

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 16:35:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354869.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_SRR22354869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354869_1.fastq.gz SRR22354869_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 16:35:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,219,686
Mapped reads	28,914,575 / 98.96%
Unmapped reads	305,111 / 1.04%
Mapped paired reads	28,914,575 / 98.96%
Mapped reads, first in pair	14,469,755 / 49.52%
Mapped reads, second in pair	14,444,820 / 49.44%
Mapped reads, both in pair	28,868,528 / 98.8%
Mapped reads, singletons	46,047 / 0.16%
Secondary alignments	0
Supplementary alignments	1,230,881 / 4.21%
Read min/max/mean length	30 / 150 / 151.53
Duplicated reads (estimated)	19,269,032 / 65.95%
Duplication rate	67.53%
Clipped reads	15,993,105 / 54.73%

2.2. ACGT Content

Number/percentage of A's	992,869,940 / 27.74%
Number/percentage of C's	763,077,456 / 21.32%
Number/percentage of T's	1,014,169,490 / 28.34%
Number/percentage of G's	808,423,276 / 22.59%
Number/percentage of N's	31,903 / 0%

GC Percentage	43.91%
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2.3. Coverage

Mean	1.1565
Standard Deviation	63.8634

2.4. Mapping Quality

Mean Mapping Quality	53.69
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2.5. Insert size

Mean	434,376.42
Standard Deviation	7,658,101.86
P25/Median/P75	100 / 151 / 222

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	19,245,358
Insertions	569,747
Mapped reads with at least one insertion	1.85%
Deletions	603,547
Mapped reads with at least one deletion	1.99%
Homopolymer indels	44.48%

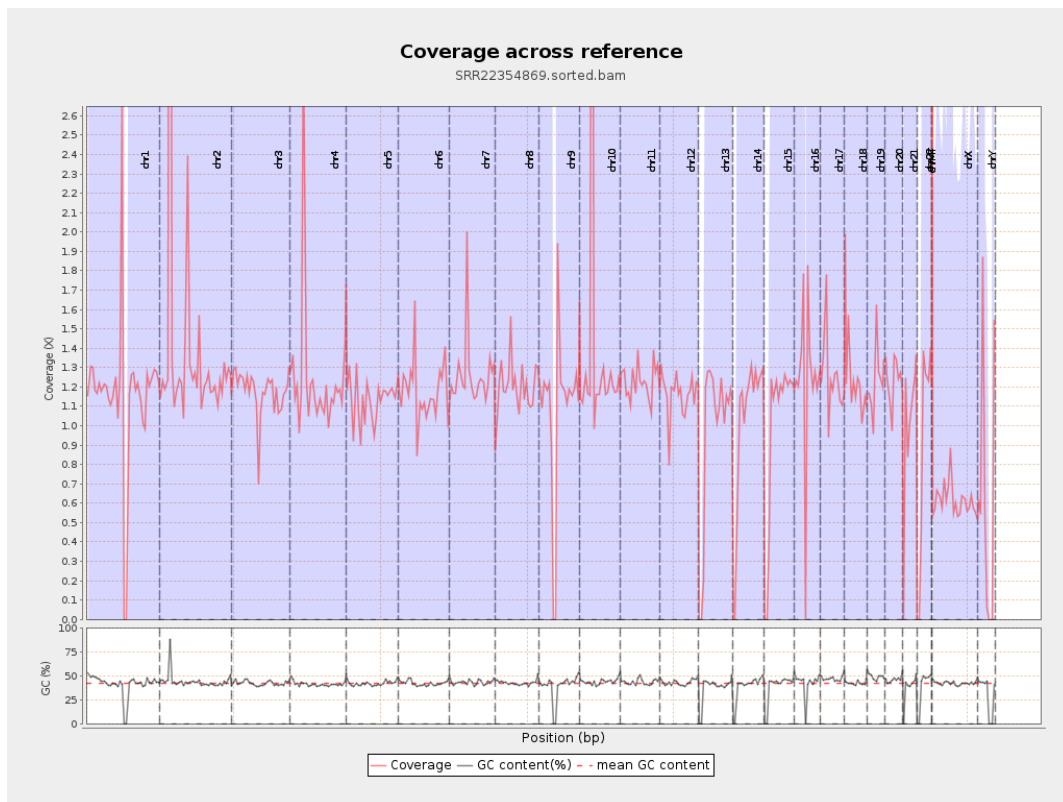
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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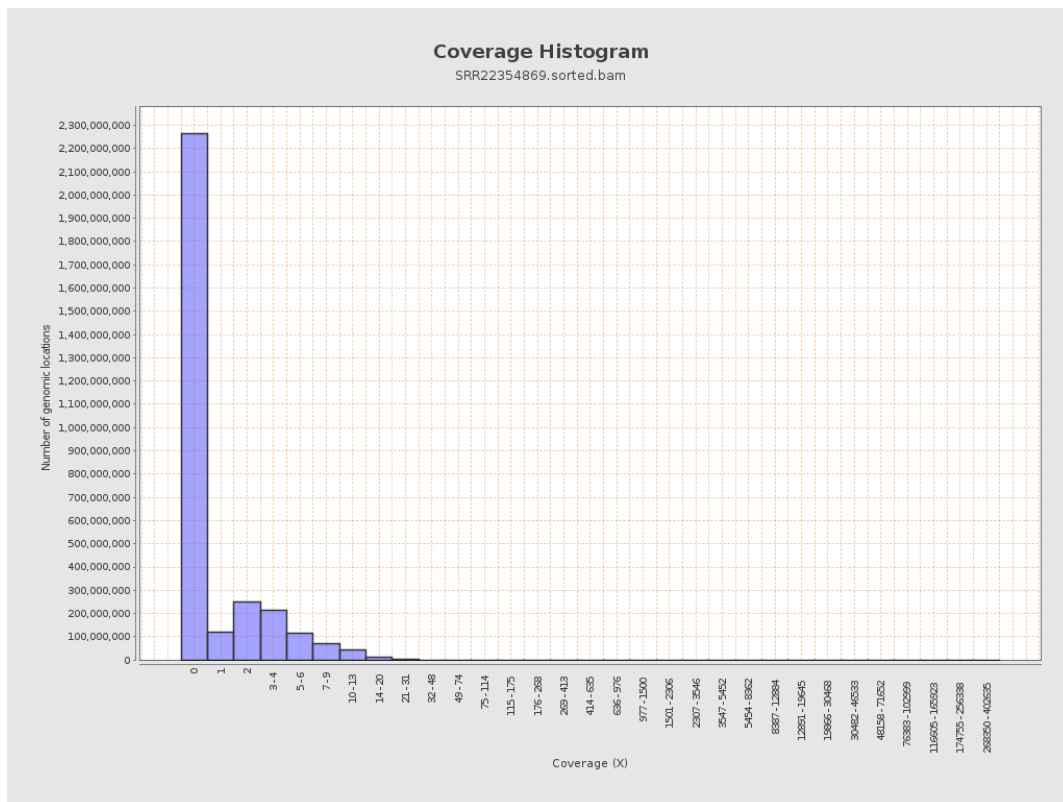
		bases	coverage	deviation
chr1	249250621	290283215	1.1646	32.4201
chr2	243199373	353369359	1.453	221.5001
chr3	198022430	232208470	1.1726	3.2801
chr4	191154276	236081846	1.235	13.579
chr5	180915260	204947185	1.1328	2.5774
chr6	171115067	201364308	1.1768	5.3914
chr7	159138663	200397639	1.2593	20.3965
chr8	146364022	177040980	1.2096	6.722
chr9	141213431	153016457	1.0836	18.1101
chr10	135534747	194133156	1.4323	36.8316
chr11	135006516	165795387	1.2281	6.6749
chr12	133851895	155753671	1.1636	2.6352
chr13	115169878	111787590	0.9706	2.3115
chr14	107349540	108537112	1.0111	8.5423
chr15	102531392	100145417	0.9767	2.3238
chr16	90354753	112479959	1.2449	6.886
chr17	81195210	101205653	1.2464	7.1155
chr18	78077248	96796738	1.2398	15.0316
chr19	59128983	72566762	1.2273	17.2616
chr20	63025520	77777867	1.2341	5.141
chr21	48129895	49144564	1.0211	7.5318
chr22	51304566	46986225	0.9158	3.7711
chrMT	16571	4499685	271.5397	58.6059
chrX	155270560	95263740	0.6135	2.8818

chrY	59373566	38663432	0.6512	17.4394
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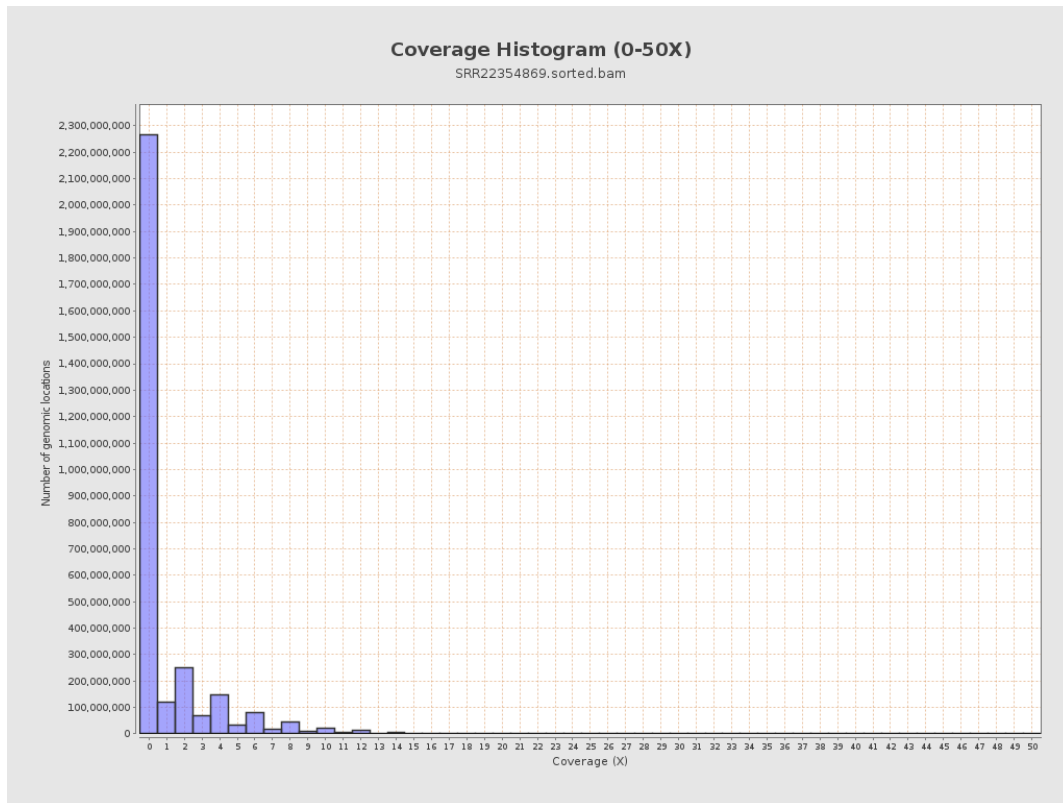
3. Results : Coverage across reference



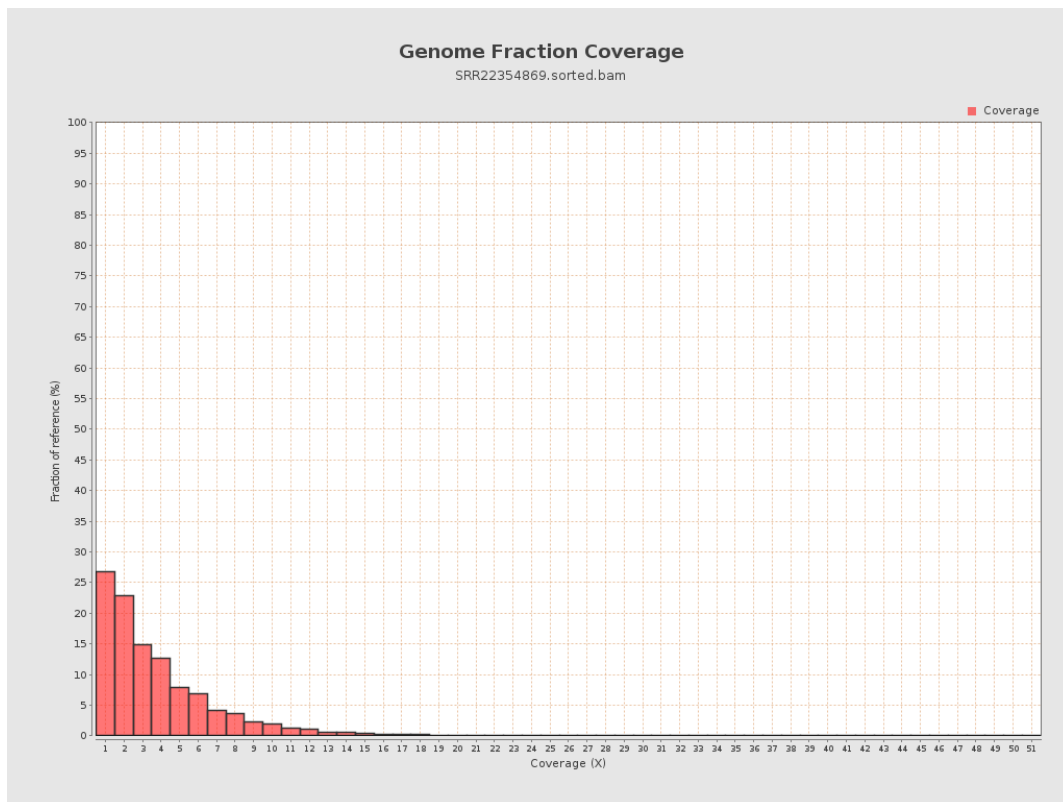
4. Results : Coverage Histogram



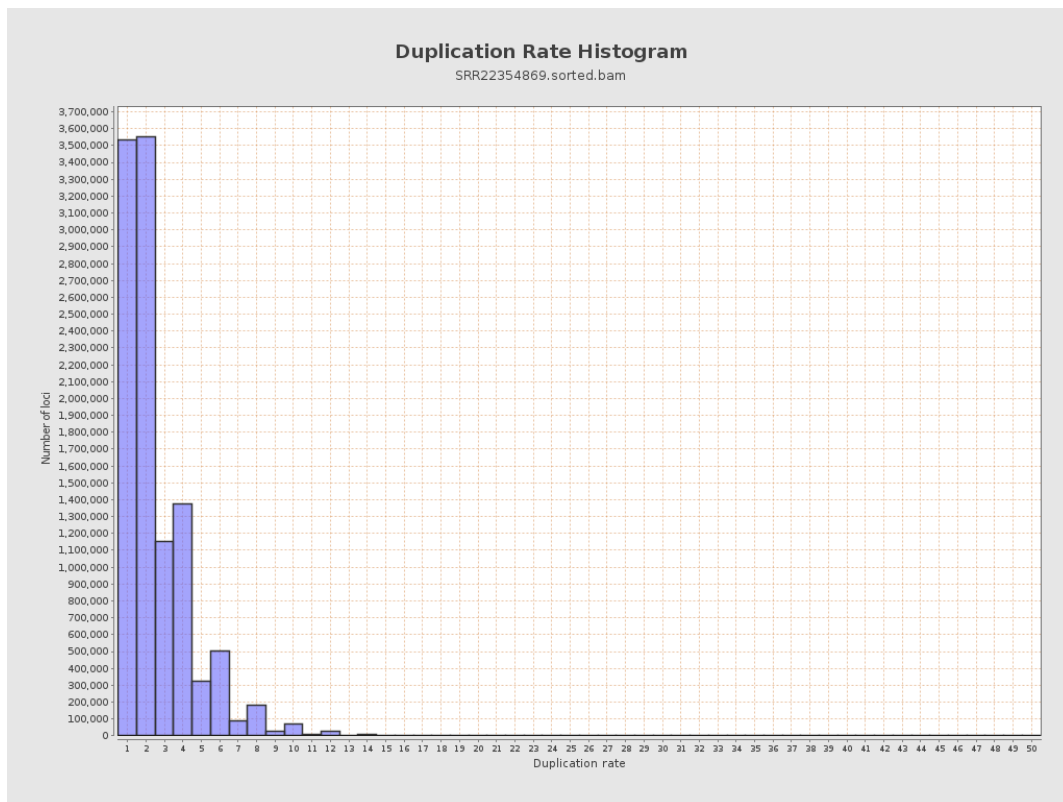
5. Results : Coverage Histogram (0-50X)



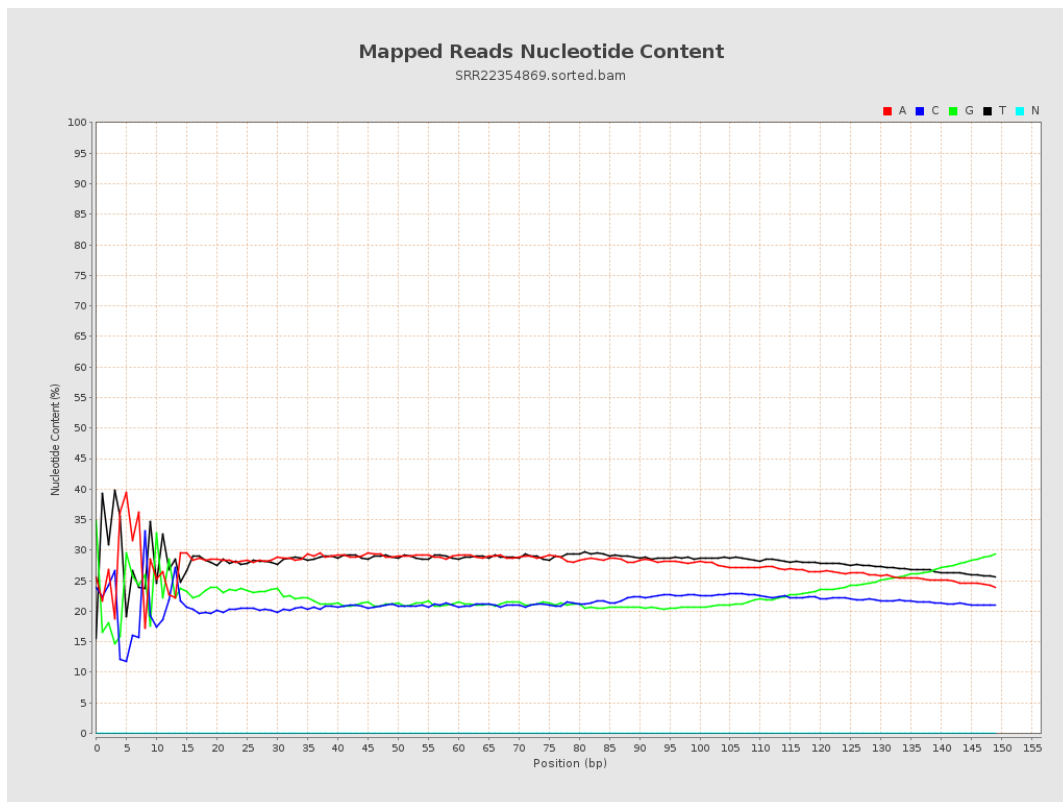
6. Results : Genome Fraction Coverage



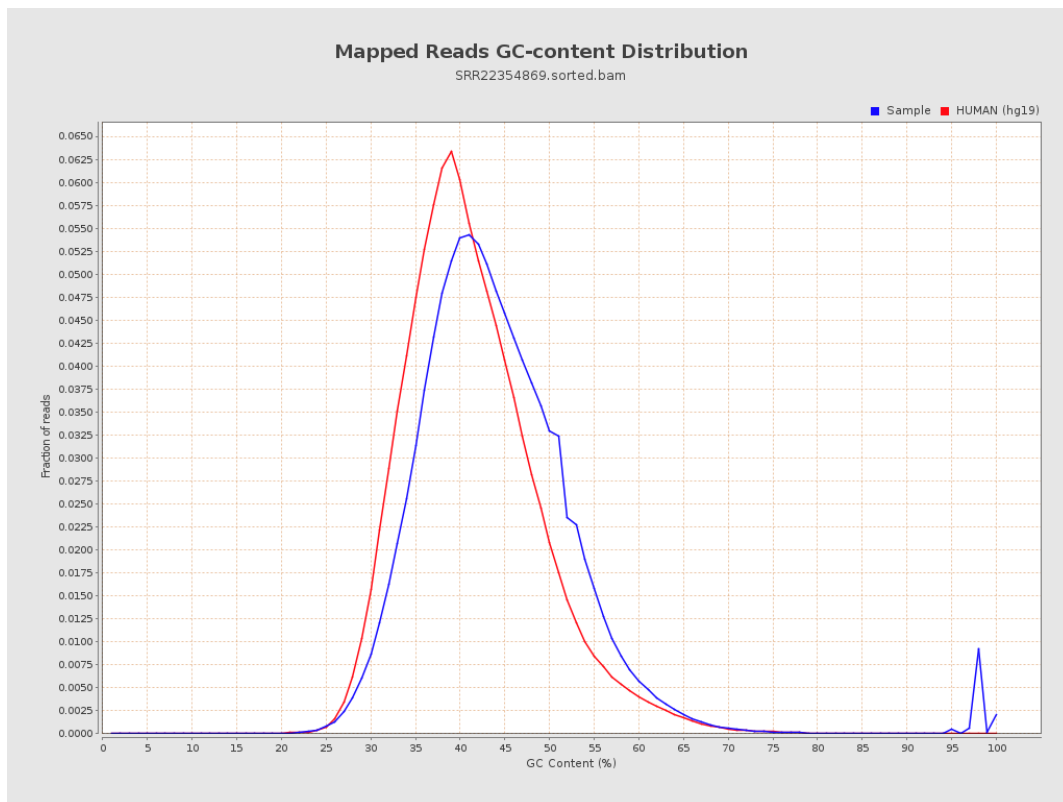
7. Results : Duplication Rate Histogram



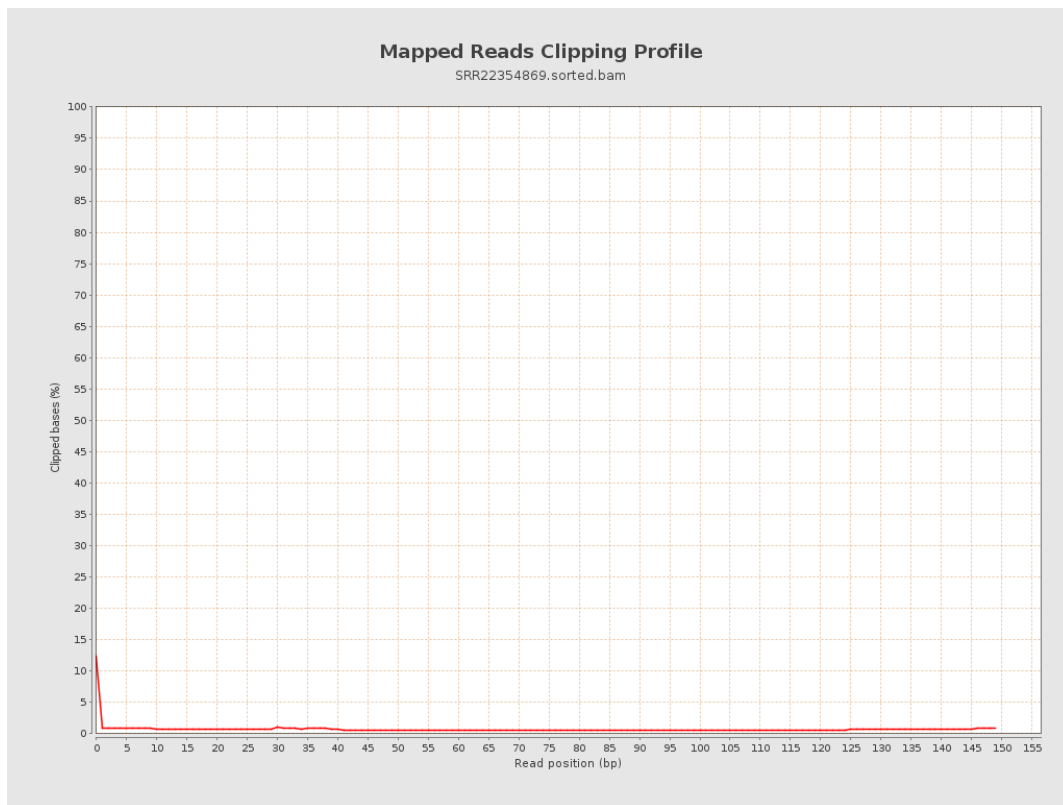
8. Results : Mapped Reads Nucleotide Content



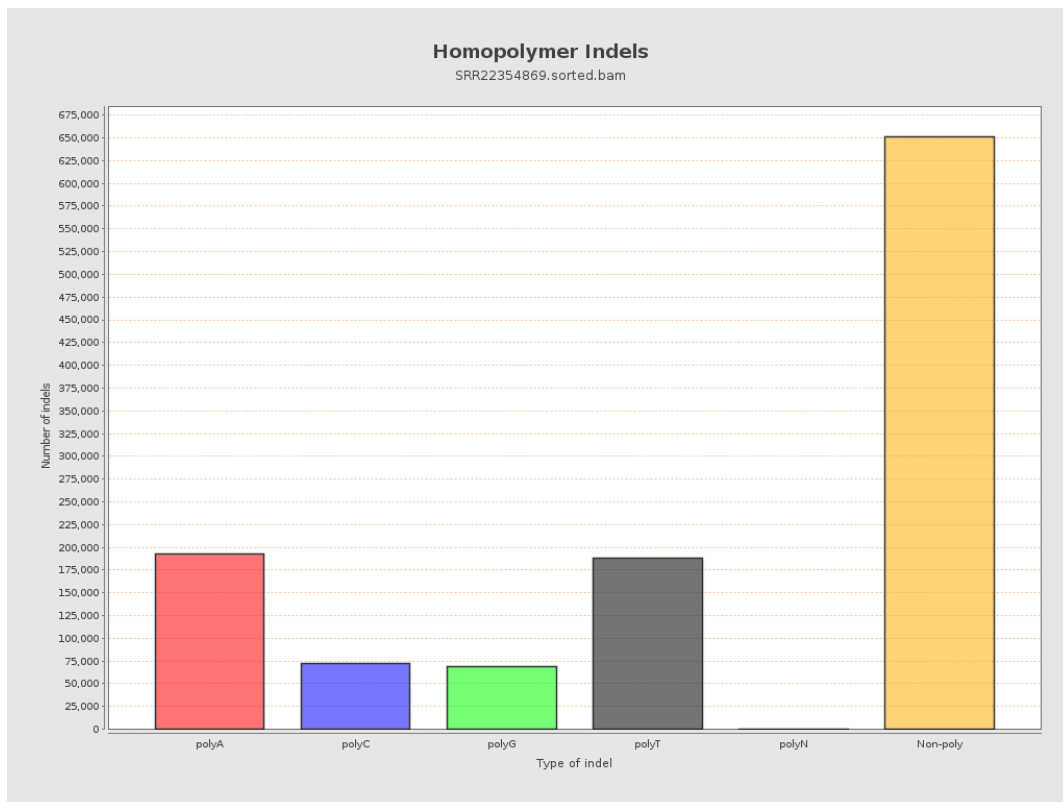
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



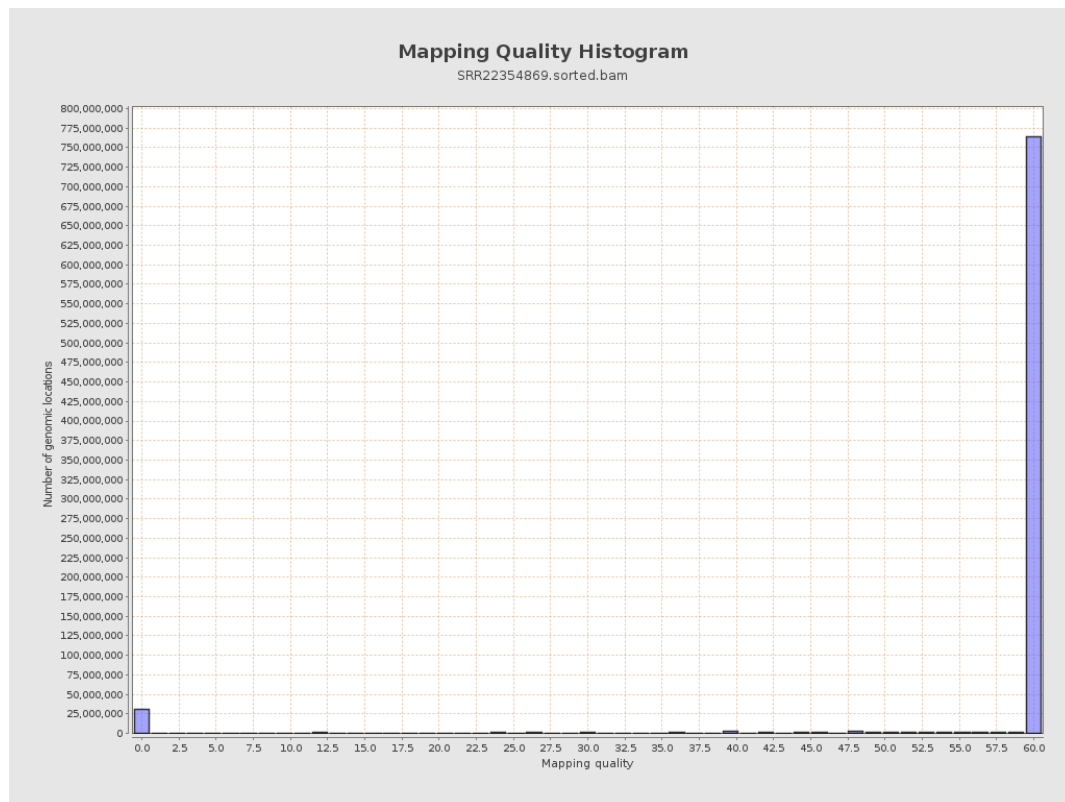
11. Results : Homopolymer Indels



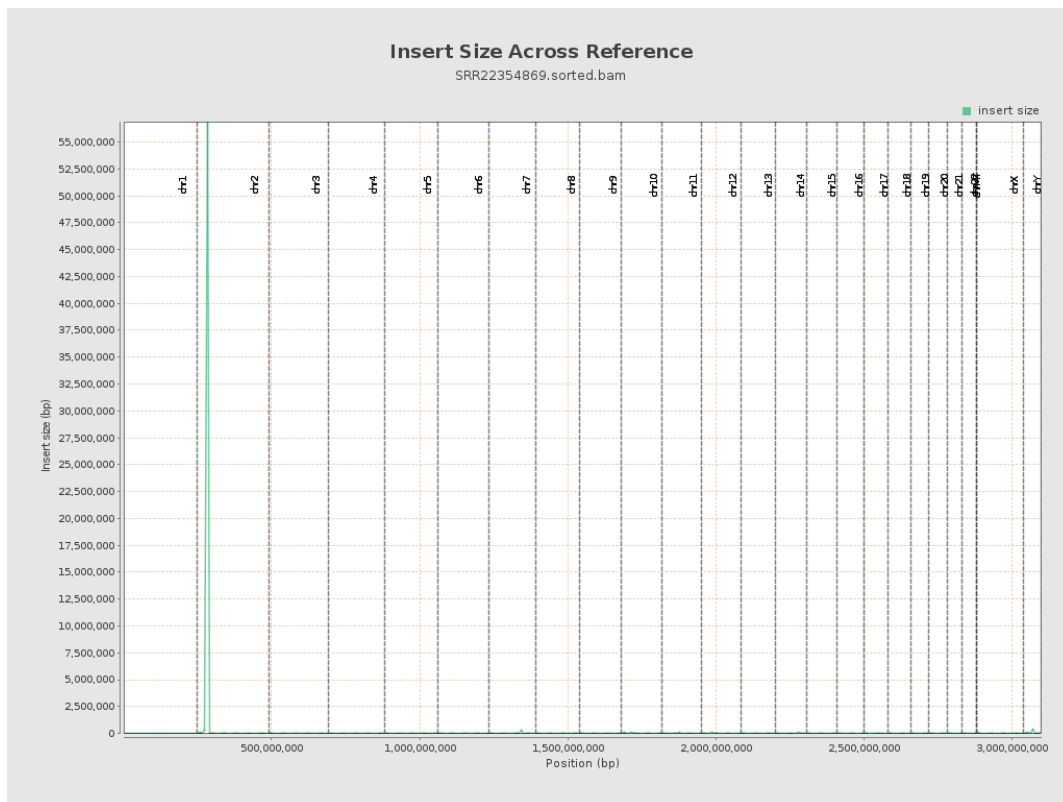
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

