Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:12:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716104.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_SRR9716104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:12:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,198,483
Mapped reads	1,085,018 / 90.53%
Unmapped reads	113,465 / 9.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,392 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	29,279 / 2.44%
Duplication rate	1.76%
Clipped reads	1,087,488 / 90.74%

2.2. ACGT Content

Number/percentage of A's	15,002,127 / 23.96%
Number/percentage of C's	11,362,752 / 18.14%
Number/percentage of T's	20,396,468 / 32.57%
Number/percentage of G's	15,860,344 / 25.33%
Number/percentage of N's	654 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2256

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

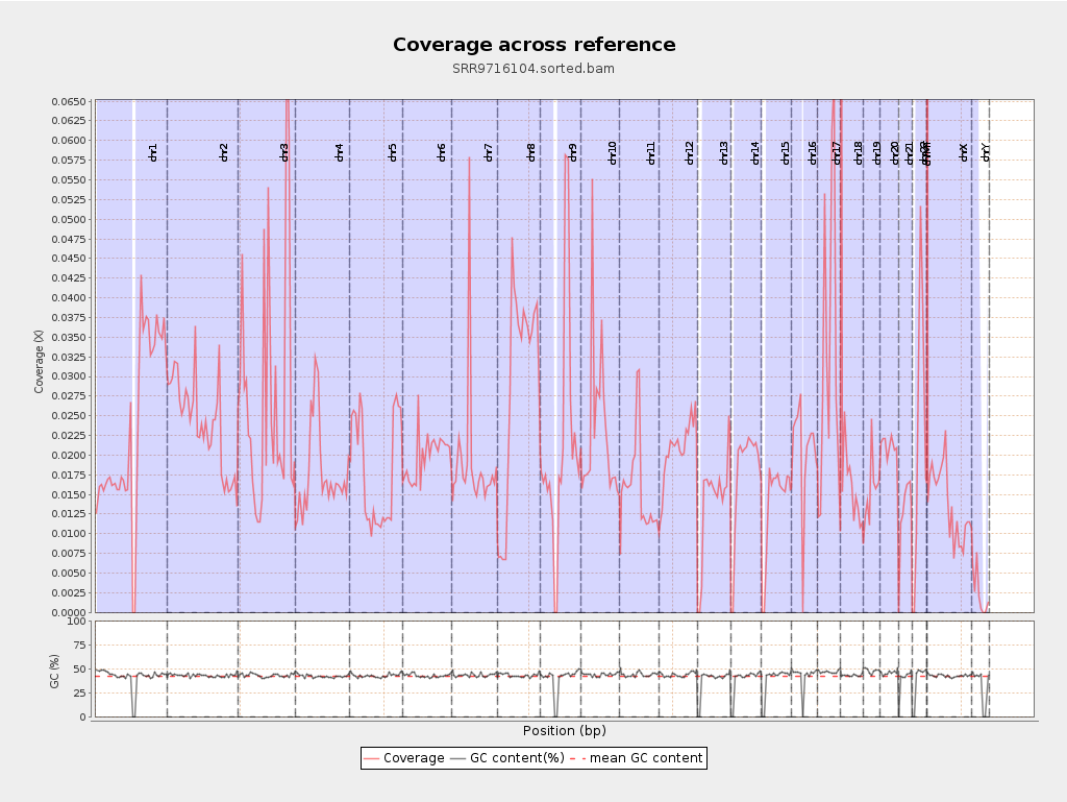
General error rate	0.51%
Mismatches	314,577
Insertions	4,158
Mapped reads with at least one insertion	0.38%
Deletions	10,547
Mapped reads with at least one deletion	0.97%
Homopolymer indels	42.22%

2.6. Chromosome stats

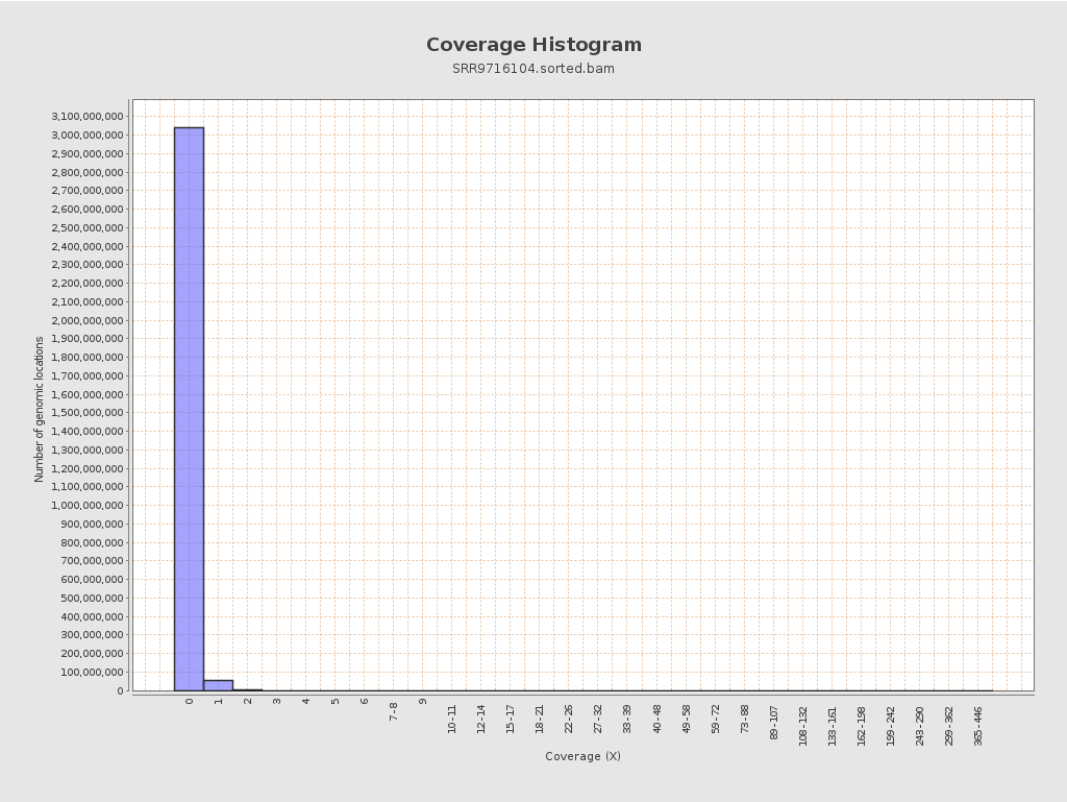
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5824465	0.0234	0.2844
chr2	243199373	5860107	0.0241	0.2531
chr3	198022430	5410220	0.0273	0.1867
chr4	191154276	3373574	0.0176	0.1468
chr5	180915260	3232295	0.0179	0.1425
chr6	171115067	3386685	0.0198	0.1599
chr7	159138663	3042496	0.0191	0.4994

chr8	146364022	4311331	0.0295	0.2406
chr9	141213431	2929004	0.0207	0.169
chr10	135534747	3100912	0.0229	0.3337
chr11	135006516	2158961	0.016	0.1606
chr12	133851895	2777614	0.0208	0.176
chr13	115169878	1621439	0.0141	0.1254
chr14	107349540	1871831	0.0174	0.1428
chr15	102531392	1399270	0.0136	0.1298
chr16	90354753	1826709	0.0202	0.1611
chr17	81195210	2629539	0.0324	0.1994
chr18	78077248	1531487	0.0196	0.2413
chr19	59128983	923489	0.0156	0.2768
chr20	63025520	1318101	0.0209	0.1642
chr21	48129895	624826	0.013	0.1236
chr22	51304566	1191837	0.0232	0.1645
chrMT	16571	7585	0.4577	0.7788
chrX	155270560	2144578	0.0138	0.1443
chrY	59373566	140330	0.0024	0.0647

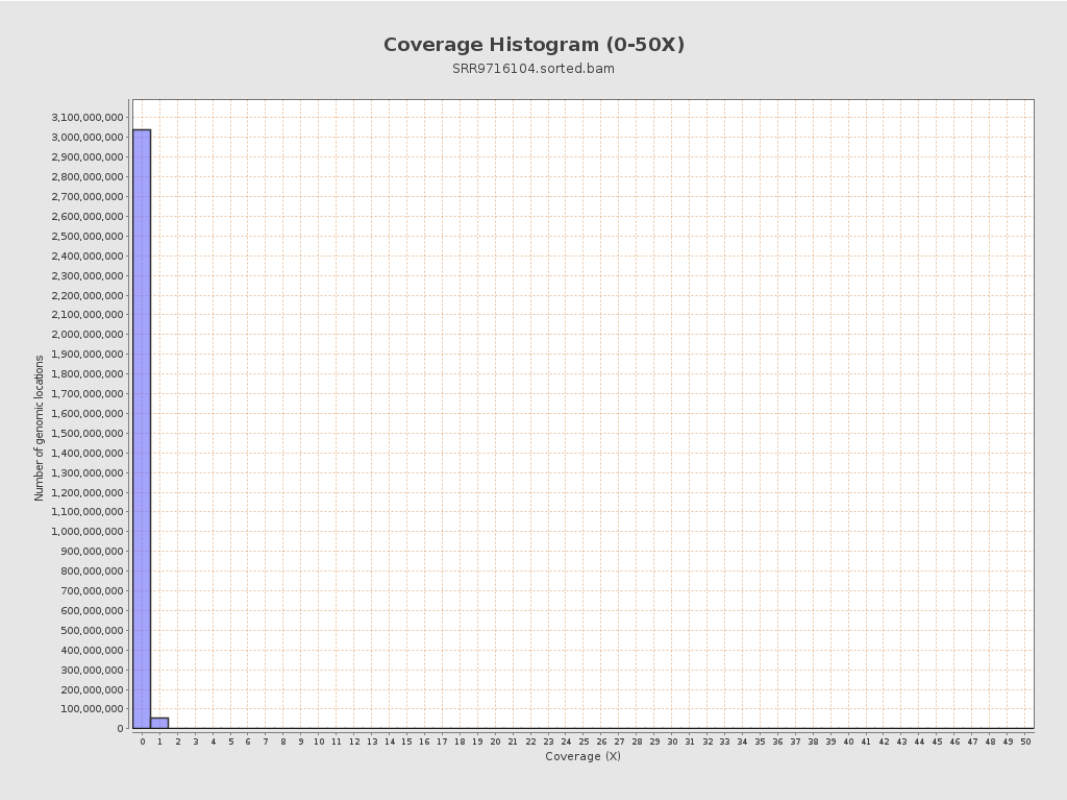
3. Results : Coverage across reference



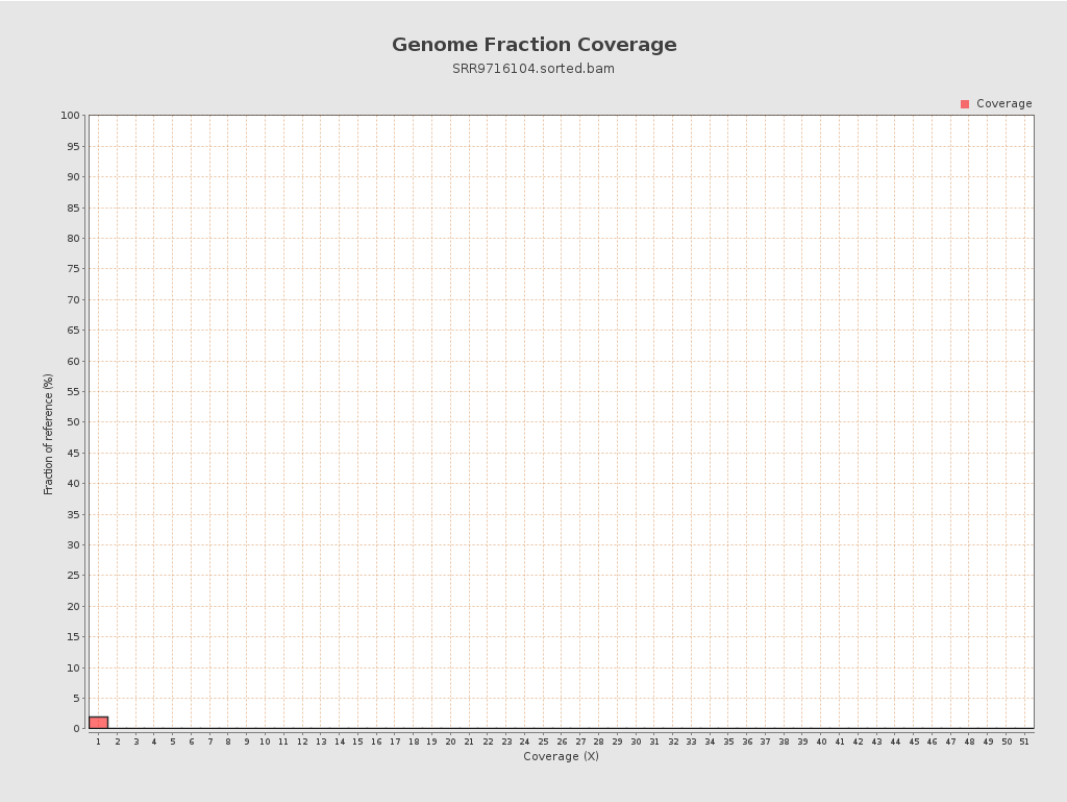
4. Results : Coverage Histogram



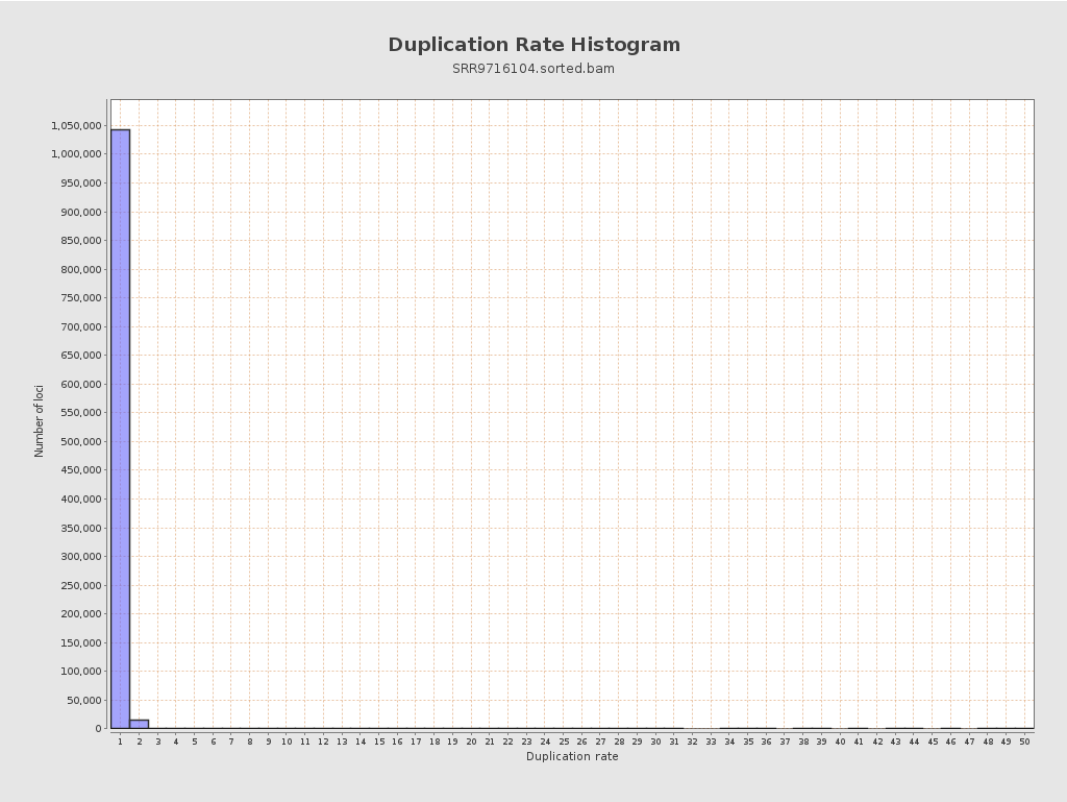
5. Results : Coverage Histogram (0-50X)



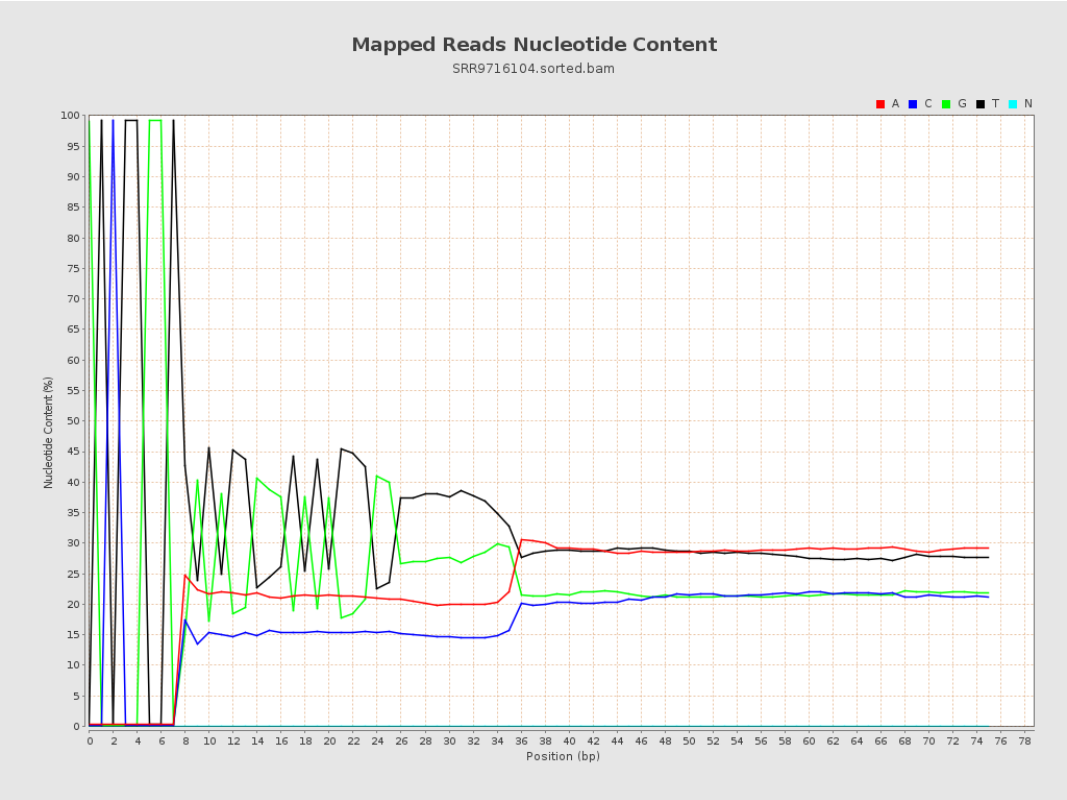
6. Results : Genome Fraction Coverage



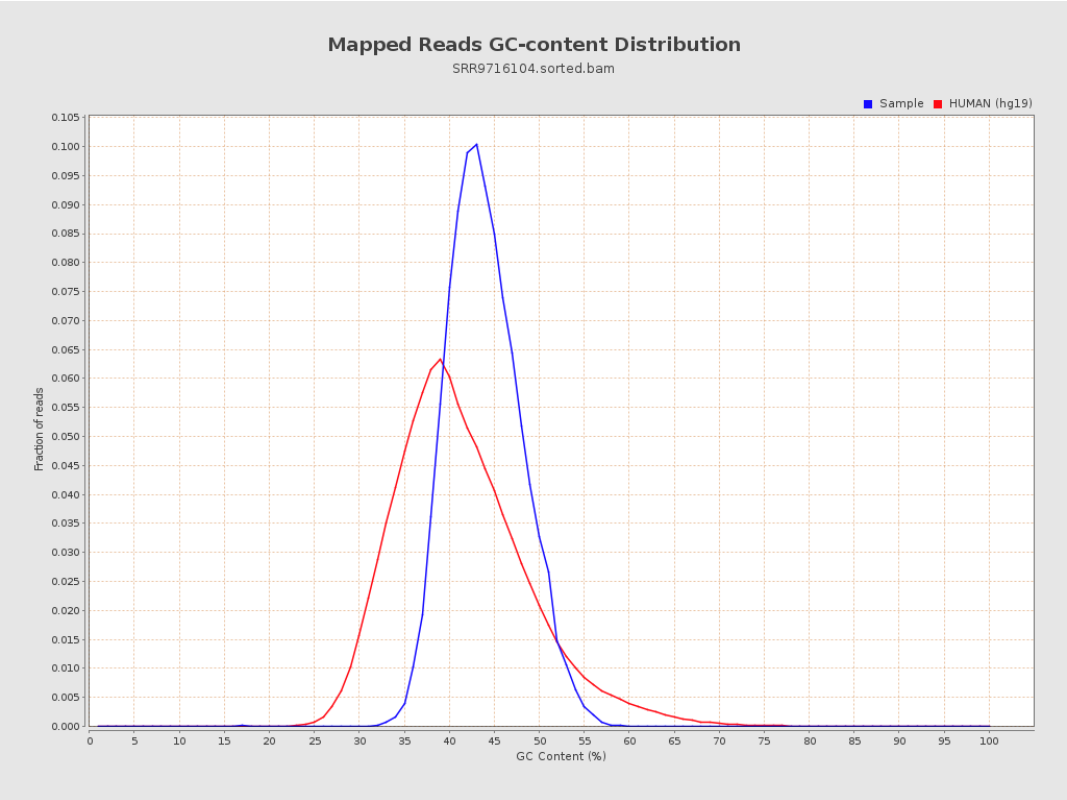
7. Results : Duplication Rate Histogram



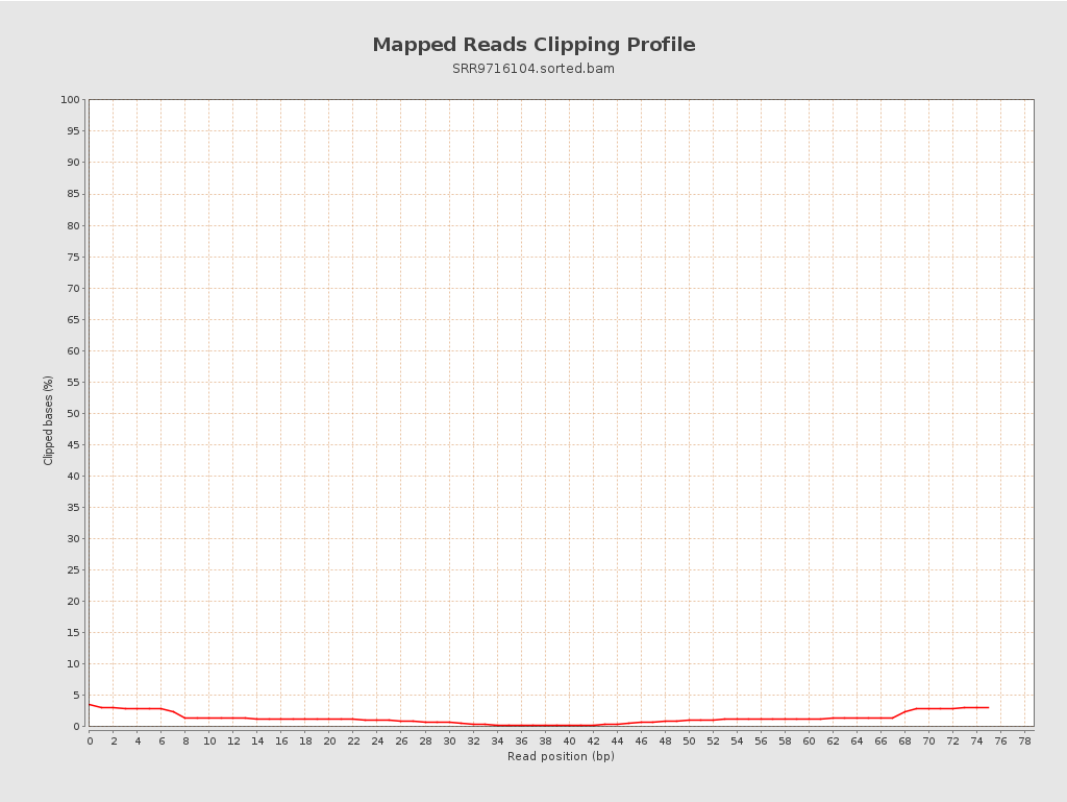
8. Results : Mapped Reads Nucleotide Content



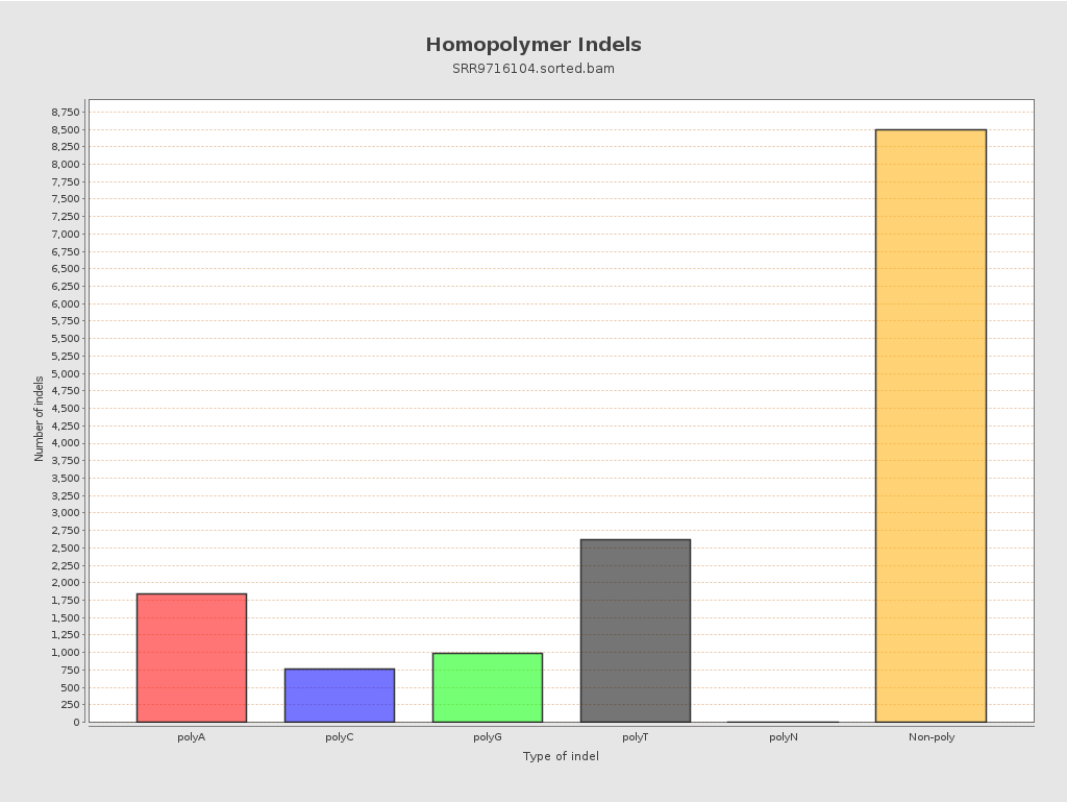
9. Results : Mapped Reads GC-content Distribution



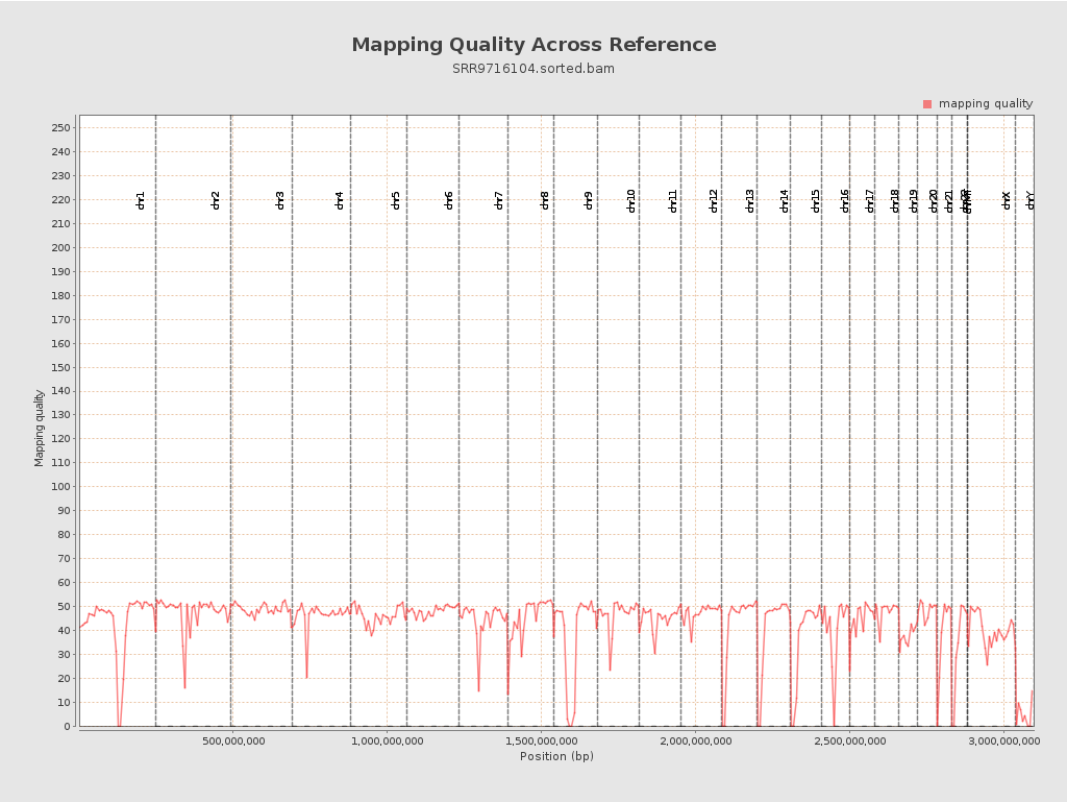
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram