Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:32:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716247.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_SRR9716247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:32:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,495,929
Mapped reads	1,344,821 / 89.9%
Unmapped reads	151,108 / 10.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,254 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	35,622 / 2.38%
Duplication rate	2%
Clipped reads	1,346,772 / 90.03%

2.2. ACGT Content

Number/percentage of A's	19,272,405 / 25.22%
Number/percentage of C's	14,683,775 / 19.21%
Number/percentage of T's	24,084,374 / 31.51%
Number/percentage of G's	18,389,730 / 24.06%
Number/percentage of N's	1,698 / 0%
GC Percentage	43.27%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2131

2.4. Mapping Quality

Mean Mapping Quality	44.41

2.5. Mismatches and indels

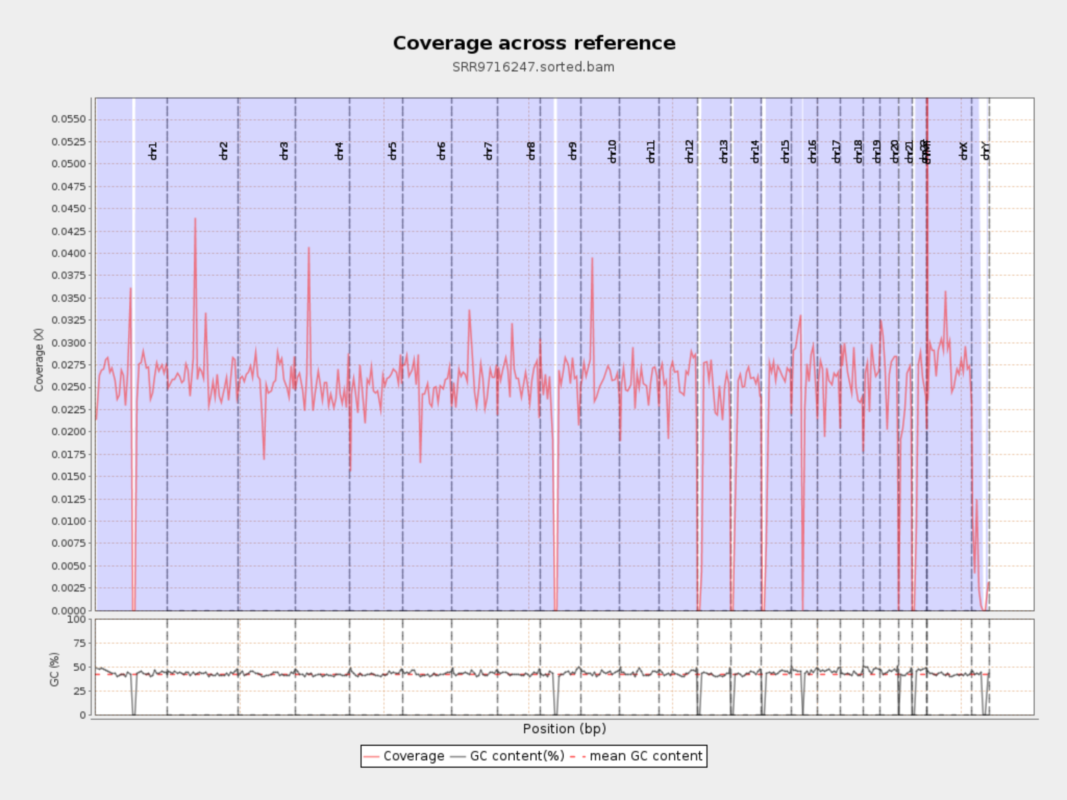
General error rate	0.51%
Mismatches	379,203
Insertions	5,204
Mapped reads with at least one insertion	0.39%
Deletions	12,050
Mapped reads with at least one deletion	0.89%
Homopolymer indels	40.54%

2.6. Chromosome stats

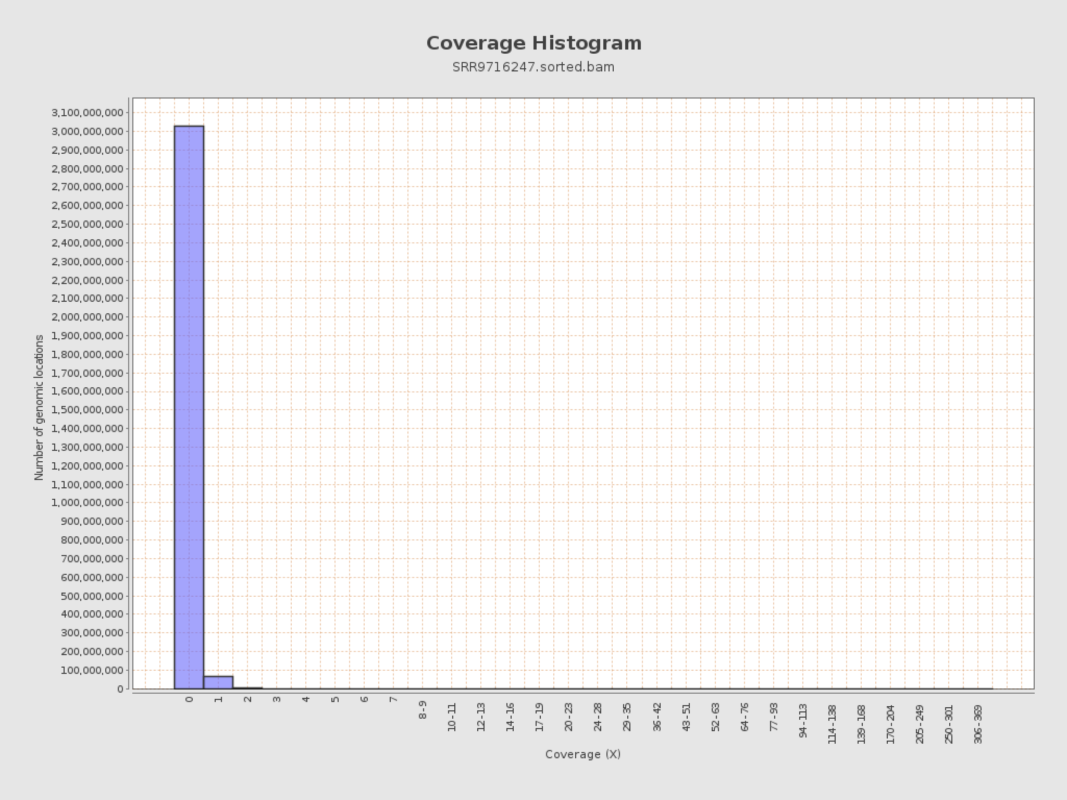
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6211828	0.0249	0.3203
chr2	243199373	6449135	0.0265	0.2426
chr3	198022430	5084249	0.0257	0.1724
chr4	191154276	4860810	0.0254	0.185
chr5	180915260	4578298	0.0253	0.1717
chr6	171115067	4326640	0.0253	0.179
chr7	159138663	4150532	0.0261	0.2332

chr8	146364022	3832278	0.0262	0.2029
chr9	141213431	3213828	0.0228	0.2159
chr10	135534747	3634191	0.0268	0.2144
chr11	135006516	3456636	0.0256	0.2151
chr12	133851895	3491469	0.0261	0.175
chr13	115169878	2414703	0.021	0.155
chr14	107349540	2309002	0.0215	0.1662
chr15	102531392	2212239	0.0216	0.1577
chr16	90354753	2288414	0.0253	0.1832
chr17	81195210	2071484	0.0255	0.1778
chr18	78077248	2042832	0.0262	0.368
chr19	59128983	1559335	0.0264	0.2505
chr20	63025520	1711696	0.0272	0.1838
chr21	48129895	1008950	0.021	0.1708
chr22	51304566	937958	0.0183	0.1462
chrMT	16571	3891	0.2348	0.5598
chrX	155270560	4374029	0.0282	0.2
chrY	59373566	228379	0.0038	0.0939

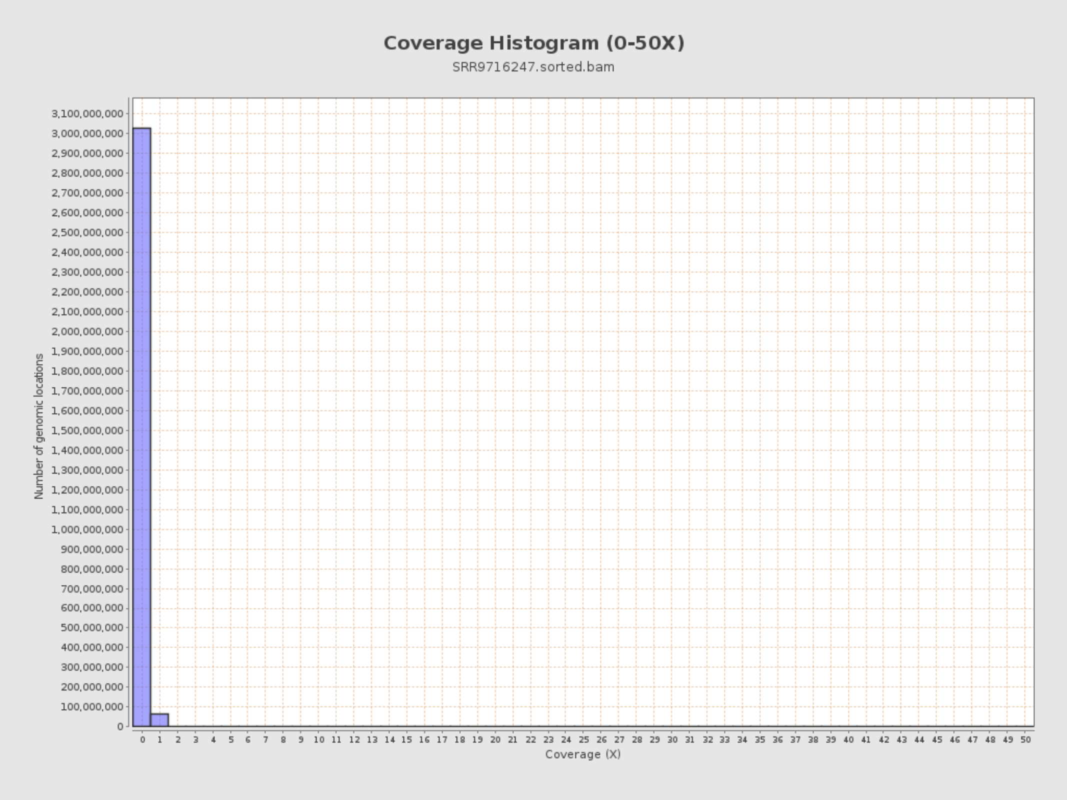
3. Results : Coverage across reference



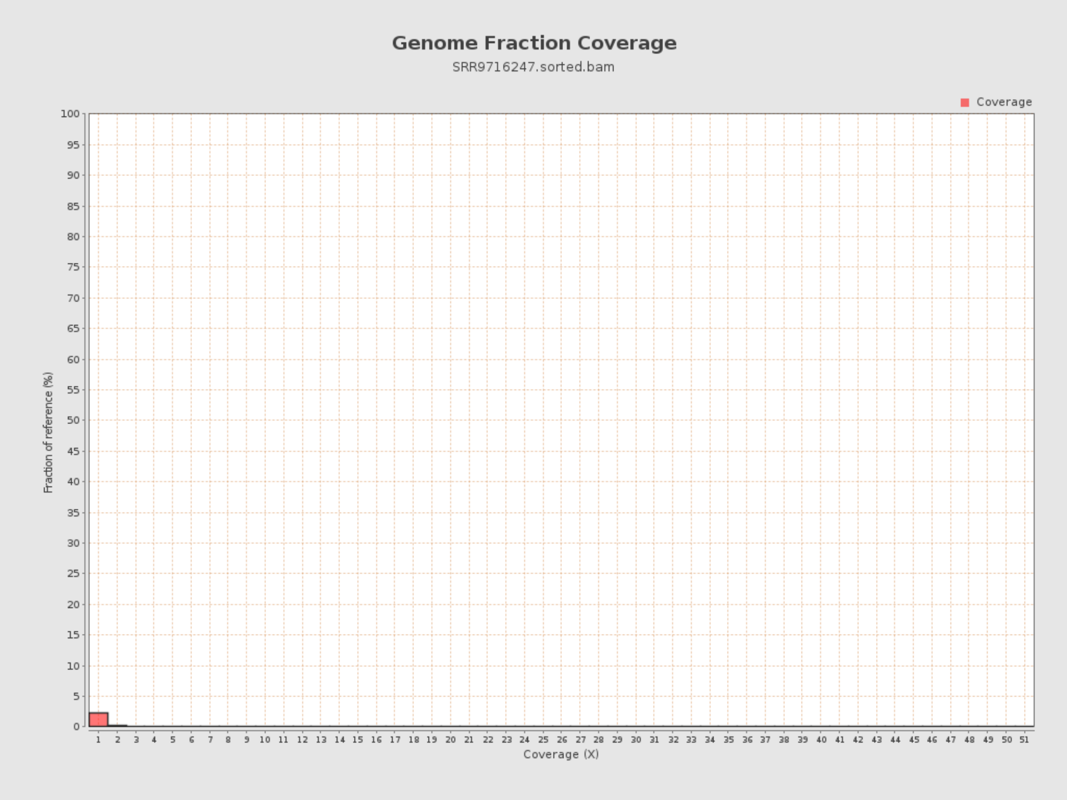
4. Results : Coverage Histogram



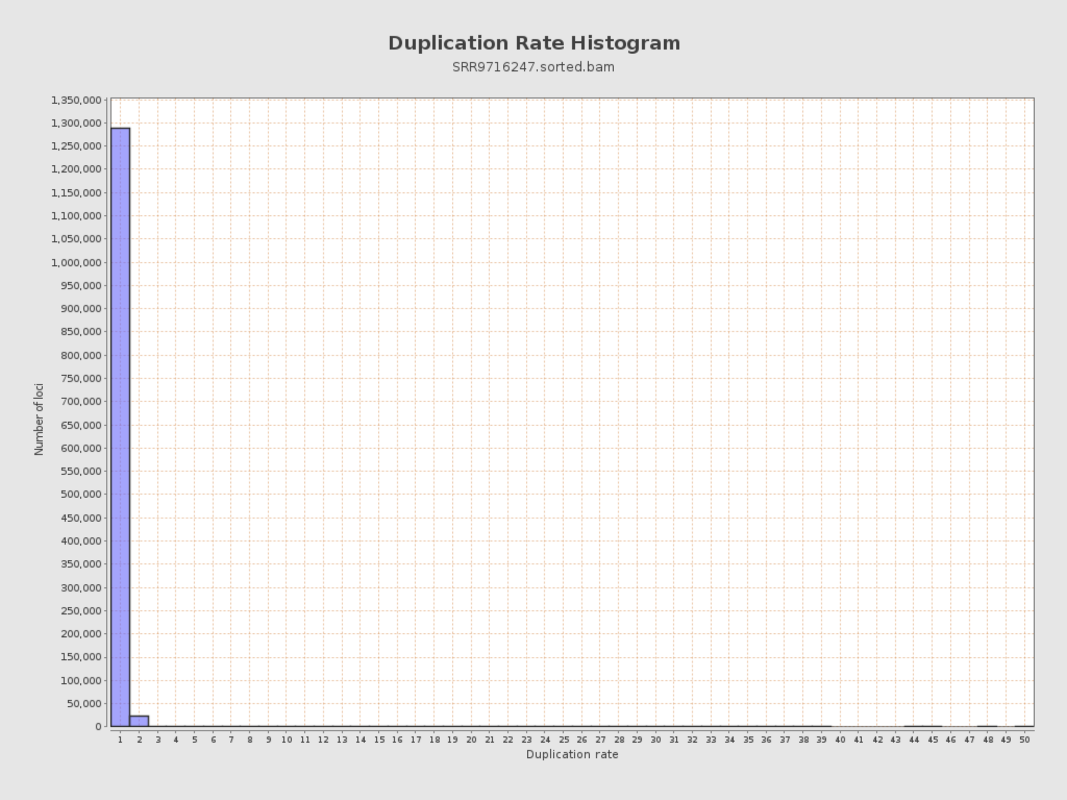
5. Results : Coverage Histogram (0-50X)



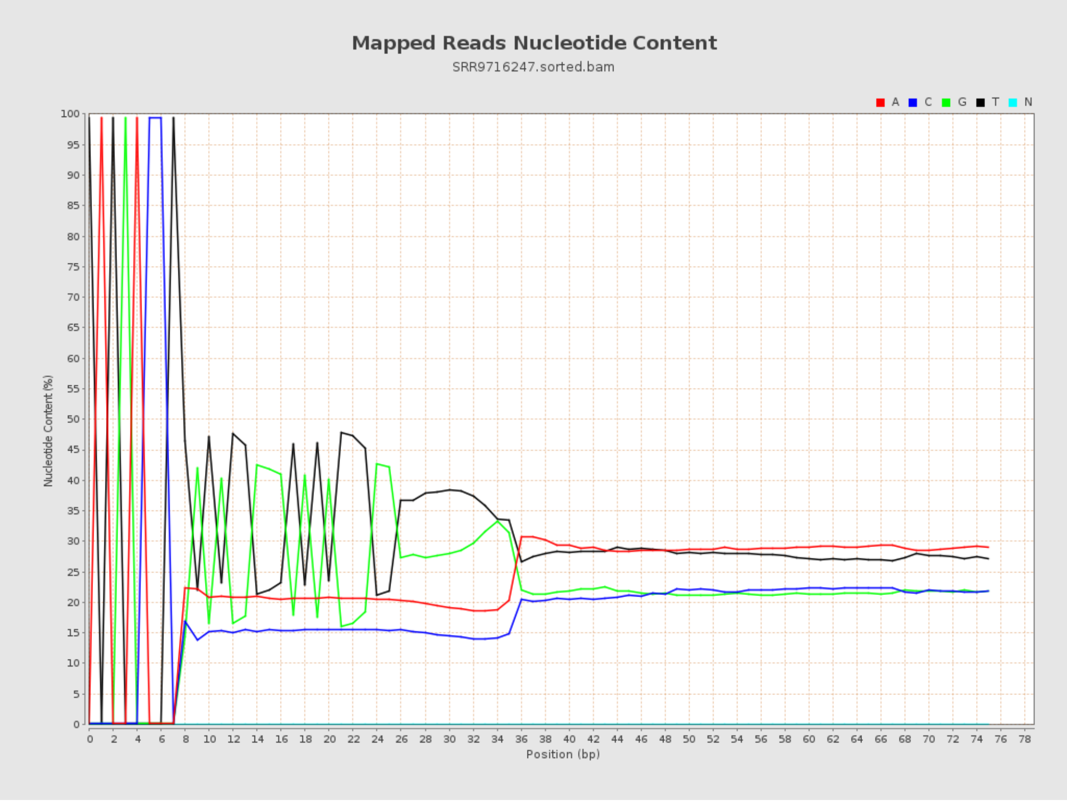
6. Results : Genome Fraction Coverage



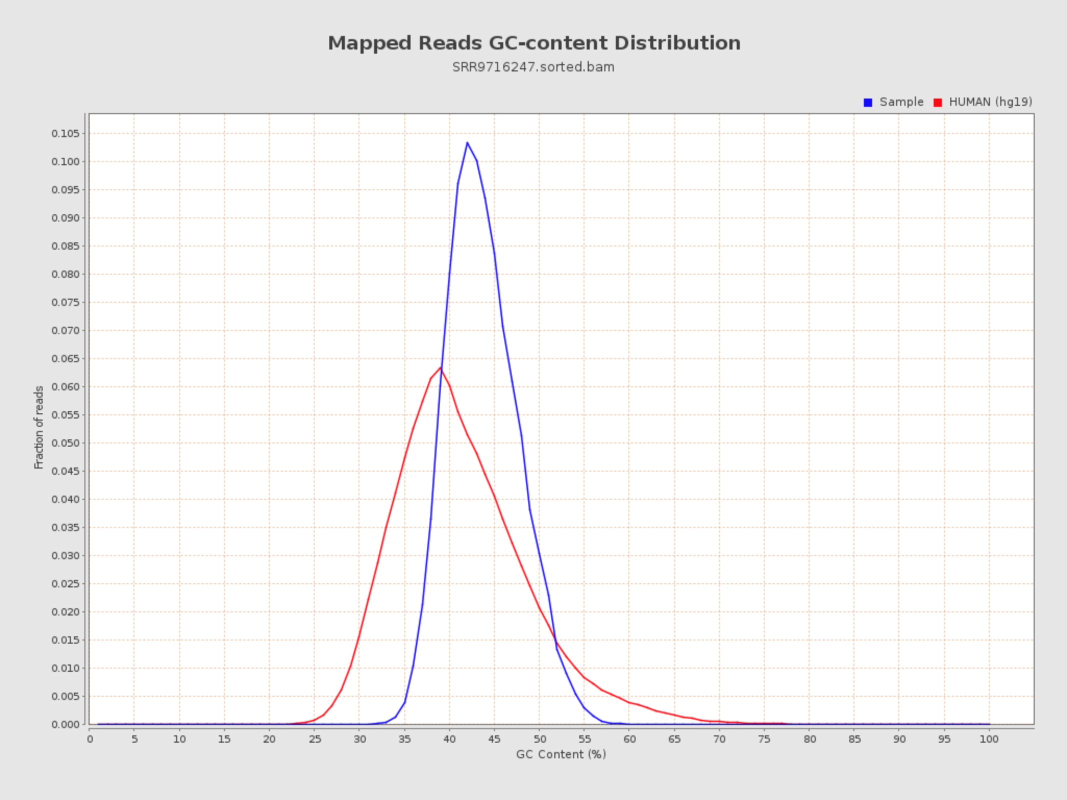
7. Results : Duplication Rate Histogram



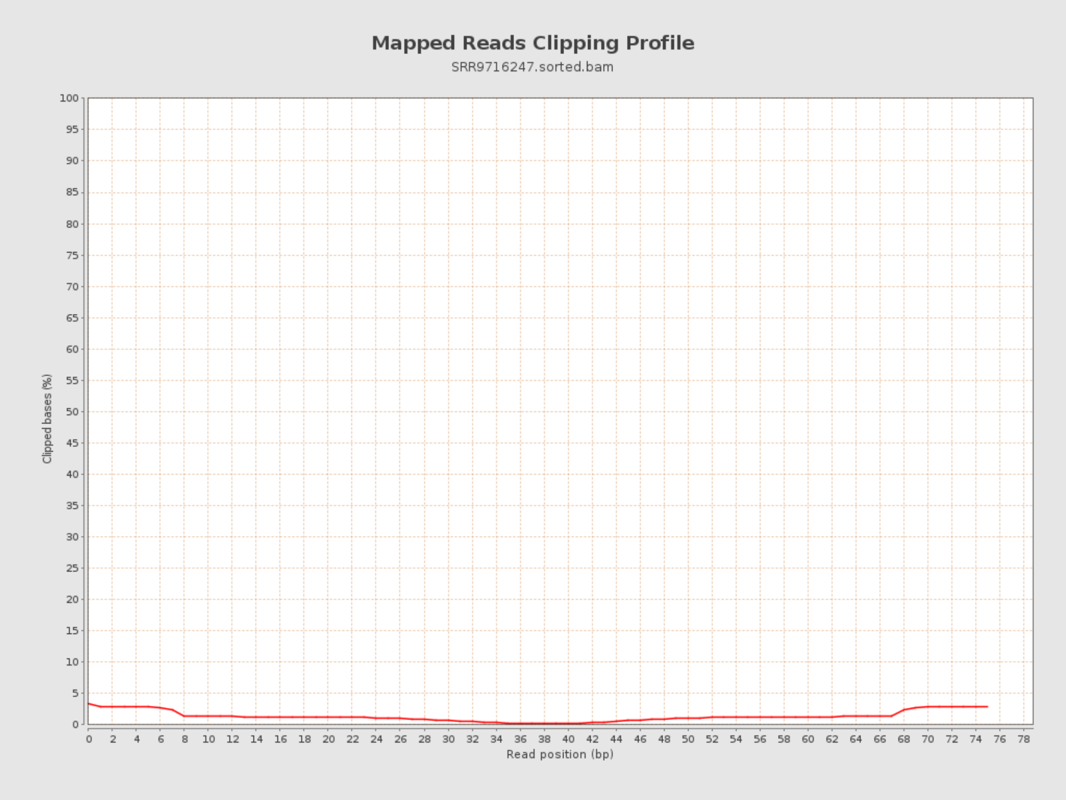
8. Results : Mapped Reads Nucleotide Content



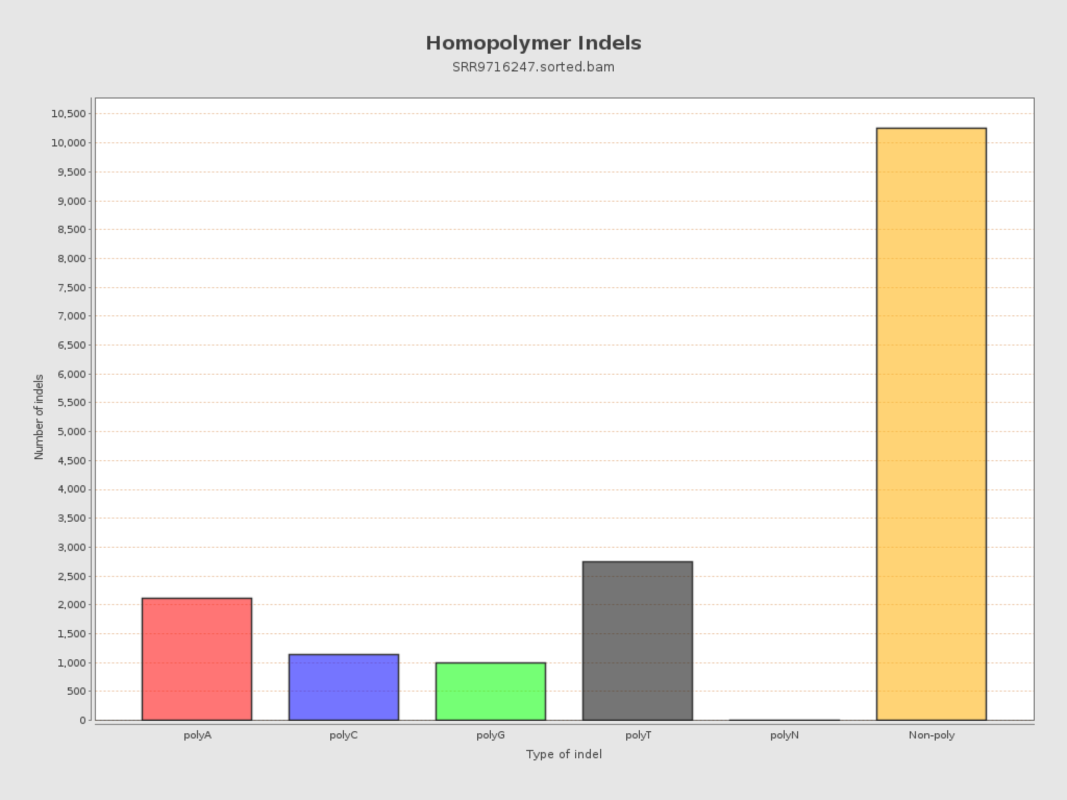
9. Results : Mapped Reads GC-content Distribution



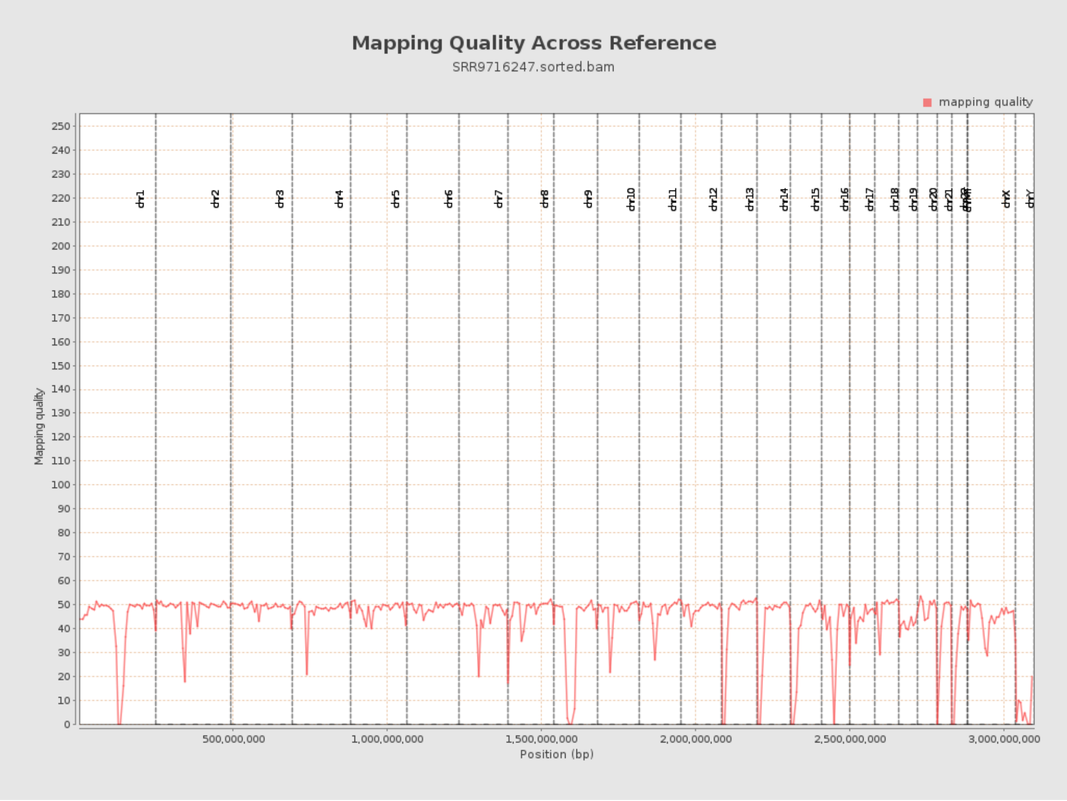
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram