Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:11:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716991.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_SRR9716991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716991.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:11:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,437,153
Mapped reads	2,097,114 / 86.05%
Unmapped reads	340,039 / 13.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,835 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	65,864 / 2.7%
Duplication rate	2.17%
Clipped reads	2,101,735 / 86.24%

2.2. ACGT Content

Number/percentage of A's	29,556,681 / 24.89%
Number/percentage of C's	24,954,951 / 21.02%
Number/percentage of T's	35,211,949 / 29.66%
Number/percentage of G's	29,001,498 / 24.43%
Number/percentage of N's	1,813 / 0%
GC Percentage	45.45%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3423

2.4. Mapping Quality

Mean Mapping Quality	42.11

2.5. Mismatches and indels

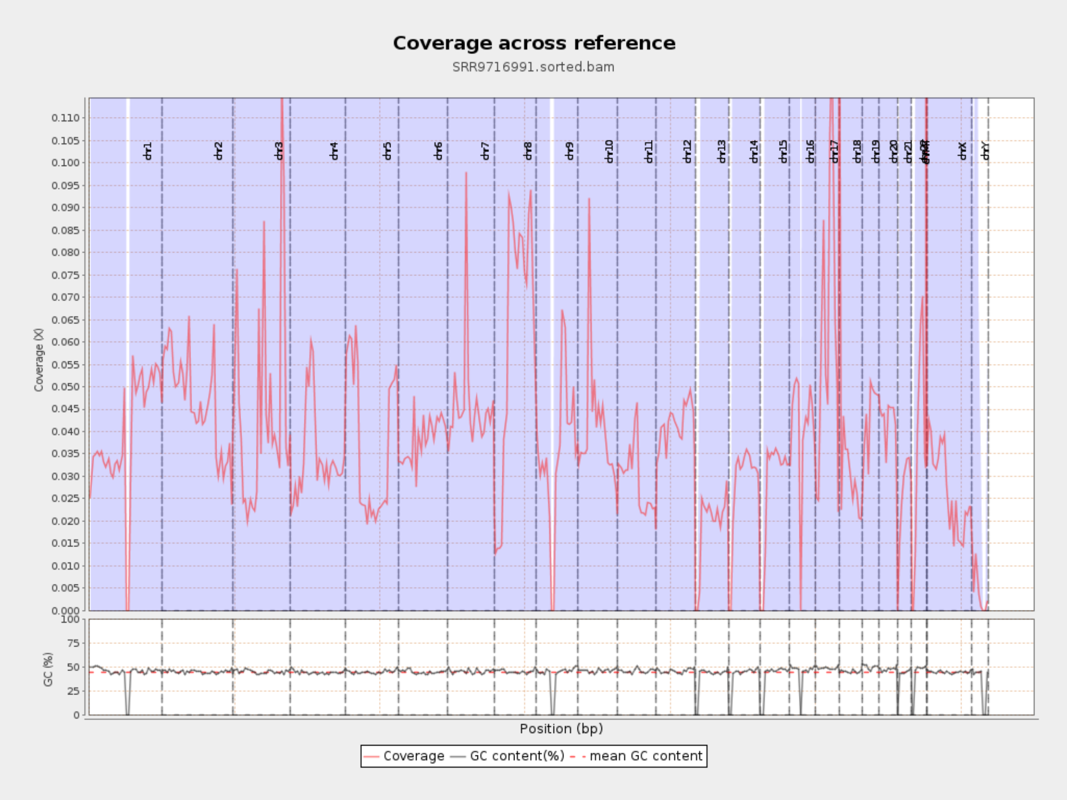
General error rate	0.53%
Mismatches	617,525
Insertions	8,341
Mapped reads with at least one insertion	0.4%
Deletions	20,937
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.19%

2.6. Chromosome stats

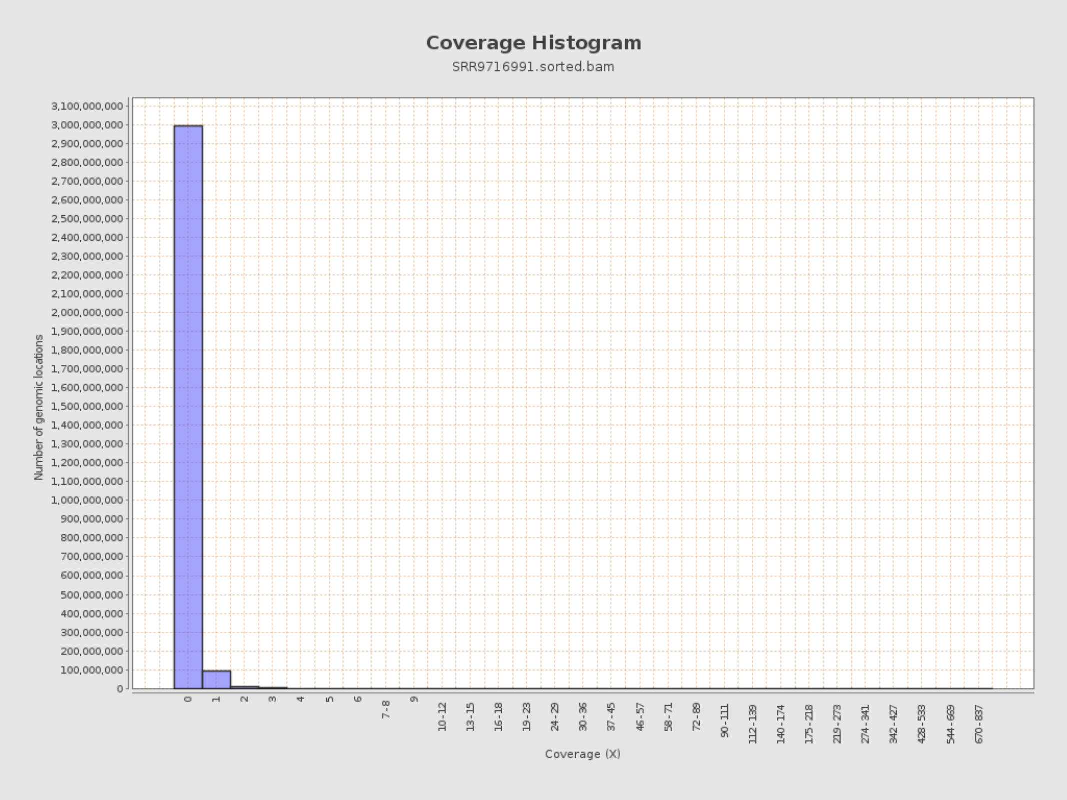
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9720529	0.039	0.4341
chr2	243199373	11434735	0.047	0.4336
chr3	198022430	8904379	0.045	0.2575
chr4	191154276	6589789	0.0345	0.2146
chr5	180915260	6751432	0.0373	0.214
chr6	171115067	6547284	0.0383	0.2452
chr7	159138663	7370144	0.0463	0.814

chr8	146364022	9169657	0.0626	0.3276
chr9	141213431	4923708	0.0349	0.2465
chr10	135534747	5565170	0.0411	0.4382
chr11	135006516	3933344	0.0291	0.231
chr12	133851895	5575481	0.0417	0.2432
chr13	115169878	2182653	0.019	0.1515
chr14	107349540	2978436	0.0277	0.1977
chr15	102531392	2846990	0.0278	0.1874
chr16	90354753	3709445	0.0411	0.2377
chr17	81195210	5096283	0.0628	0.2956
chr18	78077248	2725087	0.0349	0.3466
chr19	59128983	2560527	0.0433	0.4286
chr20	63025520	2658912	0.0422	0.2352
chr21	48129895	1212797	0.0252	0.1855
chr22	51304566	1776147	0.0346	0.2094
chrMT	16571	27835	1.6797	1.6522
chrX	155270560	4253876	0.0274	0.2163
chrY	59373566	245354	0.0041	0.0957

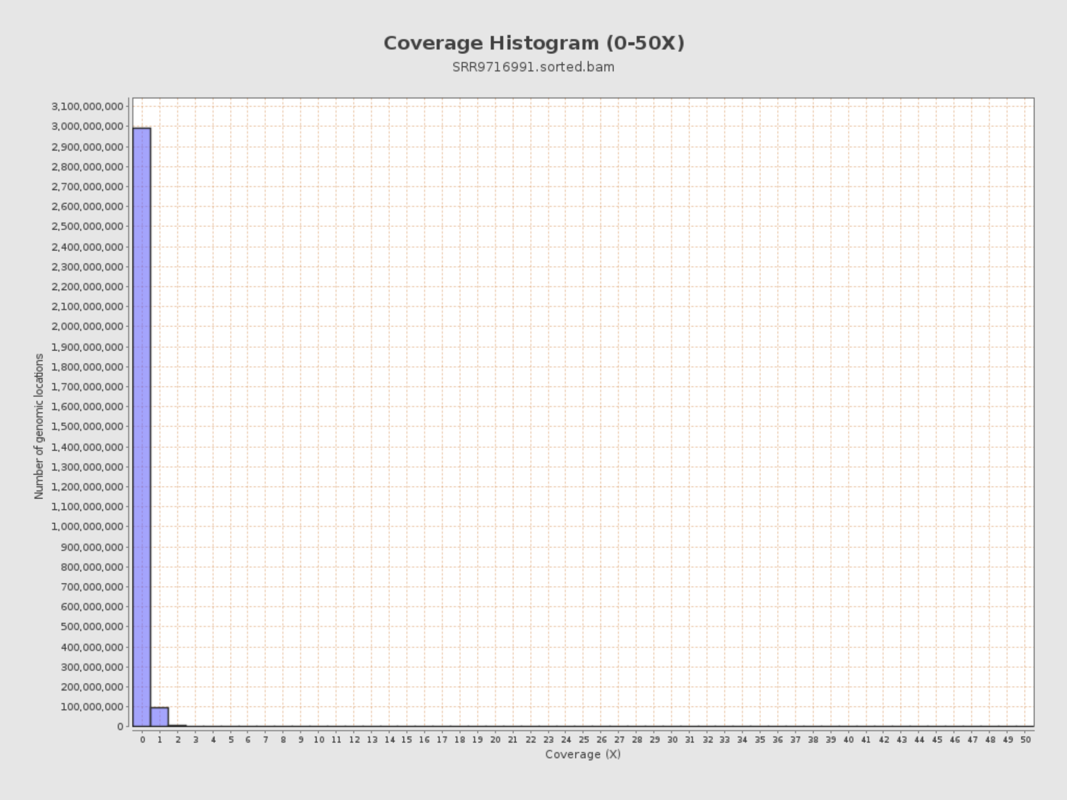
3. Results : Coverage across reference



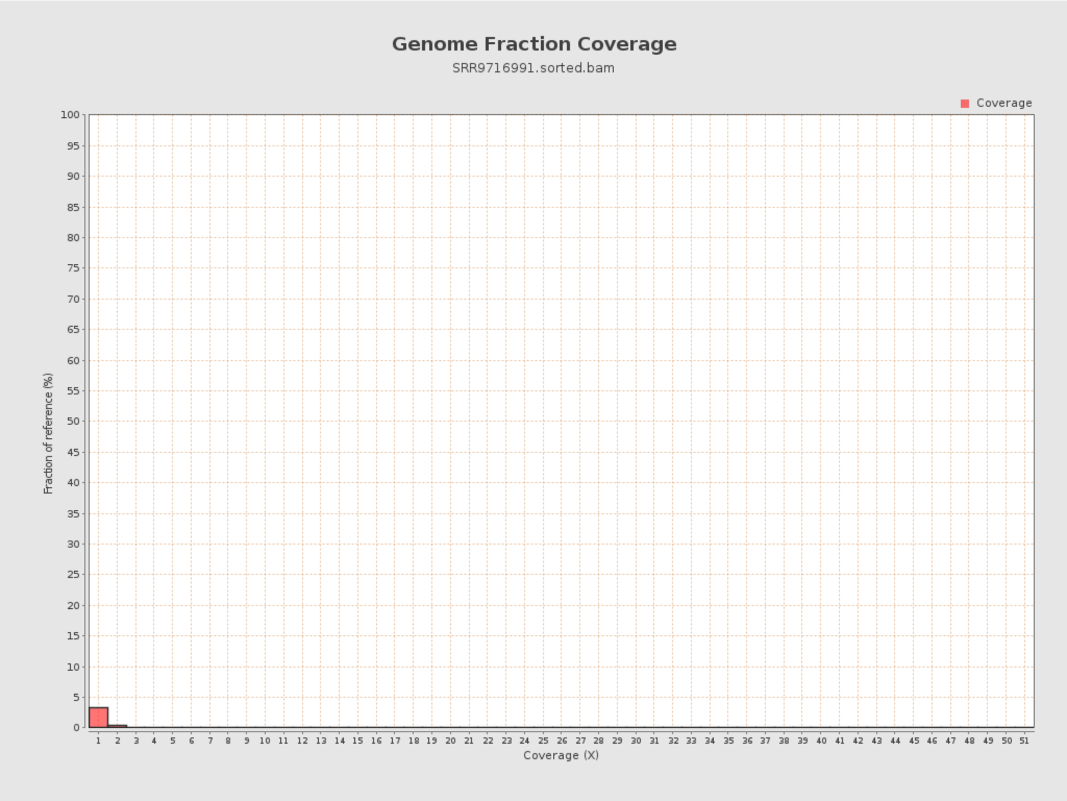
4. Results : Coverage Histogram



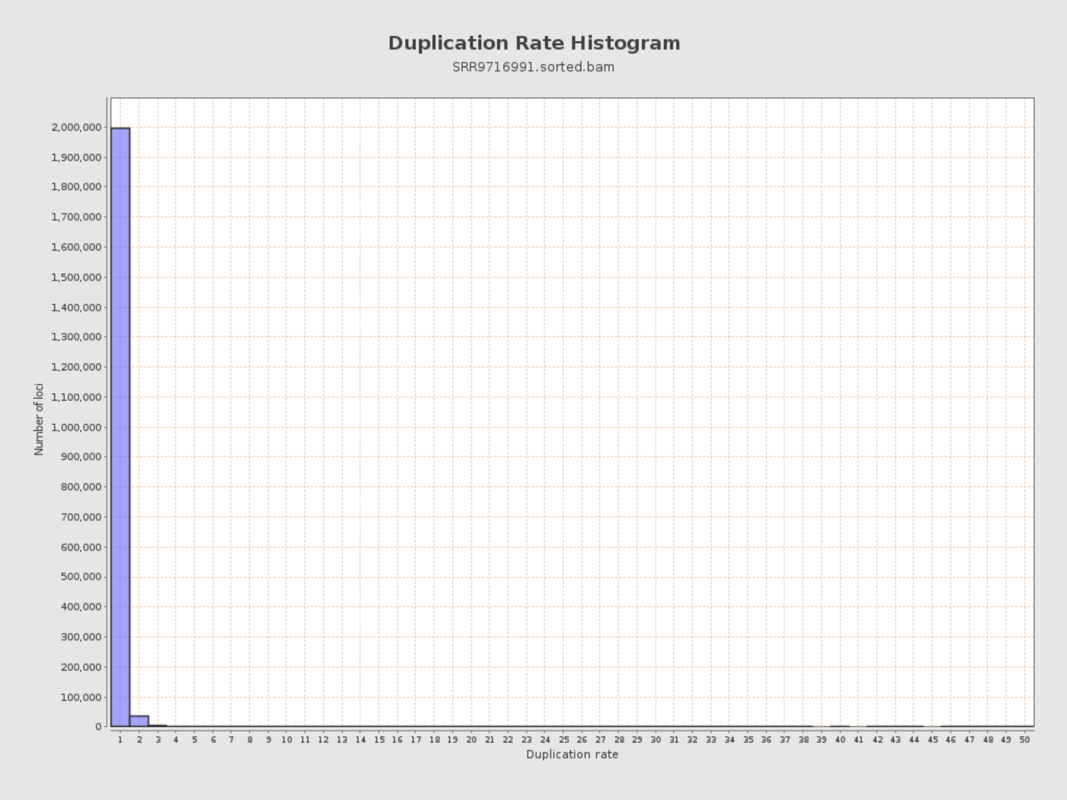
5. Results : Coverage Histogram (0-50X)



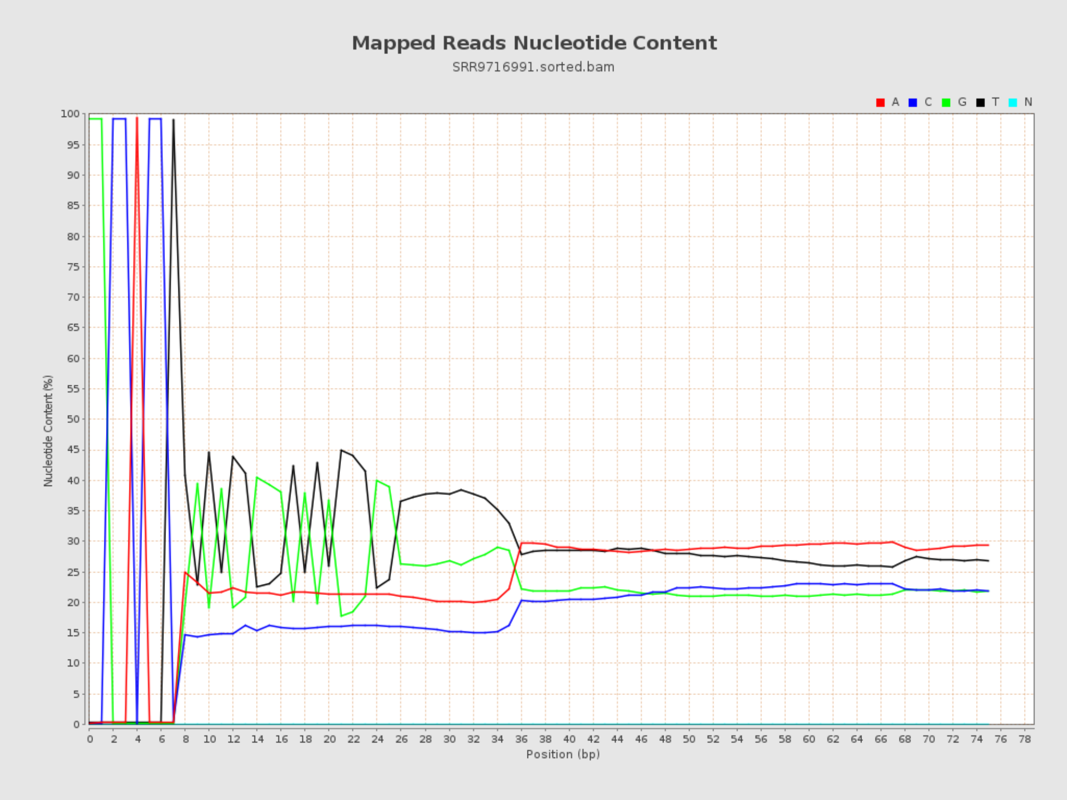
6. Results : Genome Fraction Coverage



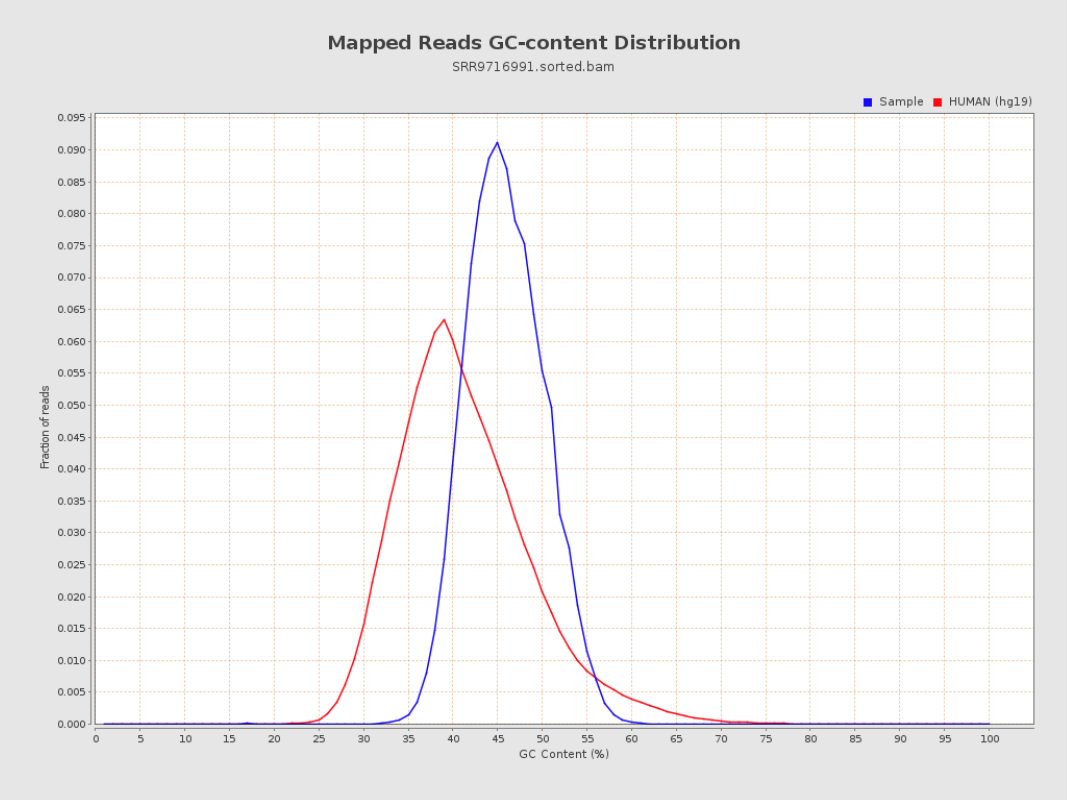
7. Results : Duplication Rate Histogram



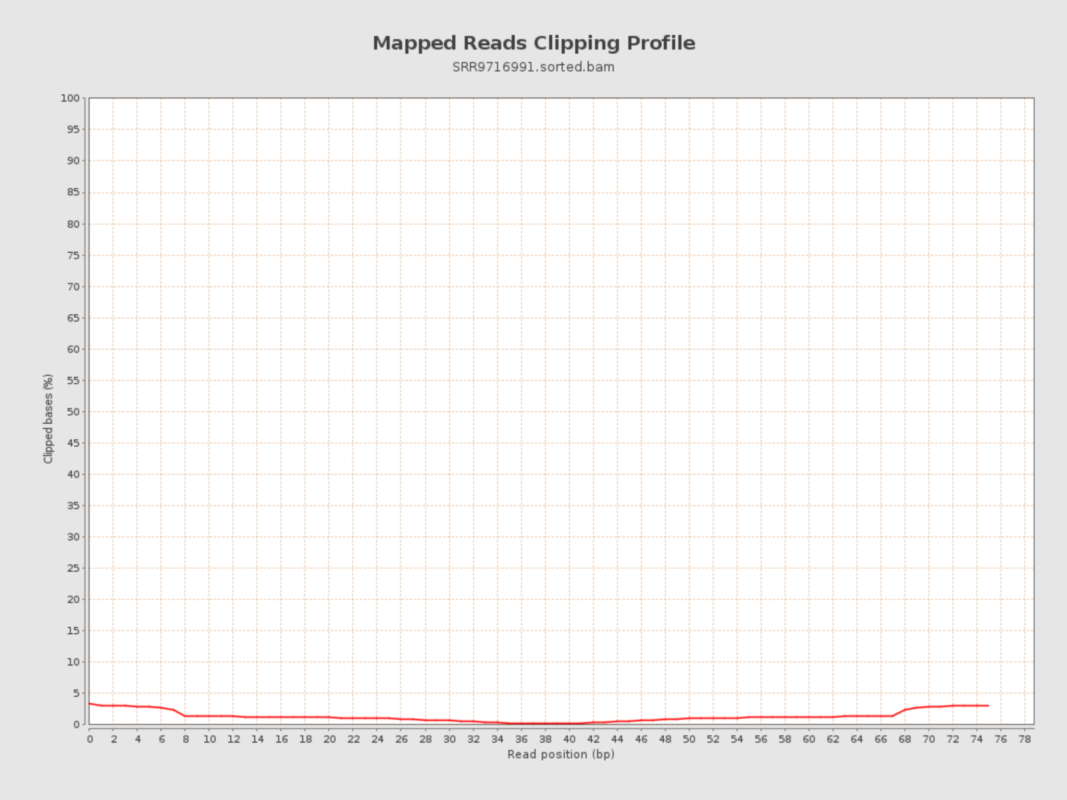
8. Results : Mapped Reads Nucleotide Content



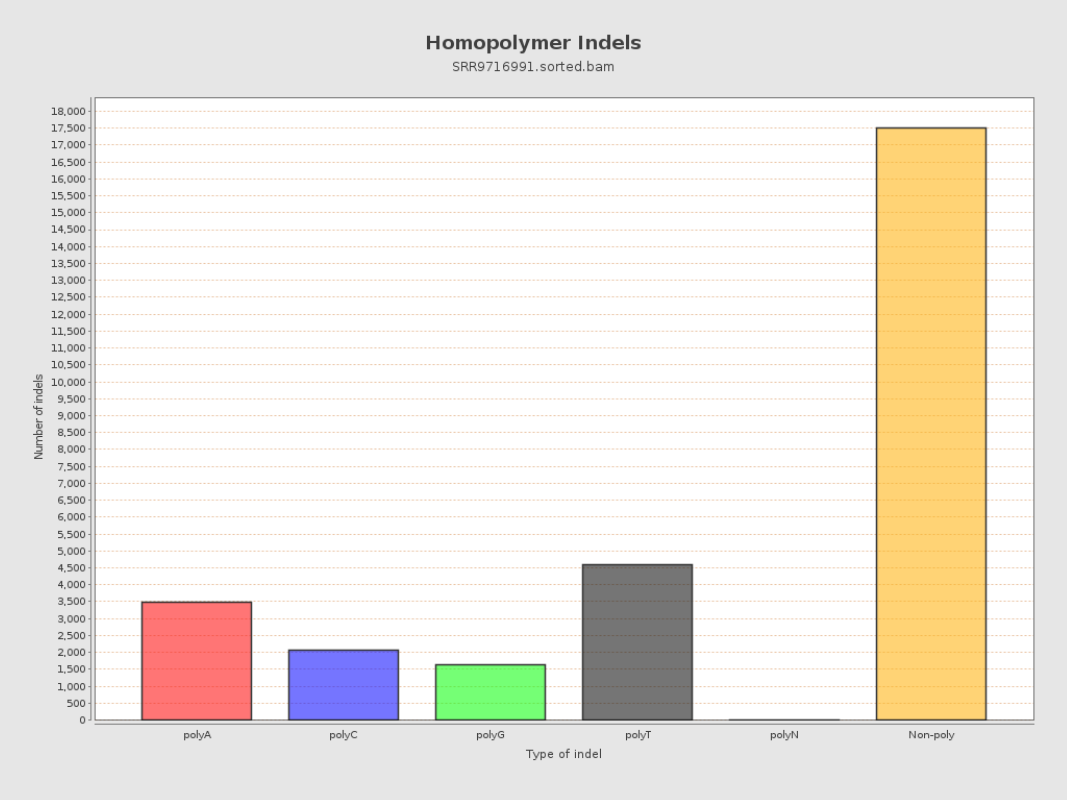
9. Results : Mapped Reads GC-content Distribution



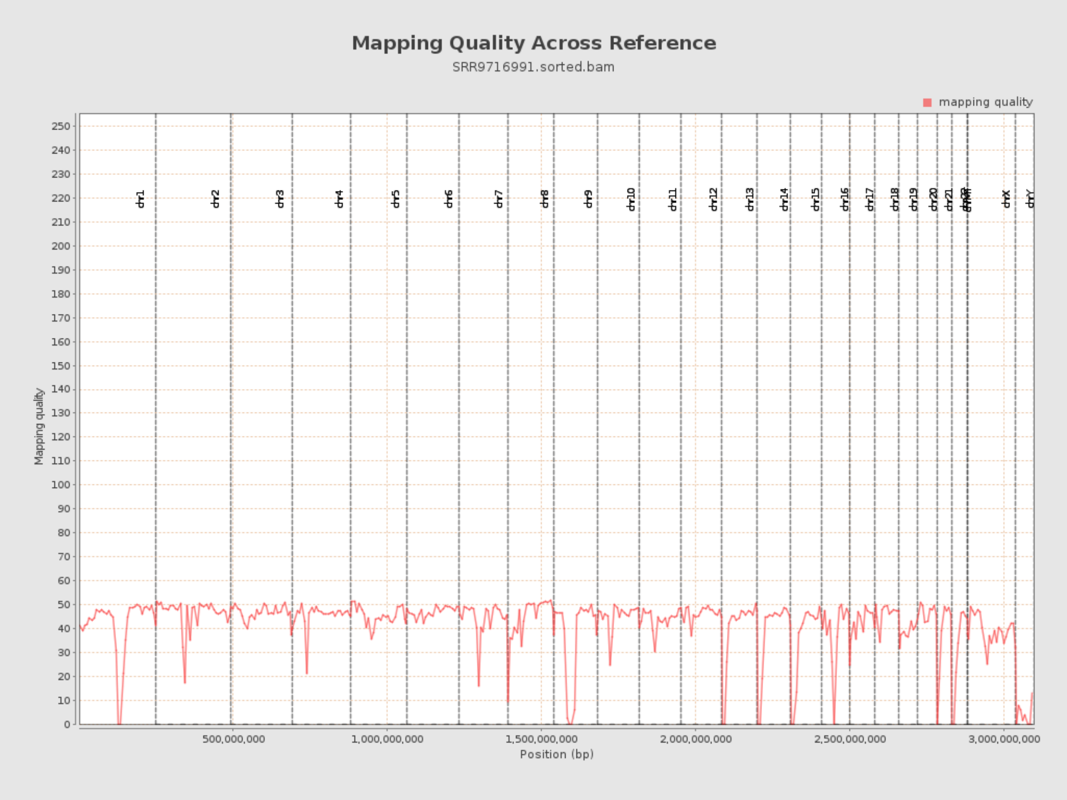
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram