

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:11:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174031.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_SRR10174031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174031_1.fastq.gz SRR10174031_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:11:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,461,048
Mapped reads	12,136,362 / 97.39%
Unmapped reads	324,686 / 2.61%
Mapped paired reads	12,136,362 / 97.39%
Mapped reads, first in pair	6,068,291 / 48.7%
Mapped reads, second in pair	6,068,071 / 48.7%
Mapped reads, both in pair	11,915,700 / 95.62%
Mapped reads, singletons	220,662 / 1.77%
Secondary alignments	0
Supplementary alignments	1,227,530 / 9.85%
Read min/max/mean length	30 / 133 / 128.16
Duplicated reads (estimated)	9,369,606 / 75.19%
Duplication rate	65.2%
Clipped reads	4,785,636 / 38.4%

2.2. ACGT Content

Number/percentage of A's	428,485,486 / 29.83%
Number/percentage of C's	284,771,356 / 19.82%
Number/percentage of T's	427,606,331 / 29.77%
Number/percentage of G's	295,579,073 / 20.58%
Number/percentage of N's	17,993 / 0%

GC Percentage	40.4%
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2.3. Coverage

Mean	0.4643
Standard Deviation	6.2889

2.4. Mapping Quality

Mean Mapping Quality	52.74
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2.5. Insert size

Mean	777,241.28
Standard Deviation	8,101,401.5
P25/Median/P75	147 / 207 / 299

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	15,016,640
Insertions	149,184
Mapped reads with at least one insertion	1.19%
Deletions	334,723
Mapped reads with at least one deletion	2.69%
Homopolymer indels	42.82%

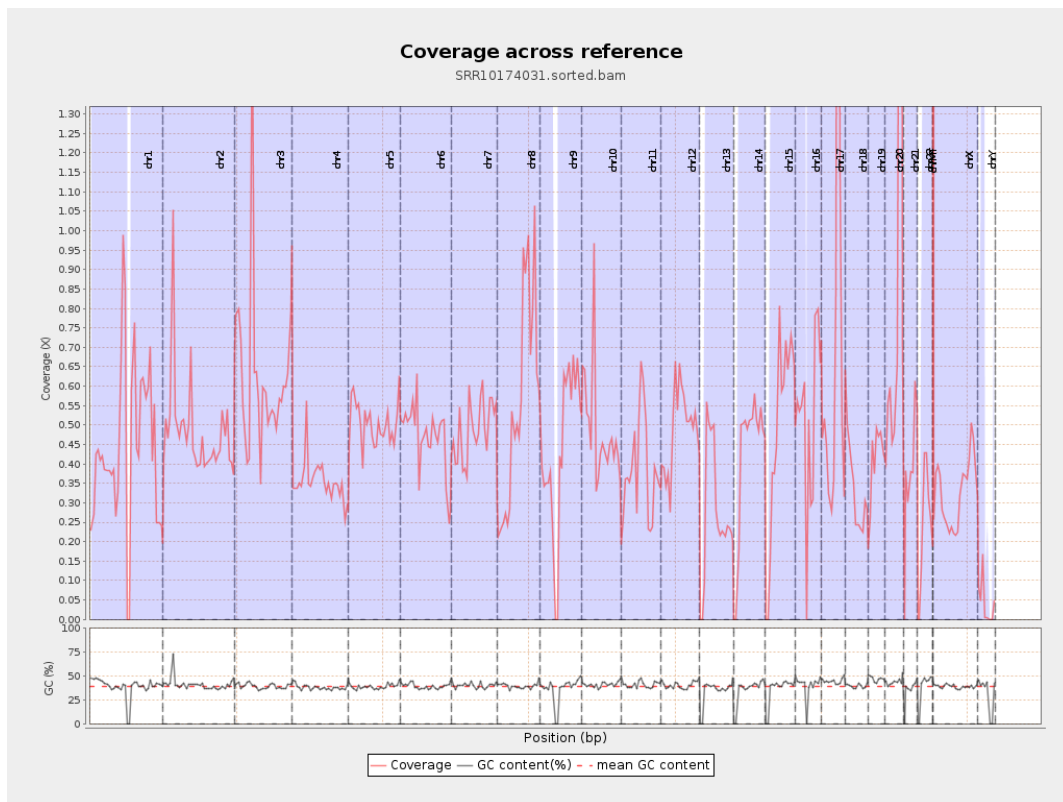
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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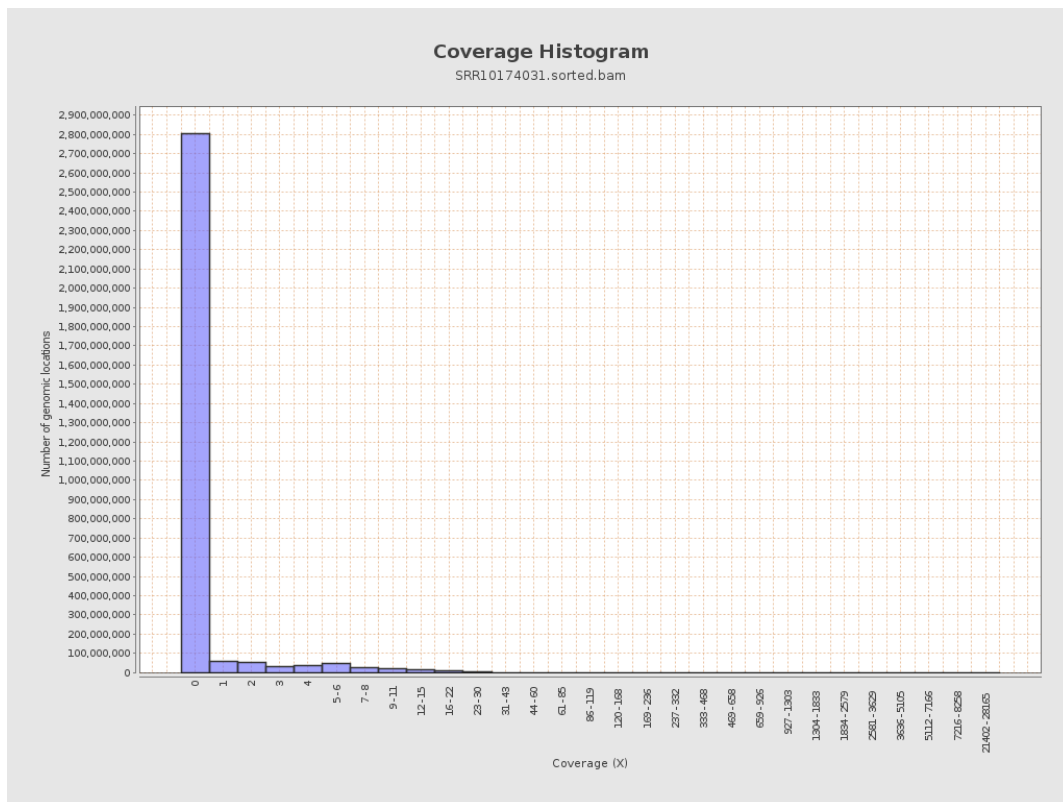
		bases	coverage	deviation
chr1	249250621	110368334	0.4428	4.497
chr2	243199373	116832986	0.4804	19.7117
chr3	198022430	122882080	0.6205	2.3111
chr4	191154276	67942422	0.3554	2.4109
chr5	180915260	90975743	0.5029	1.9978
chr6	171115067	80708072	0.4717	2.681
chr7	159138663	77886056	0.4894	3.7575
chr8	146364022	81781381	0.5588	3.2953
chr9	141213431	61536361	0.4358	2.9349
chr10	135534747	65923298	0.4864	5.8597
chr11	135006516	51772892	0.3835	1.8565
chr12	133851895	66073963	0.4936	2.0224
chr13	115169878	31538372	0.2738	1.4764
chr14	107349540	45559071	0.4244	1.8763
chr15	102531392	49342240	0.4812	1.9938
chr16	90354753	46149167	0.5108	3.1051
chr17	81195210	64520939	0.7946	3.2198
chr18	78077248	26524316	0.3397	5.0743
chr19	59128983	24354062	0.4119	3.1941
chr20	63025520	67560519	1.072	3.8069
chr21	48129895	18599608	0.3864	2.0238
chr22	51304566	12455013	0.2428	1.3785
chrMT	16571	3005717	181.3842	142.6985
chrX	155270560	50415986	0.3247	1.6302

chrY	59373566	2568942	0.0433	1.4998
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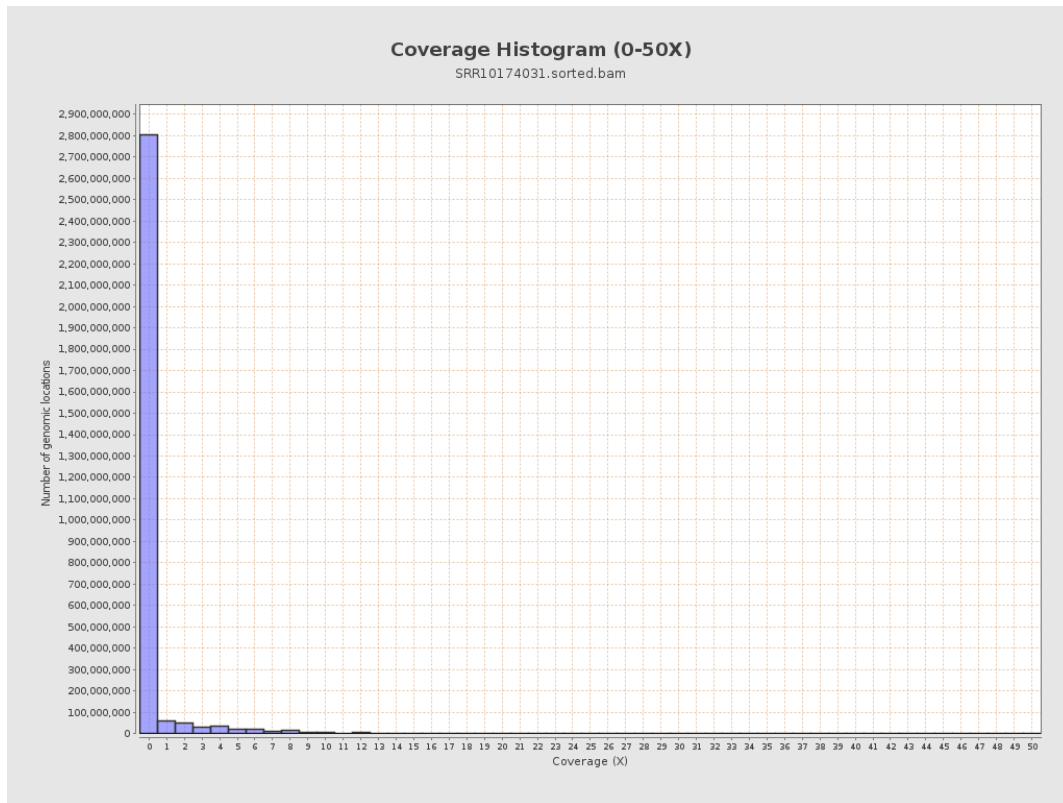
3. Results : Coverage across reference



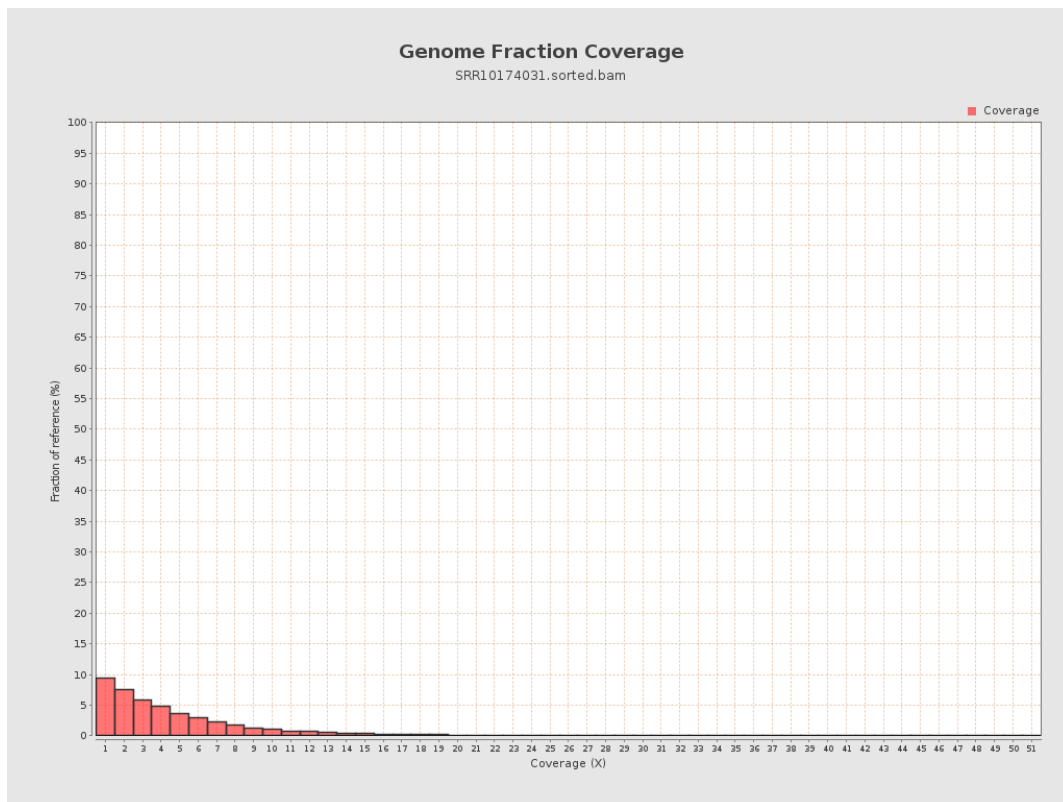
4. Results : Coverage Histogram



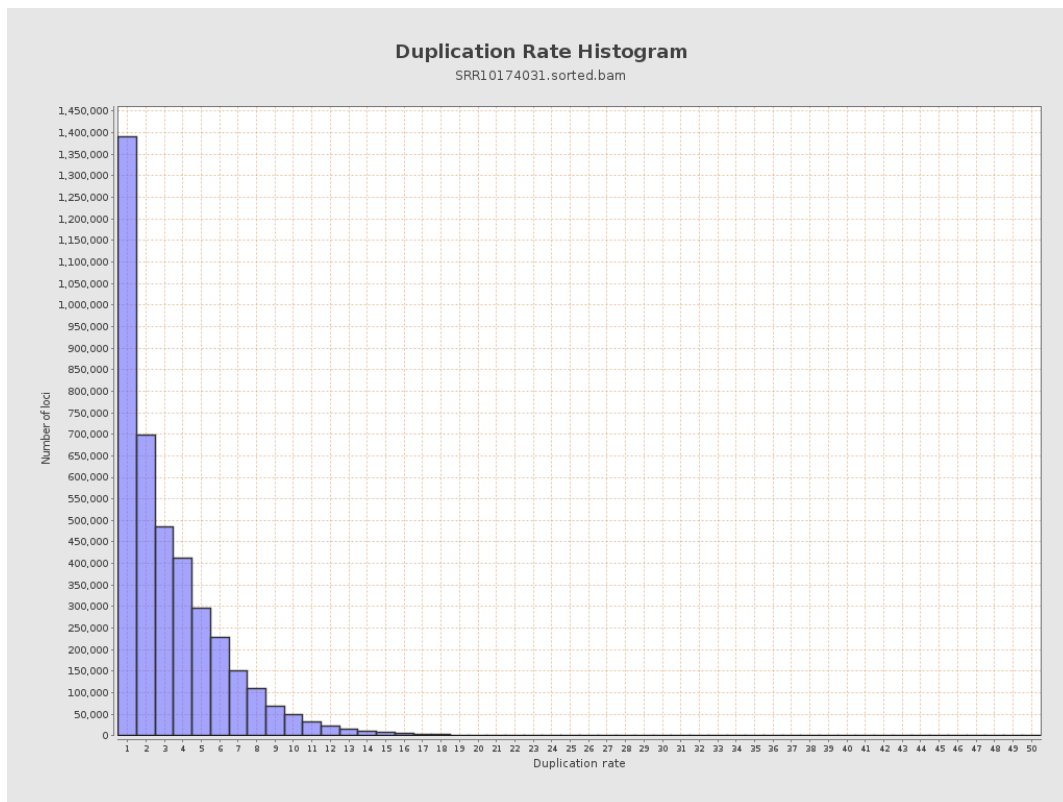
5. Results : Coverage Histogram (0-50X)



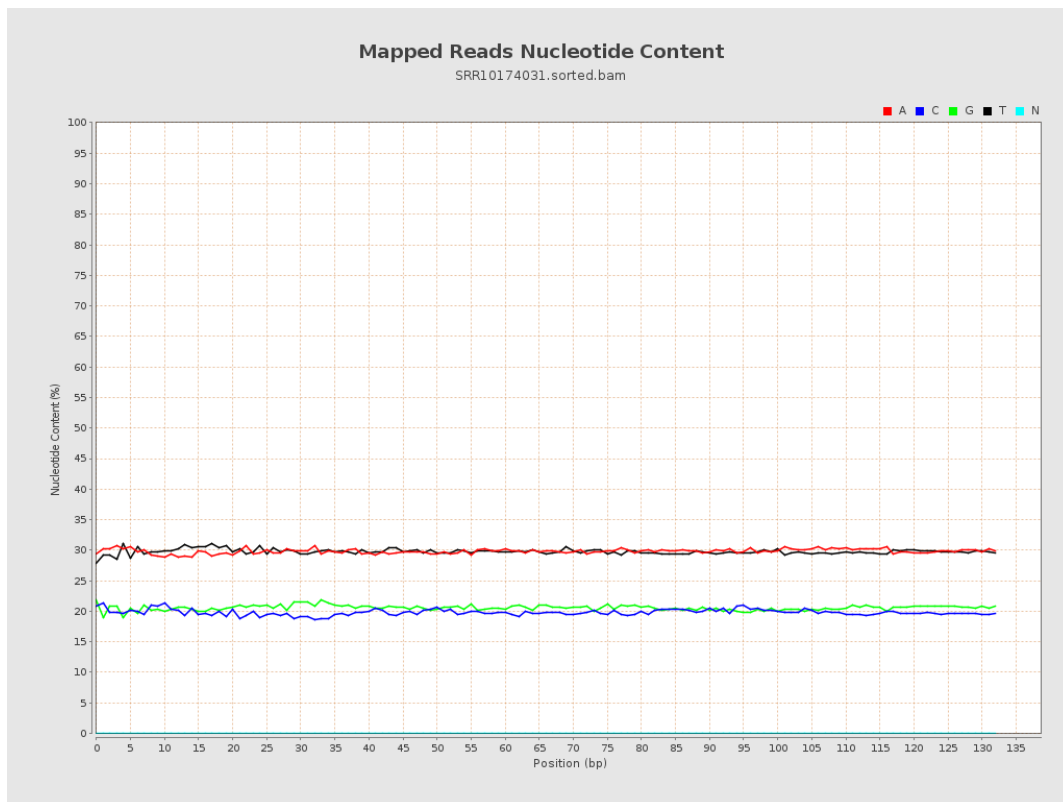
6. Results : Genome Fraction Coverage



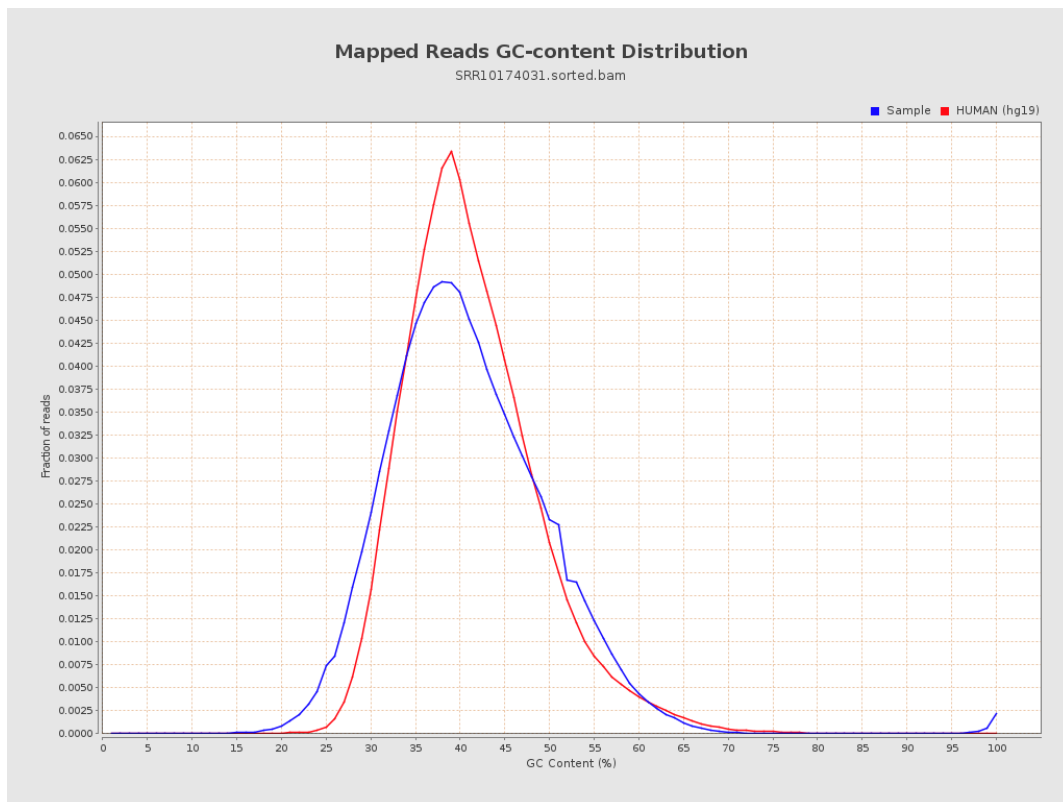
7. Results : Duplication Rate Histogram



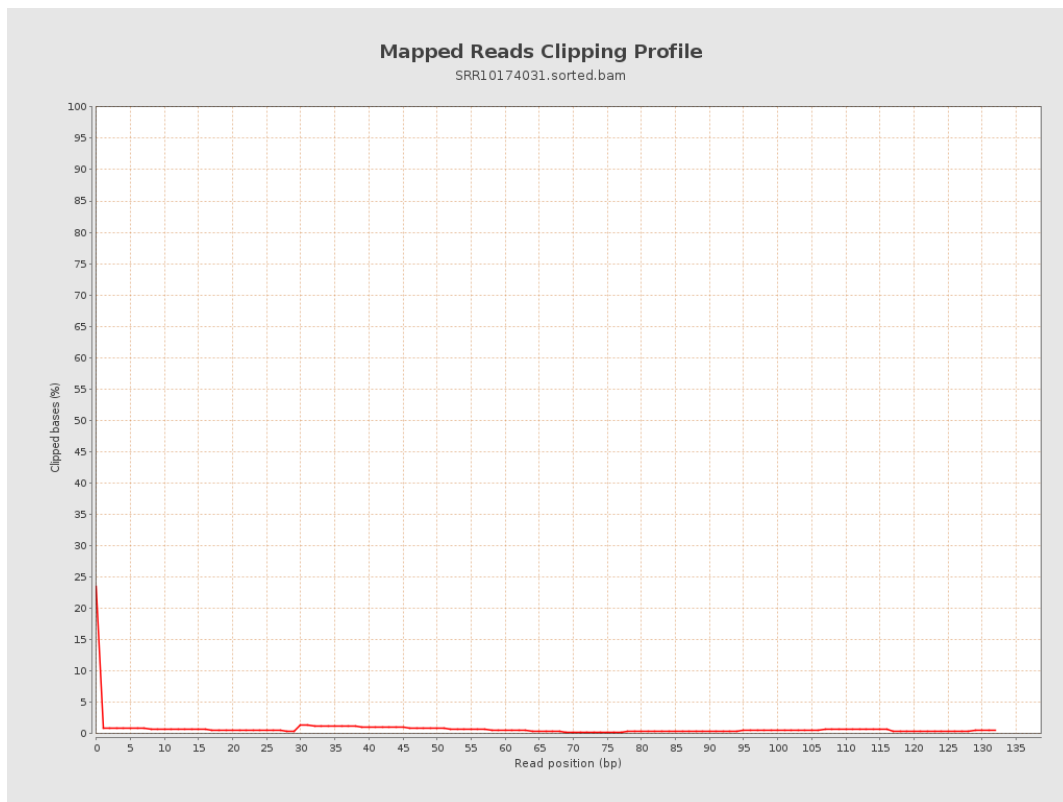
8. Results : Mapped Reads Nucleotide Content



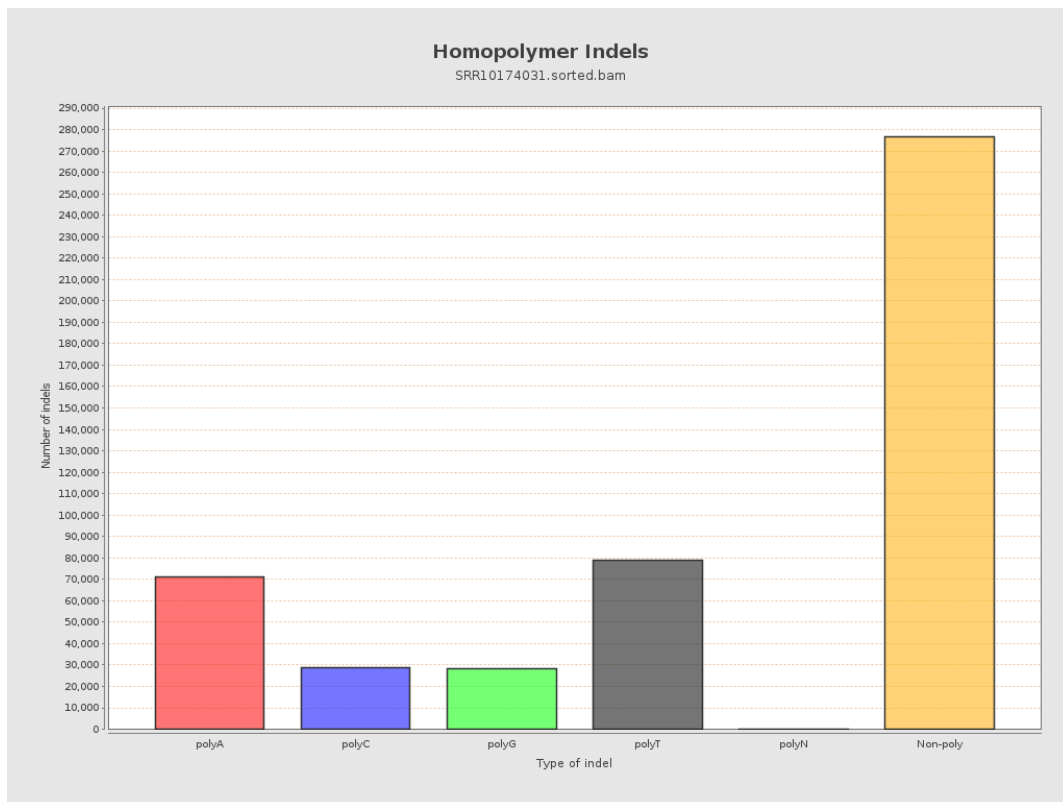
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



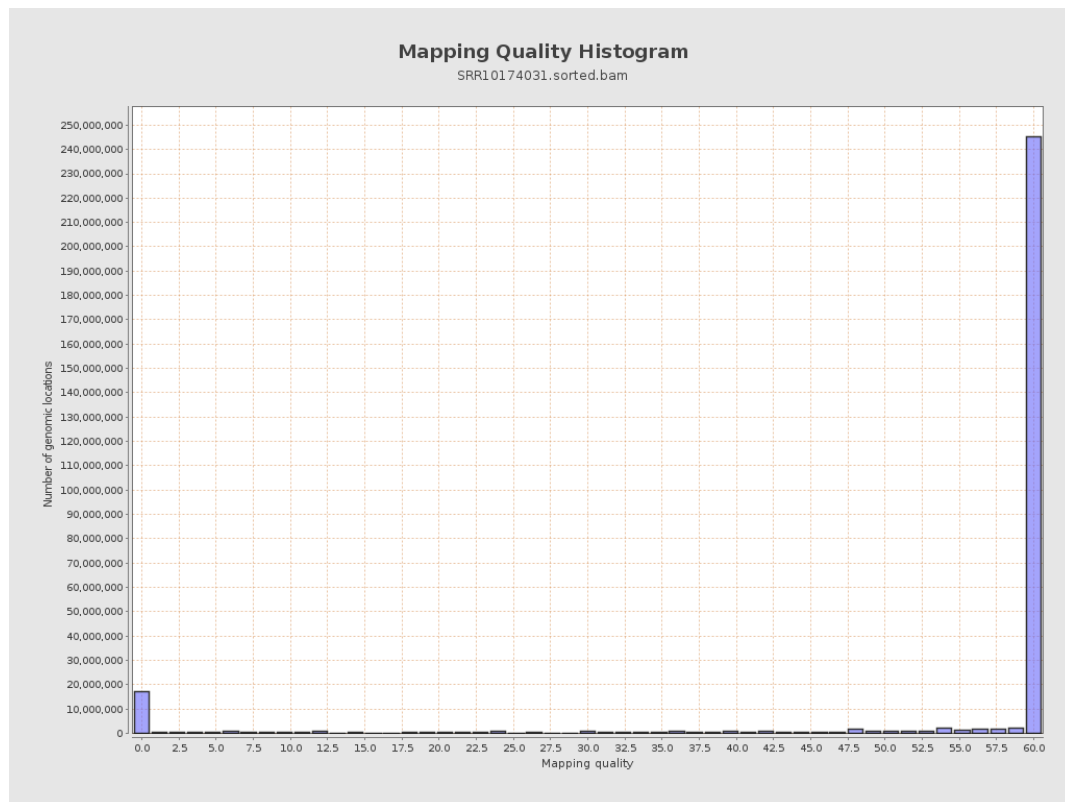
11. Results : Homopolymer Indels



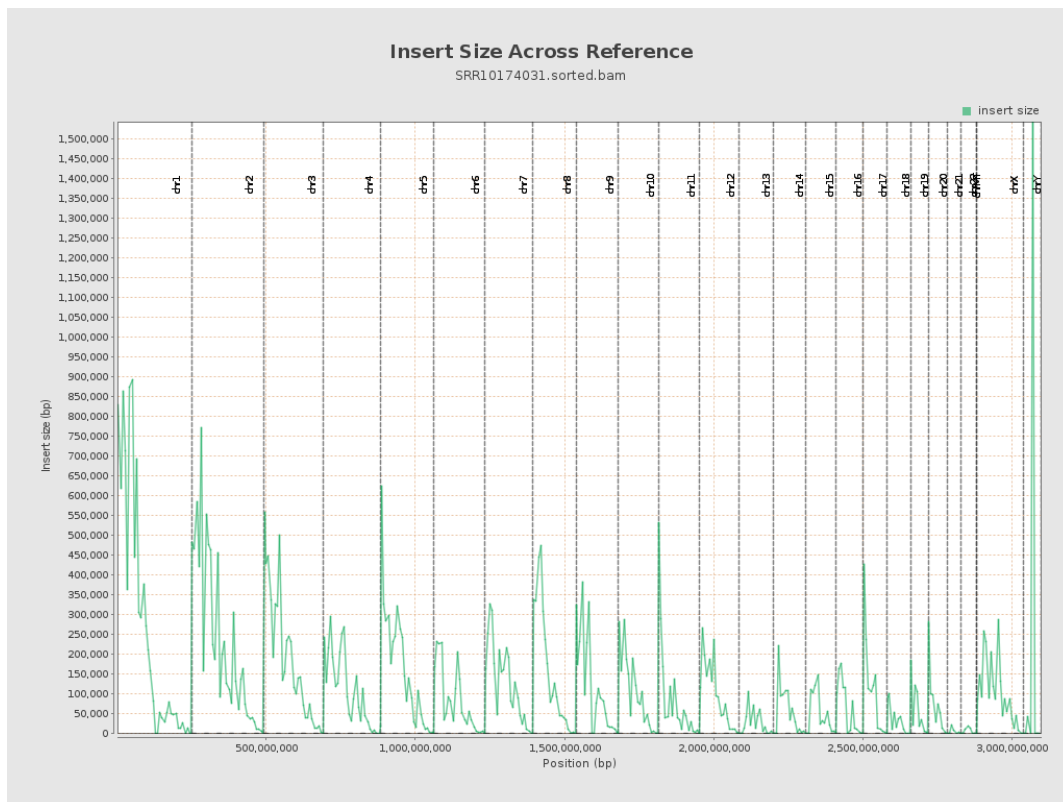
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

