Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:29:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716304.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_SRR9716304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:29:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	748,142
Mapped reads	682,757 / 91.26%
Unmapped reads	65,385 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,255 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	17,425 / 2.33%
Duplication rate	2.05%
Clipped reads	684,240 / 91.46%

2.2. ACGT Content

Number/percentage of A's	9,703,023 / 24.64%
Number/percentage of C's	6,936,903 / 17.62%
Number/percentage of T's	12,467,366 / 31.66%
Number/percentage of G's	10,267,208 / 26.08%
Number/percentage of N's	418 / 0%
GC Percentage	43.69%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1404

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

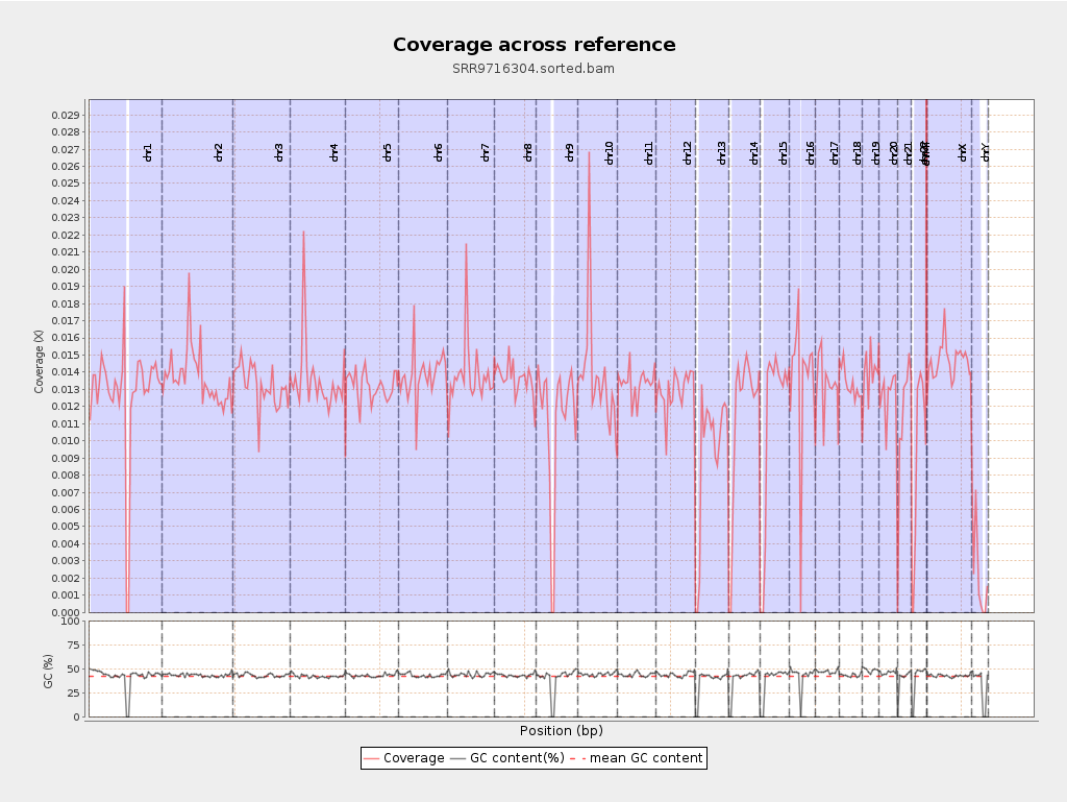
General error rate	0.5%
Mismatches	194,257
Insertions	2,206
Mapped reads with at least one insertion	0.32%
Deletions	7,517
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.57%

2.6. Chromosome stats

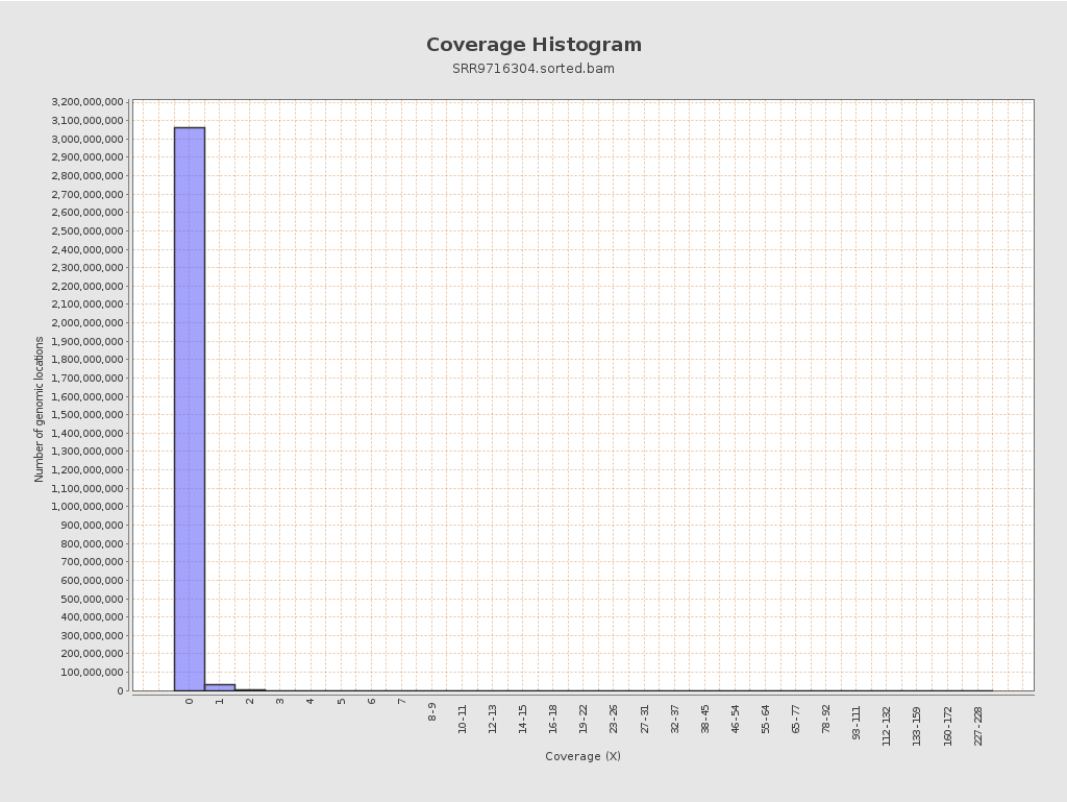
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3173793	0.0127	0.1834
chr2	243199373	3336619	0.0137	0.1664
chr3	198022430	2618279	0.0132	0.1212
chr4	191154276	2581936	0.0135	0.1287
chr5	180915260	2381015	0.0132	0.1204
chr6	171115067	2365624	0.0138	0.1336
chr7	159138663	2203646	0.0138	0.1813

chr8	146364022	1995258	0.0136	0.1444
chr9	141213431	1566318	0.0111	0.123
chr10	135534747	1864674	0.0138	0.1617
chr11	135006516	1794941	0.0133	0.1339
chr12	133851895	1722879	0.0129	0.1193
chr13	115169878	1064497	0.0092	0.1008
chr14	107349540	1212905	0.0113	0.1134
chr15	102531392	1150644	0.0112	0.1116
chr16	90354753	1222618	0.0135	0.1298
chr17	81195210	1068024	0.0132	0.1258
chr18	78077248	1044112	0.0134	0.1808
chr19	59128983	826353	0.014	0.1613
chr20	63025520	790417	0.0125	0.1204
chr21	48129895	546846	0.0114	0.1152
chr22	51304566	456865	0.0089	0.1002
chrMT	16571	1093	0.066	0.2772
chrX	155270560	2273283	0.0146	0.1328
chrY	59373566	124592	0.0021	0.0675

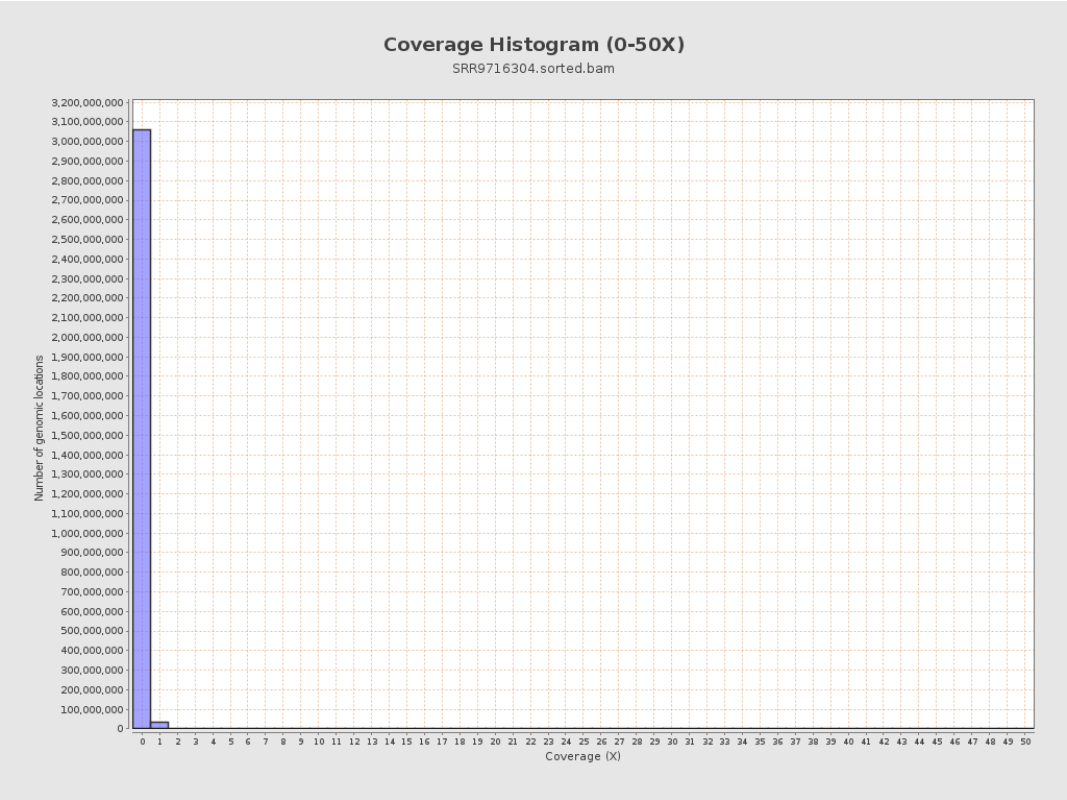
3. Results : Coverage across reference



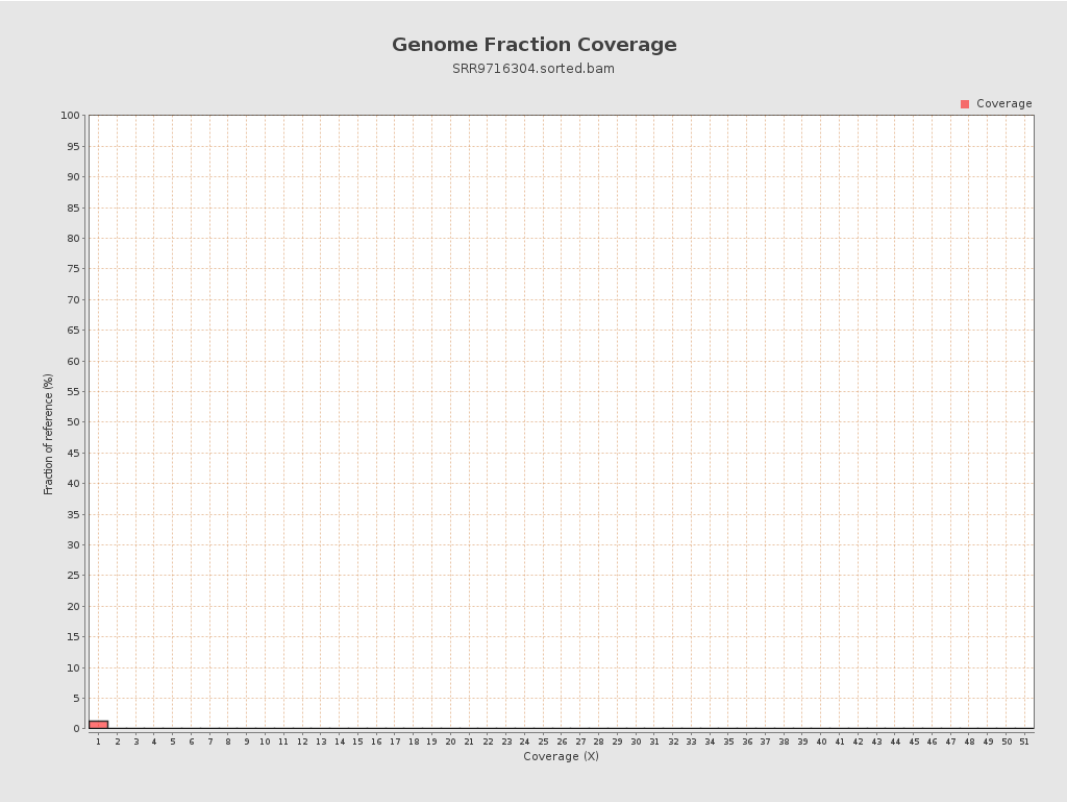
4. Results : Coverage Histogram



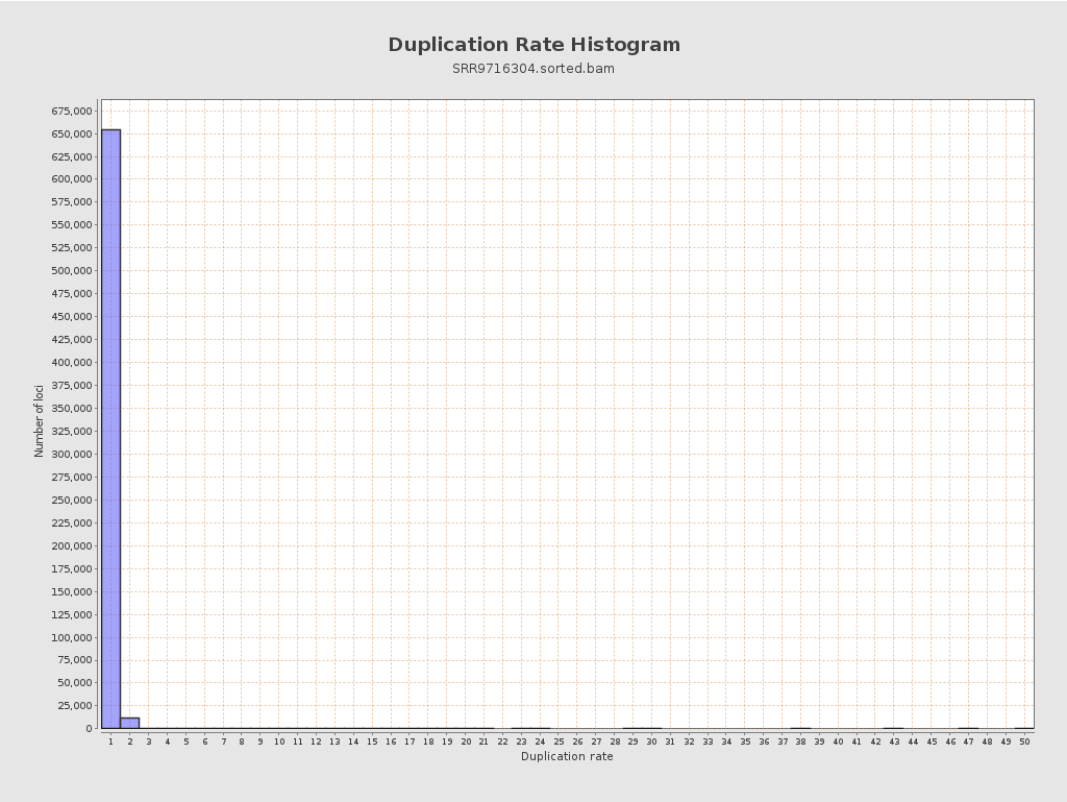
5. Results : Coverage Histogram (0-50X)



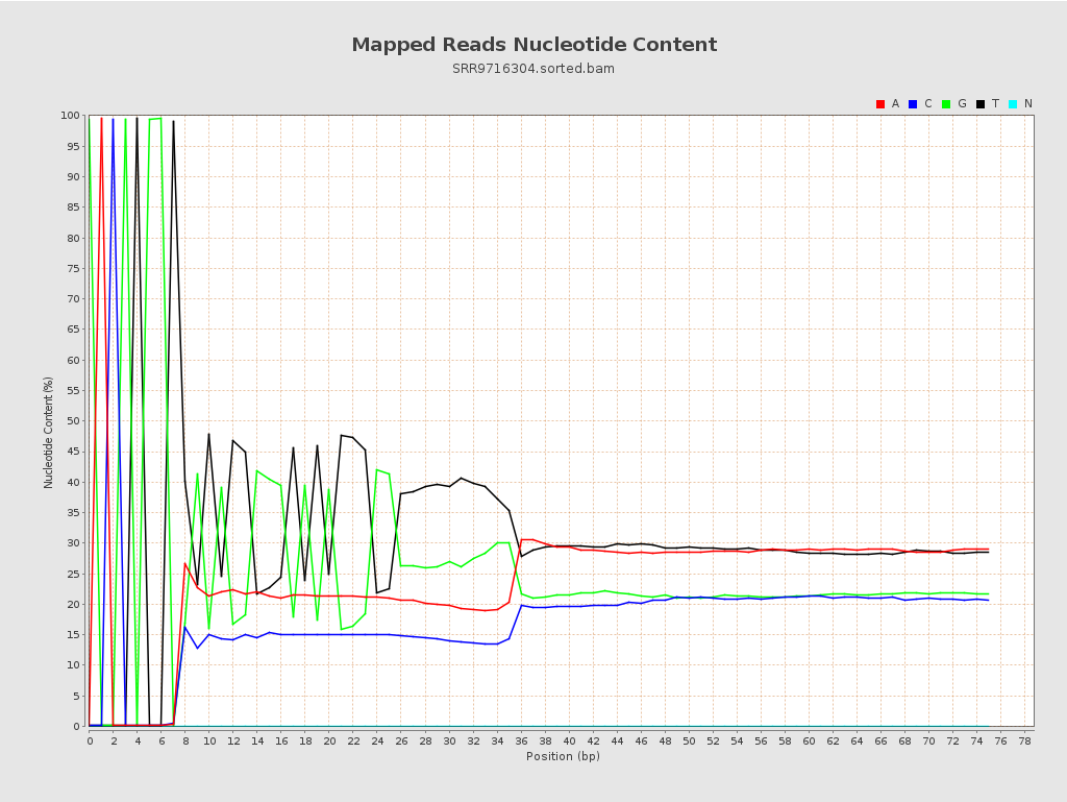
6. Results : Genome Fraction Coverage



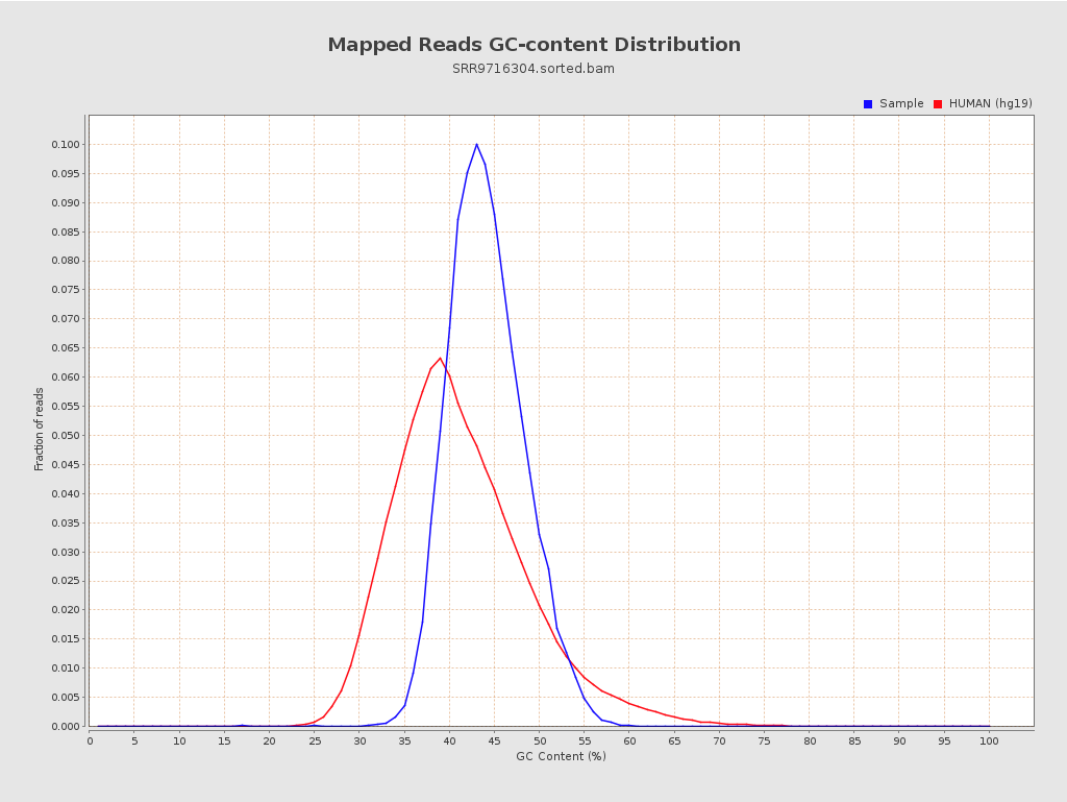
7. Results : Duplication Rate Histogram



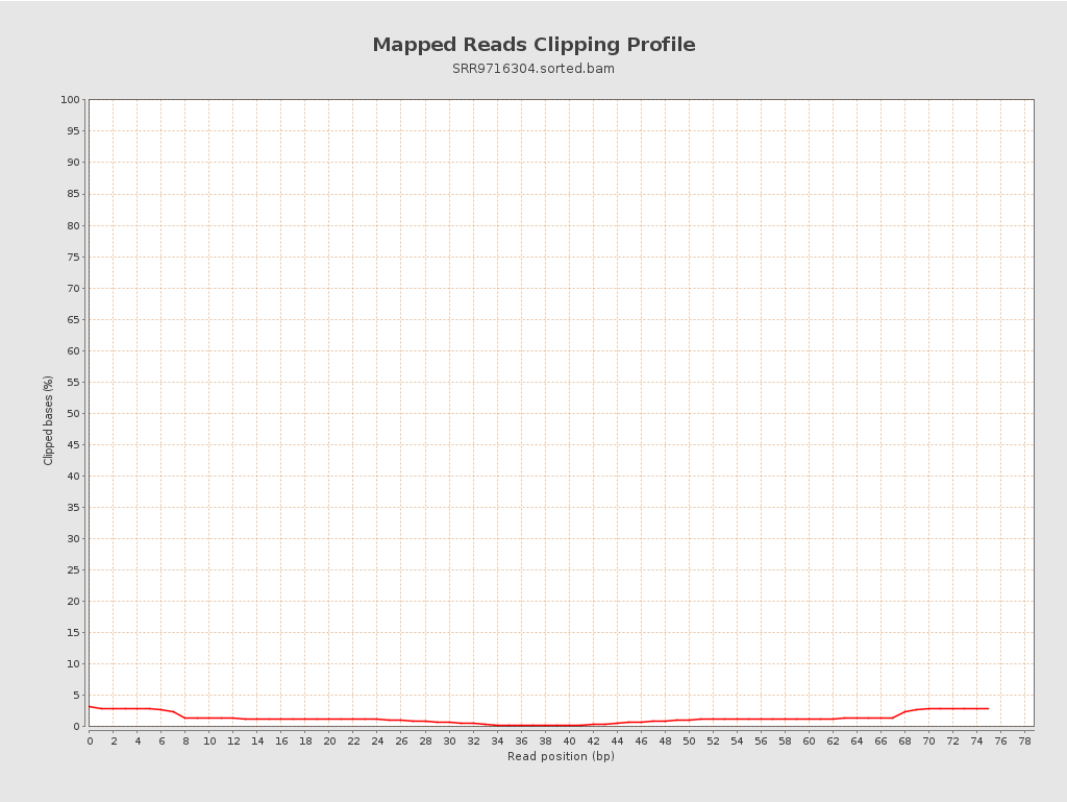
8. Results : Mapped Reads Nucleotide Content



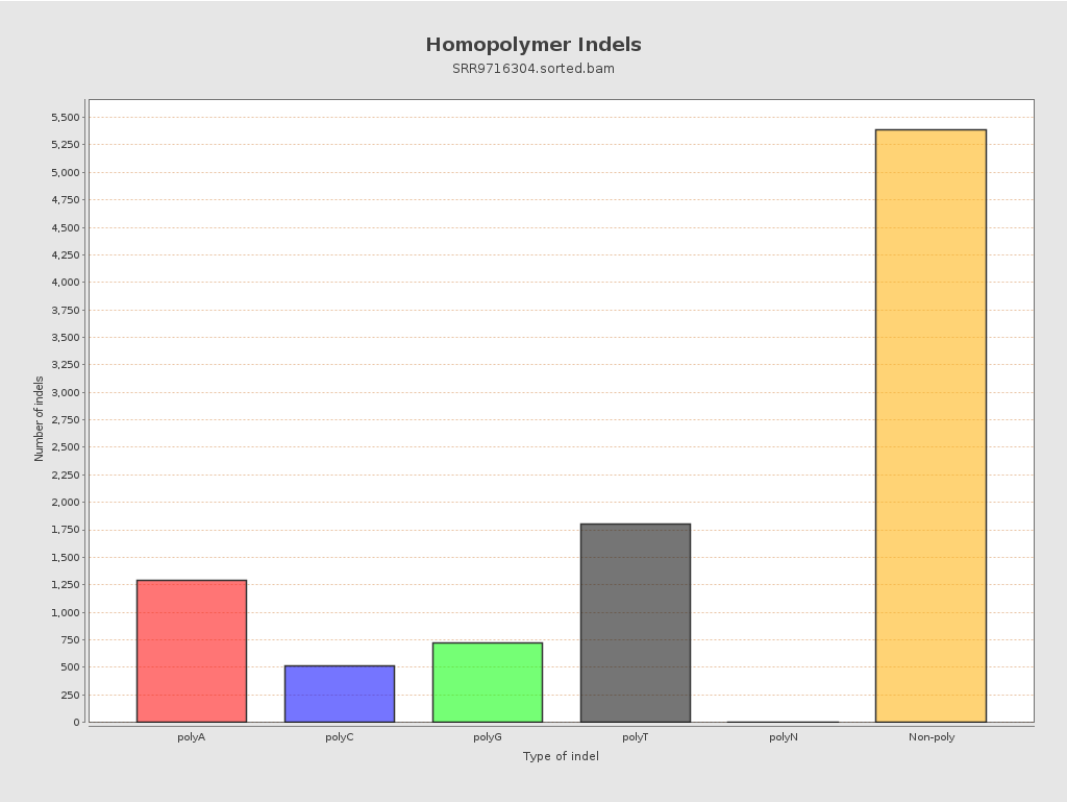
9. Results : Mapped Reads GC-content Distribution



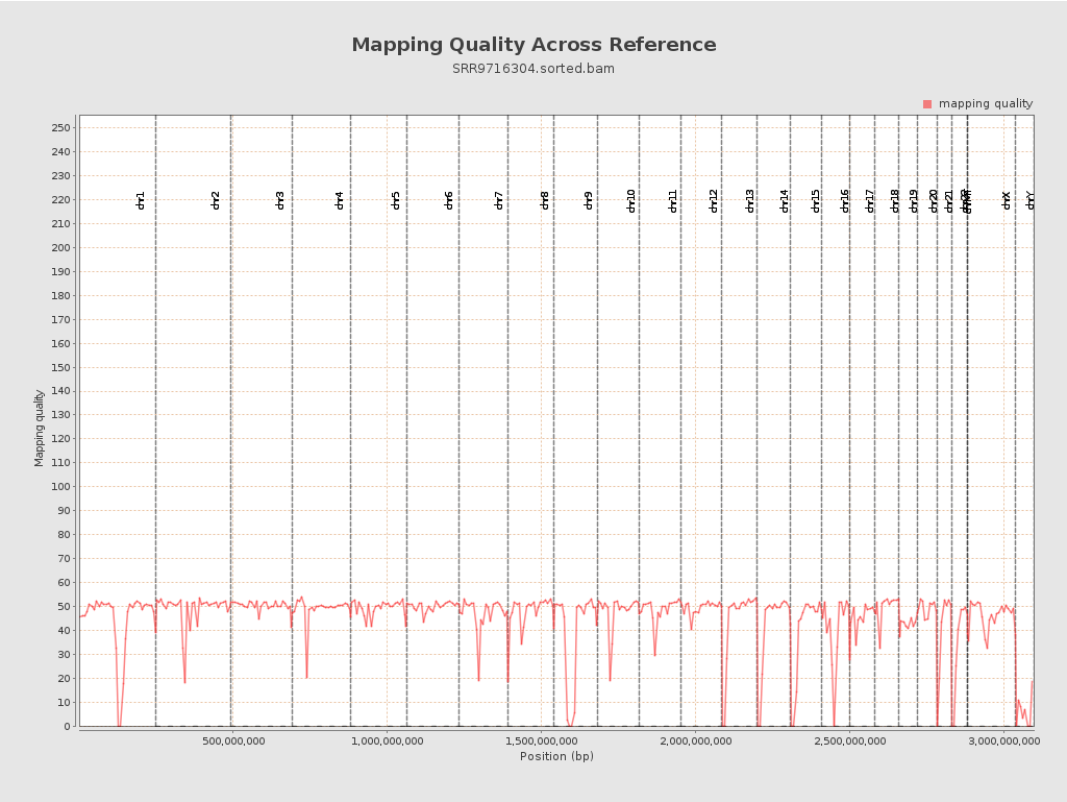
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram