

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 07:01:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174087.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_SRR10174087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174087_1.fastq.gz SRR10174087_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 07:01:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,422,926
Mapped reads	1,391,232 / 97.77%
Unmapped reads	31,694 / 2.23%
Mapped paired reads	1,391,232 / 97.77%
Mapped reads, first in pair	696,106 / 48.92%
Mapped reads, second in pair	695,126 / 48.85%
Mapped reads, both in pair	1,370,646 / 96.33%
Mapped reads, singletons	20,586 / 1.45%
Secondary alignments	0
Supplementary alignments	138,025 / 9.7%
Read min/max/mean length	30 / 133 / 128.14
Duplicated reads (estimated)	1,047,005 / 73.58%
Duplication rate	63.02%
Clipped reads	569,768 / 40.04%

2.2. ACGT Content

Number/percentage of A's	49,611,289 / 30.15%
Number/percentage of C's	32,133,194 / 19.53%
Number/percentage of T's	49,482,556 / 30.07%
Number/percentage of G's	33,324,640 / 20.25%
Number/percentage of N's	1,792 / 0%

GC Percentage	39.78%
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2.3. Coverage

Mean	0.0532
Standard Deviation	0.9356

2.4. Mapping Quality

Mean Mapping Quality	52.95
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2.5. Insert size

Mean	1,017,327.86
Standard Deviation	9,559,868.11
P25/Median/P75	146 / 202 / 285

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	1,675,058
Insertions	19,201
Mapped reads with at least one insertion	1.33%
Deletions	41,559
Mapped reads with at least one deletion	2.92%
Homopolymer indels	42.17%

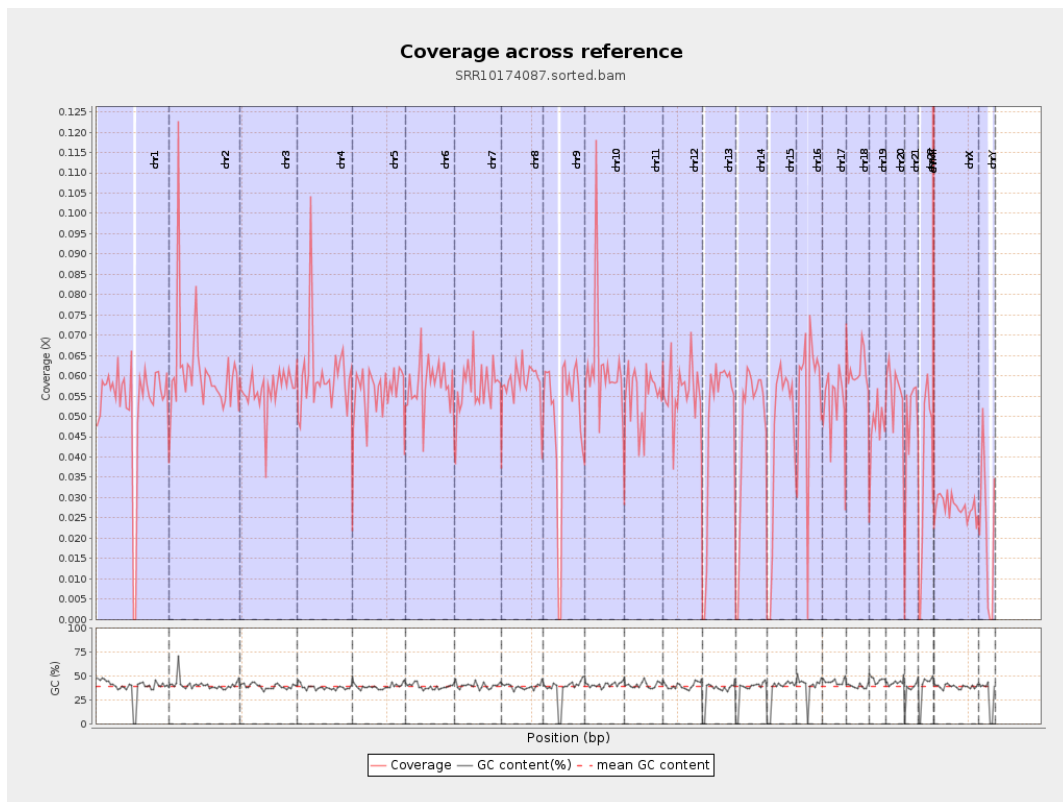
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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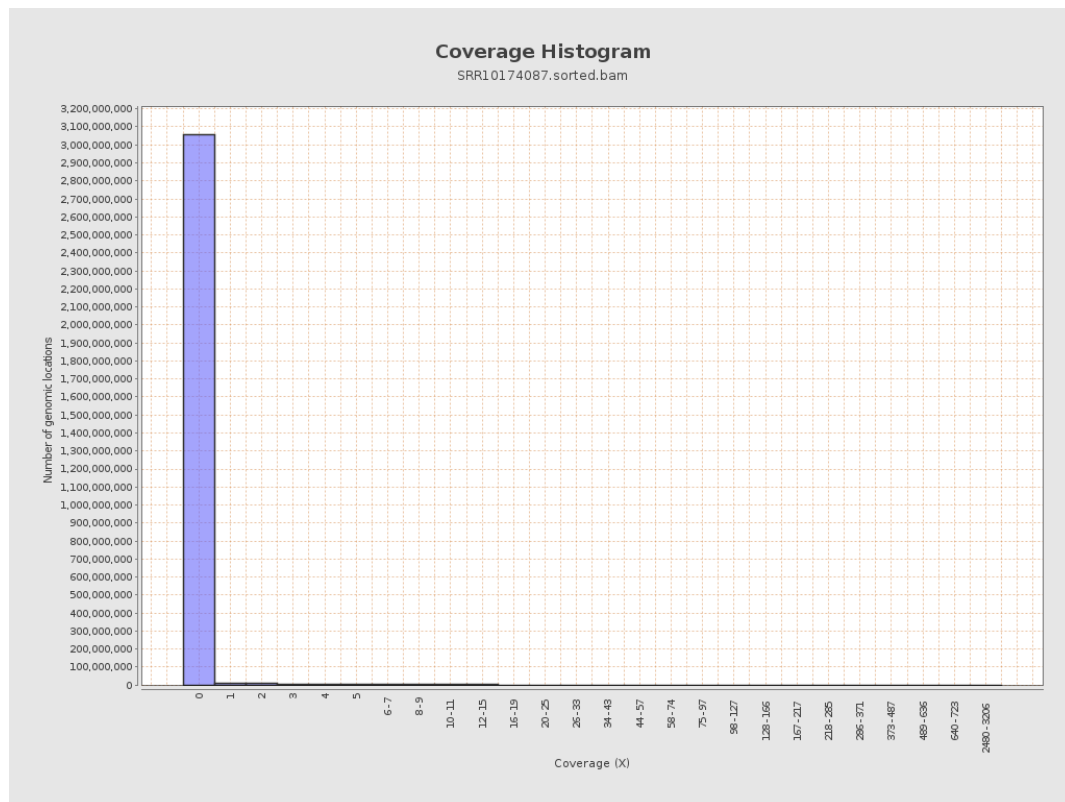
		bases	coverage	deviation
chr1	249250621	13211187	0.053	0.7418
chr2	243199373	14884529	0.0612	2.3166
chr3	198022430	11194403	0.0565	0.6664
chr4	191154276	11455421	0.0599	0.7641
chr5	180915260	10206578	0.0564	0.656
chr6	171115067	9884244	0.0578	0.6996
chr7	159138663	9148112	0.0575	0.765
chr8	146364022	8560266	0.0585	0.8103
chr9	141213431	7017016	0.0497	0.726
chr10	135534747	8422554	0.0621	0.8854
chr11	135006516	7391066	0.0547	0.6571
chr12	133851895	7467201	0.0558	0.6618
chr13	115169878	5576112	0.0484	0.6129
chr14	107349540	5072851	0.0473	0.6092
chr15	102531392	4560363	0.0445	0.5779
chr16	90354753	5074254	0.0562	0.697
chr17	81195210	4268051	0.0526	0.6452
chr18	78077248	4826939	0.0618	0.9697
chr19	59128983	2827606	0.0478	0.6253
chr20	63025520	3525874	0.0559	0.6582
chr21	48129895	2271366	0.0472	0.6699
chr22	51304566	1878484	0.0366	0.535
chrMT	16571	422363	25.4881	21.9707
chrX	155270560	4278423	0.0276	0.4562

chrY	59373566	1233874	0.0208	0.4669
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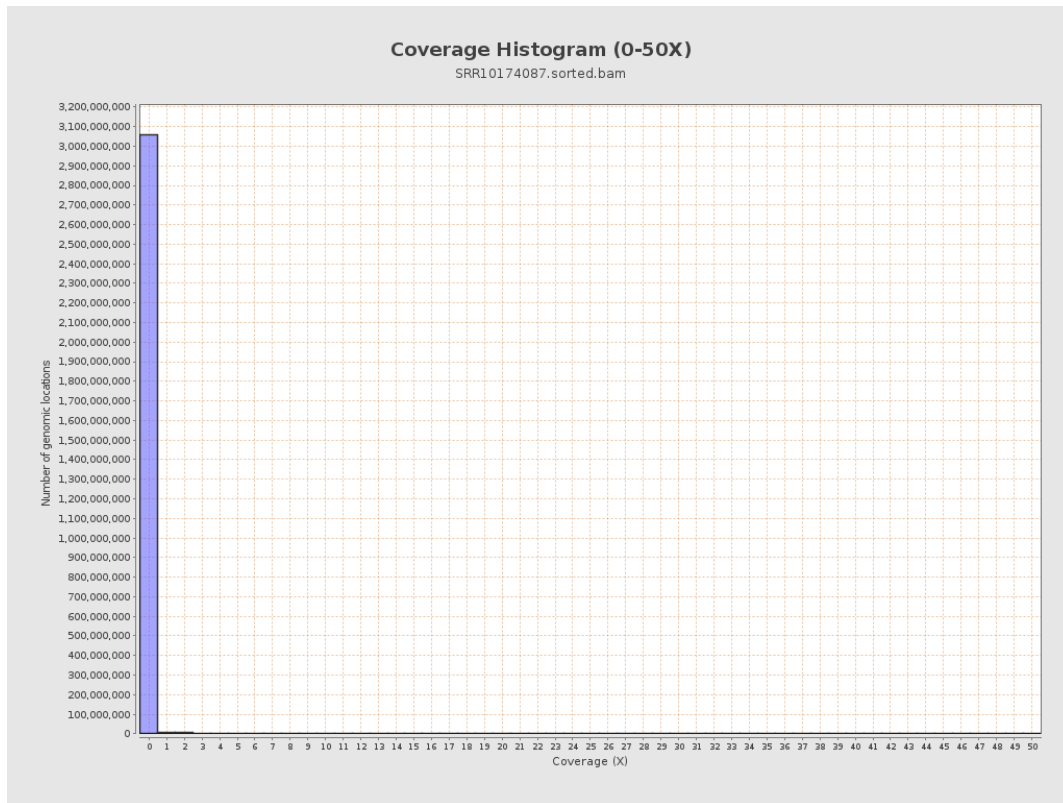
3. Results : Coverage across reference



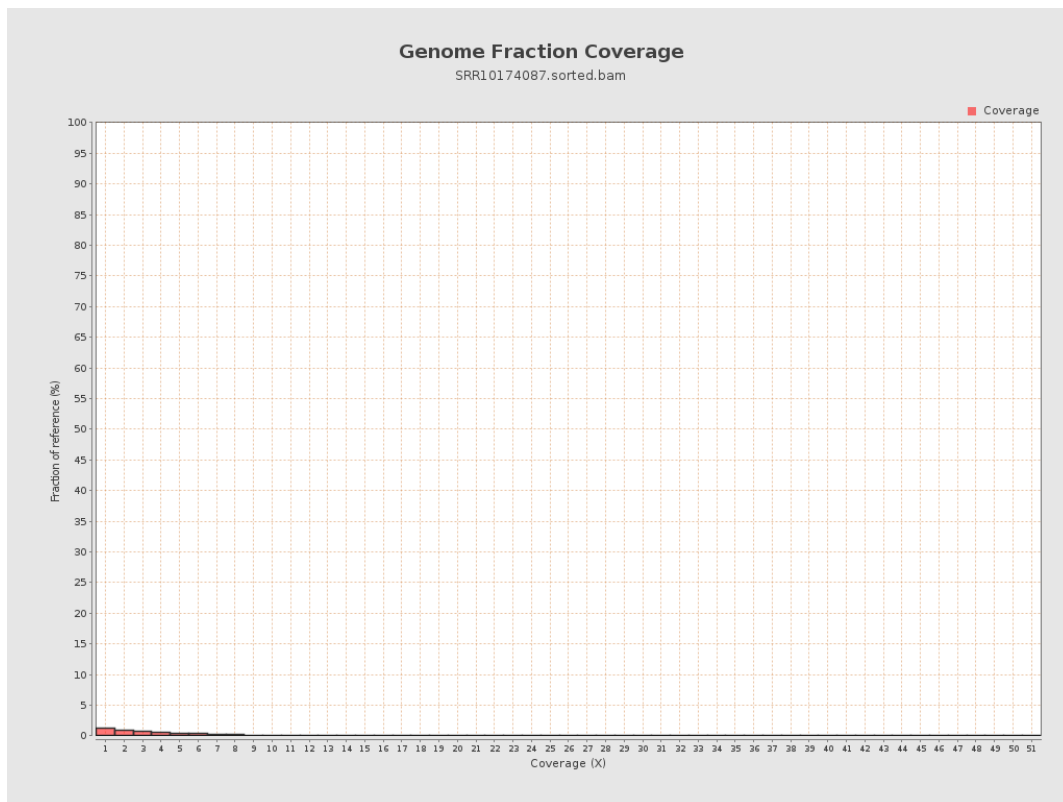
4. Results : Coverage Histogram



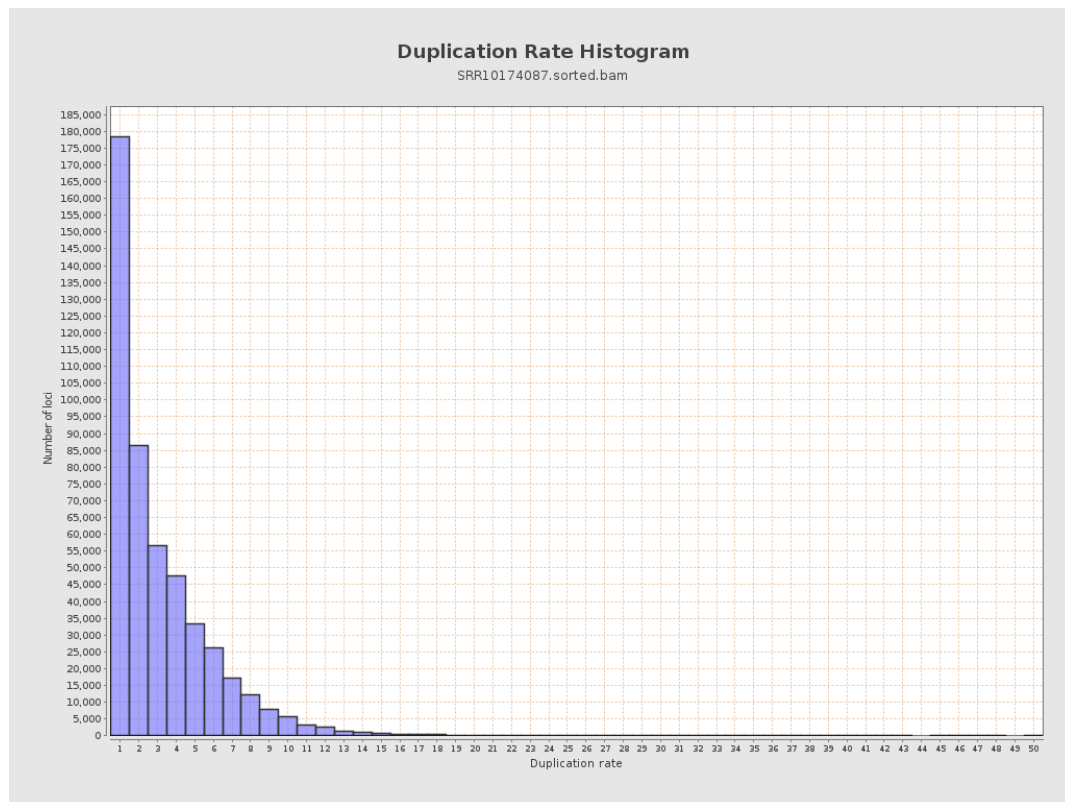
5. Results : Coverage Histogram (0-50X)



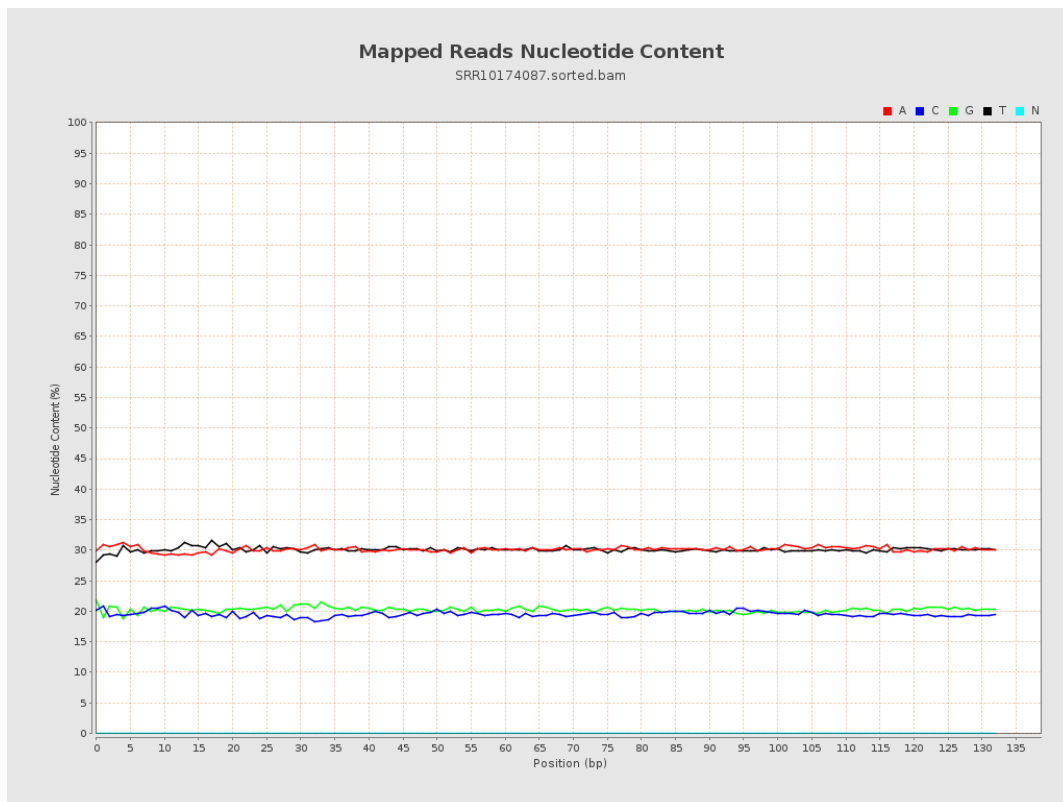
6. Results : Genome Fraction Coverage



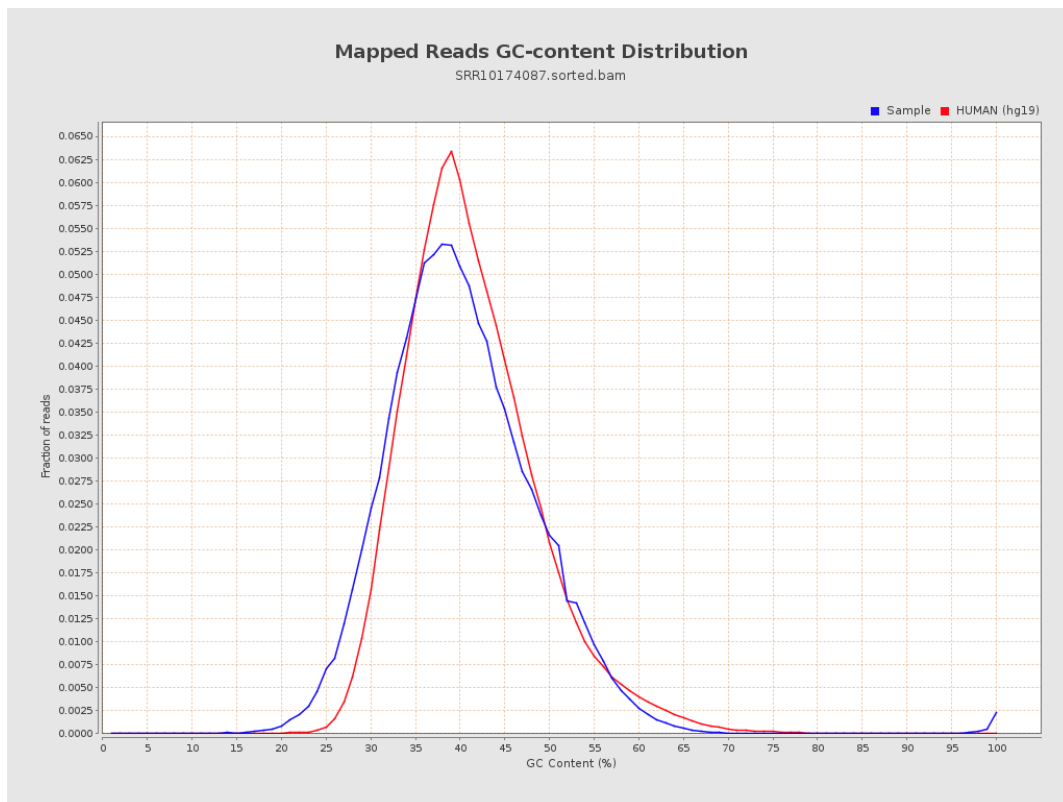
7. Results : Duplication Rate Histogram



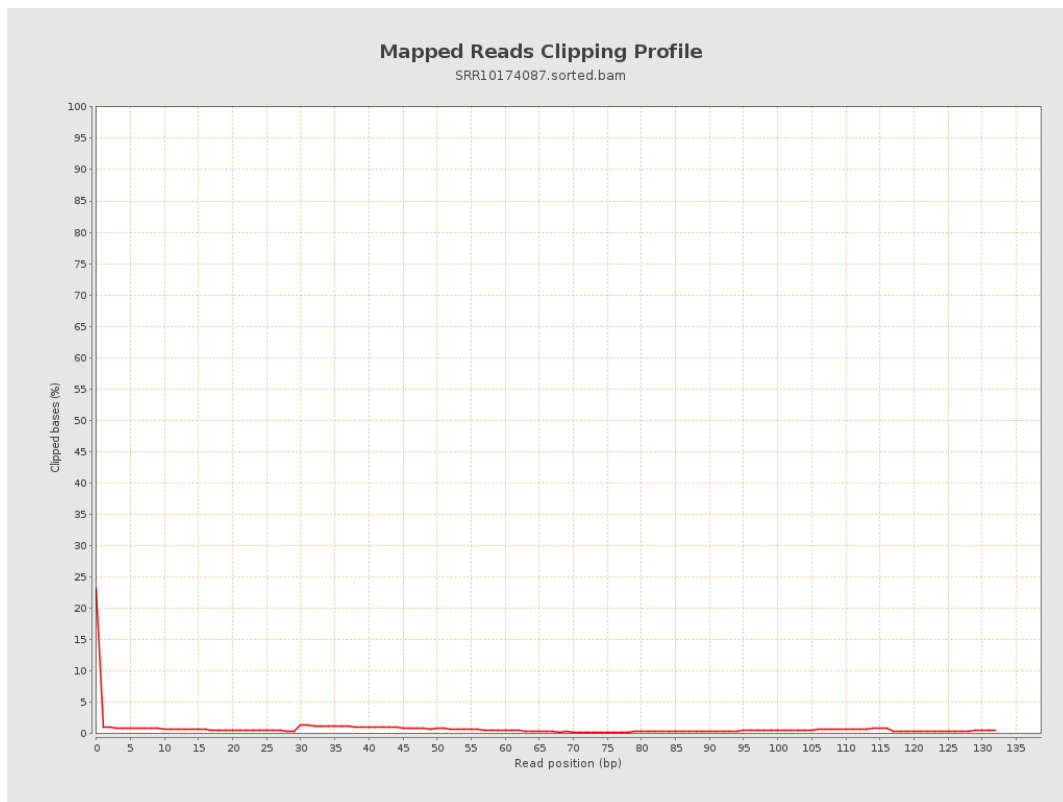
8. Results : Mapped Reads Nucleotide Content



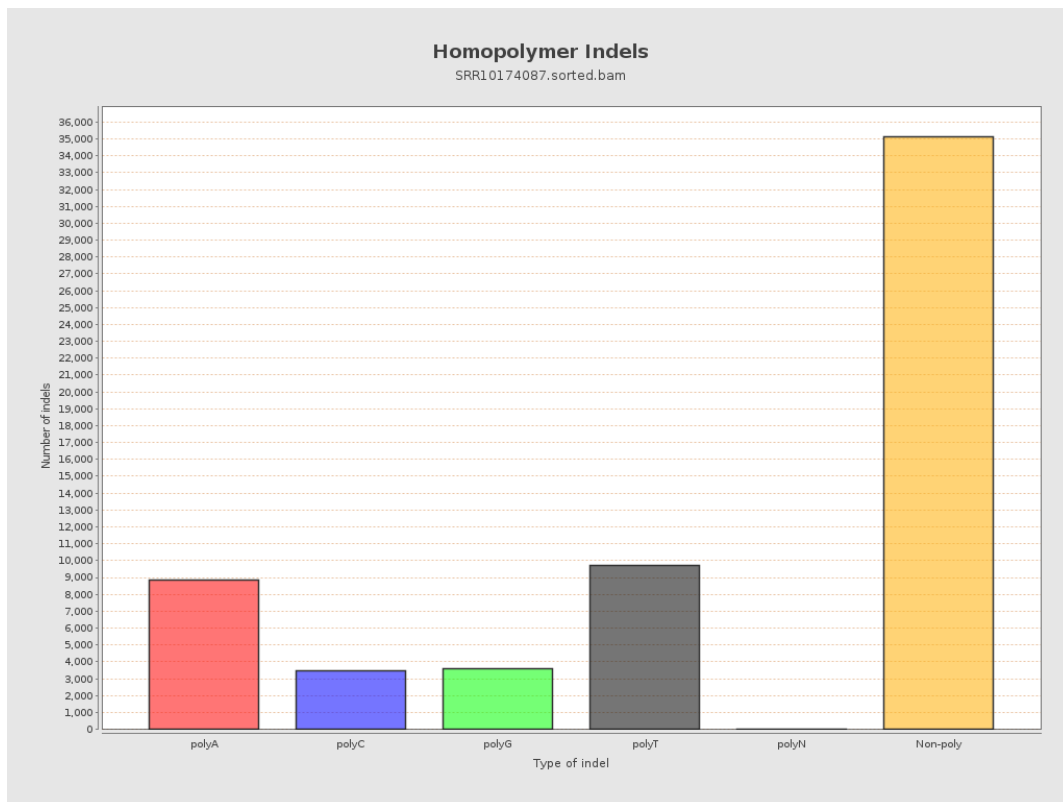
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



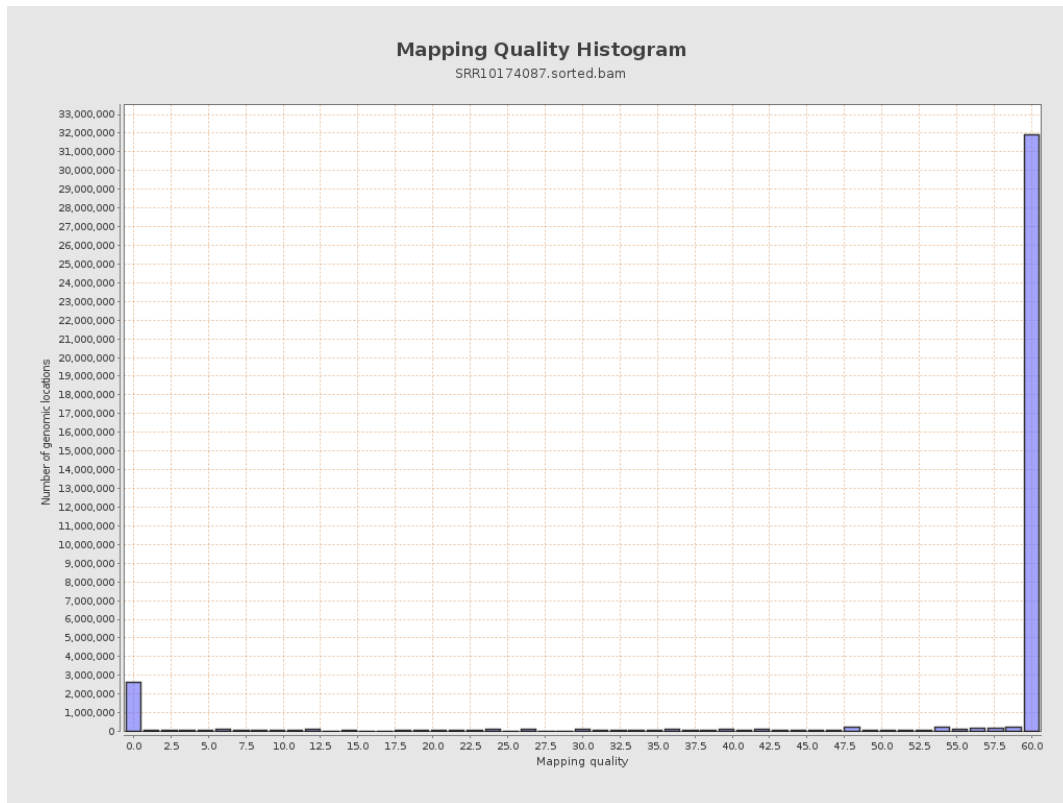
11. Results : Homopolymer Indels



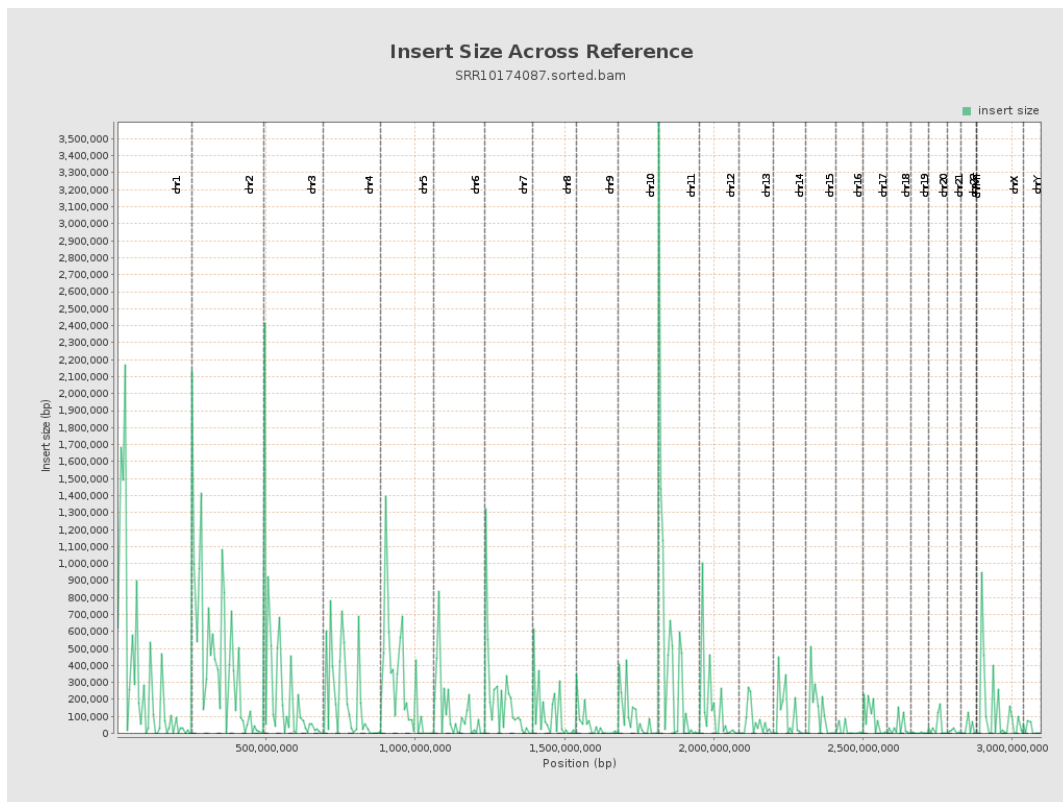
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

