Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 09:22:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716366.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_SRR9716366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716366.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 09:22:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,278,319
Mapped reads	875,278 / 68.47%
Unmapped reads	403,041 / 31.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,475 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	19,129 / 1.5%
Duplication rate	1.54%
Clipped reads	876,452 / 68.56%

2.2. ACGT Content

Number/percentage of A's	11,489,814 / 23.81%
Number/percentage of C's	9,664,733 / 20.03%
Number/percentage of T's	14,874,220 / 30.82%
Number/percentage of G's	12,231,390 / 25.34%
Number/percentage of N's	1,294 / 0%
GC Percentage	45.37%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1568

2.4. Mapping Quality

Mean Mapping Quality	39.55

2.5. Mismatches and indels

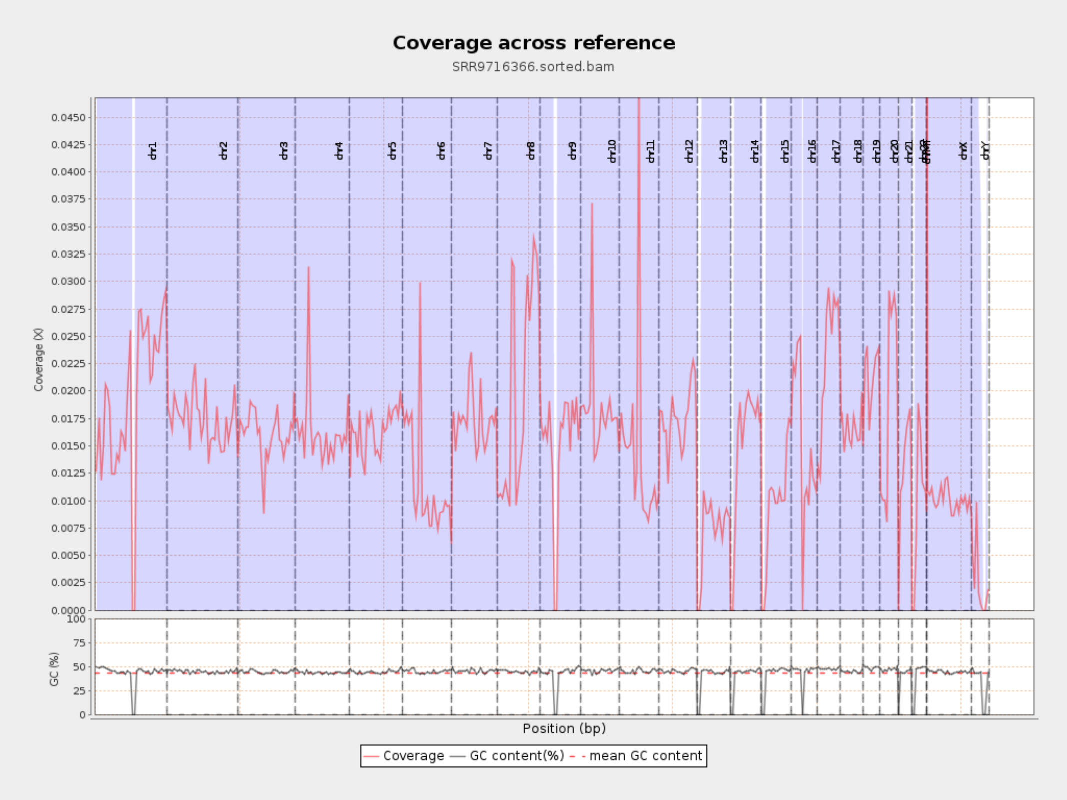
General error rate	0.56%
Mismatches	260,893
Insertions	3,626
Mapped reads with at least one insertion	0.41%
Deletions	8,115
Mapped reads with at least one deletion	0.92%
Homopolymer indels	34.68%

2.6. Chromosome stats

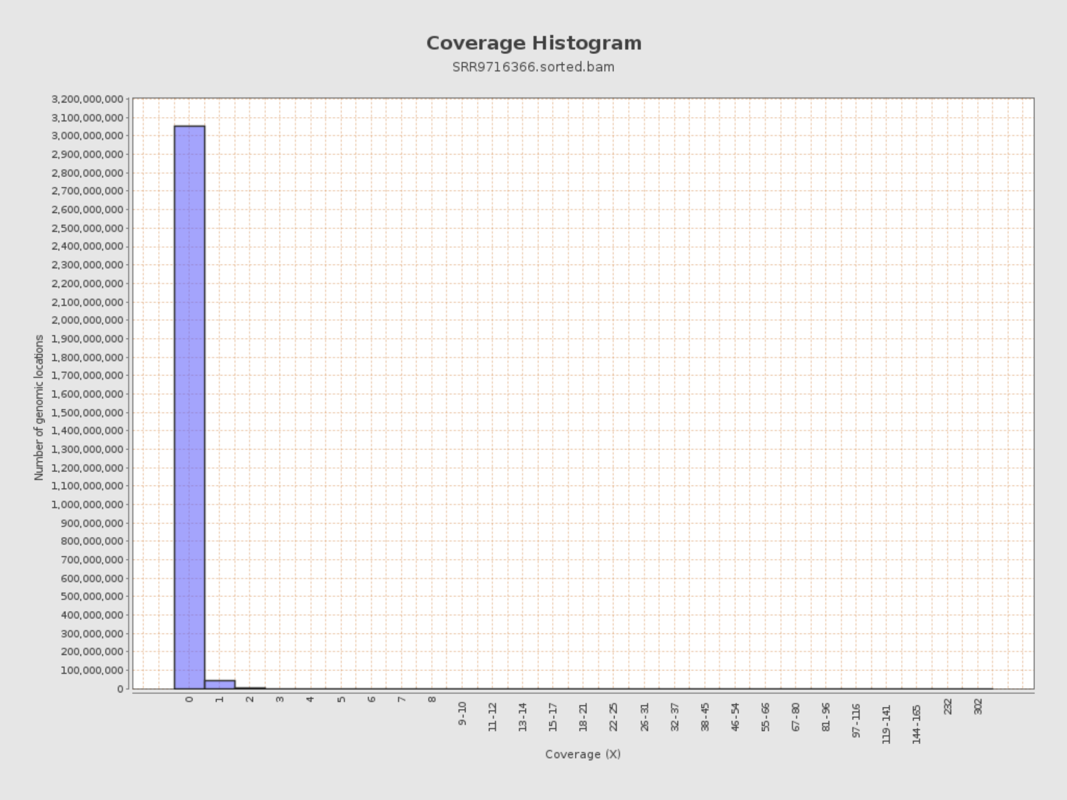
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4779318	0.0192	0.1887
chr2	243199373	4238163	0.0174	0.2008
chr3	198022430	3171174	0.016	0.1469
chr4	191154276	3132484	0.0164	0.1506
chr5	180915260	2997763	0.0166	0.1386
chr6	171115067	2026126	0.0118	0.1207
chr7	159138663	2772282	0.0174	0.1749

chr8	146364022	2958760	0.0202	0.1609
chr9	141213431	2110642	0.0149	0.1417
chr10	135534747	2499700	0.0184	0.2268
chr11	135006516	1981457	0.0147	0.1574
chr12	133851895	2354359	0.0176	0.1432
chr13	115169878	831832	0.0072	0.0933
chr14	107349540	1598931	0.0149	0.1343
chr15	102531392	973321	0.0095	0.1075
chr16	90354753	1343579	0.0149	0.1402
chr17	81195210	1883002	0.0232	0.1727
chr18	78077248	1289610	0.0165	0.171
chr19	59128983	1250541	0.0211	0.1853
chr20	63025520	1206707	0.0191	0.1538
chr21	48129895	635861	0.0132	0.1321
chr22	51304566	513513	0.01	0.1096
chrMT	16571	3107	0.1875	0.4437
chrX	155270560	1572516	0.0101	0.1198
chrY	59373566	150501	0.0025	0.0857

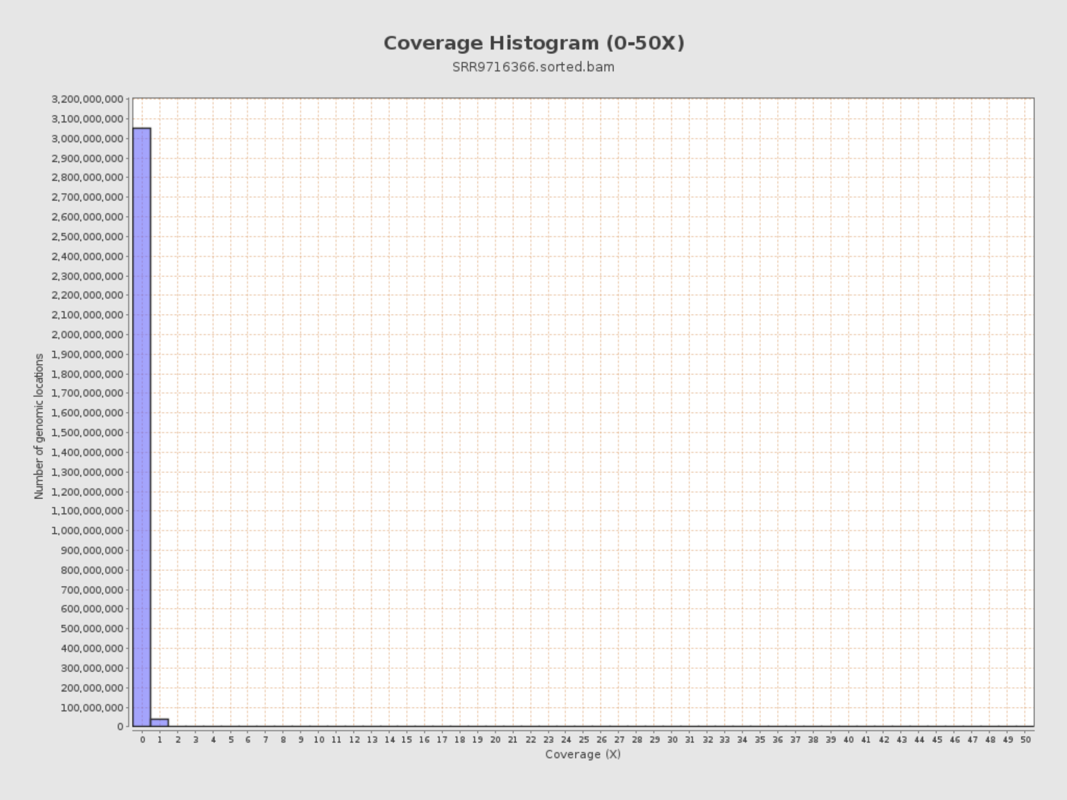
3. Results : Coverage across reference



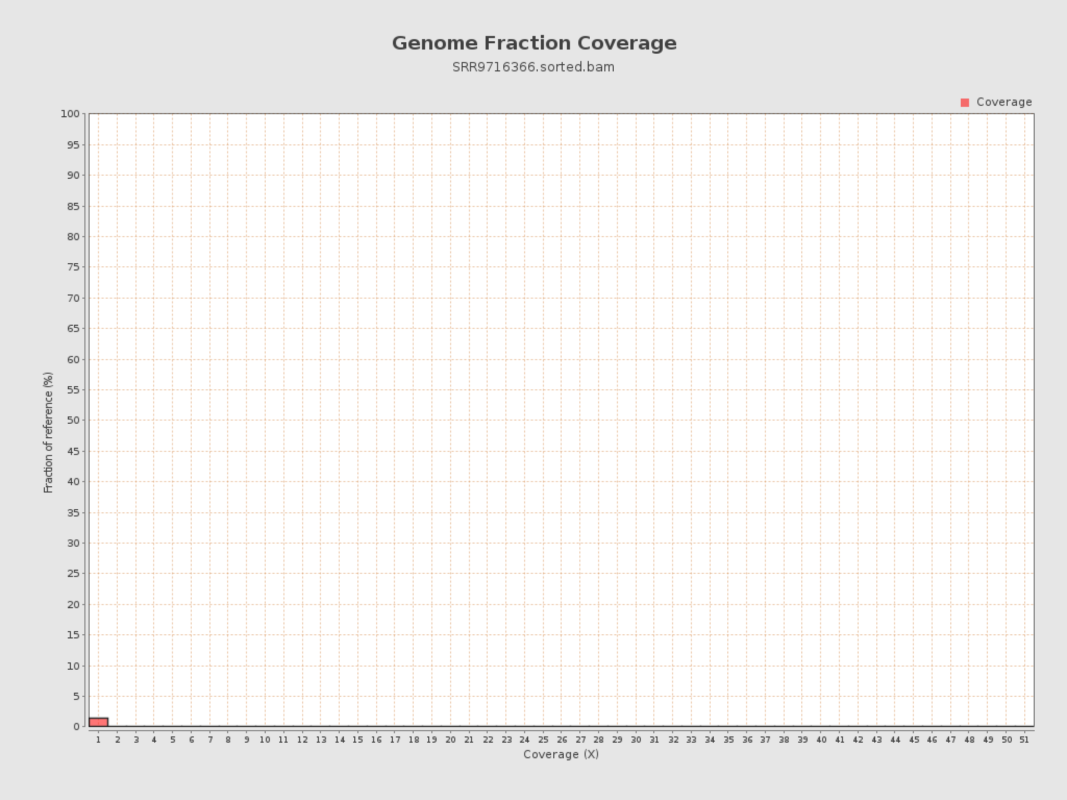
4. Results : Coverage Histogram



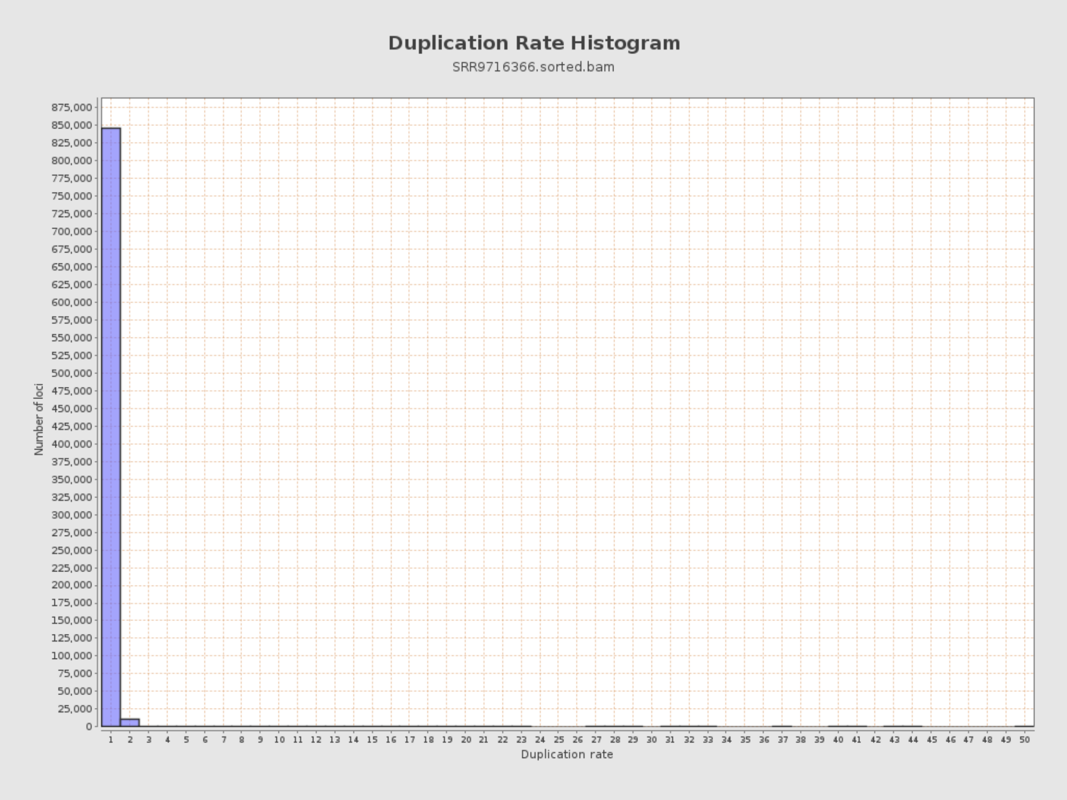
5. Results : Coverage Histogram (0-50X)



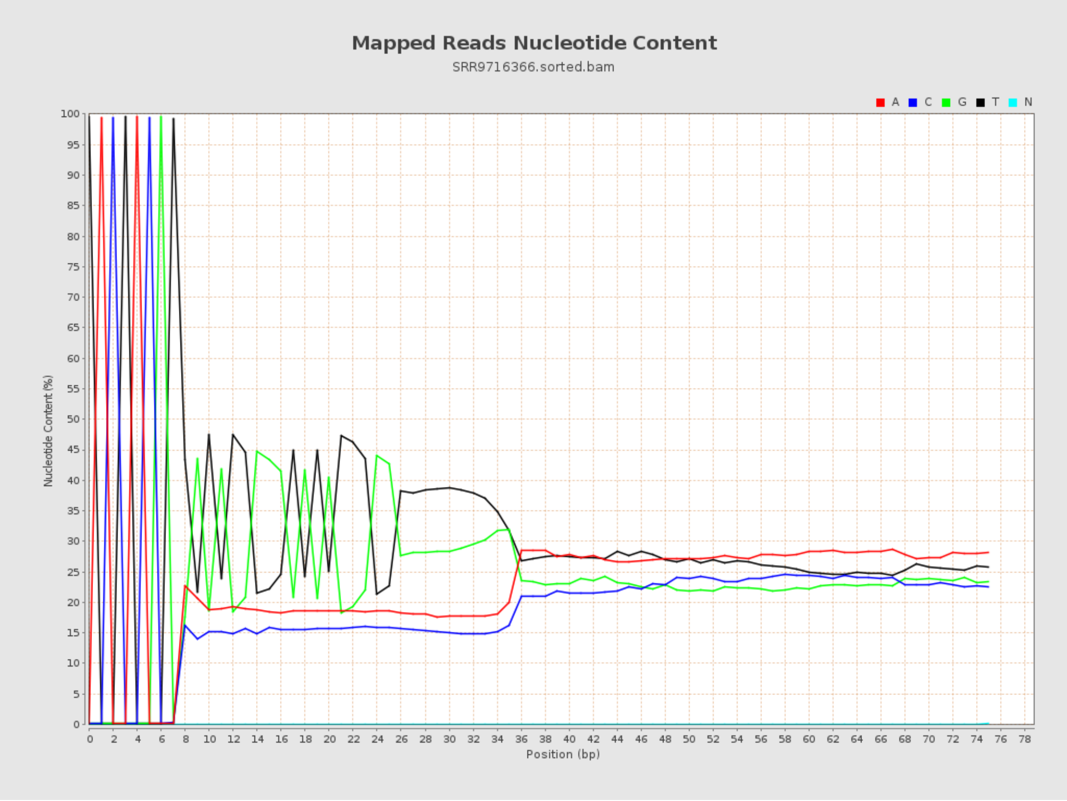
6. Results : Genome Fraction Coverage



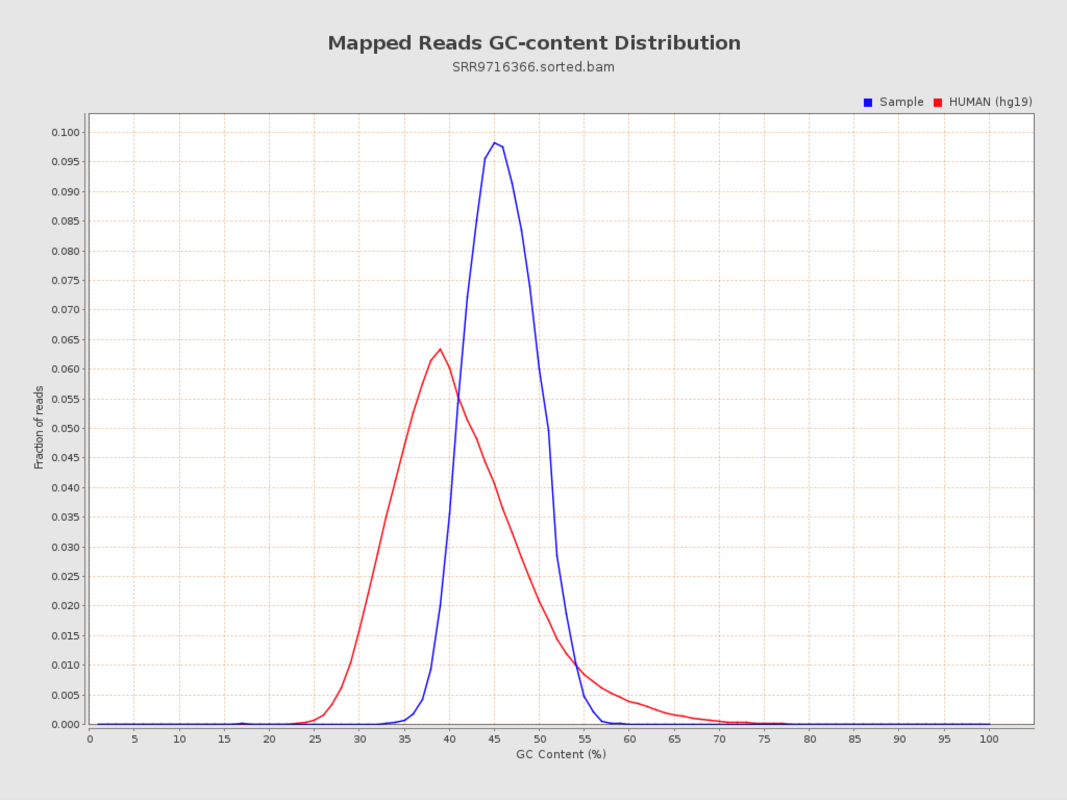
7. Results : Duplication Rate Histogram



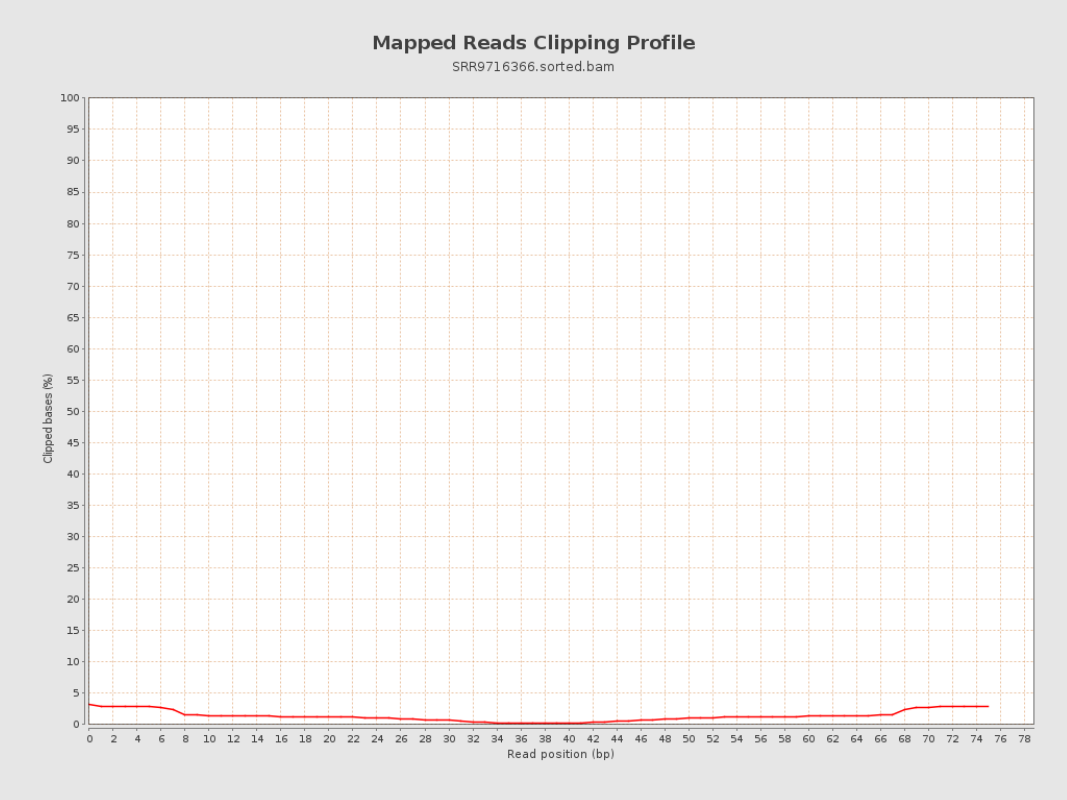
8. Results : Mapped Reads Nucleotide Content



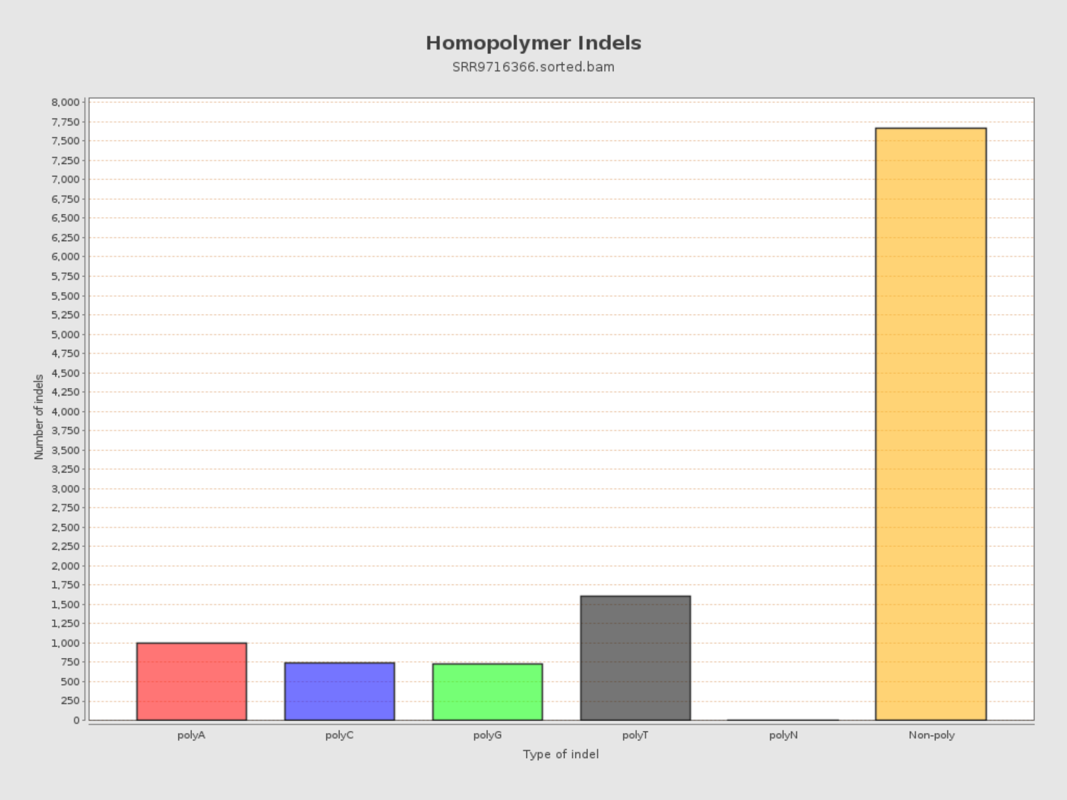
9. Results : Mapped Reads GC-content Distribution



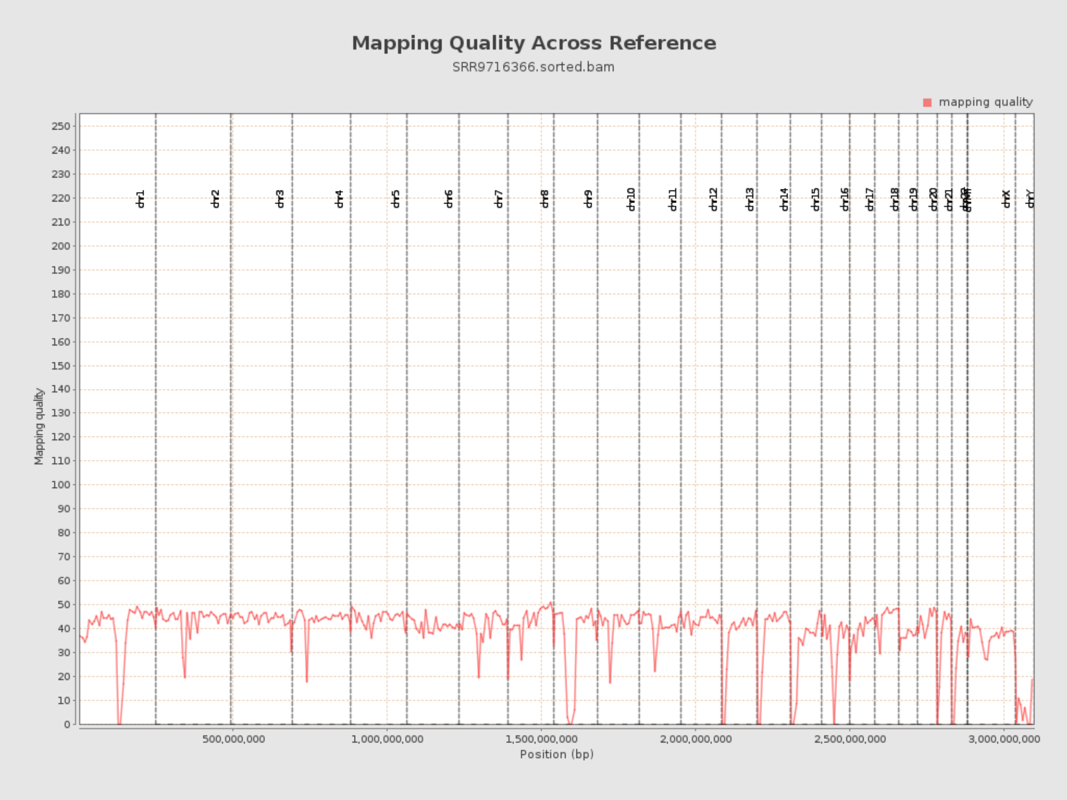
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram