

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:05:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174000.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_SRR10174000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174000_1.fastq.gz SRR10174000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:05:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,223,726
Mapped reads	3,141,923 / 97.46%
Unmapped reads	81,803 / 2.54%
Mapped paired reads	3,141,923 / 97.46%
Mapped reads, first in pair	1,572,344 / 48.77%
Mapped reads, second in pair	1,569,579 / 48.69%
Mapped reads, both in pair	3,088,390 / 95.8%
Mapped reads, singletons	53,533 / 1.66%
Secondary alignments	0
Supplementary alignments	299,111 / 9.28%
Read min/max/mean length	30 / 133 / 127.96
Duplicated reads (estimated)	2,405,628 / 74.62%
Duplication rate	64.39%
Clipped reads	1,230,427 / 38.17%

2.2. ACGT Content

Number/percentage of A's	112,174,793 / 30.17%
Number/percentage of C's	72,677,133 / 19.55%
Number/percentage of T's	111,915,316 / 30.1%
Number/percentage of G's	74,987,414 / 20.17%
Number/percentage of N's	4,293 / 0%

GC Percentage	39.72%
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2.3. Coverage

Mean	0.1202
Standard Deviation	1.8889

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	672,054.27
Standard Deviation	7,493,371.01
P25/Median/P75	145 / 199 / 281

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	3,765,921
Insertions	39,218
Mapped reads with at least one insertion	1.21%
Deletions	86,136
Mapped reads with at least one deletion	2.67%
Homopolymer indels	43.66%

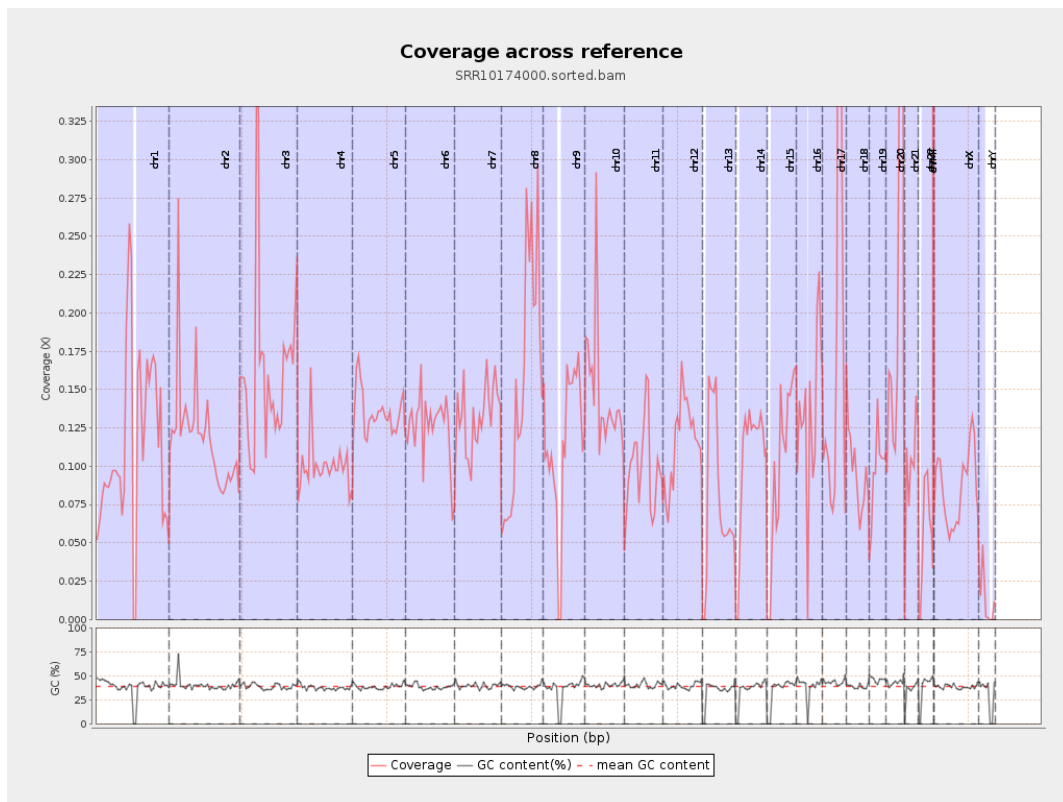
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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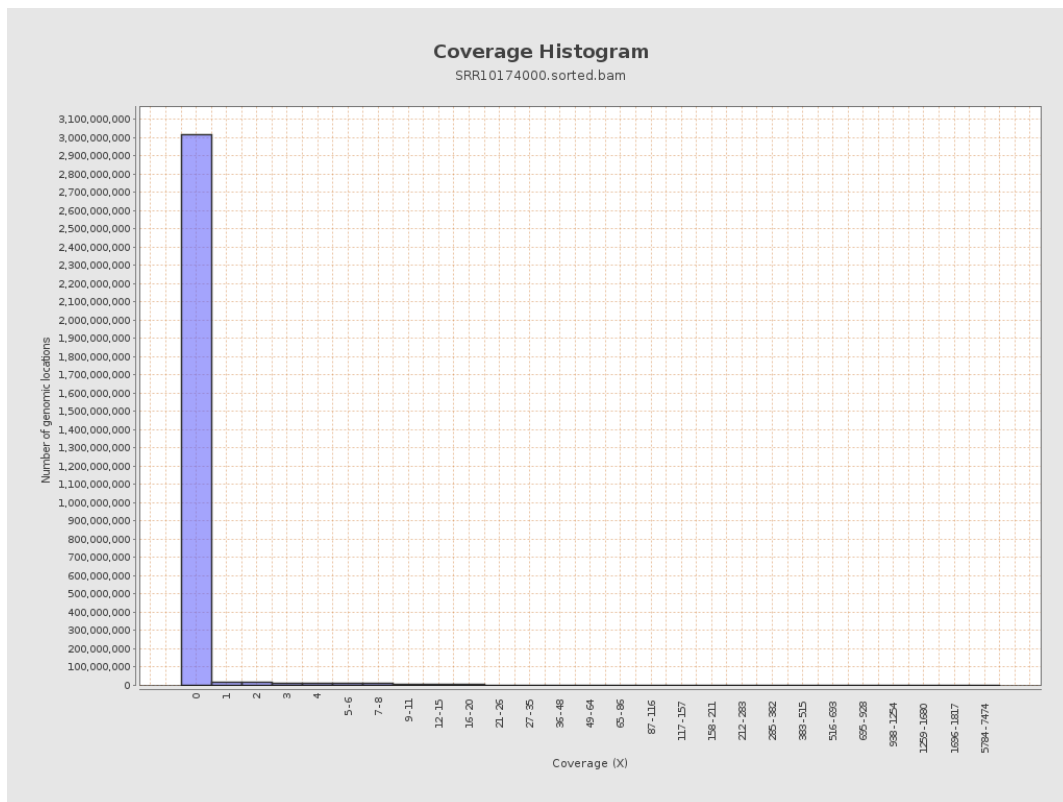
		bases	coverage	deviation
chr1	249250621	28220472	0.1132	1.6748
chr2	243199373	28937402	0.119	5.2755
chr3	198022430	31568862	0.1594	1.1533
chr4	191154276	18959954	0.0992	1.0356
chr5	180915260	24471280	0.1353	1.0507
chr6	171115067	21444973	0.1253	1.1191
chr7	159138663	21174381	0.1331	1.2811
chr8	146364022	22496714	0.1537	1.35
chr9	141213431	16016067	0.1134	1.1448
chr10	135534747	19942035	0.1471	2.0216
chr11	135006516	13425192	0.0994	0.9102
chr12	133851895	15614161	0.1167	0.9797
chr13	115169878	8901728	0.0773	0.8006
chr14	107349540	11143756	0.1038	0.9207
chr15	102531392	10382904	0.1013	0.8936
chr16	90354753	12186036	0.1349	1.2435
chr17	81195210	15196367	0.1872	1.3048
chr18	78077248	7489856	0.0959	1.5855
chr19	59128983	5810083	0.0983	1.1619
chr20	63025520	16349141	0.2594	1.5287
chr21	48129895	4778120	0.0993	0.9437
chr22	51304566	2782988	0.0542	0.6317
chrMT	16571	646957	39.0415	34.4666
chrX	155270560	13307271	0.0857	0.8318

chrY	59373566	722464	0.0122	0.582
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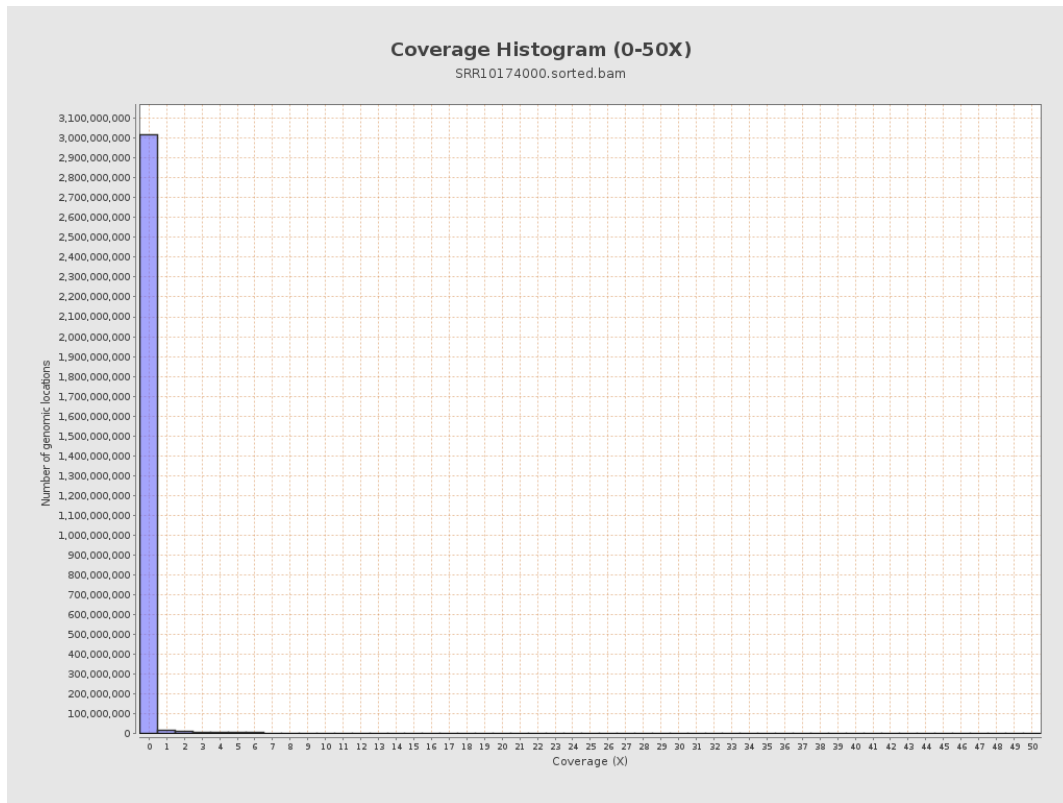
3. Results : Coverage across reference



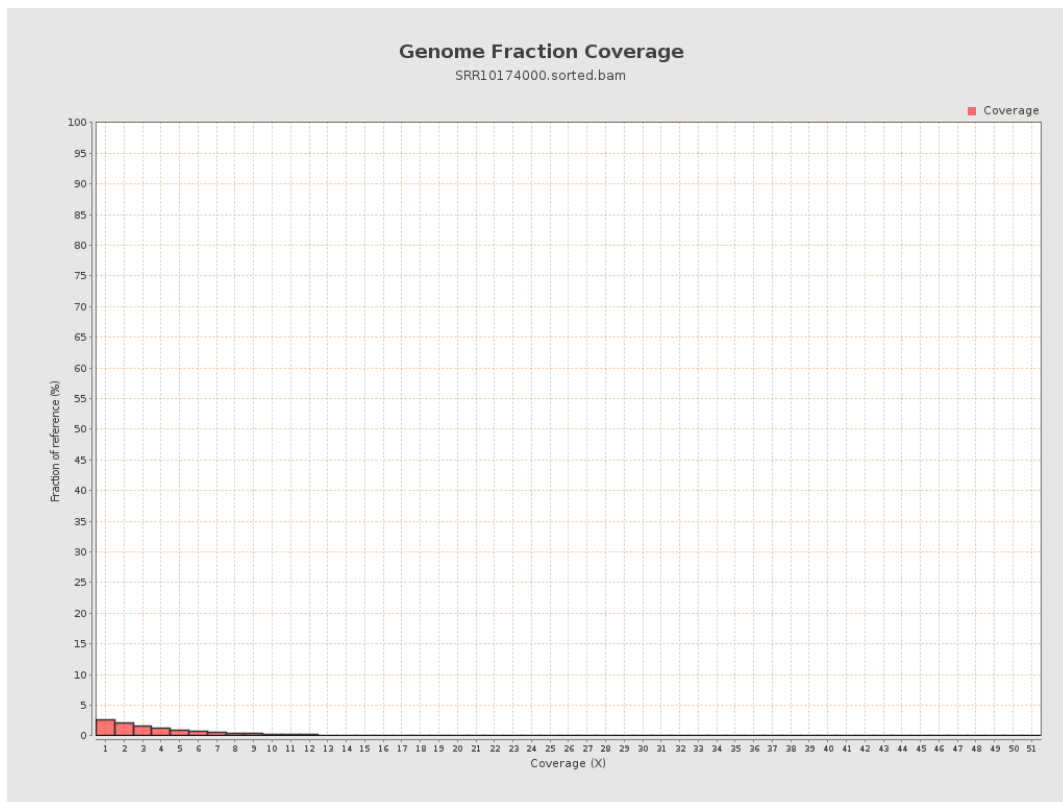
4. Results : Coverage Histogram



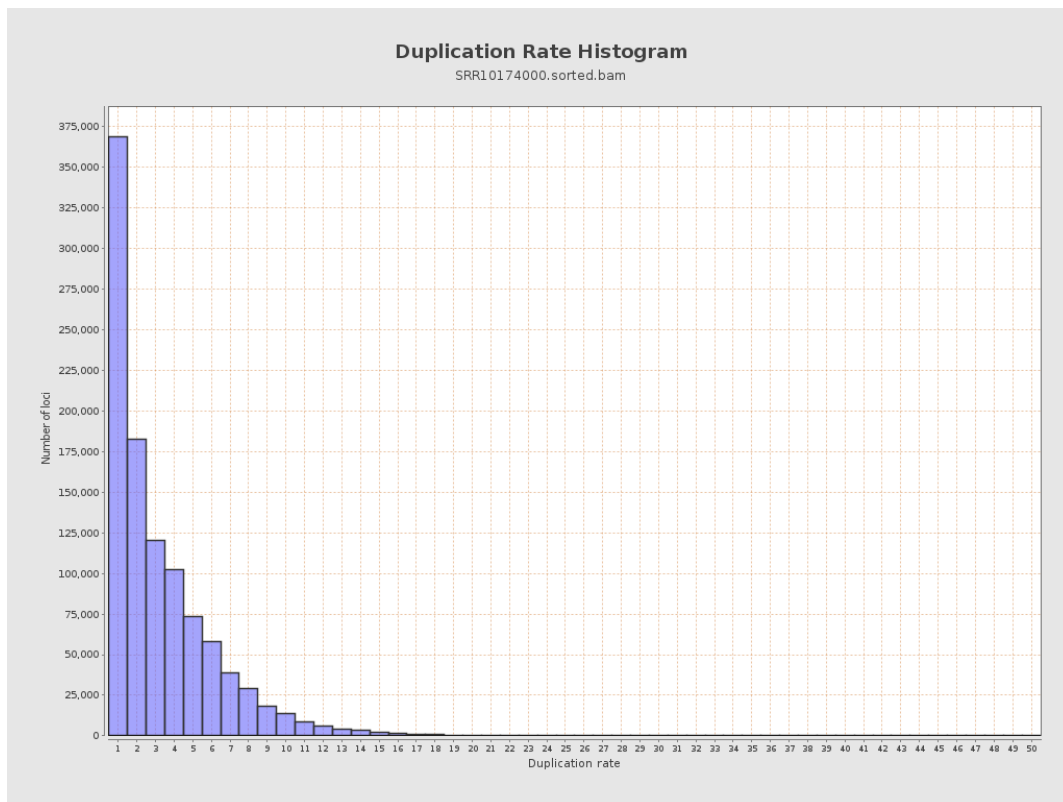
5. Results : Coverage Histogram (0-50X)



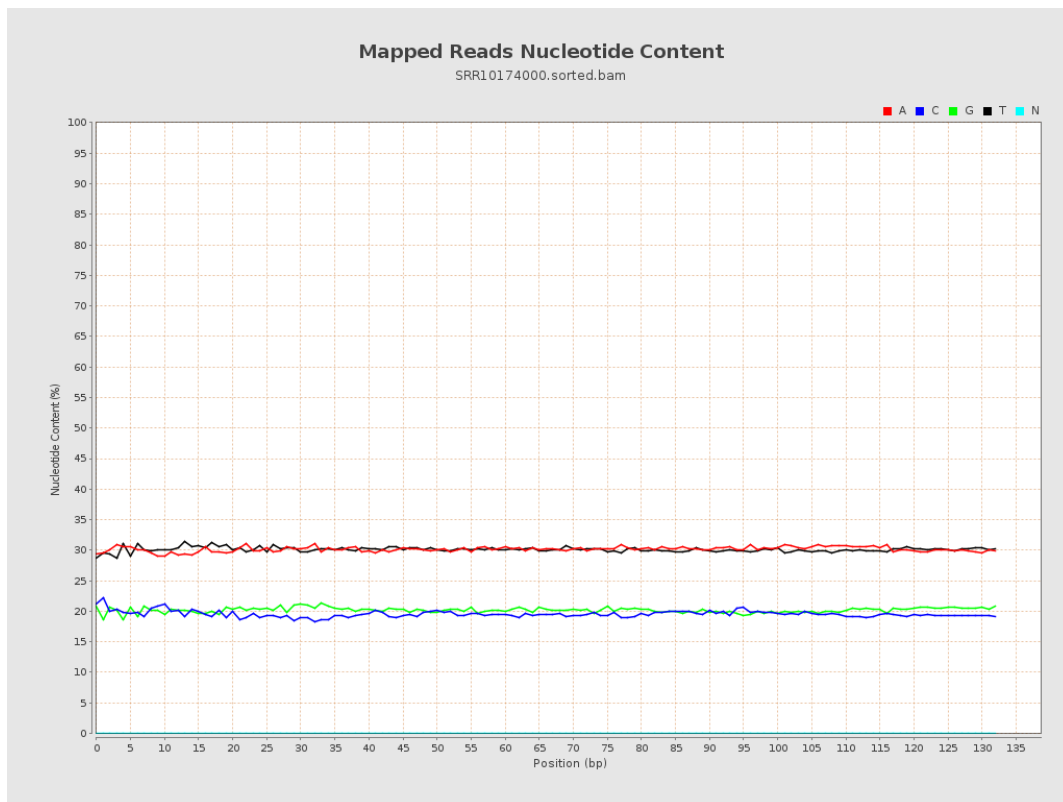
6. Results : Genome Fraction Coverage



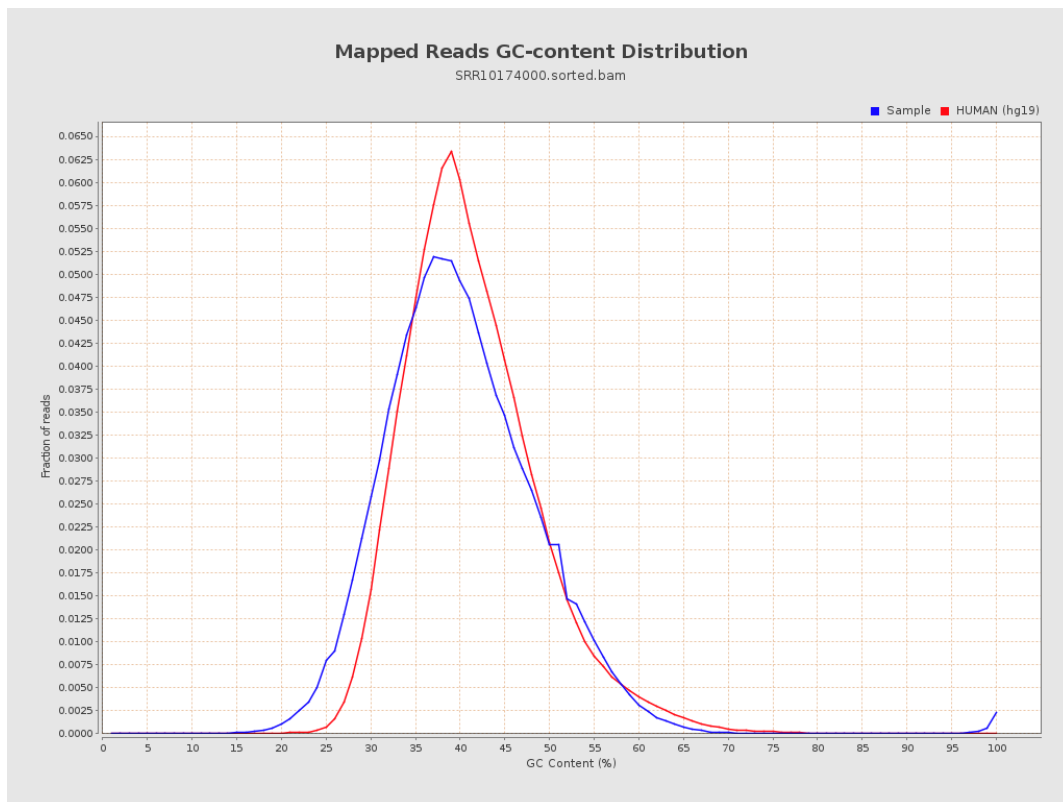
7. Results : Duplication Rate Histogram



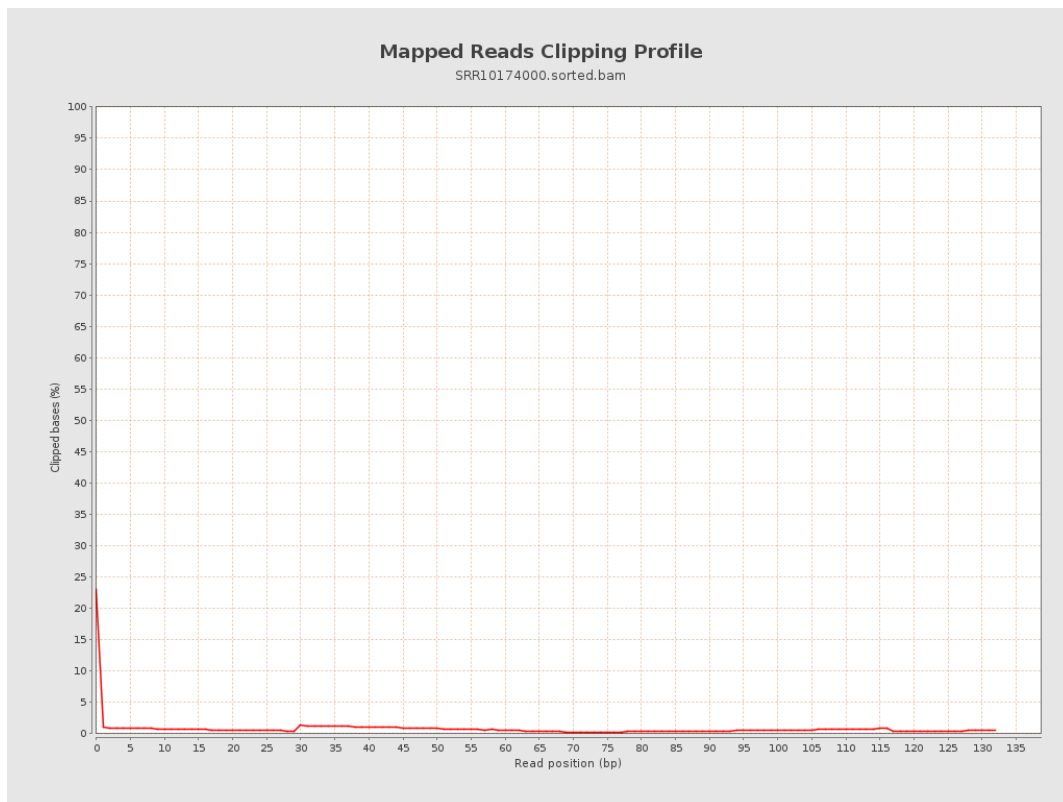
8. Results : Mapped Reads Nucleotide Content



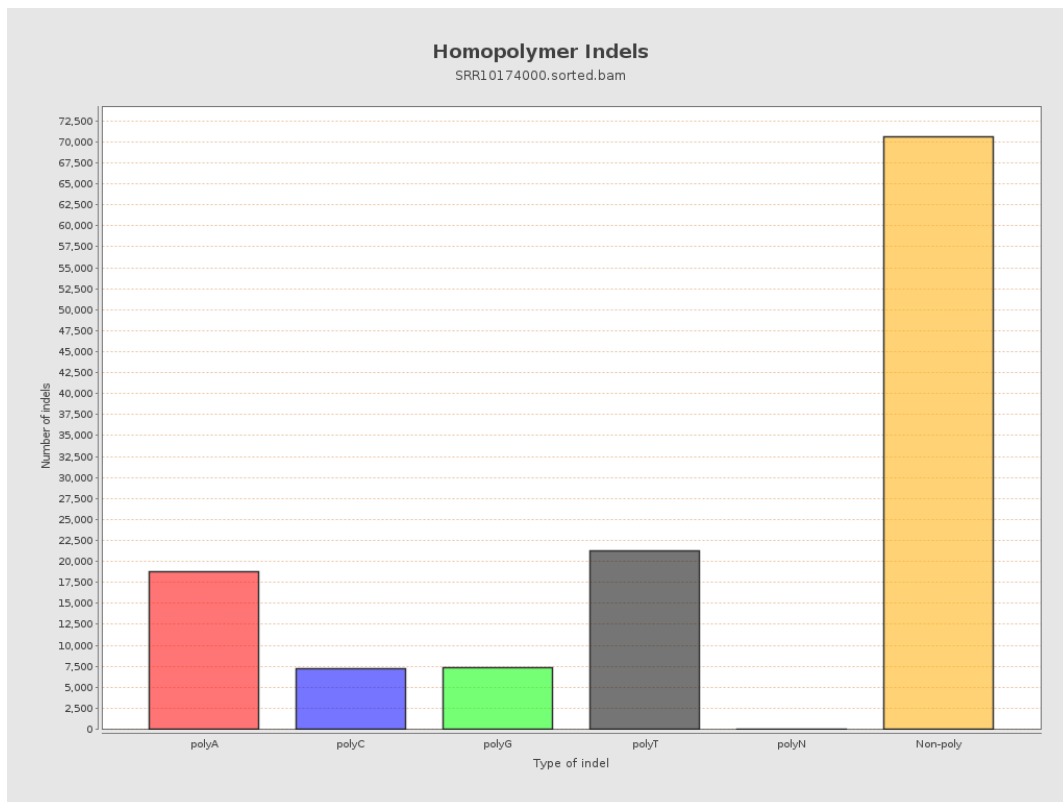
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



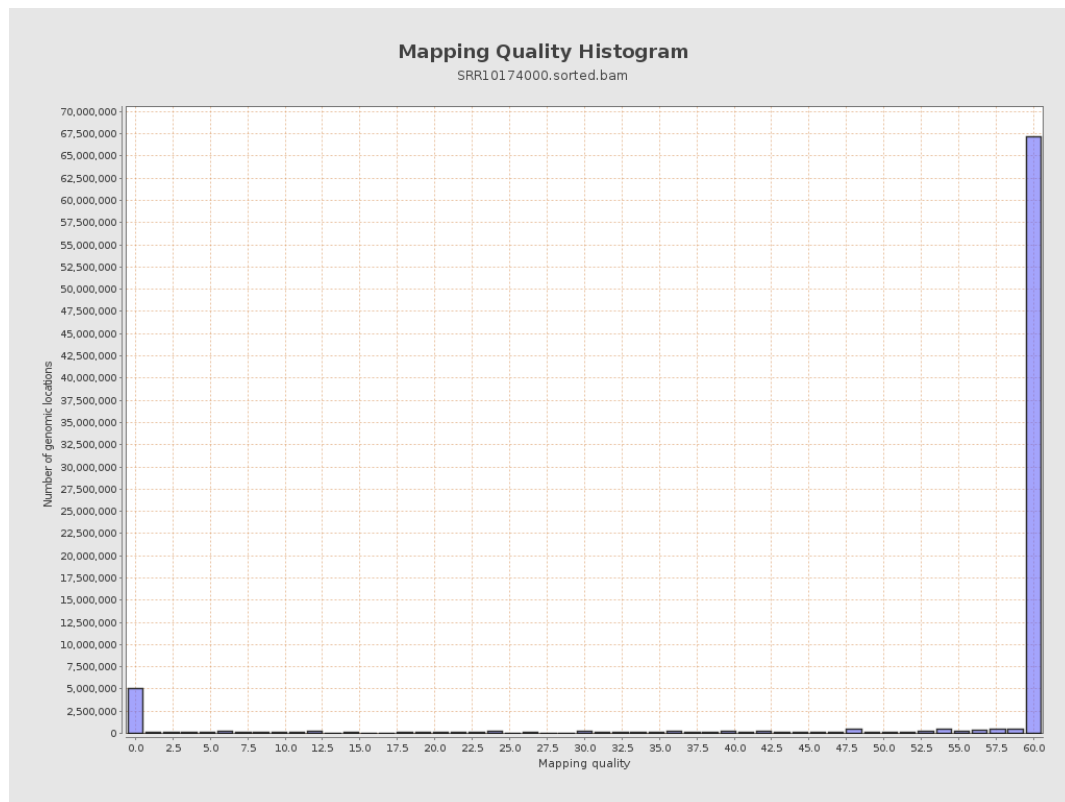
11. Results : Homopolymer Indels



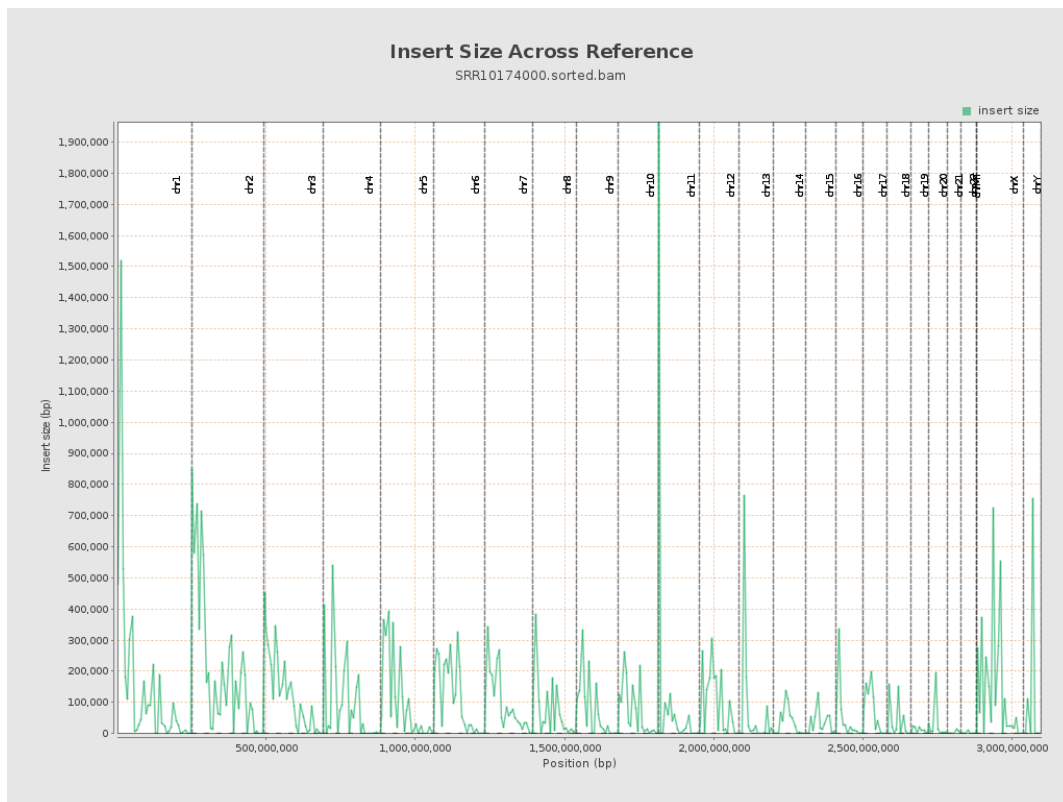
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

