Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:08:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716296.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_SRR9716296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716296.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:08:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	478,826
Mapped reads	402,478 / 84.06%
Unmapped reads	76,348 / 15.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,513 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	6,871 / 1.43%
Duplication rate	1.33%
Clipped reads	403,034 / 84.17%

2.2. ACGT Content

Number/percentage of A's	5,947,980 / 25.34%
Number/percentage of C's	4,222,604 / 17.99%
Number/percentage of T's	7,660,815 / 32.64%
Number/percentage of G's	5,640,641 / 24.03%
Number/percentage of N's	763 / 0%
GC Percentage	42.02%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.1033

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

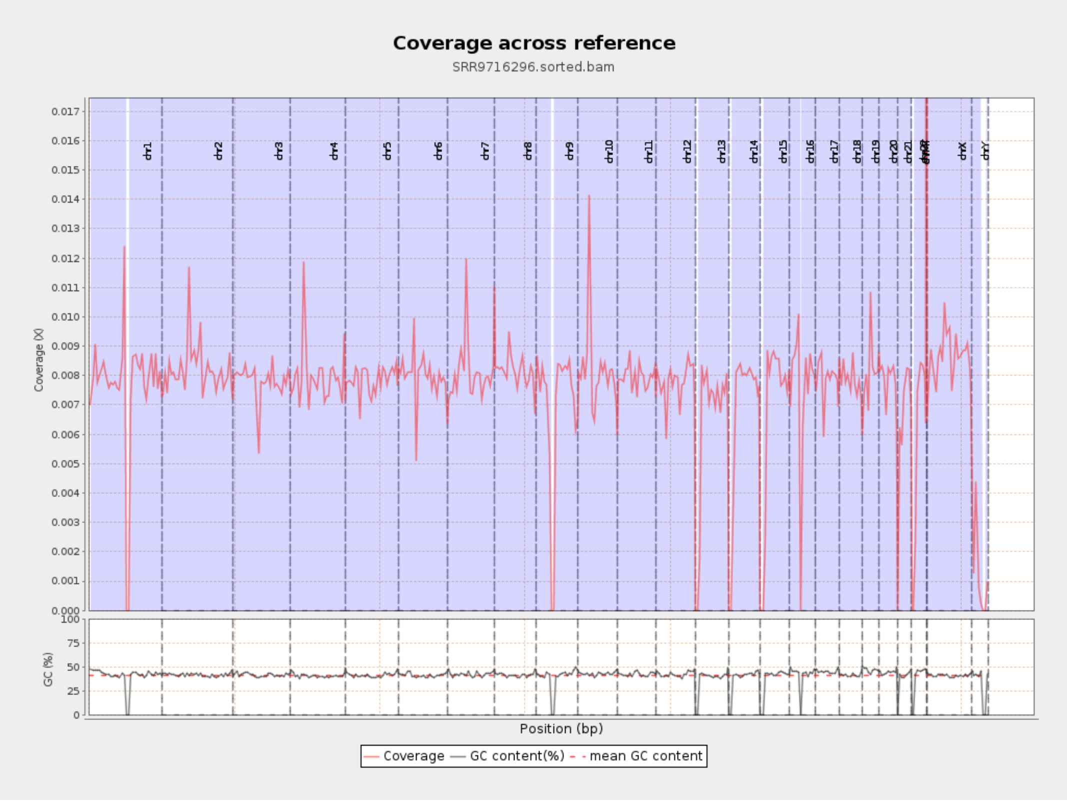
General error rate	0.52%
Mismatches	118,181
Insertions	1,647
Mapped reads with at least one insertion	0.41%
Deletions	4,460
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.98%

2.6. Chromosome stats

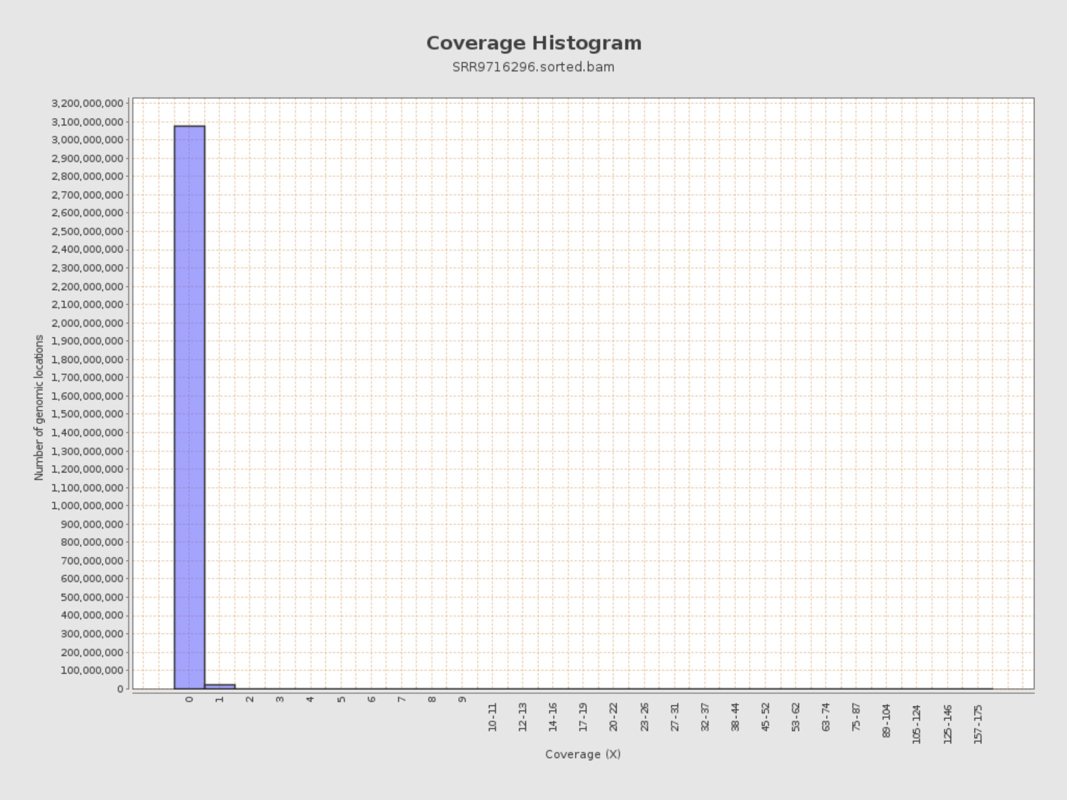
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1906867	0.0077	0.1504
chr2	243199373	2002444	0.0082	0.118
chr3	198022430	1541435	0.0078	0.0909
chr4	191154276	1518493	0.0079	0.0944
chr5	180915260	1422012	0.0079	0.0912
chr6	171115067	1364986	0.008	0.0975
chr7	159138663	1287585	0.0081	0.1148

chr8	146364022	1192369	0.0081	0.1091
chr9	141213431	969036	0.0069	0.0925
chr10	135534747	1117693	0.0082	0.1062
chr11	135006516	1070731	0.0079	0.0984
chr12	133851895	1041447	0.0078	0.0912
chr13	115169878	727935	0.0063	0.082
chr14	107349540	715066	0.0067	0.0869
chr15	102531392	680851	0.0066	0.0845
chr16	90354753	684381	0.0076	0.0914
chr17	81195210	635273	0.0078	0.092
chr18	78077248	616667	0.0079	0.1206
chr19	59128983	481889	0.0081	0.1221
chr20	63025520	494595	0.0078	0.0916
chr21	48129895	311357	0.0065	0.0849
chr22	51304566	280576	0.0055	0.076
chrMT	16571	2396	0.1446	0.3715
chrX	155270560	1338763	0.0086	0.0982
chrY	59373566	75060	0.0013	0.0448

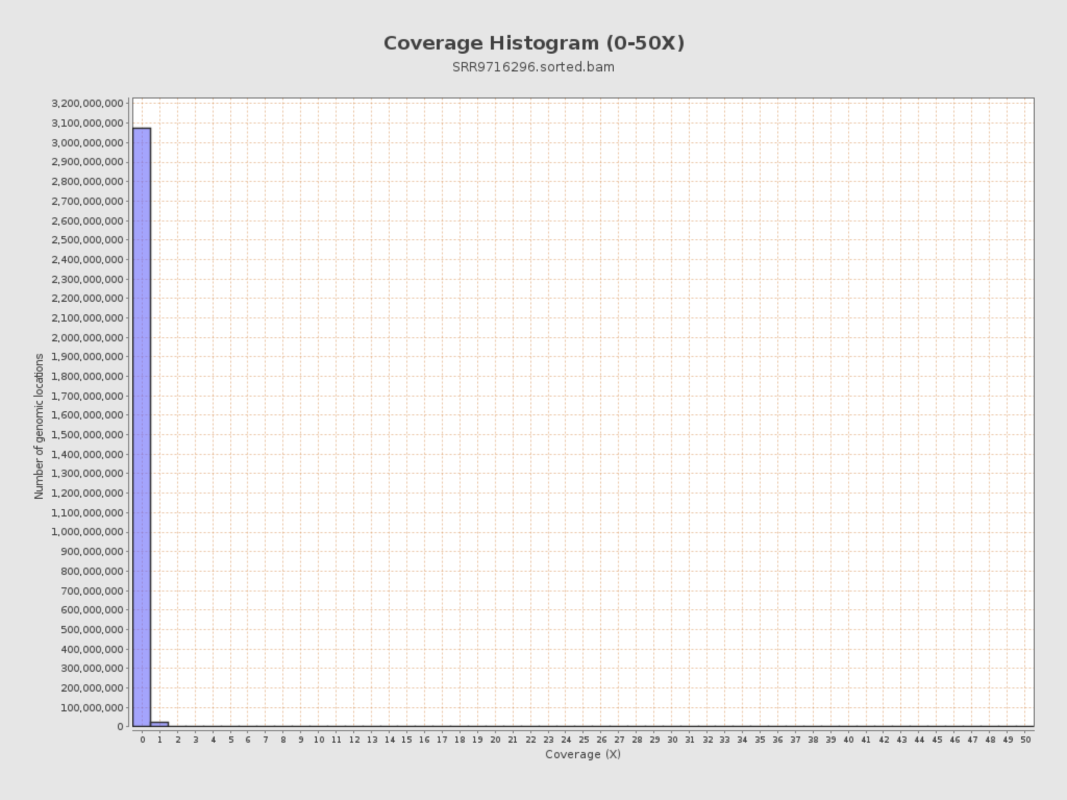
3. Results : Coverage across reference



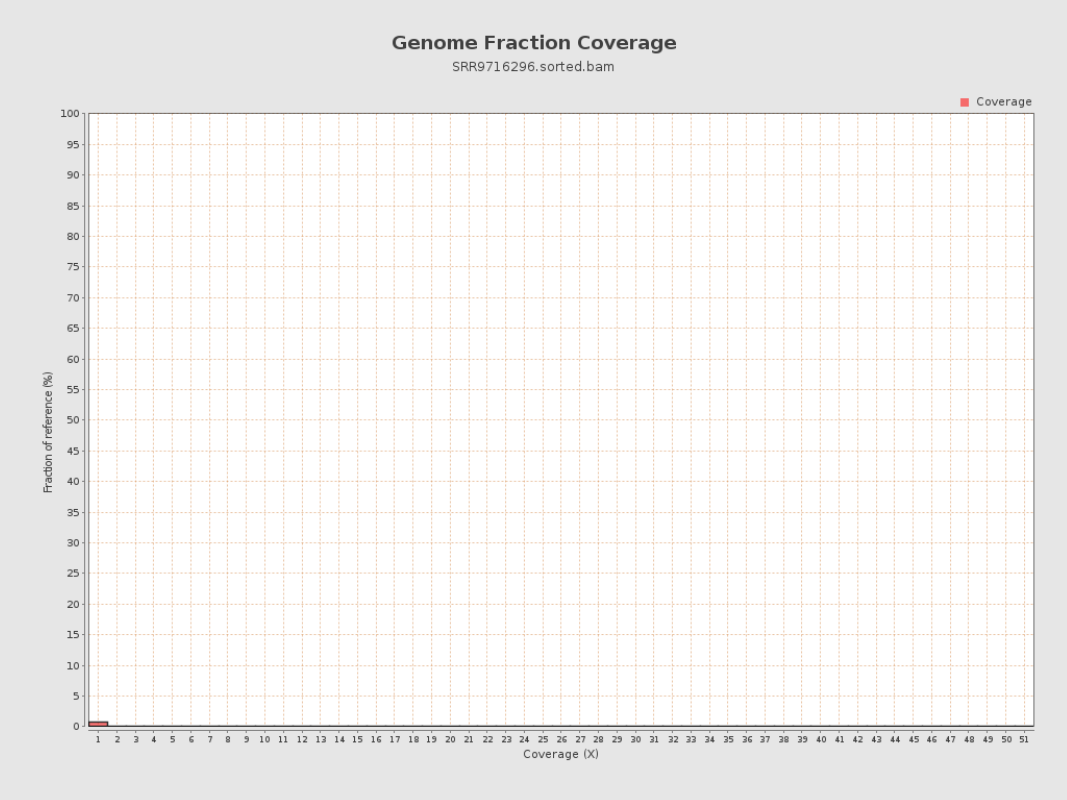
4. Results : Coverage Histogram



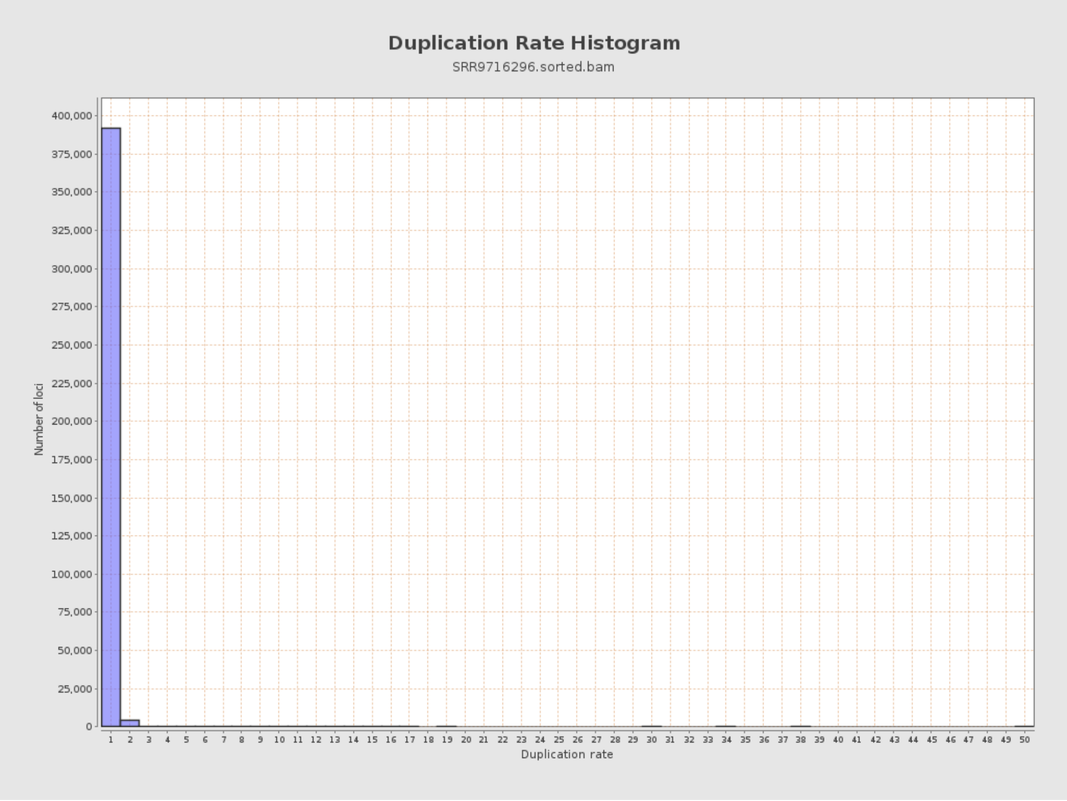
5. Results : Coverage Histogram (0-50X)



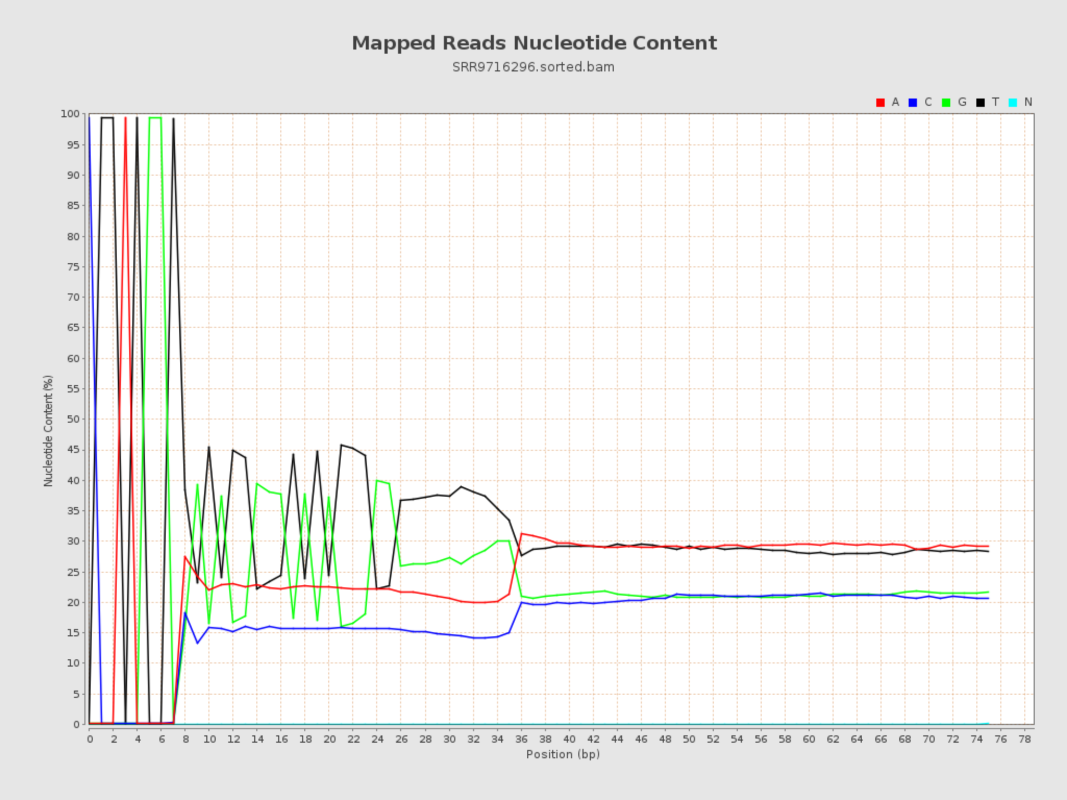
6. Results : Genome Fraction Coverage



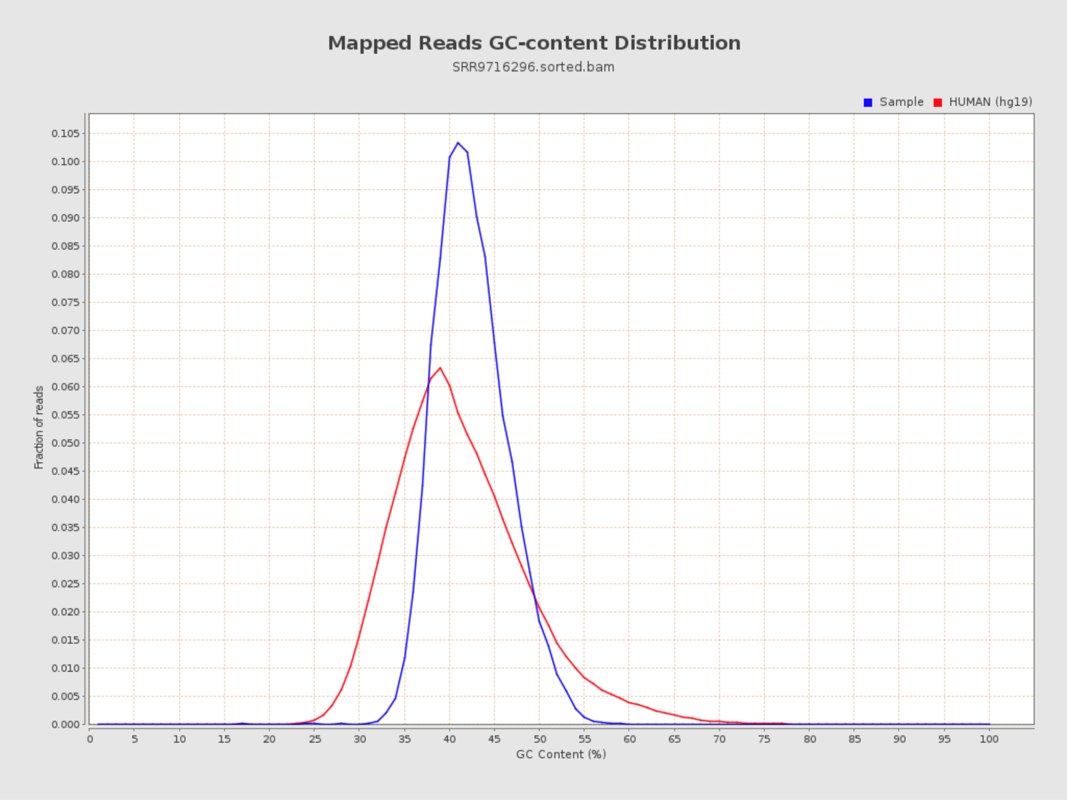
7. Results : Duplication Rate Histogram



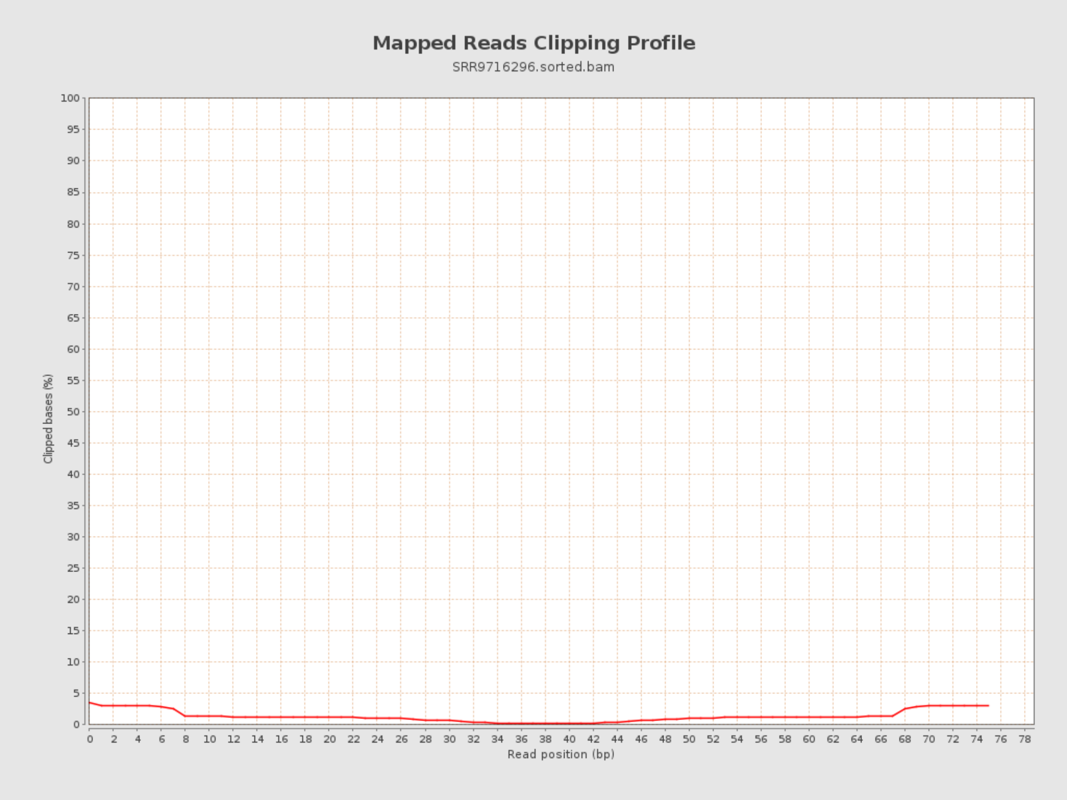
8. Results : Mapped Reads Nucleotide Content



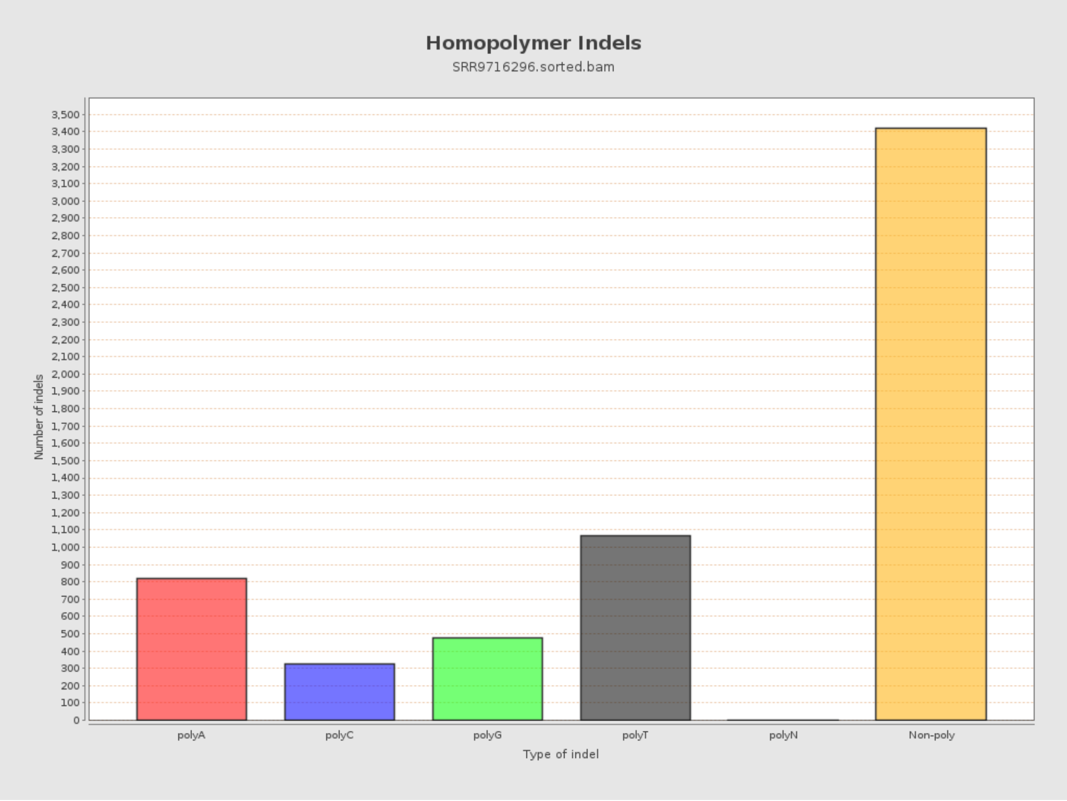
9. Results : Mapped Reads GC-content Distribution



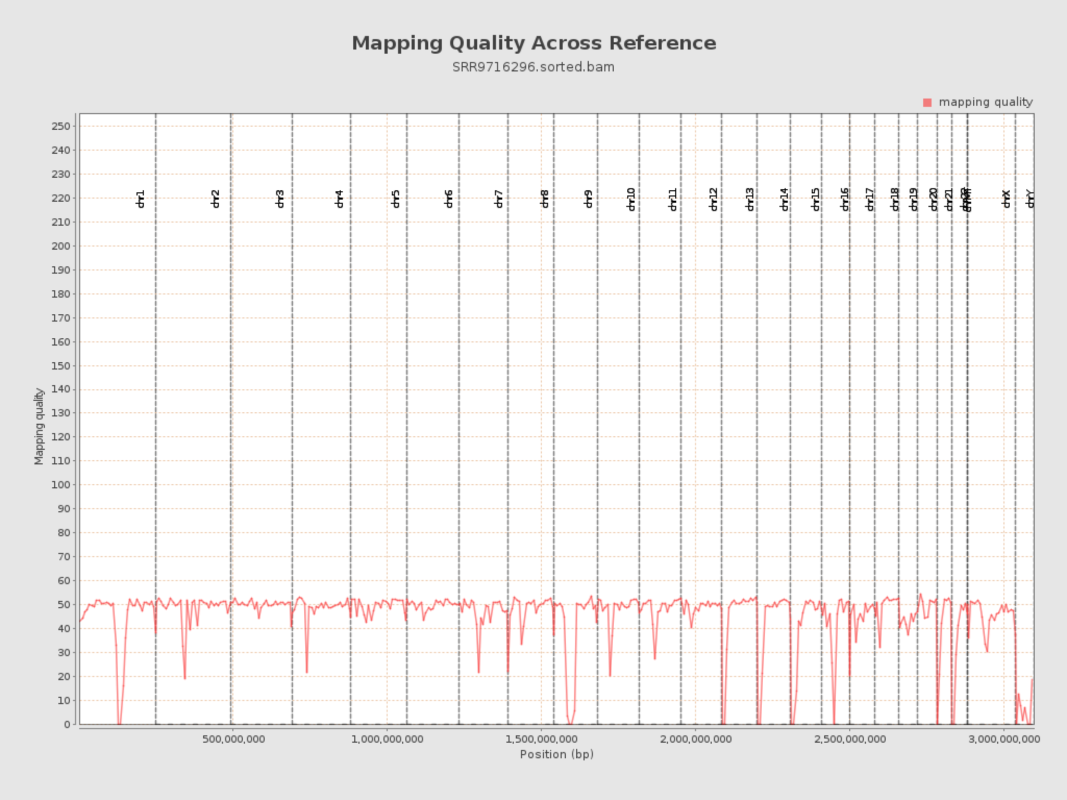
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram