Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:53:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716547.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_SRR9716547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716547.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:53:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,000,988
Mapped reads	756,707 / 75.6%
Unmapped reads	244,281 / 24.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	864 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	40,107 / 4.01%
Duplication rate	4.63%
Clipped reads	756,300 / 75.56%

2.2. ACGT Content

Number/percentage of A's	8,302,256 / 20.83%
Number/percentage of C's	6,985,728 / 17.53%
Number/percentage of T's	13,310,416 / 33.4%
Number/percentage of G's	11,250,700 / 28.23%
Number/percentage of N's	711 / 0%
GC Percentage	45.76%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1416

2.4. Mapping Quality

Mean Mapping Quality	42.67

2.5. Mismatches and indels

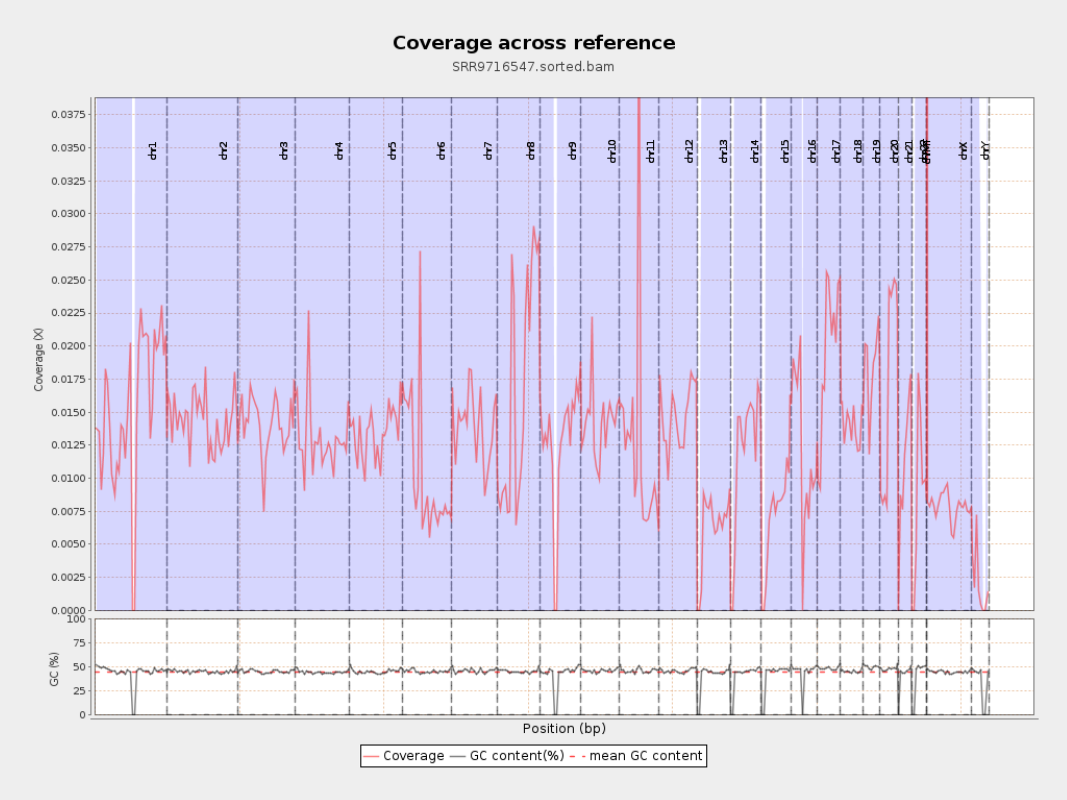
General error rate	0.71%
Mismatches	276,368
Insertions	2,787
Mapped reads with at least one insertion	0.37%
Deletions	6,040
Mapped reads with at least one deletion	0.79%
Homopolymer indels	38.34%

2.6. Chromosome stats

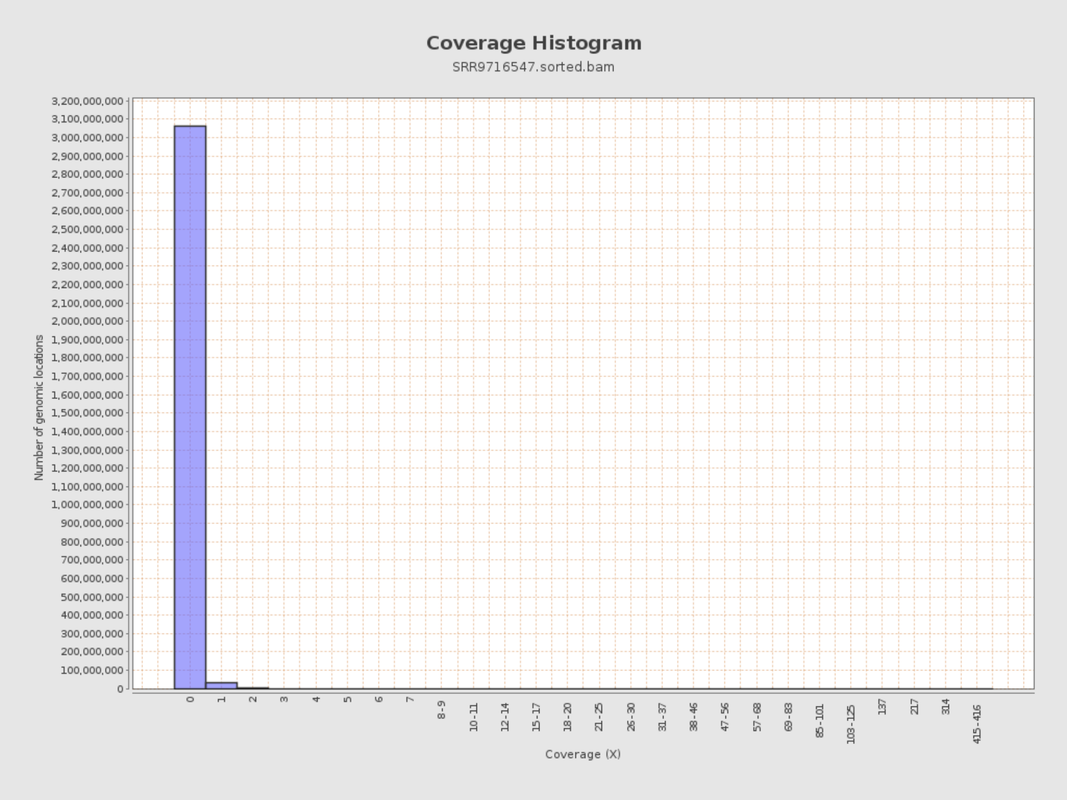
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3773426	0.0151	0.1596
chr2	243199373	3499292	0.0144	0.2129
chr3	198022430	2786343	0.0141	0.1309
chr4	191154276	2510063	0.0131	0.1308
chr5	180915260	2433175	0.0134	0.127
chr6	171115067	1758736	0.0103	0.1295
chr7	159138663	2231533	0.014	0.1524

chr8	146364022	2451914	0.0168	0.146
chr9	141213431	1755628	0.0124	0.1292
chr10	135534747	1937559	0.0143	0.1518
chr11	135006516	1741298	0.0129	0.1345
chr12	133851895	1962404	0.0147	0.1344
chr13	115169878	710149	0.0062	0.0869
chr14	107349540	1280642	0.0119	0.1215
chr15	102531392	733837	0.0072	0.0939
chr16	90354753	1069486	0.0118	0.1283
chr17	81195210	1586981	0.0195	0.1602
chr18	78077248	1088074	0.0139	0.1487
chr19	59128983	1077213	0.0182	0.1664
chr20	63025520	1070785	0.017	0.1477
chr21	48129895	545492	0.0113	0.1224
chr22	51304566	460906	0.009	0.1055
chrMT	16571	52127	3.1457	2.9428
chrX	155270560	1226170	0.0079	0.1003
chrY	59373566	116846	0.002	0.0667

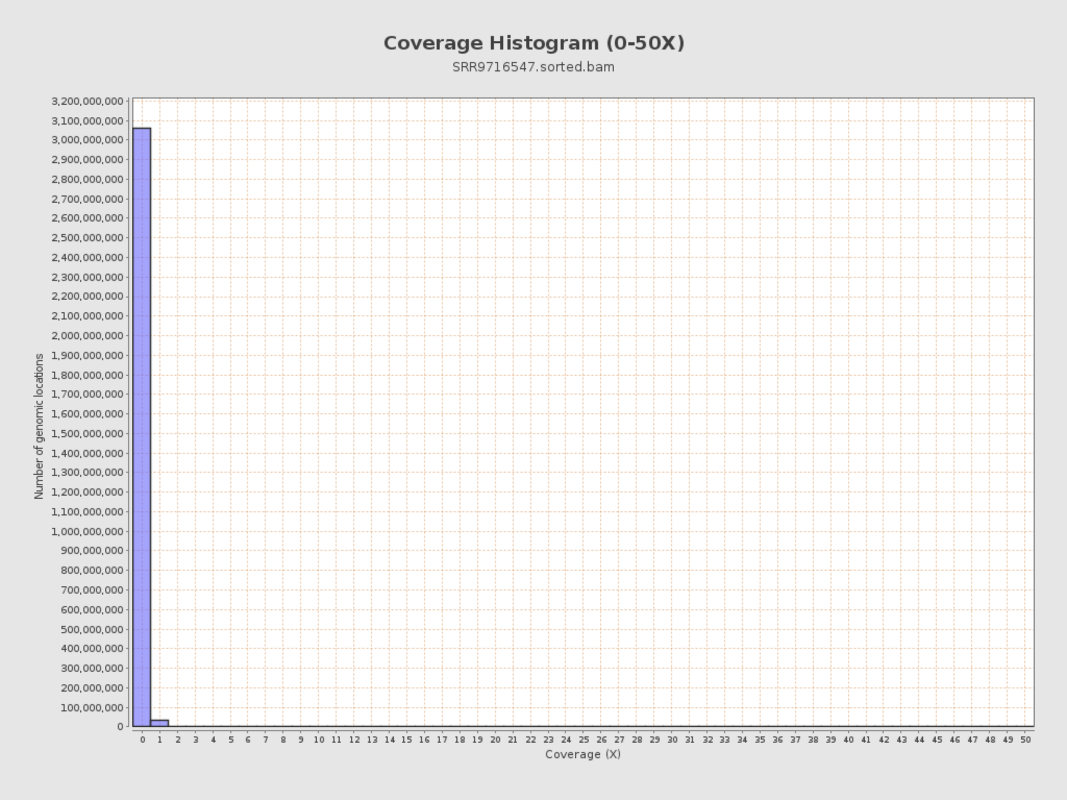
3. Results : Coverage across reference



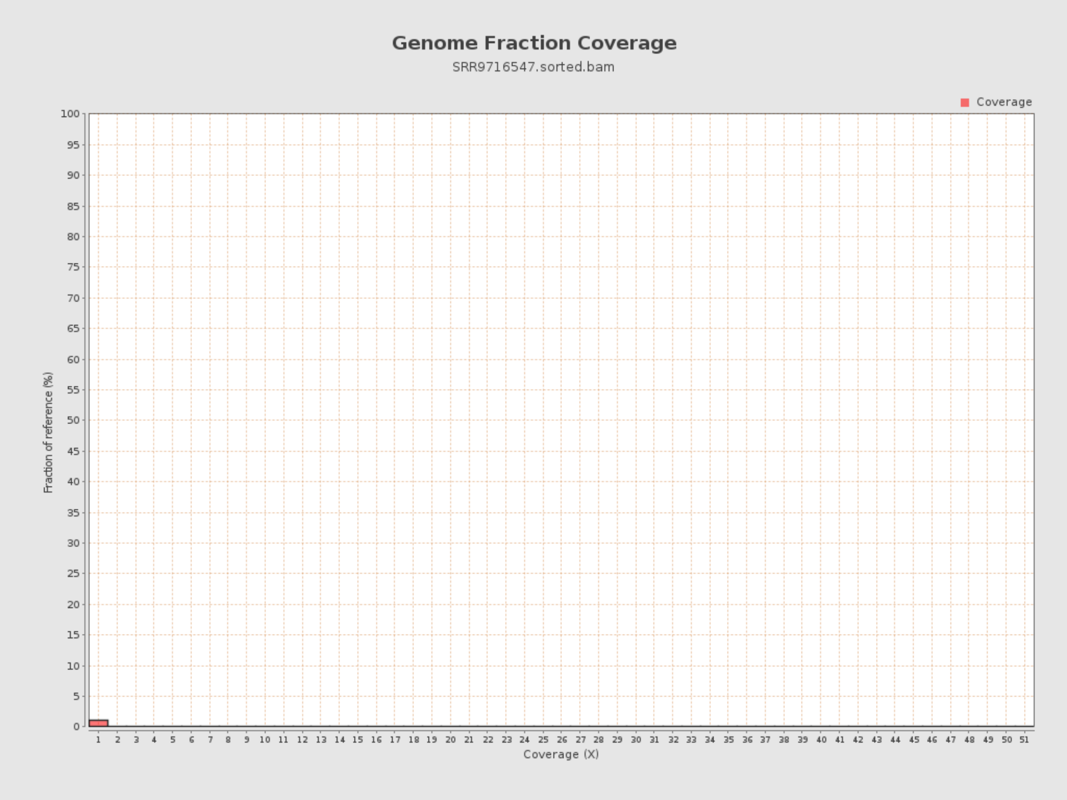
4. Results : Coverage Histogram



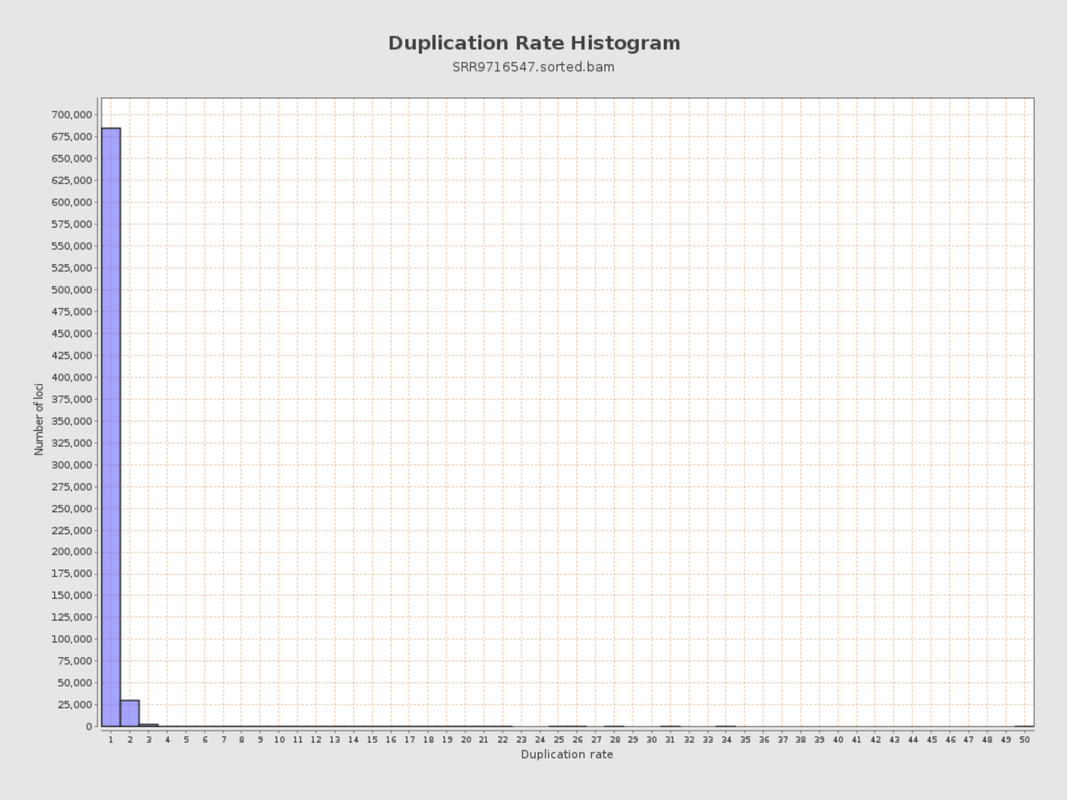
5. Results : Coverage Histogram (0-50X)



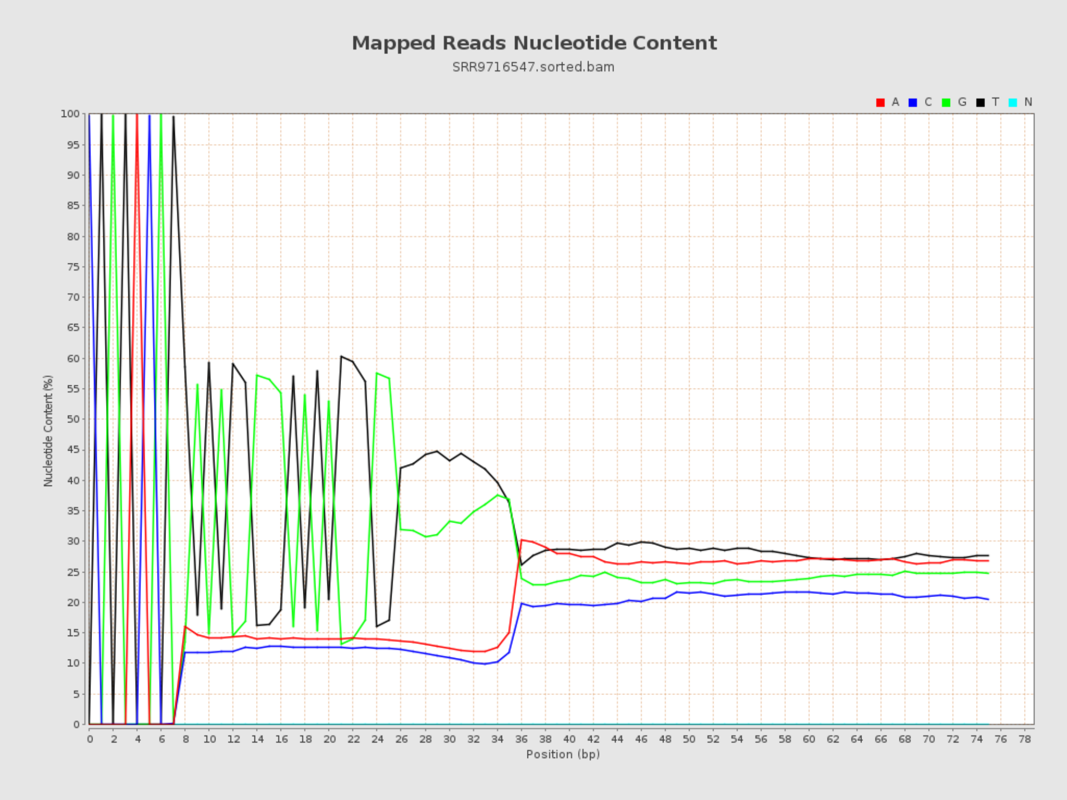
6. Results : Genome Fraction Coverage



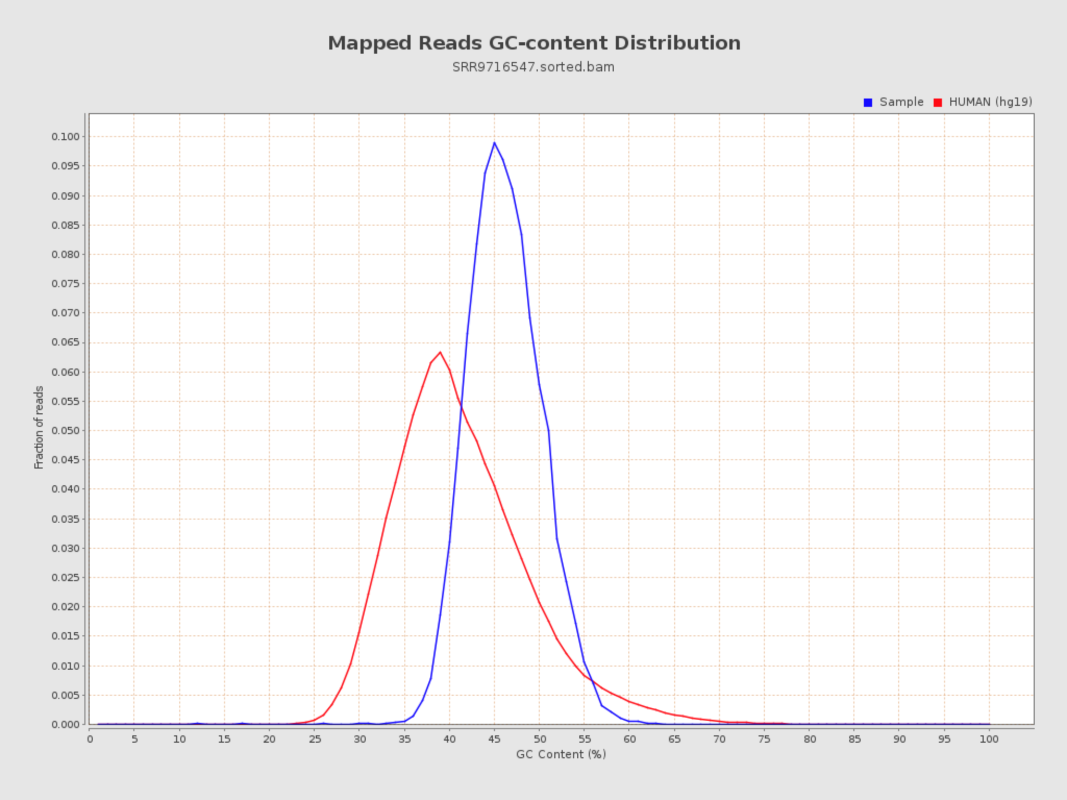
7. Results : Duplication Rate Histogram



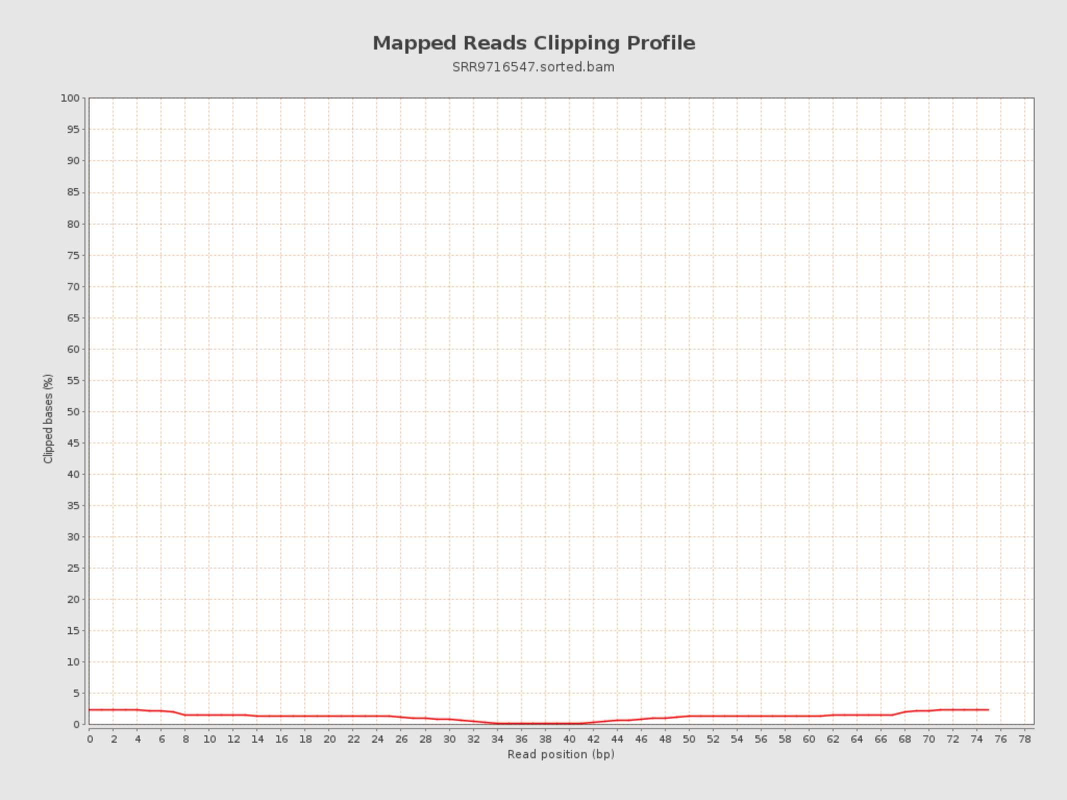
8. Results : Mapped Reads Nucleotide Content



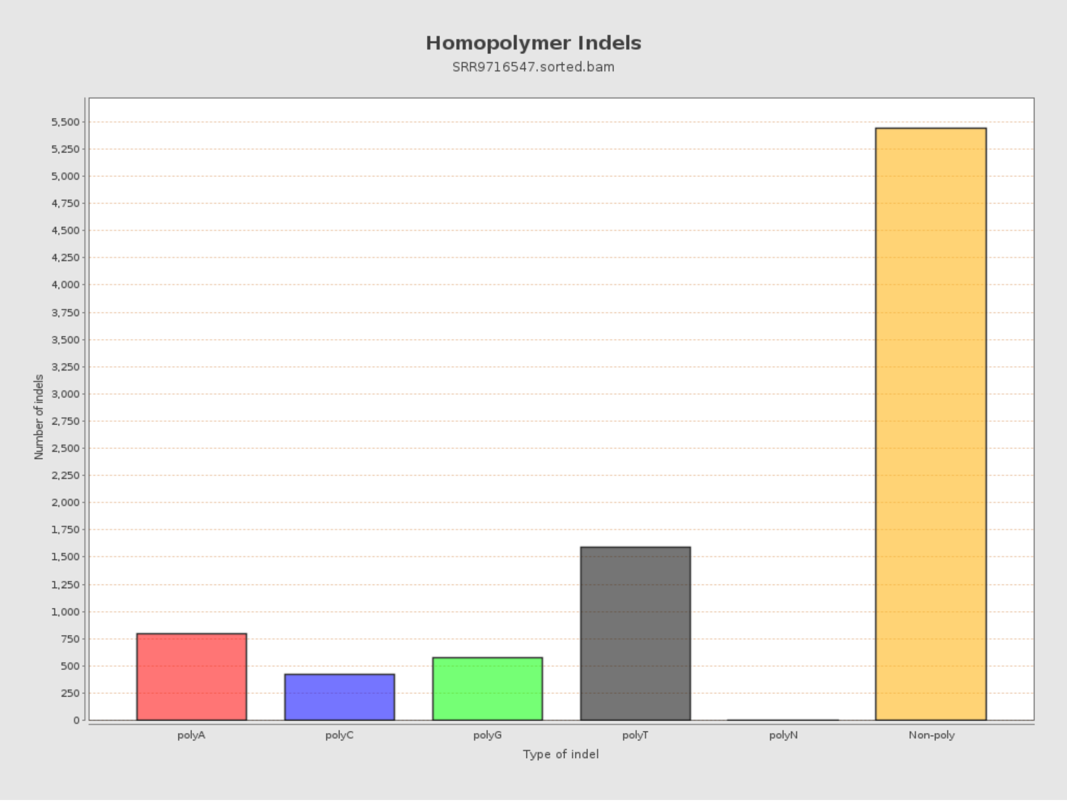
9. Results : Mapped Reads GC-content Distribution



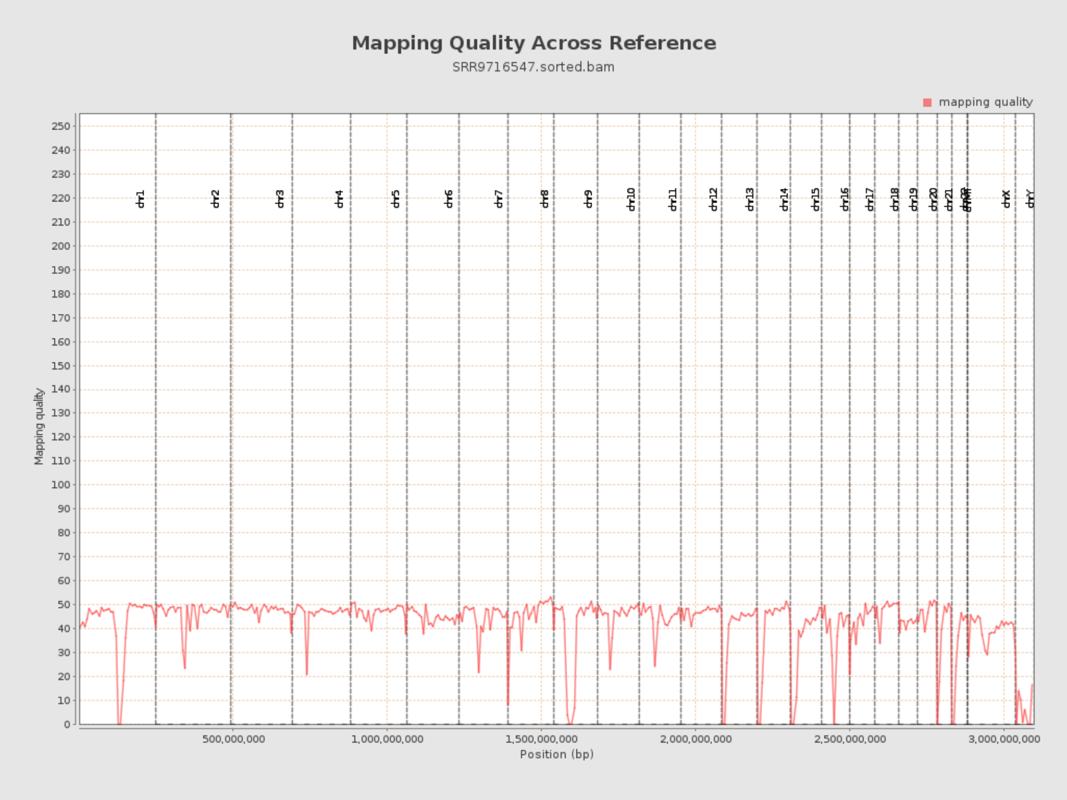
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram