Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:59:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716444.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_SRR9716444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716444.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:59:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716444.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	588,808
Mapped reads	538,835 / 91.51%
Unmapped reads	49,973 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,451 / 1.44%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	14,185 / 2.41%
Duplication rate	1.6%
Clipped reads	545,922 / 92.72%

2.2. ACGT Content

Number/percentage of A's	11,275,104 / 26.31%
Number/percentage of C's	8,130,420 / 18.97%
Number/percentage of T's	13,048,592 / 30.45%
Number/percentage of G's	10,399,027 / 24.27%
Number/percentage of N's	2,563 / 0.01%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.1848

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

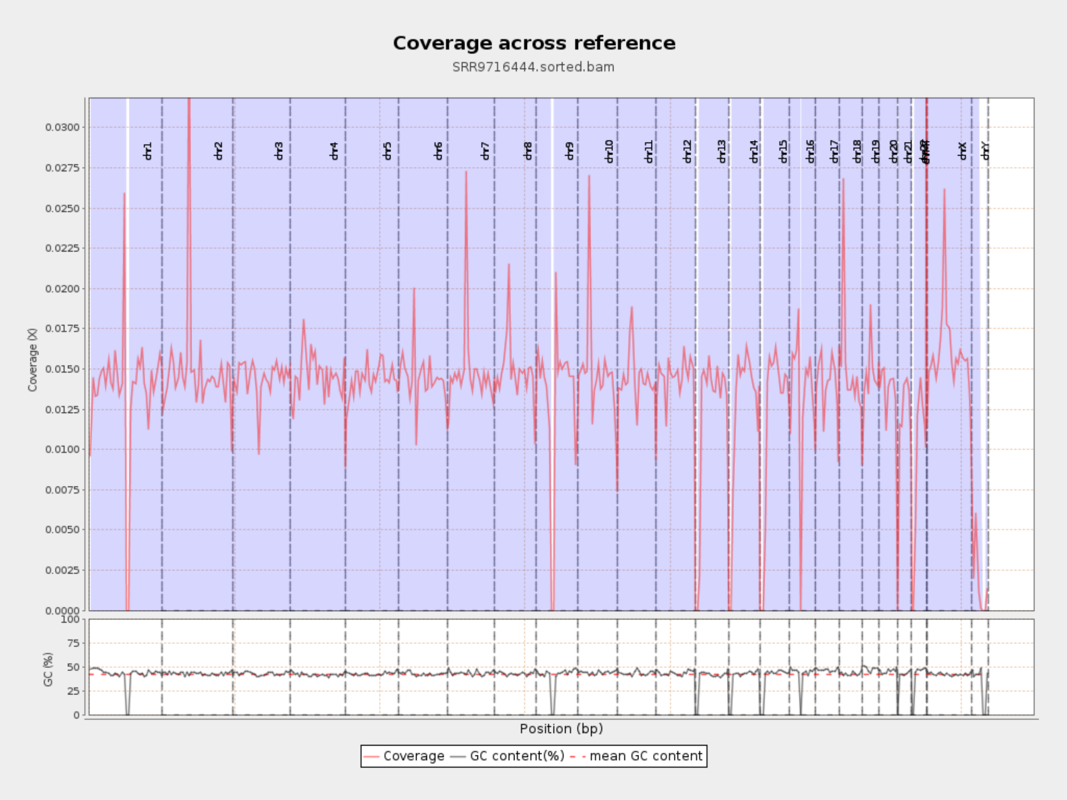
General error rate	0.84%
Mismatches	352,321
Insertions	4,196
Mapped reads with at least one insertion	0.77%
Deletions	10,872
Mapped reads with at least one deletion	1.99%
Homopolymer indels	44.2%

2.6. Chromosome stats

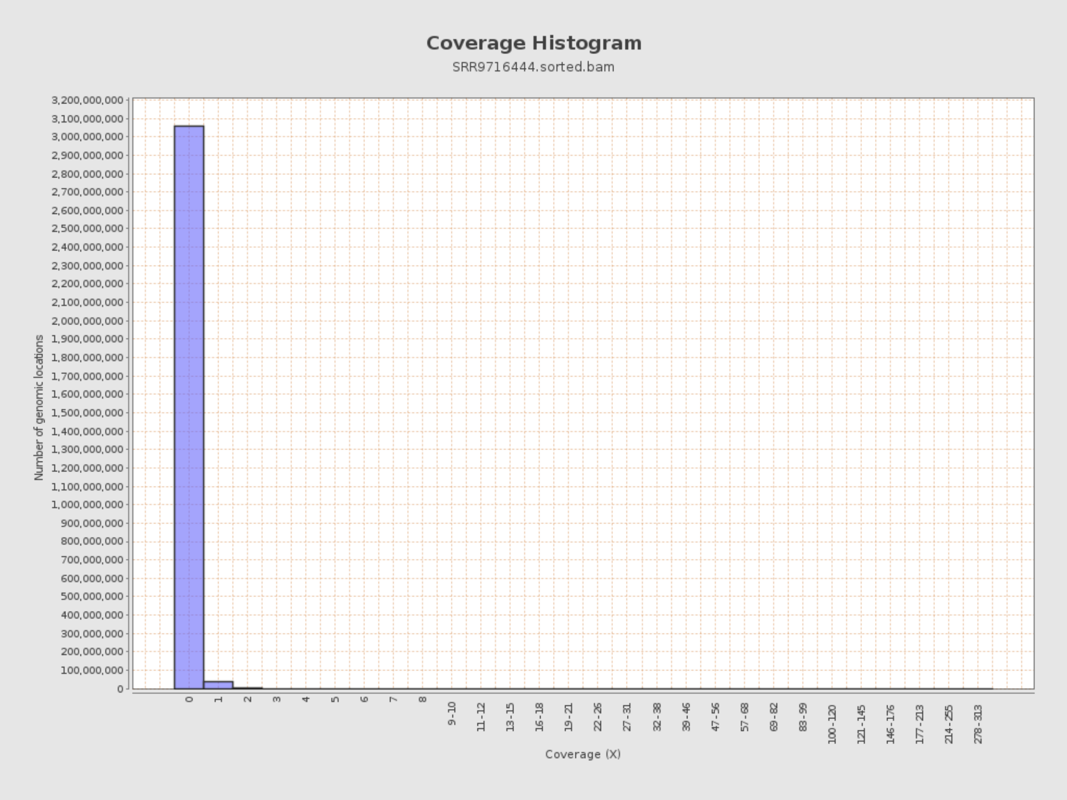
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3410890	0.0137	0.2778
chr2	243199373	3669808	0.0151	0.2414
chr3	198022430	2857522	0.0144	0.126
chr4	191154276	2790382	0.0146	0.1301
chr5	180915260	2601381	0.0144	0.1267
chr6	171115067	2475400	0.0145	0.1391
chr7	159138663	2380641	0.015	0.2259

chr8	146364022	2176674	0.0149	0.2257
chr9	141213431	1850910	0.0131	0.1947
chr10	135534747	2022703	0.0149	0.1762
chr11	135006516	1932431	0.0143	0.1875
chr12	133851895	1944980	0.0145	0.1271
chr13	115169878	1365704	0.0119	0.1133
chr14	107349540	1302784	0.0121	0.134
chr15	102531392	1217293	0.0119	0.1146
chr16	90354753	1211479	0.0134	0.1299
chr17	81195210	1134878	0.014	0.1337
chr18	78077248	1204248	0.0154	0.3721
chr19	59128983	864940	0.0146	0.2213
chr20	63025520	853518	0.0135	0.1279
chr21	48129895	551949	0.0115	0.1163
chr22	51304566	451847	0.0088	0.0975
chrMT	16571	1305	0.0788	0.2975
chrX	155270560	2492350	0.0161	0.1574
chrY	59373566	108813	0.0018	0.0621

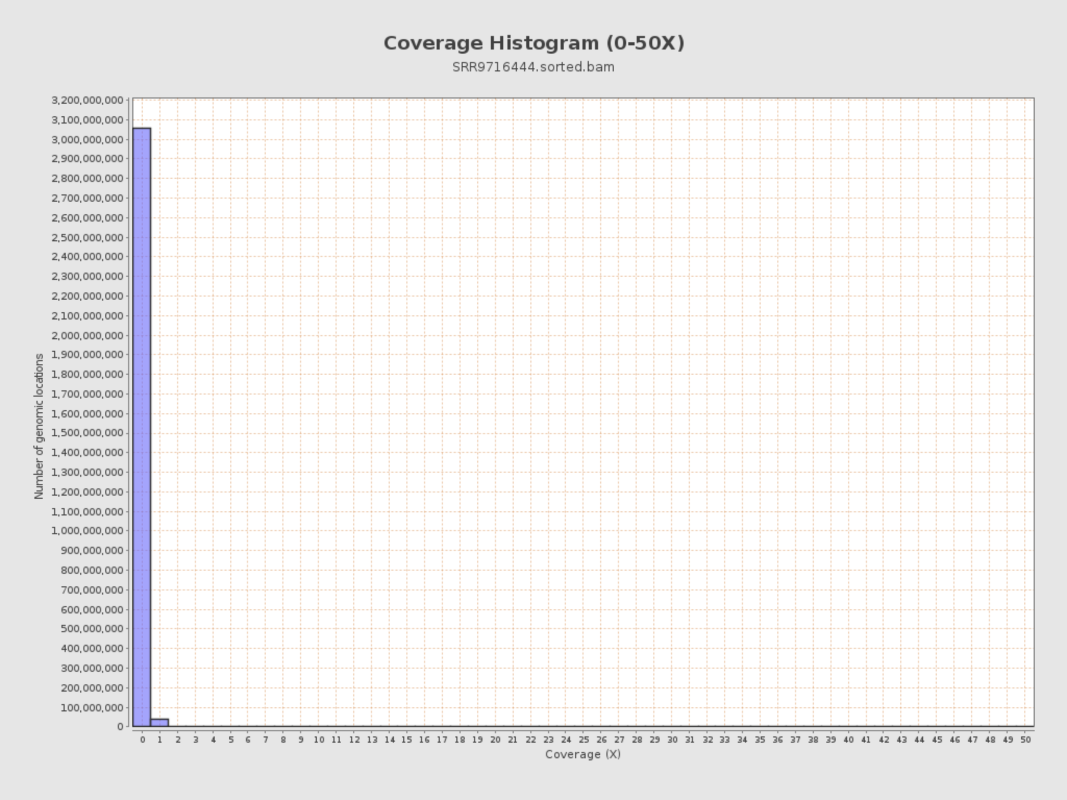
3. Results : Coverage across reference



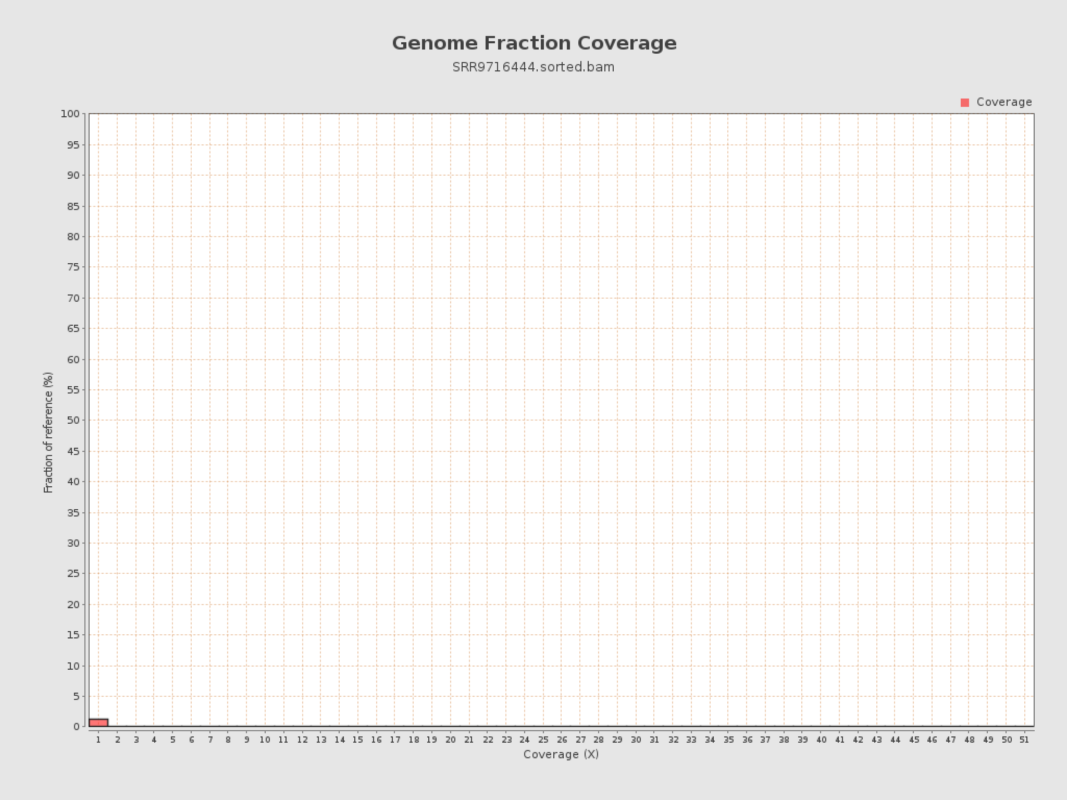
4. Results : Coverage Histogram



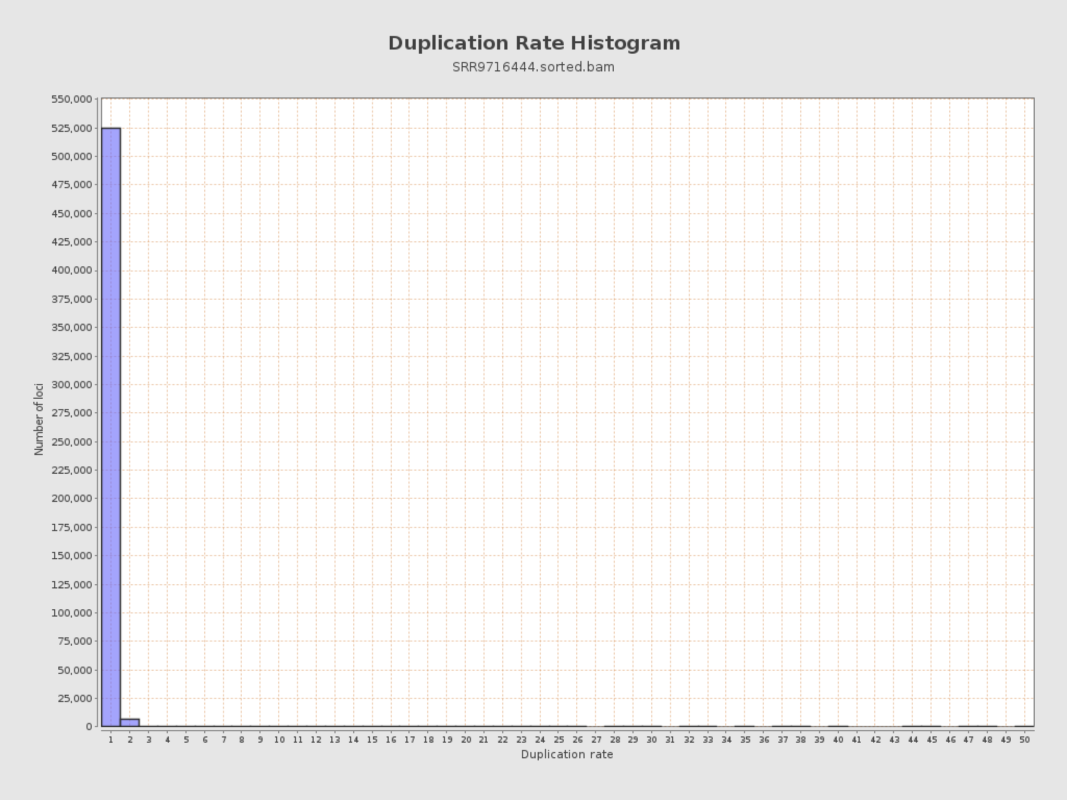
5. Results : Coverage Histogram (0-50X)



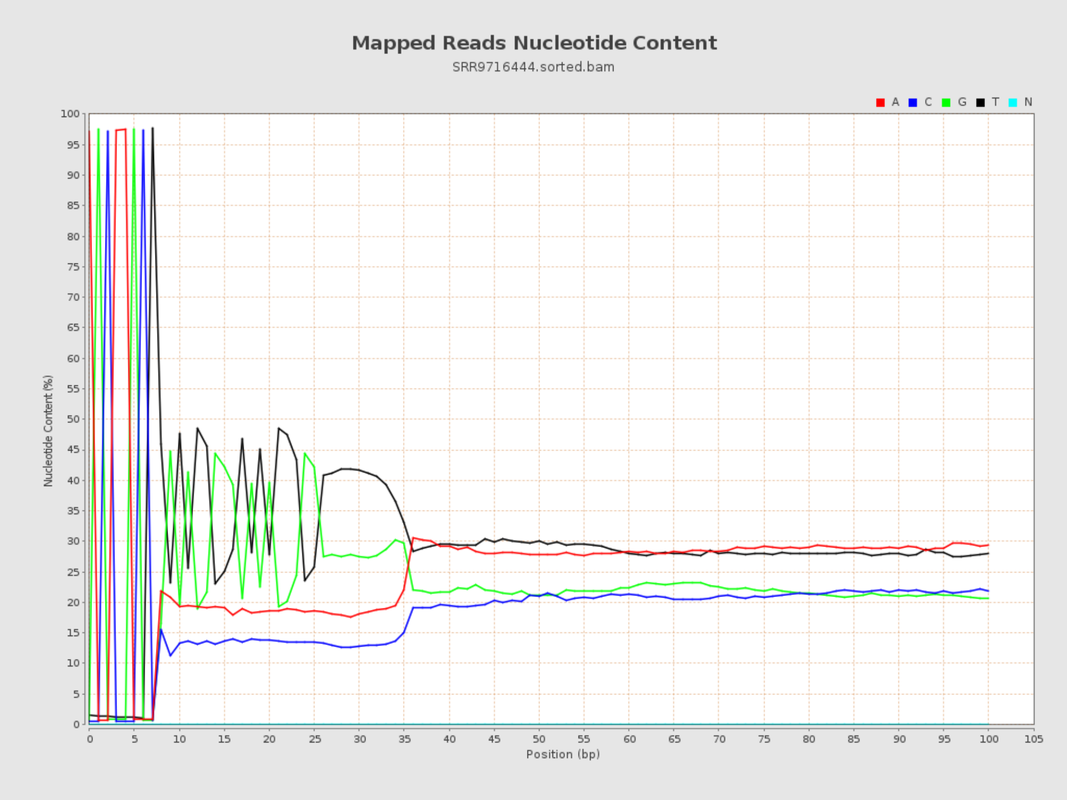
6. Results : Genome Fraction Coverage



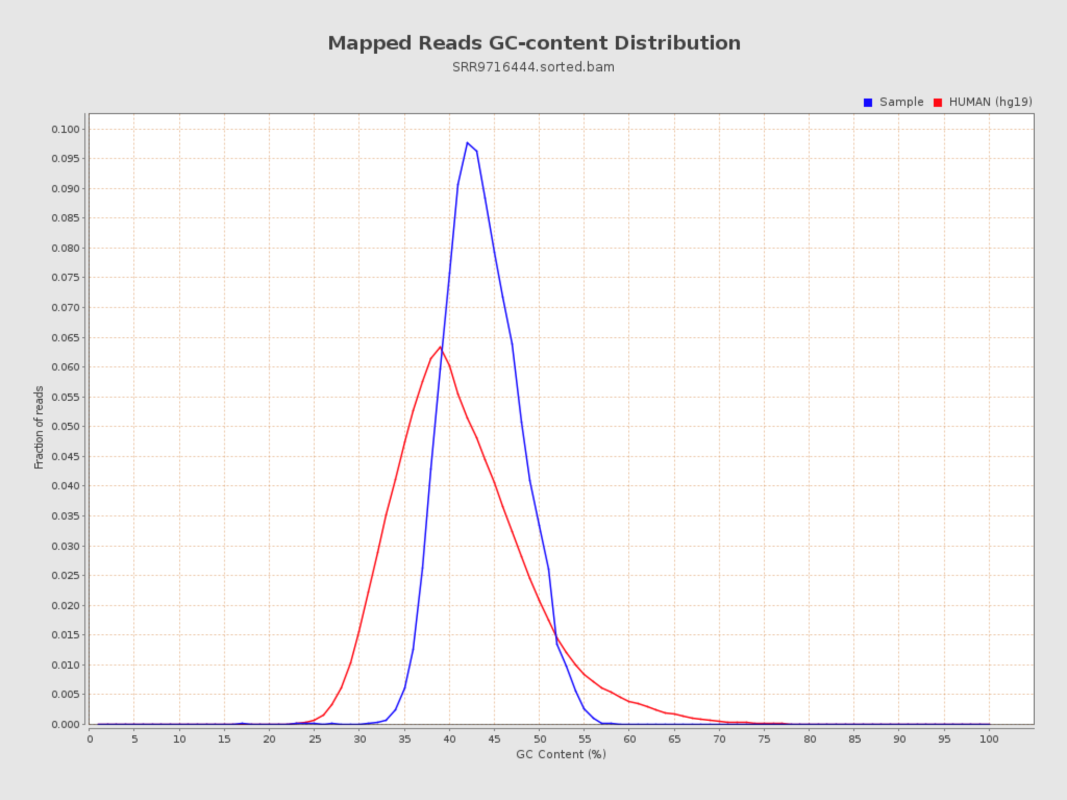
7. Results : Duplication Rate Histogram



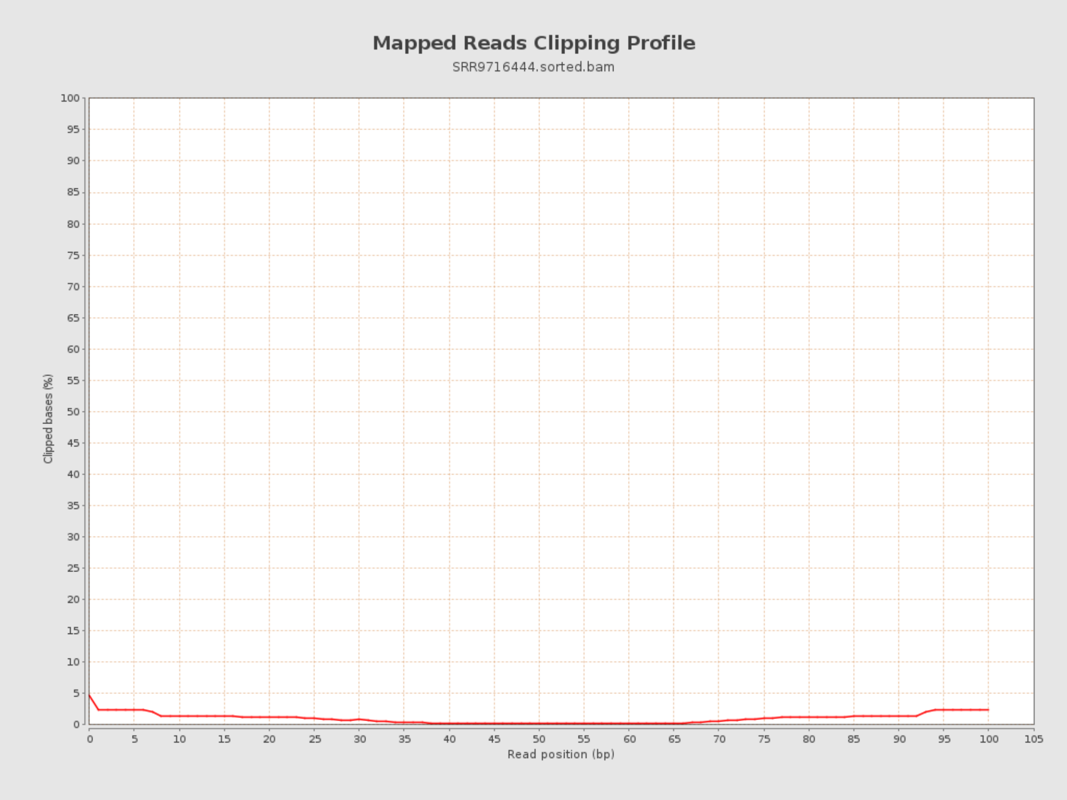
8. Results : Mapped Reads Nucleotide Content



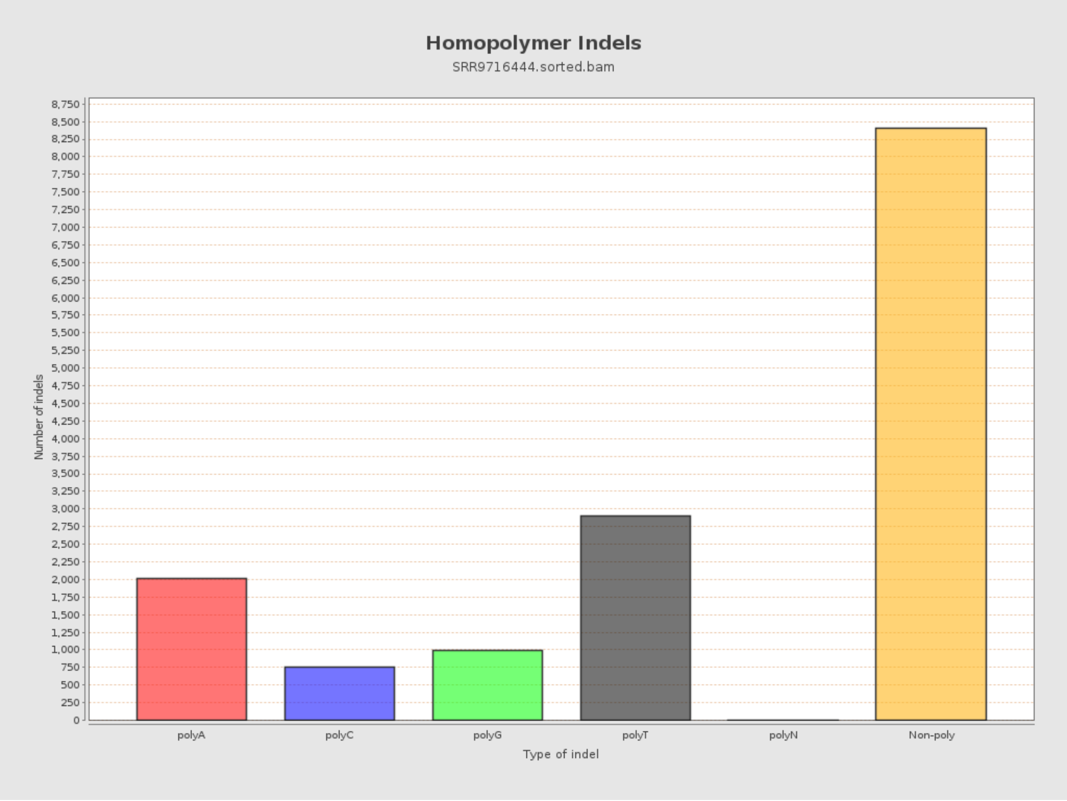
9. Results : Mapped Reads GC-content Distribution



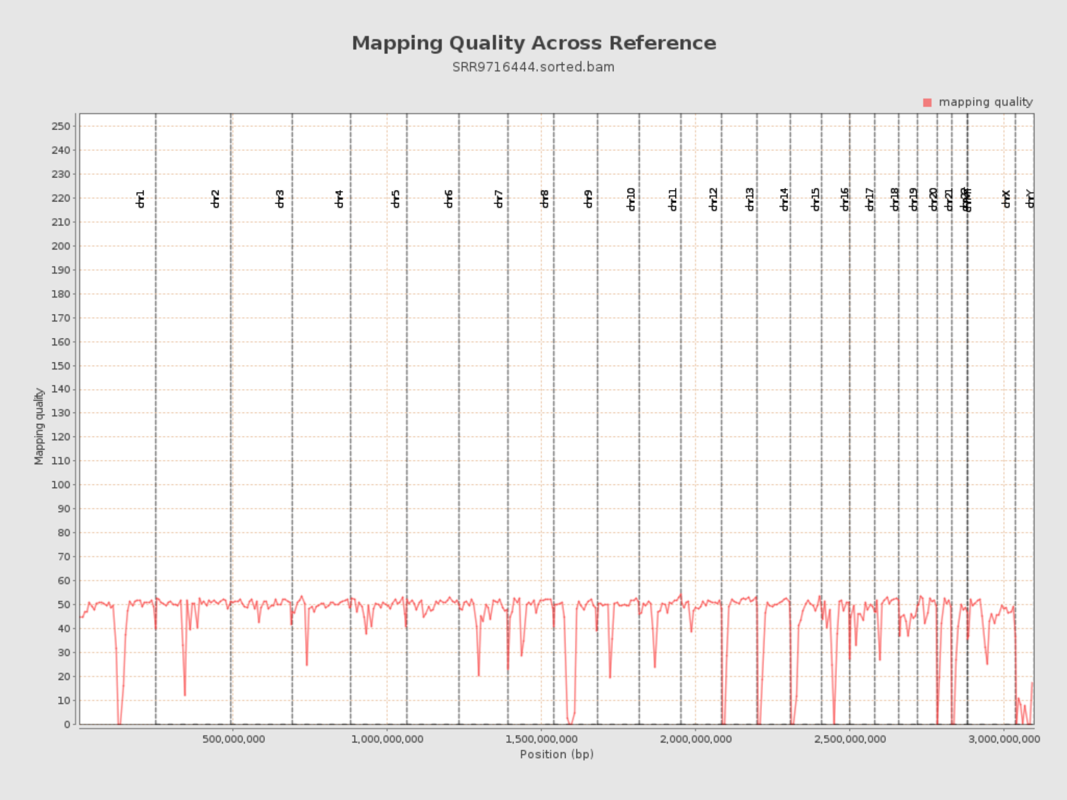
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram