Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:52:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716868.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_SRR9716868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:52:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	521,609
Mapped reads	423,872 / 81.26%
Unmapped reads	97,737 / 18.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,309 / 0.25%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	6,333 / 1.21%
Duplication rate	1.12%
Clipped reads	423,745 / 81.24%

2.2. ACGT Content

Number/percentage of A's	5,655,009 / 23.64%
Number/percentage of C's	4,725,431 / 19.75%
Number/percentage of T's	7,819,454 / 32.68%
Number/percentage of G's	5,723,865 / 23.93%
Number/percentage of N's	419 / 0%
GC Percentage	43.68%

2.3. Coverage

Mean	0.0077

Standard Deviation	0.1006

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

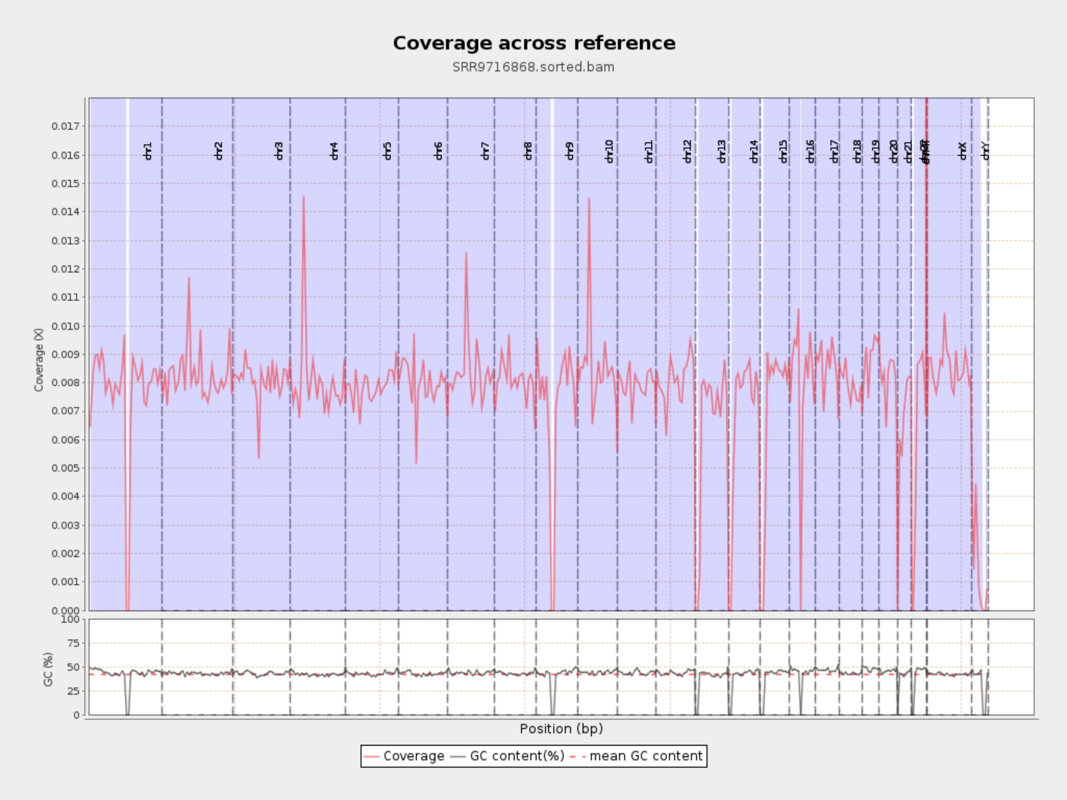
General error rate	0.55%
Mismatches	127,088
Insertions	1,953
Mapped reads with at least one insertion	0.46%
Deletions	4,846
Mapped reads with at least one deletion	1.13%
Homopolymer indels	37.84%

2.6. Chromosome stats

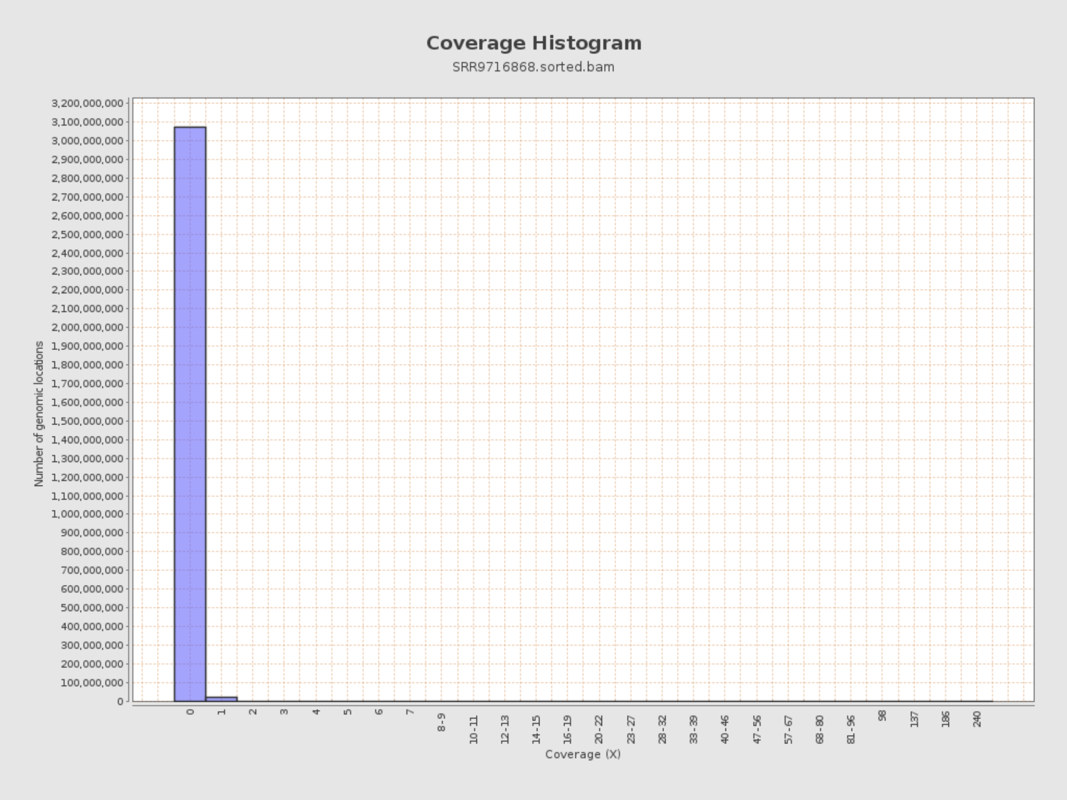
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1906625	0.0076	0.1115
chr2	243199373	2023008	0.0083	0.1356
chr3	198022430	1600997	0.0081	0.0925
chr4	191154276	1537347	0.008	0.0962
chr5	180915260	1421877	0.0079	0.0909
chr6	171115067	1368392	0.008	0.0957
chr7	159138663	1337193	0.0084	0.1152

chr8	146364022	1181233	0.0081	0.0975
chr9	141213431	993996	0.007	0.0918
chr10	135534747	1161914	0.0086	0.1096
chr11	135006516	1069210	0.0079	0.0979
chr12	133851895	1085295	0.0081	0.093
chr13	115169878	730161	0.0063	0.0818
chr14	107349540	727340	0.0068	0.0861
chr15	102531392	706563	0.0069	0.0853
chr16	90354753	722616	0.008	0.0945
chr17	81195210	695742	0.0086	0.097
chr18	78077248	620109	0.0079	0.1142
chr19	59128983	523828	0.0089	0.1109
chr20	63025520	511493	0.0081	0.0931
chr21	48129895	308957	0.0064	0.0851
chr22	51304566	305950	0.006	0.0797
chrMT	16571	1492	0.09	0.3384
chrX	155270560	1314274	0.0085	0.0977
chrY	59373566	76194	0.0013	0.0462

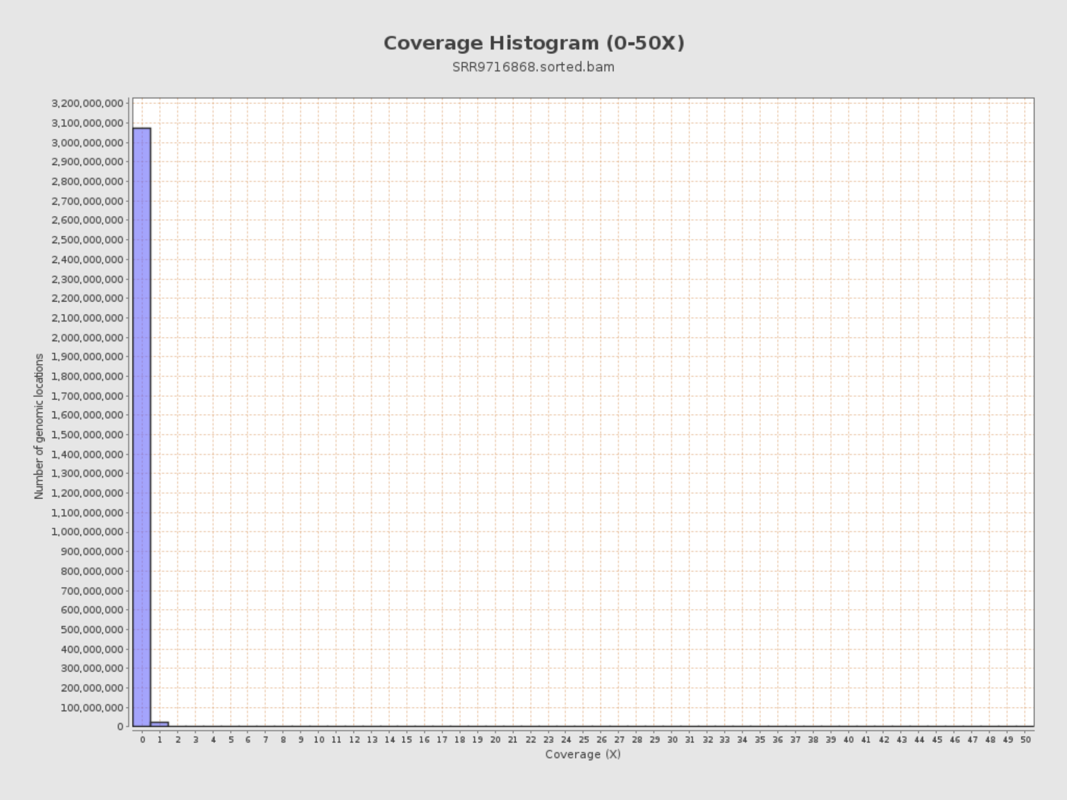
3. Results : Coverage across reference



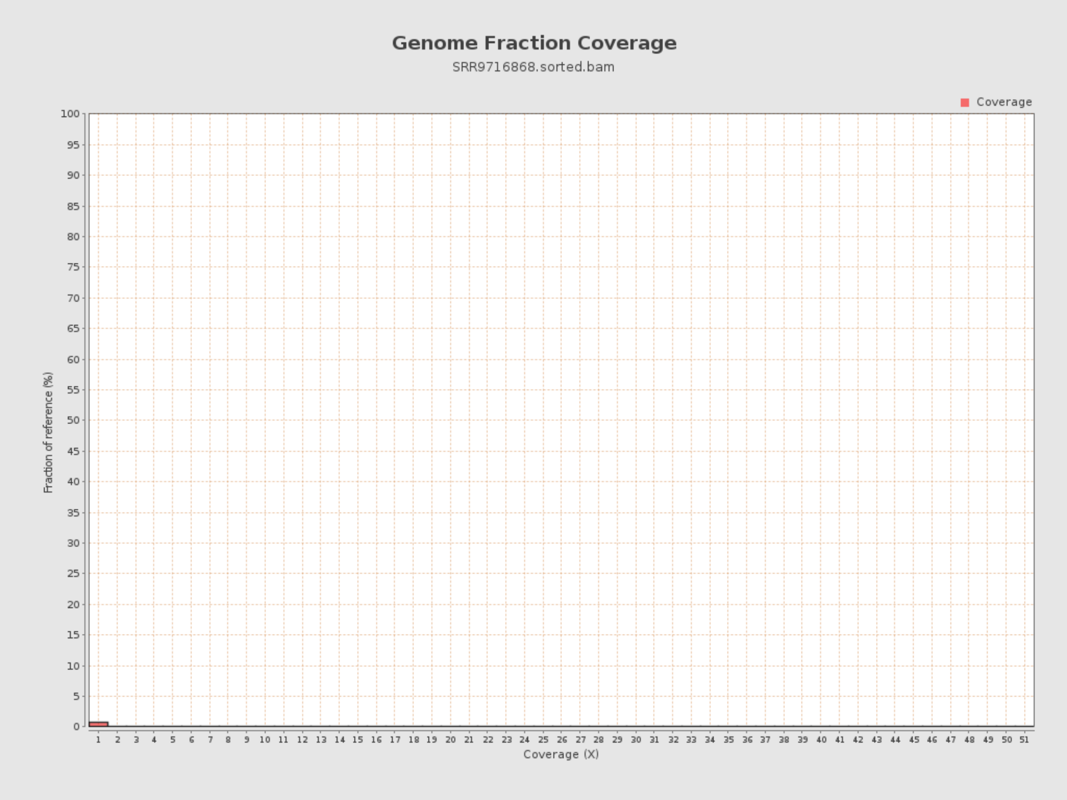
4. Results : Coverage Histogram



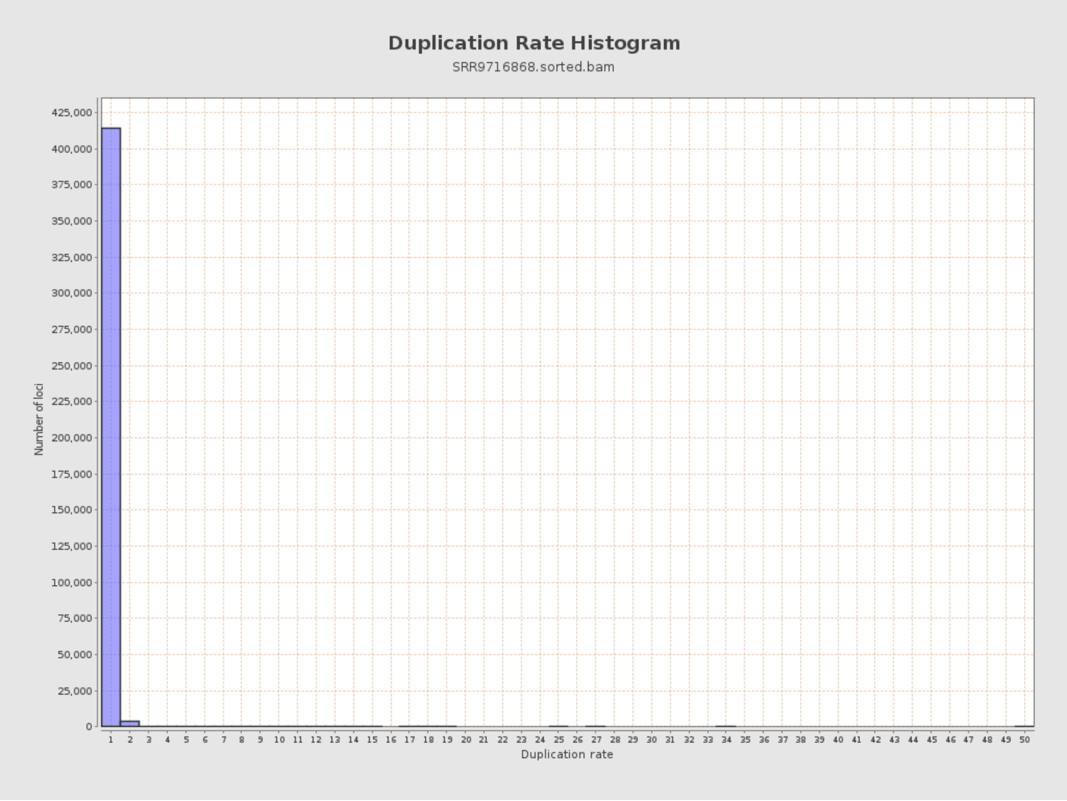
5. Results : Coverage Histogram (0-50X)



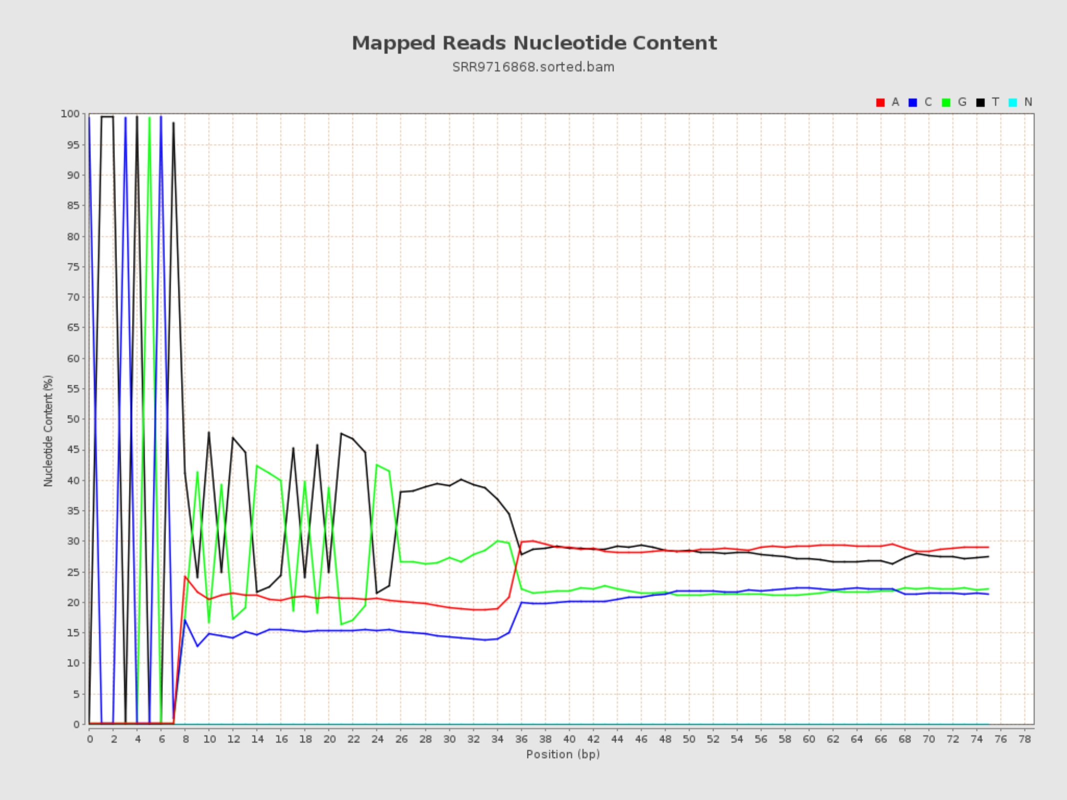
6. Results : Genome Fraction Coverage



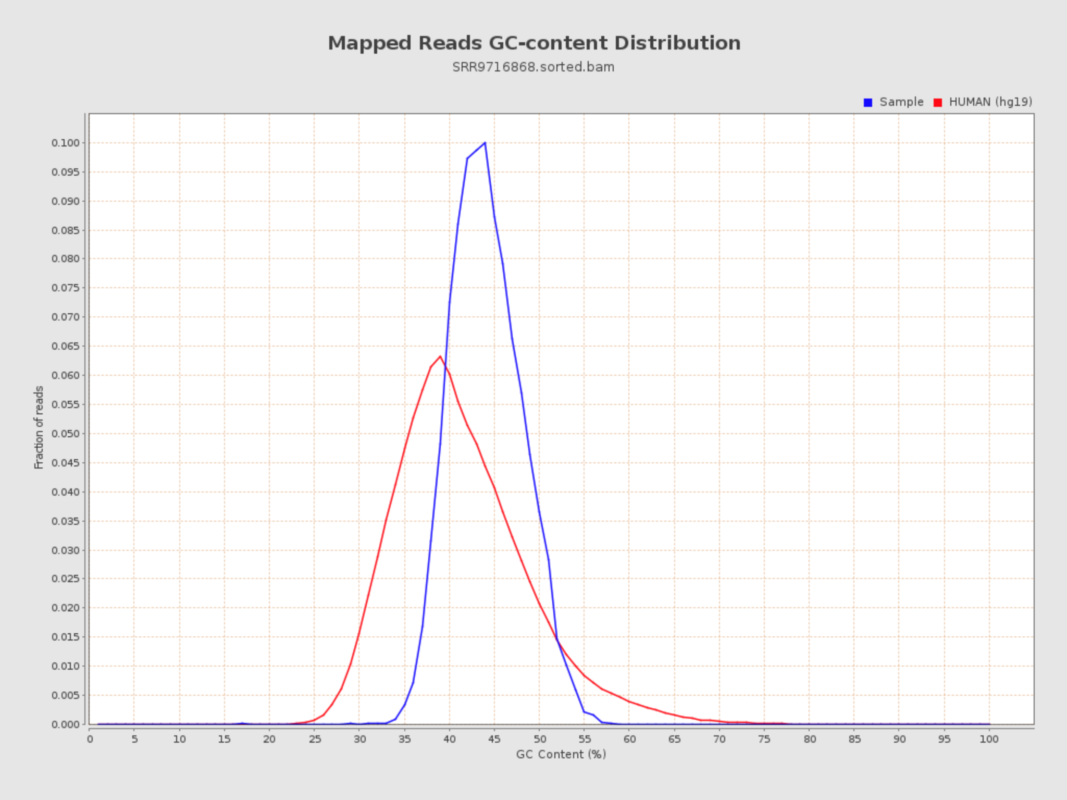
7. Results : Duplication Rate Histogram



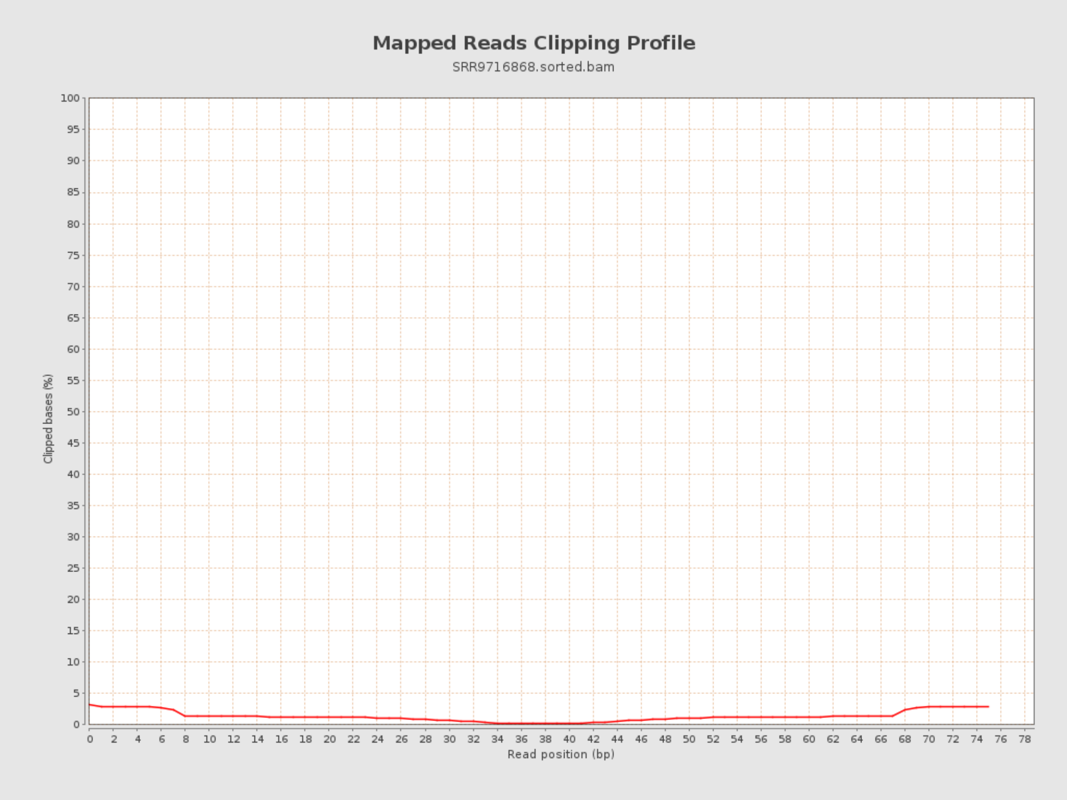
8. Results : Mapped Reads Nucleotide Content



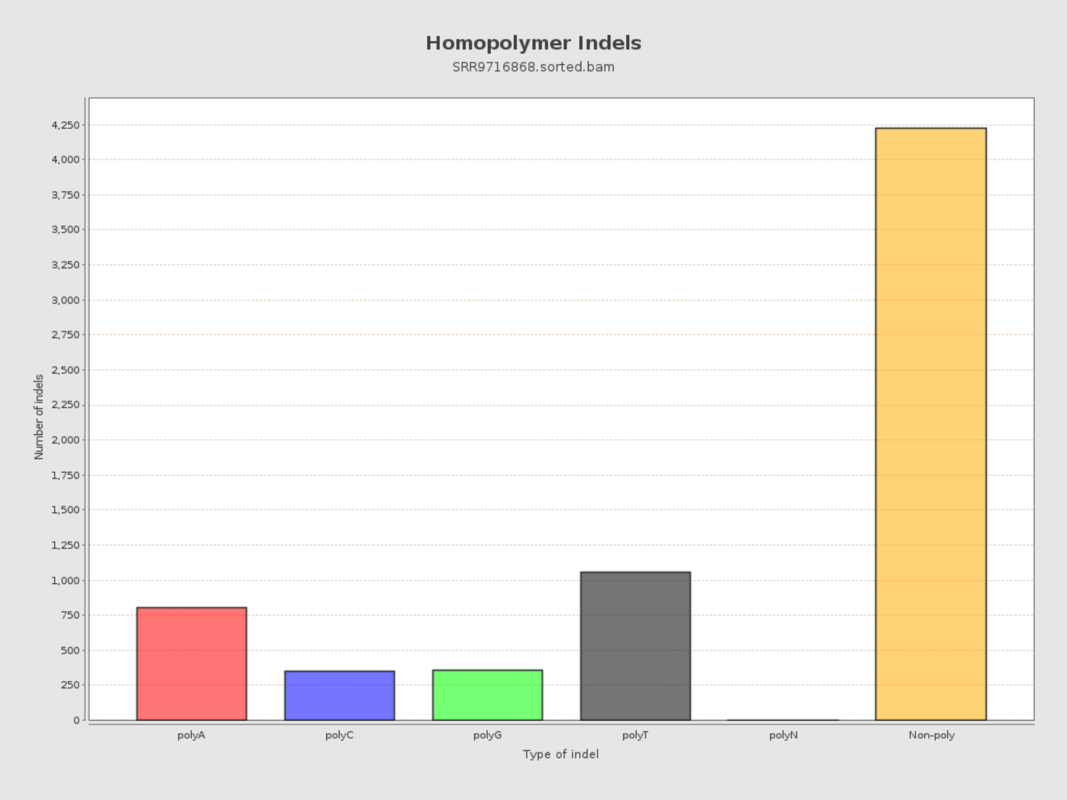
9. Results : Mapped Reads GC-content Distribution



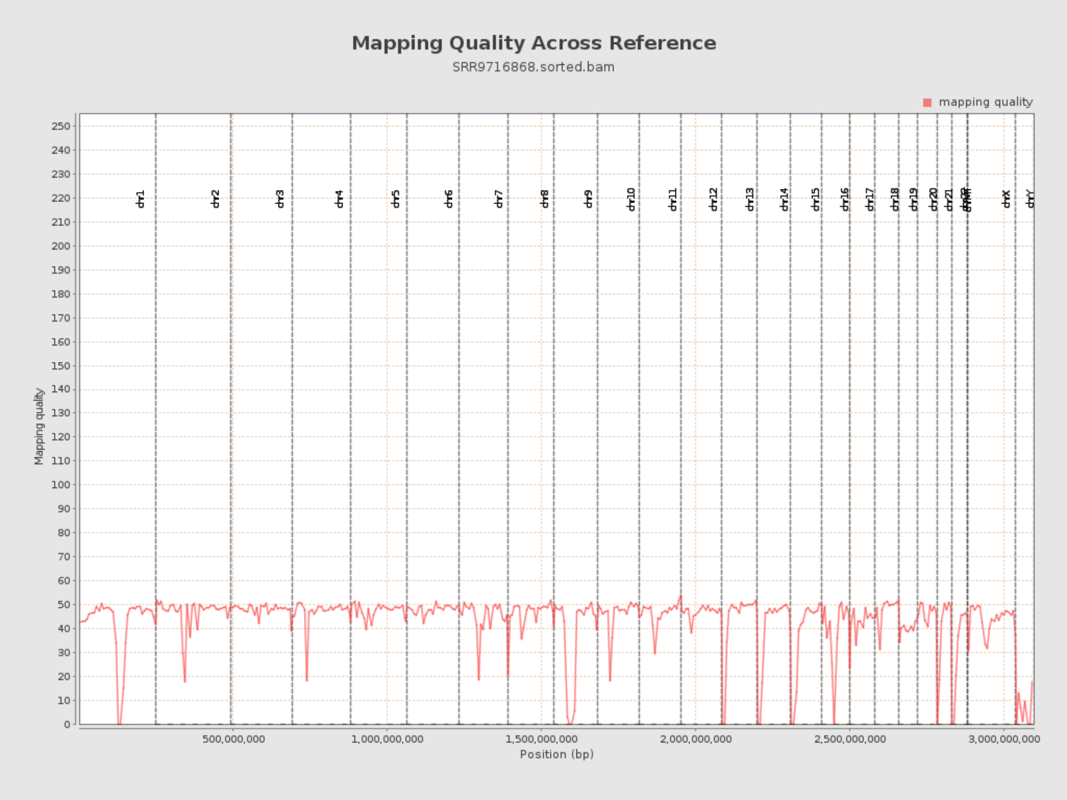
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram