

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:10:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472387.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_SRR3472387 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472387_1.fastq.gz SRR3472387_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:10:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472387.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,570,732
Mapped reads	21,399,563 / 99.21%
Unmapped reads	171,169 / 0.79%
Mapped paired reads	21,399,563 / 99.21%
Mapped reads, first in pair	10,731,433 / 49.75%
Mapped reads, second in pair	10,668,130 / 49.46%
Mapped reads, both in pair	21,297,010 / 98.73%
Mapped reads, singletons	102,553 / 0.48%
Secondary alignments	0
Supplementary alignments	83,775 / 0.39%
Read min/max/mean length	30 / 100 / 99.46
Duplicated reads (estimated)	13,935,906 / 64.61%
Duplication rate	48.29%
Clipped reads	1,391,723 / 6.45%

2.2. ACGT Content

Number/percentage of A's	566,633,673 / 26.95%
Number/percentage of C's	485,696,234 / 23.1%
Number/percentage of T's	567,872,638 / 27.01%
Number/percentage of G's	482,103,305 / 22.93%
Number/percentage of N's	260,450 / 0.01%

GC Percentage	46.03%
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2.3. Coverage

Mean	0.6793
Standard Deviation	21.2935

2.4. Mapping Quality

Mean Mapping Quality	55.15
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2.5. Insert size

Mean	17,679.88
Standard Deviation	1,293,650.27
P25/Median/P75	162 / 225 / 300

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	11,414,503
Insertions	118,950
Mapped reads with at least one insertion	0.55%
Deletions	104,484
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.96%

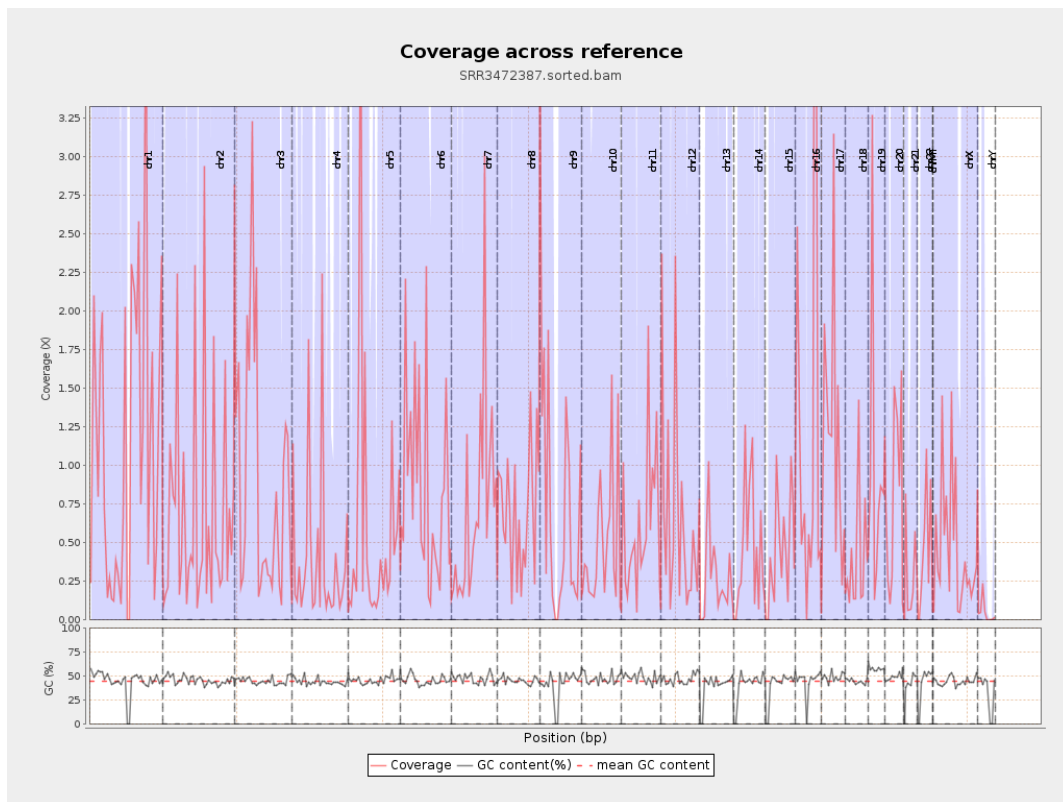
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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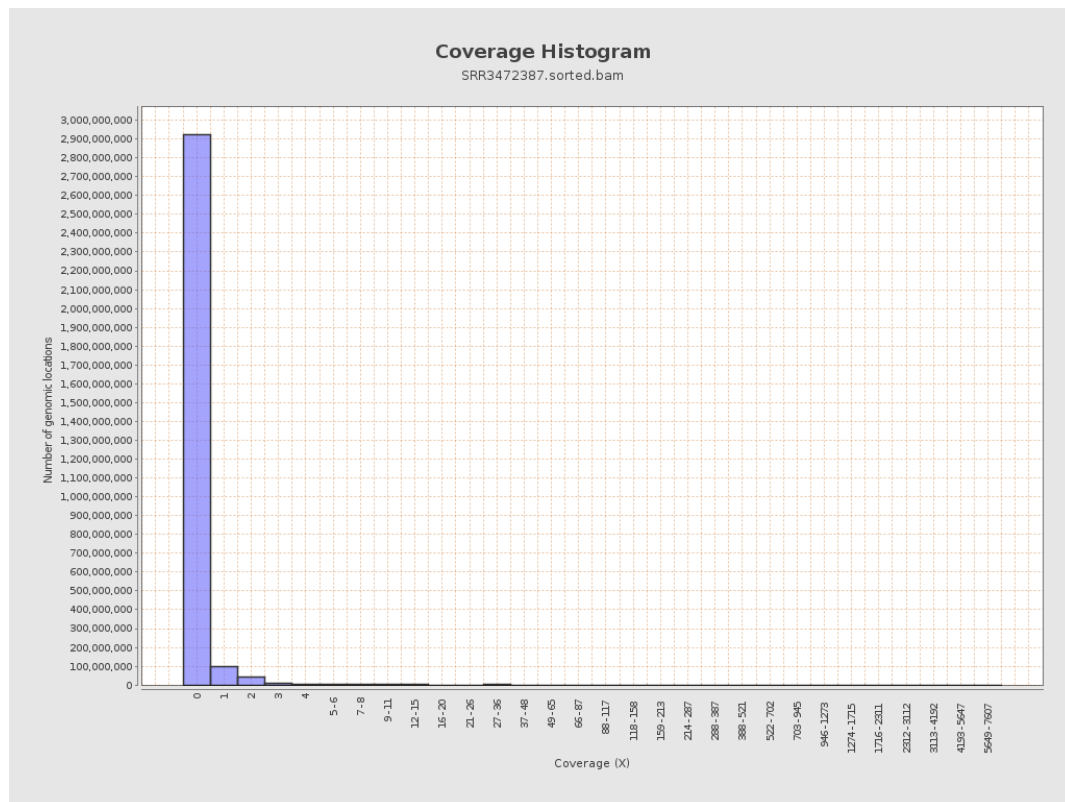
		bases	coverage	deviation
chr1	249250621	280161364	1.124	31.9865
chr2	243199373	168693126	0.6936	21.6206
chr3	198022430	179464634	0.9063	20.6919
chr4	191154276	78559318	0.411	16.2978
chr5	180915260	111658857	0.6172	22.6134
chr6	171115067	147385136	0.8613	20.332
chr7	159138663	114239732	0.7179	26.7689
chr8	146364022	102177533	0.6981	17.8777
chr9	141213431	89719584	0.6353	15.8927
chr10	135534747	68649391	0.5065	20.099
chr11	135006516	82459402	0.6108	18.1371
chr12	133851895	91375200	0.6827	17.7506
chr13	115169878	31472207	0.2733	8.1622
chr14	107349540	49148297	0.4578	13.9294
chr15	102531392	44599793	0.435	13.4024
chr16	90354753	112328495	1.2432	37.2392
chr17	81195210	98452939	1.2125	32.3848
chr18	78077248	30355186	0.3888	16.3214
chr19	59128983	57464284	0.9718	21.7048
chr20	63025520	50453667	0.8005	20.4428
chr21	48129895	14327648	0.2977	14.4141
chr22	51304566	23660449	0.4612	15.4032
chrMT	16571	2330	0.1406	0.4179
chrX	155270560	73188864	0.4714	16.6848

chrY	59373566	2844073	0.0479	2.3027
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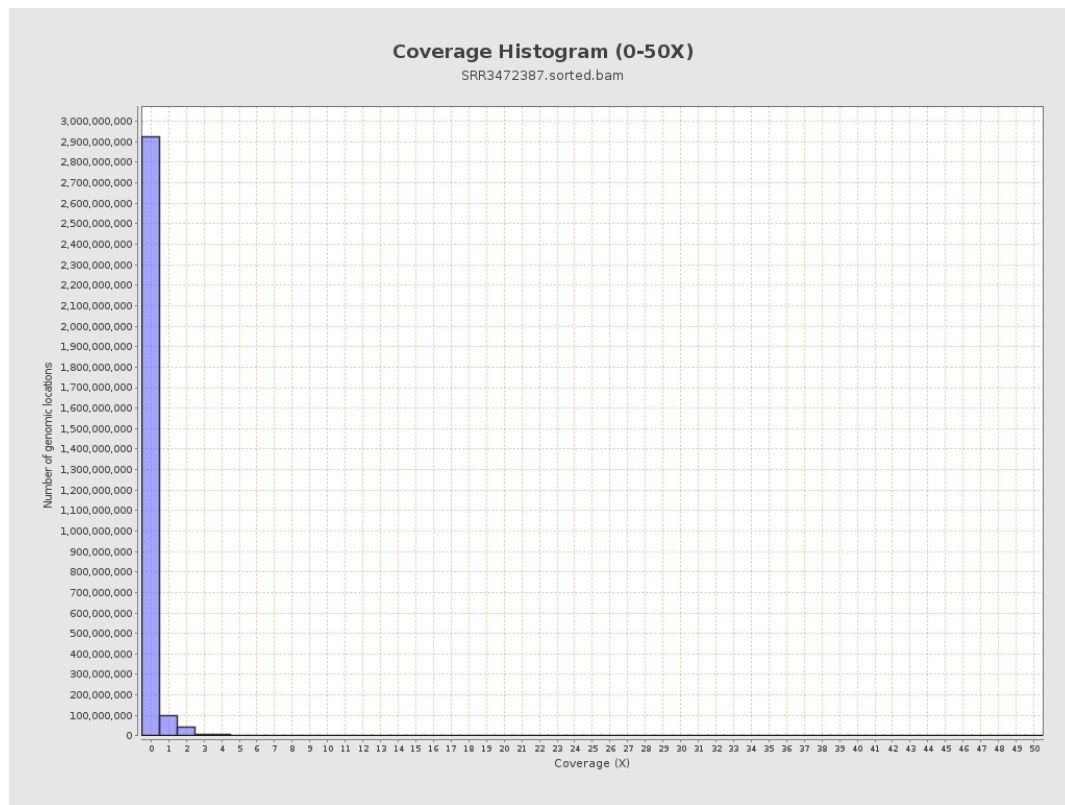
3. Results : Coverage across reference



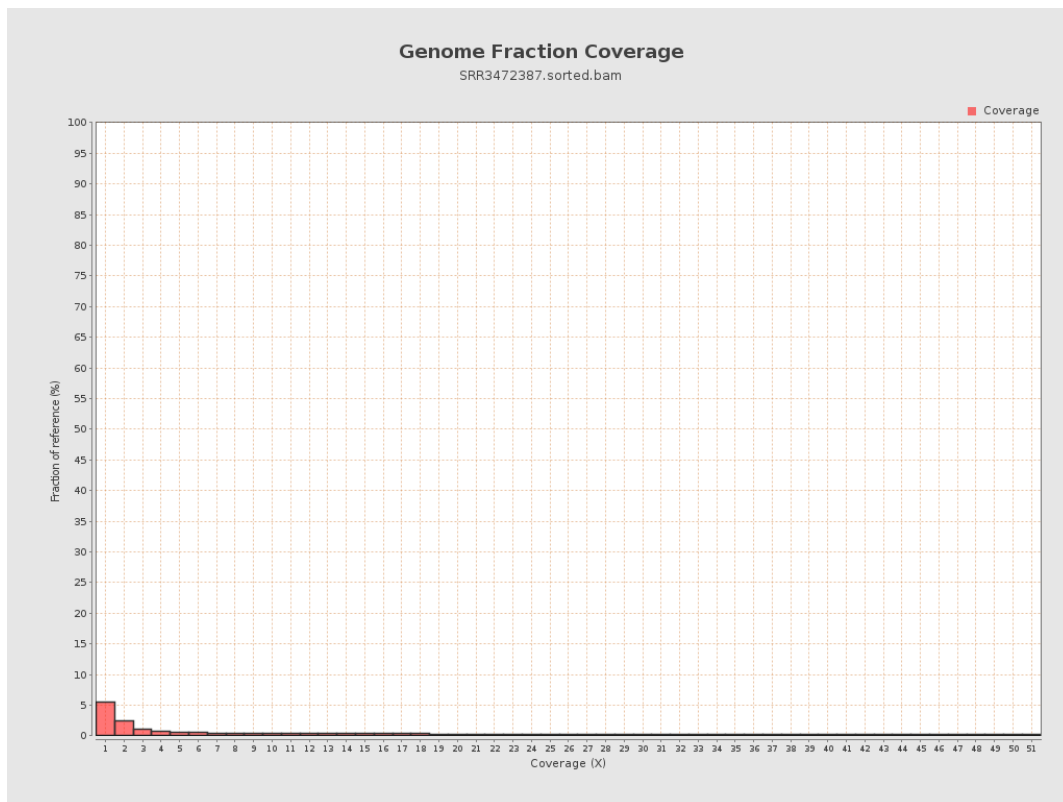
4. Results : Coverage Histogram



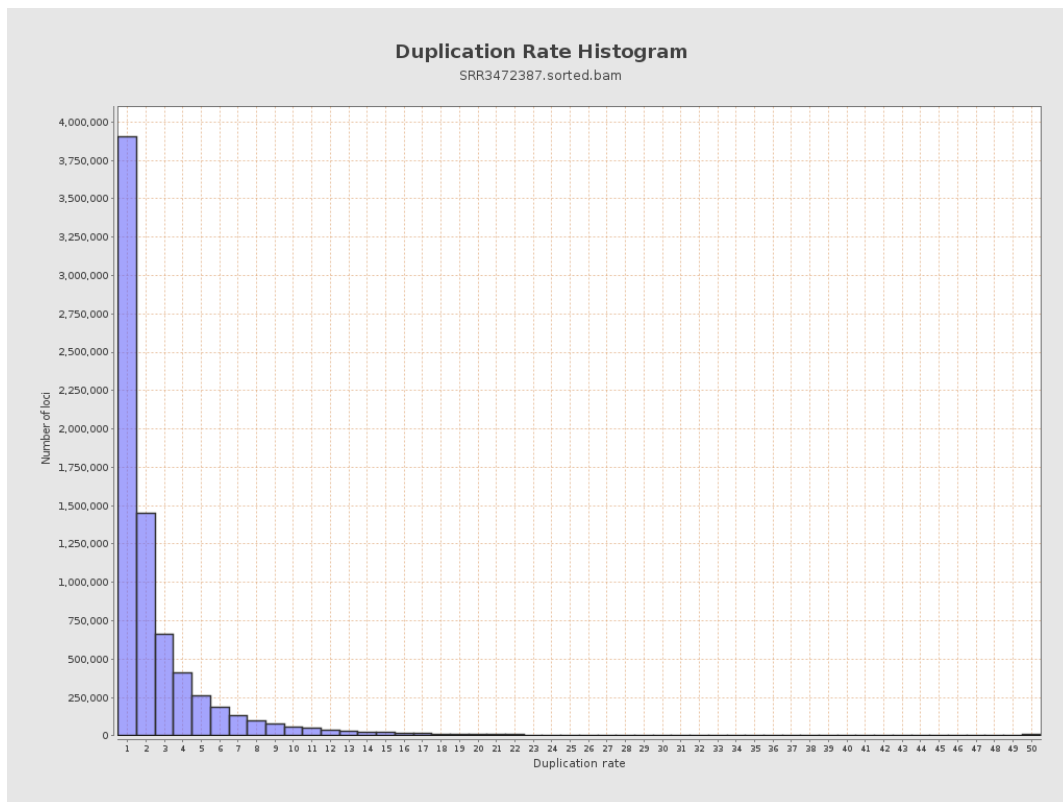
5. Results : Coverage Histogram (0-50X)



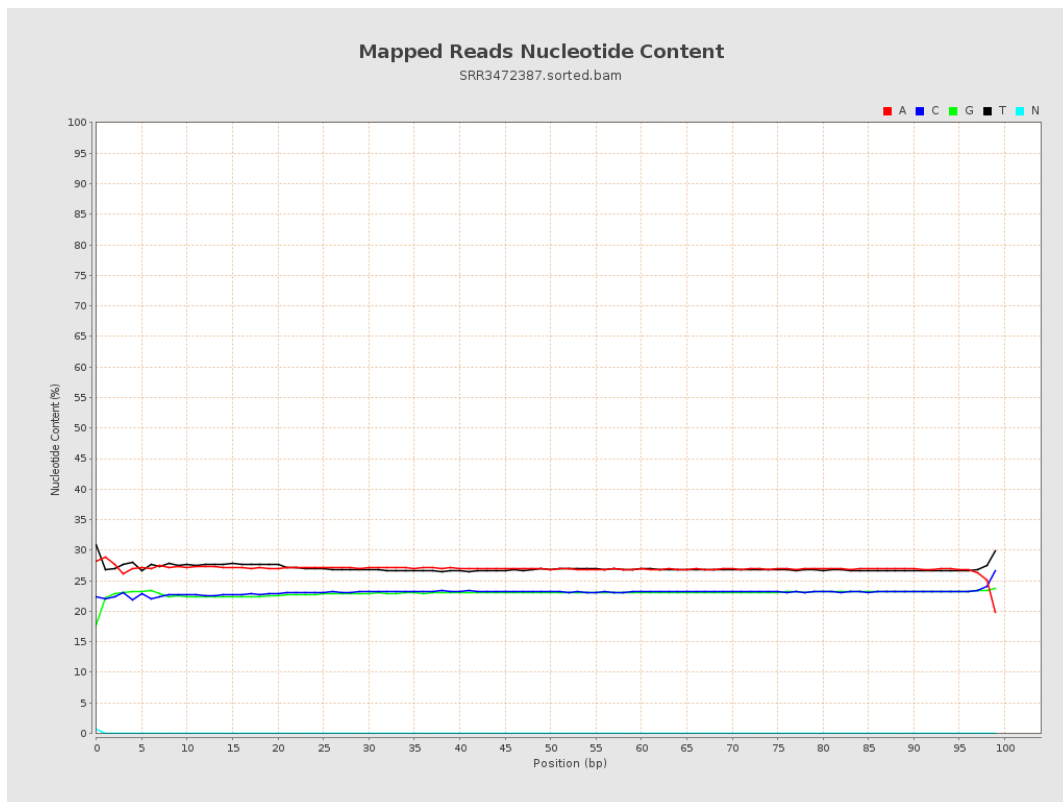
6. Results : Genome Fraction Coverage



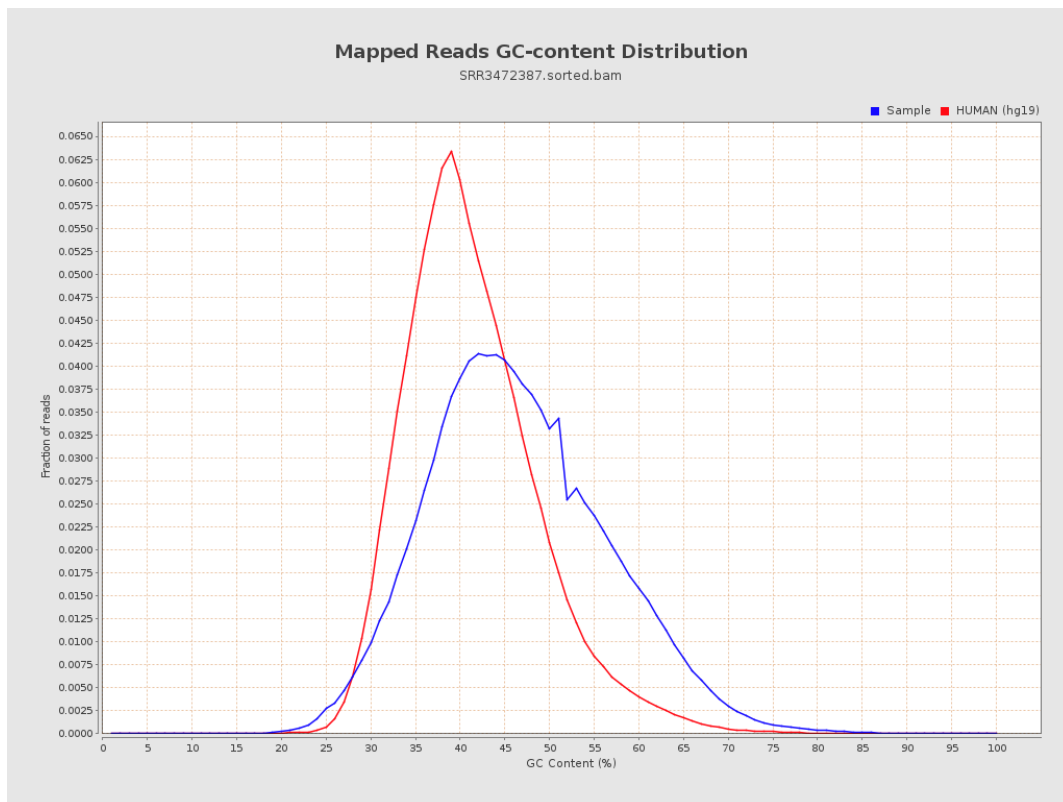
7. Results : Duplication Rate Histogram



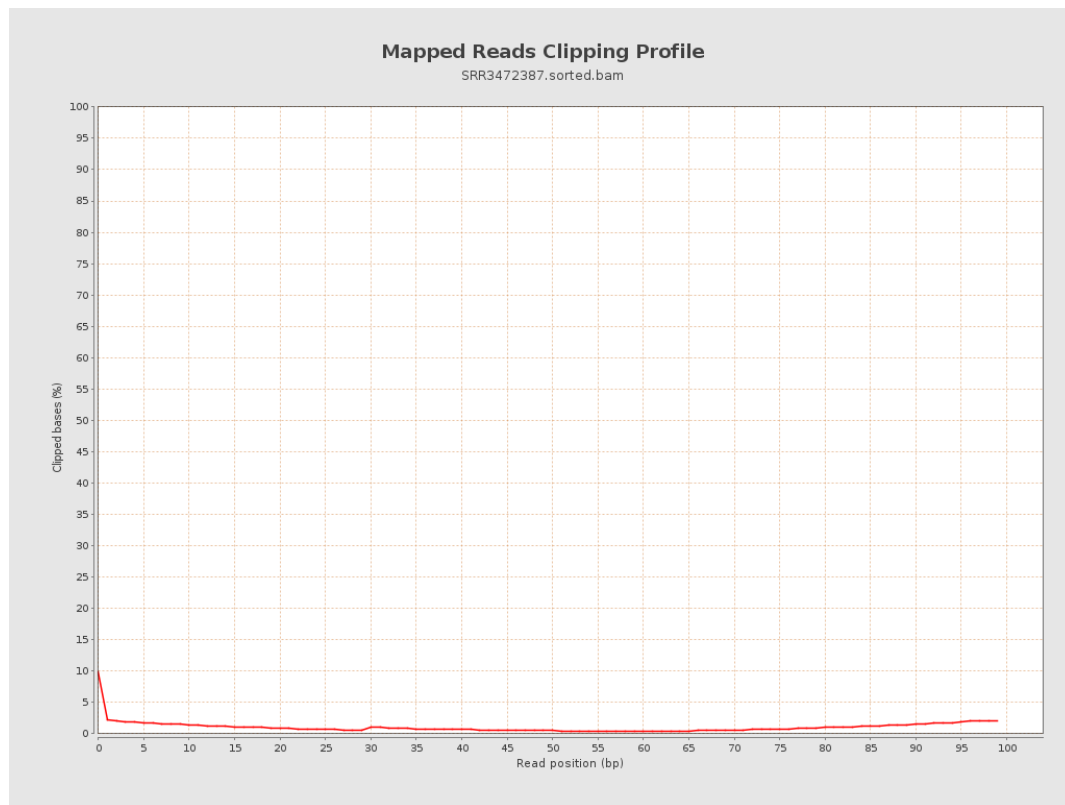
8. Results : Mapped Reads Nucleotide Content



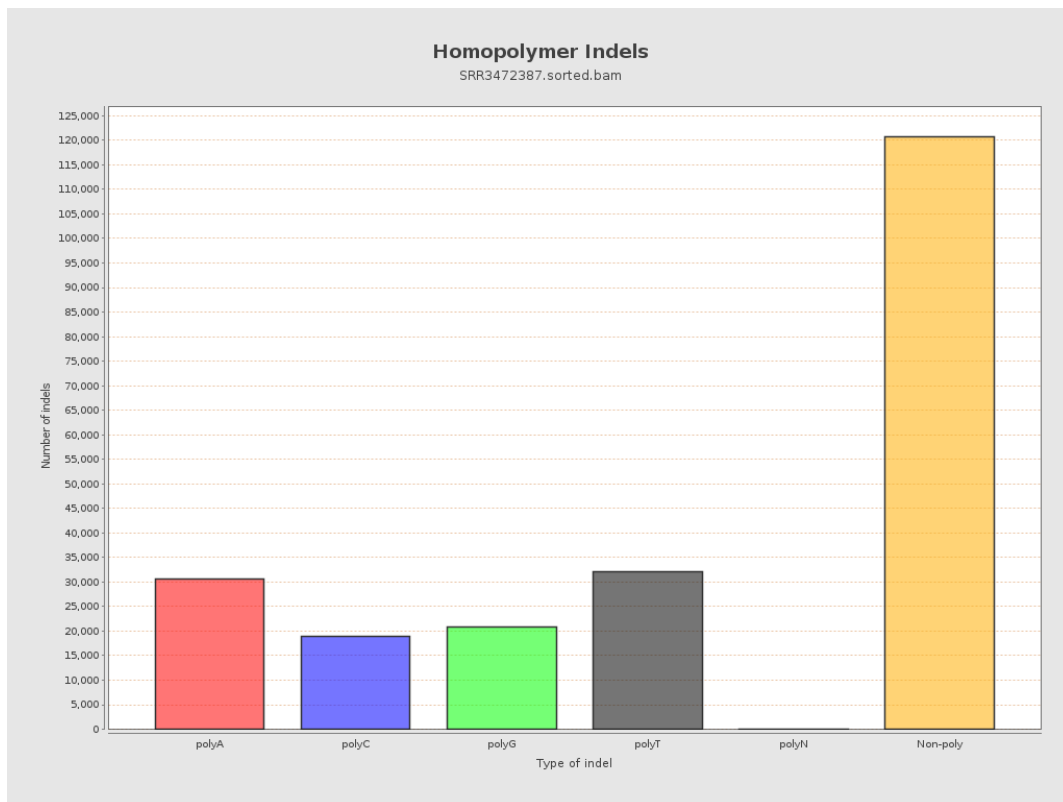
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



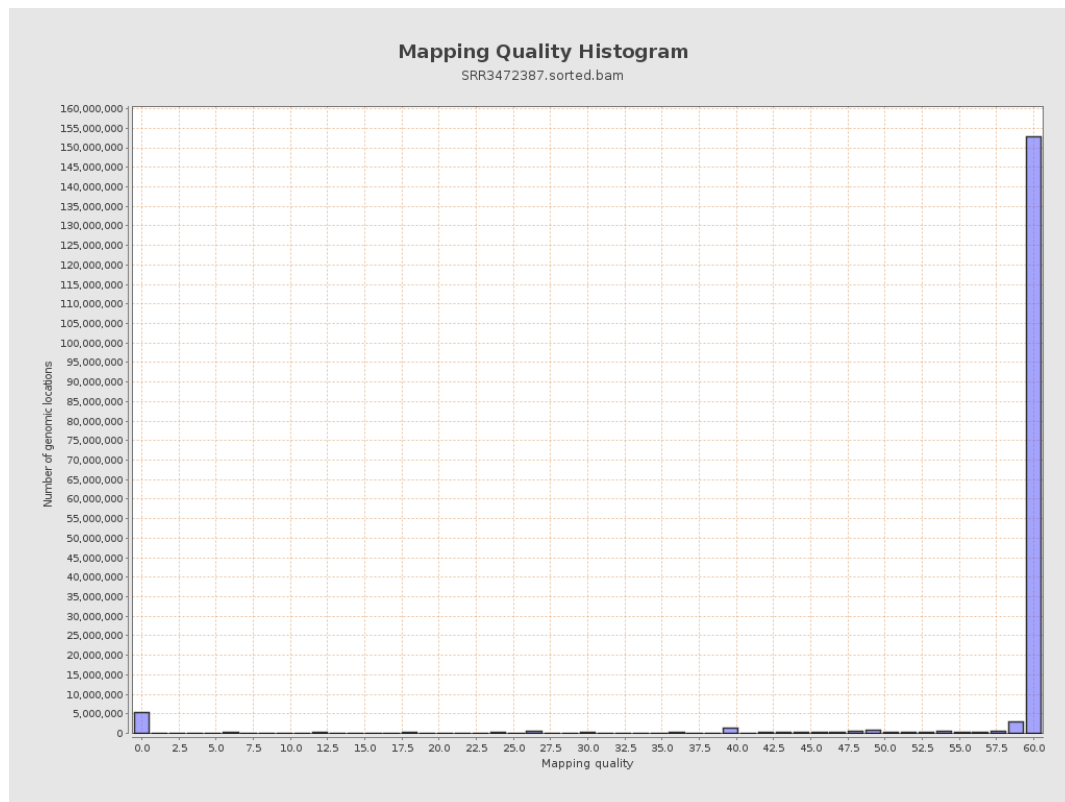
11. Results : Homopolymer Indels



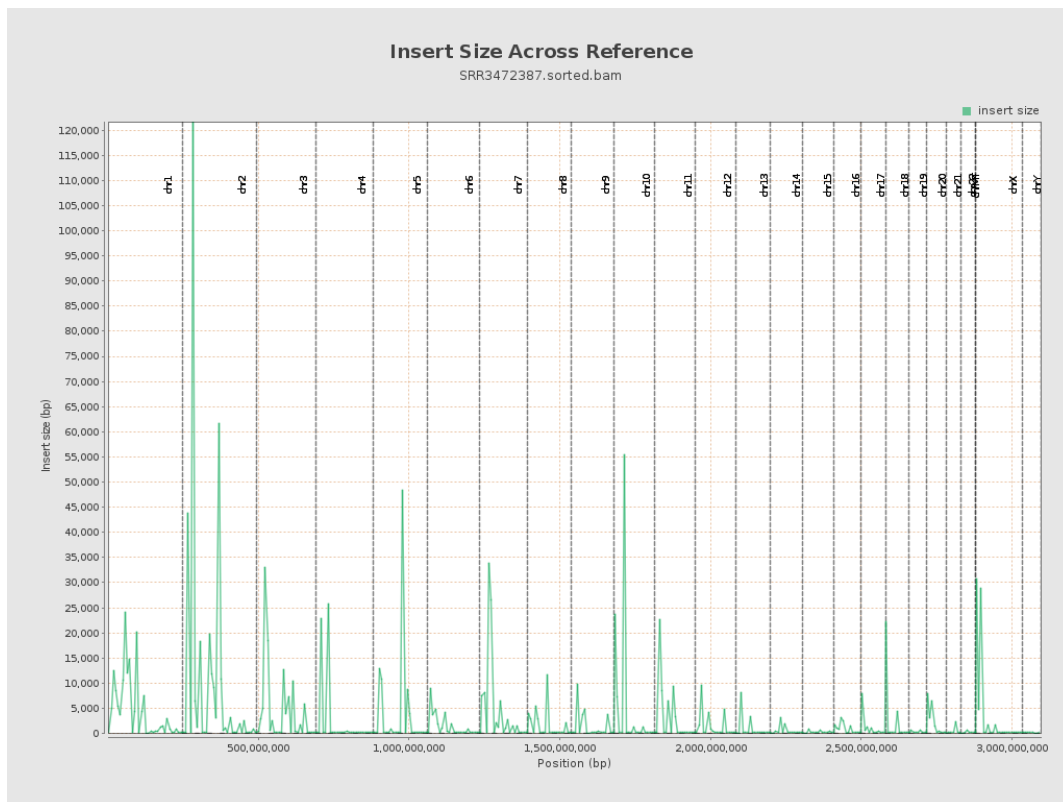
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

