Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:03:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716515.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_SRR9716515 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716515.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:03:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716515.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,060,922
Mapped reads	958,378 / 90.33%
Unmapped reads	102,544 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,195 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,218 / 2.09%
Duplication rate	1.52%
Clipped reads	959,556 / 90.45%

2.2. ACGT Content

Number/percentage of A's	14,241,967 / 25.79%
Number/percentage of C's	10,447,136 / 18.92%
Number/percentage of T's	17,618,422 / 31.91%
Number/percentage of G's	12,910,543 / 23.38%
Number/percentage of N's	644 / 0%
GC Percentage	42.3%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1994

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Mismatches and indels

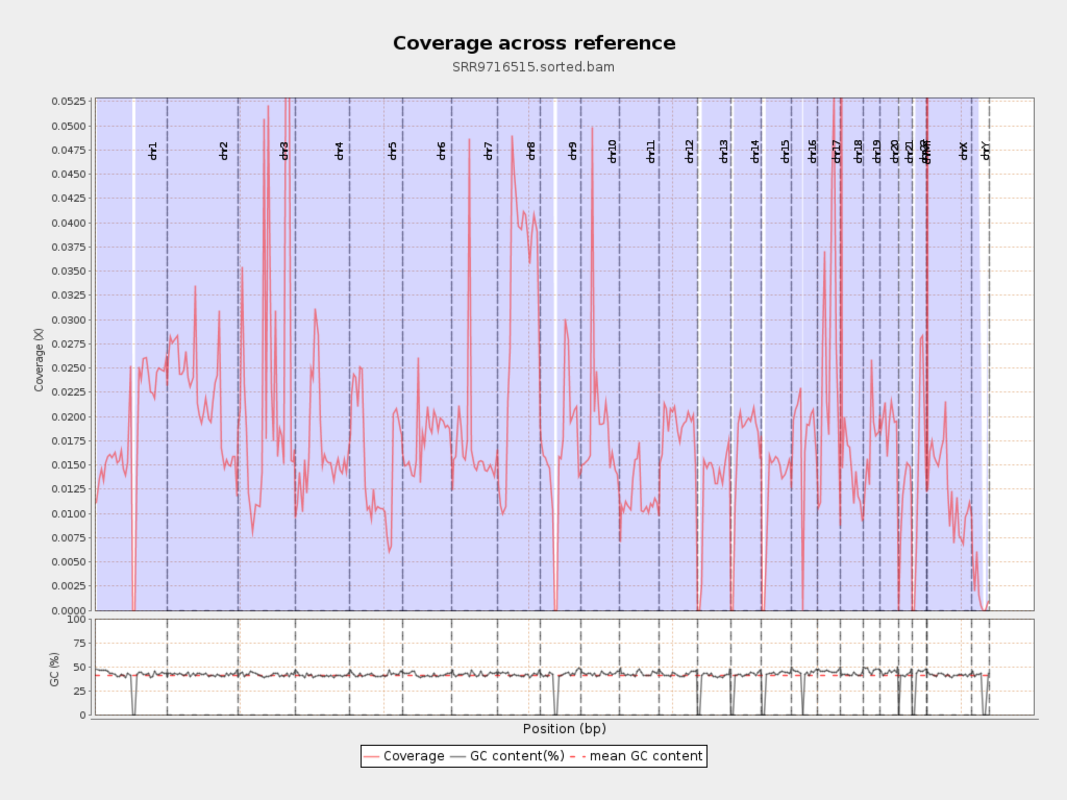
General error rate	0.51%
Mismatches	276,911
Insertions	3,904
Mapped reads with at least one insertion	0.41%
Deletions	9,602
Mapped reads with at least one deletion	1%
Homopolymer indels	41.82%

2.6. Chromosome stats

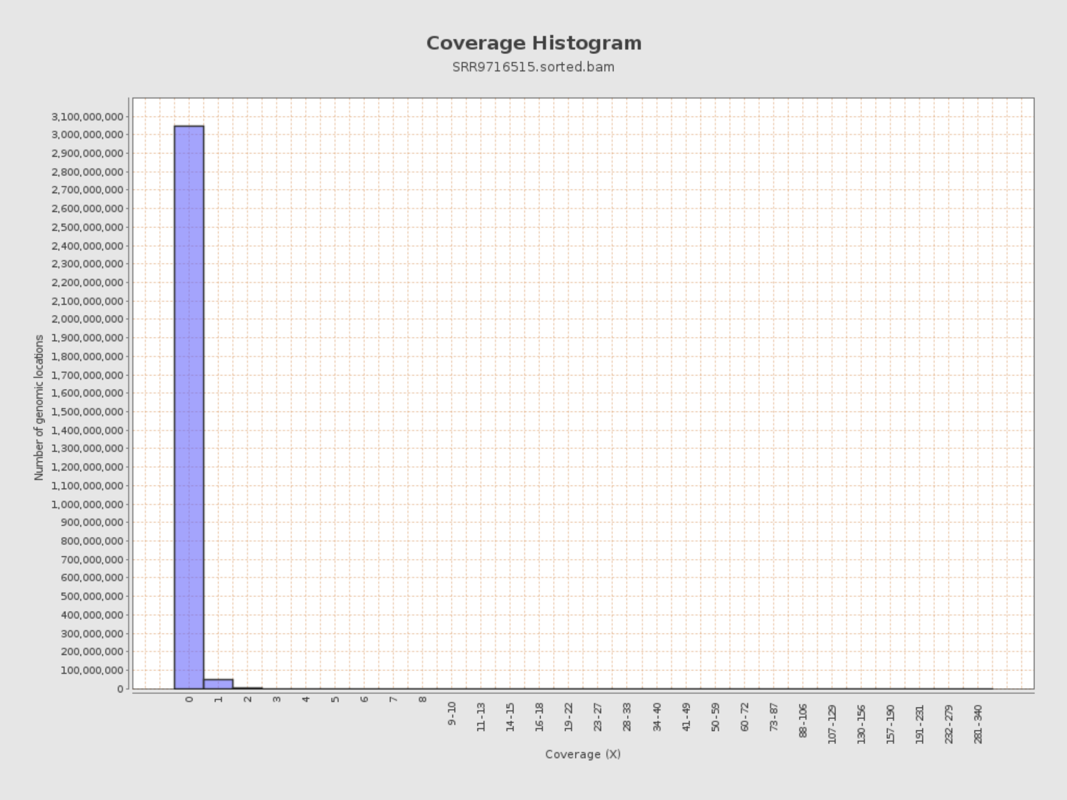
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4529539	0.0182	0.2583
chr2	243199373	5389579	0.0222	0.2175
chr3	198022430	4782860	0.0242	0.1789
chr4	191154276	3162568	0.0165	0.1402
chr5	180915260	2757023	0.0152	0.1307
chr6	171115067	3056460	0.0179	0.1489
chr7	159138663	2754824	0.0173	0.4066

chr8	146364022	4709333	0.0322	0.2199
chr9	141213431	2288683	0.0162	0.1496
chr10	135534747	2599631	0.0192	0.2933
chr11	135006516	1584261	0.0117	0.137
chr12	133851895	2518225	0.0188	0.1648
chr13	115169878	1424839	0.0124	0.1159
chr14	107349540	1736067	0.0162	0.1351
chr15	102531392	1258857	0.0123	0.1212
chr16	90354753	1585433	0.0175	0.1505
chr17	81195210	2126522	0.0262	0.175
chr18	78077248	1348363	0.0173	0.2201
chr19	59128983	1024303	0.0173	0.2602
chr20	63025520	1202728	0.0191	0.1585
chr21	48129895	549697	0.0114	0.1148
chr22	51304566	742781	0.0145	0.1267
chrMT	16571	20218	1.2201	1.2234
chrX	155270560	1965492	0.0127	0.138
chrY	59373566	115241	0.0019	0.0559

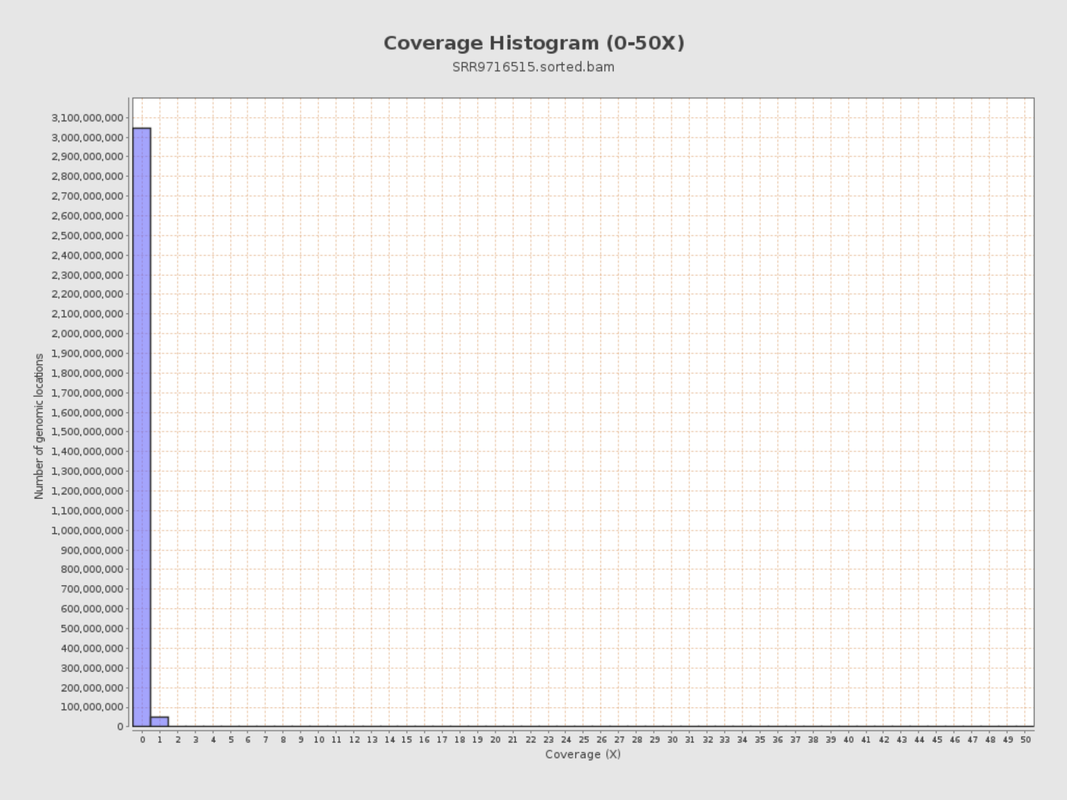
3. Results : Coverage across reference



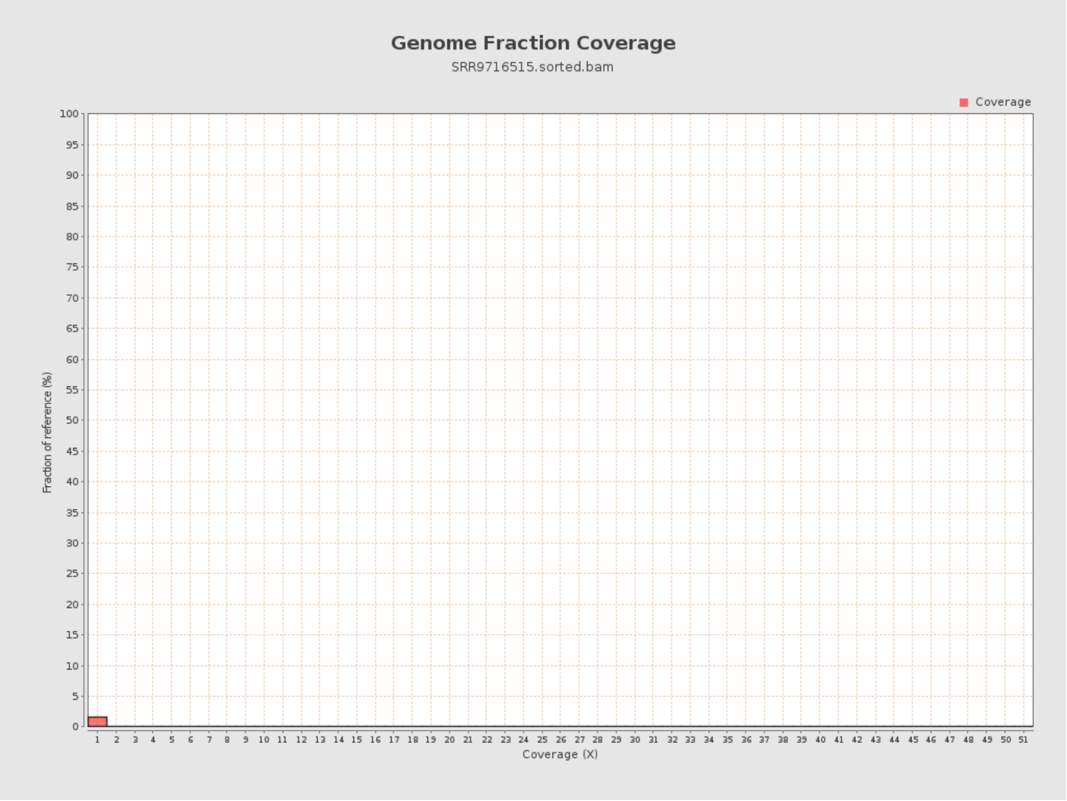
4. Results : Coverage Histogram



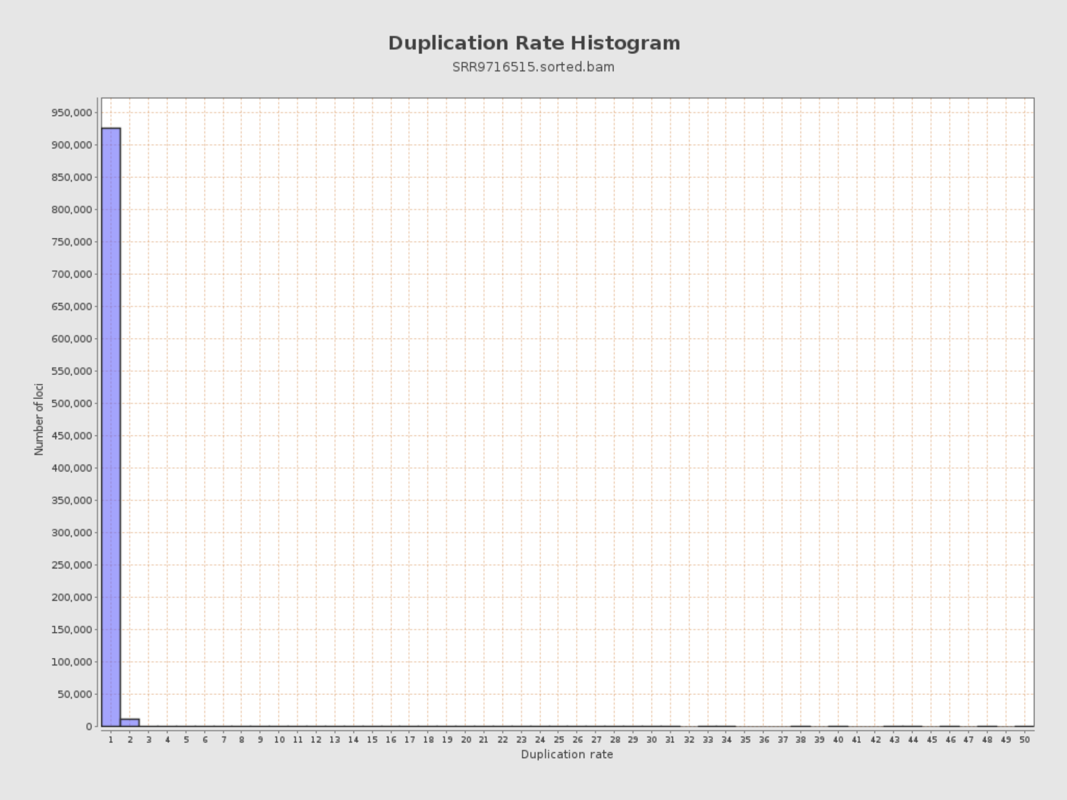
5. Results : Coverage Histogram (0-50X)



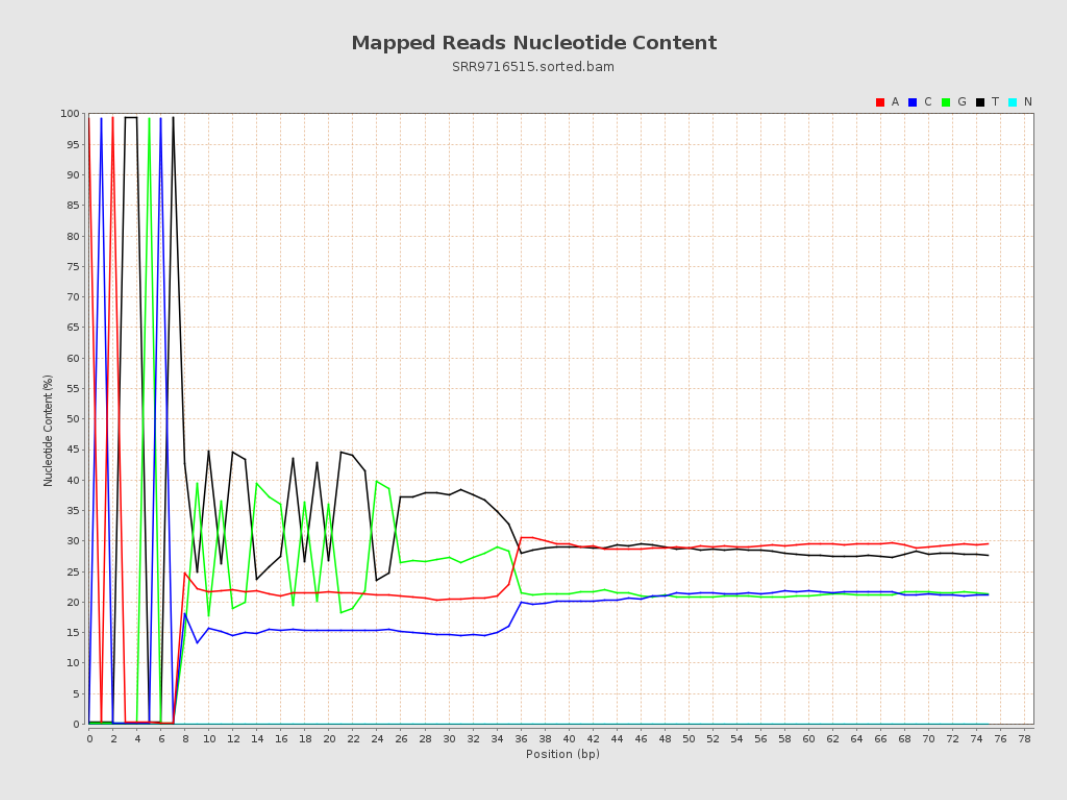
6. Results : Genome Fraction Coverage



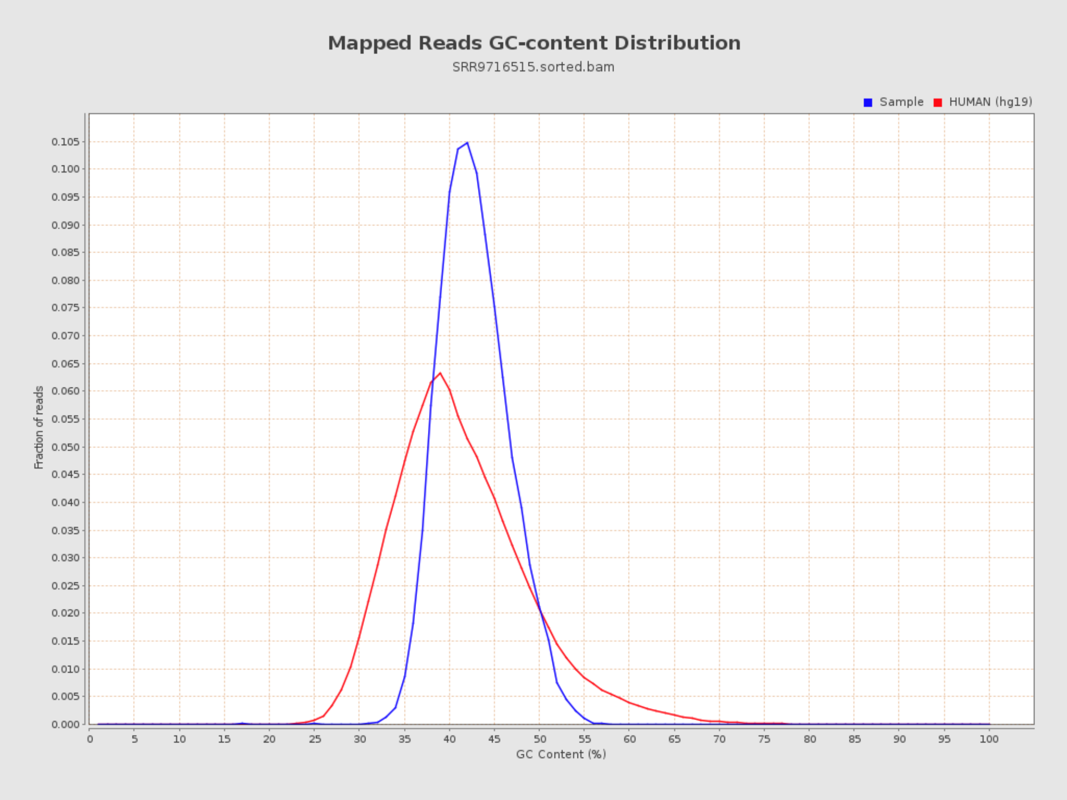
7. Results : Duplication Rate Histogram



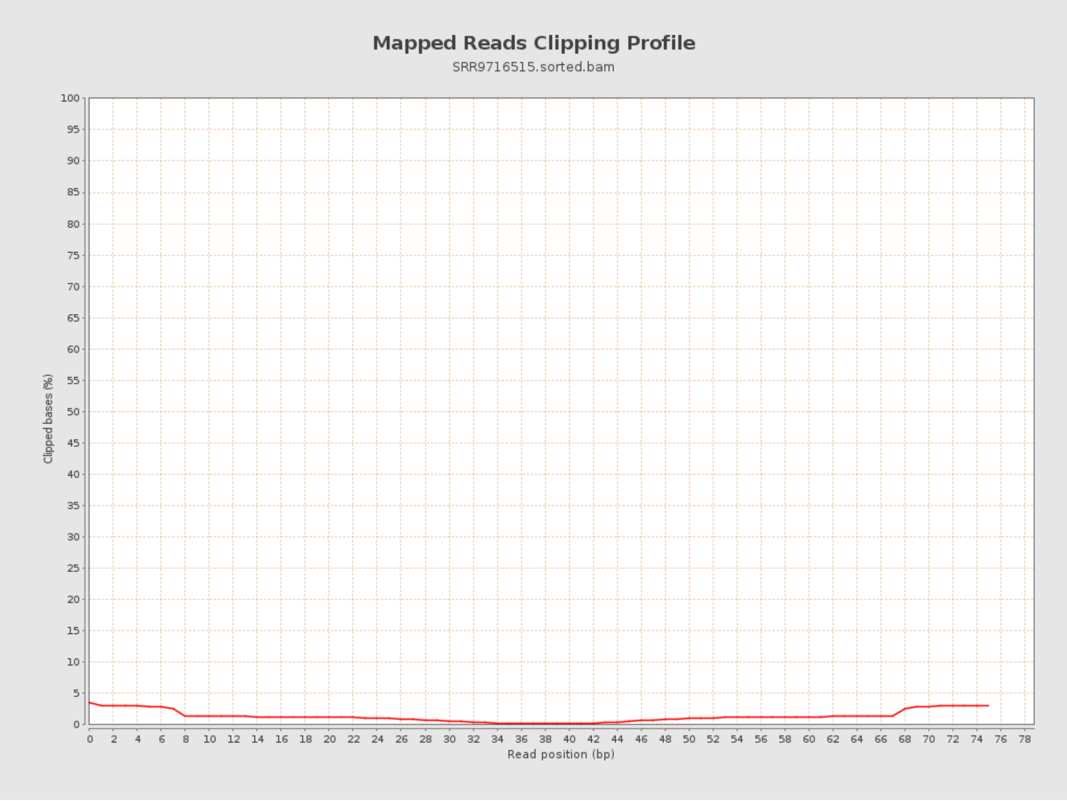
8. Results : Mapped Reads Nucleotide Content



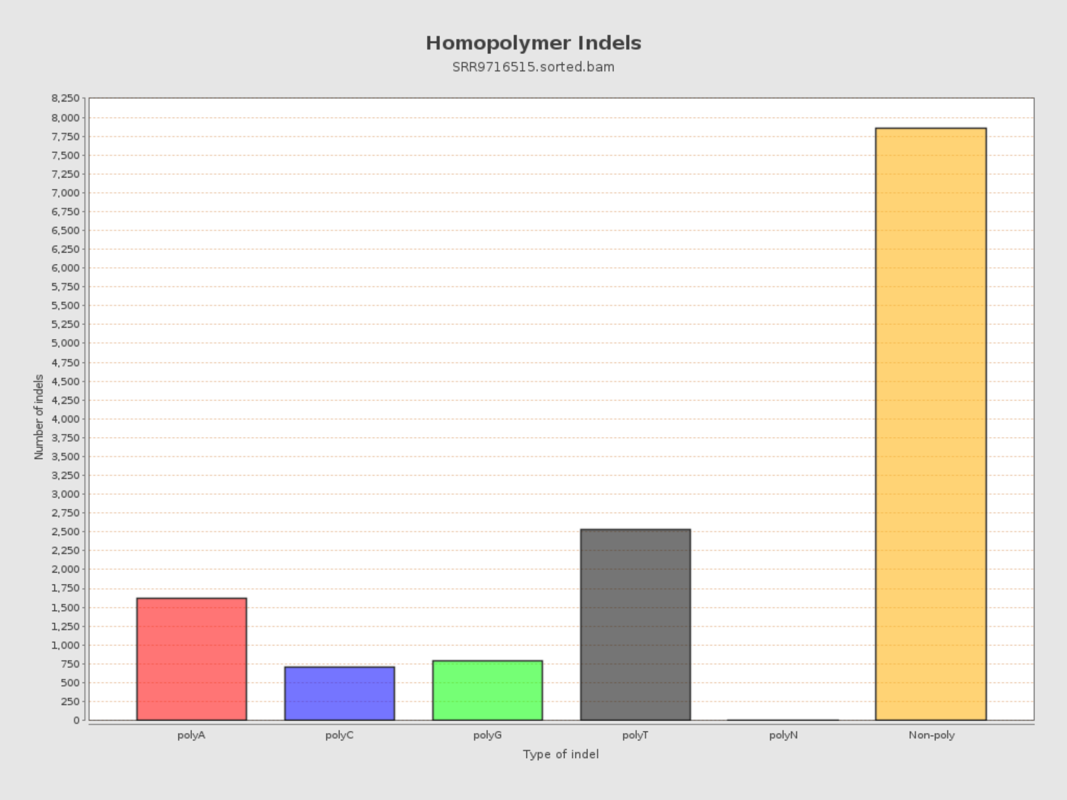
9. Results : Mapped Reads GC-content Distribution



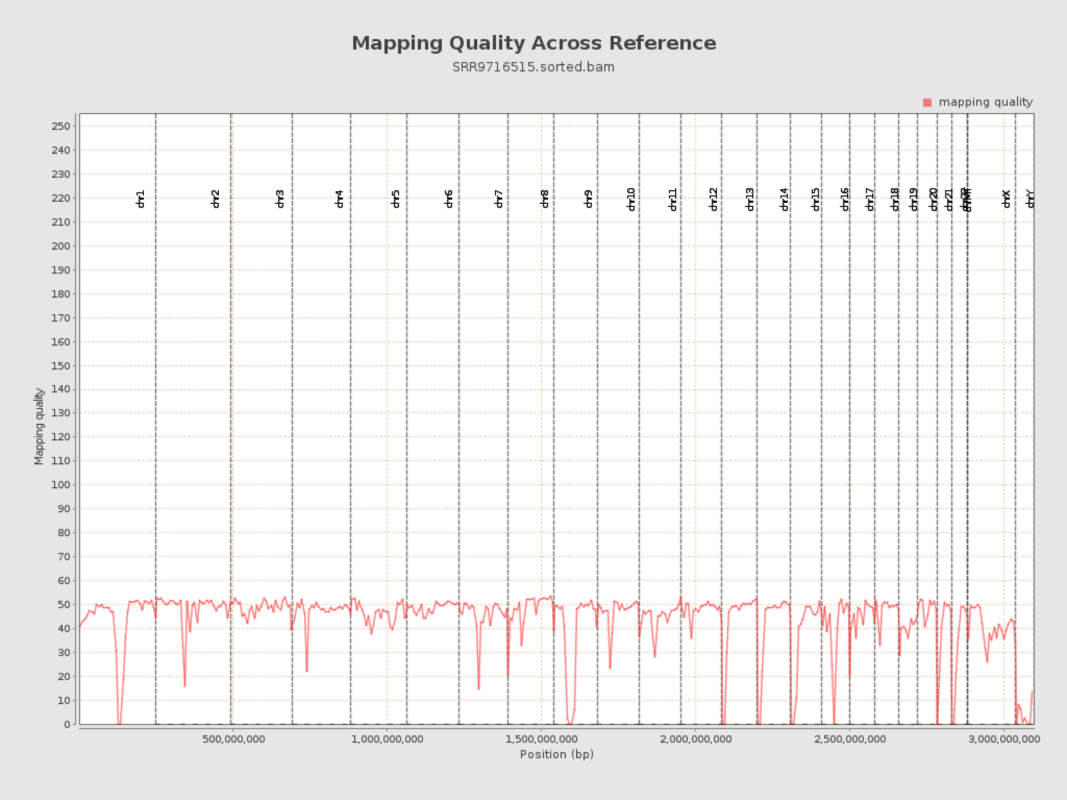
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram