Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:36:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716347.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_SRR9716347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716347.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:35:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	392,535
Mapped reads	361,759 / 92.16%
Unmapped reads	30,776 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,148 / 1.82%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	5,605 / 1.43%
Duplication rate	1.05%
Clipped reads	368,170 / 93.79%

2.2. ACGT Content

Number/percentage of A's	7,585,406 / 26.6%
Number/percentage of C's	5,650,378 / 19.81%
Number/percentage of T's	8,696,400 / 30.49%
Number/percentage of G's	6,583,984 / 23.09%
Number/percentage of N's	1,886 / 0.01%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1258

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

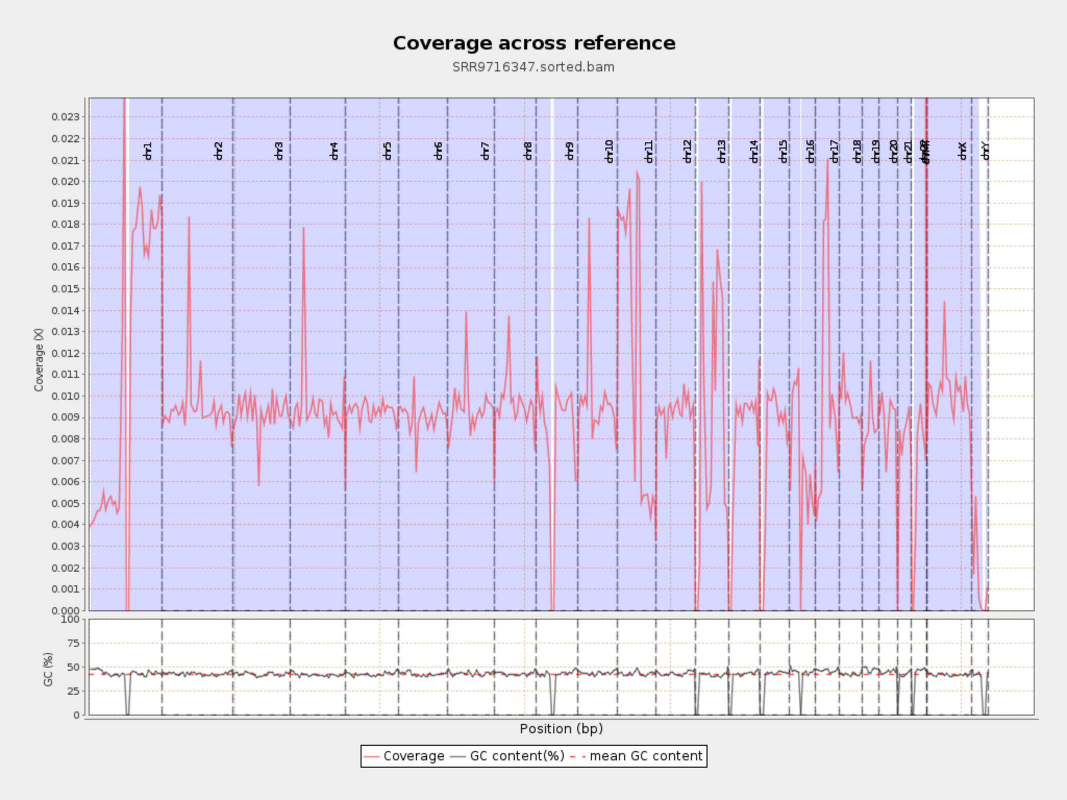
General error rate	0.68%
Mismatches	187,573
Insertions	2,423
Mapped reads with at least one insertion	0.66%
Deletions	6,540
Mapped reads with at least one deletion	1.79%
Homopolymer indels	44.42%

