Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:52:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716123.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_SRR9716123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:52:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	888,388
Mapped reads	571,587 / 64.34%
Unmapped reads	316,801 / 35.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,925 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	10,066 / 1.13%
Duplication rate	1.24%
Clipped reads	571,819 / 64.37%

2.2. ACGT Content

Number/percentage of A's	7,586,973 / 23.99%
Number/percentage of C's	6,327,546 / 20.01%
Number/percentage of T's	10,227,568 / 32.34%
Number/percentage of G's	7,482,866 / 23.66%
Number/percentage of N's	555 / 0%
GC Percentage	43.67%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1273

2.4. Mapping Quality

Mean Mapping Quality	40.98

2.5. Mismatches and indels

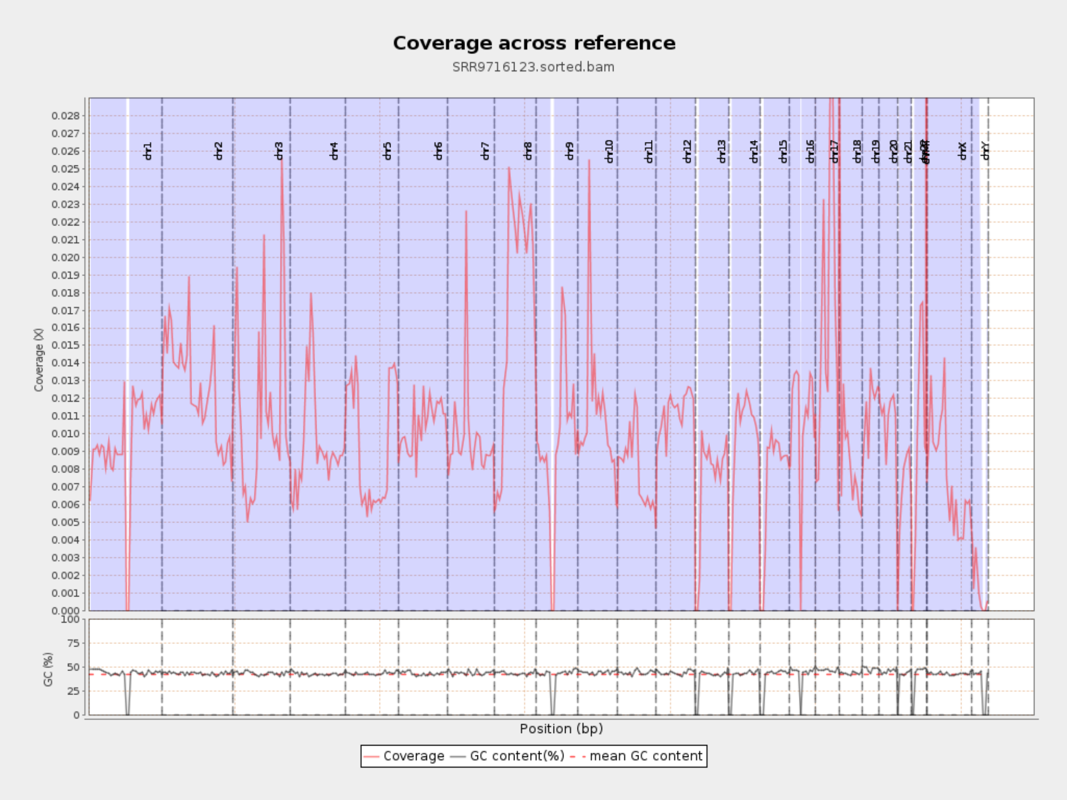
General error rate	0.54%
Mismatches	168,207
Insertions	2,408
Mapped reads with at least one insertion	0.42%
Deletions	6,065
Mapped reads with at least one deletion	1.05%
Homopolymer indels	39.3%

2.6. Chromosome stats

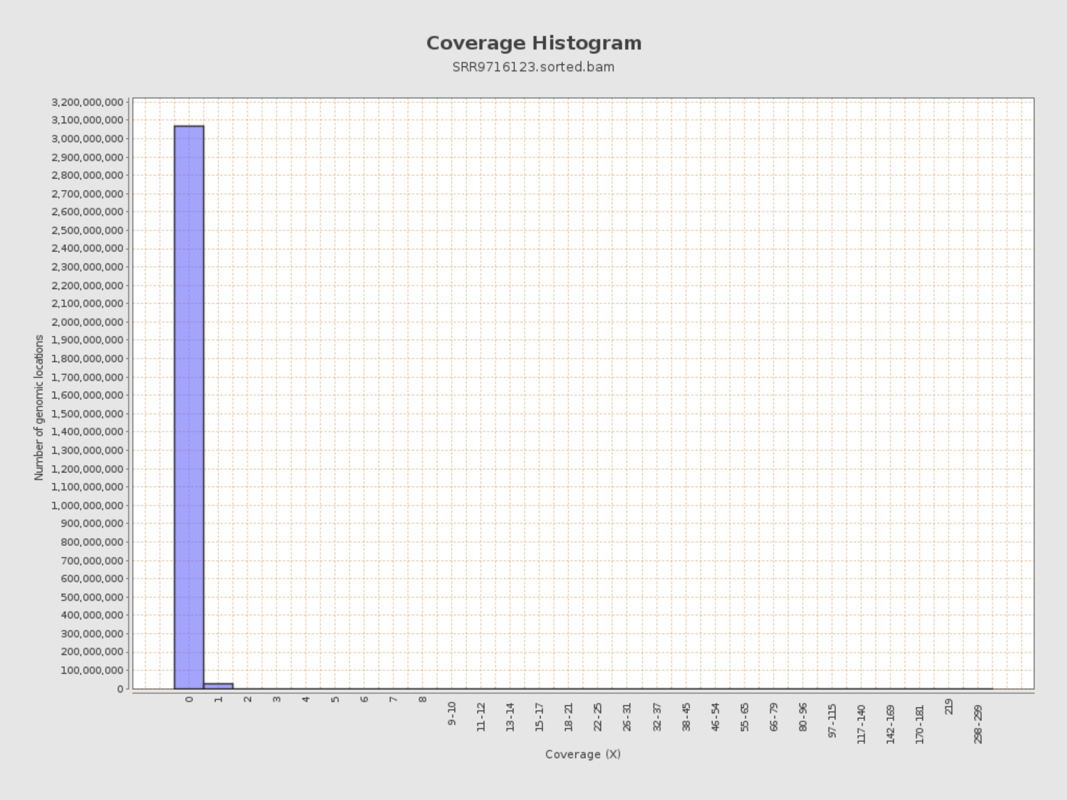
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2354411	0.0094	0.1469
chr2	243199373	3075220	0.0126	0.1708
chr3	198022430	2242232	0.0113	0.1121
chr4	191154276	1813701	0.0095	0.1026
chr5	180915260	1695537	0.0094	0.1004
chr6	171115067	1798365	0.0105	0.1118
chr7	159138663	1577092	0.0099	0.2088

chr8	146364022	2575553	0.0176	0.1457
chr9	141213431	1318049	0.0093	0.1079
chr10	135534747	1514893	0.0112	0.1434
chr11	135006516	1073295	0.0079	0.101
chr12	133851895	1502247	0.0112	0.1113
chr13	115169878	837083	0.0073	0.0885
chr14	107349540	1013152	0.0094	0.1023
chr15	102531392	757975	0.0074	0.0907
chr16	90354753	984613	0.0109	0.1119
chr17	81195210	1361448	0.0168	0.1384
chr18	78077248	717978	0.0092	0.1409
chr19	59128983	676710	0.0114	0.1457
chr20	63025520	683967	0.0109	0.1091
chr21	48129895	320414	0.0067	0.0855
chr22	51304566	466996	0.0091	0.099
chrMT	16571	2289	0.1381	0.3733
chrX	155270560	1201957	0.0077	0.1026
chrY	59373566	69783	0.0012	0.0415

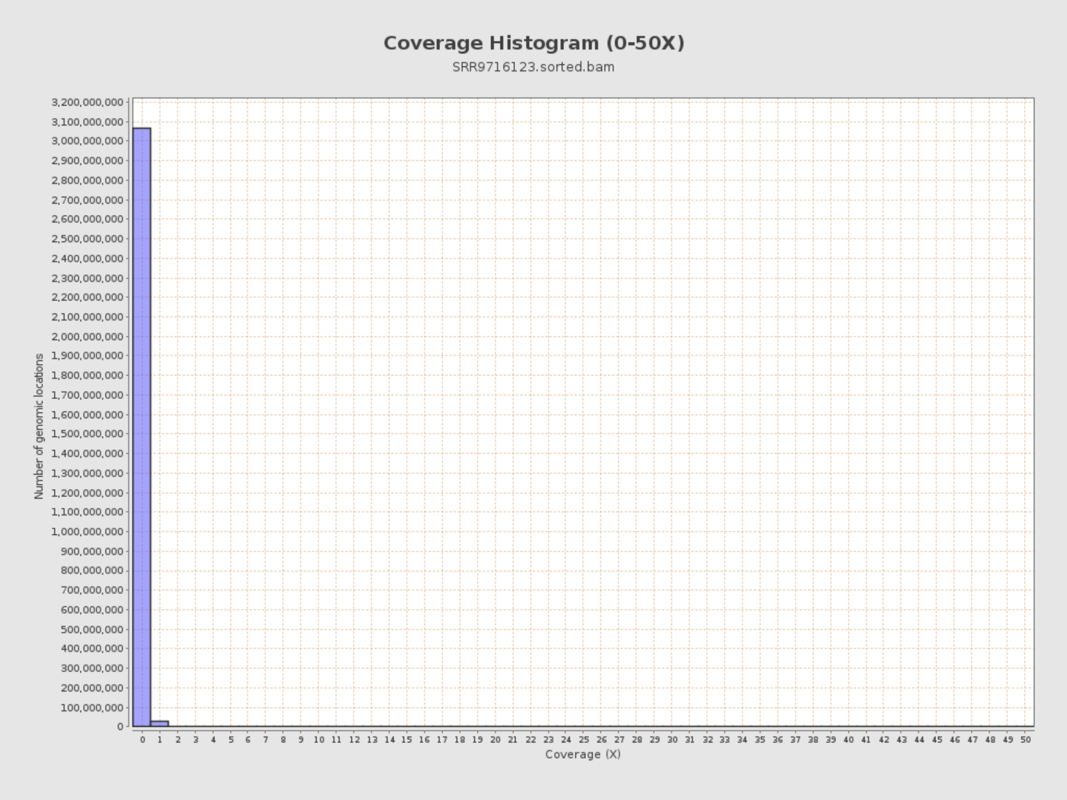
3. Results : Coverage across reference



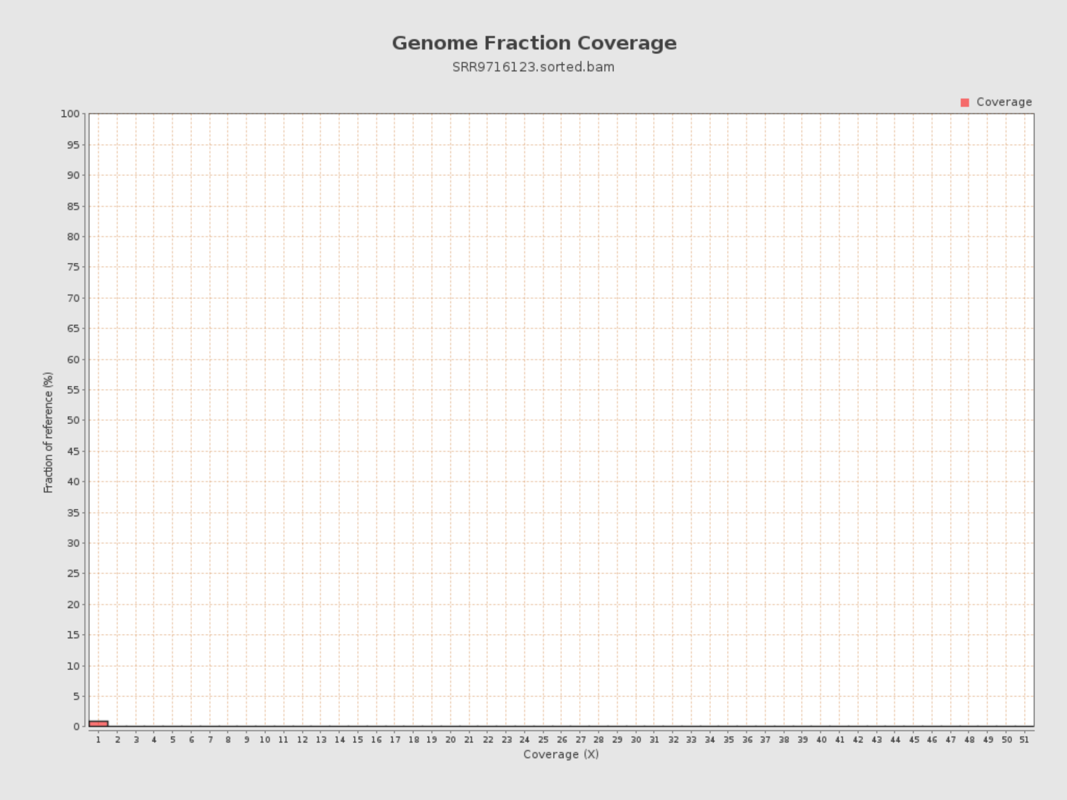
4. Results : Coverage Histogram



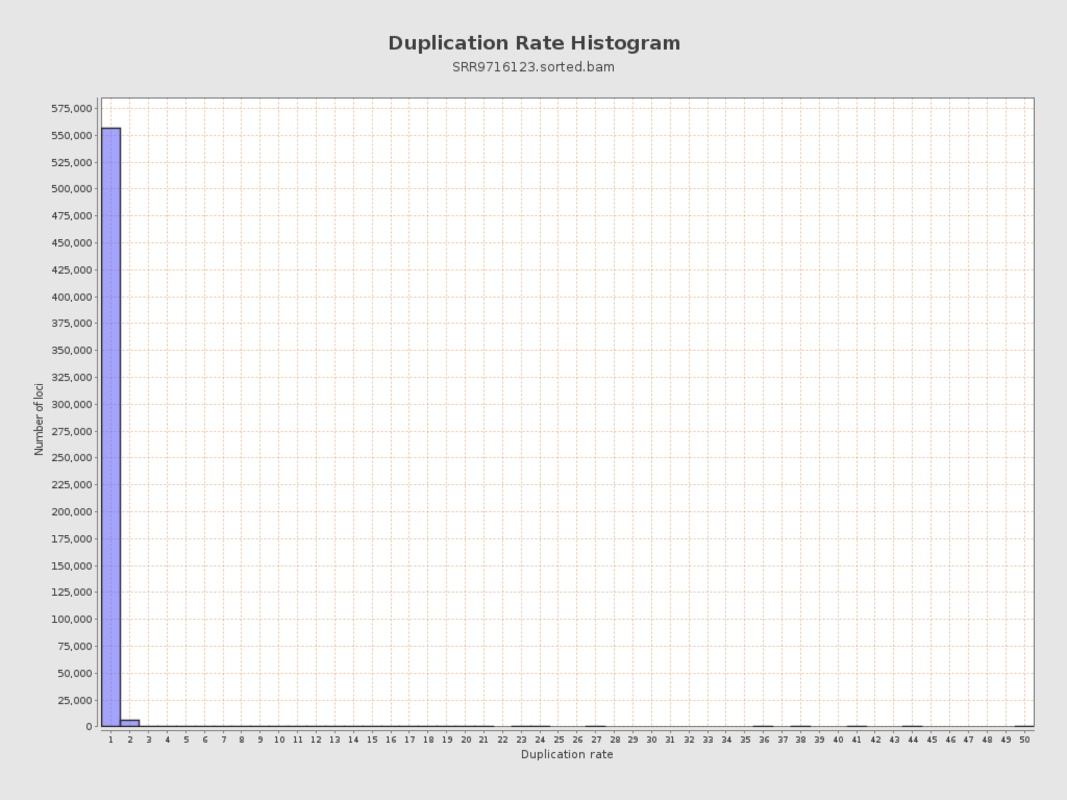
5. Results : Coverage Histogram (0-50X)



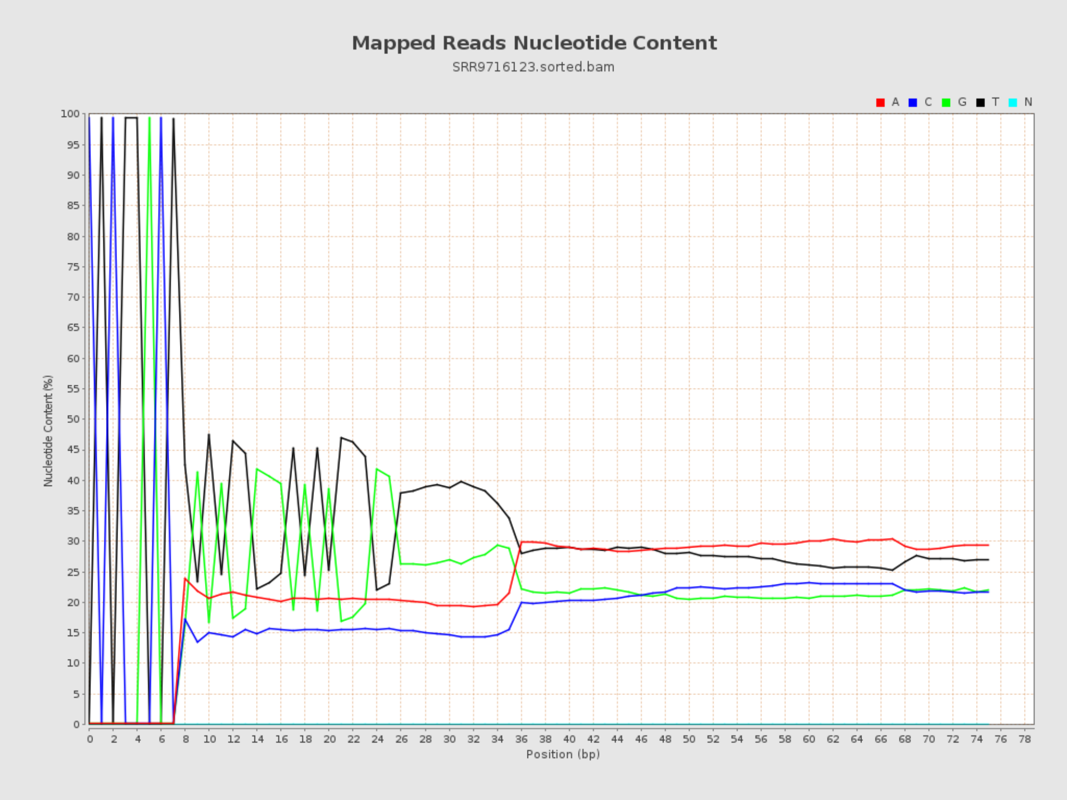
6. Results : Genome Fraction Coverage



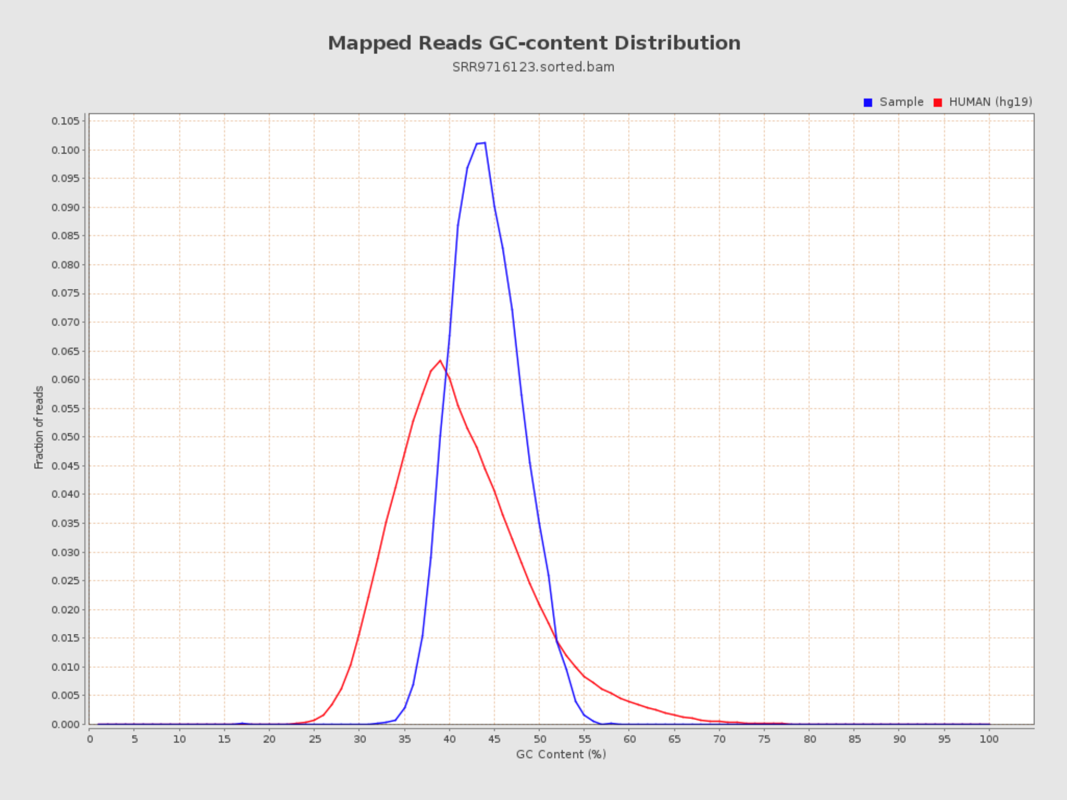
7. Results : Duplication Rate Histogram



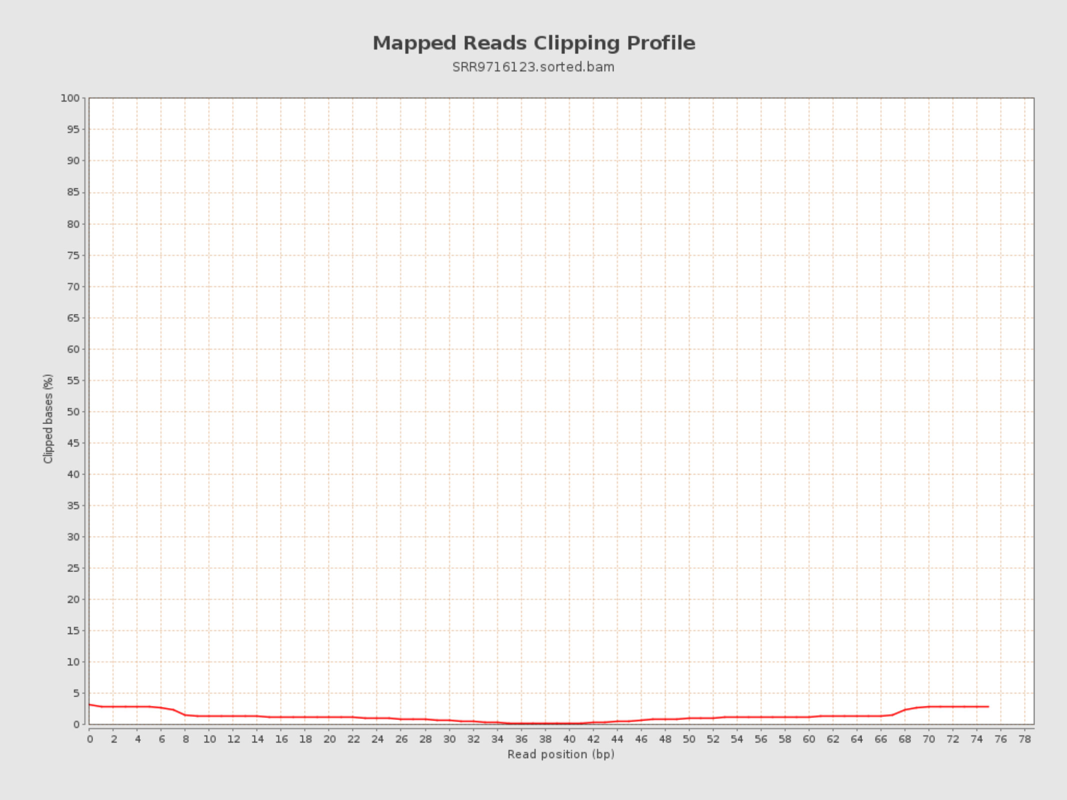
8. Results : Mapped Reads Nucleotide Content



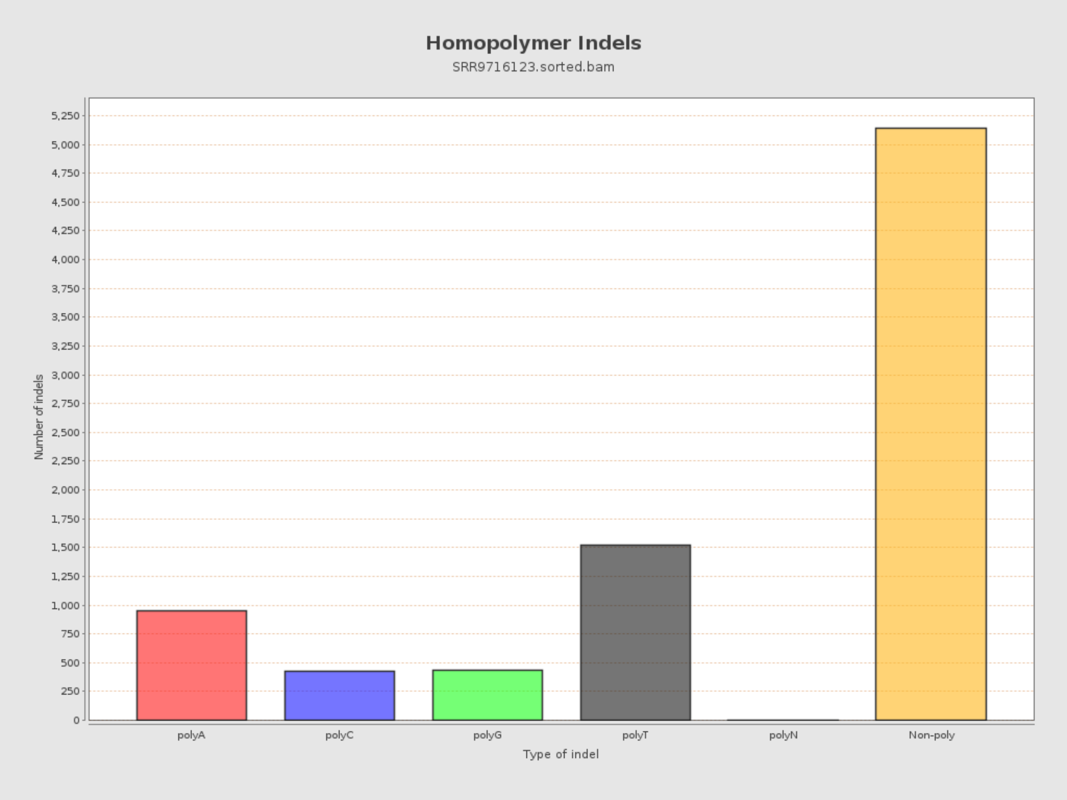
9. Results : Mapped Reads GC-content Distribution



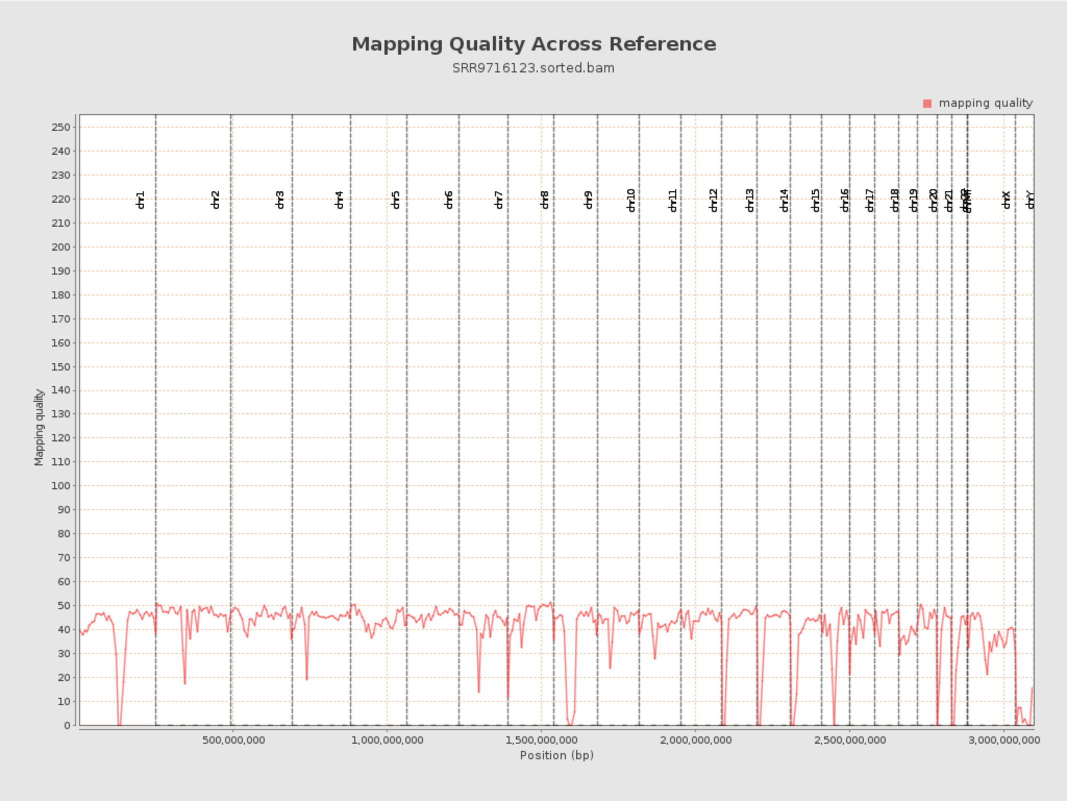
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram