

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 09:36:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354883.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_SRR22354883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354883_1.fastq.gz SRR22354883_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 09:36:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,978,854
Mapped reads	17,840,502 / 99.23%
Unmapped reads	138,352 / 0.77%
Mapped paired reads	17,840,502 / 99.23%
Mapped reads, first in pair	8,928,445 / 49.66%
Mapped reads, second in pair	8,912,057 / 49.57%
Mapped reads, both in pair	17,802,530 / 99.02%
Mapped reads, singletons	37,972 / 0.21%
Secondary alignments	0
Supplementary alignments	469,809 / 2.61%
Read min/max/mean length	30 / 150 / 151
Duplicated reads (estimated)	7,262,968 / 40.4%
Duplication rate	39.55%
Clipped reads	7,954,914 / 44.25%

2.2. ACGT Content

Number/percentage of A's	662,412,527 / 28.6%
Number/percentage of C's	484,886,243 / 20.94%
Number/percentage of T's	672,742,277 / 29.05%
Number/percentage of G's	495,901,293 / 21.41%
Number/percentage of N's	27,449 / 0%

GC Percentage	42.35%
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2.3. Coverage

Mean	0.7486
Standard Deviation	20.8002

2.4. Mapping Quality

Mean Mapping Quality	53.92
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2.5. Insert size

Mean	237,382.93
Standard Deviation	5,570,367.03
P25/Median/P75	116 / 176 / 252

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	17,932,164
Insertions	468,721
Mapped reads with at least one insertion	2.45%
Deletions	487,846
Mapped reads with at least one deletion	2.6%
Homopolymer indels	44.63%

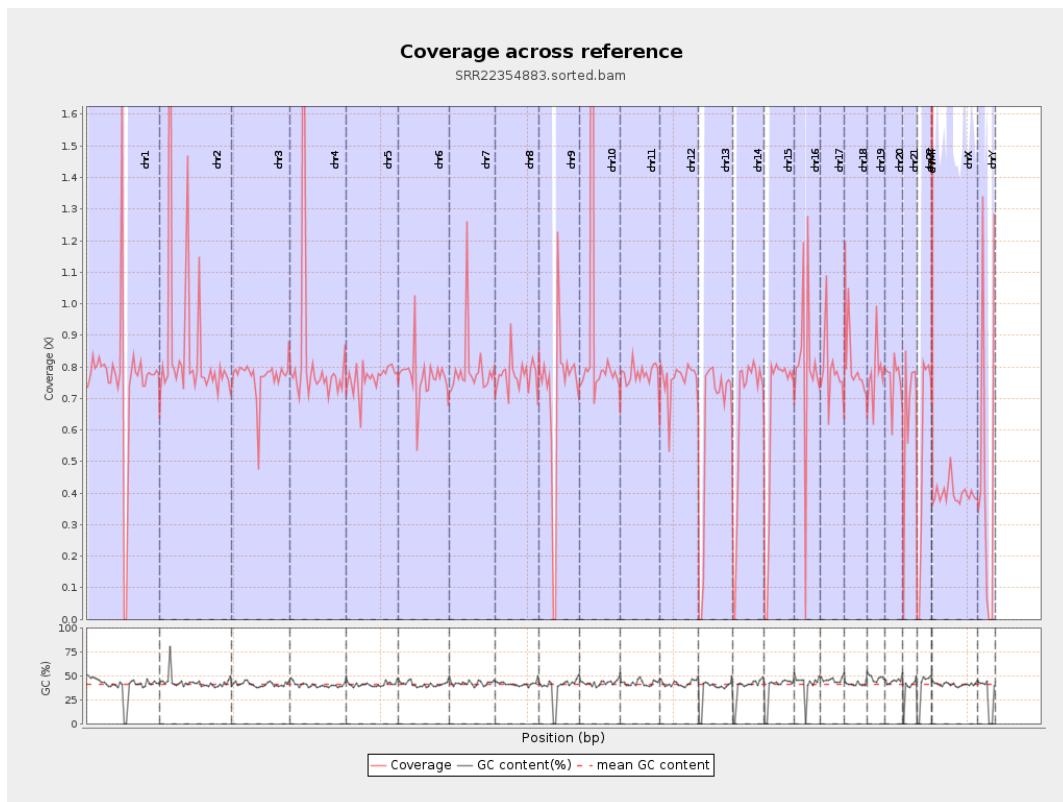
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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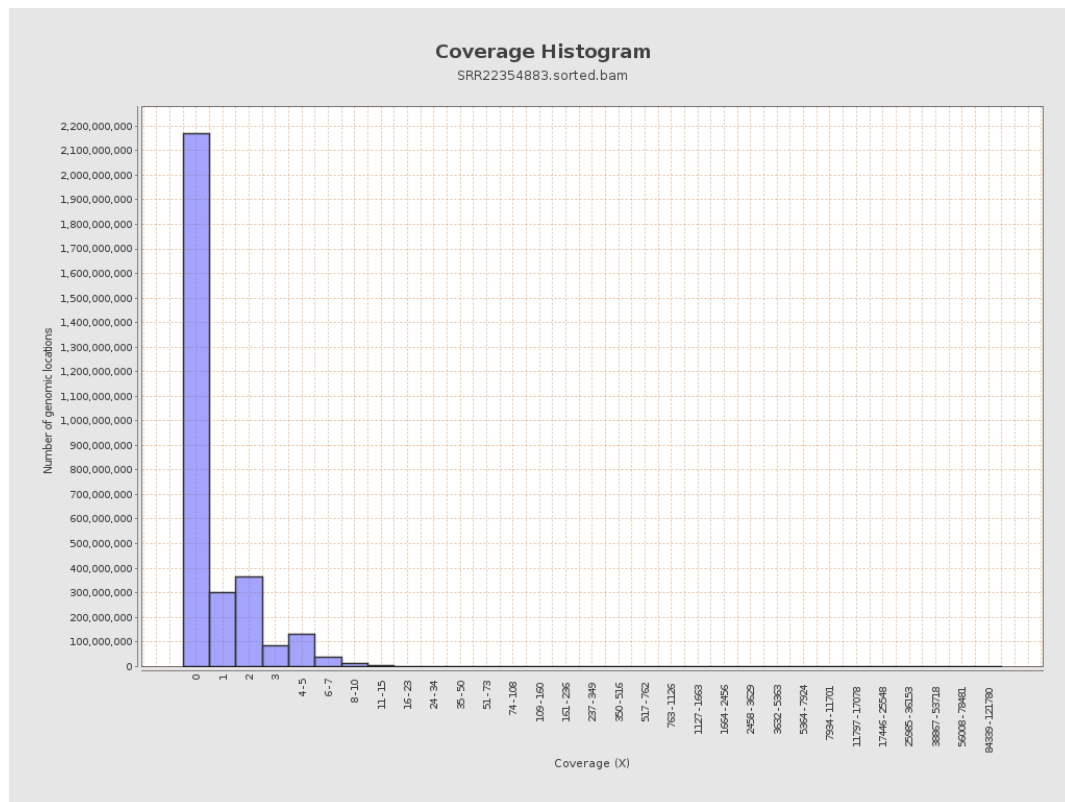
		bases	coverage	deviation
chr1	249250621	189579307	0.7606	20.3457
chr2	243199373	211638824	0.8702	64.8581
chr3	198022430	151754622	0.7664	1.8083
chr4	191154276	157284859	0.8228	11.2969
chr5	180915260	138272137	0.7643	1.5218
chr6	171115067	131576163	0.7689	3.2109
chr7	159138663	125895646	0.7911	12.2654
chr8	146364022	113531498	0.7757	2.9598
chr9	141213431	99658767	0.7057	10.9472
chr10	135534747	129238614	0.9535	27.2413
chr11	135006516	104901033	0.777	3.6934
chr12	133851895	101847878	0.7609	1.5769
chr13	115169878	72053027	0.6256	1.334
chr14	107349540	69876242	0.6509	3.1365
chr15	102531392	65556881	0.6394	1.3424
chr16	90354753	71755163	0.7941	5.1306
chr17	81195210	63651409	0.7839	4.5388
chr18	78077248	63168518	0.8091	9.4171
chr19	59128983	46064151	0.779	10.145
chr20	63025520	47822198	0.7588	3.7749
chr21	48129895	32136458	0.6677	5.9131
chr22	51304566	28277182	0.5512	2.1499
chrMT	16571	11176170	674.4415	143.2626
chrX	155270560	61828510	0.3982	1.6883

chrY	59373566	28809271	0.4852	13.8193
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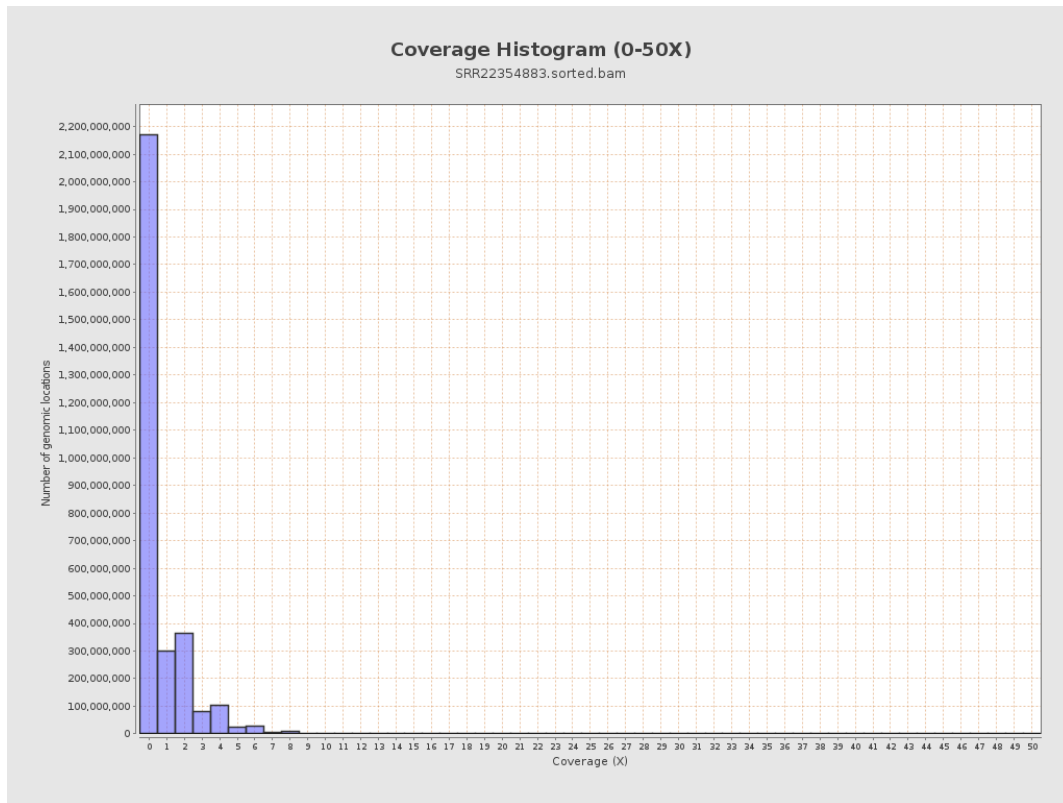
3. Results : Coverage across reference



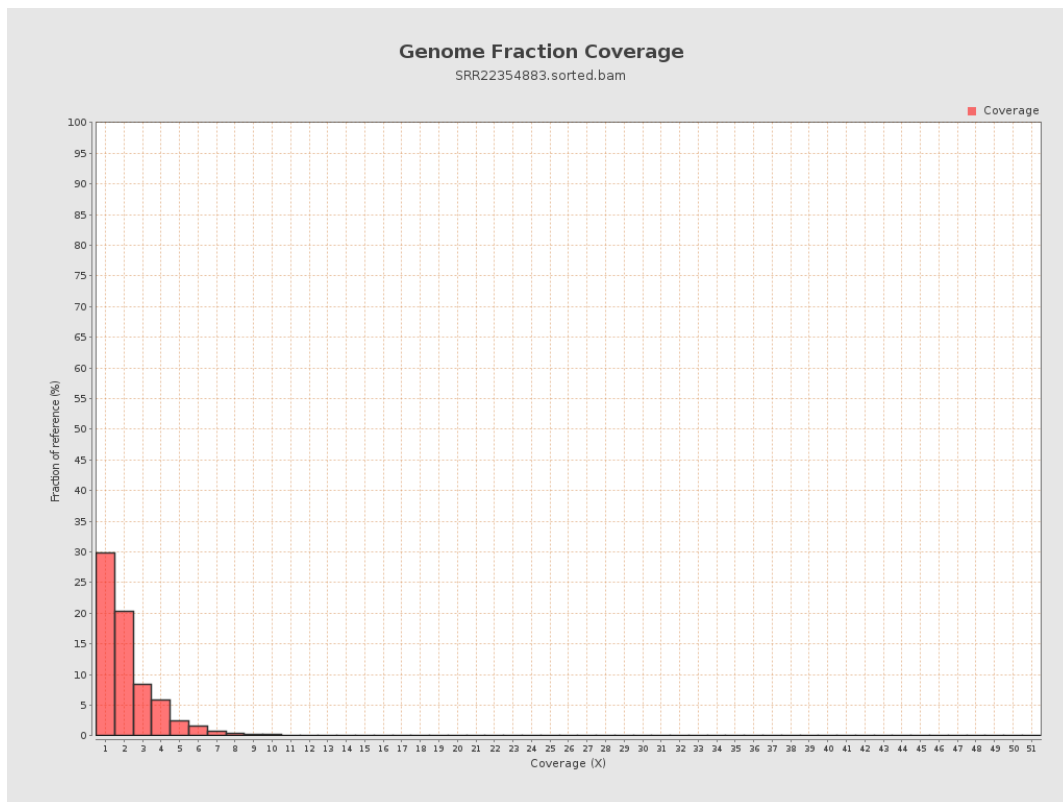
4. Results : Coverage Histogram



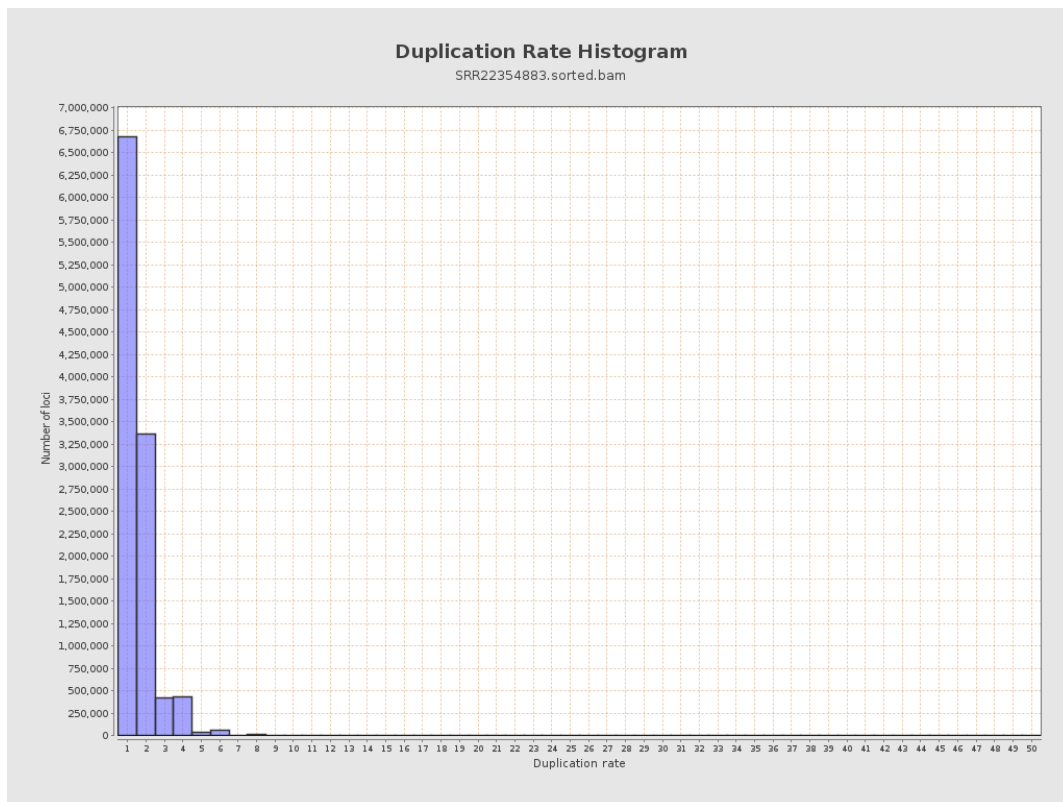
5. Results : Coverage Histogram (0-50X)



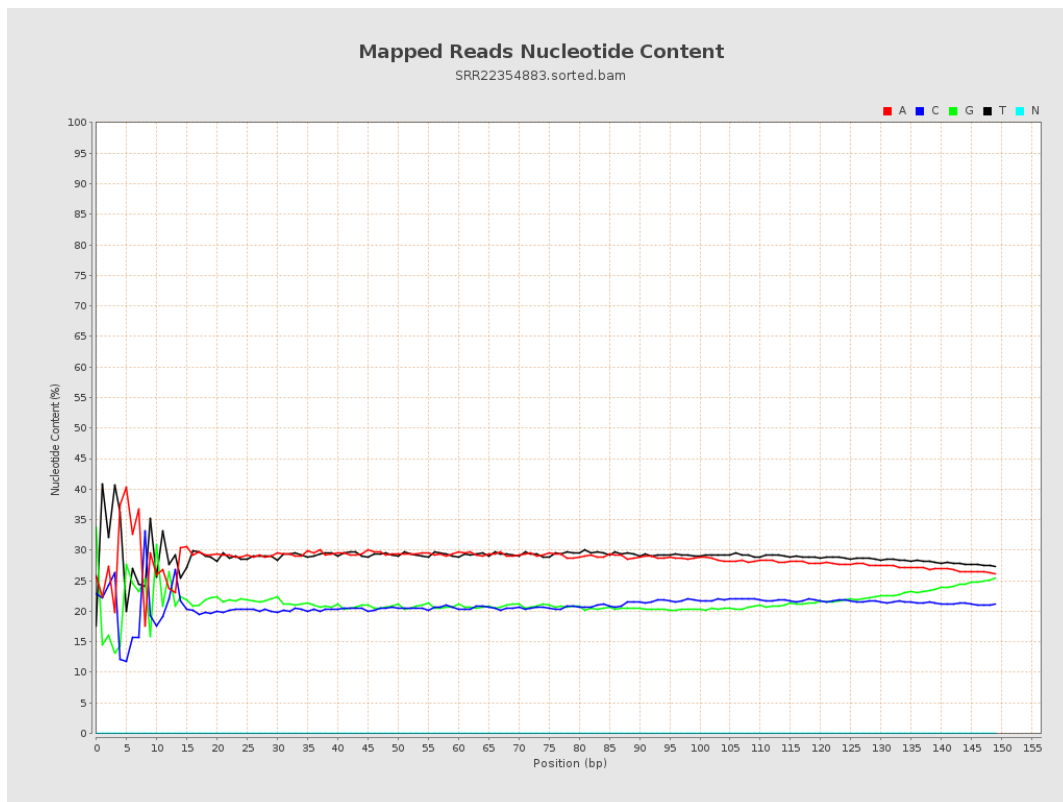
6. Results : Genome Fraction Coverage



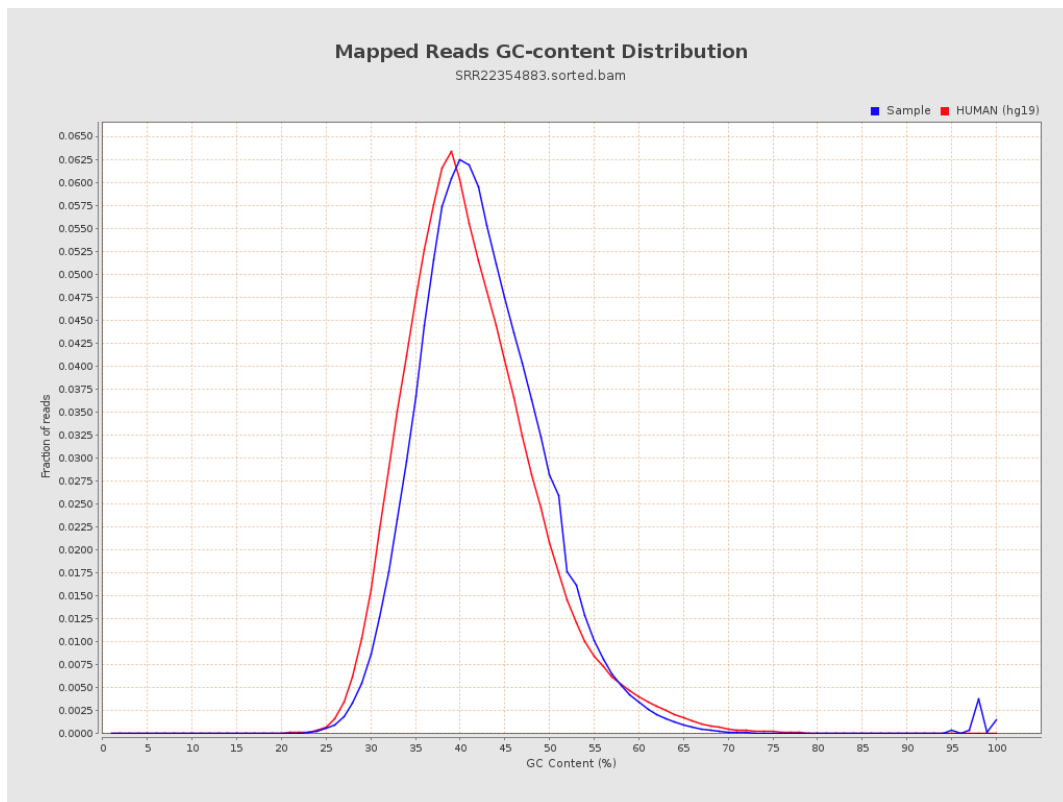
7. Results : Duplication Rate Histogram



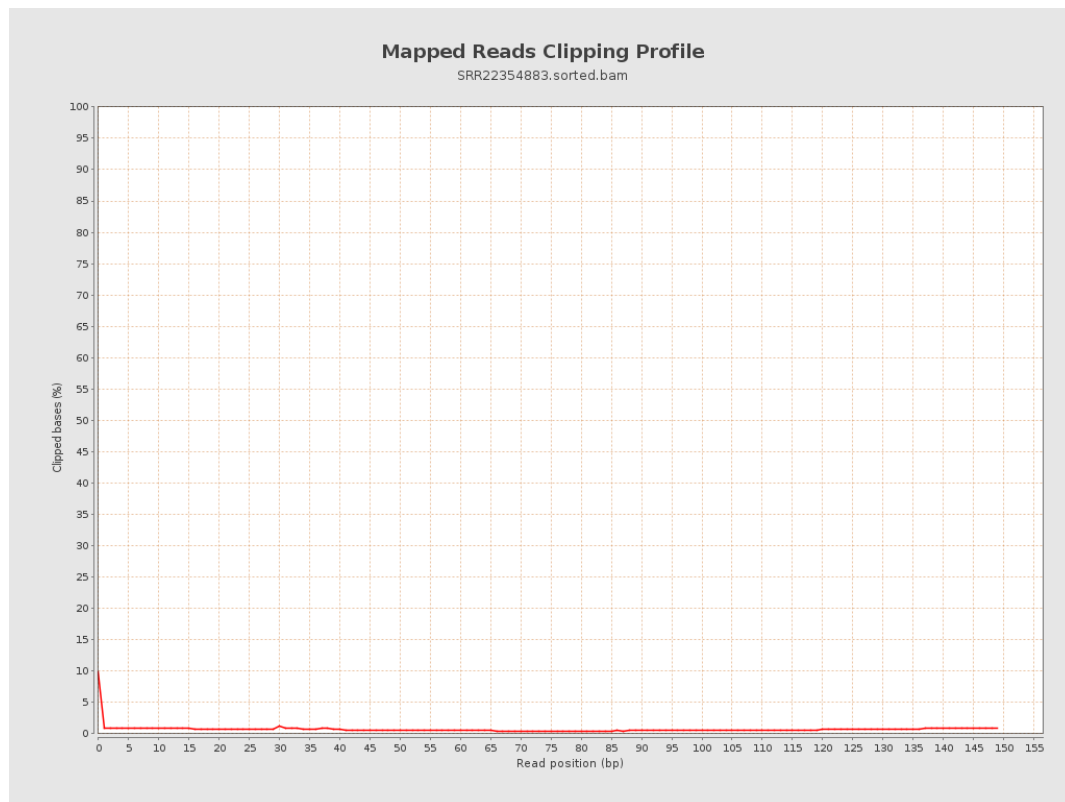
8. Results : Mapped Reads Nucleotide Content



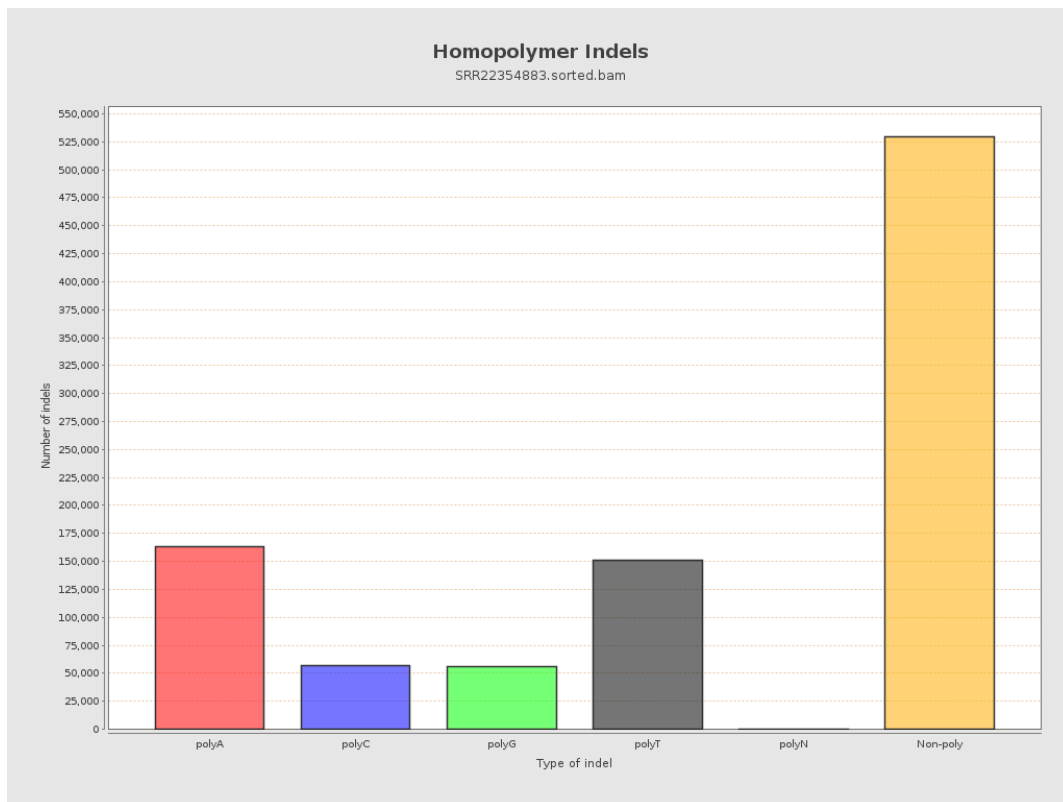
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



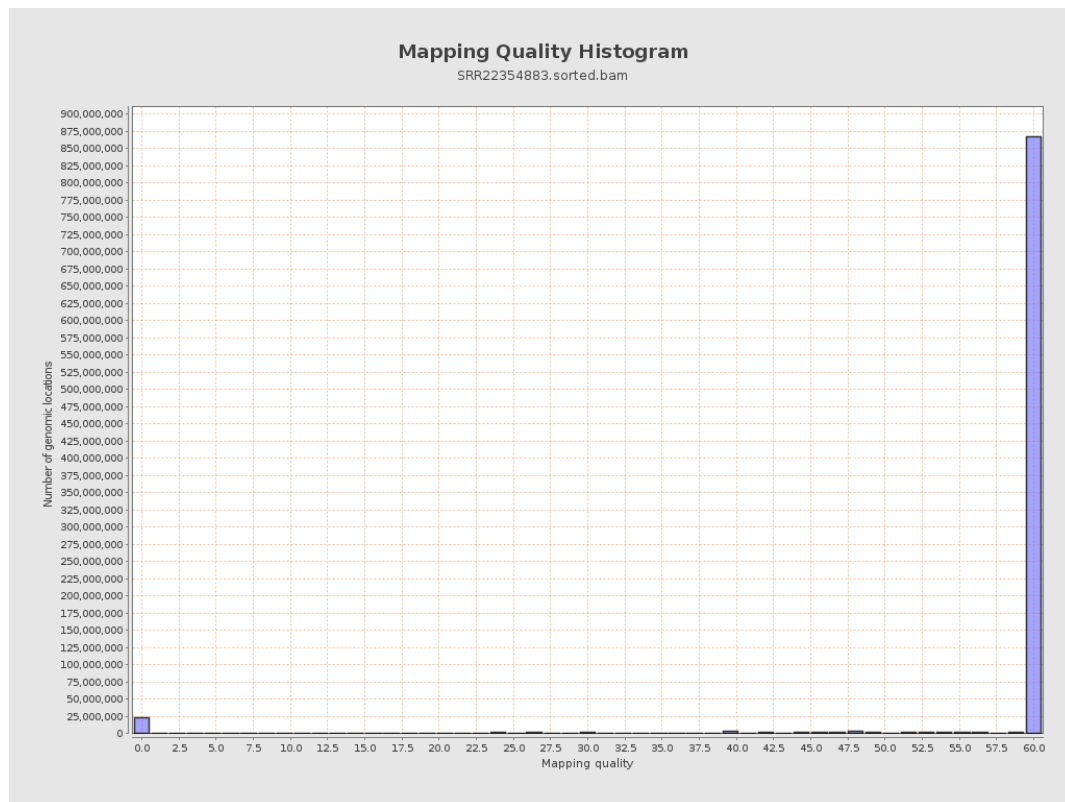
11. Results : Homopolymer Indels



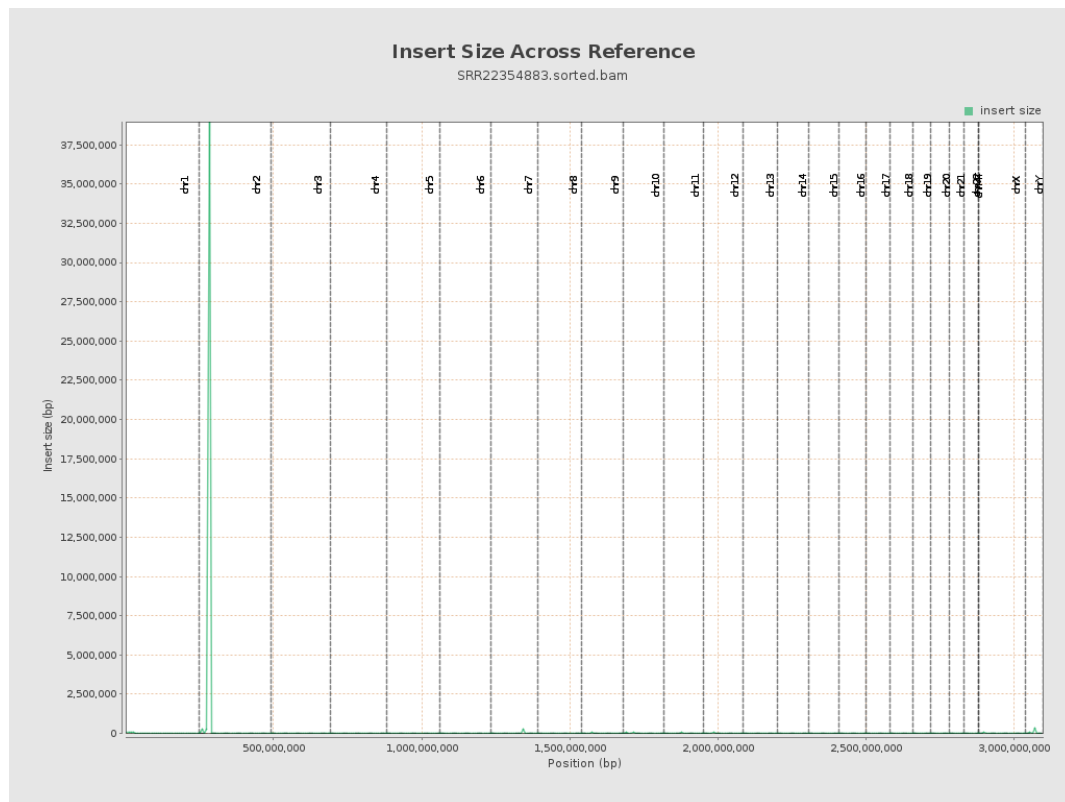
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