2.6. Chromosome stats

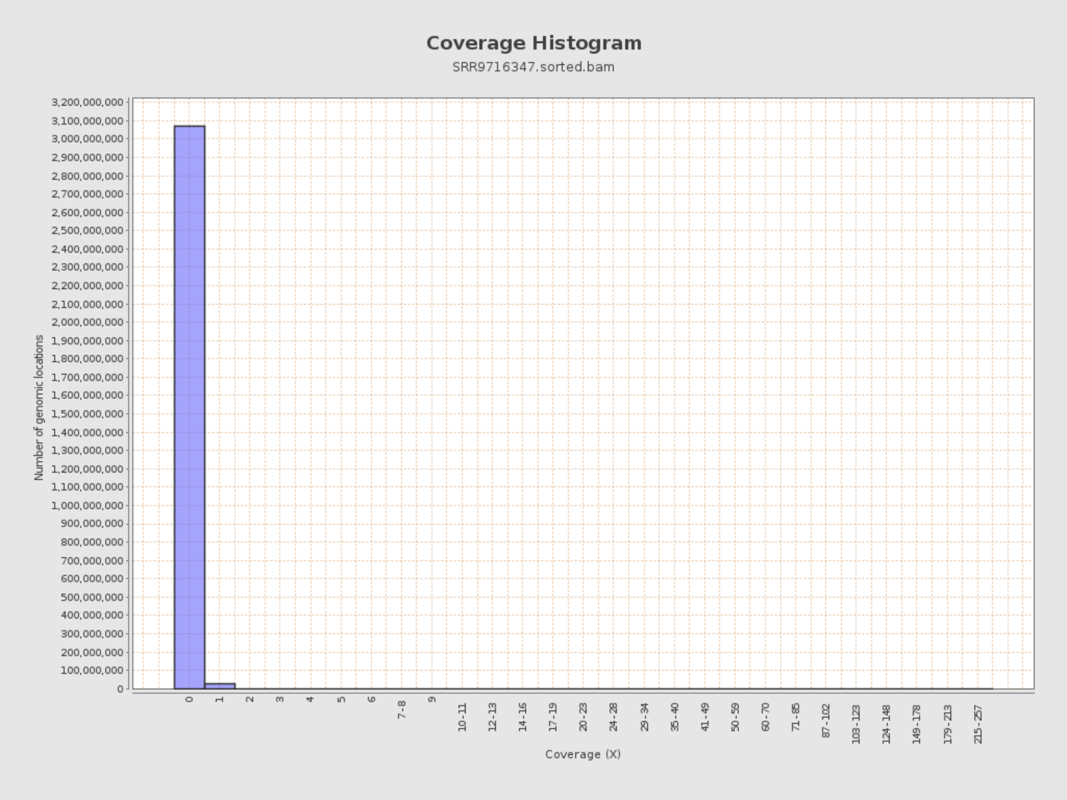
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2770087	0.0111	0.2312
chr2	243199373	2330067	0.0096	0.1302
chr3	198022430	1824449	0.0092	0.0987
chr4	191154276	1822276	0.0095	0.106
chr5	180915260	1679974	0.0093	0.099
chr6	171115067	1547540	0.009	0.1006
chr7	159138663	1511921	0.0095	0.1322

chr8	146364022	1422140	0.0097	0.1313
chr9	141213431	1152107	0.0082	0.1083
chr10	135534747	1326476	0.0098	0.1227
chr11	135006516	1630777	0.0121	0.138
chr12	133851895	1241148	0.0093	0.099
chr13	115169878	1019081	0.0088	0.0967
chr14	107349540	837043	0.0078	0.0927
chr15	102531392	780582	0.0076	0.0894
chr16	90354753	618742	0.0068	0.0871
chr17	81195210	857504	0.0106	0.1102
chr18	78077248	755426	0.0097	0.1582
chr19	59128983	512945	0.0087	0.1491
chr20	63025520	554799	0.0088	0.0977
chr21	48129895	361672	0.0075	0.0914
chr22	51304566	300474	0.0059	0.0785
chrMT	16571	8961	0.5408	0.7759
chrX	155270560	1577771	0.0102	0.1086
chrY	59373566	86375	0.0015	0.0558

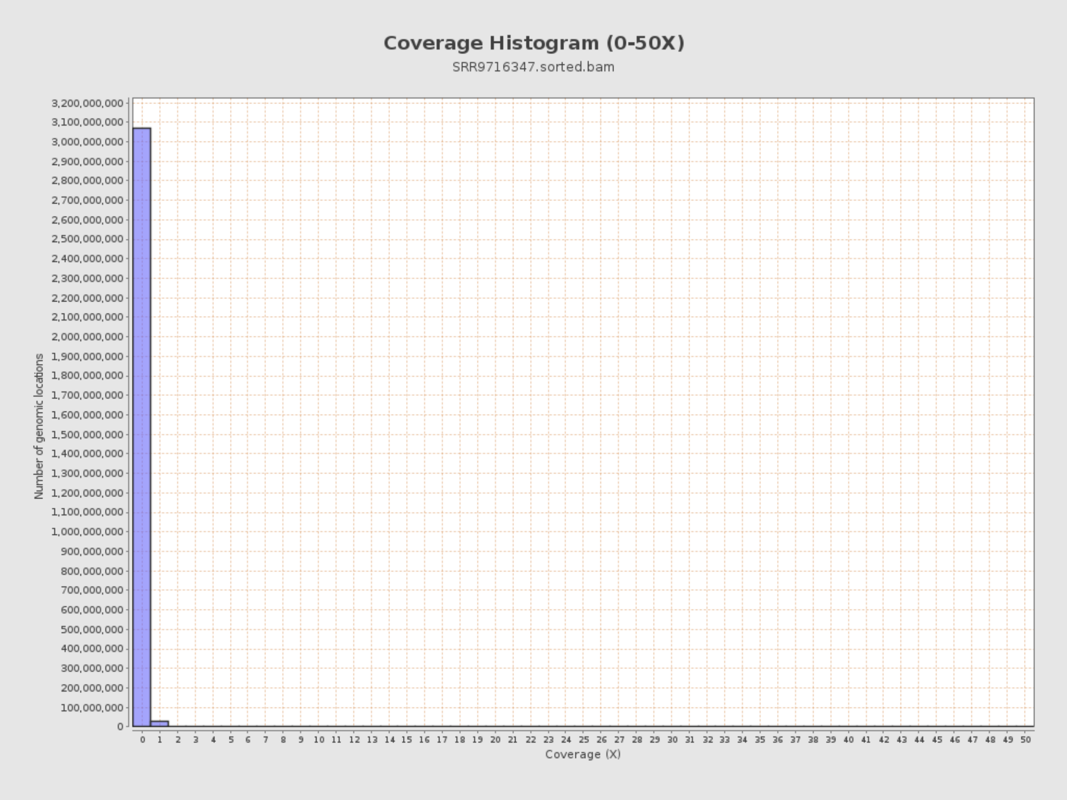
3. Results : Coverage across reference



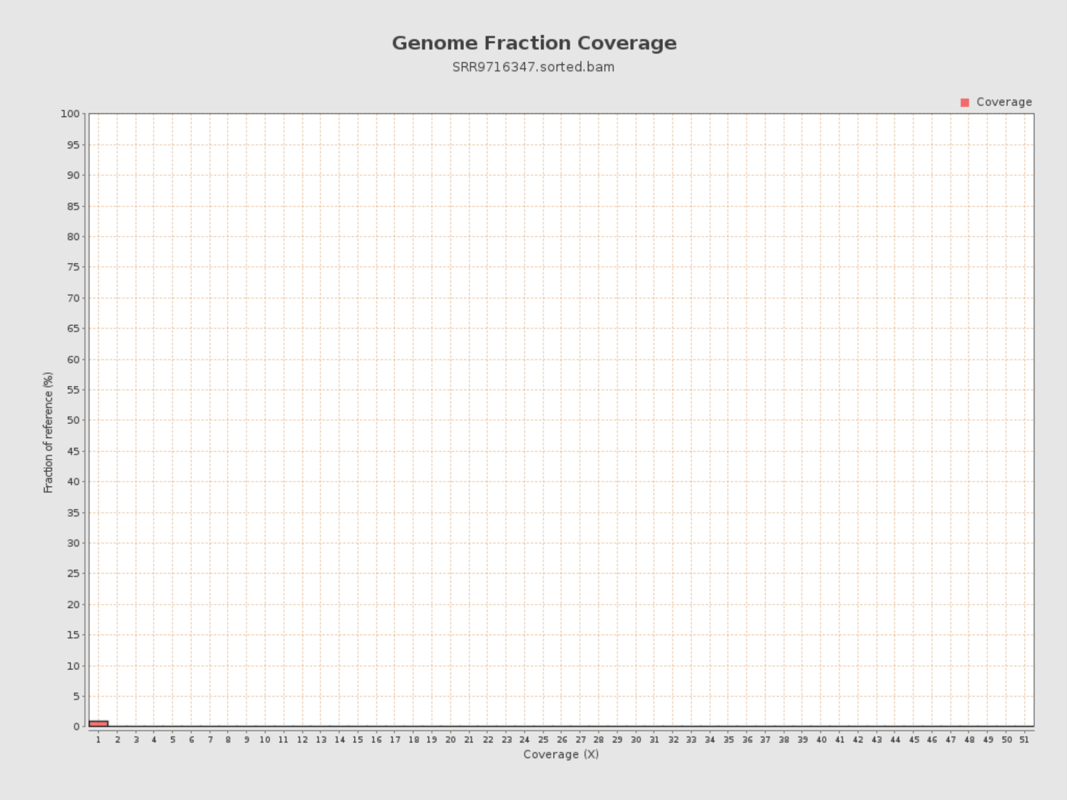
4. Results : Coverage Histogram



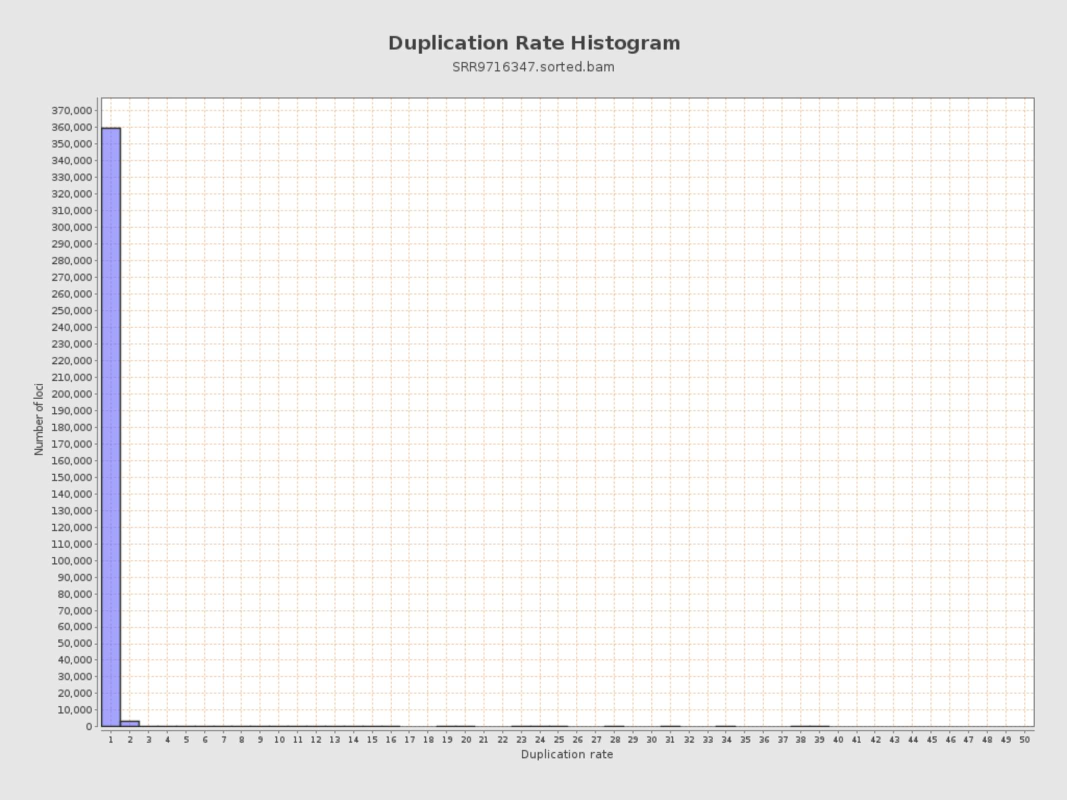
5. Results : Coverage Histogram (0-50X)



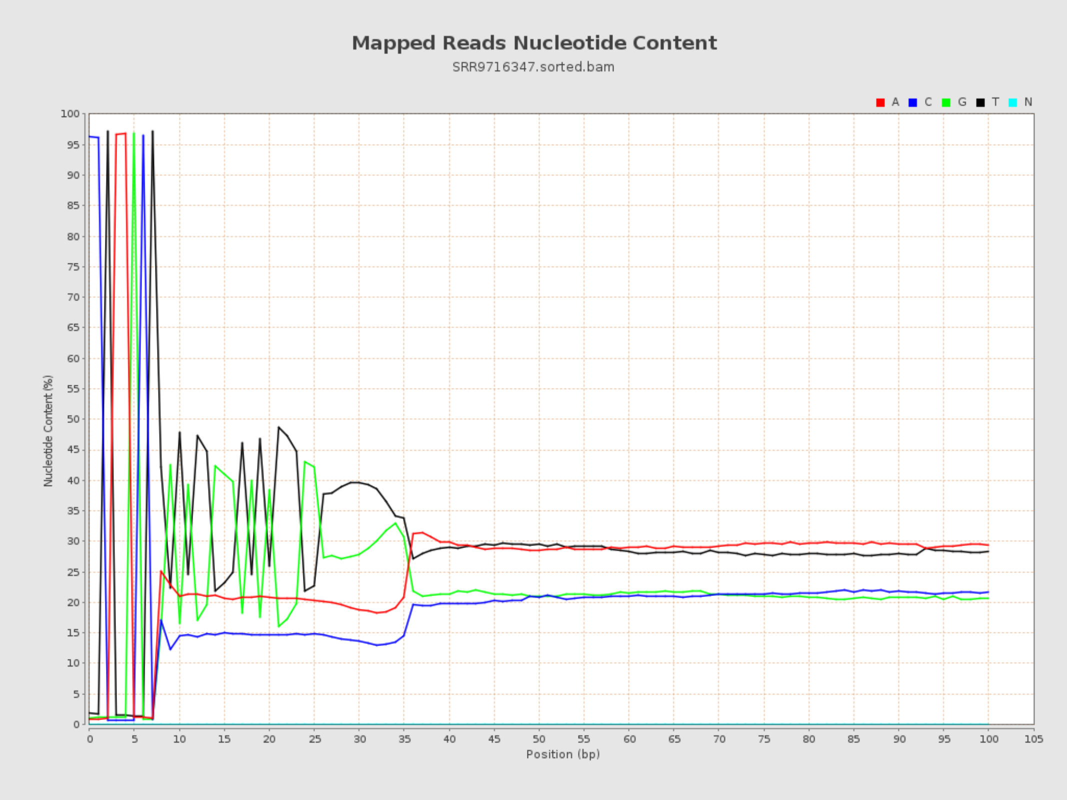
6. Results : Genome Fraction Coverage



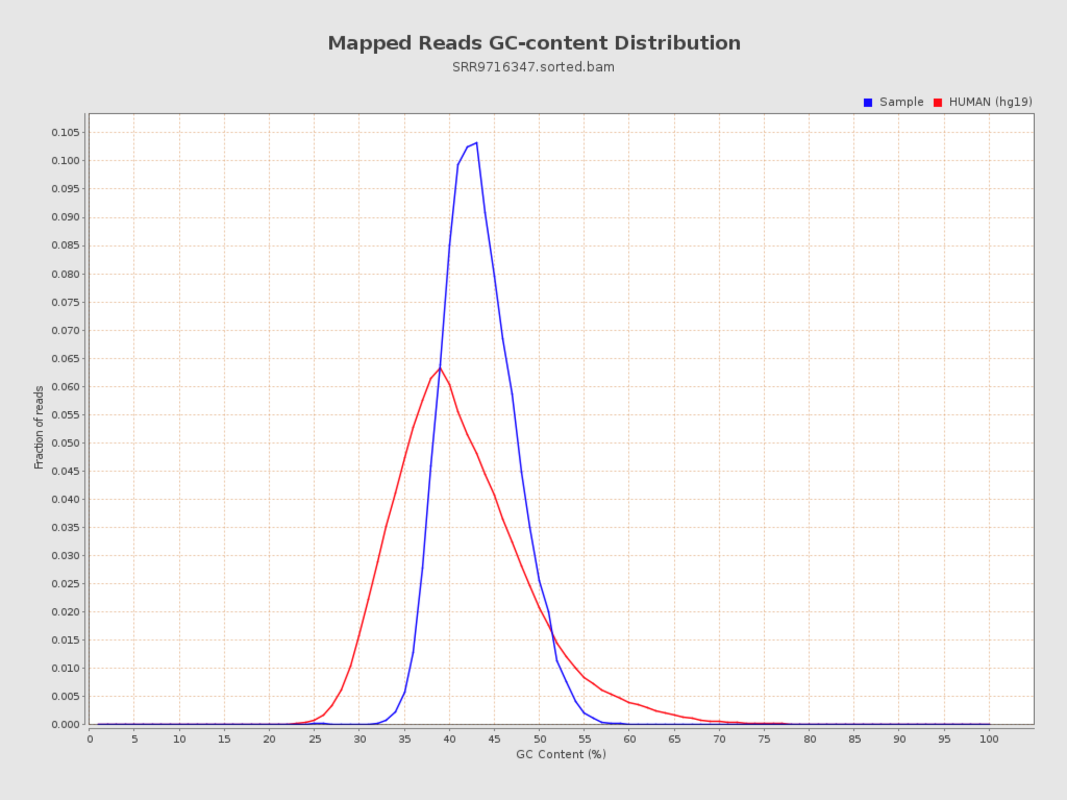
7. Results : Duplication Rate Histogram



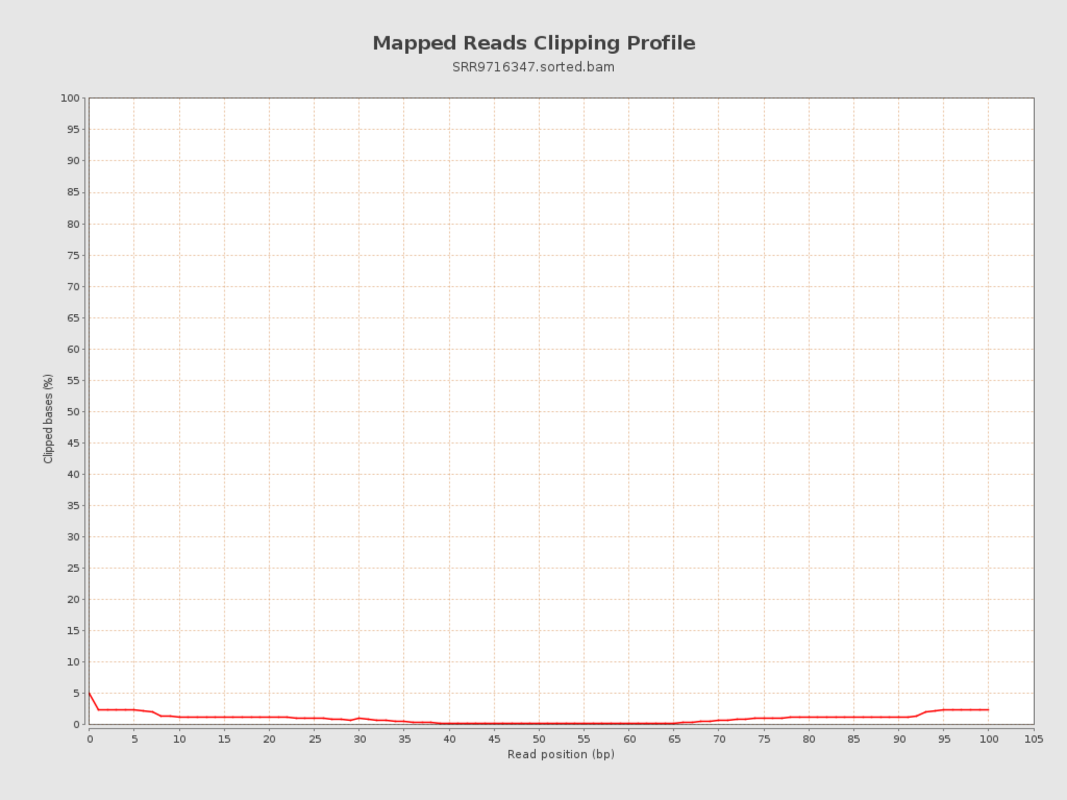
8. Results : Mapped Reads Nucleotide Content



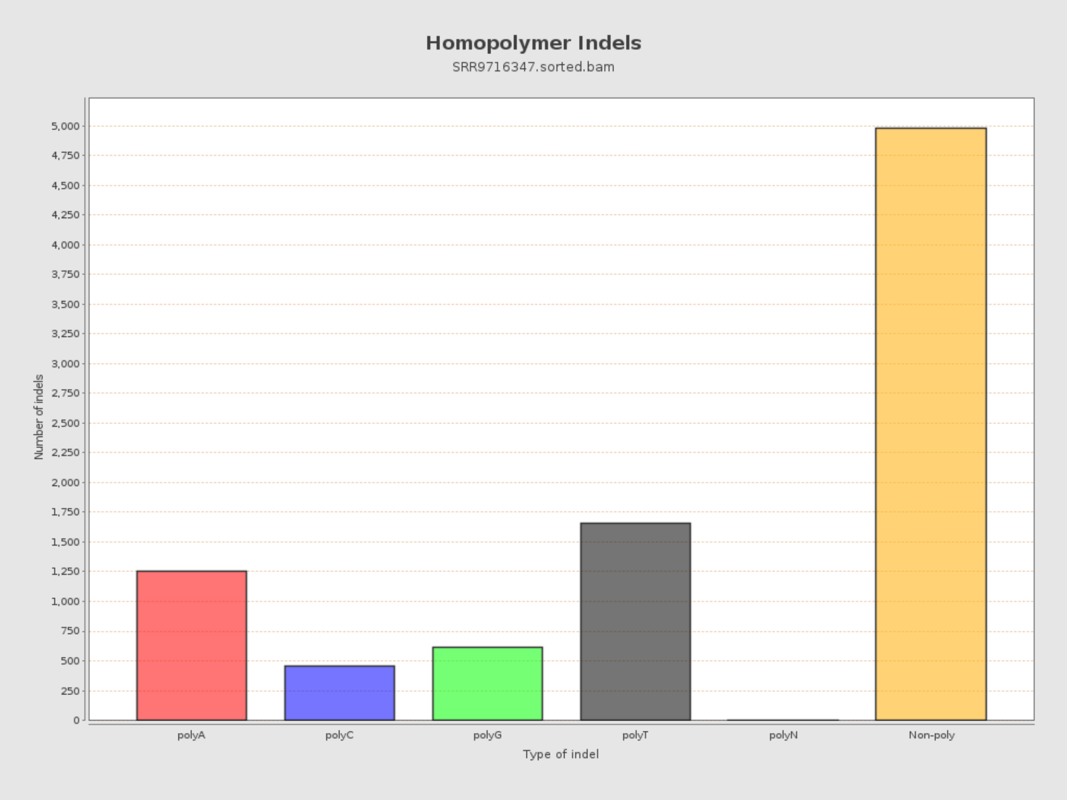
9. Results : Mapped Reads GC-content Distribution



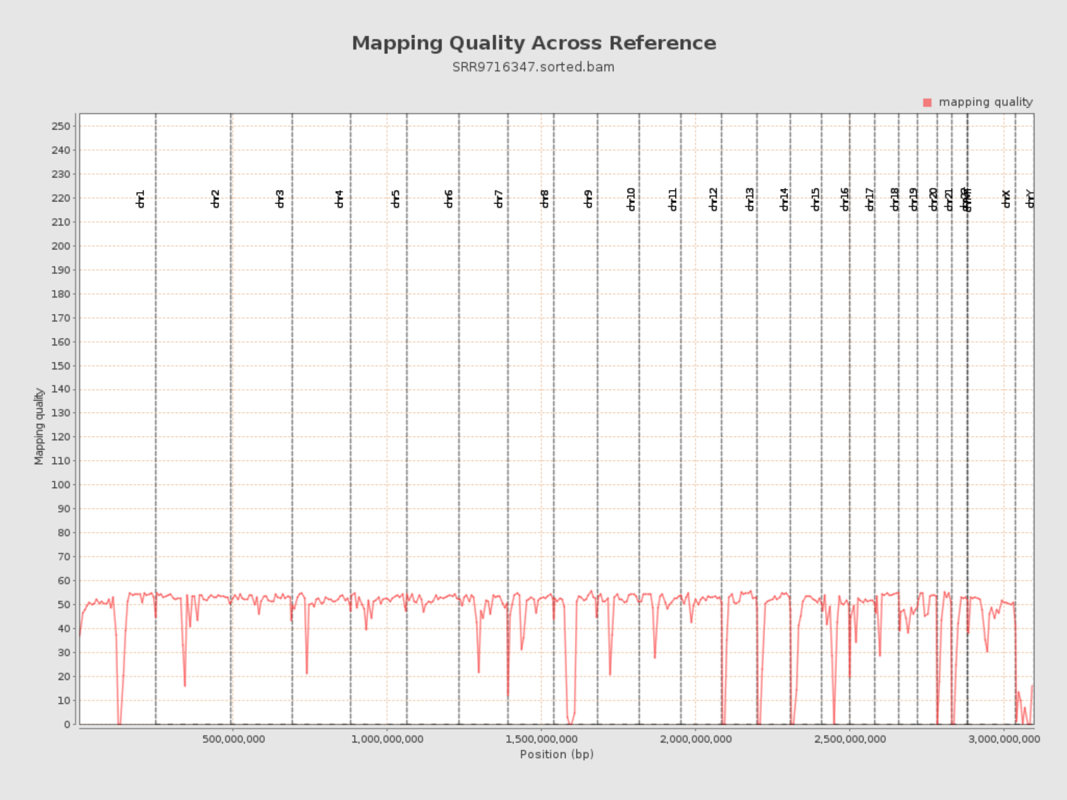
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram