Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:28:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231743.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_SRR6231743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:28:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,472,016
Mapped reads	857,244 / 58.24%
Unmapped reads	614,772 / 41.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,516 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	63,115 / 4.29%
Duplication rate	5.73%
Clipped reads	416,578 / 28.3%

2.2. ACGT Content

Number/percentage of A's	15,876,310 / 28.49%
Number/percentage of C's	9,454,935 / 16.96%
Number/percentage of T's	18,648,386 / 33.46%
Number/percentage of G's	11,750,982 / 21.08%
Number/percentage of N's	1,432 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	0.018

Standard Deviation	0.376

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

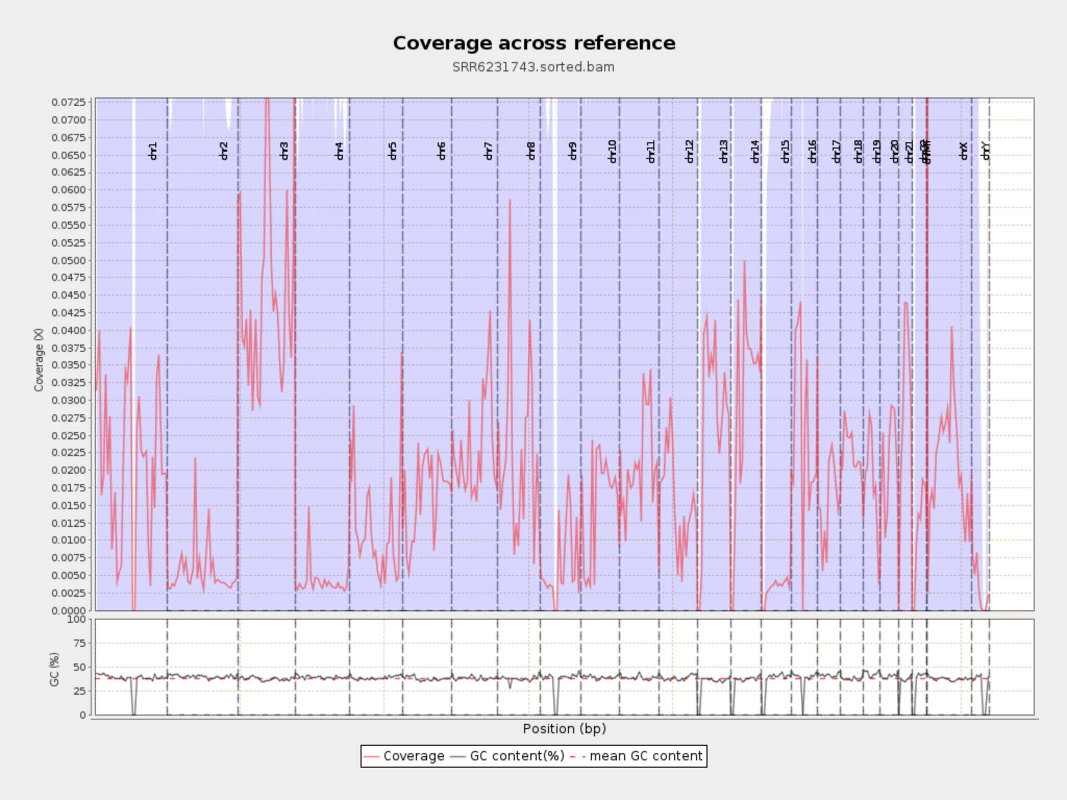
General error rate	0.9%
Mismatches	492,966
Insertions	5,111
Mapped reads with at least one insertion	0.59%
Deletions	19,199
Mapped reads with at least one deletion	2.21%
Homopolymer indels	44%

2.6. Chromosome stats

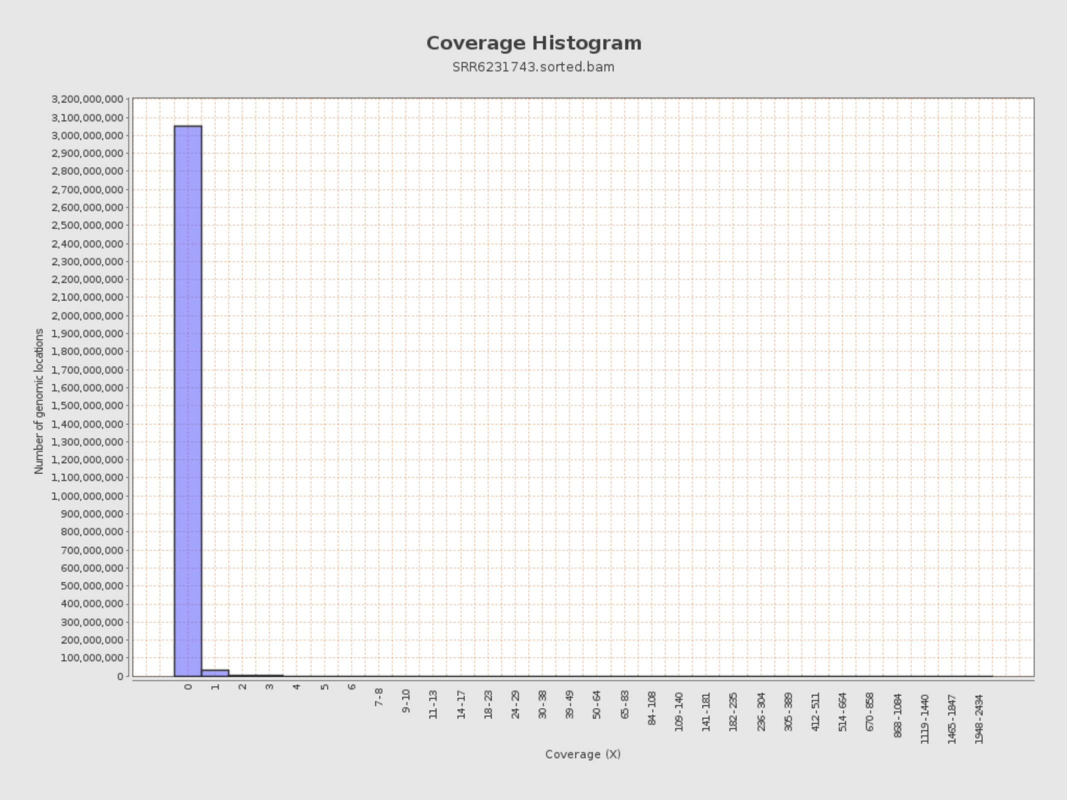
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5123187	0.0206	0.335
chr2	243199373	1368415	0.0056	0.1645
chr3	198022430	8829016	0.0446	0.266
chr4	191154276	798574	0.0042	0.0835
chr5	180915260	2097977	0.0116	0.1321
chr6	171115067	2822045	0.0165	0.1671
chr7	159138663	3686917	0.0232	0.2505

chr8	146364022	3329123	0.0227	1.4439
chr9	141213431	907009	0.0064	0.136
chr10	135534747	2048663	0.0151	0.2336
chr11	135006516	2810778	0.0208	0.1914
chr12	133851895	2147579	0.016	0.195
chr13	115169878	3137435	0.0272	0.2085
chr14	107349540	3157942	0.0294	0.2198
chr15	102531392	325093	0.0032	0.0764
chr16	90354753	2248642	0.0249	0.2034
chr17	81195210	1232295	0.0152	0.15
chr18	78077248	1772137	0.0227	0.3977
chr19	59128983	1073834	0.0182	0.2589
chr20	63025520	1335151	0.0212	0.1895
chr21	48129895	1432677	0.0298	0.2171
chr22	51304566	585664	0.0114	0.1277
chrMT	16571	65034	3.9246	3.163
chrX	155270560	3243563	0.0209	0.1899
chrY	59373566	187136	0.0032	0.0729

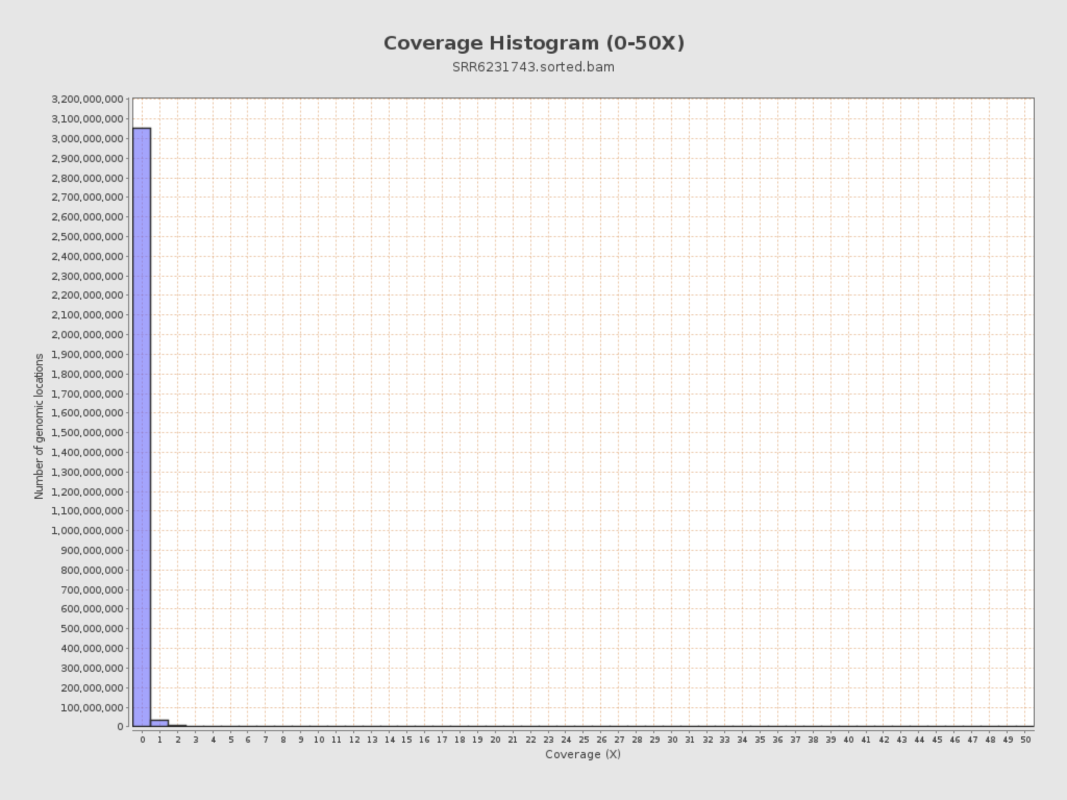
3. Results : Coverage across reference



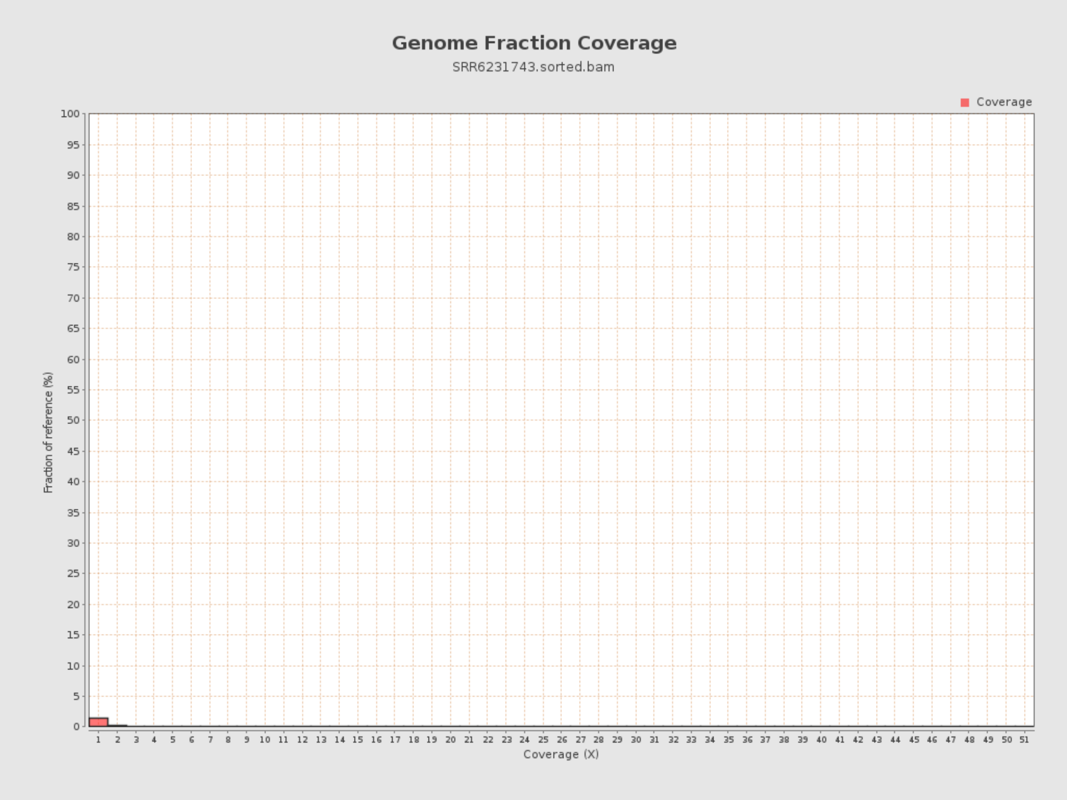
4. Results : Coverage Histogram



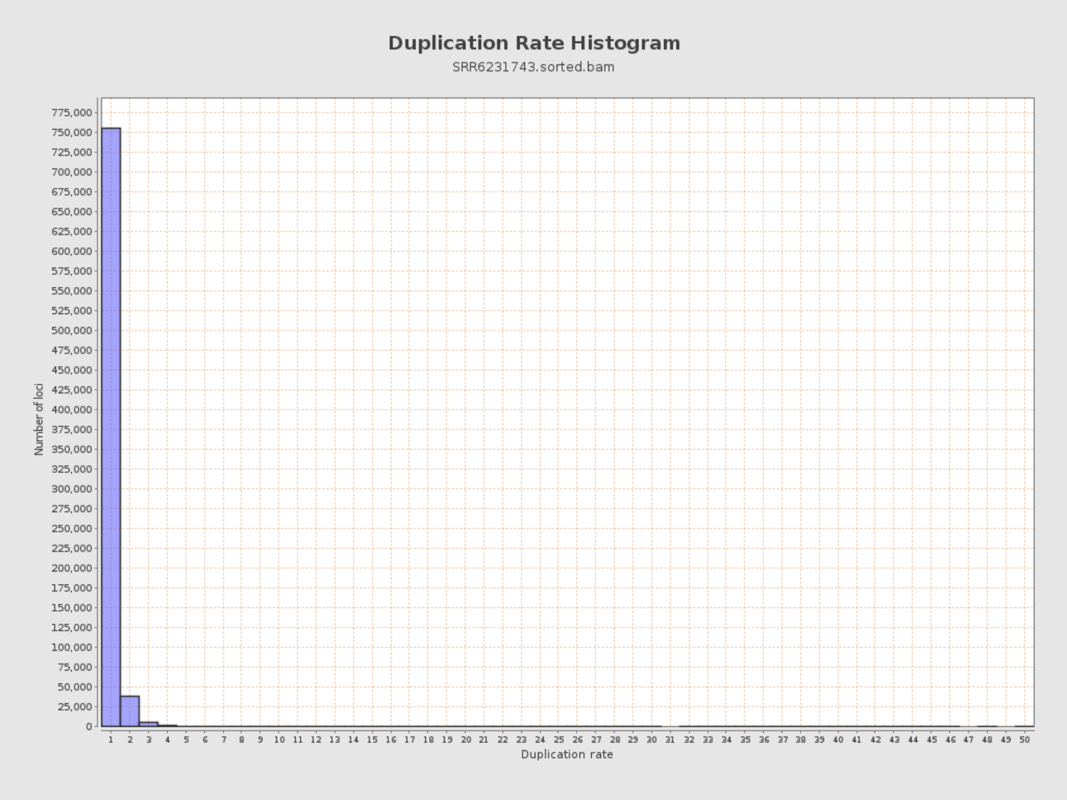
5. Results : Coverage Histogram (0-50X)



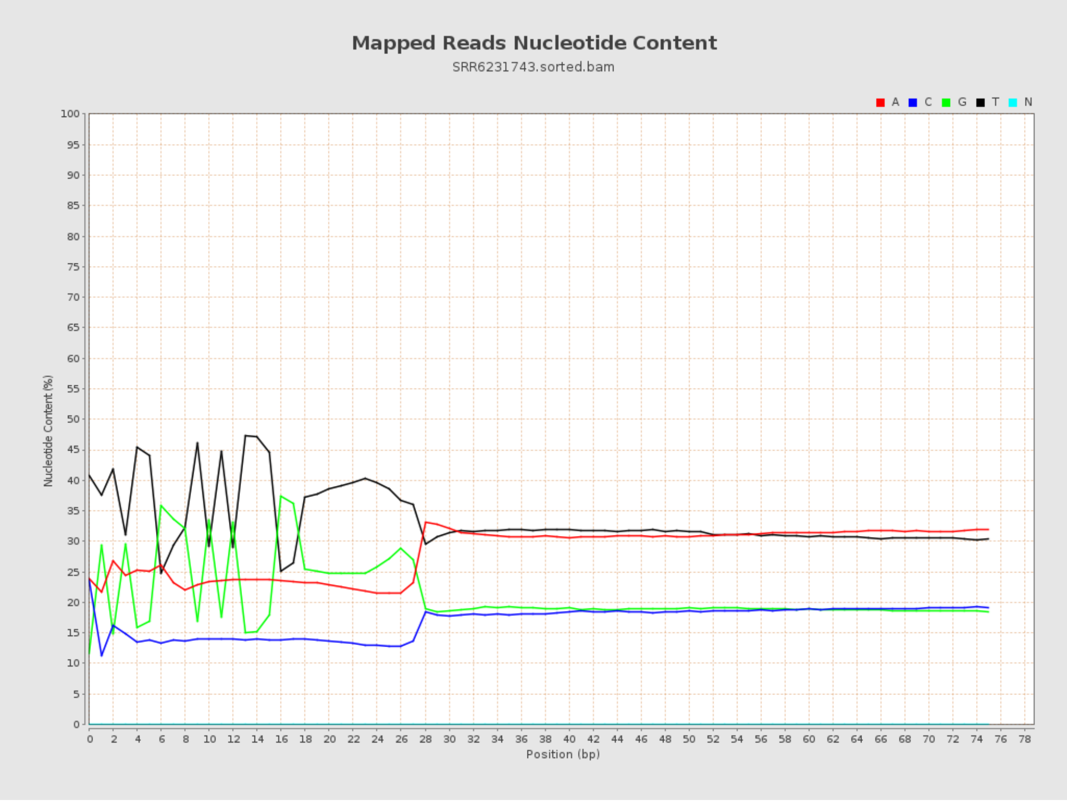
6. Results : Genome Fraction Coverage



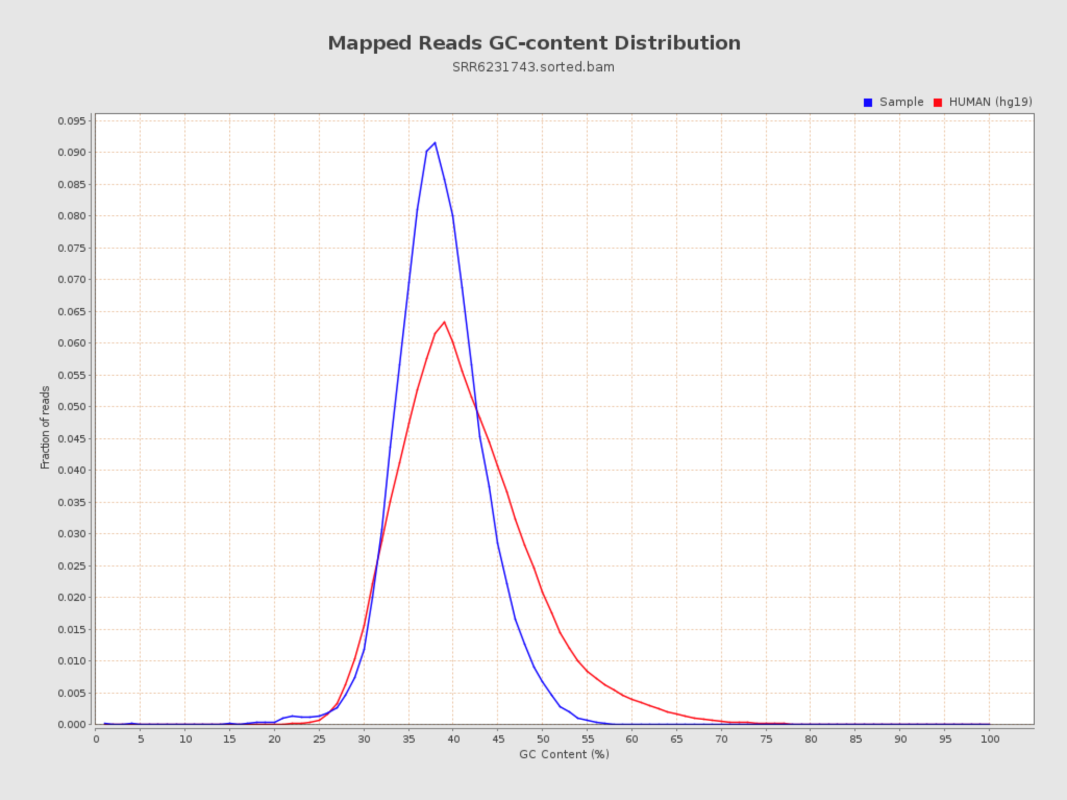
7. Results : Duplication Rate Histogram



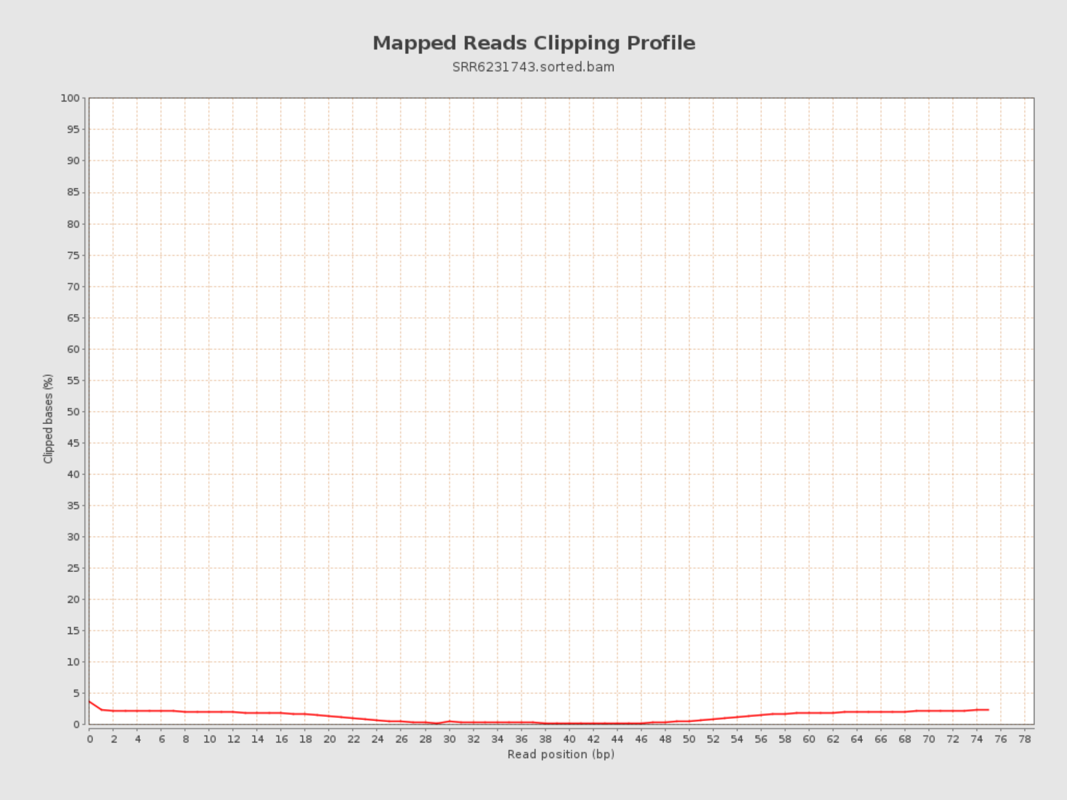
8. Results : Mapped Reads Nucleotide Content



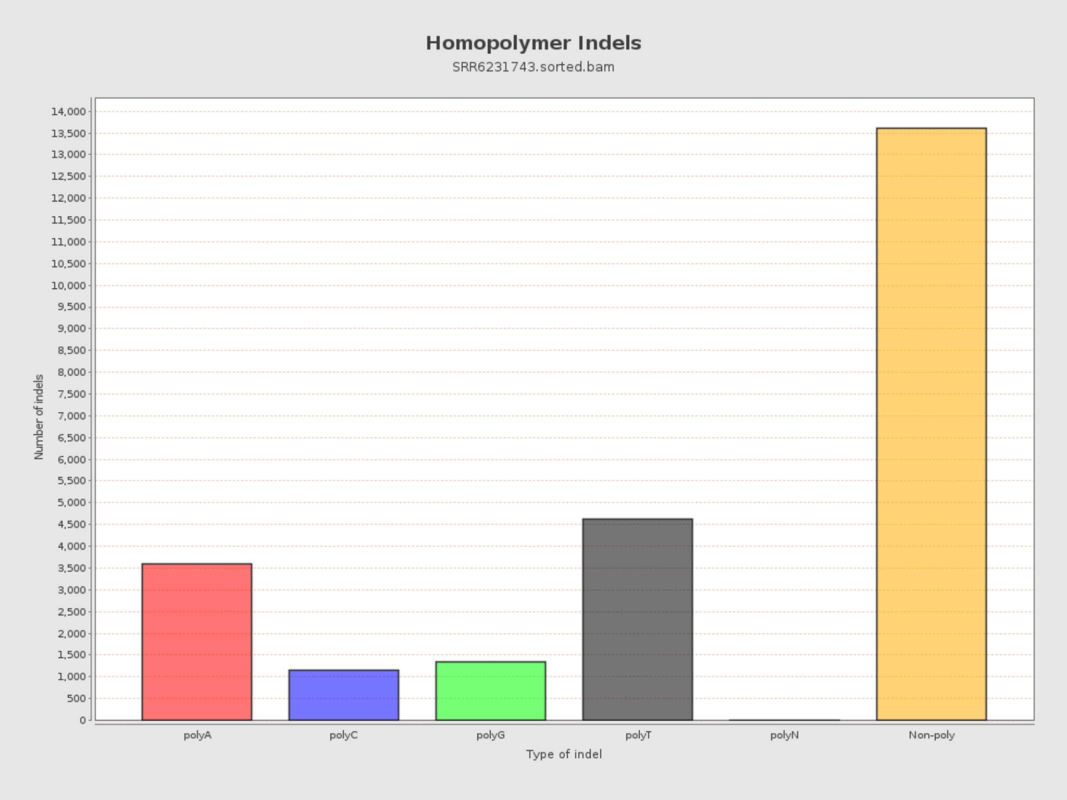
9. Results : Mapped Reads GC-content Distribution



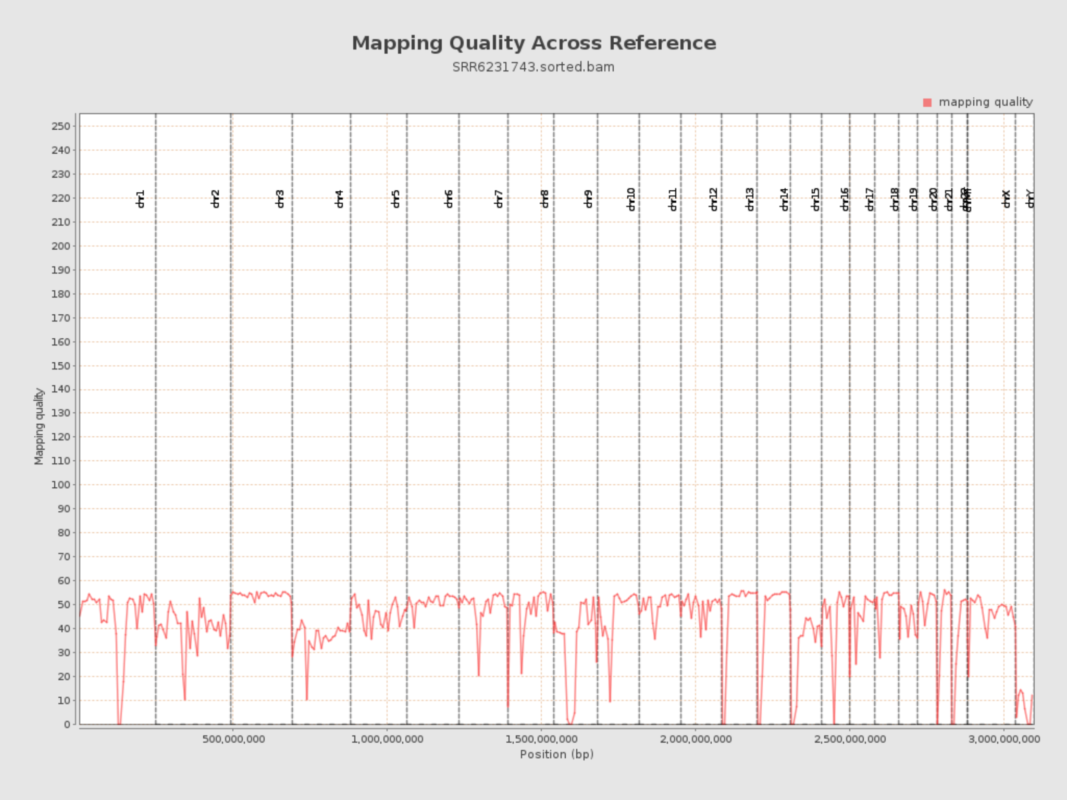
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram