Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:29:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716344.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_SRR9716344 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716344.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:29:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716344.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,103,711
Mapped reads	986,437 / 89.37%
Unmapped reads	117,274 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,878 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	28,452 / 2.58%
Duplication rate	2.24%
Clipped reads	989,763 / 89.68%

2.2. ACGT Content

Number/percentage of A's	14,671,734 / 25.8%
Number/percentage of C's	10,932,921 / 19.22%
Number/percentage of T's	17,938,390 / 31.54%
Number/percentage of G's	13,334,145 / 23.44%
Number/percentage of N's	734 / 0%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.1814

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

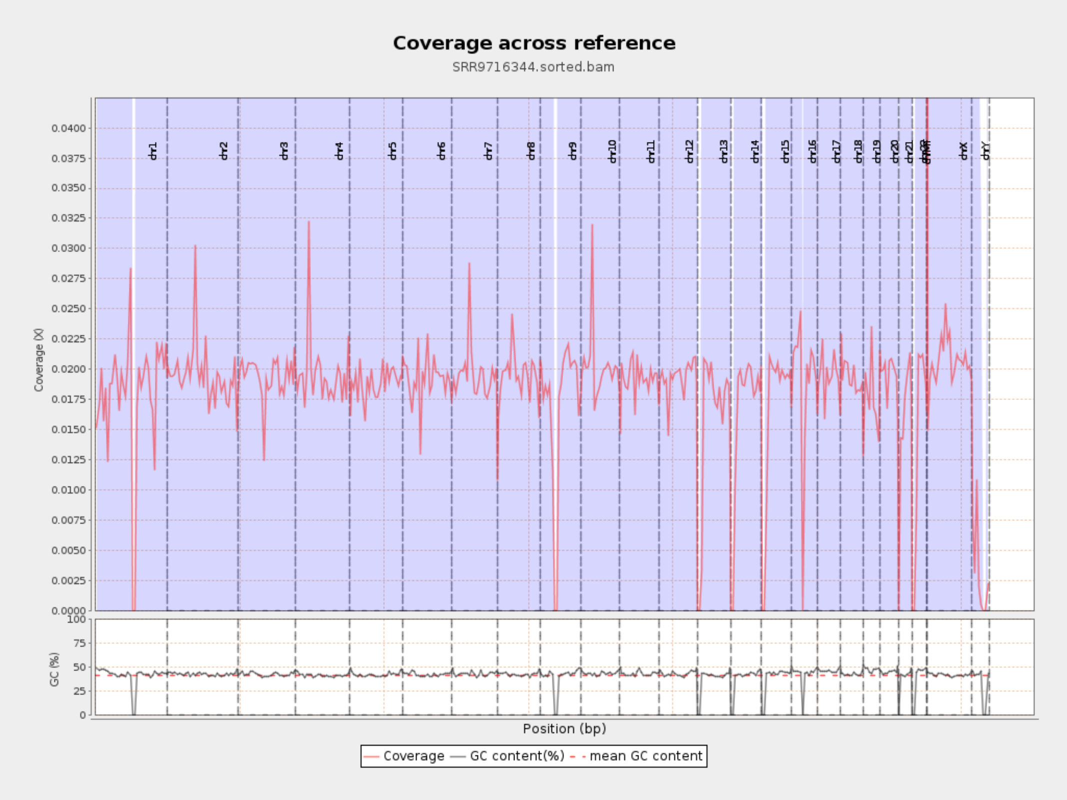
General error rate	0.51%
Mismatches	284,772
Insertions	3,980
Mapped reads with at least one insertion	0.4%
Deletions	10,225
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.62%

2.6. Chromosome stats

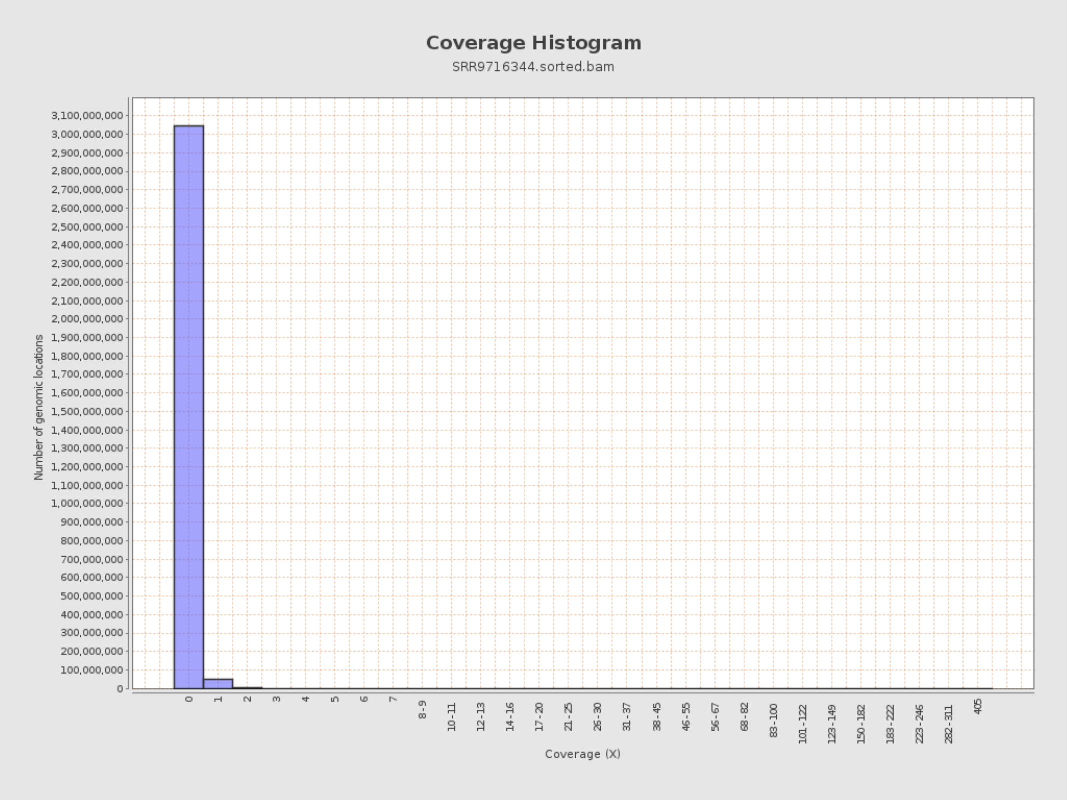
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4424389	0.0178	0.2683
chr2	243199373	4742863	0.0195	0.2331
chr3	198022430	3827053	0.0193	0.1487
chr4	191154276	3750285	0.0196	0.1635
chr5	180915260	3422018	0.0189	0.1471
chr6	171115067	3290527	0.0192	0.1551
chr7	159138663	3135410	0.0197	0.2202

chr8	146364022	2852824	0.0195	0.1834
chr9	141213431	2380055	0.0169	0.1595
chr10	135534747	2752671	0.0203	0.1919
chr11	135006516	2607309	0.0193	0.1708
chr12	133851895	2584767	0.0193	0.1501
chr13	115169878	1786119	0.0155	0.1327
chr14	107349540	1728763	0.0161	0.1408
chr15	102531392	1659175	0.0162	0.138
chr16	90354753	1676472	0.0186	0.1505
chr17	81195210	1581343	0.0195	0.1573
chr18	78077248	1508936	0.0193	0.242
chr19	59128983	1049928	0.0178	0.2011
chr20	63025520	1232978	0.0196	0.1511
chr21	48129895	762342	0.0158	0.1421
chr22	51304566	728688	0.0142	0.1274
chrMT	16571	19439	1.1731	1.2764
chrX	155270560	3205677	0.0206	0.161
chrY	59373566	184208	0.0031	0.0948

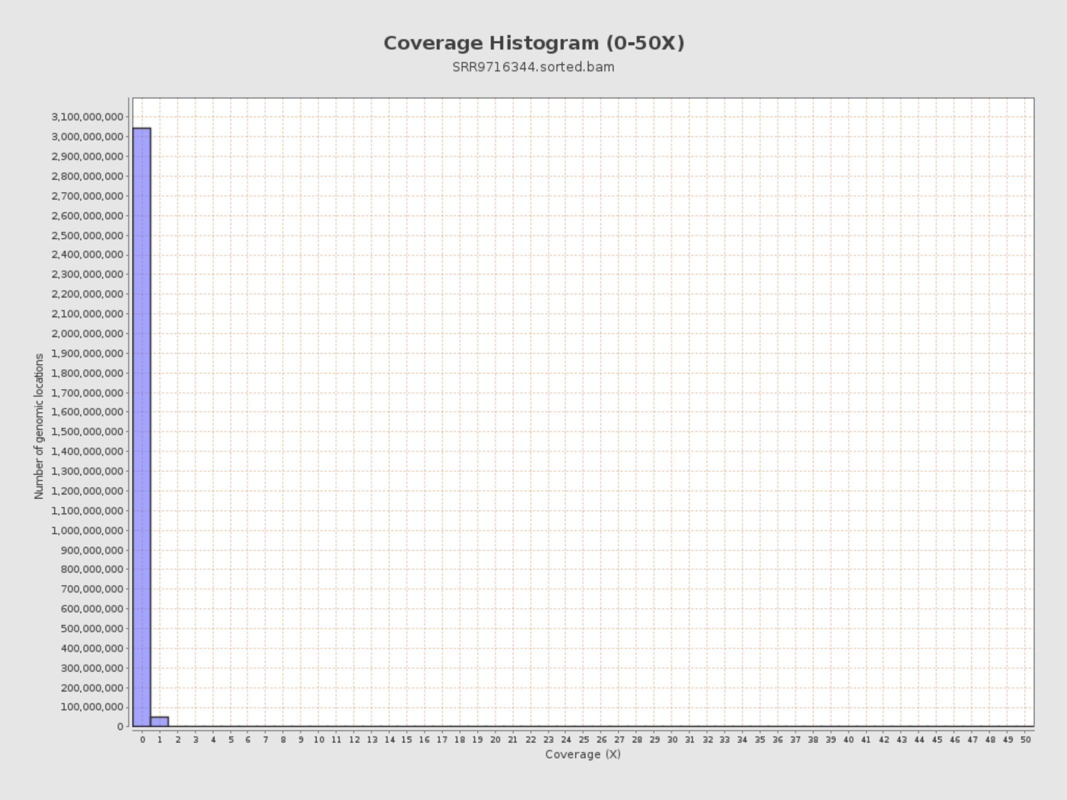
3. Results : Coverage across reference



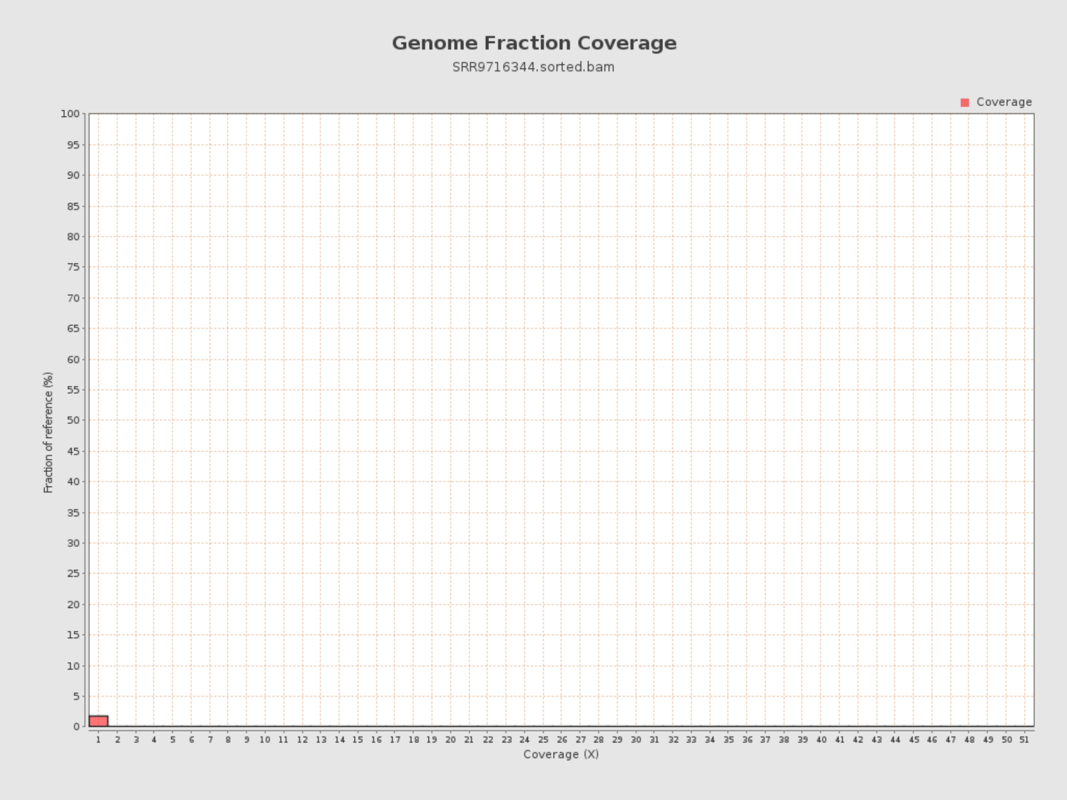
4. Results : Coverage Histogram



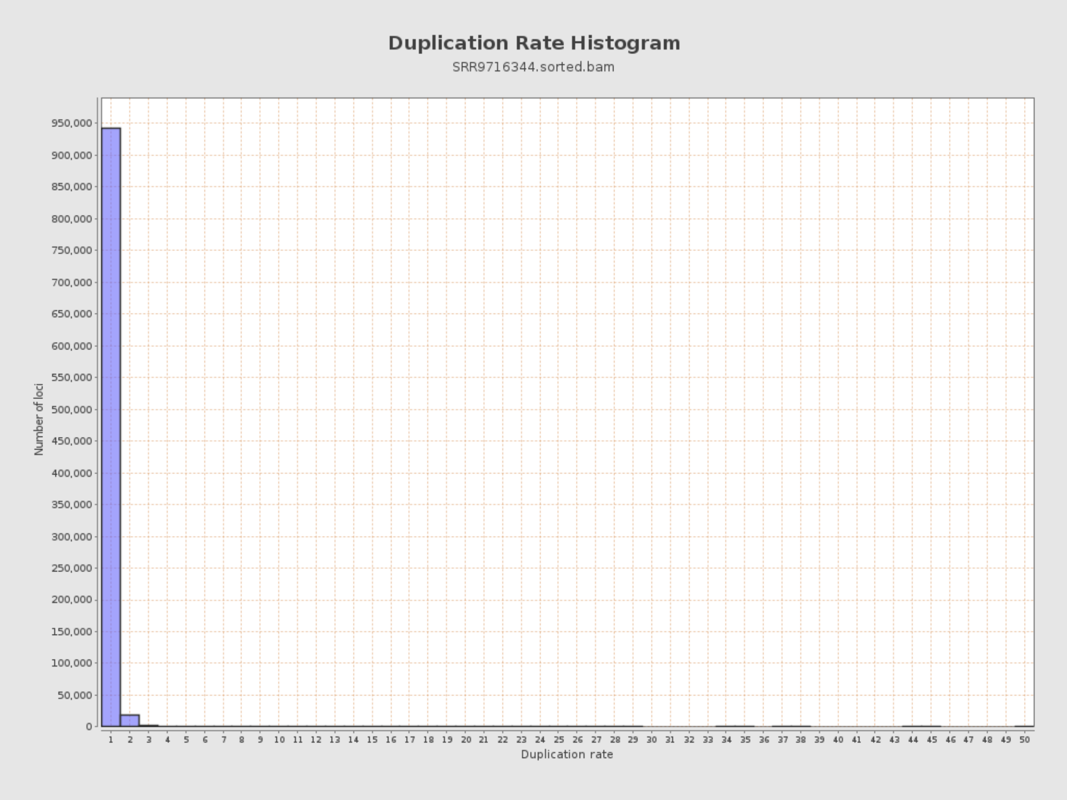
5. Results : Coverage Histogram (0-50X)



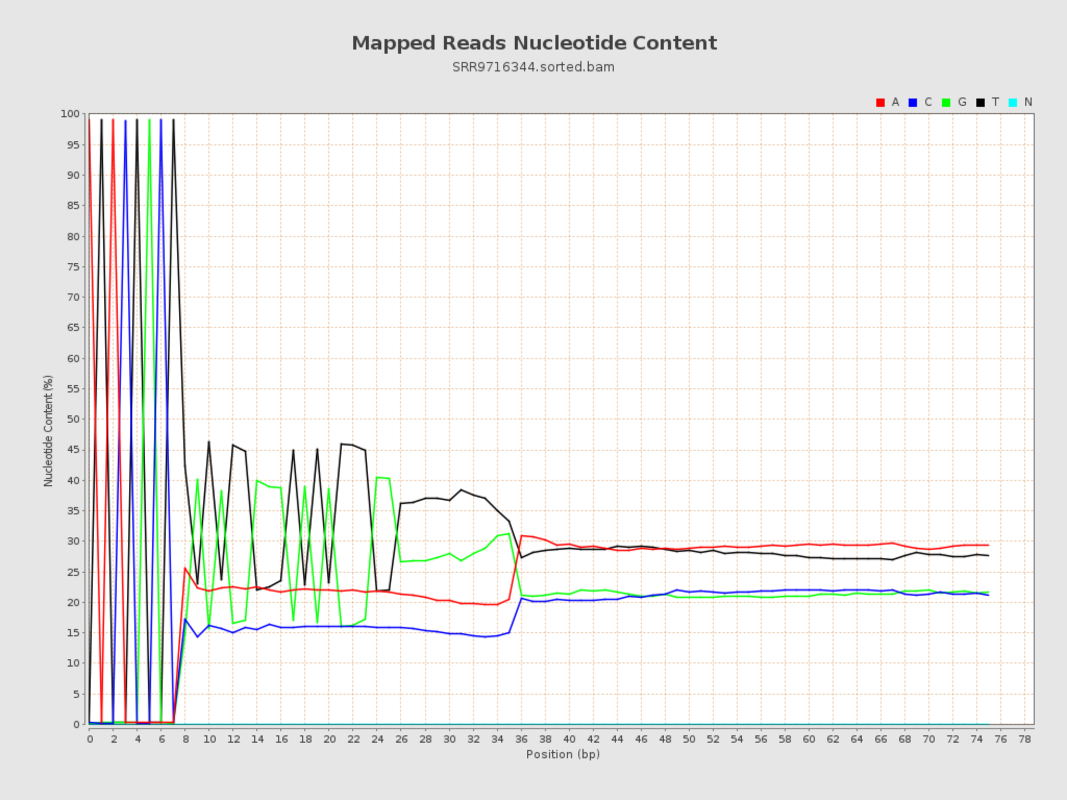
6. Results : Genome Fraction Coverage



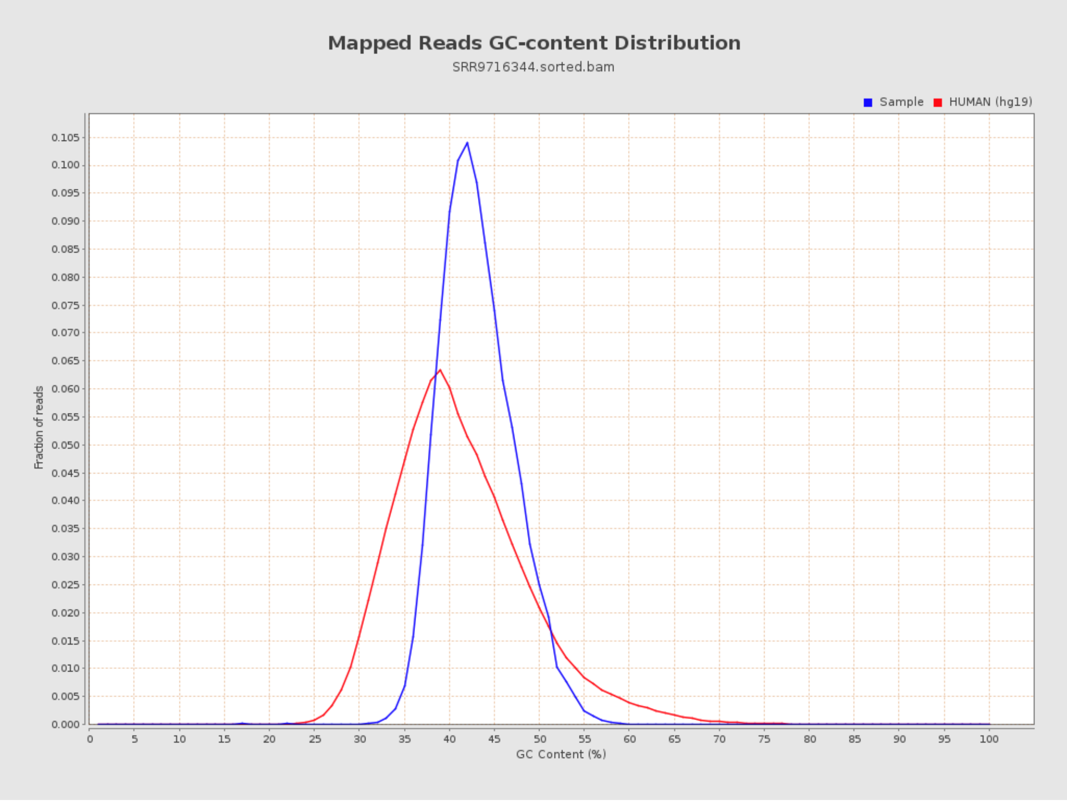
7. Results : Duplication Rate Histogram



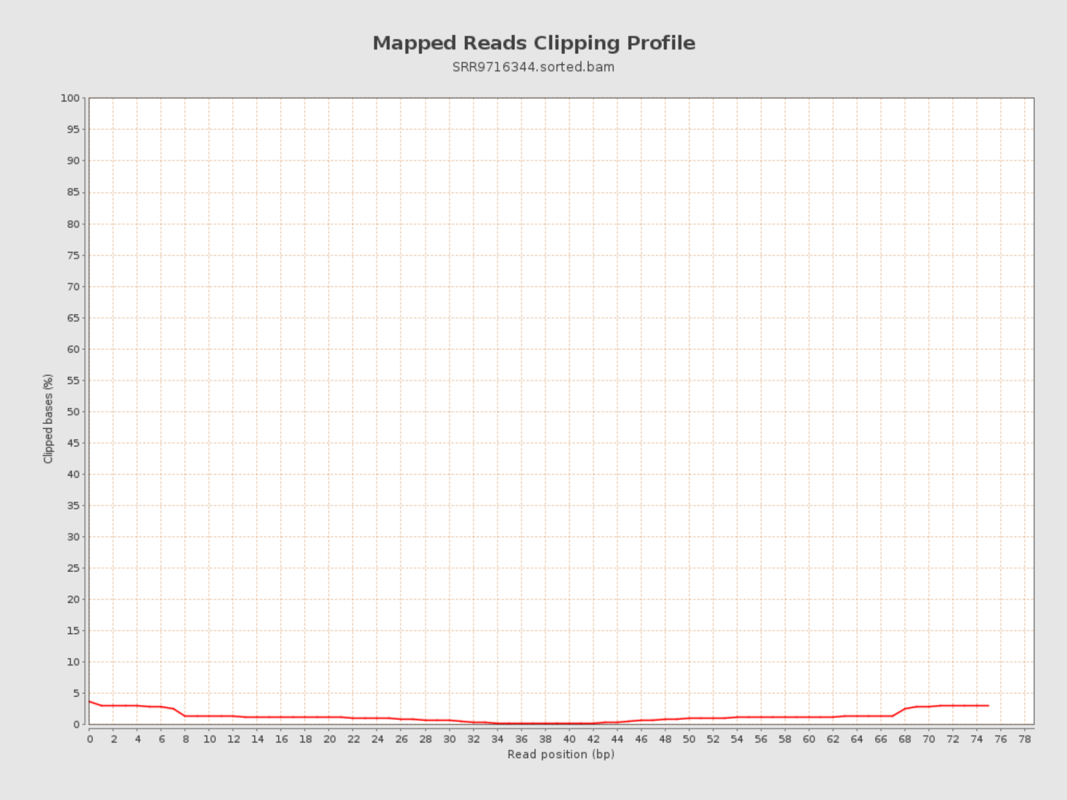
8. Results : Mapped Reads Nucleotide Content



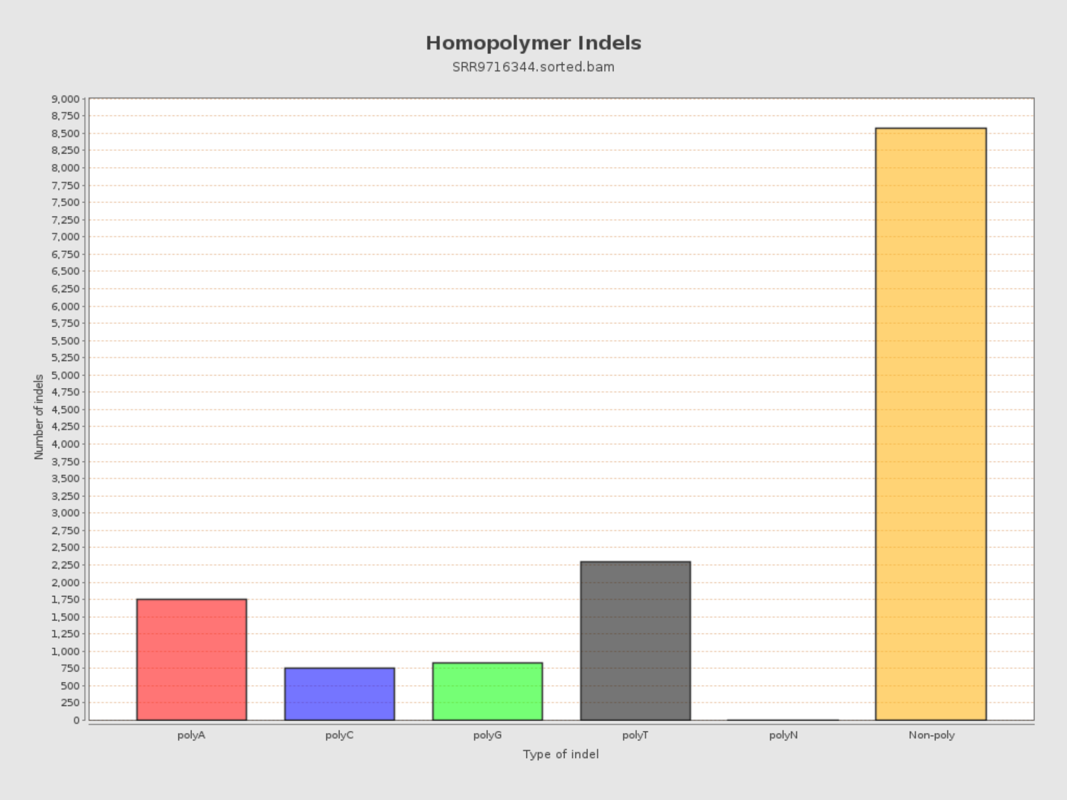
9. Results : Mapped Reads GC-content Distribution



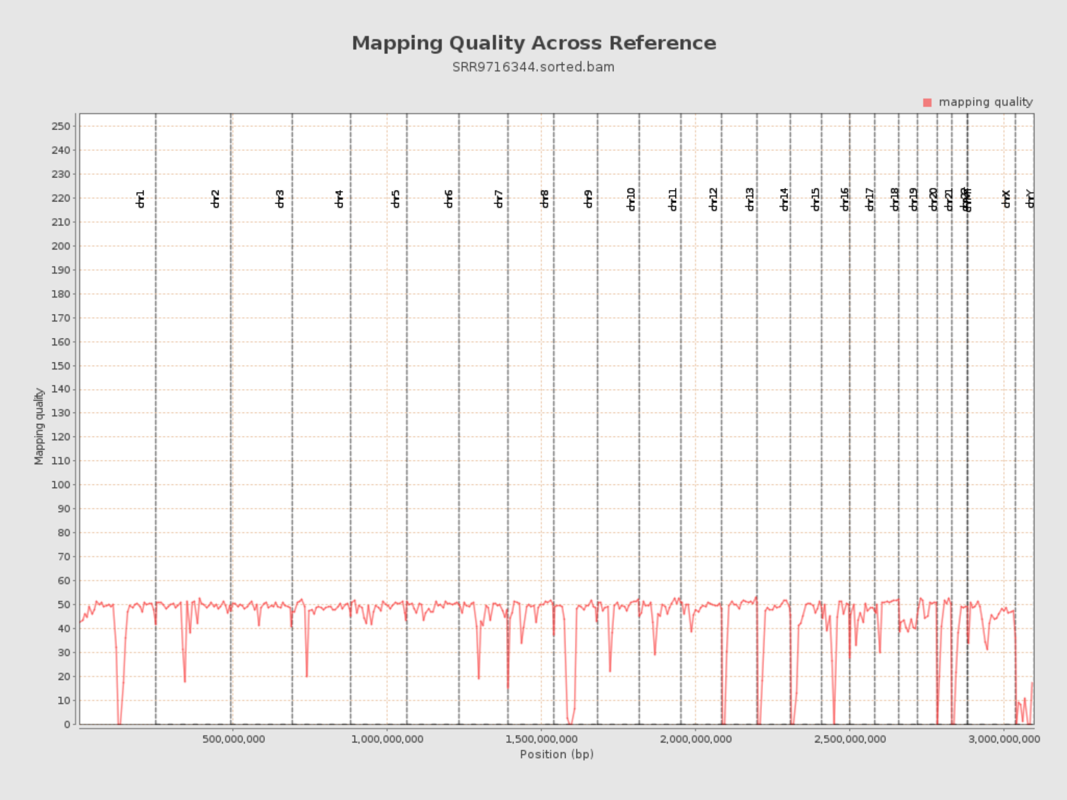
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram