

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 16:15:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472710.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_SRR3472710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472710_1.fastq.gz SRR3472710_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 16:15:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,744,586
Mapped reads	16,637,260 / 99.36%
Unmapped reads	107,326 / 0.64%
Mapped paired reads	16,637,260 / 99.36%
Mapped reads, first in pair	8,335,043 / 49.78%
Mapped reads, second in pair	8,302,217 / 49.58%
Mapped reads, both in pair	16,573,578 / 98.98%
Mapped reads, singletons	63,682 / 0.38%
Secondary alignments	0
Supplementary alignments	69,461 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	11,615,325 / 69.37%
Duplication rate	46.06%
Clipped reads	1,378,971 / 8.24%

2.2. ACGT Content

Number/percentage of A's	455,381,668 / 27.77%
Number/percentage of C's	367,471,945 / 22.41%
Number/percentage of T's	451,755,261 / 27.55%
Number/percentage of G's	364,872,506 / 22.25%
Number/percentage of N's	327,751 / 0.02%

GC Percentage	44.66%
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2.3. Coverage

Mean	0.5298
Standard Deviation	29.3616

2.4. Mapping Quality

Mean Mapping Quality	54.82
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2.5. Insert size

Mean	22,410.49
Standard Deviation	1,433,779.71
P25/Median/P75	158 / 216 / 288

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	8,724,653
Insertions	86,537
Mapped reads with at least one insertion	0.51%
Deletions	83,181
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.55%

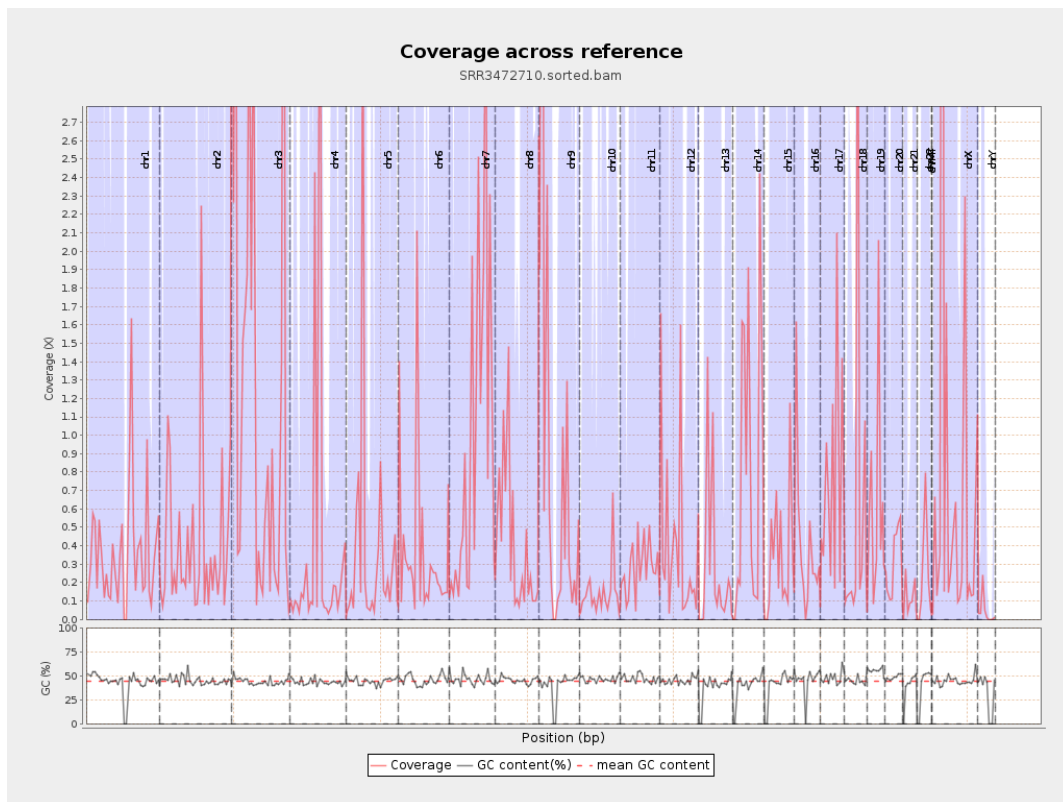
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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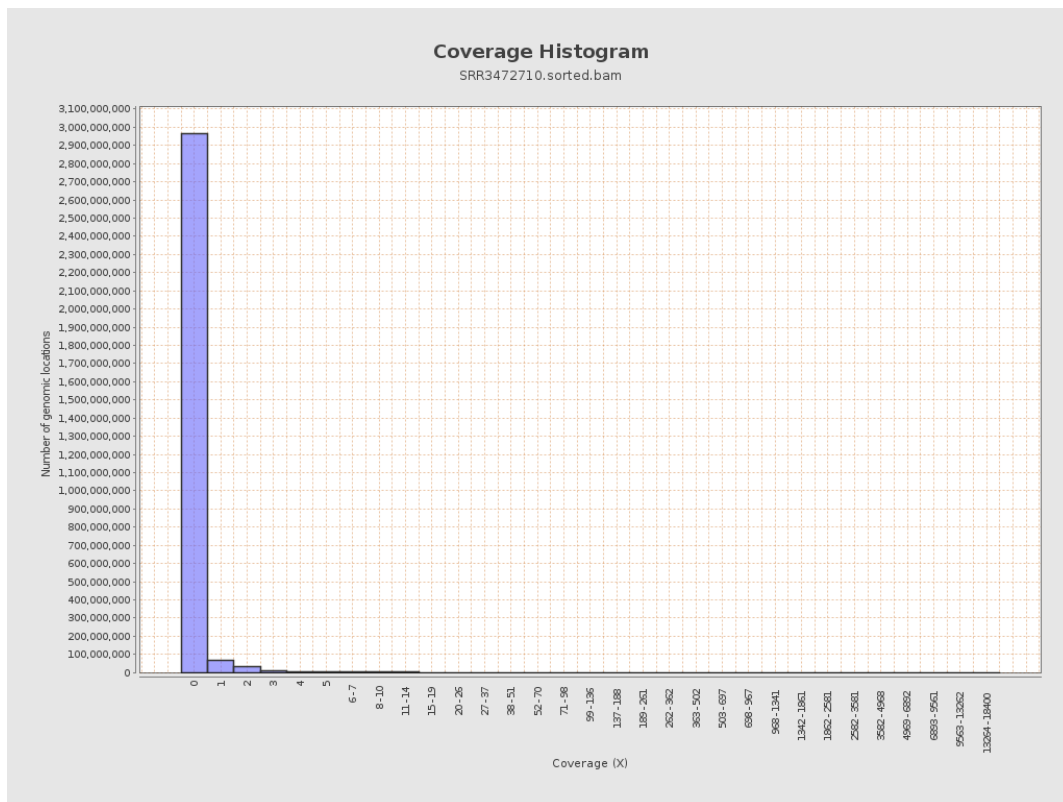
		bases	coverage	deviation
chr1	249250621	90518439	0.3632	15.5755
chr2	243199373	94989787	0.3906	18.4599
chr3	198022430	267730891	1.352	49.5108
chr4	191154276	73440916	0.3842	51.2025
chr5	180915260	68593766	0.3791	15.8887
chr6	171115067	60240364	0.352	10.7497
chr7	159138663	159231468	1.0006	40.4264
chr8	146364022	60399340	0.4127	17.3712
chr9	141213431	143420639	1.0156	35.4212
chr10	135534747	20238779	0.1493	8.8819
chr11	135006516	38000308	0.2815	11.0088
chr12	133851895	53830498	0.4022	15.6504
chr13	115169878	32939139	0.286	12.6785
chr14	107349540	80703334	0.7518	31.2402
chr15	102531392	35452877	0.3458	18.3582
chr16	90354753	34307561	0.3797	12.0516
chr17	81195210	61581427	0.7584	34.1767
chr18	78077248	50000898	0.6404	52.2181
chr19	59128983	39117186	0.6616	33.6504
chr20	63025520	20127765	0.3194	12.442
chr21	48129895	5816890	0.1209	8.7854
chr22	51304566	12352071	0.2408	11.0942
chrMT	16571	1532	0.0925	0.3361
chrX	155270560	134226402	0.8645	48.558

chrY	59373566	2769288	0.0466	2.3448
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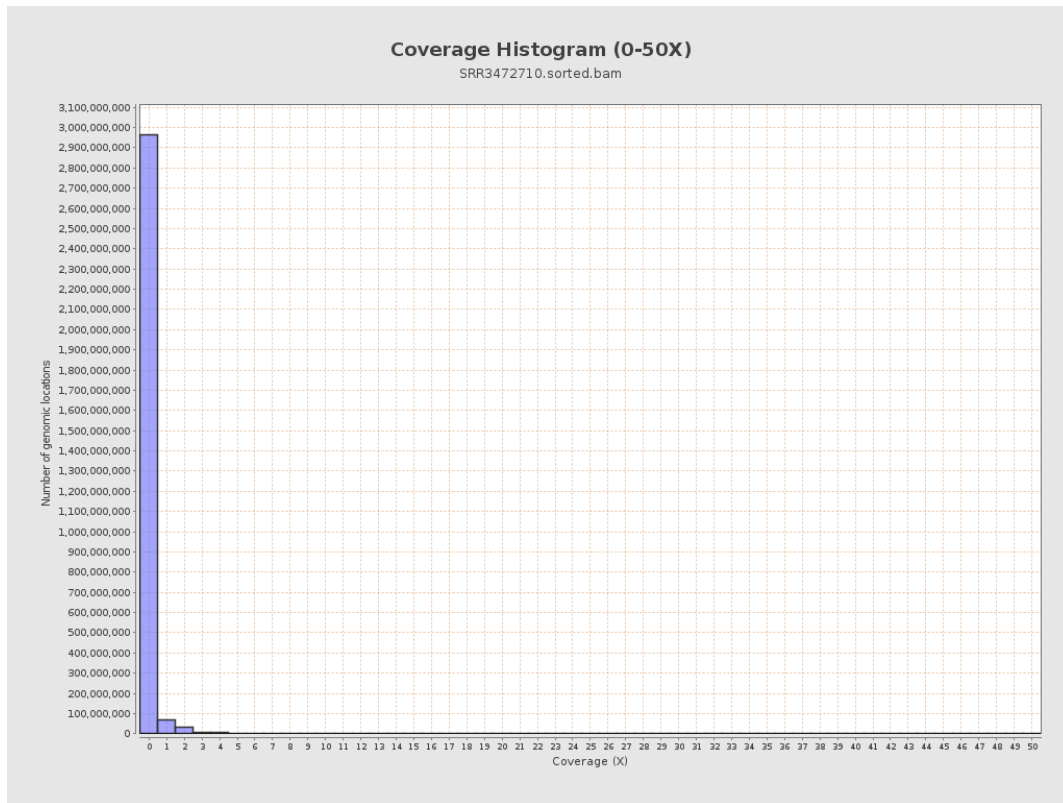
3. Results : Coverage across reference



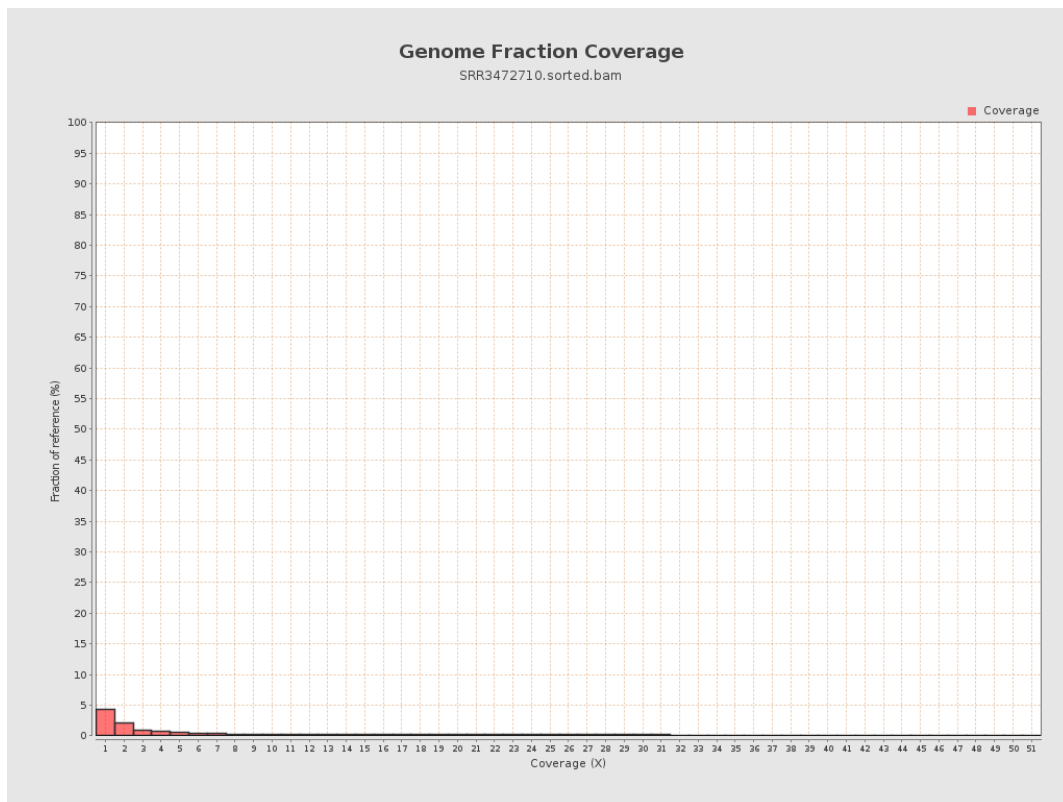
4. Results : Coverage Histogram



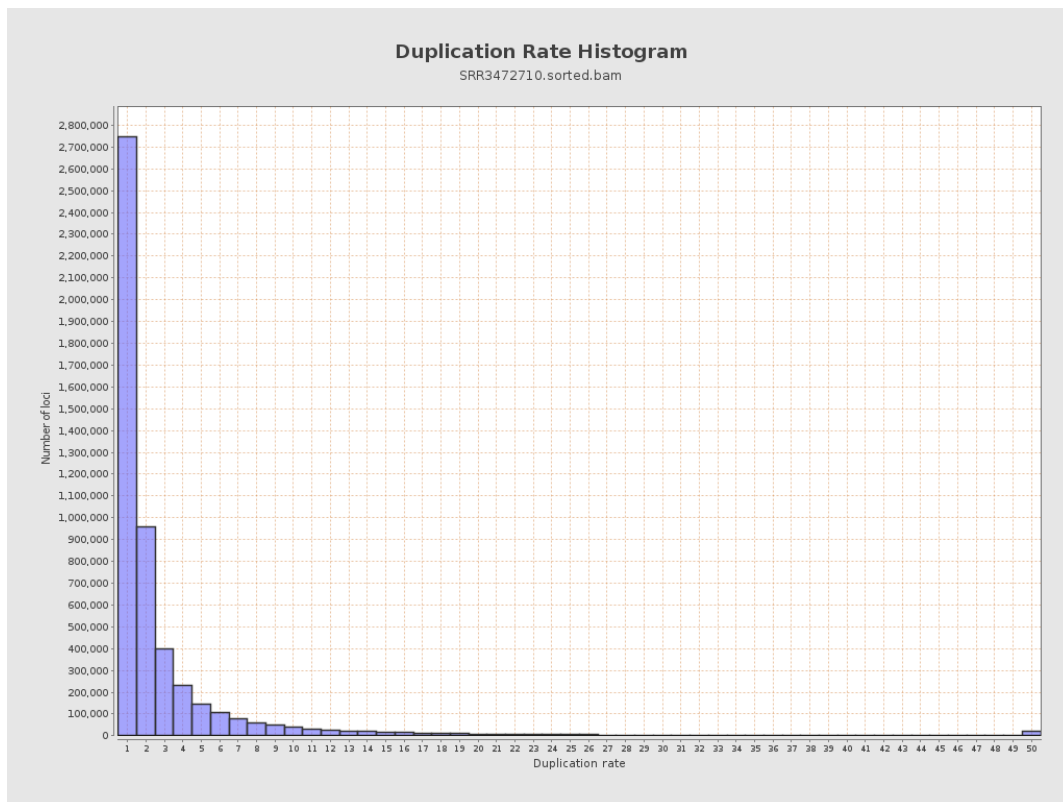
5. Results : Coverage Histogram (0-50X)



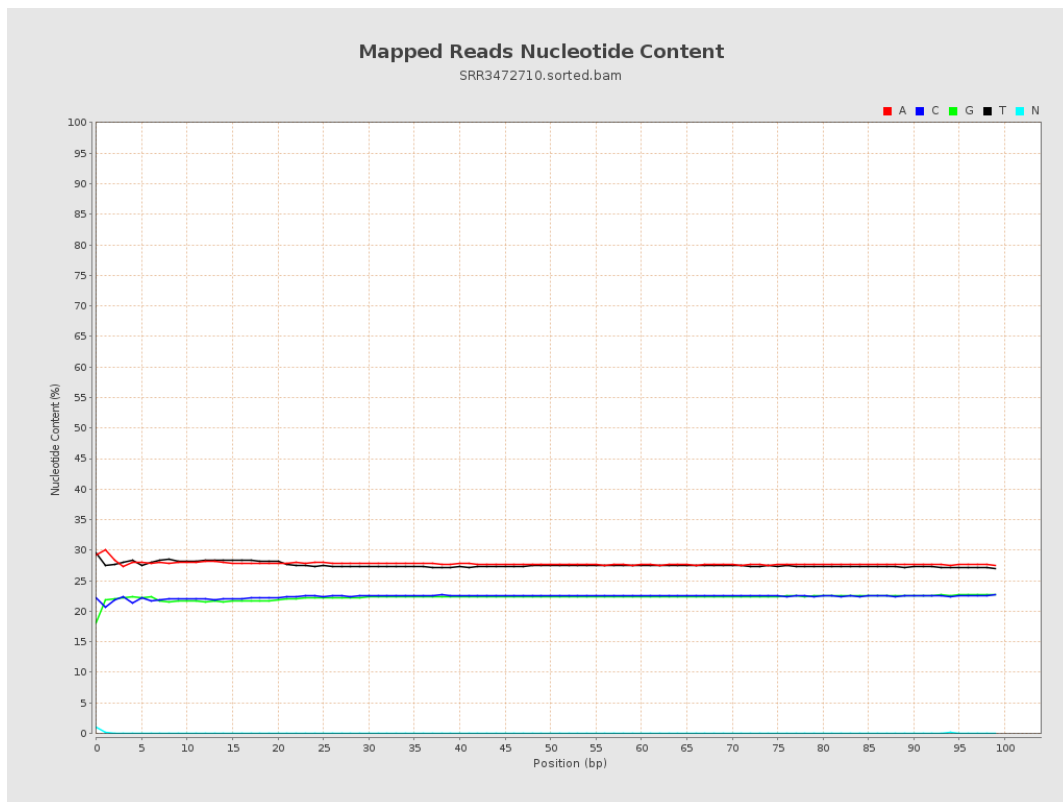
6. Results : Genome Fraction Coverage



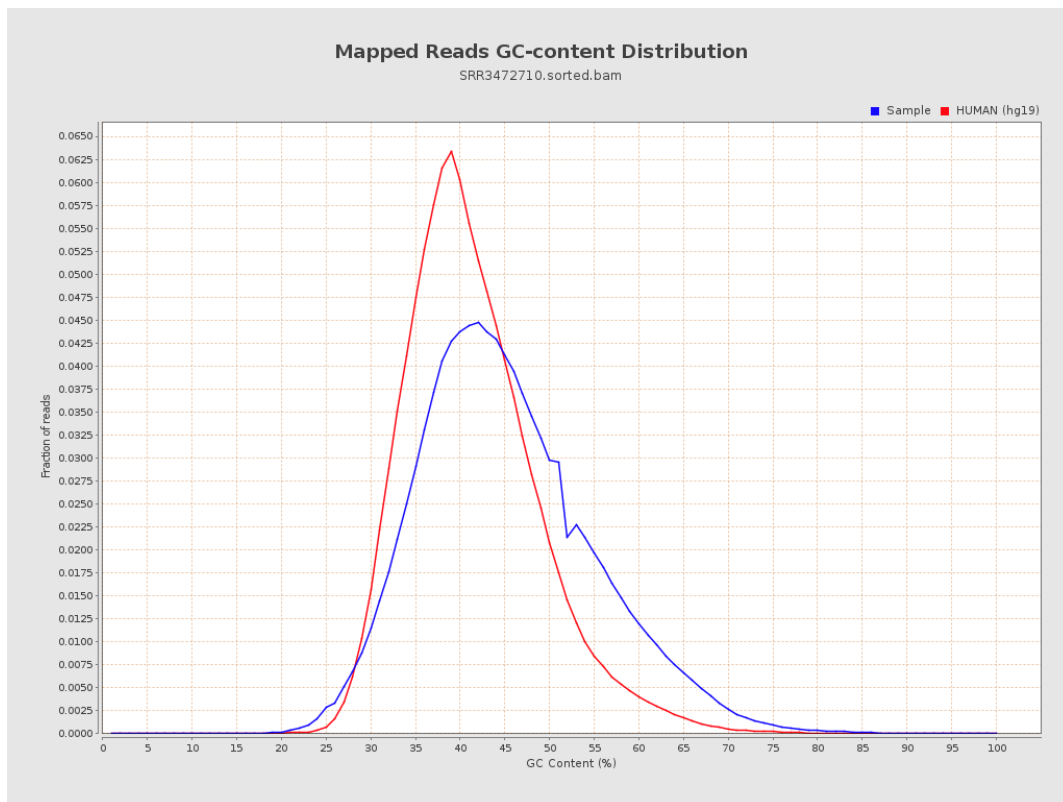
7. Results : Duplication Rate Histogram



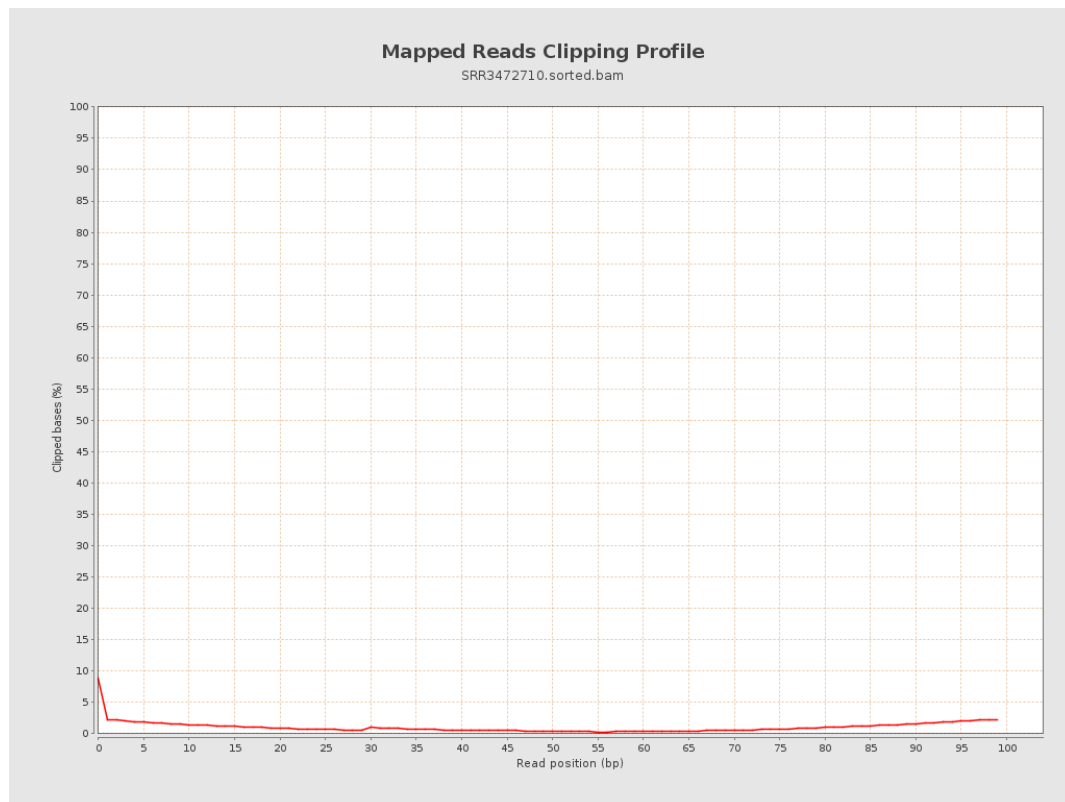
8. Results : Mapped Reads Nucleotide Content



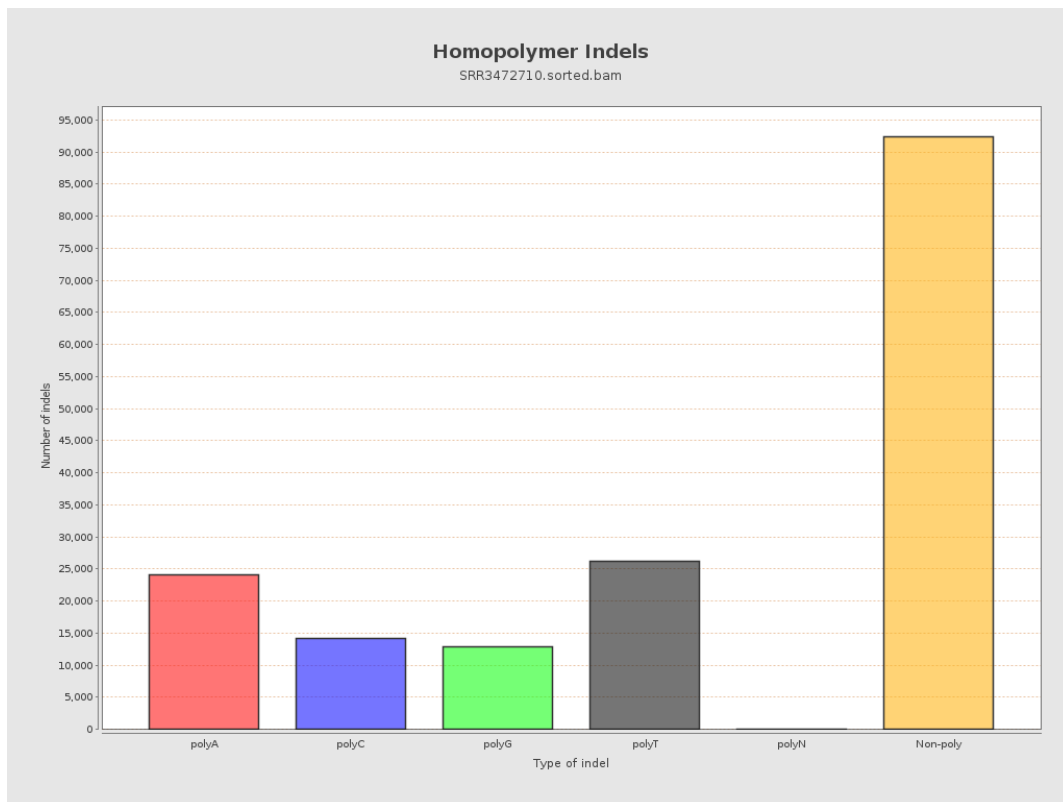
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



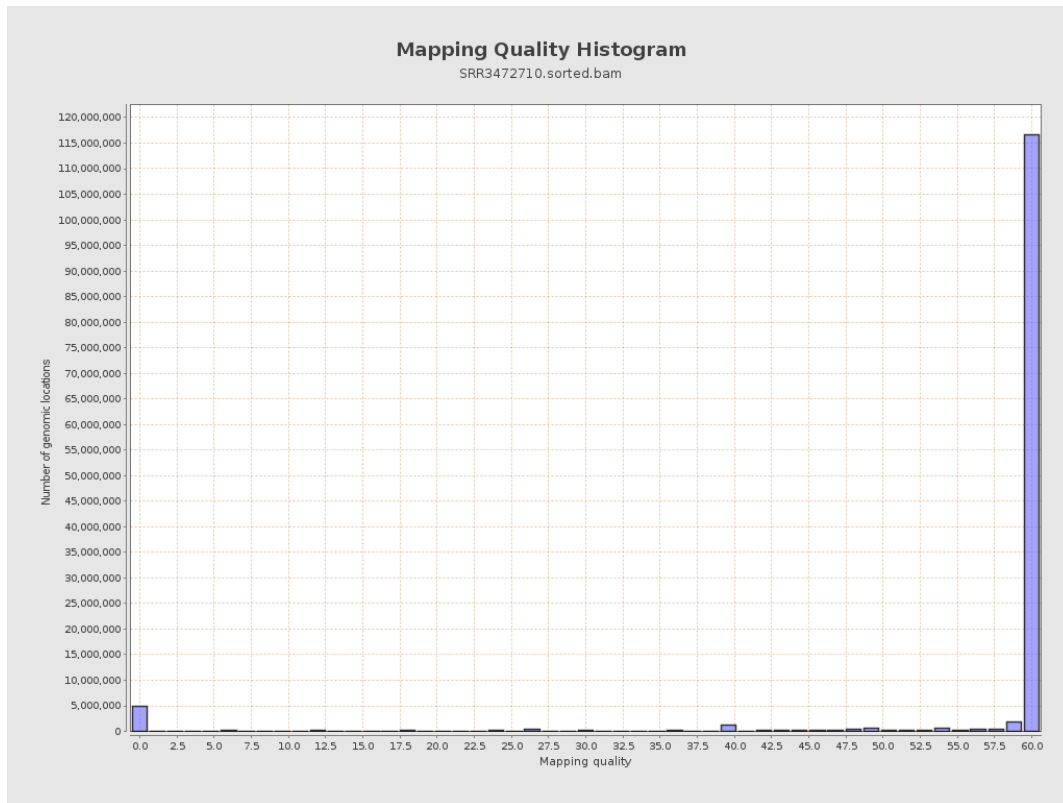
11. Results : Homopolymer Indels



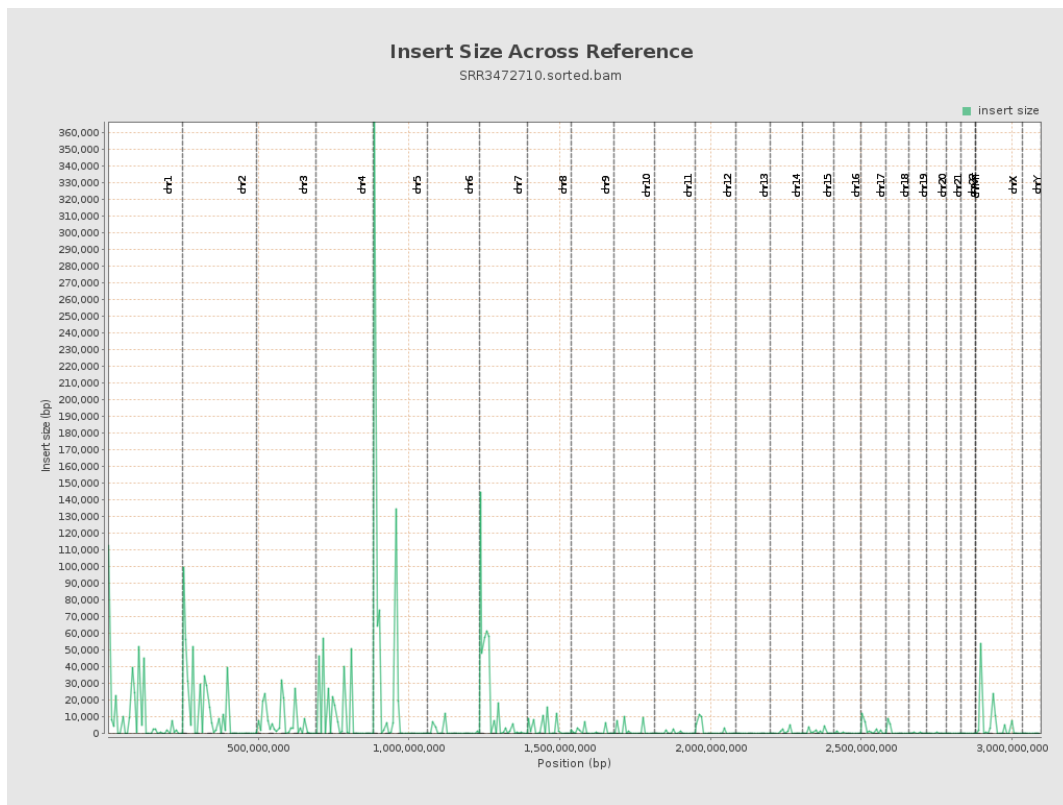
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

