Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:26:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716210.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_SRR9716210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:26:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,397,965
Mapped reads	1,026,490 / 73.43%
Unmapped reads	371,475 / 26.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,459 / 1.82%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	21,900 / 1.57%
Duplication rate	1.46%
Clipped reads	1,049,855 / 75.1%

2.2. ACGT Content

Number/percentage of A's	20,271,981 / 26.73%
Number/percentage of C's	15,344,221 / 20.23%
Number/percentage of T's	22,293,010 / 29.39%
Number/percentage of G's	17,926,350 / 23.64%
Number/percentage of N's	8,633 / 0.01%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2132

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

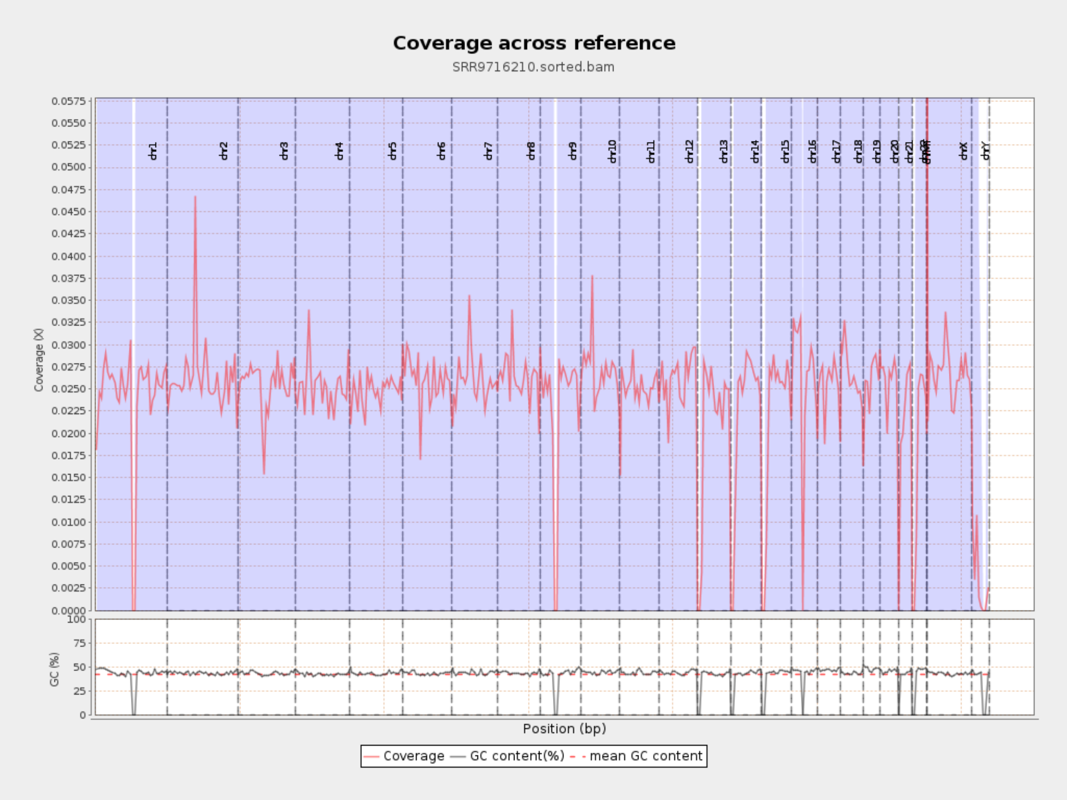
General error rate	0.76%
Mismatches	557,773
Insertions	7,061
Mapped reads with at least one insertion	0.68%
Deletions	14,559
Mapped reads with at least one deletion	1.4%
Homopolymer indels	38.27%

2.6. Chromosome stats

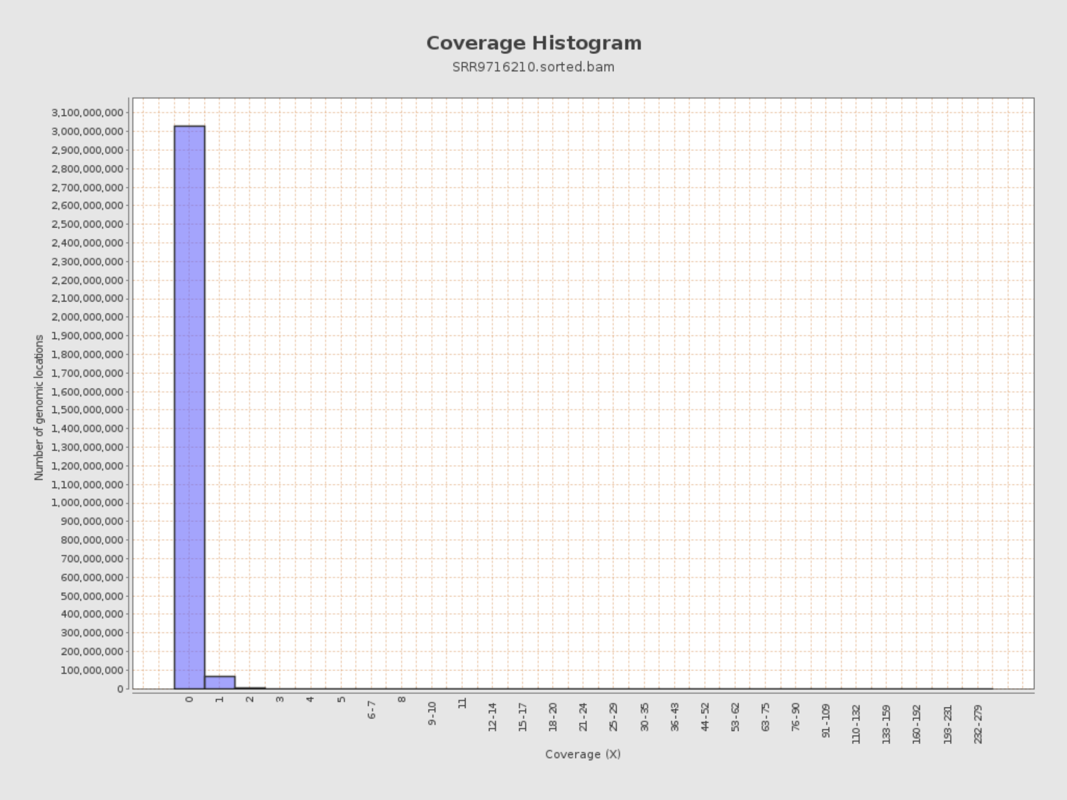
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5988745	0.024	0.2325
chr2	243199373	6422567	0.0264	0.2866
chr3	198022430	5045602	0.0255	0.1711
chr4	191154276	4829506	0.0253	0.1809
chr5	180915260	4506752	0.0249	0.17
chr6	171115067	4456099	0.026	0.1852
chr7	159138663	4148617	0.0261	0.251

chr8	146364022	3847617	0.0263	0.2552
chr9	141213431	3222270	0.0228	0.2229
chr10	135534747	3681579	0.0272	0.2232
chr11	135006516	3409414	0.0253	0.2266
chr12	133851895	3485795	0.026	0.175
chr13	115169878	2369467	0.0206	0.1535
chr14	107349540	2363270	0.022	0.1815
chr15	102531392	2189998	0.0214	0.1573
chr16	90354753	2325941	0.0257	0.1811
chr17	81195210	2068104	0.0255	0.1815
chr18	78077248	2092565	0.0268	0.3776
chr19	59128983	1539707	0.026	0.2225
chr20	63025520	1615507	0.0256	0.1796
chr21	48129895	1002621	0.0208	0.1661
chr22	51304566	898350	0.0175	0.1432
chrMT	16571	2926	0.1766	0.429
chrX	155270560	4161942	0.0268	0.1991
chrY	59373566	195257	0.0033	0.1057

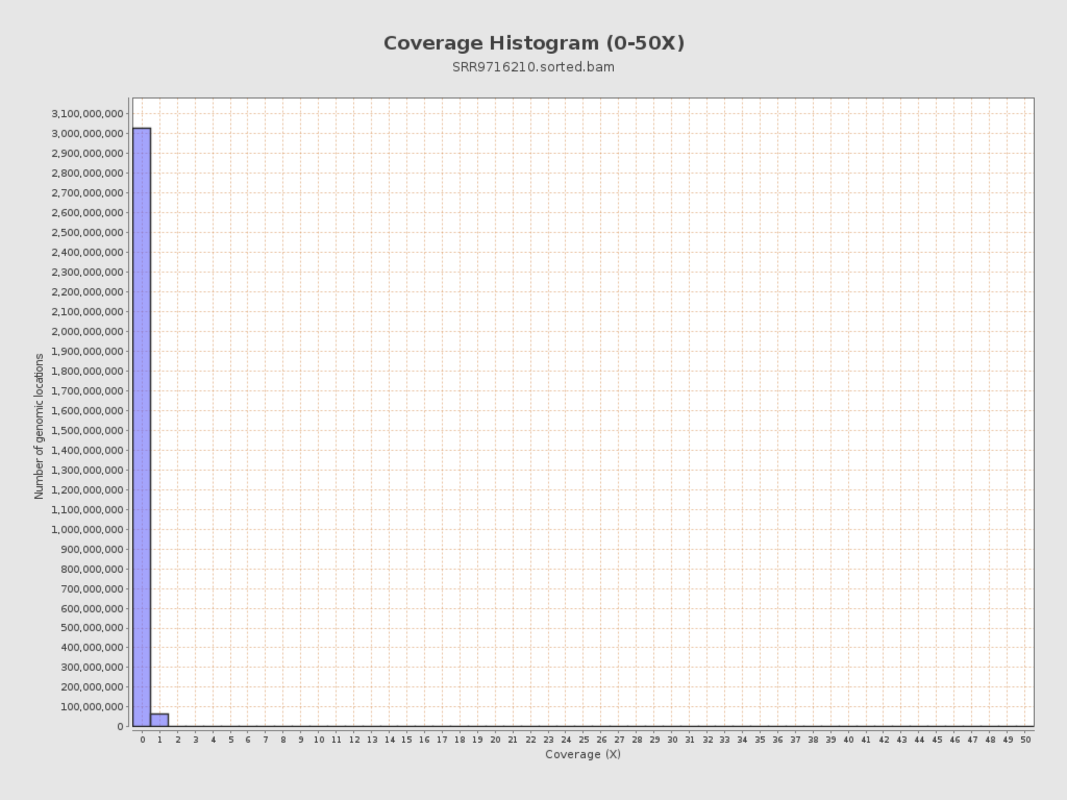
3. Results : Coverage across reference



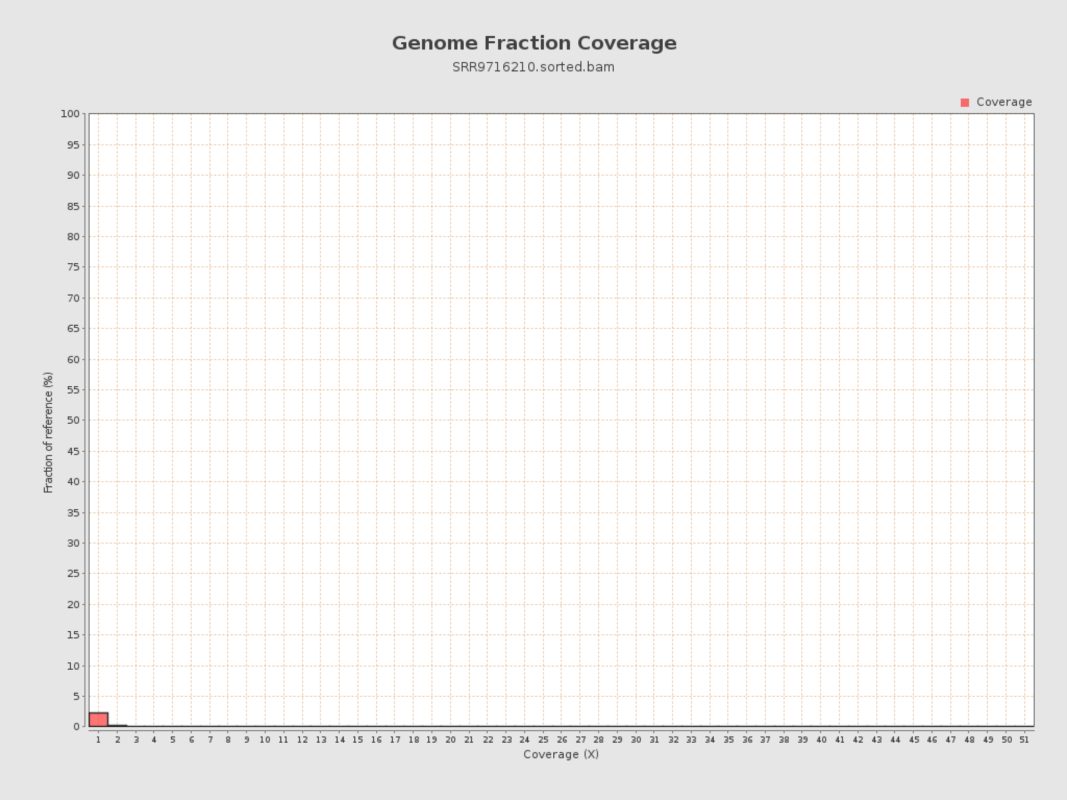
4. Results : Coverage Histogram



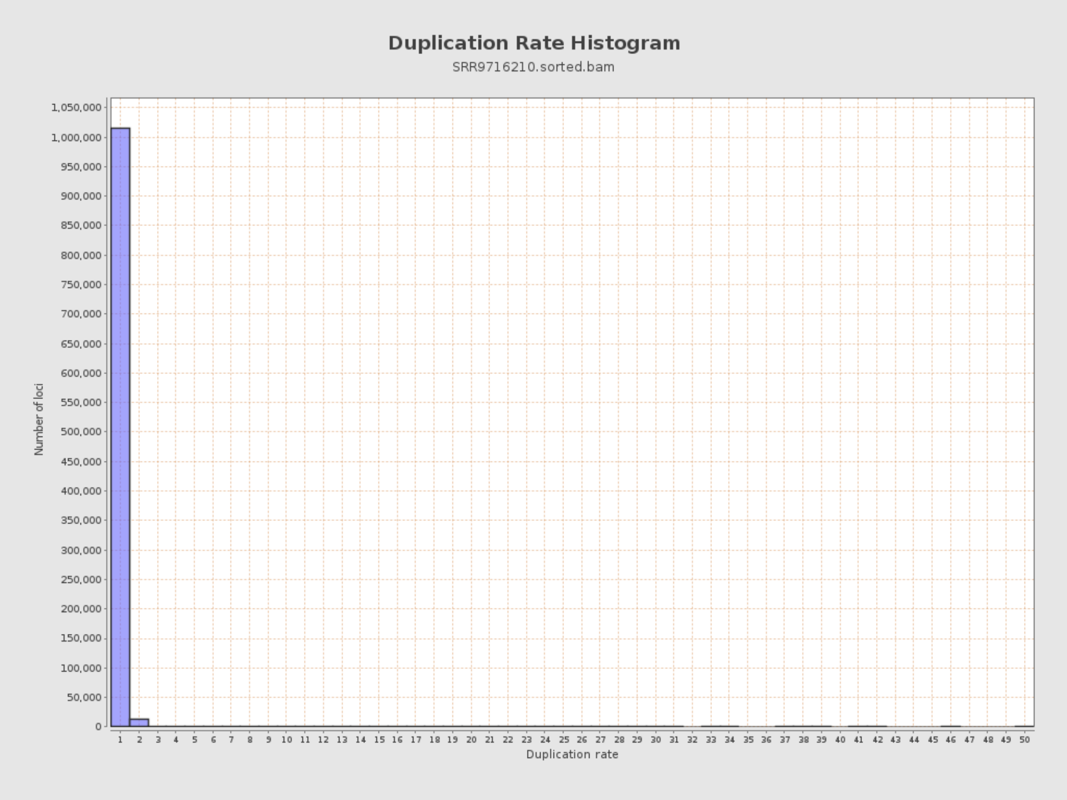
5. Results : Coverage Histogram (0-50X)



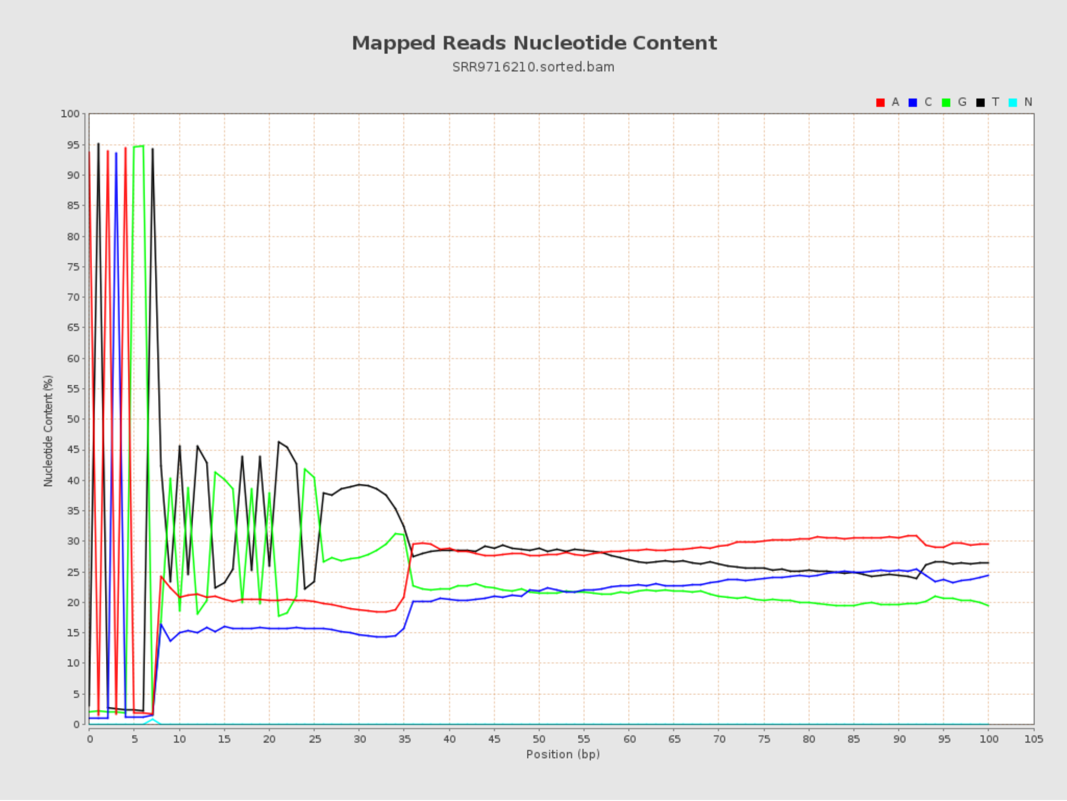
6. Results : Genome Fraction Coverage



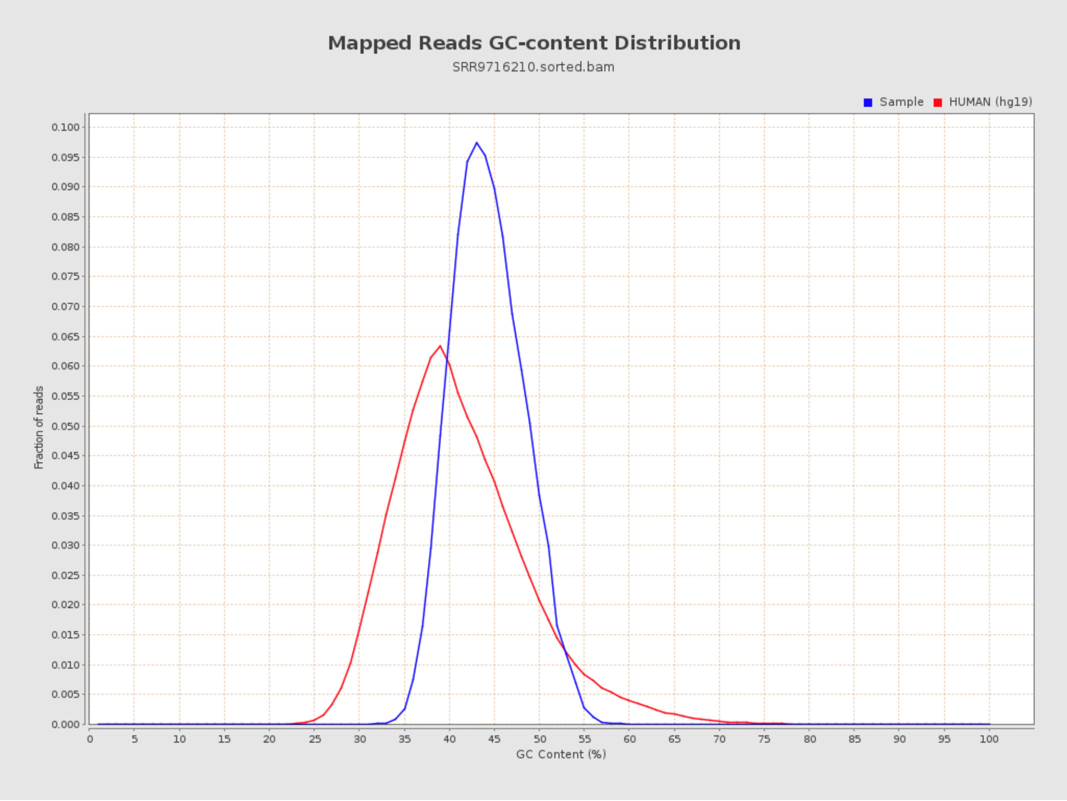
7. Results : Duplication Rate Histogram



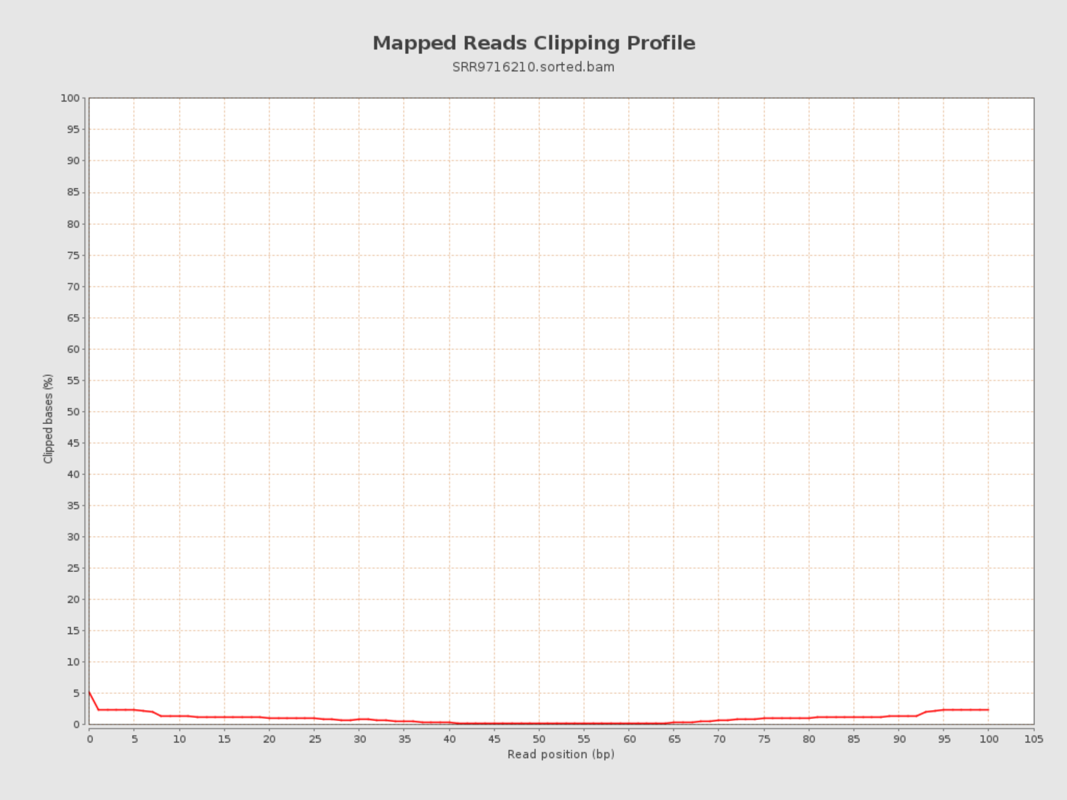
8. Results : Mapped Reads Nucleotide Content



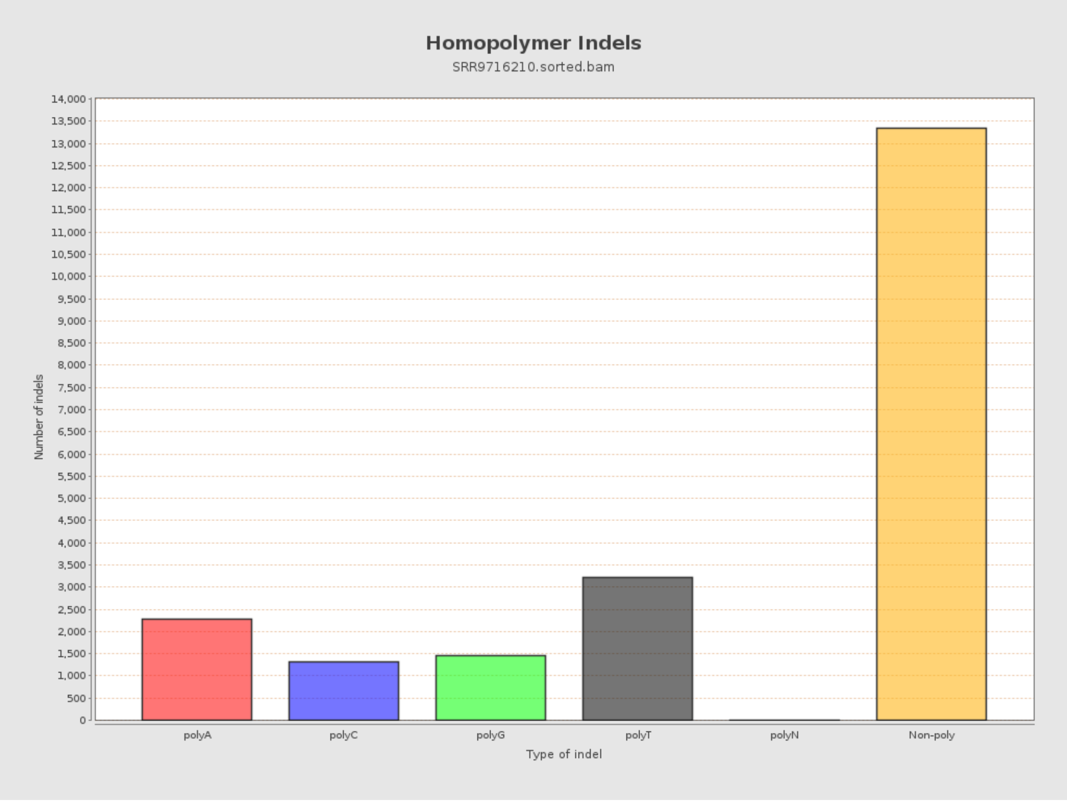
9. Results : Mapped Reads GC-content Distribution



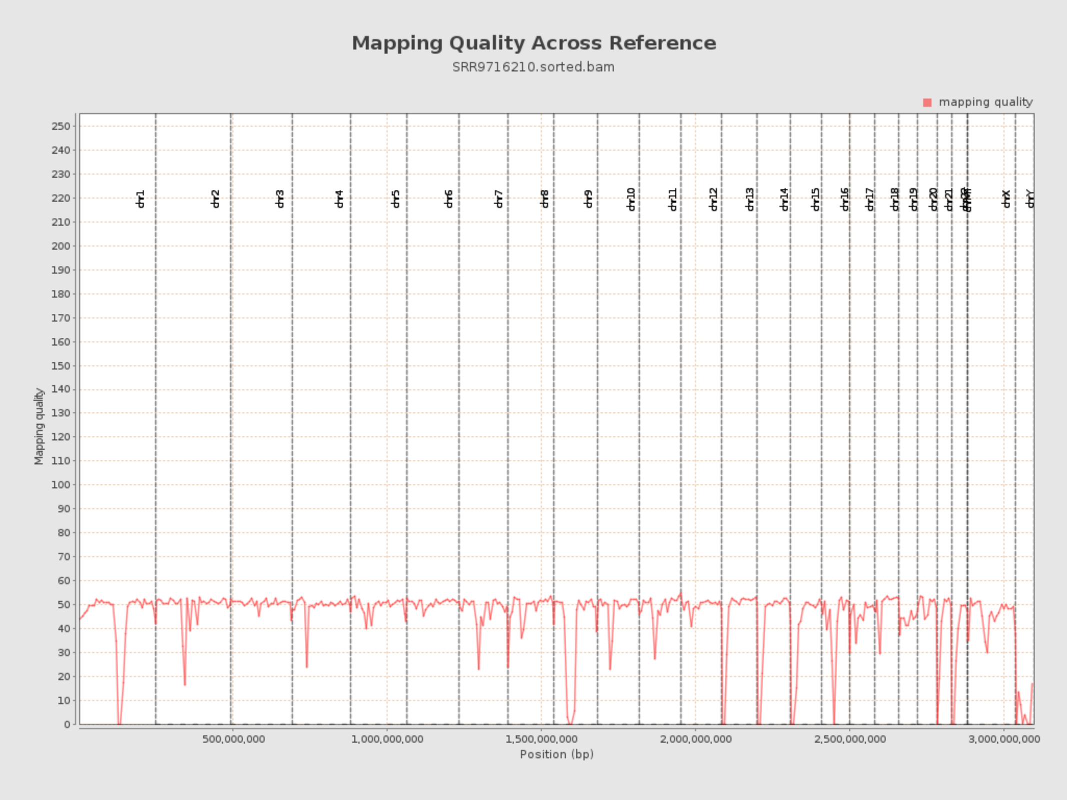
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram