Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:46:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716598.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_SRR9716598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:46:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	948,509
Mapped reads	840,965 / 88.66%
Unmapped reads	107,544 / 11.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,650 / 0.6%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	20,498 / 2.16%
Duplication rate	1.9%
Clipped reads	844,222 / 89.01%

2.2. ACGT Content

Number/percentage of A's	12,292,464 / 25.12%
Number/percentage of C's	9,499,769 / 19.41%
Number/percentage of T's	15,307,494 / 31.28%
Number/percentage of G's	11,841,733 / 24.2%
Number/percentage of N's	595 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0158

Standard Deviation	0.1584

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

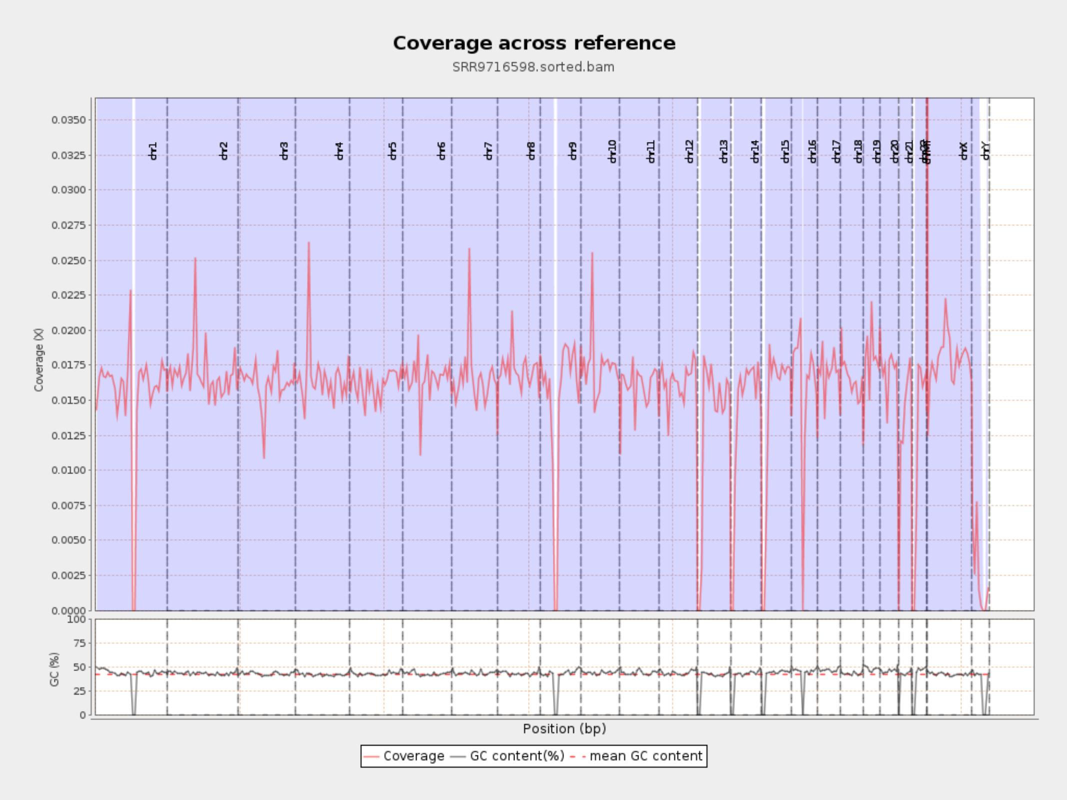
General error rate	0.52%
Mismatches	247,345
Insertions	3,407
Mapped reads with at least one insertion	0.4%
Deletions	8,891
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.62%

2.6. Chromosome stats

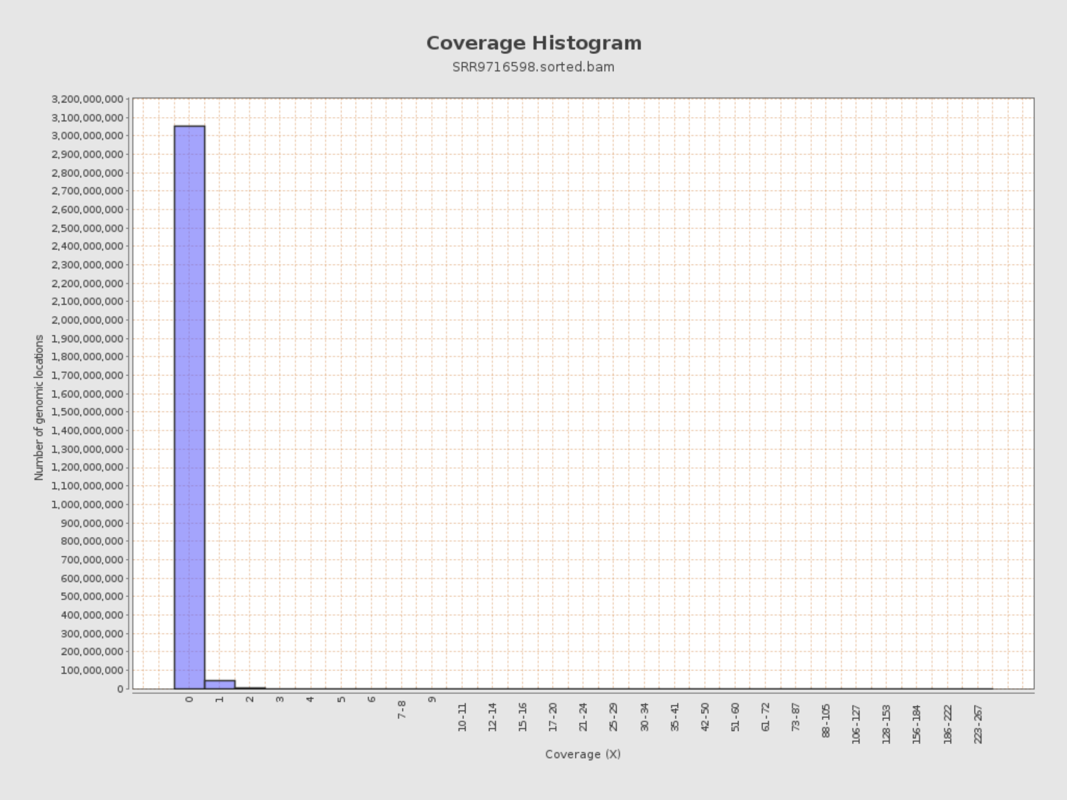
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3836812	0.0154	0.2165
chr2	243199373	4116303	0.0169	0.1885
chr3	198022430	3198142	0.0162	0.1338
chr4	191154276	3183028	0.0167	0.1458
chr5	180915260	2926768	0.0162	0.1344
chr6	171115067	2837901	0.0166	0.1438
chr7	159138663	2655501	0.0167	0.1994

chr8	146364022	2508032	0.0171	0.1664
chr9	141213431	2095549	0.0148	0.1426
chr10	135534747	2365167	0.0175	0.1651
chr11	135006516	2178305	0.0161	0.154
chr12	133851895	2184863	0.0163	0.136
chr13	115169878	1528135	0.0133	0.1221
chr14	107349540	1488490	0.0139	0.1287
chr15	102531392	1445864	0.0141	0.127
chr16	90354753	1419069	0.0157	0.137
chr17	81195210	1379990	0.017	0.1433
chr18	78077248	1287250	0.0165	0.2013
chr19	59128983	1066174	0.018	0.1912
chr20	63025520	1064038	0.0169	0.1397
chr21	48129895	645297	0.0134	0.1293
chr22	51304566	603582	0.0118	0.1142
chrMT	16571	15529	0.9371	1.1041
chrX	155270560	2786953	0.0179	0.148
chrY	59373566	139517	0.0023	0.0742

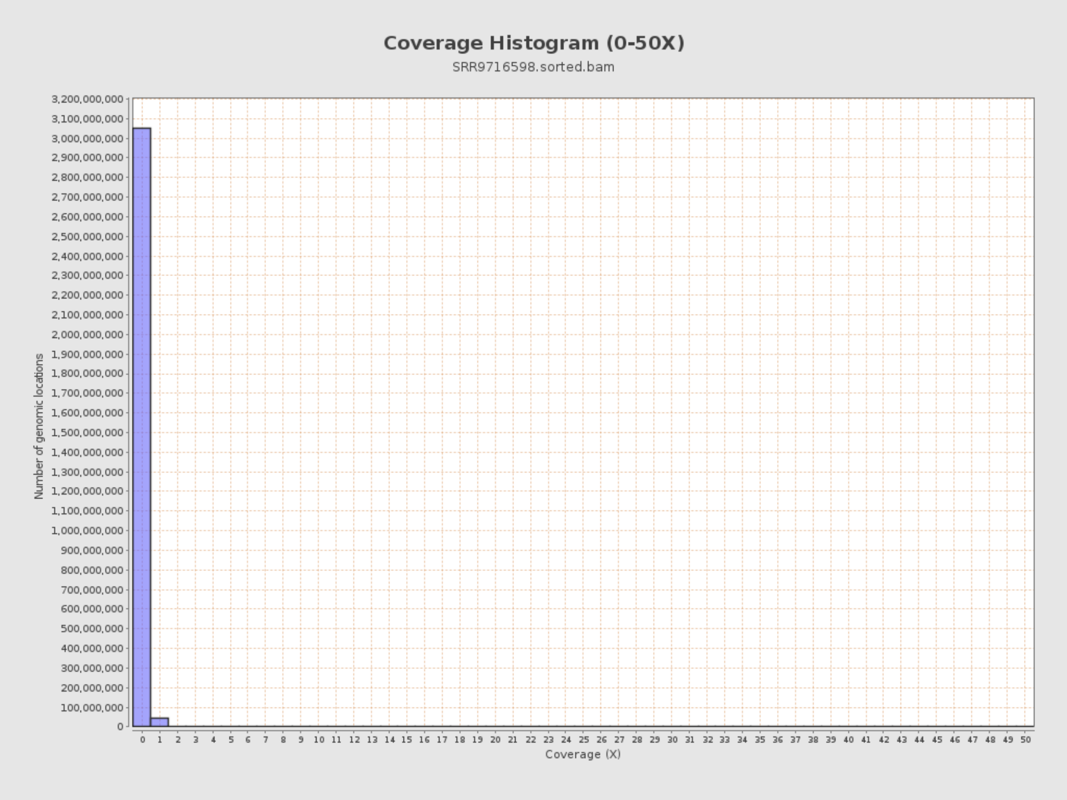
3. Results : Coverage across reference



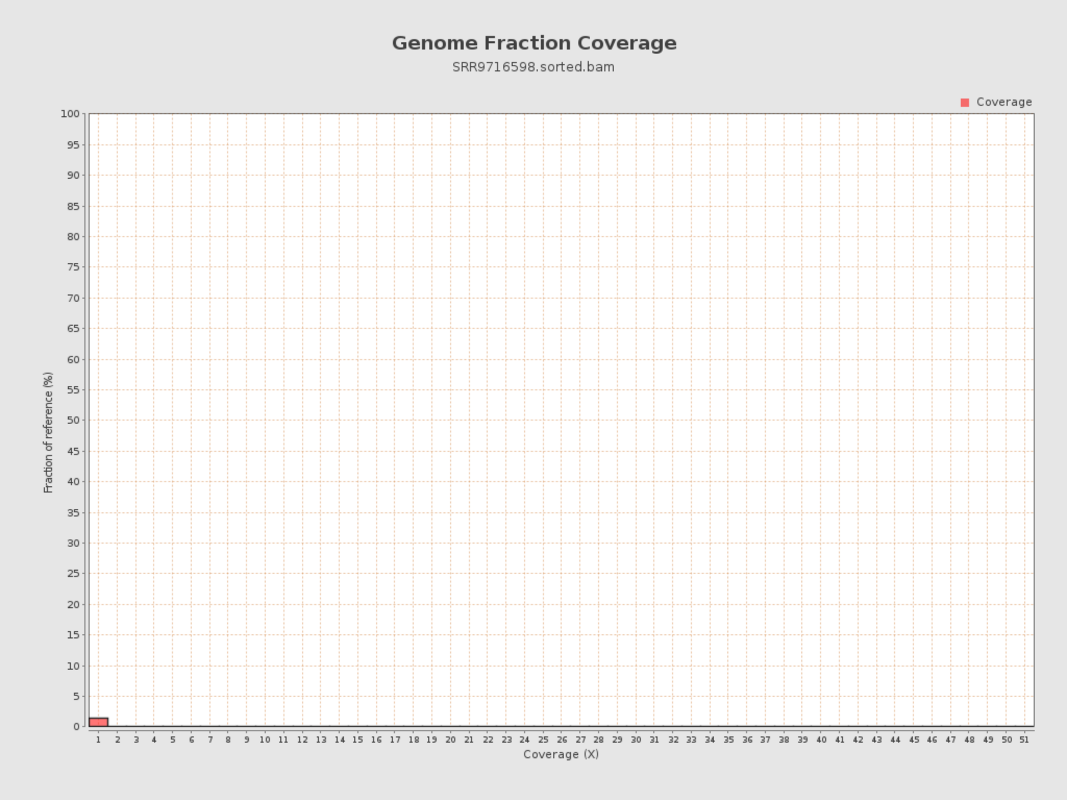
4. Results : Coverage Histogram



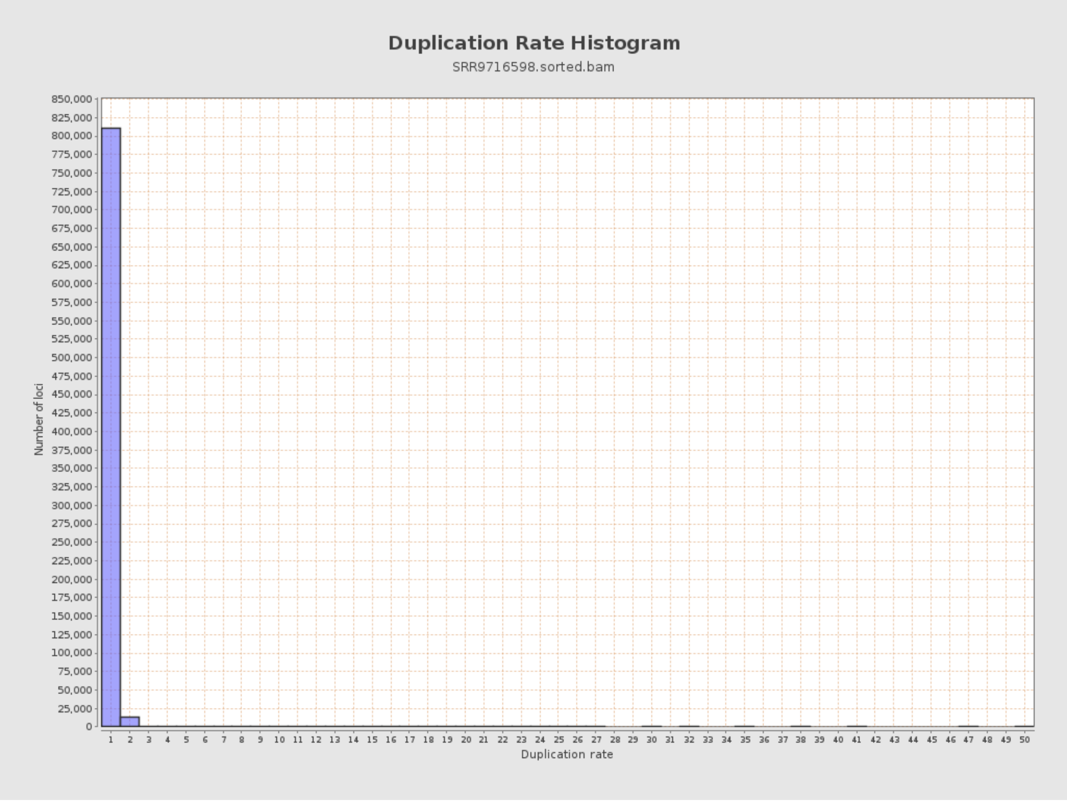
5. Results : Coverage Histogram (0-50X)



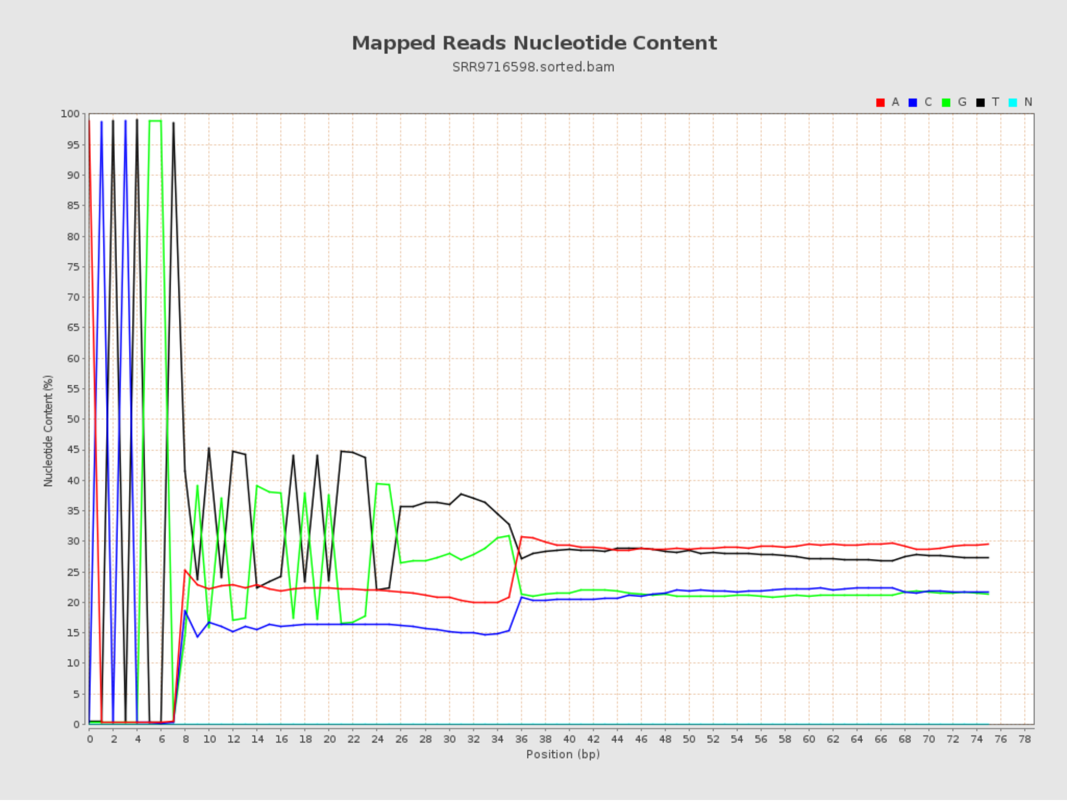
6. Results : Genome Fraction Coverage



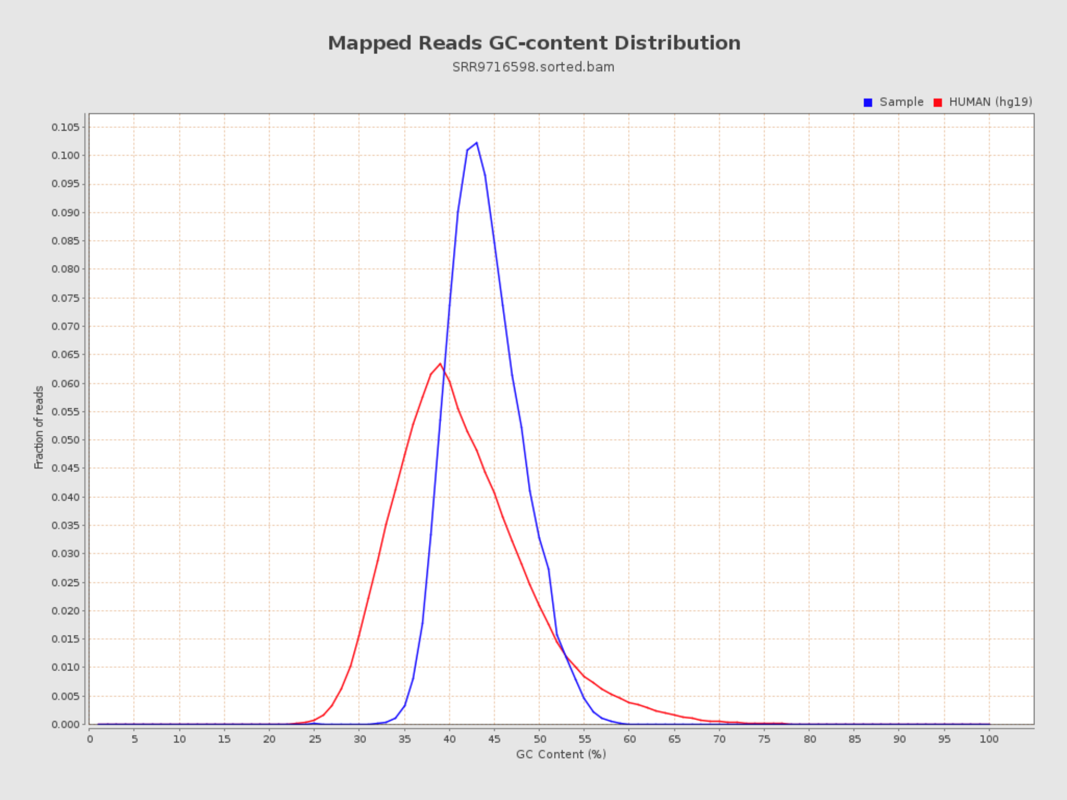
7. Results : Duplication Rate Histogram



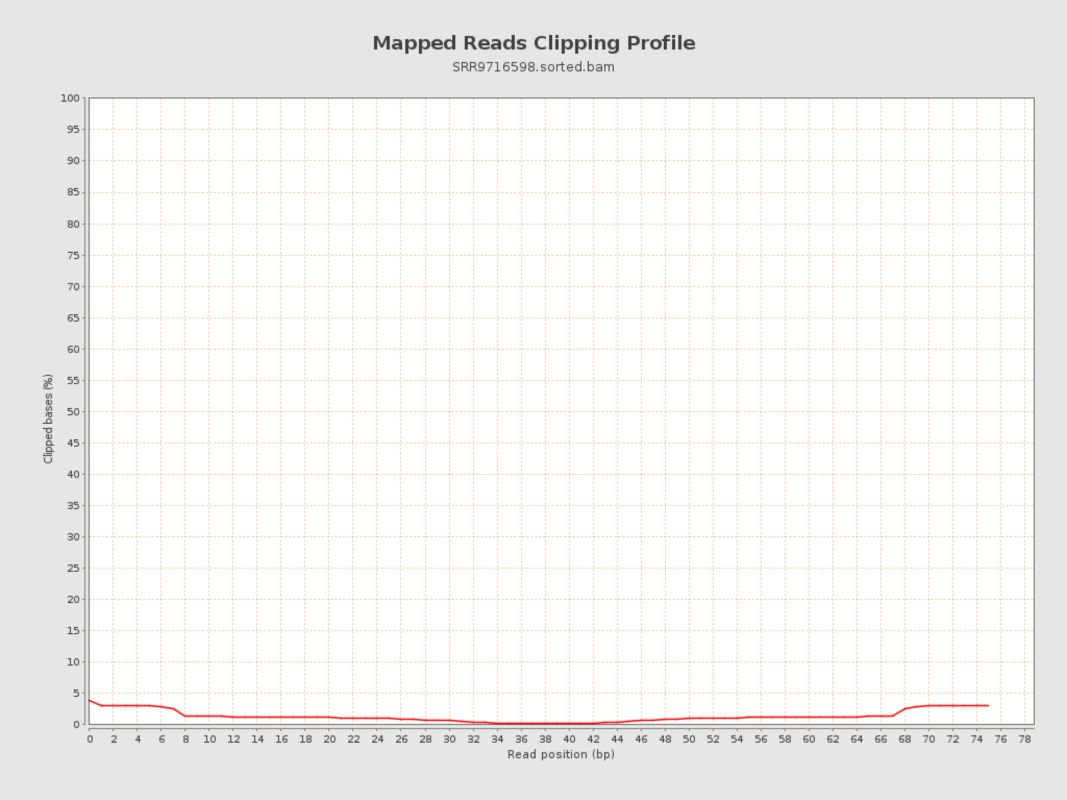
8. Results : Mapped Reads Nucleotide Content



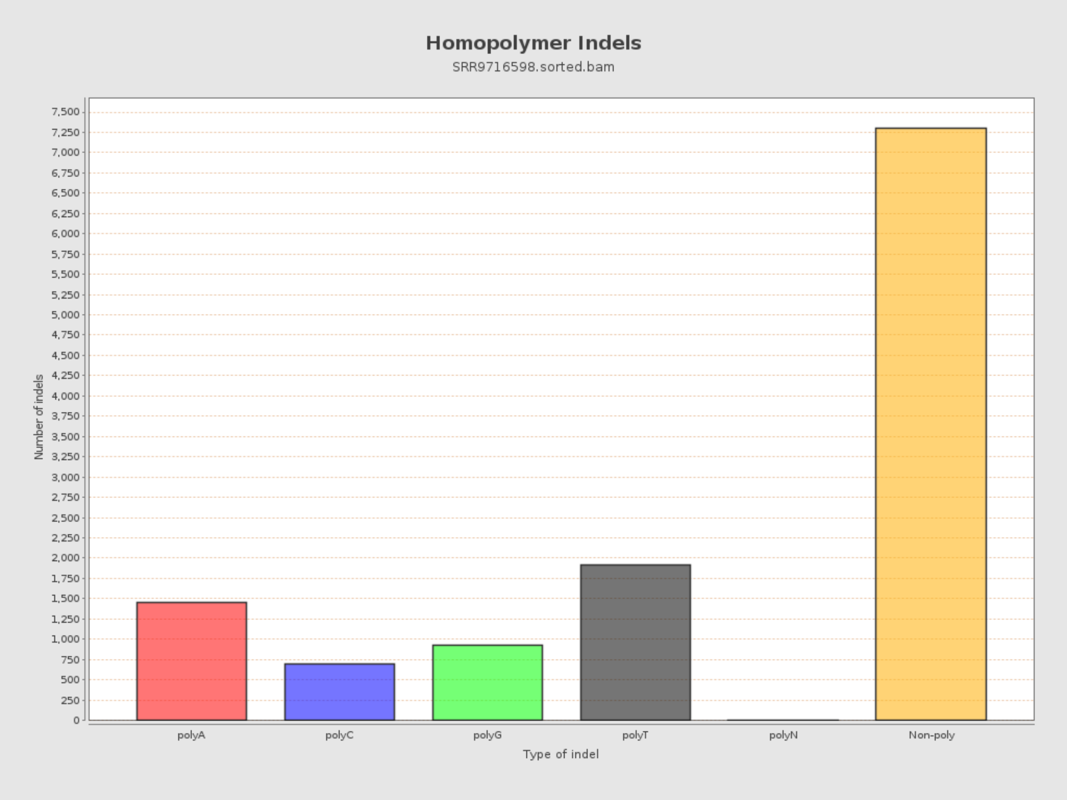
9. Results : Mapped Reads GC-content Distribution



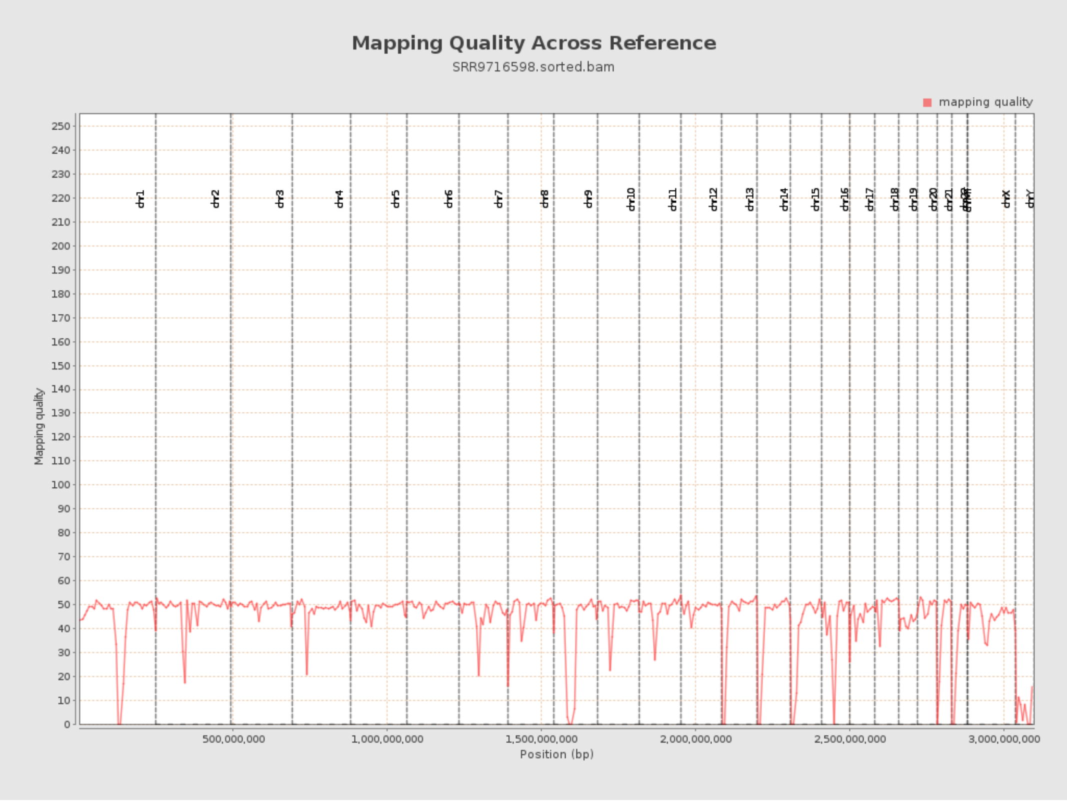
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram