Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:25:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716537.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_SRR9716537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:25:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	561,071
Mapped reads	493,840 / 88.02%
Unmapped reads	67,231 / 11.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,972 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,856 / 1.76%
Duplication rate	1.57%
Clipped reads	494,730 / 88.18%

2.2. ACGT Content

Number/percentage of A's	7,335,446 / 25.8%
Number/percentage of C's	5,291,053 / 18.61%
Number/percentage of T's	9,192,573 / 32.33%
Number/percentage of G's	6,610,246 / 23.25%
Number/percentage of N's	793 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1167

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

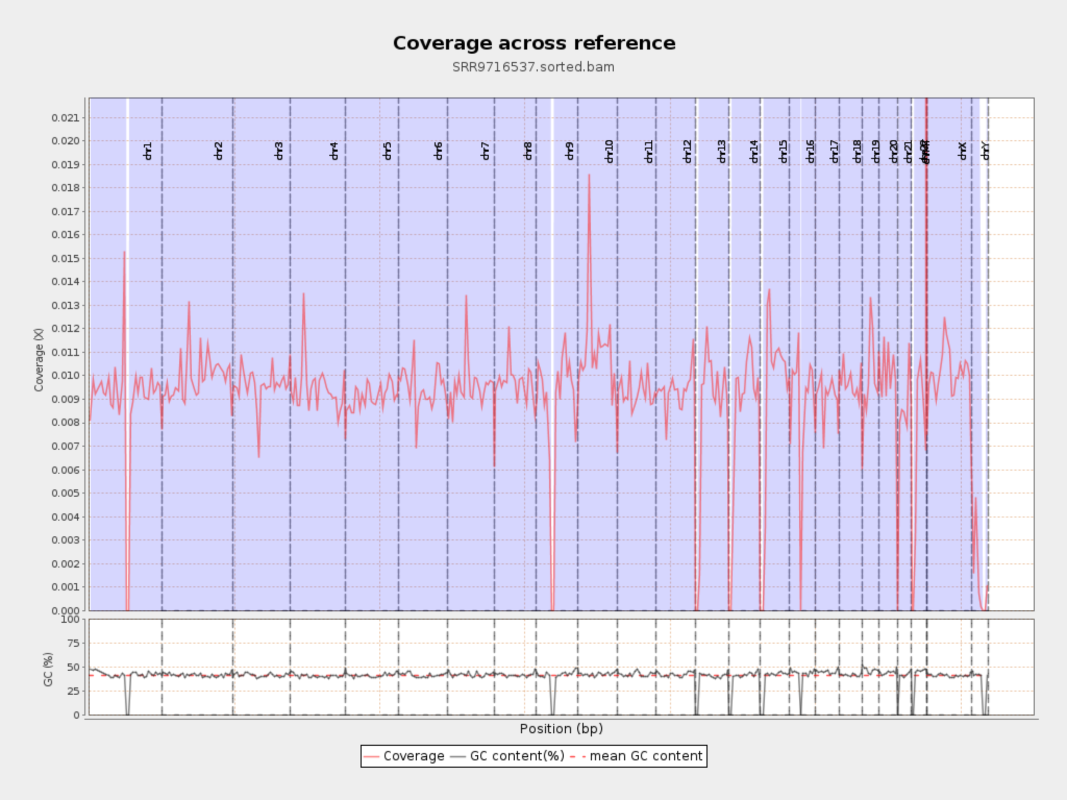
General error rate	0.51%
Mismatches	142,278
Insertions	2,103
Mapped reads with at least one insertion	0.42%
Deletions	5,181
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.85%

2.6. Chromosome stats

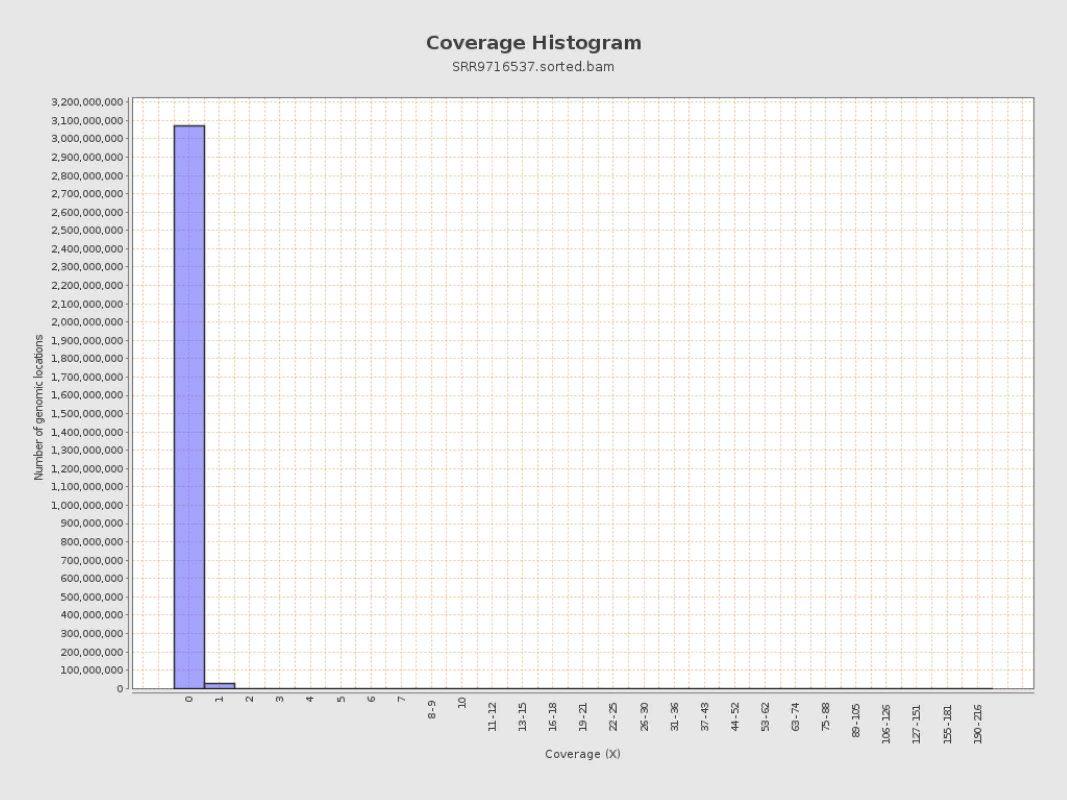
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2229100	0.0089	0.1765
chr2	243199373	2425988	0.01	0.1399
chr3	198022430	1898627	0.0096	0.1014
chr4	191154276	1806517	0.0095	0.103
chr5	180915260	1649640	0.0091	0.0989
chr6	171115067	1624894	0.0095	0.1059
chr7	159138663	1528053	0.0096	0.1256

chr8	146364022	1423709	0.0097	0.1127
chr9	141213431	1201937	0.0085	0.1059
chr10	135534747	1512019	0.0112	0.1241
chr11	135006516	1252943	0.0093	0.1069
chr12	133851895	1256160	0.0094	0.1007
chr13	115169878	940776	0.0082	0.0934
chr14	107349540	880647	0.0082	0.0961
chr15	102531392	918757	0.009	0.0984
chr16	90354753	788866	0.0087	0.1002
chr17	81195210	739243	0.0091	0.1002
chr18	78077248	756001	0.0097	0.1477
chr19	59128983	595563	0.0101	0.1359
chr20	63025520	628870	0.01	0.1037
chr21	48129895	386526	0.008	0.0959
chr22	51304566	329462	0.0064	0.0829
chrMT	16571	8031	0.4846	0.748
chrX	155270560	1570254	0.0101	0.1073
chrY	59373566	85799	0.0014	0.0483

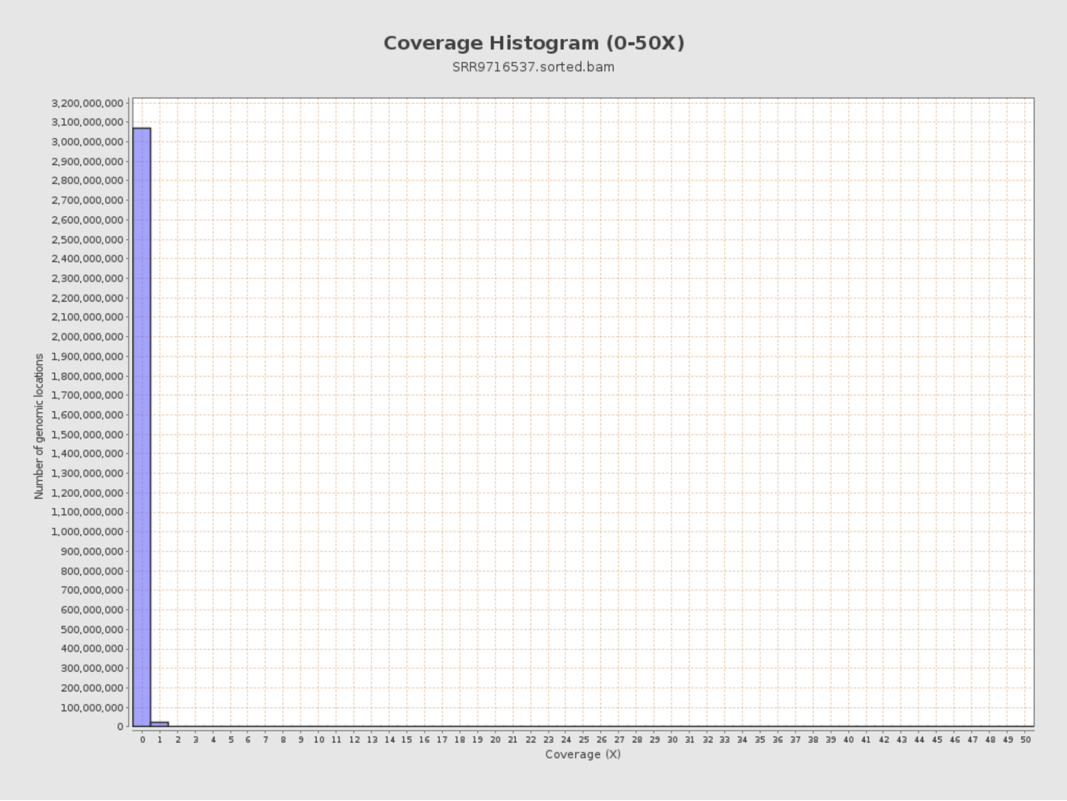
3. Results : Coverage across reference



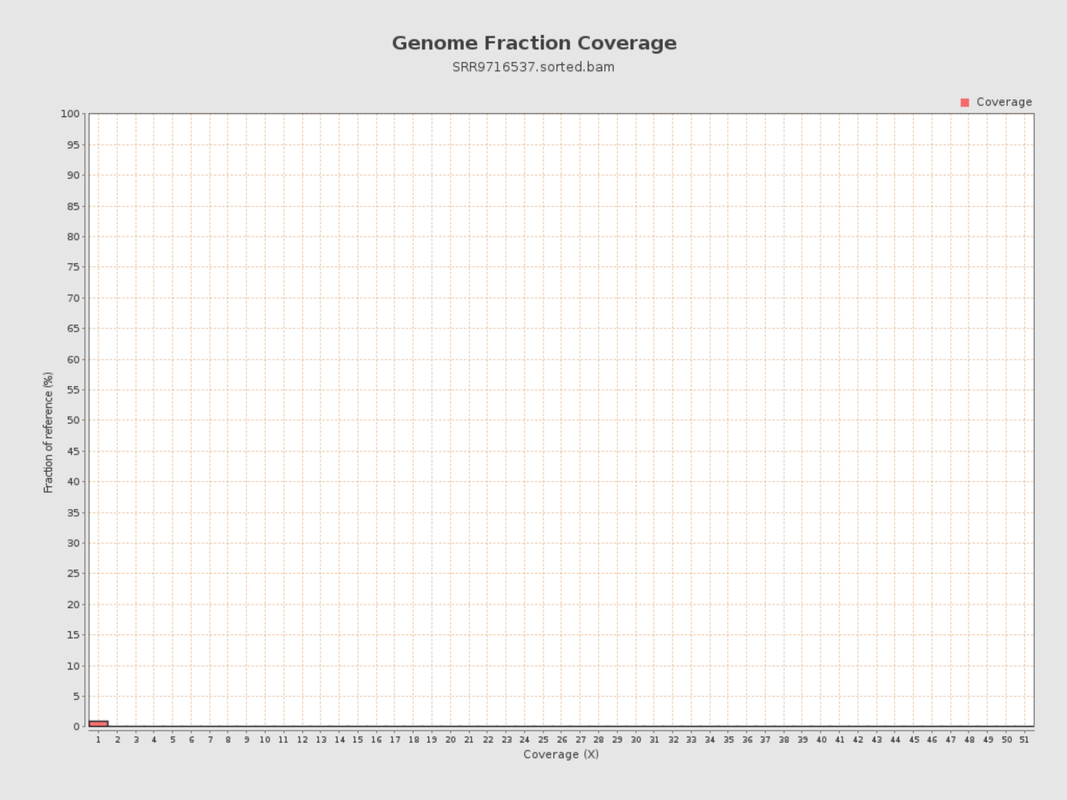
4. Results : Coverage Histogram



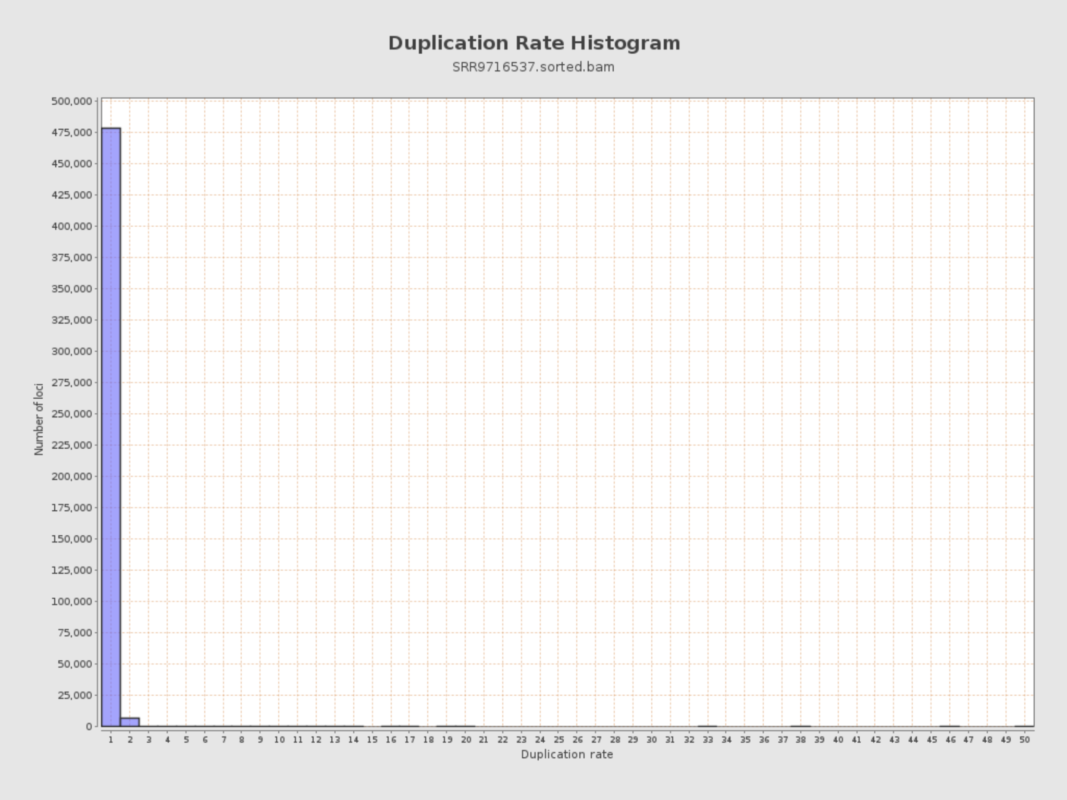
5. Results : Coverage Histogram (0-50X)



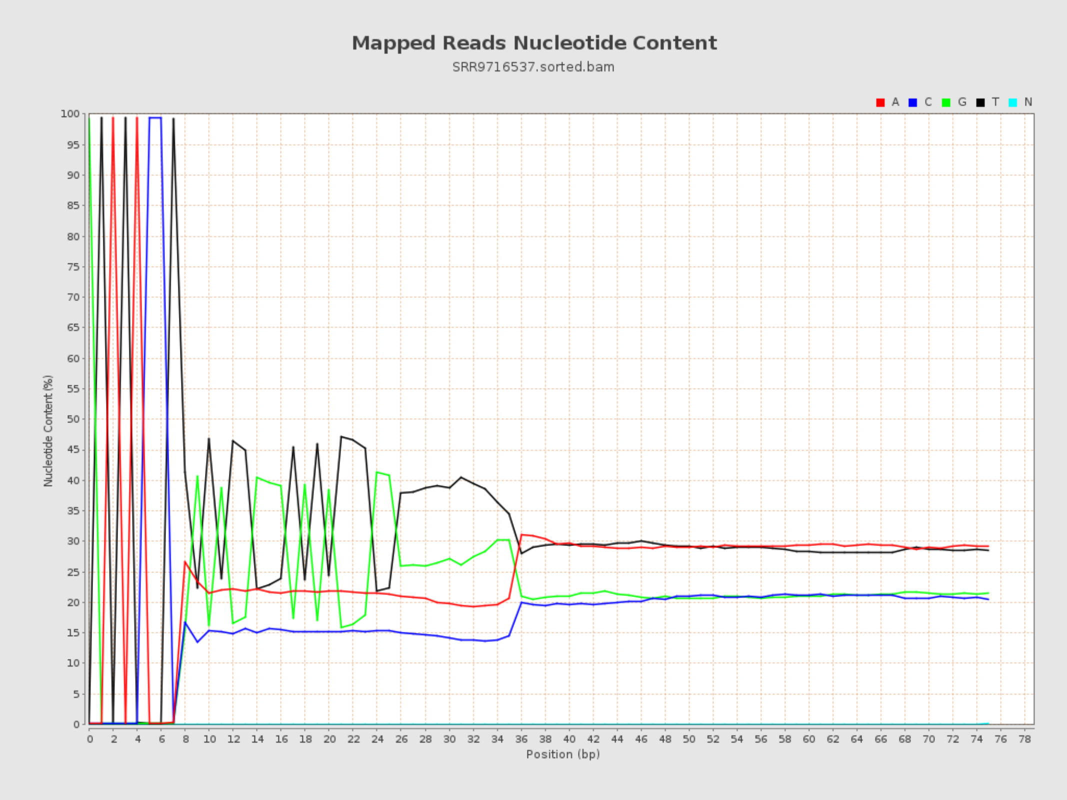
6. Results : Genome Fraction Coverage



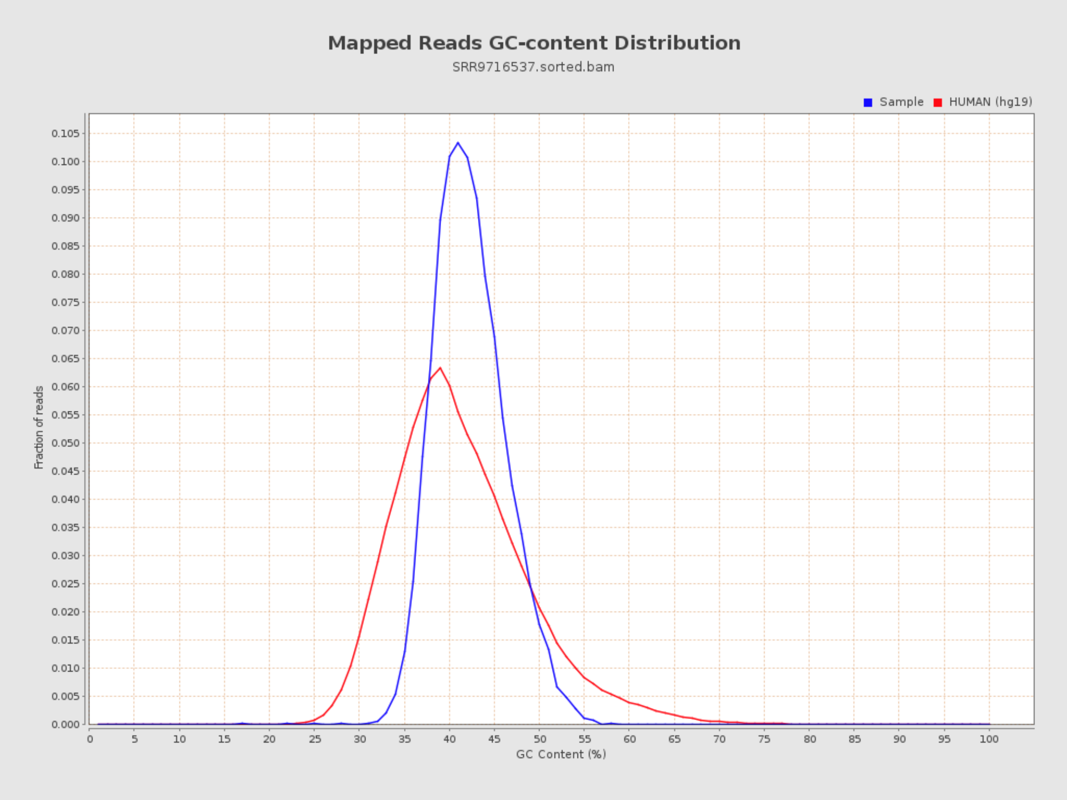
7. Results : Duplication Rate Histogram



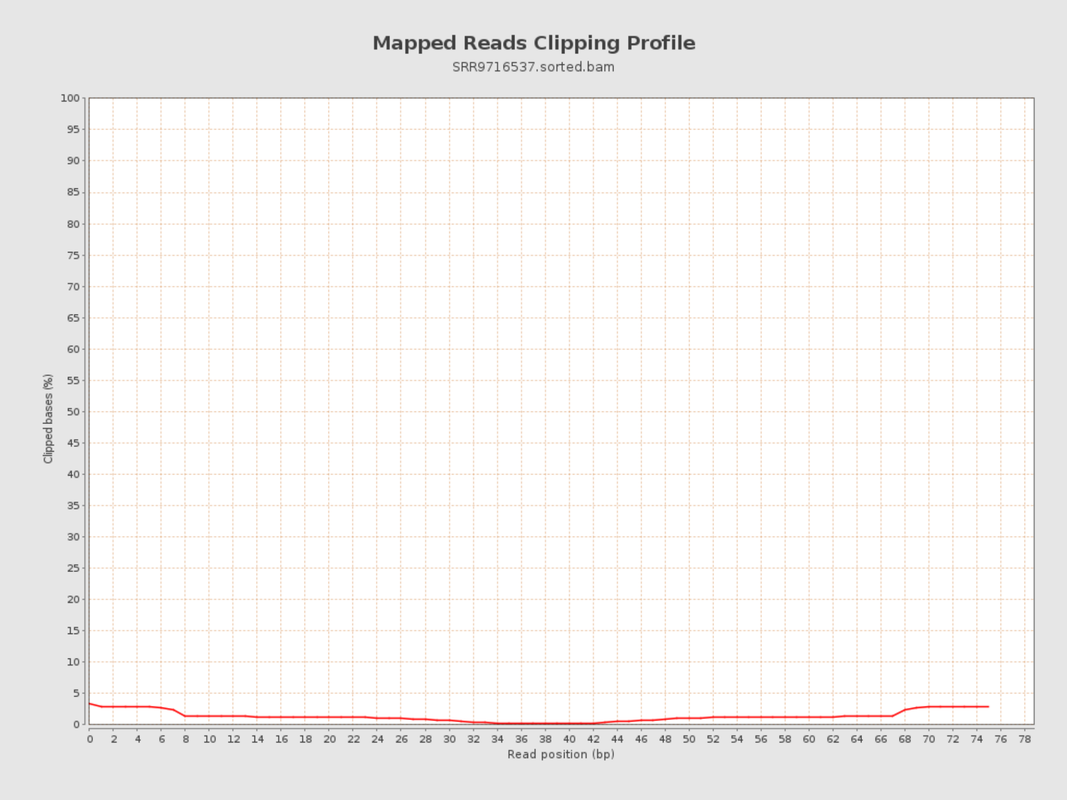
8. Results : Mapped Reads Nucleotide Content



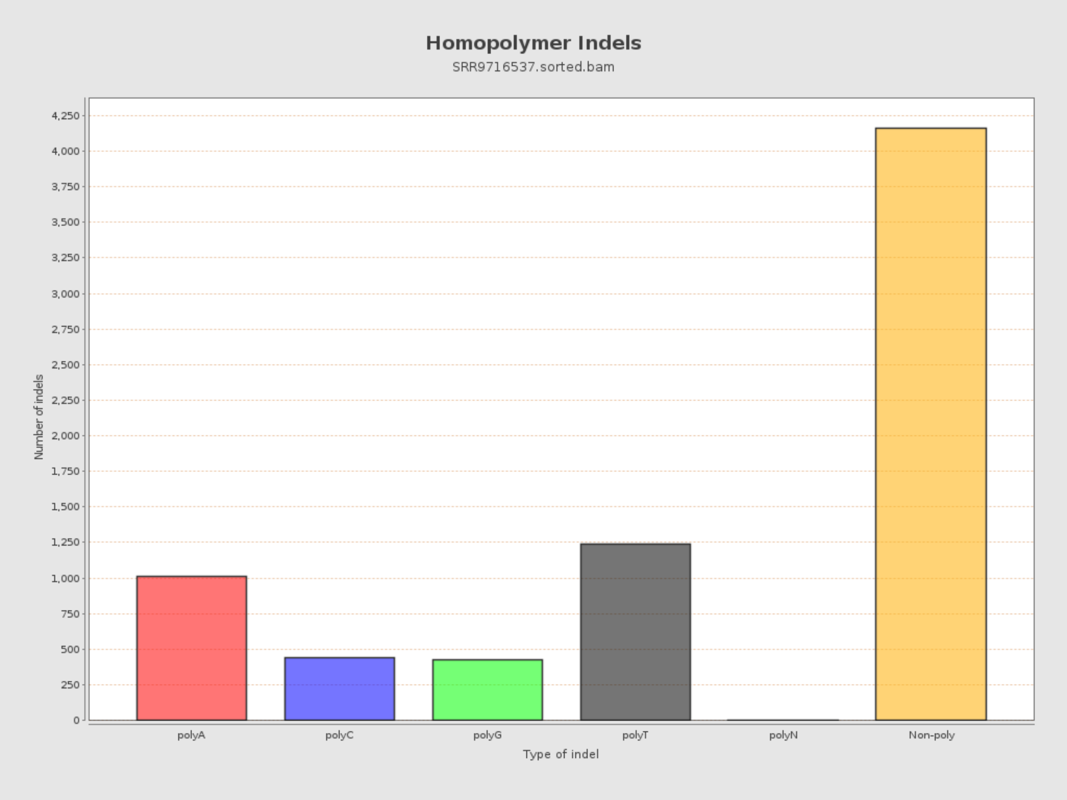
9. Results : Mapped Reads GC-content Distribution



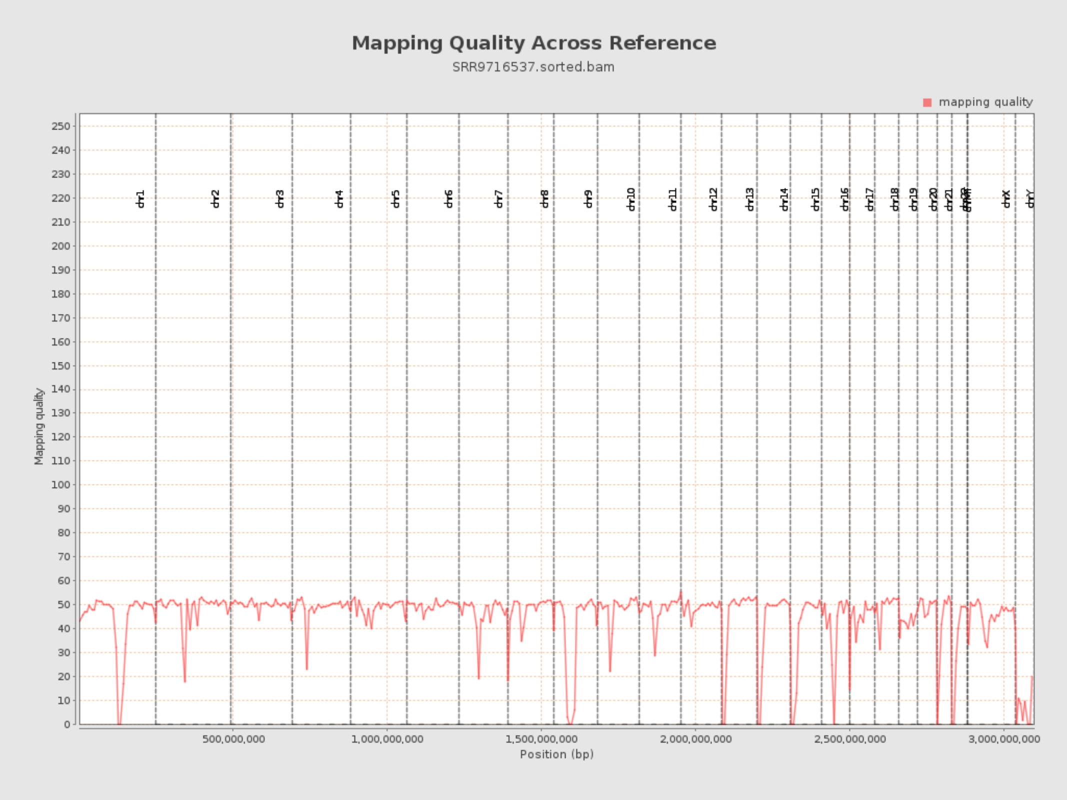
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram