

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:28:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354855.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_SRR22354855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354855_1.fastq.gz SRR22354855_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:28:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,308,442
Mapped reads	28,750,751 / 98.1%
Unmapped reads	557,691 / 1.9%
Mapped paired reads	28,750,751 / 98.1%
Mapped reads, first in pair	14,418,141 / 49.19%
Mapped reads, second in pair	14,332,610 / 48.9%
Mapped reads, both in pair	28,626,006 / 97.67%
Mapped reads, singletons	124,745 / 0.43%
Secondary alignments	0
Supplementary alignments	637,295 / 2.17%
Read min/max/mean length	30 / 150 / 150.87
Duplicated reads (estimated)	16,882,223 / 57.6%
Duplication rate	57.86%
Clipped reads	7,734,955 / 26.39%

2.2. ACGT Content

Number/percentage of A's	1,145,884,991 / 28.9%
Number/percentage of C's	819,180,789 / 20.66%
Number/percentage of T's	1,153,144,030 / 29.08%
Number/percentage of G's	847,074,821 / 21.36%
Number/percentage of N's	19,661 / 0%

GC Percentage	42.02%
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2.3. Coverage

Mean	1.2815
Standard Deviation	30.3346

2.4. Mapping Quality

Mean Mapping Quality	53.96
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2.5. Insert size

Mean	182,074.67
Standard Deviation	4,844,987.67
P25/Median/P75	171 / 304 / 477

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	30,113,577
Insertions	641,665
Mapped reads with at least one insertion	2.08%
Deletions	682,216
Mapped reads with at least one deletion	2.26%
Homopolymer indels	43.77%

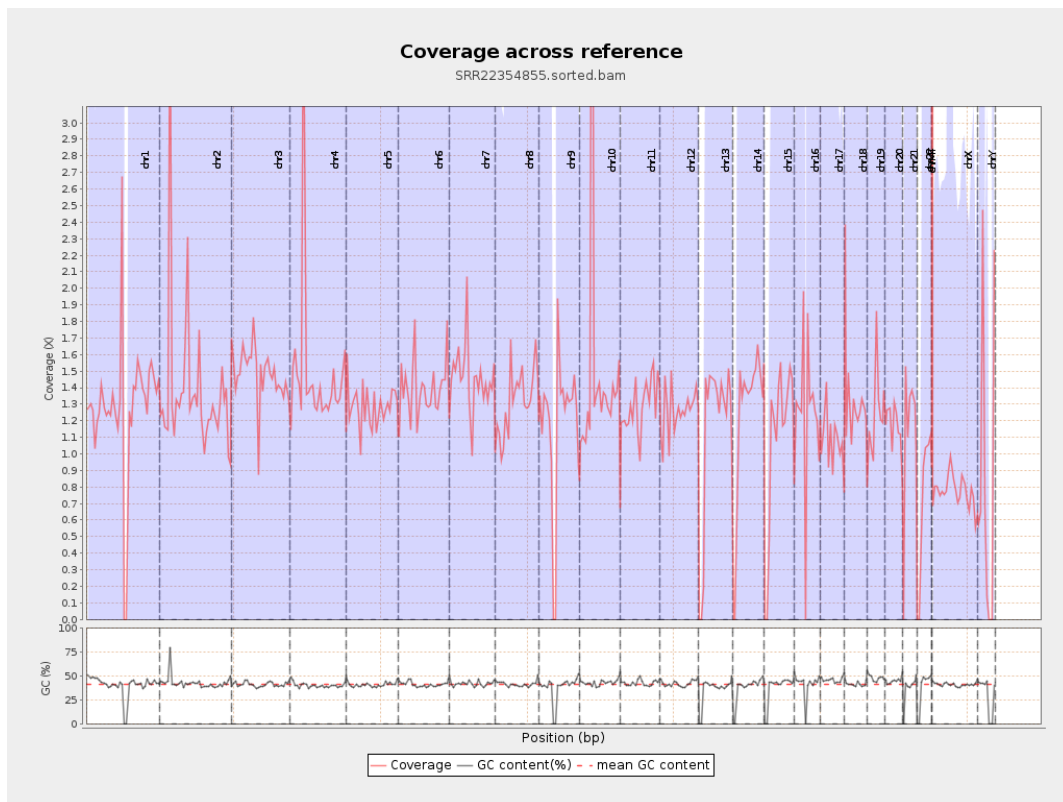
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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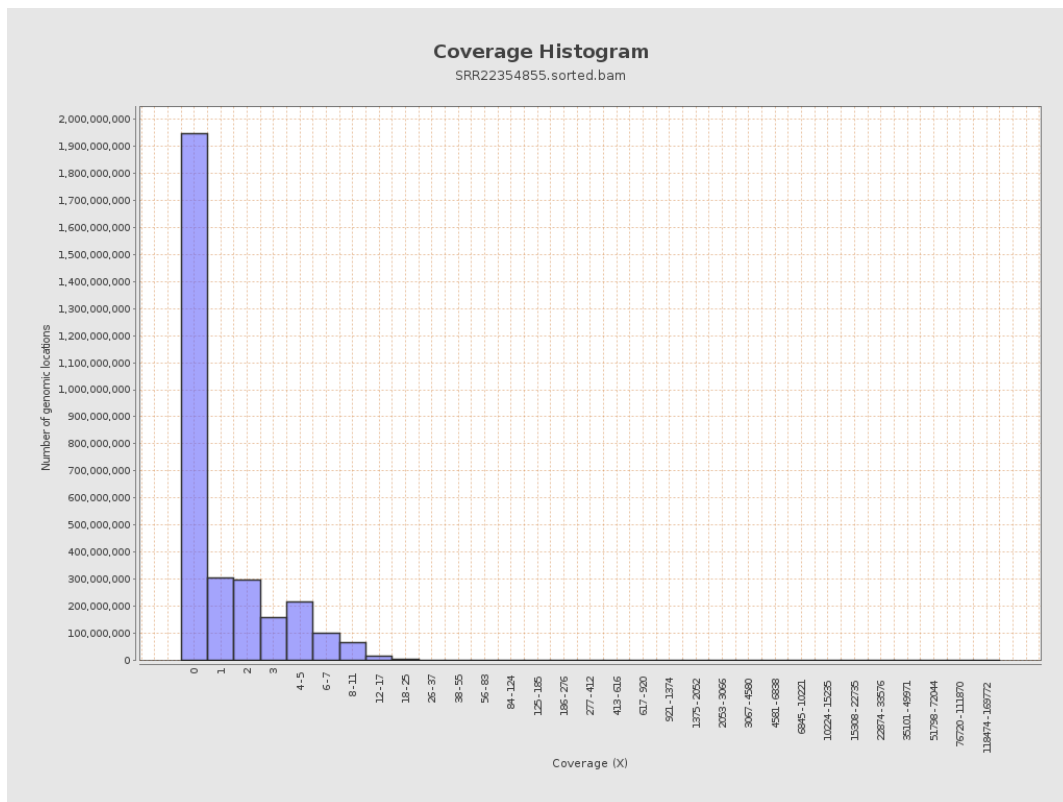
		bases	coverage	deviation
chr1	249250621	319833559	1.2832	31.2139
chr2	243199373	339301696	1.3952	93.1122
chr3	198022430	292966052	1.4795	2.6447
chr4	191154276	282282795	1.4767	20.2975
chr5	180915260	232011937	1.2824	2.3693
chr6	171115067	238880130	1.396	4.9468
chr7	159138663	232205161	1.4591	15.6404
chr8	146364022	193634358	1.323	7.4378
chr9	141213431	164460237	1.1646	16.7807
chr10	135534747	209193631	1.5435	32.9072
chr11	135006516	172564942	1.2782	7.1617
chr12	133851895	168052816	1.2555	2.3085
chr13	115169878	132093800	1.1469	2.1907
chr14	107349540	131840419	1.2281	4.0168
chr15	102531392	110569118	1.0784	2.1232
chr16	90354753	111056761	1.2291	6.7012
chr17	81195210	87317855	1.0754	5.8253
chr18	78077248	101718057	1.3028	16.814
chr19	59128983	72739430	1.2302	17.7431
chr20	63025520	73885419	1.1723	7.4483
chr21	48129895	56573013	1.1754	11.0552
chr22	51304566	37602443	0.7329	3.8147
chrMT	16571	35883817	2,165.4588	340.5721
chrX	155270560	119749424	0.7712	2.7662

chrY	59373566	50839229	0.8563	22.2987
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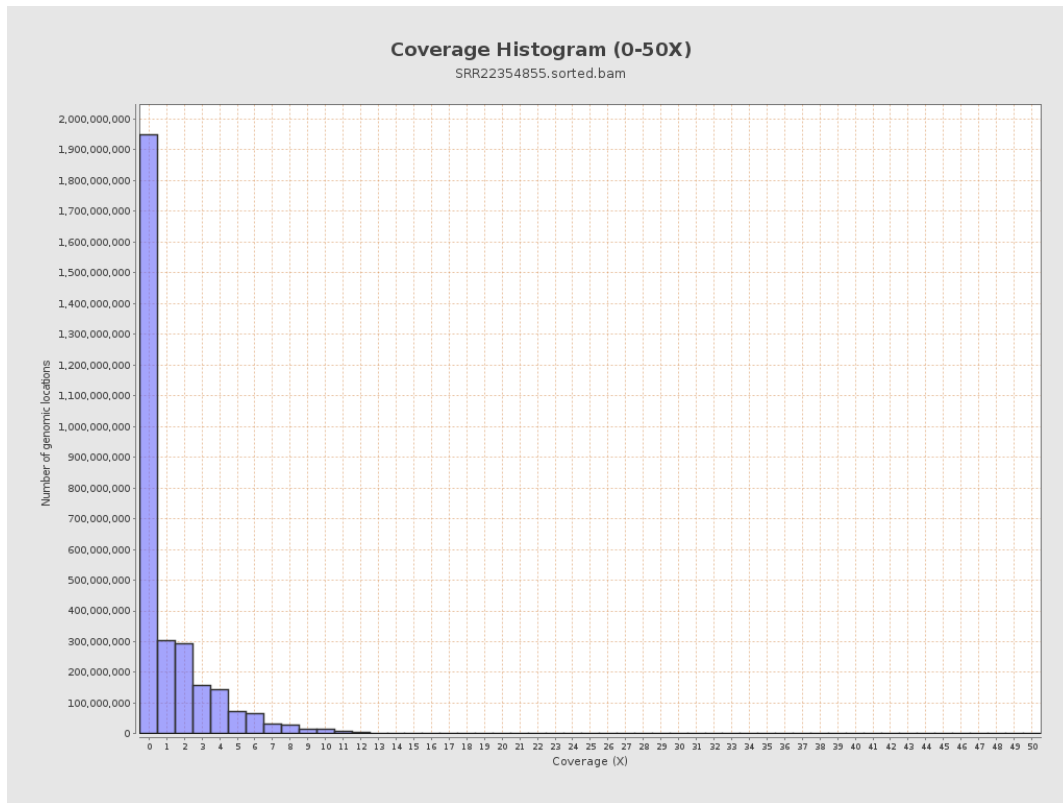
3. Results : Coverage across reference



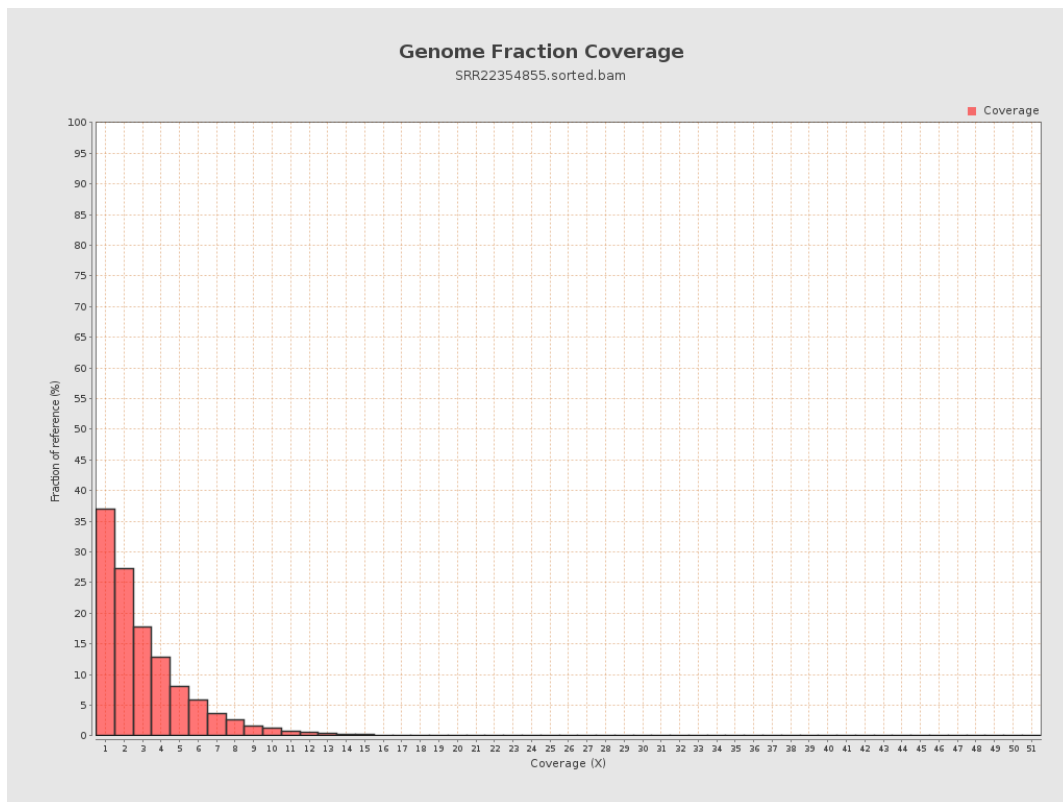
4. Results : Coverage Histogram



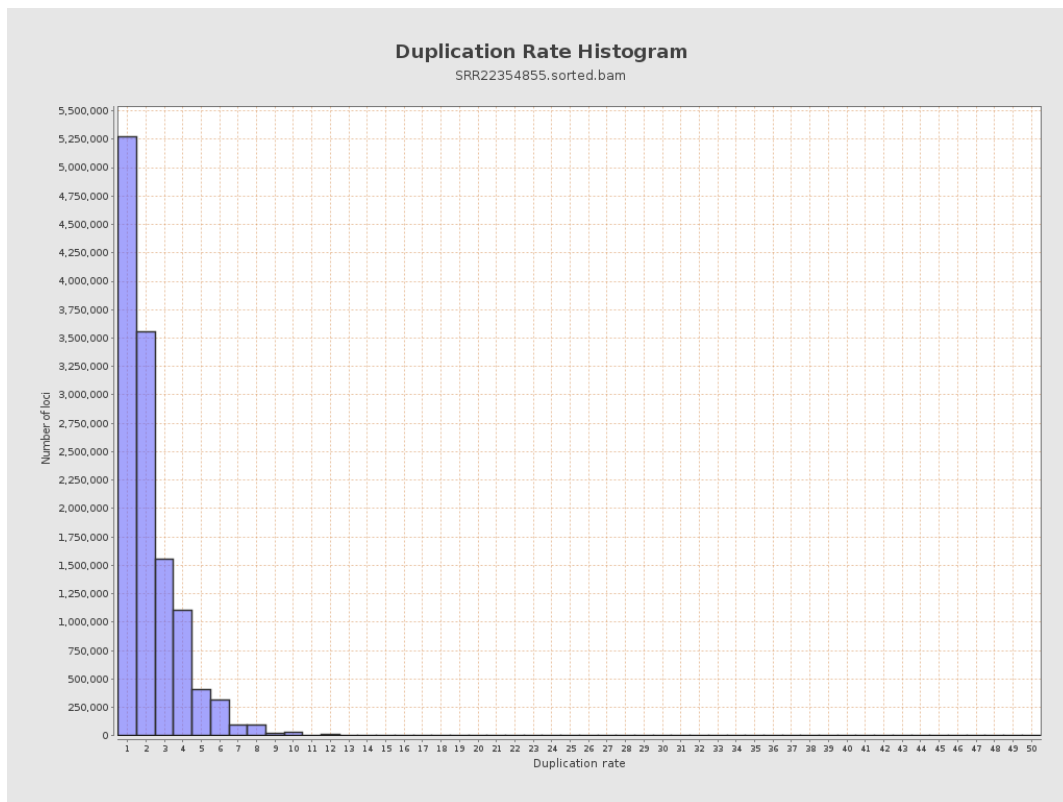
5. Results : Coverage Histogram (0-50X)



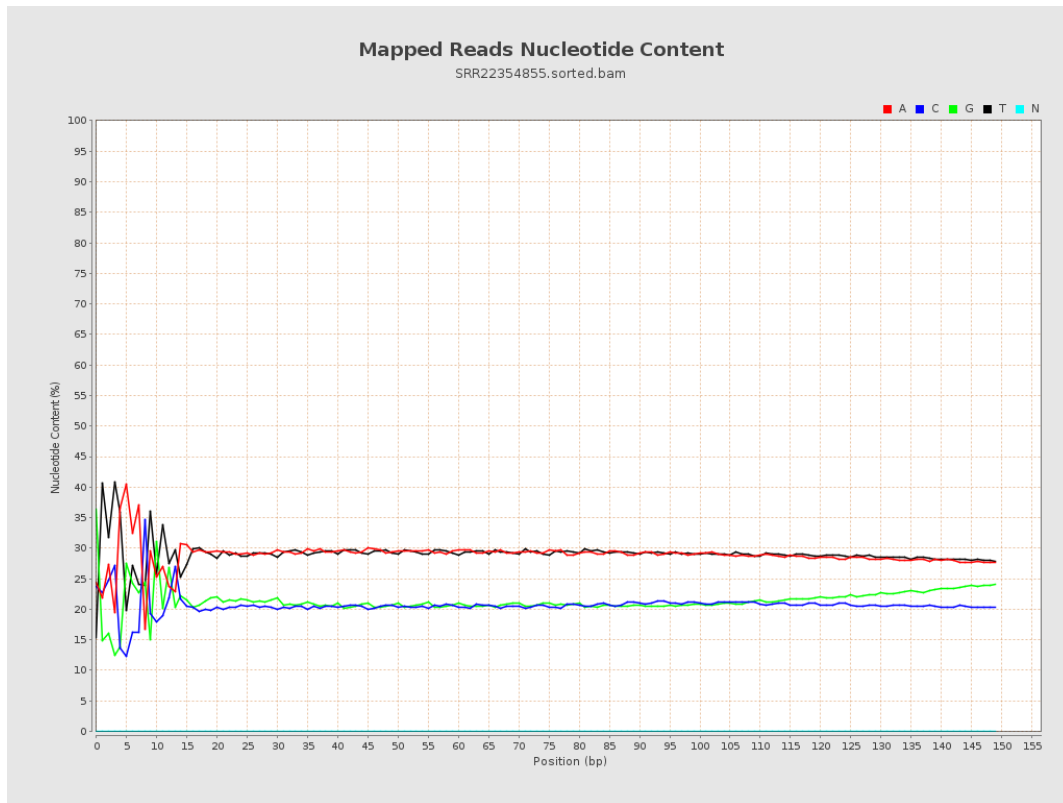
6. Results : Genome Fraction Coverage



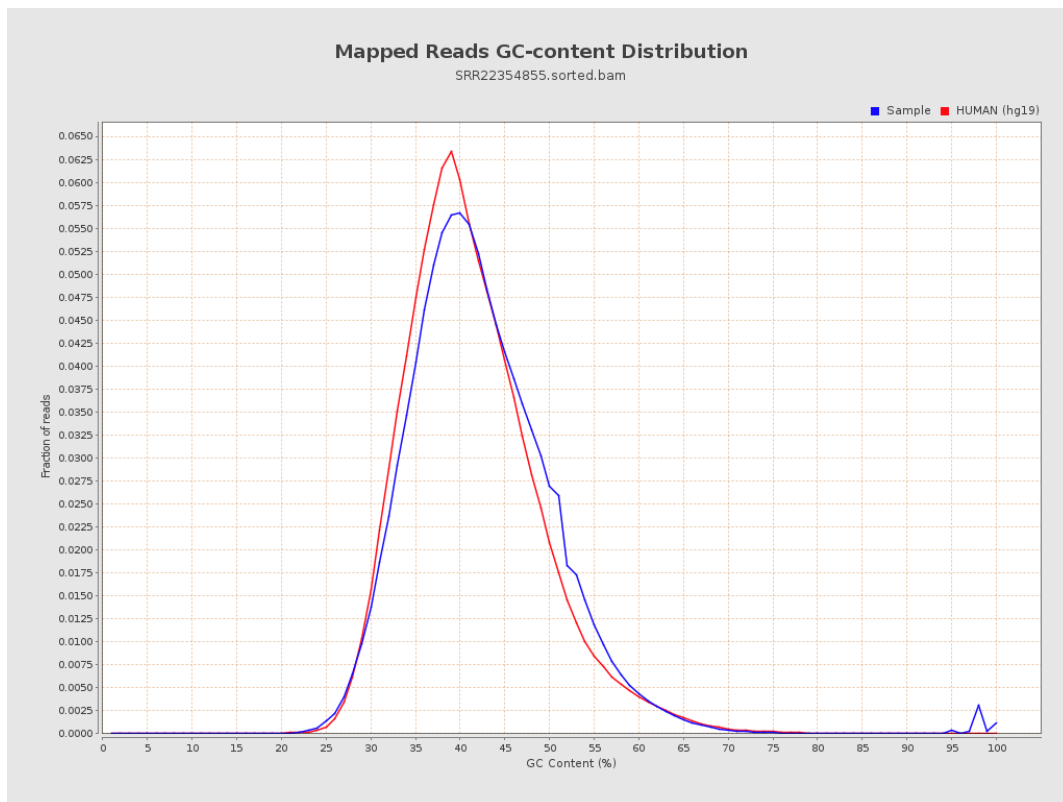
7. Results : Duplication Rate Histogram



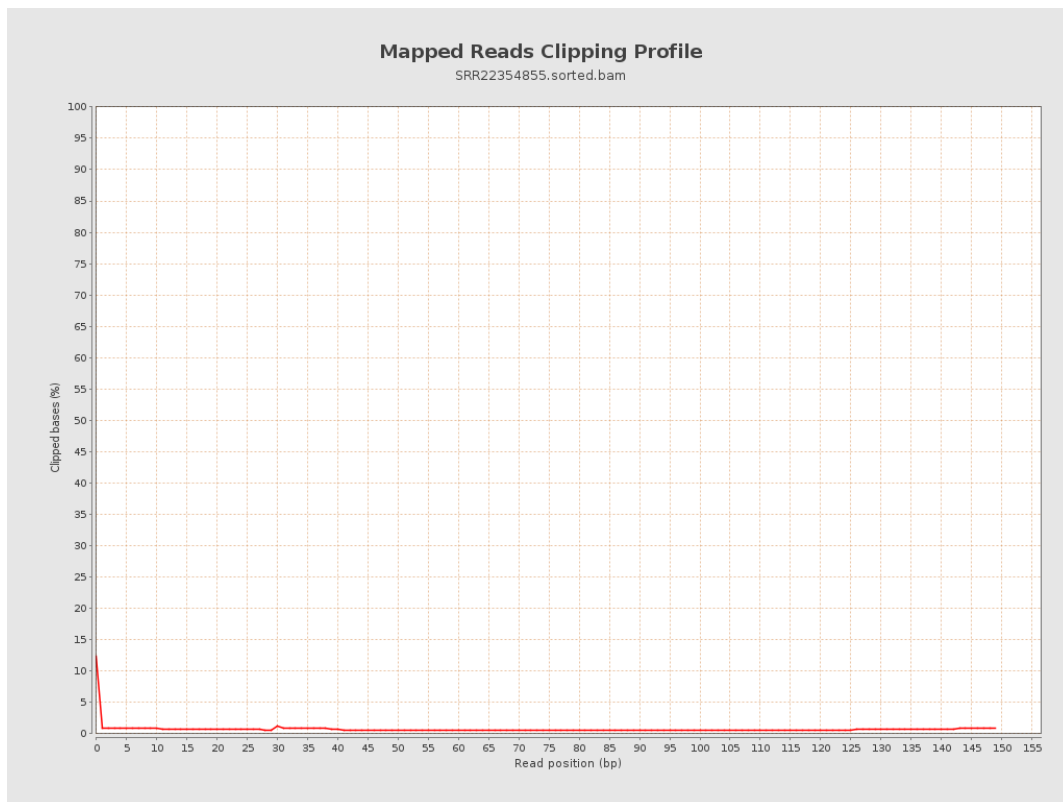
8. Results : Mapped Reads Nucleotide Content



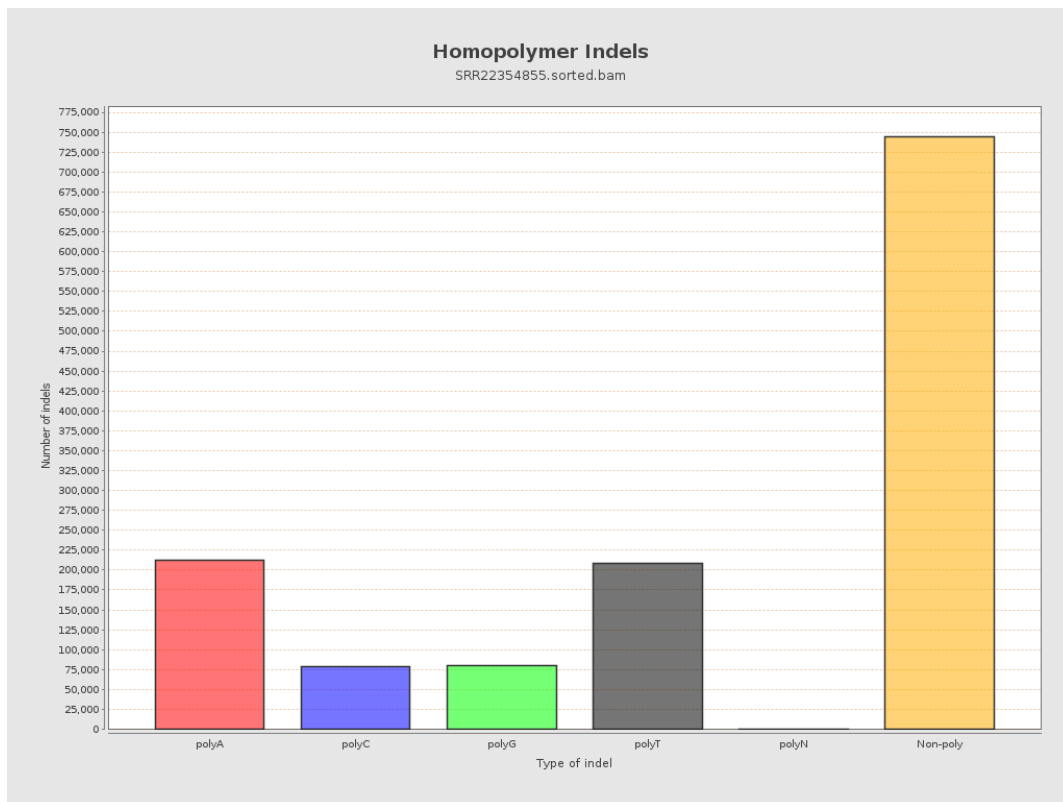
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



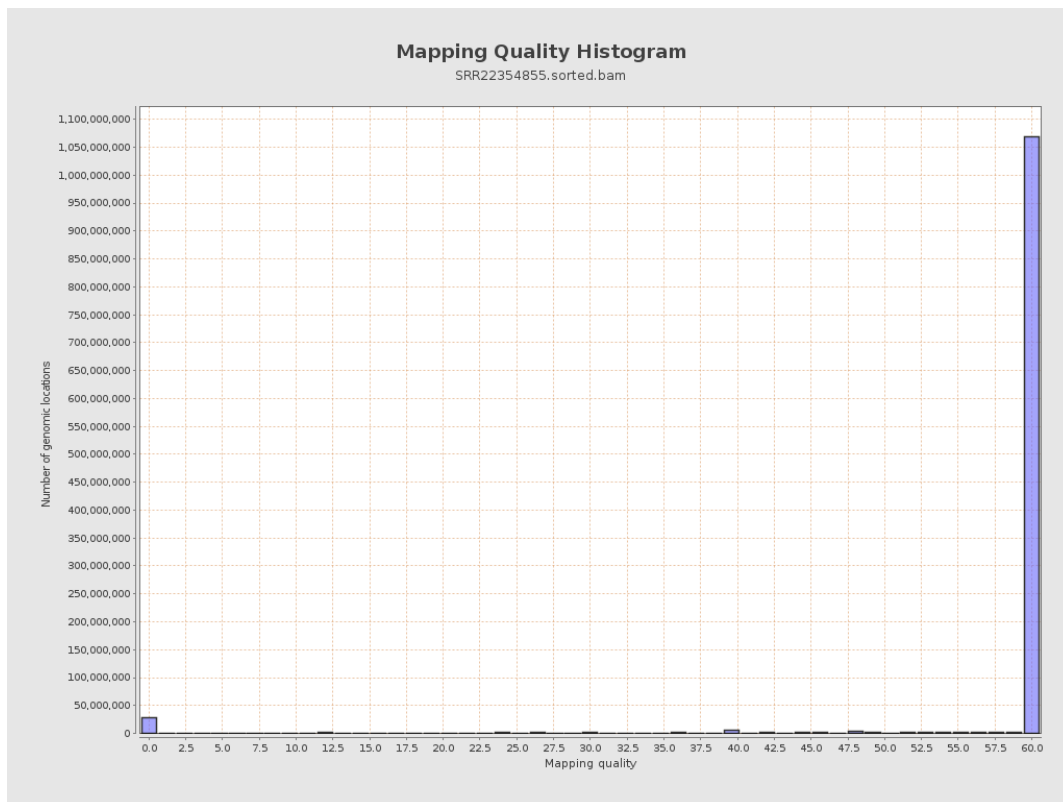
11. Results : Homopolymer Indels



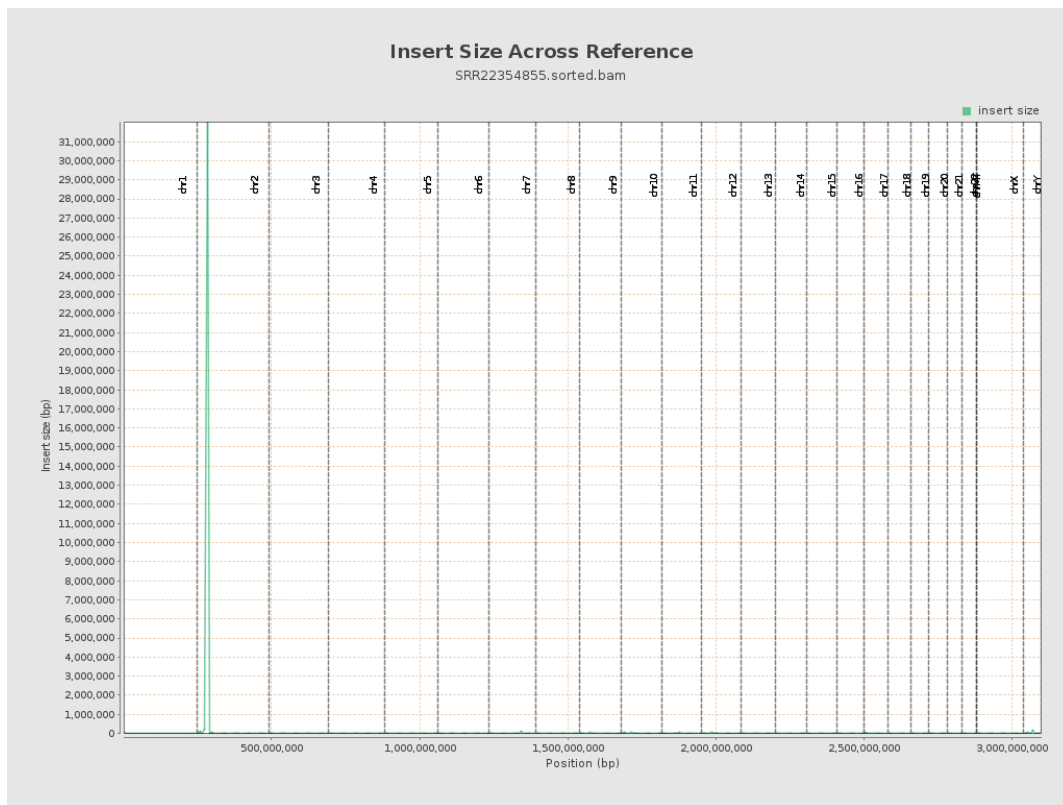
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

