Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:58:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716237.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_SRR9716237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:58:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	572,574
Mapped reads	508,227 / 88.76%
Unmapped reads	64,347 / 11.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,844 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	7,515 / 1.31%
Duplication rate	1.1%
Clipped reads	509,808 / 89.04%

2.2. ACGT Content

Number/percentage of A's	7,070,016 / 24.54%
Number/percentage of C's	5,310,547 / 18.44%
Number/percentage of T's	9,274,355 / 32.2%
Number/percentage of G's	7,150,449 / 24.82%
Number/percentage of N's	625 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1114

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Mismatches and indels

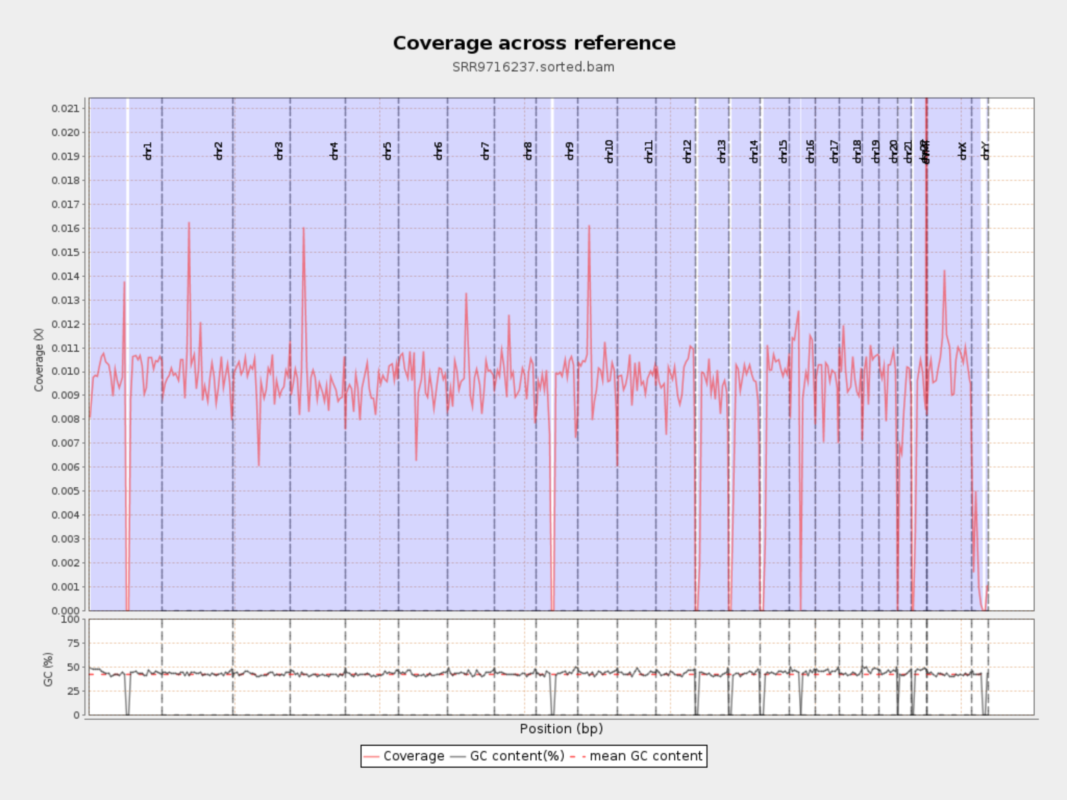
General error rate	0.52%
Mismatches	144,387
Insertions	2,117
Mapped reads with at least one insertion	0.41%
Deletions	4,639
Mapped reads with at least one deletion	0.91%
Homopolymer indels	39.74%

2.6. Chromosome stats

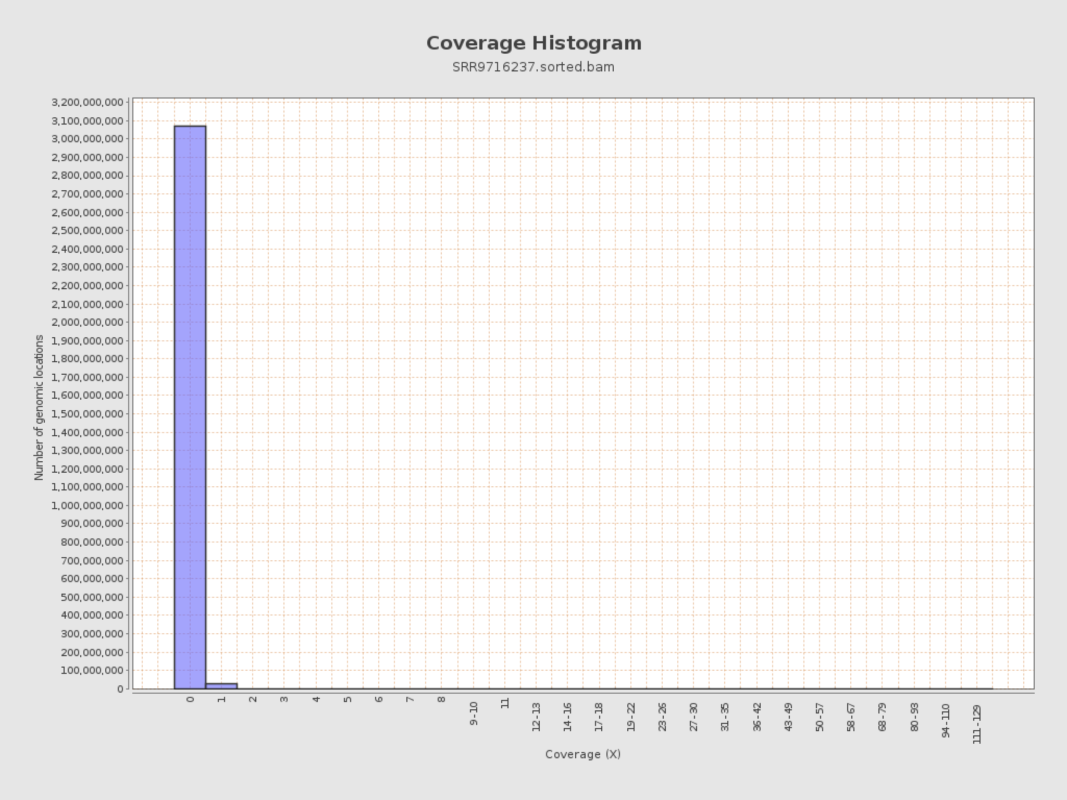
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2369627	0.0095	0.1432
chr2	243199373	2435990	0.01	0.1236
chr3	198022430	1909010	0.0096	0.1012
chr4	191154276	1839946	0.0096	0.1045
chr5	180915260	1709736	0.0095	0.1005
chr6	171115067	1657056	0.0097	0.1042
chr7	159138663	1552414	0.0098	0.1167

chr8	146364022	1437744	0.0098	0.1081
chr9	141213431	1207746	0.0086	0.1118
chr10	135534747	1386431	0.0102	0.1161
chr11	135006516	1302468	0.0096	0.111
chr12	133851895	1300613	0.0097	0.1032
chr13	115169878	911979	0.0079	0.0912
chr14	107349540	870835	0.0081	0.0952
chr15	102531392	848988	0.0083	0.0938
chr16	90354753	875850	0.0097	0.1057
chr17	81195210	775820	0.0096	0.1025
chr18	78077248	777511	0.01	0.16
chr19	59128983	601712	0.0102	0.1254
chr20	63025520	614935	0.0098	0.1038
chr21	48129895	370960	0.0077	0.0937
chr22	51304566	342634	0.0067	0.0839
chrMT	16571	1295	0.0781	0.285
chrX	155270560	1622767	0.0105	0.1133
chrY	59373566	89757	0.0015	0.0496

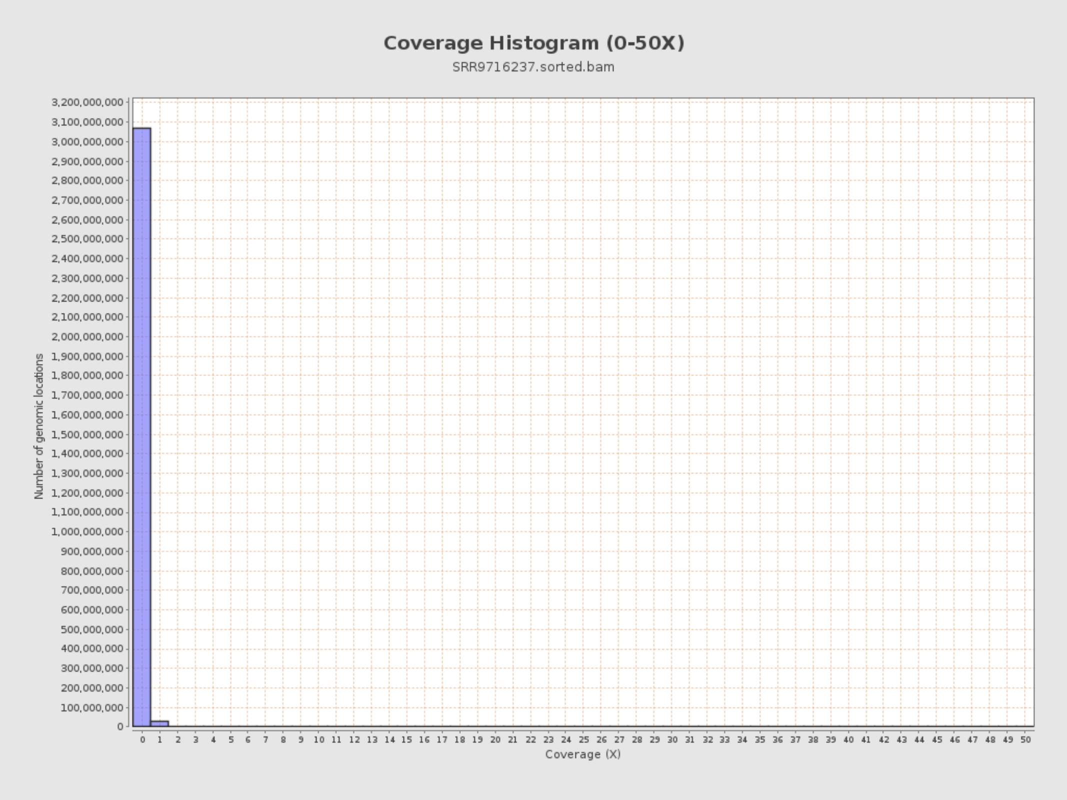
3. Results : Coverage across reference



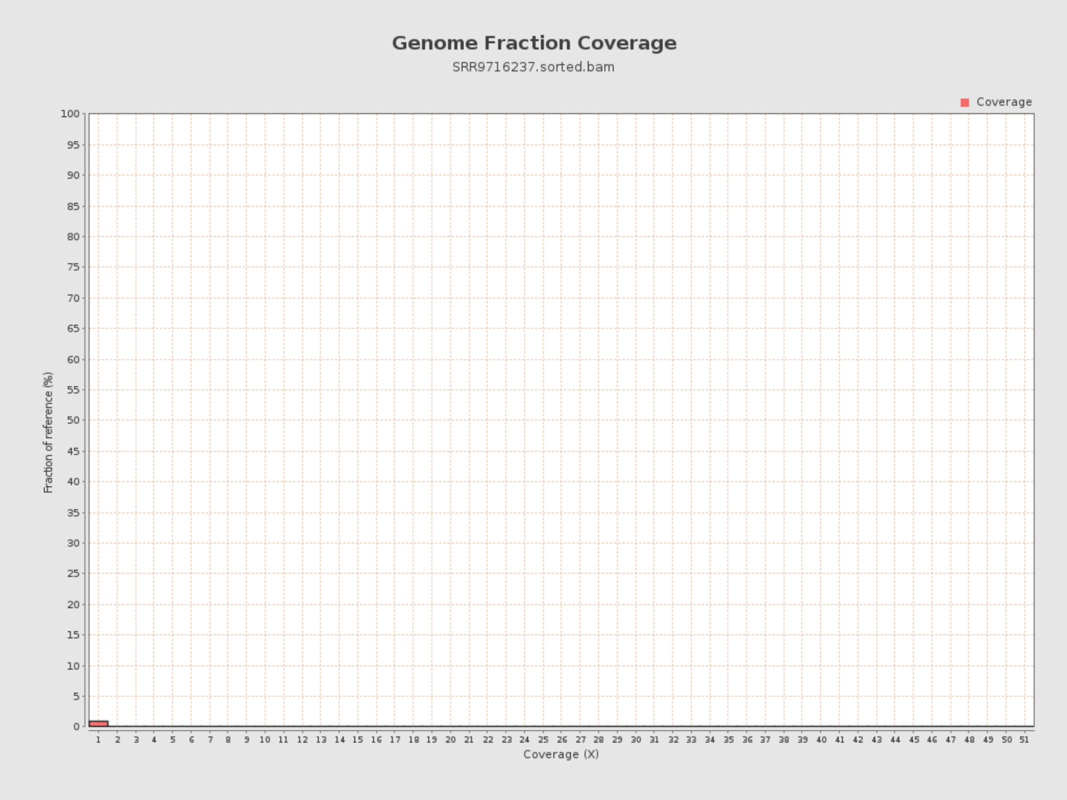
4. Results : Coverage Histogram



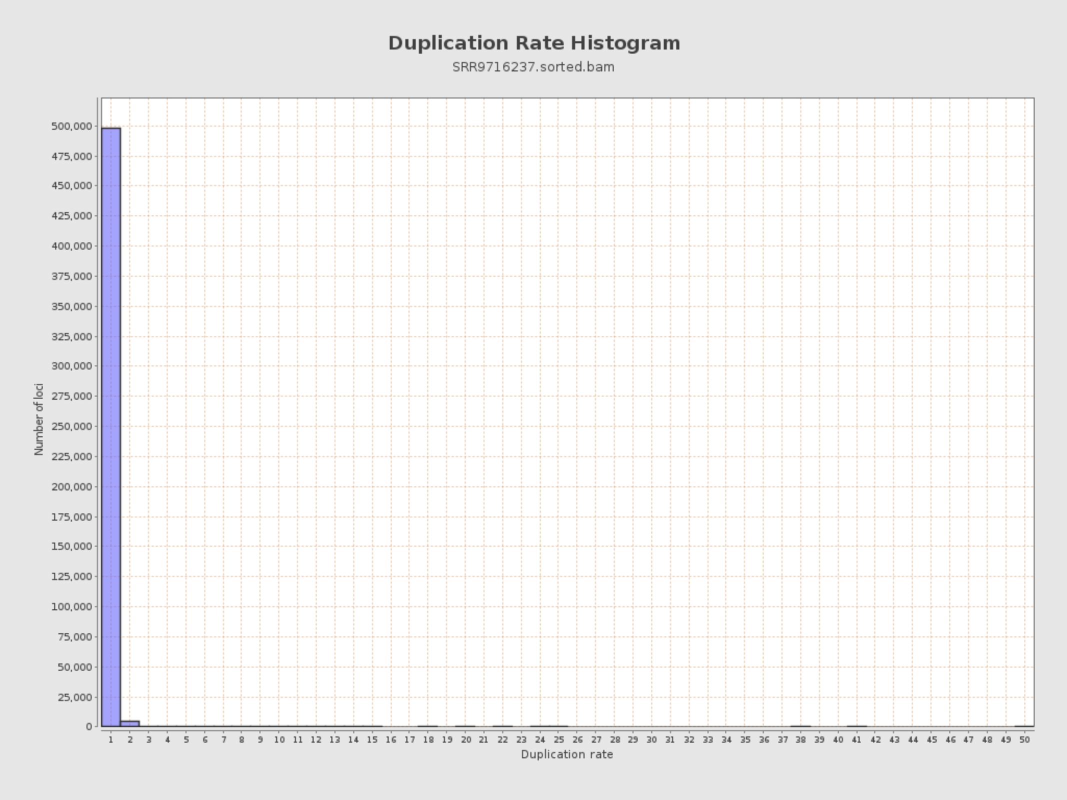
5. Results : Coverage Histogram (0-50X)



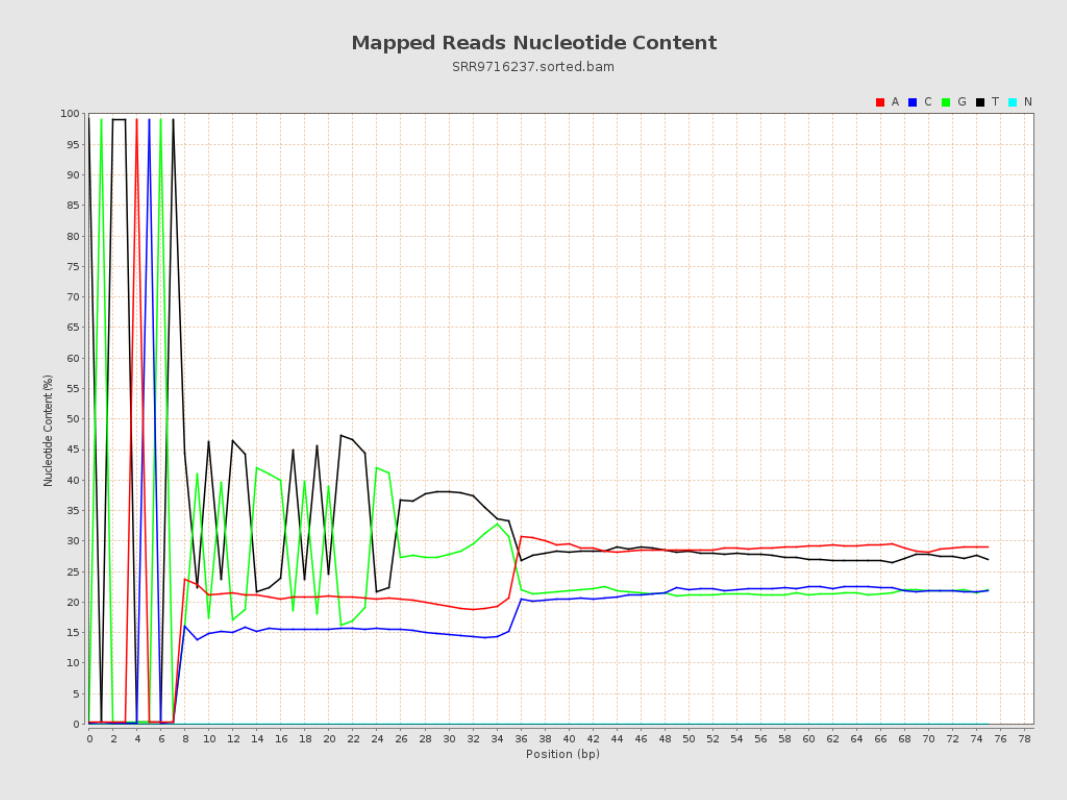
6. Results : Genome Fraction Coverage



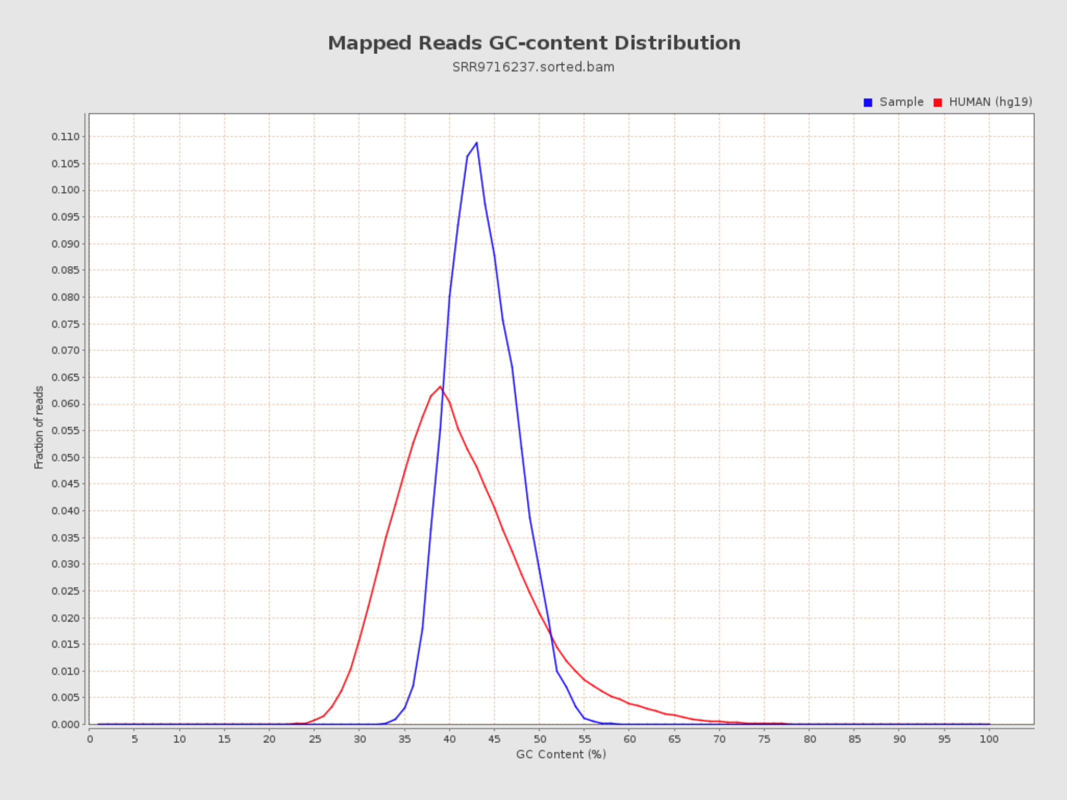
7. Results : Duplication Rate Histogram



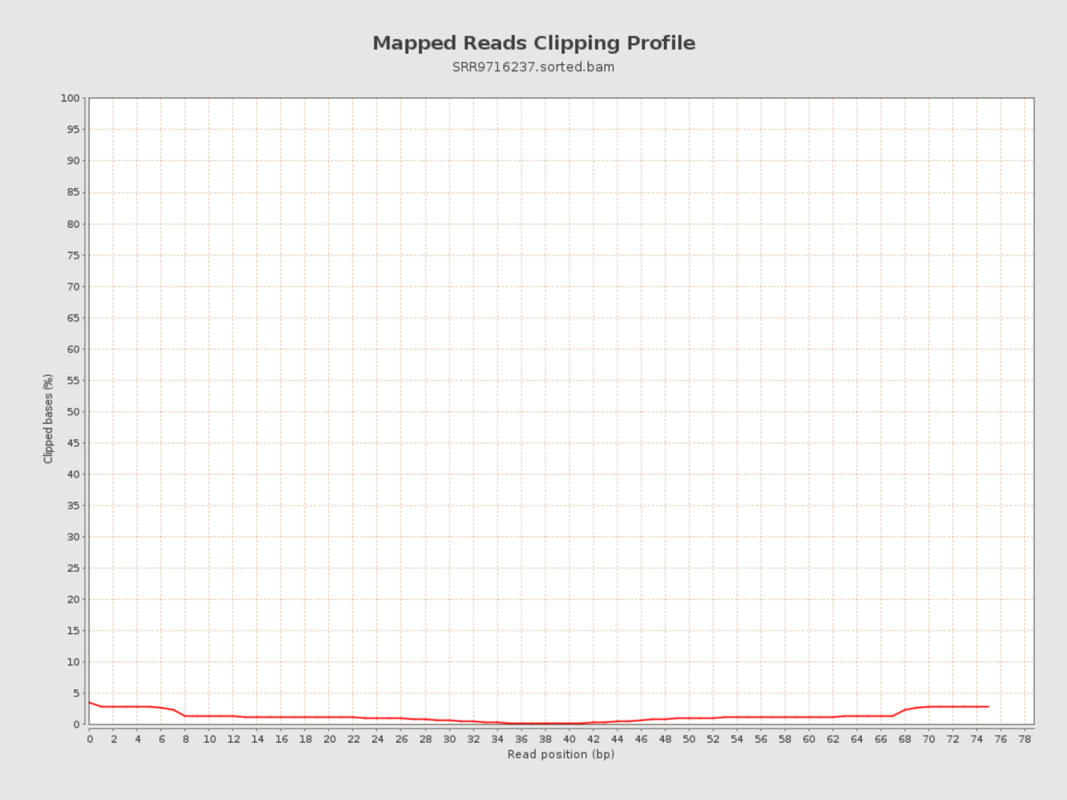
8. Results : Mapped Reads Nucleotide Content



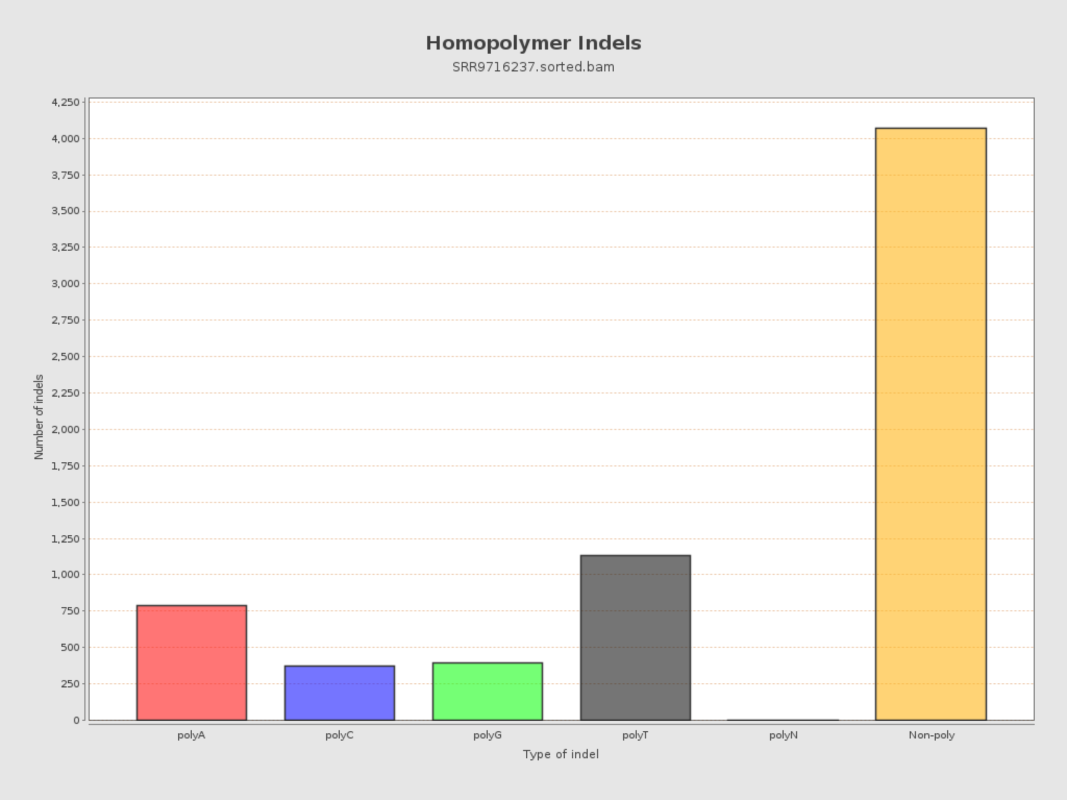
9. Results : Mapped Reads GC-content Distribution



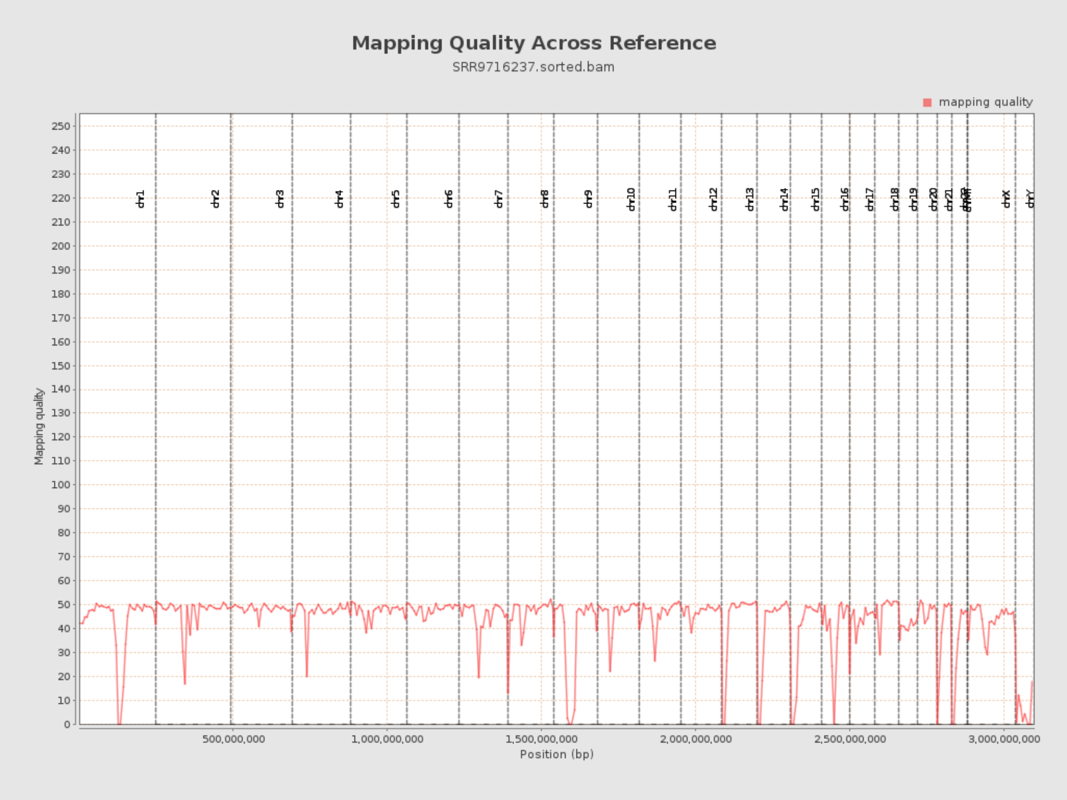
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram