Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:33:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716179.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_SRR9716179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:33:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	572,043
Mapped reads	524,778 / 91.74%
Unmapped reads	47,265 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,864 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	13,458 / 2.35%
Duplication rate	1.9%
Clipped reads	525,998 / 91.95%

2.2. ACGT Content

Number/percentage of A's	7,413,651 / 24.4%
Number/percentage of C's	5,953,620 / 19.6%
Number/percentage of T's	9,511,824 / 31.31%
Number/percentage of G's	7,502,874 / 24.69%
Number/percentage of N's	615 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0098

Standard Deviation	0.1264

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

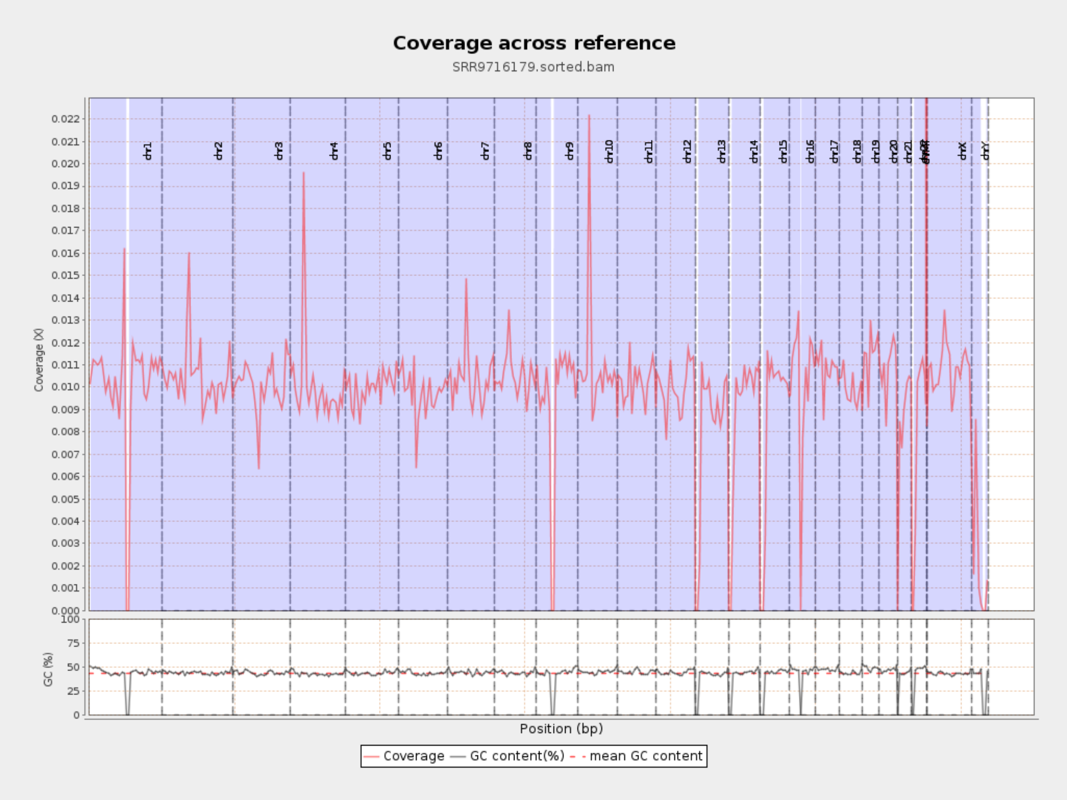
General error rate	0.52%
Mismatches	152,492
Insertions	1,904
Mapped reads with at least one insertion	0.36%
Deletions	5,845
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.64%

2.6. Chromosome stats

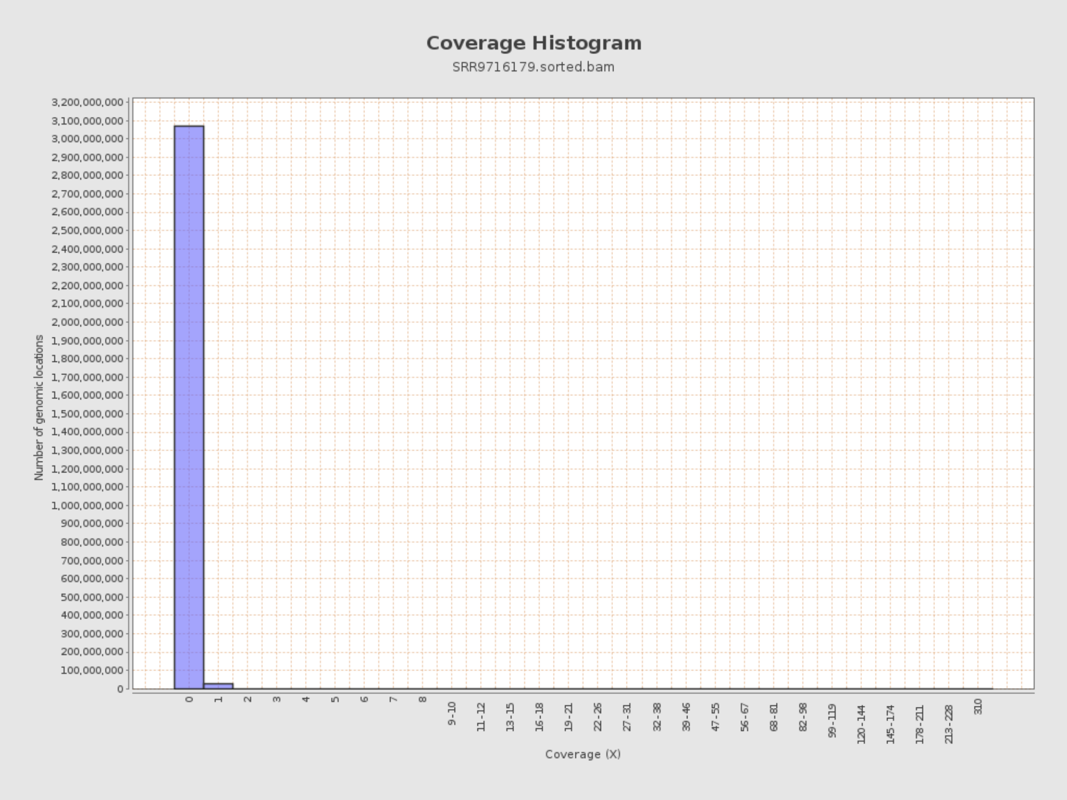
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2510844	0.0101	0.1786
chr2	243199373	2551850	0.0105	0.1672
chr3	198022430	1998297	0.0101	0.1054
chr4	191154276	1914427	0.01	0.1155
chr5	180915260	1807347	0.01	0.1042
chr6	171115067	1671344	0.0098	0.1083
chr7	159138663	1655576	0.0104	0.1362

chr8	146364022	1540040	0.0105	0.1422
chr9	141213431	1309414	0.0093	0.1094
chr10	135534747	1480598	0.0109	0.1409
chr11	135006516	1374840	0.0102	0.1149
chr12	133851895	1338810	0.01	0.1048
chr13	115169878	919546	0.008	0.0932
chr14	107349540	927031	0.0086	0.0986
chr15	102531392	875294	0.0085	0.0962
chr16	90354753	917384	0.0102	0.1085
chr17	81195210	878132	0.0108	0.111
chr18	78077248	777416	0.01	0.1505
chr19	59128983	675387	0.0114	0.151
chr20	63025520	685324	0.0109	0.1092
chr21	48129895	401976	0.0084	0.1051
chr22	51304566	379007	0.0074	0.0897
chrMT	16571	5777	0.3486	0.6256
chrX	155270560	1675022	0.0108	0.1128
chrY	59373566	121470	0.002	0.1006

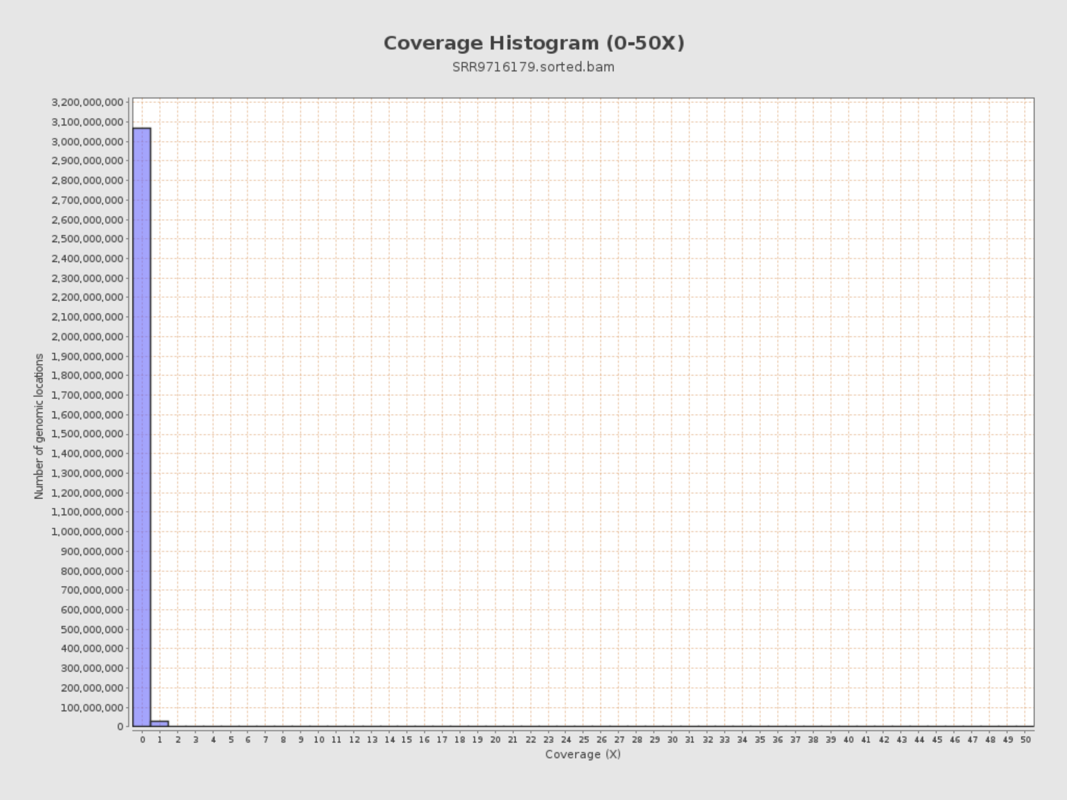
3. Results : Coverage across reference



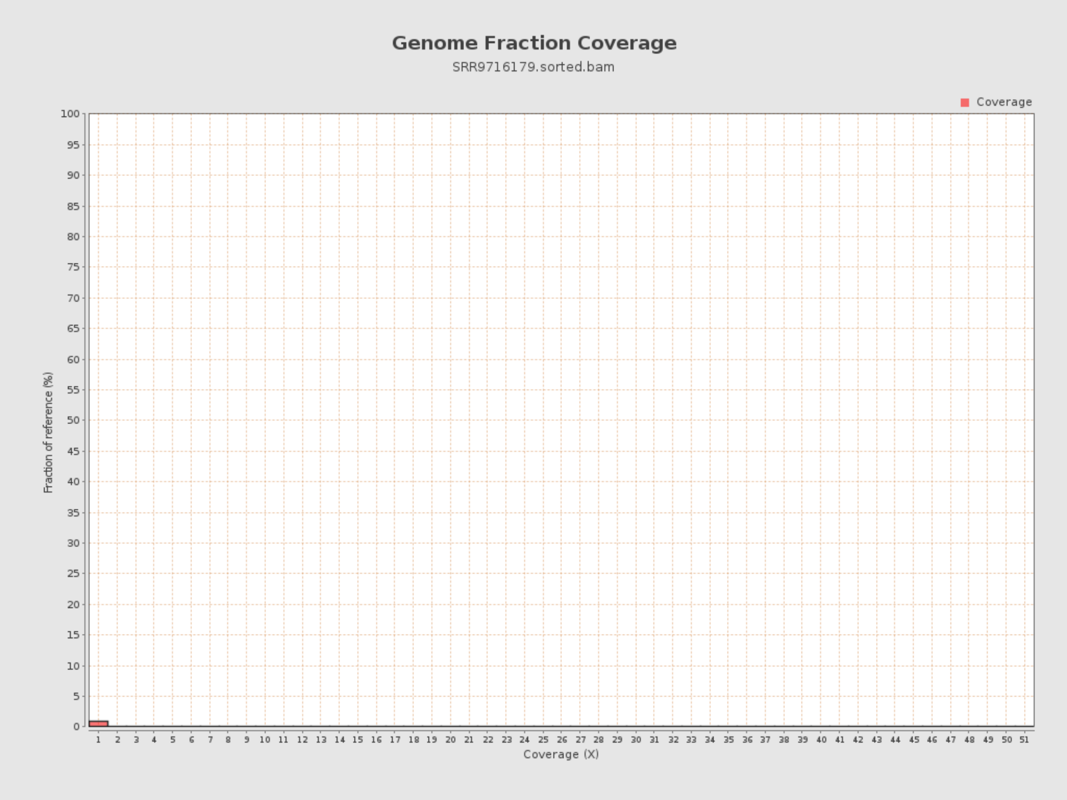
4. Results : Coverage Histogram



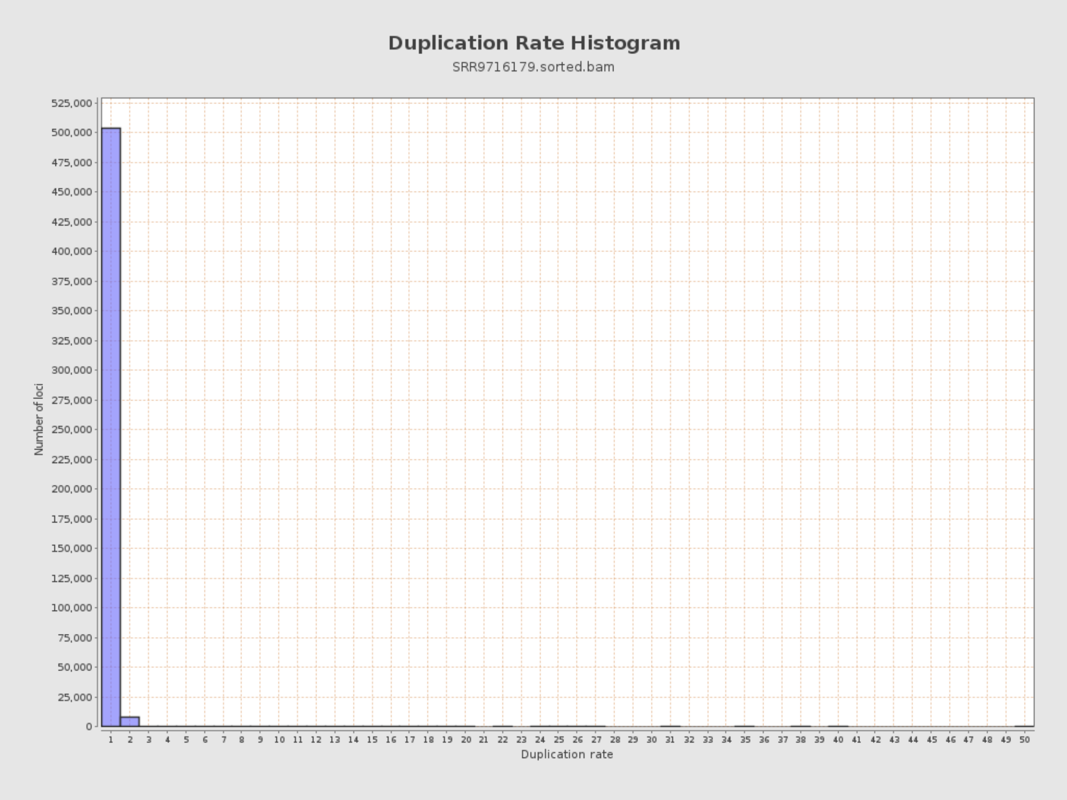
5. Results : Coverage Histogram (0-50X)



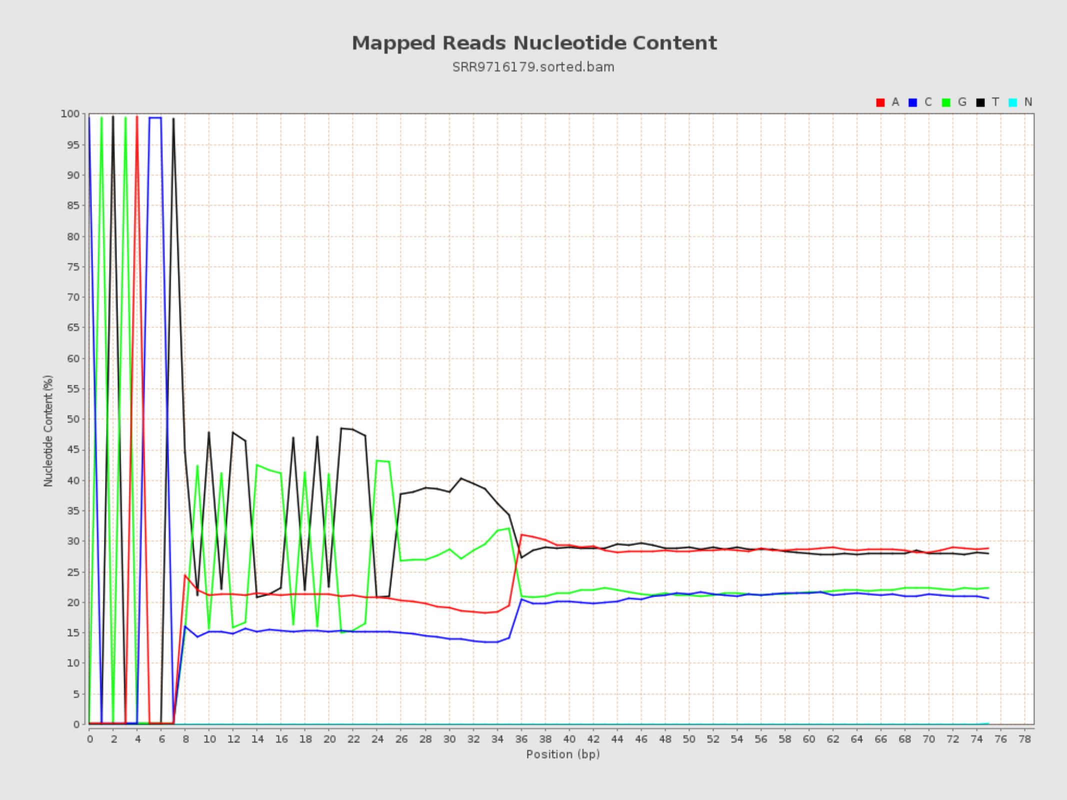
6. Results : Genome Fraction Coverage



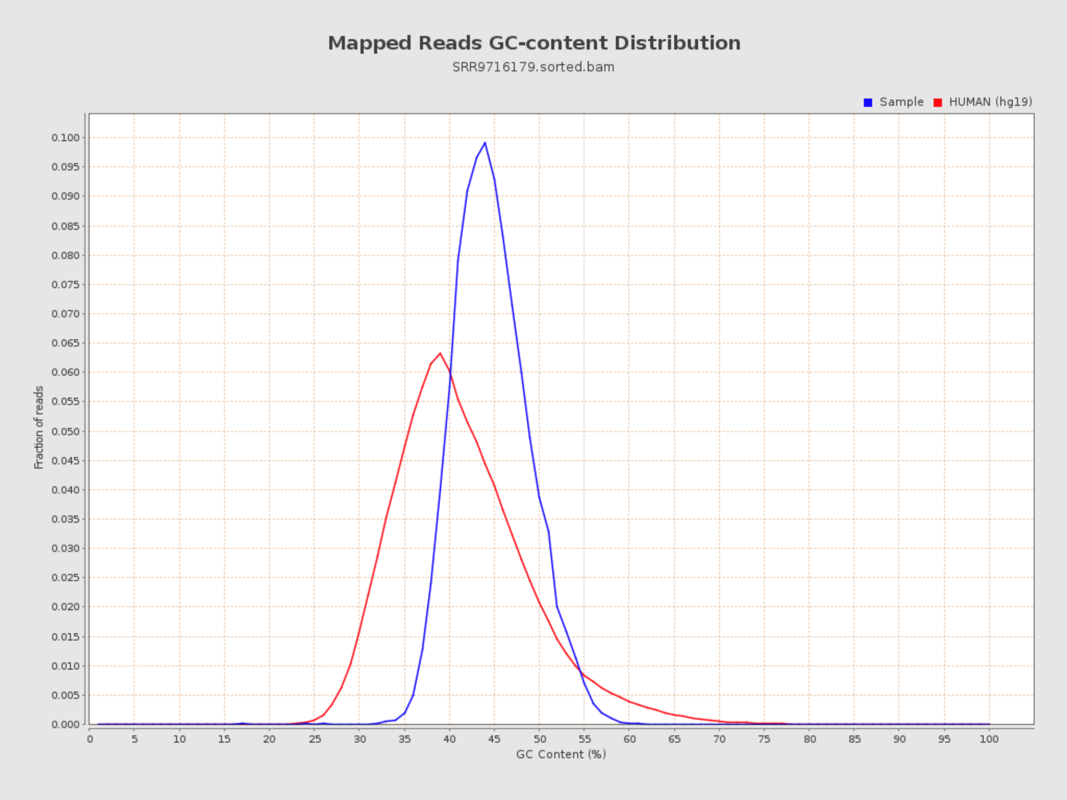
7. Results : Duplication Rate Histogram



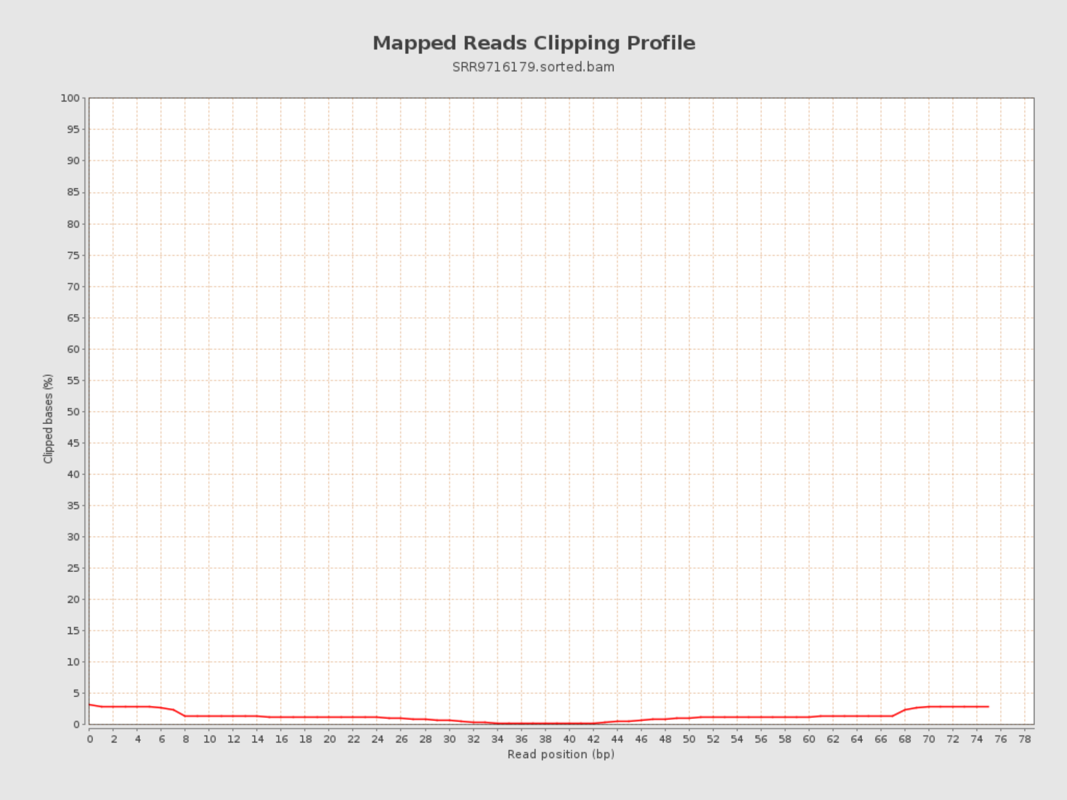
8. Results : Mapped Reads Nucleotide Content



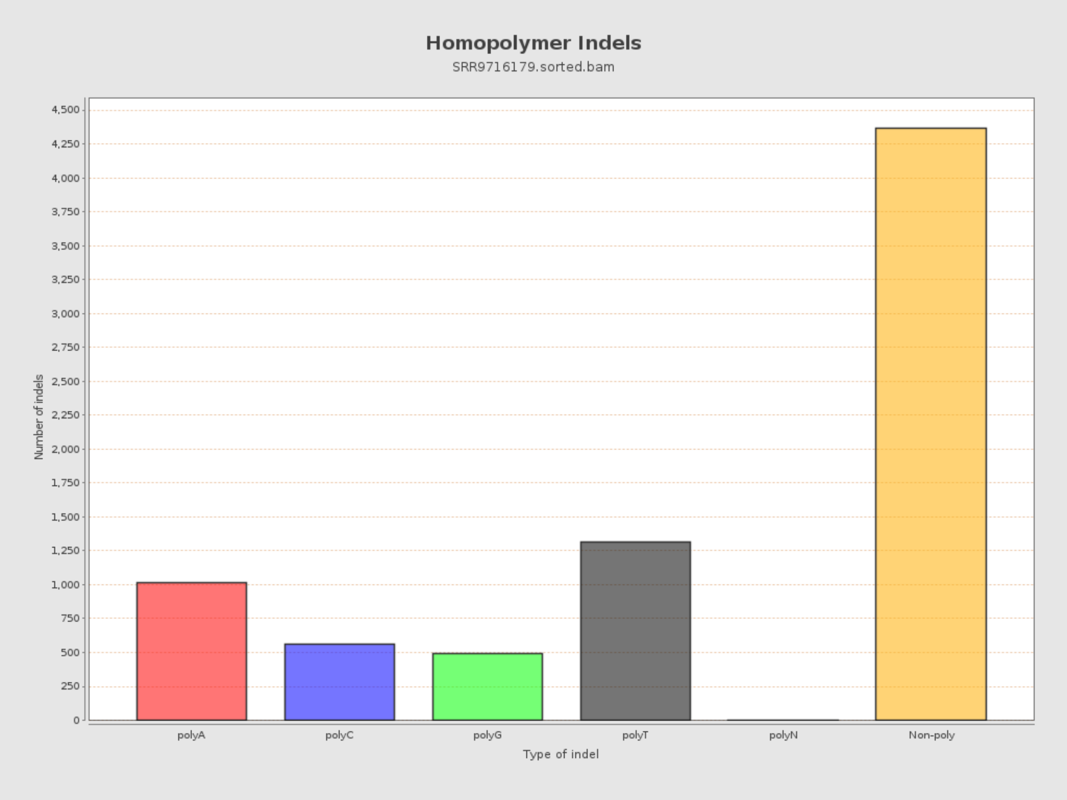
9. Results : Mapped Reads GC-content Distribution



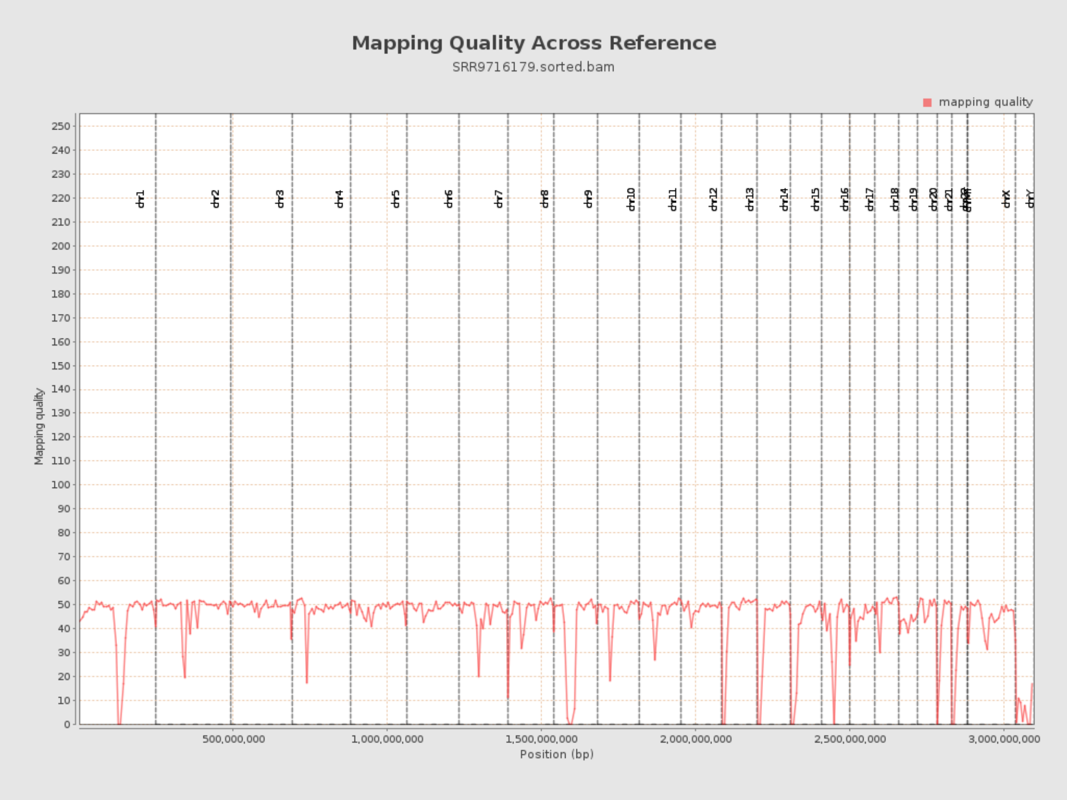
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram