

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174051.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_SRR10174051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174051_1.fastq.gz SRR10174051_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:34:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,790,574
Mapped reads	1,747,286 / 97.58%
Unmapped reads	43,288 / 2.42%
Mapped paired reads	1,747,286 / 97.58%
Mapped reads, first in pair	873,111 / 48.76%
Mapped reads, second in pair	874,175 / 48.82%
Mapped reads, both in pair	1,718,202 / 95.96%
Mapped reads, singletons	29,084 / 1.62%
Secondary alignments	0
Supplementary alignments	194,362 / 10.85%
Read min/max/mean length	30 / 133 / 128.72
Duplicated reads (estimated)	1,328,209 / 74.18%
Duplication rate	62.7%
Clipped reads	739,851 / 41.32%

2.2. ACGT Content

Number/percentage of A's	62,011,820 / 29.98%
Number/percentage of C's	40,826,009 / 19.73%
Number/percentage of T's	61,771,017 / 29.86%
Number/percentage of G's	42,265,871 / 20.43%
Number/percentage of N's	2,648 / 0%

GC Percentage	40.16%
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2.3. Coverage

Mean	0.0669
Standard Deviation	1.1272

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	1,178,673.21
Standard Deviation	9,772,142.76
P25/Median/P75	143 / 199 / 280

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	2,078,597
Insertions	20,872
Mapped reads with at least one insertion	1.16%
Deletions	47,692
Mapped reads with at least one deletion	2.66%
Homopolymer indels	42.48%

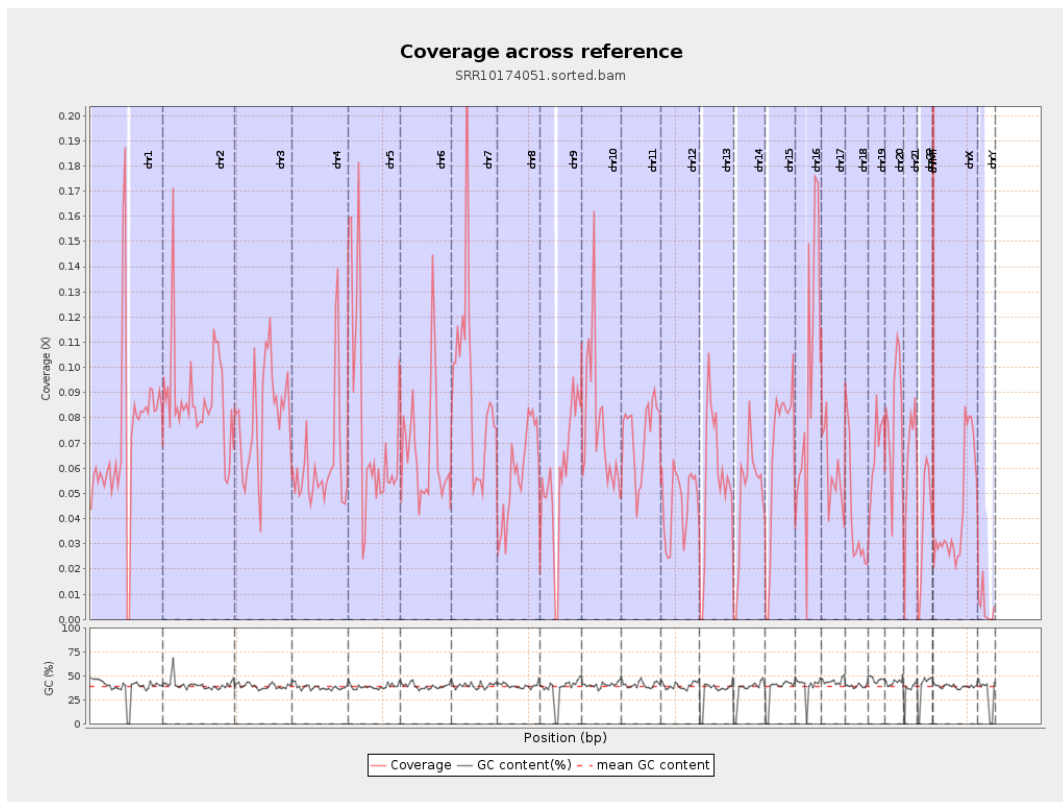
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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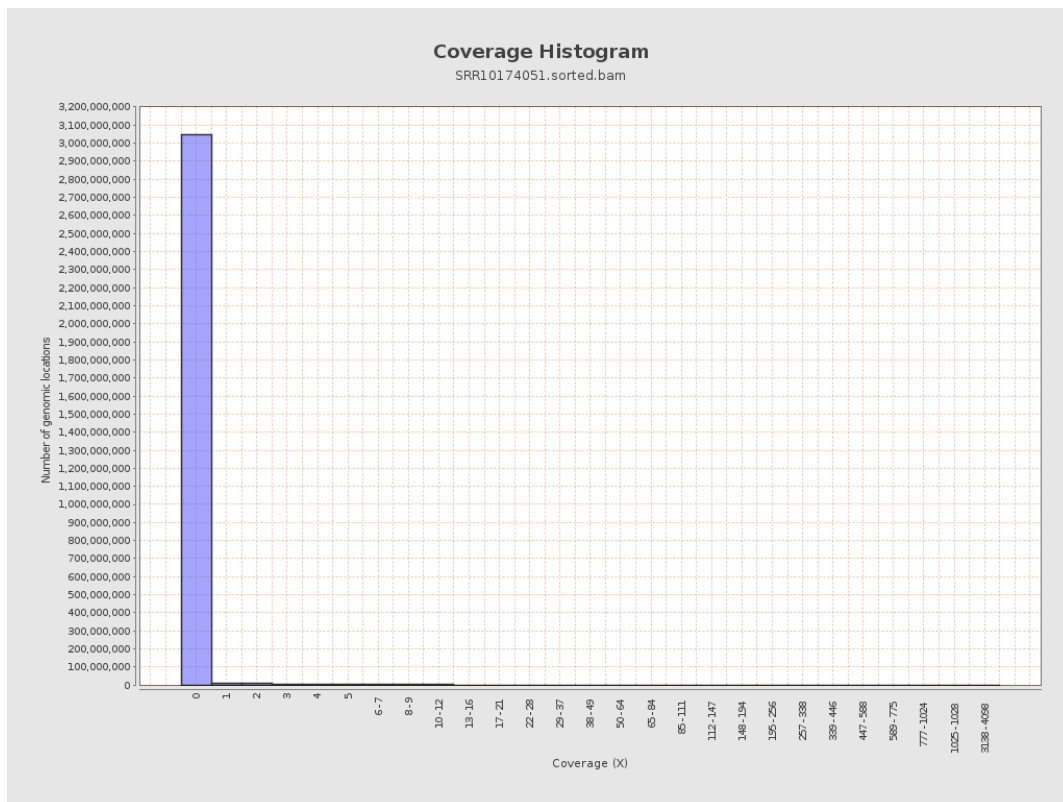
		bases	coverage	deviation
chr1	249250621	18012858	0.0723	1.0349
chr2	243199373	21337808	0.0877	2.9465
chr3	198022430	15885241	0.0802	0.7913
chr4	191154276	11779109	0.0616	0.726
chr5	180915260	14134260	0.0781	0.7775
chr6	171115067	11401212	0.0666	0.7216
chr7	159138663	14590173	0.0917	0.9977
chr8	146364022	8524972	0.0582	0.7236
chr9	141213431	8364936	0.0592	0.7301
chr10	135534747	10321276	0.0762	1.0435
chr11	135006516	9908076	0.0734	0.7458
chr12	133851895	6249736	0.0467	0.5918
chr13	115169878	6478809	0.0563	0.6661
chr14	107349540	5293073	0.0493	0.6133
chr15	102531392	6811766	0.0664	0.7029
chr16	90354753	8240215	0.0912	0.9328
chr17	81195210	4764195	0.0587	0.6786
chr18	78077248	3186196	0.0408	0.8485
chr19	59128983	3913897	0.0662	0.9235
chr20	63025520	5115117	0.0812	0.777
chr21	48129895	2994220	0.0622	0.6951
chr22	51304566	1993406	0.0389	0.522
chrMT	16571	740622	44.6939	37.7922
chrX	155270560	6669924	0.043	0.5701

chrY	59373566	278102	0.0047	0.2498
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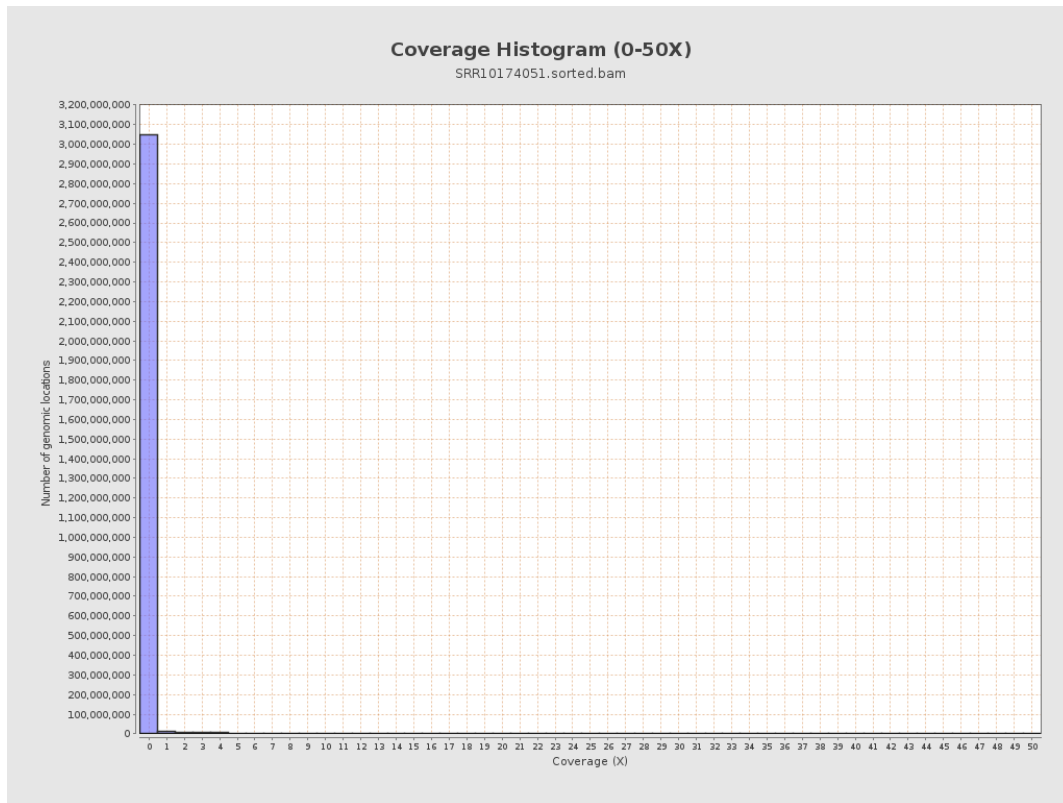
3. Results : Coverage across reference



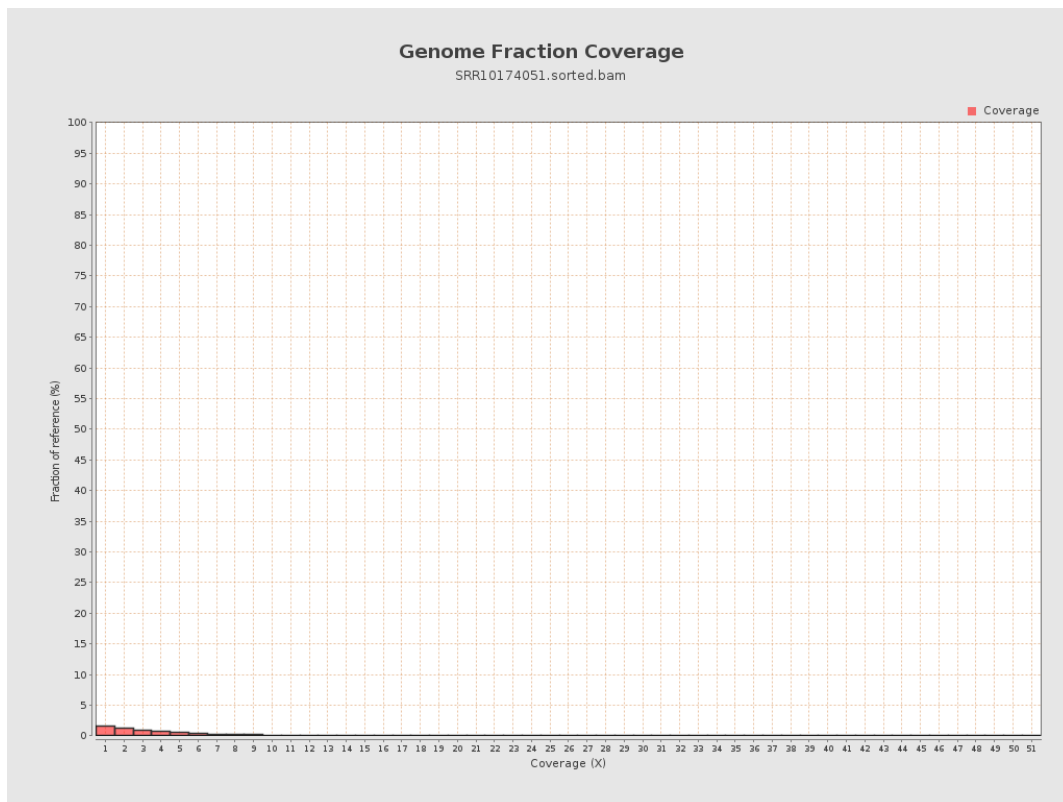
4. Results : Coverage Histogram



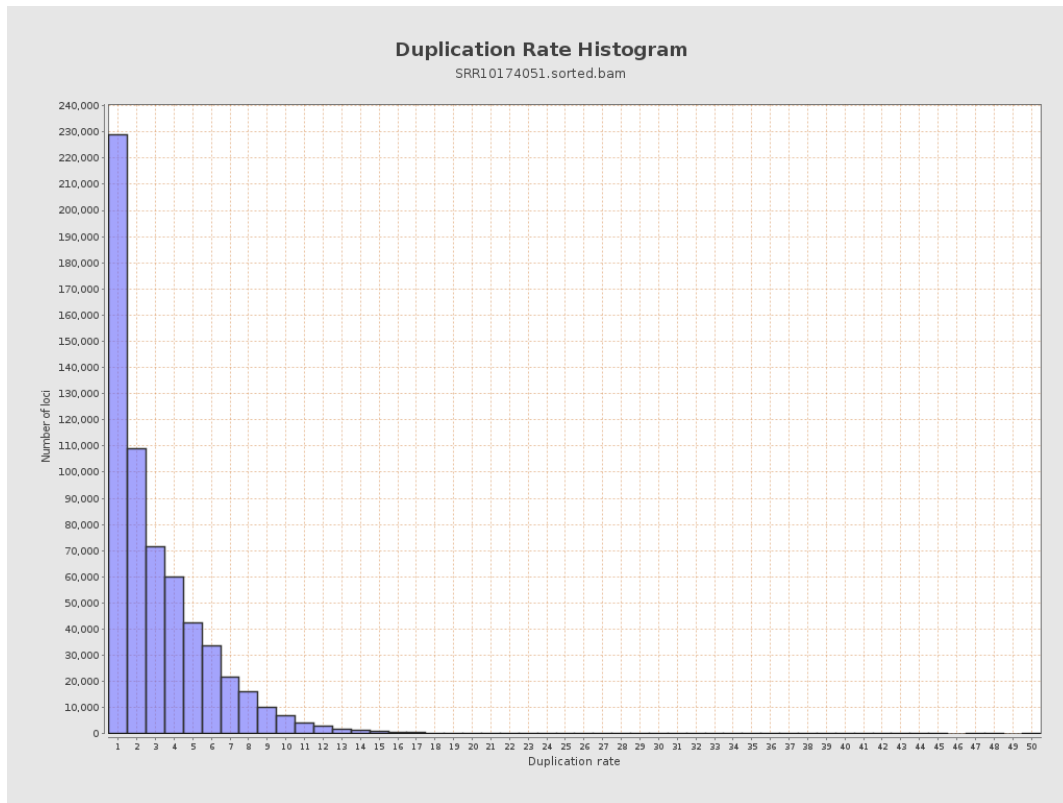
5. Results : Coverage Histogram (0-50X)



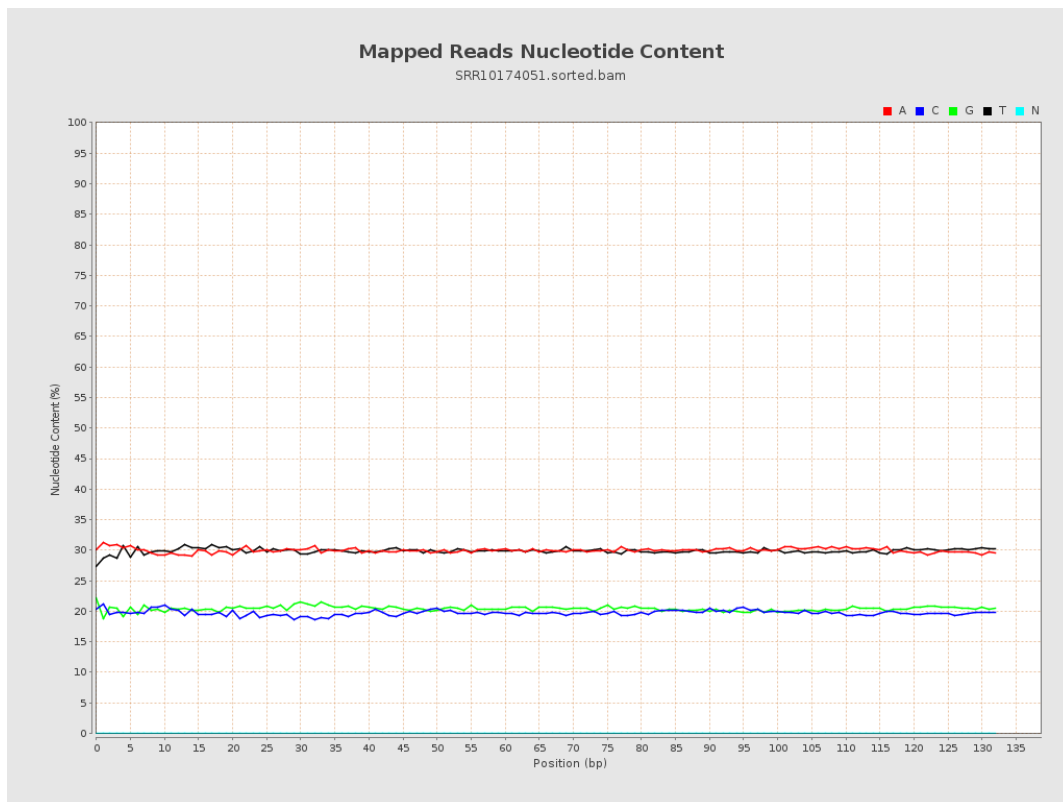
6. Results : Genome Fraction Coverage



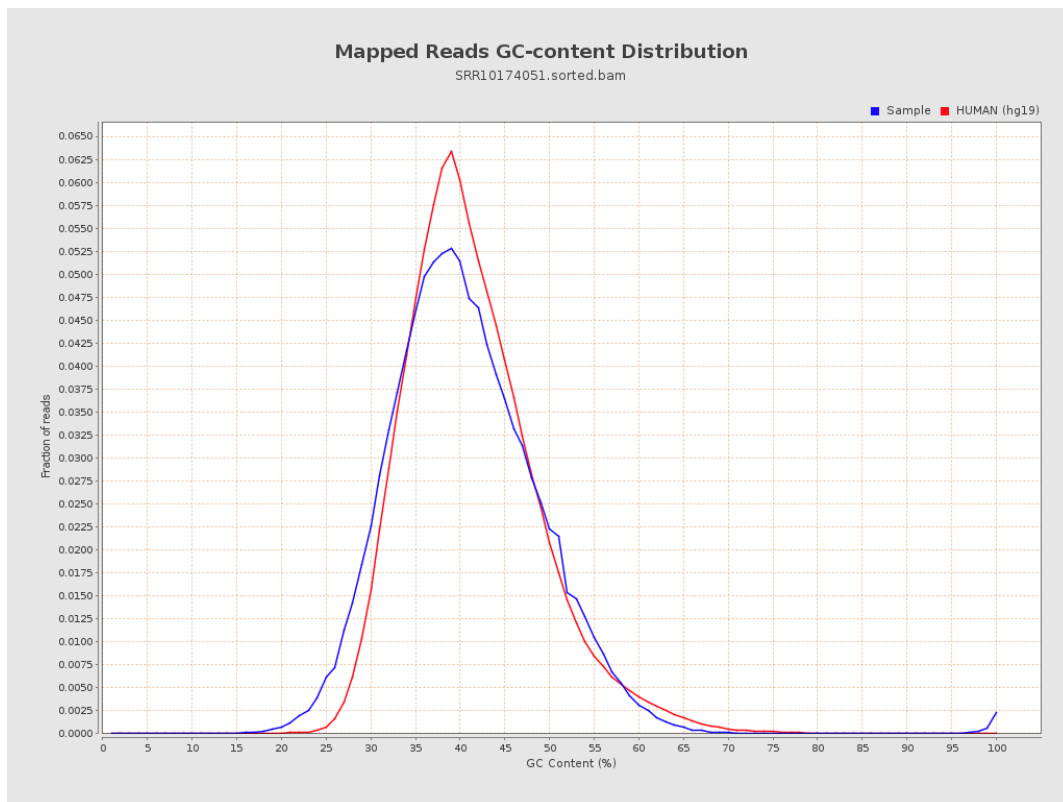
7. Results : Duplication Rate Histogram



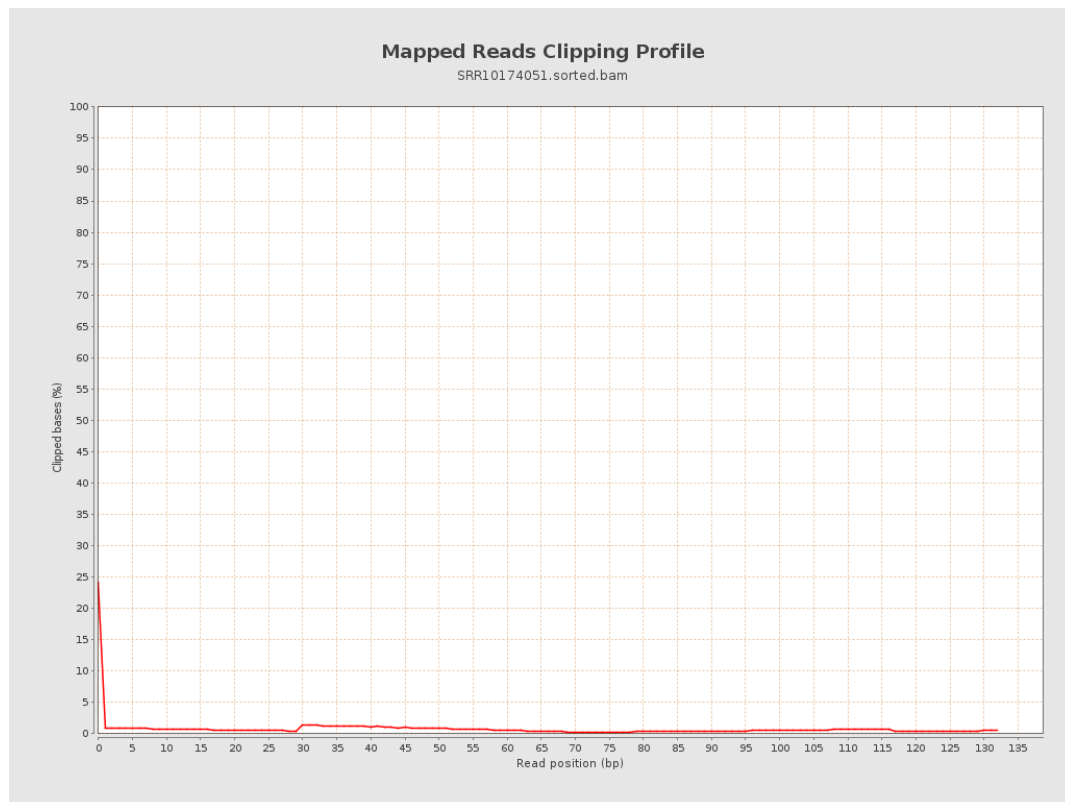
8. Results : Mapped Reads Nucleotide Content



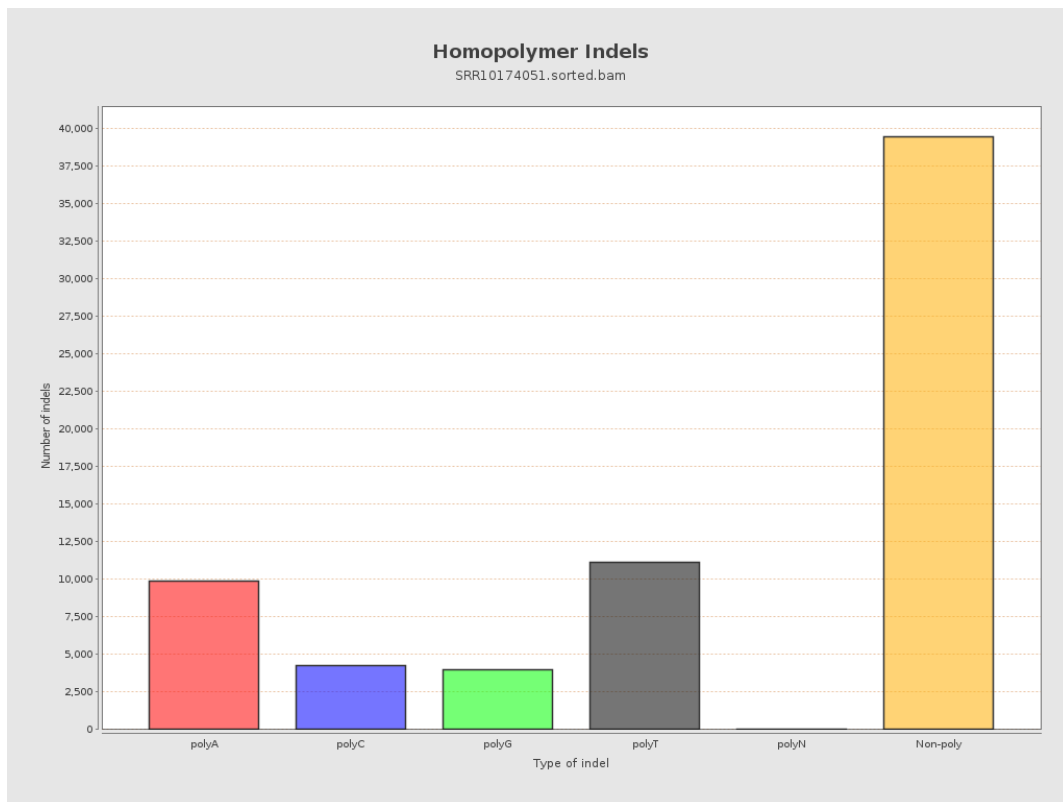
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



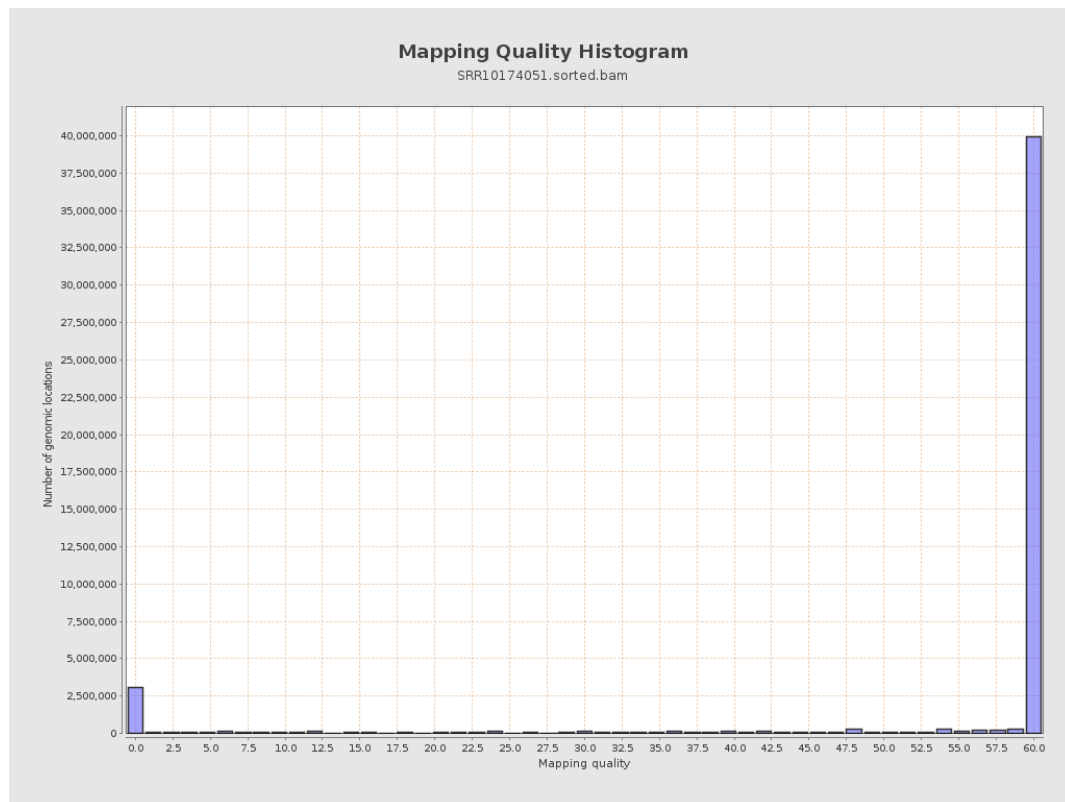
11. Results : Homopolymer Indels



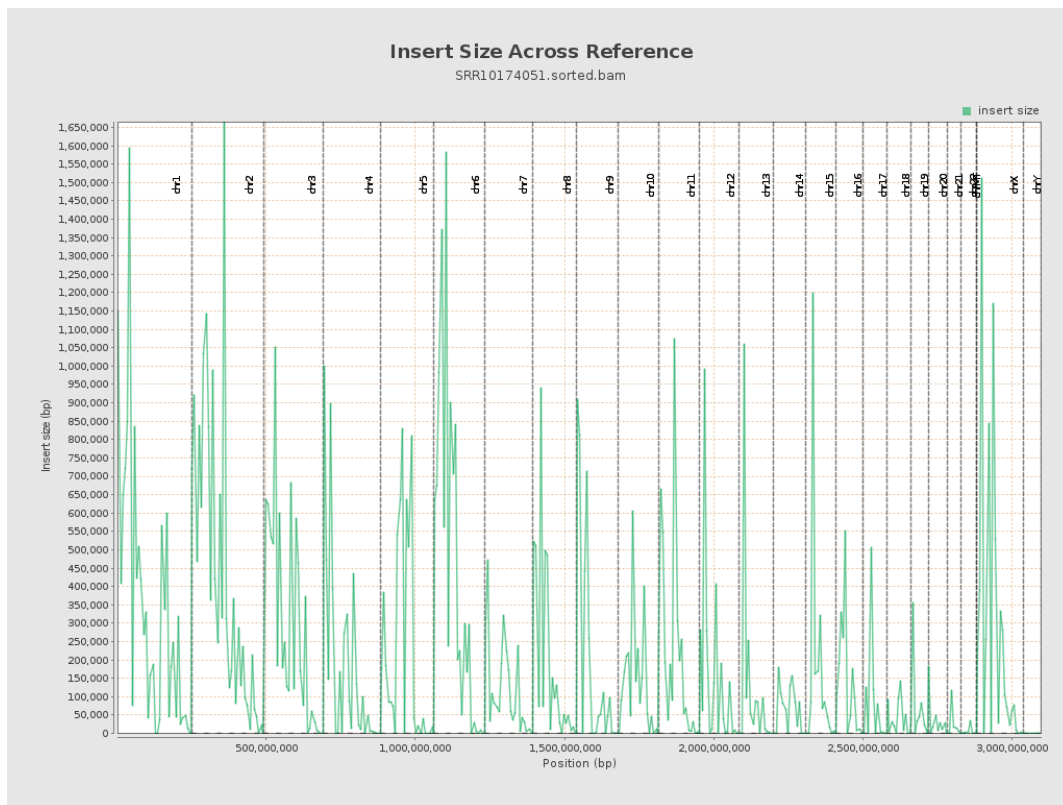
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

