

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 20:42:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174009.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_SRR10174009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174009_1.fastq.gz SRR10174009_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 20:42:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,229,952
Mapped reads	2,181,943 / 97.85%
Unmapped reads	48,009 / 2.15%
Mapped paired reads	2,181,943 / 97.85%
Mapped reads, first in pair	1,089,663 / 48.86%
Mapped reads, second in pair	1,092,280 / 48.98%
Mapped reads, both in pair	2,151,478 / 96.48%
Mapped reads, singletons	30,465 / 1.37%
Secondary alignments	0
Supplementary alignments	206,254 / 9.25%
Read min/max/mean length	30 / 133 / 128.16
Duplicated reads (estimated)	1,727,089 / 77.45%
Duplication rate	65.62%
Clipped reads	778,351 / 34.9%

2.2. ACGT Content

Number/percentage of A's	78,451,290 / 30.11%
Number/percentage of C's	51,231,086 / 19.66%
Number/percentage of T's	78,139,965 / 29.99%
Number/percentage of G's	52,726,937 / 20.24%
Number/percentage of N's	3,462 / 0%

GC Percentage	39.9%
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2.3. Coverage

Mean	0.0842
Standard Deviation	1.3697

2.4. Mapping Quality

Mean Mapping Quality	52.83
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2.5. Insert size

Mean	729,978.24
Standard Deviation	7,816,628.66
P25/Median/P75	151 / 207 / 291

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	2,588,474
Insertions	27,753
Mapped reads with at least one insertion	1.23%
Deletions	50,470
Mapped reads with at least one deletion	2.26%
Homopolymer indels	44.96%

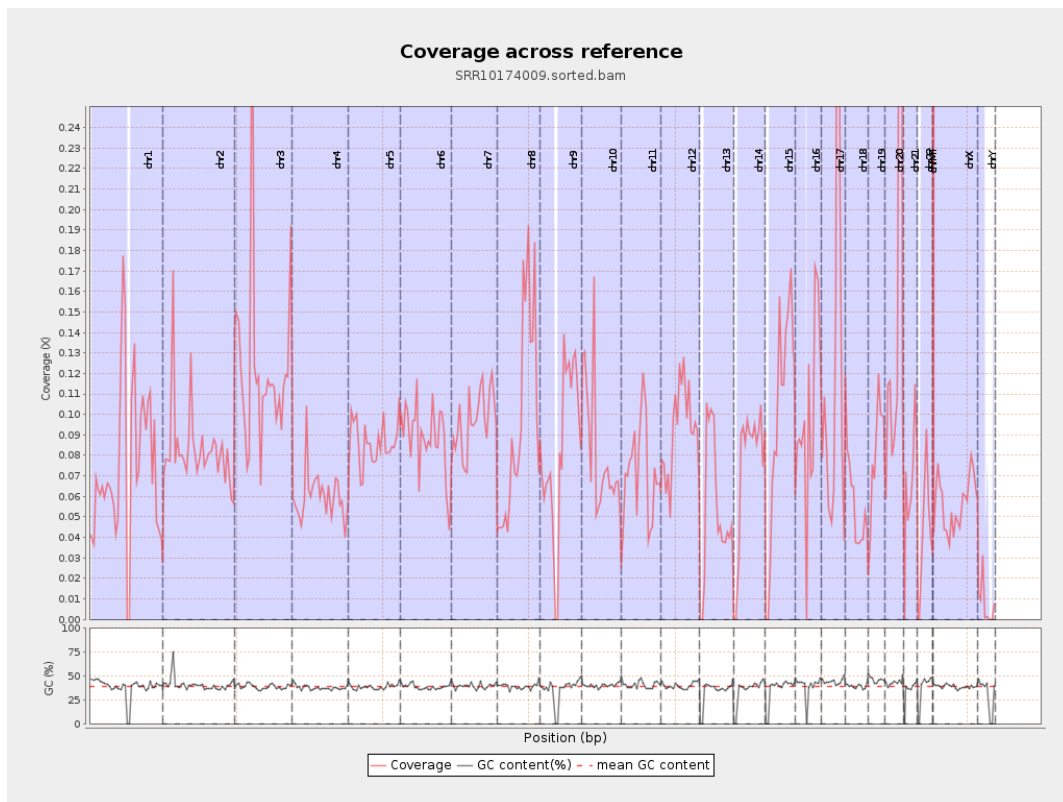
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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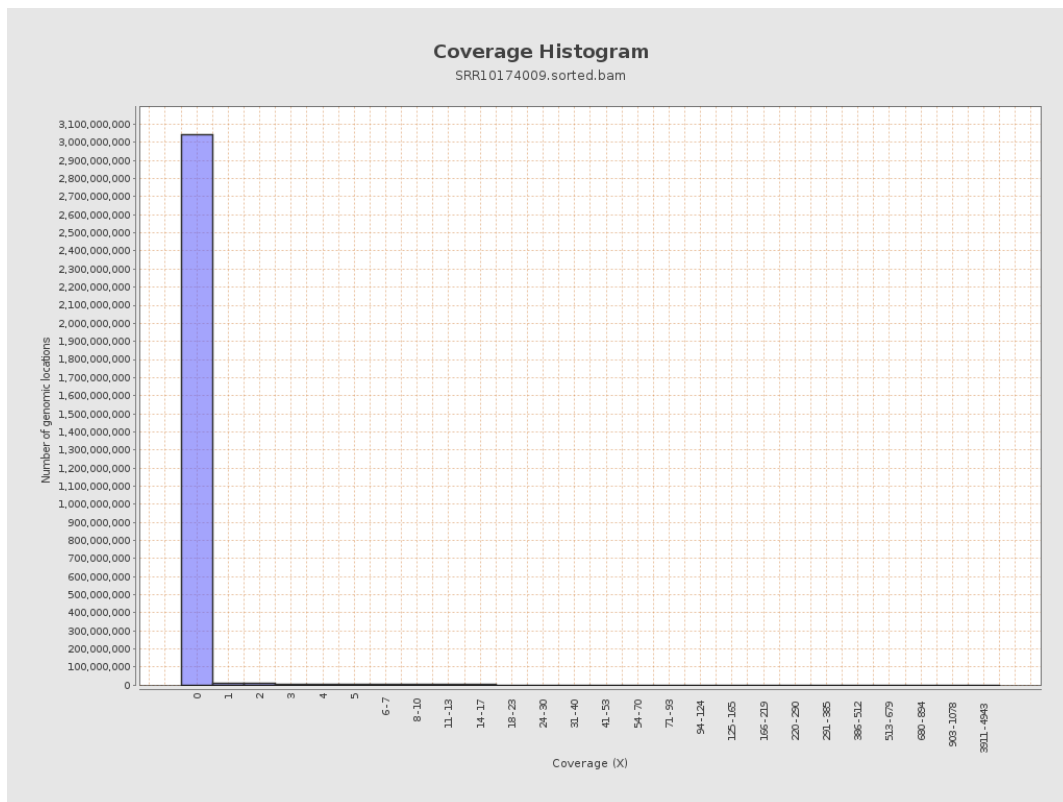
		bases	coverage	deviation
chr1	249250621	18534514	0.0744	1.0066
chr2	243199373	20140321	0.0828	3.5598
chr3	198022430	24110184	0.1218	1.057
chr4	191154276	11518838	0.0603	0.8137
chr5	180915260	15557537	0.086	0.8716
chr6	171115067	15145634	0.0885	0.9601
chr7	159138663	15397657	0.0968	1.0977
chr8	146364022	14151591	0.0967	1.086
chr9	141213431	11715525	0.083	0.9727
chr10	135534747	10971692	0.081	1.2509
chr11	135006516	9622057	0.0713	0.7944
chr12	133851895	12453398	0.093	0.9101
chr13	115169878	6099072	0.053	0.6934
chr14	107349540	8061428	0.0751	0.8169
chr15	102531392	9913578	0.0967	0.9208
chr16	90354753	8773091	0.0971	1.0418
chr17	81195210	11745971	0.1447	1.1766
chr18	78077248	4460336	0.0571	1.0718
chr19	59128983	4807824	0.0813	0.9452
chr20	63025520	11793647	0.1871	1.3339
chr21	48129895	3240623	0.0673	0.7802
chr22	51304566	2225331	0.0434	0.5925
chrMT	16571	956250	57.7062	57.4995
chrX	155270560	8829186	0.0569	0.7114

chrY	59373566	457313	0.0077	0.3516
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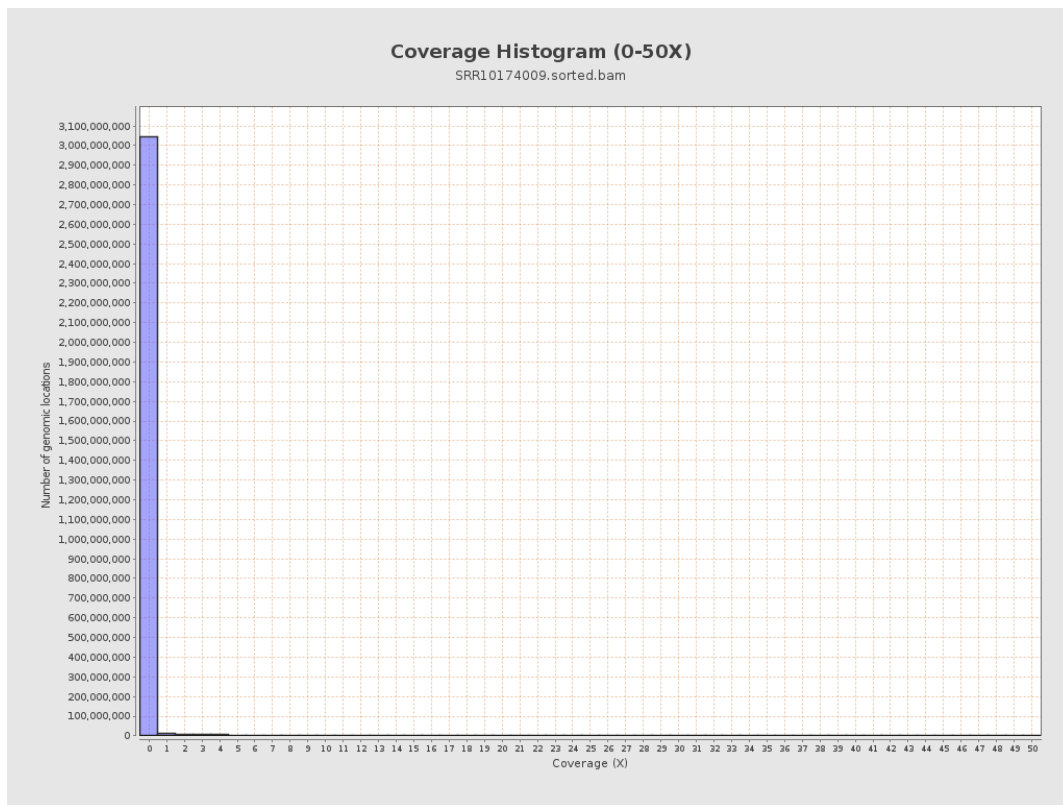
3. Results : Coverage across reference



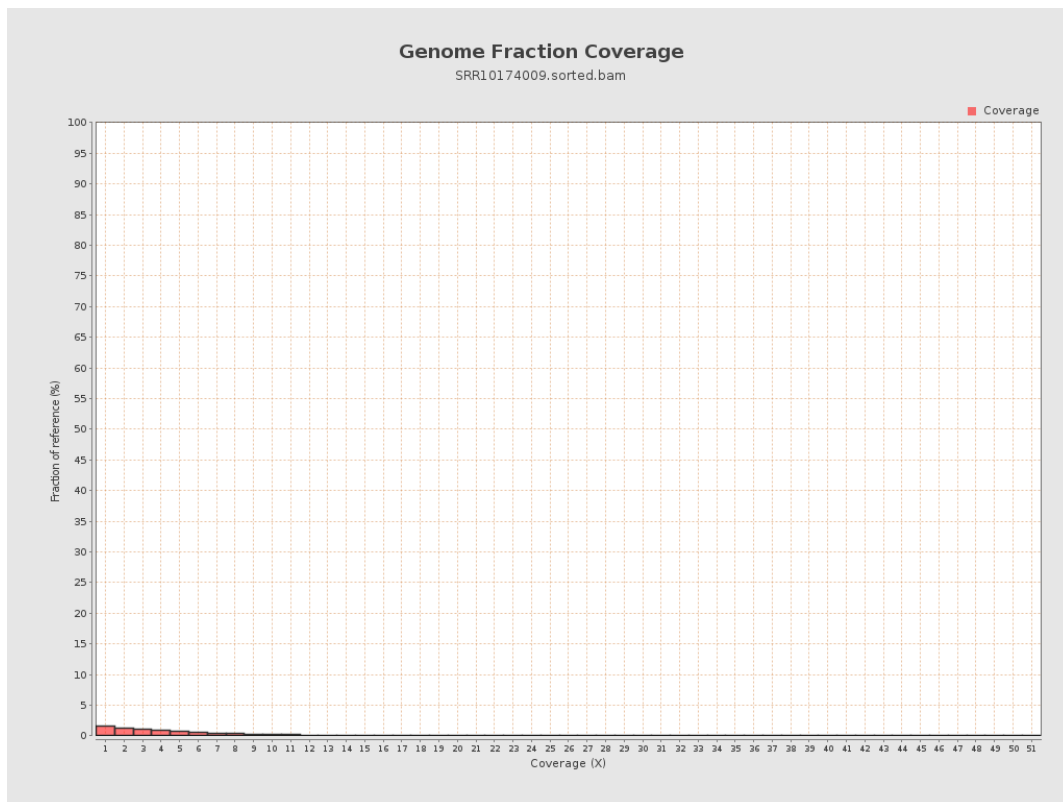
4. Results : Coverage Histogram



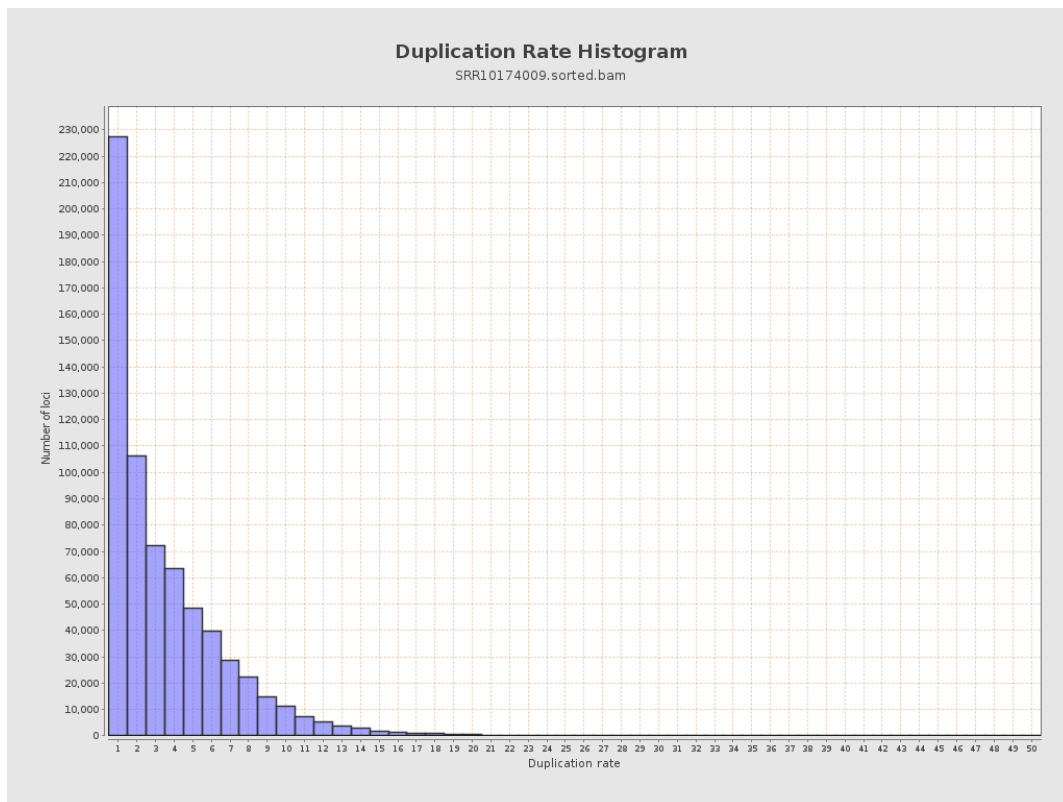
5. Results : Coverage Histogram (0-50X)



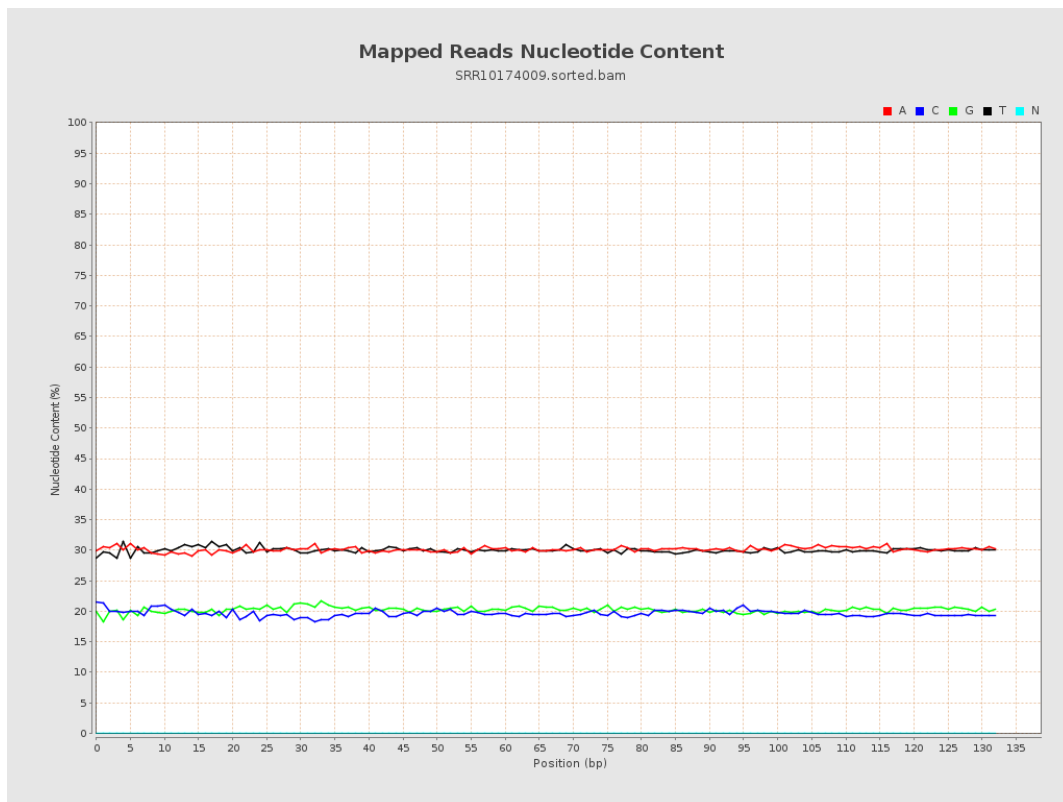
6. Results : Genome Fraction Coverage



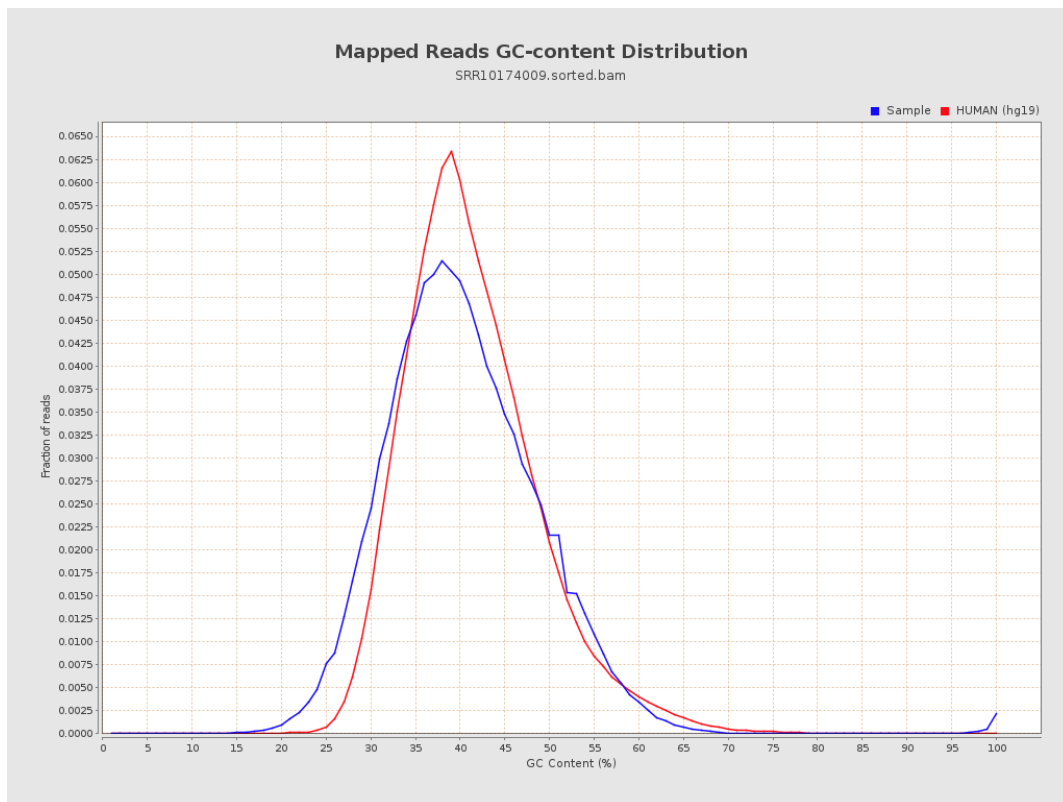
7. Results : Duplication Rate Histogram



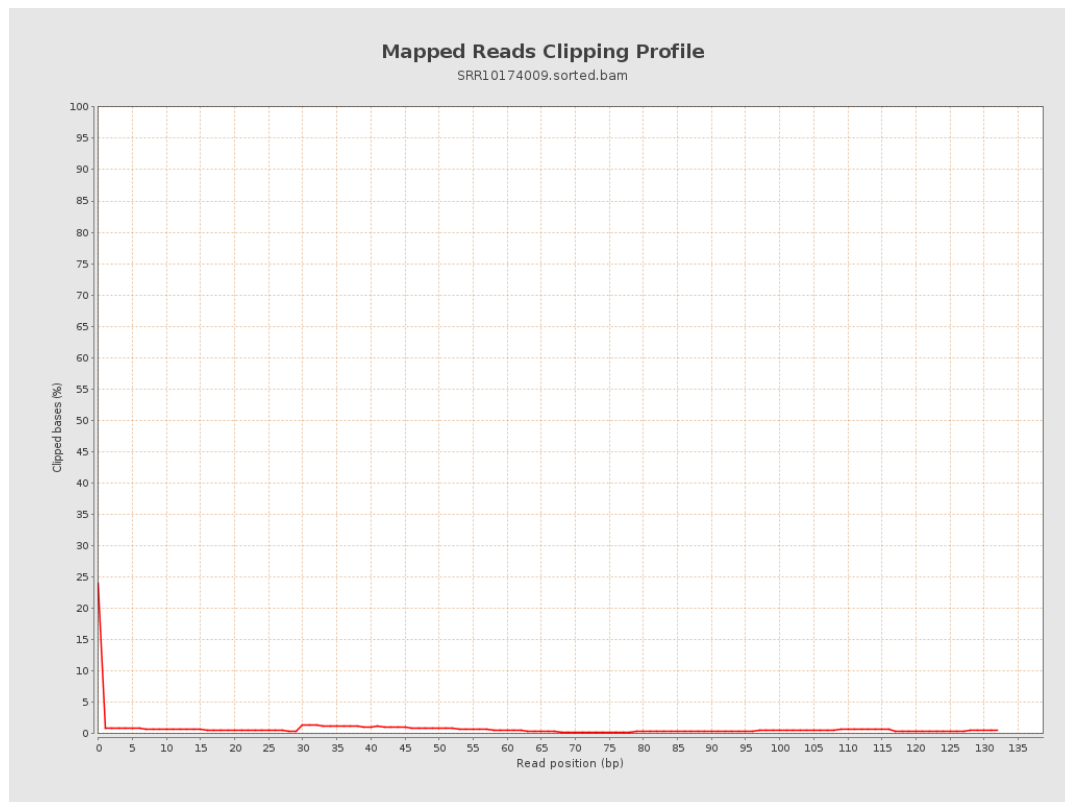
8. Results : Mapped Reads Nucleotide Content



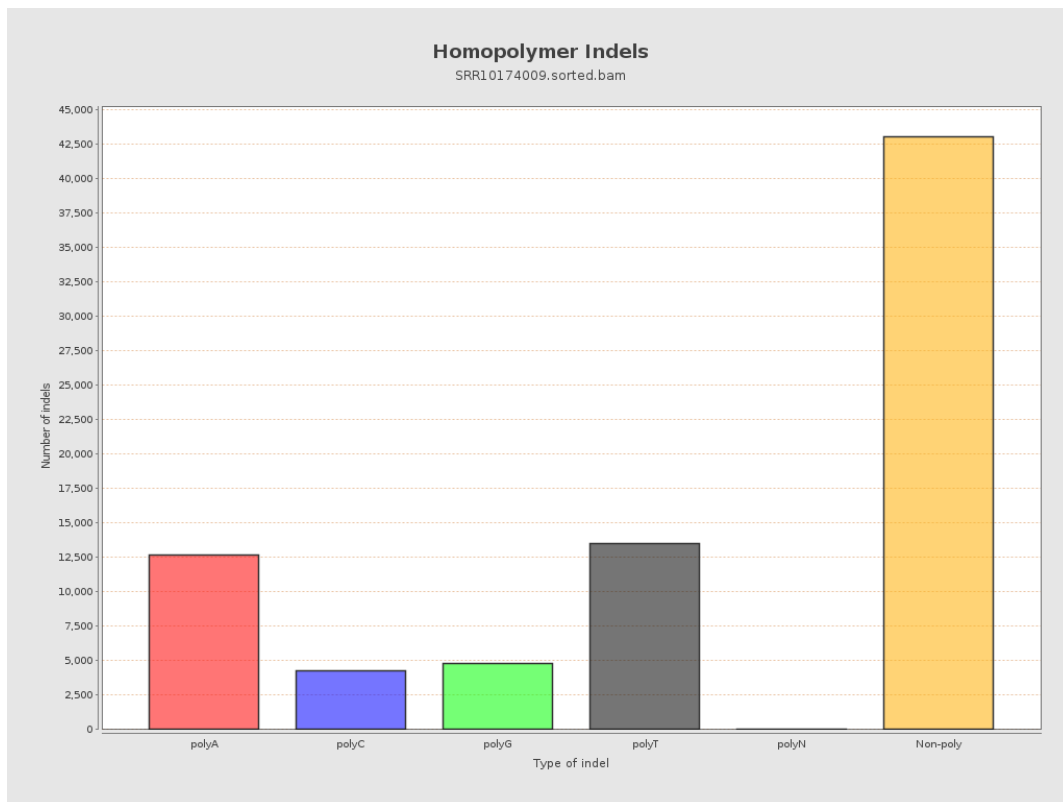
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



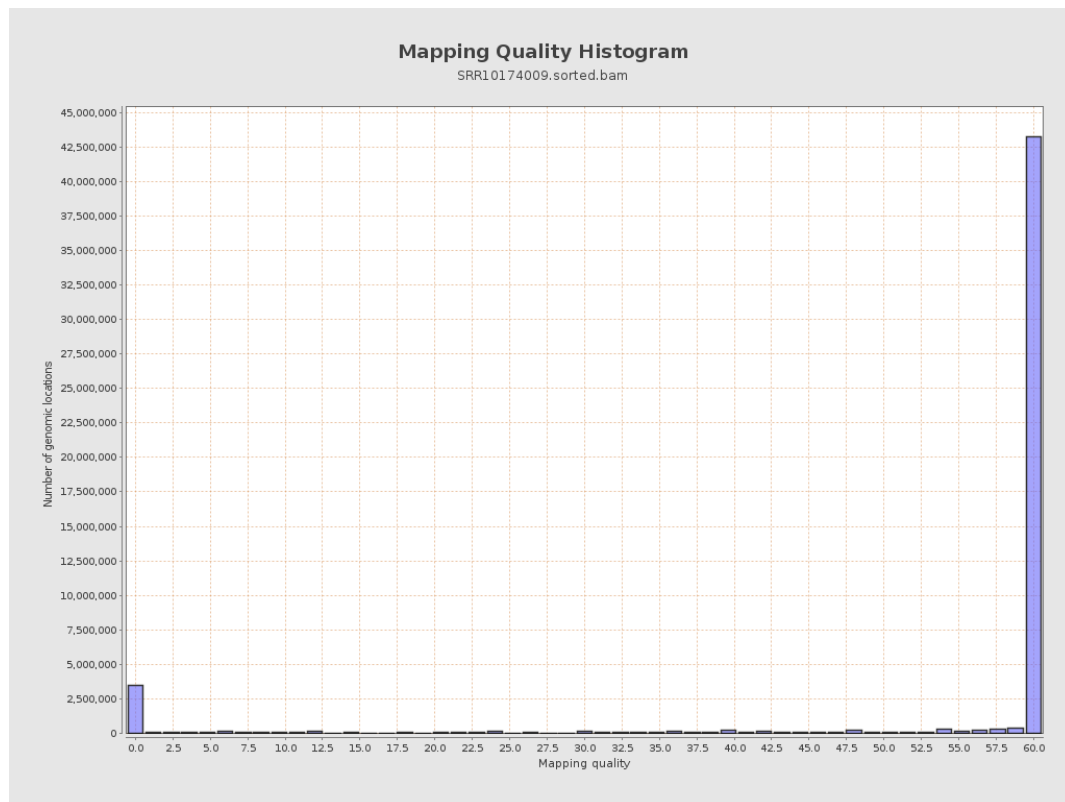
11. Results : Homopolymer Indels



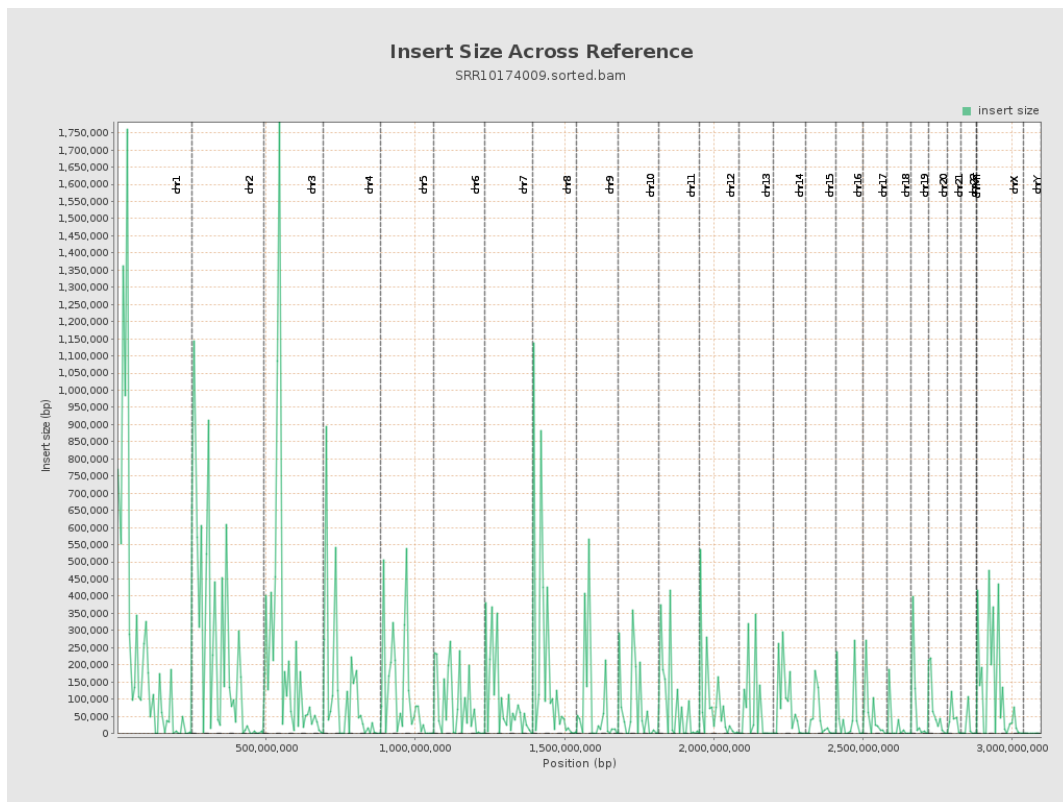
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

