

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:34:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716793.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_SRR9716793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:34:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	600,310
Mapped reads	516,204 / 85.99%
Unmapped reads	84,106 / 14.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	534 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	31,383 / 5.23%
Duplication rate	5.42%
Clipped reads	516,278 / 86%

2.2. ACGT Content

Number/percentage of A's	5,645,136 / 20.68%
Number/percentage of C's	4,875,531 / 17.86%
Number/percentage of T's	8,474,765 / 31.05%
Number/percentage of G's	8,301,349 / 30.41%
Number/percentage of N's	450 / 0%
GC Percentage	48.27%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1103
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2.4. Mapping Quality

Mean Mapping Quality	44.02
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2.5. Mismatches and indels

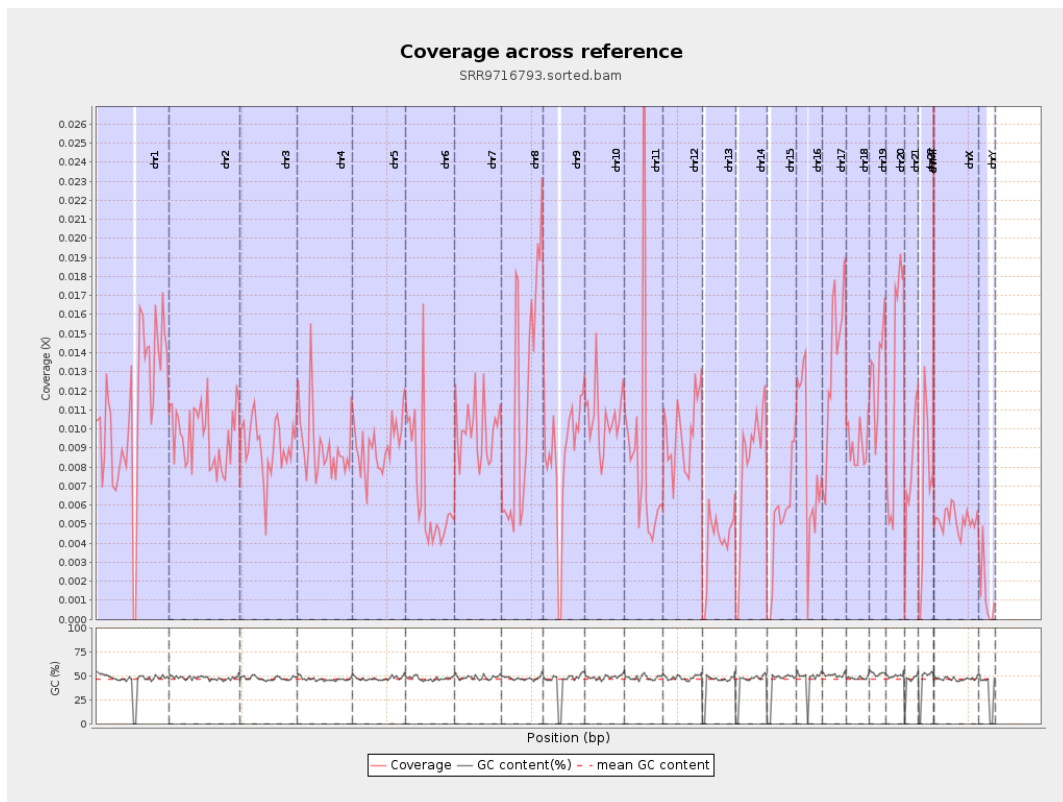
General error rate	0.63%
Mismatches	168,707
Insertions	1,421
Mapped reads with at least one insertion	0.27%
Deletions	4,241
Mapped reads with at least one deletion	0.81%
Homopolymer indels	42.83%

2.6. Chromosome stats

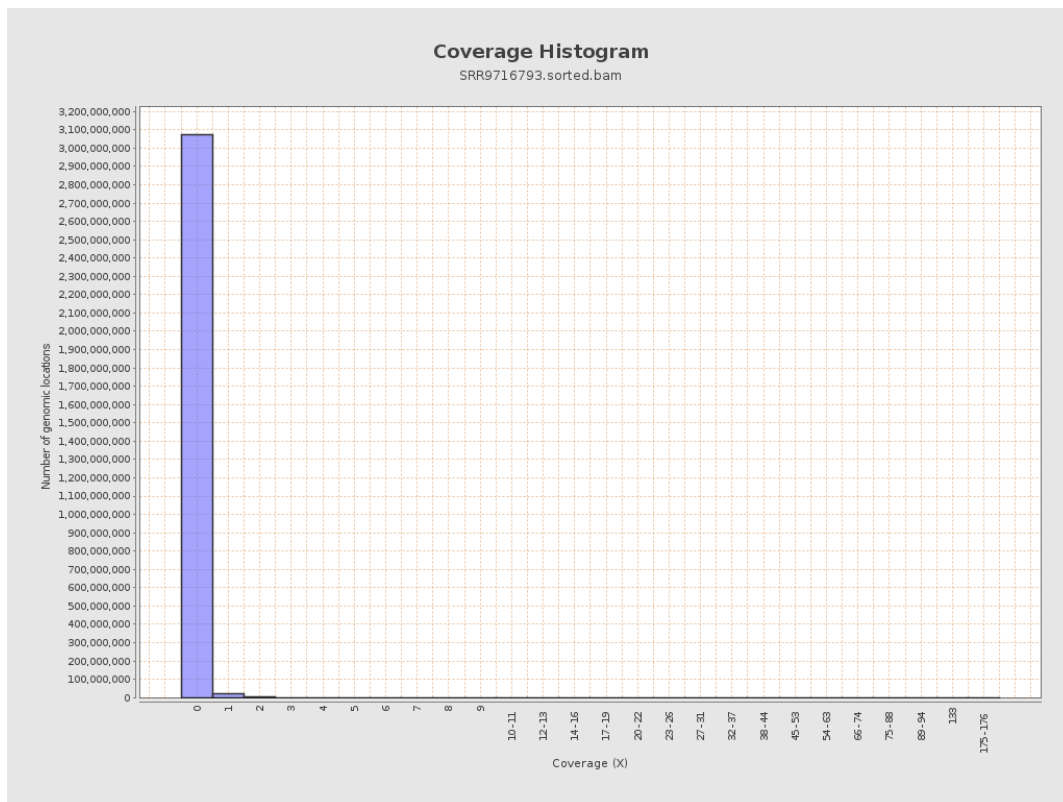
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2702679	0.0108	0.1298
chr2	243199373	2342047	0.0096	0.1329
chr3	198022430	1794365	0.0091	0.1046
chr4	191154276	1726466	0.009	0.1072
chr5	180915260	1642161	0.0091	0.1047
chr6	171115067	1149124	0.0067	0.0937
chr7	159138663	1571001	0.0099	0.1167

chr8	146364022	1680966	0.0115	0.1201
chr9	141213431	1192424	0.0084	0.1057
chr10	135534747	1419911	0.0105	0.1235
chr11	135006516	1184846	0.0088	0.1092
chr12	133851895	1308617	0.0098	0.1095
chr13	115169878	464224	0.004	0.0709
chr14	107349540	871456	0.0081	0.099
chr15	102531392	535162	0.0052	0.0797
chr16	90354753	752978	0.0083	0.1062
chr17	81195210	1115706	0.0137	0.1347
chr18	78077248	713647	0.0091	0.114
chr19	59128983	767909	0.013	0.1463
chr20	63025520	770466	0.0122	0.1284
chr21	48129895	381172	0.0079	0.1021
chr22	51304566	330259	0.0064	0.0934
chrMT	16571	502	0.0303	0.1714
chrX	155270560	809463	0.0052	0.0798
chrY	59373566	77138	0.0013	0.0498

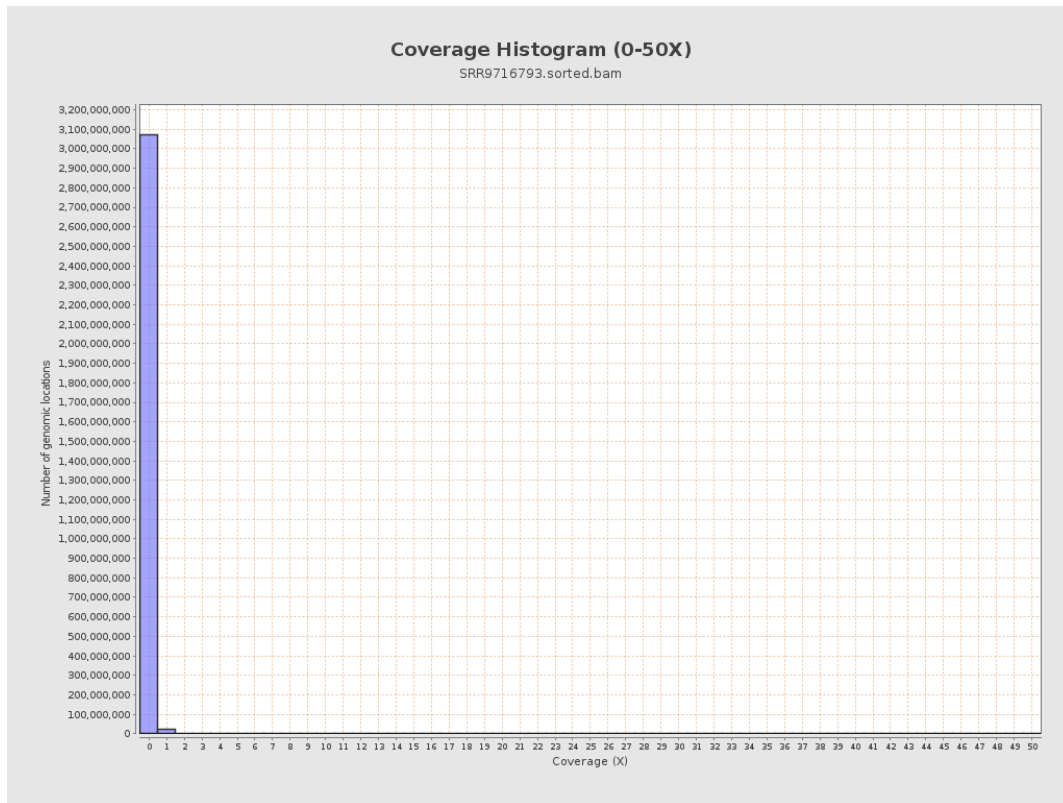
3. Results : Coverage across reference



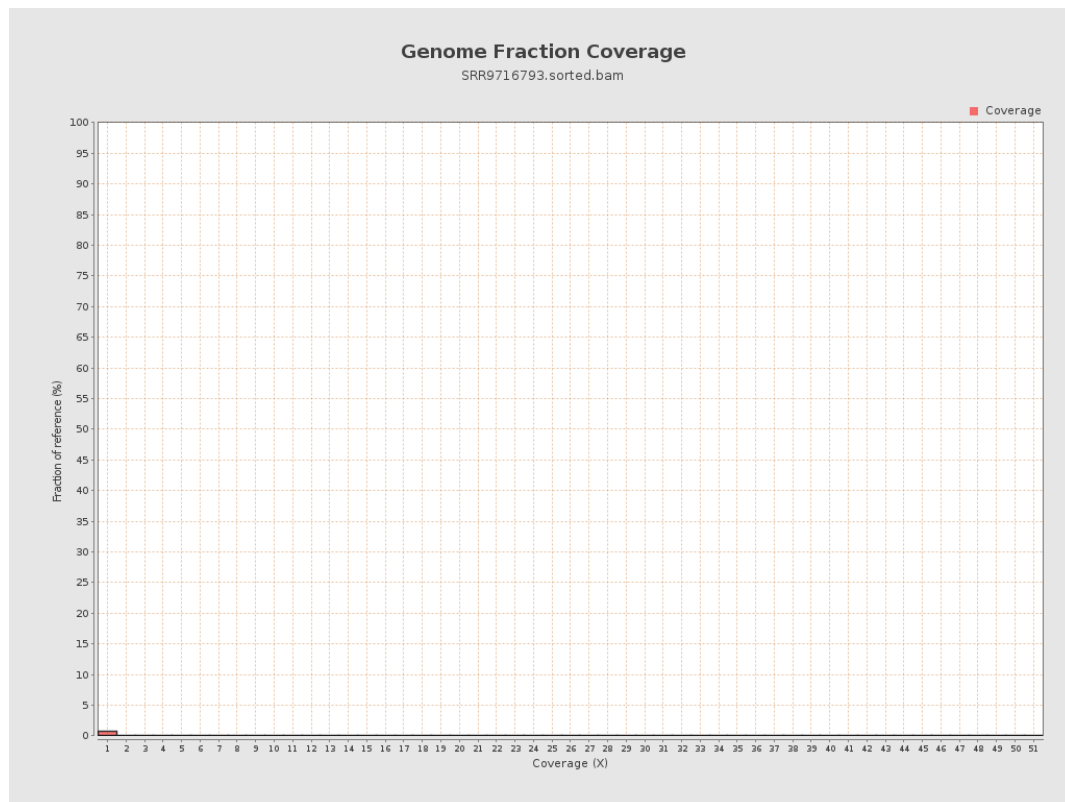
4. Results : Coverage Histogram



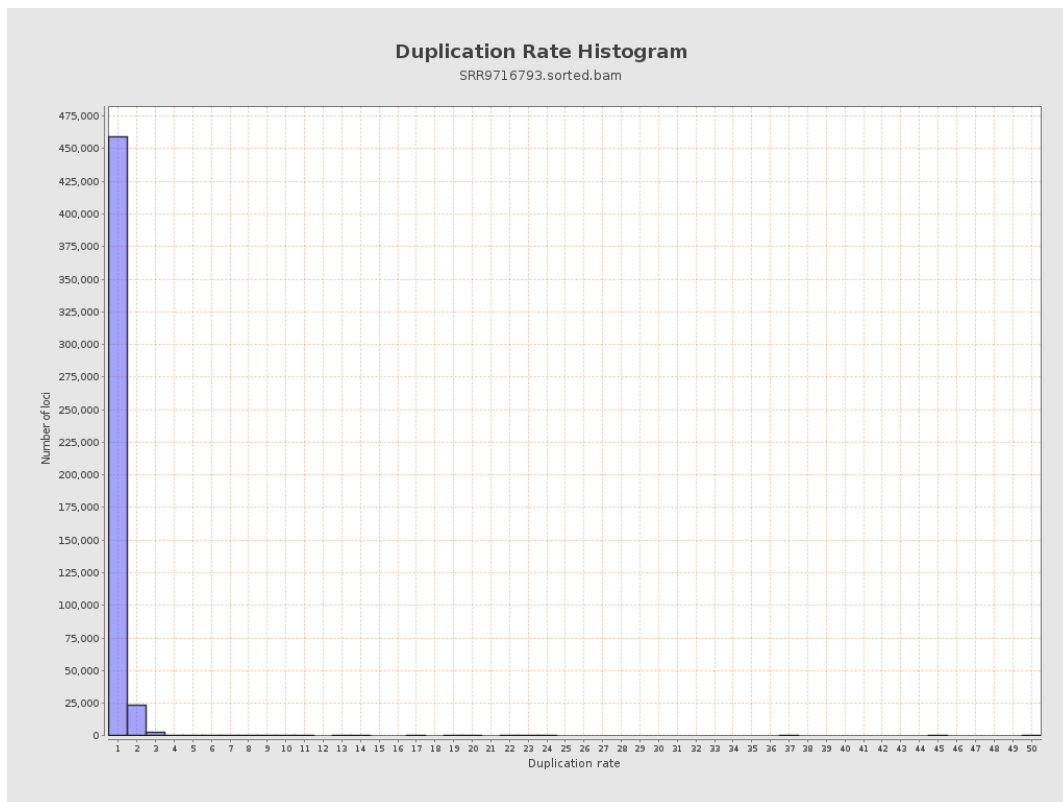
5. Results : Coverage Histogram (0-50X)



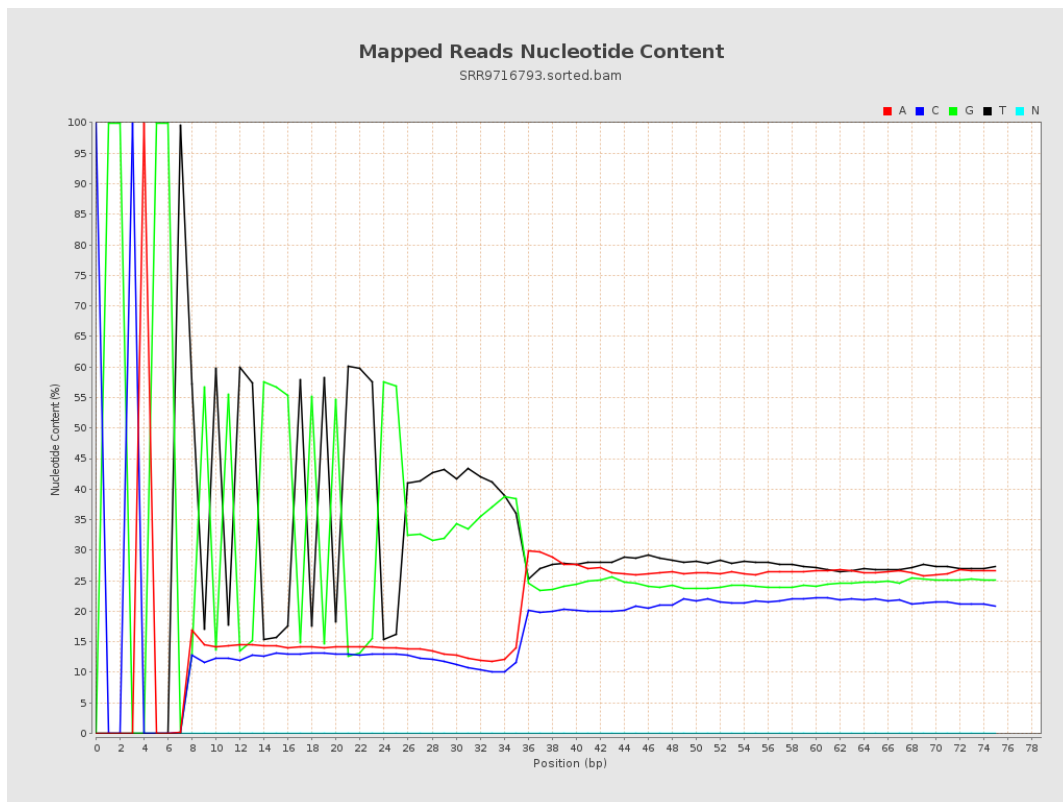
6. Results : Genome Fraction Coverage



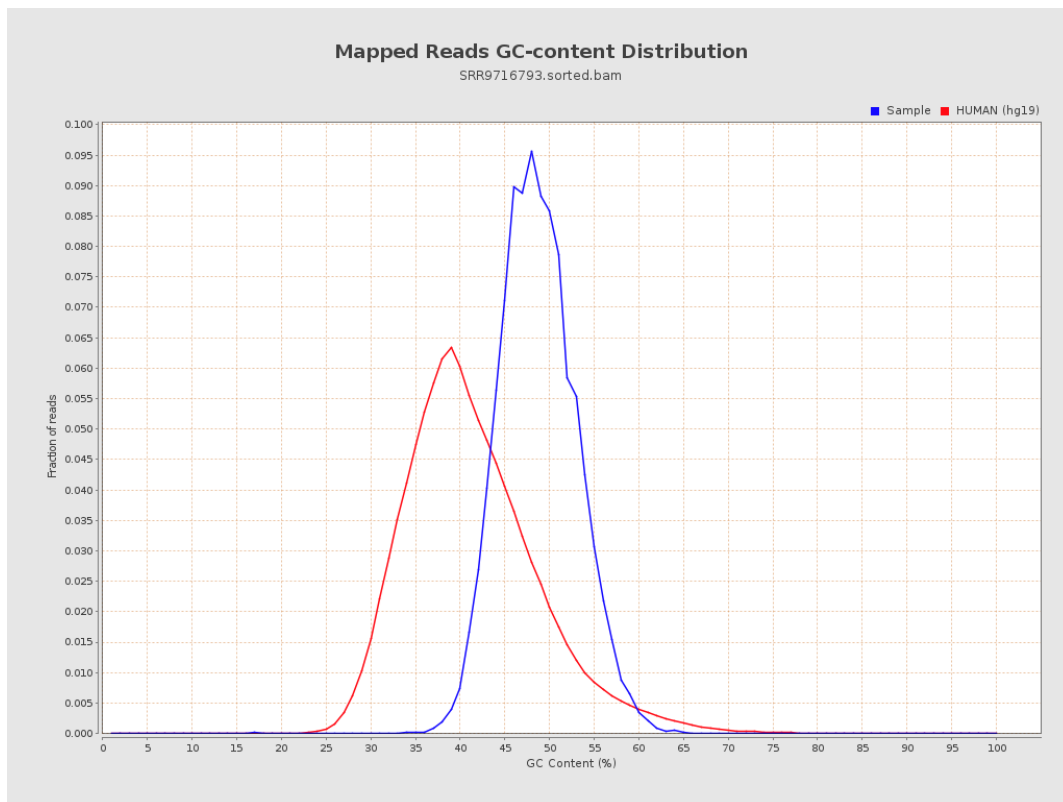
7. Results : Duplication Rate Histogram



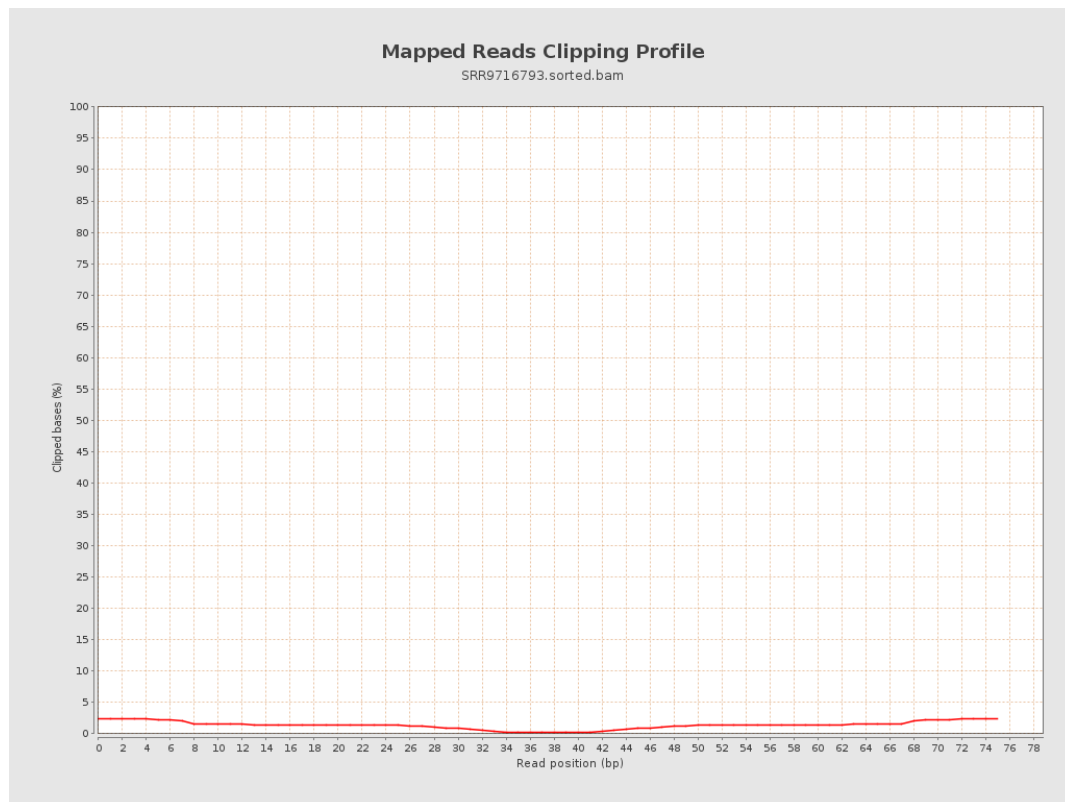
8. Results : Mapped Reads Nucleotide Content



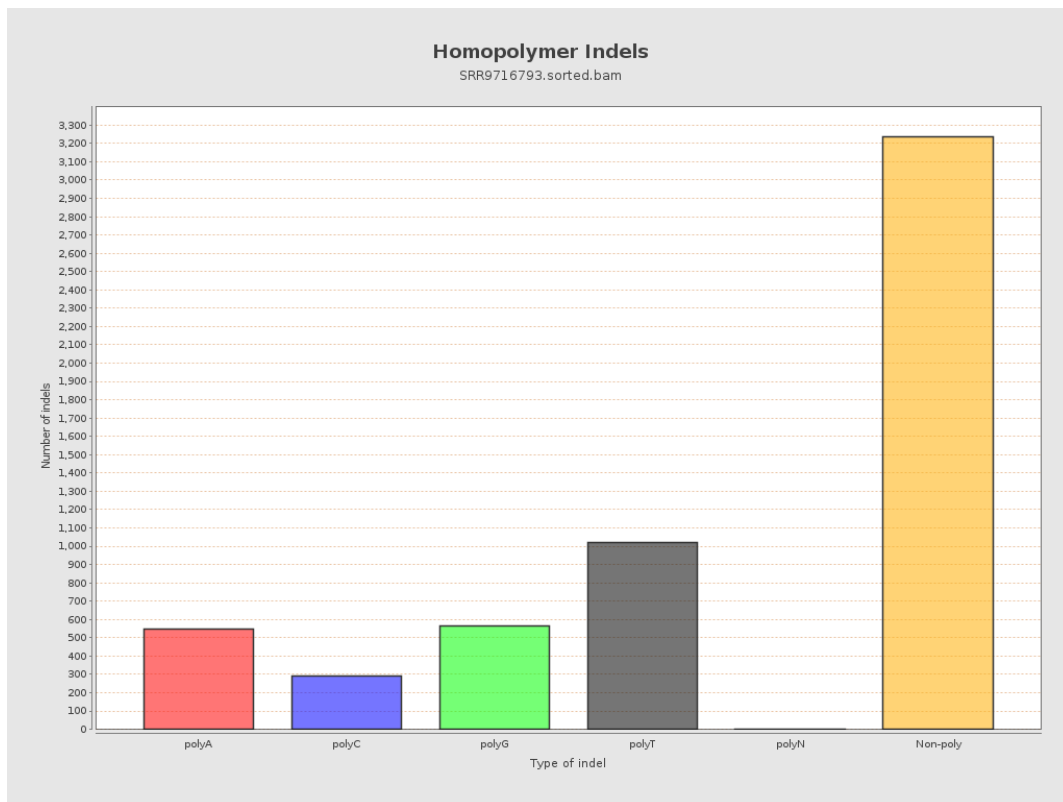
9. Results : Mapped Reads GC-content Distribution



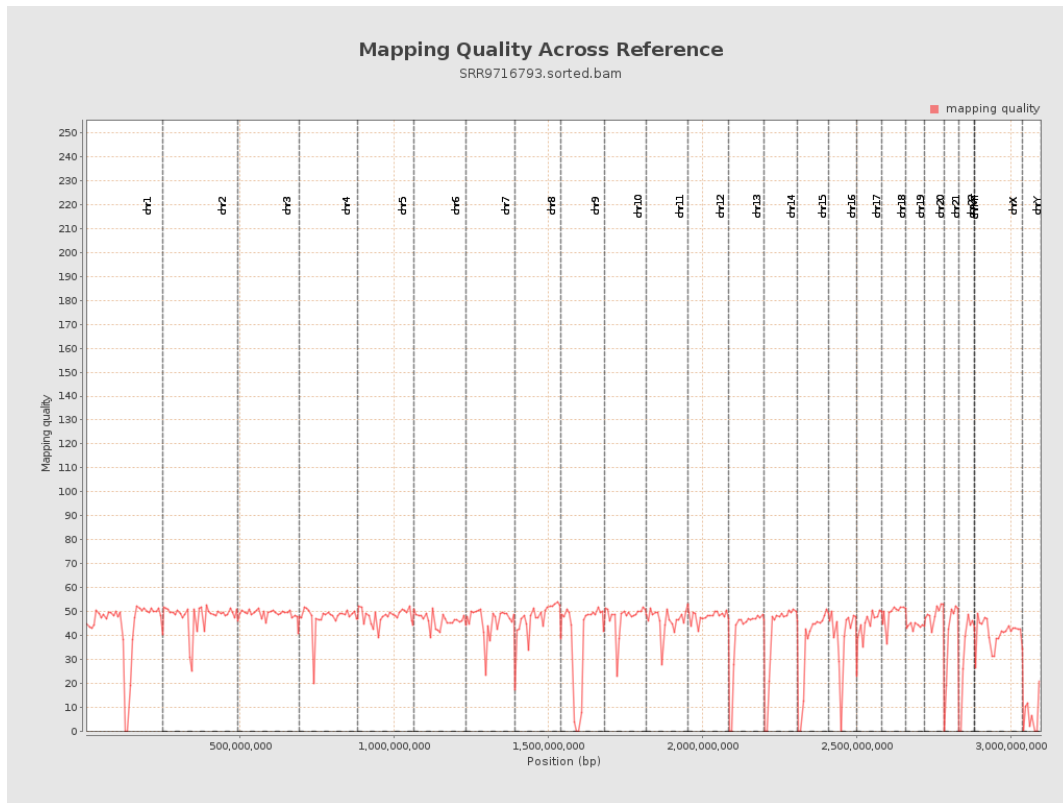
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

