

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:58:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251059.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_SRR10251059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251059_1.fastq.gz SRR10251059_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:58:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,800,008
Mapped reads	1,467,591 / 81.53%
Unmapped reads	332,417 / 18.47%
Mapped paired reads	1,467,591 / 81.53%
Mapped reads, first in pair	735,138 / 40.84%
Mapped reads, second in pair	732,453 / 40.69%
Mapped reads, both in pair	1,457,812 / 80.99%
Mapped reads, singletons	9,779 / 0.54%
Secondary alignments	0
Supplementary alignments	41,131 / 2.29%
Read min/max/mean length	30 / 127 / 128.03
Duplicated reads (estimated)	243,013 / 13.5%
Duplication rate	14.86%
Clipped reads	423,834 / 23.55%

2.2. ACGT Content

Number/percentage of A's	52,246,741 / 29.33%
Number/percentage of C's	36,276,151 / 20.37%
Number/percentage of T's	52,243,790 / 29.33%
Number/percentage of G's	37,347,145 / 20.97%
Number/percentage of N's	5,459 / 0%

GC Percentage	41.33%
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2.3. Coverage

Mean	0.0576
Standard Deviation	0.7276

2.4. Mapping Quality

Mean Mapping Quality	52.88
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2.5. Insert size

Mean	99,229.91
Standard Deviation	3,027,014.59
P25/Median/P75	139 / 177 / 238

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	1,287,465
Insertions	30,811
Mapped reads with at least one insertion	1.96%
Deletions	74,287
Mapped reads with at least one deletion	4.85%
Homopolymer indels	43.03%

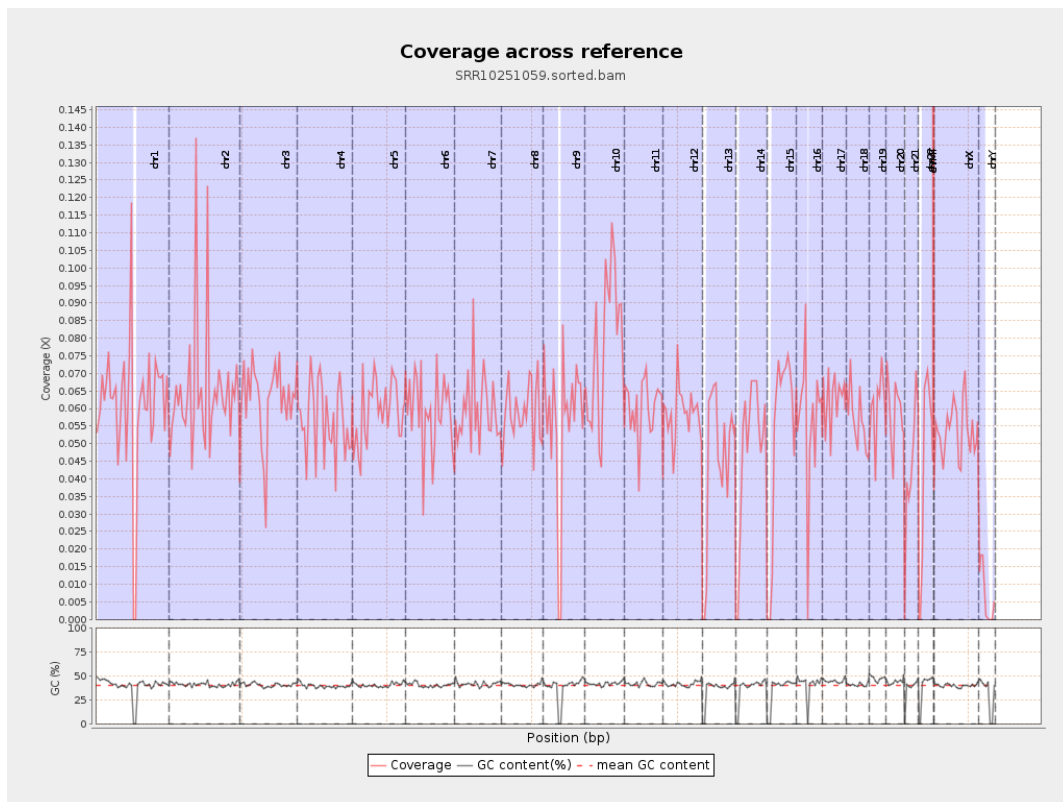
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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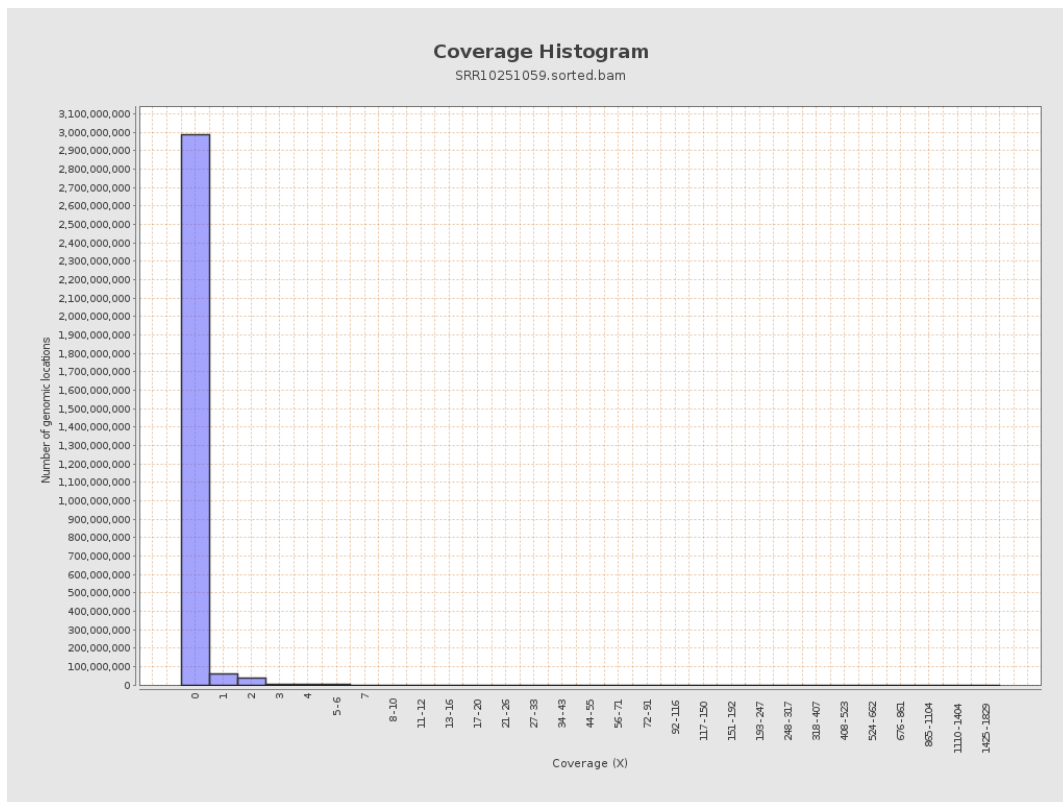
		bases	coverage	deviation
chr1	249250621	15157910	0.0608	1.534
chr2	243199373	15798553	0.065	1.0752
chr3	198022430	12315252	0.0622	0.3616
chr4	191154276	10743349	0.0562	0.4307
chr5	180915260	10726802	0.0593	0.3641
chr6	171115067	10105577	0.0591	0.407
chr7	159138663	9488460	0.0596	0.9559
chr8	146364022	8603127	0.0588	0.4267
chr9	141213431	7838585	0.0555	0.8872
chr10	135534747	10524972	0.0777	0.8356
chr11	135006516	8147492	0.0603	0.4498
chr12	133851895	7856420	0.0587	0.3604
chr13	115169878	5133589	0.0446	0.3115
chr14	107349540	5200246	0.0484	0.3431
chr15	102531392	5407954	0.0527	0.3334
chr16	90354753	5130477	0.0568	0.6822
chr17	81195210	5088258	0.0627	0.4282
chr18	78077248	4472880	0.0573	0.7815
chr19	59128983	3561619	0.0602	0.789
chr20	63025520	3702040	0.0587	0.3665
chr21	48129895	2126942	0.0442	0.3284
chr22	51304566	2215517	0.0432	0.3158
chrMT	16571	234167	14.1311	8.1398
chrX	155270560	8291770	0.0534	0.3549

chrY	59373566	404472	0.0068	0.5085
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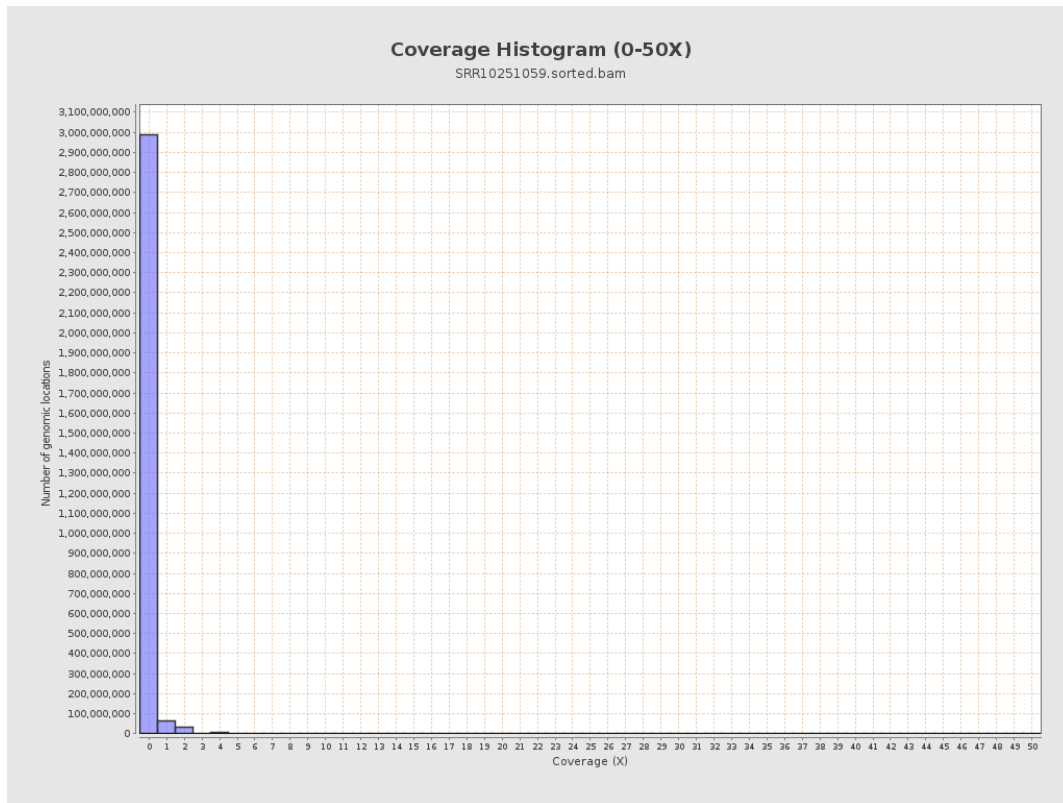
3. Results : Coverage across reference



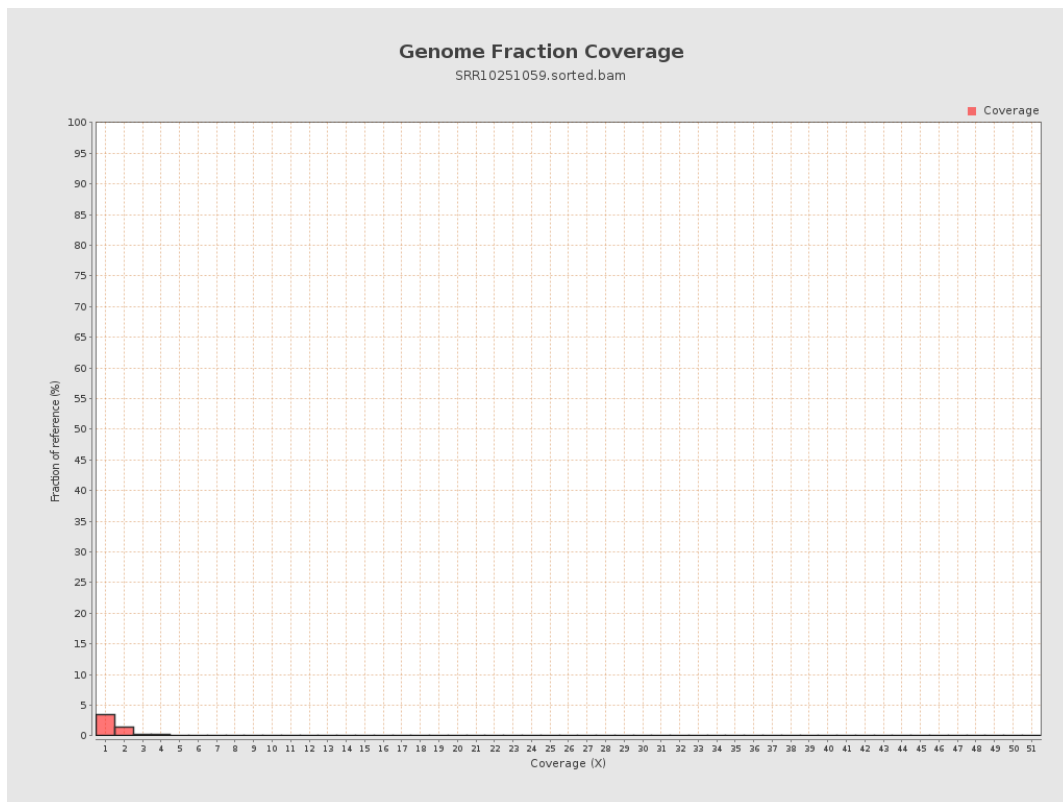
4. Results : Coverage Histogram



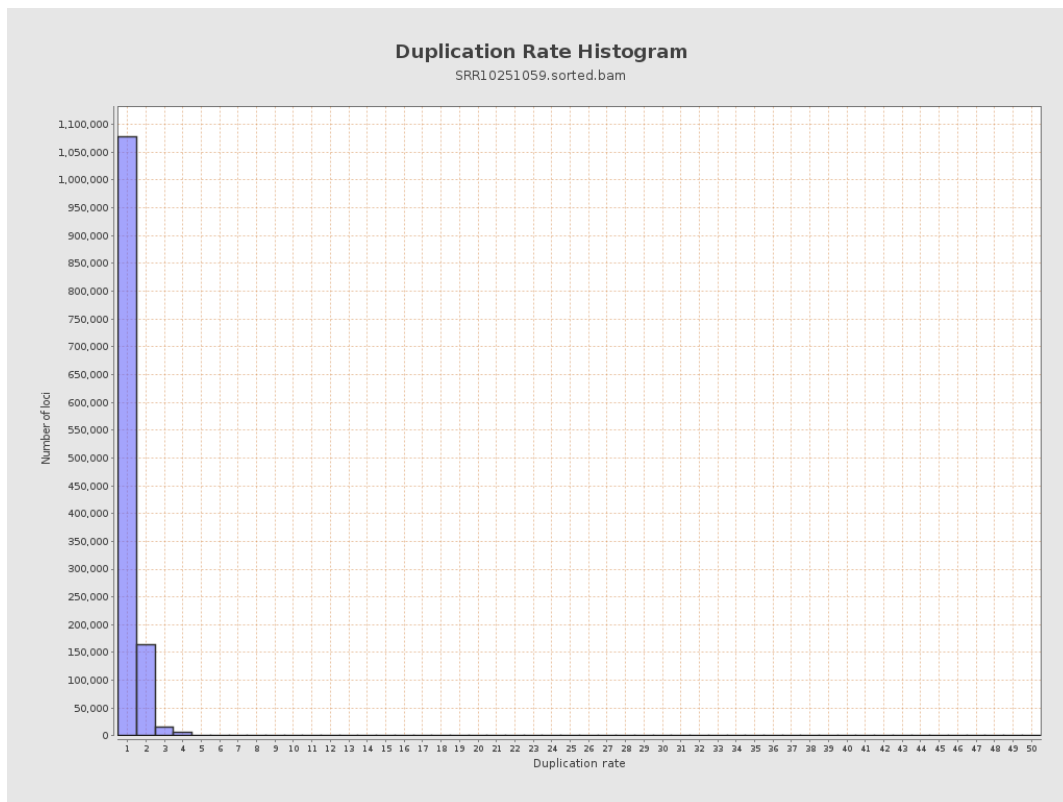
5. Results : Coverage Histogram (0-50X)



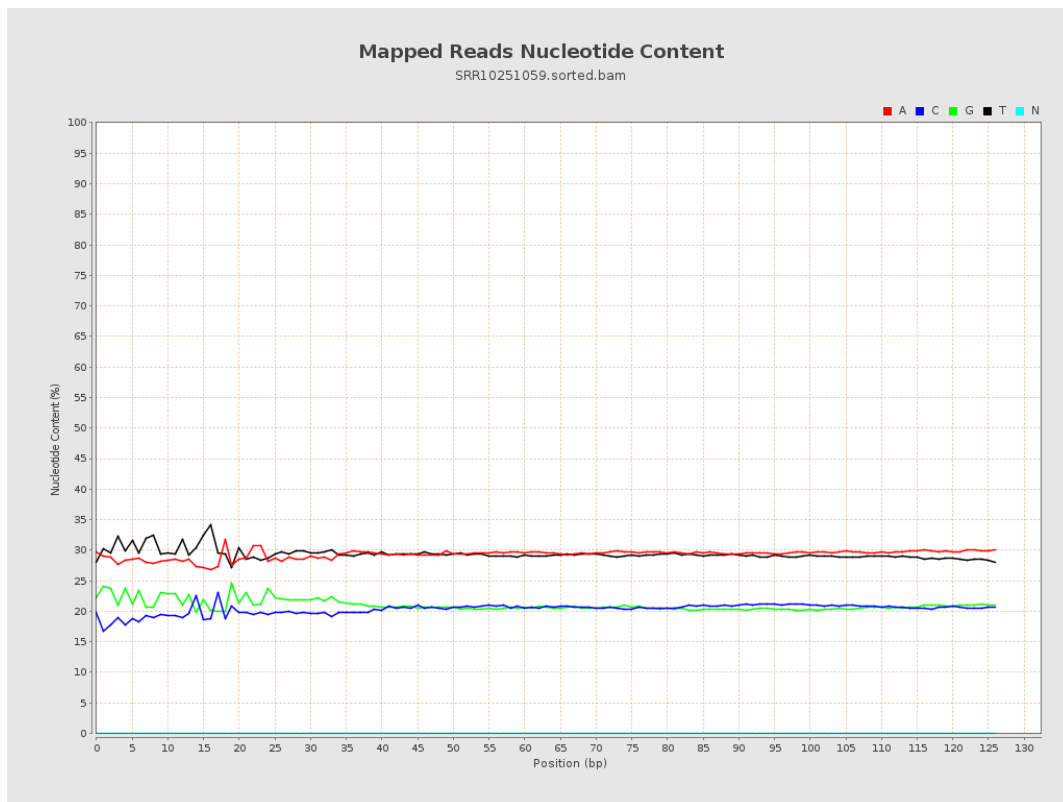
6. Results : Genome Fraction Coverage



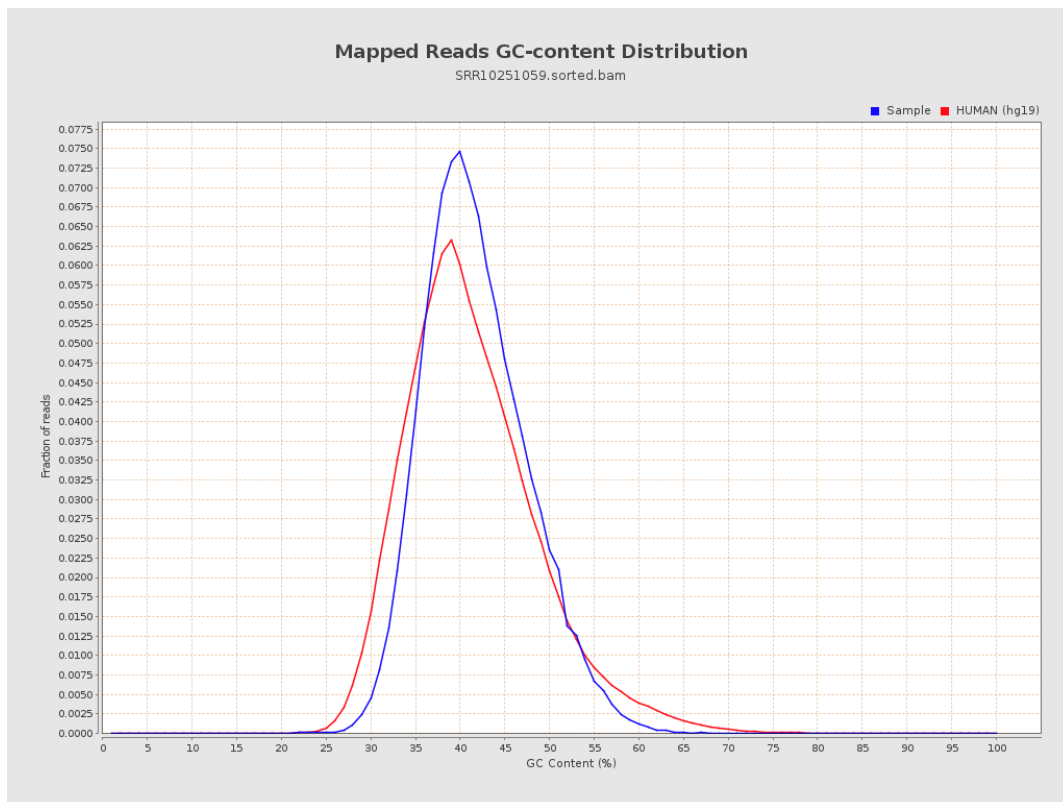
7. Results : Duplication Rate Histogram



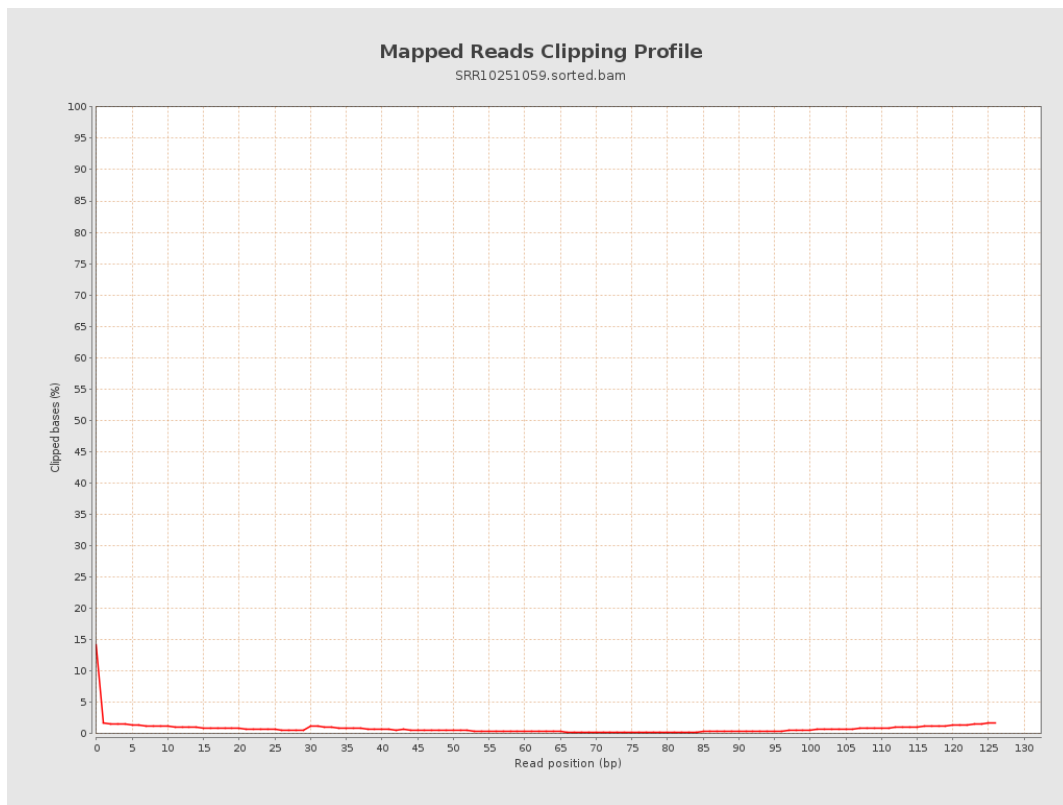
8. Results : Mapped Reads Nucleotide Content



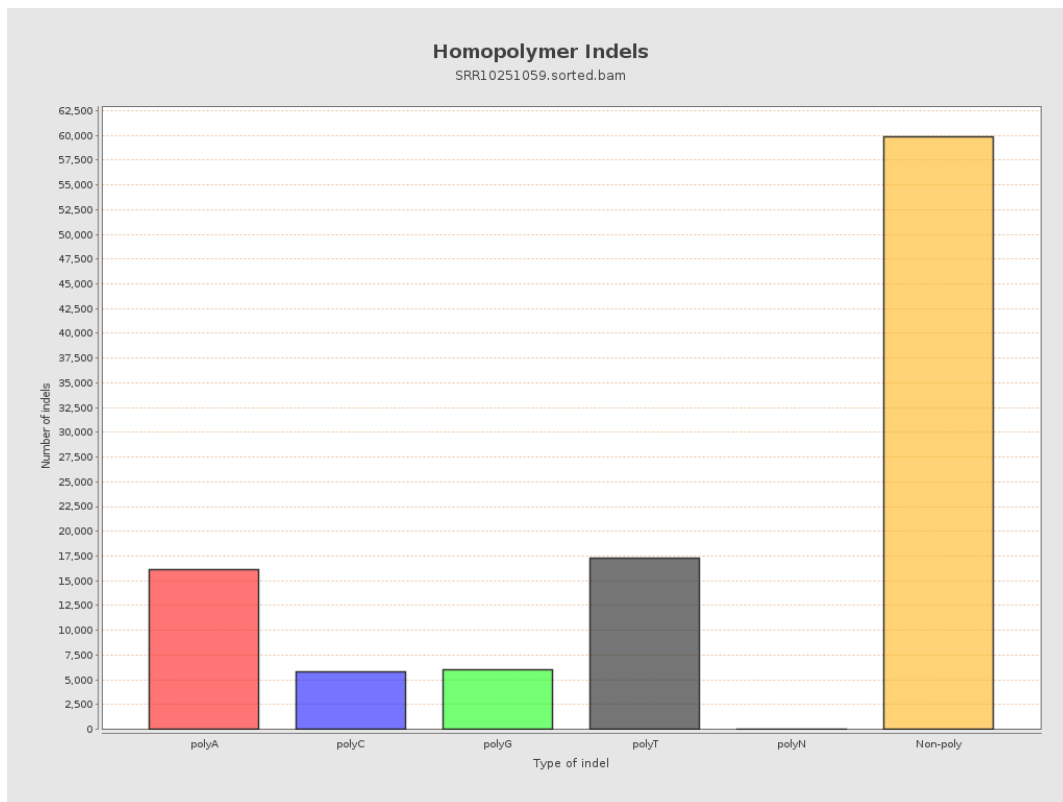
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



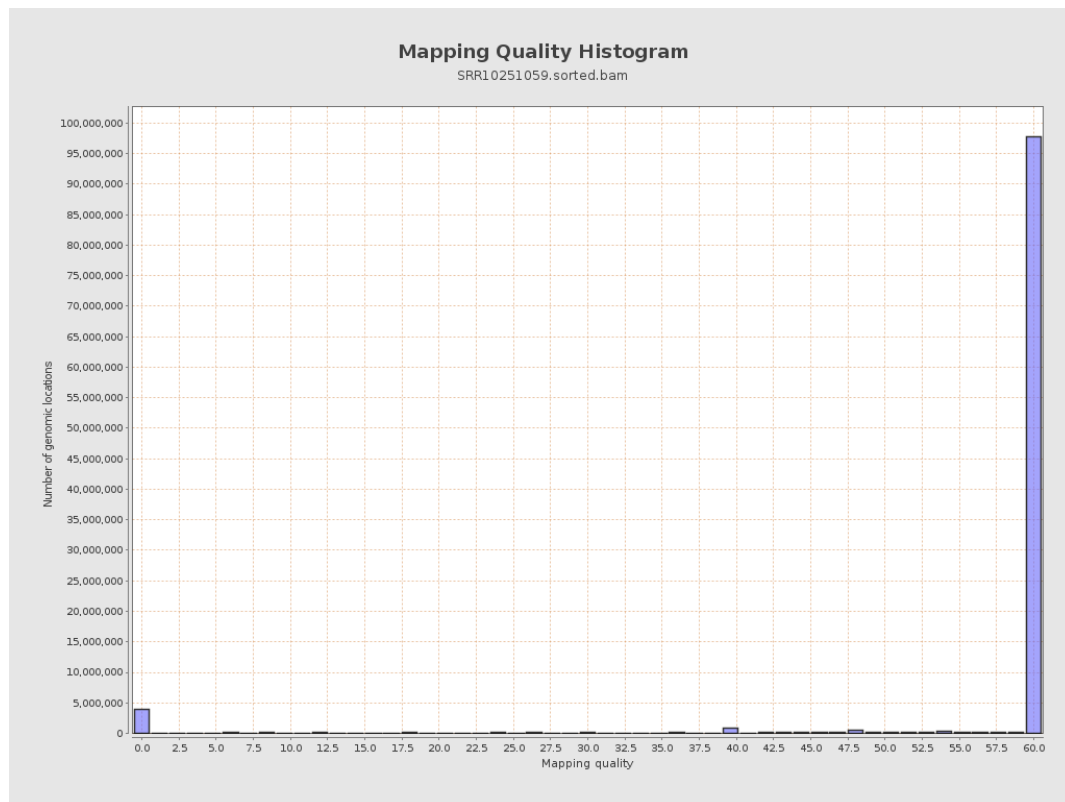
11. Results : Homopolymer Indels



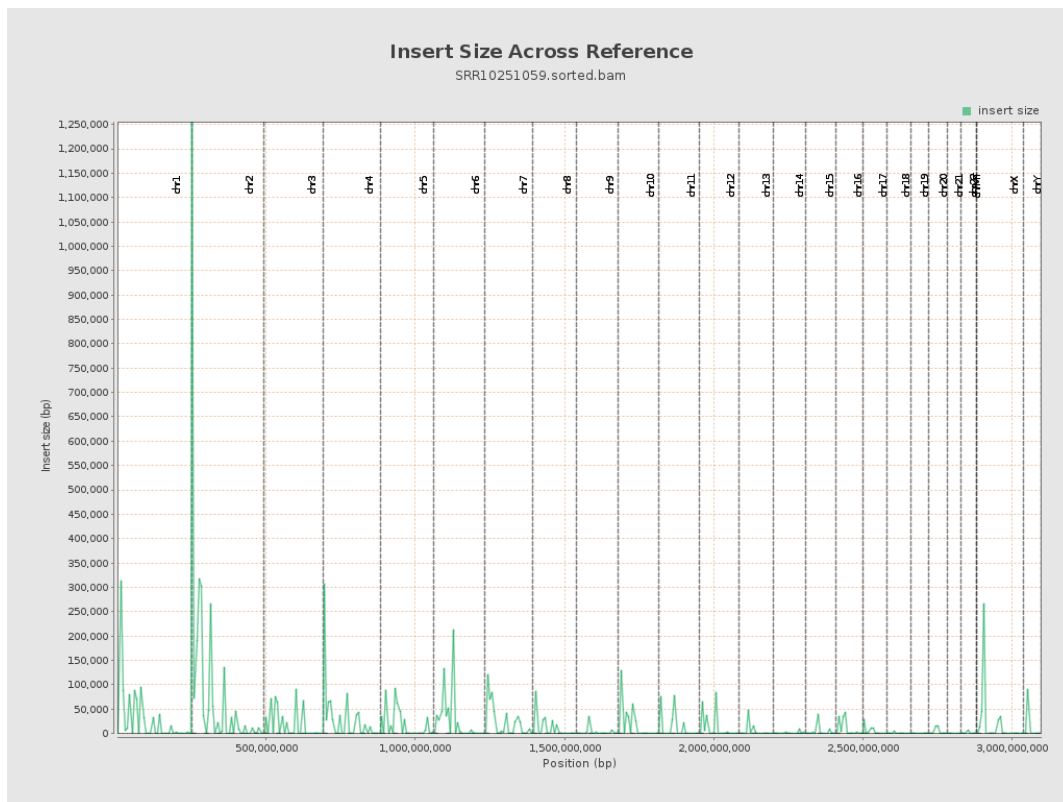
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

