Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:30:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716915.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_SRR9716915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716915.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:30:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	660,021
Mapped reads	533,276 / 80.8%
Unmapped reads	126,745 / 19.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,410 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,901 / 1.2%
Duplication rate	1.07%
Clipped reads	534,722 / 81.02%

2.2. ACGT Content

Number/percentage of A's	7,081,103 / 24.19%
Number/percentage of C's	6,105,693 / 20.86%
Number/percentage of T's	8,796,428 / 30.05%
Number/percentage of G's	7,290,767 / 24.9%
Number/percentage of N's	733 / 0%
GC Percentage	45.76%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.113

2.4. Mapping Quality

Mean Mapping Quality	39.2

2.5. Mismatches and indels

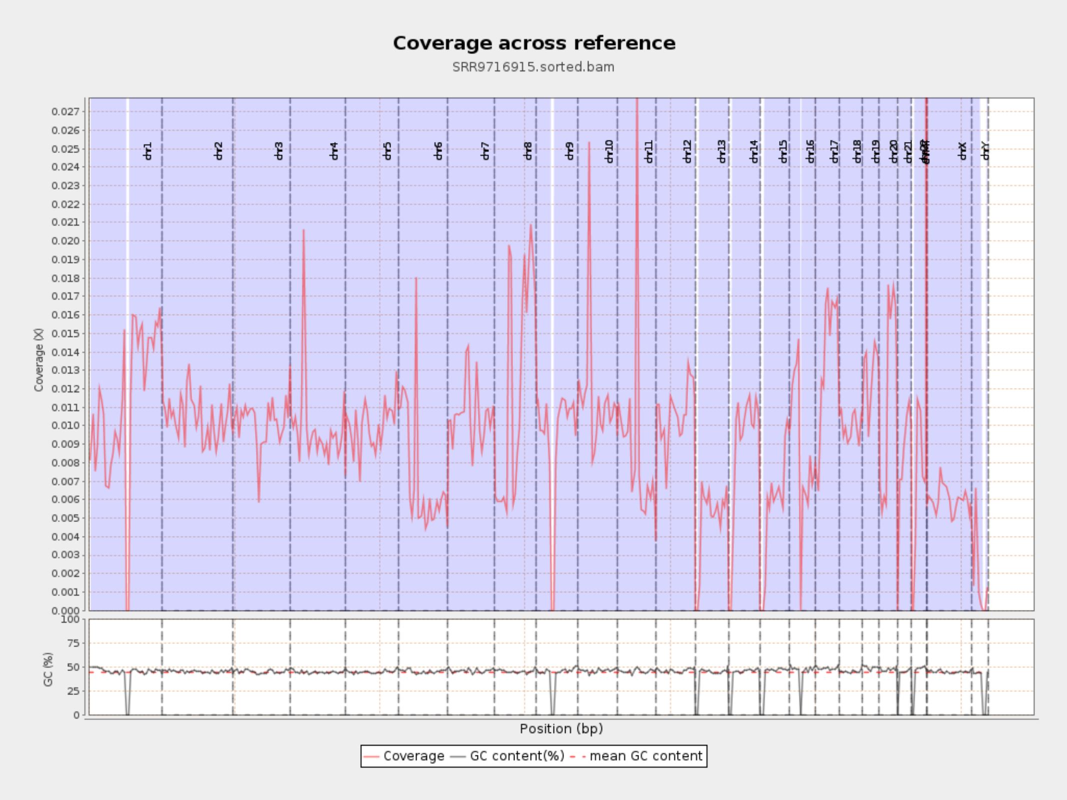
General error rate	0.56%
Mismatches	158,635
Insertions	2,232
Mapped reads with at least one insertion	0.42%
Deletions	4,973
Mapped reads with at least one deletion	0.92%
Homopolymer indels	32.94%

2.6. Chromosome stats

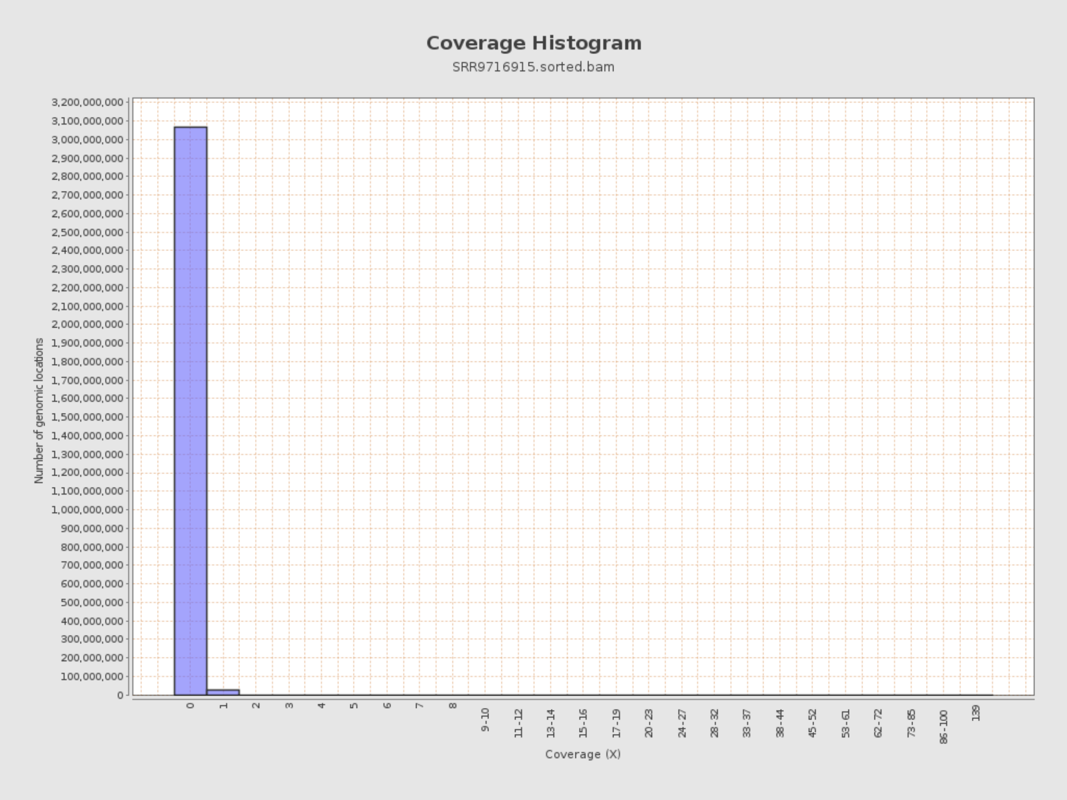
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2791985	0.0112	0.1321
chr2	243199373	2547185	0.0105	0.1292
chr3	198022430	2005032	0.0101	0.1069
chr4	191154276	1886023	0.0099	0.1145
chr5	180915260	1806489	0.01	0.1045
chr6	171115067	1260302	0.0074	0.091
chr7	159138663	1688708	0.0106	0.1225

chr8	146364022	1790978	0.0122	0.1193
chr9	141213431	1299839	0.0092	0.1051
chr10	135534747	1565520	0.0116	0.1694
chr11	135006516	1220415	0.009	0.1087
chr12	133851895	1424143	0.0106	0.1083
chr13	115169878	559898	0.0049	0.0743
chr14	107349540	937168	0.0087	0.0997
chr15	102531392	571587	0.0056	0.0793
chr16	90354753	783276	0.0087	0.1034
chr17	81195210	1118817	0.0138	0.1276
chr18	78077248	776792	0.0099	0.1205
chr19	59128983	751499	0.0127	0.1286
chr20	63025520	737285	0.0117	0.1173
chr21	48129895	398093	0.0083	0.1029
chr22	51304566	324693	0.0063	0.0857
chrMT	16571	4186	0.2526	0.5413
chrX	155270560	933632	0.006	0.0842
chrY	59373566	99634	0.0017	0.0675

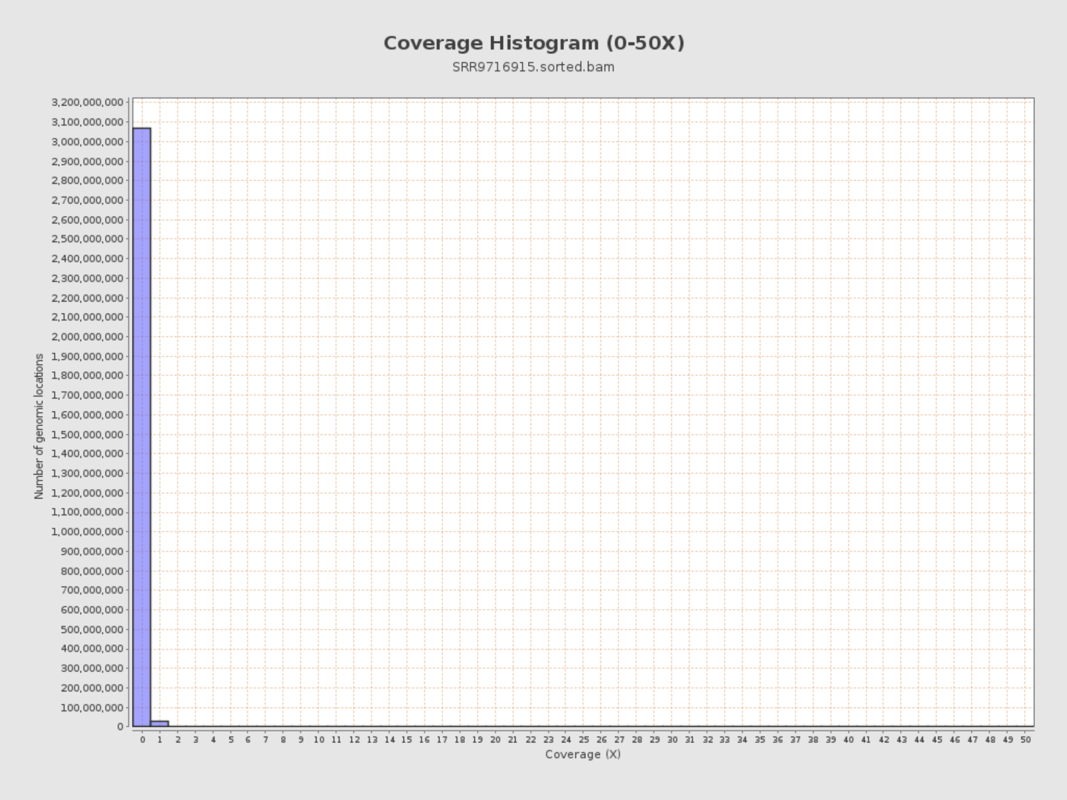
3. Results : Coverage across reference



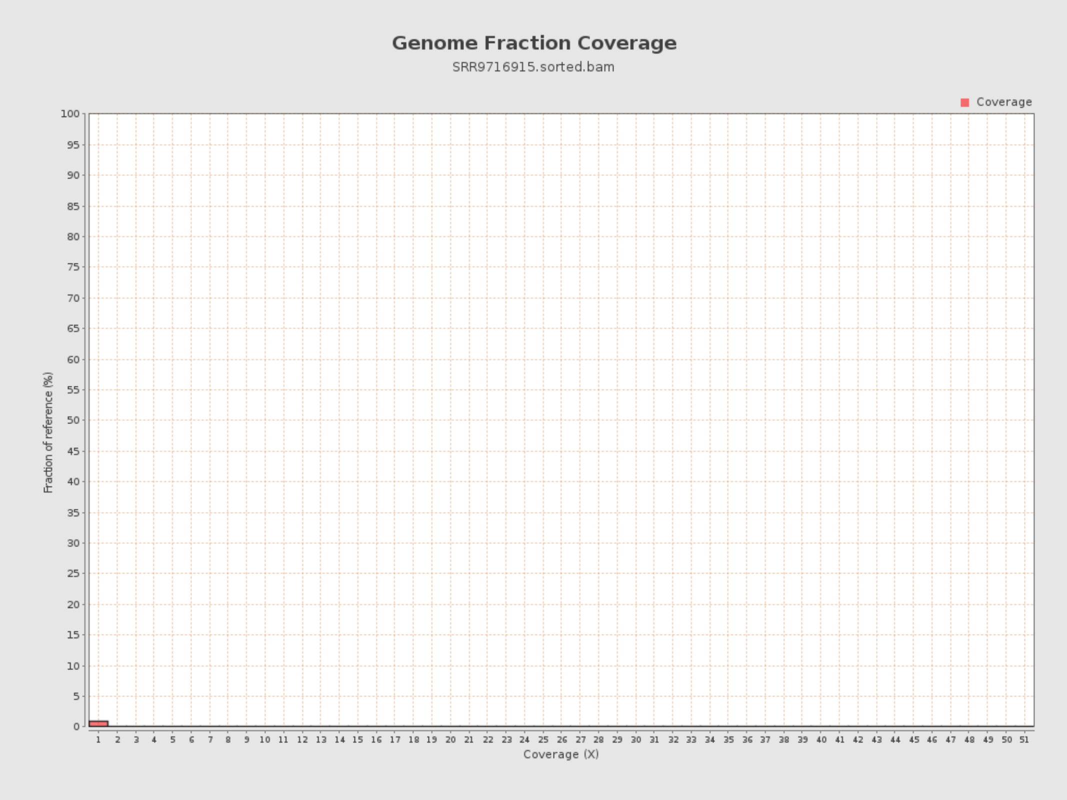
4. Results : Coverage Histogram



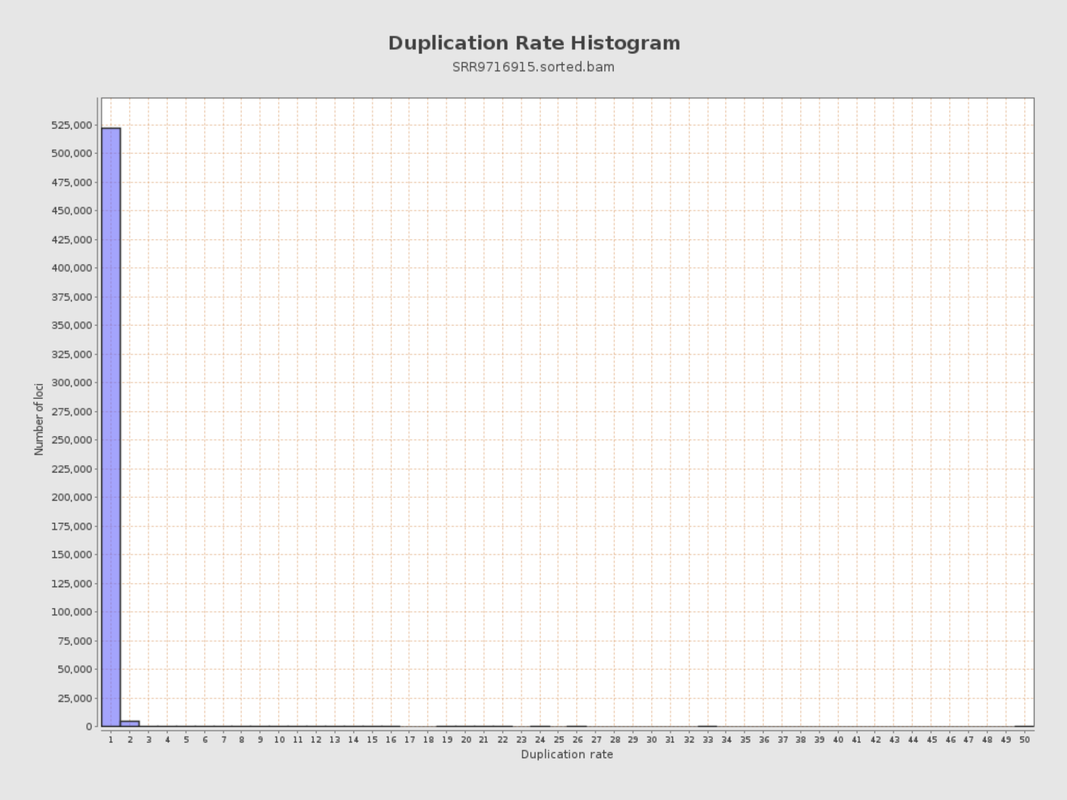
5. Results : Coverage Histogram (0-50X)



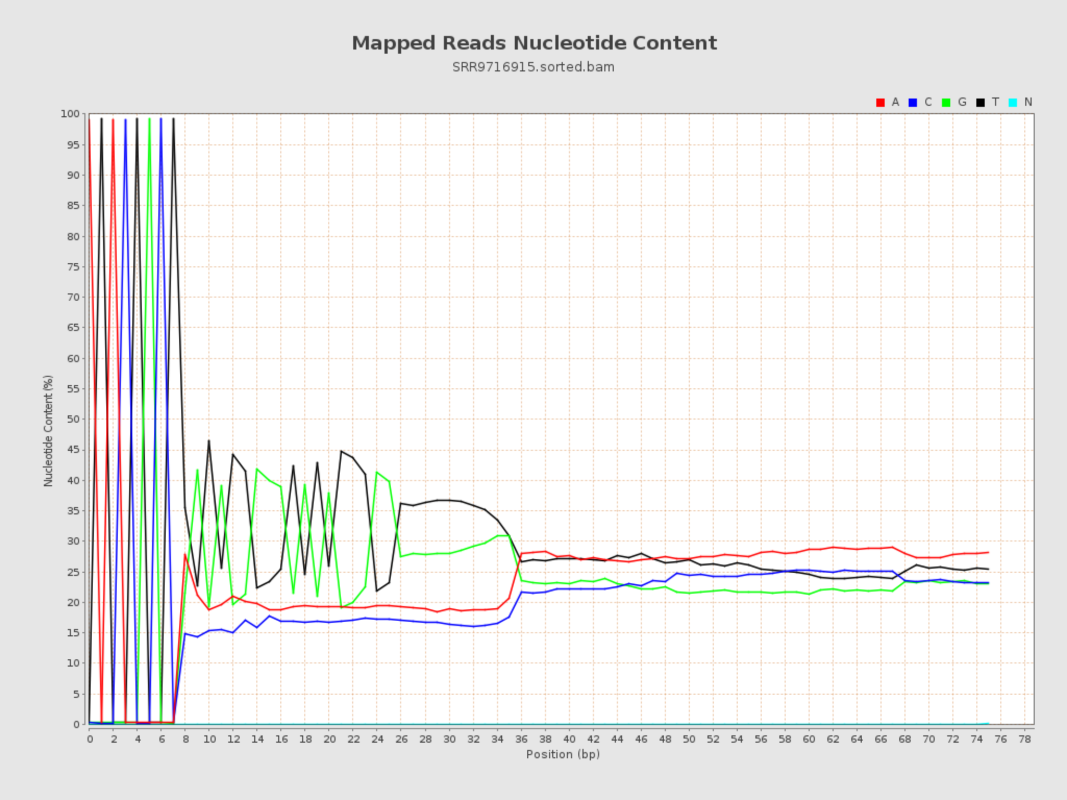
6. Results : Genome Fraction Coverage



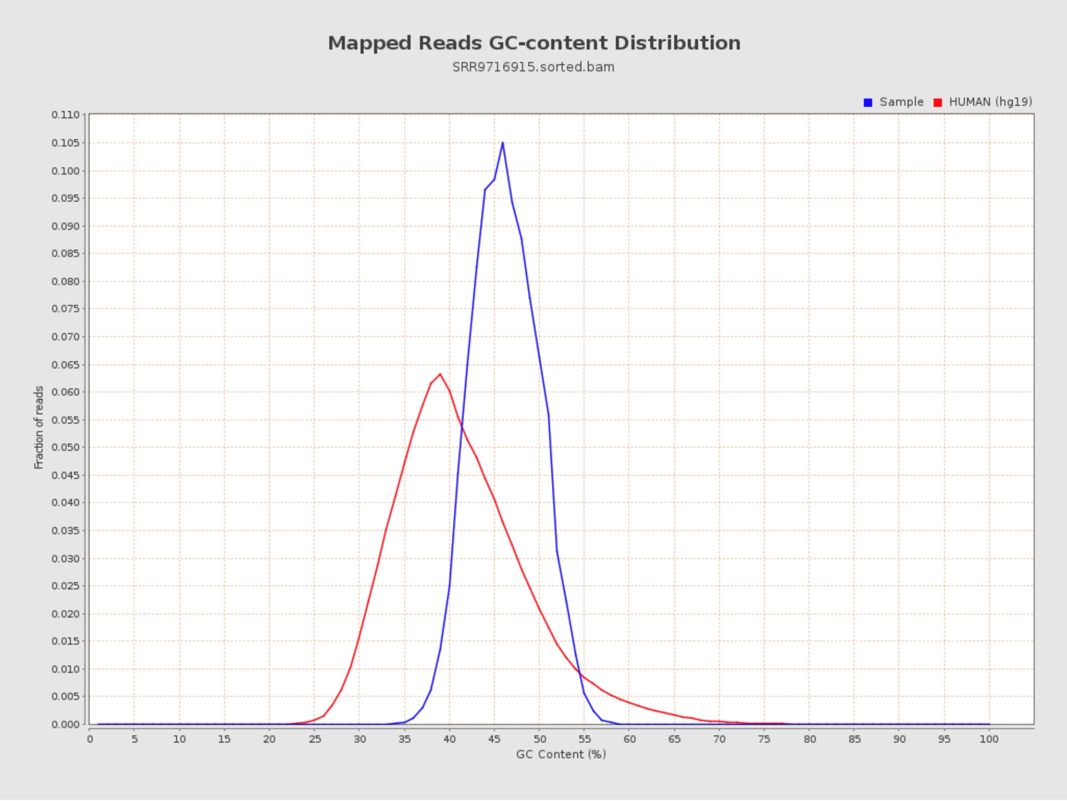
7. Results : Duplication Rate Histogram



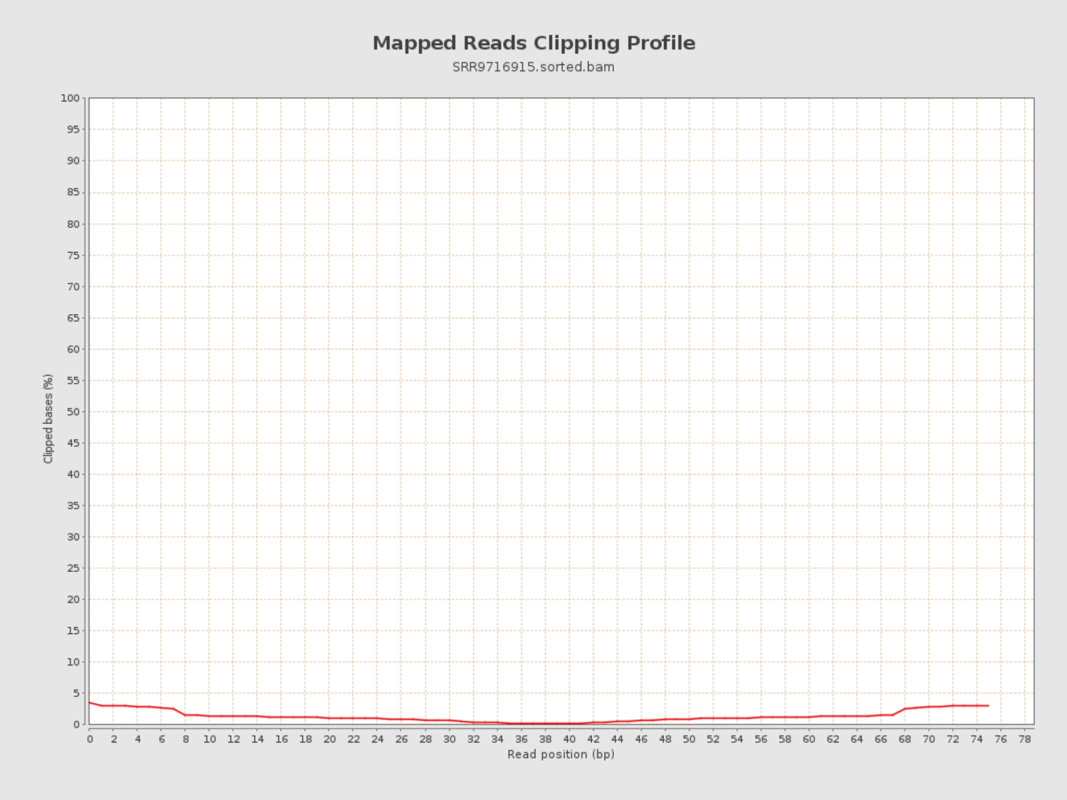
8. Results : Mapped Reads Nucleotide Content



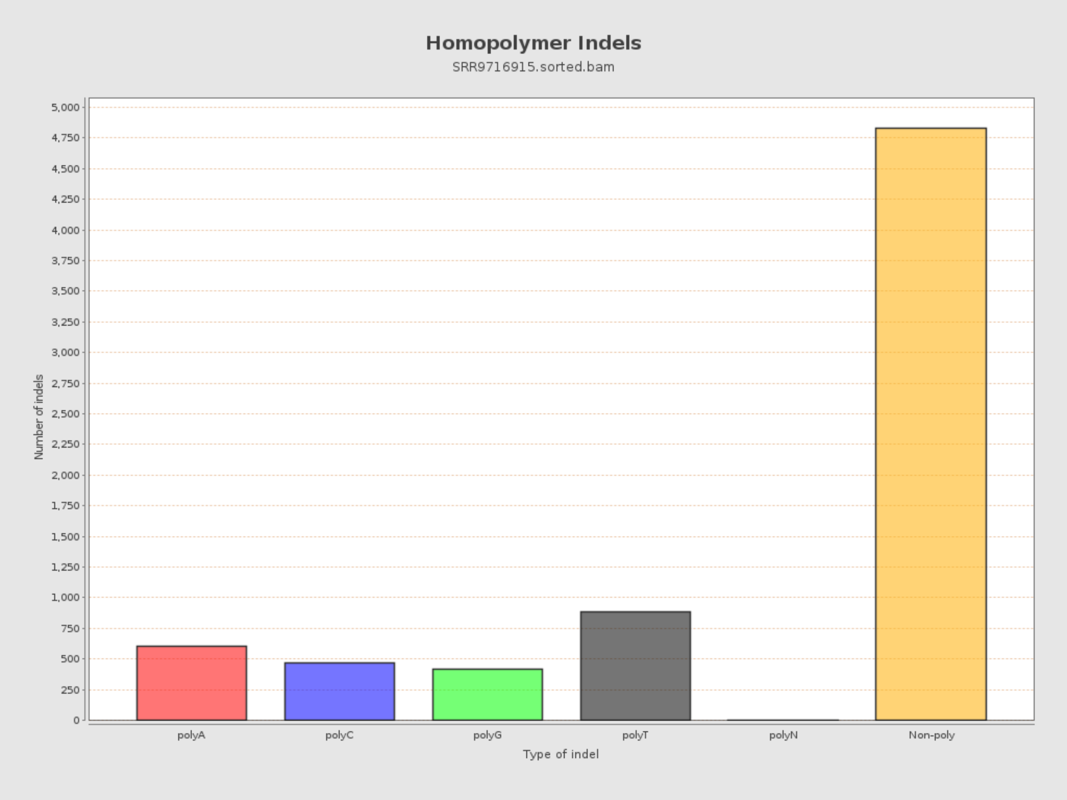
9. Results : Mapped Reads GC-content Distribution



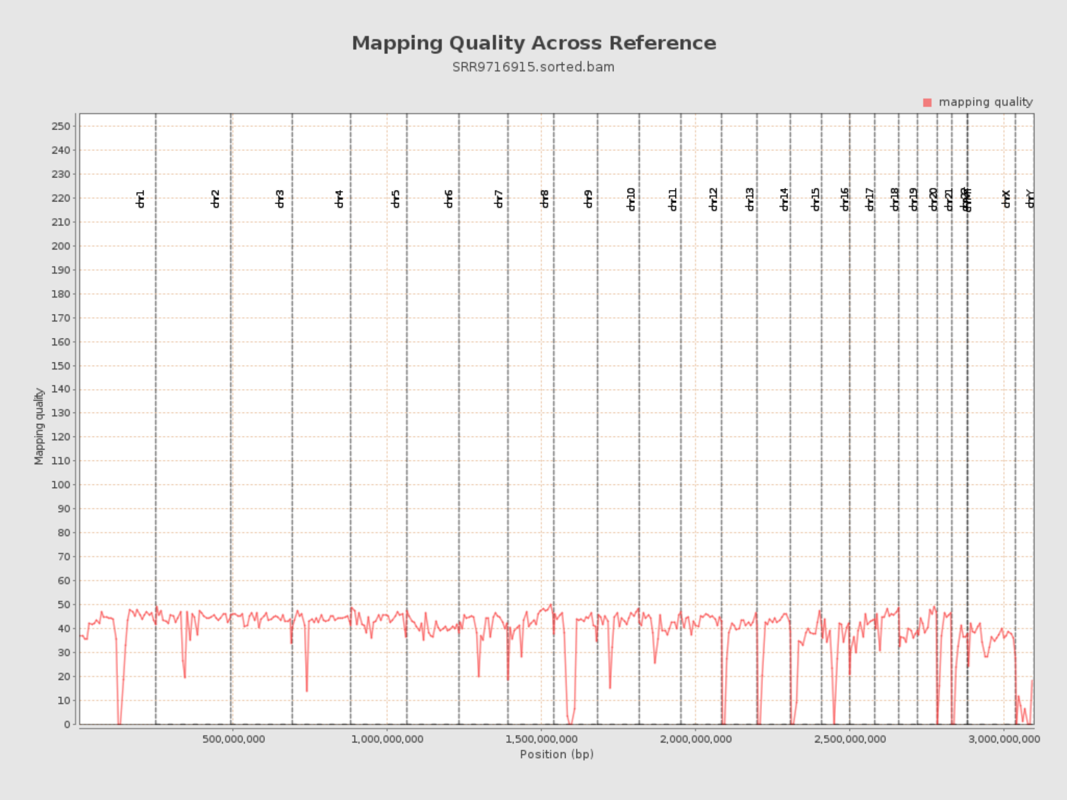
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram