

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:16:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716481.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_SRR9716481 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716481.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:16:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716481.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,717,586
Mapped reads	1,585,279 / 92.3%
Unmapped reads	132,307 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,208 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	70,319 / 4.09%
Duplication rate	3.49%
Clipped reads	1,590,344 / 92.59%

2.2. ACGT Content

Number/percentage of A's	22,867,662 / 24.71%
Number/percentage of C's	17,680,140 / 19.1%
Number/percentage of T's	29,410,156 / 31.78%
Number/percentage of G's	22,597,167 / 24.41%
Number/percentage of N's	623 / 0%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.2629
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2.4. Mapping Quality

Mean Mapping Quality	44.91
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2.5. Mismatches and indels

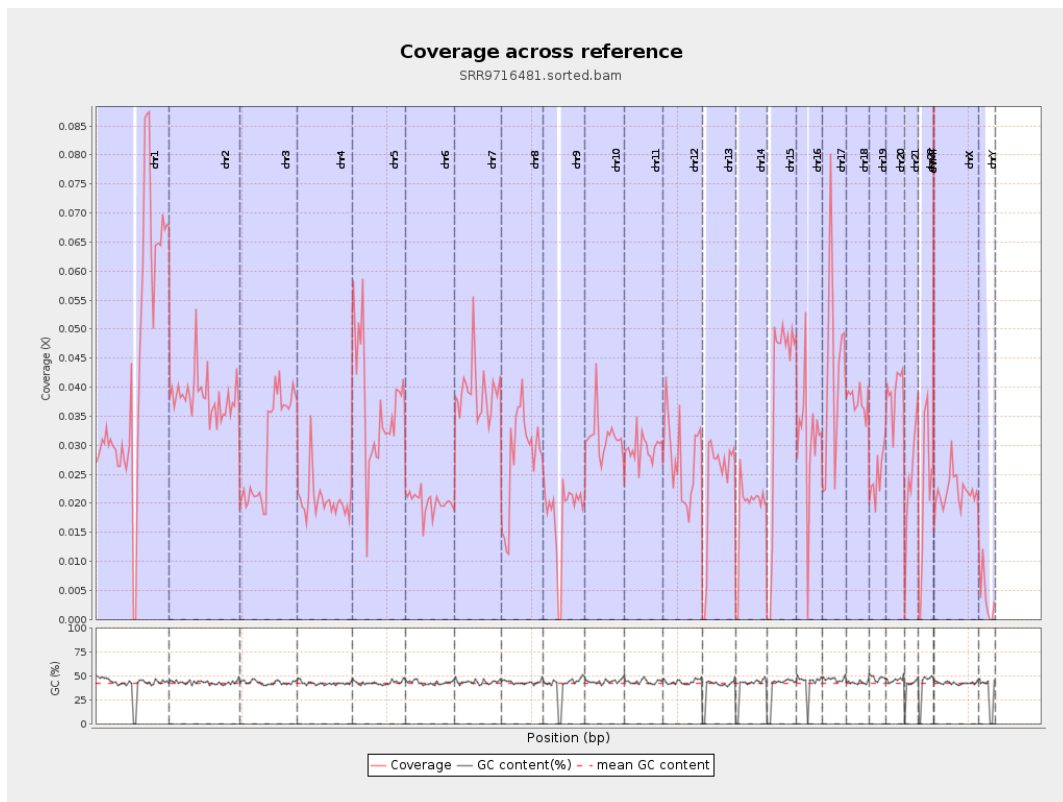
General error rate	0.5%
Mismatches	455,889
Insertions	6,166
Mapped reads with at least one insertion	0.39%
Deletions	16,548
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.51%

2.6. Chromosome stats

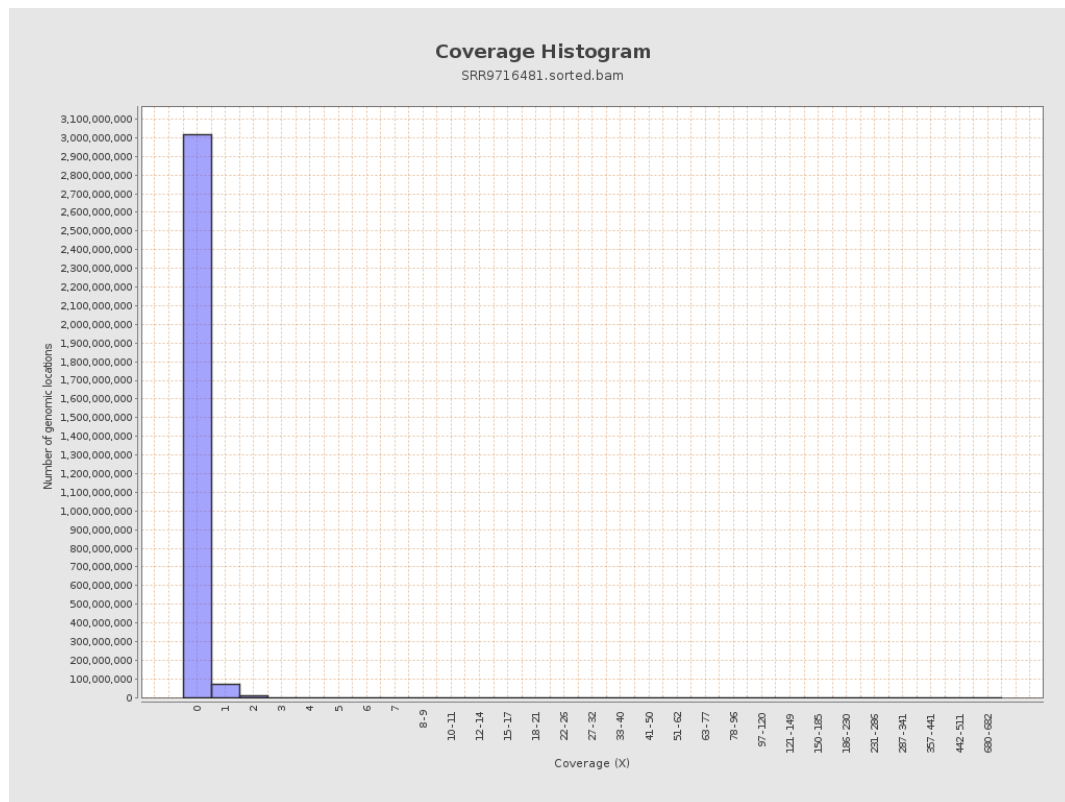
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10872235	0.0436	0.4074
chr2	243199373	9324520	0.0383	0.3777
chr3	198022430	5857672	0.0296	0.1903
chr4	191154276	3908922	0.0204	0.182
chr5	180915260	6624598	0.0366	0.2128
chr6	171115067	3453840	0.0202	0.1748
chr7	159138663	6247001	0.0393	0.3946

chr8	146364022	4104103	0.028	0.2437
chr9	141213431	2536781	0.018	0.2007
chr10	135534747	4249986	0.0314	0.2429
chr11	135006516	3959858	0.0293	0.2522
chr12	133851895	3674590	0.0275	0.1859
chr13	115169878	2687070	0.0233	0.1685
chr14	107349540	1997533	0.0186	0.1589
chr15	102531392	3972545	0.0387	0.2201
chr16	90354753	2821334	0.0312	0.2072
chr17	81195210	3502537	0.0431	0.2479
chr18	78077248	2942200	0.0377	0.4097
chr19	59128983	1471630	0.0249	0.3011
chr20	63025520	2471040	0.0392	0.224
chr21	48129895	1189132	0.0247	0.1847
chr22	51304566	1075604	0.021	0.16
chrMT	16571	1640	0.099	0.3474
chrX	155270560	3412880	0.022	0.1846
chrY	59373566	222723	0.0038	0.1002

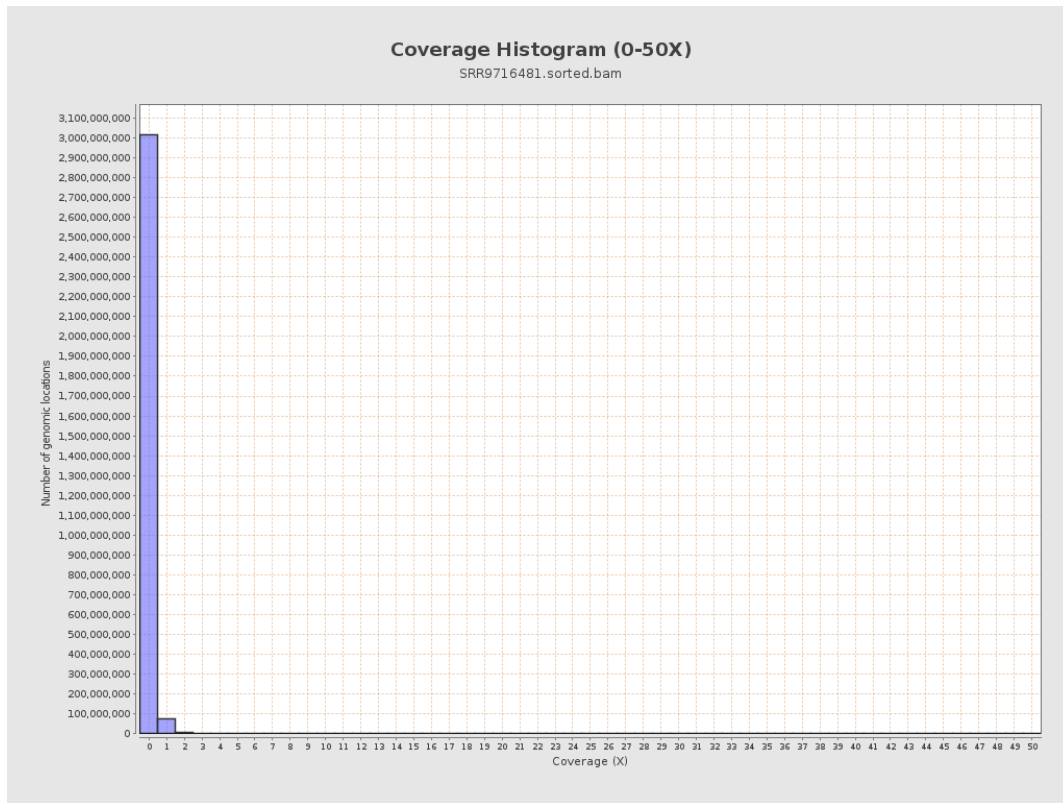
3. Results : Coverage across reference



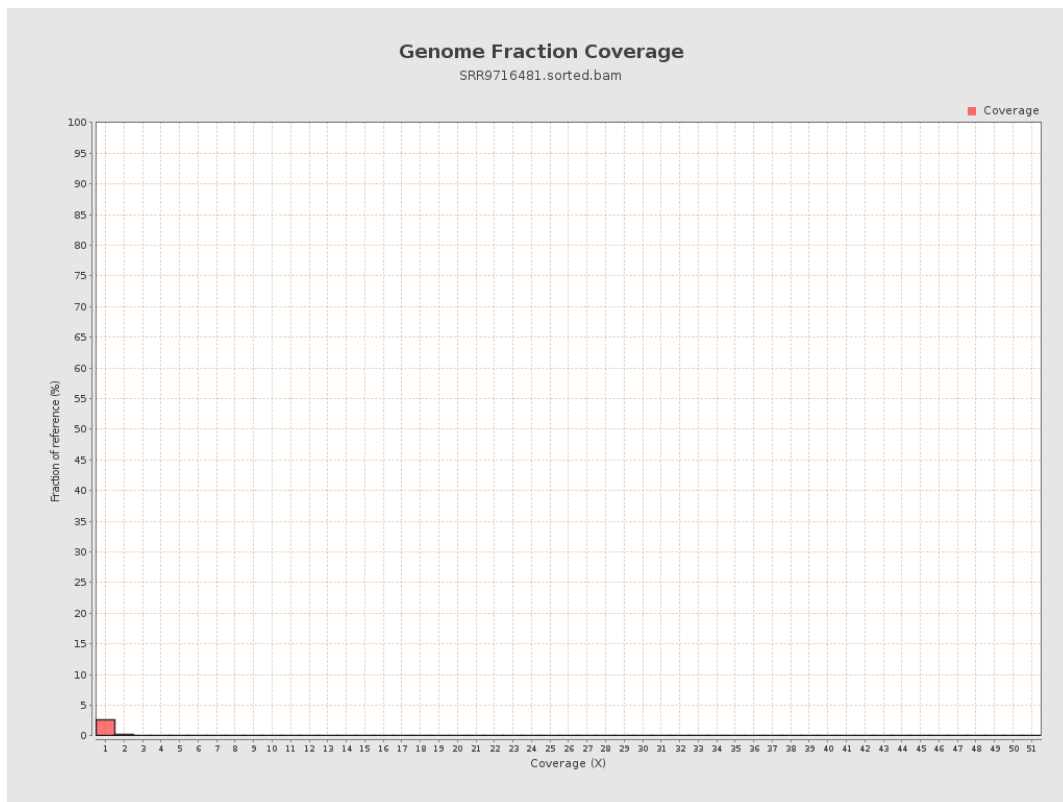
4. Results : Coverage Histogram



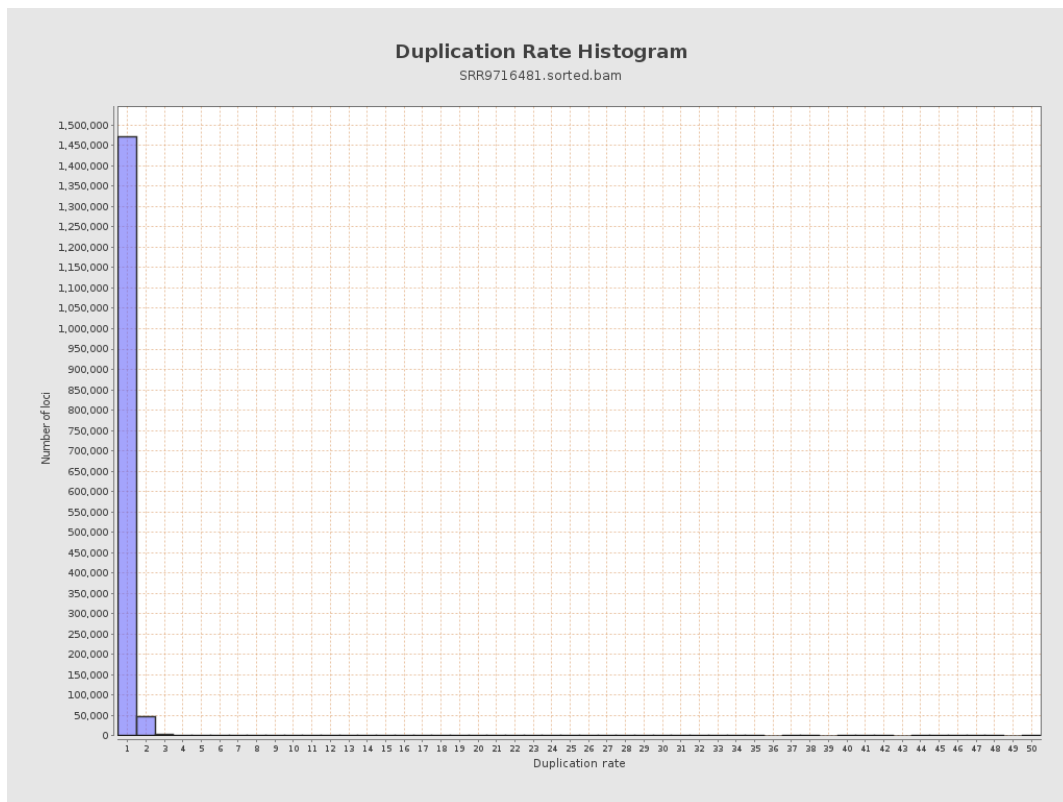
5. Results : Coverage Histogram (0-50X)



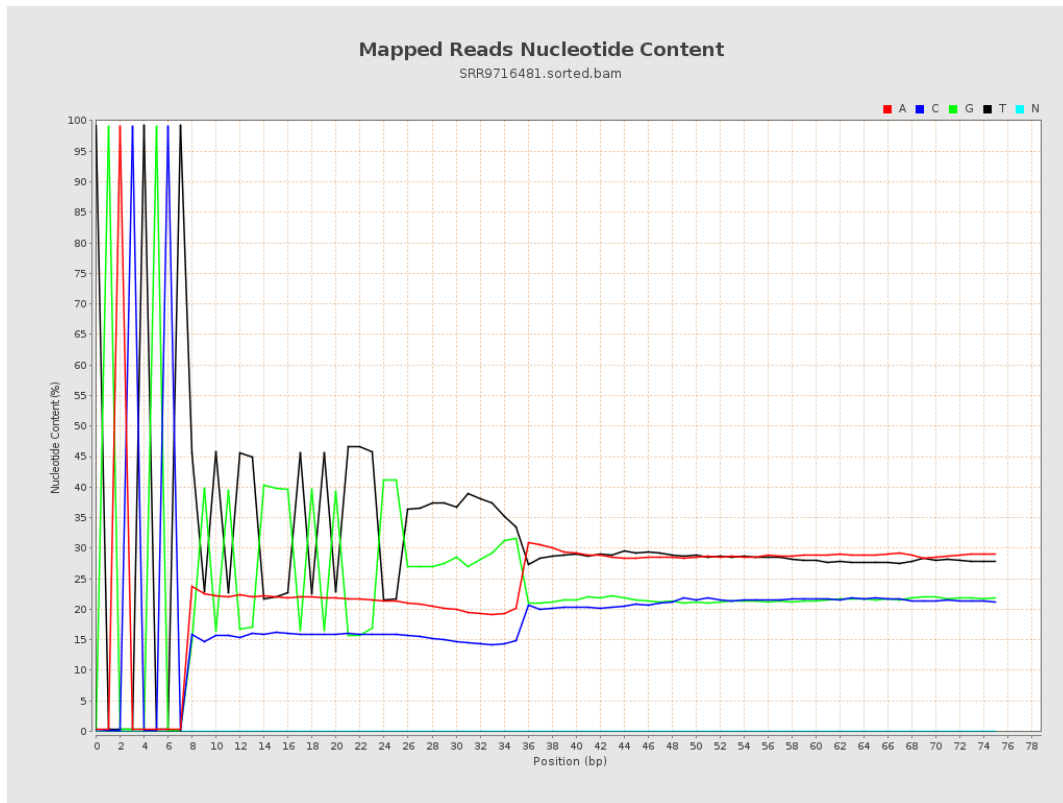
6. Results : Genome Fraction Coverage



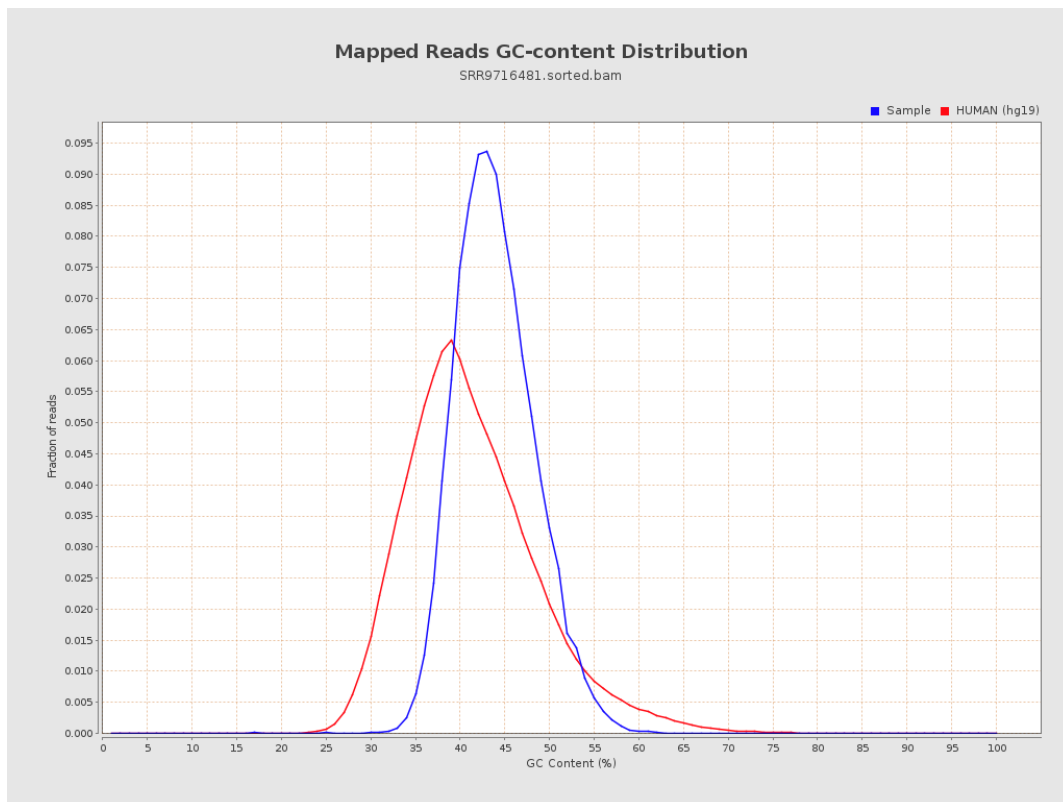
7. Results : Duplication Rate Histogram



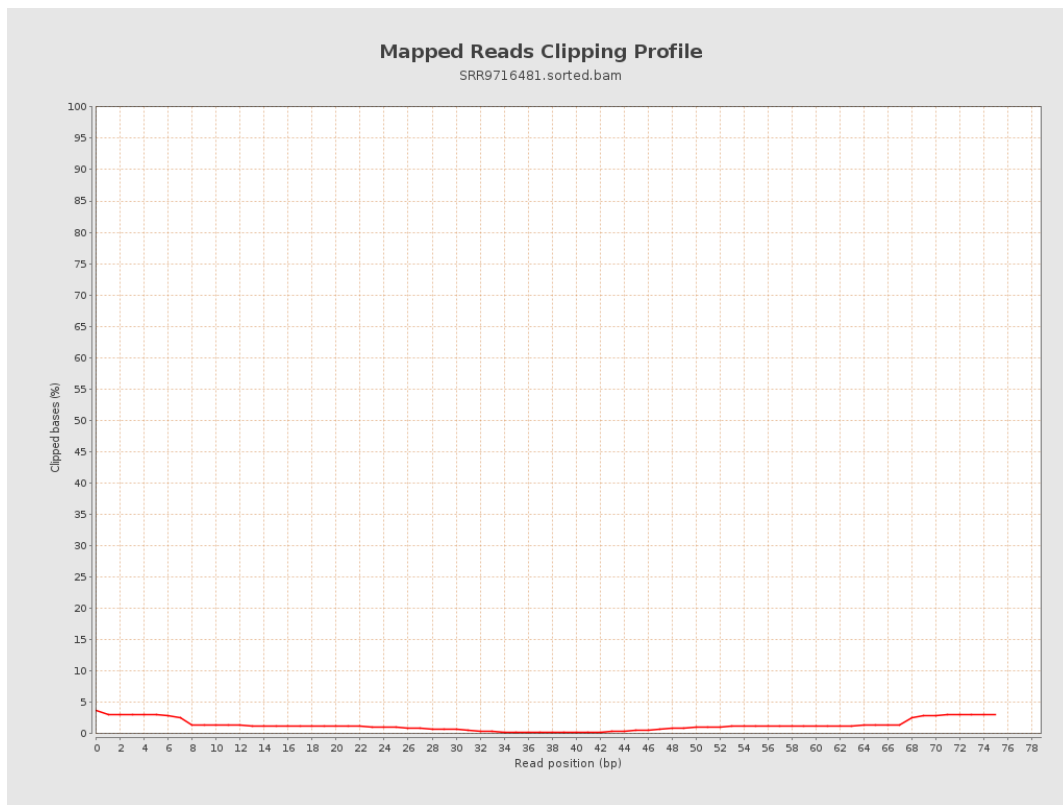
8. Results : Mapped Reads Nucleotide Content



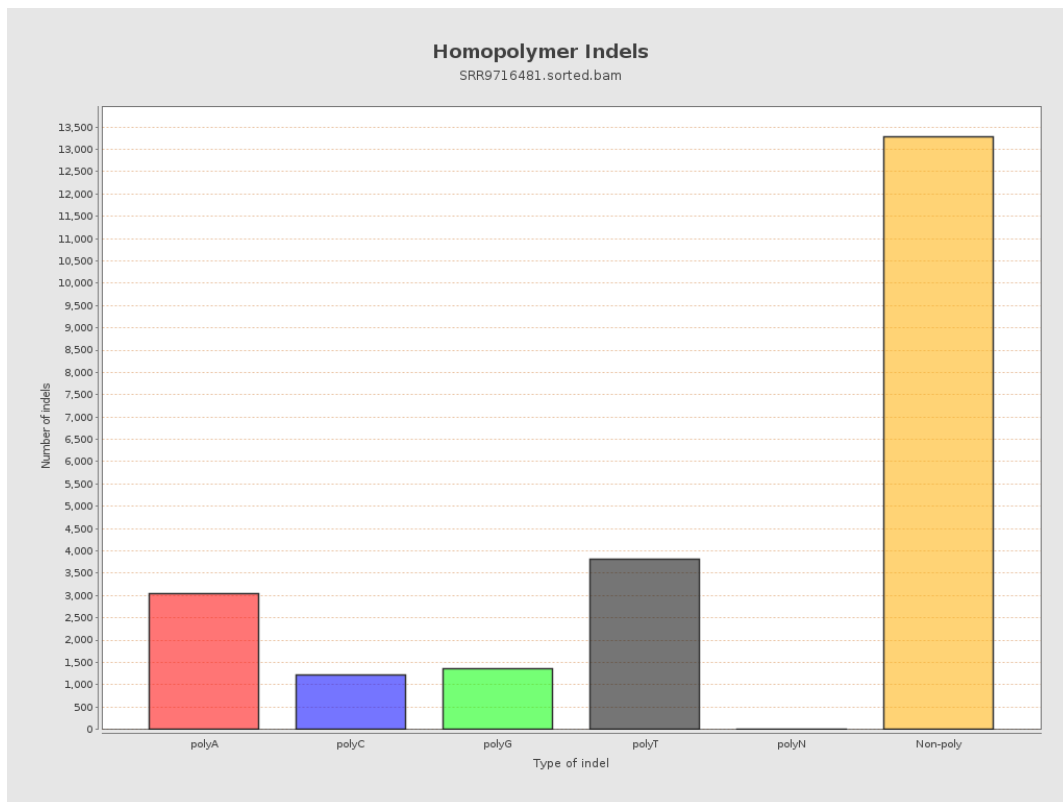
9. Results : Mapped Reads GC-content Distribution



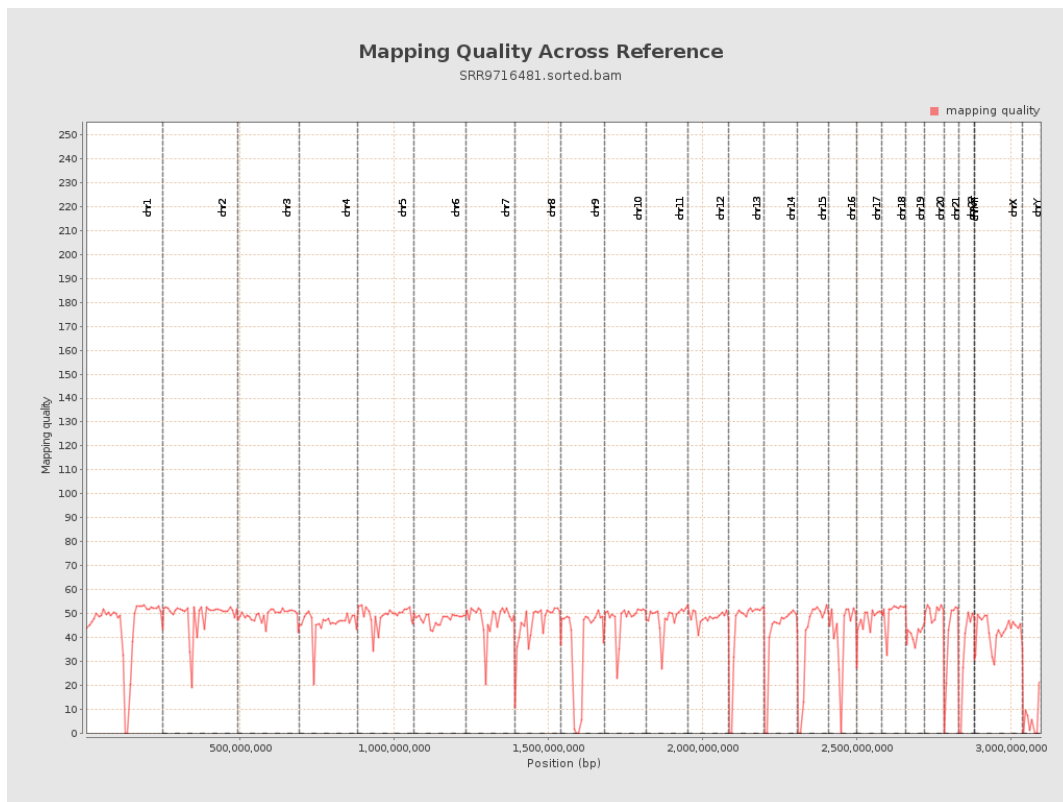
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

