

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:25:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174049.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_SRR10174049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174049_1.fastq.gz SRR10174049_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:25:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,017,448
Mapped reads	3,921,034 / 97.6%
Unmapped reads	96,414 / 2.4%
Mapped paired reads	3,921,034 / 97.6%
Mapped reads, first in pair	1,959,304 / 48.77%
Mapped reads, second in pair	1,961,730 / 48.83%
Mapped reads, both in pair	3,855,814 / 95.98%
Mapped reads, singletons	65,220 / 1.62%
Secondary alignments	0
Supplementary alignments	417,894 / 10.4%
Read min/max/mean length	30 / 133 / 128.5
Duplicated reads (estimated)	2,988,590 / 74.39%
Duplication rate	63.55%
Clipped reads	1,593,195 / 39.66%

2.2. ACGT Content

Number/percentage of A's	140,377,107 / 30.22%
Number/percentage of C's	90,453,483 / 19.47%
Number/percentage of T's	140,073,507 / 30.15%
Number/percentage of G's	93,618,086 / 20.15%
Number/percentage of N's	5,713 / 0%

GC Percentage	39.63%
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2.3. Coverage

Mean	0.1501
Standard Deviation	2.2637

2.4. Mapping Quality

Mean Mapping Quality	52.61
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2.5. Insert size

Mean	872,227.29
Standard Deviation	8,459,399.63
P25/Median/P75	145 / 203 / 292

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	4,708,754
Insertions	48,342
Mapped reads with at least one insertion	1.19%
Deletions	106,405
Mapped reads with at least one deletion	2.65%
Homopolymer indels	42.26%

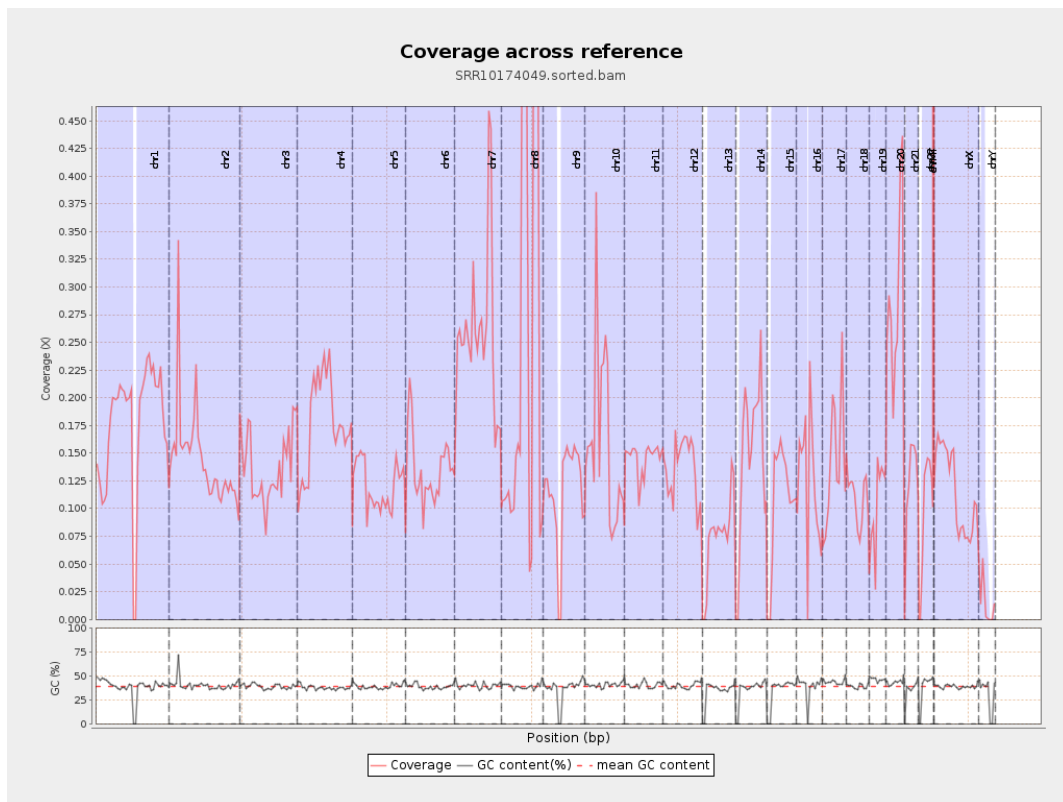
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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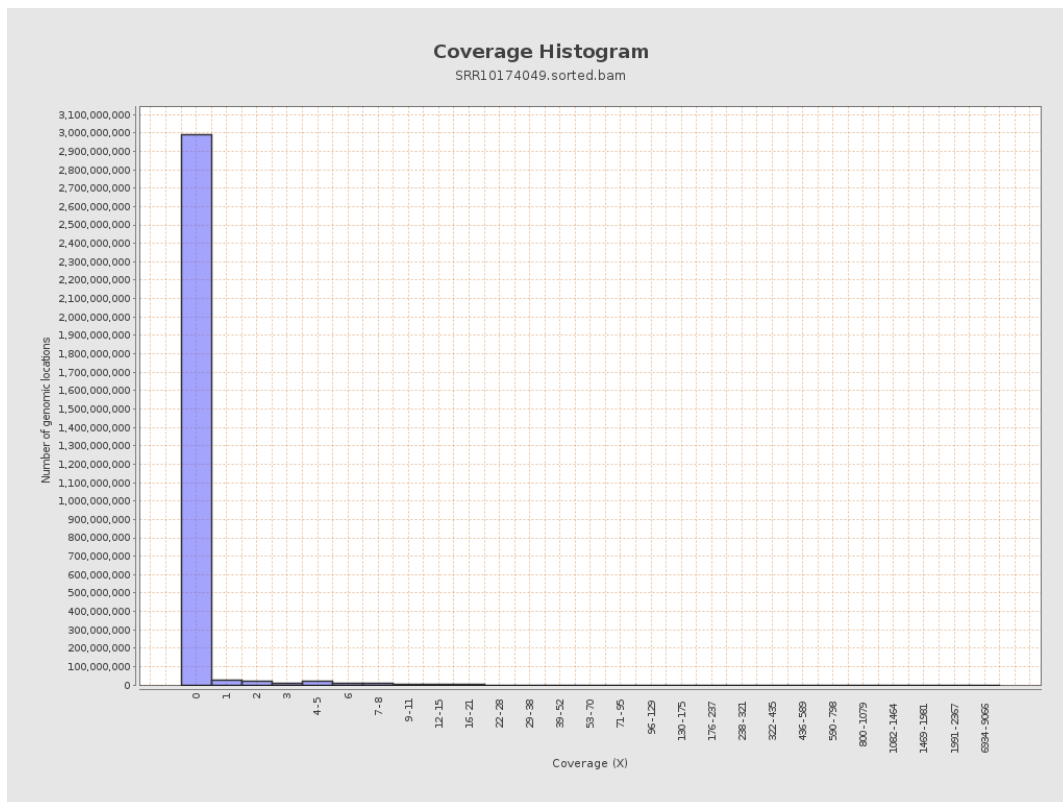
		bases	coverage	deviation
chr1	249250621	43641959	0.1751	1.405
chr2	243199373	35156430	0.1446	6.3835
chr3	198022430	27095555	0.1368	1.0304
chr4	191154276	33776564	0.1767	1.3766
chr5	180915260	21756725	0.1203	0.9643
chr6	171115067	22879083	0.1337	1.0533
chr7	159138663	41478613	0.2606	2.7098
chr8	146364022	41713116	0.285	1.8155
chr9	141213431	16368393	0.1159	1.2251
chr10	135534747	21754434	0.1605	2.8343
chr11	135006516	19539059	0.1447	1.0685
chr12	133851895	18334996	0.137	1.0287
chr13	115169878	8601284	0.0747	0.7653
chr14	107349540	15768860	0.1469	1.0764
chr15	102531392	11080436	0.1081	0.903
chr16	90354753	11058247	0.1224	1.3007
chr17	81195210	11554506	0.1423	1.1907
chr18	78077248	8520406	0.1091	1.4559
chr19	59128983	6052622	0.1024	1.035
chr20	63025520	18087594	0.287	1.5127
chr21	48129895	5829301	0.1211	1.0571
chr22	51304566	4838420	0.0943	0.8211
chrMT	16571	997176	60.176	55.1685
chrX	155270560	18053993	0.1163	0.9505

chrY	59373566	856485	0.0144	0.5625
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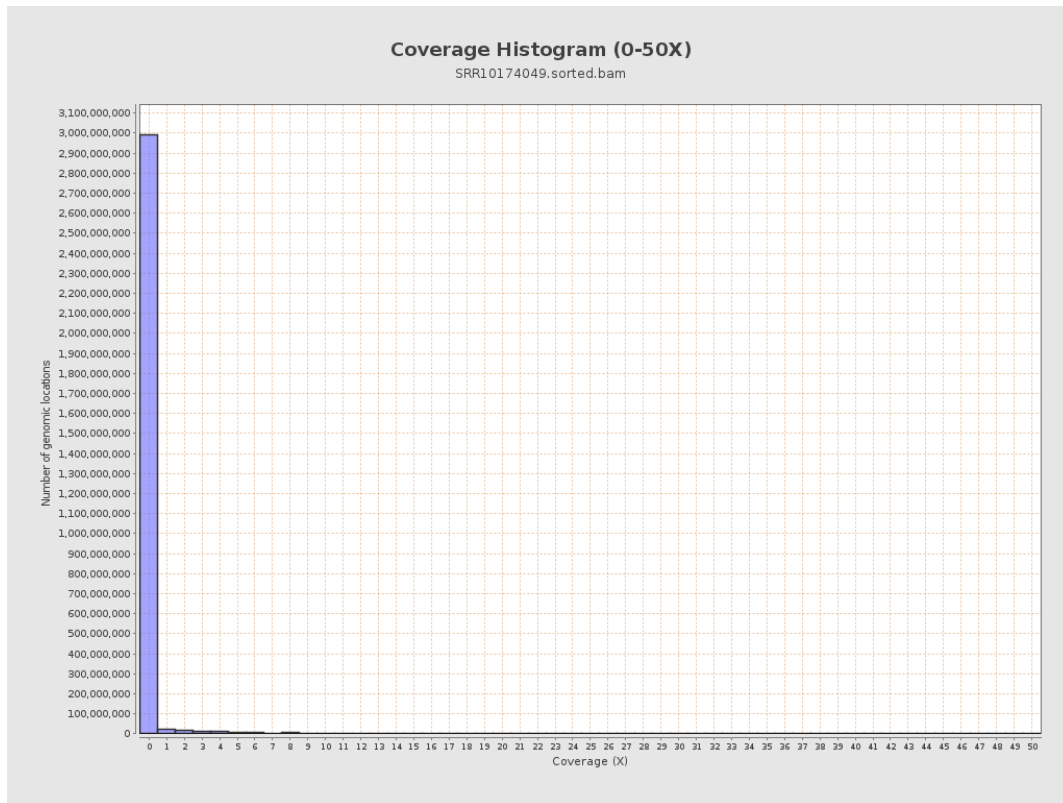
3. Results : Coverage across reference



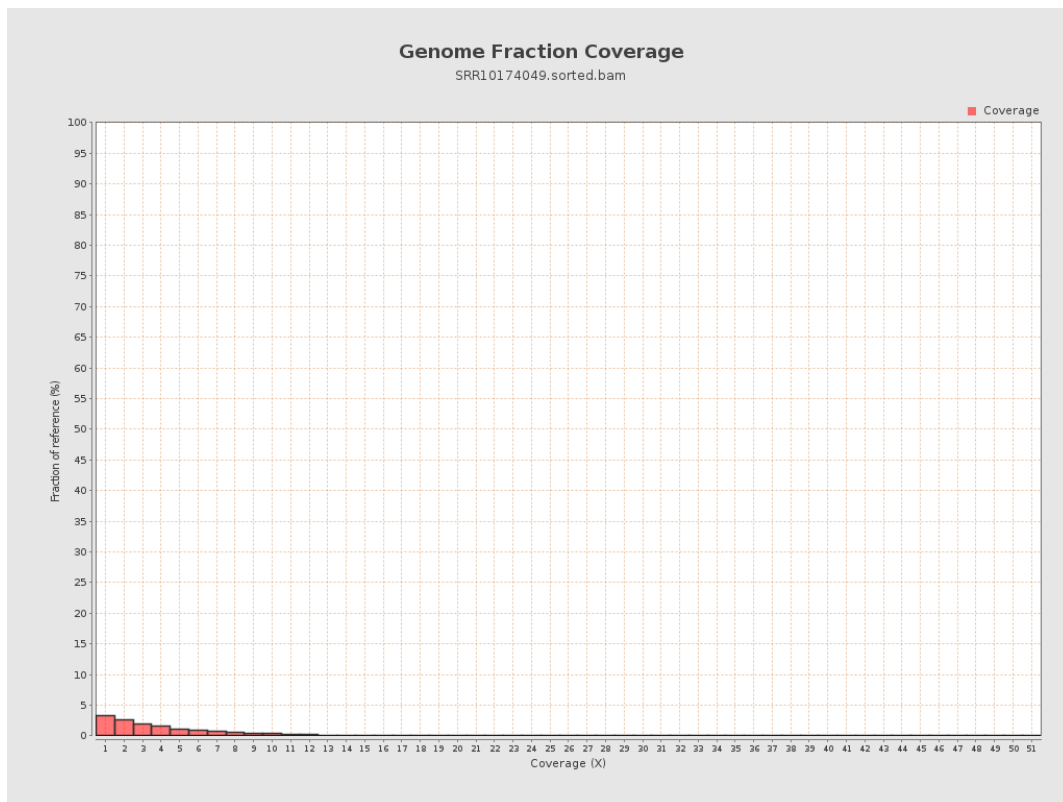
4. Results : Coverage Histogram



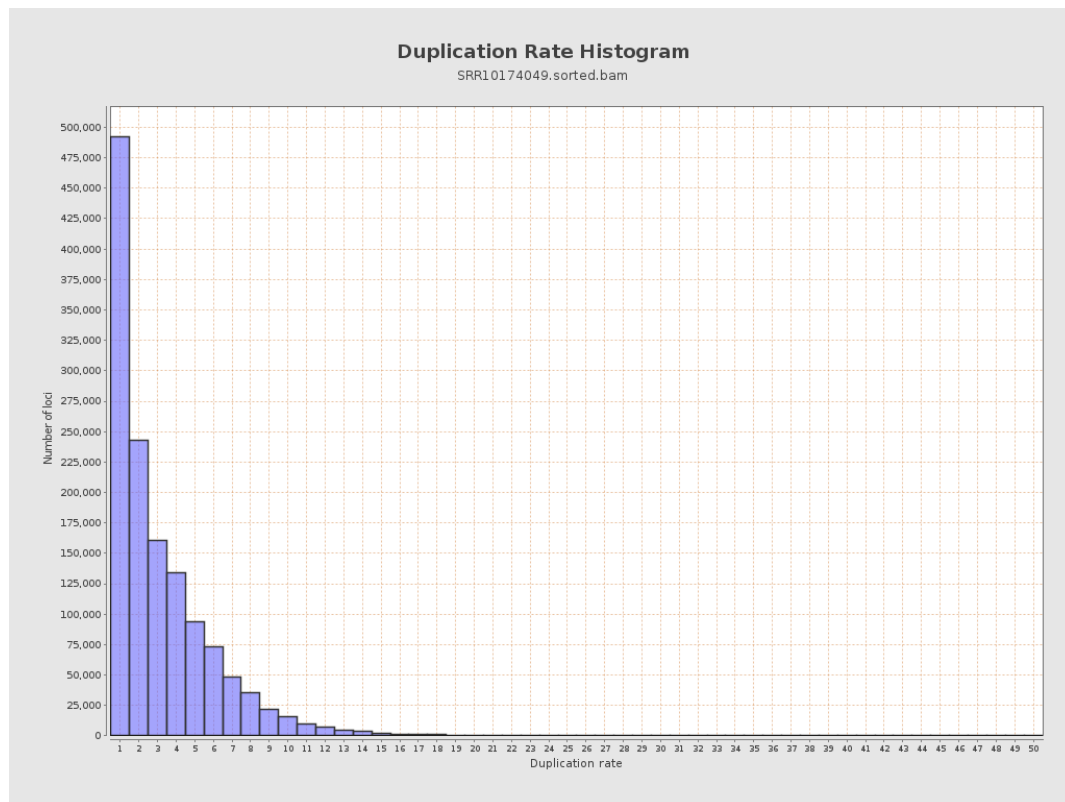
5. Results : Coverage Histogram (0-50X)



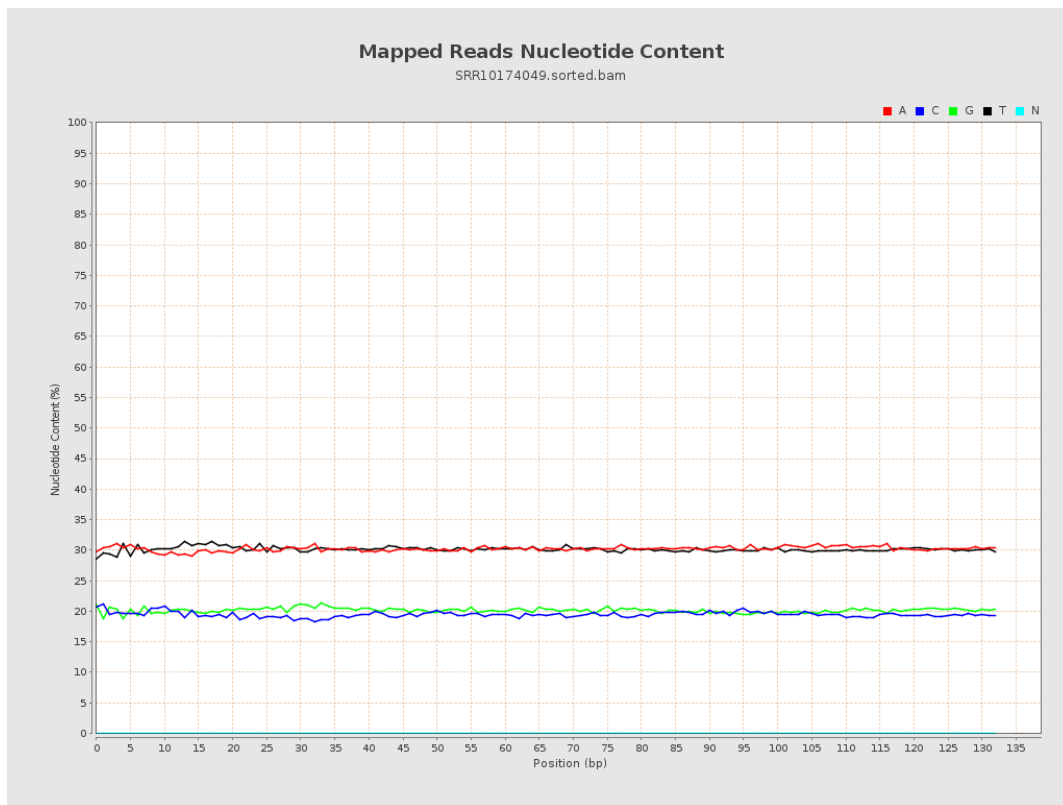
6. Results : Genome Fraction Coverage



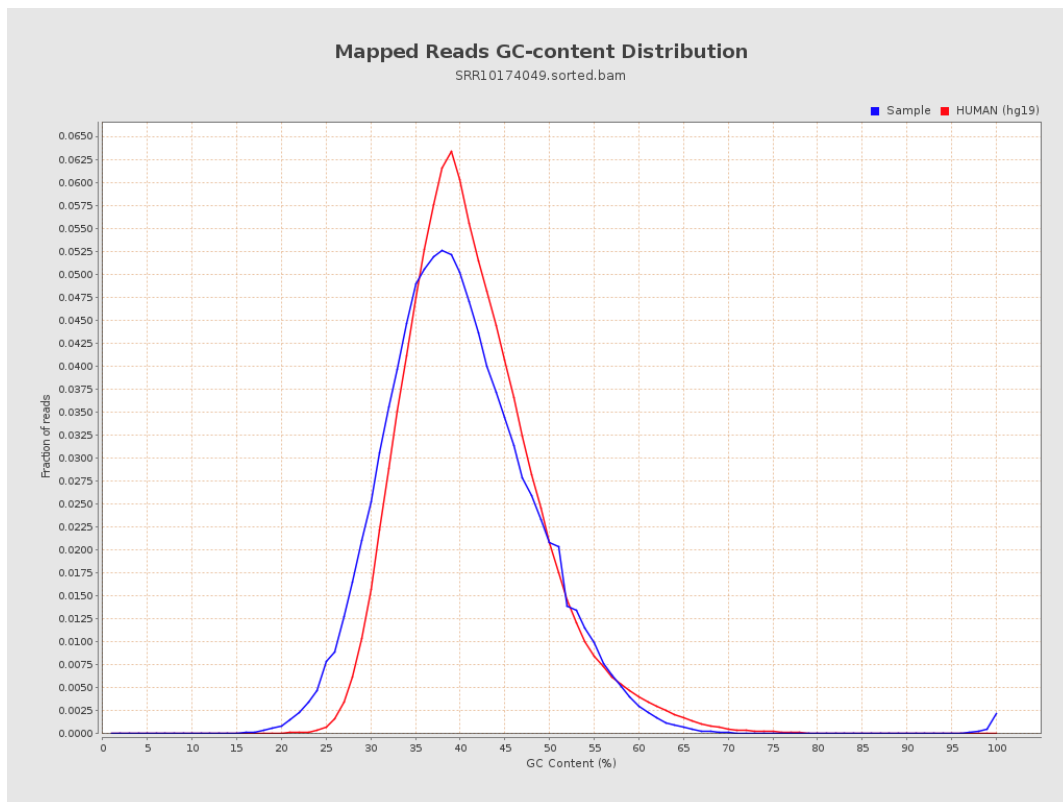
7. Results : Duplication Rate Histogram



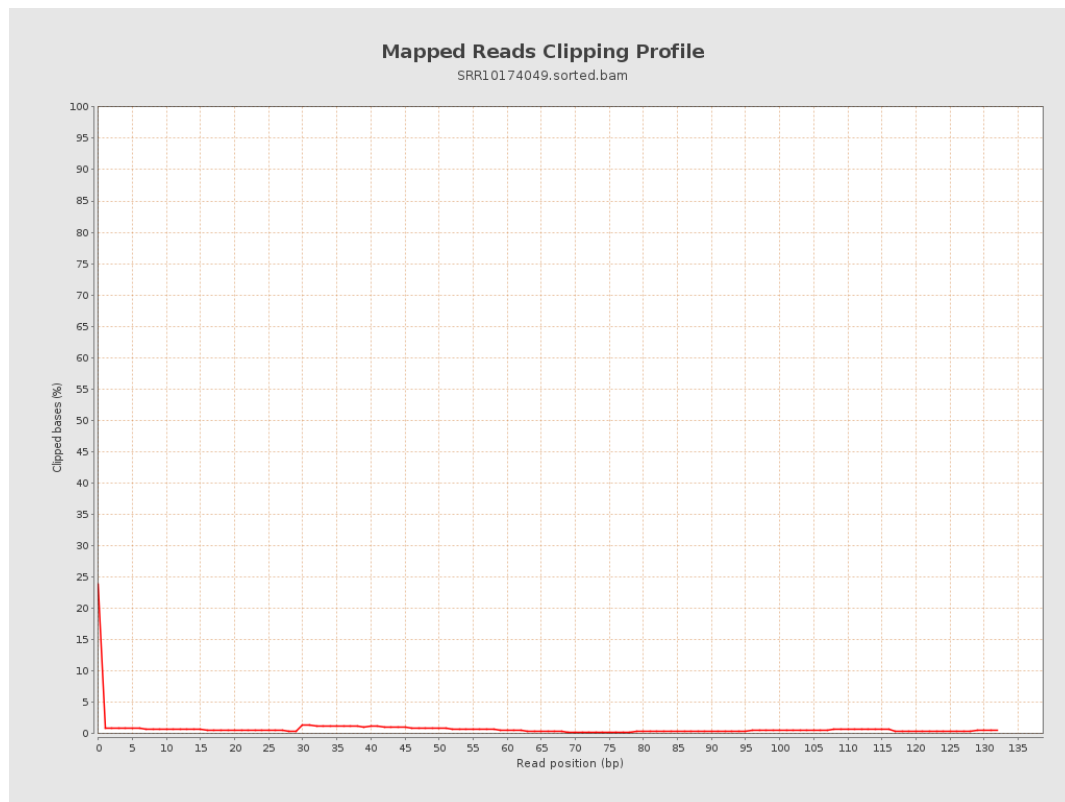
8. Results : Mapped Reads Nucleotide Content



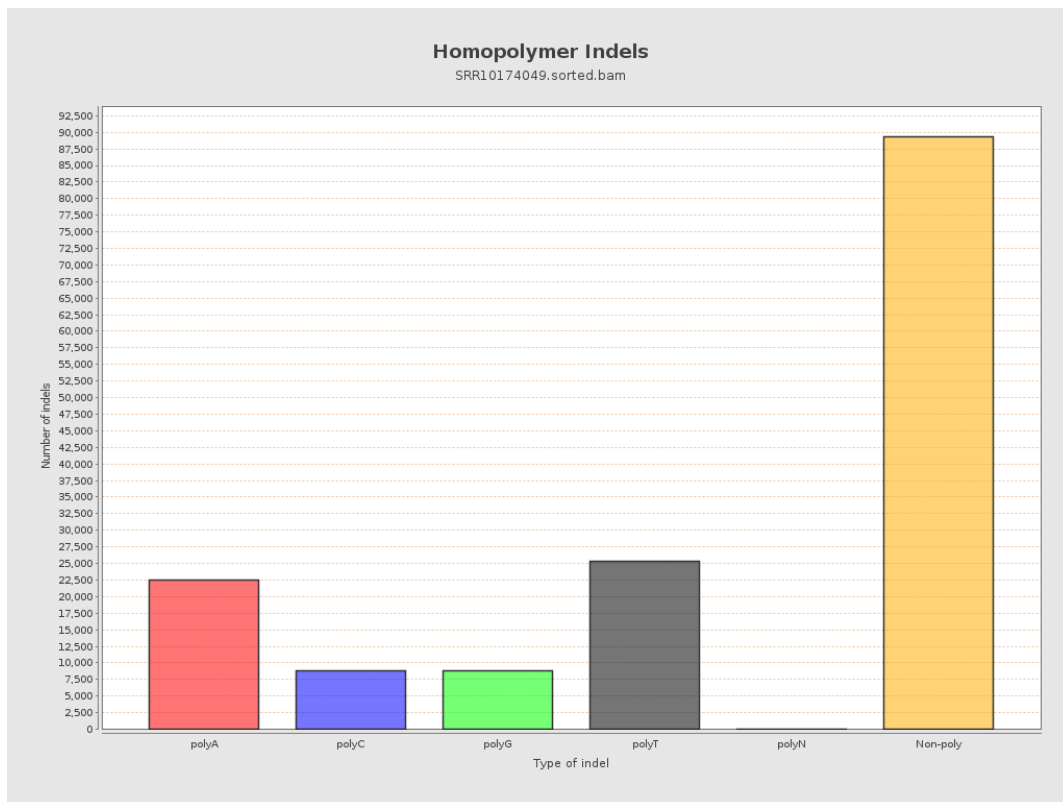
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



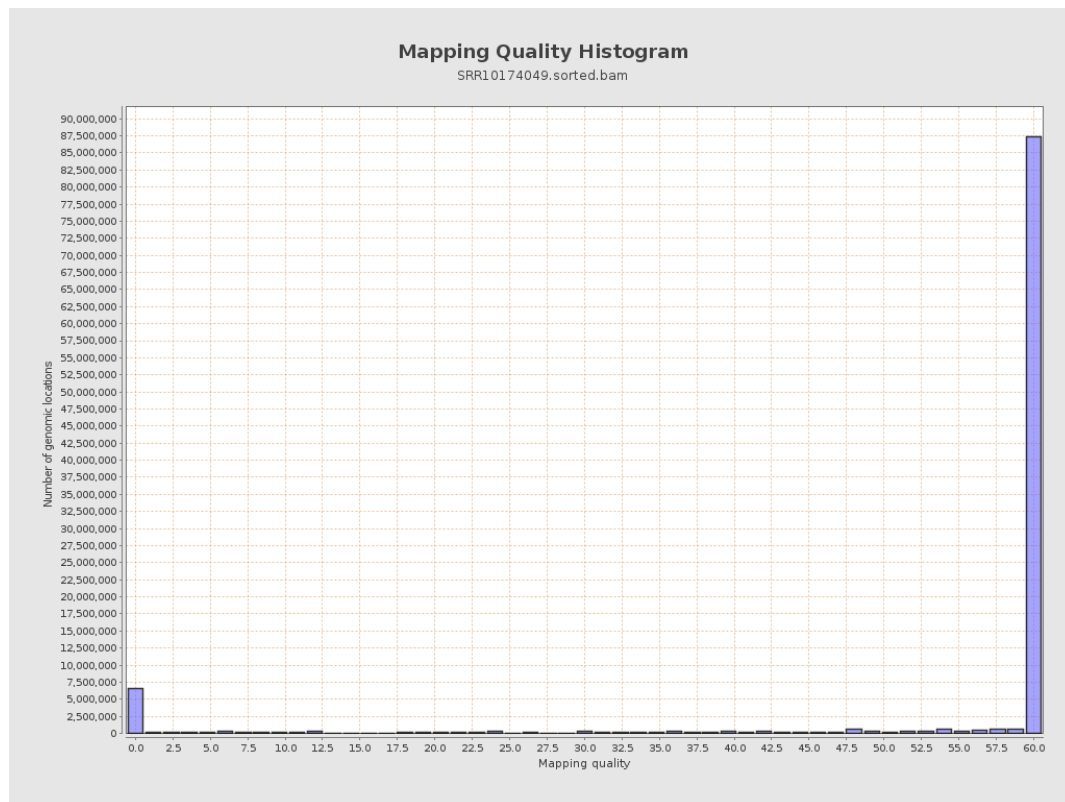
11. Results : Homopolymer Indels



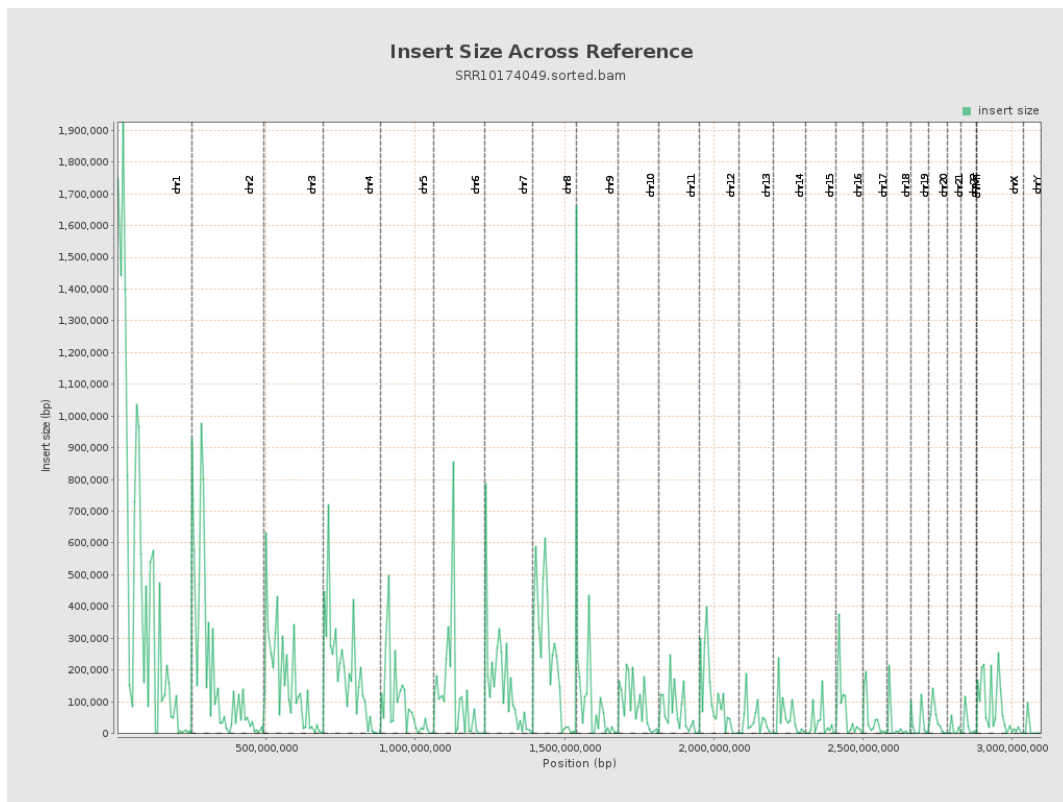
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

