Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:27:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716714.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_SRR9716714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:27:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,107,248
Mapped reads	1,027,129 / 92.76%
Unmapped reads	80,119 / 7.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,621 / 2.31%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	33,294 / 3.01%
Duplication rate	2.49%
Clipped reads	1,052,121 / 95.02%

2.2. ACGT Content

Number/percentage of A's	19,789,459 / 25.27%
Number/percentage of C's	16,584,880 / 21.18%
Number/percentage of T's	22,779,144 / 29.09%
Number/percentage of G's	19,156,836 / 24.46%
Number/percentage of N's	2,674 / 0%
GC Percentage	45.64%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.218

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

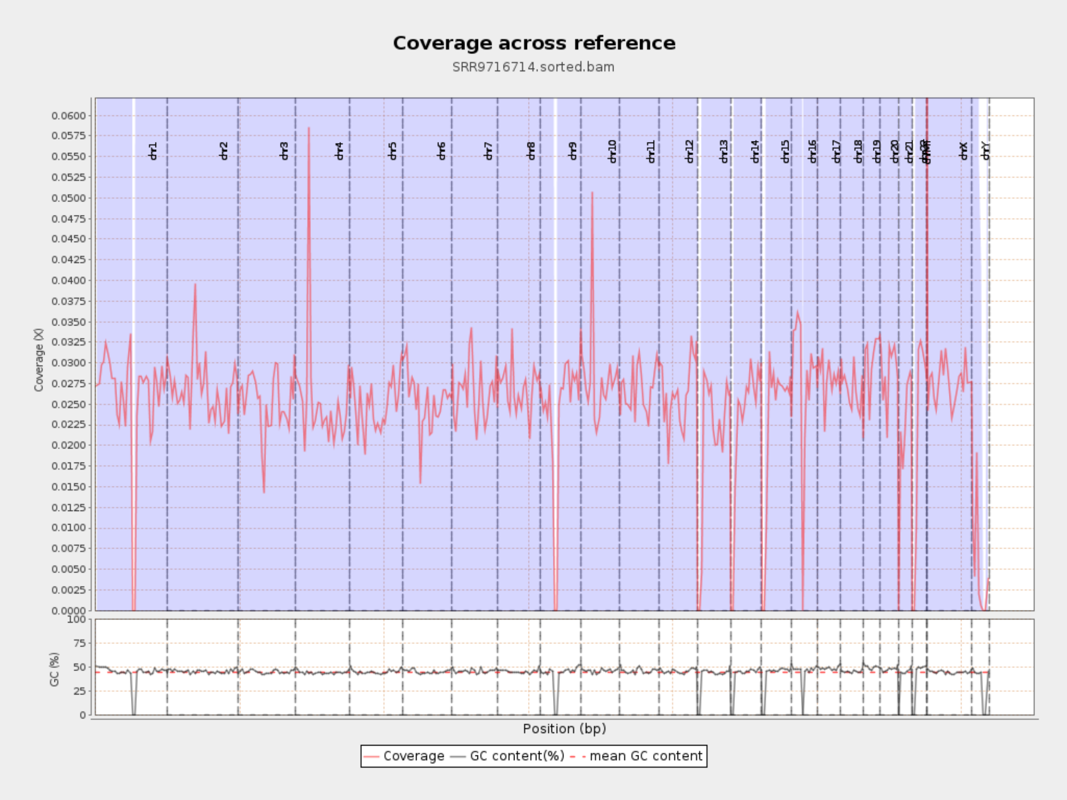
General error rate	0.67%
Mismatches	510,631
Insertions	6,657
Mapped reads with at least one insertion	0.64%
Deletions	14,344
Mapped reads with at least one deletion	1.38%
Homopolymer indels	39.26%

2.6. Chromosome stats

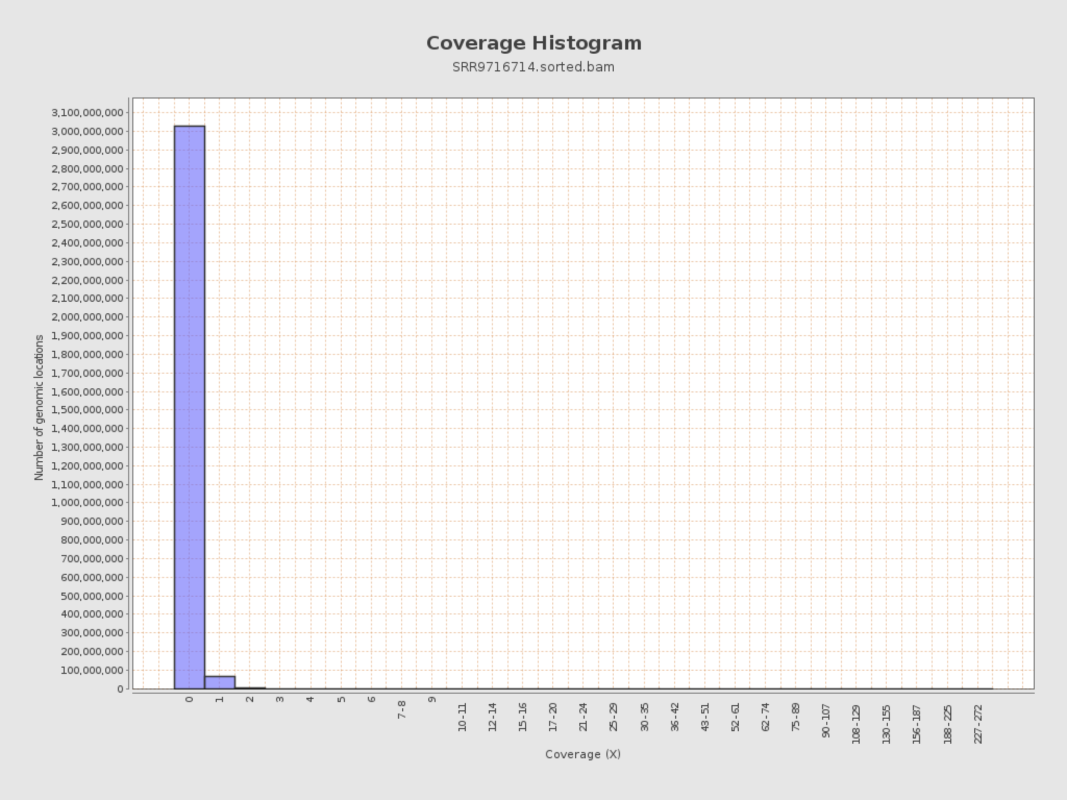
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6415125	0.0257	0.2759
chr2	243199373	6545217	0.0269	0.24
chr3	198022430	4995765	0.0252	0.1737
chr4	191154276	4861678	0.0254	0.2408
chr5	180915260	4529530	0.025	0.1731
chr6	171115067	4353320	0.0254	0.1802
chr7	159138663	4218101	0.0265	0.2461

chr8	146364022	3932992	0.0269	0.2201
chr9	141213431	3309180	0.0234	0.1996
chr10	135534747	3817575	0.0282	0.3077
chr11	135006516	3639227	0.027	0.2238
chr12	133851895	3502508	0.0262	0.1797
chr13	115169878	2352125	0.0204	0.1565
chr14	107349540	2399685	0.0224	0.174
chr15	102531392	2291712	0.0224	0.1644
chr16	90354753	2481558	0.0275	0.1939
chr17	81195210	2291601	0.0282	0.1986
chr18	78077248	2088191	0.0267	0.2961
chr19	59128983	1781341	0.0301	0.2453
chr20	63025520	1814194	0.0288	0.1952
chr21	48129895	1040815	0.0216	0.2033
chr22	51304566	1102793	0.0215	0.1658
chrMT	16571	1430	0.0863	0.2883
chrX	155270560	4287639	0.0276	0.1911
chrY	59373566	289740	0.0049	0.2043

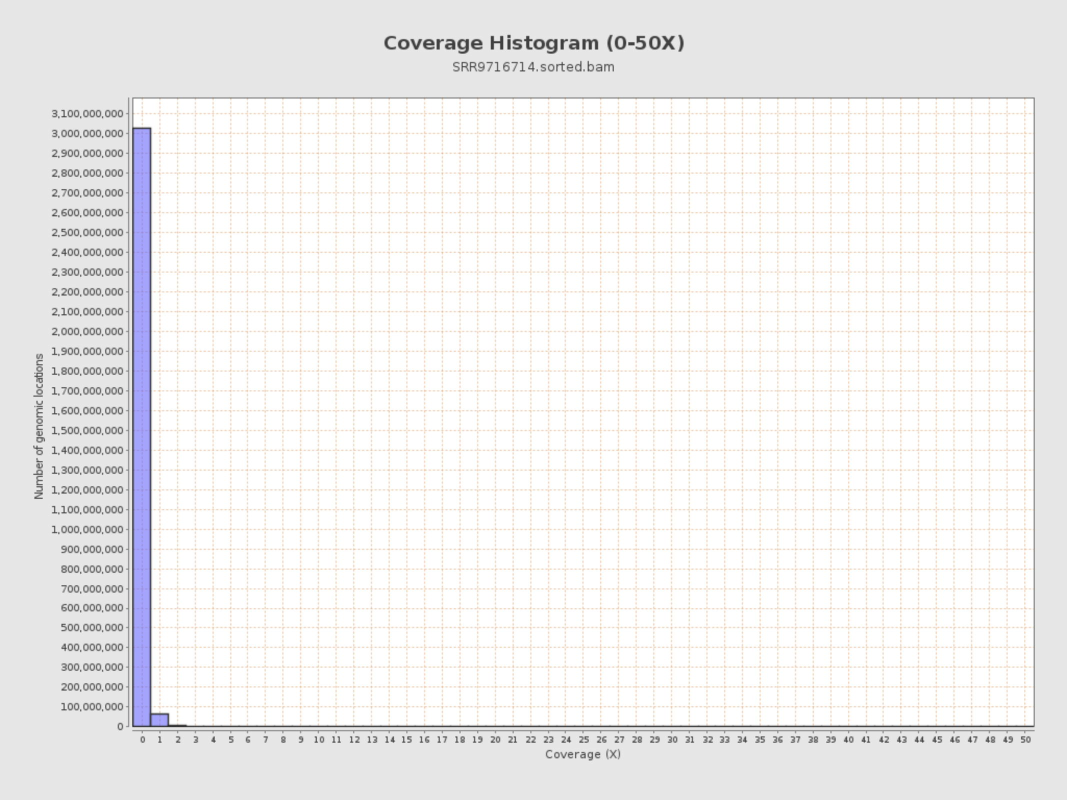
3. Results : Coverage across reference



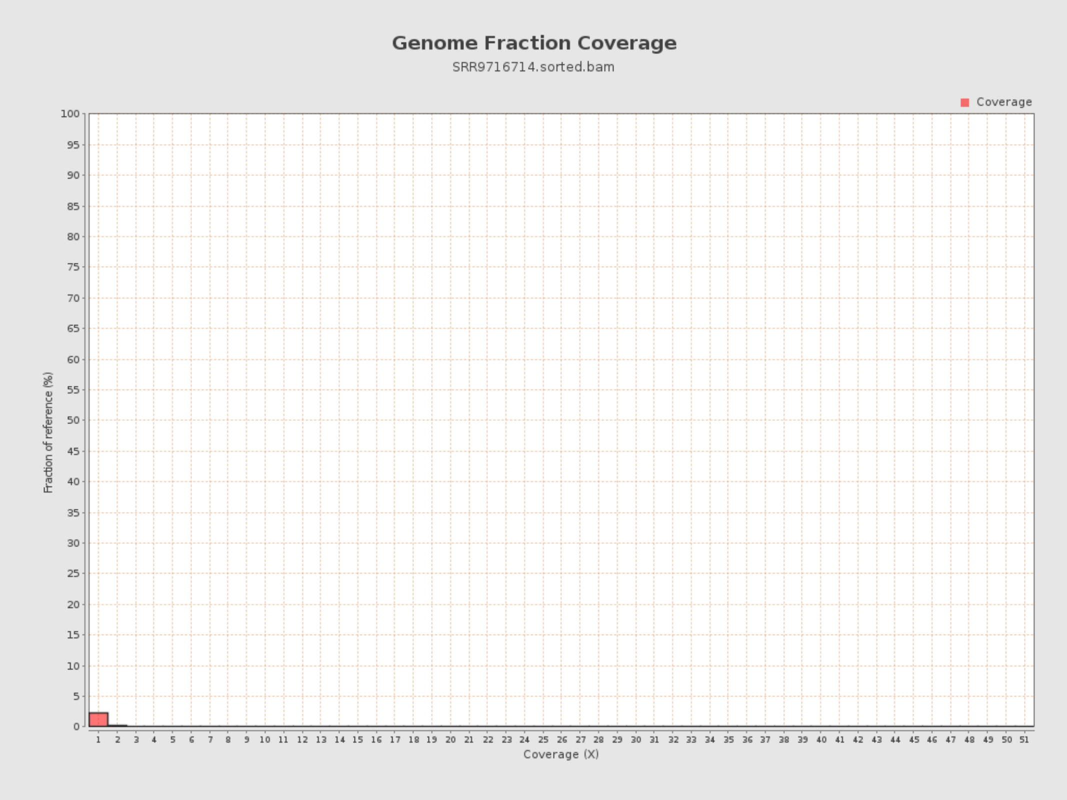
4. Results : Coverage Histogram



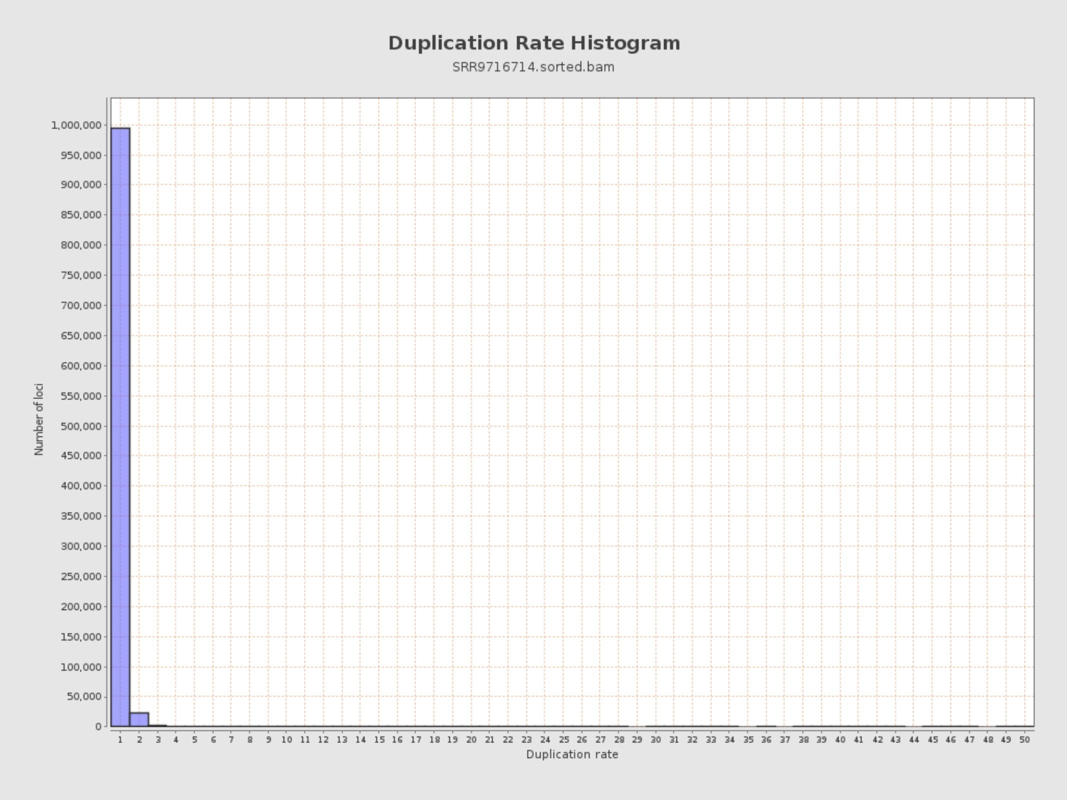
5. Results : Coverage Histogram (0-50X)



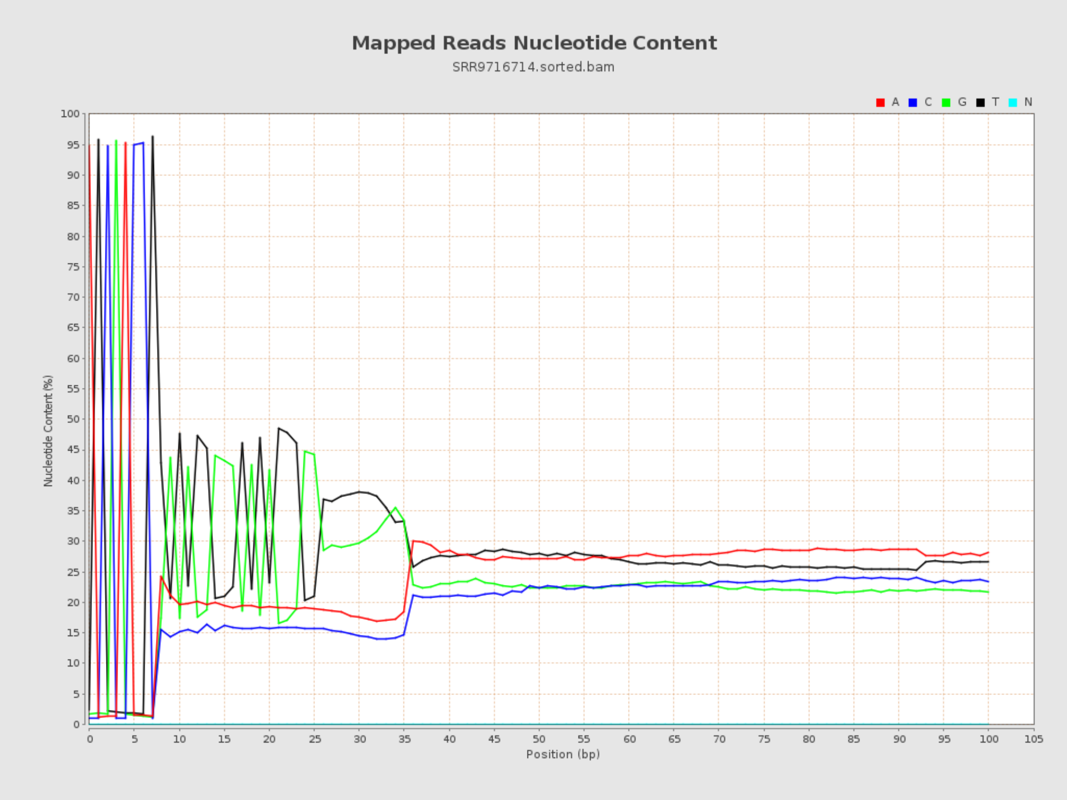
6. Results : Genome Fraction Coverage



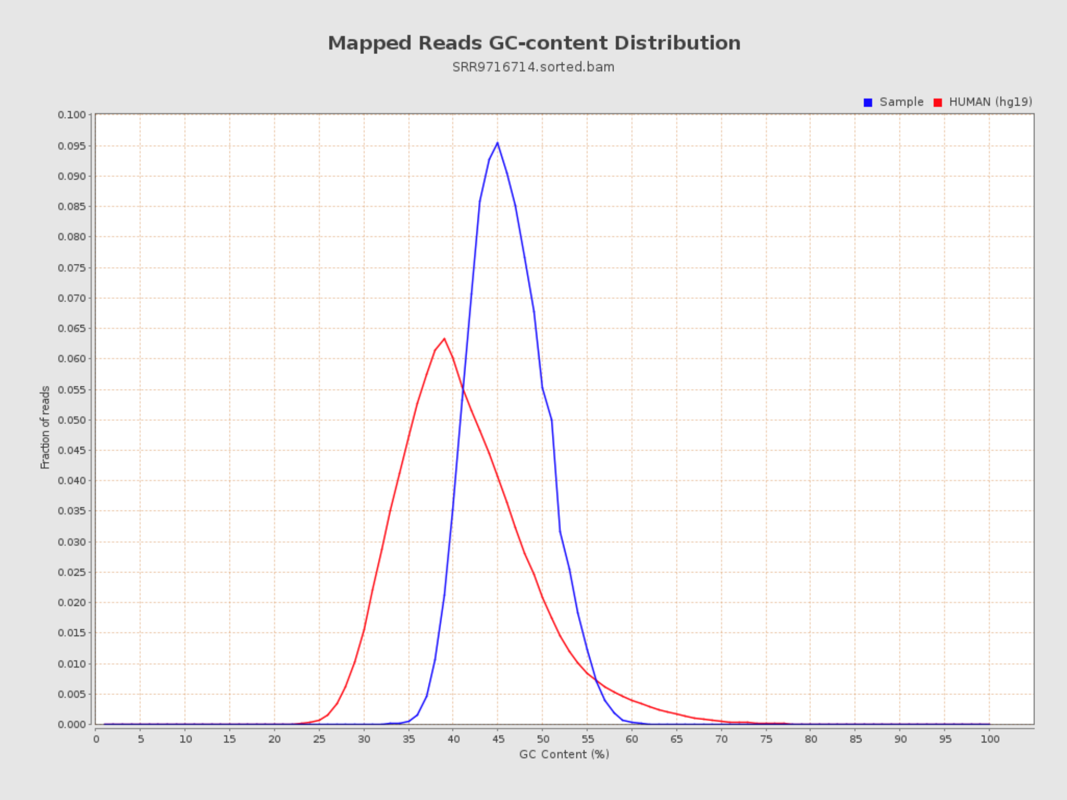
7. Results : Duplication Rate Histogram



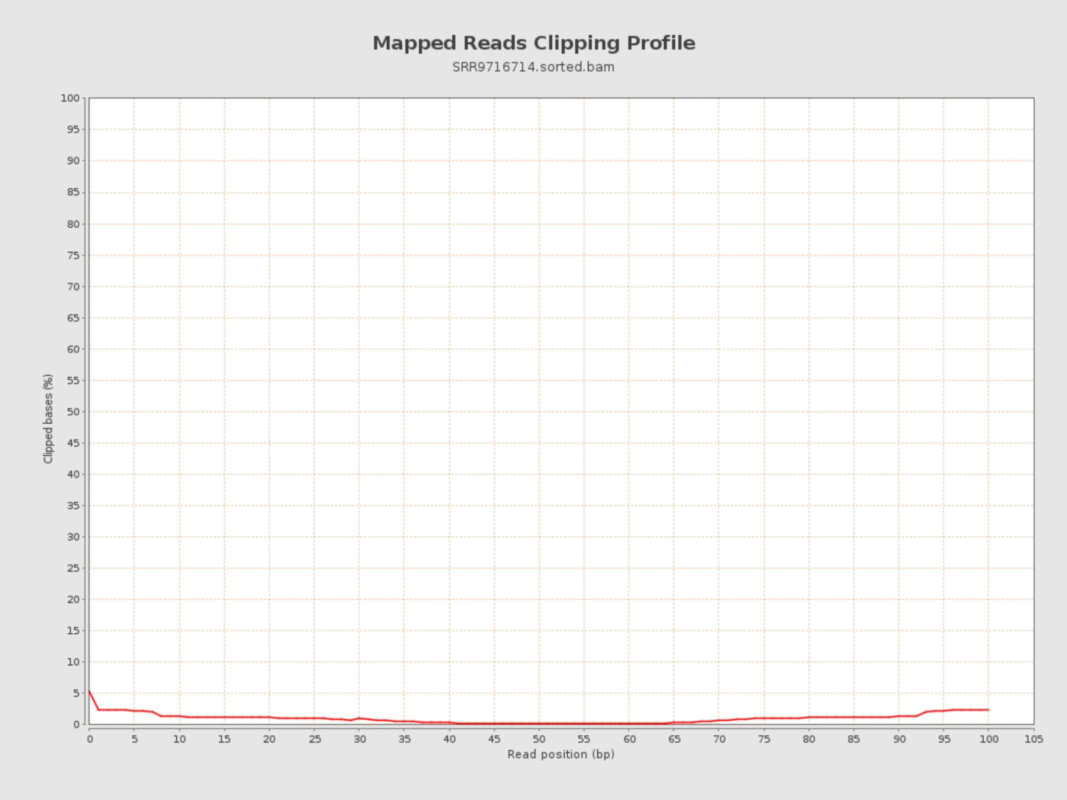
8. Results : Mapped Reads Nucleotide Content



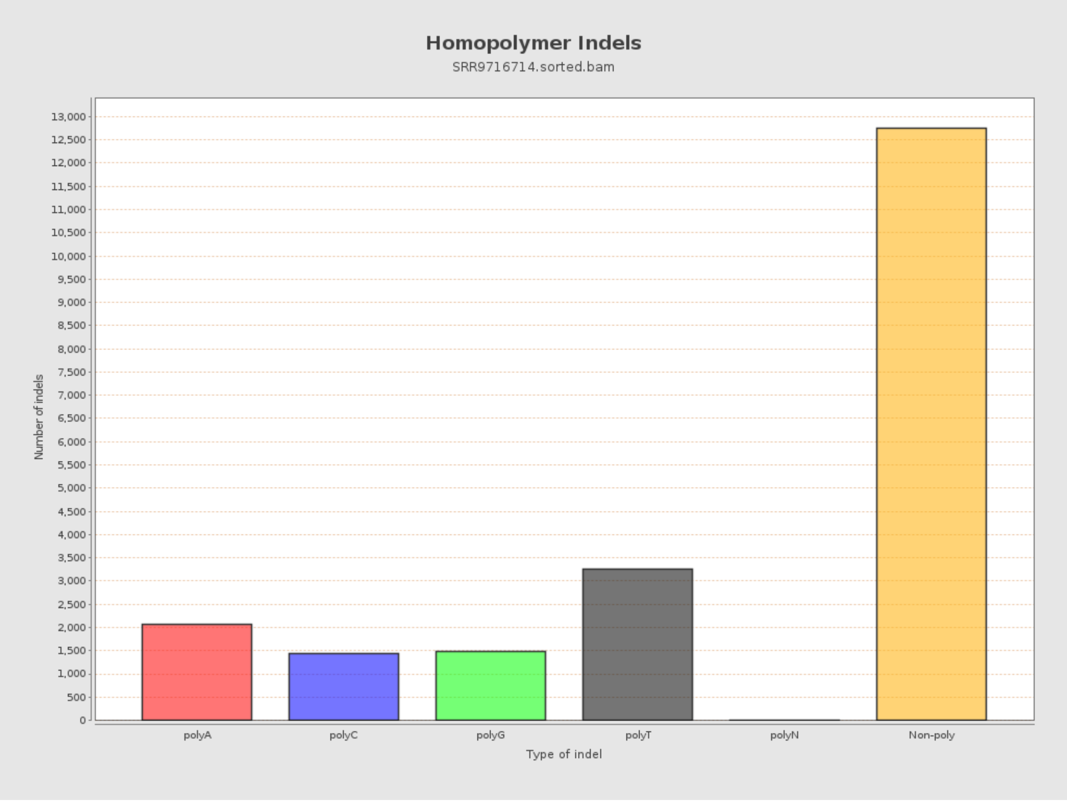
9. Results : Mapped Reads GC-content Distribution



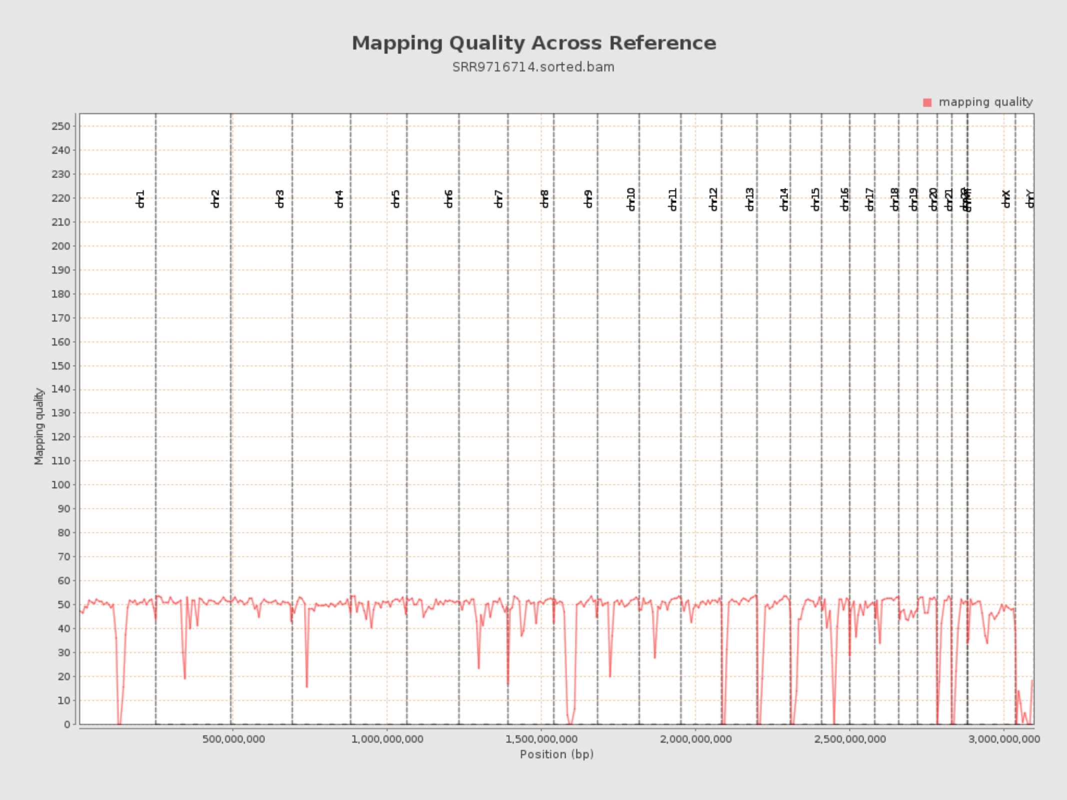
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram