Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:11:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716193.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_SRR9716193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:11:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	889,086
Mapped reads	834,366 / 93.85%
Unmapped reads	54,720 / 6.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,069 / 2.14%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	25,613 / 2.88%
Duplication rate	2.38%
Clipped reads	851,348 / 95.76%

2.2. ACGT Content

Number/percentage of A's	16,433,778 / 25.33%
Number/percentage of C's	12,850,009 / 19.8%
Number/percentage of T's	19,233,730 / 29.64%
Number/percentage of G's	16,369,123 / 25.23%
Number/percentage of N's	2,416 / 0%
GC Percentage	45.03%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2136

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

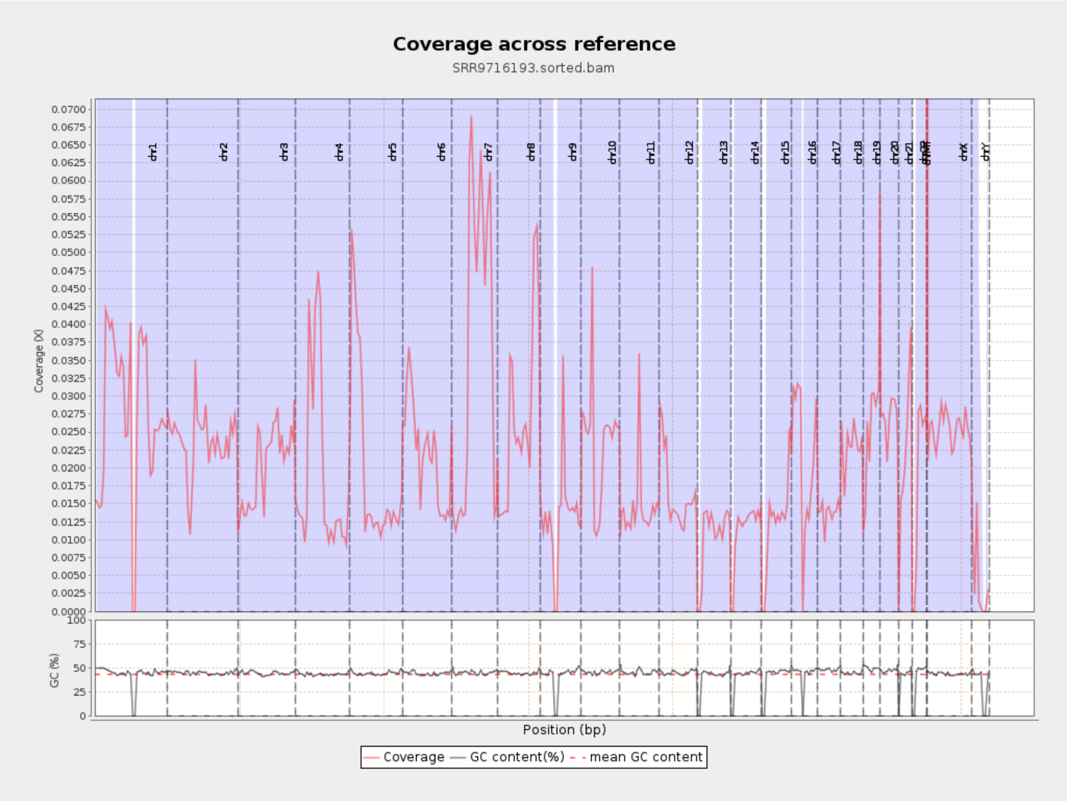
General error rate	0.66%
Mismatches	409,502
Insertions	6,276
Mapped reads with at least one insertion	0.74%
Deletions	12,149
Mapped reads with at least one deletion	1.43%
Homopolymer indels	37.6%

2.6. Chromosome stats

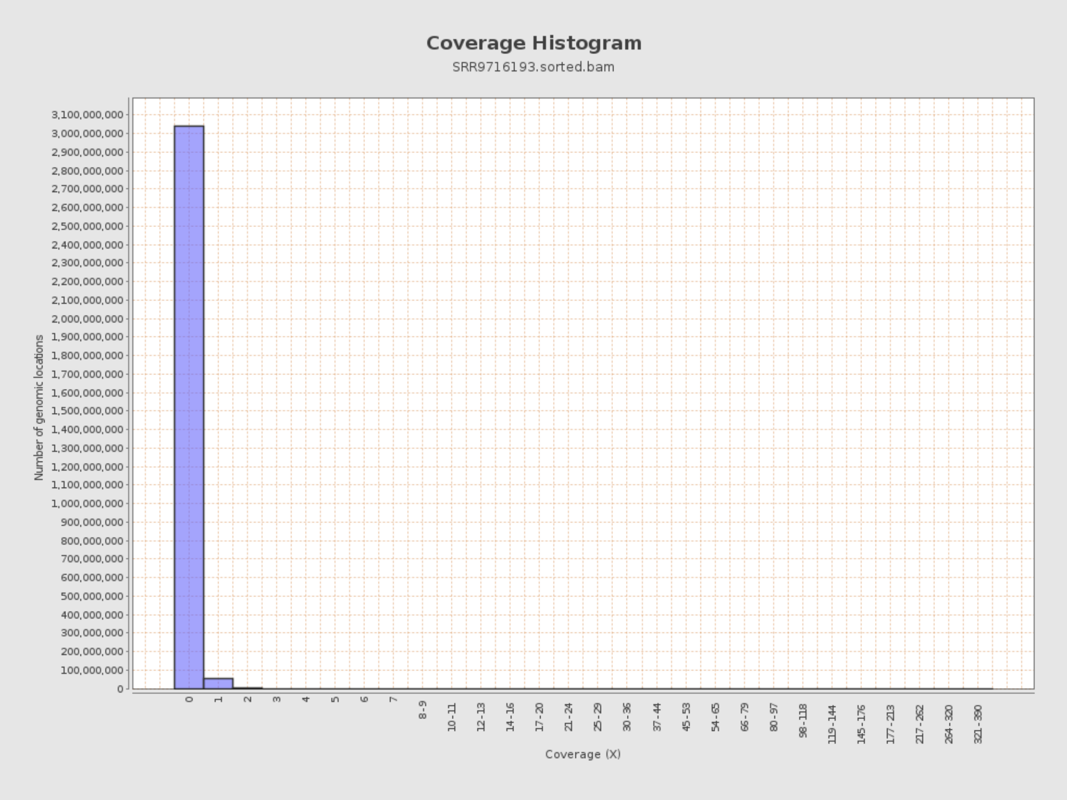
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6906623	0.0277	0.3803
chr2	243199373	5804017	0.0239	0.2088
chr3	198022430	4022674	0.0203	0.1552
chr4	191154276	3699005	0.0194	0.188
chr5	180915260	3696572	0.0204	0.1572
chr6	171115067	3758511	0.022	0.1654
chr7	159138663	5757267	0.0362	0.3586

chr8	146364022	3910310	0.0267	0.2122
chr9	141213431	1867396	0.0132	0.1474
chr10	135534747	3270614	0.0241	0.2648
chr11	135006516	1976956	0.0146	0.1516
chr12	133851895	2225556	0.0166	0.1394
chr13	115169878	1199025	0.0104	0.1095
chr14	107349540	1197052	0.0112	0.1198
chr15	102531392	1250798	0.0122	0.1189
chr16	90354753	1888133	0.0209	0.1642
chr17	81195210	1120874	0.0138	0.1348
chr18	78077248	1809966	0.0232	0.2166
chr19	59128983	1559406	0.0264	0.2788
chr20	63025520	1694339	0.0269	0.1848
chr21	48129895	1087296	0.0226	0.1809
chr22	51304566	948146	0.0185	0.1503
chrMT	16571	88613	5.3475	4.1318
chrX	155270560	3947477	0.0254	0.1791
chrY	59373566	228285	0.0038	0.1489

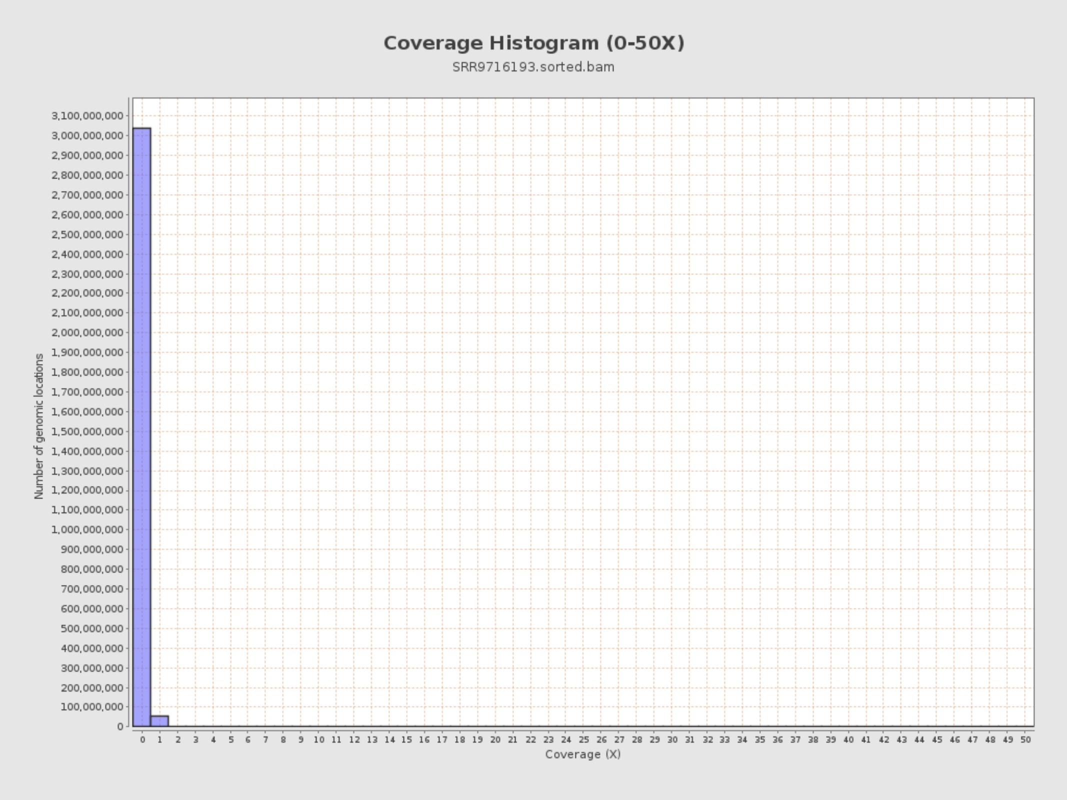
3. Results : Coverage across reference



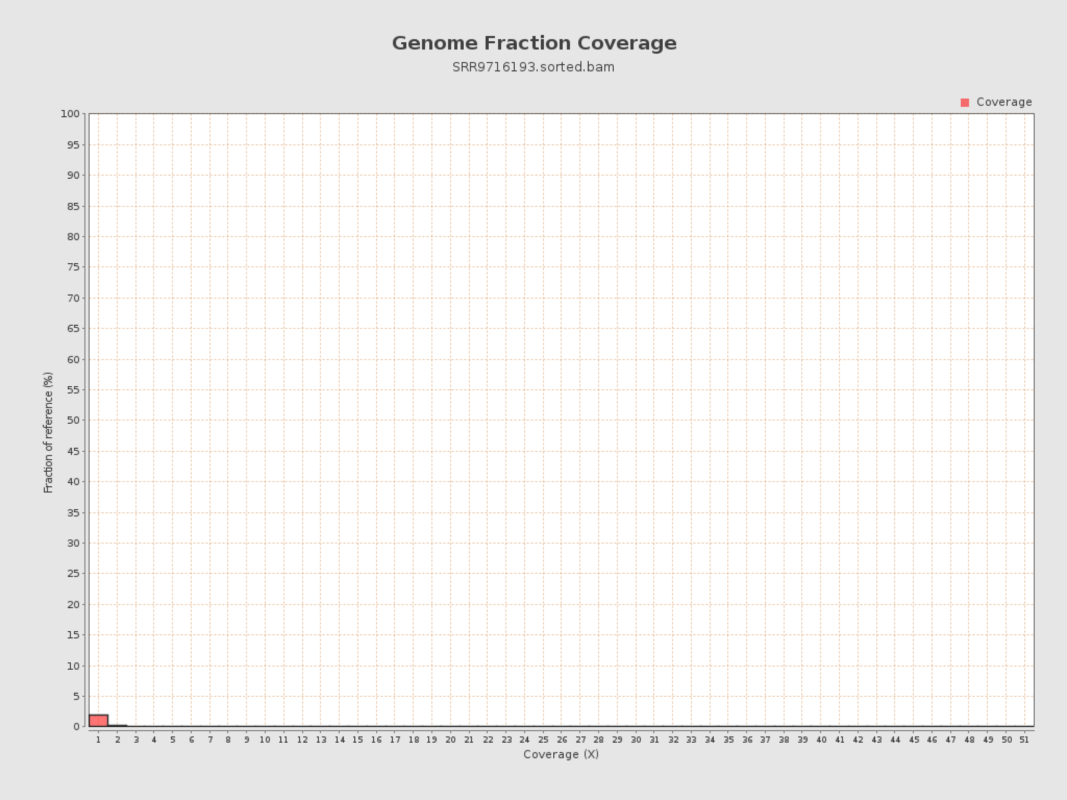
4. Results : Coverage Histogram



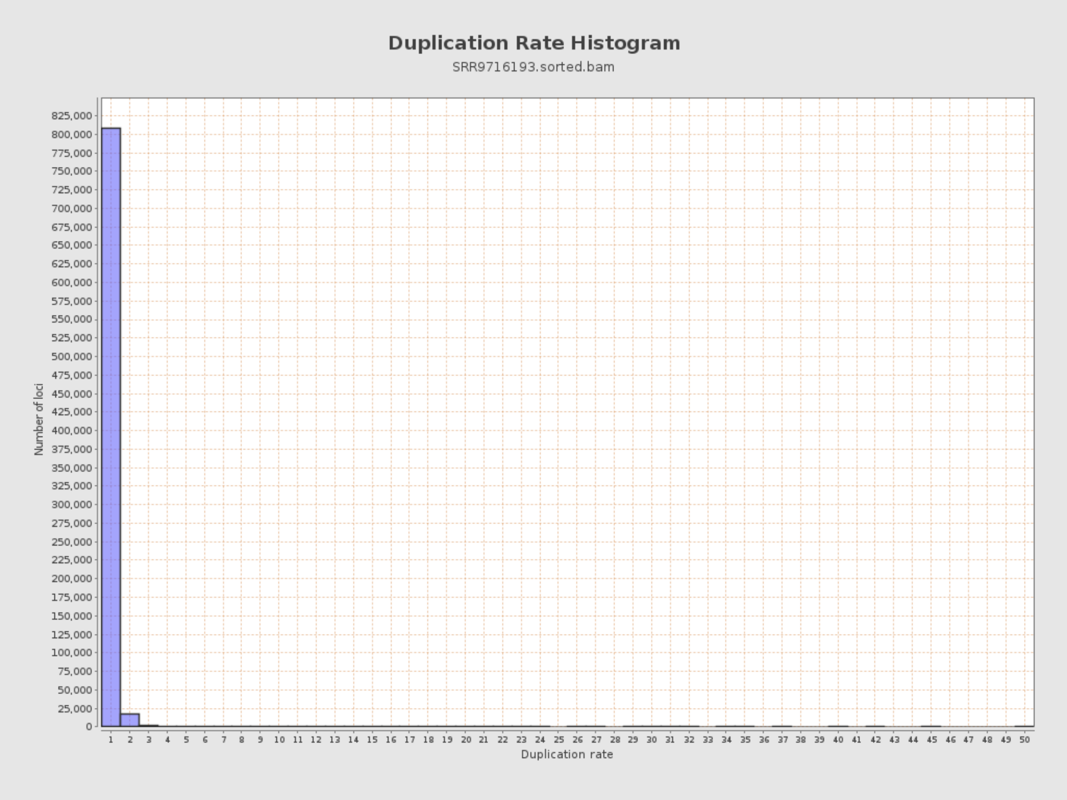
5. Results : Coverage Histogram (0-50X)



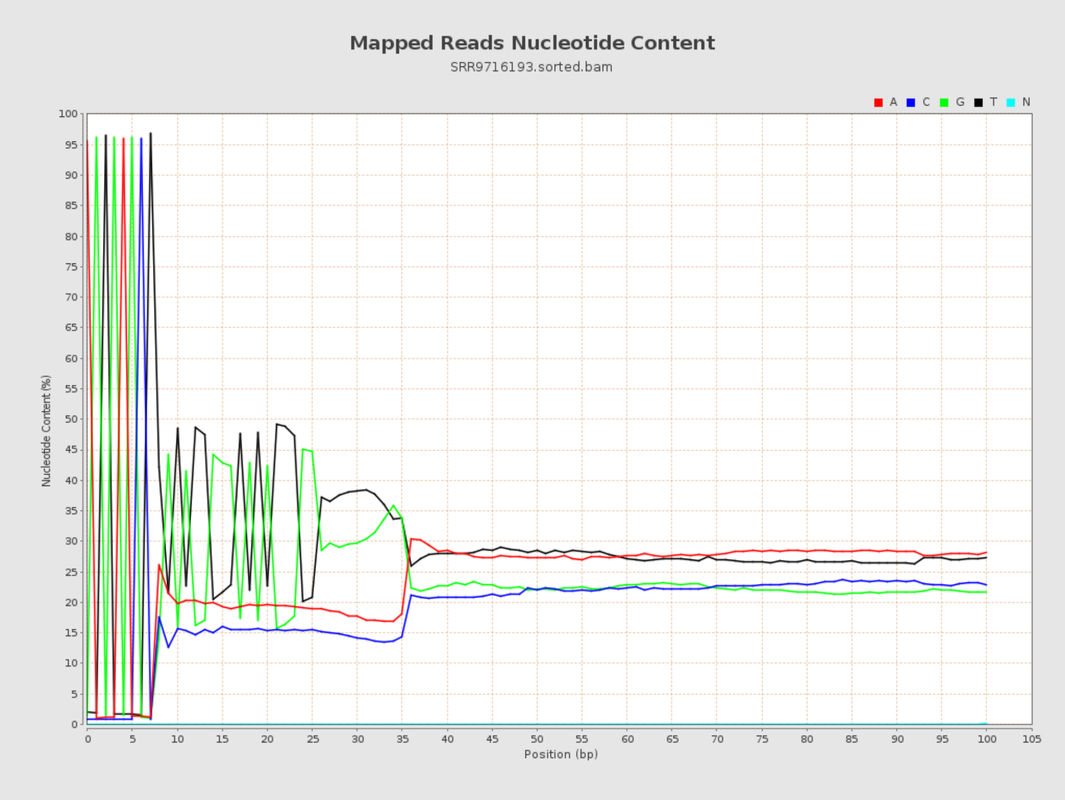
6. Results : Genome Fraction Coverage



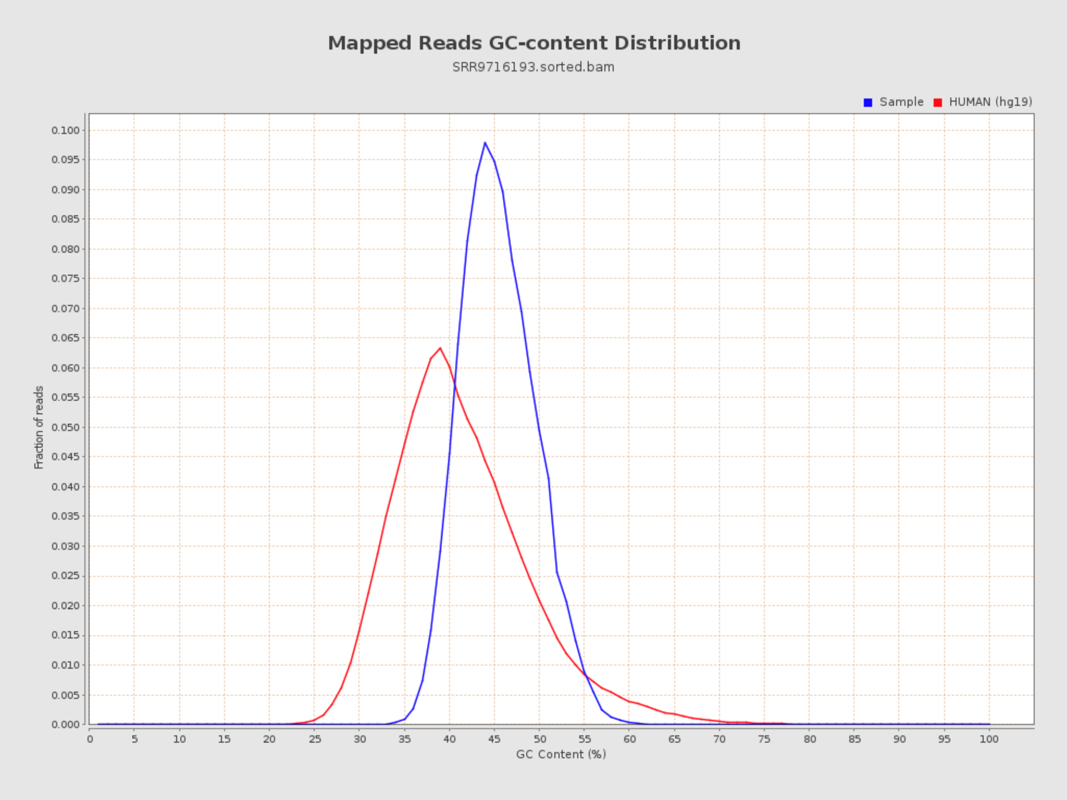
7. Results : Duplication Rate Histogram



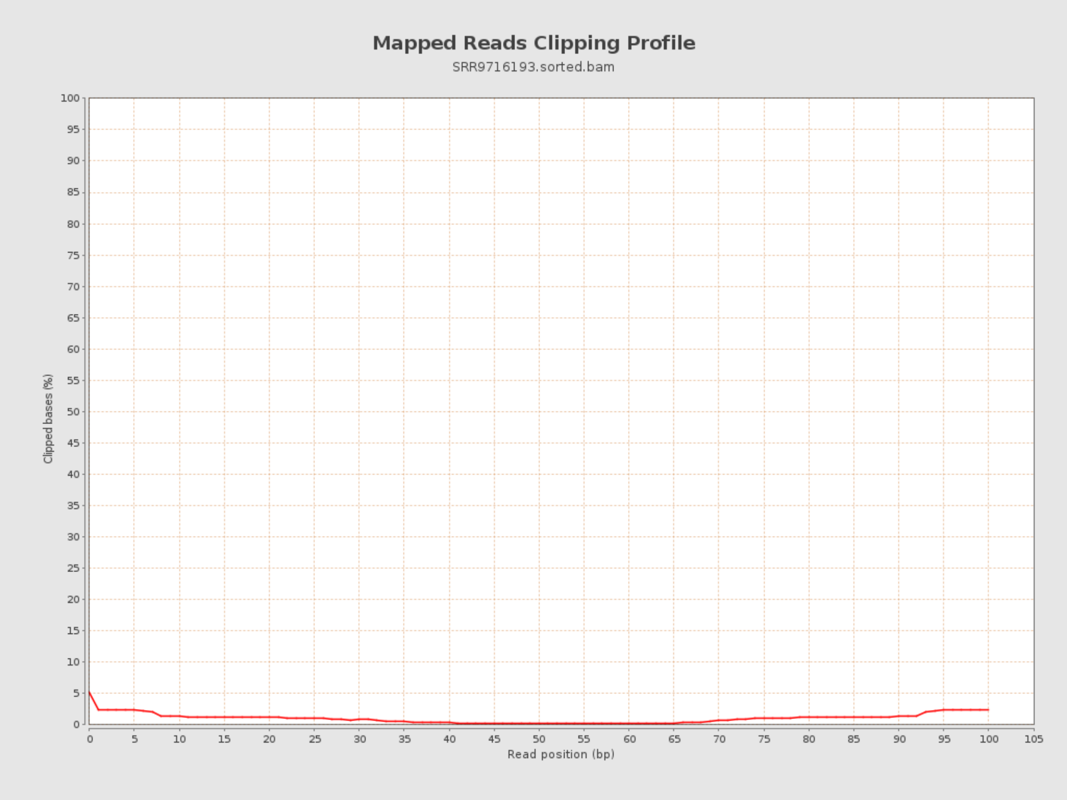
8. Results : Mapped Reads Nucleotide Content



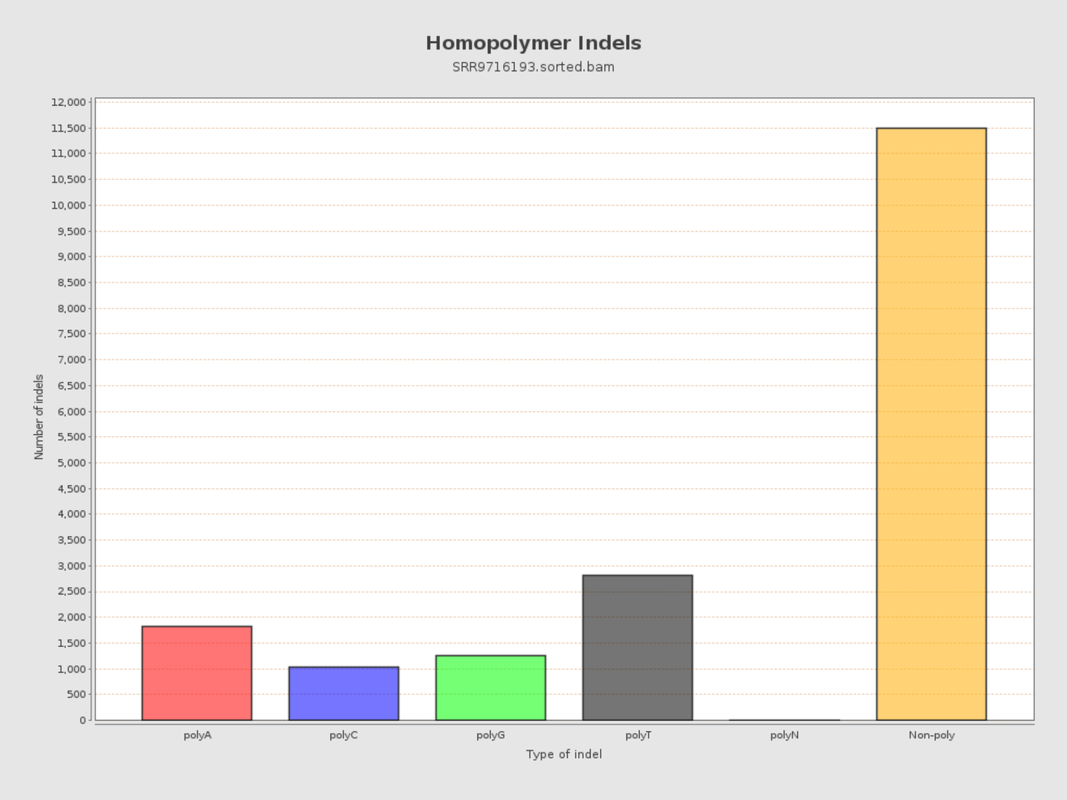
9. Results : Mapped Reads GC-content Distribution



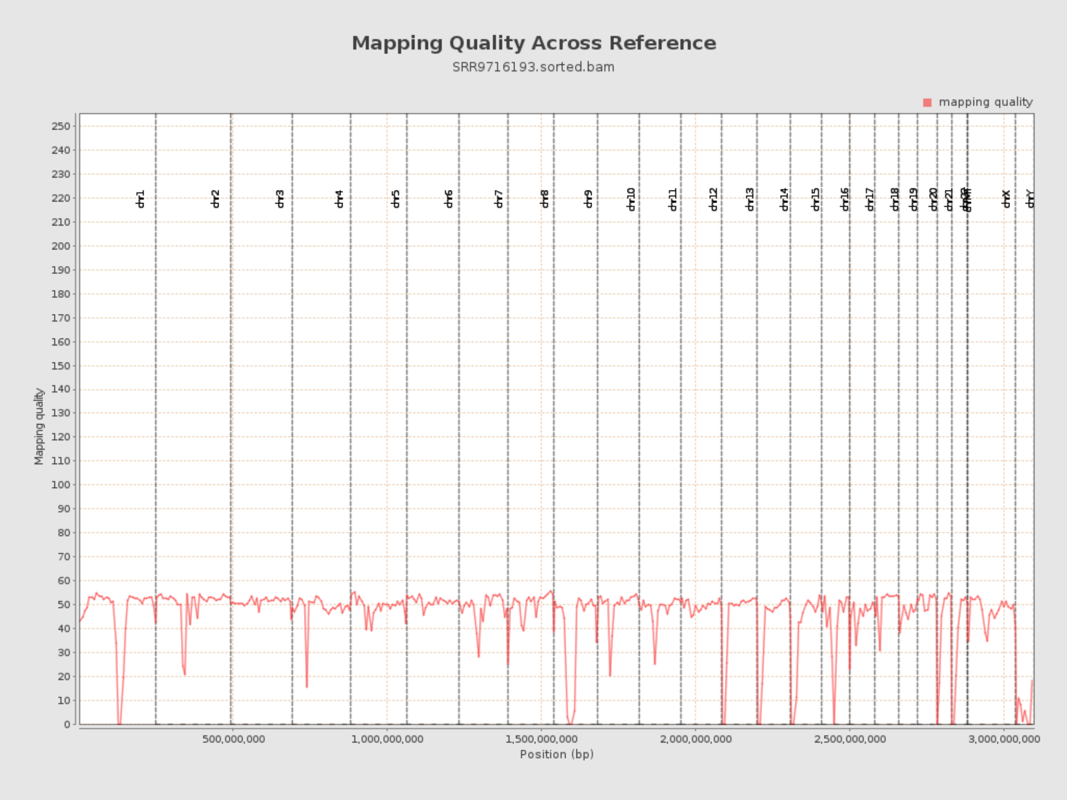
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram