Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:04:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716584.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_SRR9716584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716584.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:04:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,001,554
Mapped reads	922,105 / 92.07%
Unmapped reads	79,449 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,139 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	23,079 / 2.3%
Duplication rate	1.85%
Clipped reads	924,039 / 92.26%

2.2. ACGT Content

Number/percentage of A's	13,472,814 / 24.94%
Number/percentage of C's	11,274,240 / 20.87%
Number/percentage of T's	17,024,625 / 31.52%
Number/percentage of G's	12,242,727 / 22.67%
Number/percentage of N's	641 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0175

Standard Deviation	0.1777

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

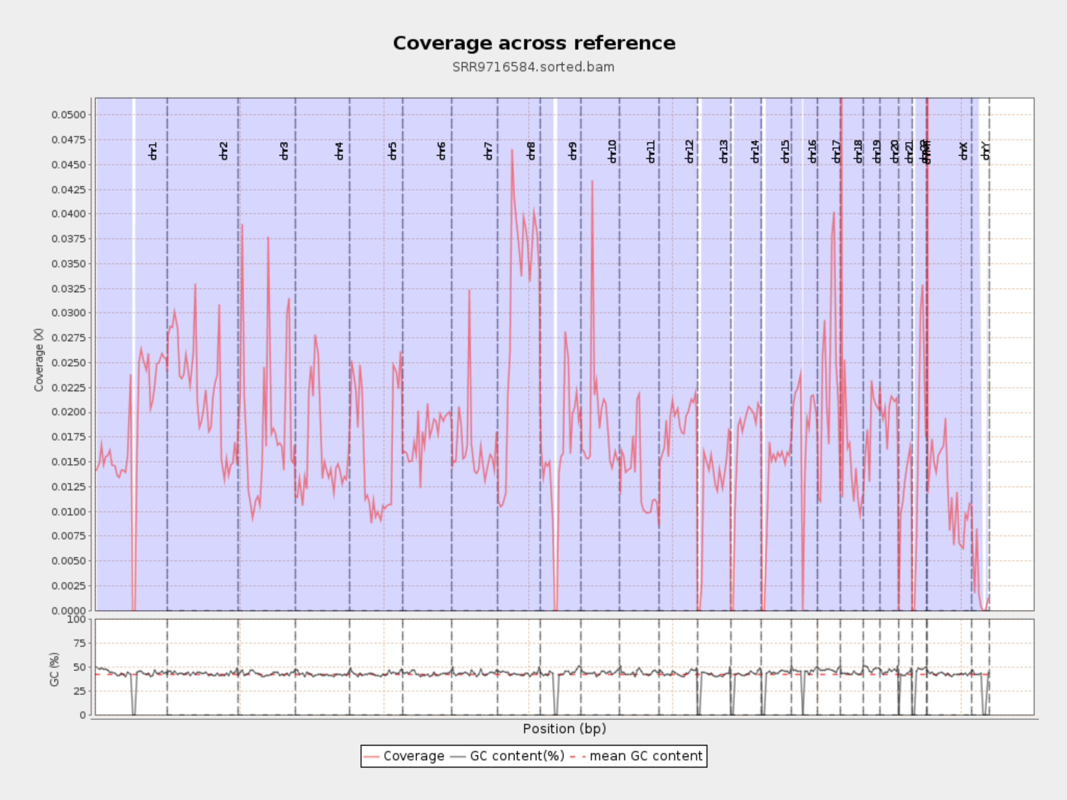
General error rate	0.51%
Mismatches	265,175
Insertions	4,270
Mapped reads with at least one insertion	0.46%
Deletions	10,424
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.69%

2.6. Chromosome stats

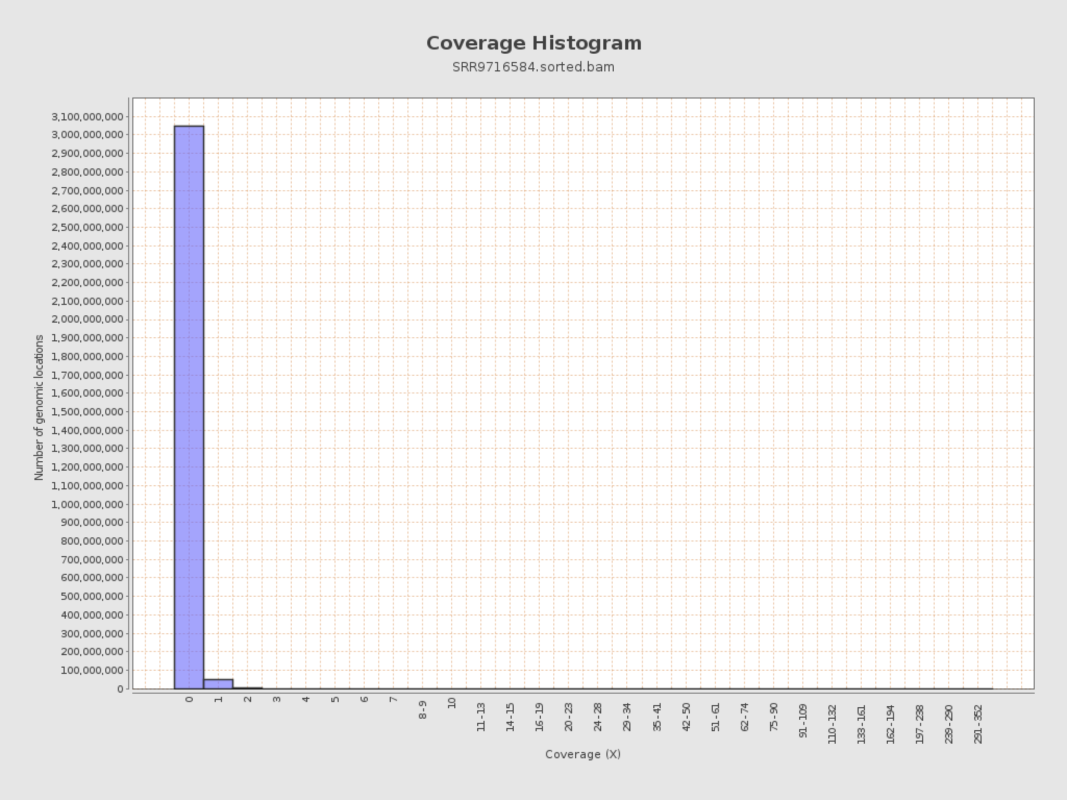
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4521445	0.0181	0.2517
chr2	243199373	5348725	0.022	0.2272
chr3	198022430	3703733	0.0187	0.1449
chr4	191154276	3028601	0.0158	0.1468
chr5	180915260	2925864	0.0162	0.1335
chr6	171115067	3036399	0.0177	0.1466
chr7	159138663	2620566	0.0165	0.2582

chr8	146364022	4526623	0.0309	0.2255
chr9	141213431	2201757	0.0156	0.1445
chr10	135534747	2590769	0.0191	0.2128
chr11	135006516	1841972	0.0136	0.1404
chr12	133851895	2535295	0.0189	0.1488
chr13	115169878	1404749	0.0122	0.1162
chr14	107349540	1769005	0.0165	0.1374
chr15	102531392	1310575	0.0128	0.1199
chr16	90354753	1666123	0.0184	0.1471
chr17	81195210	1893564	0.0233	0.1644
chr18	78077248	1297001	0.0166	0.2176
chr19	59128983	1109102	0.0188	0.2086
chr20	63025520	1260469	0.02	0.1516
chr21	48129895	573599	0.0119	0.129
chr22	51304566	853488	0.0166	0.1362
chrMT	16571	8488	0.5122	0.7891
chrX	155270560	1867947	0.012	0.1241
chrY	59373566	135745	0.0023	0.0723

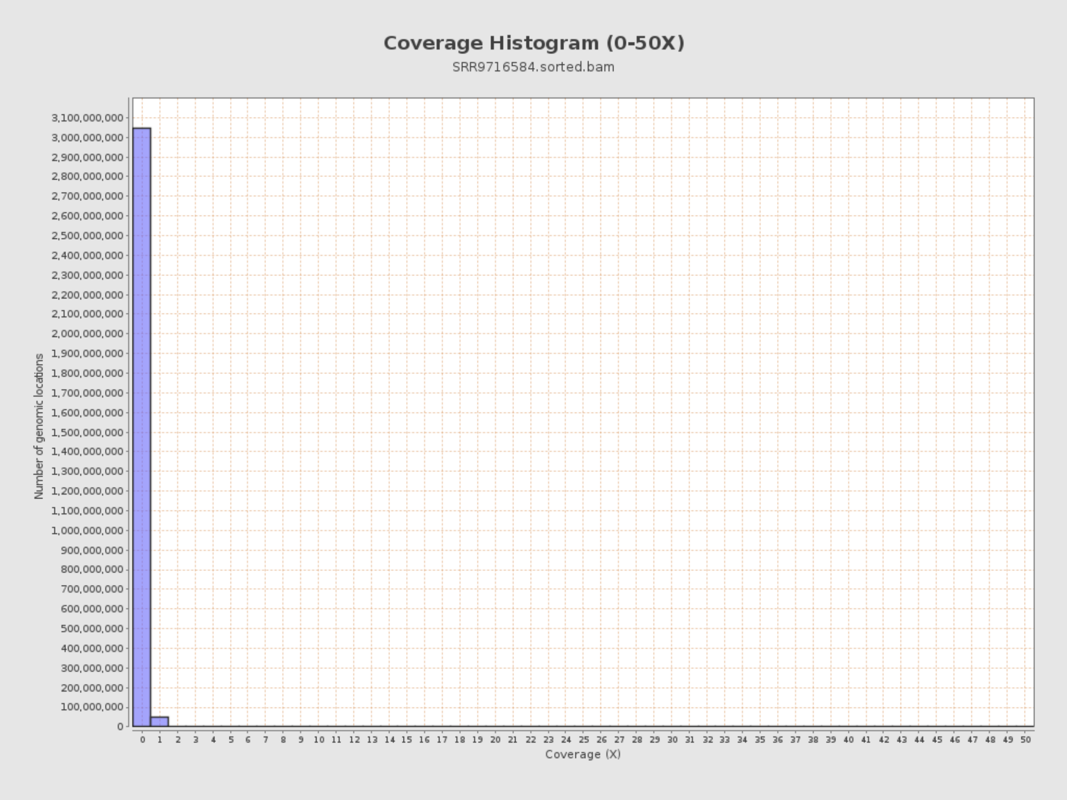
3. Results : Coverage across reference



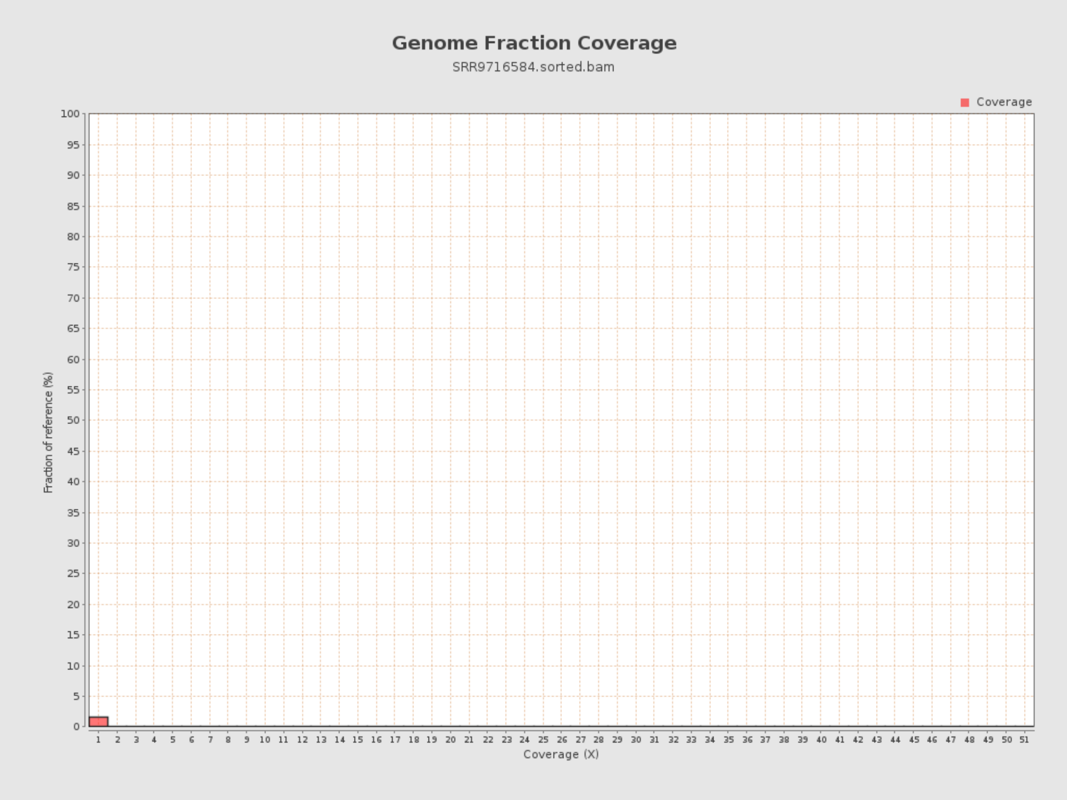
4. Results : Coverage Histogram



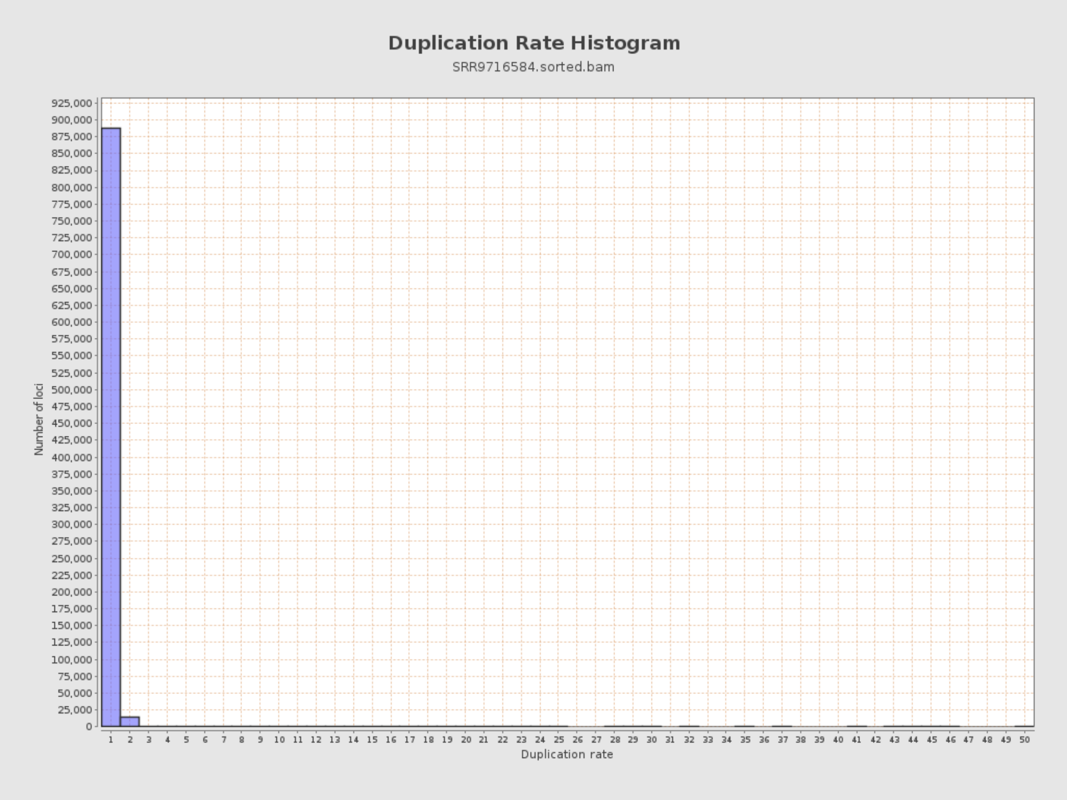
5. Results : Coverage Histogram (0-50X)



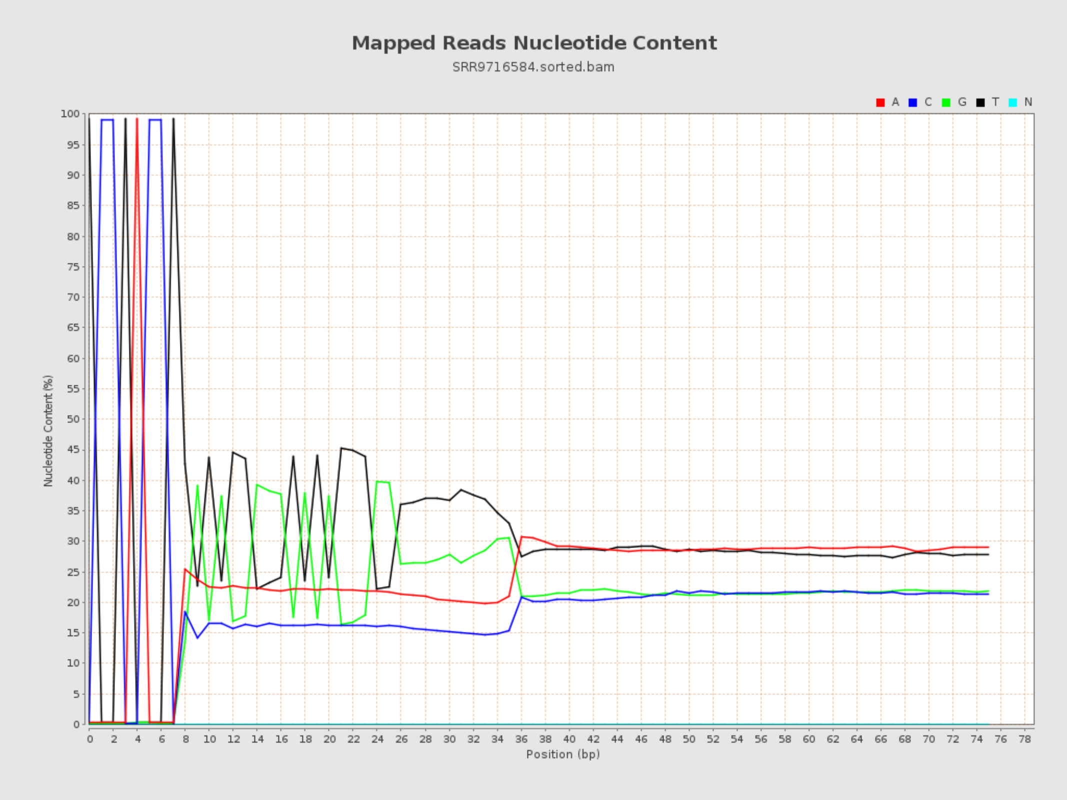
6. Results : Genome Fraction Coverage



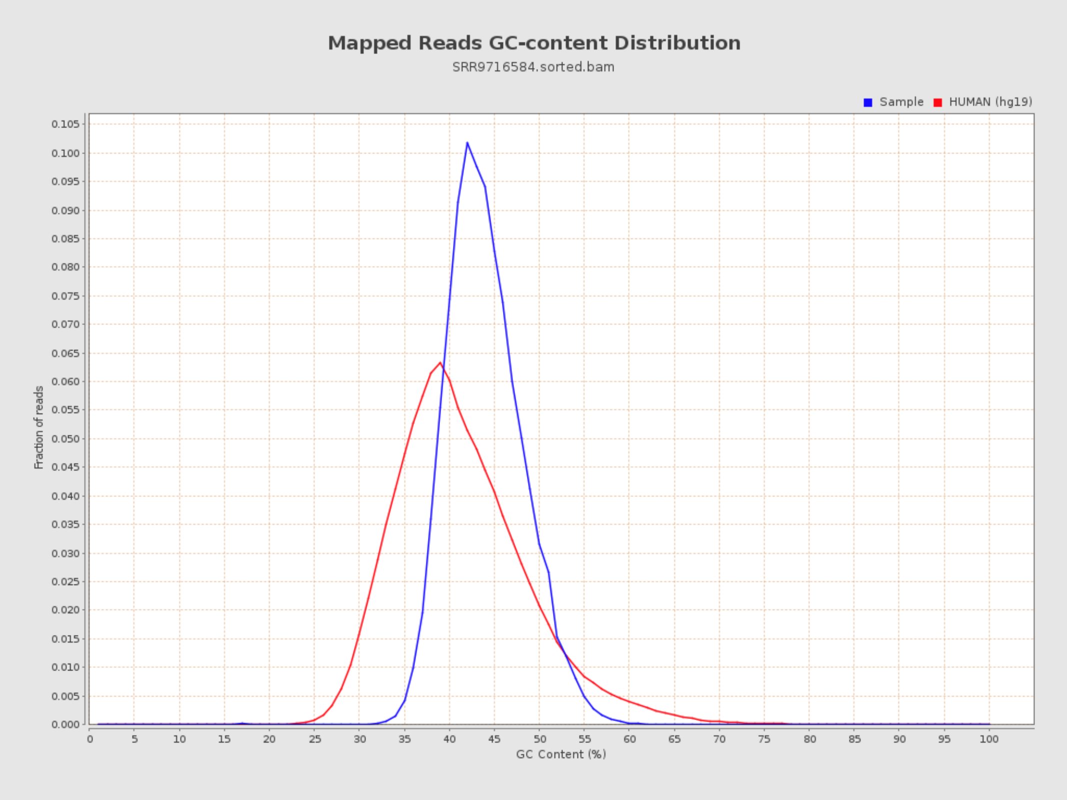
7. Results : Duplication Rate Histogram



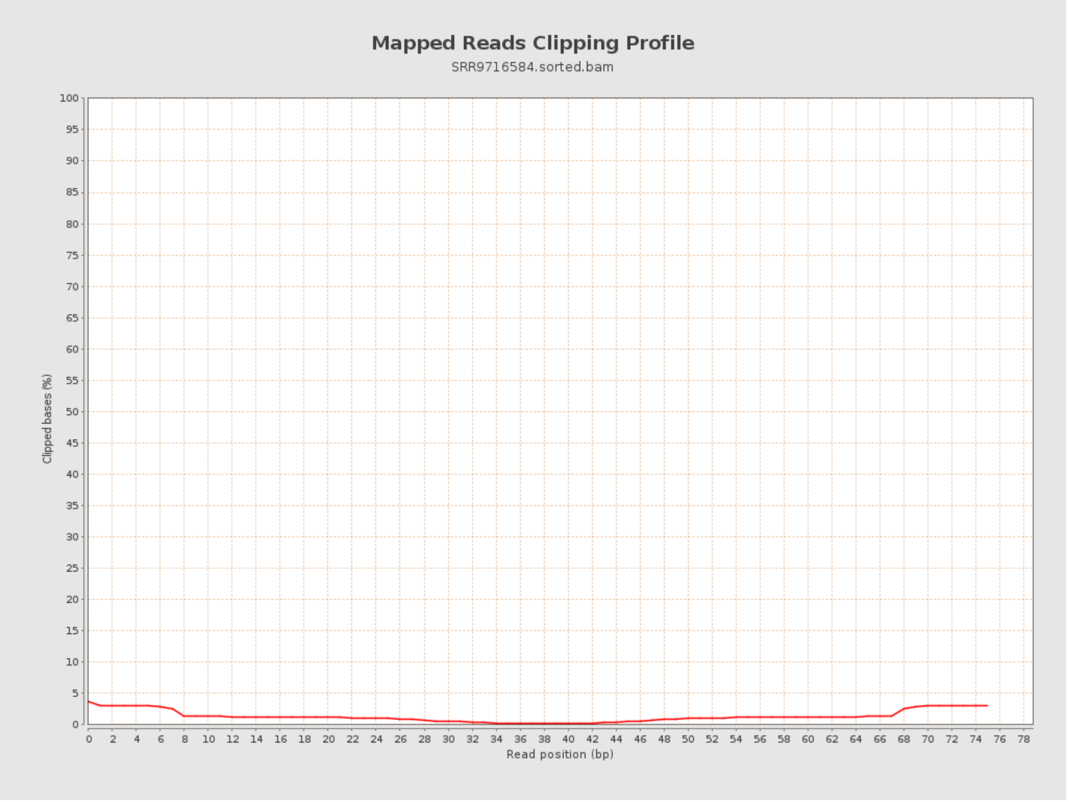
8. Results : Mapped Reads Nucleotide Content



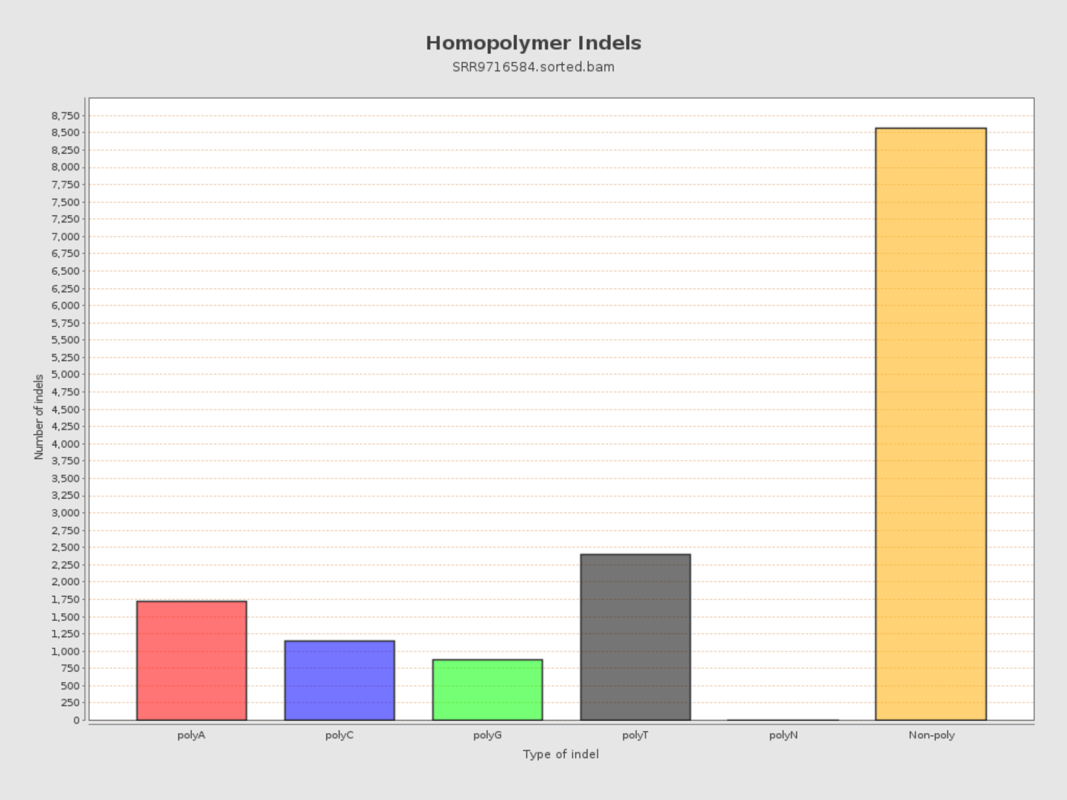
9. Results : Mapped Reads GC-content Distribution



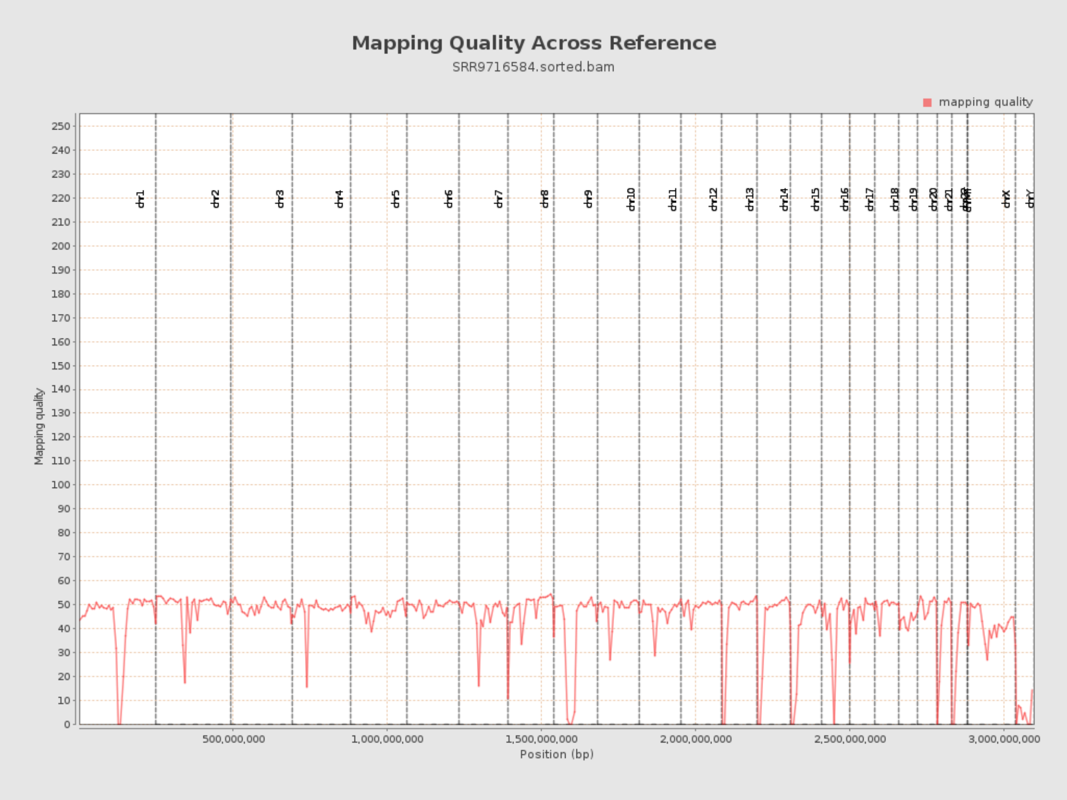
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram