Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:33:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716468.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_SRR9716468 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716468.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:33:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716468.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	621,326
Mapped reads	465,276 / 74.88%
Unmapped reads	156,050 / 25.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,160 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	5,896 / 0.95%
Duplication rate	0.91%
Clipped reads	465,284 / 74.89%

2.2. ACGT Content

Number/percentage of A's	7,559,154 / 27.35%
Number/percentage of C's	5,106,090 / 18.47%
Number/percentage of T's	8,368,078 / 30.27%
Number/percentage of G's	6,609,723 / 23.91%
Number/percentage of N's	173 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1119

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

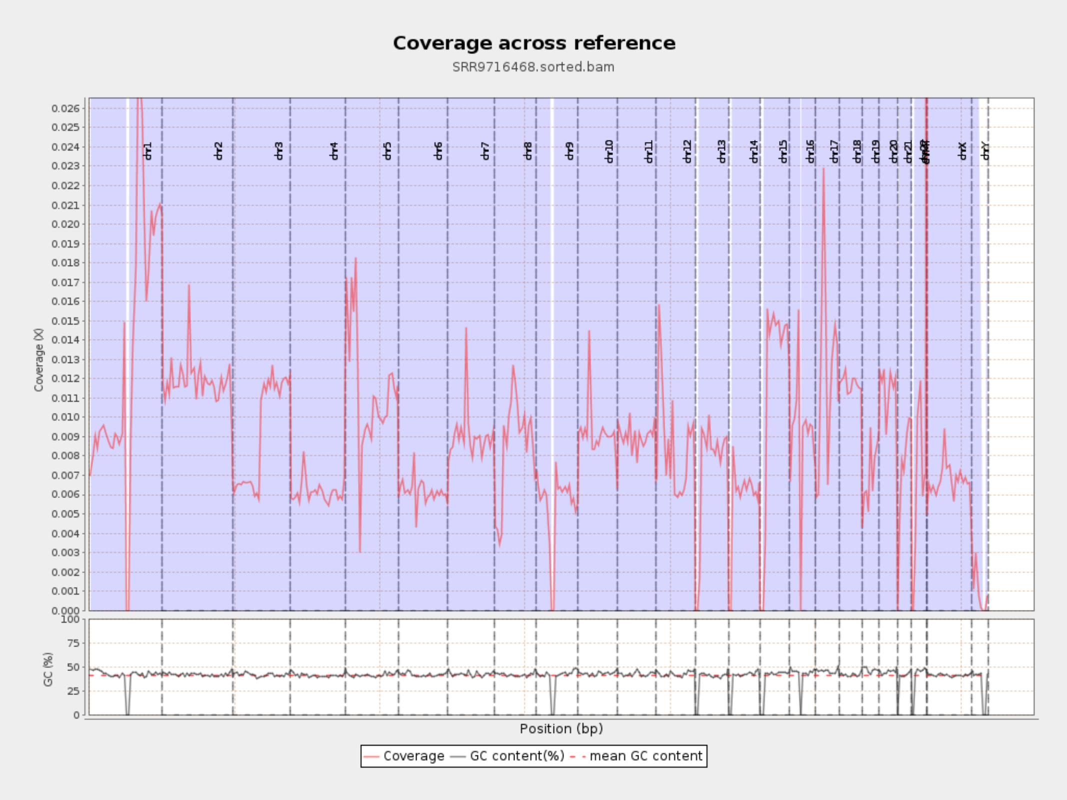
General error rate	0.51%
Mismatches	135,695
Insertions	2,441
Mapped reads with at least one insertion	0.52%
Deletions	5,164
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.42%

2.6. Chromosome stats

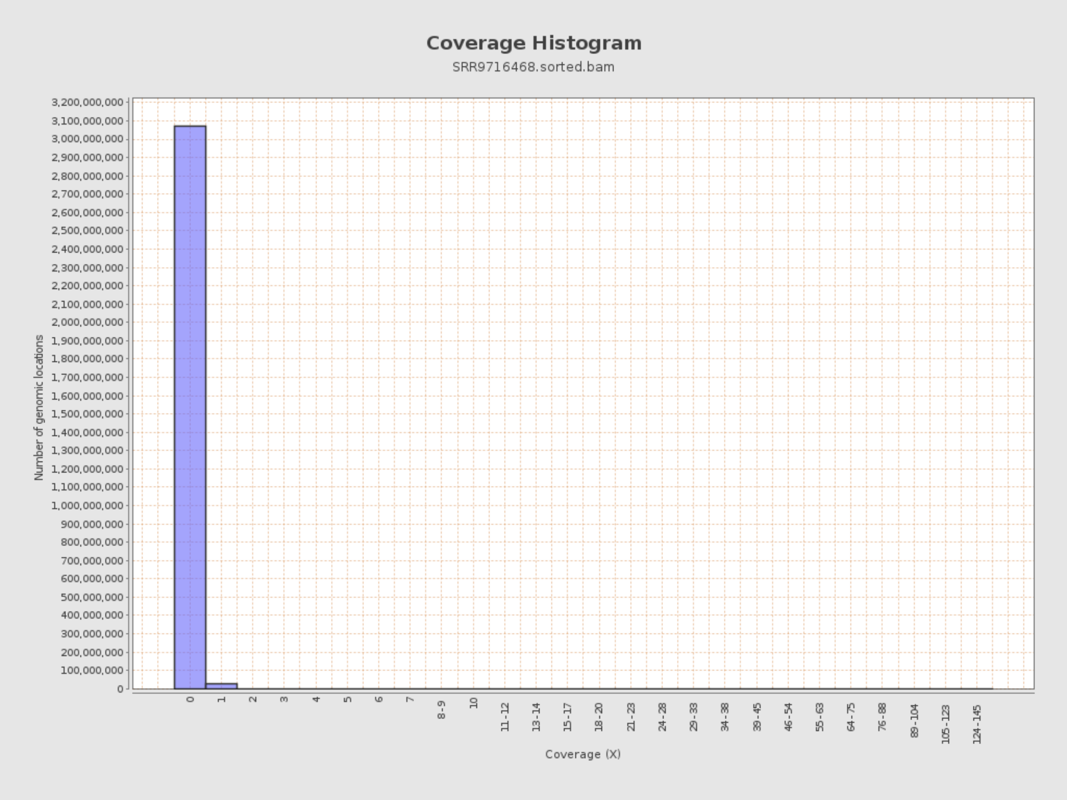
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3311177	0.0133	0.1729
chr2	243199373	2900752	0.0119	0.1335
chr3	198022430	1809046	0.0091	0.0984
chr4	191154276	1168995	0.0061	0.0811
chr5	180915260	2056069	0.0114	0.1093
chr6	171115067	1055233	0.0062	0.0842
chr7	159138663	1447957	0.0091	0.1299

chr8	146364022	1250882	0.0085	0.1023
chr9	141213431	753937	0.0053	0.0882
chr10	135534747	1256498	0.0093	0.1111
chr11	135006516	1208584	0.009	0.1103
chr12	133851895	1134728	0.0085	0.0944
chr13	115169878	835812	0.0073	0.0871
chr14	107349540	606297	0.0056	0.0775
chr15	102531392	1206866	0.0118	0.1115
chr16	90354753	822095	0.0091	0.1006
chr17	81195210	1006310	0.0124	0.1169
chr18	78077248	920591	0.0118	0.1611
chr19	59128983	416654	0.007	0.1314
chr20	63025520	716346	0.0114	0.1091
chr21	48129895	350323	0.0073	0.0881
chr22	51304566	310365	0.006	0.0794
chrMT	16571	3078	0.1857	0.4525
chrX	155270560	1046054	0.0067	0.0887
chrY	59373566	56934	0.001	0.0351

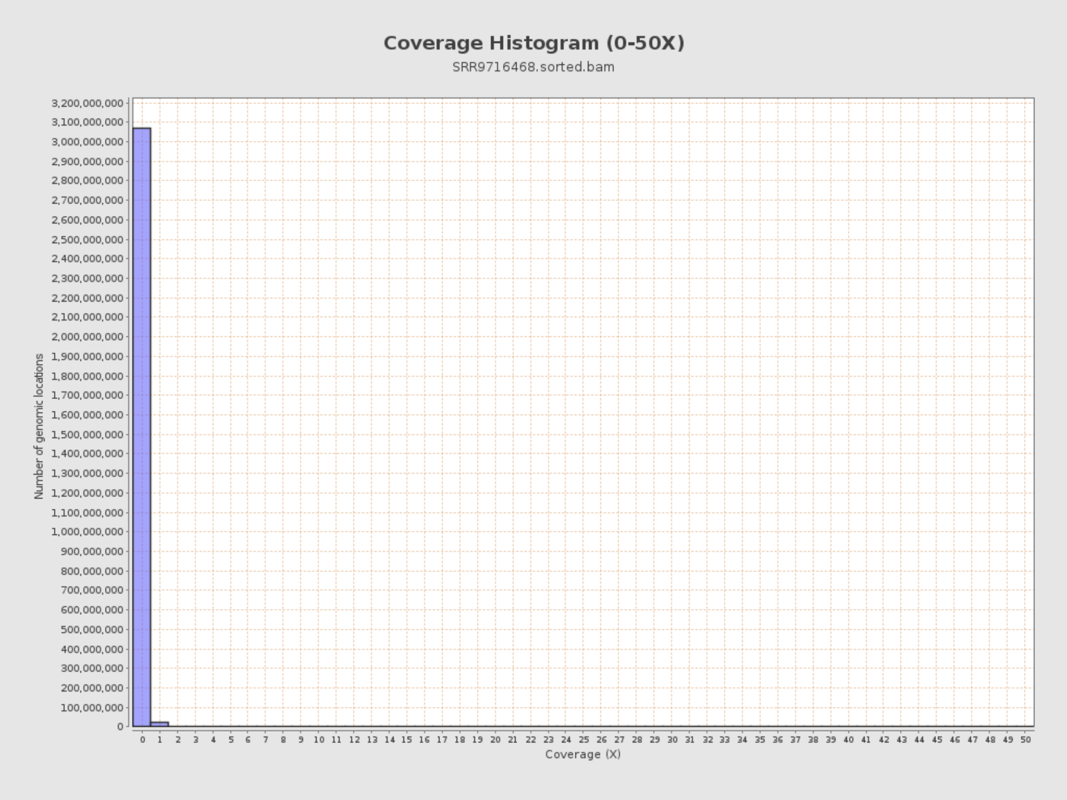
3. Results : Coverage across reference



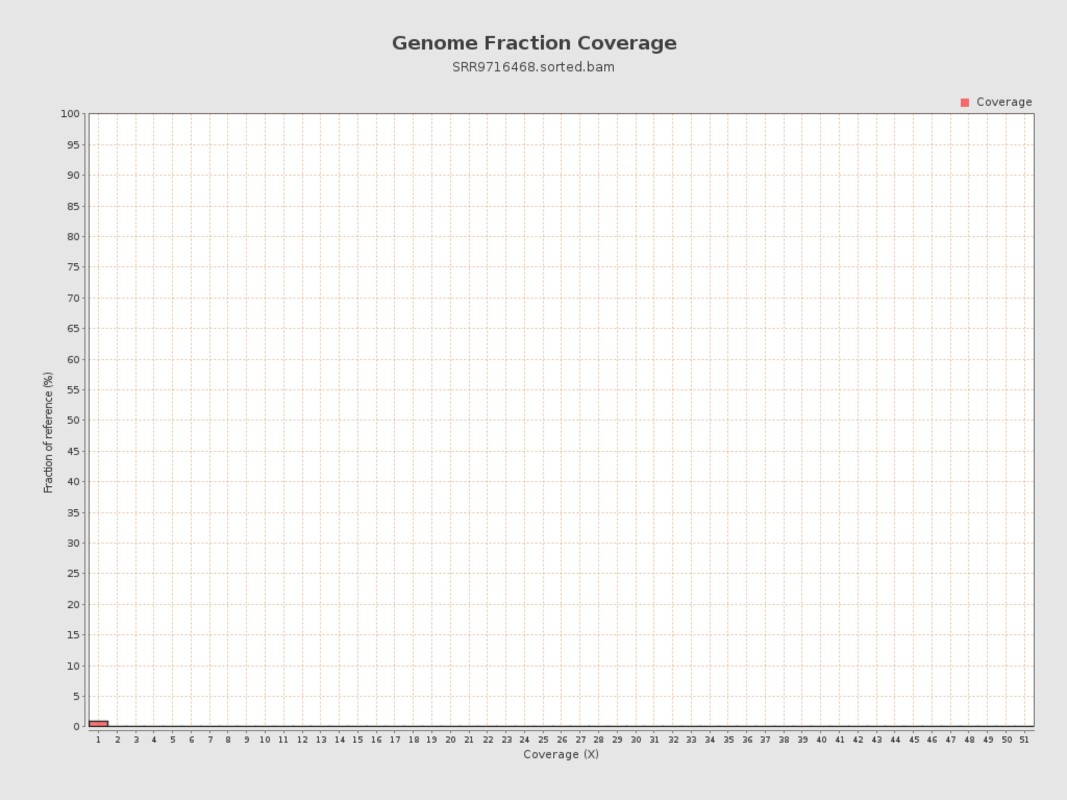
4. Results : Coverage Histogram



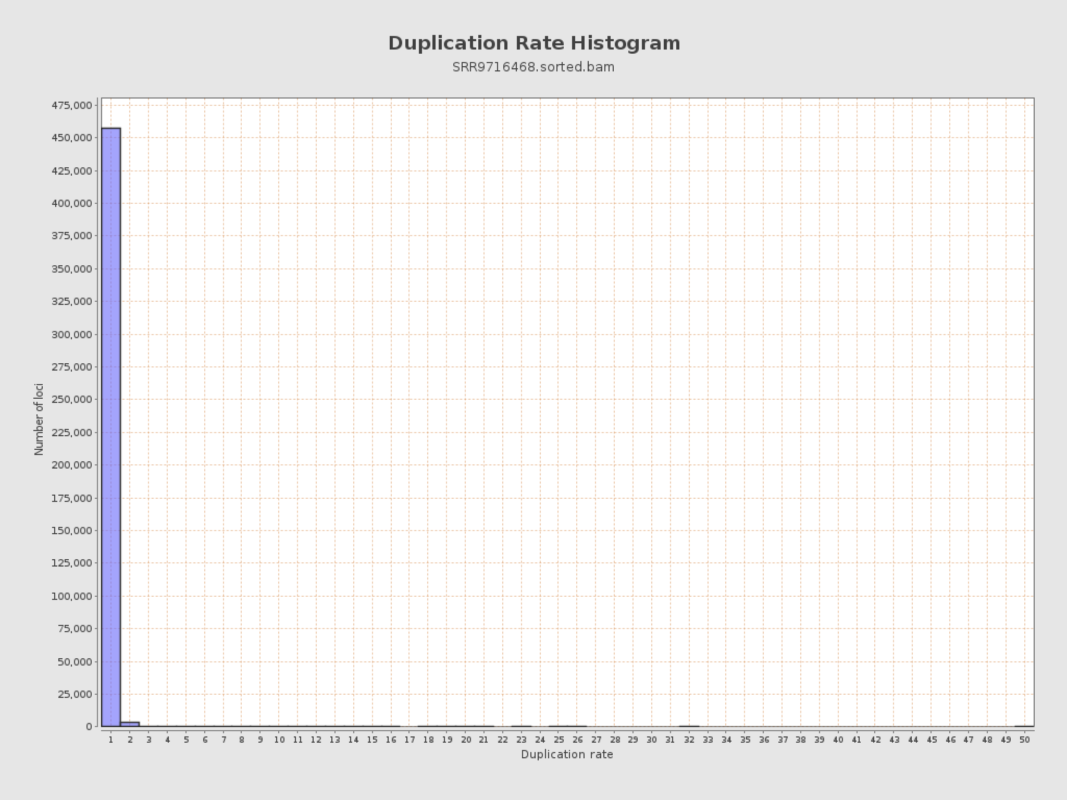
5. Results : Coverage Histogram (0-50X)



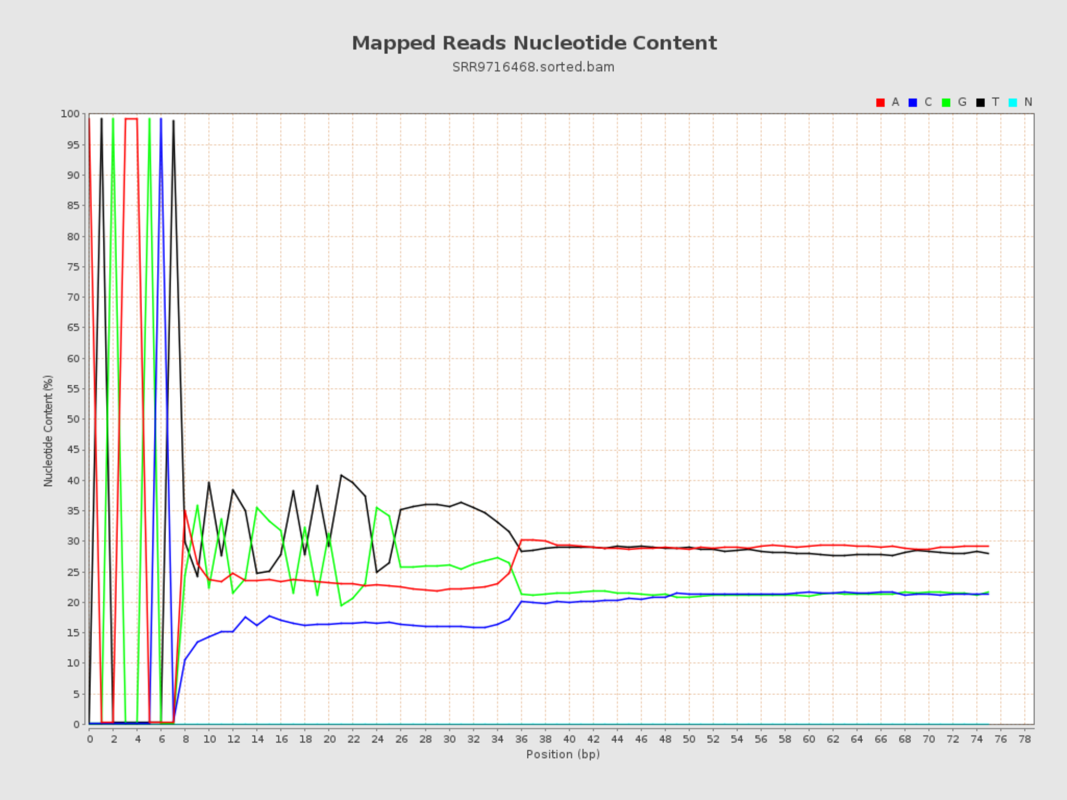
6. Results : Genome Fraction Coverage



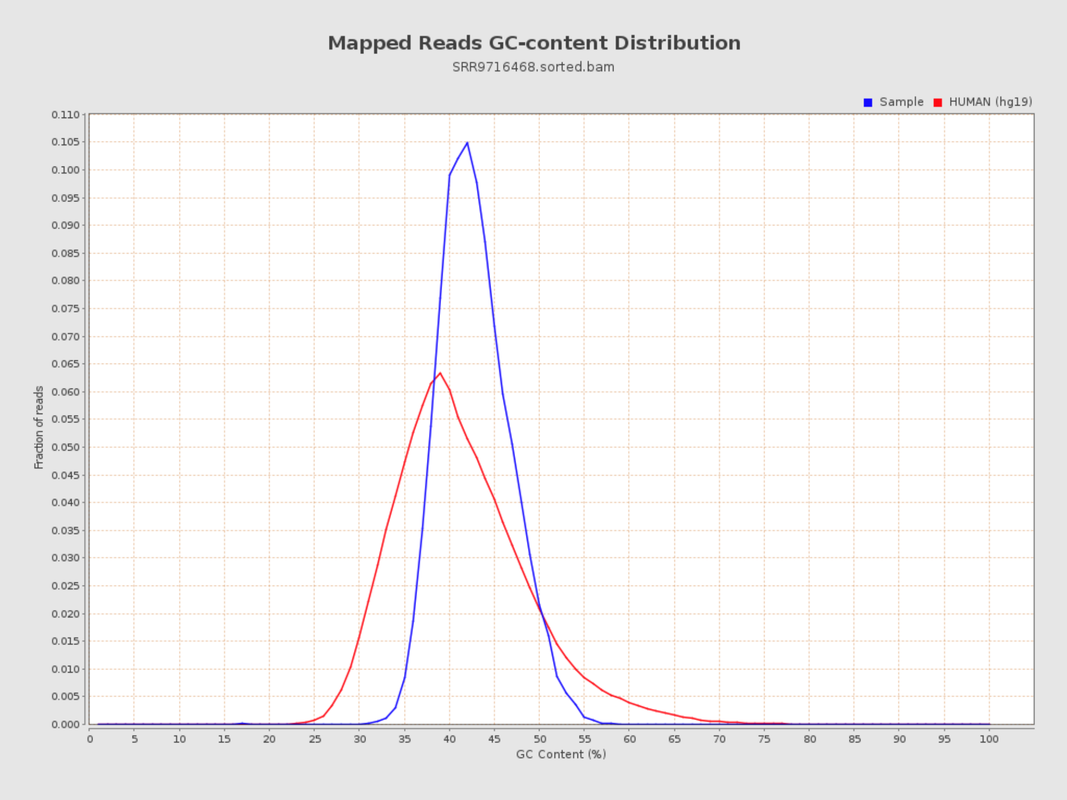
7. Results : Duplication Rate Histogram



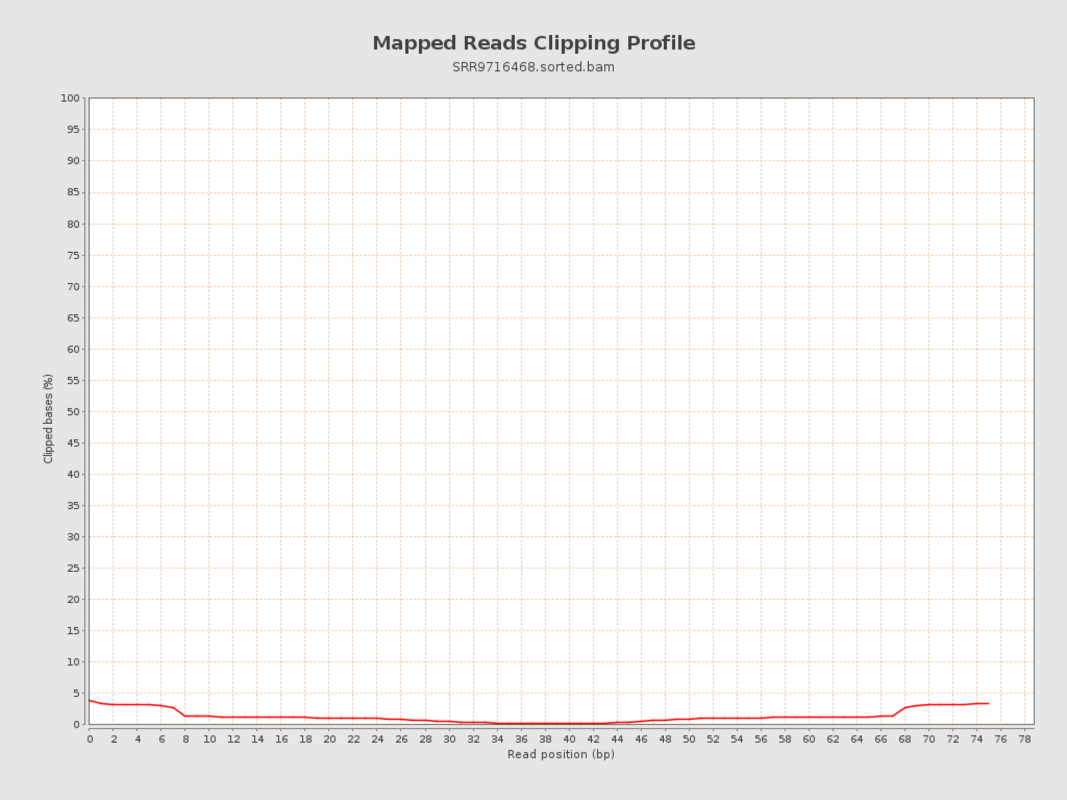
8. Results : Mapped Reads Nucleotide Content



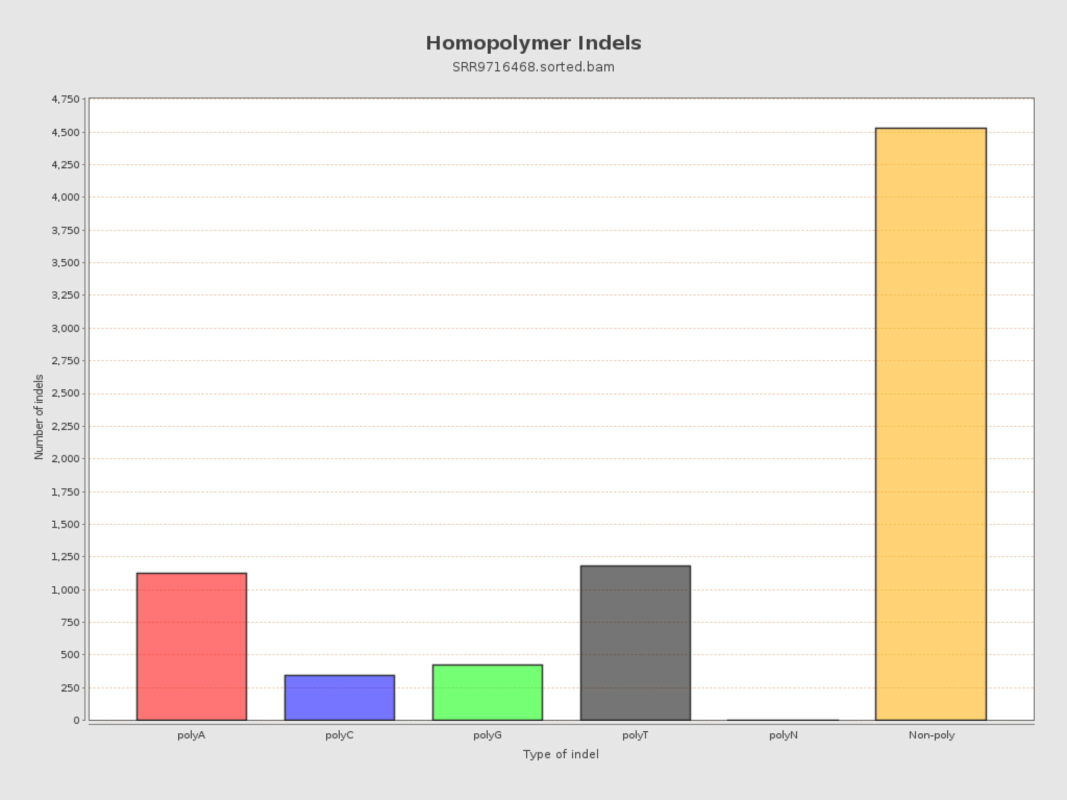
9. Results : Mapped Reads GC-content Distribution



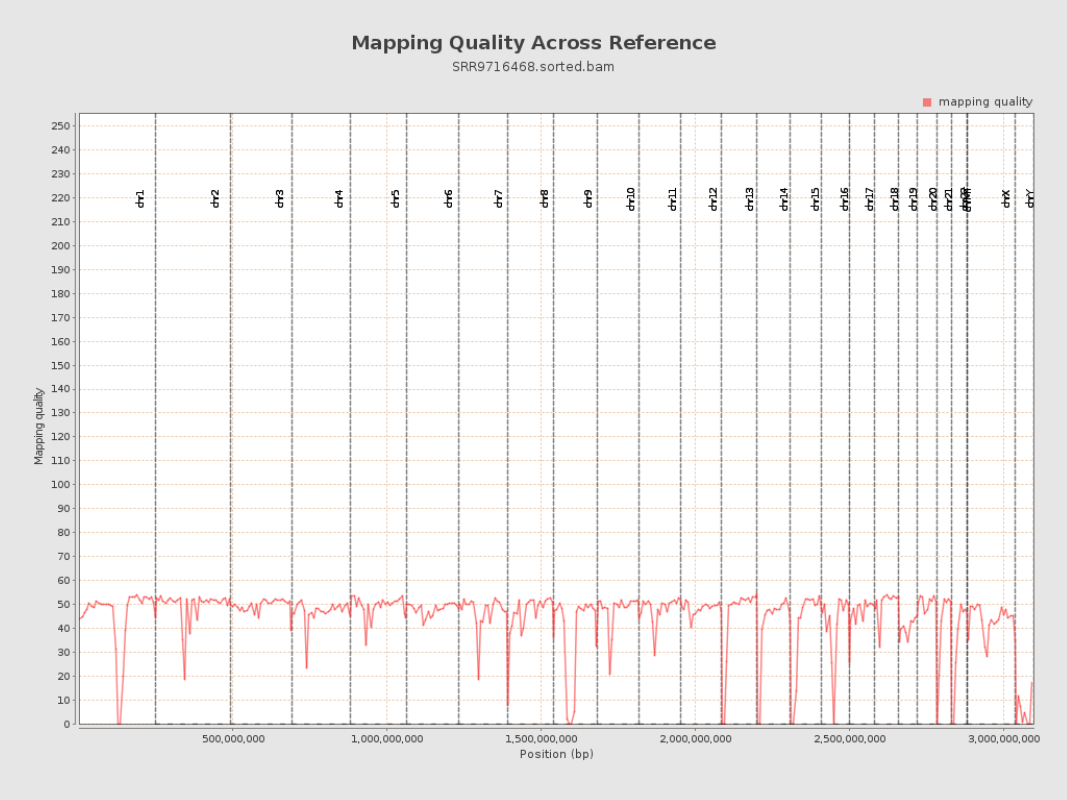
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram