Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:57:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716443.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_SRR9716443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716443.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:57:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	905,686
Mapped reads	818,759 / 90.4%
Unmapped reads	86,927 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,391 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	19,675 / 2.17%
Duplication rate	1.67%
Clipped reads	820,967 / 90.65%

2.2. ACGT Content

Number/percentage of A's	11,400,569 / 24.07%
Number/percentage of C's	9,118,584 / 19.26%
Number/percentage of T's	14,917,793 / 31.5%
Number/percentage of G's	11,917,218 / 25.17%
Number/percentage of N's	493 / 0%
GC Percentage	44.42%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1764

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

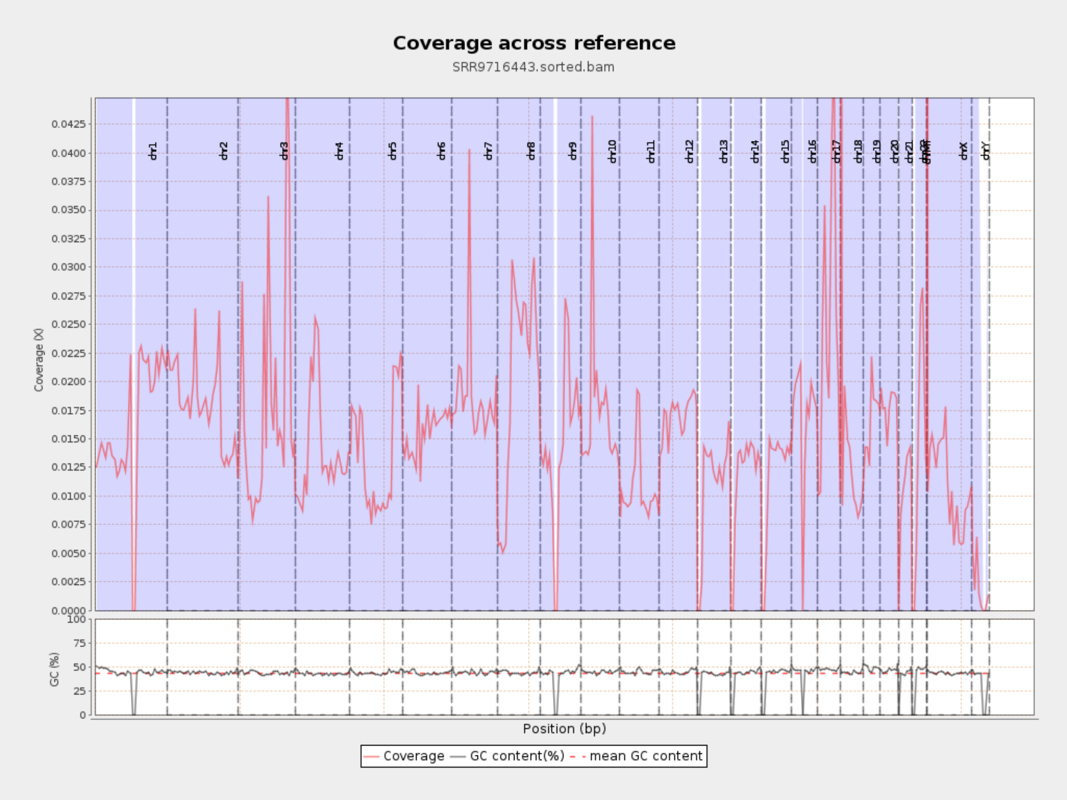
General error rate	0.52%
Mismatches	239,956
Insertions	3,143
Mapped reads with at least one insertion	0.38%
Deletions	8,995
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.3%

2.6. Chromosome stats

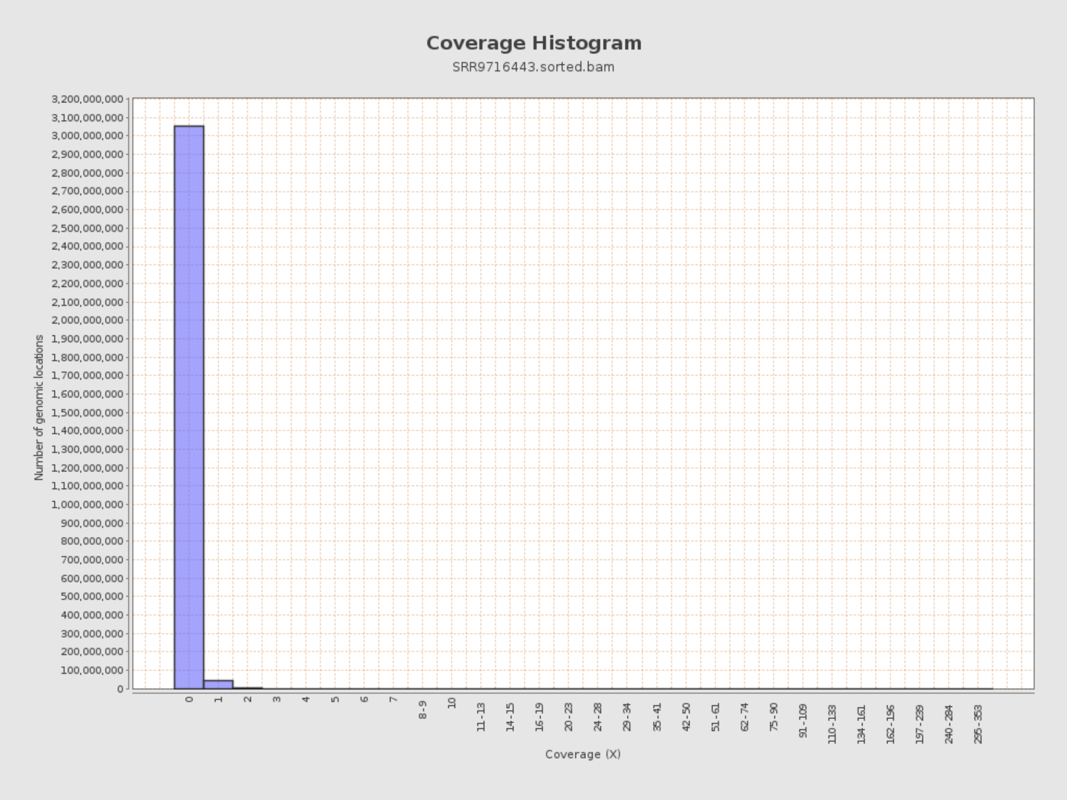
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4022636	0.0161	0.2475
chr2	243199373	4409706	0.0181	0.2056
chr3	198022430	3555314	0.018	0.1461
chr4	191154276	2673411	0.014	0.1323
chr5	180915260	2431745	0.0134	0.1218
chr6	171115067	2677306	0.0156	0.1375
chr7	159138663	3011134	0.0189	0.341

chr8	146364022	3005024	0.0205	0.1872
chr9	141213431	2020053	0.0143	0.1366
chr10	135534747	2355954	0.0174	0.235
chr11	135006516	1461216	0.0108	0.1246
chr12	133851895	2272006	0.017	0.1453
chr13	115169878	1260782	0.0109	0.1094
chr14	107349540	1235101	0.0115	0.1141
chr15	102531392	1177455	0.0115	0.1146
chr16	90354753	1505790	0.0167	0.139
chr17	81195210	2036721	0.0251	0.1703
chr18	78077248	1099846	0.0141	0.1829
chr19	59128983	984081	0.0166	0.2107
chr20	63025520	1115624	0.0177	0.1428
chr21	48129895	511004	0.0106	0.1123
chr22	51304566	722540	0.0141	0.1245
chrMT	16571	12059	0.7277	0.9548
chrX	155270560	1696788	0.0109	0.1186
chrY	59373566	115381	0.0019	0.064

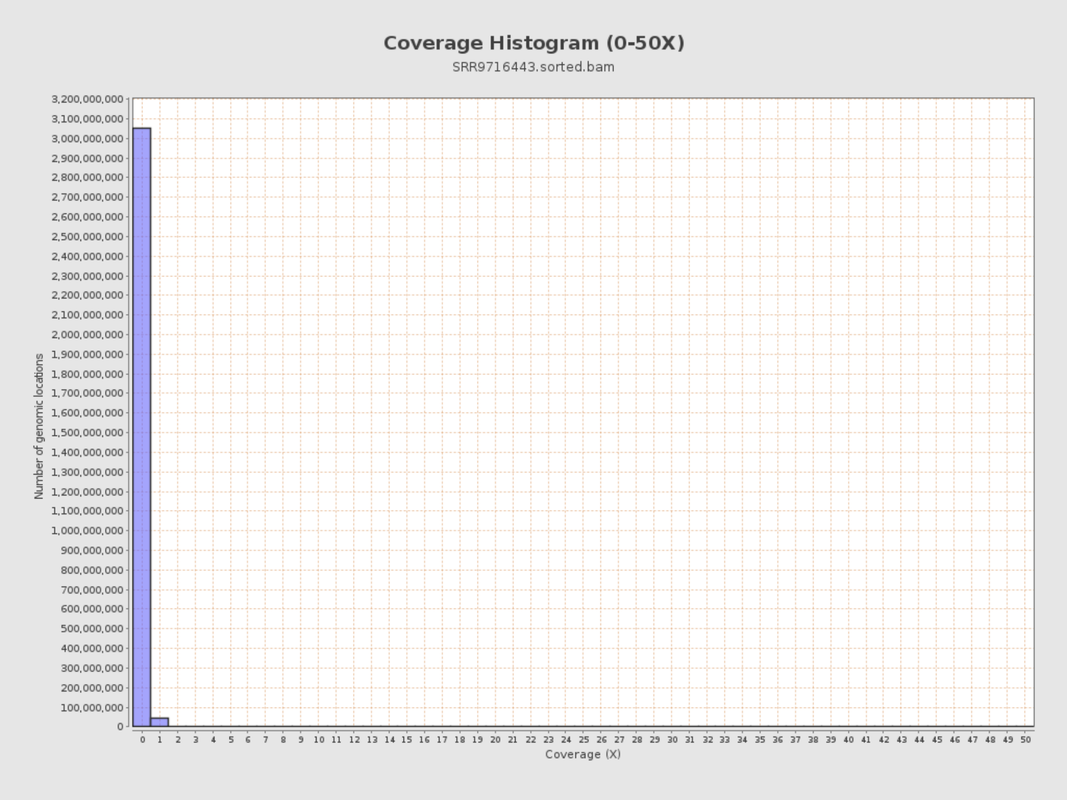
3. Results : Coverage across reference



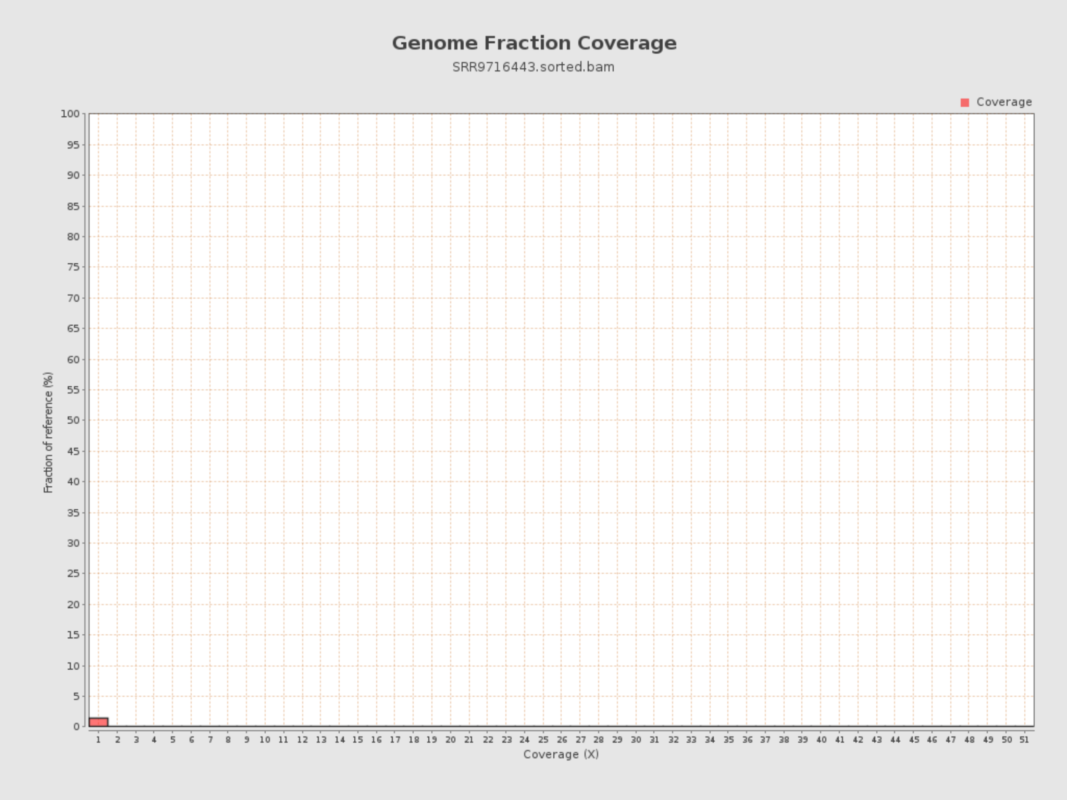
4. Results : Coverage Histogram



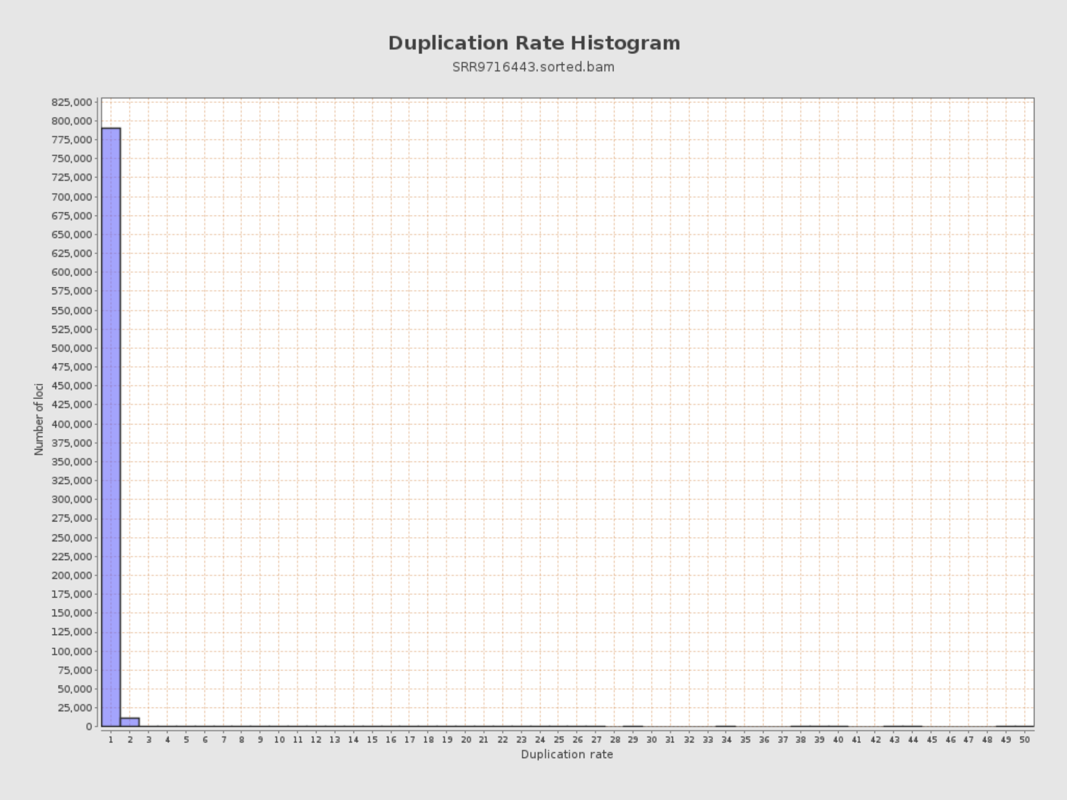
5. Results : Coverage Histogram (0-50X)



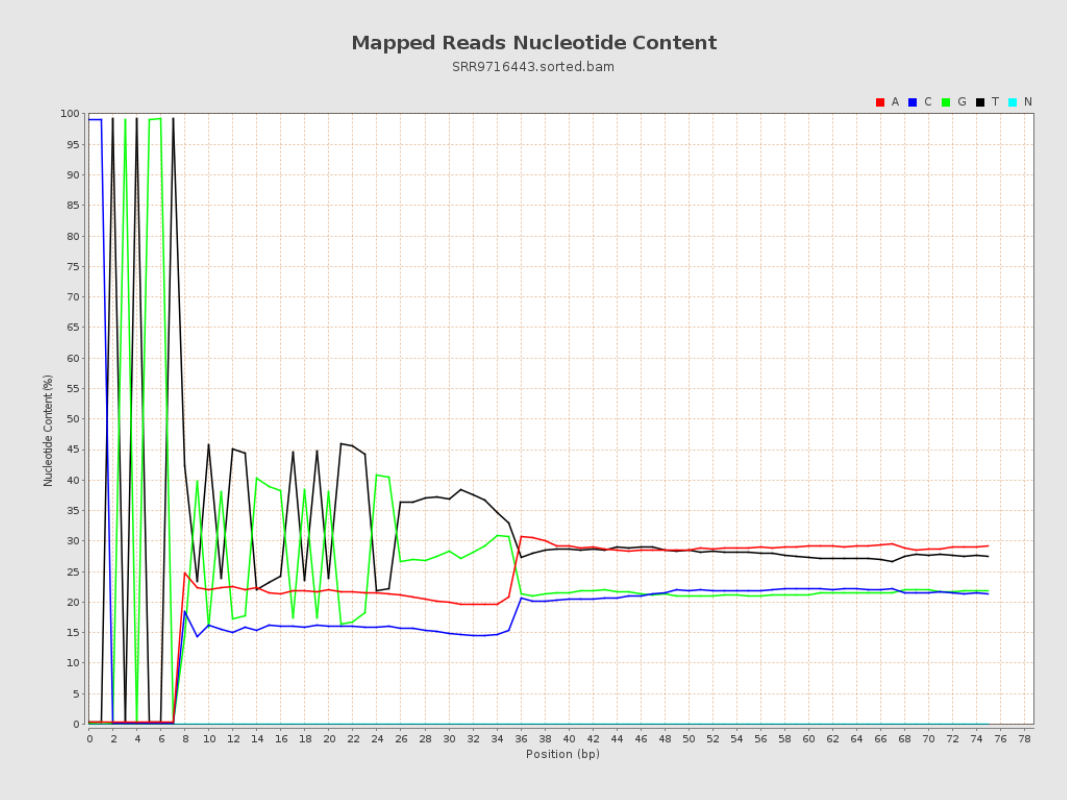
6. Results : Genome Fraction Coverage



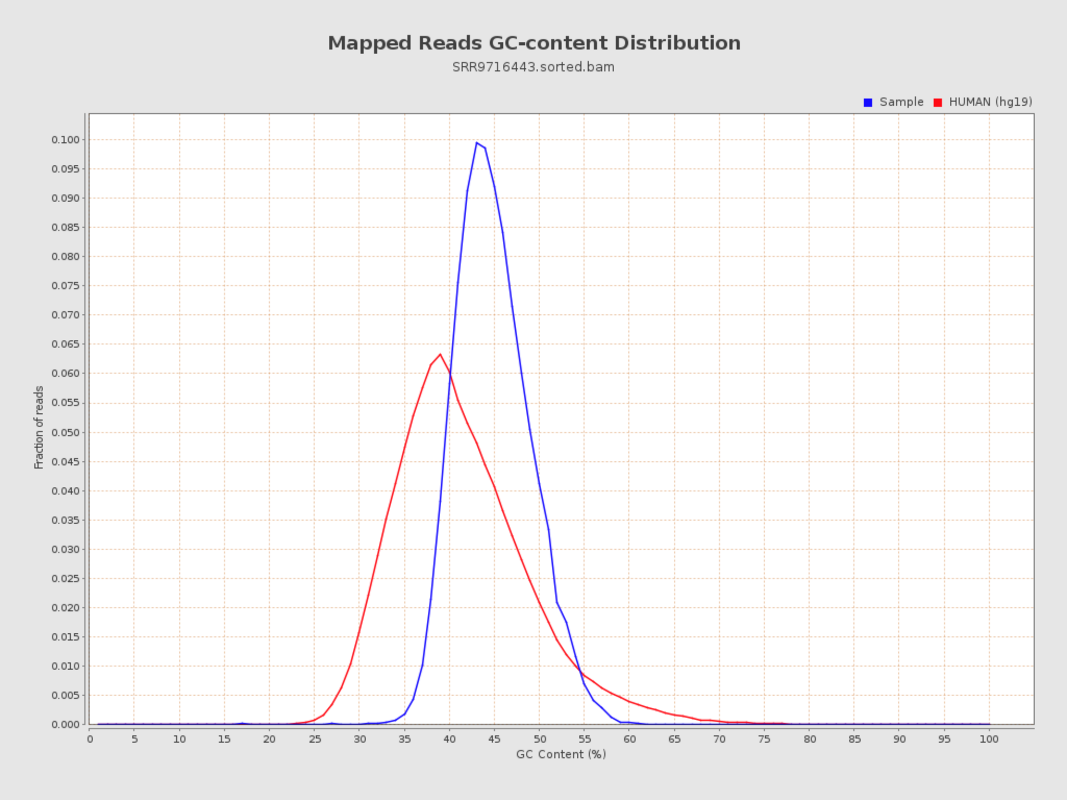
7. Results : Duplication Rate Histogram



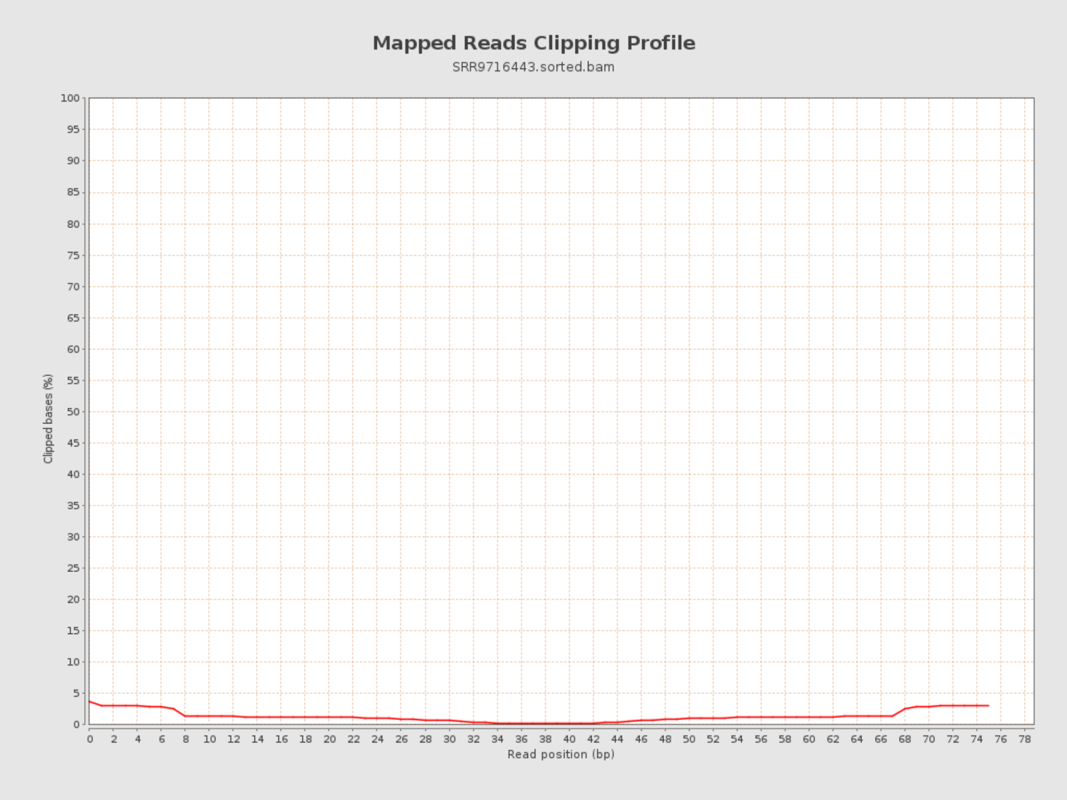
8. Results : Mapped Reads Nucleotide Content



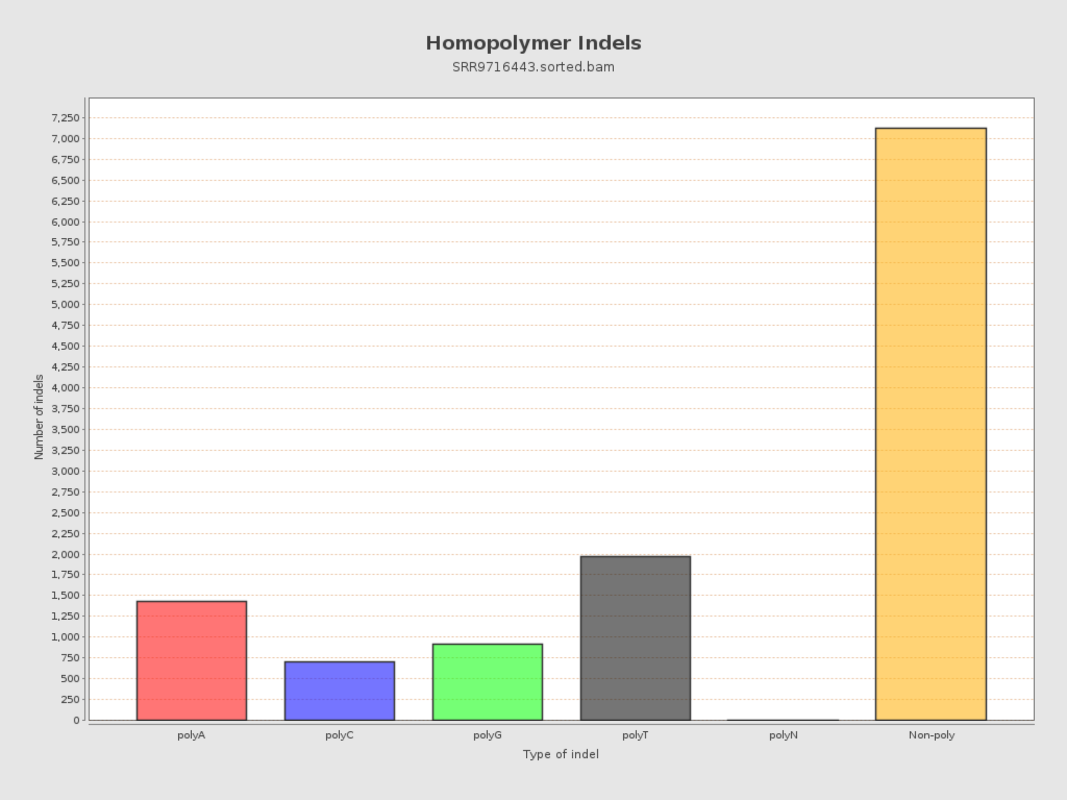
9. Results : Mapped Reads GC-content Distribution



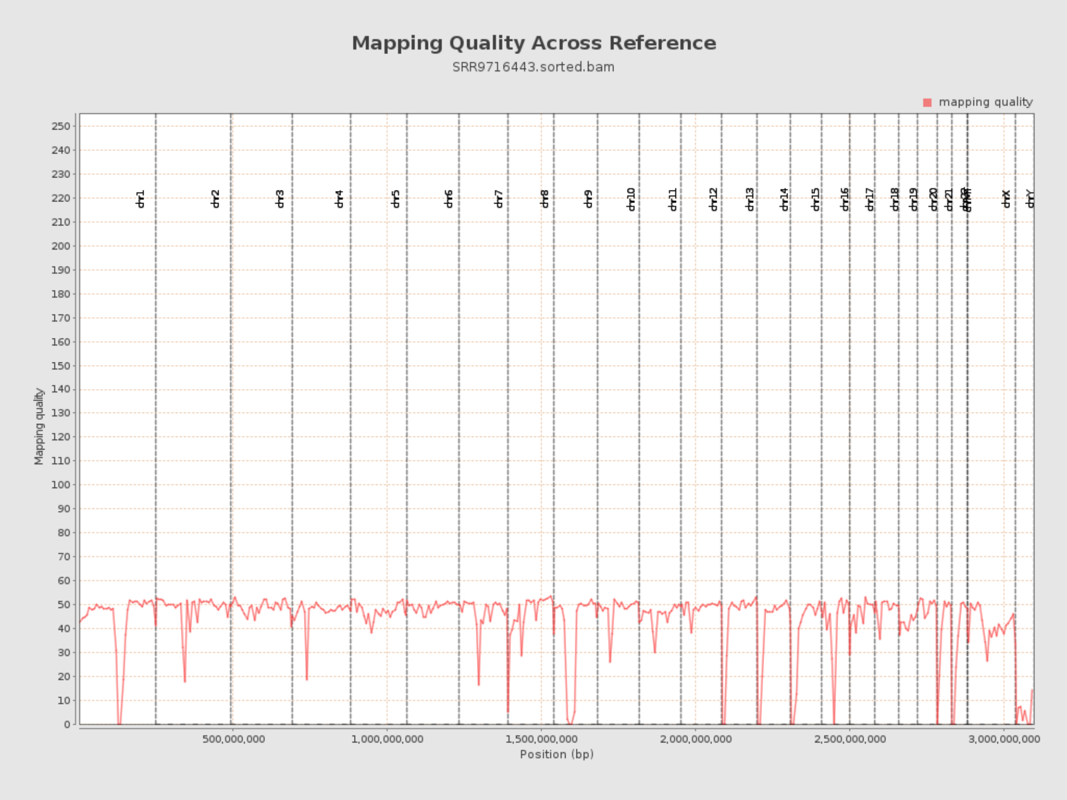
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram