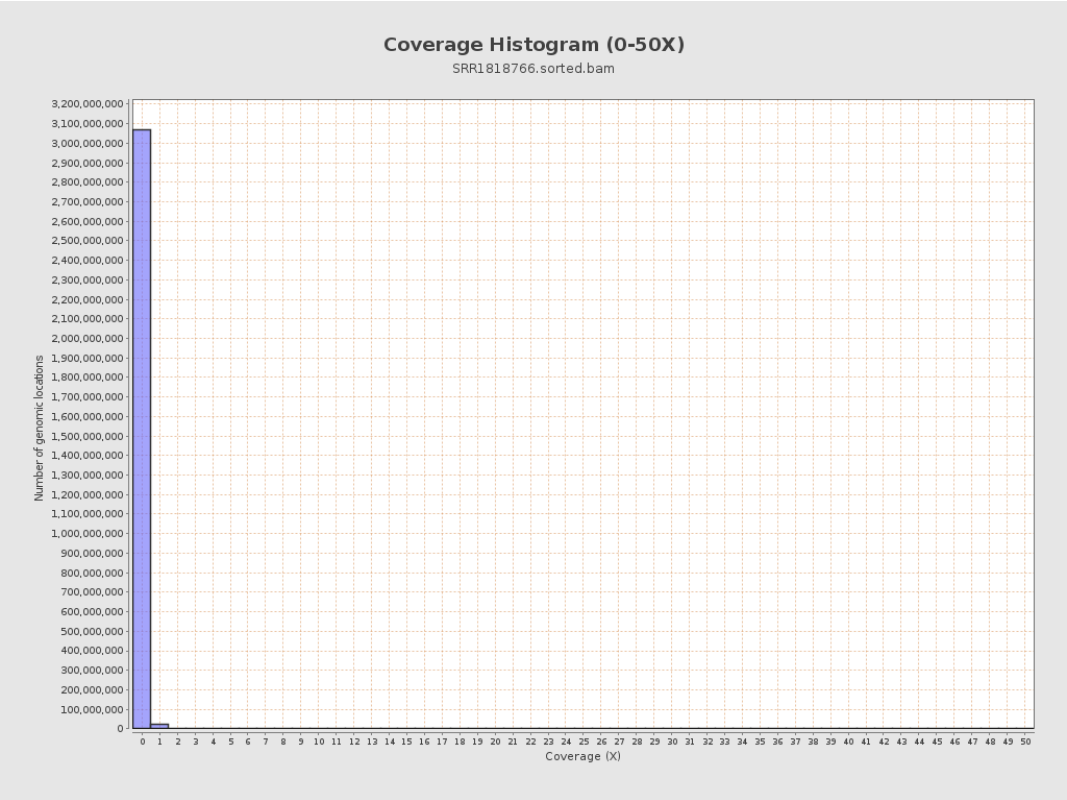
3. Results : Coverage across reference



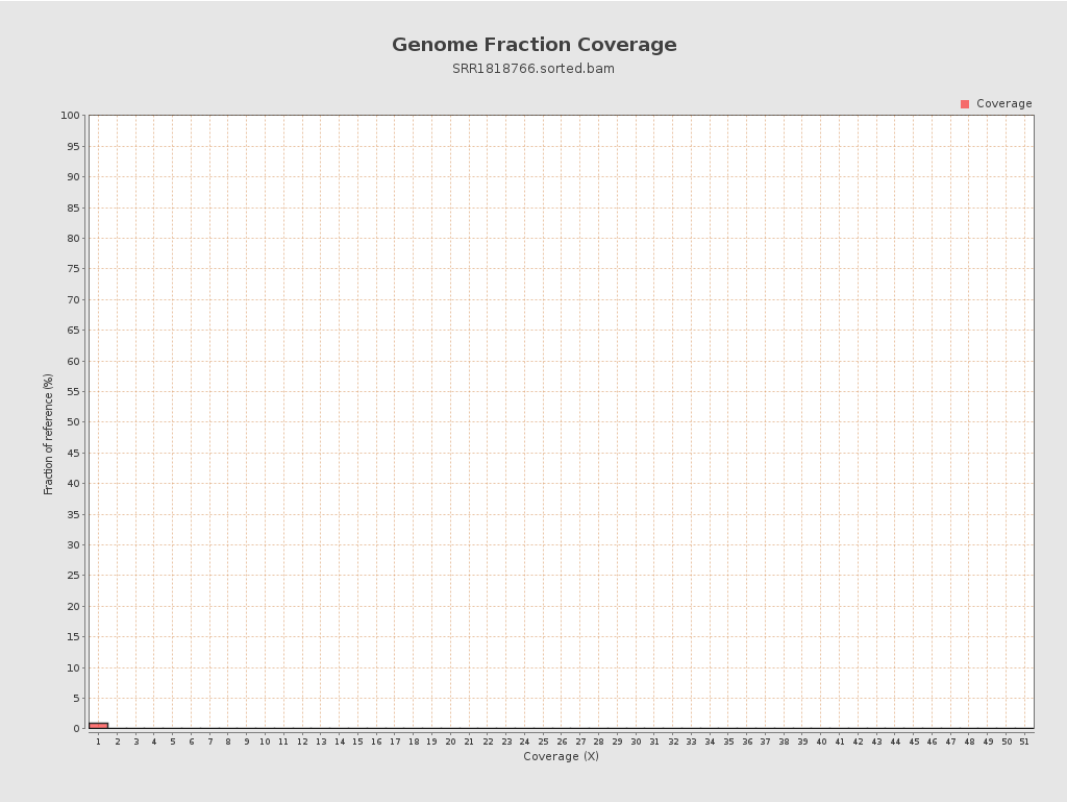
4. Results : Coverage Histogram



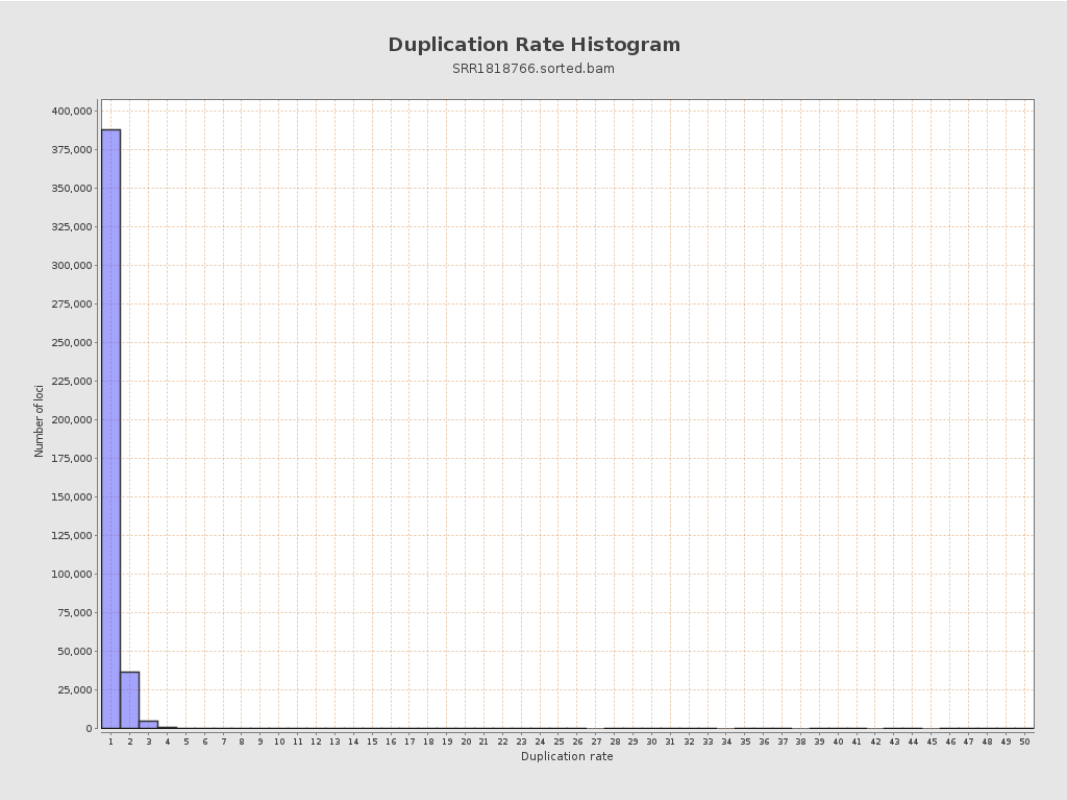
5. Results : Coverage Histogram (0-50X)



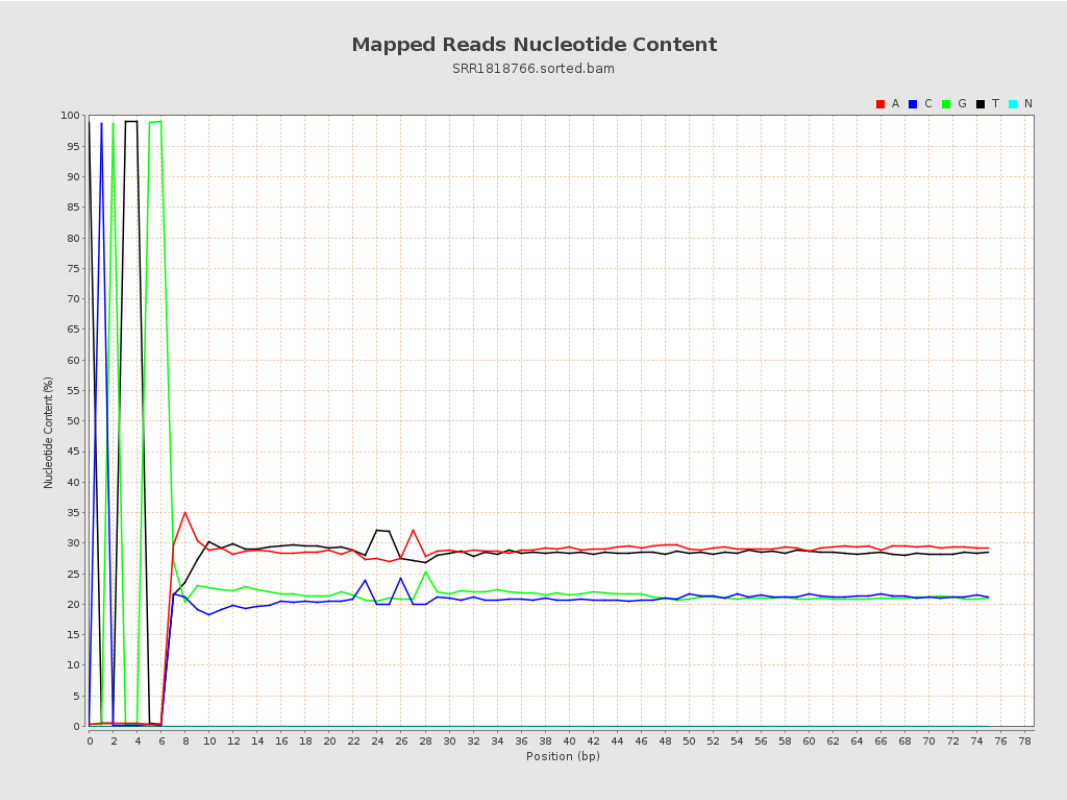
6. Results : Genome Fraction Coverage



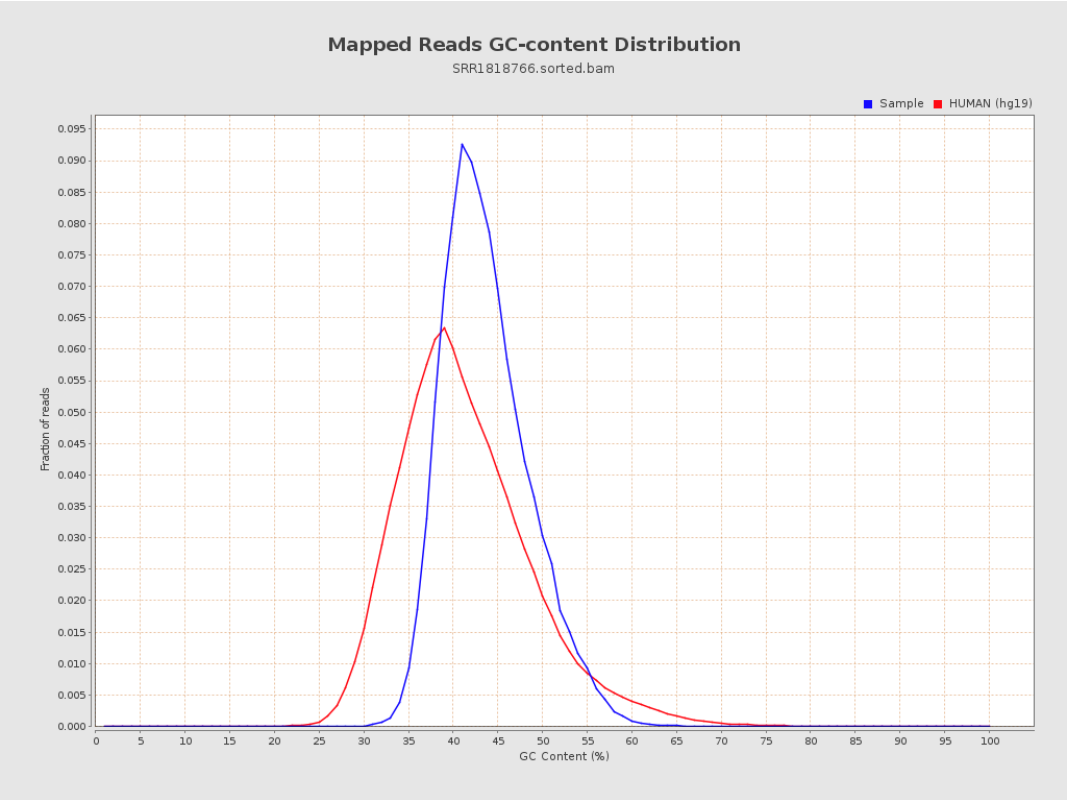
7. Results : Duplication Rate Histogram



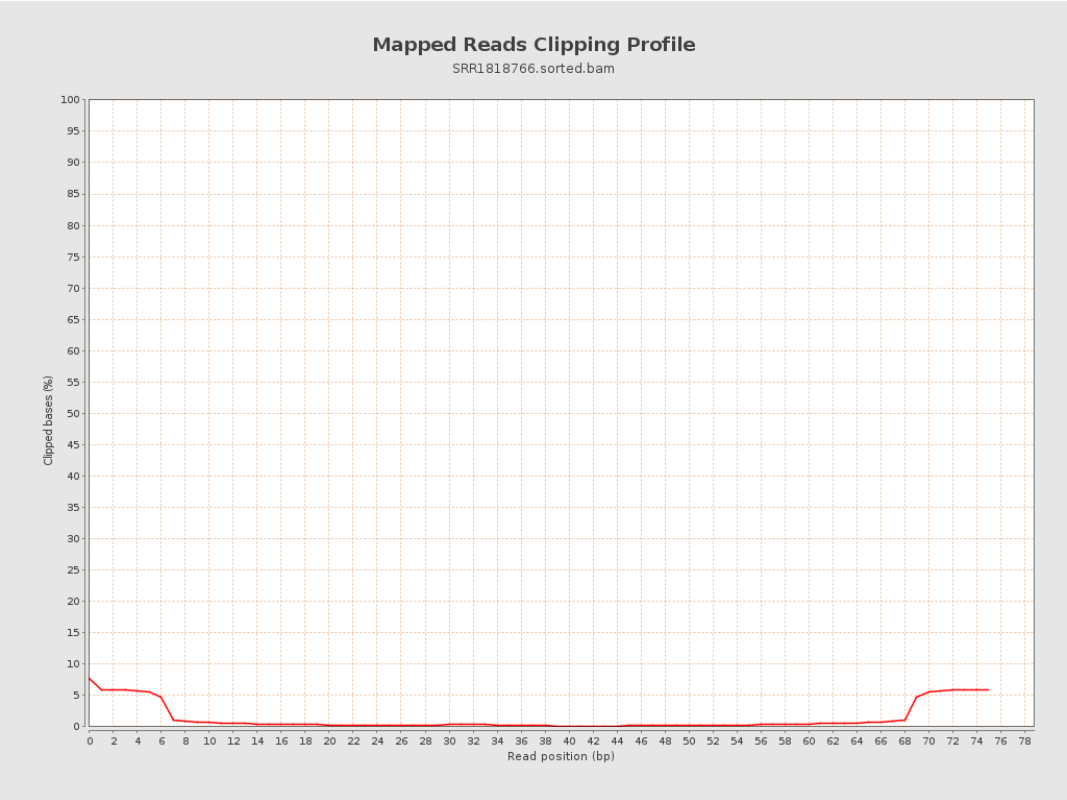
8. Results : Mapped Reads Nucleotide Content



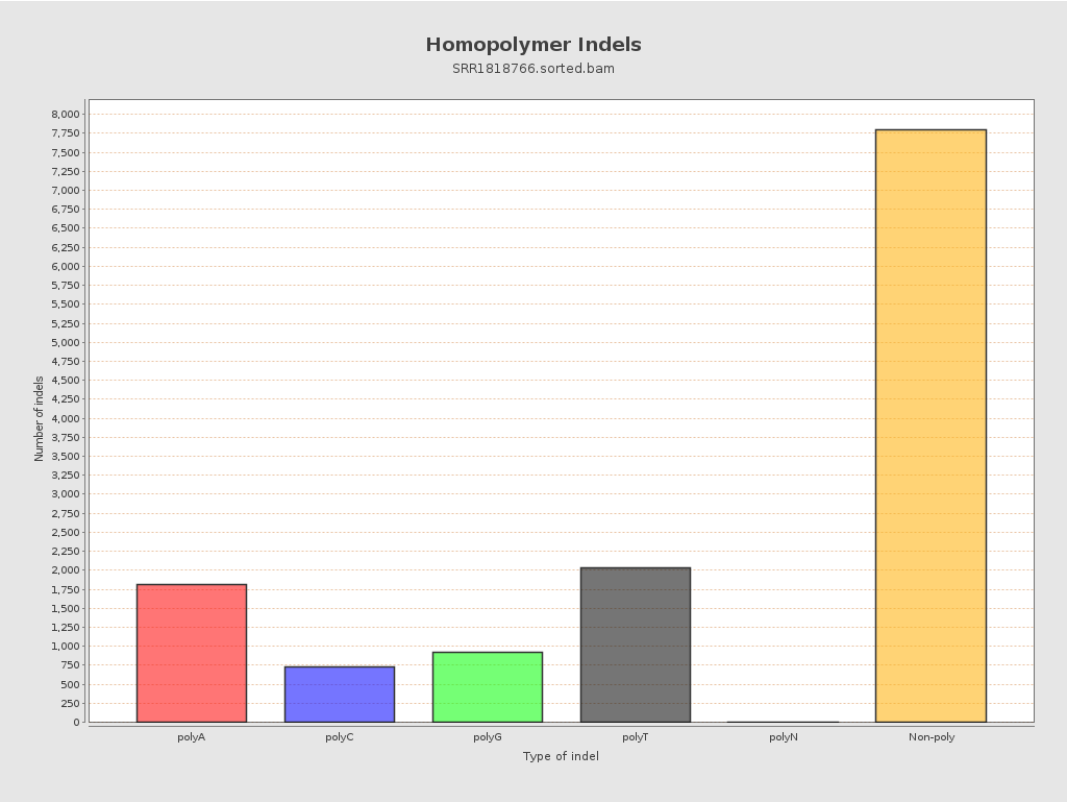
9. Results : Mapped Reads GC-content Distribution



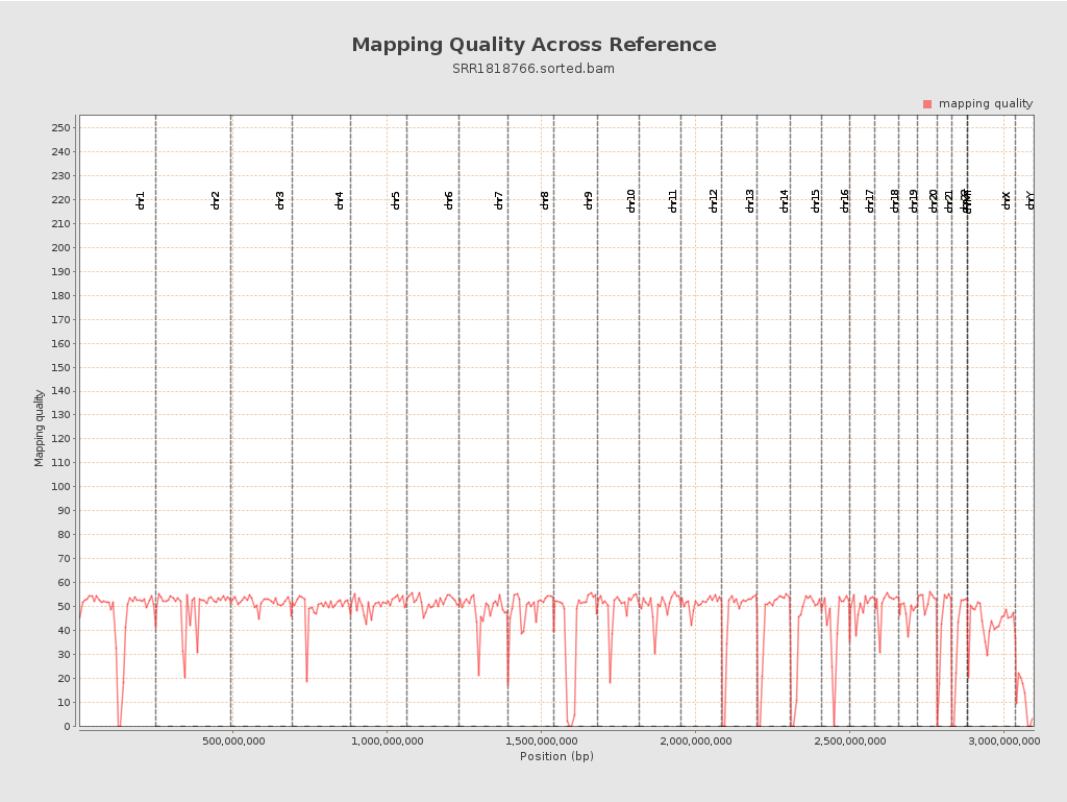
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram