

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:41:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818964.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_SRR1818964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:41:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,074,150
Mapped reads	2,046,187 / 98.65%
Unmapped reads	27,963 / 1.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,696 / 1.58%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	941,030 / 45.37%
Duplication rate	39.81%
Clipped reads	2,065,042 / 99.56%

2.2. ACGT Content

Number/percentage of A's	55,111,845 / 29.12%
Number/percentage of C's	38,783,844 / 20.49%
Number/percentage of T's	53,845,922 / 28.45%
Number/percentage of G's	41,520,667 / 21.94%
Number/percentage of N's	8,925 / 0%
GC Percentage	42.43%

2.3. Coverage

Mean	0.0612

Standard Deviation	0.7186
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2.4. Mapping Quality

Mean Mapping Quality	48.99
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2.5. Mismatches and indels

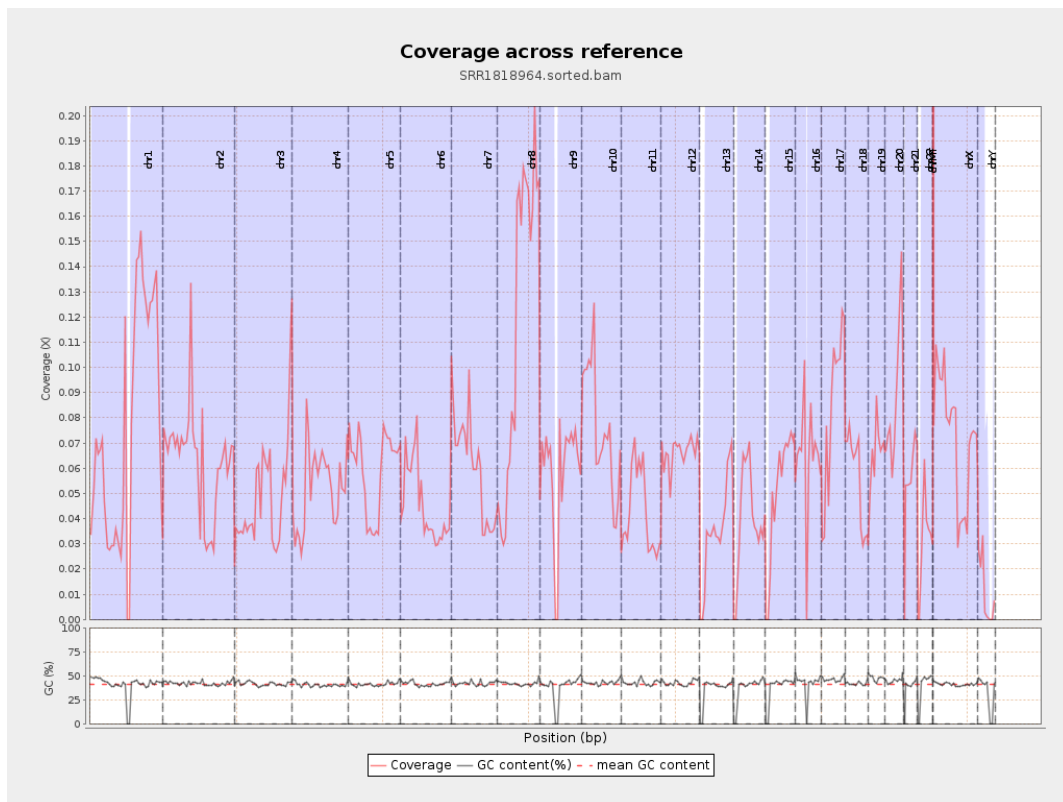
General error rate	0.65%
Mismatches	1,160,149
Insertions	29,326
Mapped reads with at least one insertion	1.39%
Deletions	61,233
Mapped reads with at least one deletion	2.93%
Homopolymer indels	41.23%

2.6. Chromosome stats

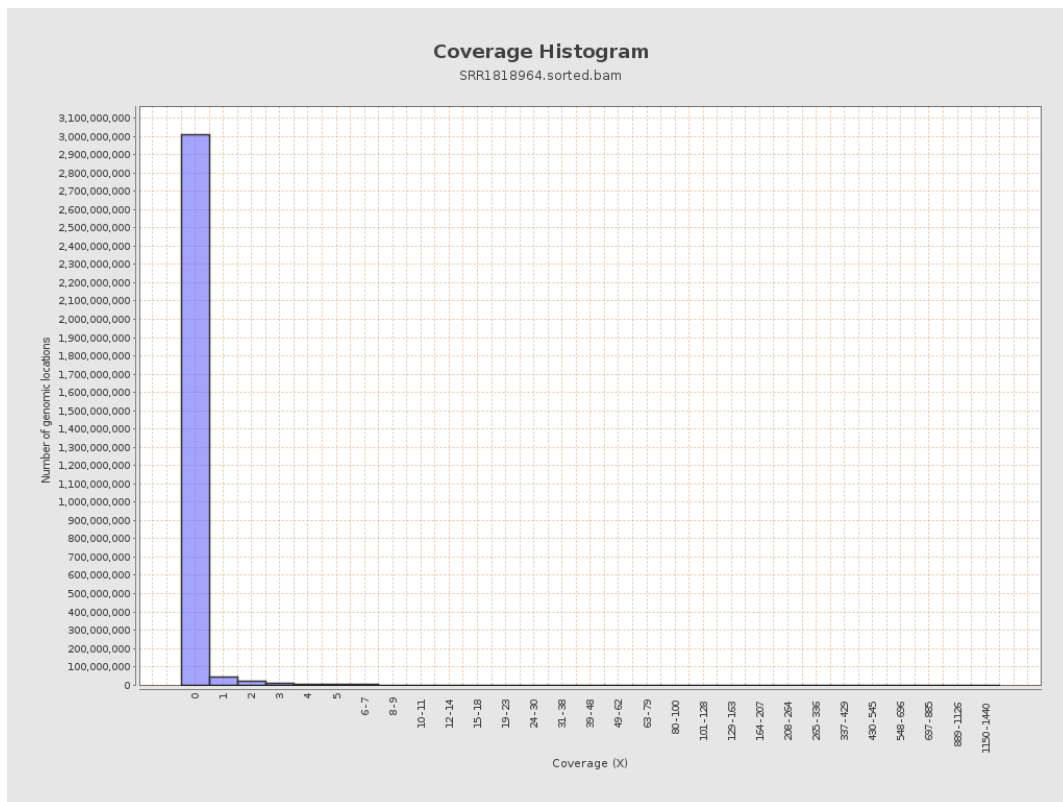
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18909640	0.0759	1.2849
chr2	243199373	15335487	0.0631	1.0239
chr3	198022430	9607774	0.0485	0.403
chr4	191154276	10060721	0.0526	0.4851
chr5	180915260	10727623	0.0593	0.4667
chr6	171115067	7815516	0.0457	0.4452
chr7	159138663	9597869	0.0603	0.7825

chr8	146364022	17671303	0.1207	0.7311
chr9	141213431	8333962	0.059	0.6646
chr10	135534747	10135688	0.0748	0.8418
chr11	135006516	5730019	0.0424	0.47
chr12	133851895	8917363	0.0666	0.4861
chr13	115169878	4160826	0.0361	0.3489
chr14	107349540	4325304	0.0403	0.3973
chr15	102531392	5101036	0.0498	0.4131
chr16	90354753	5773045	0.0639	0.8202
chr17	81195210	6801771	0.0838	0.6161
chr18	78077248	4406049	0.0564	0.779
chr19	59128983	3896680	0.0659	1.1331
chr20	63025520	5716912	0.0907	0.6045
chr21	48129895	2672999	0.0555	0.4738
chr22	51304566	1573035	0.0307	0.3542
chrMT	16571	102268	6.1715	5.6465
chrX	155270560	11361891	0.0732	0.5826
chrY	59373566	649621	0.0109	0.6777

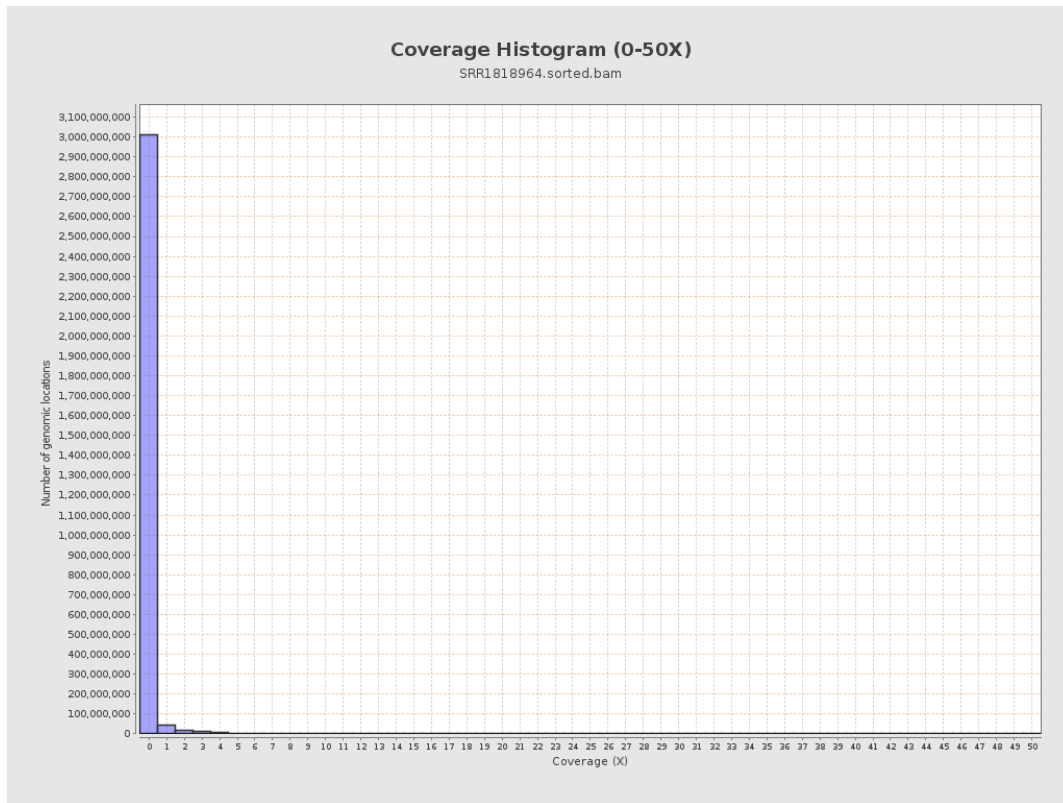
3. Results : Coverage across reference



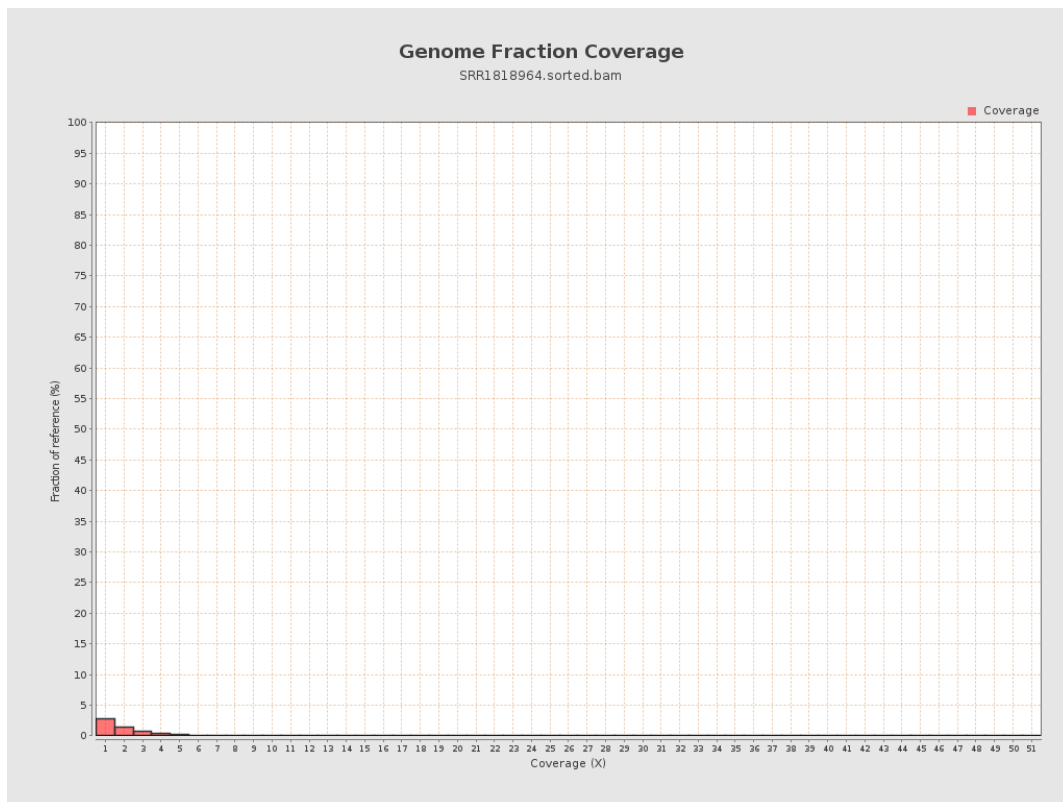
4. Results : Coverage Histogram



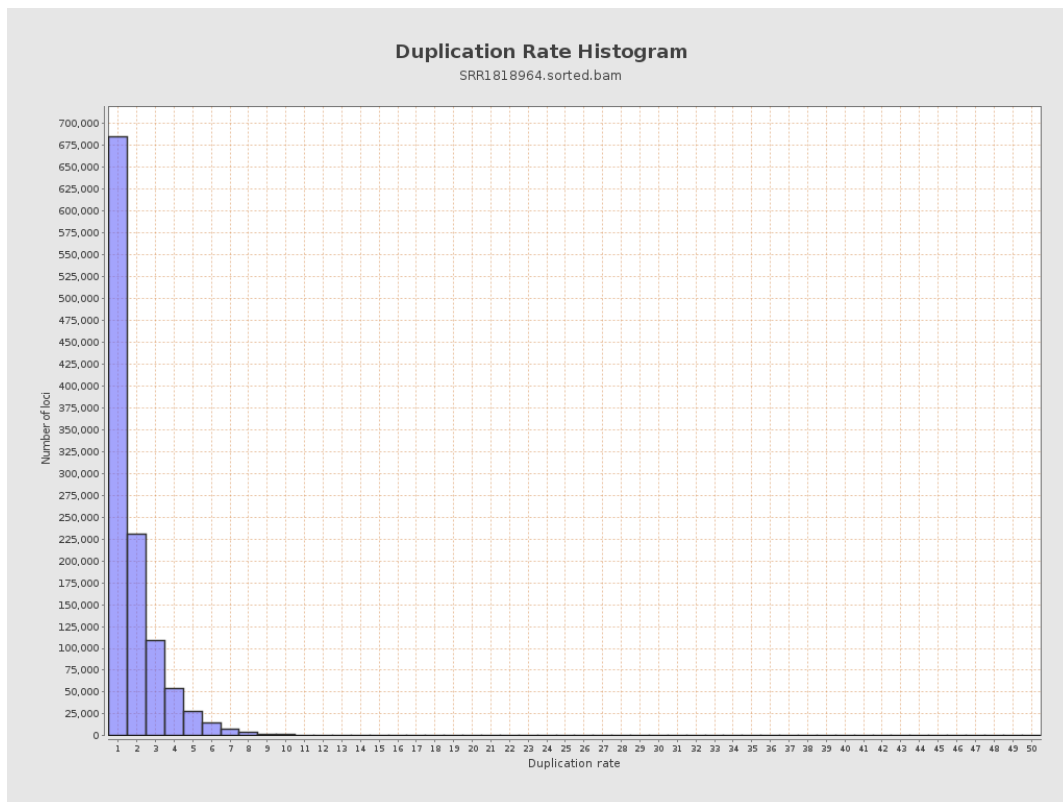
5. Results : Coverage Histogram (0-50X)



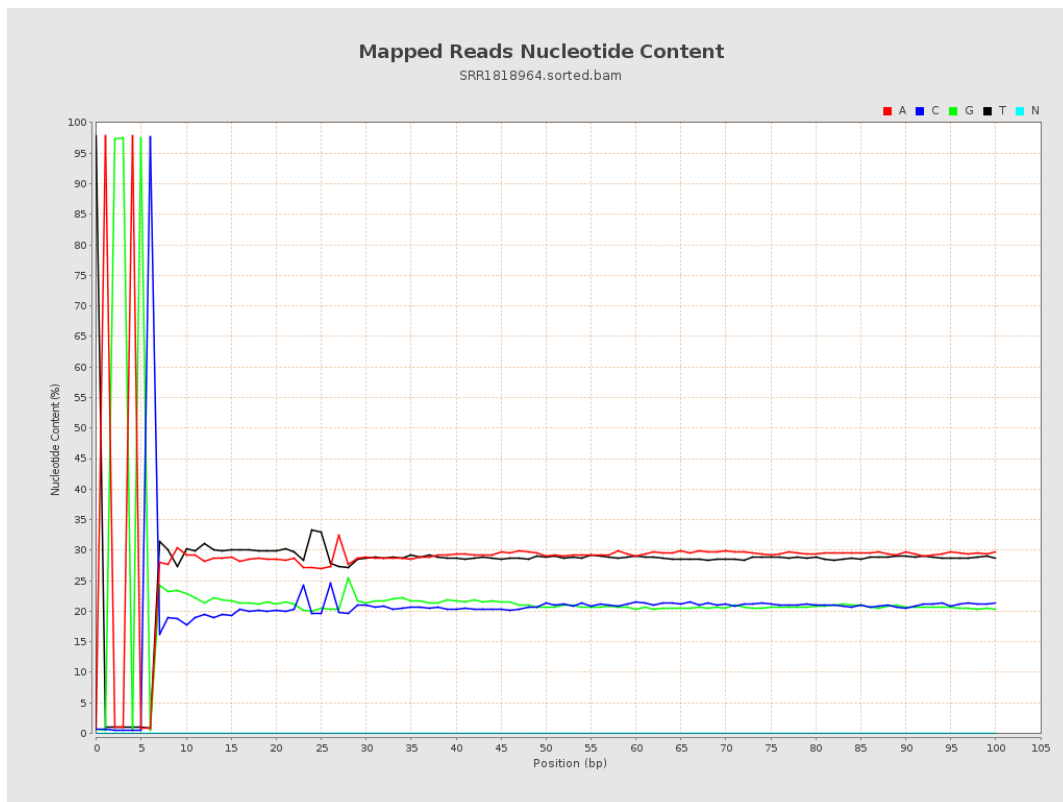
6. Results : Genome Fraction Coverage



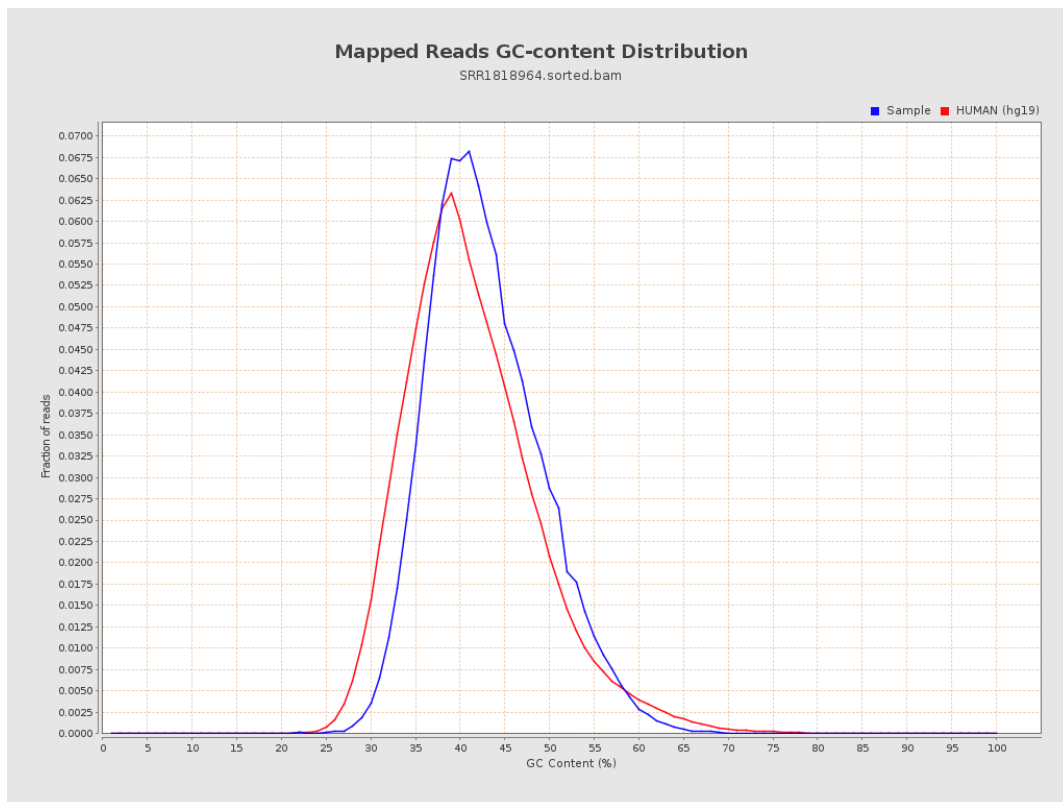
7. Results : Duplication Rate Histogram



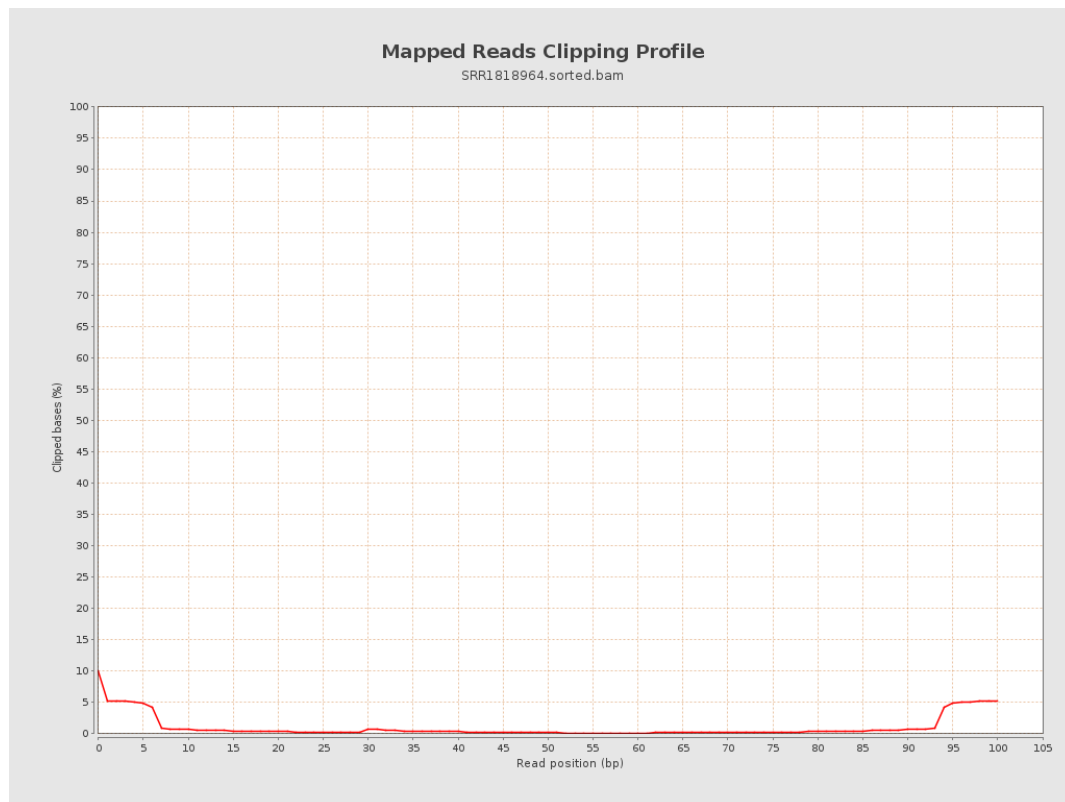
8. Results : Mapped Reads Nucleotide Content



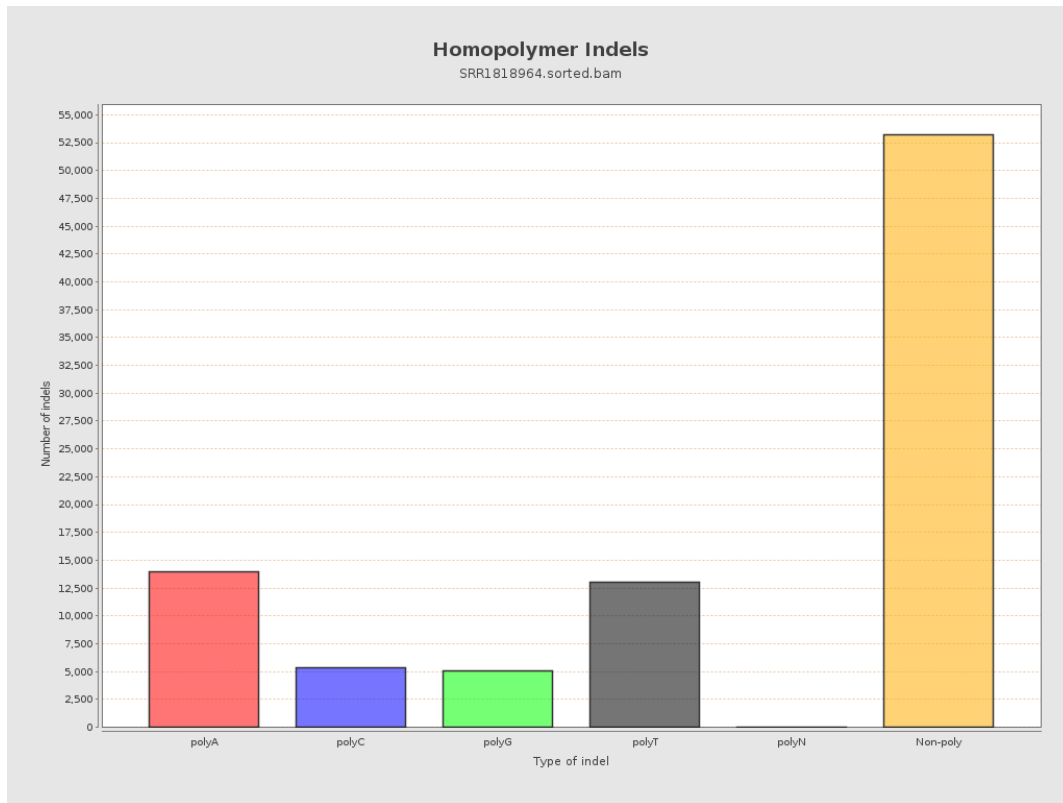
9. Results : Mapped Reads GC-content Distribution



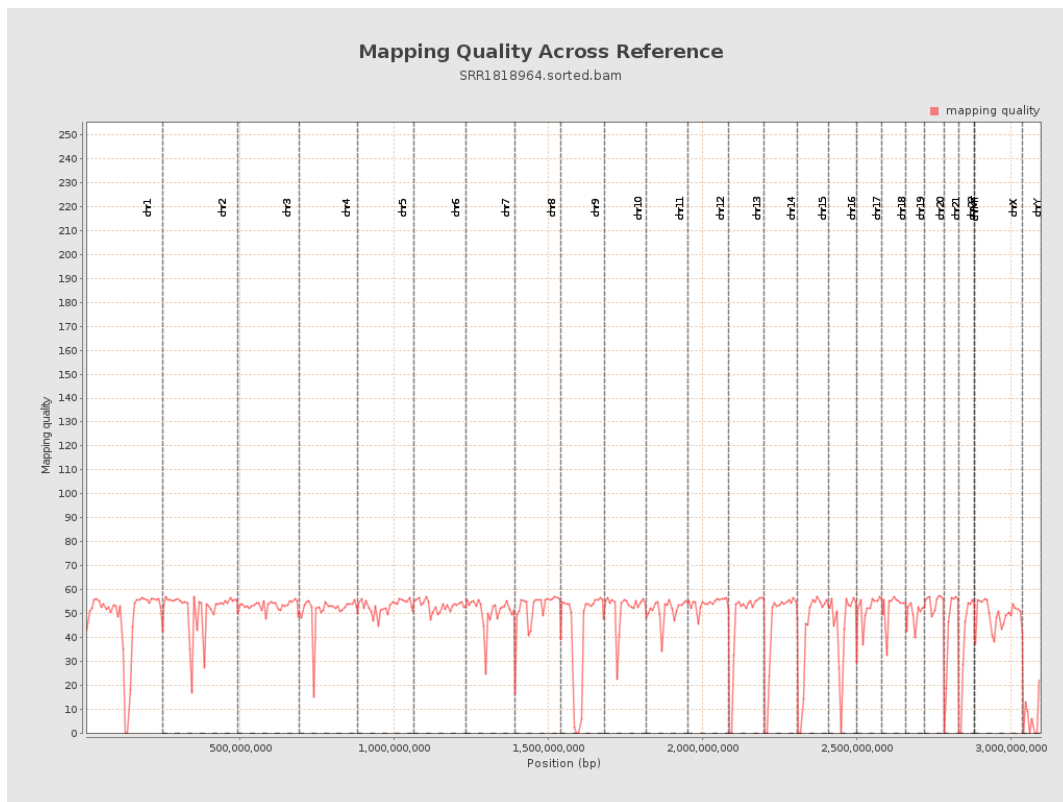
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

