

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:02:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251060.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_SRR10251060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251060_1.fastq.gz SRR10251060_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:02:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,598,292
Mapped reads	1,517,717 / 94.96%
Unmapped reads	80,575 / 5.04%
Mapped paired reads	1,517,717 / 94.96%
Mapped reads, first in pair	760,789 / 47.6%
Mapped reads, second in pair	756,928 / 47.36%
Mapped reads, both in pair	1,510,540 / 94.51%
Mapped reads, singletons	7,177 / 0.45%
Secondary alignments	0
Supplementary alignments	41,616 / 2.6%
Read min/max/mean length	30 / 127 / 128.18
Duplicated reads (estimated)	252,640 / 15.81%
Duplication rate	15.08%
Clipped reads	359,364 / 22.48%

2.2. ACGT Content

Number/percentage of A's	54,775,319 / 29.33%
Number/percentage of C's	37,945,601 / 20.32%
Number/percentage of T's	54,876,939 / 29.39%
Number/percentage of G's	39,125,121 / 20.95%
Number/percentage of N's	5,841 / 0%

GC Percentage	41.27%
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2.3. Coverage

Mean	0.0604
Standard Deviation	0.6667

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	94,827.56
Standard Deviation	2,919,108.21
P25/Median/P75	150 / 192 / 257

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	1,313,946
Insertions	31,453
Mapped reads with at least one insertion	1.94%
Deletions	75,213
Mapped reads with at least one deletion	4.76%
Homopolymer indels	44.45%

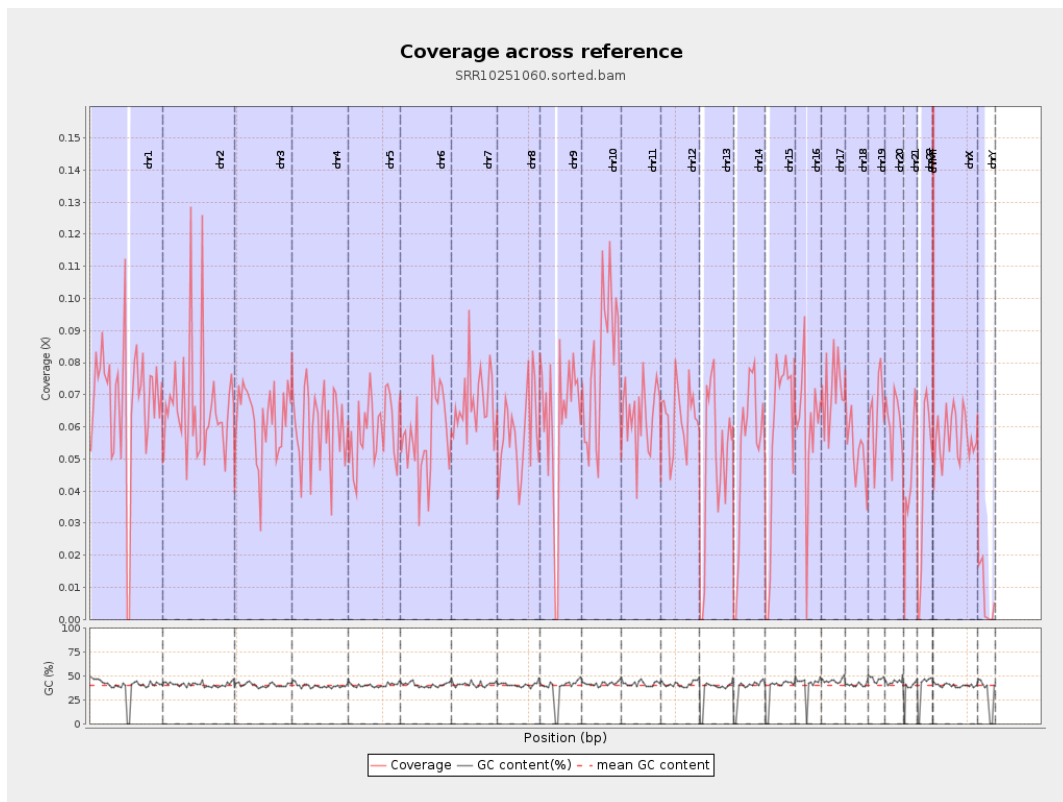
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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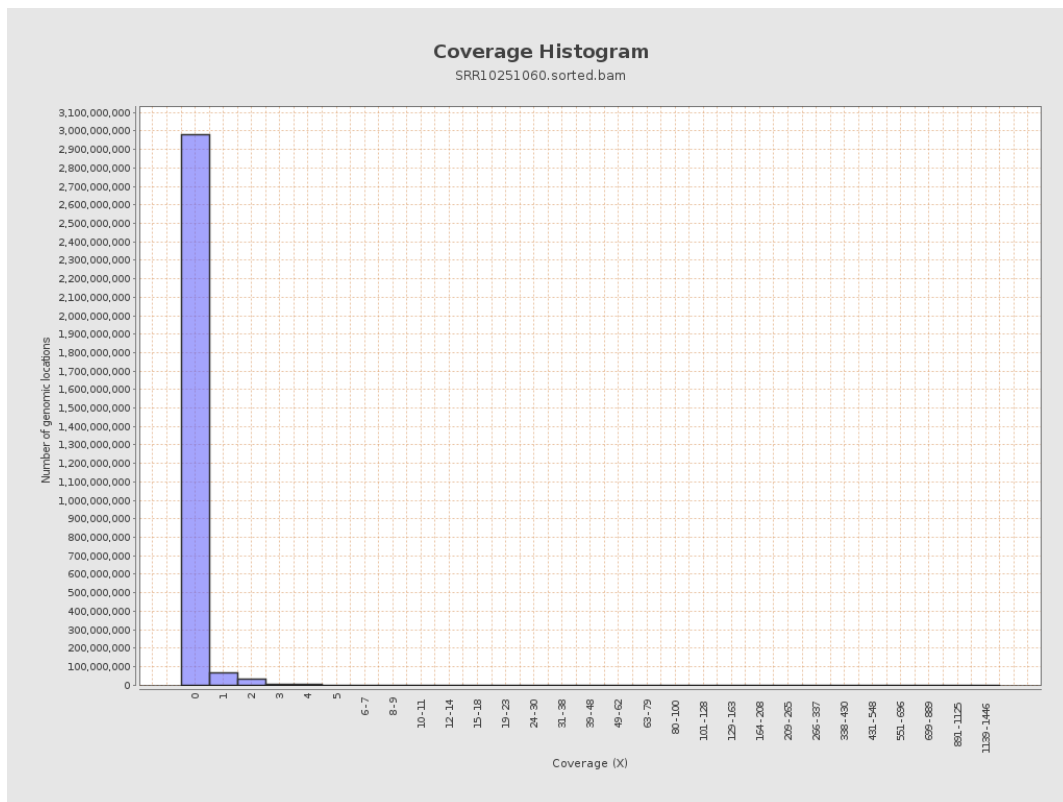
		bases	coverage	deviation
chr1	249250621	16869257	0.0677	1.2514
chr2	243199373	16224484	0.0667	1.0387
chr3	198022430	12288878	0.0621	0.3646
chr4	191154276	11466146	0.06	0.4346
chr5	180915260	10732217	0.0593	0.3662
chr6	171115067	9747970	0.057	0.3783
chr7	159138663	10713147	0.0673	0.9533
chr8	146364022	8427902	0.0576	0.4121
chr9	141213431	8698002	0.0616	0.8521
chr10	135534747	10745867	0.0793	0.7836
chr11	135006516	8535906	0.0632	0.4481
chr12	133851895	8533555	0.0638	0.3758
chr13	115169878	5551076	0.0482	0.3221
chr14	107349540	5721164	0.0533	0.3485
chr15	102531392	5792454	0.0565	0.3512
chr16	90354753	5425457	0.06	0.6813
chr17	81195210	5823452	0.0717	0.4822
chr18	78077248	4175686	0.0535	0.6249
chr19	59128983	3799252	0.0643	0.6555
chr20	63025520	3863924	0.0613	0.3754
chr21	48129895	2177807	0.0452	0.3391
chr22	51304566	2235036	0.0436	0.3139
chrMT	16571	80523	4.8593	3.8135
chrX	155270560	8833785	0.0569	0.3617

chrY	59373566	425936	0.0072	0.5185
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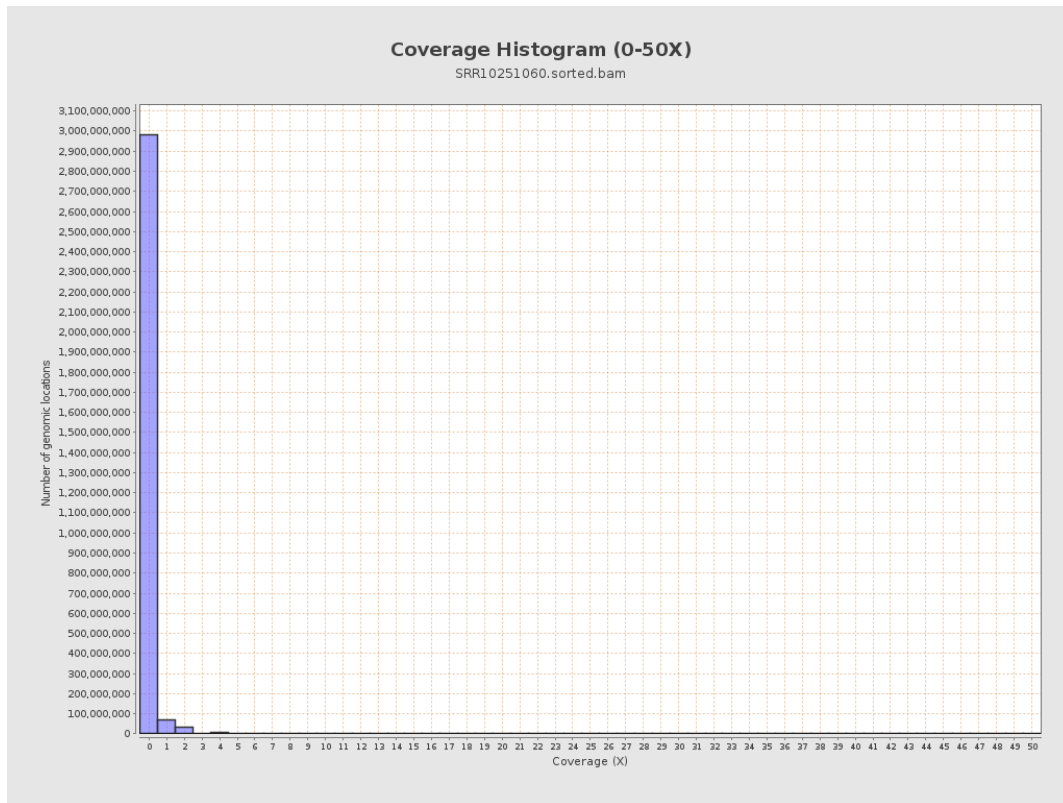
3. Results : Coverage across reference



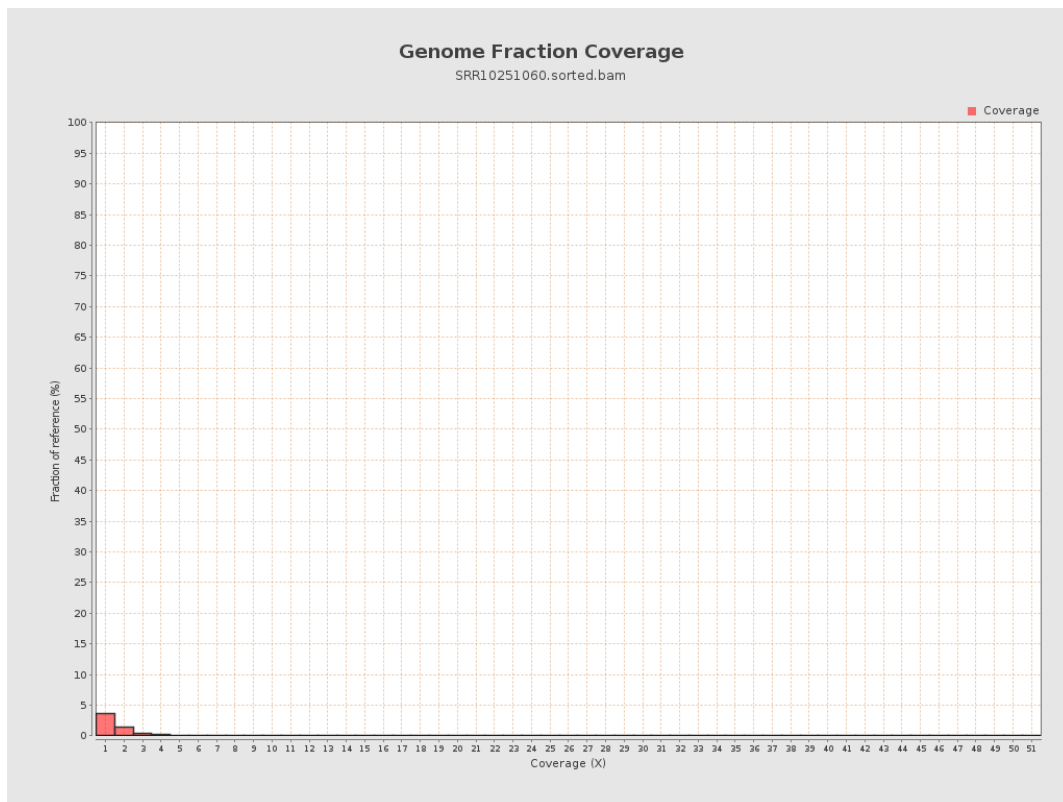
4. Results : Coverage Histogram



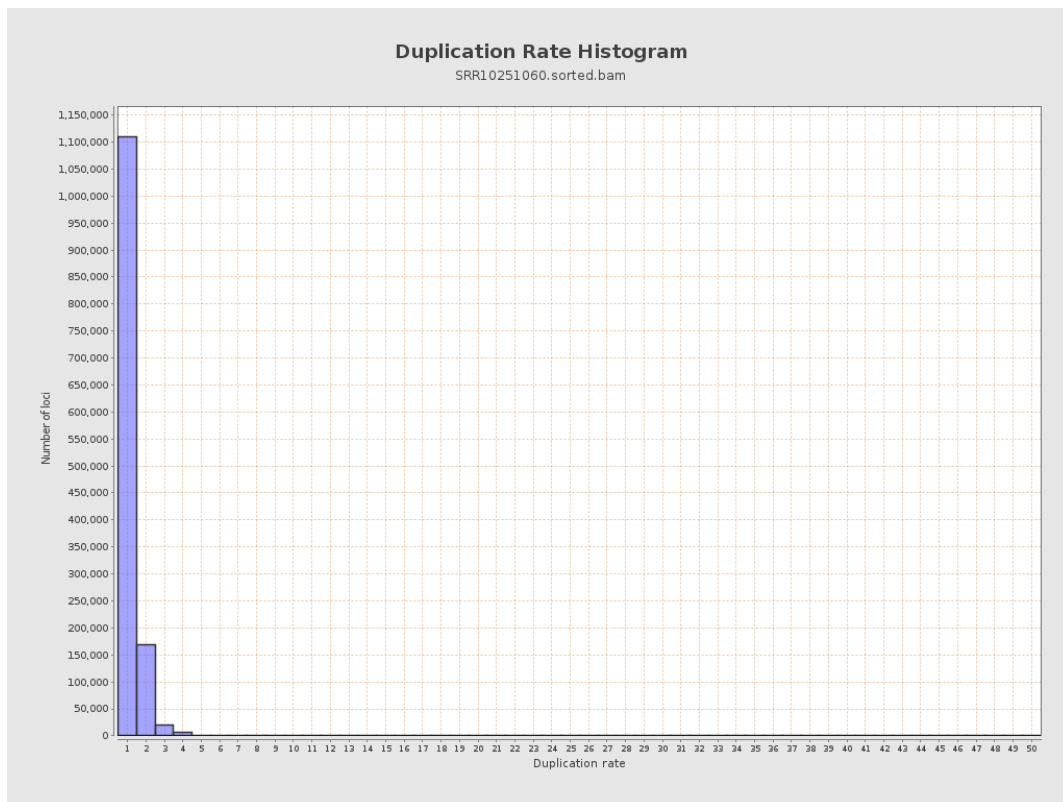
5. Results : Coverage Histogram (0-50X)



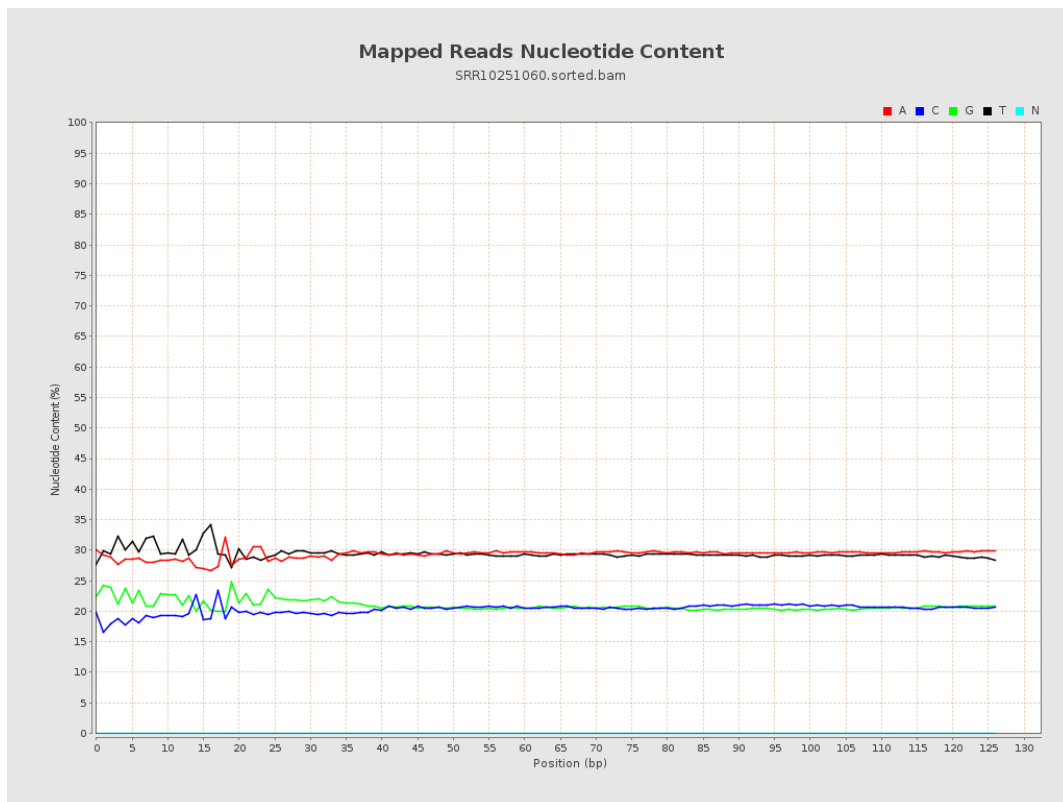
6. Results : Genome Fraction Coverage



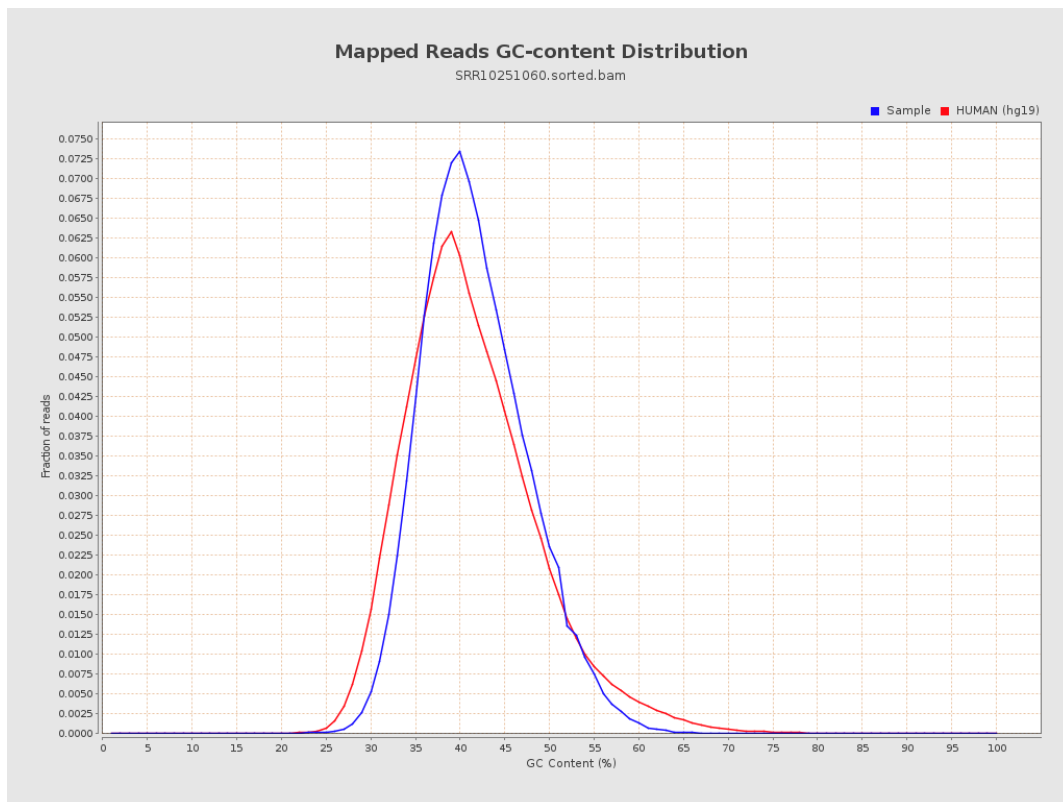
7. Results : Duplication Rate Histogram



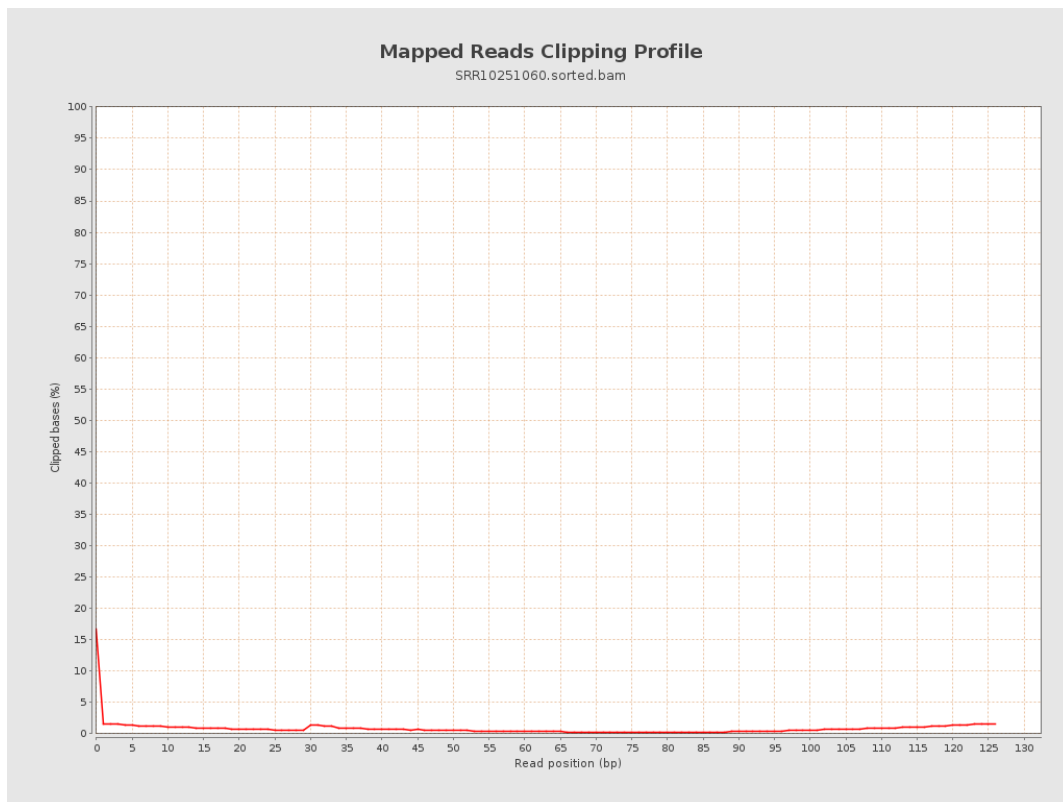
8. Results : Mapped Reads Nucleotide Content



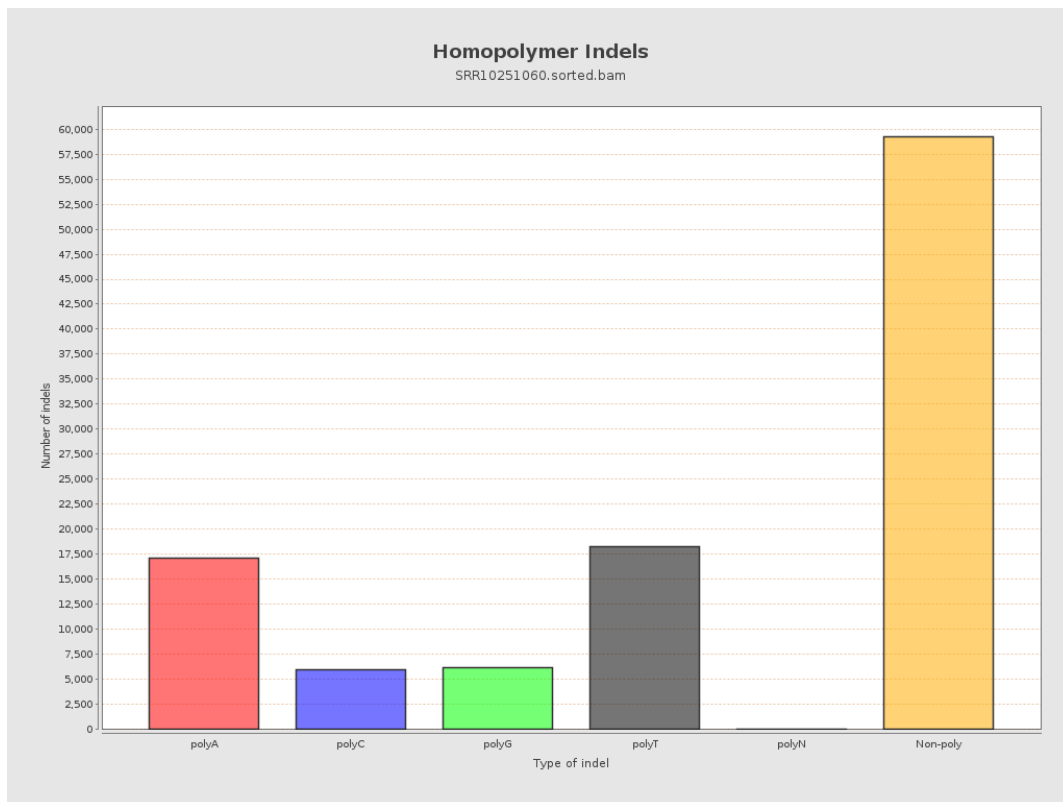
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



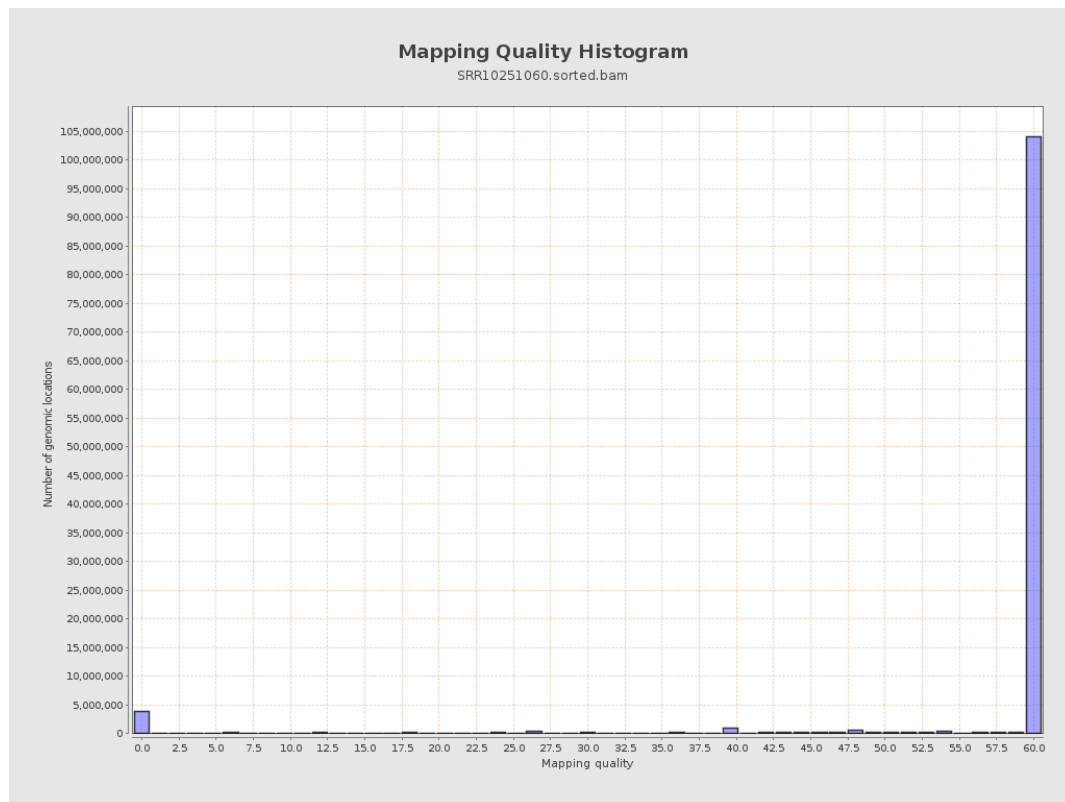
11. Results : Homopolymer Indels



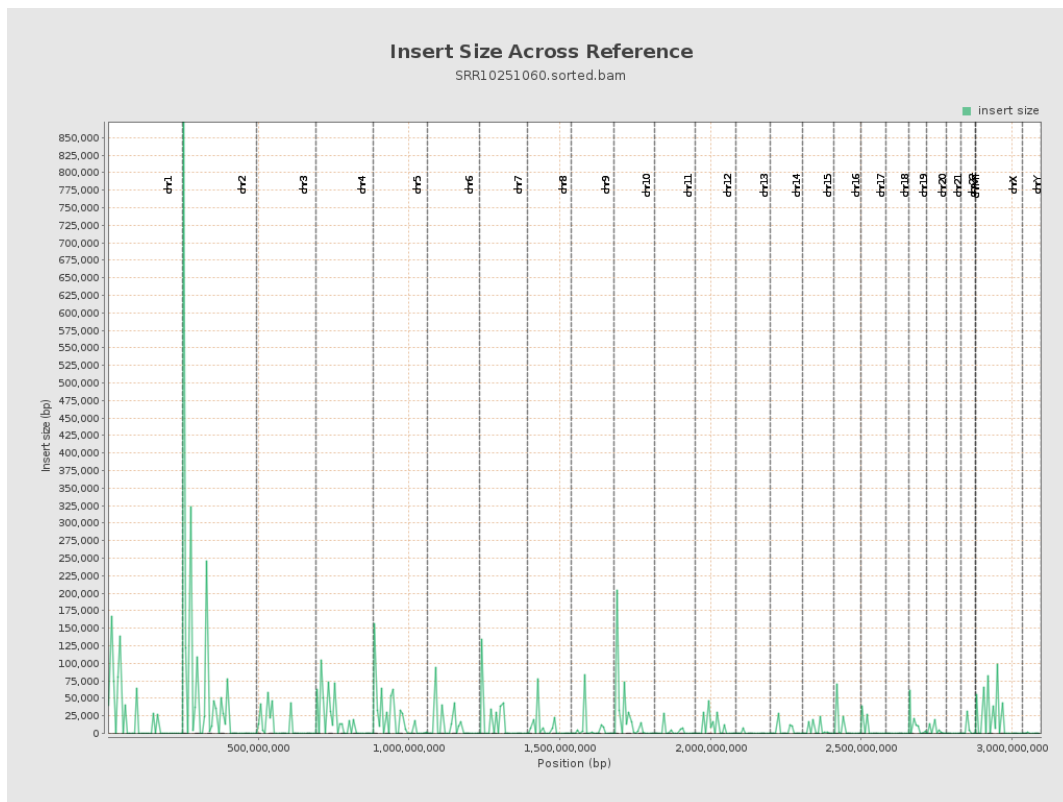
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

