Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:09:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716103.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_SRR9716103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:09:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,299,508
Mapped reads	1,053,327 / 81.06%
Unmapped reads	246,181 / 18.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,362 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	23,022 / 1.77%
Duplication rate	1.57%
Clipped reads	1,054,188 / 81.12%

2.2. ACGT Content

Number/percentage of A's	13,407,978 / 22.99%
Number/percentage of C's	12,451,497 / 21.35%
Number/percentage of T's	17,159,347 / 29.42%
Number/percentage of G's	15,303,436 / 26.24%
Number/percentage of N's	1,559 / 0%
GC Percentage	47.59%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.1712

2.4. Mapping Quality

Mean Mapping Quality	39.08

2.5. Mismatches and indels

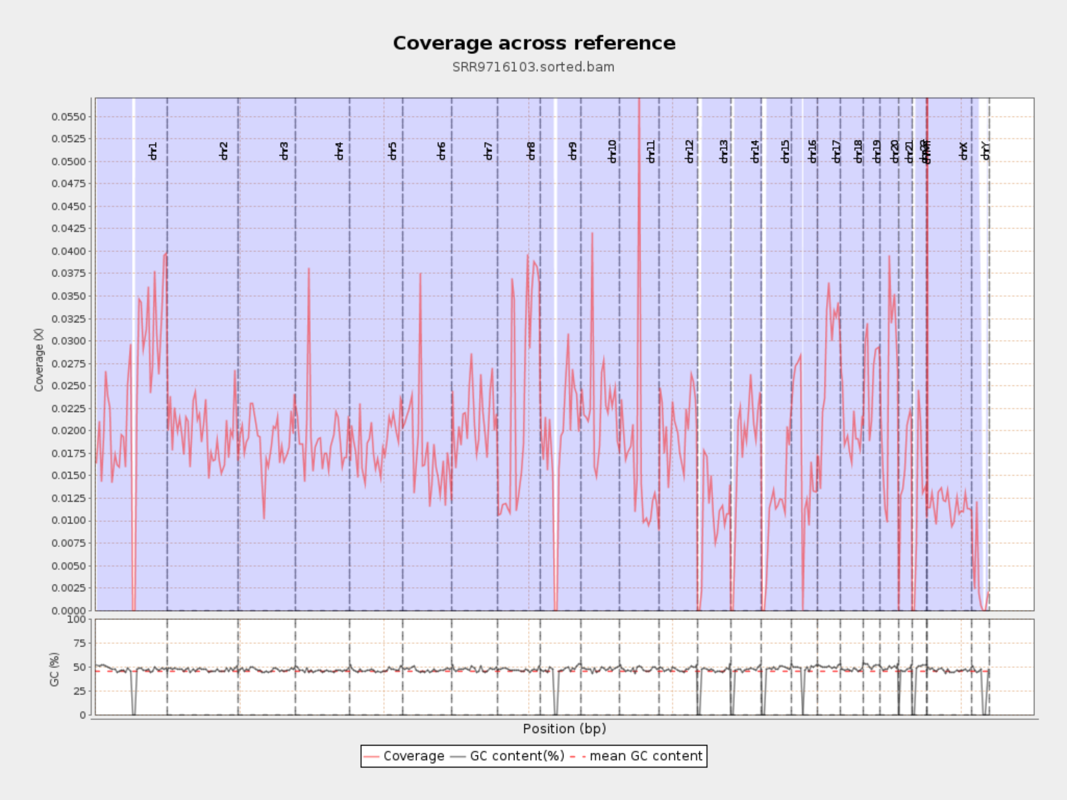
General error rate	0.55%
Mismatches	309,376
Insertions	5,126
Mapped reads with at least one insertion	0.48%
Deletions	9,705
Mapped reads with at least one deletion	0.91%
Homopolymer indels	33.39%

2.6. Chromosome stats

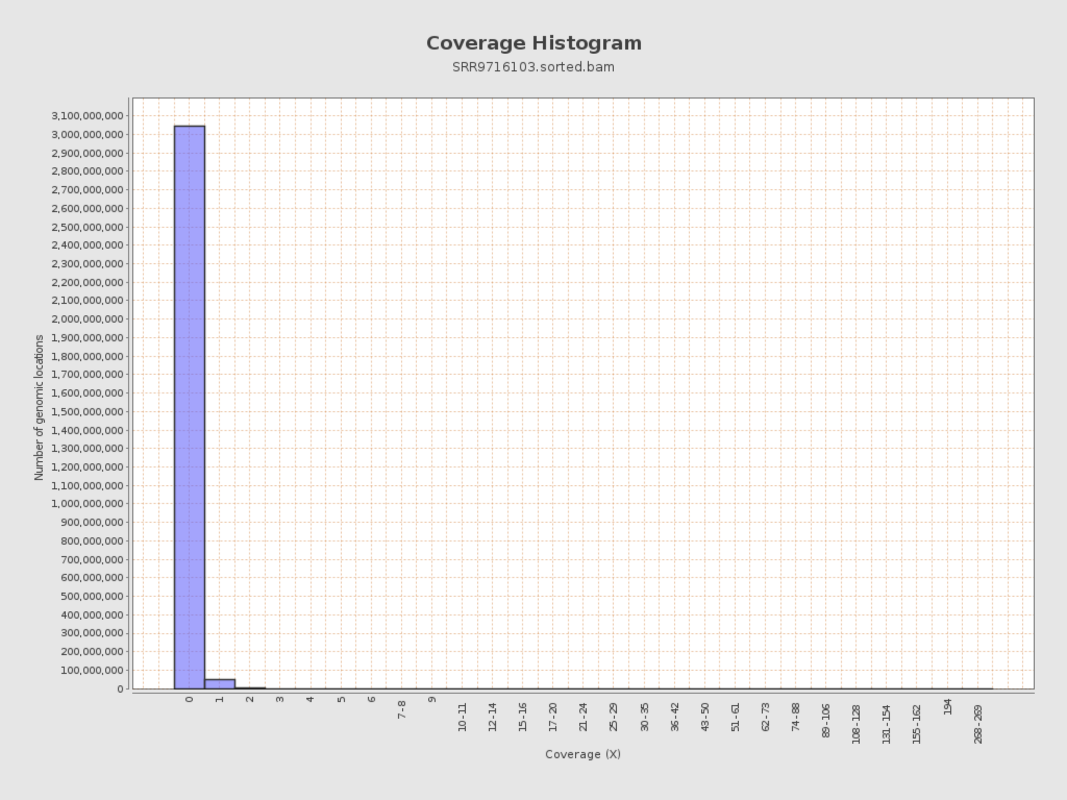
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5970009	0.024	0.2039
chr2	243199373	4805419	0.0198	0.2081
chr3	198022430	3713720	0.0188	0.1541
chr4	191154276	3700497	0.0194	0.1727
chr5	180915260	3388554	0.0187	0.1491
chr6	171115067	3058200	0.0179	0.1493
chr7	159138663	3411730	0.0214	0.189

chr8	146364022	3421714	0.0234	0.1751
chr9	141213431	2650262	0.0188	0.1613
chr10	135534747	3105038	0.0229	0.2422
chr11	135006516	2329648	0.0173	0.1713
chr12	133851895	2738616	0.0205	0.1561
chr13	115169878	1146552	0.01	0.1082
chr14	107349540	1897410	0.0177	0.1473
chr15	102531392	1128150	0.011	0.1155
chr16	90354753	1546943	0.0171	0.1541
chr17	81195210	2260695	0.0278	0.1928
chr18	78077248	1559143	0.02	0.1862
chr19	59128983	1569754	0.0265	0.2106
chr20	63025520	1543290	0.0245	0.1771
chr21	48129895	762653	0.0158	0.1509
chr22	51304566	637897	0.0124	0.1253
chrMT	16571	3851	0.2324	0.5252
chrX	155270560	1810201	0.0117	0.1255
chrY	59373566	180354	0.003	0.1061

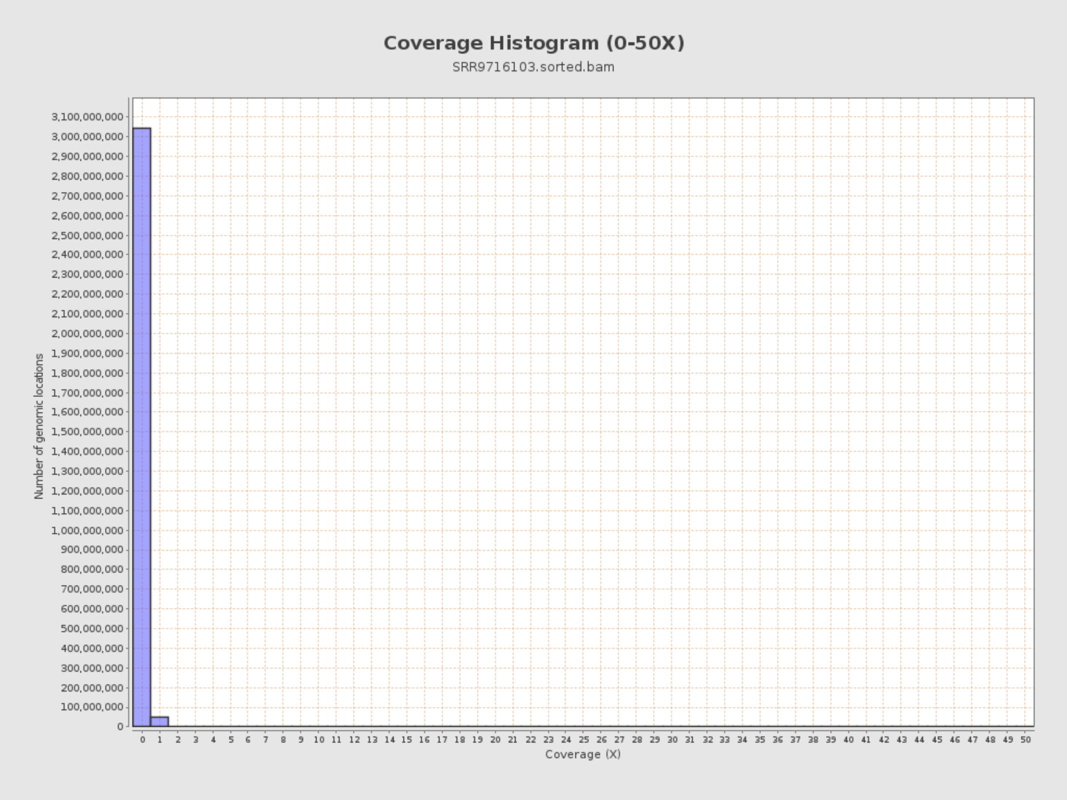
3. Results : Coverage across reference



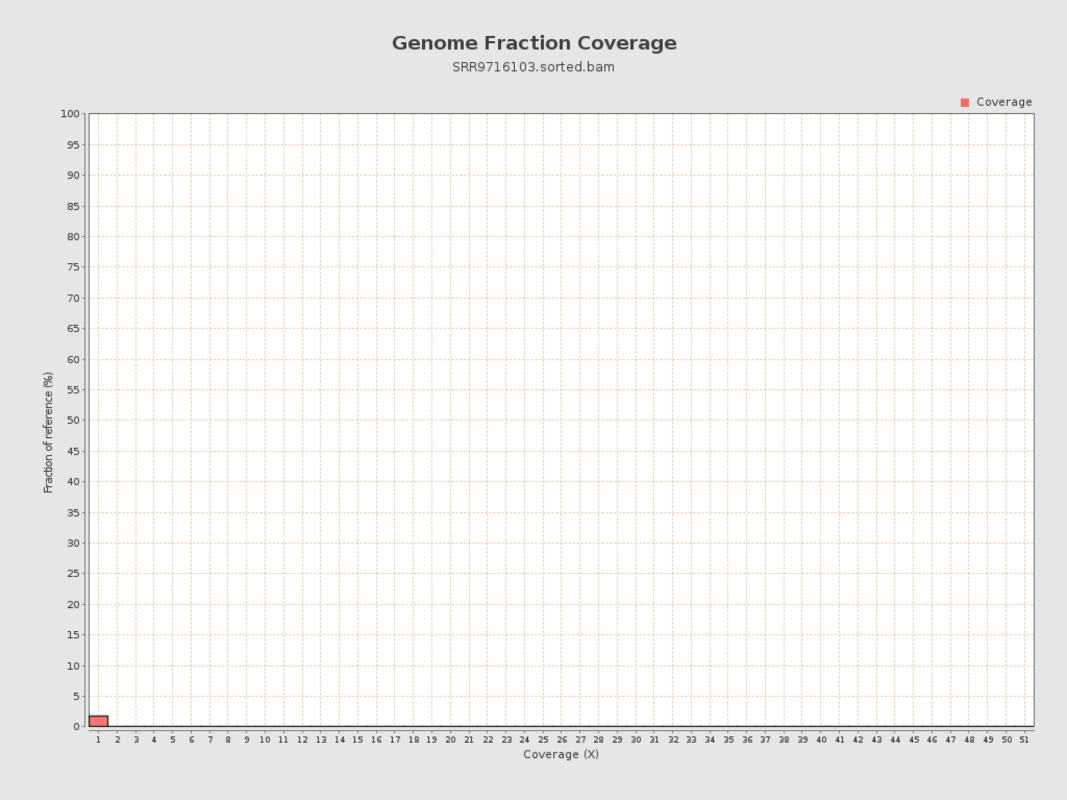
4. Results : Coverage Histogram



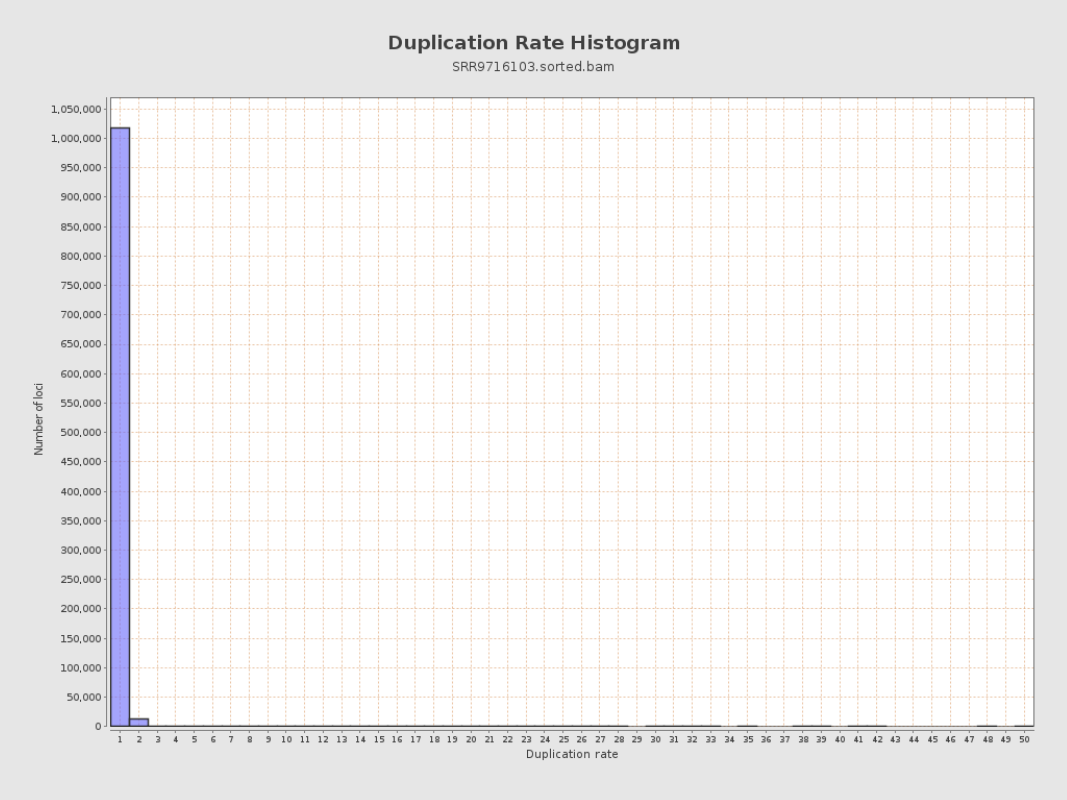
5. Results : Coverage Histogram (0-50X)



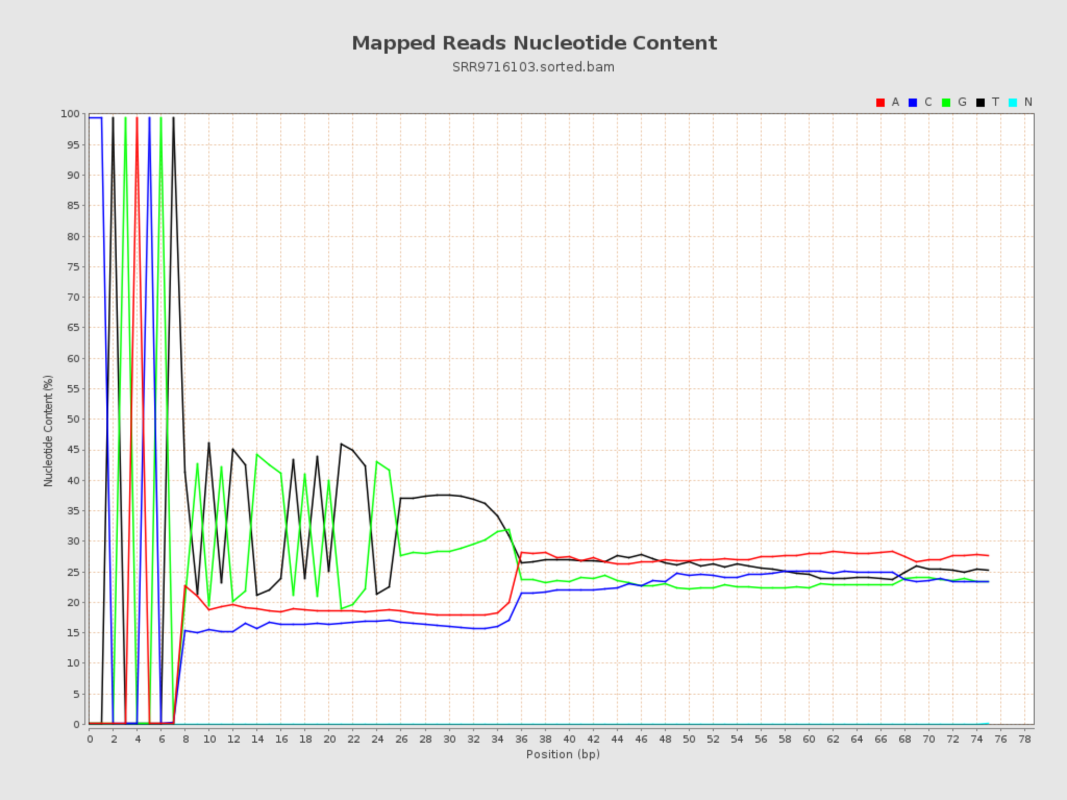
6. Results : Genome Fraction Coverage



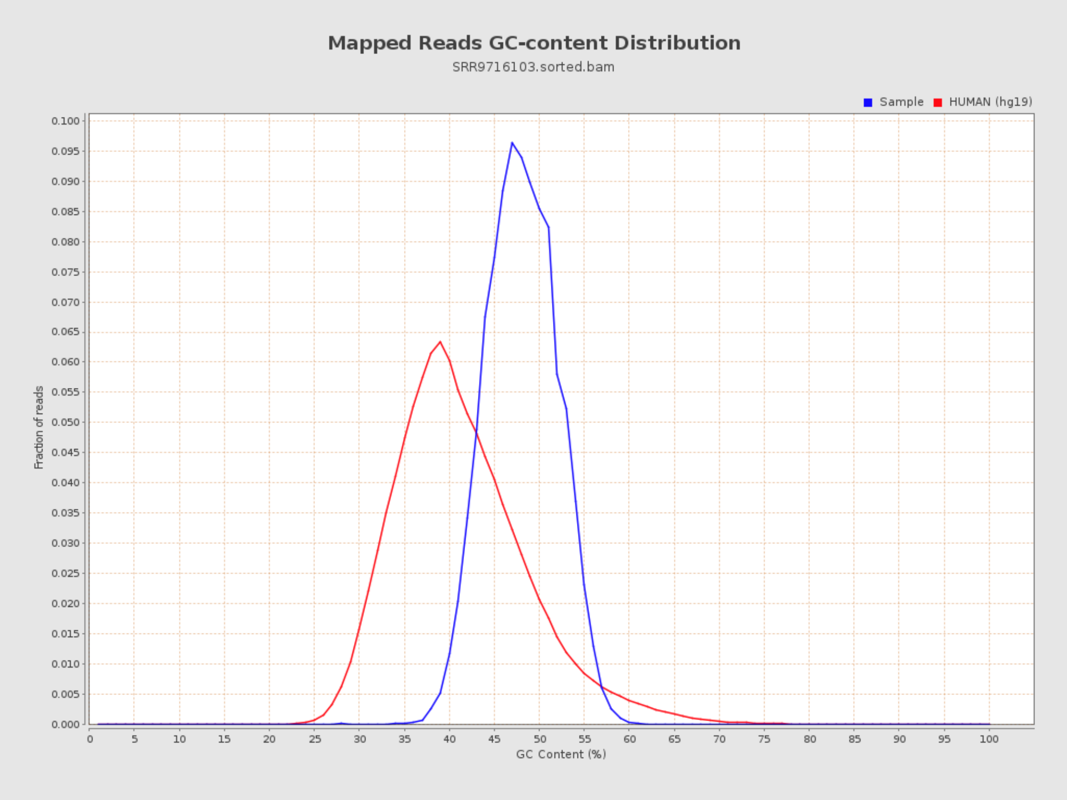
7. Results : Duplication Rate Histogram



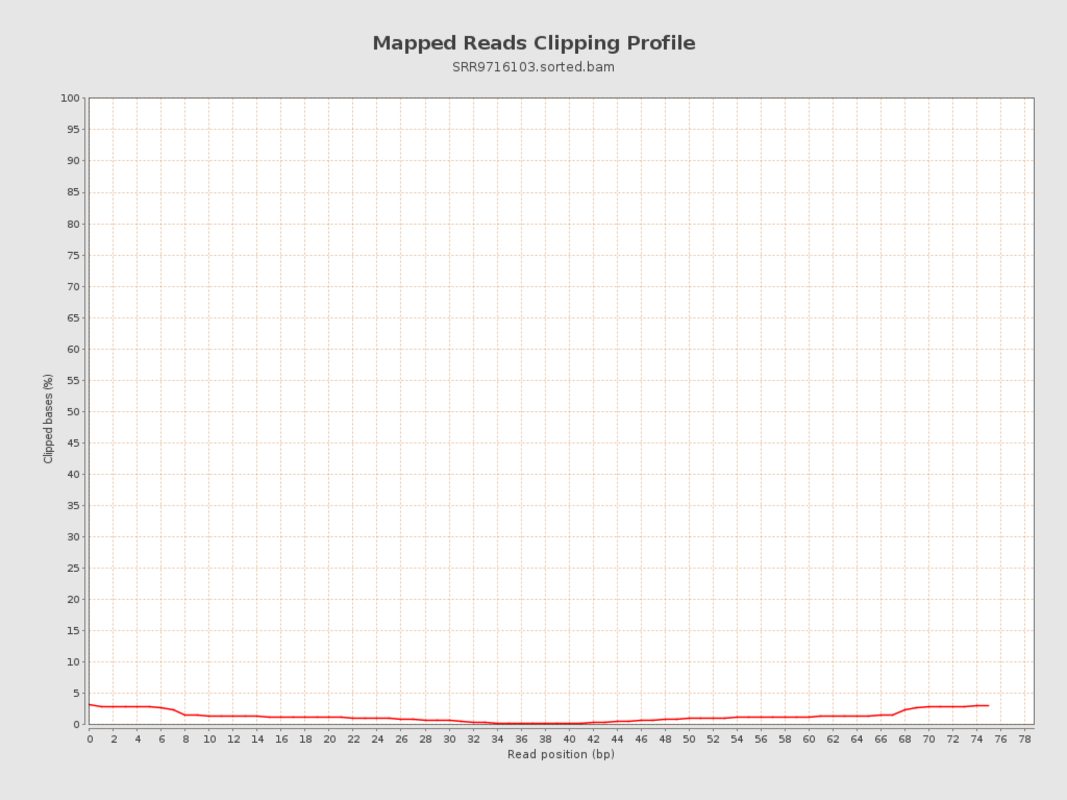
8. Results : Mapped Reads Nucleotide Content



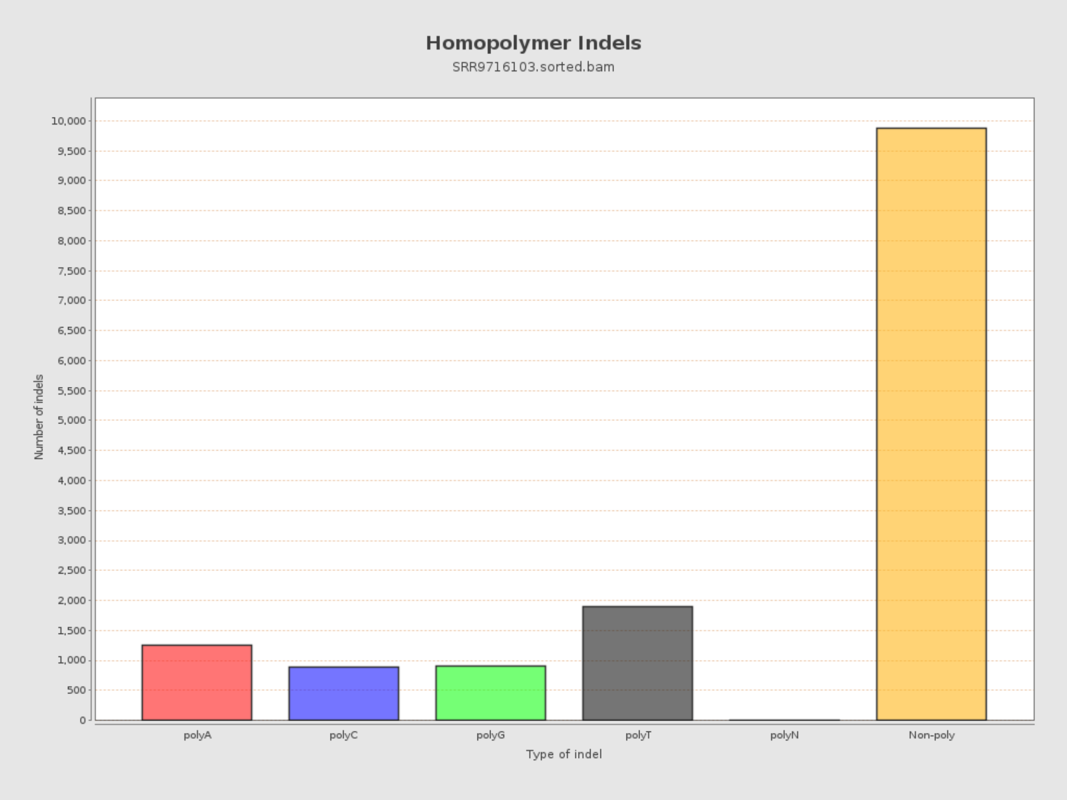
9. Results : Mapped Reads GC-content Distribution



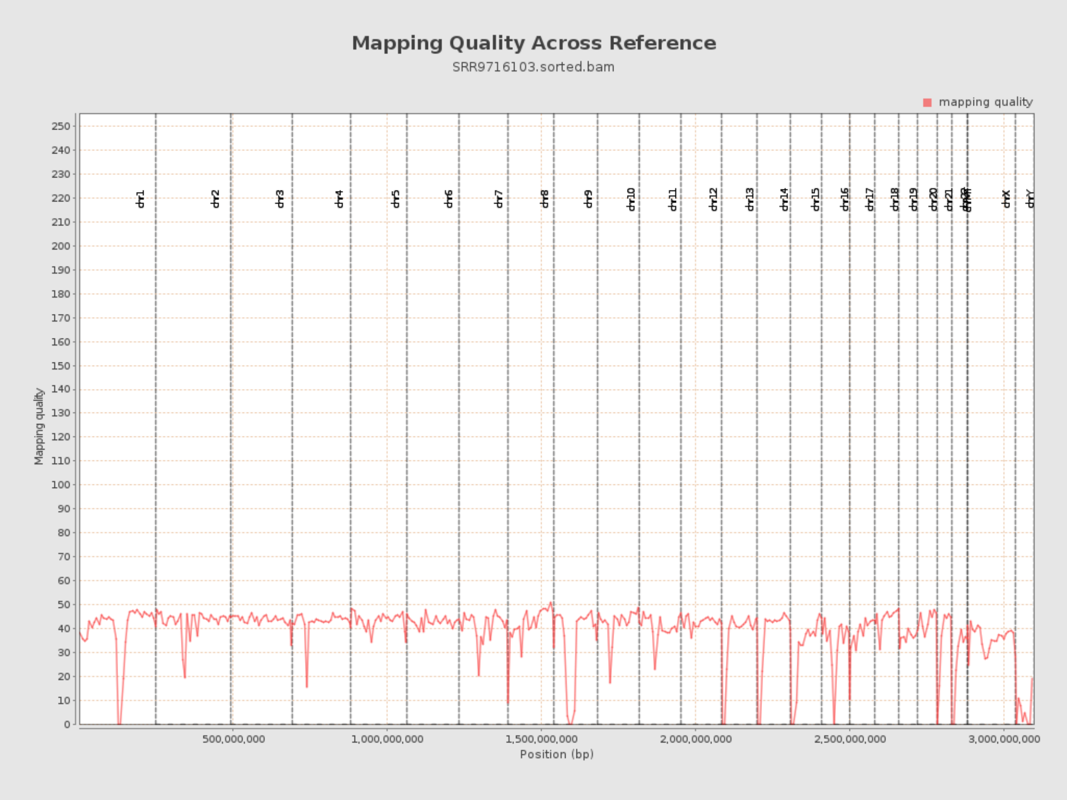
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram