

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 01:26:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472663.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_SRR3472663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472663_1.fastq.gz SRR3472663_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 01:26:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,990,548
Mapped reads	15,887,274 / 99.35%
Unmapped reads	103,274 / 0.65%
Mapped paired reads	15,887,274 / 99.35%
Mapped reads, first in pair	7,961,913 / 49.79%
Mapped reads, second in pair	7,925,361 / 49.56%
Mapped reads, both in pair	15,819,580 / 98.93%
Mapped reads, singletons	67,694 / 0.42%
Secondary alignments	0
Supplementary alignments	102,861 / 0.64%
Read min/max/mean length	30 / 101 / 99.67
Duplicated reads (estimated)	11,324,041 / 70.82%
Duplication rate	49.88%
Clipped reads	1,175,861 / 7.35%

2.2. ACGT Content

Number/percentage of A's	421,394,422 / 26.99%
Number/percentage of C's	360,678,745 / 23.1%
Number/percentage of T's	423,250,170 / 27.11%
Number/percentage of G's	355,667,447 / 22.78%
Number/percentage of N's	298,724 / 0.02%

GC Percentage	45.88%
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2.3. Coverage

Mean	0.5044
Standard Deviation	26.6349

2.4. Mapping Quality

Mean Mapping Quality	54.72
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2.5. Insert size

Mean	19,346.17
Standard Deviation	1,337,670.54
P25/Median/P75	148 / 202 / 270

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	8,665,748
Insertions	101,354
Mapped reads with at least one insertion	0.63%
Deletions	79,967
Mapped reads with at least one deletion	0.5%
Homopolymer indels	43.76%

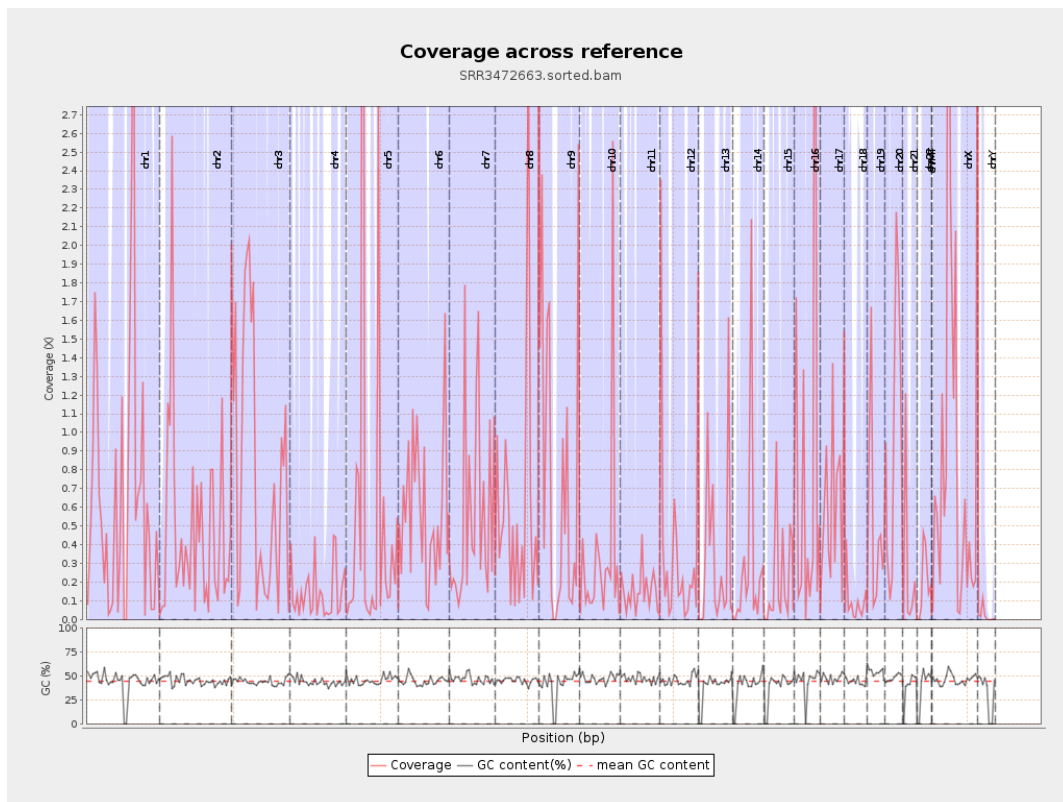
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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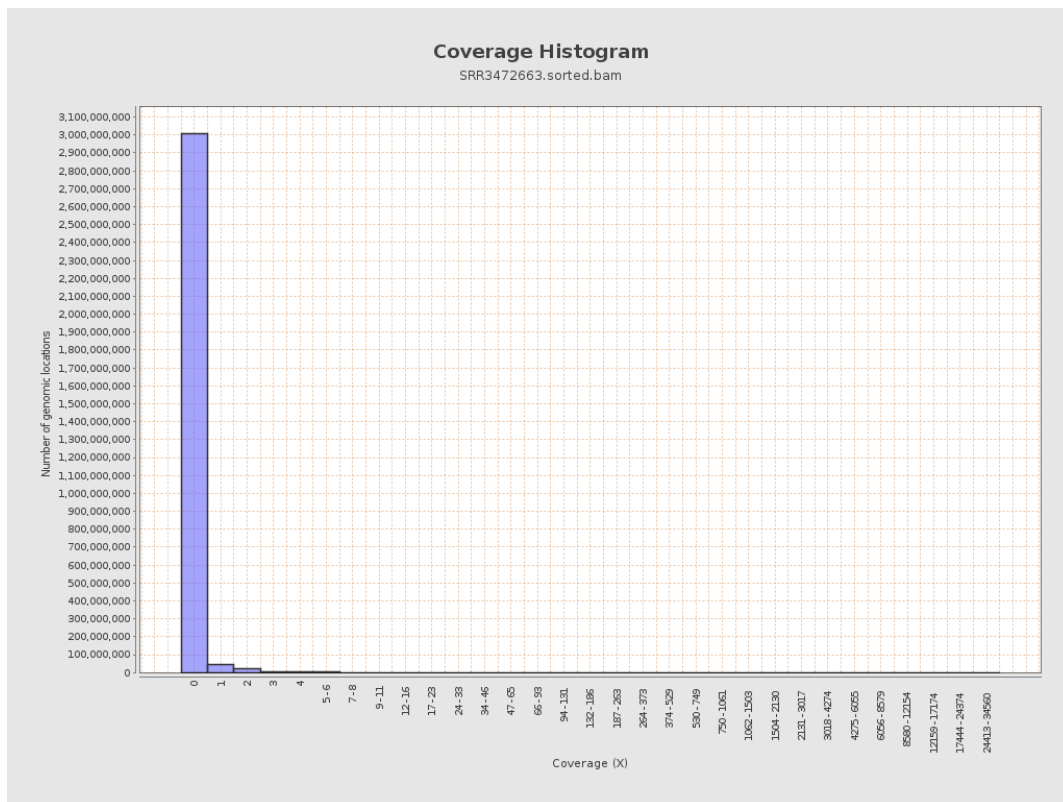
		bases	coverage	deviation
chr1	249250621	166929766	0.6697	30.3031
chr2	243199373	117278075	0.4822	23.5851
chr3	198022430	159719602	0.8066	27.4012
chr4	191154276	27793200	0.1454	9.5983
chr5	180915260	106343566	0.5878	40.2055
chr6	171115067	97633567	0.5706	18.7461
chr7	159138663	89401070	0.5618	24.6707
chr8	146364022	90965117	0.6215	38.0175
chr9	141213431	110522161	0.7827	32.4852
chr10	135534747	44785017	0.3304	28.7441
chr11	135006516	20809276	0.1541	6.8803
chr12	133851895	47144228	0.3522	13.8139
chr13	115169878	38352232	0.333	19.6198
chr14	107349540	29525734	0.275	18.9261
chr15	102531392	22170584	0.2162	11.683
chr16	90354753	78404445	0.8677	33.344
chr17	81195210	49831184	0.6137	18.9331
chr18	78077248	7764803	0.0995	4.2881
chr19	59128983	31514139	0.533	15.5302
chr20	63025520	63510106	1.0077	30.4318
chr21	48129895	12252398	0.2546	24.7387
chr22	51304566	9799288	0.191	6.3981
chrMT	16571	2832	0.1709	0.5312
chrX	155270560	137705171	0.8869	49.4322

chrY	59373566	1334679	0.0225	1.8766
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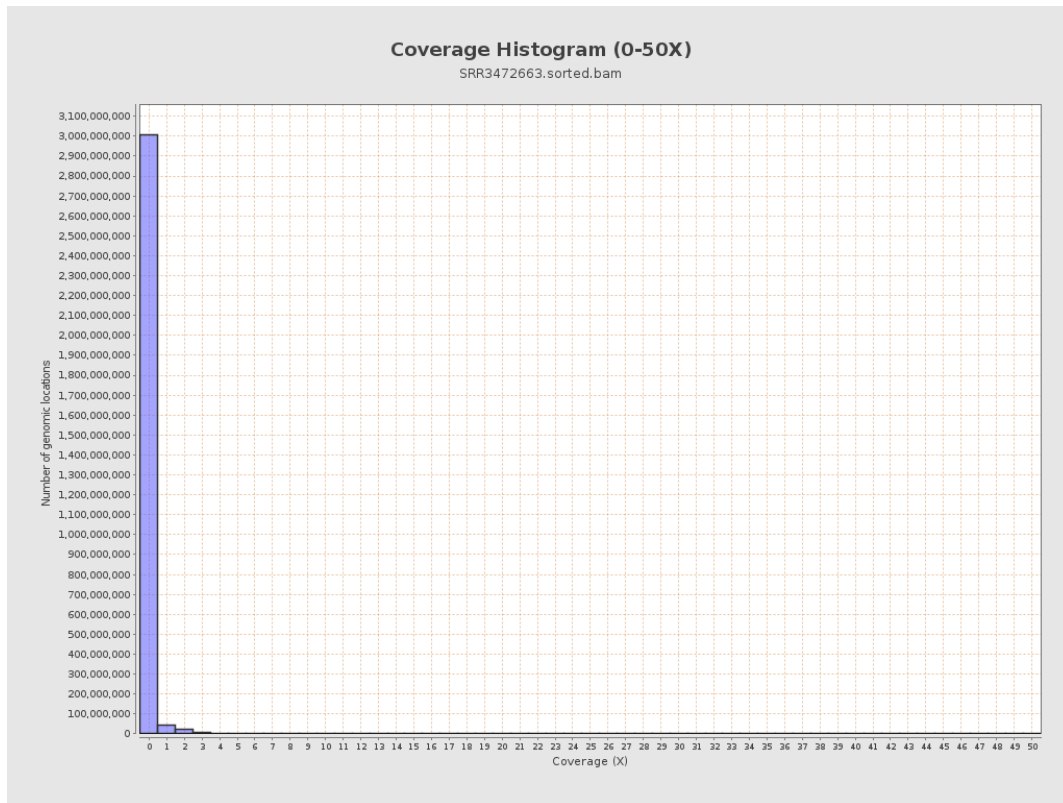
3. Results : Coverage across reference



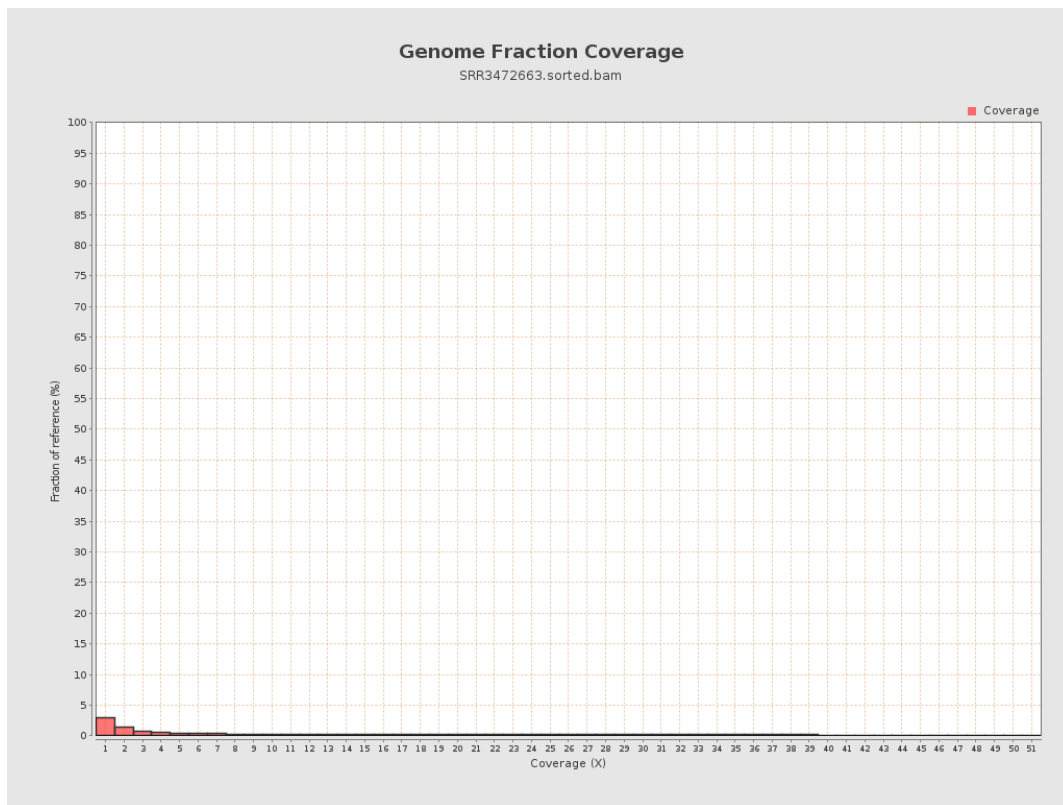
4. Results : Coverage Histogram



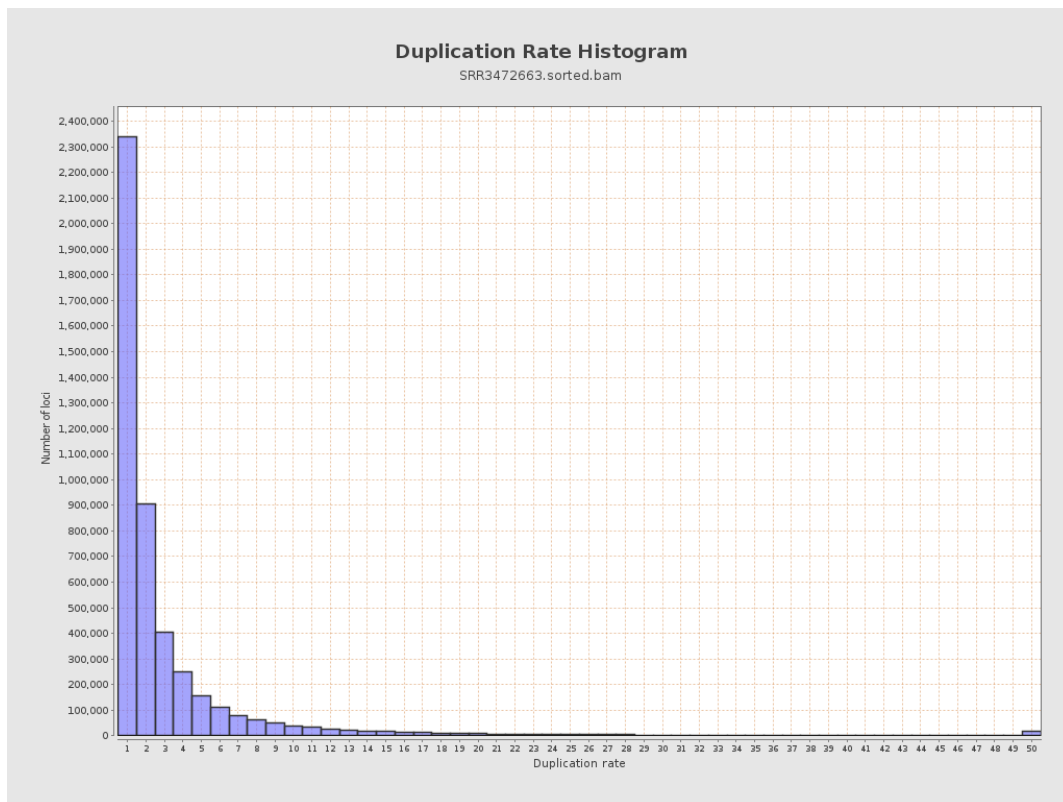
5. Results : Coverage Histogram (0-50X)



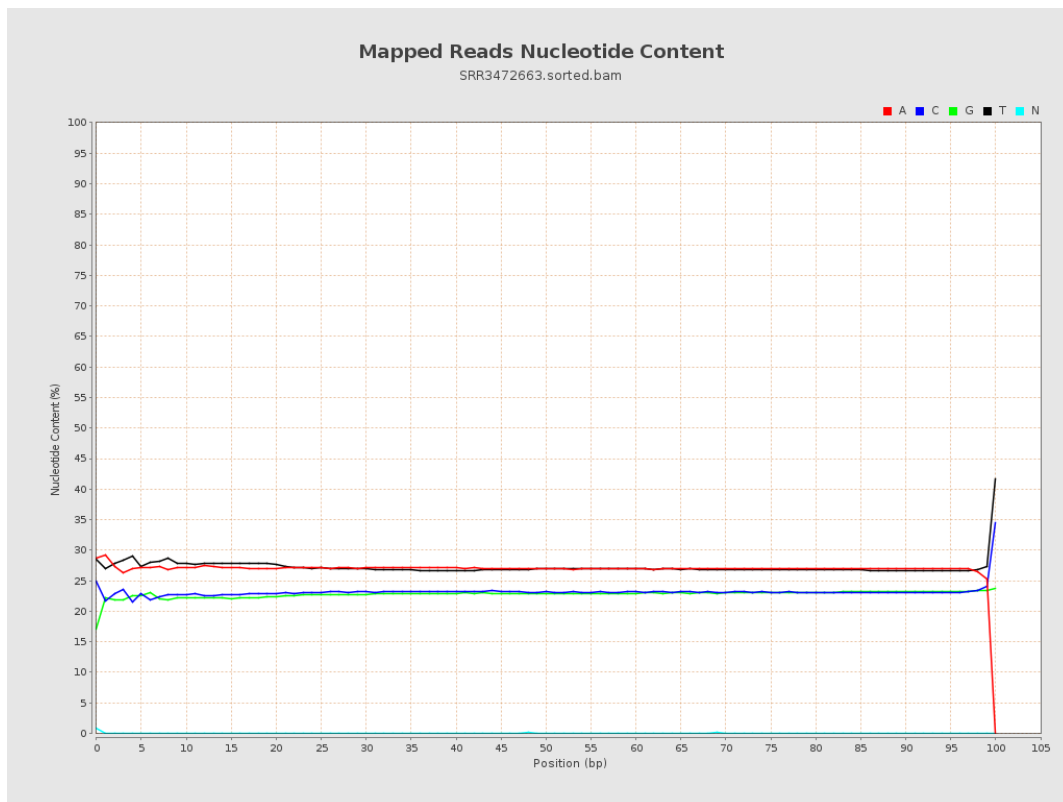
6. Results : Genome Fraction Coverage



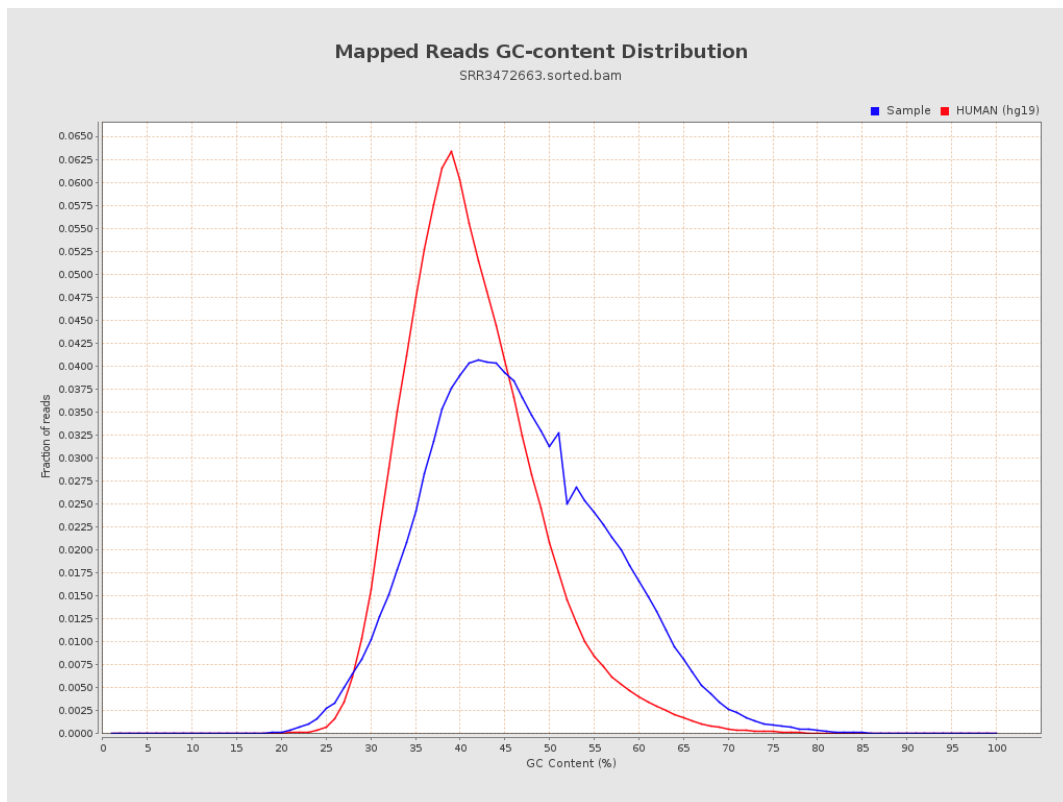
7. Results : Duplication Rate Histogram



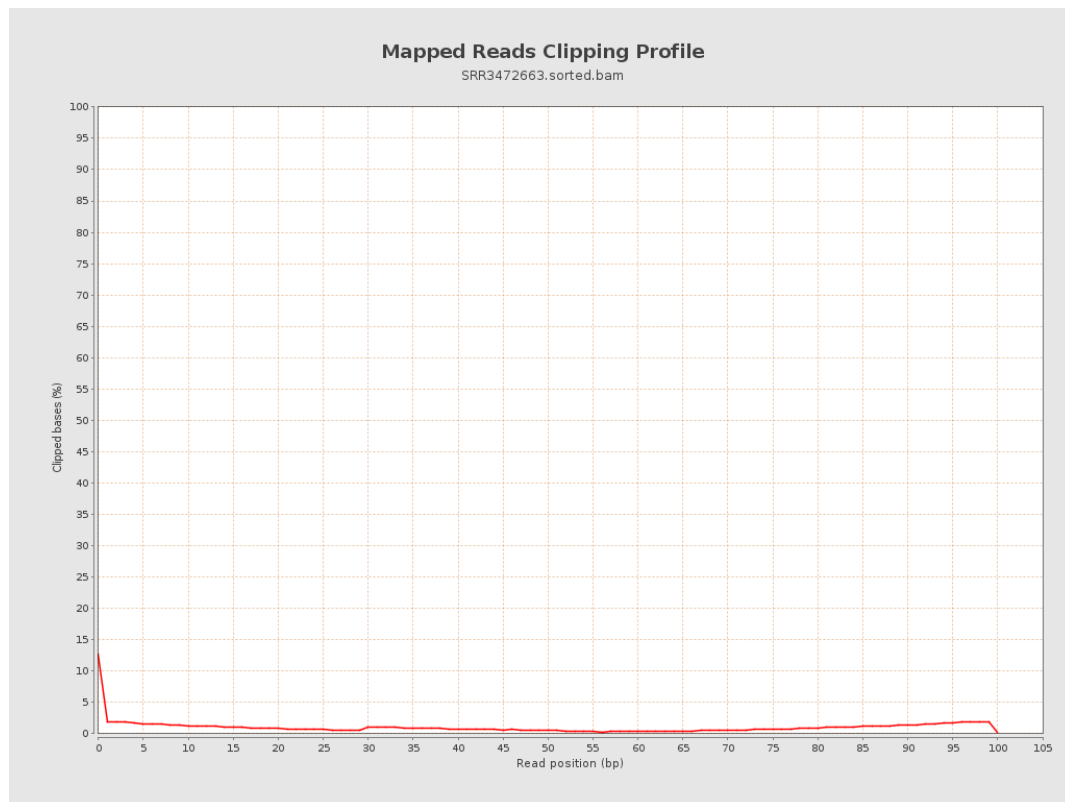
8. Results : Mapped Reads Nucleotide Content



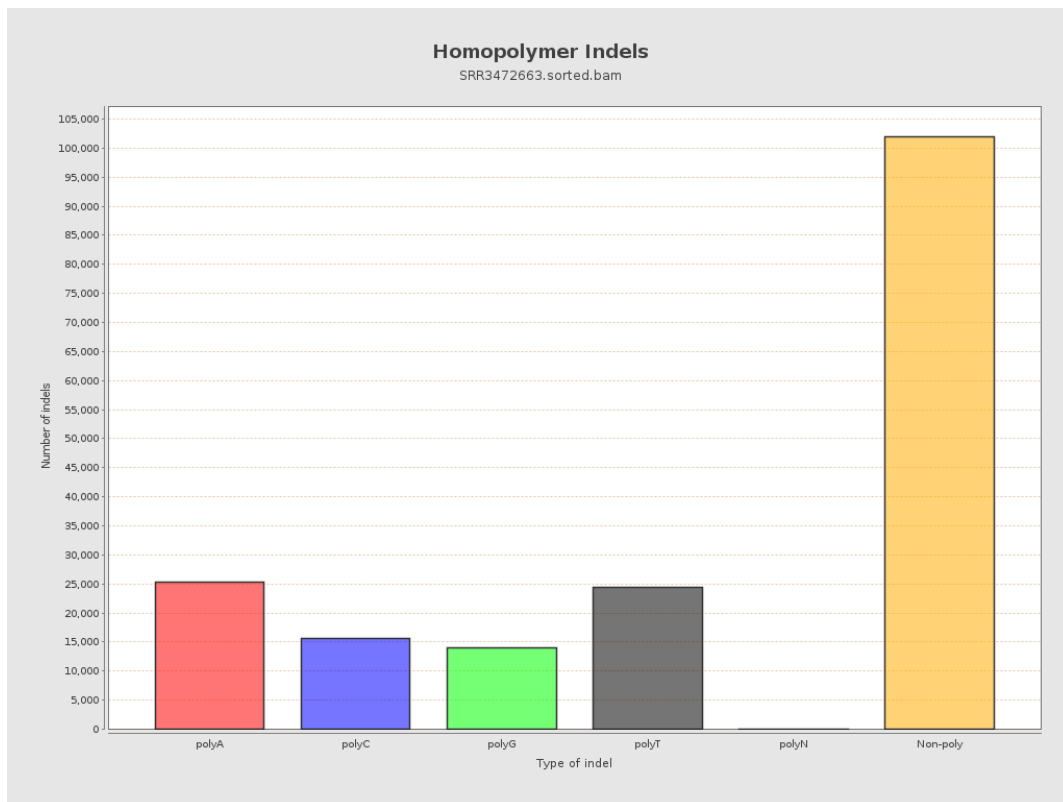
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



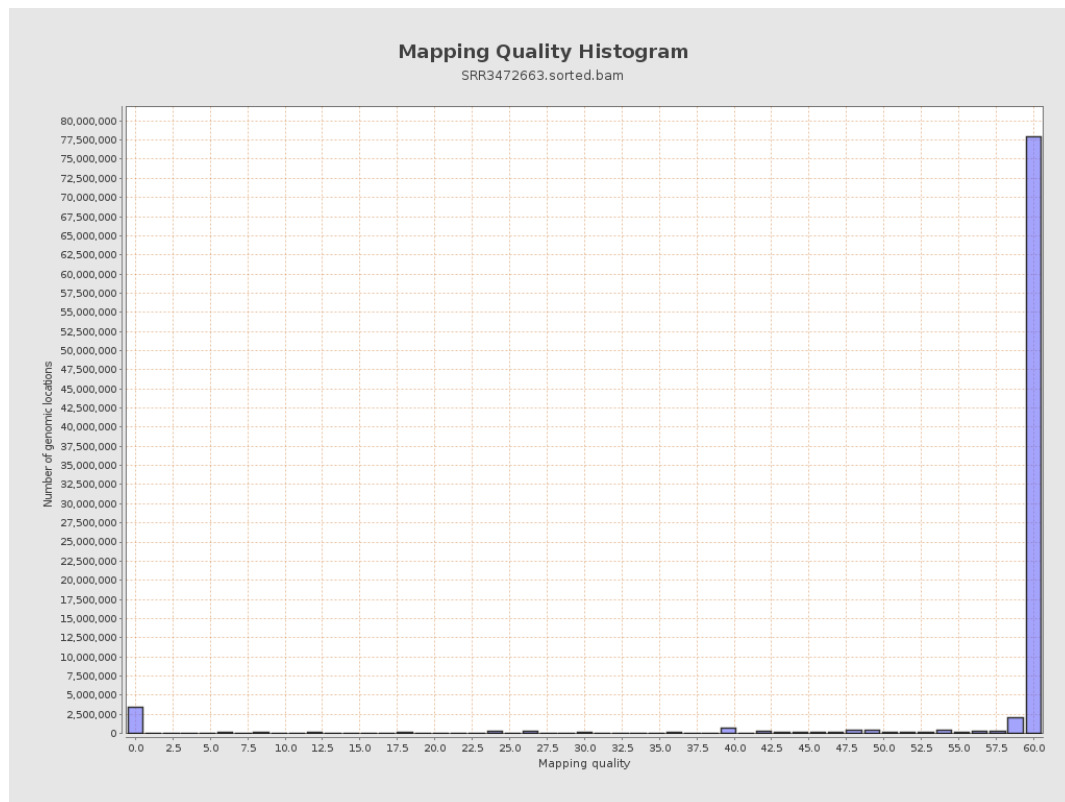
11. Results : Homopolymer Indels



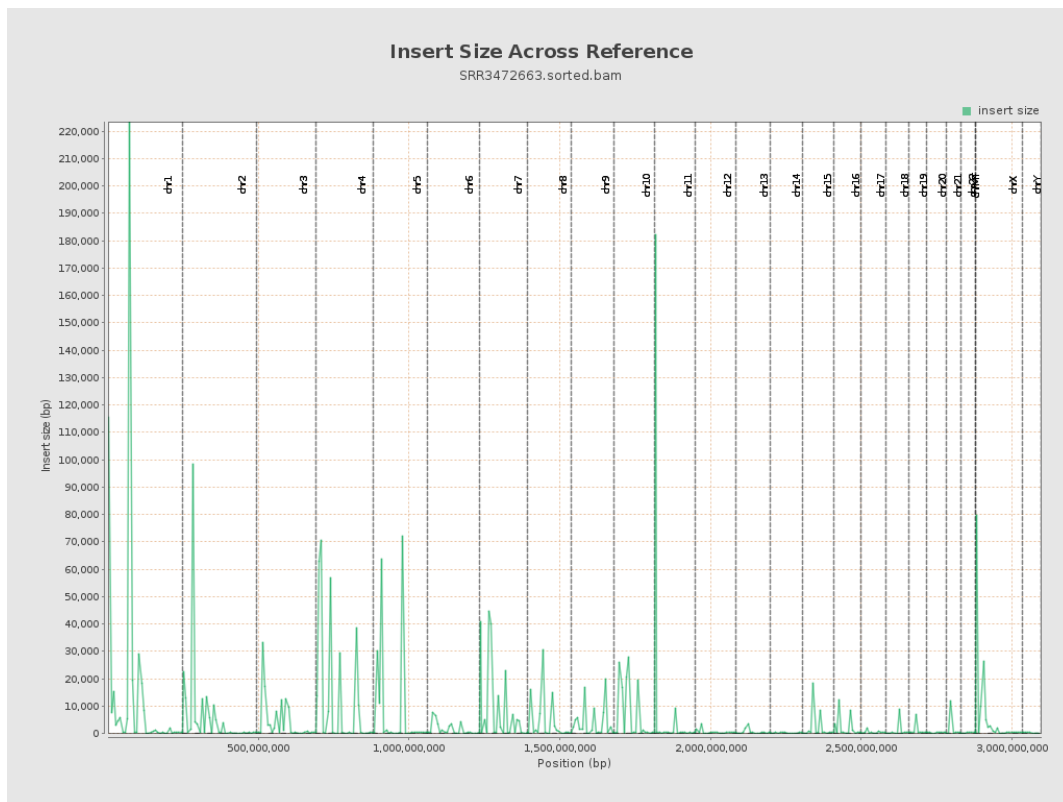
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

