

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:06:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251061.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_SRR10251061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251061_1.fastq.gz SRR10251061_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:06:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,635,576
Mapped reads	1,552,591 / 94.93%
Unmapped reads	82,985 / 5.07%
Mapped paired reads	1,552,591 / 94.93%
Mapped reads, first in pair	778,312 / 47.59%
Mapped reads, second in pair	774,279 / 47.34%
Mapped reads, both in pair	1,545,042 / 94.46%
Mapped reads, singletons	7,549 / 0.46%
Secondary alignments	0
Supplementary alignments	42,516 / 2.6%
Read min/max/mean length	30 / 127 / 128.18
Duplicated reads (estimated)	261,079 / 15.96%
Duplication rate	15.24%
Clipped reads	367,247 / 22.45%

2.2. ACGT Content

Number/percentage of A's	56,029,281 / 29.33%
Number/percentage of C's	38,848,670 / 20.34%
Number/percentage of T's	56,131,733 / 29.38%
Number/percentage of G's	40,013,279 / 20.95%
Number/percentage of N's	5,727 / 0%

GC Percentage	41.28%
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2.3. Coverage

Mean	0.0618
Standard Deviation	0.6849

2.4. Mapping Quality

Mean Mapping Quality	53.23
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2.5. Insert size

Mean	87,236.73
Standard Deviation	2,787,250.31
P25/Median/P75	150 / 192 / 257

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	1,334,964
Insertions	32,128
Mapped reads with at least one insertion	1.94%
Deletions	76,800
Mapped reads with at least one deletion	4.75%
Homopolymer indels	44.16%

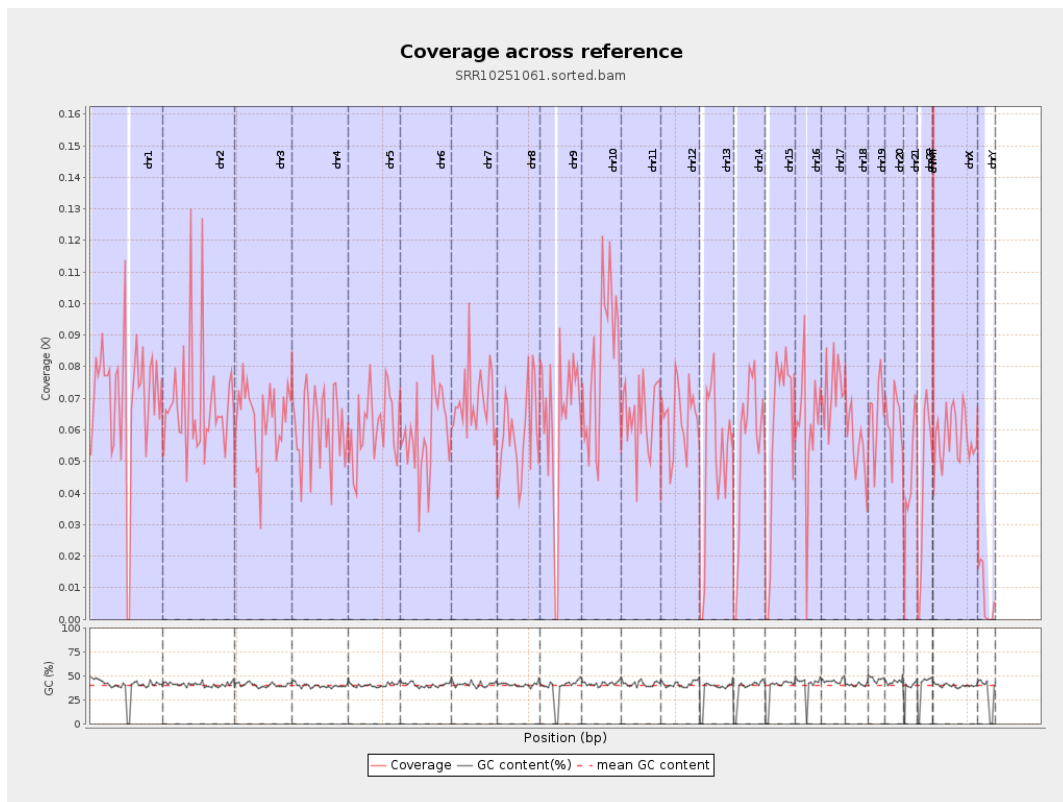
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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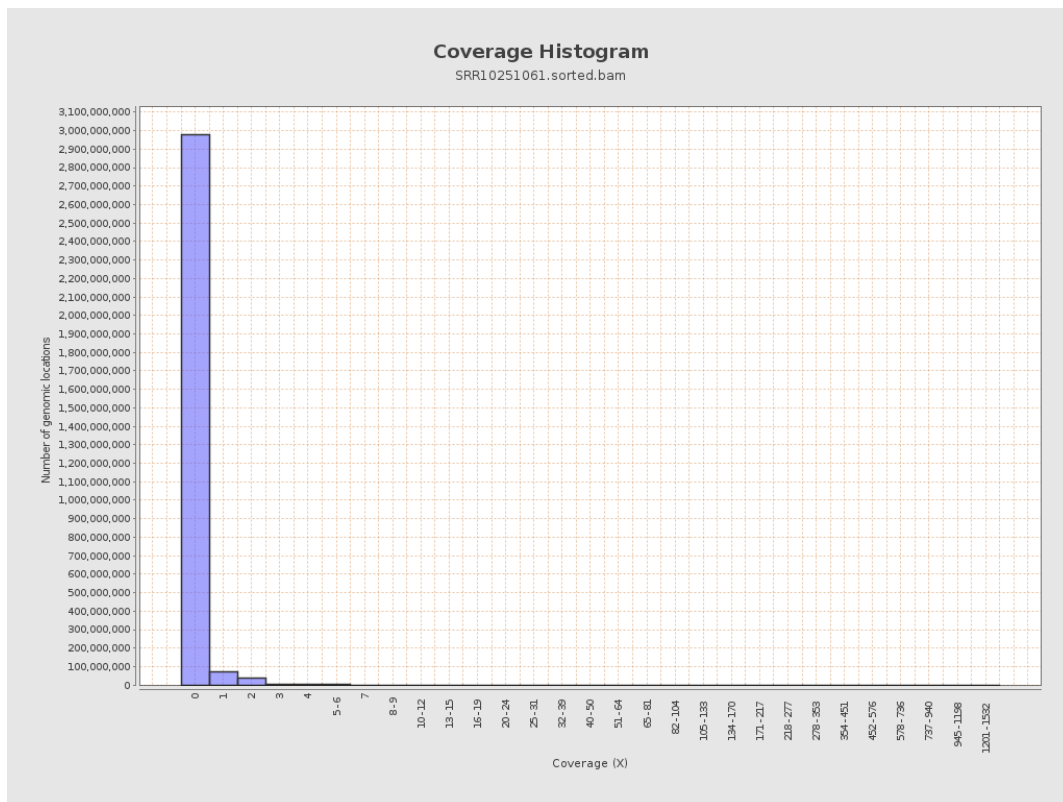
		bases	coverage	deviation
chr1	249250621	17370128	0.0697	1.3256
chr2	243199373	16581446	0.0682	1.056
chr3	198022430	12628855	0.0638	0.37
chr4	191154276	11628478	0.0608	0.442
chr5	180915260	11116154	0.0614	0.3755
chr6	171115067	9986078	0.0584	0.3874
chr7	159138663	10984886	0.069	0.9841
chr8	146364022	8566860	0.0585	0.4175
chr9	141213431	8919141	0.0632	0.8519
chr10	135534747	11062968	0.0816	0.7674
chr11	135006516	8702690	0.0645	0.456
chr12	133851895	8645741	0.0646	0.3825
chr13	115169878	5684913	0.0494	0.3242
chr14	107349540	5928883	0.0552	0.3581
chr15	102531392	5907641	0.0576	0.3537
chr16	90354753	5482578	0.0607	0.6756
chr17	81195210	5935048	0.0731	0.4806
chr18	78077248	4368295	0.0559	0.6499
chr19	59128983	3847531	0.0651	0.6659
chr20	63025520	3927958	0.0623	0.3794
chr21	48129895	2176308	0.0452	0.3342
chr22	51304566	2262461	0.0441	0.3183
chrMT	16571	90921	5.4868	4.2311
chrX	155270560	8956431	0.0577	0.3654

chrY	59373566	429807	0.0072	0.5534
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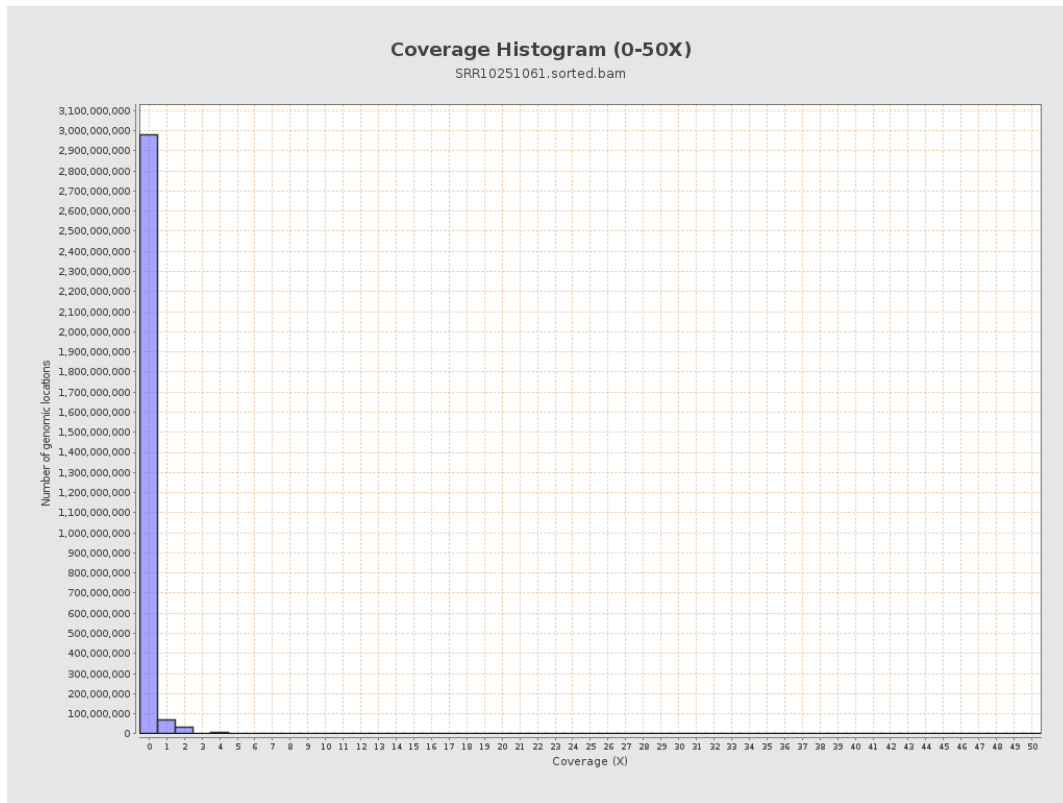
3. Results : Coverage across reference



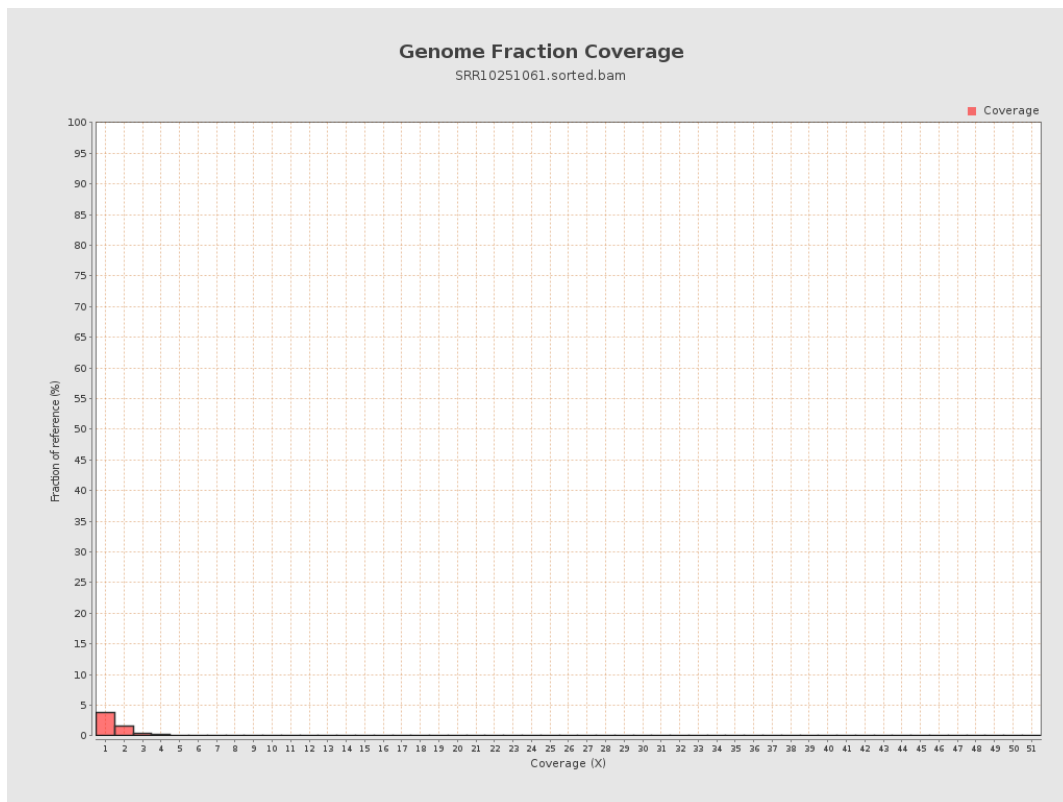
4. Results : Coverage Histogram



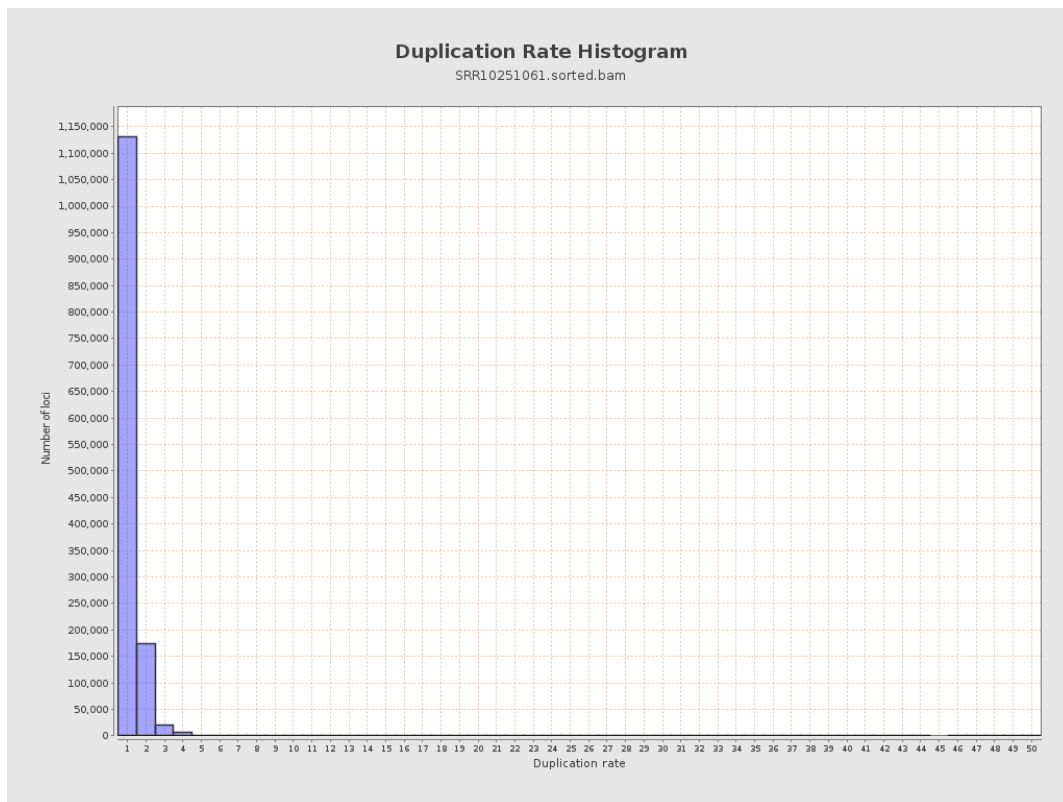
5. Results : Coverage Histogram (0-50X)



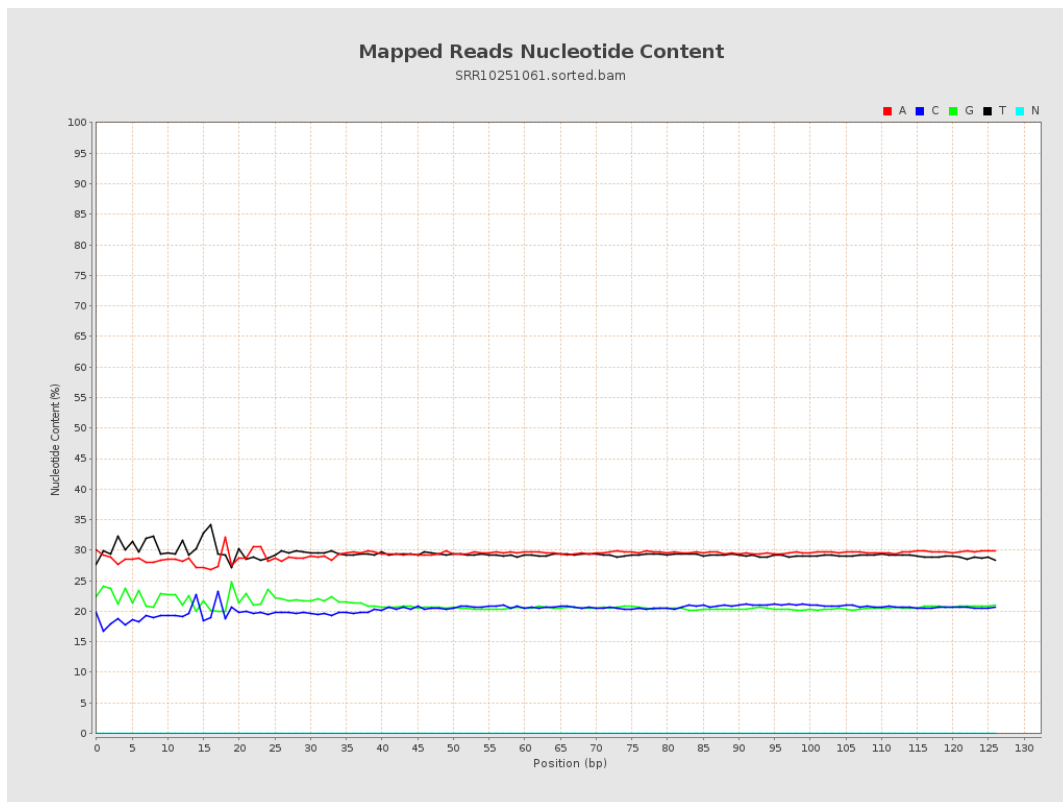
6. Results : Genome Fraction Coverage



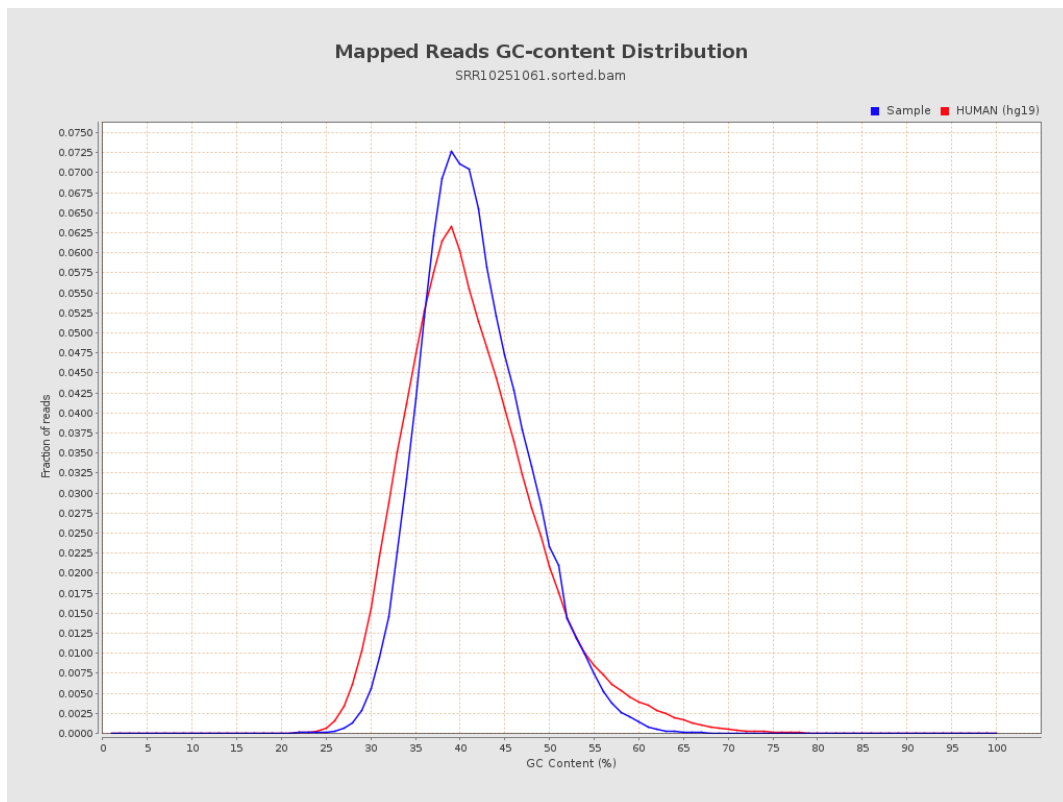
7. Results : Duplication Rate Histogram



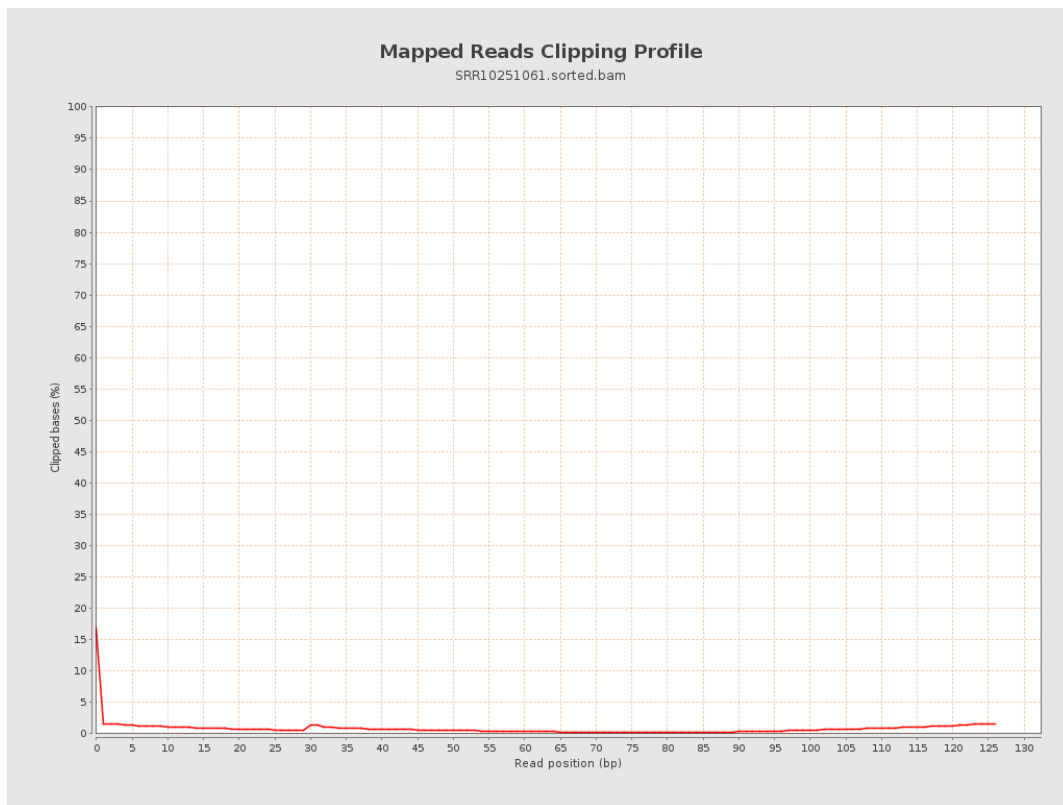
8. Results : Mapped Reads Nucleotide Content



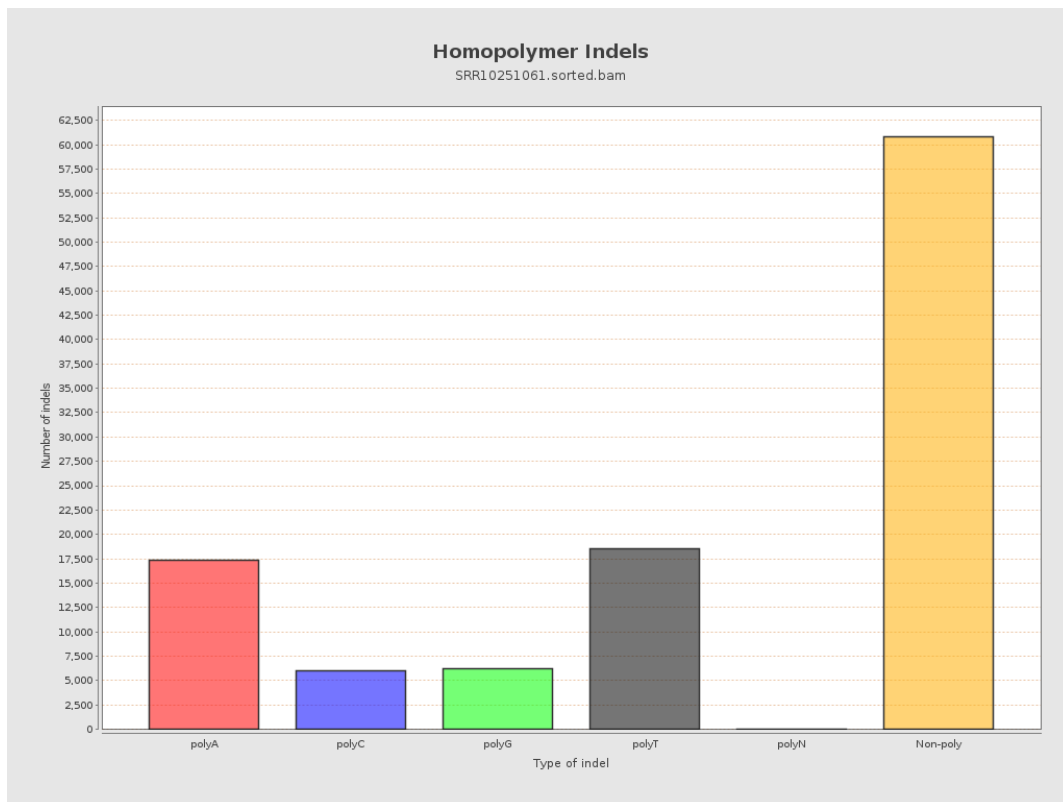
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



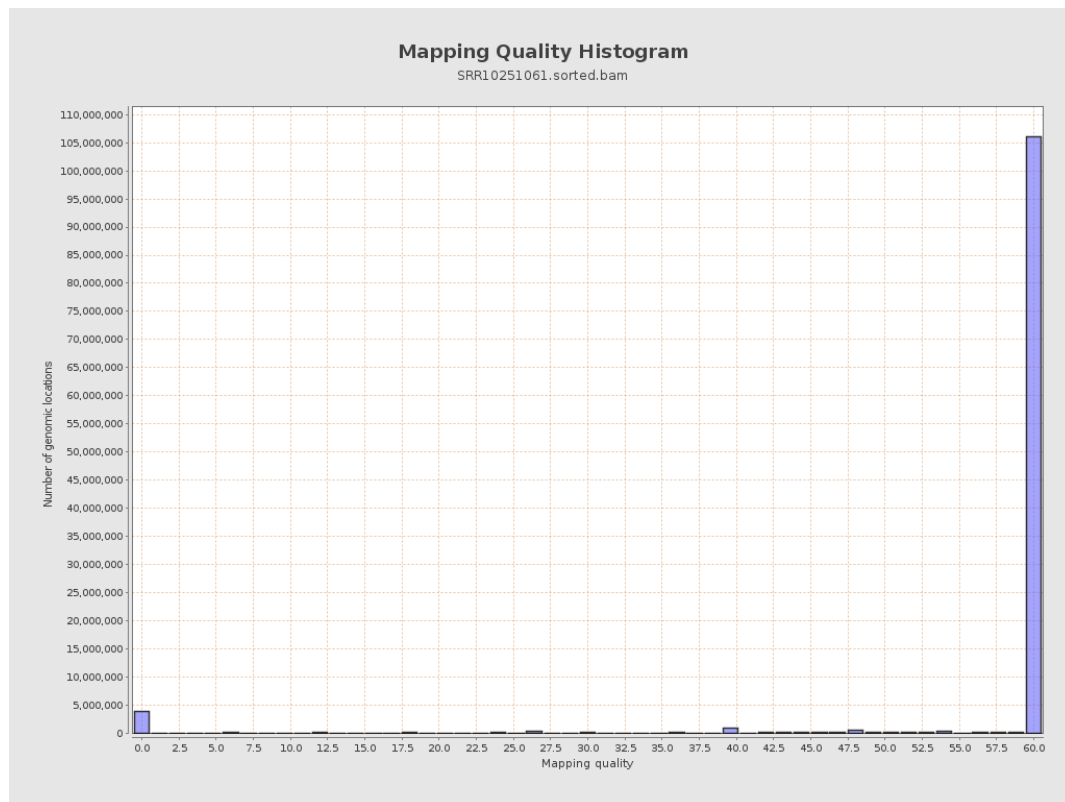
11. Results : Homopolymer Indels



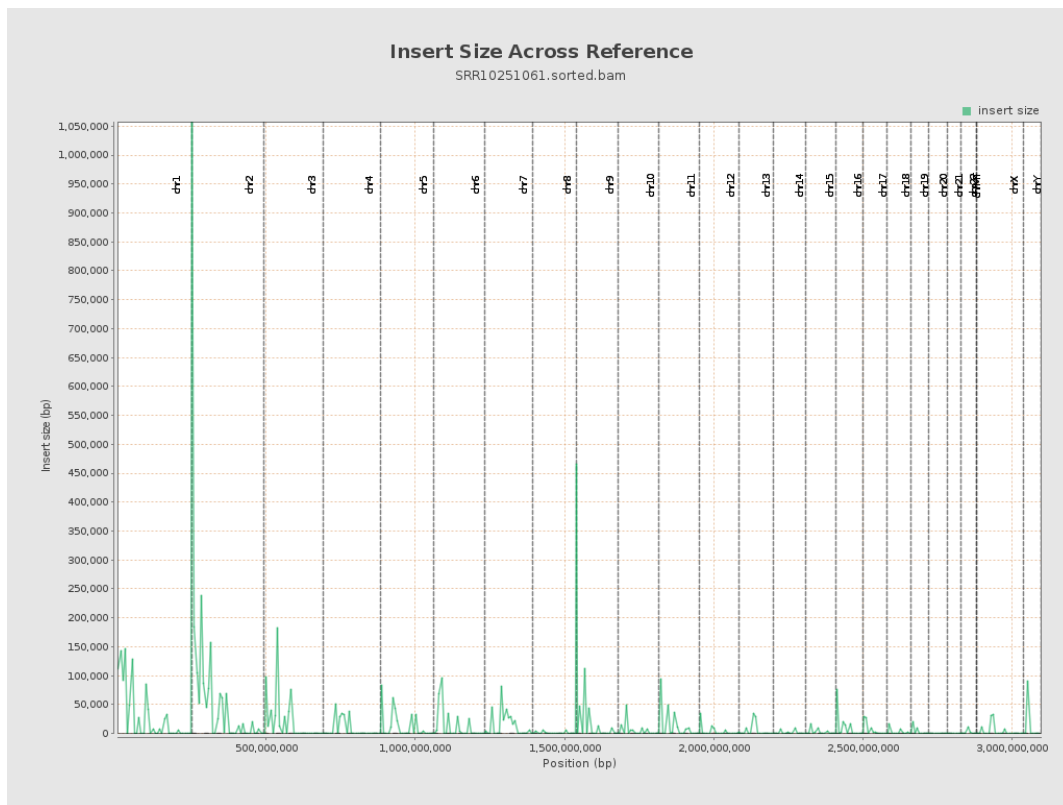
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

