Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:11:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716518.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_SRR9716518 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716518.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:11:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716518.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,276,495
Mapped reads	1,166,915 / 91.42%
Unmapped reads	109,580 / 8.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,771 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	39,115 / 3.06%
Duplication rate	2.57%
Clipped reads	1,169,398 / 91.61%

2.2. ACGT Content

Number/percentage of A's	16,863,580 / 24.88%
Number/percentage of C's	12,196,189 / 17.99%
Number/percentage of T's	21,149,085 / 31.2%
Number/percentage of G's	17,570,777 / 25.92%
Number/percentage of N's	1,918 / 0%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0219

Standard Deviation	0.2168

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

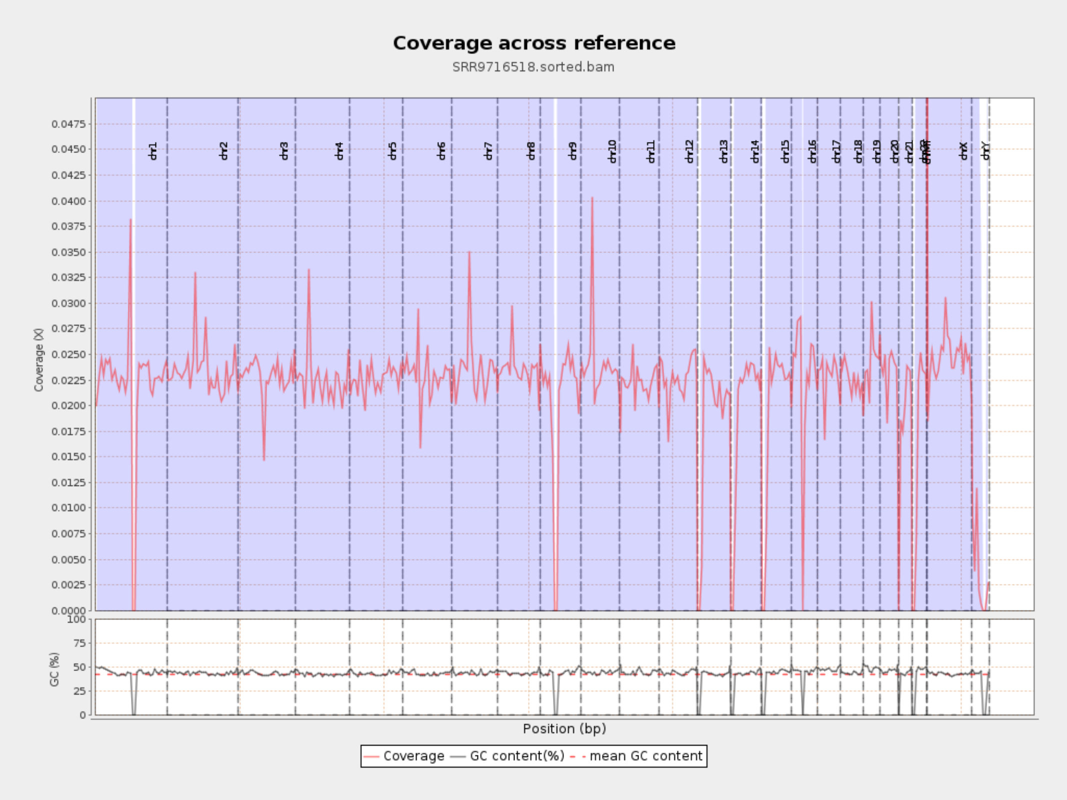
General error rate	0.52%
Mismatches	343,862
Insertions	4,551
Mapped reads with at least one insertion	0.39%
Deletions	12,981
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.09%

2.6. Chromosome stats

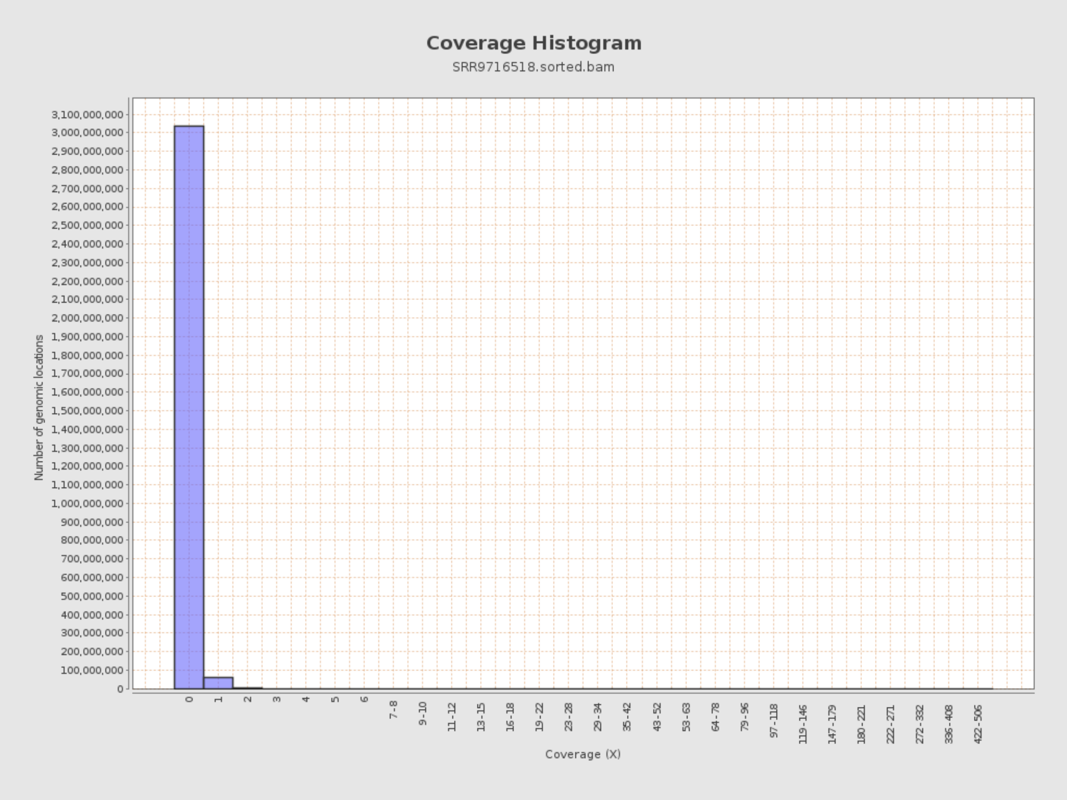
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5471314	0.022	0.3867
chr2	243199373	5700817	0.0234	0.2735
chr3	198022430	4510693	0.0228	0.163
chr4	191154276	4317458	0.0226	0.1705
chr5	180915260	4103136	0.0227	0.163
chr6	171115067	3921919	0.0229	0.1846
chr7	159138663	3774520	0.0237	0.2552

chr8	146364022	3447957	0.0236	0.2034
chr9	141213431	2838721	0.0201	0.1836
chr10	135534747	3279230	0.0242	0.2149
chr11	135006516	3015203	0.0223	0.1898
chr12	133851895	3034091	0.0227	0.1636
chr13	115169878	2090661	0.0182	0.1459
chr14	107349540	2038062	0.019	0.1505
chr15	102531392	1953360	0.0191	0.1501
chr16	90354753	1993773	0.0221	0.1683
chr17	81195210	1854814	0.0228	0.1692
chr18	78077248	1769606	0.0227	0.2791
chr19	59128983	1443526	0.0244	0.284
chr20	63025520	1464177	0.0232	0.1658
chr21	48129895	902552	0.0188	0.1596
chr22	51304566	822219	0.016	0.1362
chrMT	16571	2831	0.1708	0.4181
chrX	155270560	3841479	0.0247	0.1828
chrY	59373566	210215	0.0035	0.099

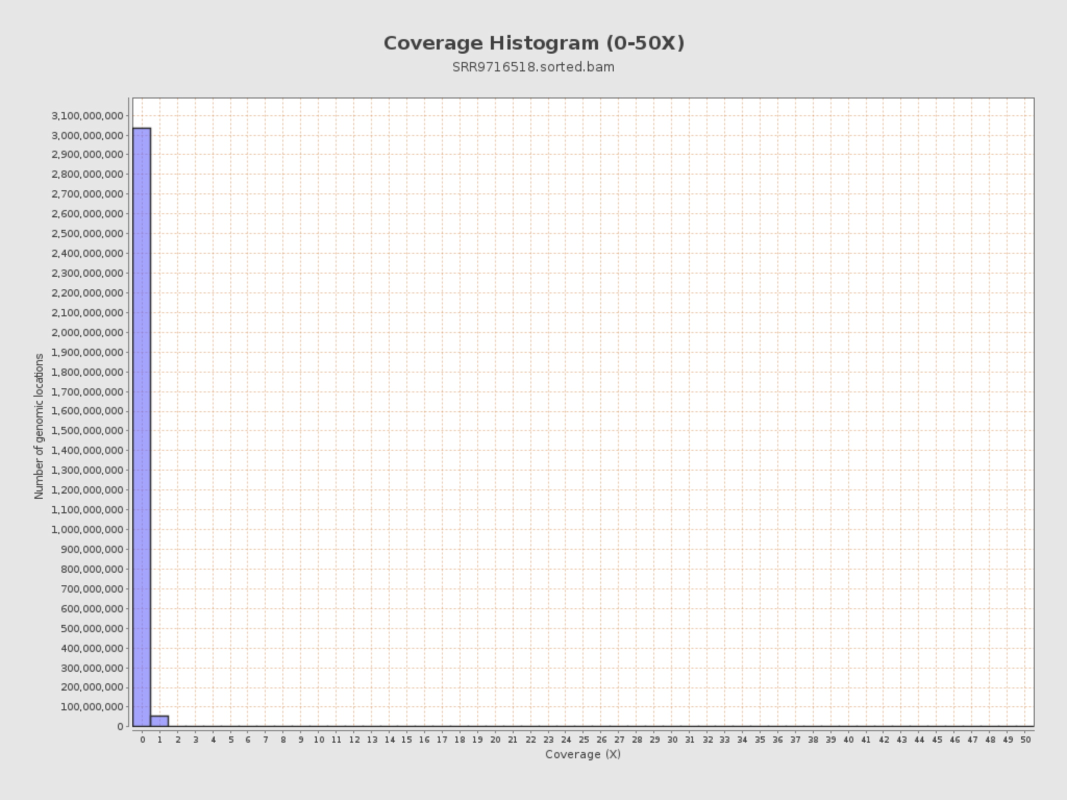
3. Results : Coverage across reference



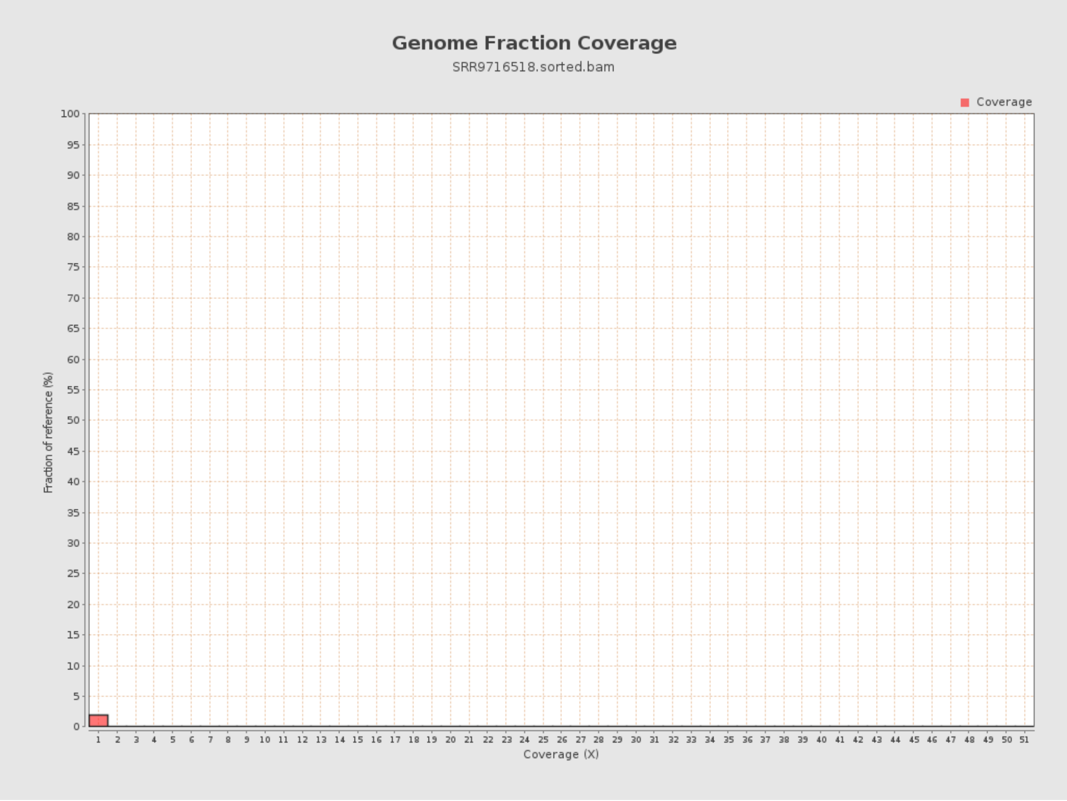
4. Results : Coverage Histogram



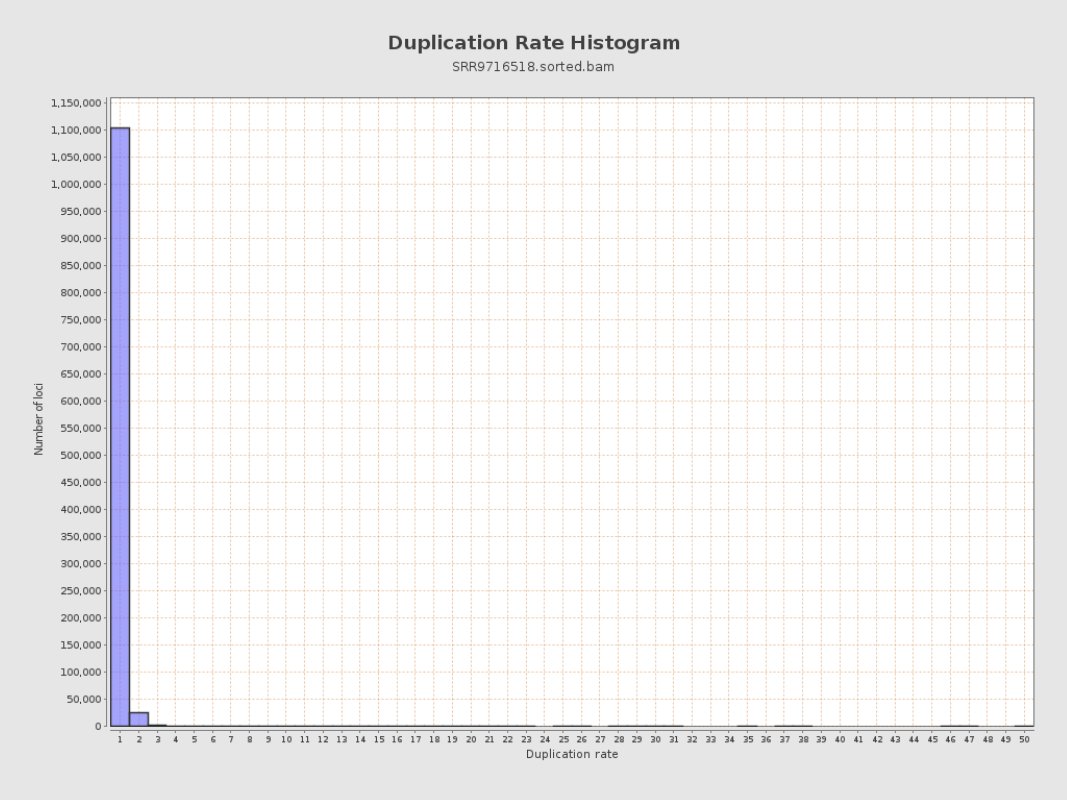
5. Results : Coverage Histogram (0-50X)



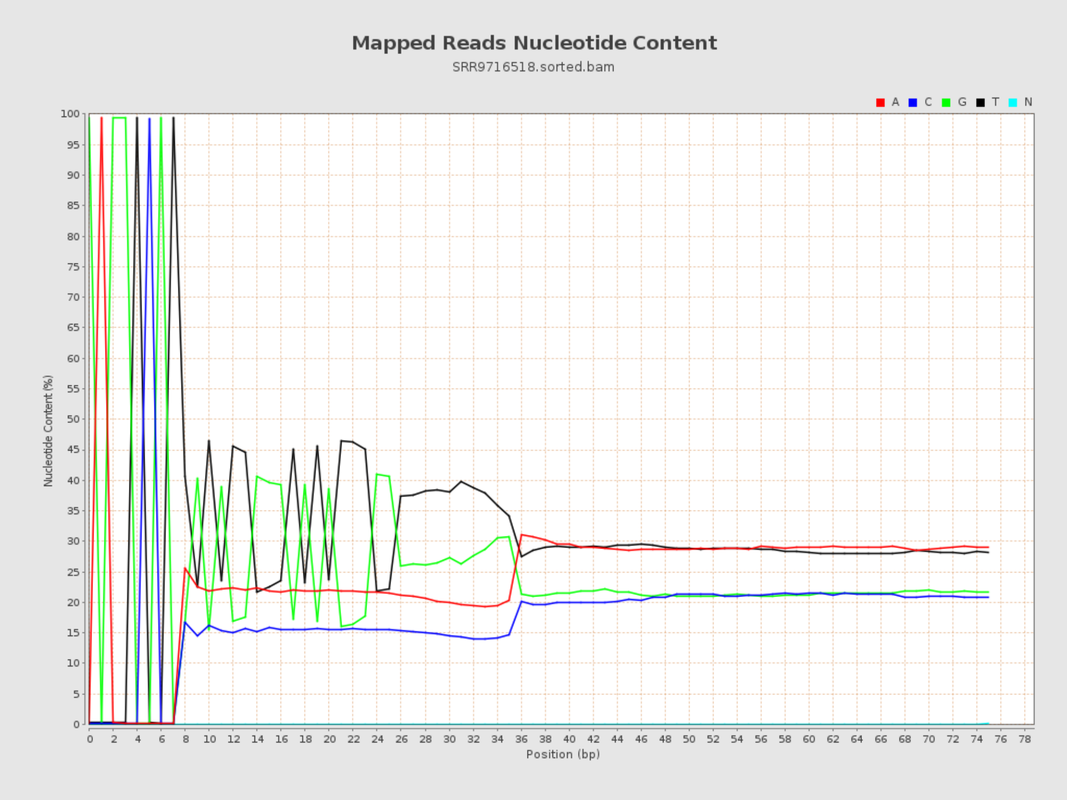
6. Results : Genome Fraction Coverage



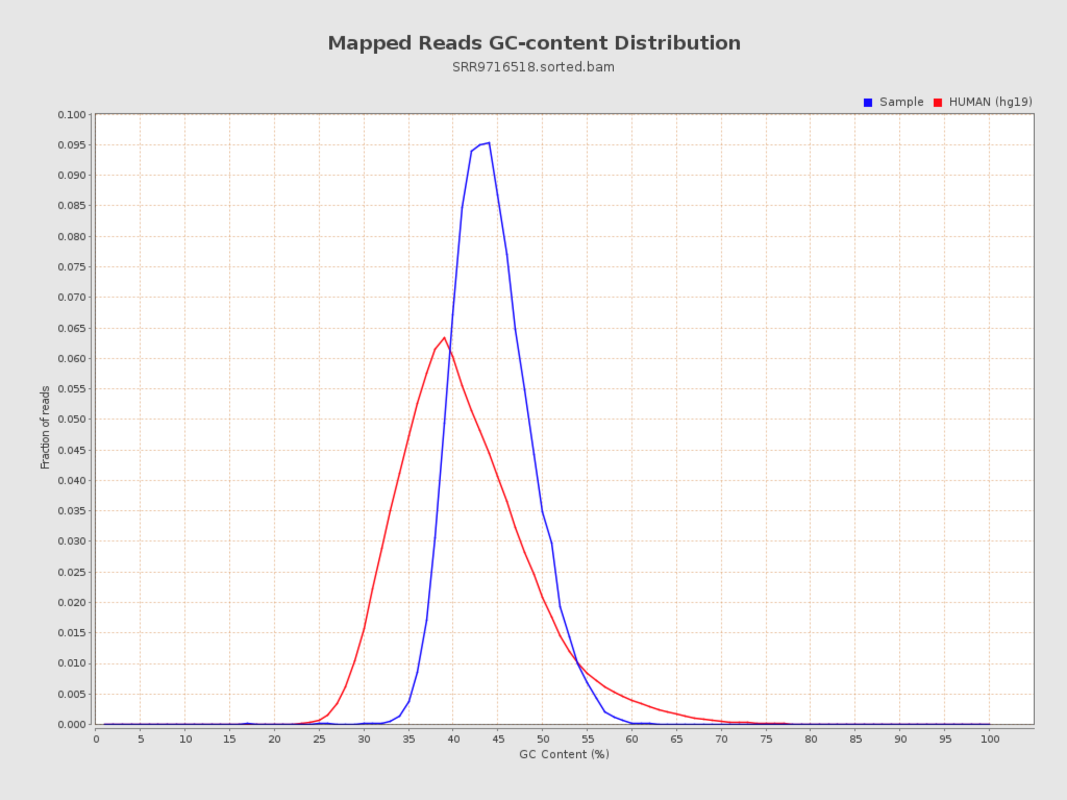
7. Results : Duplication Rate Histogram



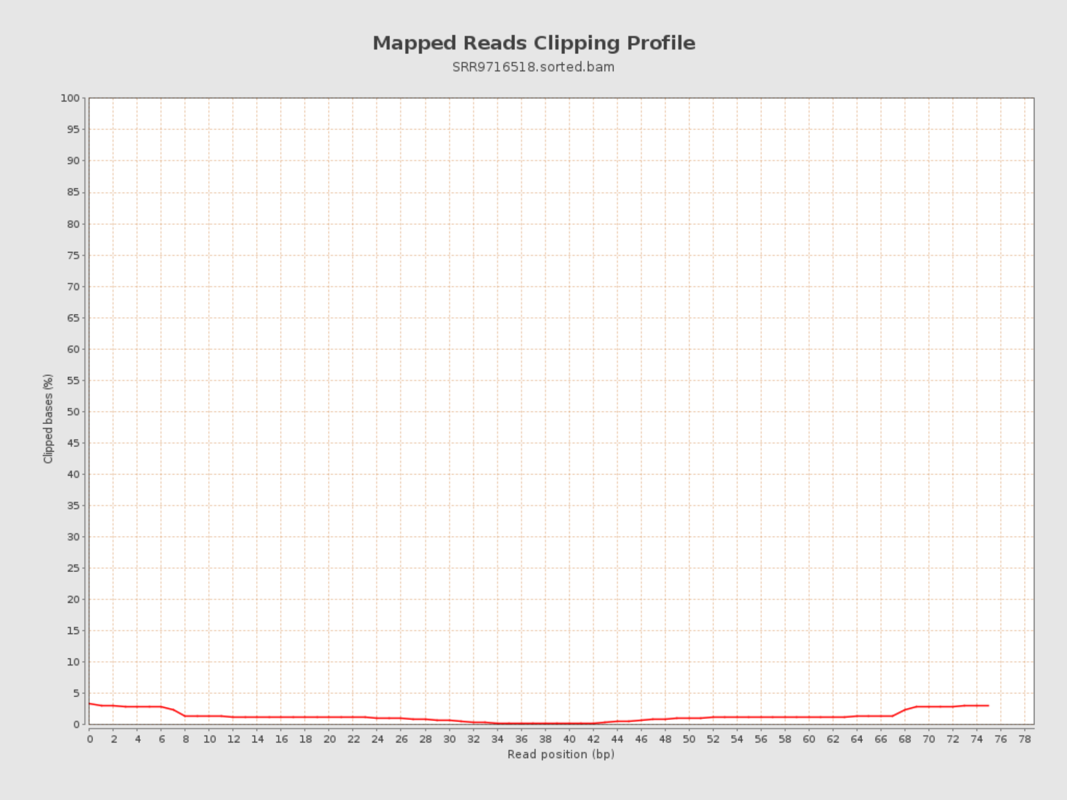
8. Results : Mapped Reads Nucleotide Content



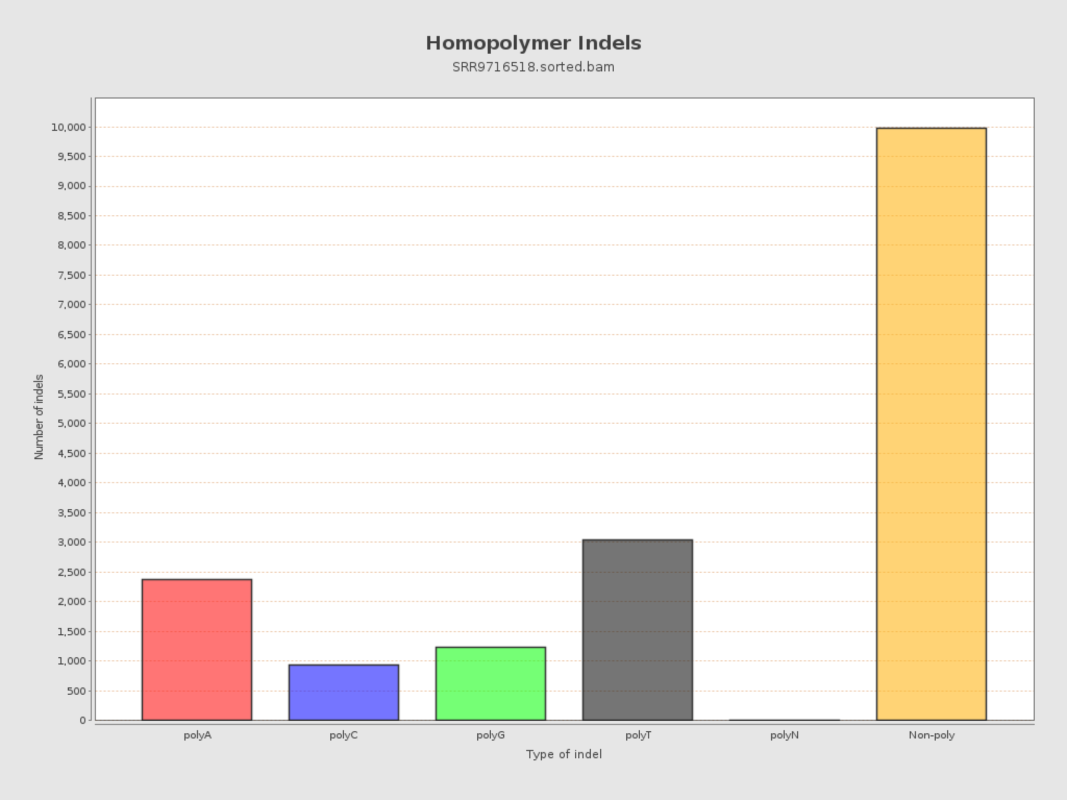
9. Results : Mapped Reads GC-content Distribution



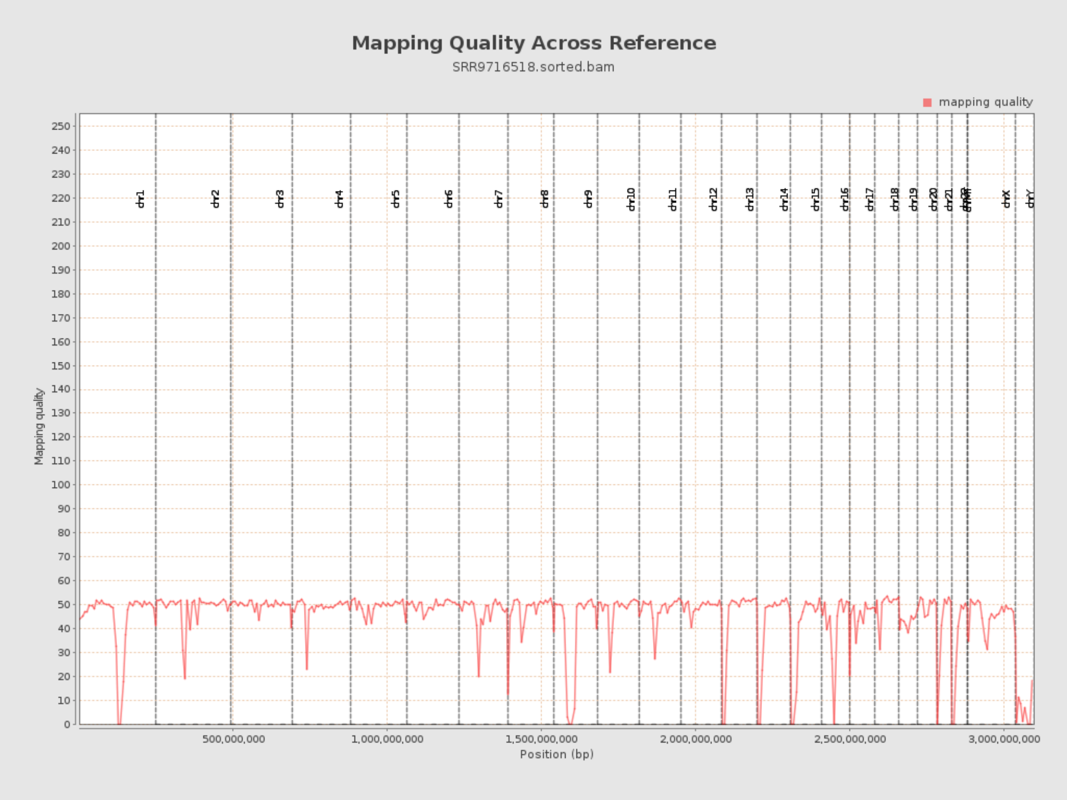
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram