Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:01:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716583.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_SRR9716583 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716583.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:01:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716583.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,201,601
Mapped reads	1,942,936 / 88.25%
Unmapped reads	258,665 / 11.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,226 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	53,949 / 2.45%
Duplication rate	1.93%
Clipped reads	1,946,332 / 88.41%

2.2. ACGT Content

Number/percentage of A's	27,137,992 / 24.53%
Number/percentage of C's	20,870,994 / 18.86%
Number/percentage of T's	33,730,222 / 30.49%
Number/percentage of G's	28,899,515 / 26.12%
Number/percentage of N's	741 / 0%
GC Percentage	44.98%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.2872

2.4. Mapping Quality

Mean Mapping Quality	42.19

2.5. Mismatches and indels

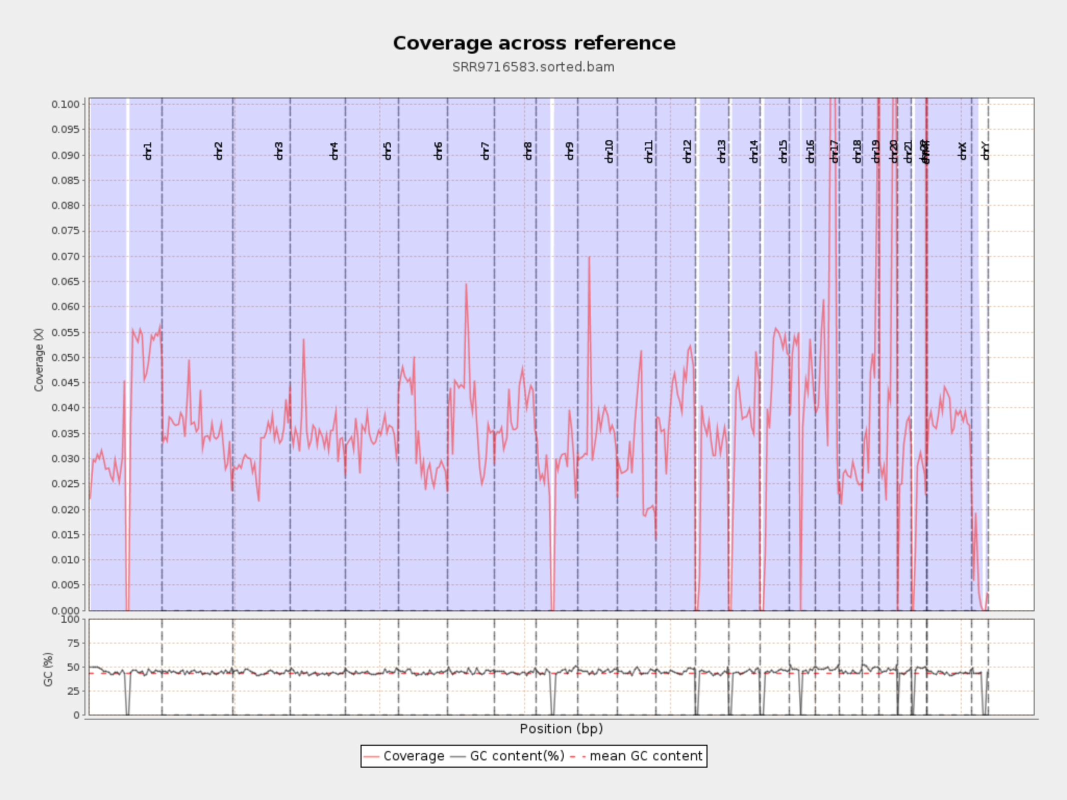
General error rate	0.54%
Mismatches	586,167
Insertions	7,847
Mapped reads with at least one insertion	0.4%
Deletions	20,003
Mapped reads with at least one deletion	1.02%
Homopolymer indels	38.74%

2.6. Chromosome stats

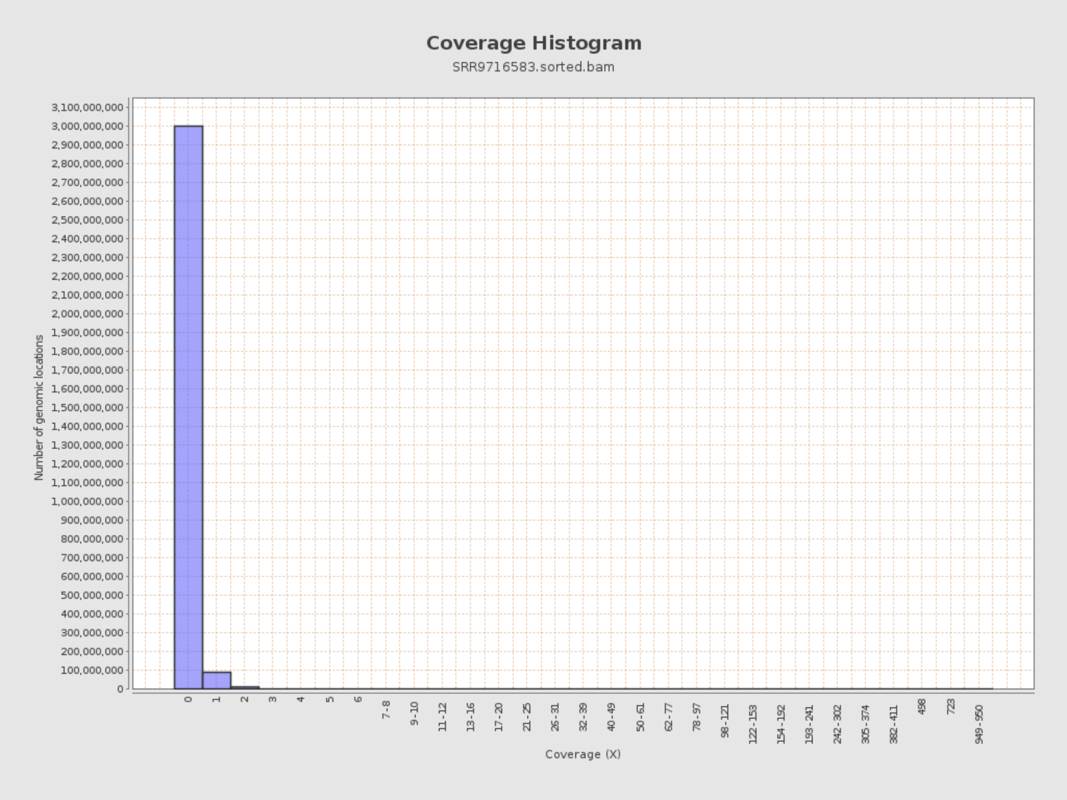
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9327461	0.0374	0.364
chr2	243199373	8676497	0.0357	0.44
chr3	198022430	6368943	0.0322	0.2018
chr4	191154276	6697458	0.035	0.2264
chr5	180915260	6254848	0.0346	0.2031
chr6	171115067	5872026	0.0343	0.2417
chr7	159138663	6359481	0.04	0.4258

chr8	146364022	5692274	0.0389	0.2761
chr9	141213431	3683323	0.0261	0.2118
chr10	135534747	4913468	0.0363	0.3631
chr11	135006516	3915695	0.029	0.2446
chr12	133851895	5591651	0.0418	0.2273
chr13	115169878	3307094	0.0287	0.186
chr14	107349540	3713382	0.0346	0.2131
chr15	102531392	4064185	0.0396	0.2233
chr16	90354753	3916933	0.0434	0.2505
chr17	81195210	5002871	0.0616	0.2927
chr18	78077248	2044379	0.0262	0.3373
chr19	59128983	2997235	0.0507	0.3426
chr20	63025520	3555123	0.0564	0.2783
chr21	48129895	1386165	0.0288	0.2029
chr22	51304566	1029853	0.0201	0.1563
chrMT	16571	9277	0.5598	0.9164
chrX	155270560	5953913	0.0383	0.234
chrY	59373566	337892	0.0057	0.1566

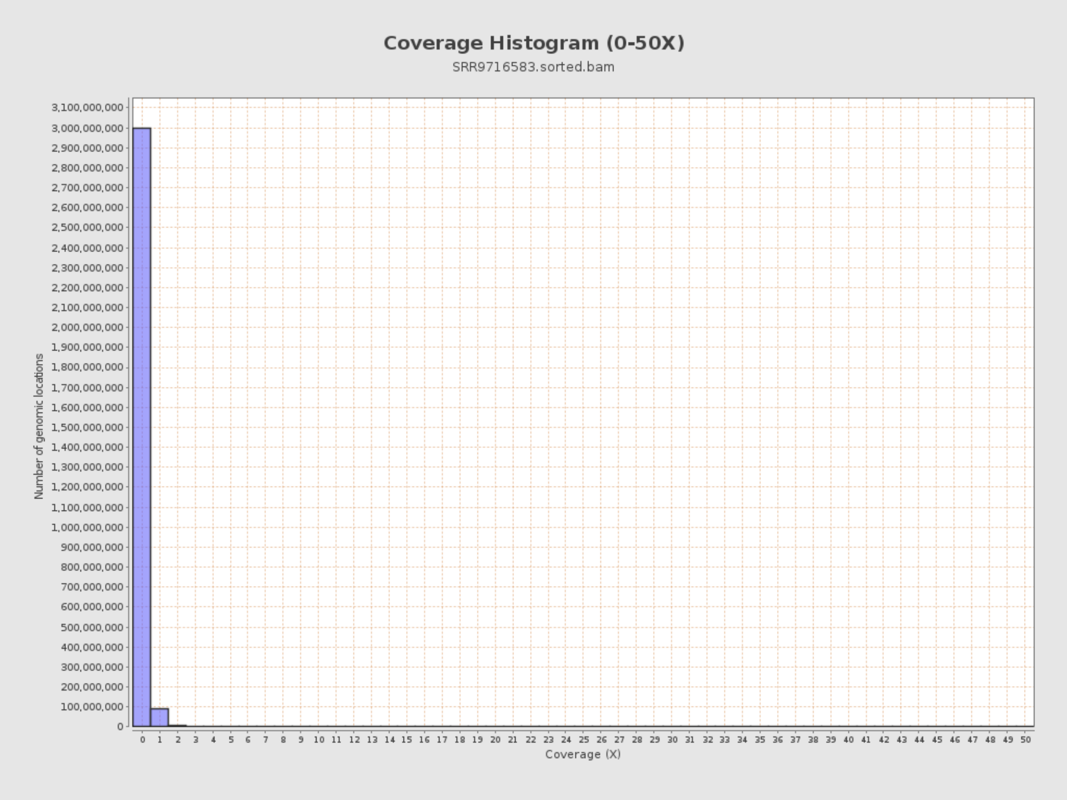
3. Results : Coverage across reference



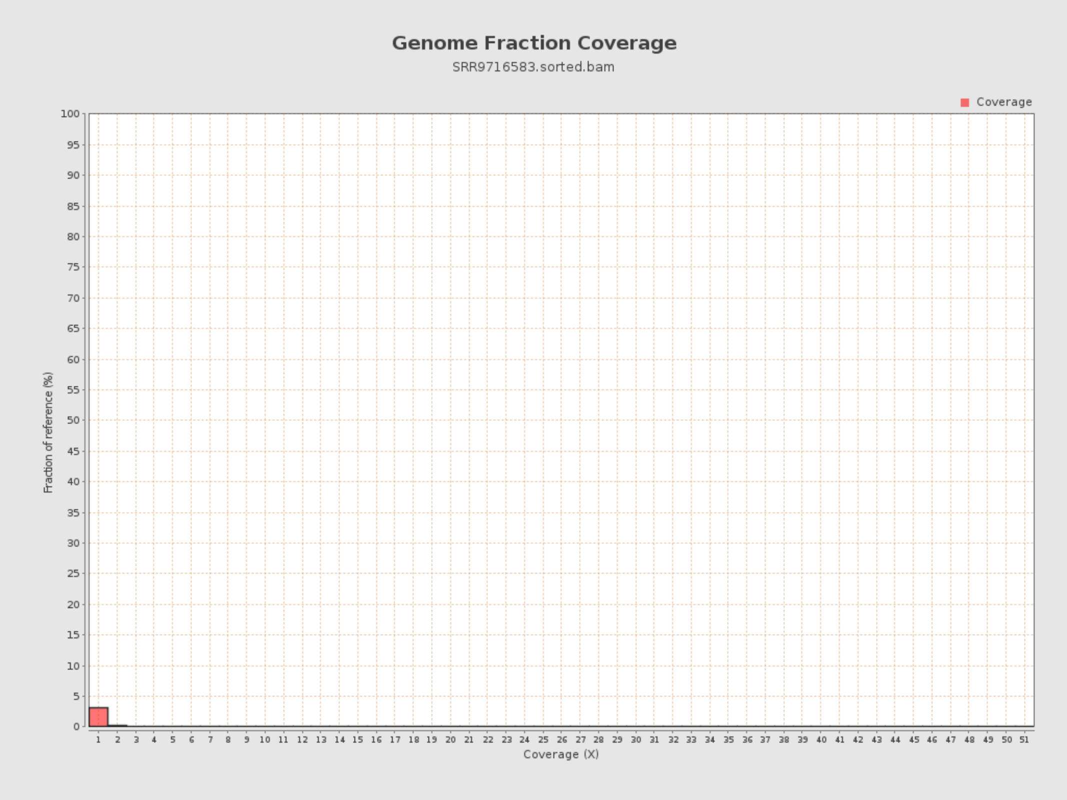
4. Results : Coverage Histogram



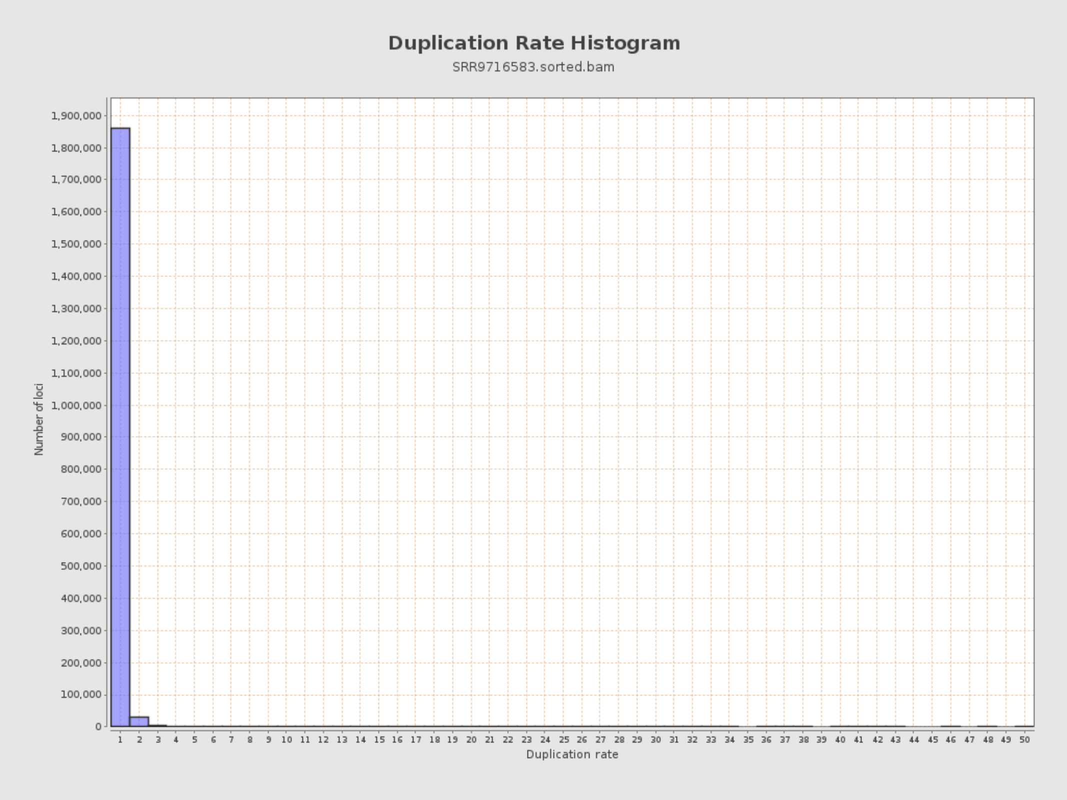
5. Results : Coverage Histogram (0-50X)



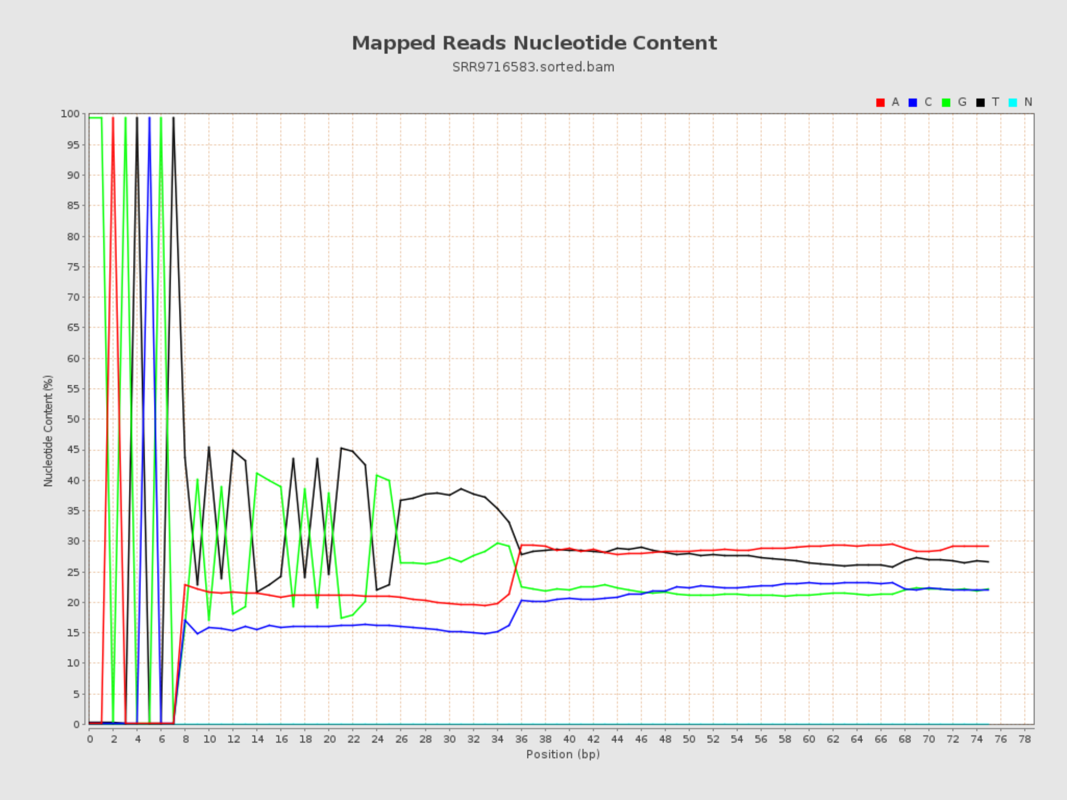
6. Results : Genome Fraction Coverage



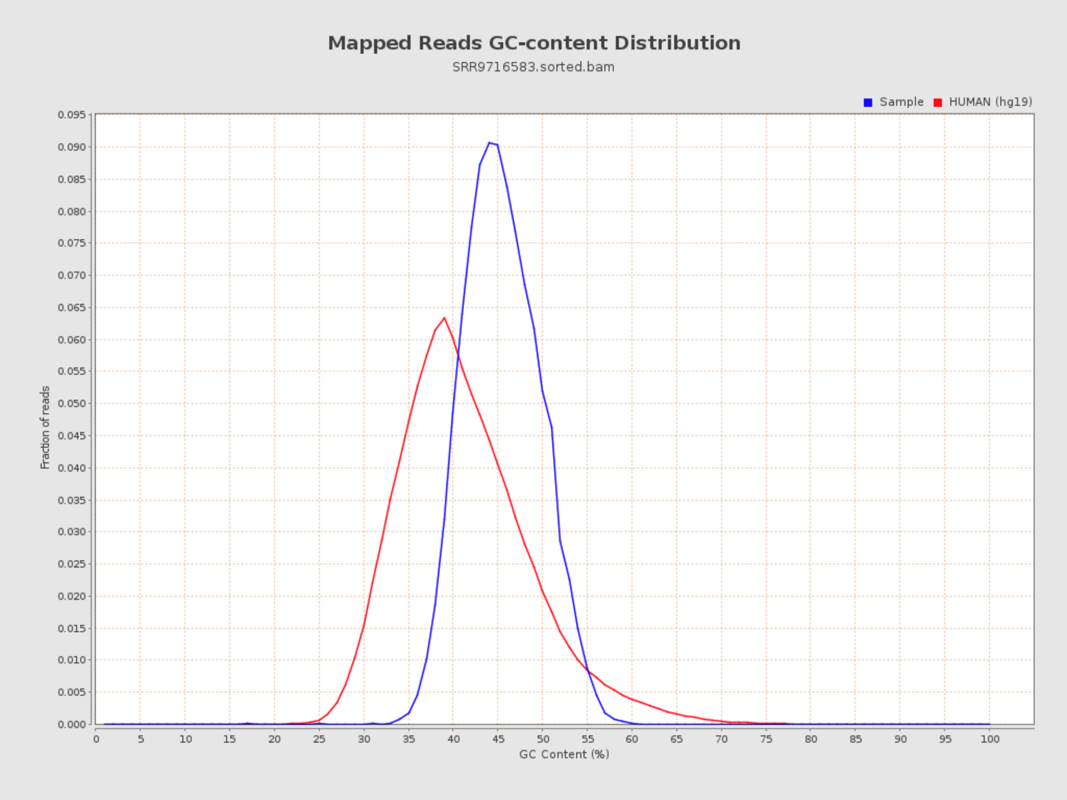
7. Results : Duplication Rate Histogram



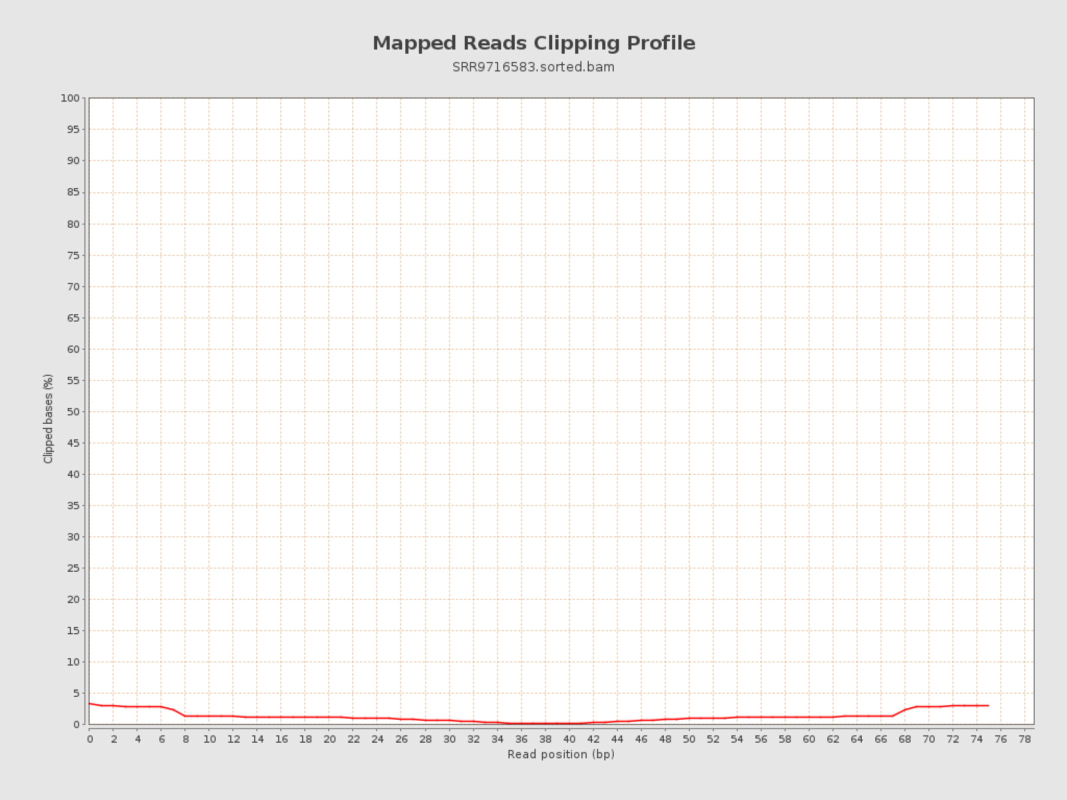
8. Results : Mapped Reads Nucleotide Content



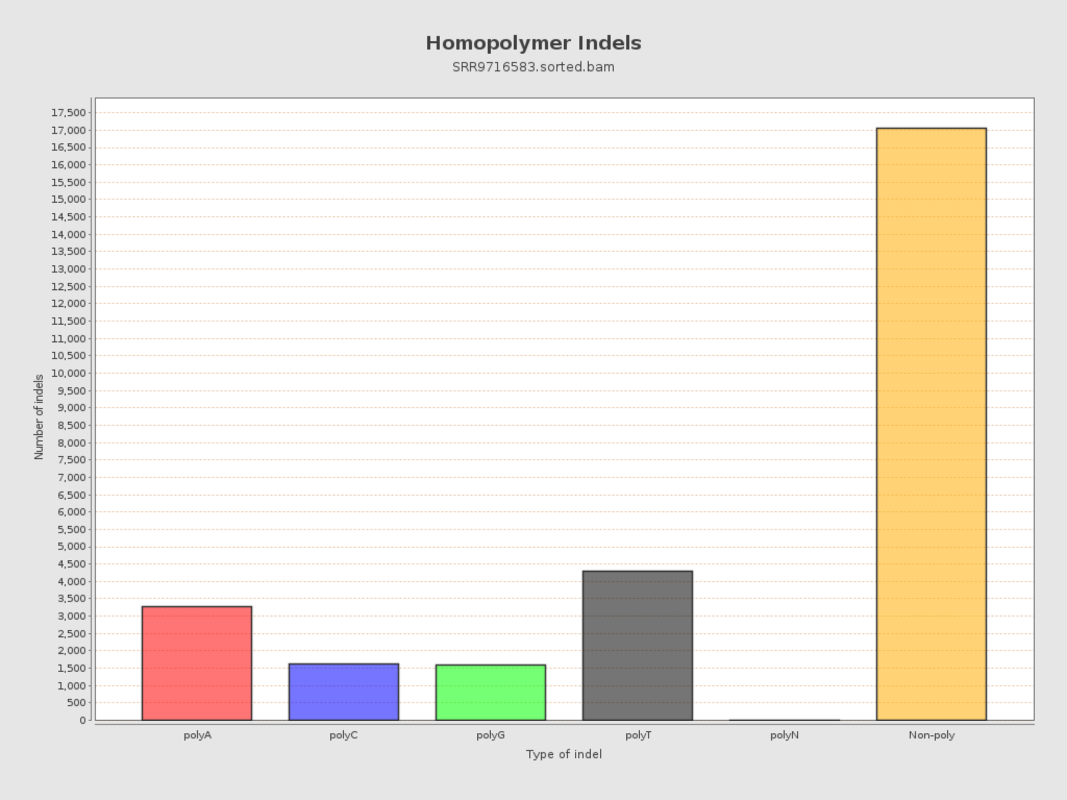
9. Results : Mapped Reads GC-content Distribution



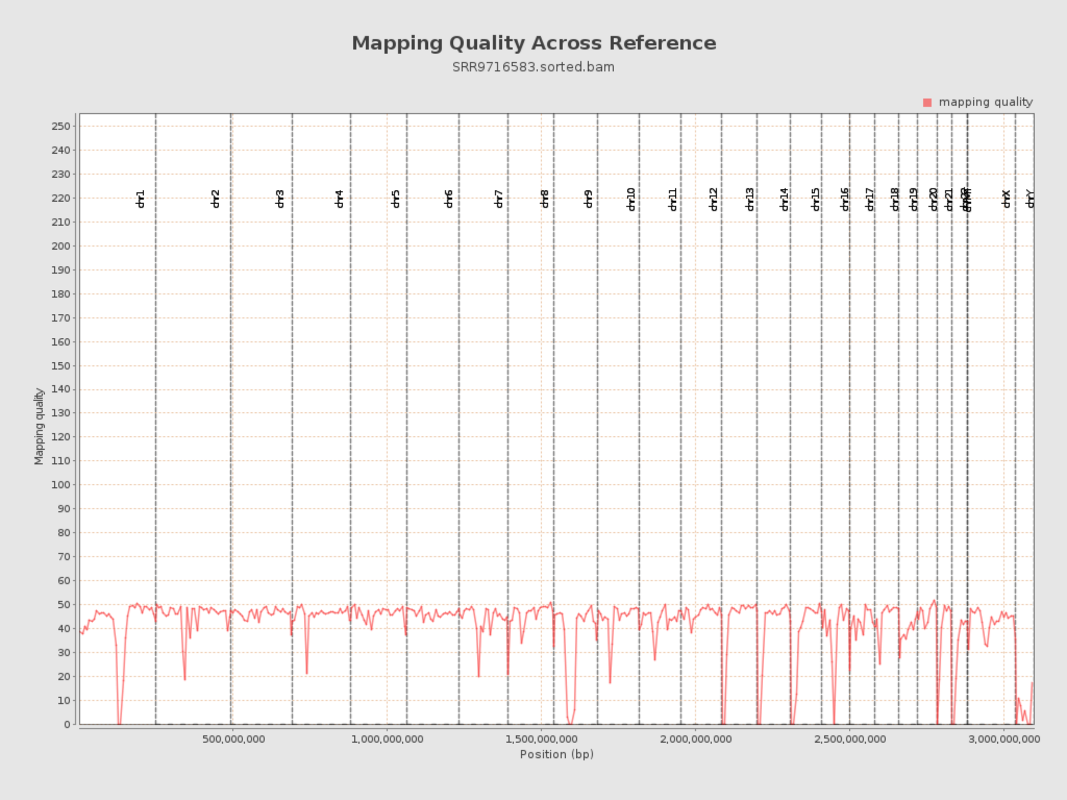
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram