

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:33:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354859.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_SRR22354859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354859_1.fastq.gz SRR22354859_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:33:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,656,616
Mapped reads	36,182,431 / 98.71%
Unmapped reads	474,185 / 1.29%
Mapped paired reads	36,182,431 / 98.71%
Mapped reads, first in pair	18,119,149 / 49.43%
Mapped reads, second in pair	18,063,282 / 49.28%
Mapped reads, both in pair	36,067,860 / 98.39%
Mapped reads, singletons	114,571 / 0.31%
Secondary alignments	0
Supplementary alignments	921,022 / 2.51%
Read min/max/mean length	30 / 150 / 150.98
Duplicated reads (estimated)	24,902,444 / 67.93%
Duplication rate	67.15%
Clipped reads	13,172,821 / 35.94%

2.2. ACGT Content

Number/percentage of A's	1,320,571,253 / 27.42%
Number/percentage of C's	1,064,309,314 / 22.1%
Number/percentage of T's	1,333,877,923 / 27.69%
Number/percentage of G's	1,097,814,189 / 22.79%
Number/percentage of N's	114,166 / 0%

GC Percentage	44.89%
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2.3. Coverage

Mean	1.5568
Standard Deviation	40.1948

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	229,825.83
Standard Deviation	5,504,578.59
P25/Median/P75	131 / 233 / 362

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	36,990,491
Insertions	852,530
Mapped reads with at least one insertion	2.16%
Deletions	837,534
Mapped reads with at least one deletion	2.18%
Homopolymer indels	41.45%

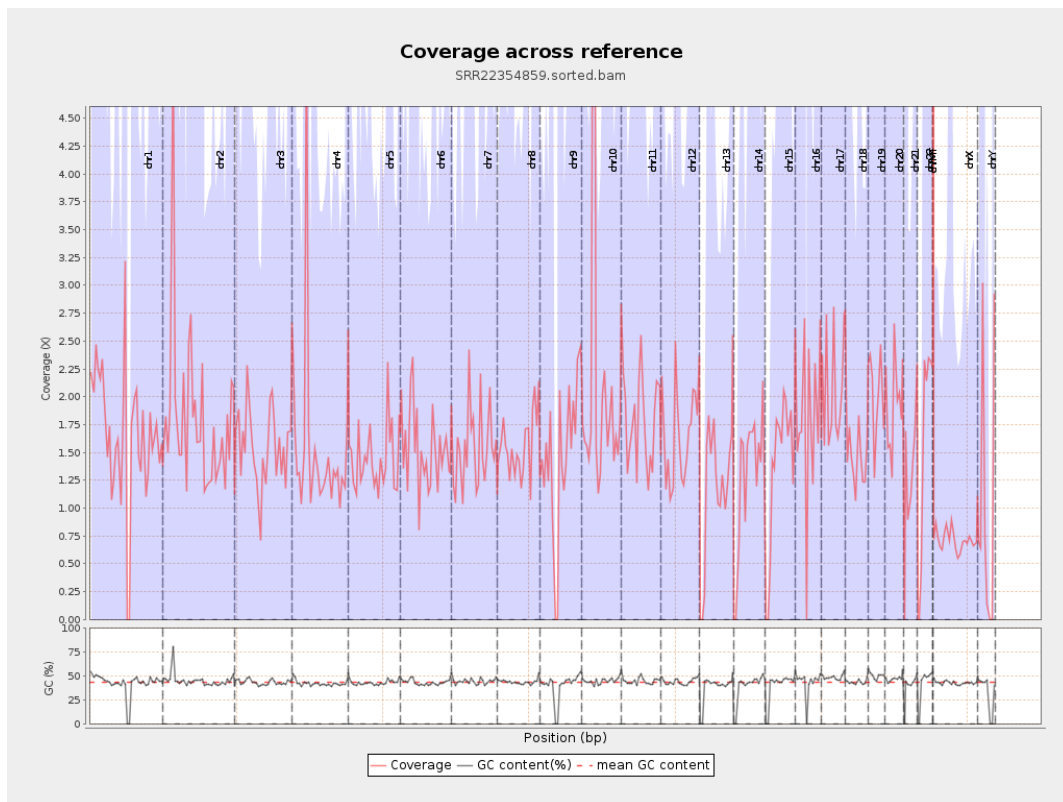
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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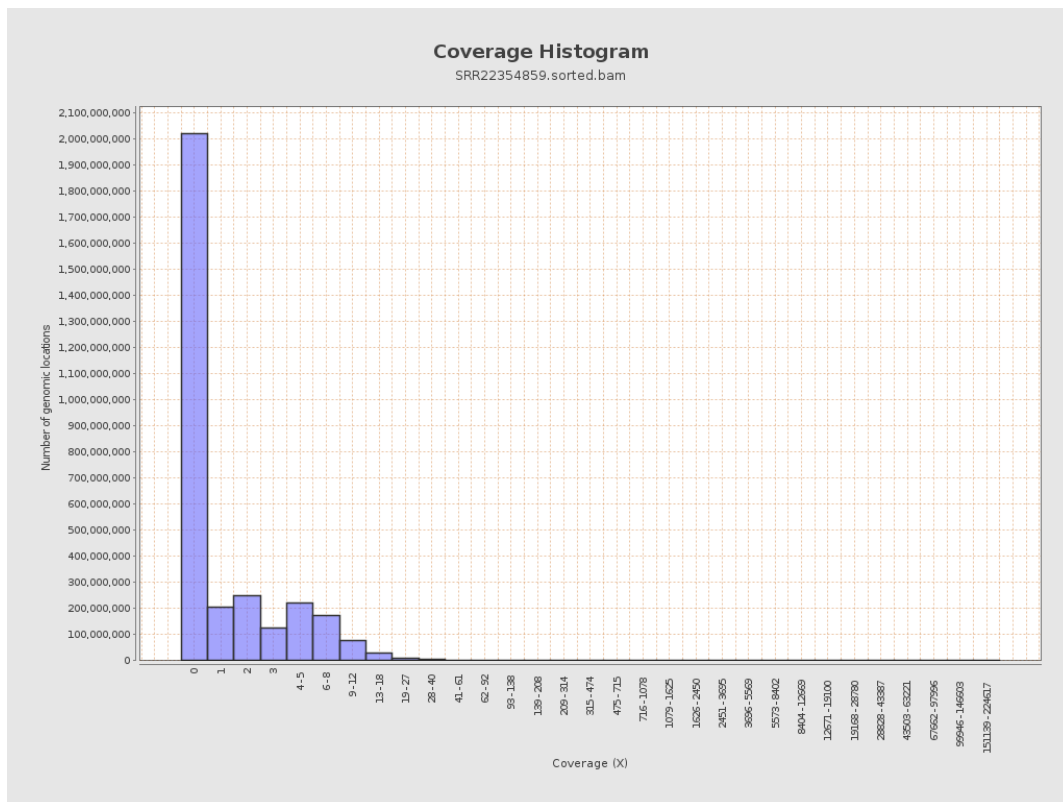
		bases	coverage	deviation
chr1	249250621	411109426	1.6494	36.0113
chr2	243199373	435588144	1.7911	123.5826
chr3	198022430	306850465	1.5496	3.8164
chr4	191154276	290405025	1.5192	30.5638
chr5	180915260	263321388	1.4555	3.0217
chr6	171115067	259665137	1.5175	5.9037
chr7	159138663	246830323	1.551	21.6991
chr8	146364022	228625308	1.562	4.4714
chr9	141213431	207221537	1.4674	19.996
chr10	135534747	276827905	2.0425	57.9536
chr11	135006516	242102869	1.7933	6.9098
chr12	133851895	223281483	1.6681	3.1829
chr13	115169878	136033544	1.1812	2.6045
chr14	107349540	138389898	1.2892	6.5572
chr15	102531392	137154421	1.3377	2.7951
chr16	90354753	164742835	1.8233	10.2635
chr17	81195210	166094225	2.0456	8.602
chr18	78077248	116194698	1.4882	18.2417
chr19	59128983	117584388	1.9886	19.2002
chr20	63025520	119712636	1.8994	10.2441
chr21	48129895	64200766	1.3339	14.6596
chr22	51304566	78868058	1.5373	4.4082
chrMT	16571	15299574	923.274	248.1342
chrX	155270560	111793592	0.72	2.7545

chrY	59373566	61389212	1.0339	35.196
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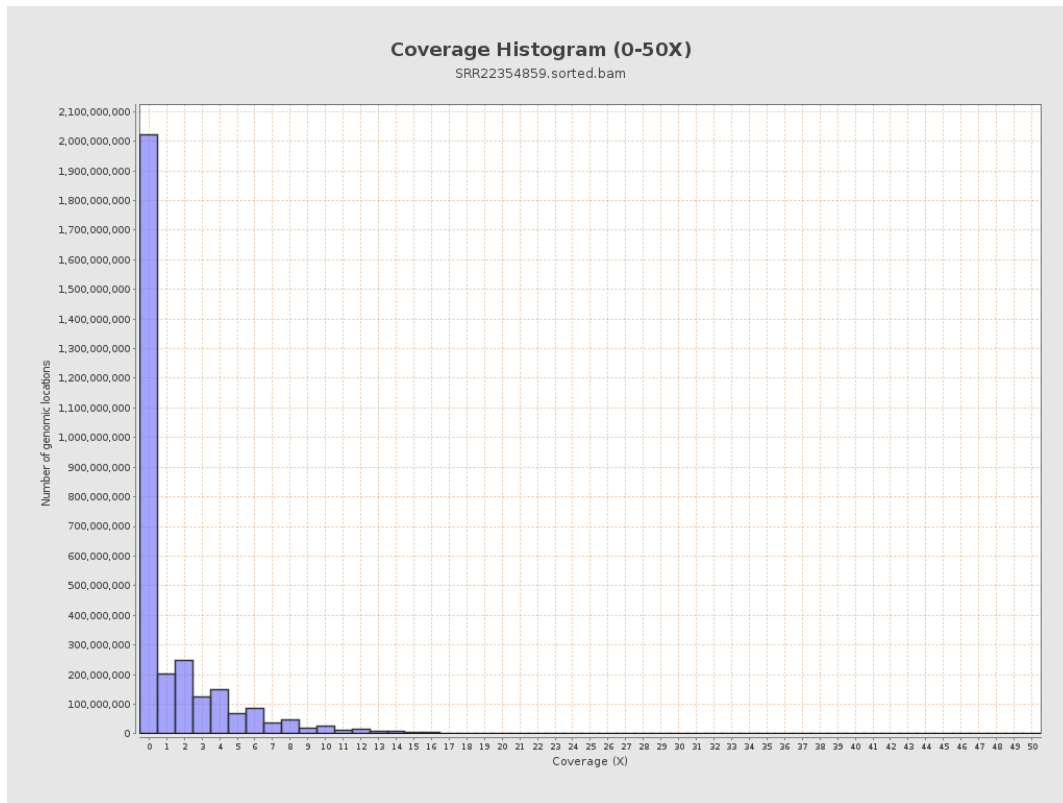
3. Results : Coverage across reference



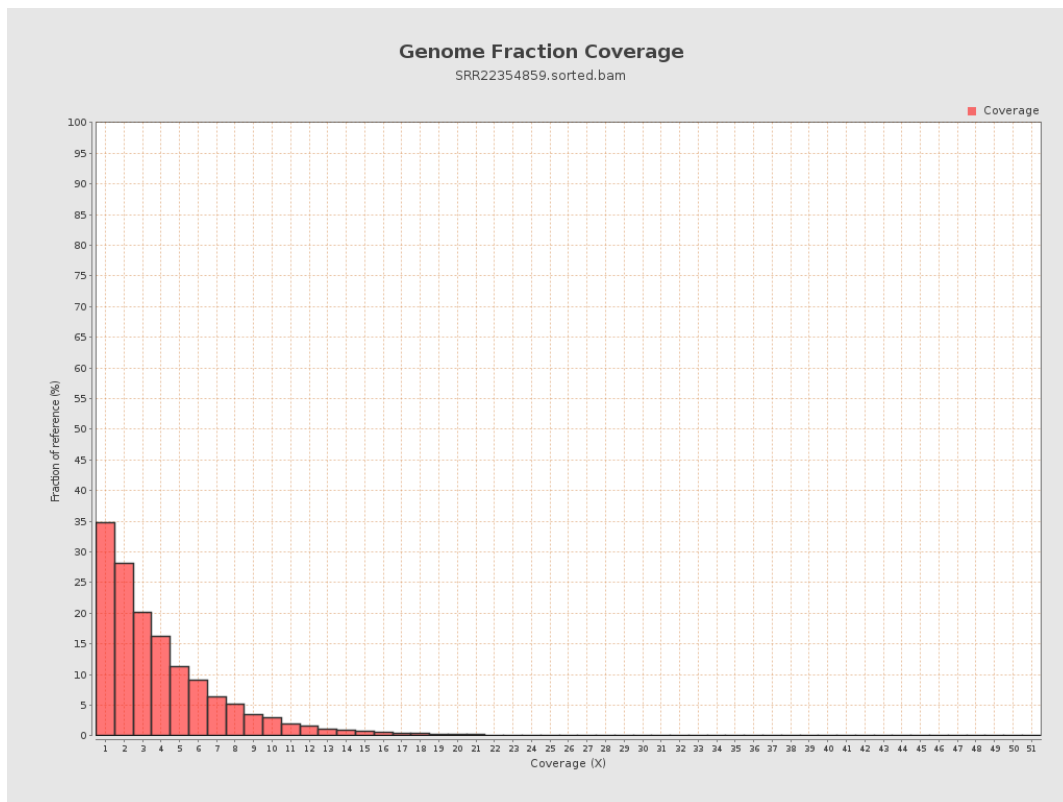
4. Results : Coverage Histogram



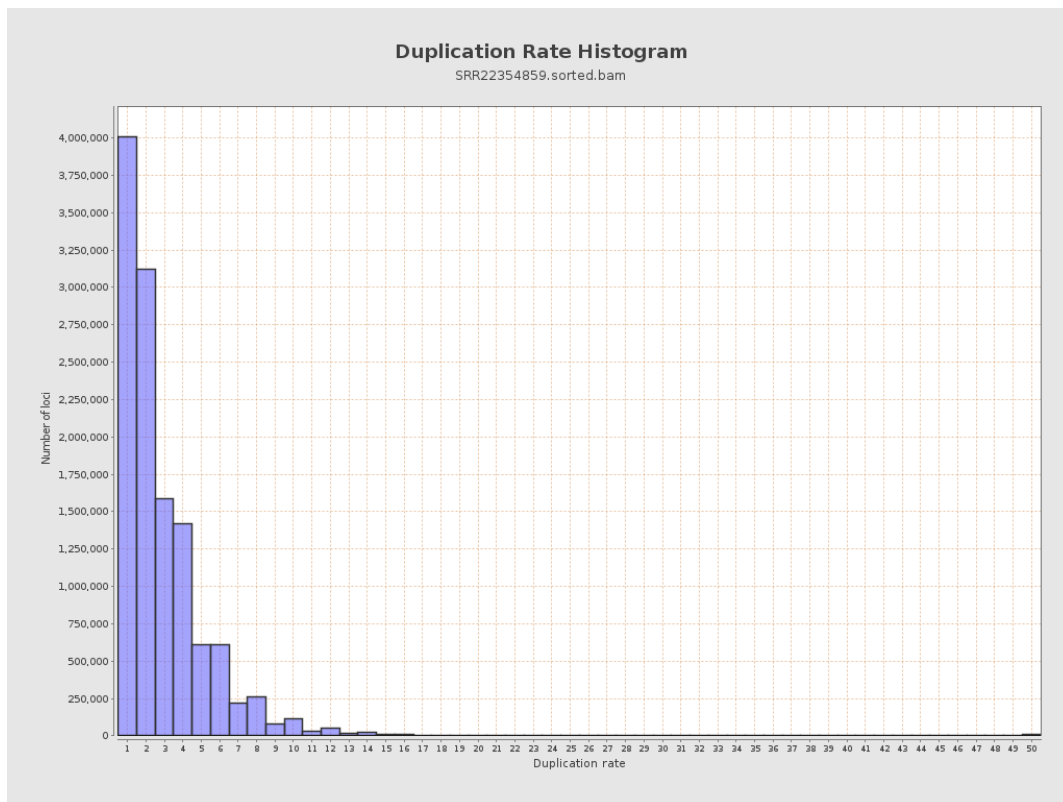
5. Results : Coverage Histogram (0-50X)



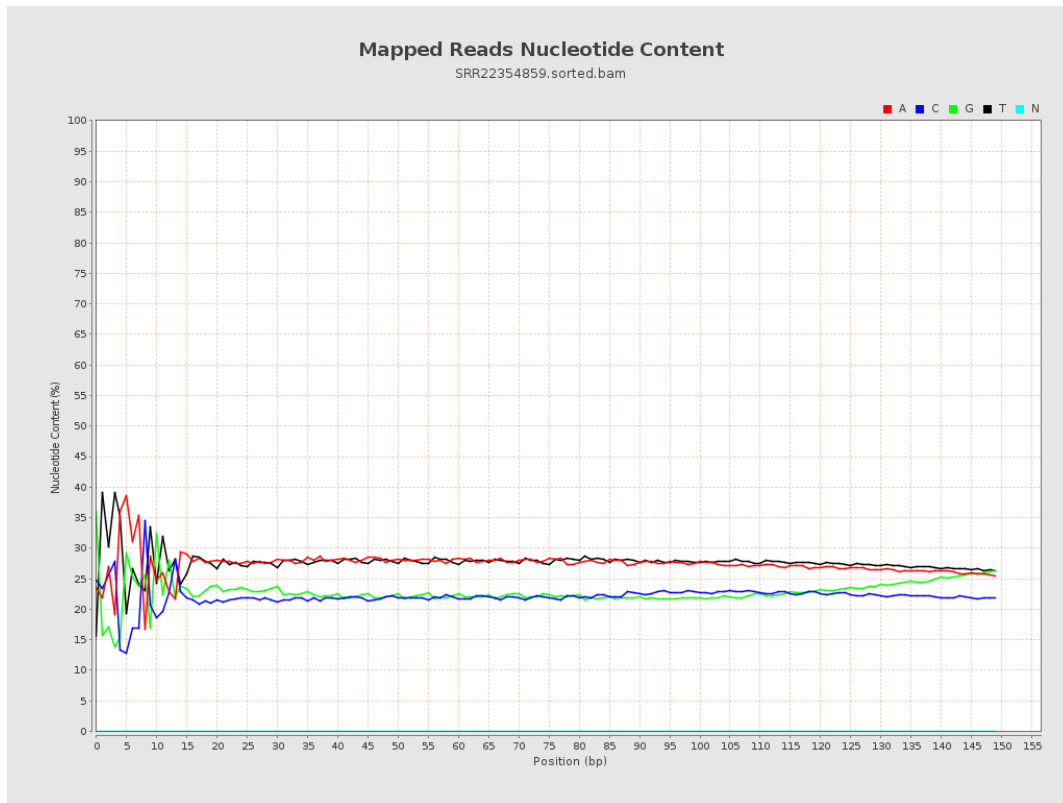
6. Results : Genome Fraction Coverage



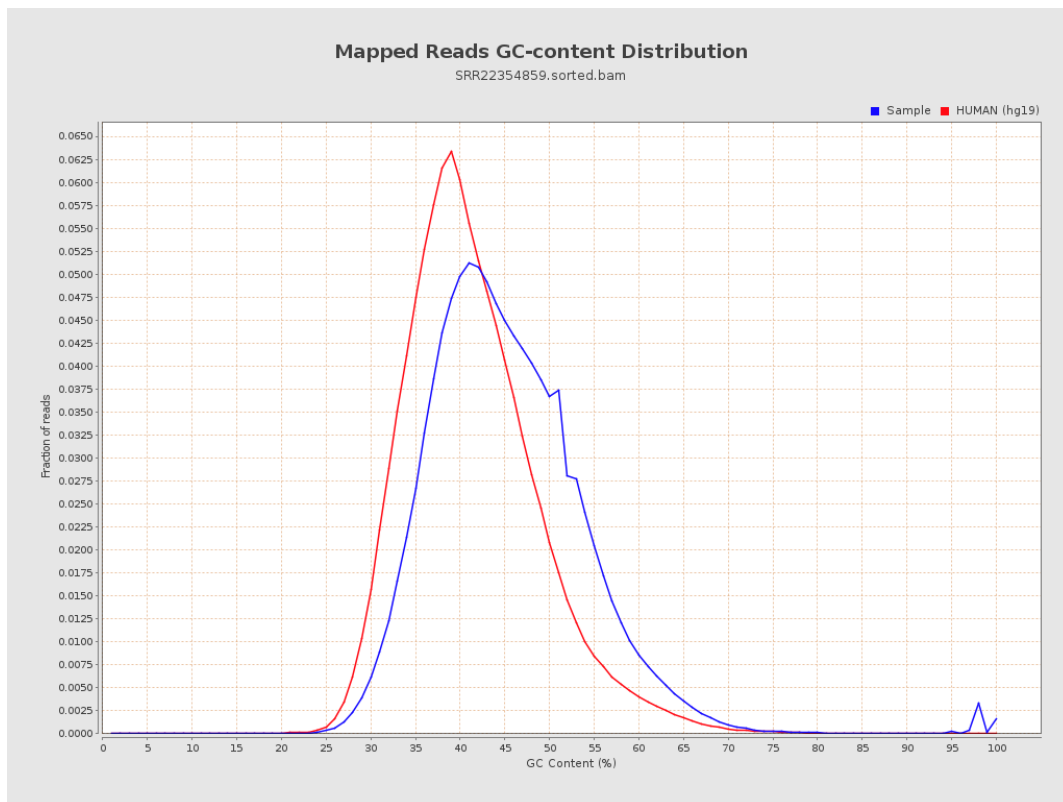
7. Results : Duplication Rate Histogram



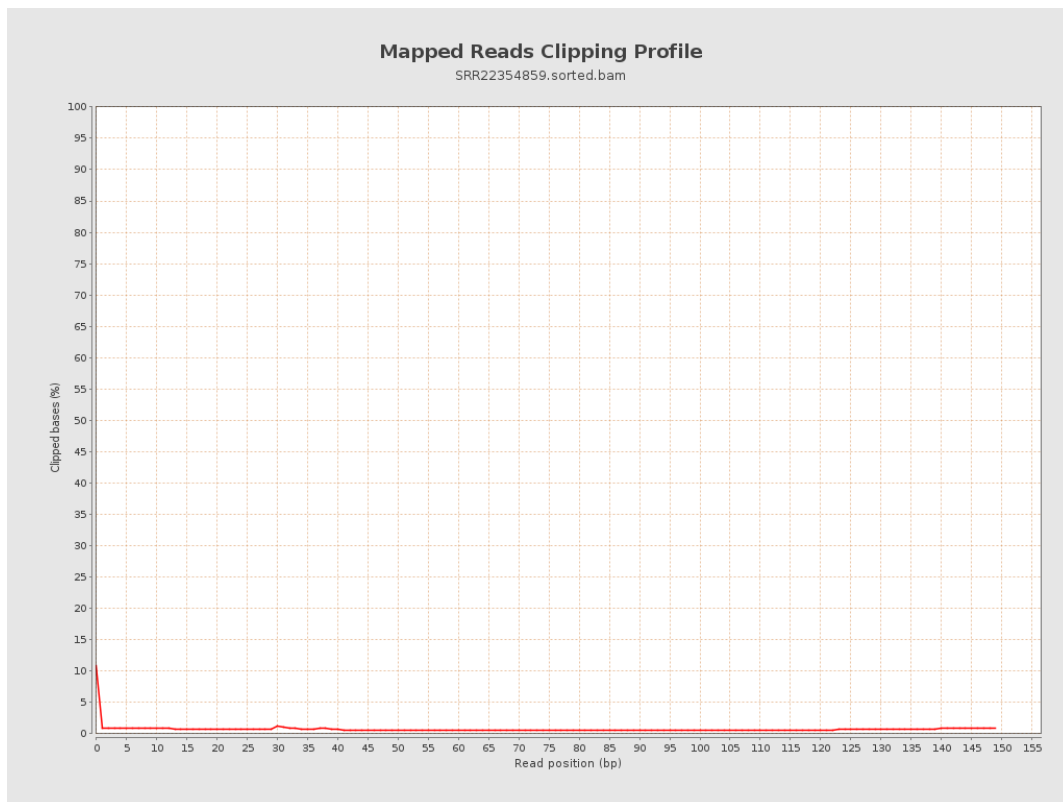
8. Results : Mapped Reads Nucleotide Content



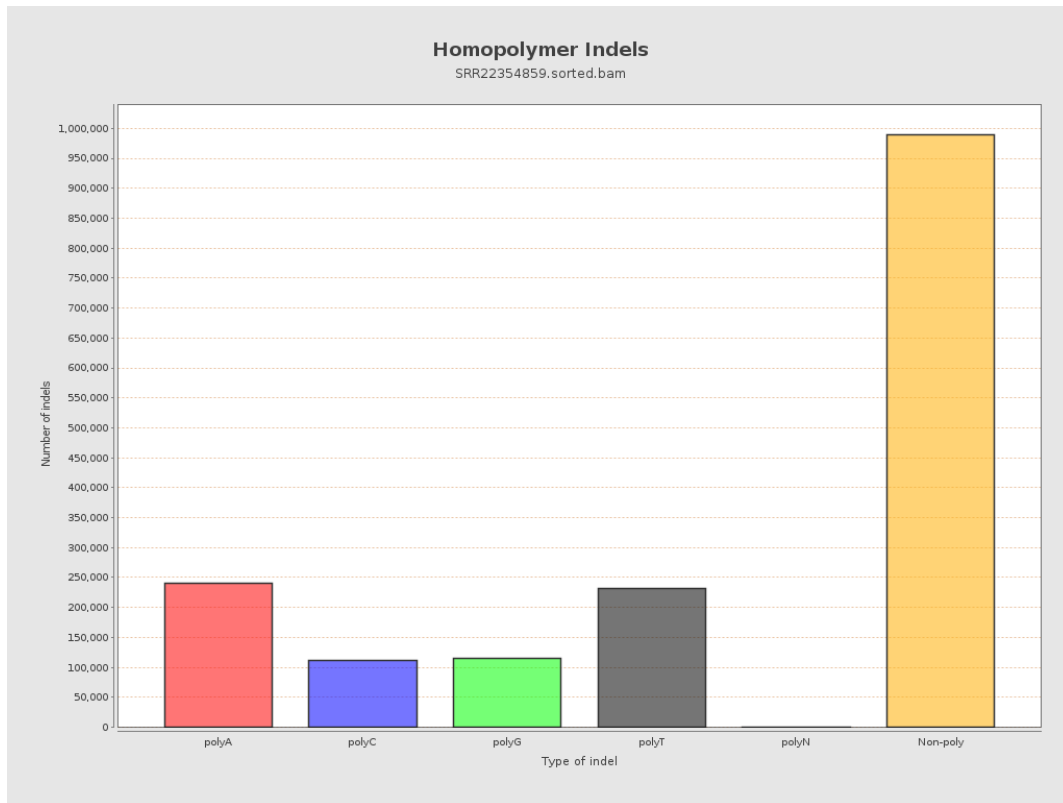
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



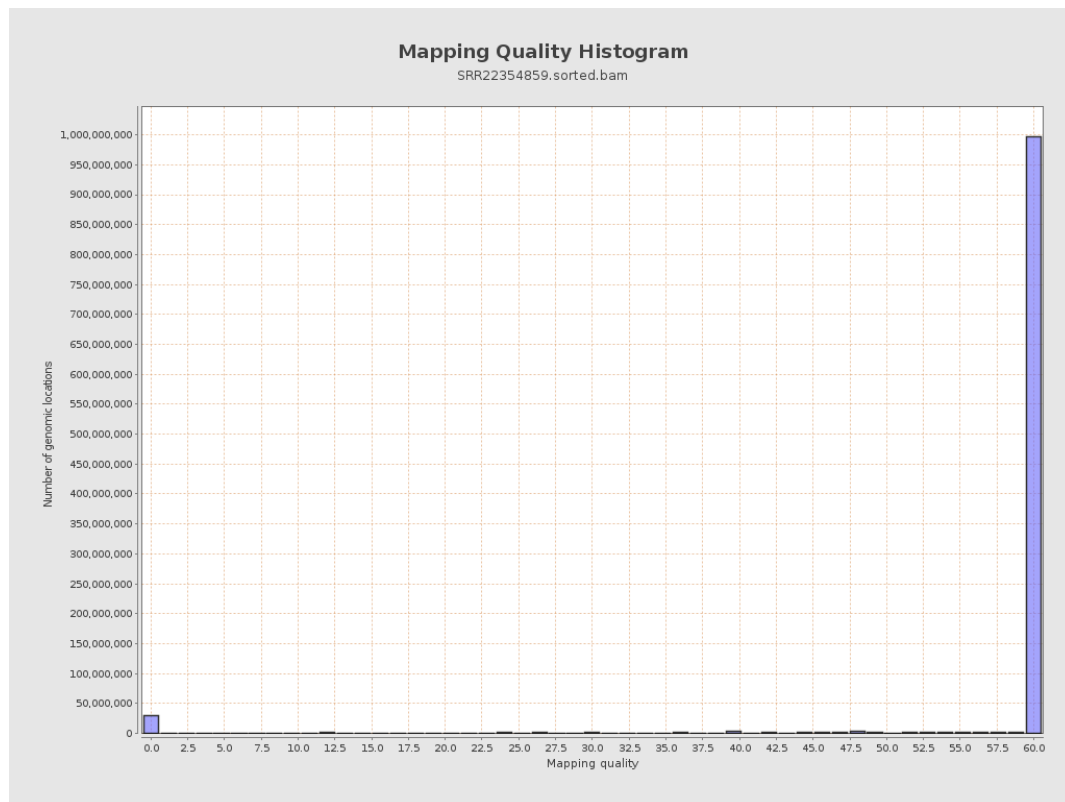
11. Results : Homopolymer Indels



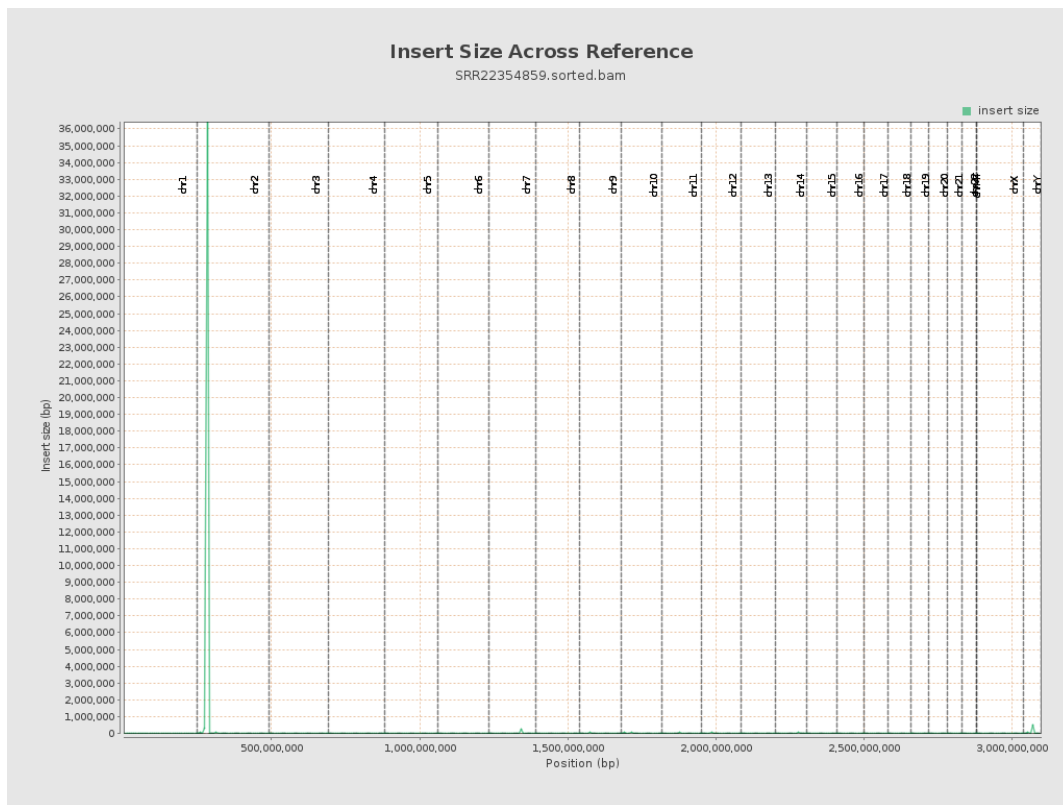
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

