

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:34:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472482.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_SRR3472482 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472482_1.fastq.gz SRR3472482_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:34:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472482.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	301,816
Mapped reads	297,720 / 98.64%
Unmapped reads	4,096 / 1.36%
Mapped paired reads	297,720 / 98.64%
Mapped reads, first in pair	149,501 / 49.53%
Mapped reads, second in pair	148,219 / 49.11%
Mapped reads, both in pair	295,626 / 97.95%
Mapped reads, singletons	2,094 / 0.69%
Secondary alignments	0
Supplementary alignments	1,128 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	52,323 / 17.34%
Duplication rate	17.26%
Clipped reads	24,282 / 8.05%

2.2. ACGT Content

Number/percentage of A's	8,139,929 / 27.77%
Number/percentage of C's	6,555,159 / 22.36%
Number/percentage of T's	8,104,350 / 27.65%
Number/percentage of G's	6,506,276 / 22.2%
Number/percentage of N's	4,534 / 0.02%

GC Percentage	44.56%
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2.3. Coverage

Mean	0.0095
Standard Deviation	0.2543

2.4. Mapping Quality

Mean Mapping Quality	55.1
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2.5. Insert size

Mean	27,140.04
Standard Deviation	1,567,337.2
P25/Median/P75	171 / 238 / 323

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	183,812
Insertions	1,672
Mapped reads with at least one insertion	0.55%
Deletions	1,497
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.23%

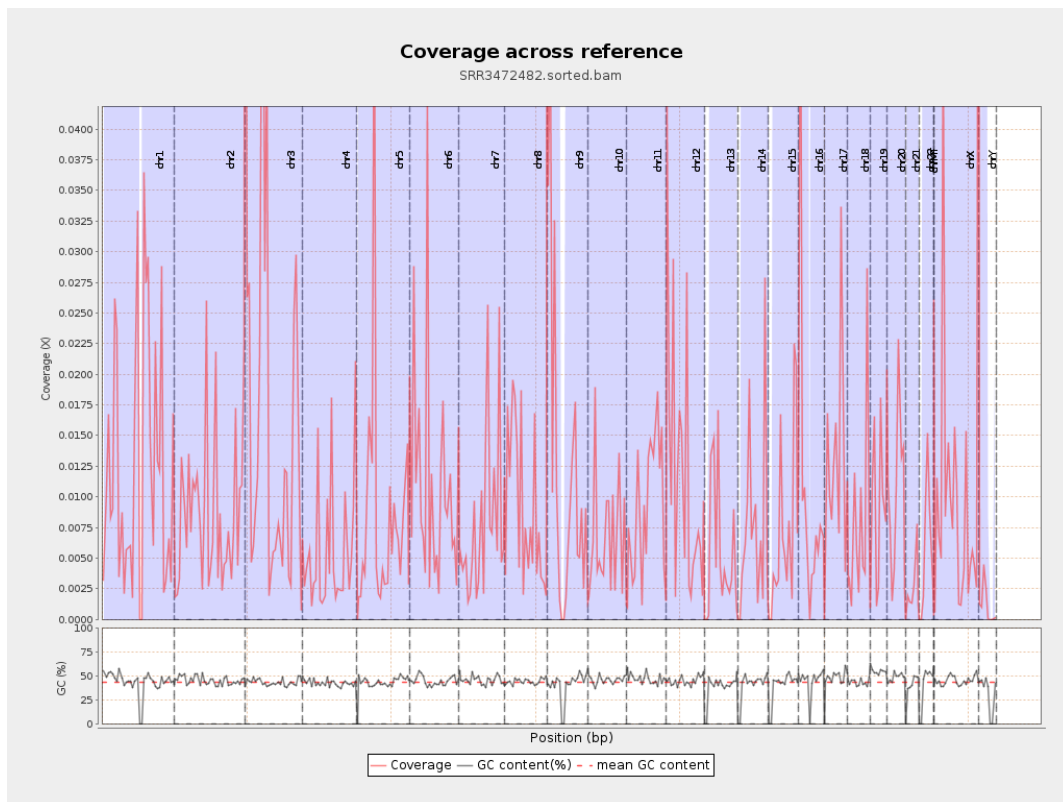
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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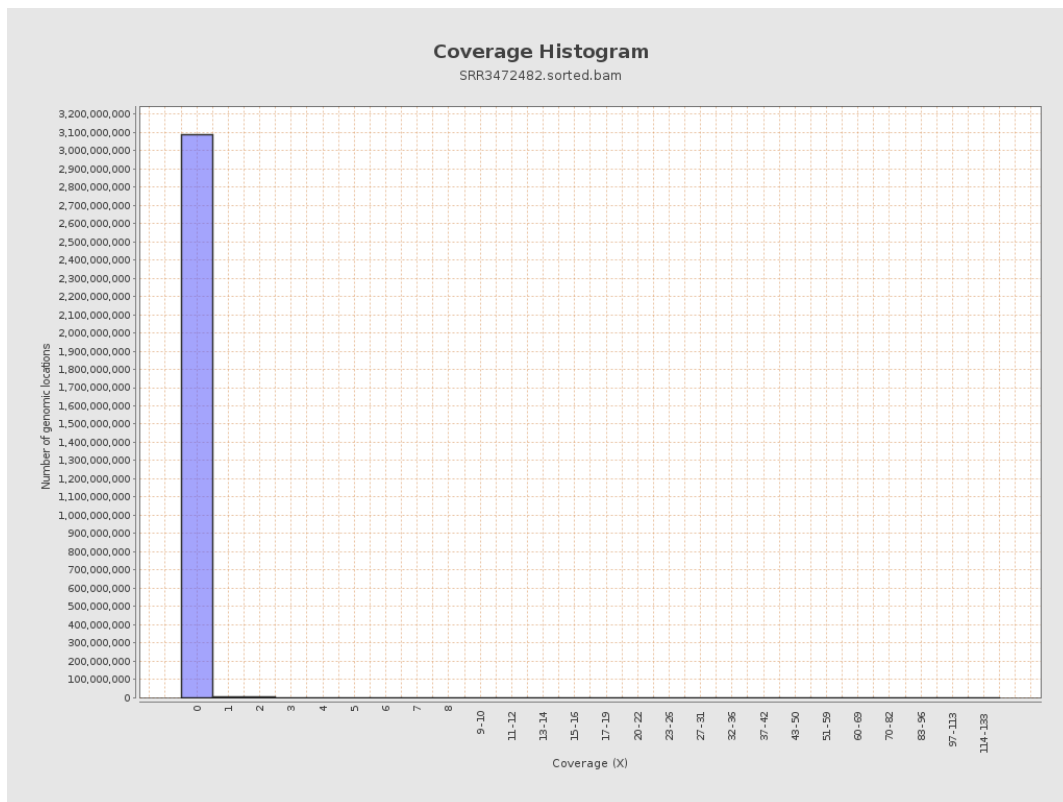
		bases	coverage	deviation
chr1	249250621	3135279	0.0126	0.3179
chr2	243199373	2078865	0.0085	0.2419
chr3	198022430	3287026	0.0166	0.3096
chr4	191154276	1099676	0.0058	0.1841
chr5	180915260	1583759	0.0088	0.2224
chr6	171115067	1911751	0.0112	0.271
chr7	159138663	1249363	0.0079	0.2107
chr8	146364022	1312515	0.009	0.2411
chr9	141213431	1766168	0.0125	0.2688
chr10	135534747	891111	0.0066	0.267
chr11	135006516	1280020	0.0095	0.2543
chr12	133851895	1600537	0.012	0.3181
chr13	115169878	618619	0.0054	0.1708
chr14	107349540	807808	0.0075	0.333
chr15	102531392	749271	0.0073	0.212
chr16	90354753	959289	0.0106	0.2436
chr17	81195210	1070689	0.0132	0.271
chr18	78077248	598622	0.0077	0.2439
chr19	59128983	570278	0.0096	0.2433
chr20	63025520	646419	0.0103	0.2702
chr21	48129895	123964	0.0026	0.0967
chr22	51304566	297747	0.0058	0.1756
chrMT	16571	432	0.0261	0.1856
chrX	155270560	1603676	0.0103	0.252

chrY	59373566	70907	0.0012	0.0594
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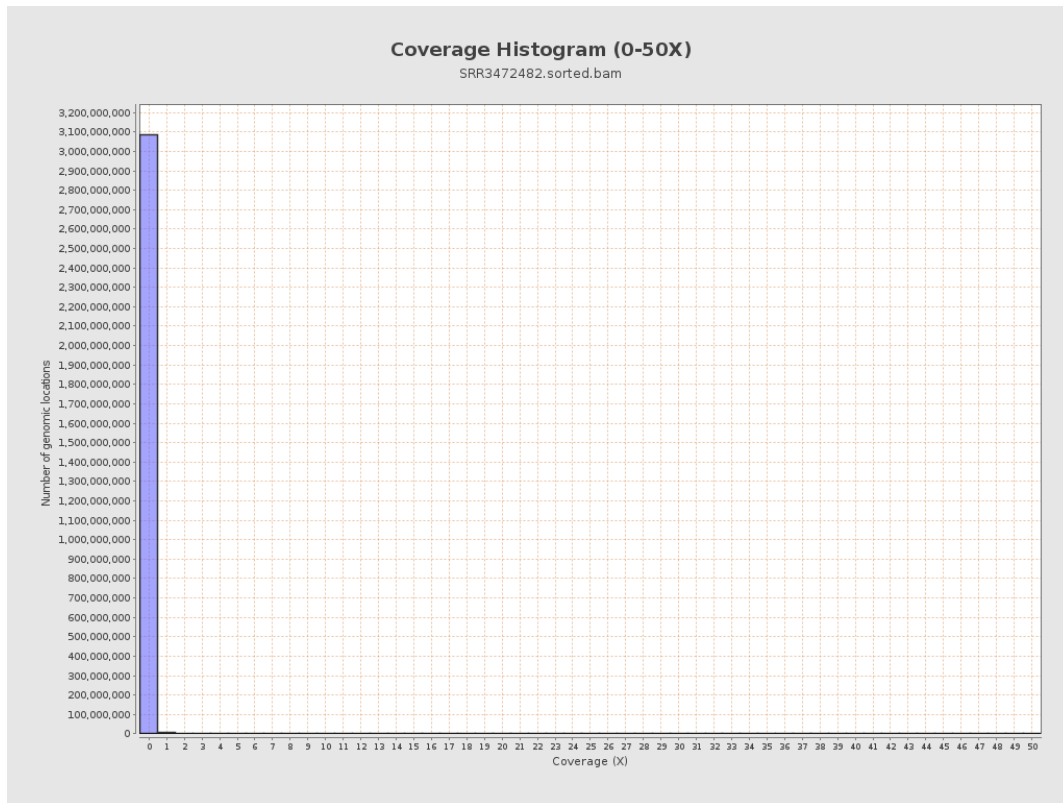
3. Results : Coverage across reference



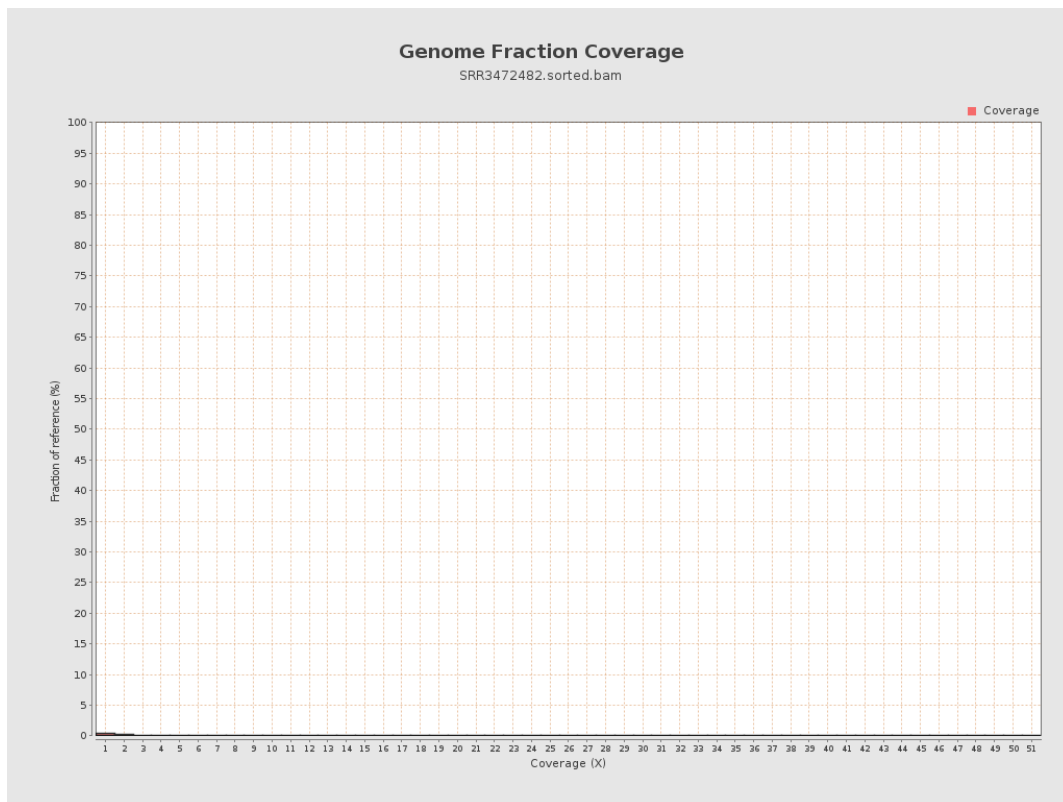
4. Results : Coverage Histogram



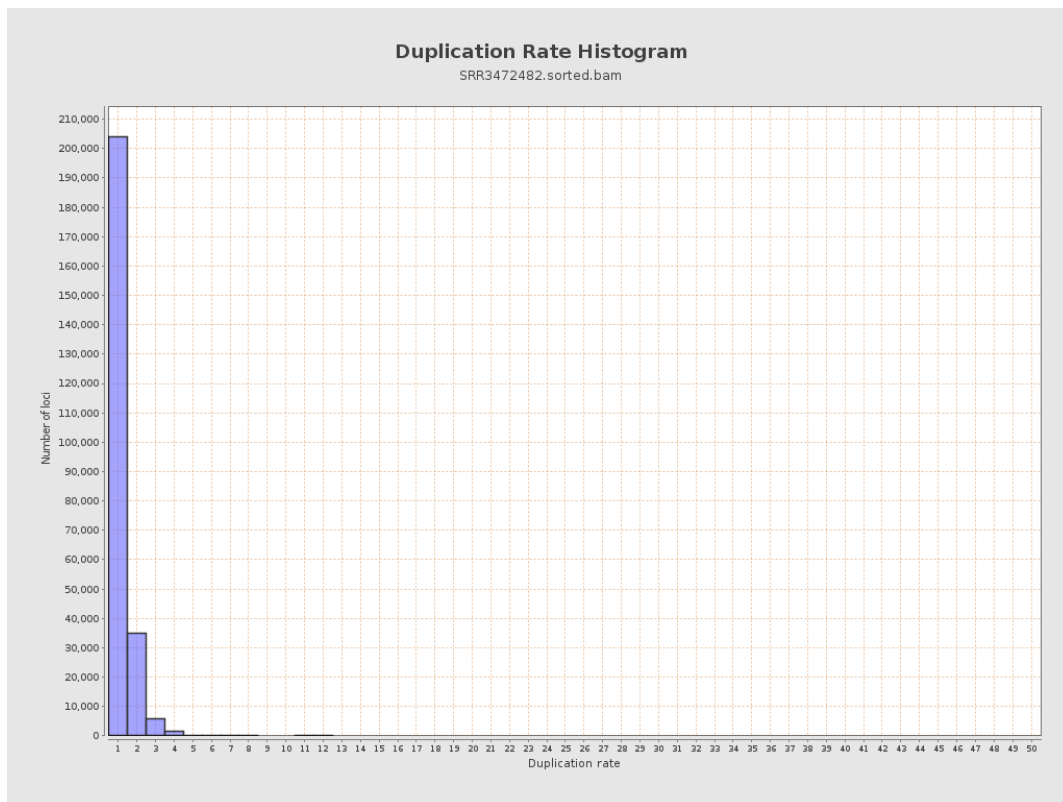
5. Results : Coverage Histogram (0-50X)



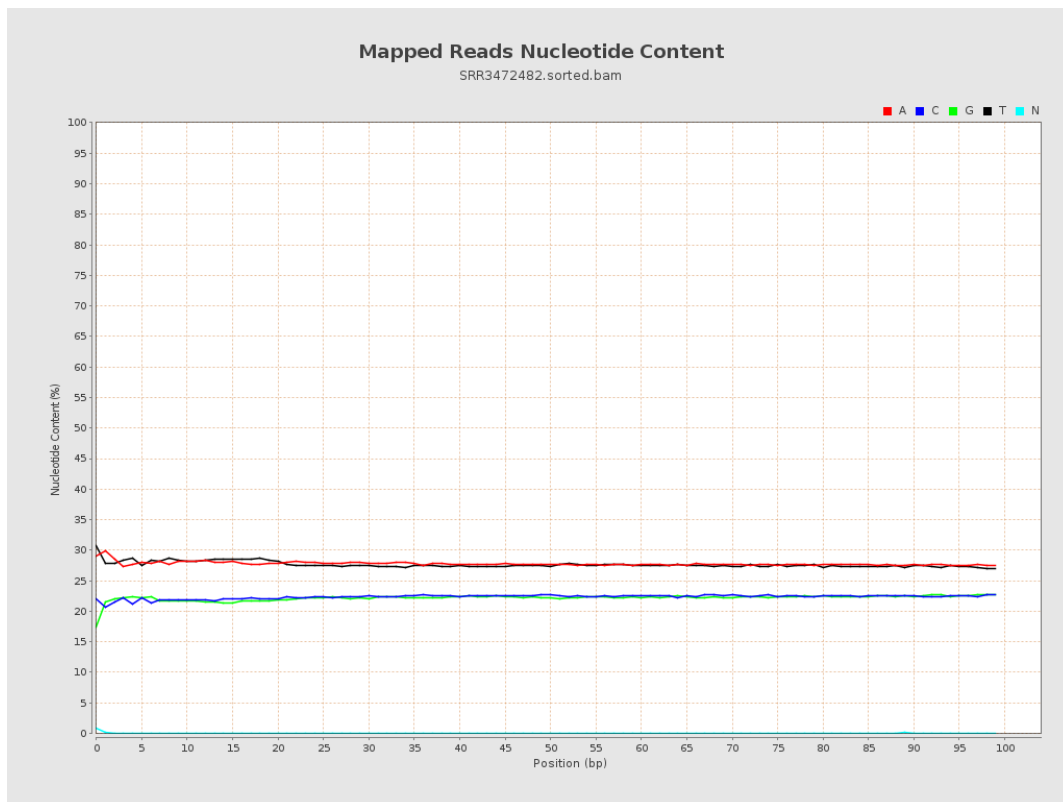
6. Results : Genome Fraction Coverage



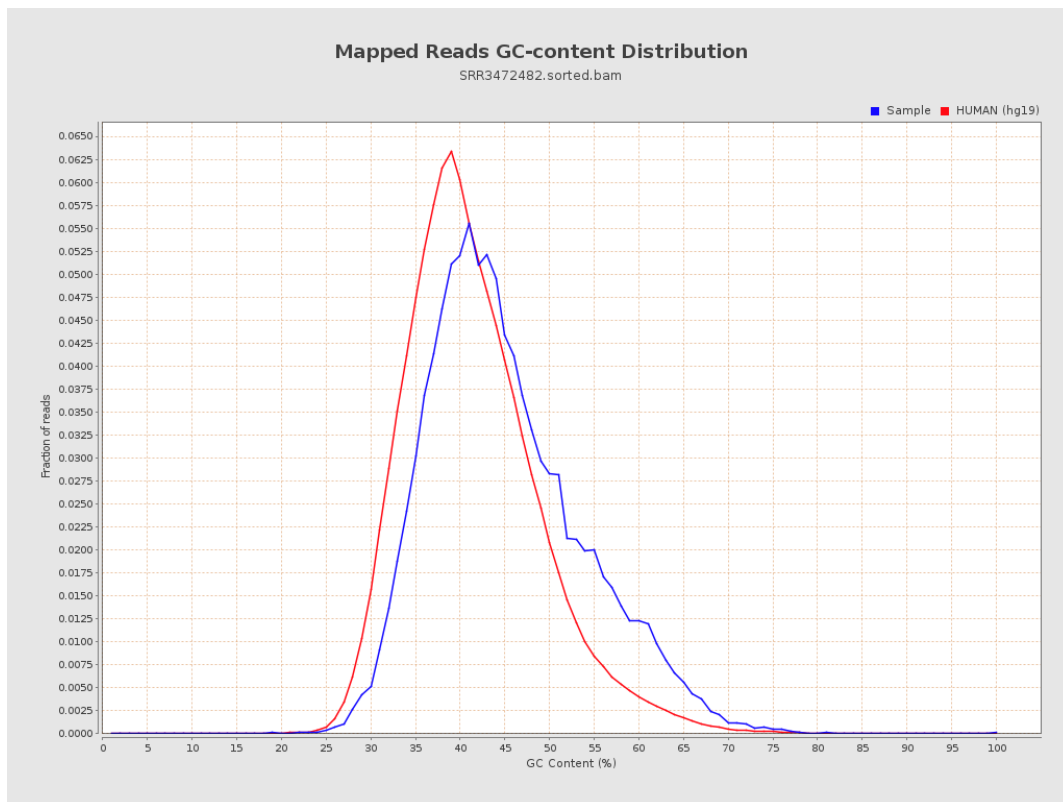
7. Results : Duplication Rate Histogram



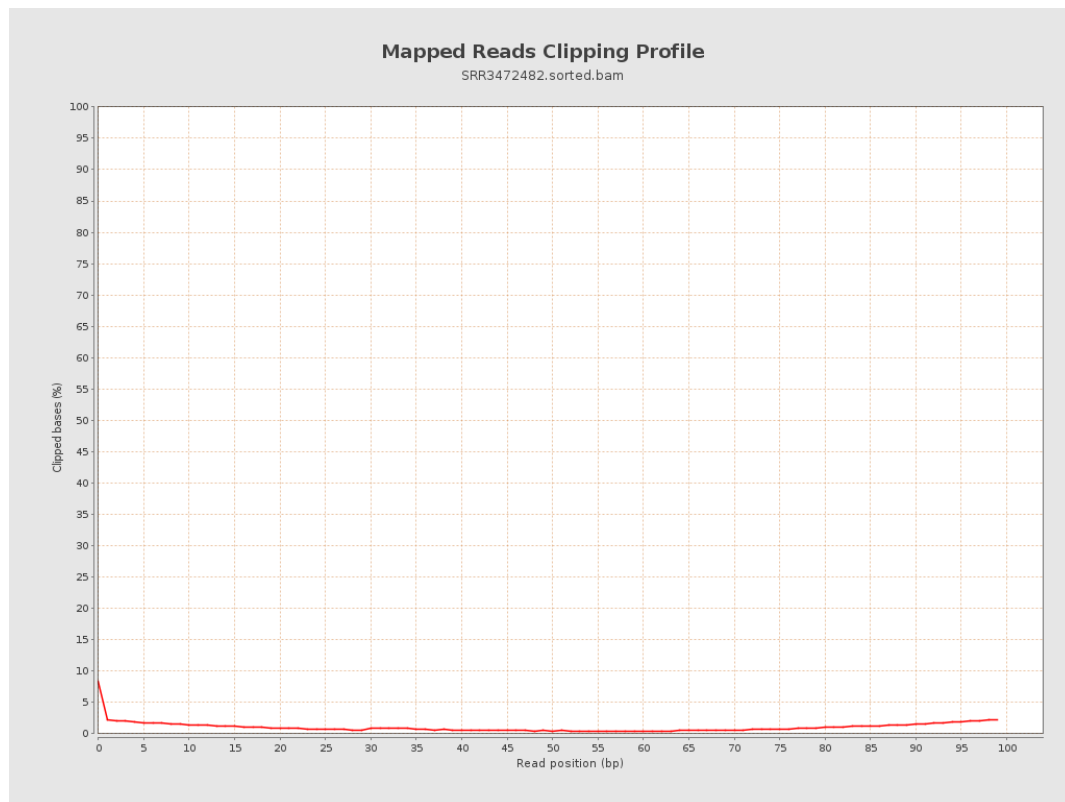
8. Results : Mapped Reads Nucleotide Content



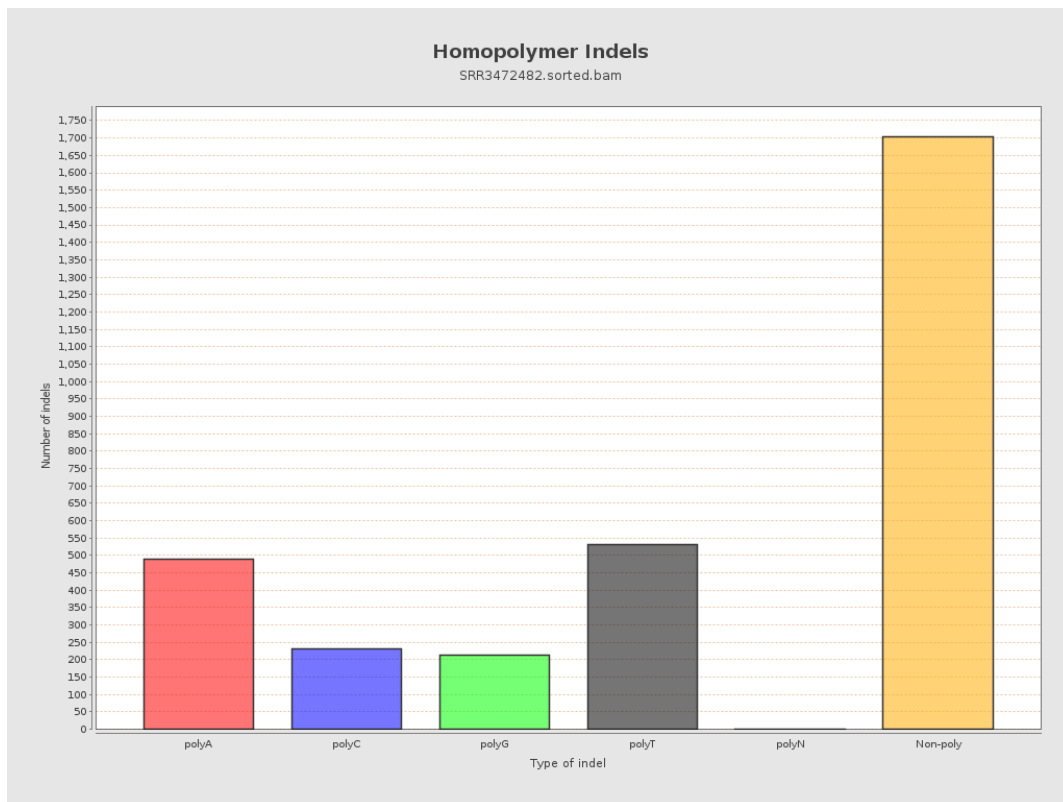
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



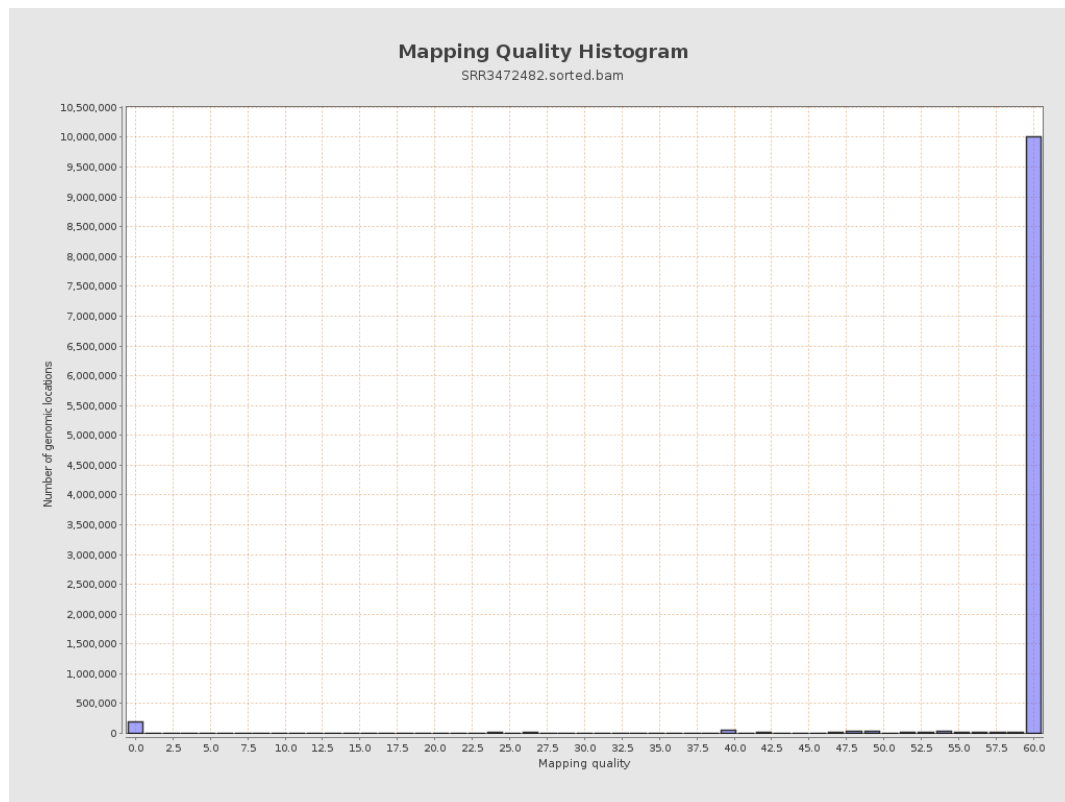
11. Results : Homopolymer Indels



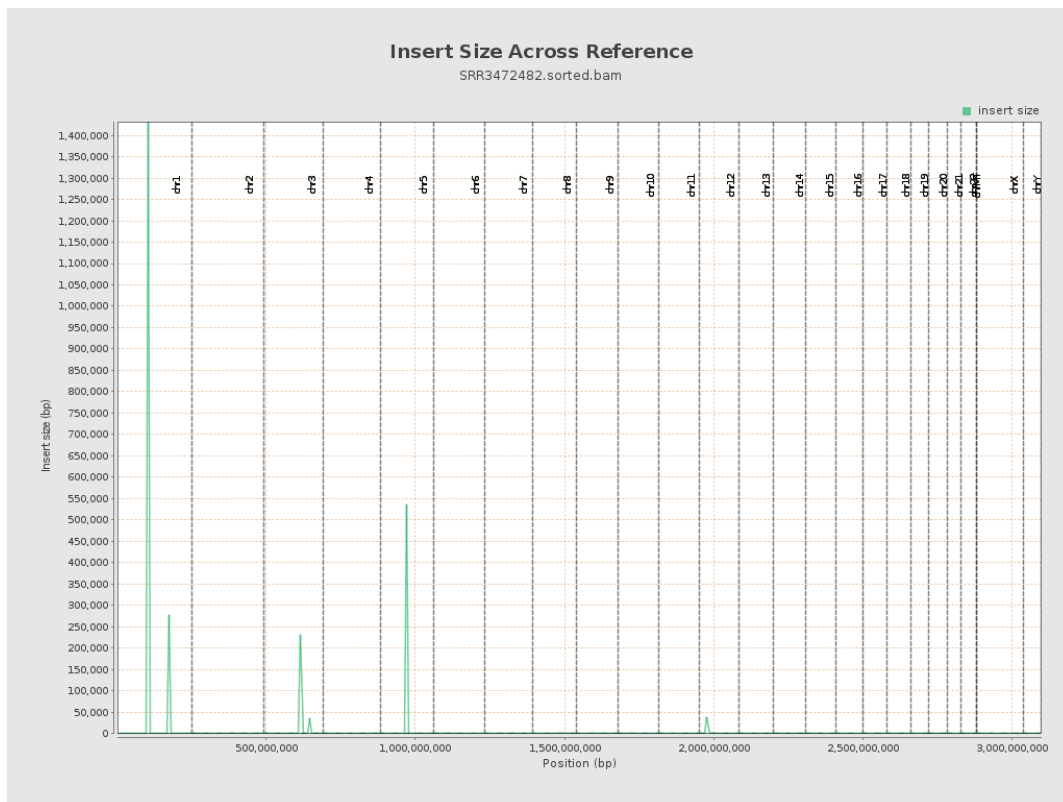
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

