Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:16:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716908.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_SRR9716908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:16:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,098,603
Mapped reads	890,049 / 81.02%
Unmapped reads	208,554 / 18.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,927 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	21,678 / 1.97%
Duplication rate	1.71%
Clipped reads	891,308 / 81.13%

2.2. ACGT Content

Number/percentage of A's	11,121,763 / 22.69%
Number/percentage of C's	9,723,383 / 19.83%
Number/percentage of T's	14,534,151 / 29.65%
Number/percentage of G's	13,645,624 / 27.83%
Number/percentage of N's	1,357 / 0%
GC Percentage	47.67%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1597

2.4. Mapping Quality

Mean Mapping Quality	38.08

2.5. Mismatches and indels

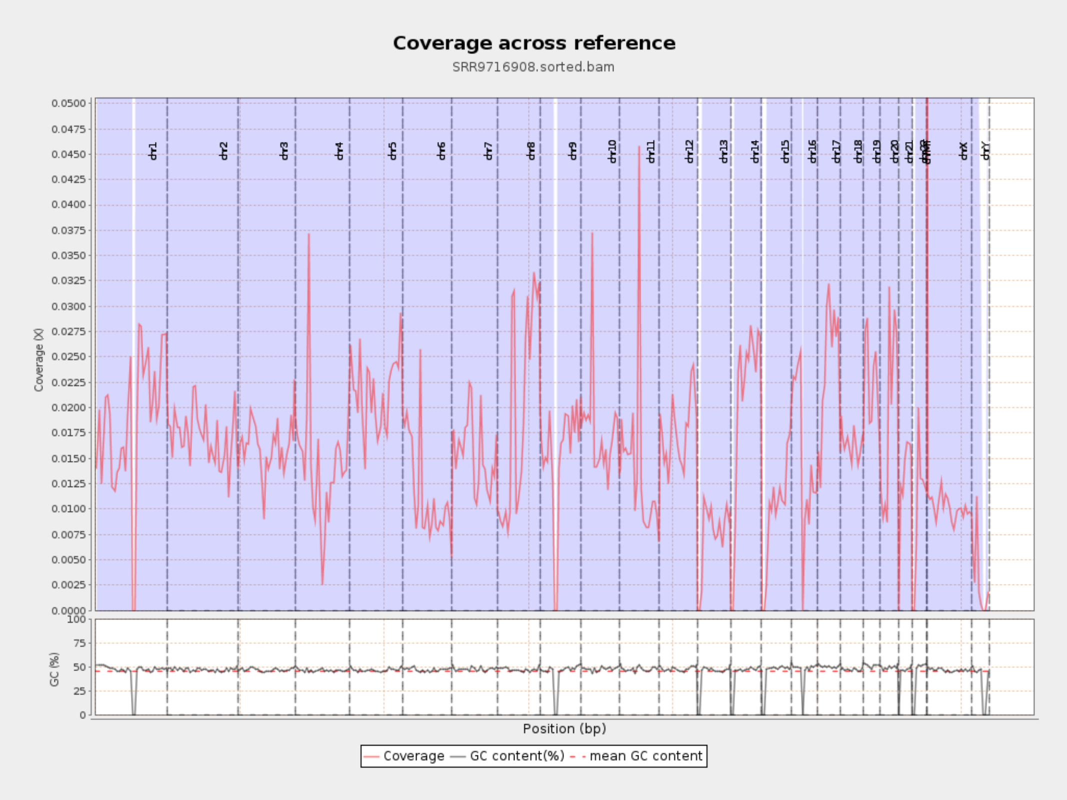
General error rate	0.55%
Mismatches	261,486
Insertions	4,035
Mapped reads with at least one insertion	0.45%
Deletions	8,230
Mapped reads with at least one deletion	0.92%
Homopolymer indels	34.59%

2.6. Chromosome stats

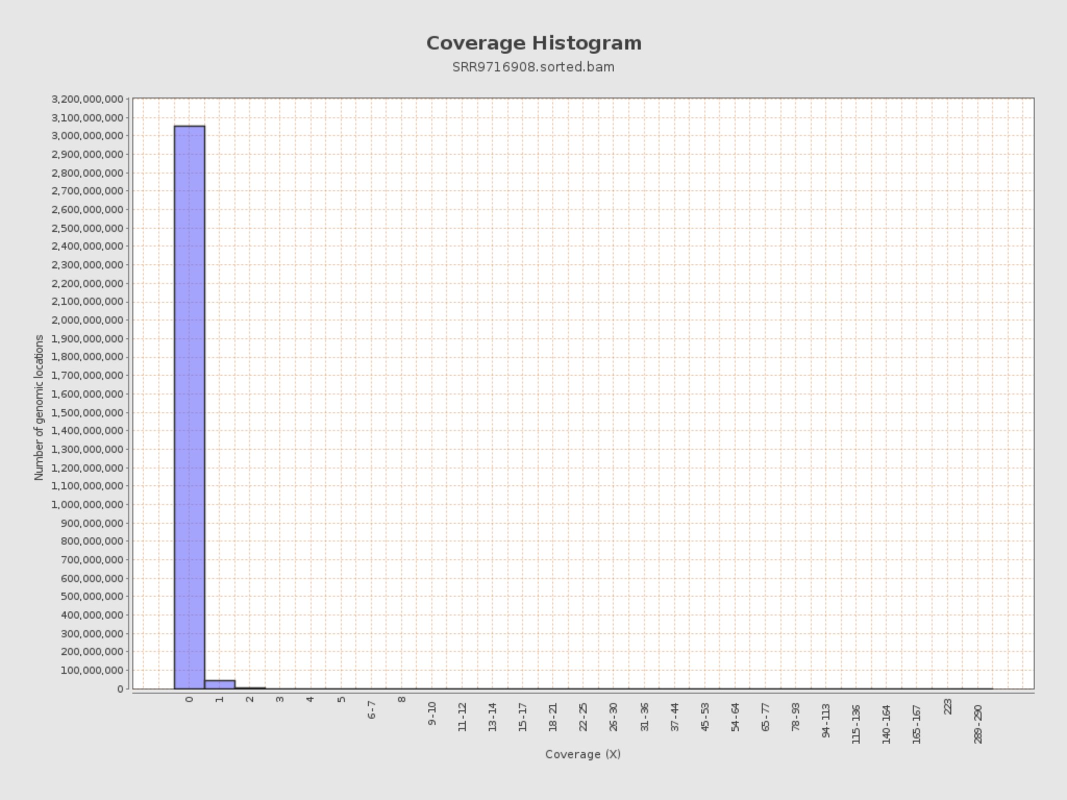
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4668824	0.0187	0.1903
chr2	243199373	4171396	0.0172	0.2056
chr3	198022430	3183687	0.0161	0.146
chr4	191154276	2737864	0.0143	0.1535
chr5	180915260	3929537	0.0217	0.1605
chr6	171115067	2021630	0.0118	0.1212
chr7	159138663	2489479	0.0156	0.1693

chr8	146364022	2894930	0.0198	0.163
chr9	141213431	2128592	0.0151	0.1427
chr10	135534747	2407212	0.0178	0.2139
chr11	135006516	1956509	0.0145	0.1559
chr12	133851895	2364623	0.0177	0.1442
chr13	115169878	857493	0.0074	0.093
chr14	107349540	2208775	0.0206	0.1595
chr15	102531392	998732	0.0097	0.1091
chr16	90354753	1354141	0.015	0.1444
chr17	81195210	1952204	0.024	0.1766
chr18	78077248	1274015	0.0163	0.1782
chr19	59128983	1331676	0.0225	0.197
chr20	63025520	1205420	0.0191	0.157
chr21	48129895	629927	0.0131	0.1353
chr22	51304566	520834	0.0102	0.1116
chrMT	16571	2251	0.1358	0.3932
chrX	155270560	1577078	0.0102	0.1227
chrY	59373566	173527	0.0029	0.0995

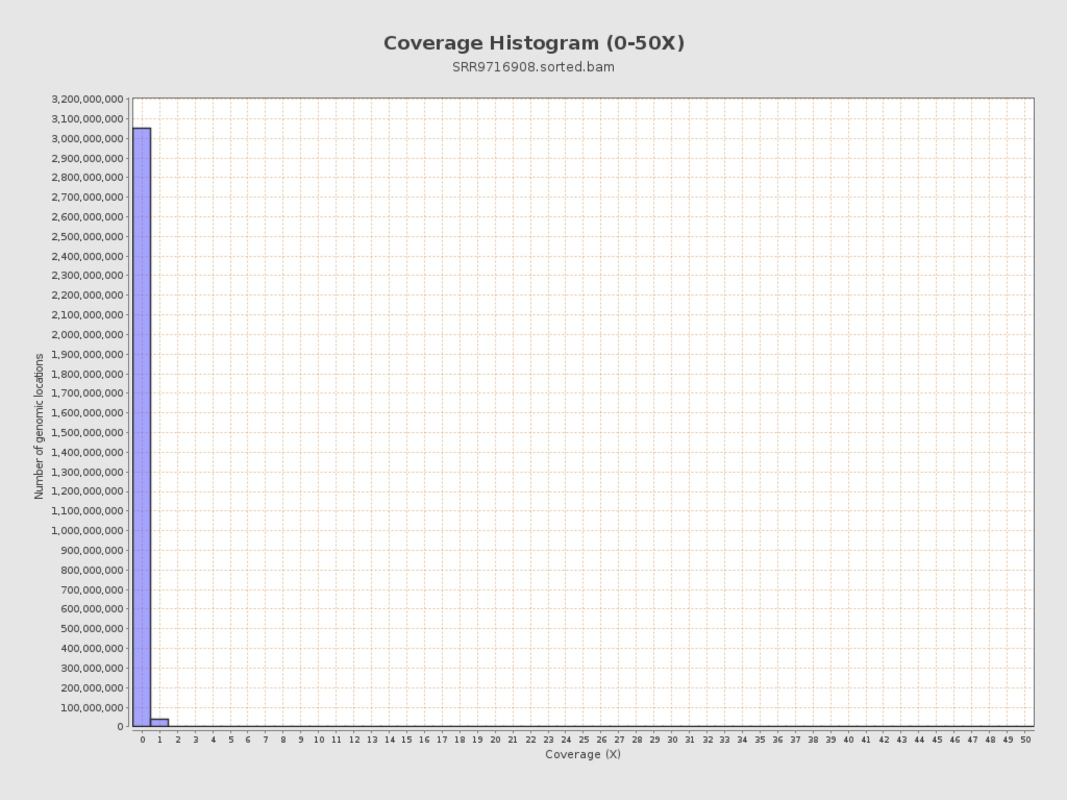
3. Results : Coverage across reference



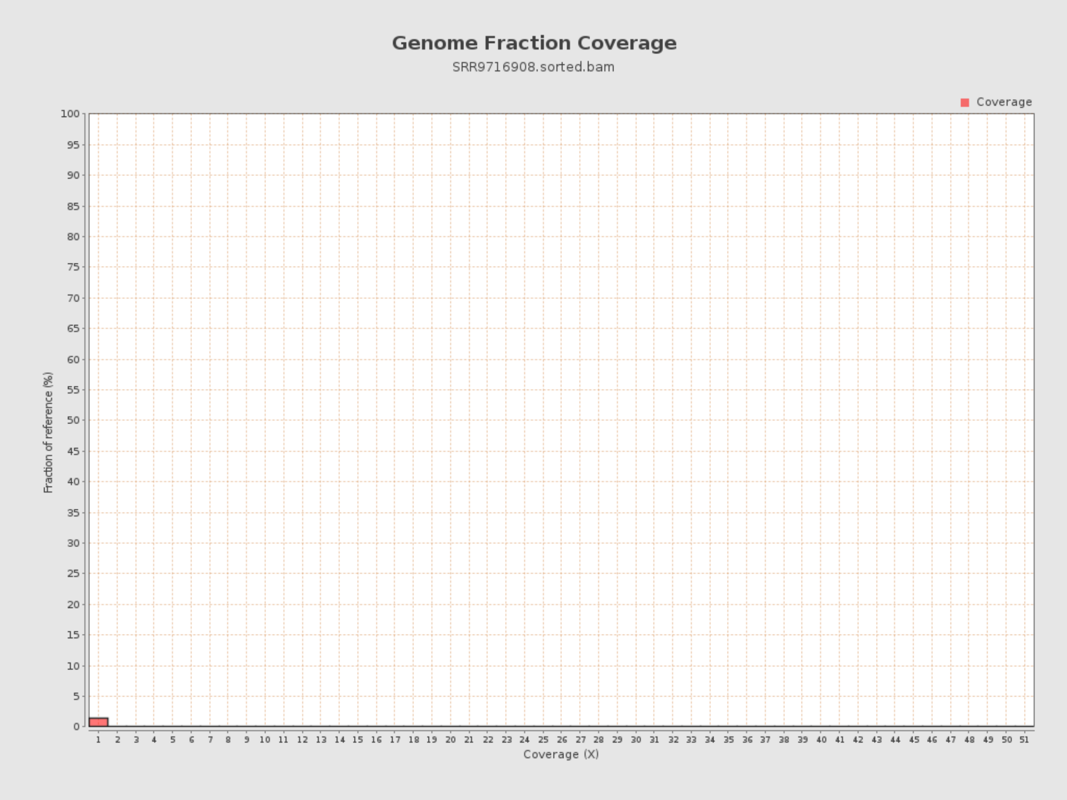
4. Results : Coverage Histogram



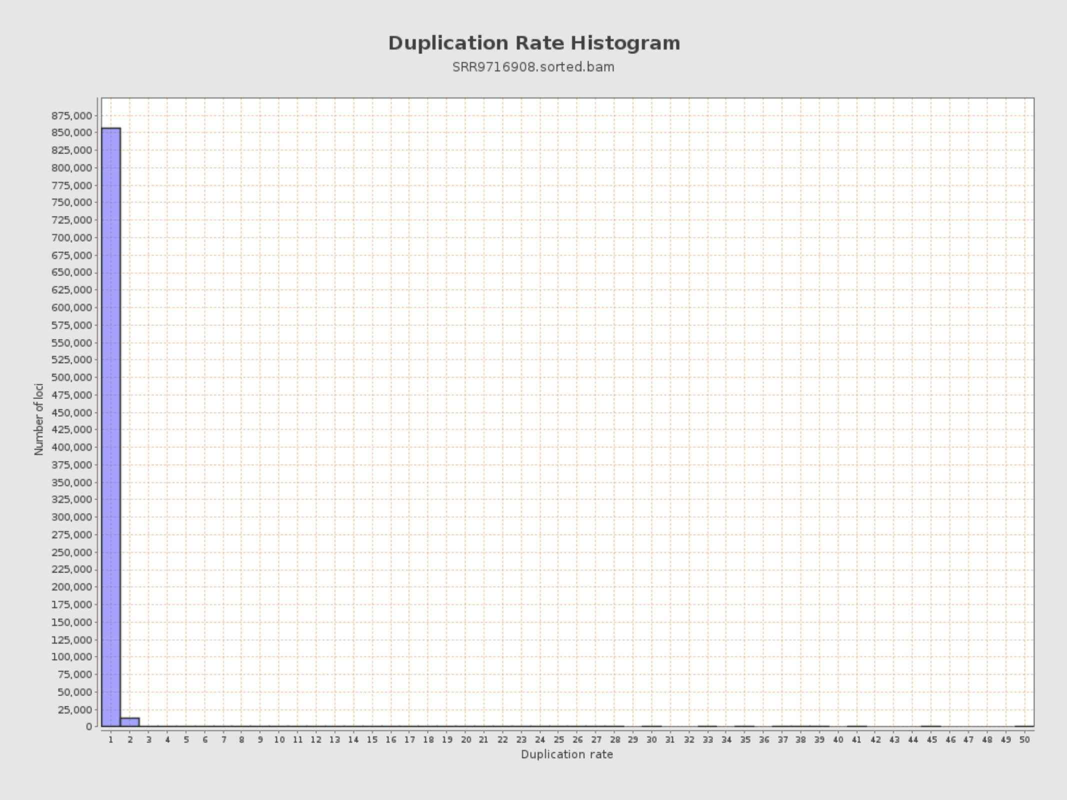
5. Results : Coverage Histogram (0-50X)



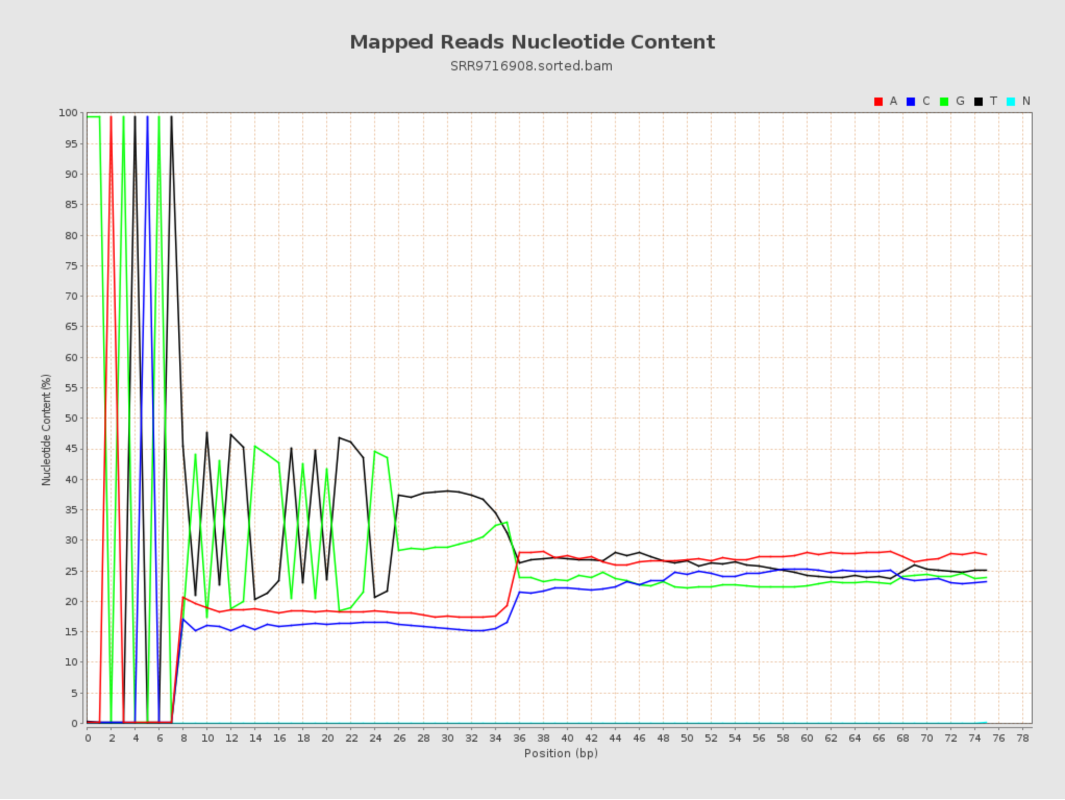
6. Results : Genome Fraction Coverage



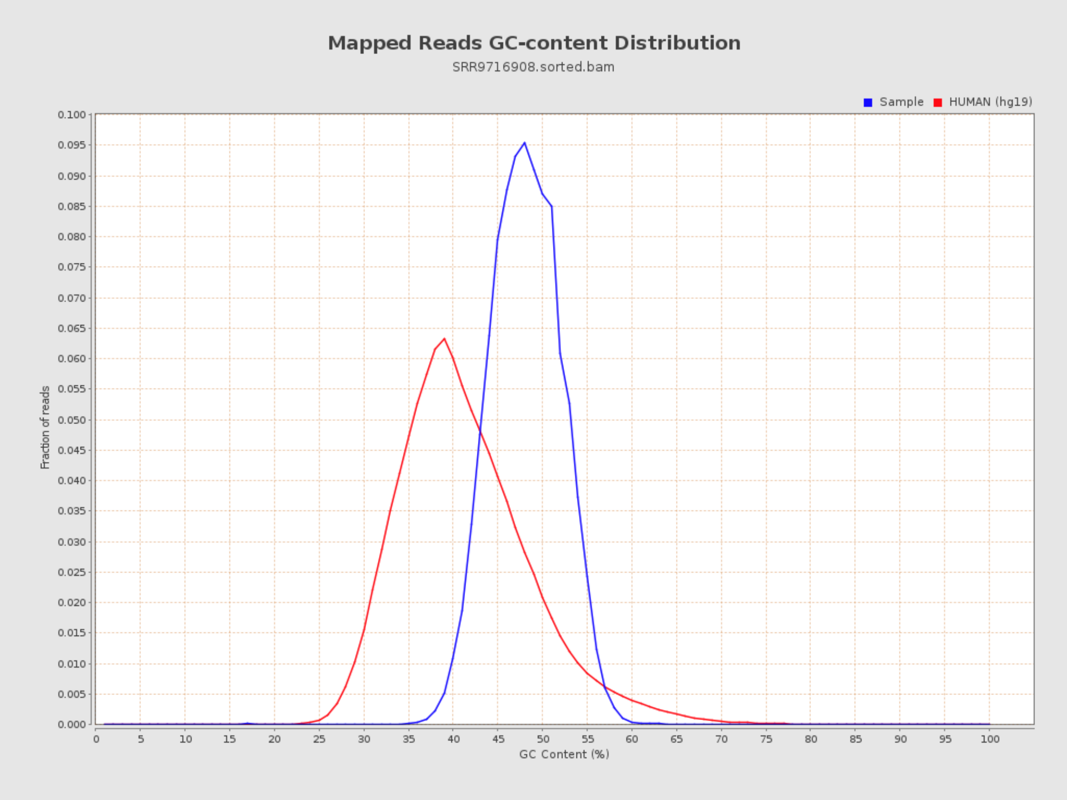
7. Results : Duplication Rate Histogram



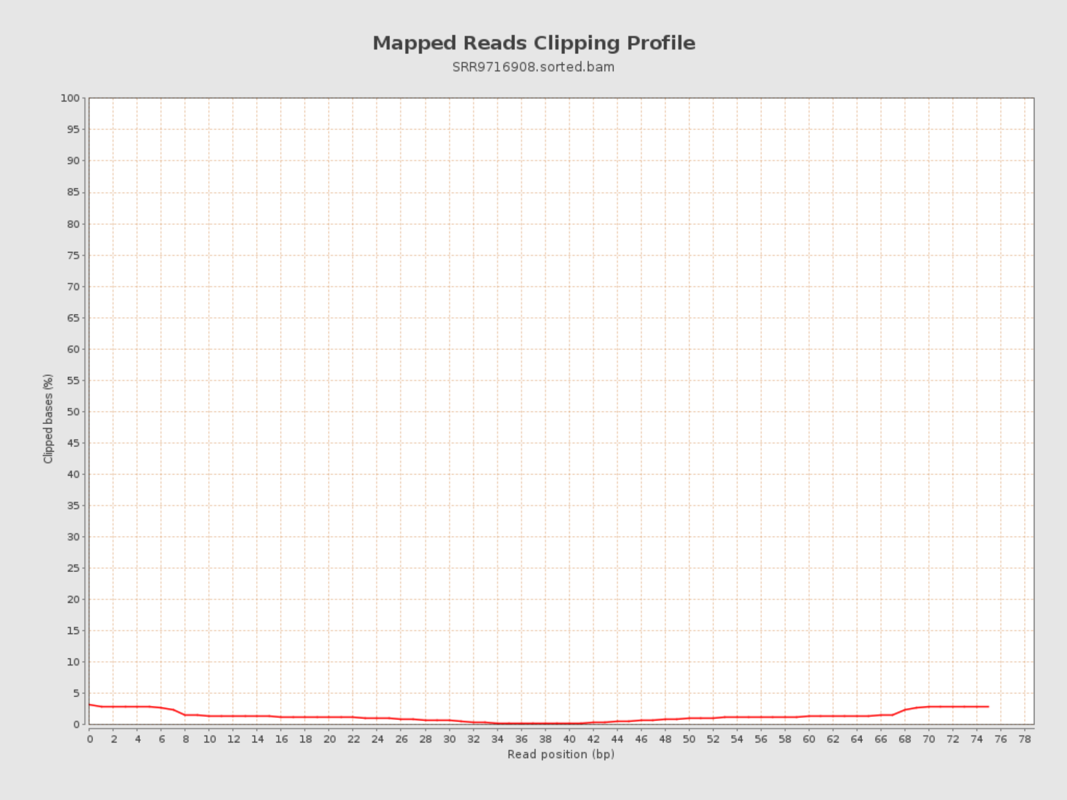
8. Results : Mapped Reads Nucleotide Content



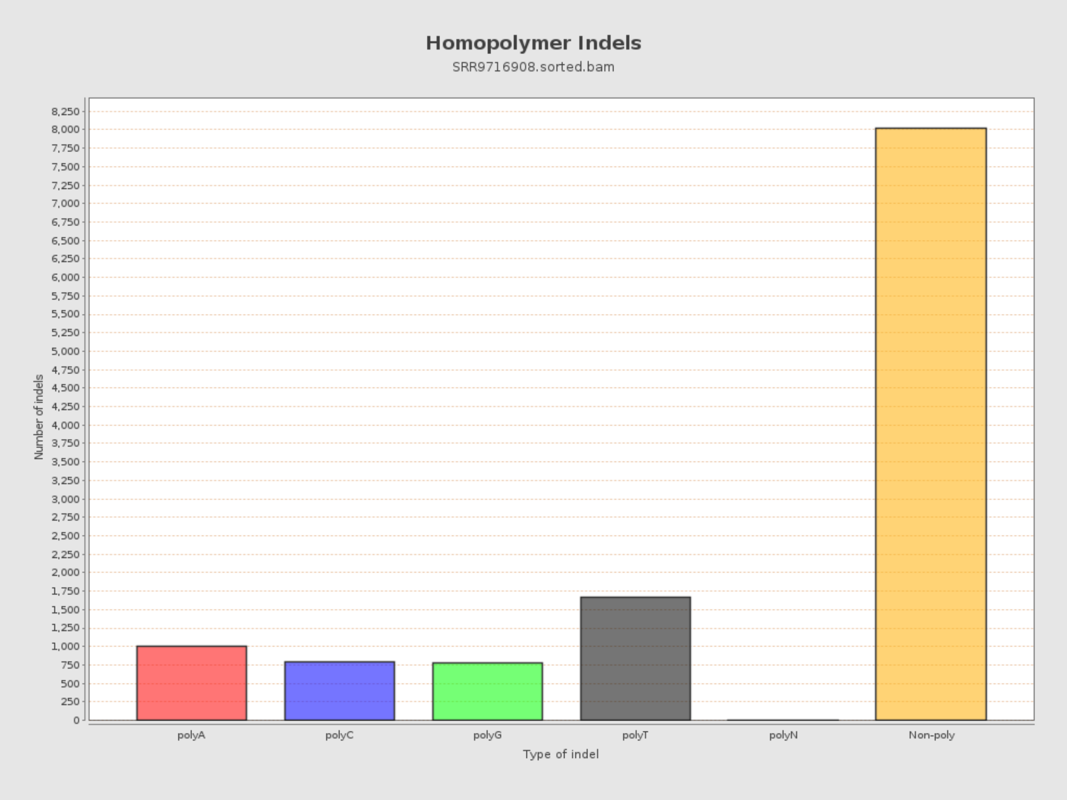
9. Results : Mapped Reads GC-content Distribution



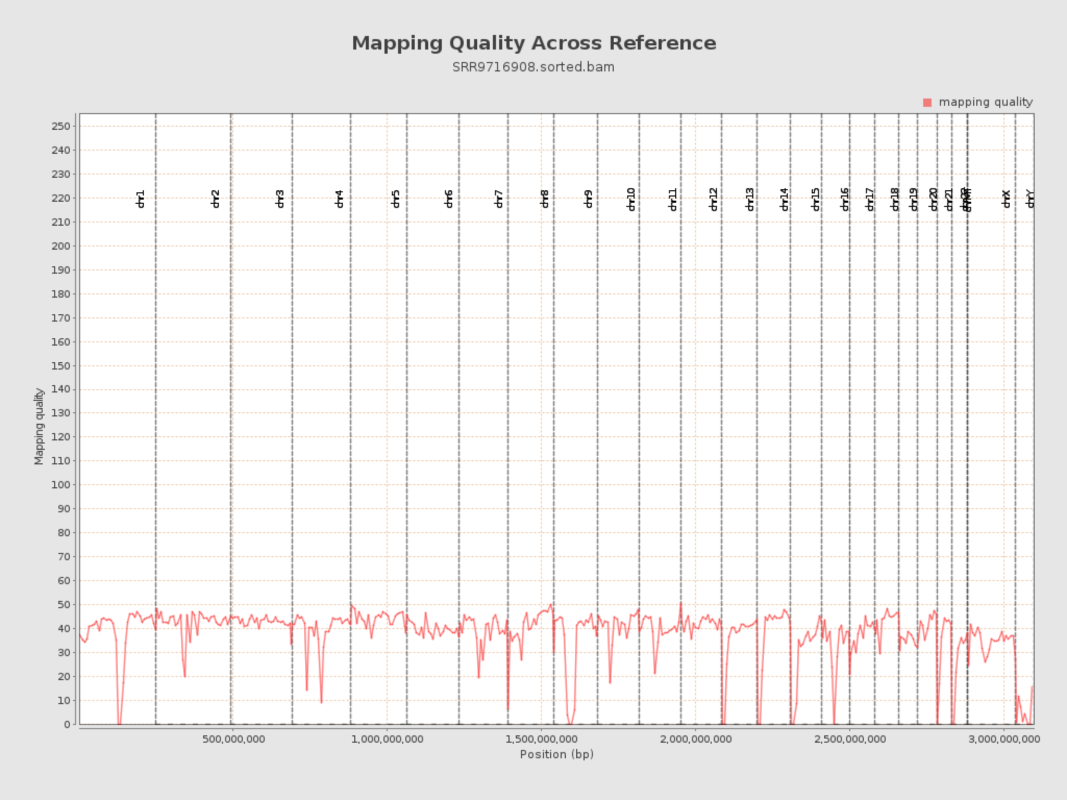
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram