Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:02:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716496.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_SRR9716496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716496.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:02:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,256,426
Mapped reads	1,080,733 / 86.02%
Unmapped reads	175,693 / 13.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,974 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	31,771 / 2.53%
Duplication rate	2.2%
Clipped reads	1,083,016 / 86.2%

2.2. ACGT Content

Number/percentage of A's	15,633,178 / 24.99%
Number/percentage of C's	11,563,838 / 18.49%
Number/percentage of T's	20,210,659 / 32.31%
Number/percentage of G's	15,140,576 / 24.21%
Number/percentage of N's	1,636 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2084

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

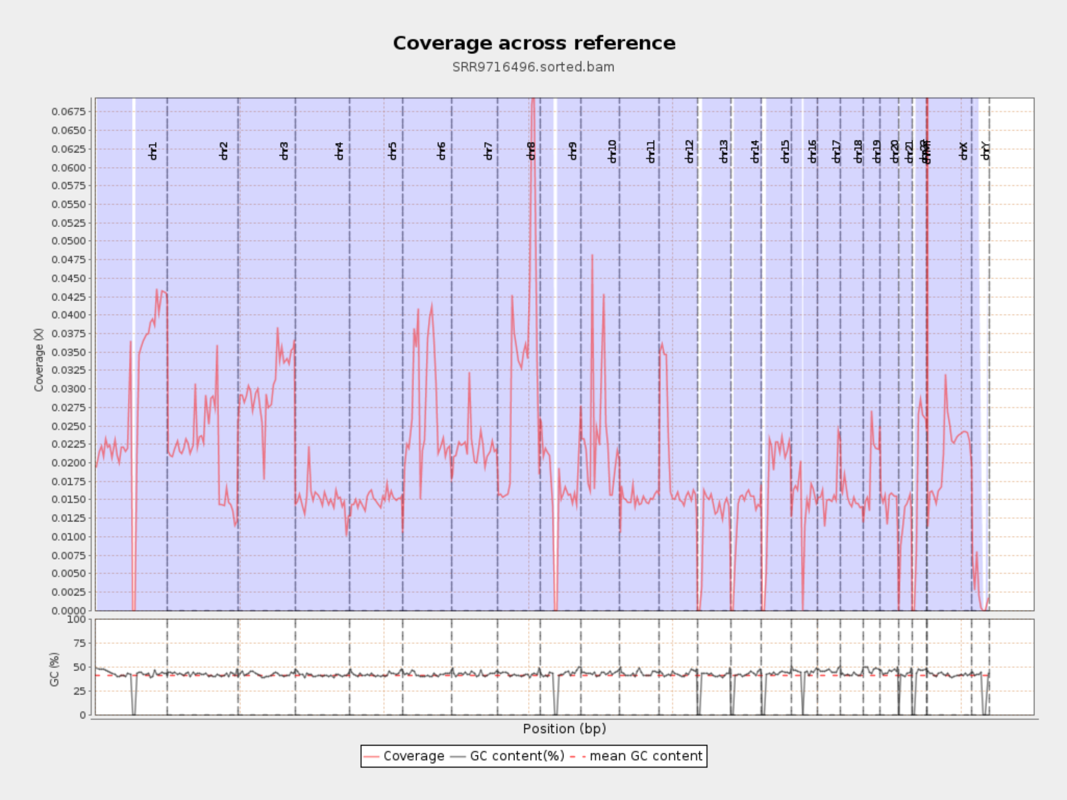
General error rate	0.5%
Mismatches	305,026
Insertions	4,368
Mapped reads with at least one insertion	0.4%
Deletions	11,177
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.05%

2.6. Chromosome stats

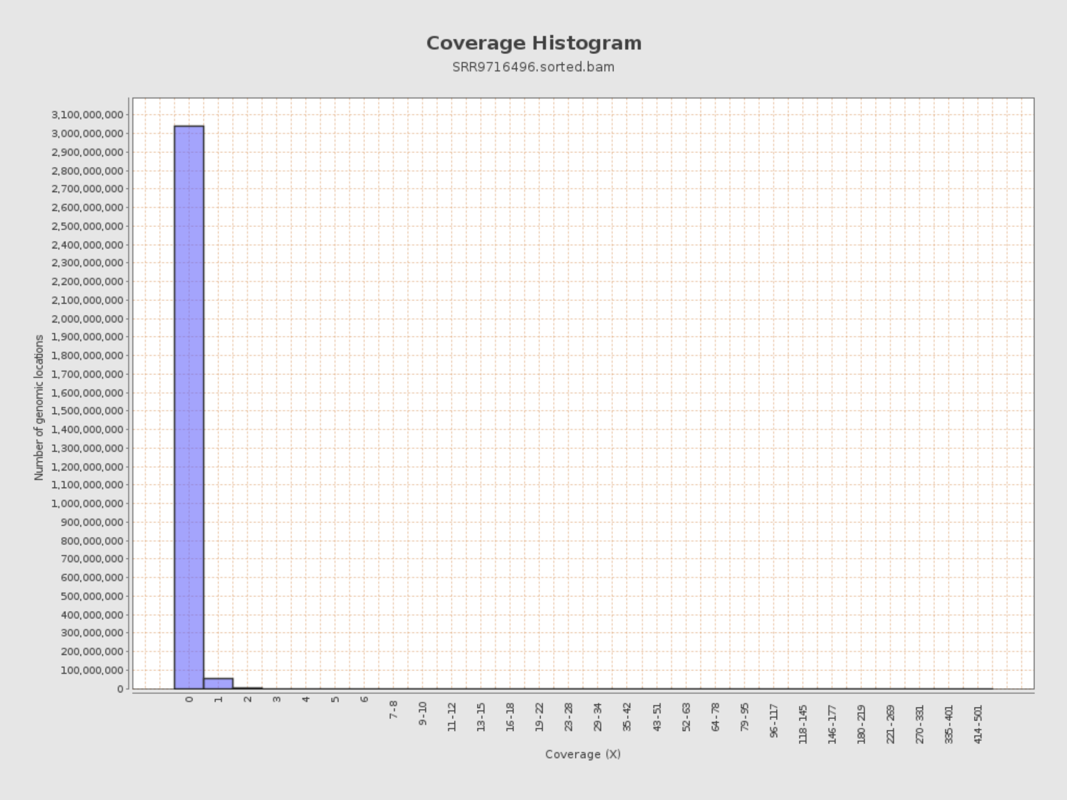
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6990339	0.028	0.3707
chr2	243199373	5243122	0.0216	0.2555
chr3	198022430	6012911	0.0304	0.1872
chr4	191154276	2871406	0.015	0.1378
chr5	180915260	2725984	0.0151	0.1323
chr6	171115067	4617769	0.027	0.2334
chr7	159138663	3534204	0.0222	0.2485

chr8	146364022	4782996	0.0327	0.2116
chr9	141213431	2289196	0.0162	0.1714
chr10	135534747	3251379	0.024	0.2278
chr11	135006516	2038829	0.0151	0.1572
chr12	133851895	2715964	0.0203	0.1553
chr13	115169878	1396186	0.0121	0.1169
chr14	107349540	1350551	0.0126	0.1295
chr15	102531392	1810525	0.0177	0.1428
chr16	90354753	1289325	0.0143	0.1377
chr17	81195210	1315754	0.0162	0.1393
chr18	78077248	1184387	0.0152	0.2635
chr19	59128983	1146988	0.0194	0.269
chr20	63025520	932642	0.0148	0.1301
chr21	48129895	566995	0.0118	0.1273
chr22	51304566	943784	0.0184	0.1448
chrMT	16571	96062	5.797	3.8379
chrX	155270560	3308206	0.0213	0.1719
chrY	59373566	151868	0.0026	0.0697

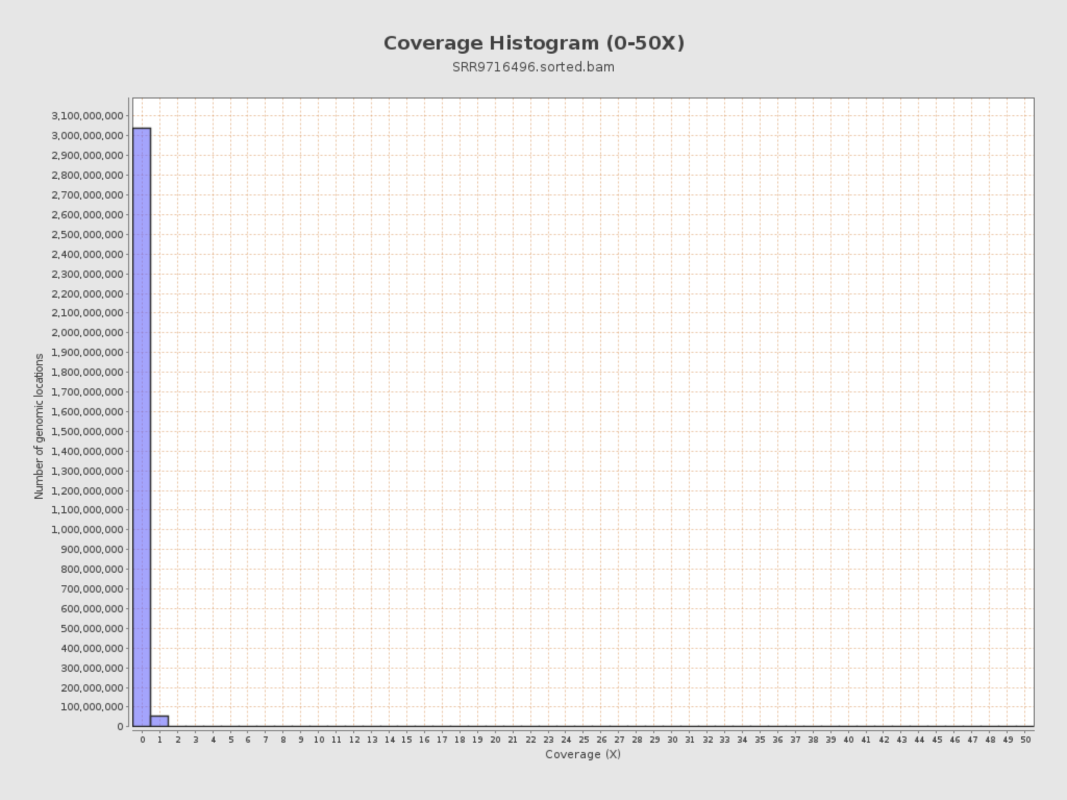
3. Results : Coverage across reference



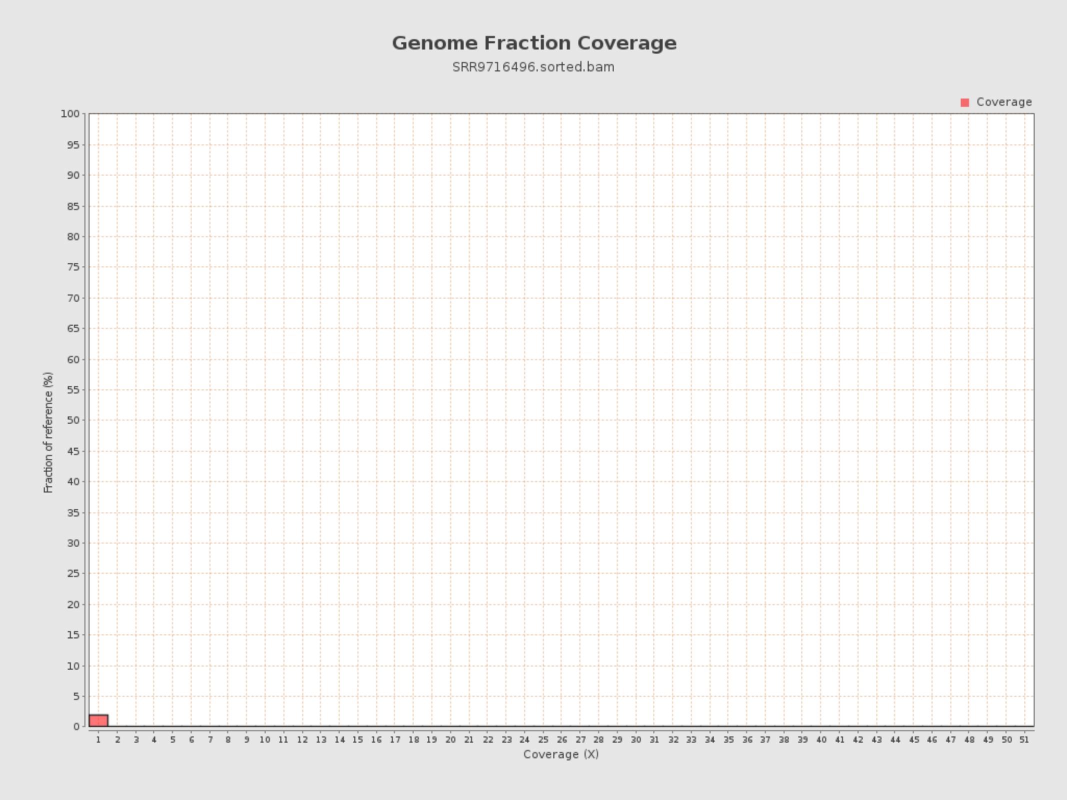
4. Results : Coverage Histogram



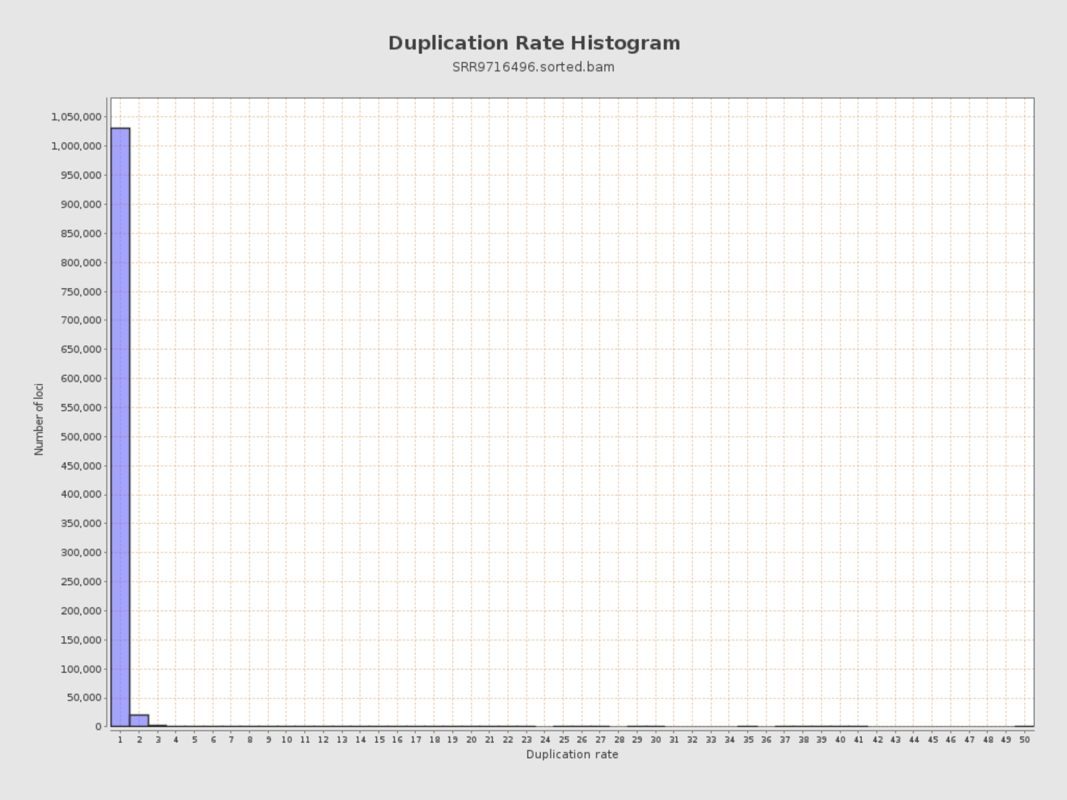
5. Results : Coverage Histogram (0-50X)



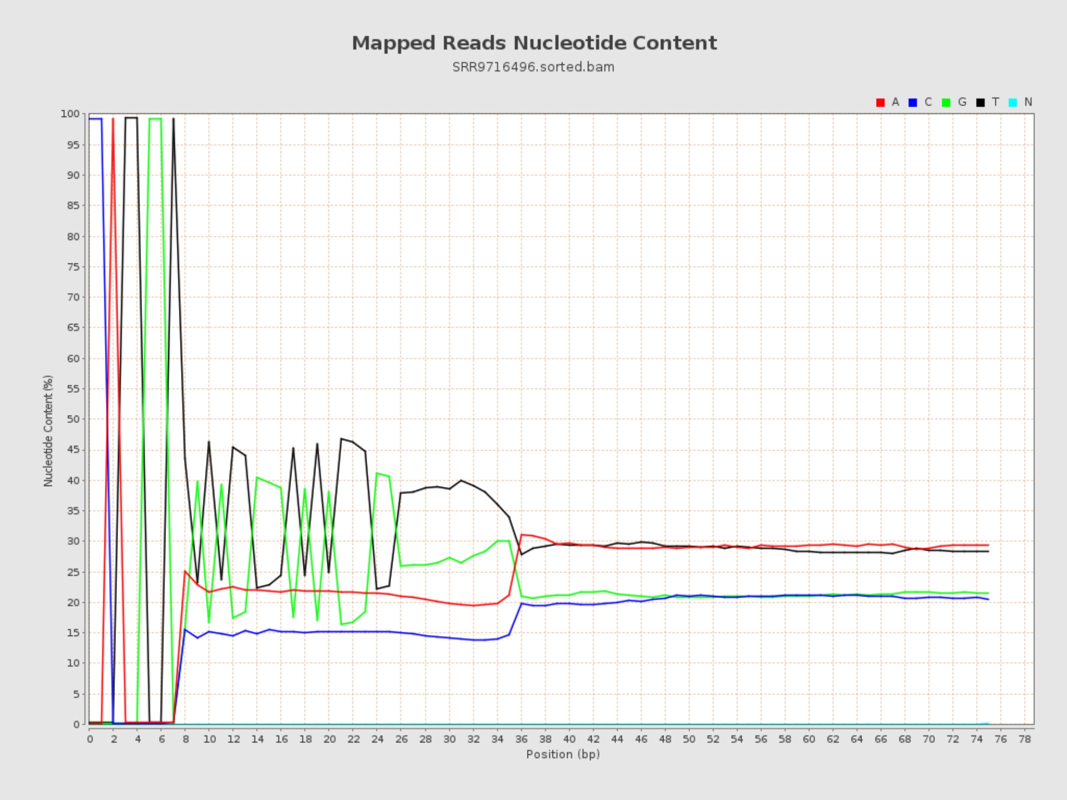
6. Results : Genome Fraction Coverage



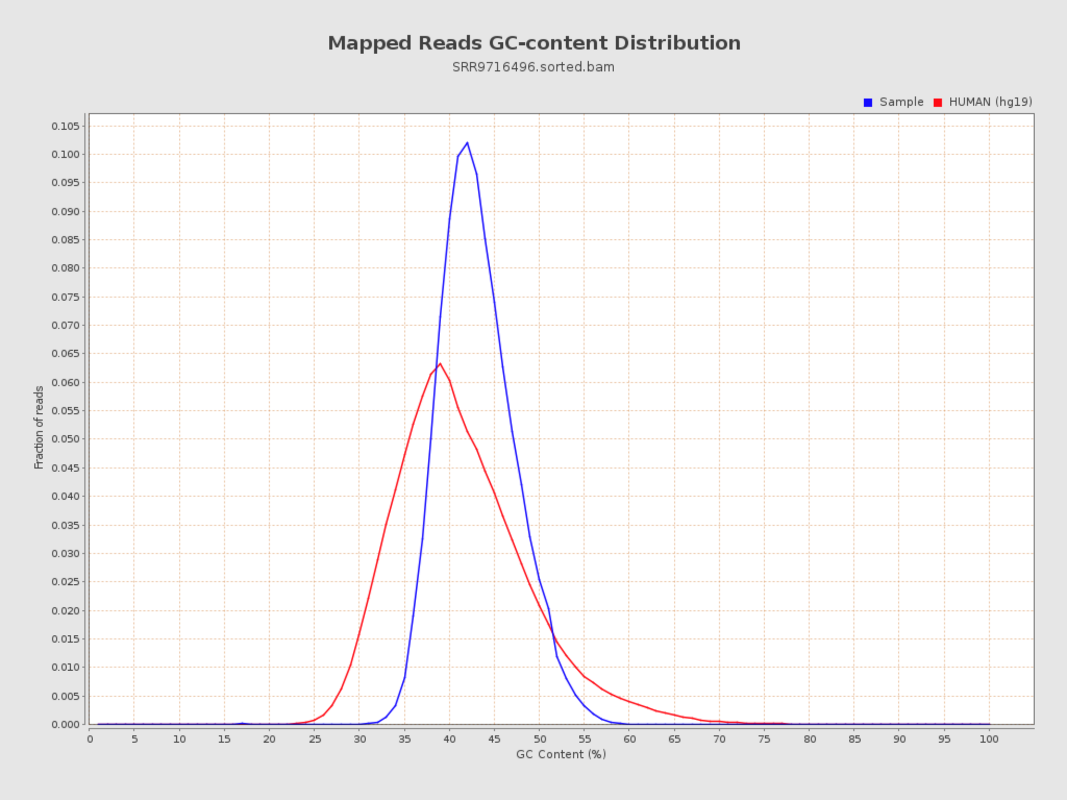
7. Results : Duplication Rate Histogram



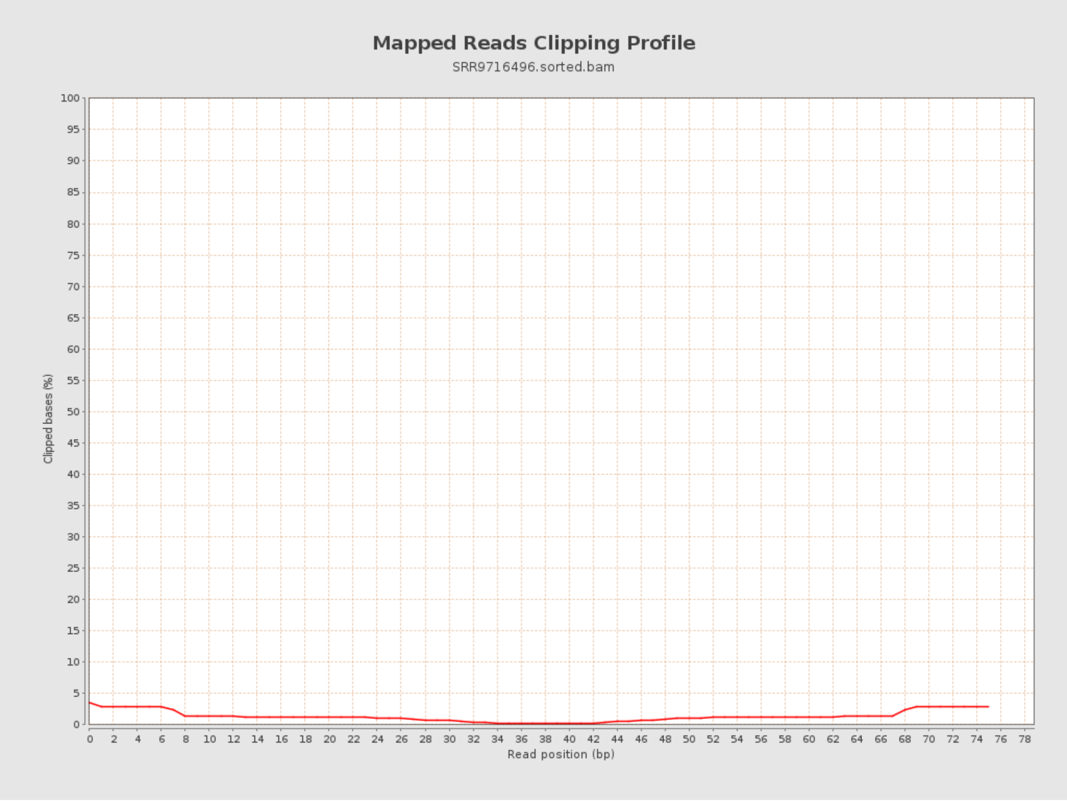
8. Results : Mapped Reads Nucleotide Content



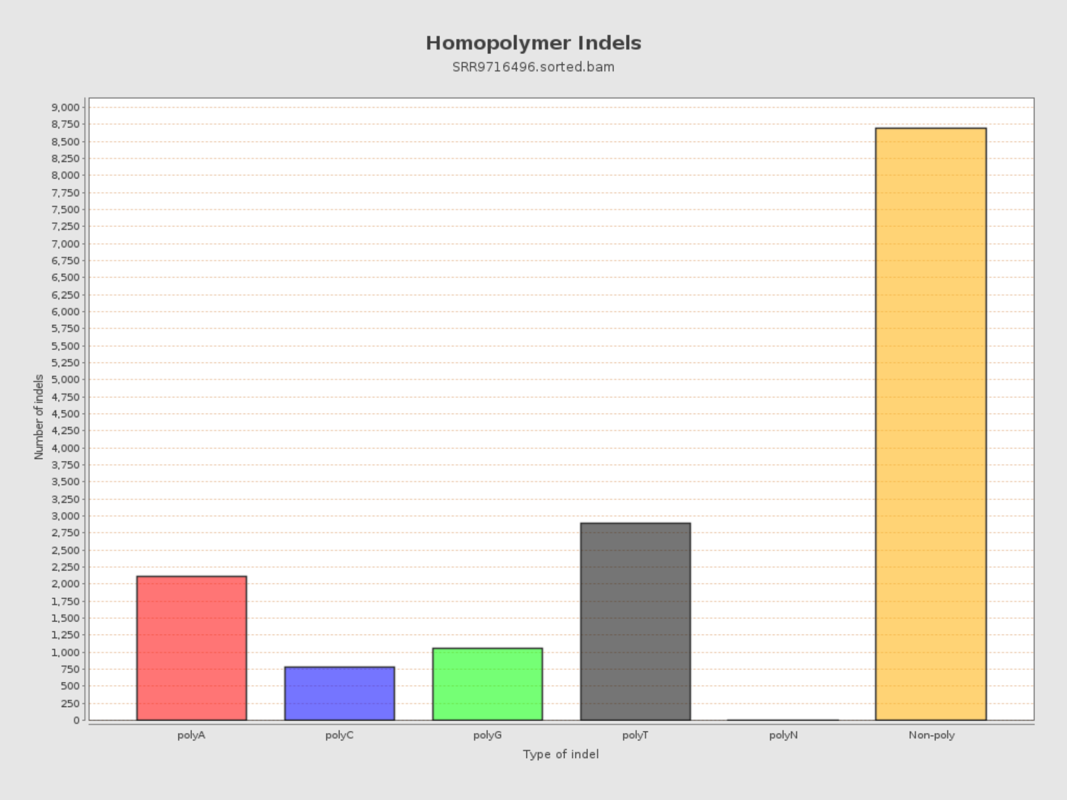
9. Results : Mapped Reads GC-content Distribution



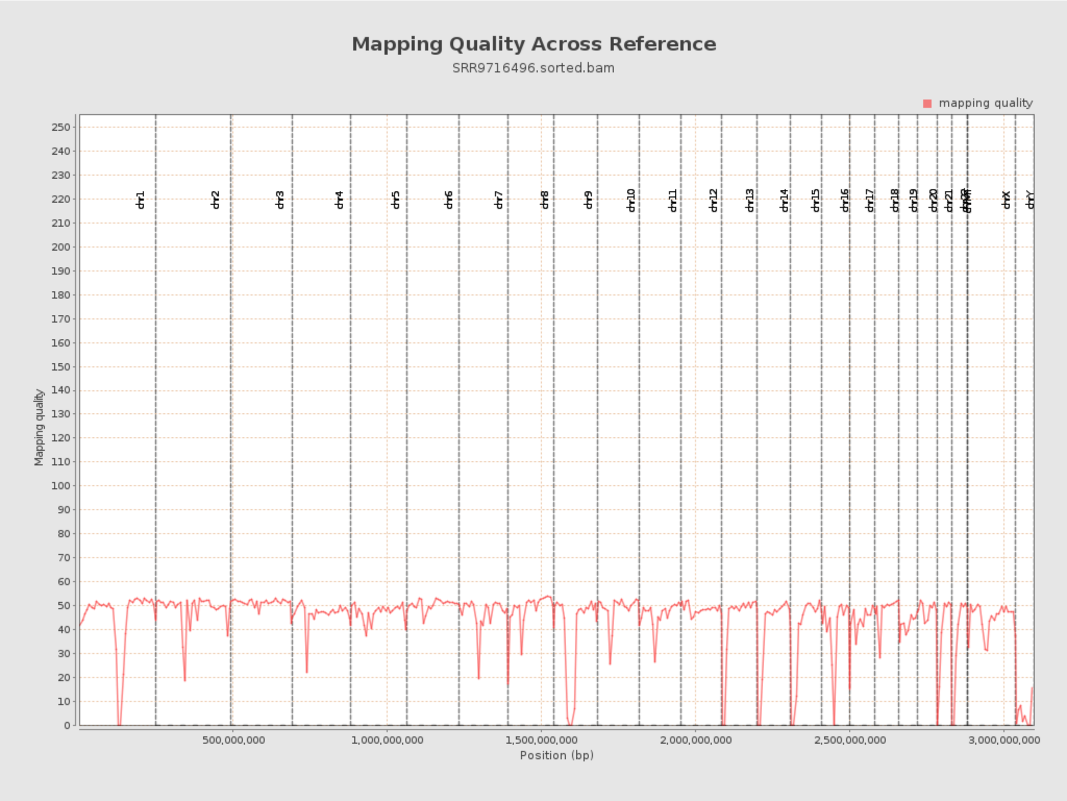
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram