Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:55:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716802.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_SRR9716802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	980,910
Mapped reads	834,524 / 85.08%
Unmapped reads	146,386 / 14.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,200 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	22,251 / 2.27%
Duplication rate	2.06%
Clipped reads	835,405 / 85.17%

2.2. ACGT Content

Number/percentage of A's	11,538,008 / 23.96%
Number/percentage of C's	9,598,010 / 19.93%
Number/percentage of T's	15,665,053 / 32.53%
Number/percentage of G's	11,353,896 / 23.58%
Number/percentage of N's	707 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1681

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

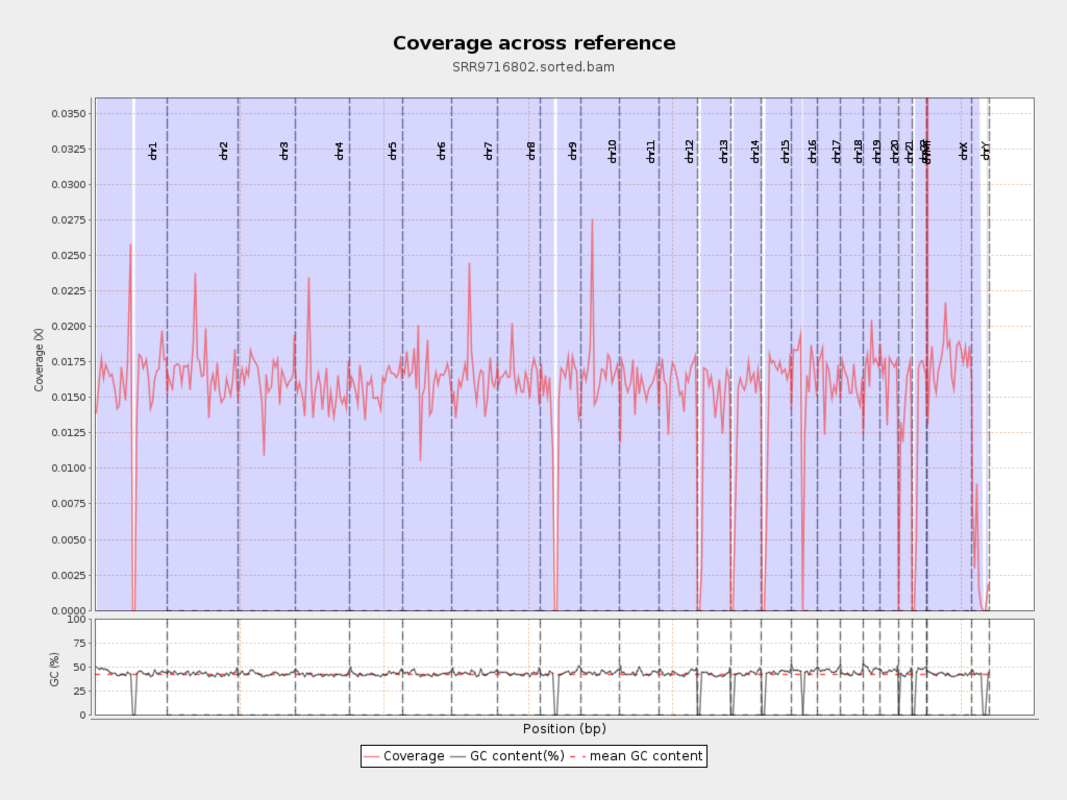
General error rate	0.52%
Mismatches	243,659
Insertions	3,752
Mapped reads with at least one insertion	0.45%
Deletions	8,862
Mapped reads with at least one deletion	1.05%
Homopolymer indels	39.35%

2.6. Chromosome stats

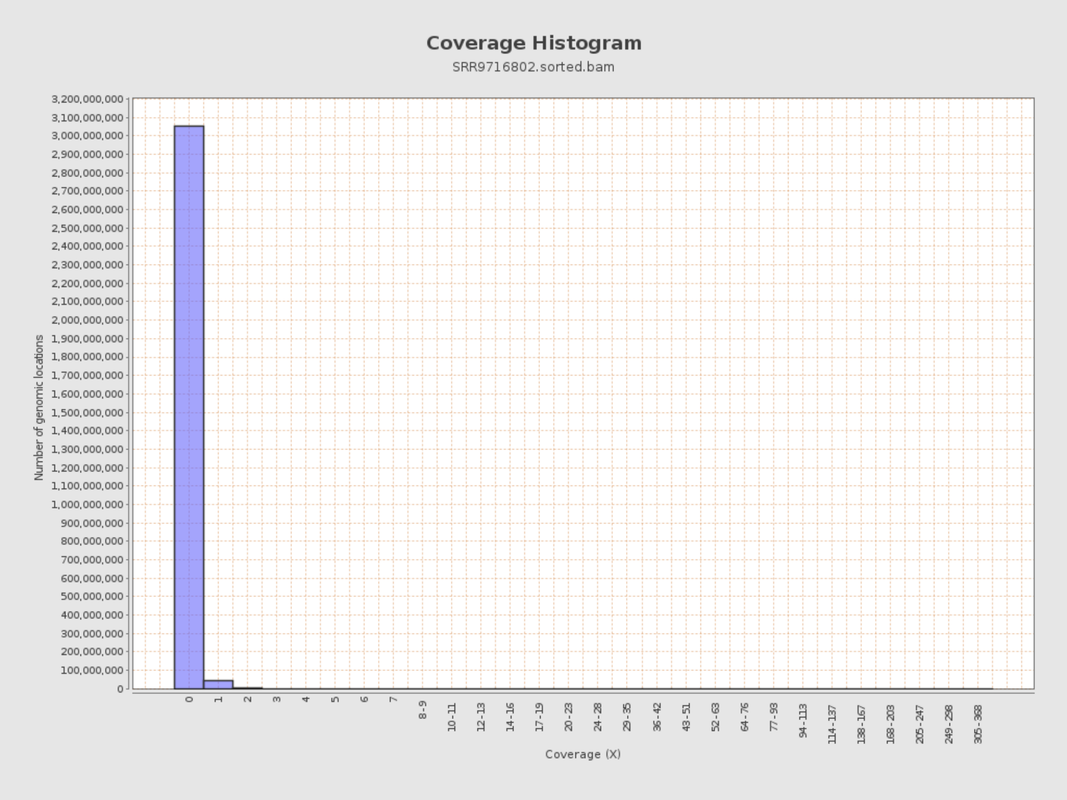
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3909051	0.0157	0.2921
chr2	243199373	4077084	0.0168	0.2059
chr3	198022430	3233067	0.0163	0.135
chr4	191154276	2999661	0.0157	0.1387
chr5	180915260	2890058	0.016	0.1342
chr6	171115067	2797108	0.0163	0.146
chr7	159138663	2609194	0.0164	0.1901

chr8	146364022	2405471	0.0164	0.154
chr9	141213431	2011702	0.0142	0.1429
chr10	135534747	2338006	0.0173	0.1662
chr11	135006516	2164952	0.016	0.1503
chr12	133851895	2164024	0.0162	0.1357
chr13	115169878	1503359	0.0131	0.1206
chr14	107349540	1437938	0.0134	0.1259
chr15	102531392	1420983	0.0139	0.1257
chr16	90354753	1395231	0.0154	0.1367
chr17	81195210	1323942	0.0163	0.1398
chr18	78077248	1249624	0.016	0.2019
chr19	59128983	1032479	0.0175	0.2013
chr20	63025520	1055000	0.0167	0.1402
chr21	48129895	640896	0.0133	0.1292
chr22	51304566	599354	0.0117	0.1142
chrMT	16571	13384	0.8077	1.0324
chrX	155270560	2740211	0.0176	0.1474
chrY	59373566	157743	0.0027	0.0794

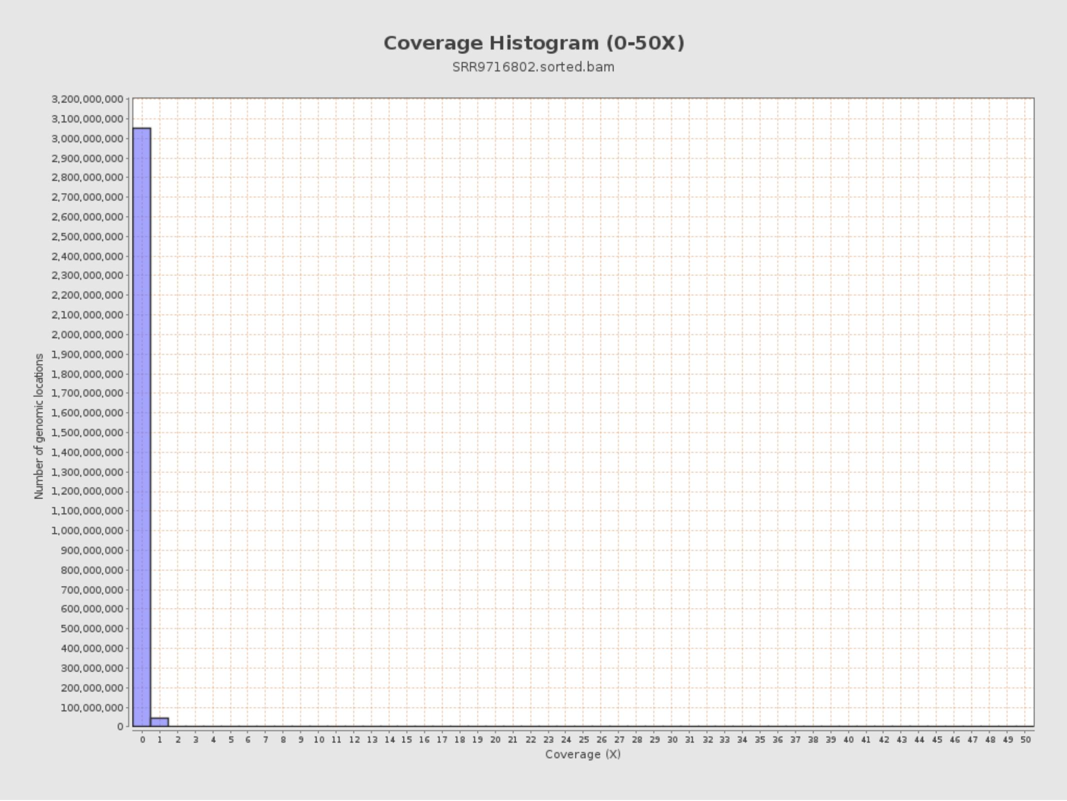
3. Results : Coverage across reference



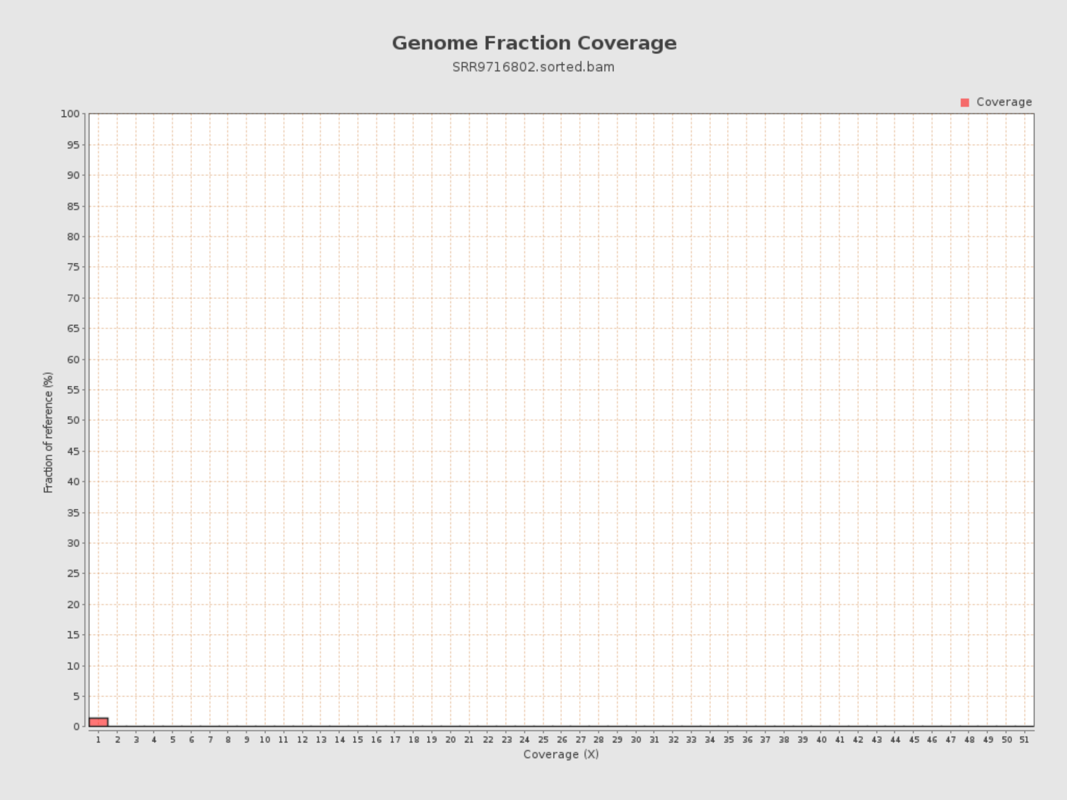
4. Results : Coverage Histogram



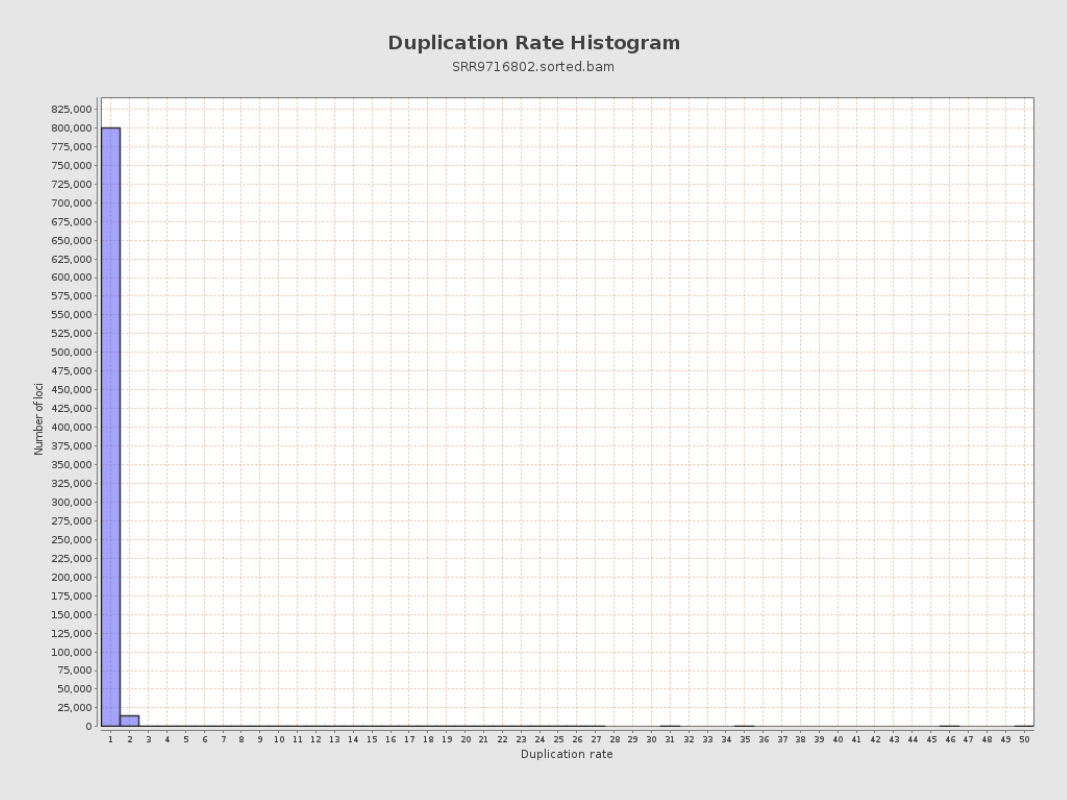
5. Results : Coverage Histogram (0-50X)



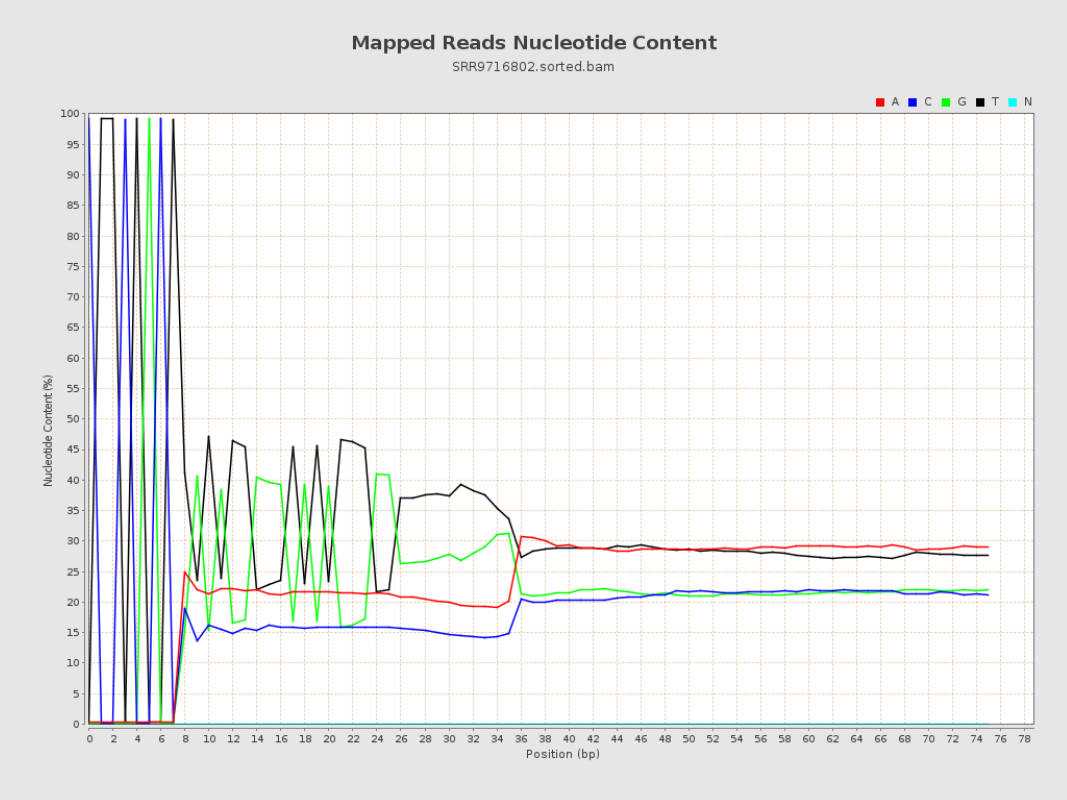
6. Results : Genome Fraction Coverage



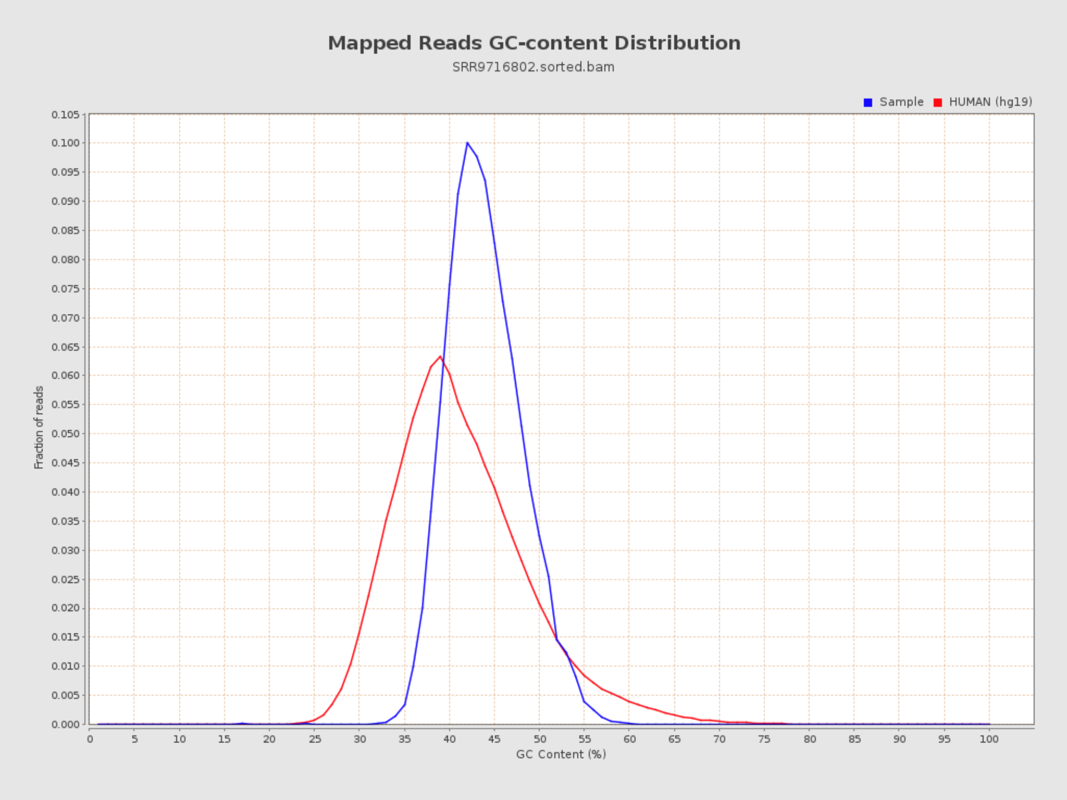
7. Results : Duplication Rate Histogram



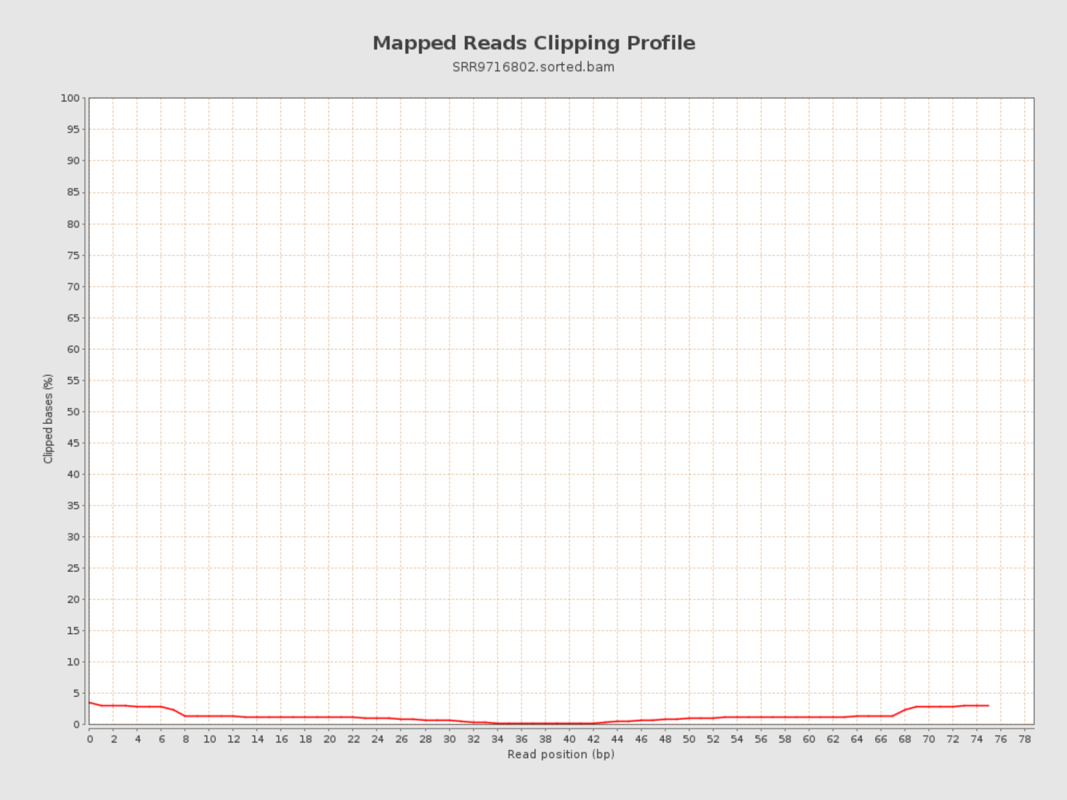
8. Results : Mapped Reads Nucleotide Content



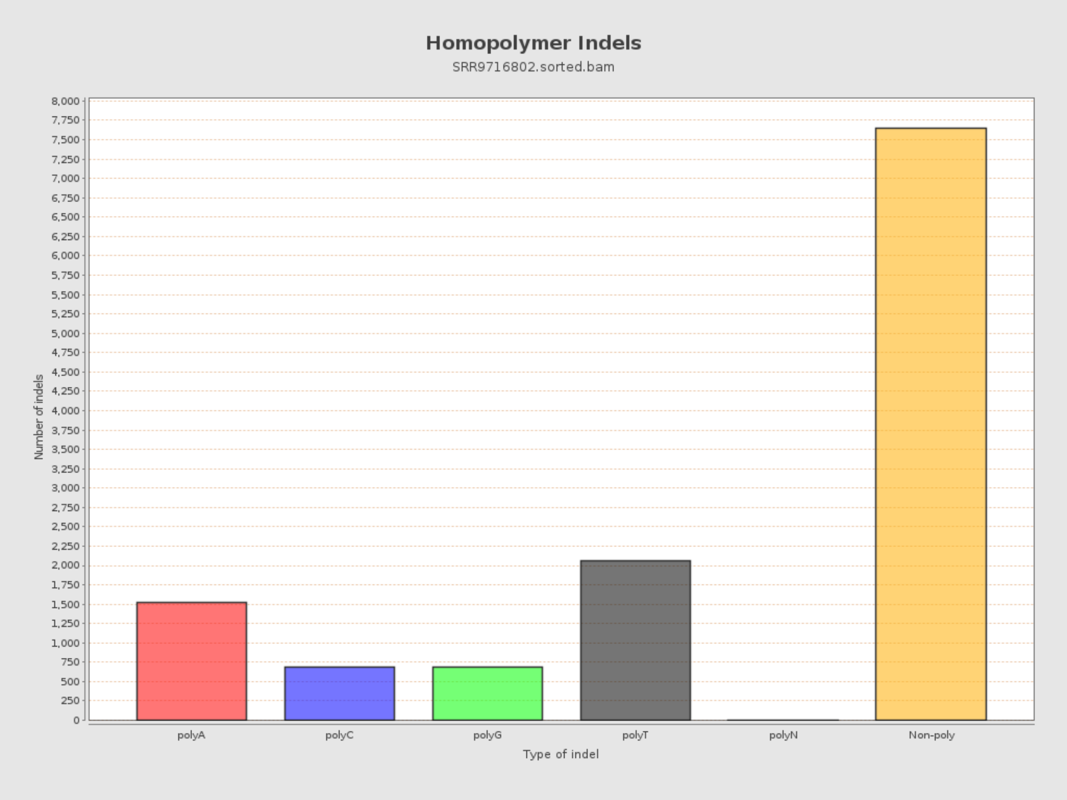
9. Results : Mapped Reads GC-content Distribution



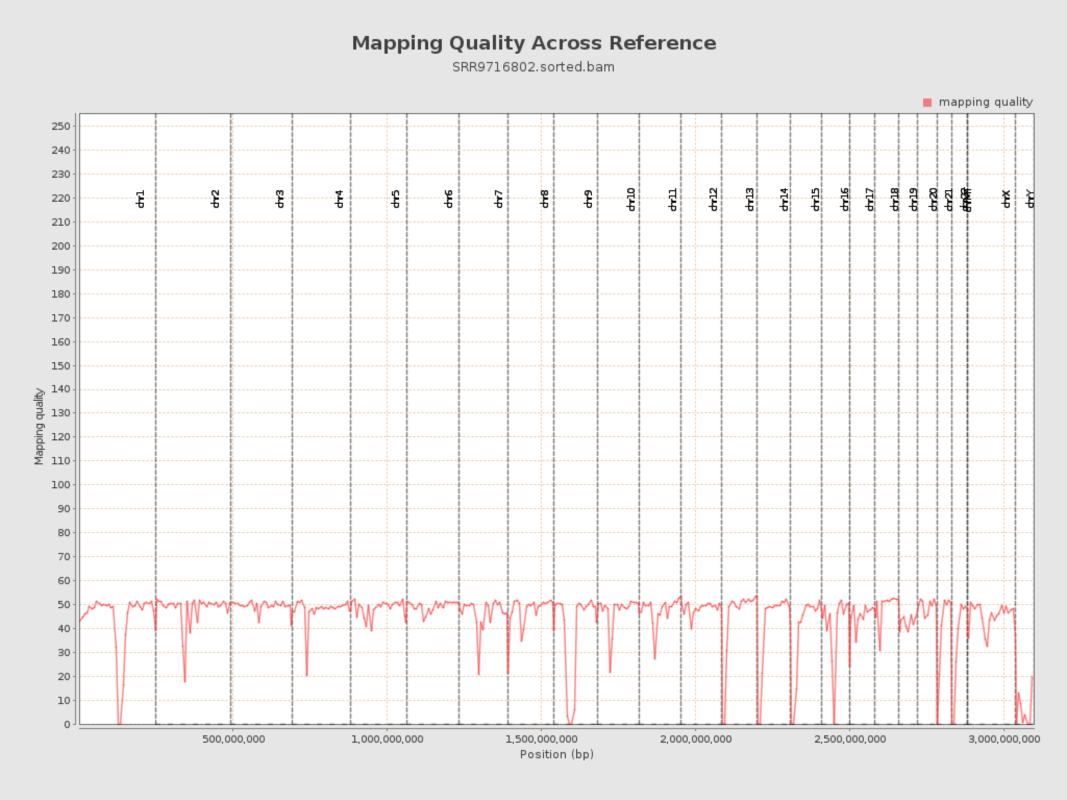
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram