Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:39:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716895.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_SRR9716895 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716895.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:39:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716895.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	943,704
Mapped reads	821,559 / 87.06%
Unmapped reads	122,145 / 12.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,844 / 2%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	15,753 / 1.67%
Duplication rate	1.28%
Clipped reads	839,006 / 88.91%

2.2. ACGT Content

Number/percentage of A's	15,789,501 / 25.94%
Number/percentage of C's	12,982,206 / 21.32%
Number/percentage of T's	18,135,785 / 29.79%
Number/percentage of G's	13,963,540 / 22.94%
Number/percentage of N's	7,292 / 0.01%
GC Percentage	44.26%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.1866

2.4. Mapping Quality

Mean Mapping Quality	45.96

2.5. Mismatches and indels

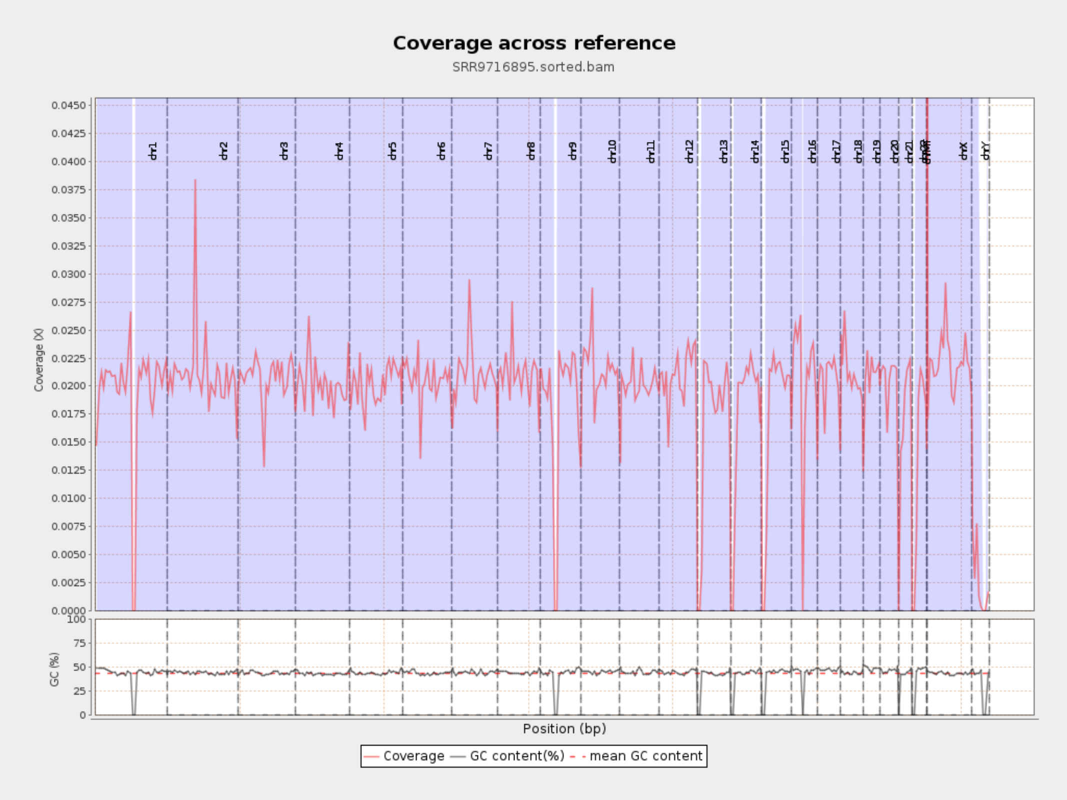
General error rate	0.77%
Mismatches	459,696
Insertions	4,803
Mapped reads with at least one insertion	0.58%
Deletions	12,517
Mapped reads with at least one deletion	1.5%
Homopolymer indels	40.16%

2.6. Chromosome stats

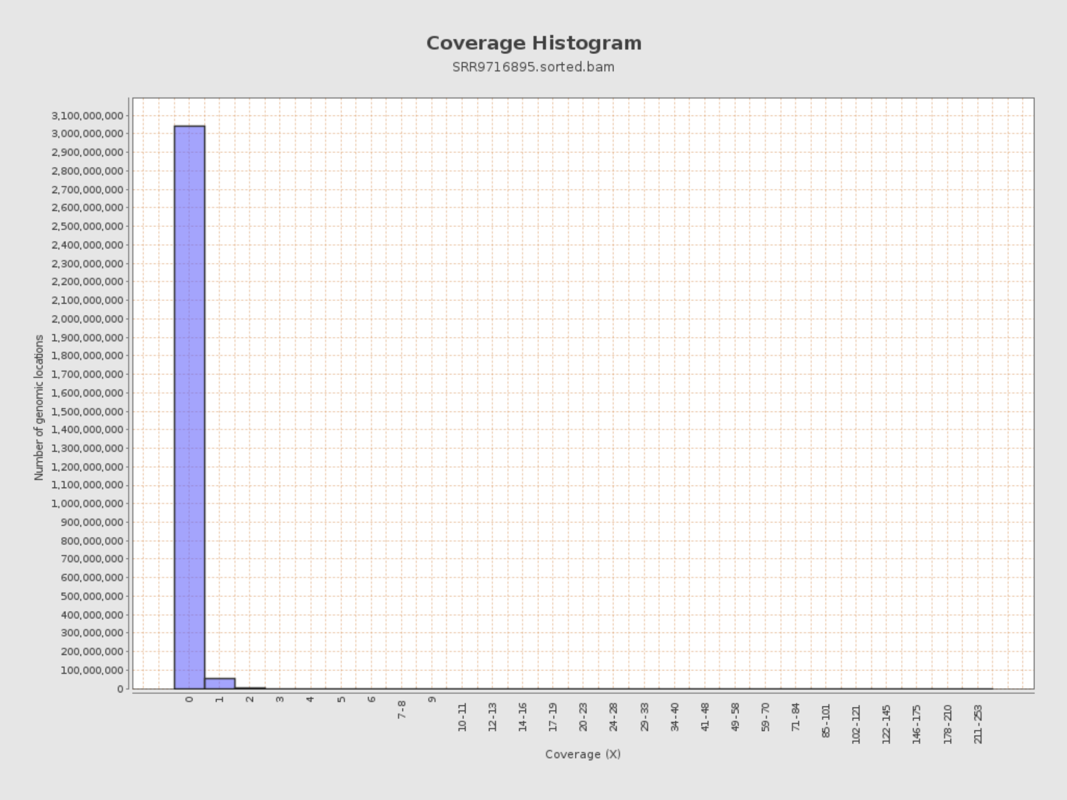
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4836434	0.0194	0.2083
chr2	243199373	5149325	0.0212	0.246
chr3	198022430	4113147	0.0208	0.1527
chr4	191154276	3862683	0.0202	0.1566
chr5	180915260	3673823	0.0203	0.1514
chr6	171115067	3517857	0.0206	0.1659
chr7	159138663	3365964	0.0212	0.2334

chr8	146364022	3076726	0.021	0.2213
chr9	141213431	2568748	0.0182	0.1955
chr10	135534747	2927271	0.0216	0.1897
chr11	135006516	2725810	0.0202	0.1904
chr12	133851895	2790433	0.0208	0.1545
chr13	115169878	1909305	0.0166	0.136
chr14	107349540	1843786	0.0172	0.1527
chr15	102531392	1768573	0.0172	0.1392
chr16	90354753	1820259	0.0201	0.1605
chr17	81195210	1668478	0.0205	0.1575
chr18	78077248	1658582	0.0212	0.32
chr19	59128983	1240701	0.021	0.1918
chr20	63025520	1283089	0.0204	0.1542
chr21	48129895	802291	0.0167	0.1427
chr22	51304566	694849	0.0135	0.1234
chrMT	16571	10824	0.6532	0.9055
chrX	155270560	3445742	0.0222	0.1818
chrY	59373566	145213	0.0024	0.0792

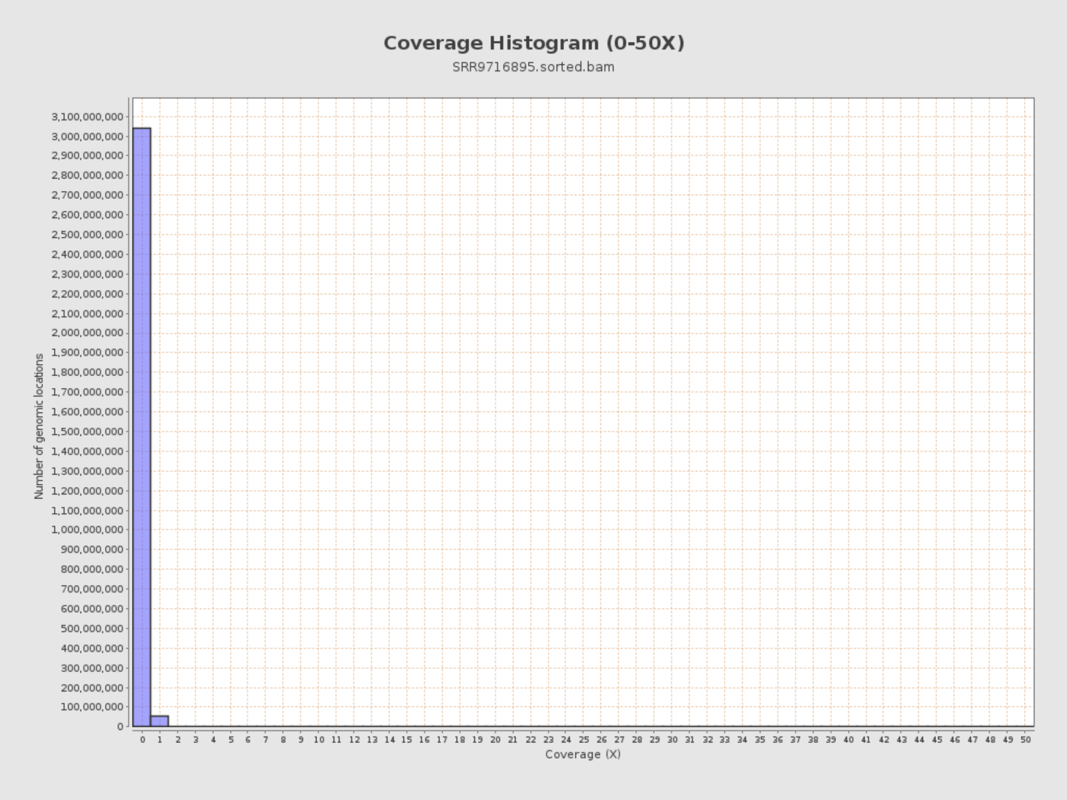
3. Results : Coverage across reference



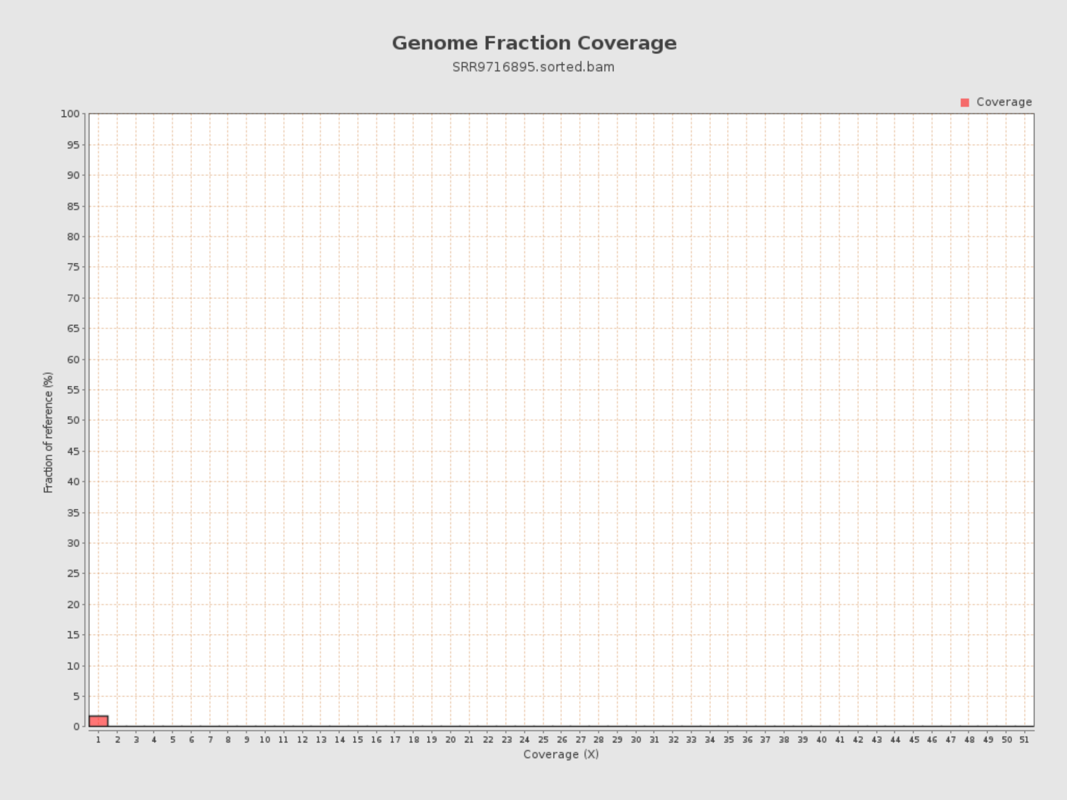
4. Results : Coverage Histogram



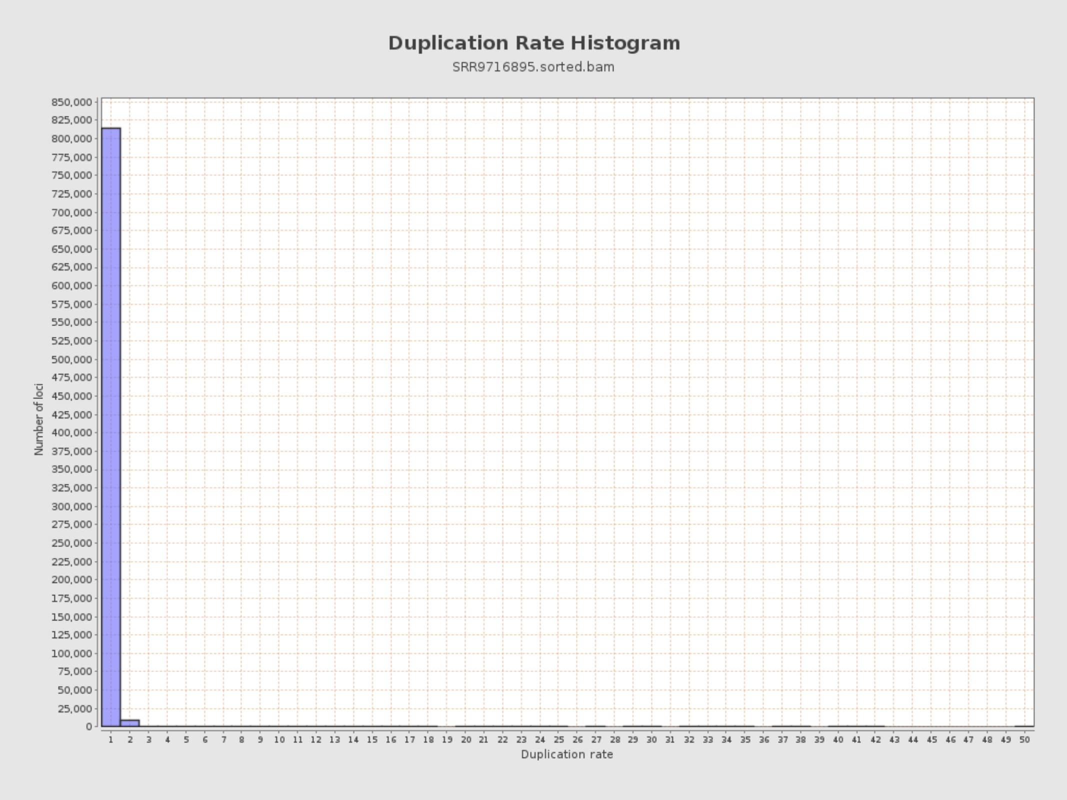
5. Results : Coverage Histogram (0-50X)



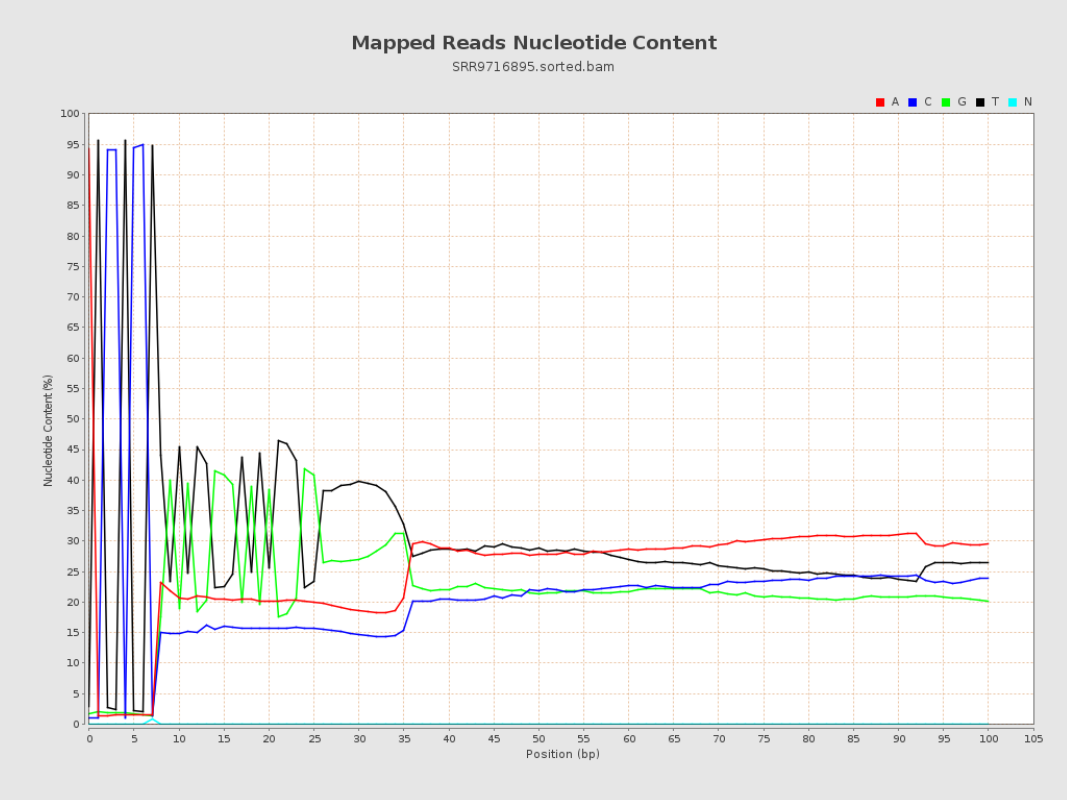
6. Results : Genome Fraction Coverage



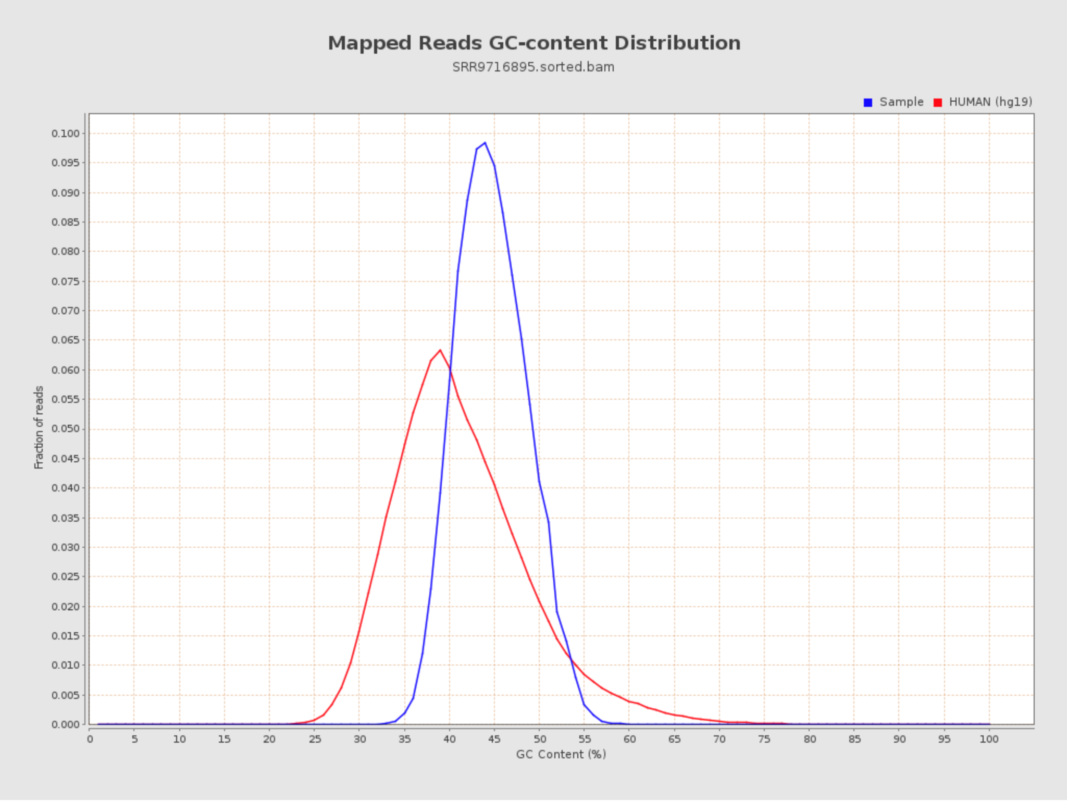
7. Results : Duplication Rate Histogram



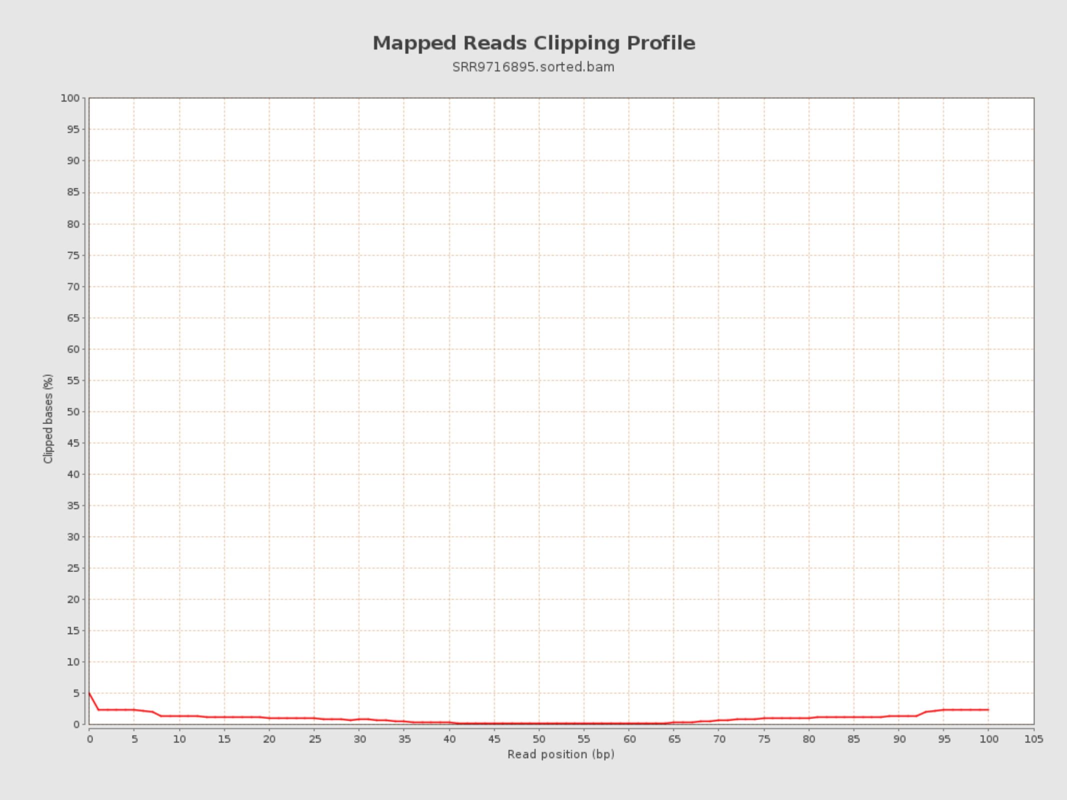
8. Results : Mapped Reads Nucleotide Content



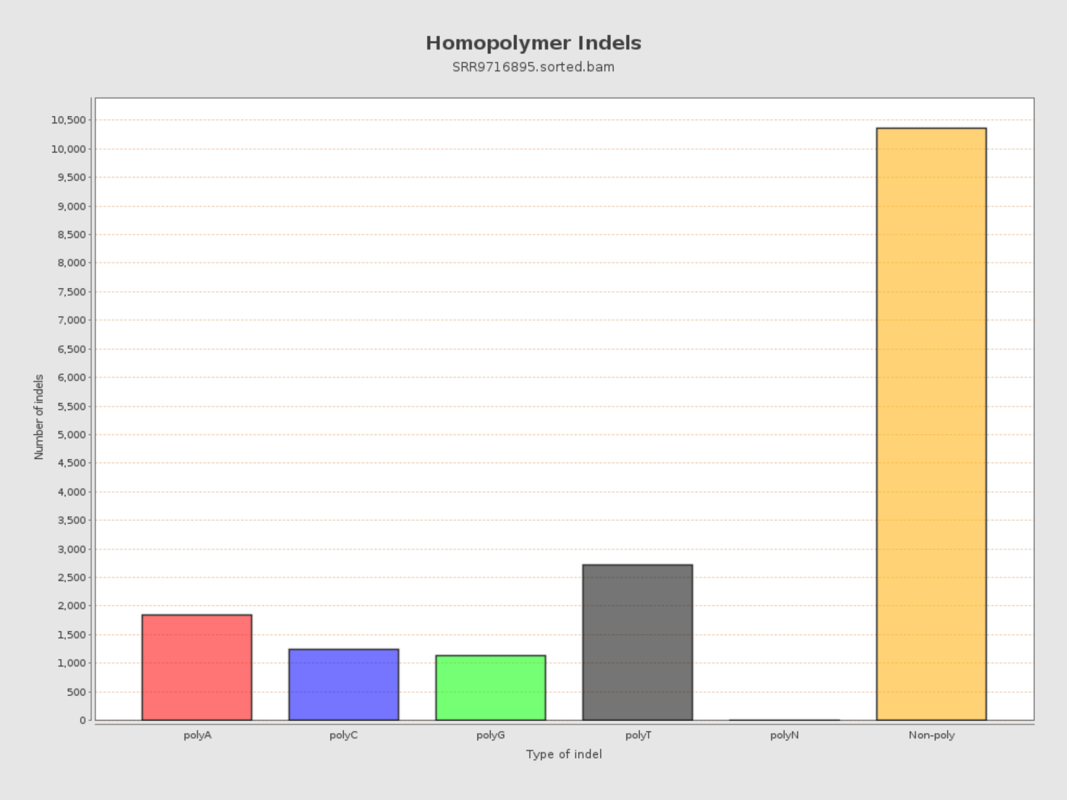
9. Results : Mapped Reads GC-content Distribution



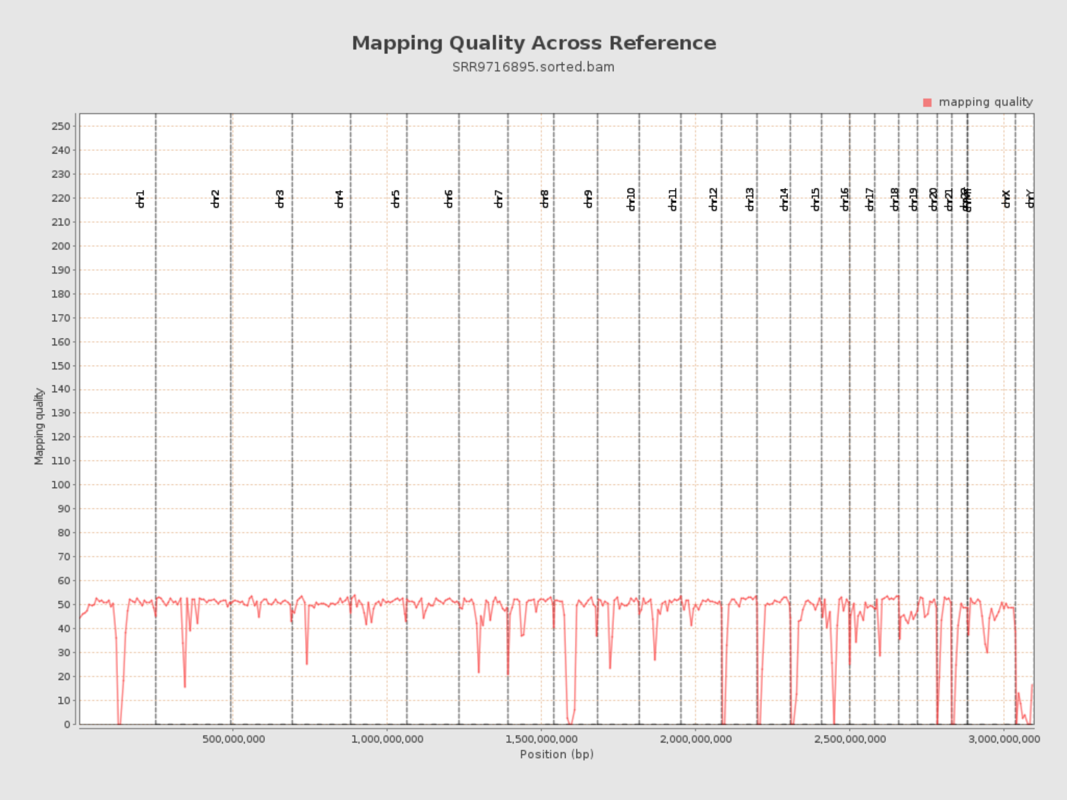
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram