Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:49:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716097.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_SRR9716097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:49:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	718,394
Mapped reads	662,192 / 92.18%
Unmapped reads	56,202 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,212 / 1.42%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	18,263 / 2.54%
Duplication rate	1.71%
Clipped reads	671,066 / 93.41%

2.2. ACGT Content

Number/percentage of A's	12,933,018 / 24.72%
Number/percentage of C's	10,383,193 / 19.85%
Number/percentage of T's	16,037,284 / 30.66%
Number/percentage of G's	12,956,619 / 24.77%
Number/percentage of N's	2,860 / 0.01%
GC Percentage	44.62%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.2096

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

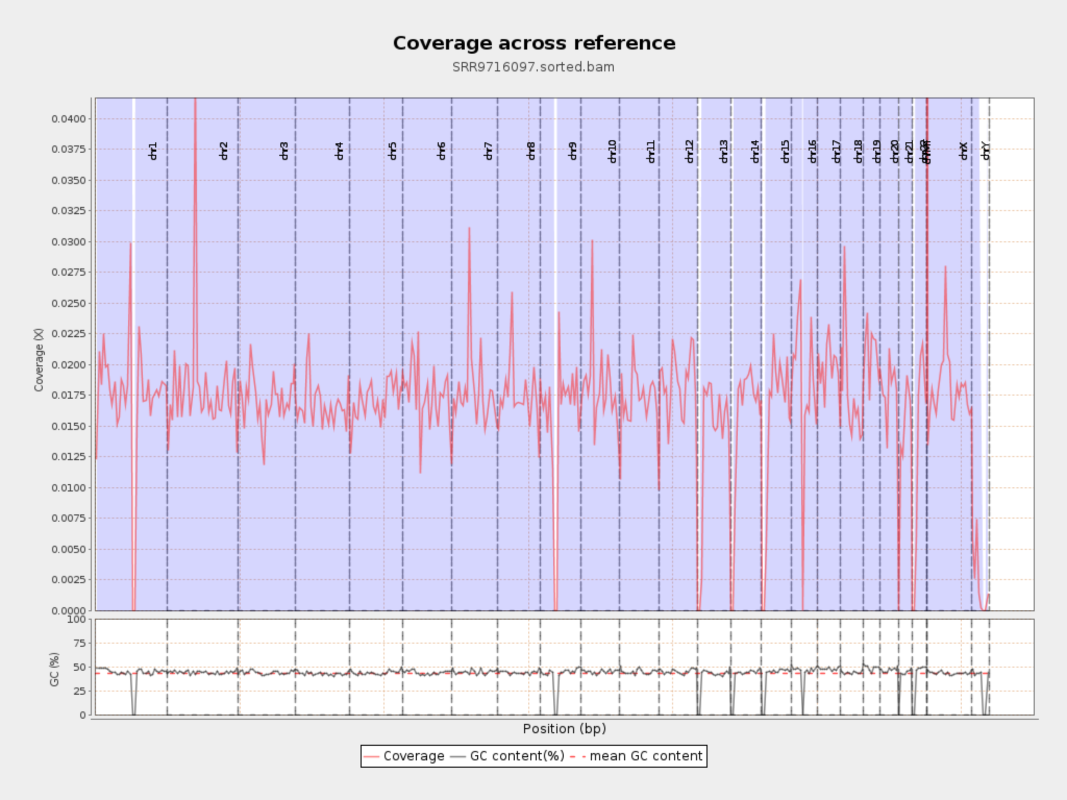
General error rate	0.82%
Mismatches	419,857
Insertions	5,145
Mapped reads with at least one insertion	0.77%
Deletions	12,395
Mapped reads with at least one deletion	1.85%
Homopolymer indels	43.52%

2.6. Chromosome stats

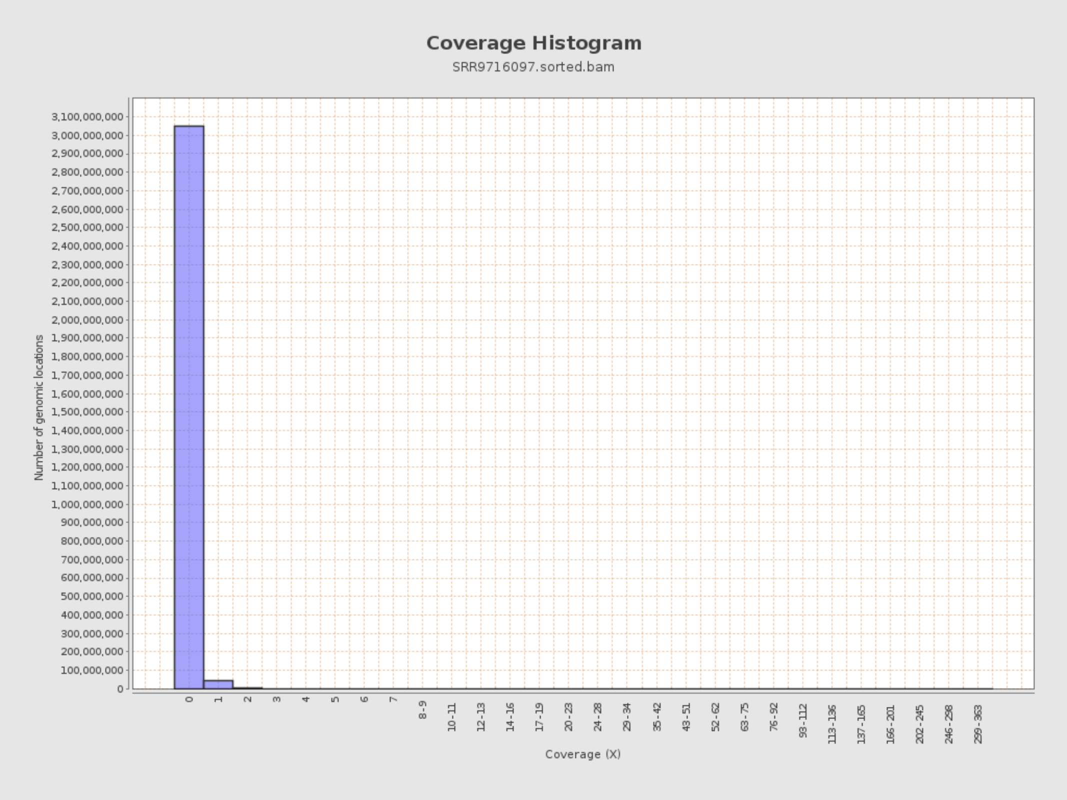
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4308513	0.0173	0.3076
chr2	243199373	4439331	0.0183	0.2954
chr3	198022430	3387923	0.0171	0.1387
chr4	191154276	3207408	0.0168	0.1427
chr5	180915260	3103126	0.0172	0.1404
chr6	171115067	2995810	0.0175	0.1545
chr7	159138663	2849403	0.0179	0.2534

chr8	146364022	2562007	0.0175	0.2777
chr9	141213431	2182560	0.0155	0.221
chr10	135534747	2463804	0.0182	0.1956
chr11	135006516	2359905	0.0175	0.2004
chr12	133851895	2473489	0.0185	0.1457
chr13	115169878	1558355	0.0135	0.122
chr14	107349540	1622326	0.0151	0.1471
chr15	102531392	1536523	0.015	0.131
chr16	90354753	1630241	0.018	0.1516
chr17	81195210	1606644	0.0198	0.156
chr18	78077248	1366899	0.0175	0.3958
chr19	59128983	1245110	0.0211	0.2602
chr20	63025520	1112781	0.0177	0.1471
chr21	48129895	678280	0.0141	0.1304
chr22	51304566	677682	0.0132	0.1223
chrMT	16571	16280	0.9824	1.1751
chrX	155270560	2820022	0.0182	0.172
chrY	59373566	129980	0.0022	0.0697

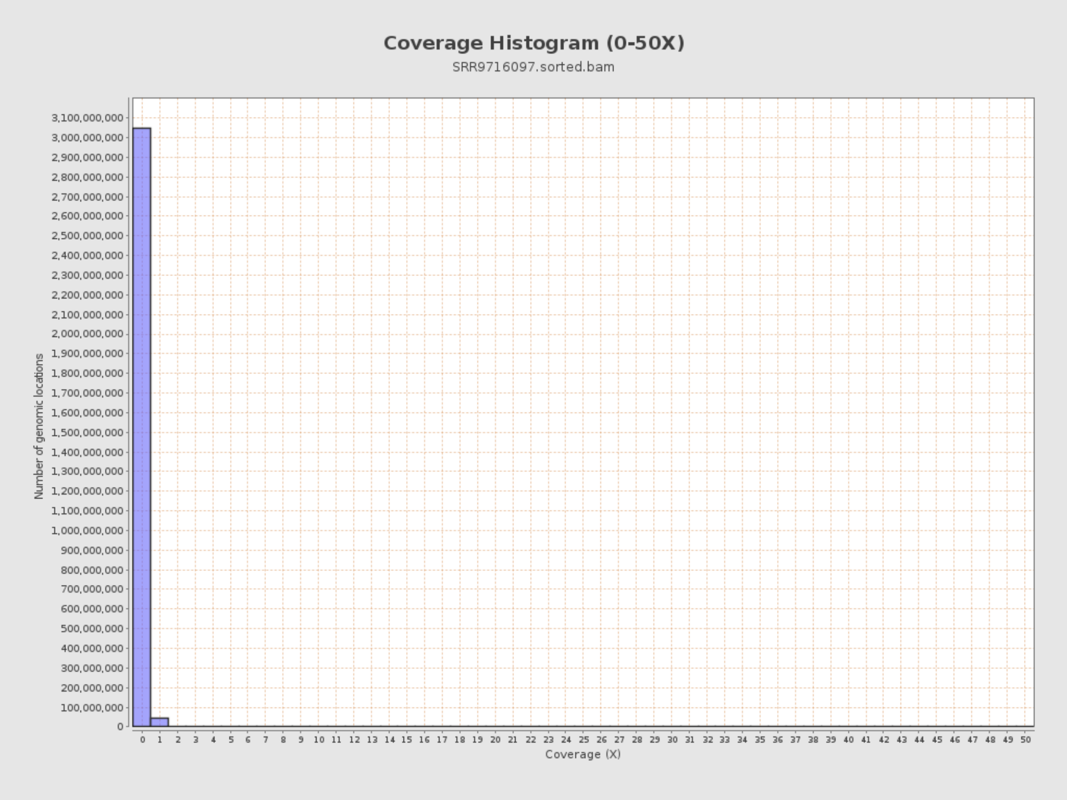
3. Results : Coverage across reference



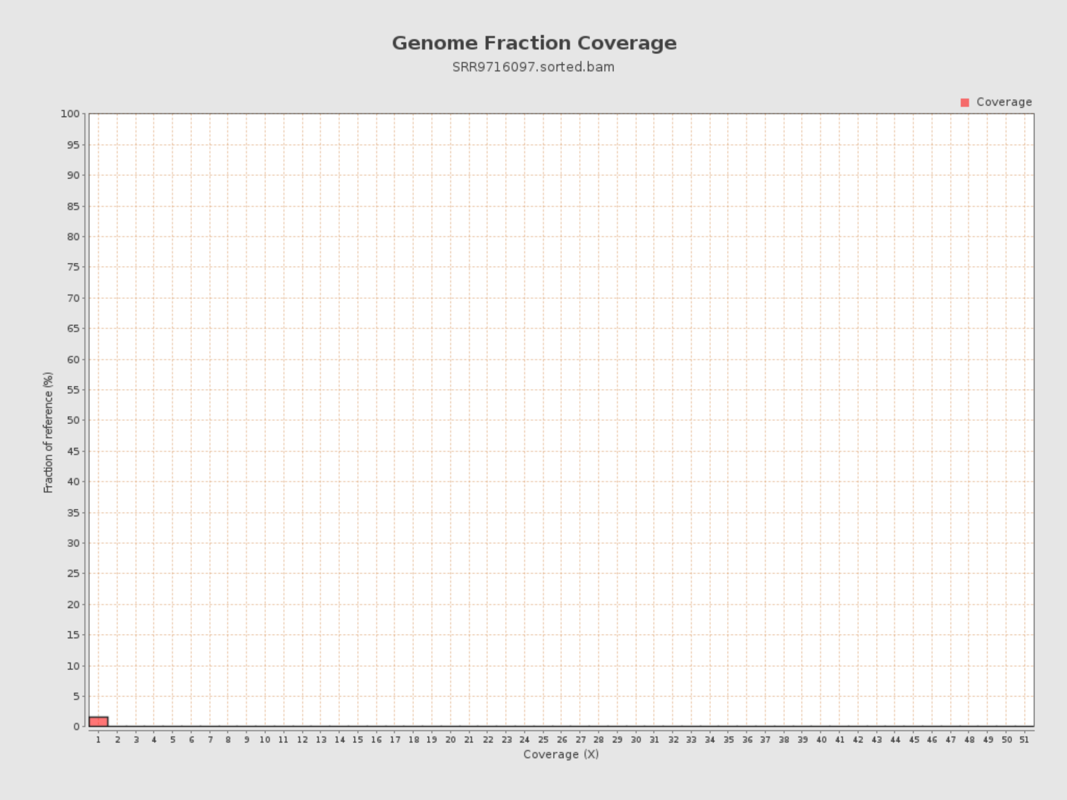
4. Results : Coverage Histogram



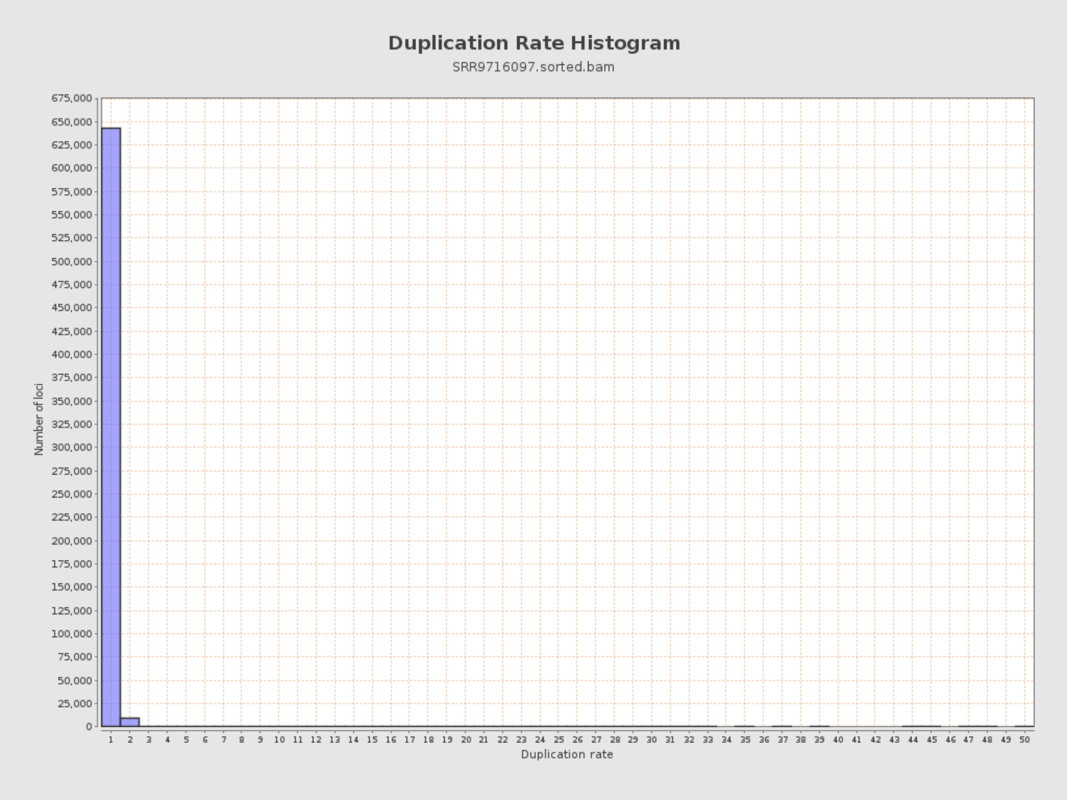
5. Results : Coverage Histogram (0-50X)



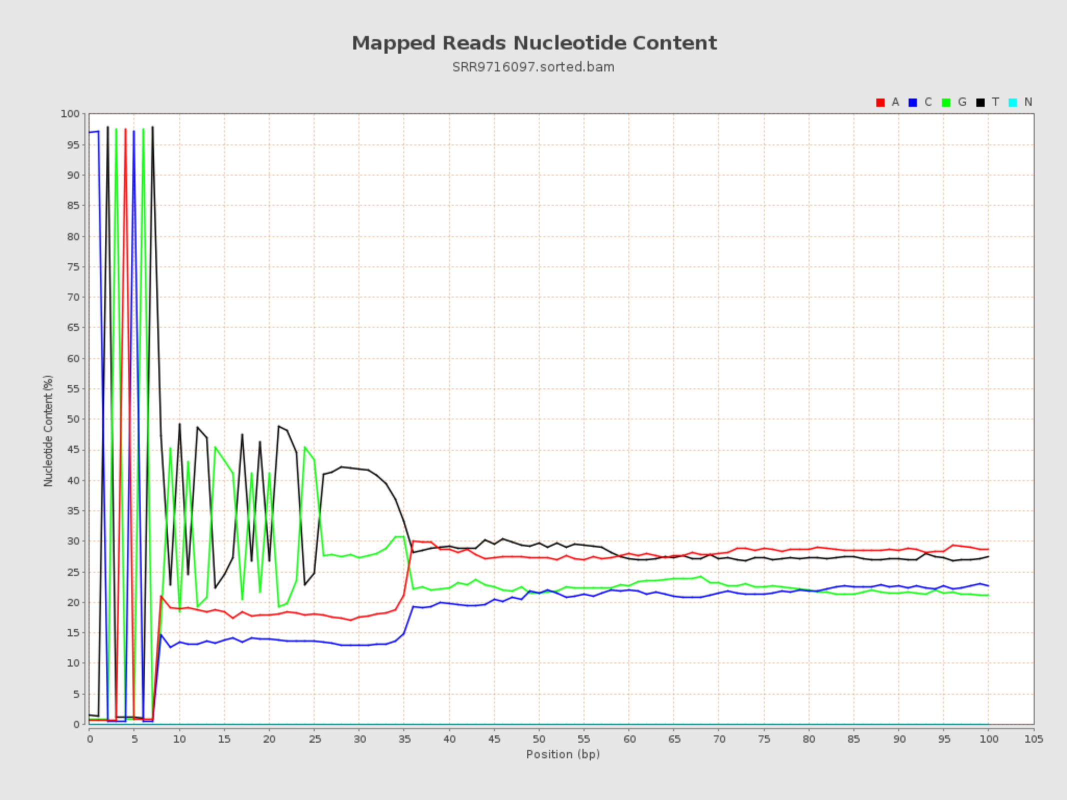
6. Results : Genome Fraction Coverage



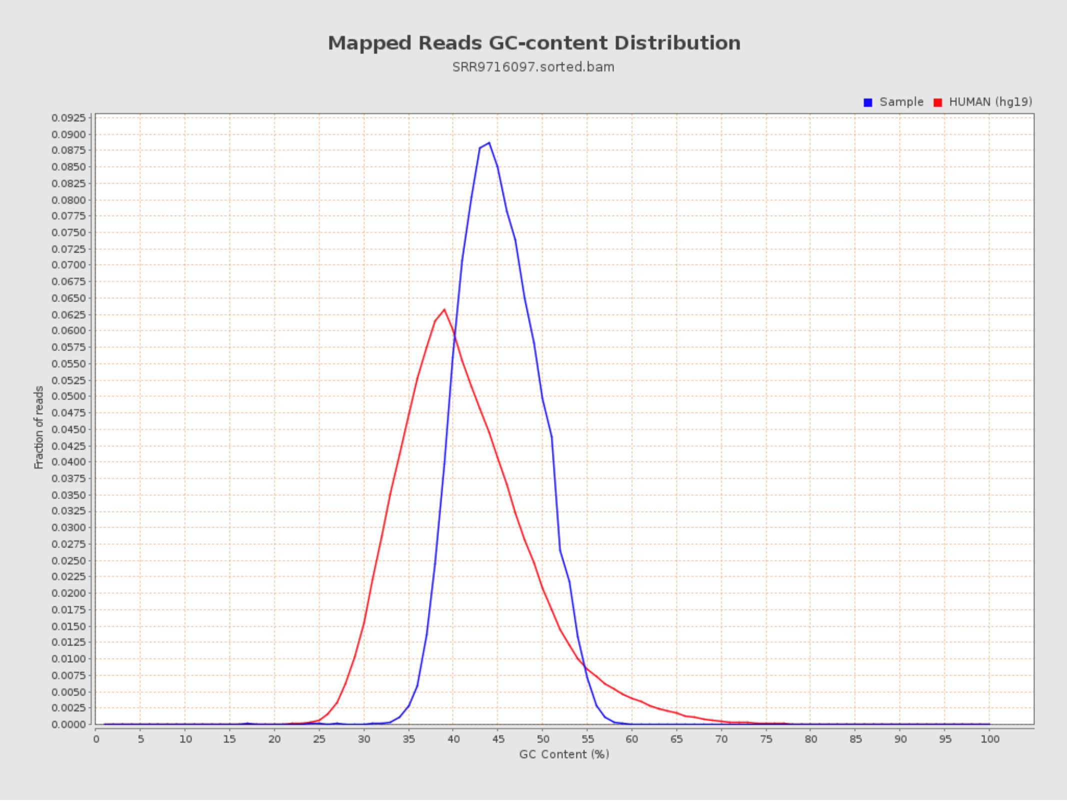
7. Results : Duplication Rate Histogram



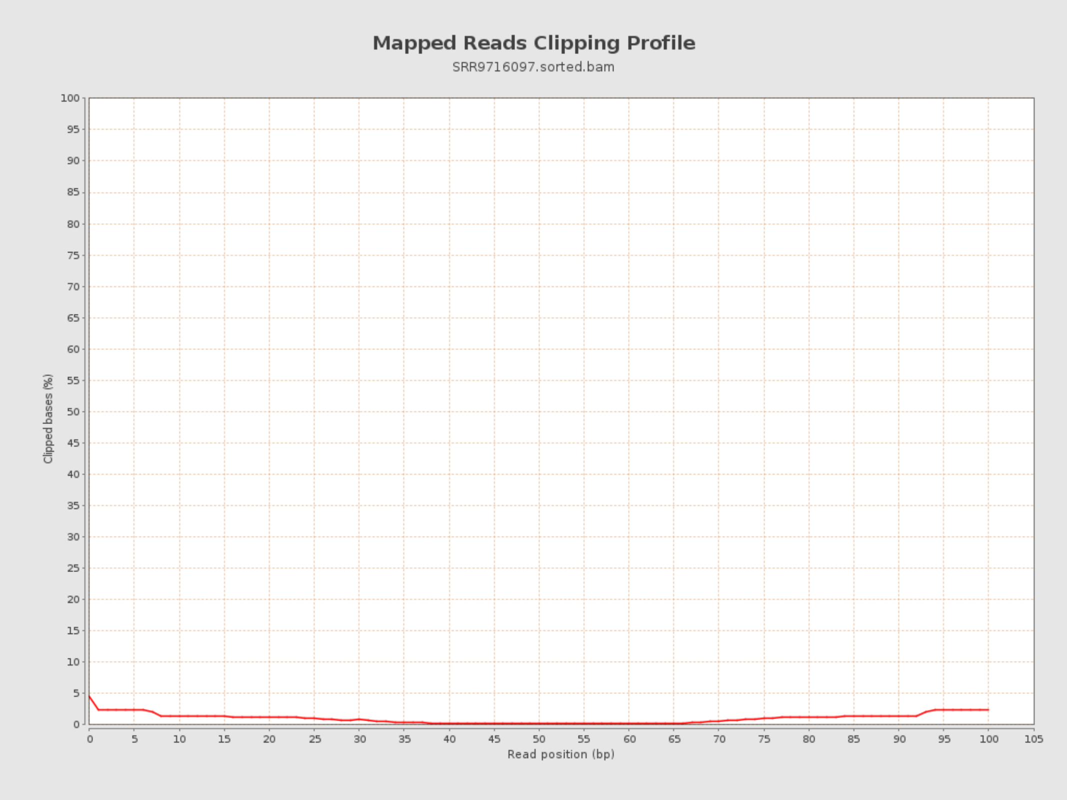
8. Results : Mapped Reads Nucleotide Content



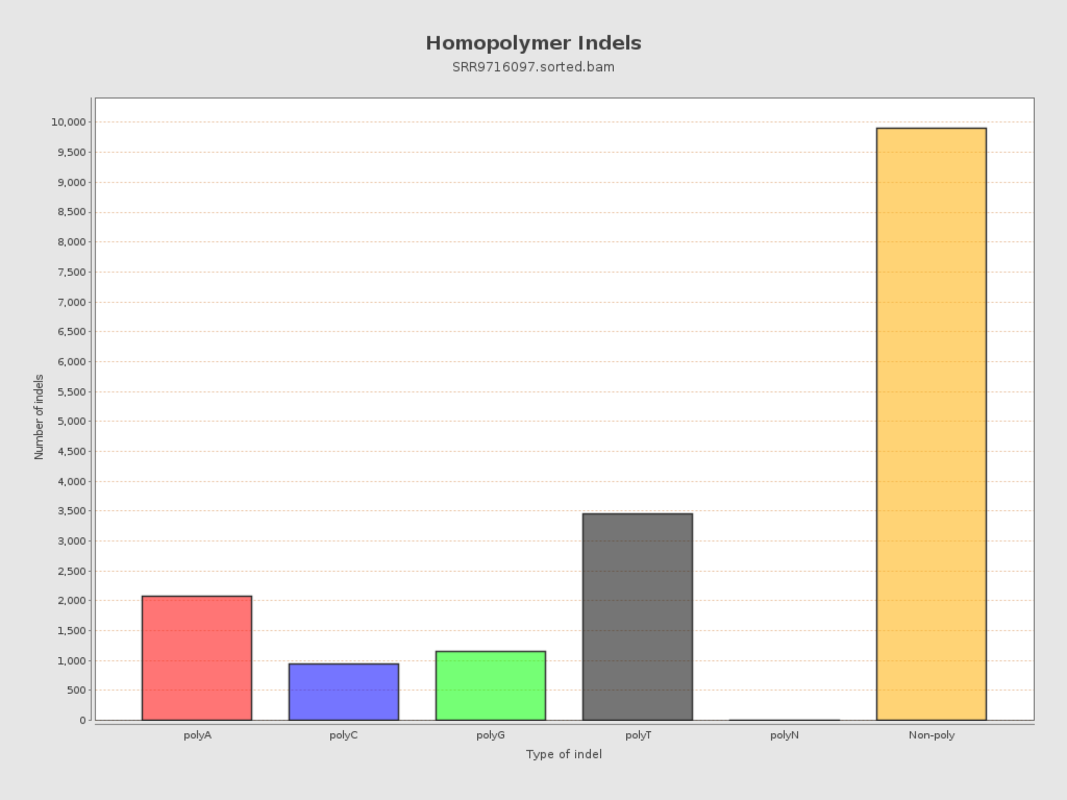
9. Results : Mapped Reads GC-content Distribution



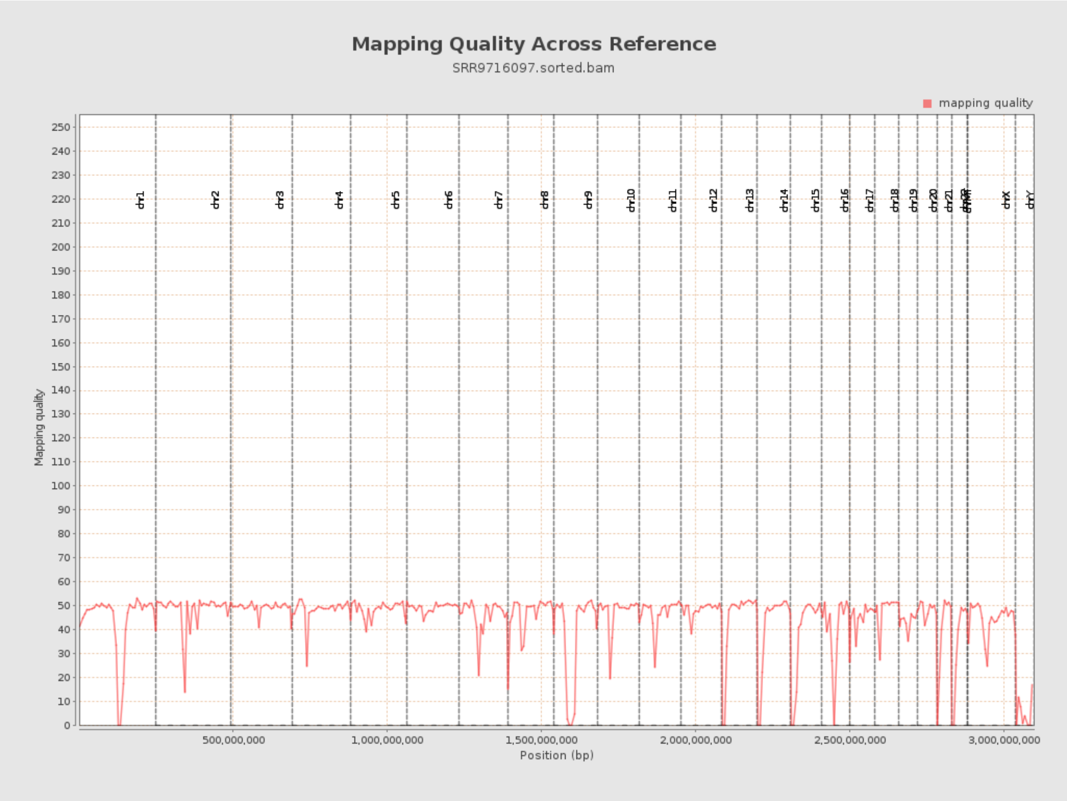
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram