Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:54:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716829.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_SRR9716829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:54:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	665,919
Mapped reads	473,436 / 71.1%
Unmapped reads	192,483 / 28.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	478 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	21,838 / 3.28%
Duplication rate	4.12%
Clipped reads	473,315 / 71.08%

2.2. ACGT Content

Number/percentage of A's	5,200,348 / 21.19%
Number/percentage of C's	4,224,569 / 17.21%
Number/percentage of T's	8,286,580 / 33.76%
Number/percentage of G's	6,835,238 / 27.85%
Number/percentage of N's	391 / 0%
GC Percentage	45.06%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1045

2.4. Mapping Quality

Mean Mapping Quality	42.04

2.5. Mismatches and indels

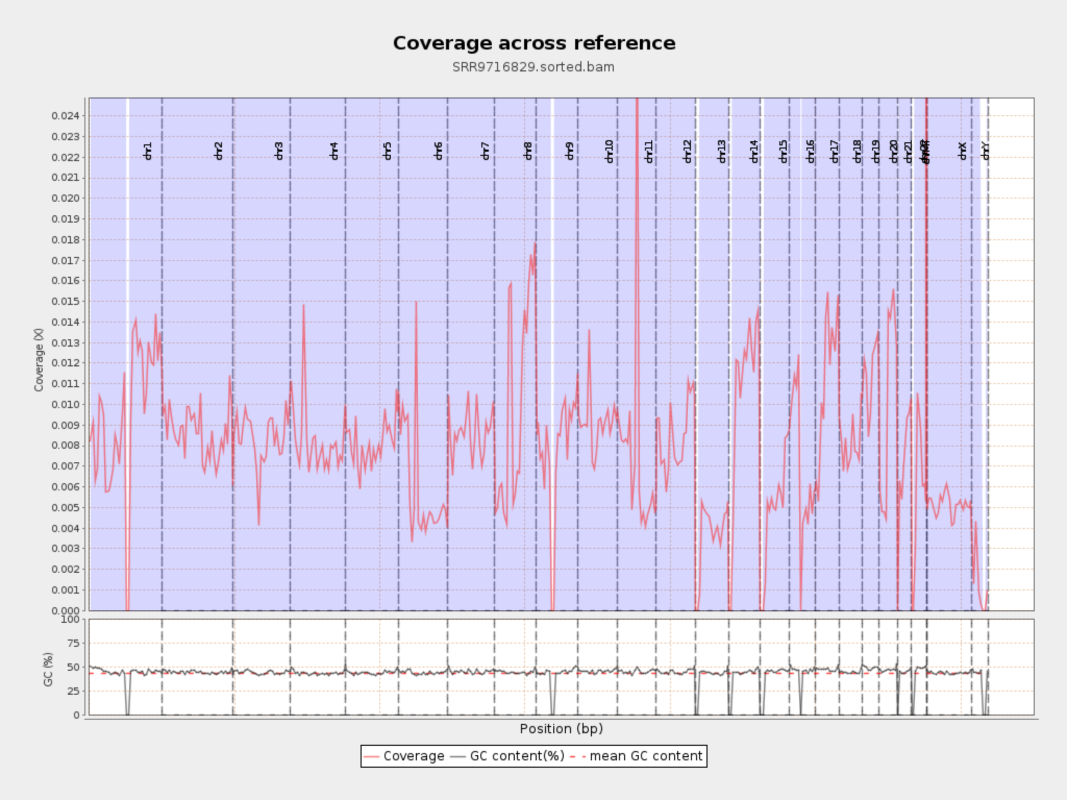
General error rate	0.73%
Mismatches	176,142
Insertions	1,535
Mapped reads with at least one insertion	0.32%
Deletions	3,659
Mapped reads with at least one deletion	0.77%
Homopolymer indels	39.6%

2.6. Chromosome stats

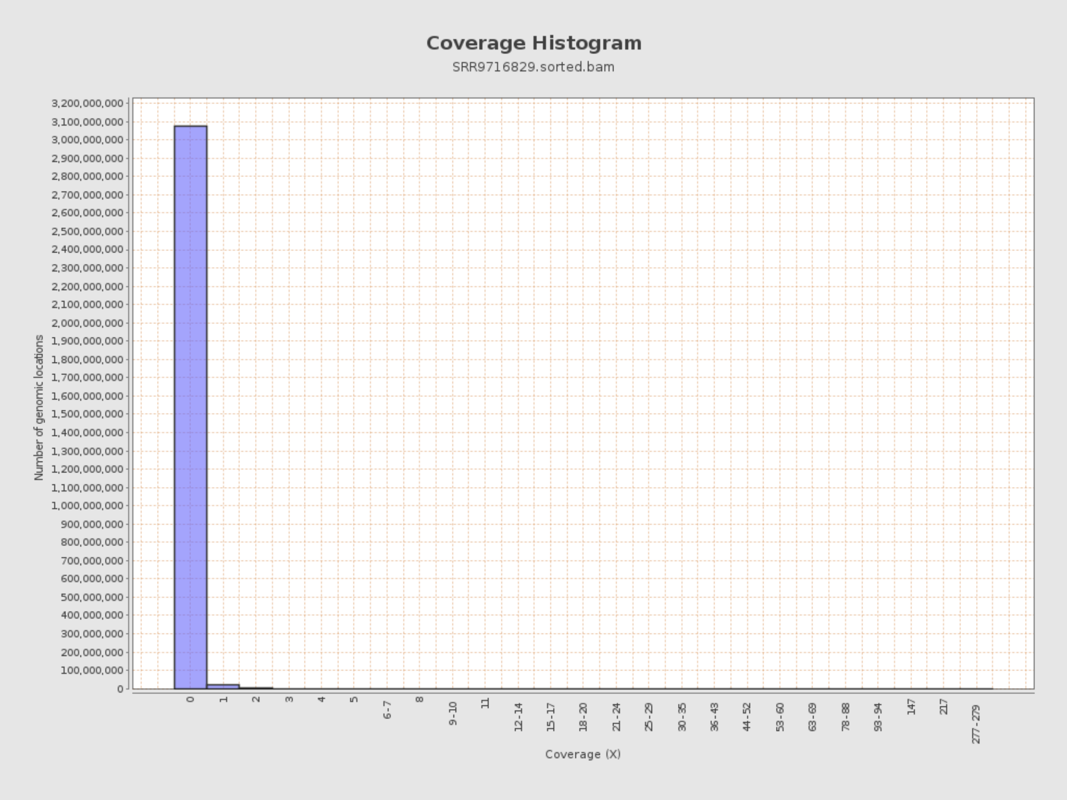
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2356025	0.0095	0.1152
chr2	243199373	2104471	0.0087	0.1496
chr3	198022430	1649054	0.0083	0.0982
chr4	191154276	1563699	0.0082	0.1002
chr5	180915260	1462652	0.0081	0.0968
chr6	171115067	1029786	0.006	0.0897
chr7	159138663	1368513	0.0086	0.1068

chr8	146364022	1492330	0.0102	0.1101
chr9	141213431	1072945	0.0076	0.0977
chr10	135534747	1231069	0.0091	0.113
chr11	135006516	1070512	0.0079	0.1021
chr12	133851895	1135713	0.0085	0.0996
chr13	115169878	414769	0.0036	0.0657
chr14	107349540	1110213	0.0103	0.1111
chr15	102531392	493701	0.0048	0.075
chr16	90354753	628183	0.007	0.0925
chr17	81195210	939607	0.0116	0.118
chr18	78077248	626433	0.008	0.1046
chr19	59128983	675530	0.0114	0.1269
chr20	63025520	632921	0.01	0.1099
chr21	48129895	343065	0.0071	0.0952
chr22	51304566	278691	0.0054	0.0811
chrMT	16571	2249	0.1357	0.4014
chrX	155270560	798127	0.0051	0.0796
chrY	59373566	73143	0.0012	0.0451

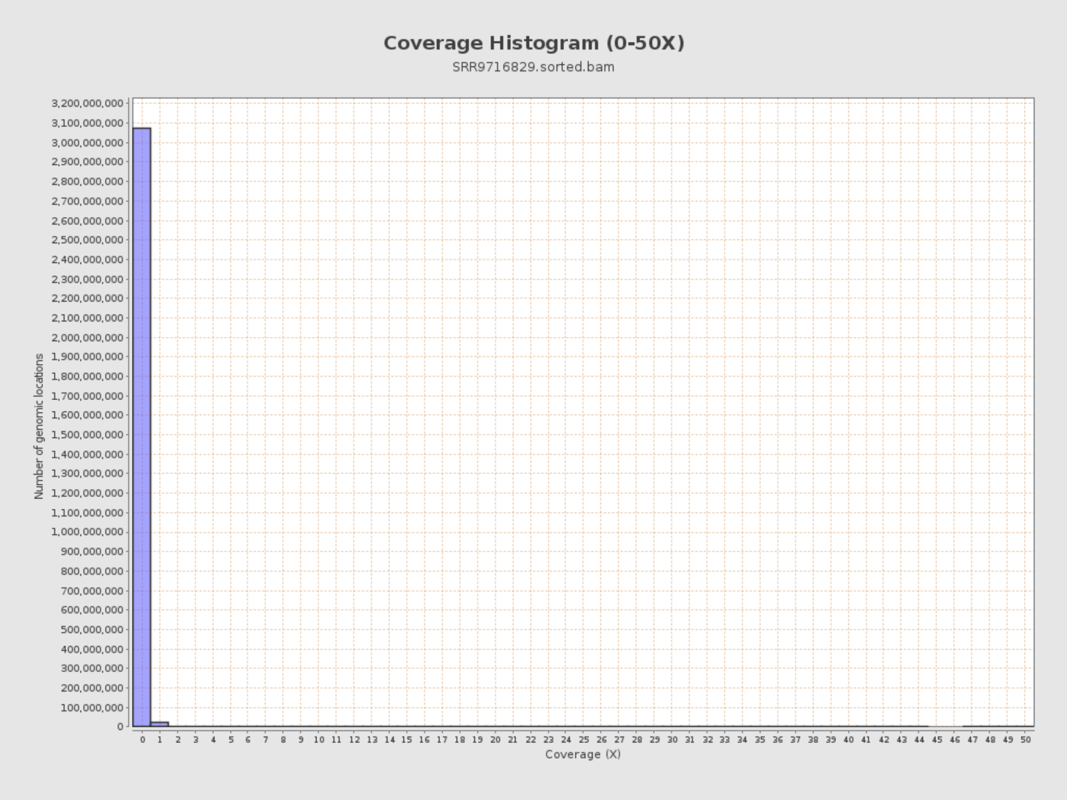
3. Results : Coverage across reference



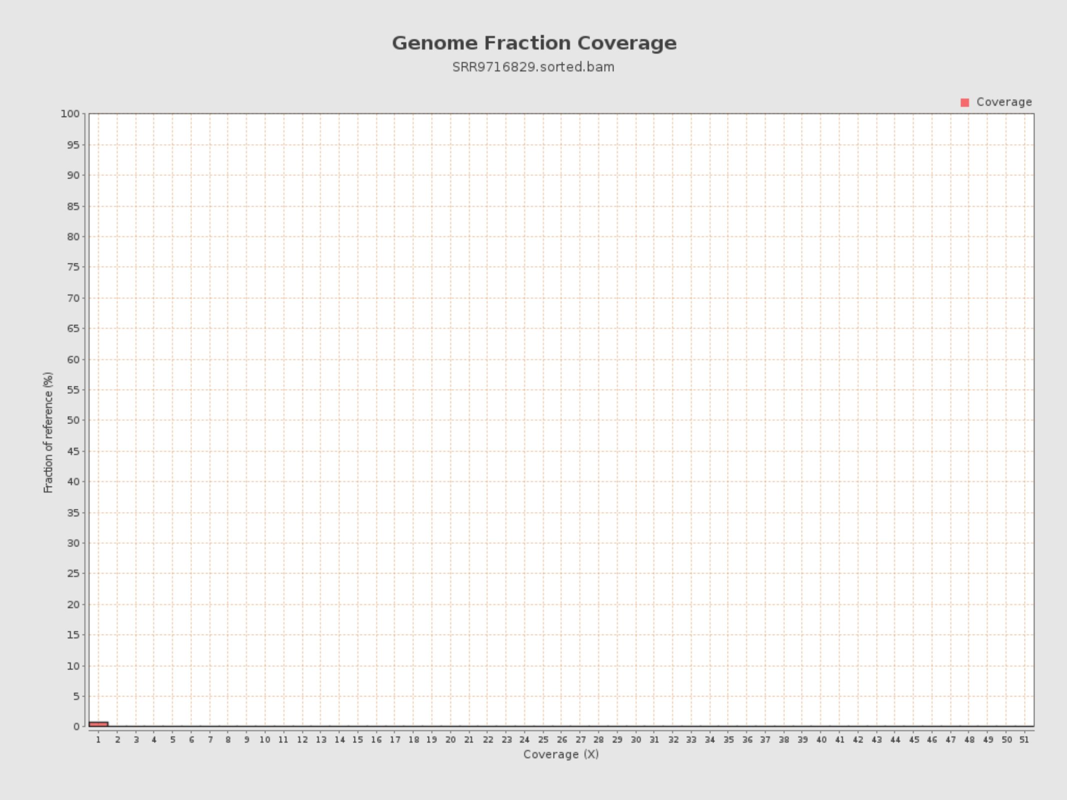
4. Results : Coverage Histogram



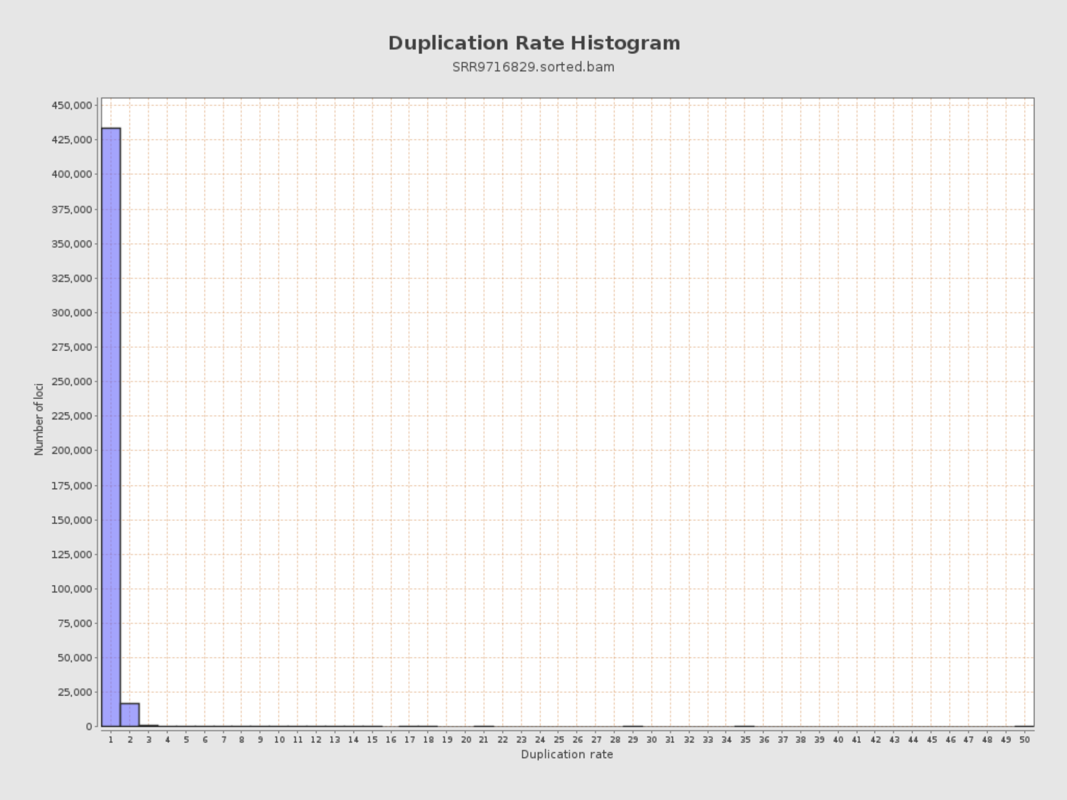
5. Results : Coverage Histogram (0-50X)



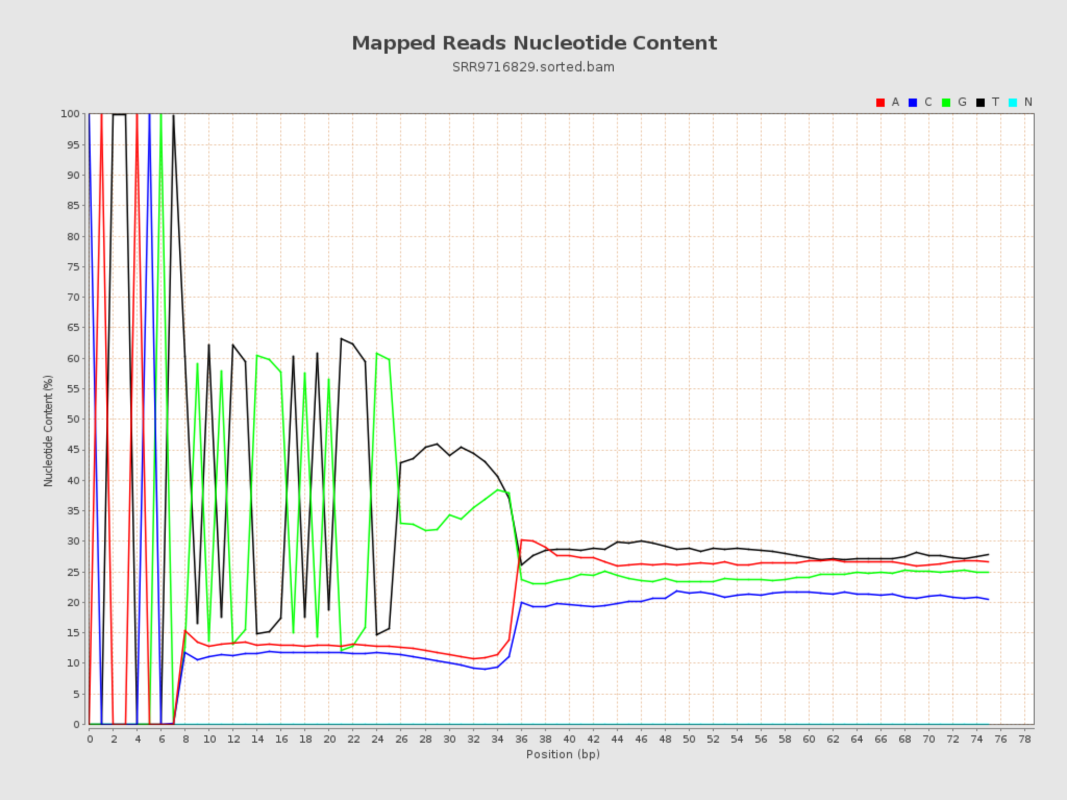
6. Results : Genome Fraction Coverage



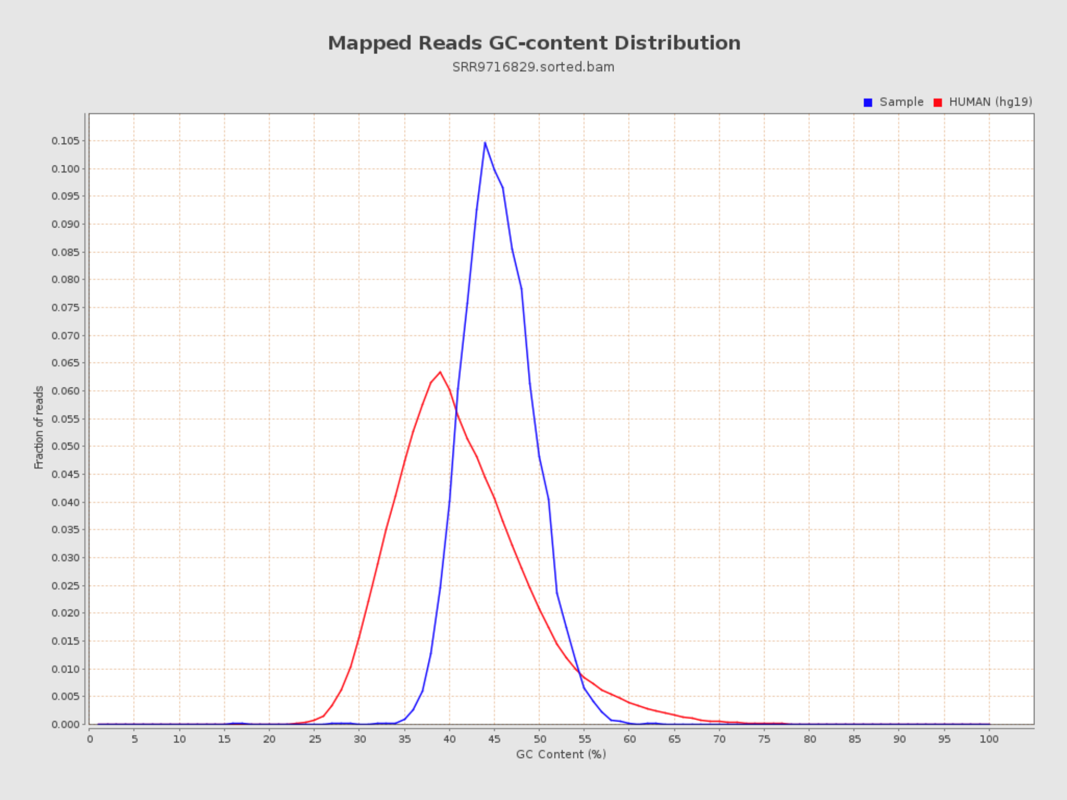
7. Results : Duplication Rate Histogram



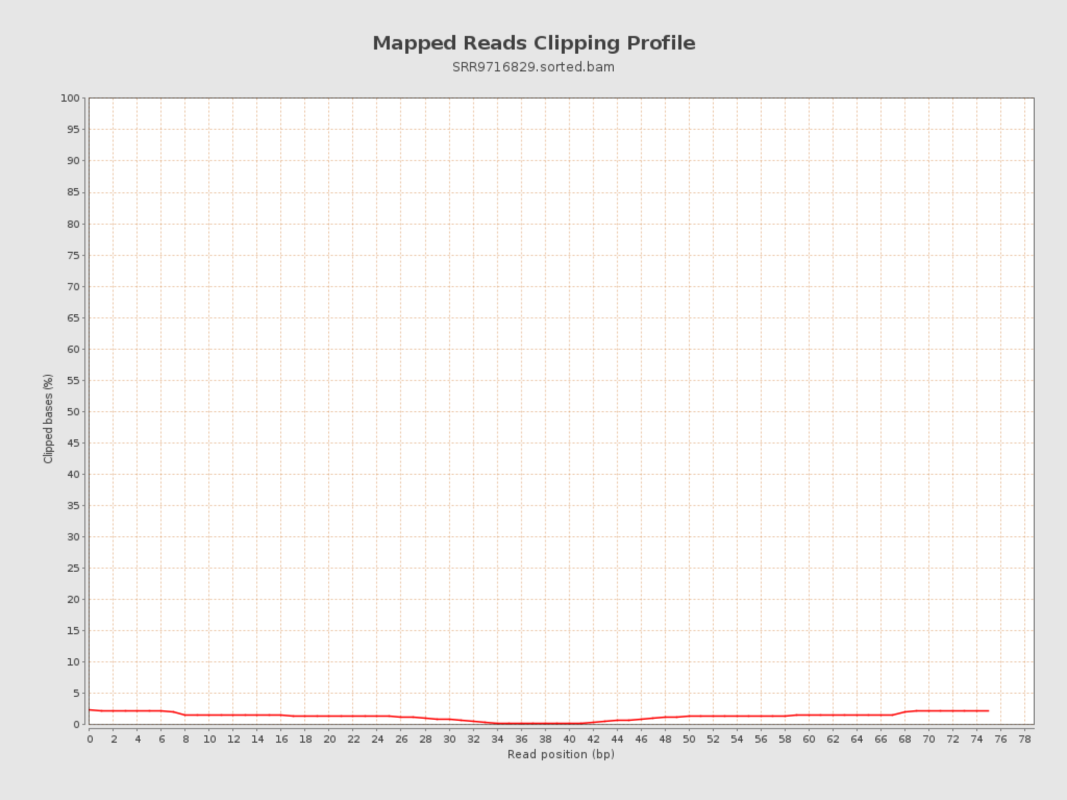
8. Results : Mapped Reads Nucleotide Content



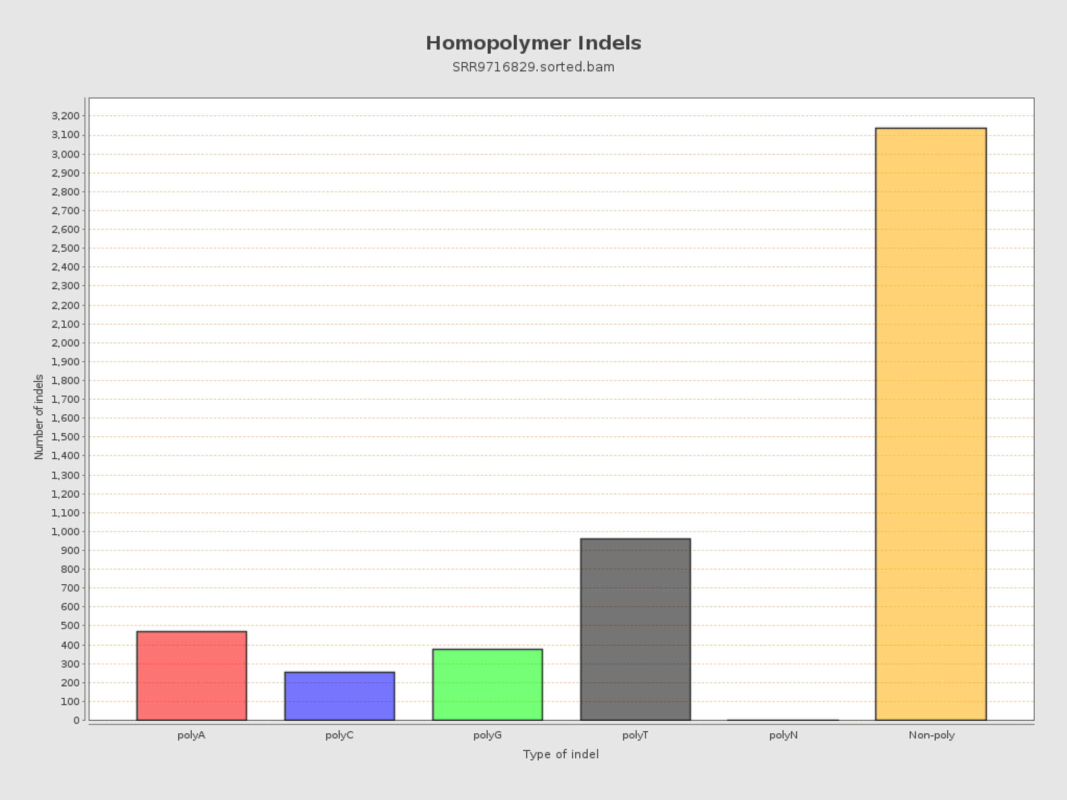
9. Results : Mapped Reads GC-content Distribution



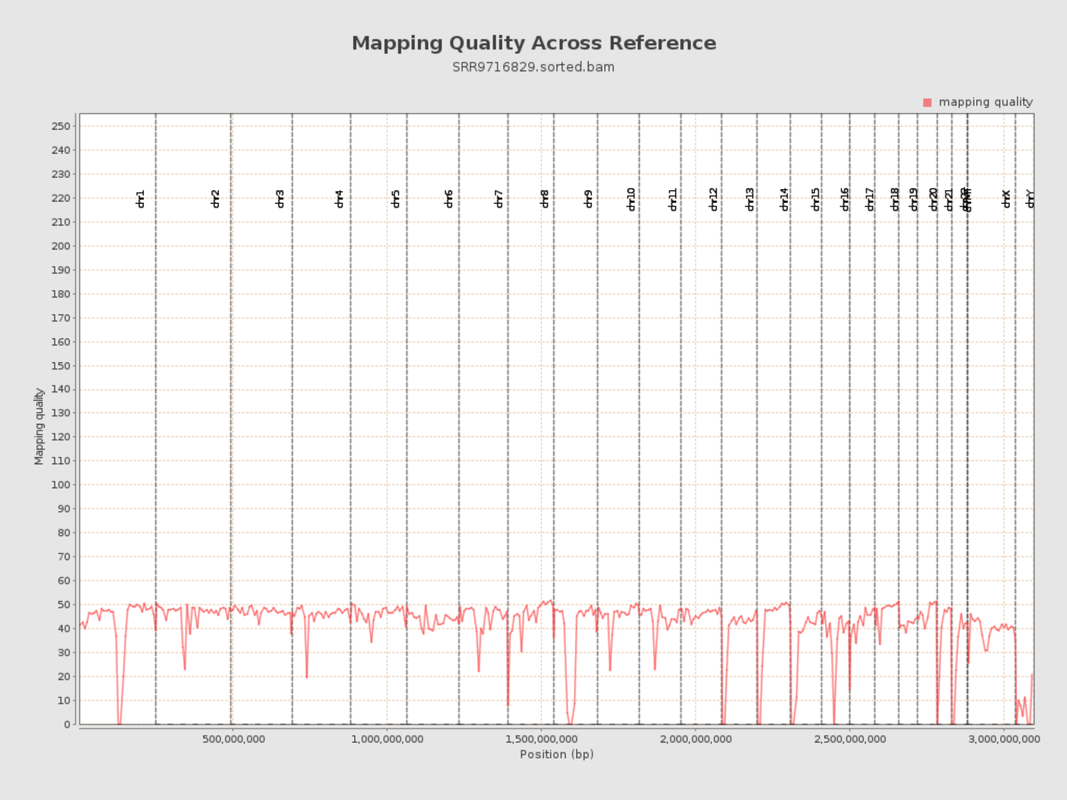
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram