

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:30:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716887.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_SRR9716887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716887.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:30:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,067,149
Mapped reads	921,528 / 86.35%
Unmapped reads	145,621 / 13.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,523 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	24,697 / 2.31%
Duplication rate	1.94%
Clipped reads	924,260 / 86.61%

2.2. ACGT Content

Number/percentage of A's	13,504,360 / 25.62%
Number/percentage of C's	9,663,819 / 18.33%
Number/percentage of T's	17,154,315 / 32.54%
Number/percentage of G's	12,392,791 / 23.51%
Number/percentage of N's	1,451 / 0%
GC Percentage	41.84%

2.3. Coverage

Mean	0.017

Standard Deviation	0.1859
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2.4. Mapping Quality

Mean Mapping Quality	44.32
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2.5. Mismatches and indels

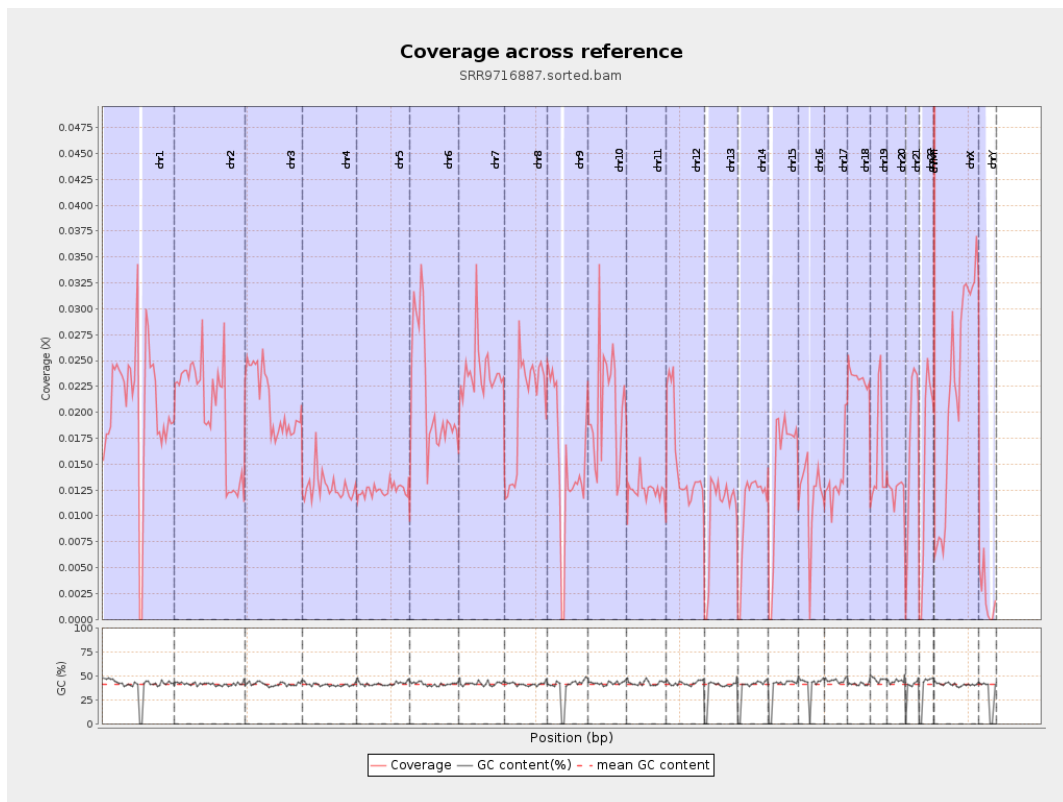
General error rate	0.52%
Mismatches	267,586
Insertions	3,719
Mapped reads with at least one insertion	0.4%
Deletions	9,971
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.18%

2.6. Chromosome stats

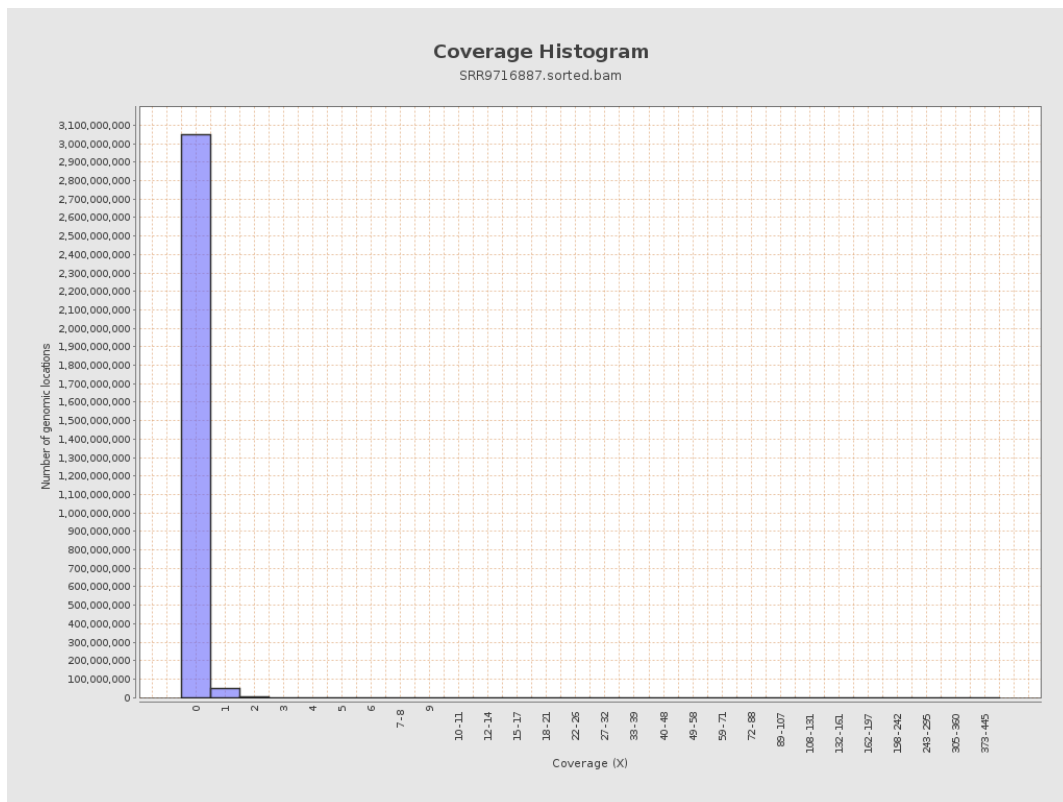
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5104955	0.0205	0.3165
chr2	243199373	4888688	0.0201	0.2437
chr3	198022430	4150352	0.021	0.1534
chr4	191154276	2442072	0.0128	0.1238
chr5	180915260	2257939	0.0125	0.1195
chr6	171115067	3632125	0.0212	0.17
chr7	159138663	3794750	0.0238	0.2554

chr8	146364022	2973996	0.0203	0.1709
chr9	141213431	2114893	0.015	0.1614
chr10	135534747	2771874	0.0205	0.1897
chr11	135006516	1694309	0.0125	0.1435
chr12	133851895	2054754	0.0154	0.1344
chr13	115169878	1174319	0.0102	0.1071
chr14	107349540	1146504	0.0107	0.1161
chr15	102531392	1502099	0.0147	0.129
chr16	90354753	1076250	0.0119	0.1221
chr17	81195210	1109983	0.0137	0.1258
chr18	78077248	1826328	0.0234	0.2727
chr19	59128983	930248	0.0157	0.2196
chr20	63025520	780183	0.0124	0.1178
chr21	48129895	849092	0.0176	0.1448
chr22	51304566	792971	0.0155	0.1312
chrMT	16571	69691	4.2056	3.0186
chrX	155270560	3465918	0.0223	0.1748
chrY	59373566	128333	0.0022	0.0615

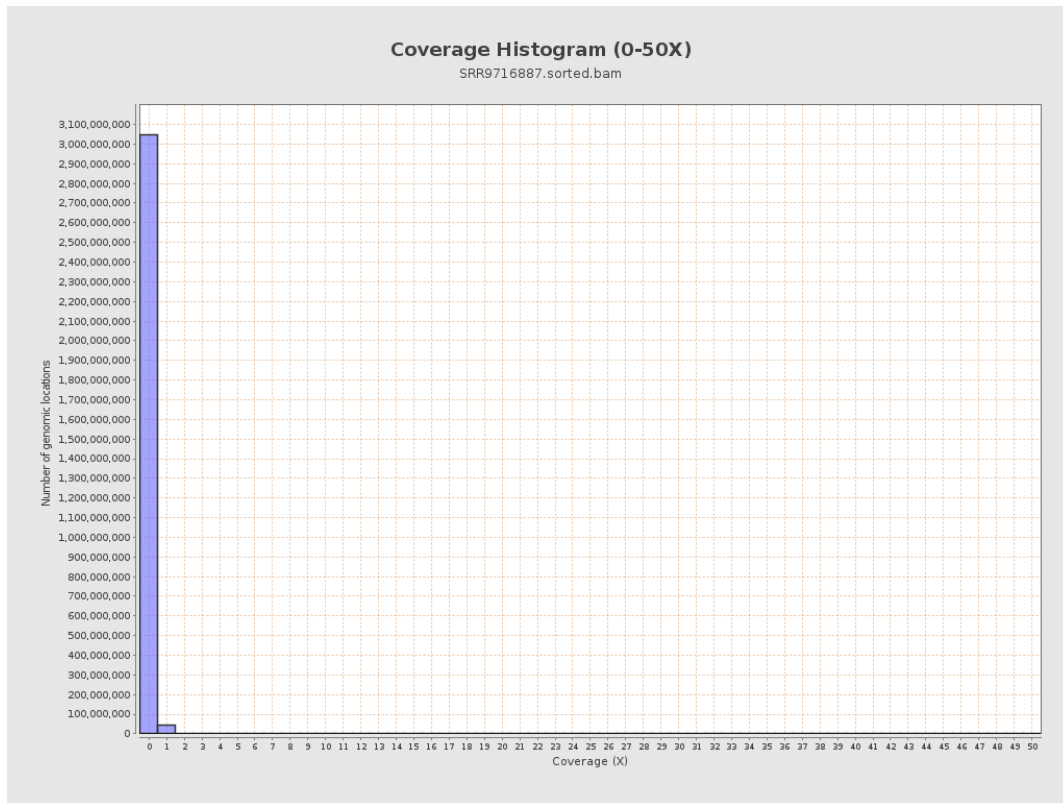
3. Results : Coverage across reference



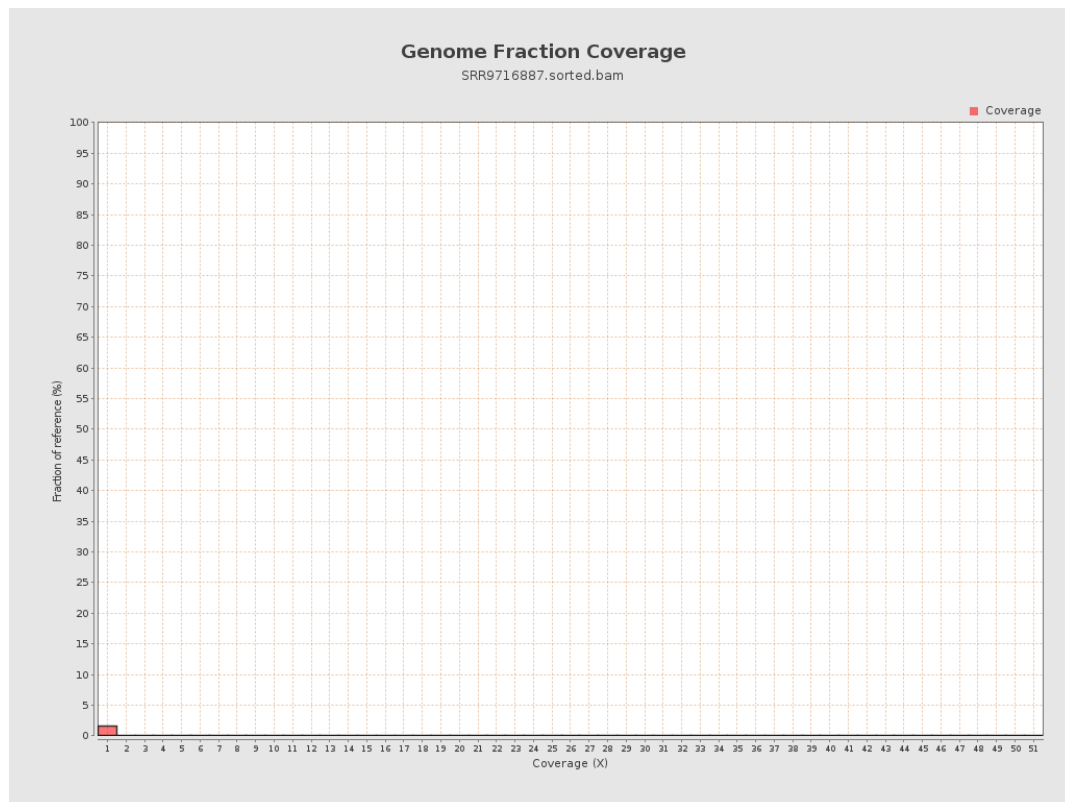
4. Results : Coverage Histogram



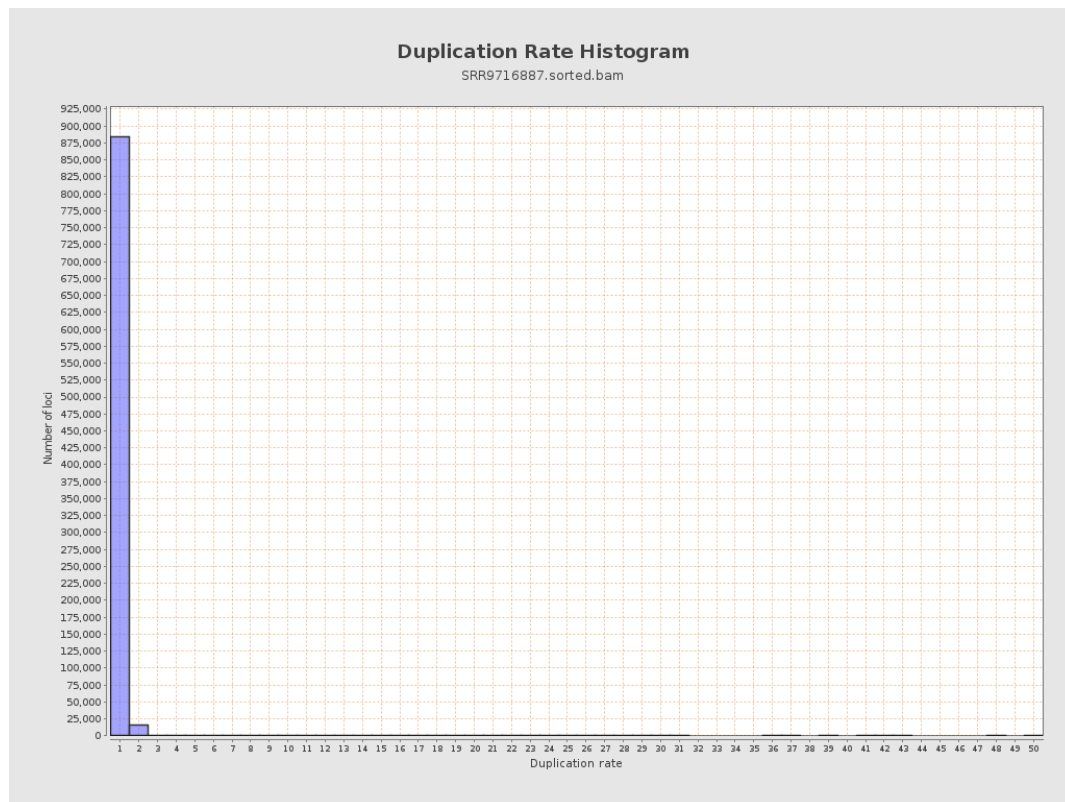
5. Results : Coverage Histogram (0-50X)



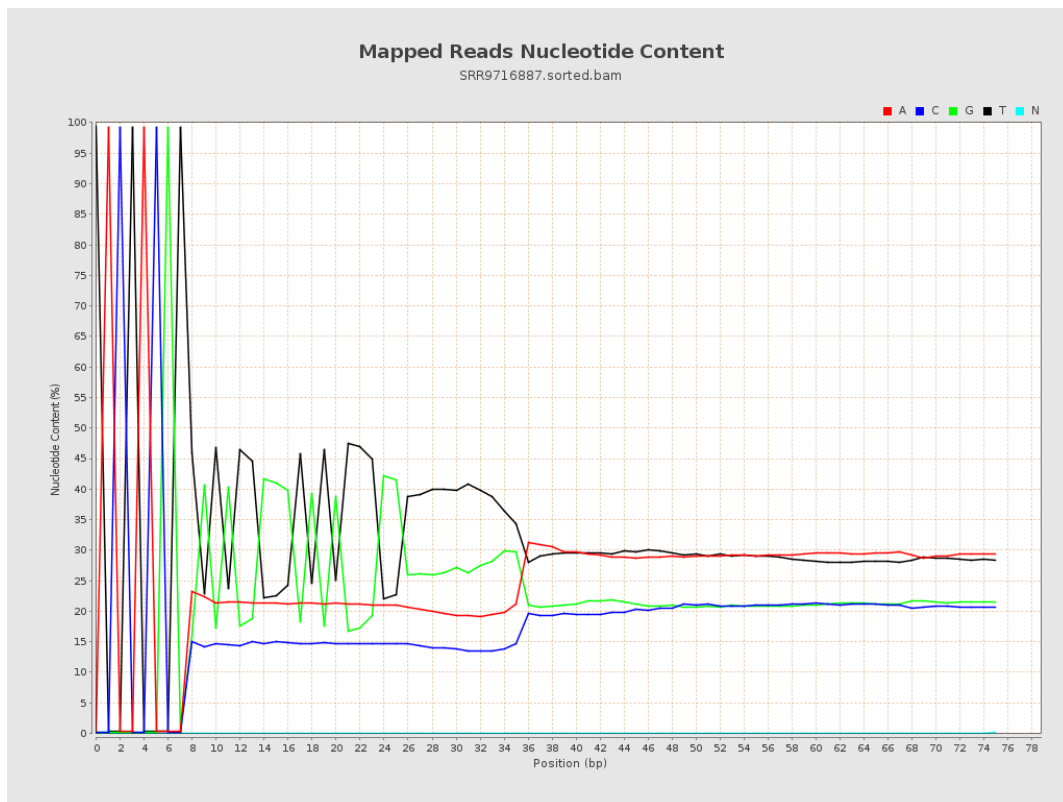
6. Results : Genome Fraction Coverage



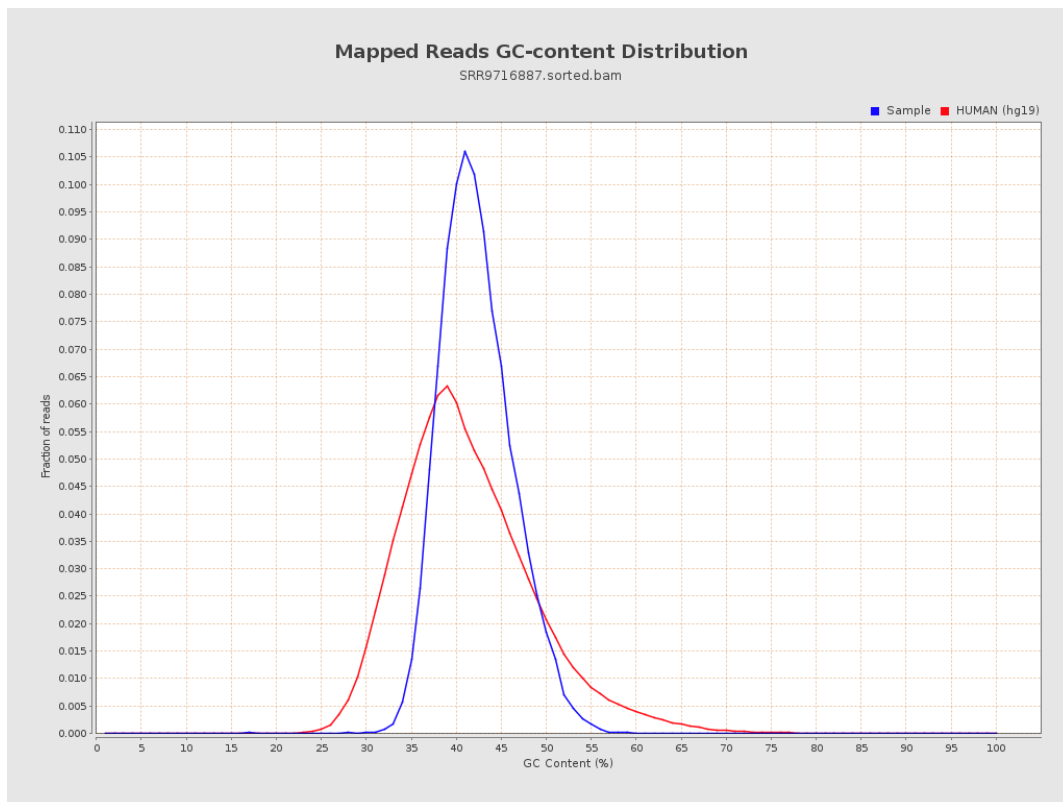
7. Results : Duplication Rate Histogram



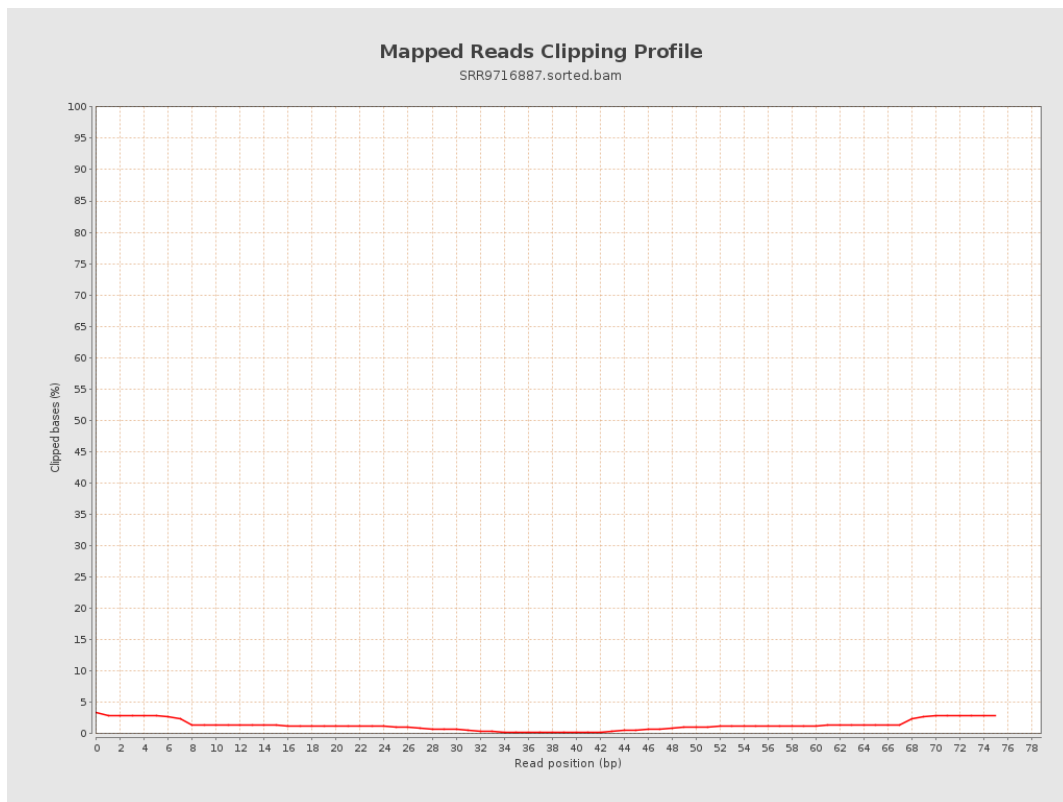
8. Results : Mapped Reads Nucleotide Content



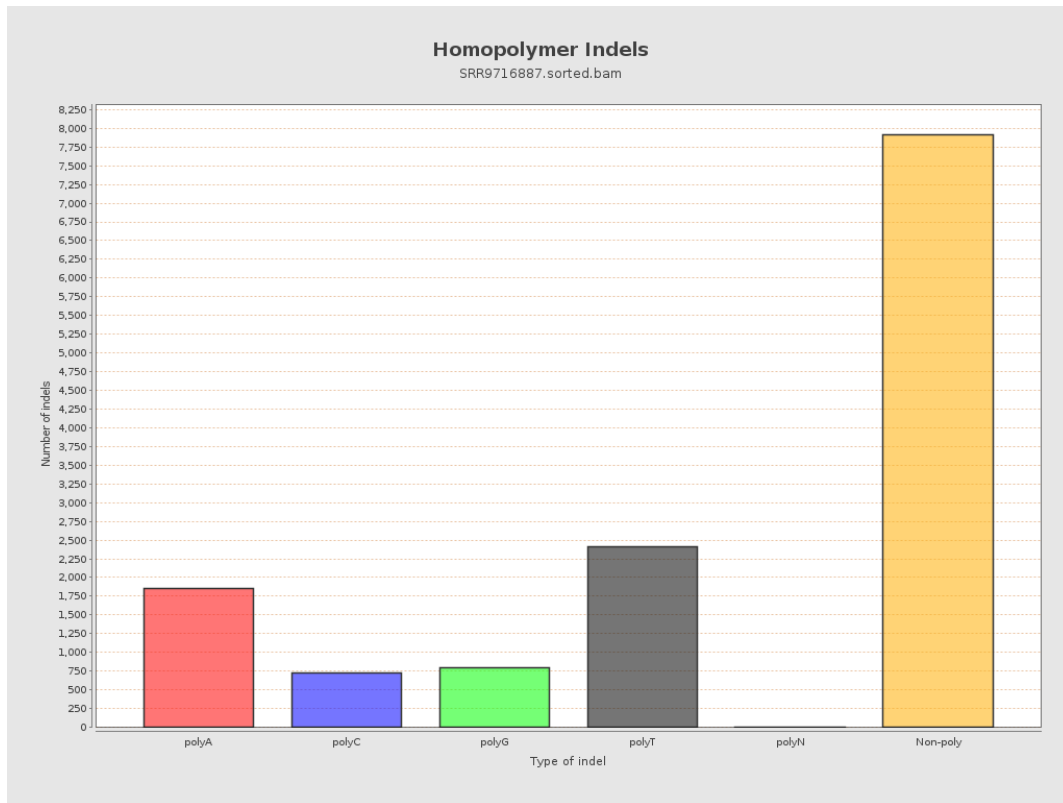
9. Results : Mapped Reads GC-content Distribution



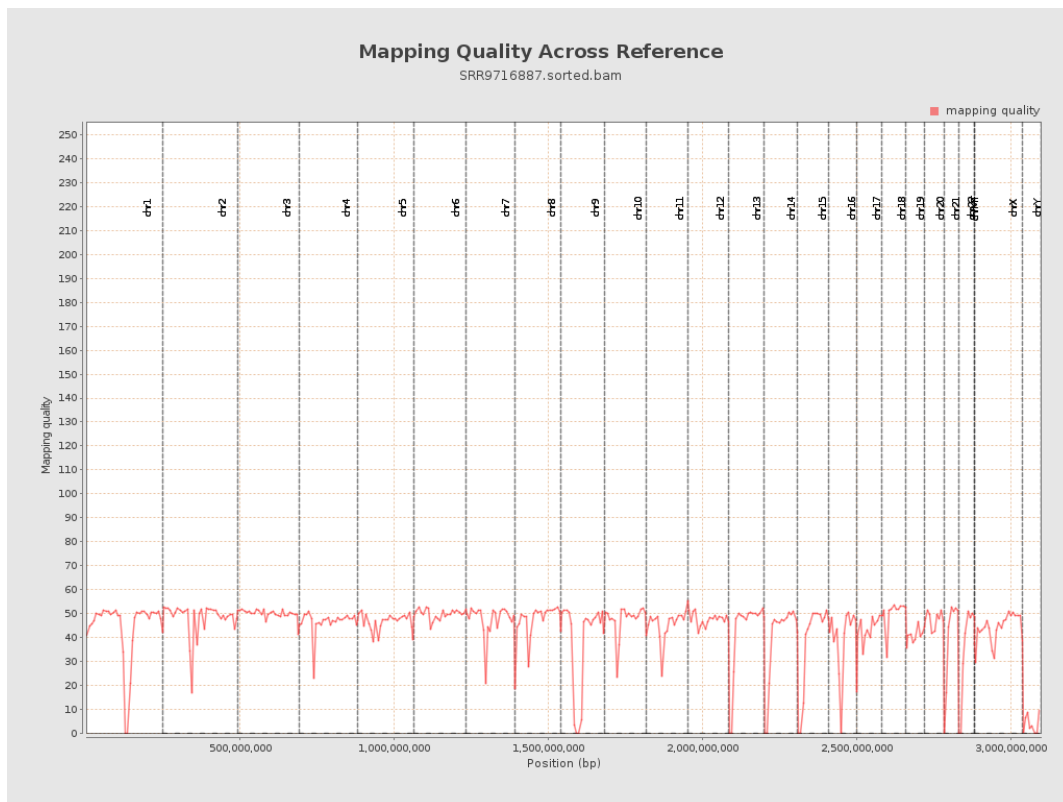
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

