Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 13:18:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716436.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_SRR9716436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716436.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 13:18:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	983,718
Mapped reads	907,924 / 92.3%
Unmapped reads	75,794 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,196 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	23,474 / 2.39%
Duplication rate	1.81%
Clipped reads	910,216 / 92.53%

2.2. ACGT Content

Number/percentage of A's	13,432,451 / 25.38%
Number/percentage of C's	10,769,128 / 20.35%
Number/percentage of T's	16,209,828 / 30.63%
Number/percentage of G's	12,509,636 / 23.64%
Number/percentage of N's	1,100 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.183

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

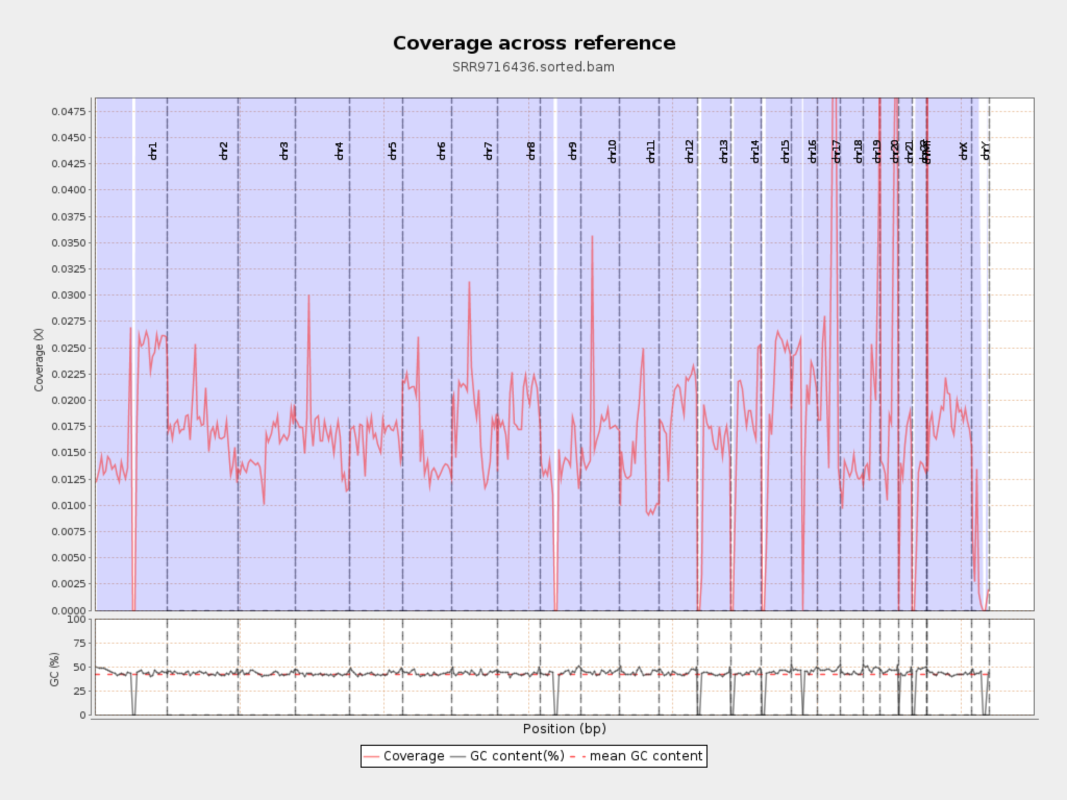
General error rate	0.51%
Mismatches	264,750
Insertions	3,303
Mapped reads with at least one insertion	0.36%
Deletions	10,979
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.82%

2.6. Chromosome stats

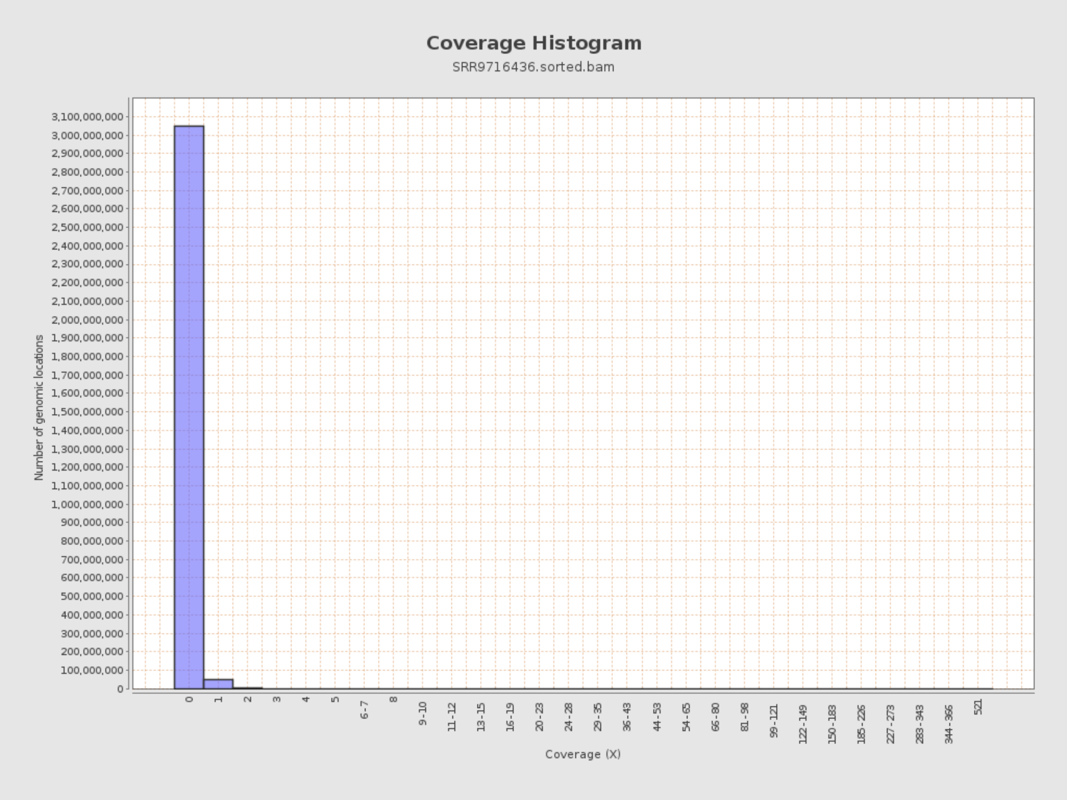
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4500796	0.0181	0.2748
chr2	243199373	4213894	0.0173	0.2535
chr3	198022430	3033912	0.0153	0.1307
chr4	191154276	3215109	0.0168	0.1519
chr5	180915260	3026369	0.0167	0.1357
chr6	171115067	2832049	0.0166	0.1516
chr7	159138663	3004335	0.0189	0.2311

chr8	146364022	2817439	0.0192	0.2249
chr9	141213431	1770169	0.0125	0.1381
chr10	135534747	2383277	0.0176	0.1891
chr11	135006516	1890027	0.014	0.1436
chr12	133851895	2628123	0.0196	0.148
chr13	115169878	1610330	0.014	0.1246
chr14	107349540	1820724	0.017	0.1386
chr15	102531392	1938153	0.0189	0.1441
chr16	90354753	1826681	0.0202	0.1542
chr17	81195210	2305779	0.0284	0.1814
chr18	78077248	1005921	0.0129	0.2031
chr19	59128983	1307087	0.0221	0.2255
chr20	63025520	1576719	0.025	0.1705
chr21	48129895	691321	0.0144	0.1438
chr22	51304566	492459	0.0096	0.1029
chrMT	16571	4058	0.2449	0.5309
chrX	155270560	2852534	0.0184	0.1493
chrY	59373566	192605	0.0032	0.137

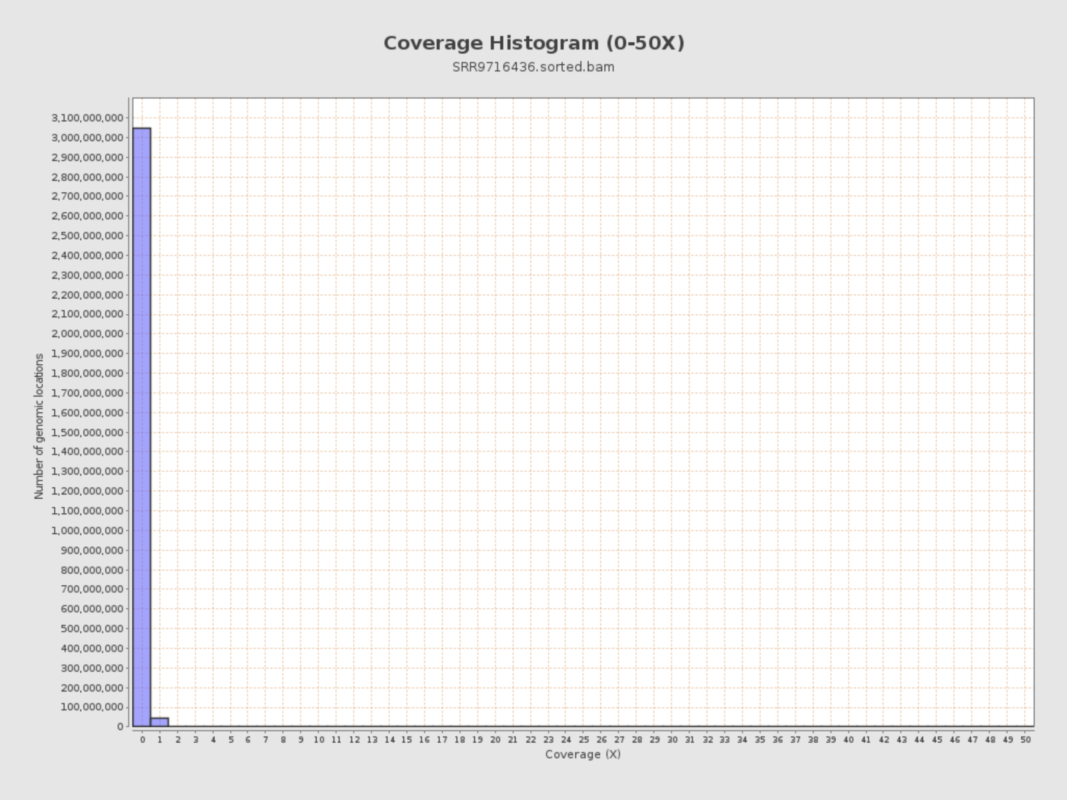
3. Results : Coverage across reference



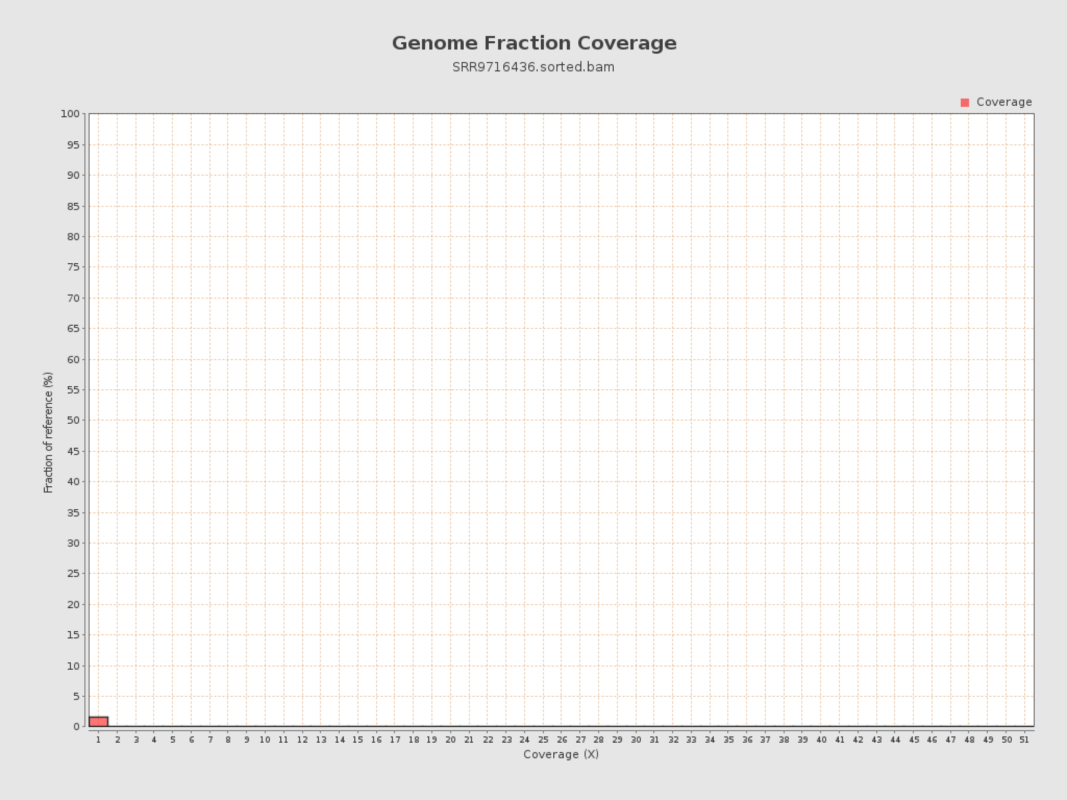
4. Results : Coverage Histogram



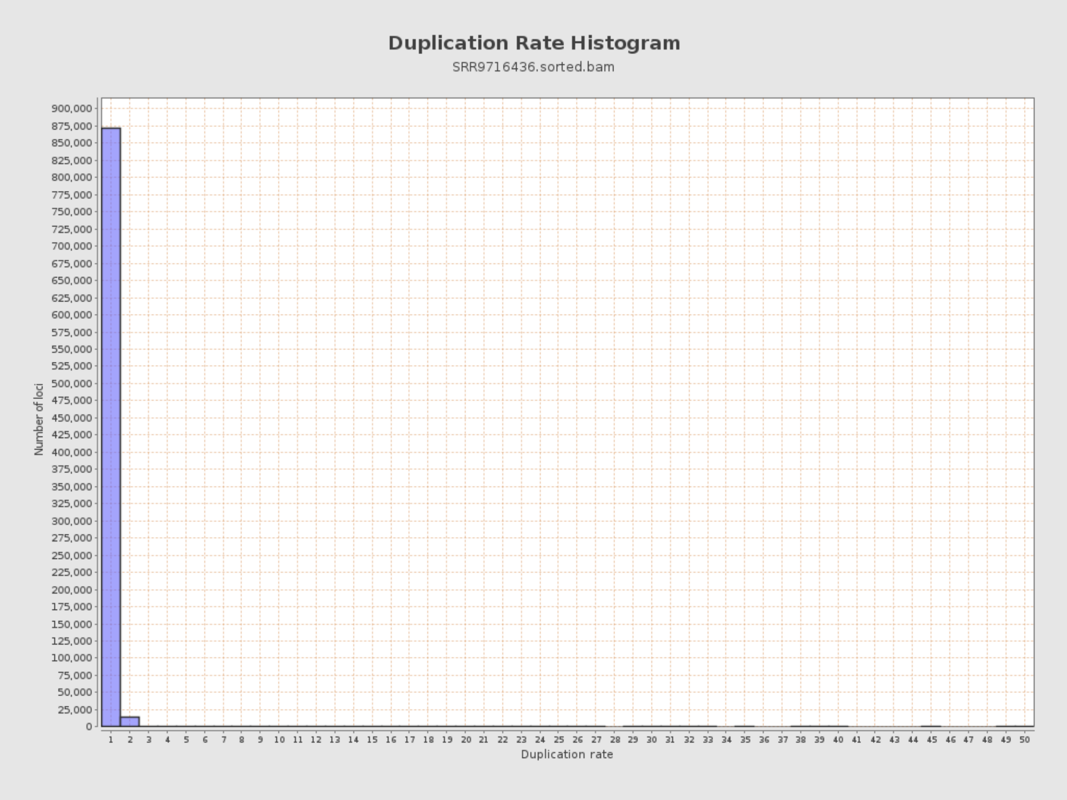
5. Results : Coverage Histogram (0-50X)



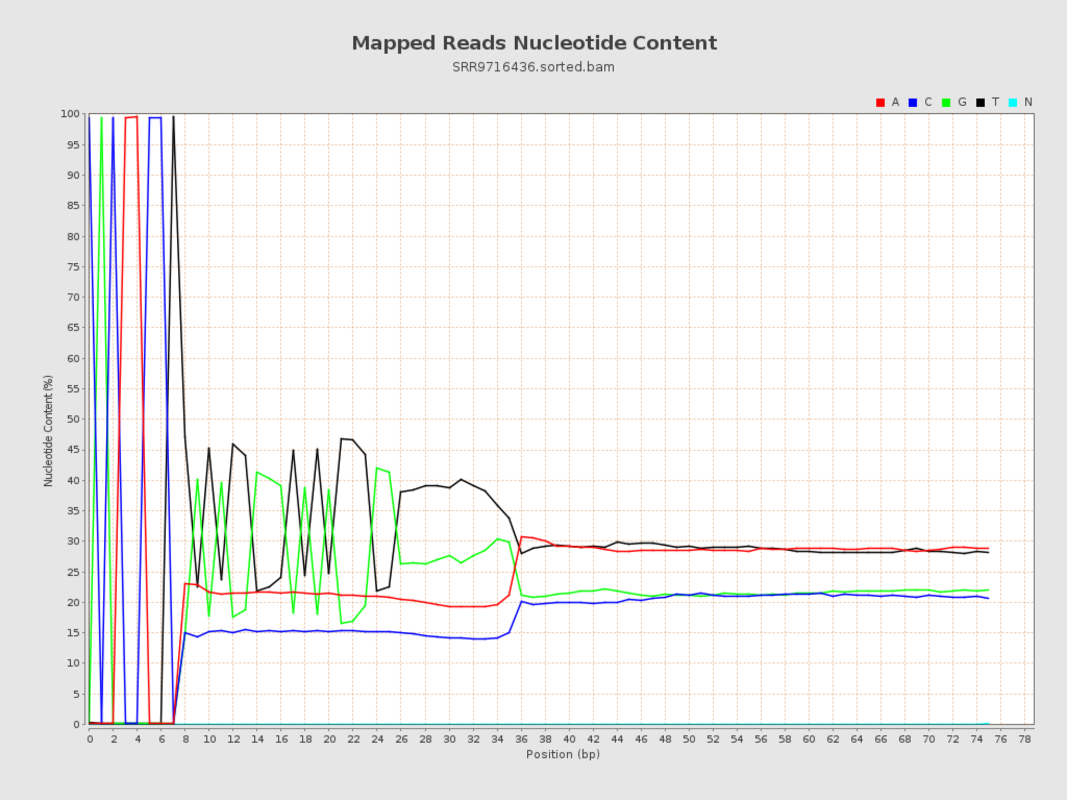
6. Results : Genome Fraction Coverage



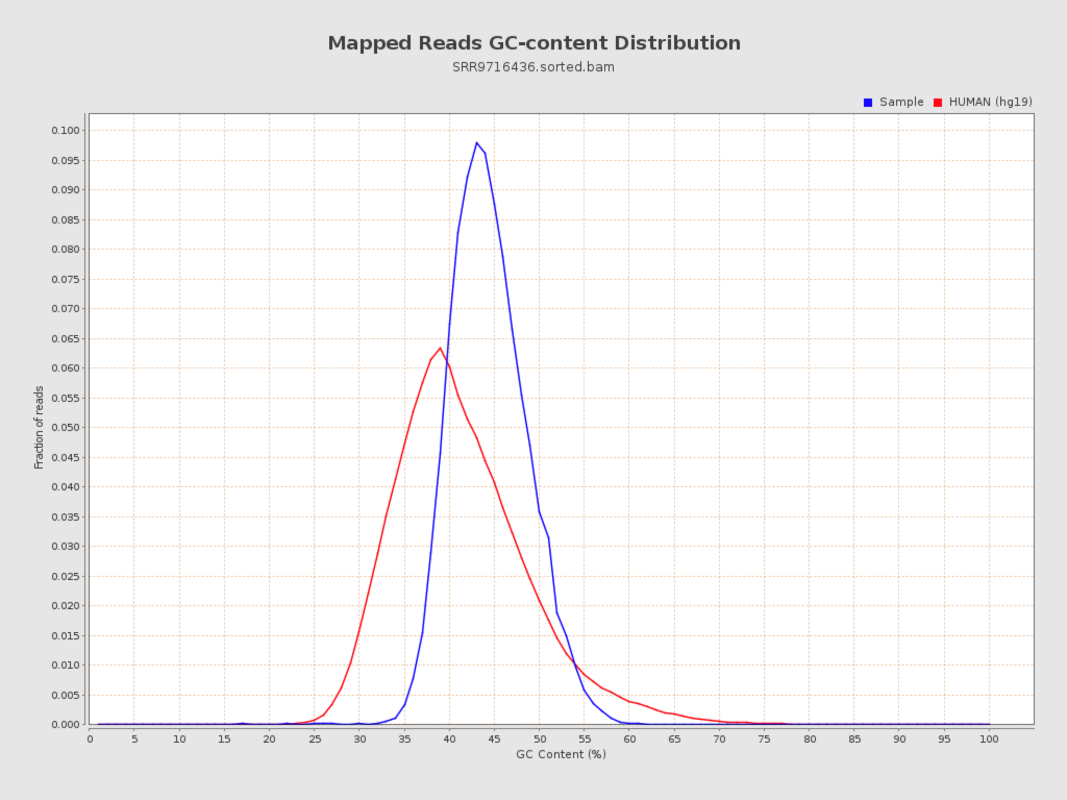
7. Results : Duplication Rate Histogram



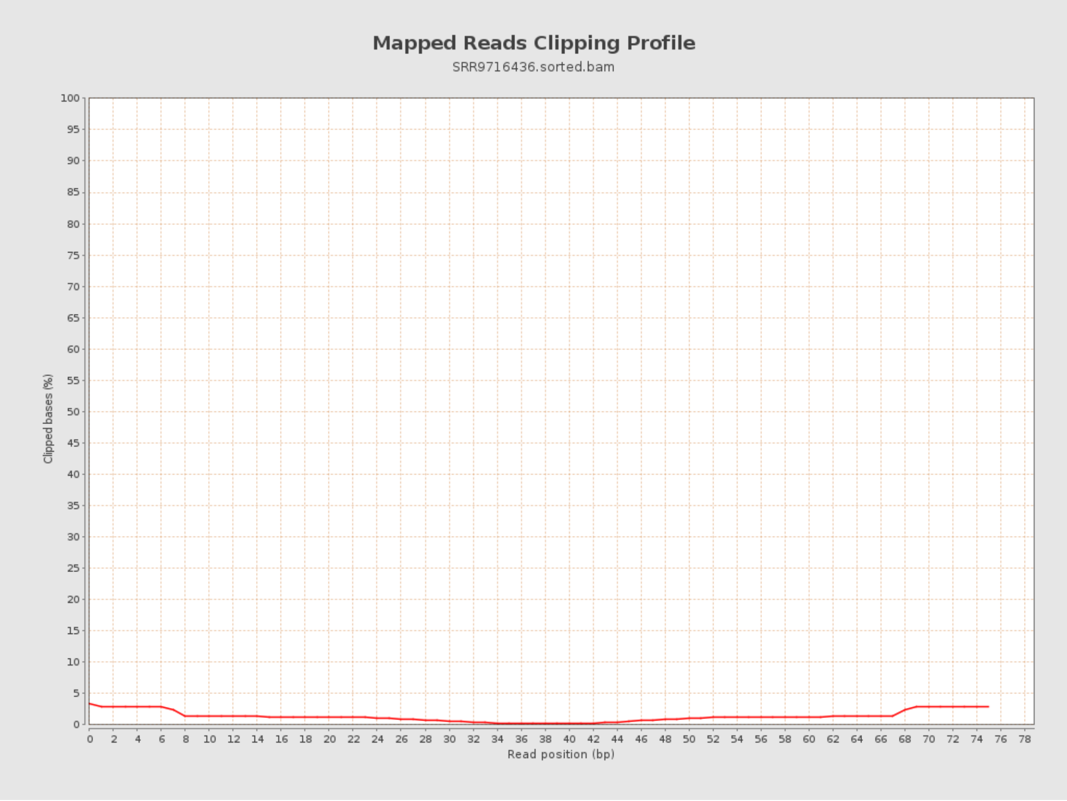
8. Results : Mapped Reads Nucleotide Content



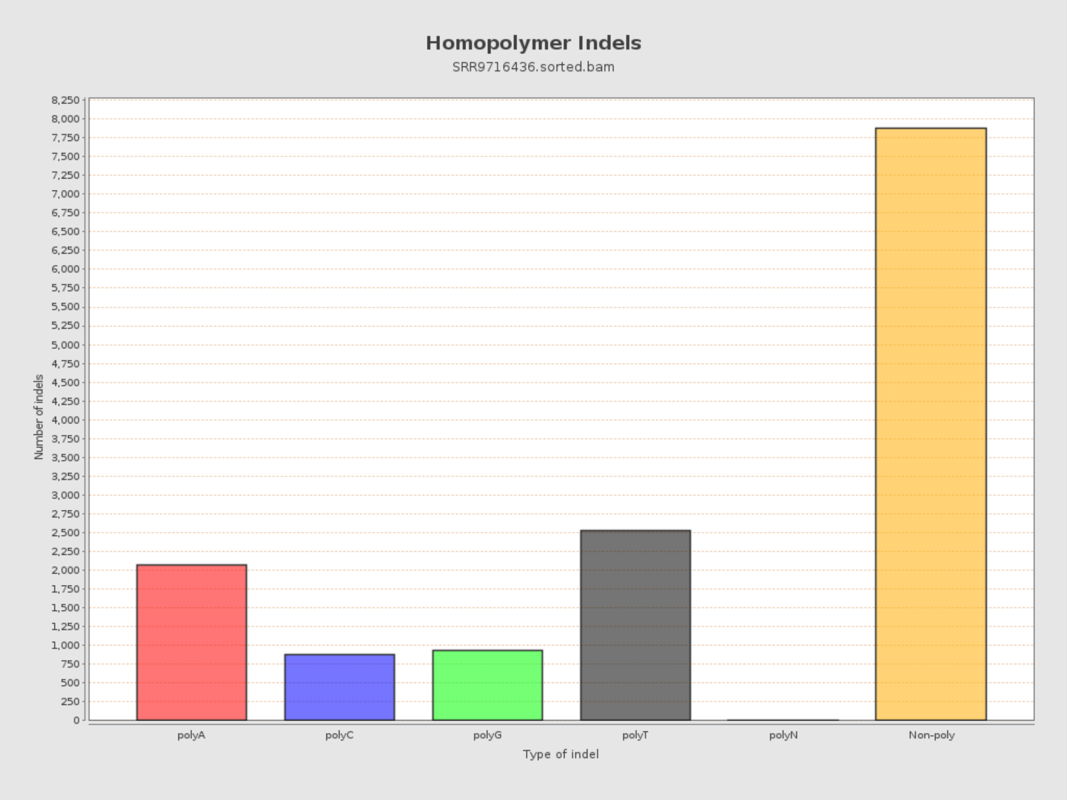
9. Results : Mapped Reads GC-content Distribution



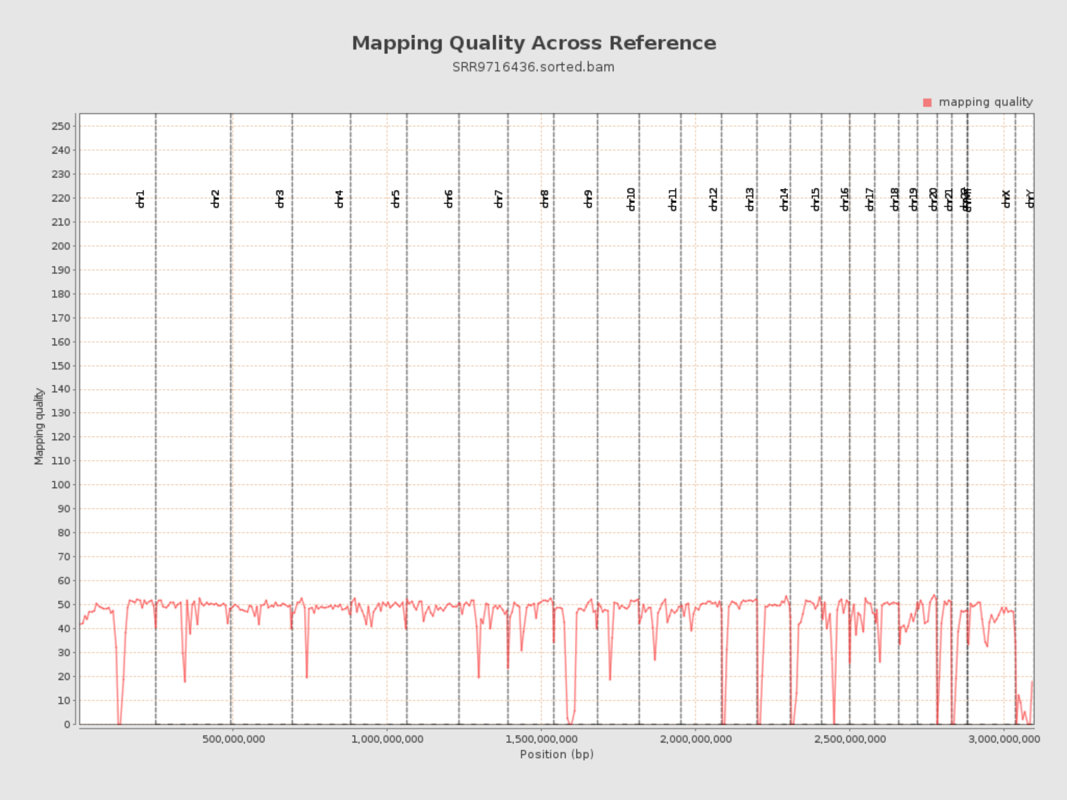
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram