Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:14:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716412.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_SRR9716412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716412.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:14:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,274,525
Mapped reads	1,851,988 / 81.42%
Unmapped reads	422,537 / 18.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,744 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	74,035 / 3.25%
Duplication rate	3.02%
Clipped reads	1,856,744 / 81.63%

2.2. ACGT Content

Number/percentage of A's	26,486,343 / 24.69%
Number/percentage of C's	22,115,193 / 20.61%
Number/percentage of T's	34,116,996 / 31.8%
Number/percentage of G's	24,562,962 / 22.9%
Number/percentage of N's	1,406 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0347

Standard Deviation	0.31

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

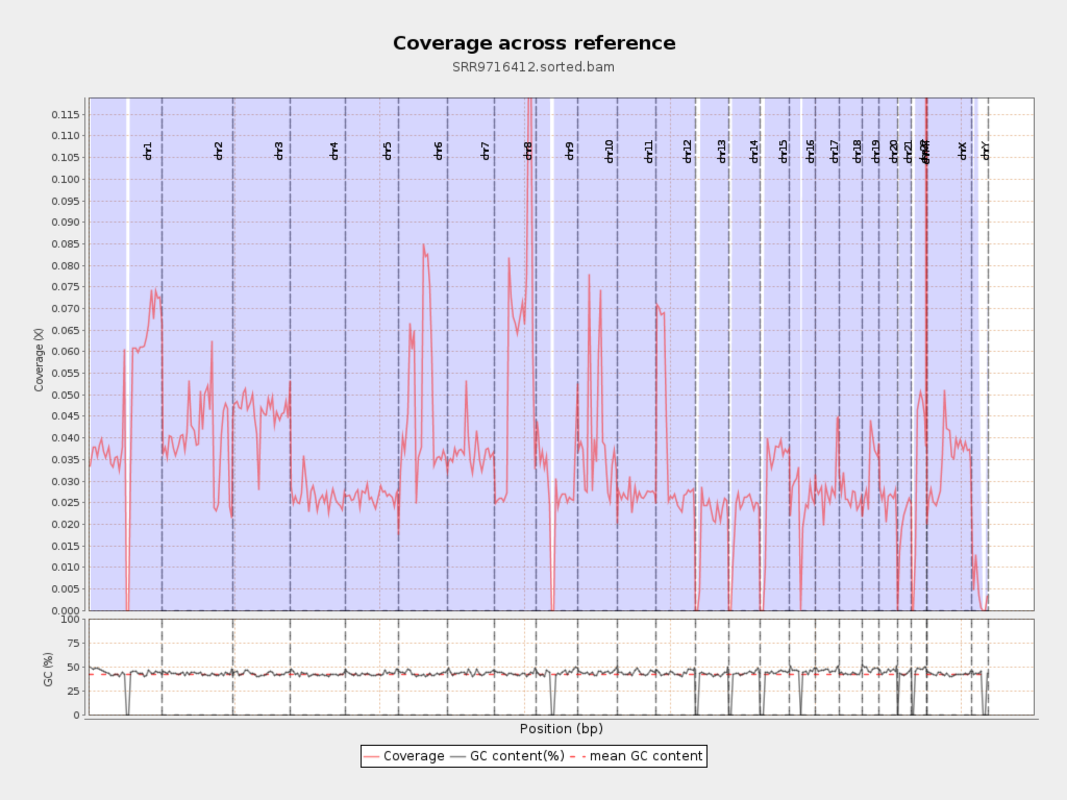
General error rate	0.51%
Mismatches	530,942
Insertions	6,862
Mapped reads with at least one insertion	0.37%
Deletions	19,362
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.02%

2.6. Chromosome stats

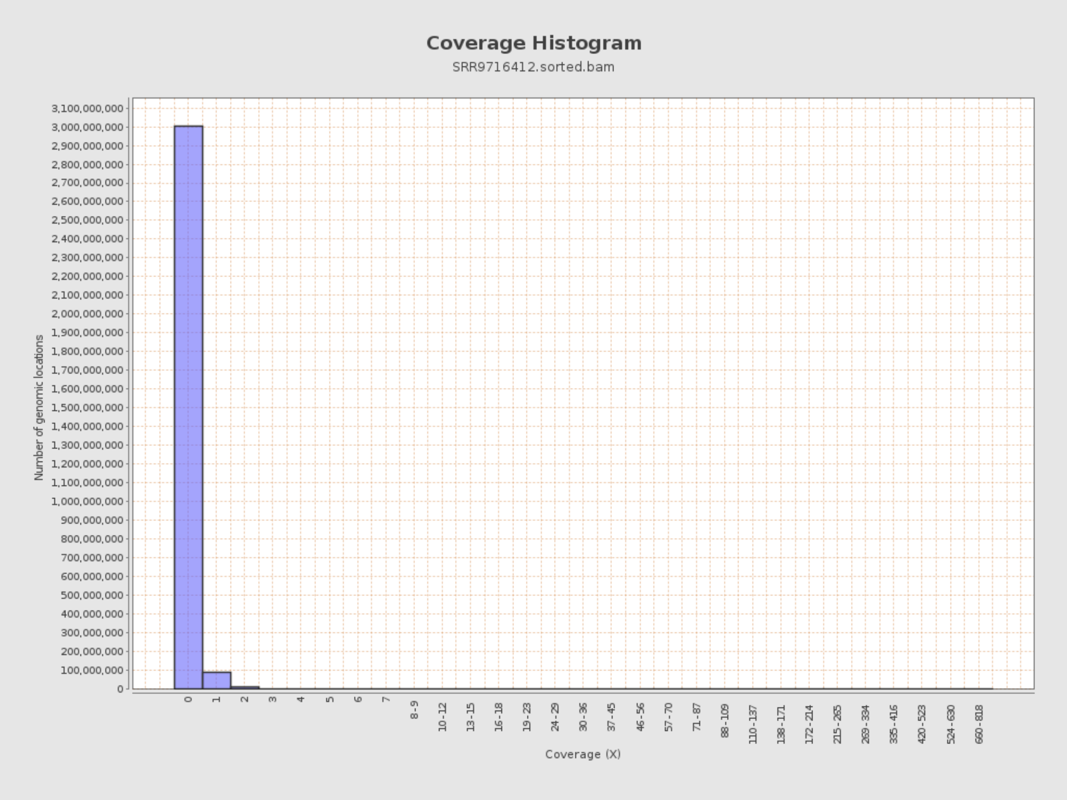
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11656169	0.0468	0.5826
chr2	243199373	9791831	0.0403	0.4038
chr3	198022430	9134534	0.0461	0.2393
chr4	191154276	5024924	0.0263	0.1942
chr5	180915260	4806045	0.0266	0.1836
chr6	171115067	8256966	0.0483	0.3421
chr7	159138663	5880761	0.037	0.3721

chr8	146364022	8770795	0.0599	0.2997
chr9	141213431	3829817	0.0271	0.2429
chr10	135534747	5422871	0.04	0.32
chr11	135006516	3615085	0.0268	0.2456
chr12	133851895	4947841	0.037	0.219
chr13	115169878	2314218	0.0201	0.1568
chr14	107349540	2265686	0.0211	0.1793
chr15	102531392	3048284	0.0297	0.1991
chr16	90354753	2206608	0.0244	0.1936
chr17	81195210	2377006	0.0293	0.2012
chr18	78077248	2078390	0.0266	0.4267
chr19	59128983	1960756	0.0332	0.4007
chr20	63025520	1630147	0.0259	0.1798
chr21	48129895	940357	0.0195	0.1723
chr22	51304566	1654489	0.0322	0.1999
chrMT	16571	73451	4.4325	3.1246
chrX	155270560	5366864	0.0346	0.2395
chrY	59373566	259045	0.0044	0.1002

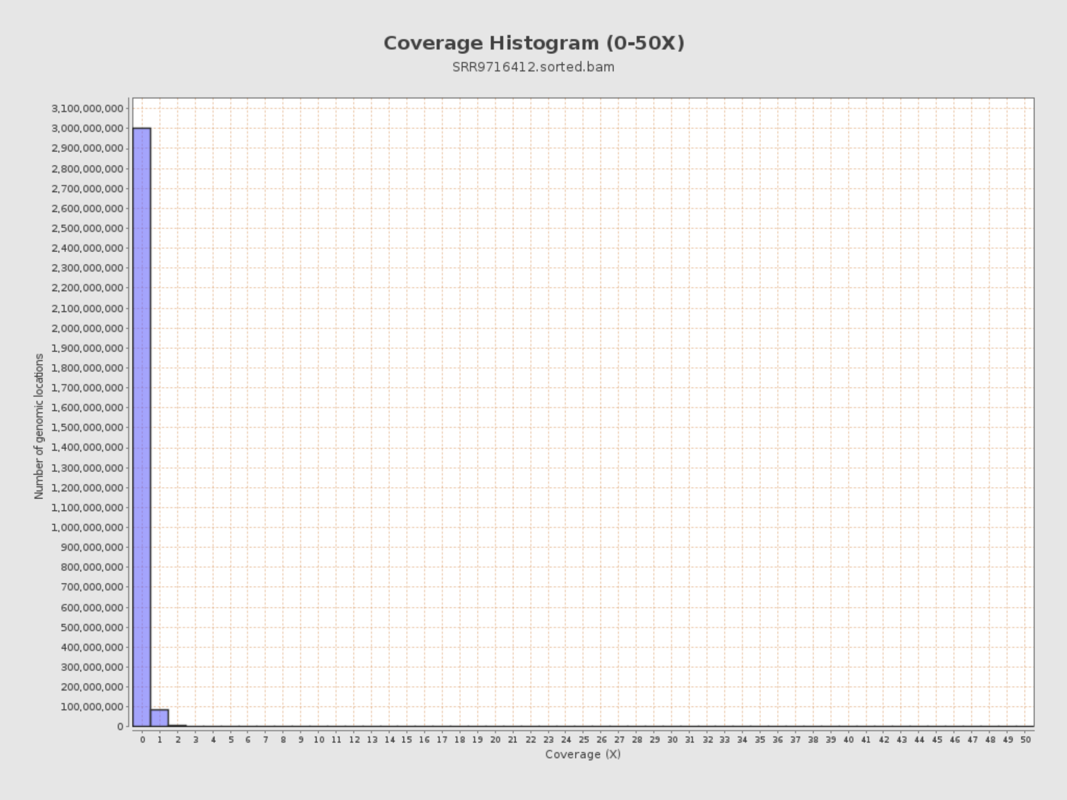
3. Results : Coverage across reference



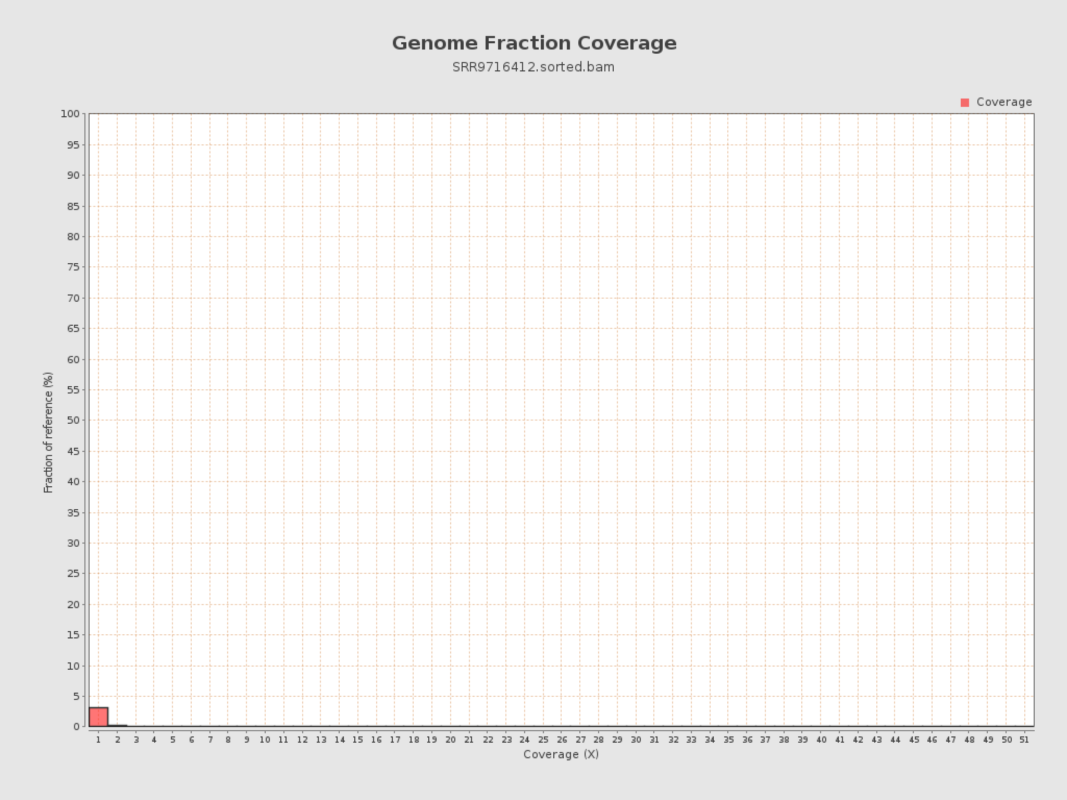
4. Results : Coverage Histogram



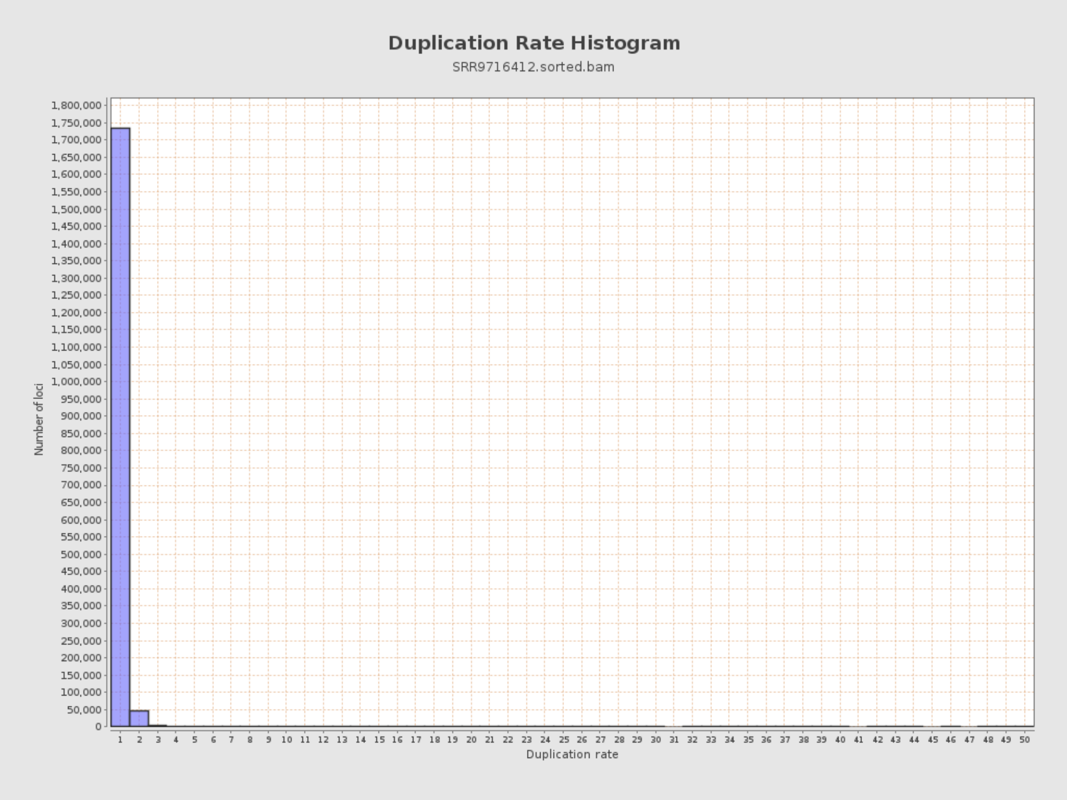
5. Results : Coverage Histogram (0-50X)



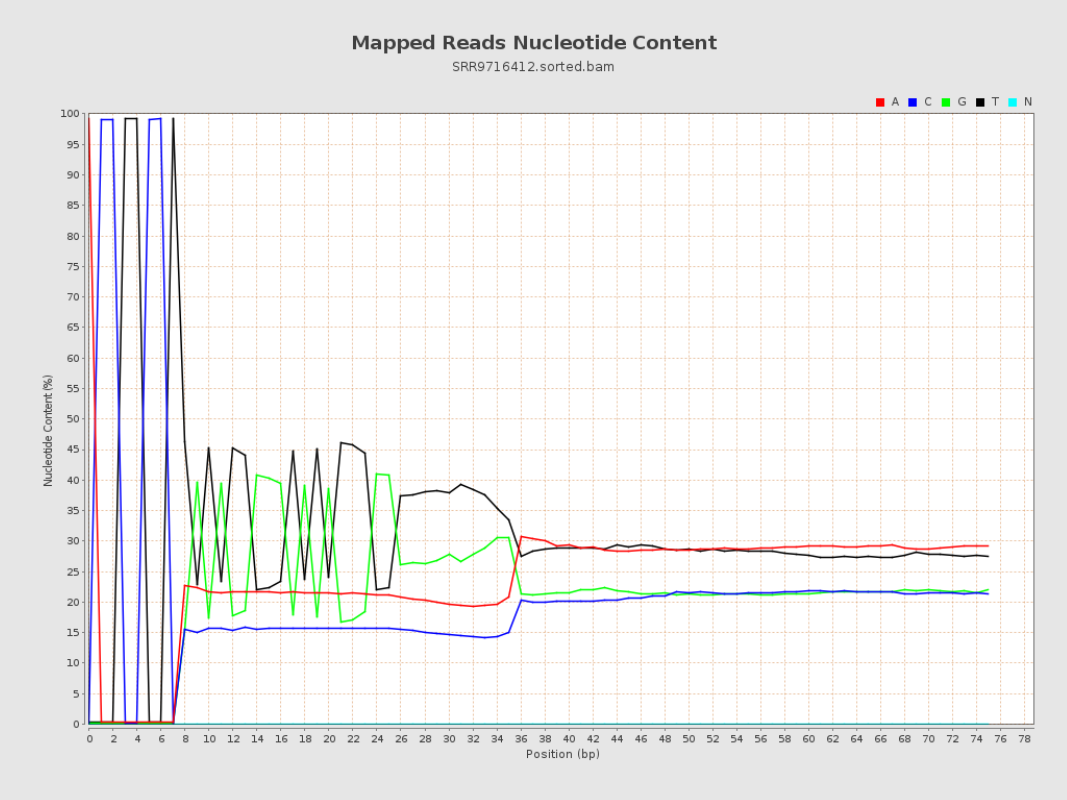
6. Results : Genome Fraction Coverage



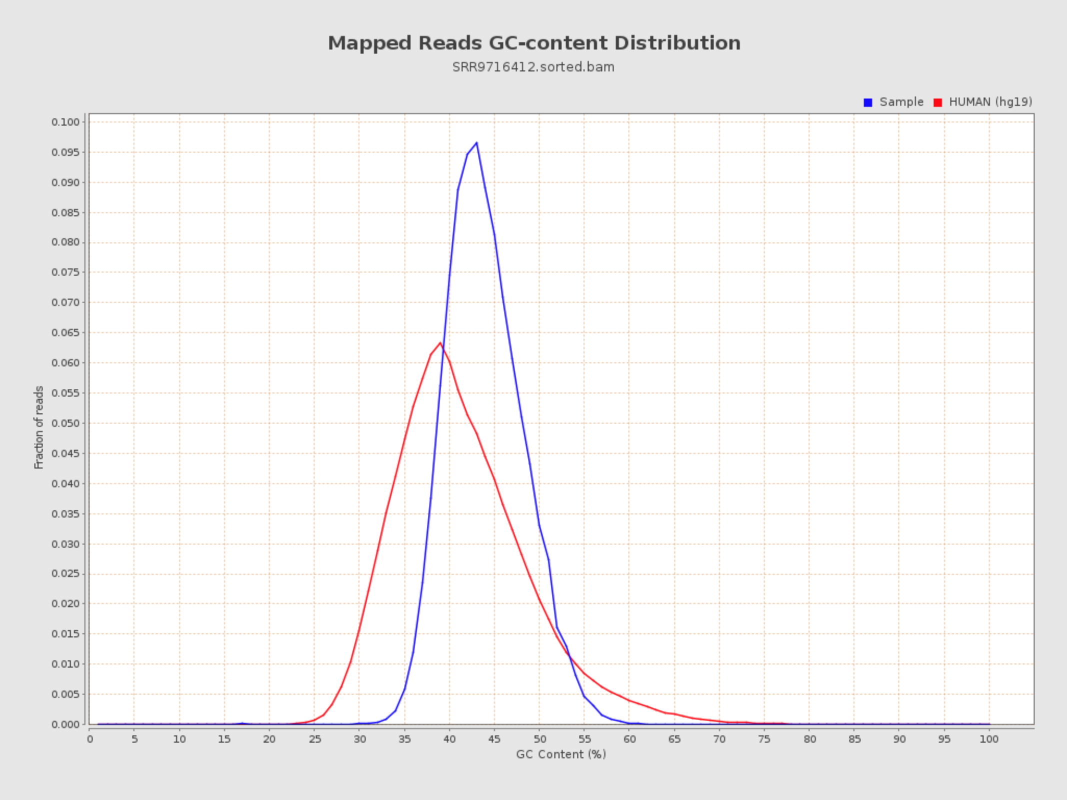
7. Results : Duplication Rate Histogram



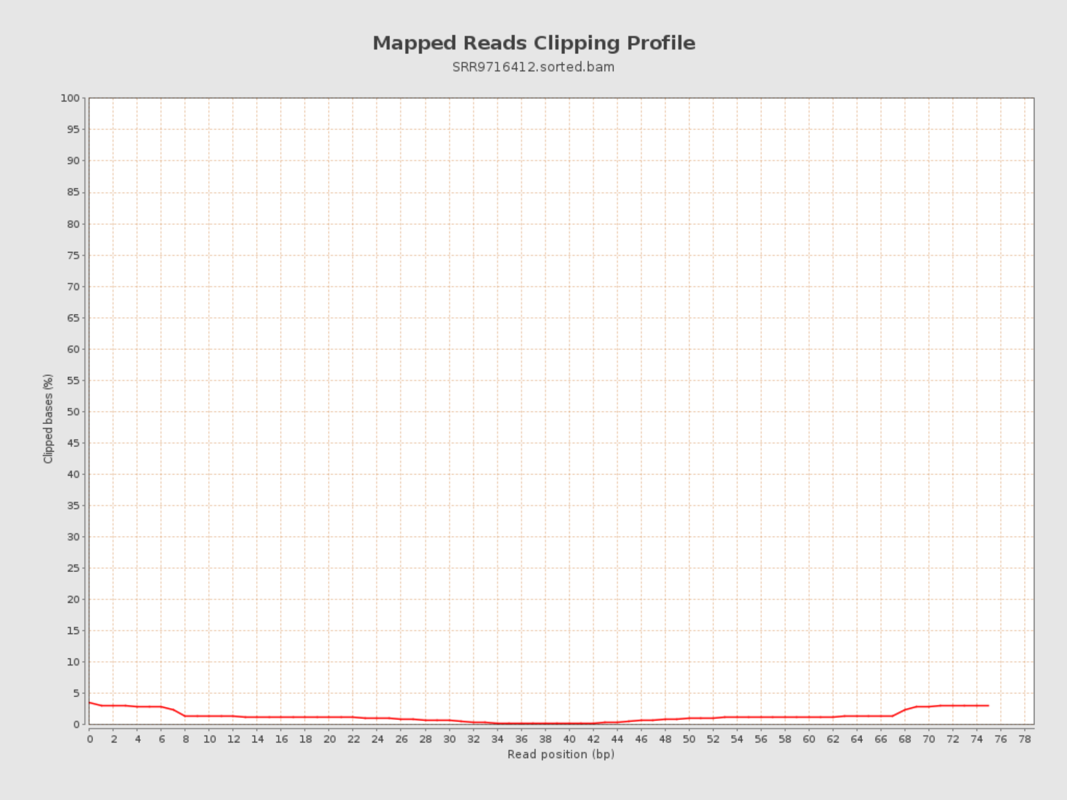
8. Results : Mapped Reads Nucleotide Content



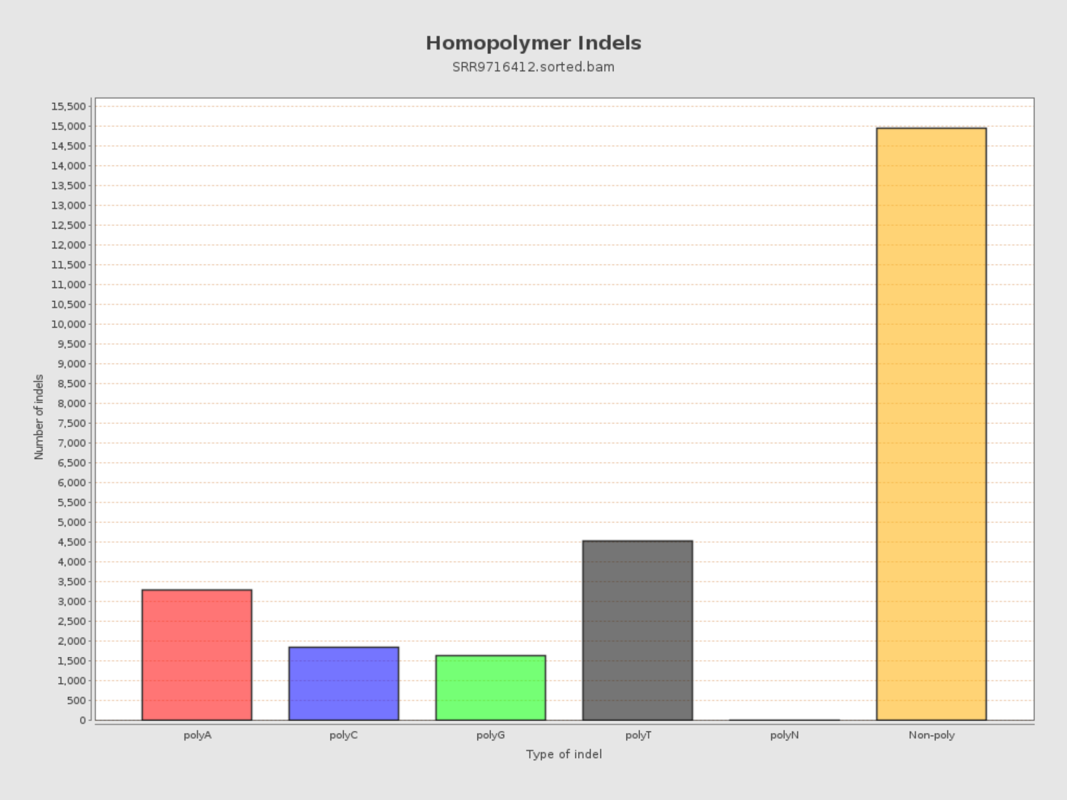
9. Results : Mapped Reads GC-content Distribution



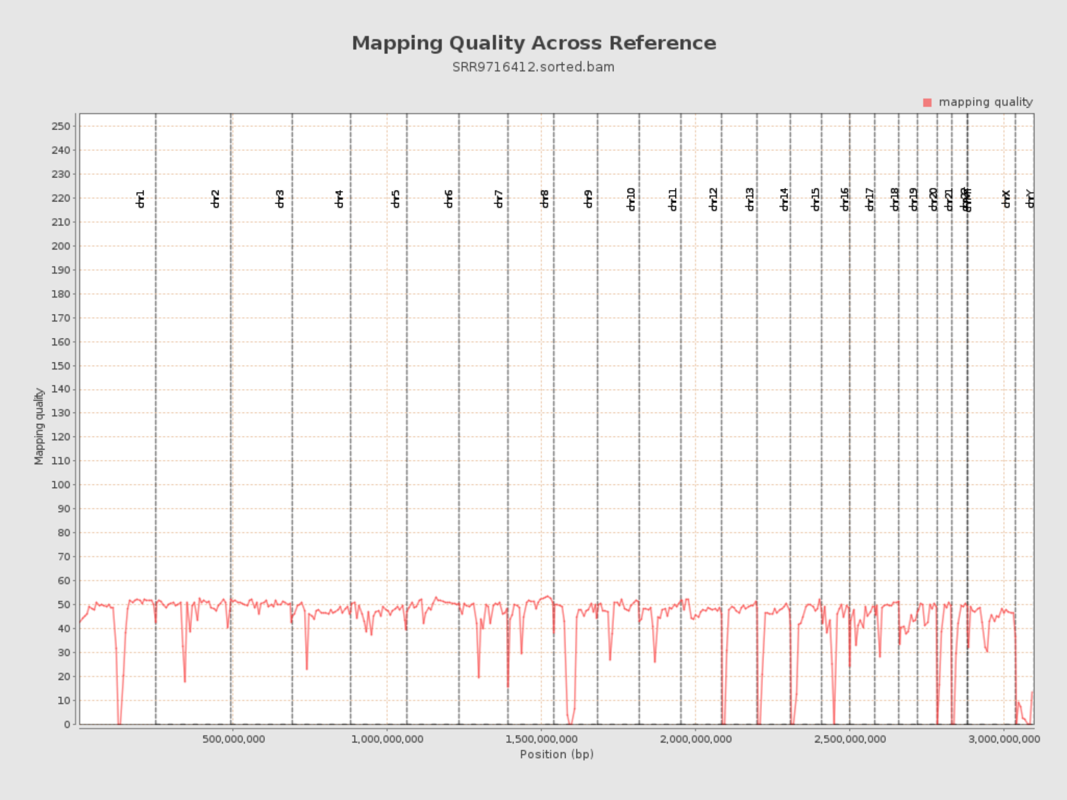
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram