

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:55:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716291.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_SRR9716291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:55:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,129,650
Mapped reads	926,926 / 82.05%
Unmapped reads	202,724 / 17.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,915 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	19,657 / 1.74%
Duplication rate	1.52%
Clipped reads	929,153 / 82.25%

2.2. ACGT Content

Number/percentage of A's	12,164,231 / 23.75%
Number/percentage of C's	10,841,457 / 21.17%
Number/percentage of T's	15,283,919 / 29.84%
Number/percentage of G's	12,930,871 / 25.24%
Number/percentage of N's	1,282 / 0%
GC Percentage	46.41%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.157
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	40.08
----------------------	-------

2.5. Mismatches and indels

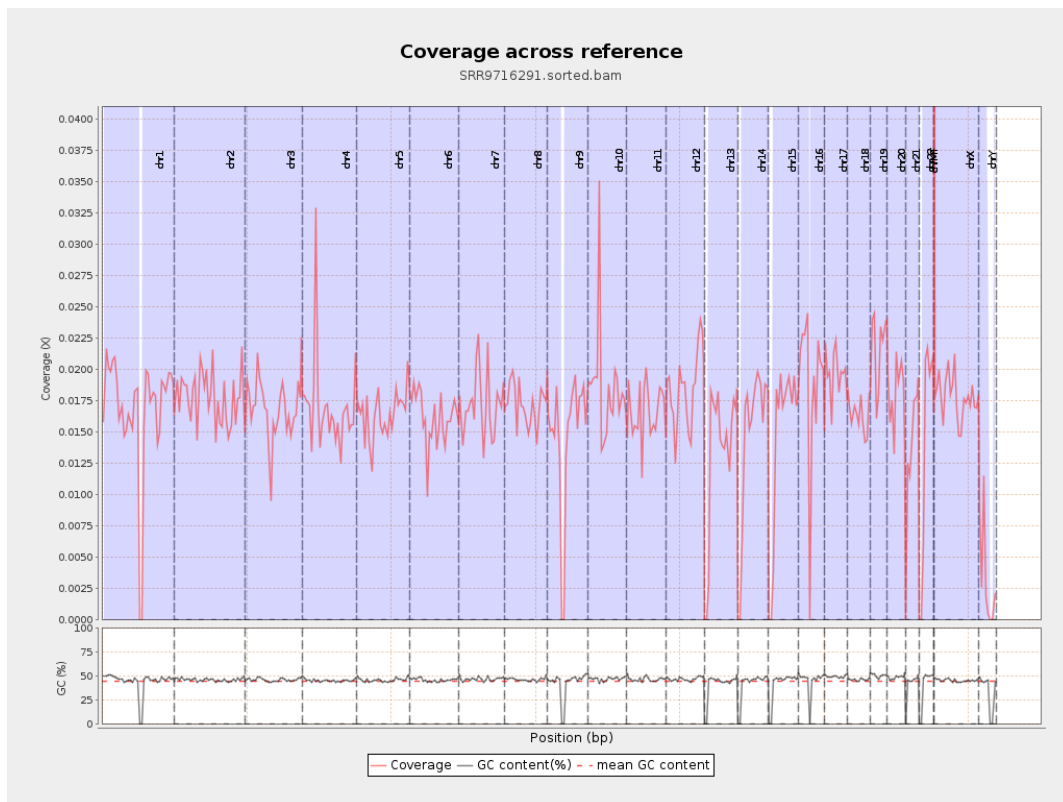
General error rate	0.54%
Mismatches	271,809
Insertions	3,179
Mapped reads with at least one insertion	0.34%
Deletions	8,729
Mapped reads with at least one deletion	0.93%
Homopolymer indels	36.87%

2.6. Chromosome stats

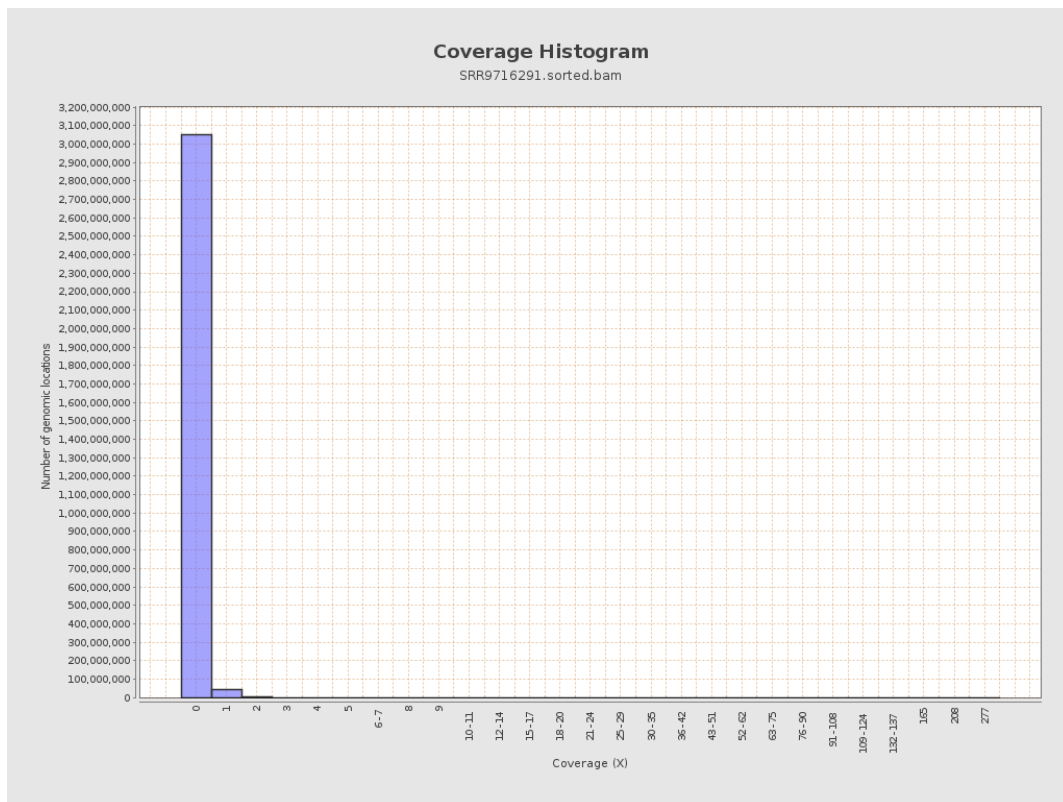
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4186413	0.0168	0.166
chr2	243199373	4320542	0.0178	0.1975
chr3	198022430	3324241	0.0168	0.1453
chr4	191154276	3240911	0.017	0.1582
chr5	180915260	2977727	0.0165	0.1388
chr6	171115067	2762613	0.0161	0.14
chr7	159138663	2731699	0.0172	0.1656

chr8	146364022	2507093	0.0171	0.1477
chr9	141213431	2056842	0.0146	0.1391
chr10	135534747	2515151	0.0186	0.2087
chr11	135006516	2259998	0.0167	0.1575
chr12	133851895	2456463	0.0184	0.1473
chr13	115169878	1524931	0.0132	0.1246
chr14	107349540	1571575	0.0146	0.1331
chr15	102531392	1485268	0.0145	0.133
chr16	90354753	1689051	0.0187	0.1573
chr17	81195210	1601318	0.0197	0.1587
chr18	78077248	1266818	0.0162	0.1752
chr19	59128983	1279753	0.0216	0.1806
chr20	63025520	1134329	0.018	0.1512
chr21	48129895	664547	0.0138	0.1437
chr22	51304566	722642	0.0141	0.1349
chrMT	16571	4587	0.2768	0.5698
chrX	155270560	2763540	0.0178	0.1522
chrY	59373566	188305	0.0032	0.0998

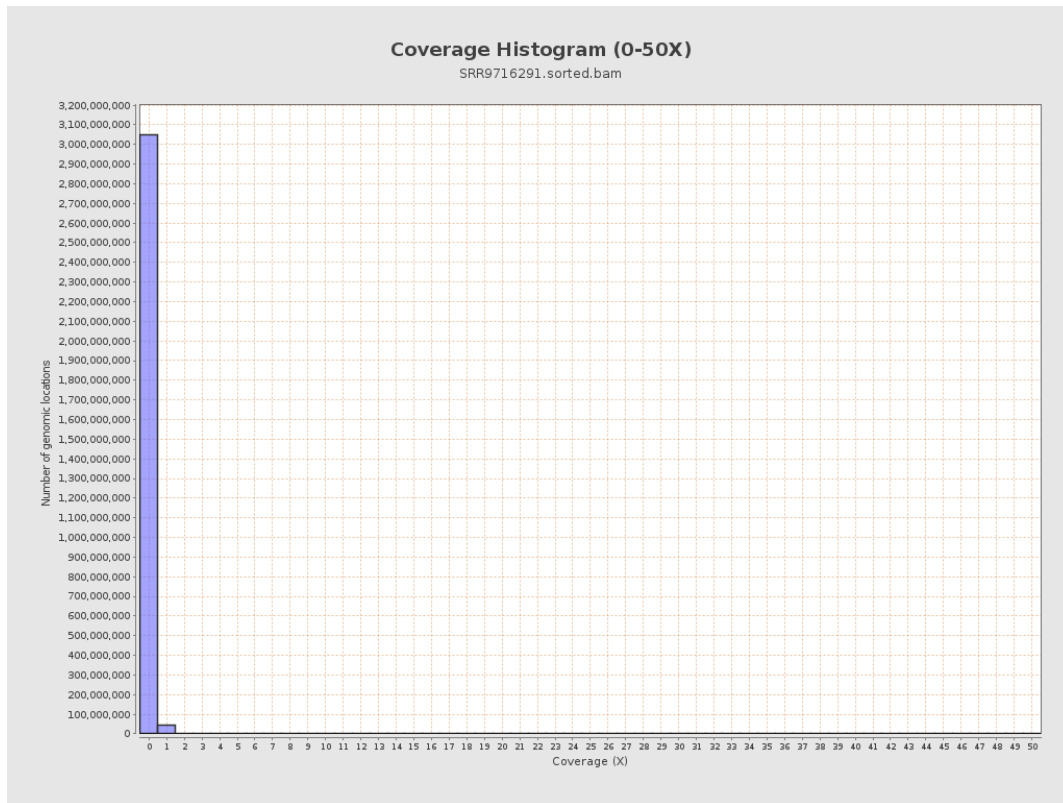
3. Results : Coverage across reference



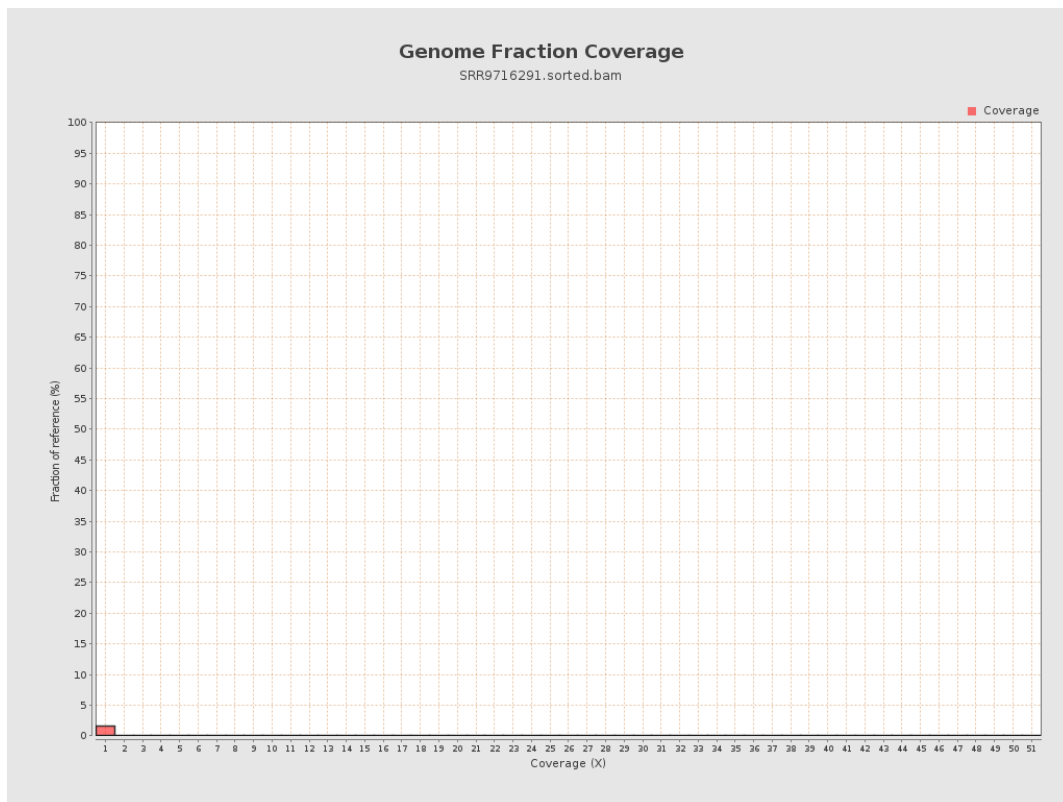
4. Results : Coverage Histogram



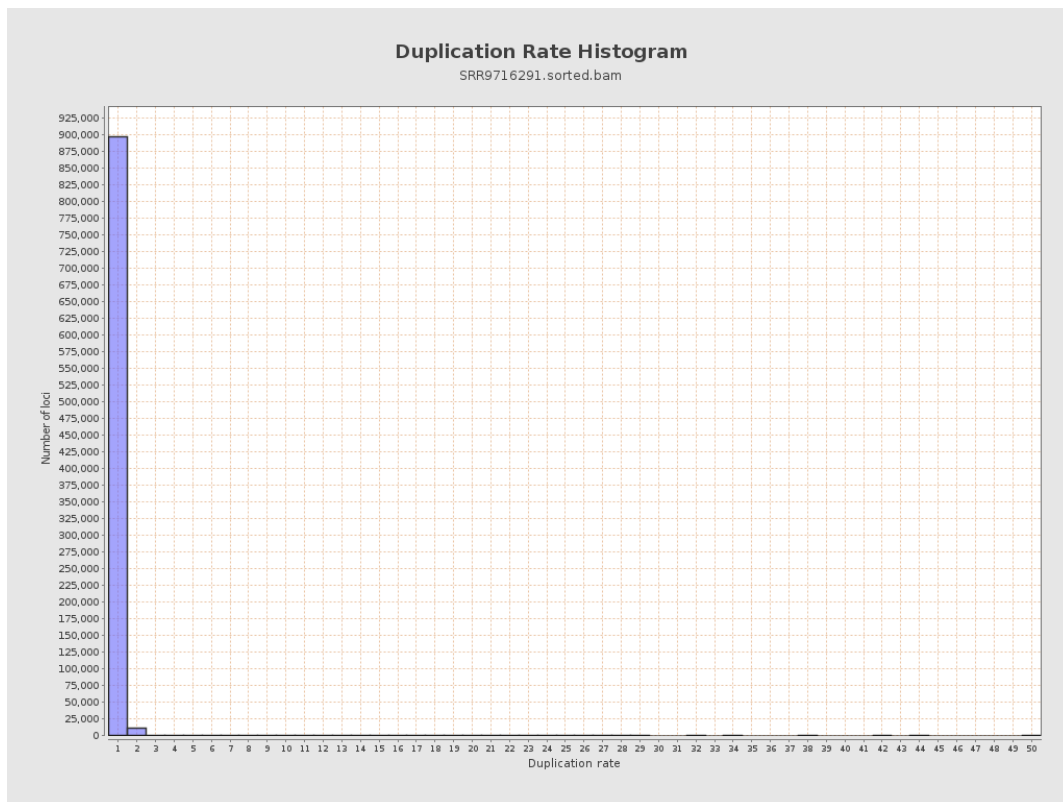
5. Results : Coverage Histogram (0-50X)



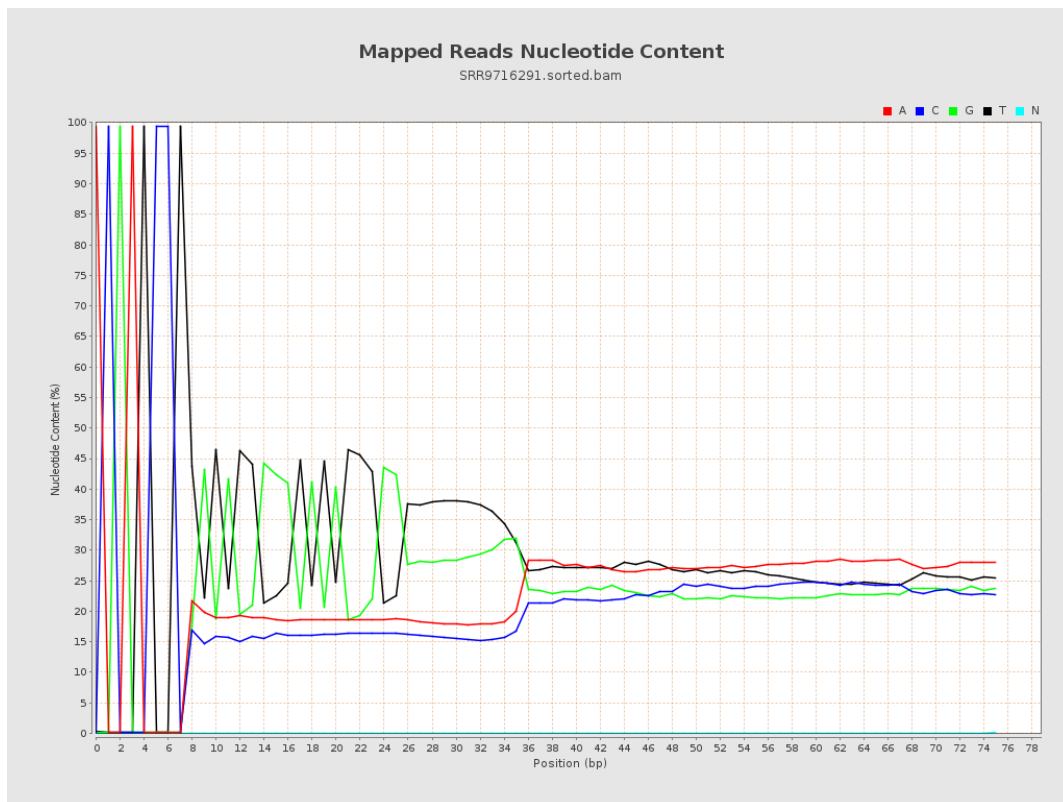
6. Results : Genome Fraction Coverage



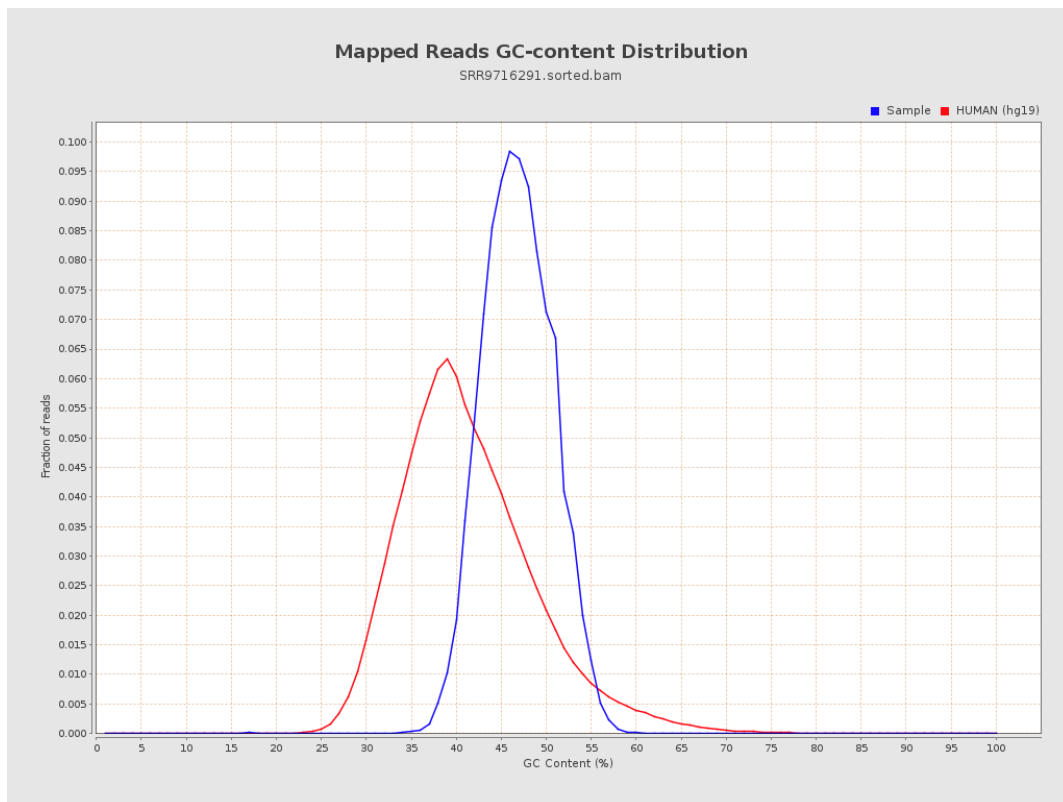
7. Results : Duplication Rate Histogram



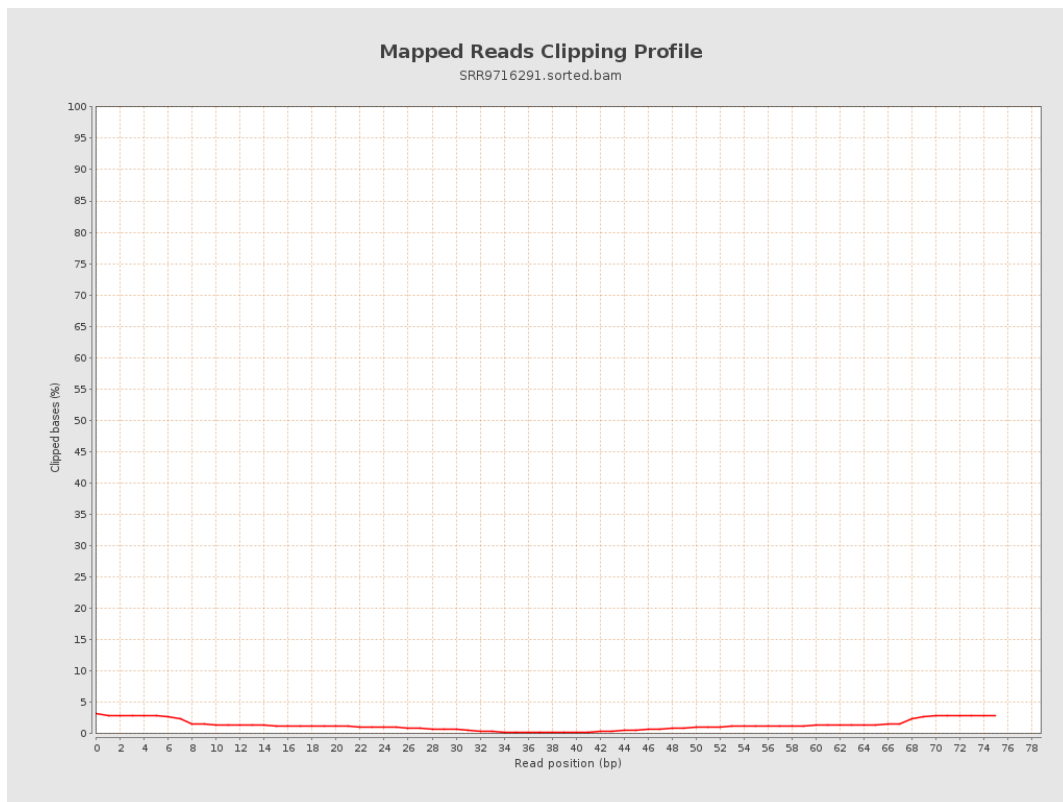
8. Results : Mapped Reads Nucleotide Content



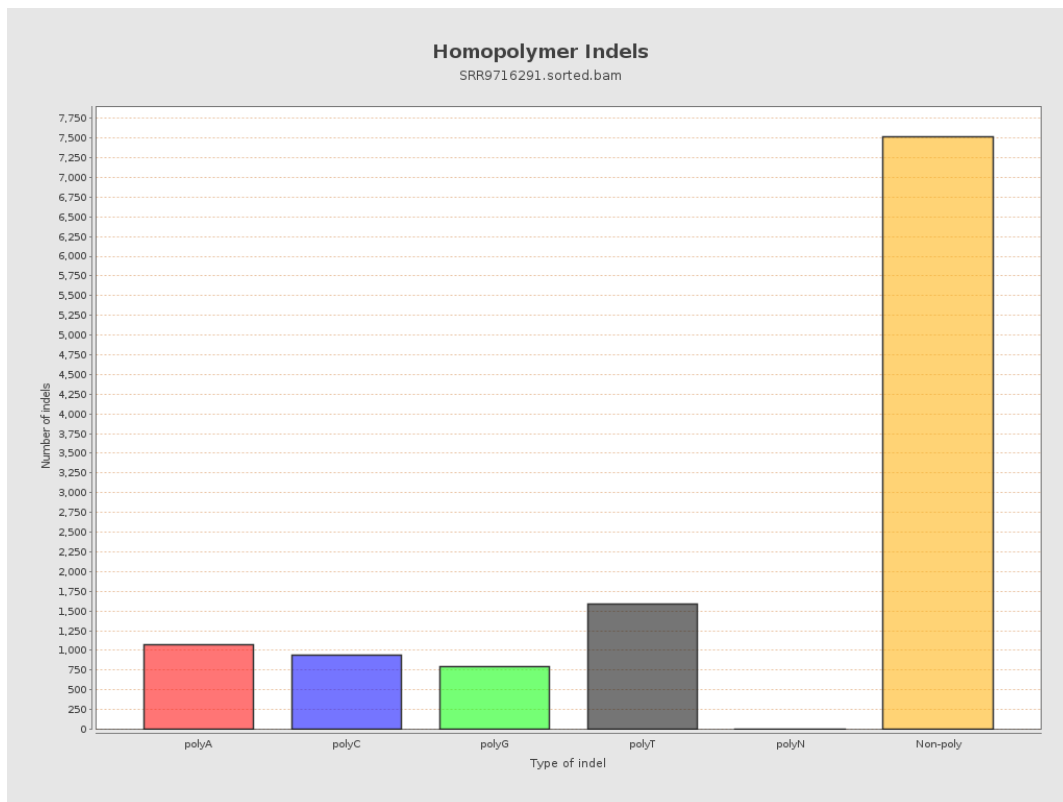
9. Results : Mapped Reads GC-content Distribution



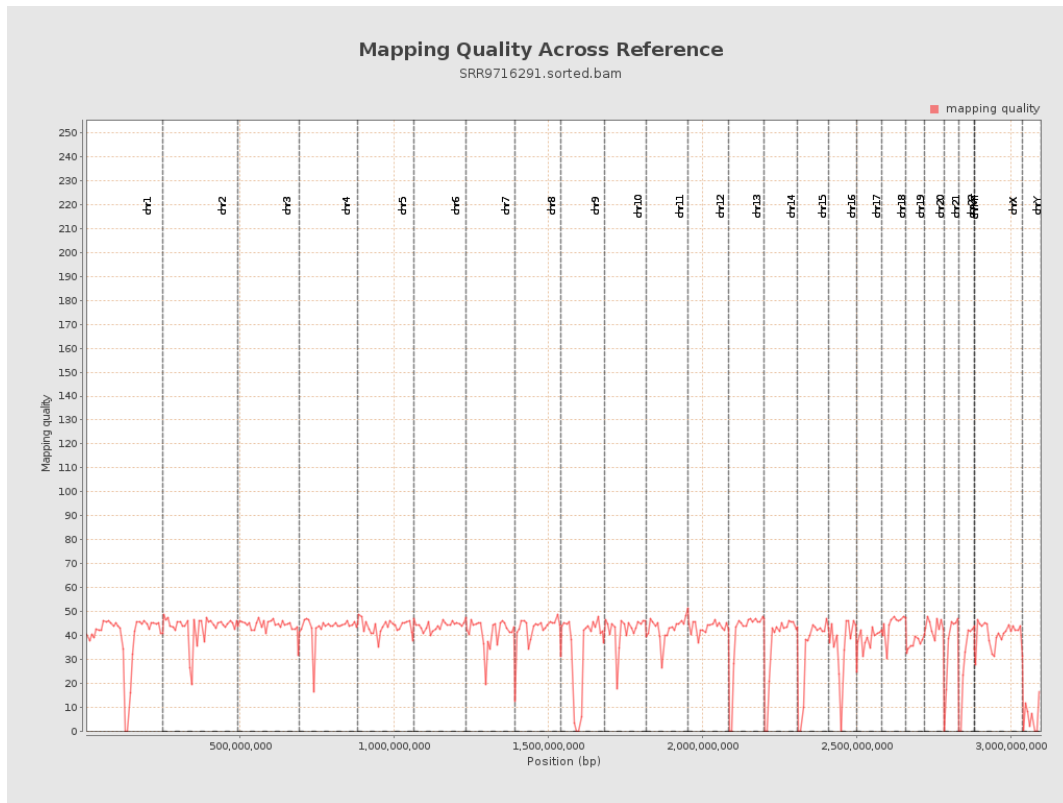
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

