

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:44:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354847.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_SRR22354847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354847_1.fastq.gz SRR22354847_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:44:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,880,488
Mapped reads	22,680,210 / 99.12%
Unmapped reads	200,278 / 0.88%
Mapped paired reads	22,680,210 / 99.12%
Mapped reads, first in pair	11,351,134 / 49.61%
Mapped reads, second in pair	11,329,076 / 49.51%
Mapped reads, both in pair	22,631,262 / 98.91%
Mapped reads, singletons	48,948 / 0.21%
Secondary alignments	0
Supplementary alignments	551,858 / 2.41%
Read min/max/mean length	30 / 150 / 150.92
Duplicated reads (estimated)	9,259,334 / 40.47%
Duplication rate	39.62%
Clipped reads	9,718,560 / 42.48%

2.2. ACGT Content

Number/percentage of A's	837,620,591 / 28.28%
Number/percentage of C's	628,233,808 / 21.21%
Number/percentage of T's	848,897,954 / 28.66%
Number/percentage of G's	646,934,659 / 21.84%
Number/percentage of N's	35,119 / 0%

GC Percentage	43.05%
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2.3. Coverage

Mean	0.9572
Standard Deviation	25.0348

2.4. Mapping Quality

Mean Mapping Quality	53.9
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2.5. Insert size

Mean	224,768.33
Standard Deviation	5,432,509.53
P25/Median/P75	118 / 181 / 263

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	22,795,686
Insertions	532,917
Mapped reads with at least one insertion	2.19%
Deletions	563,265
Mapped reads with at least one deletion	2.37%
Homopolymer indels	43.74%

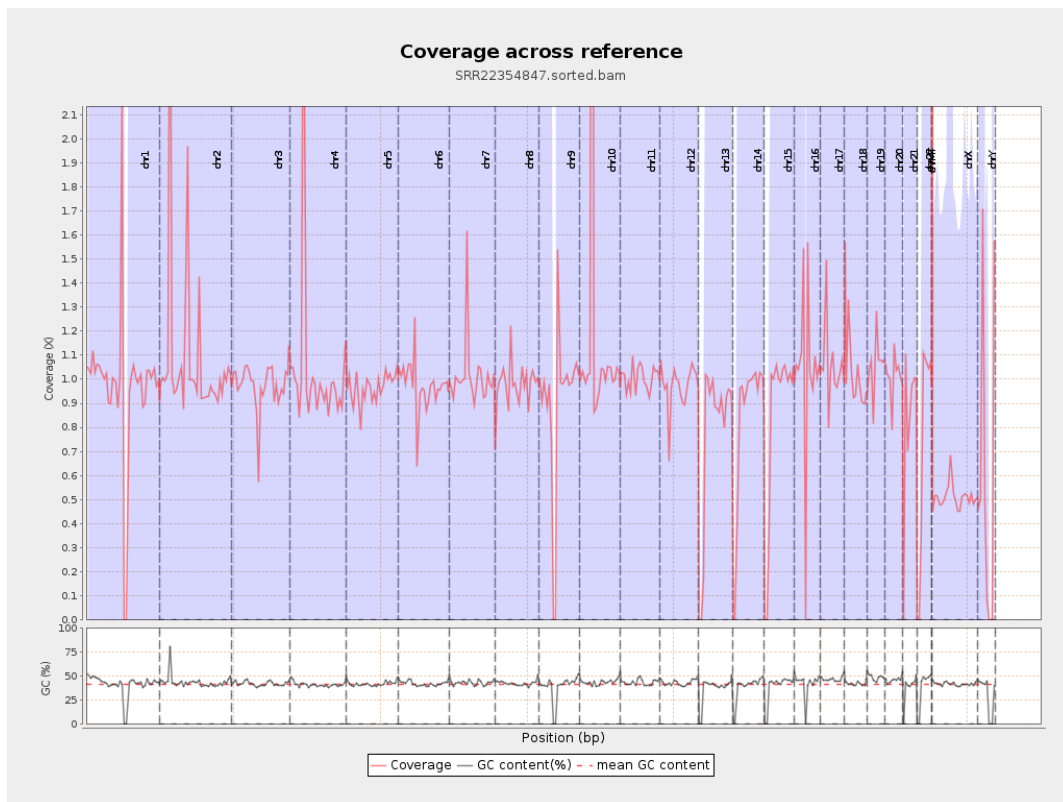
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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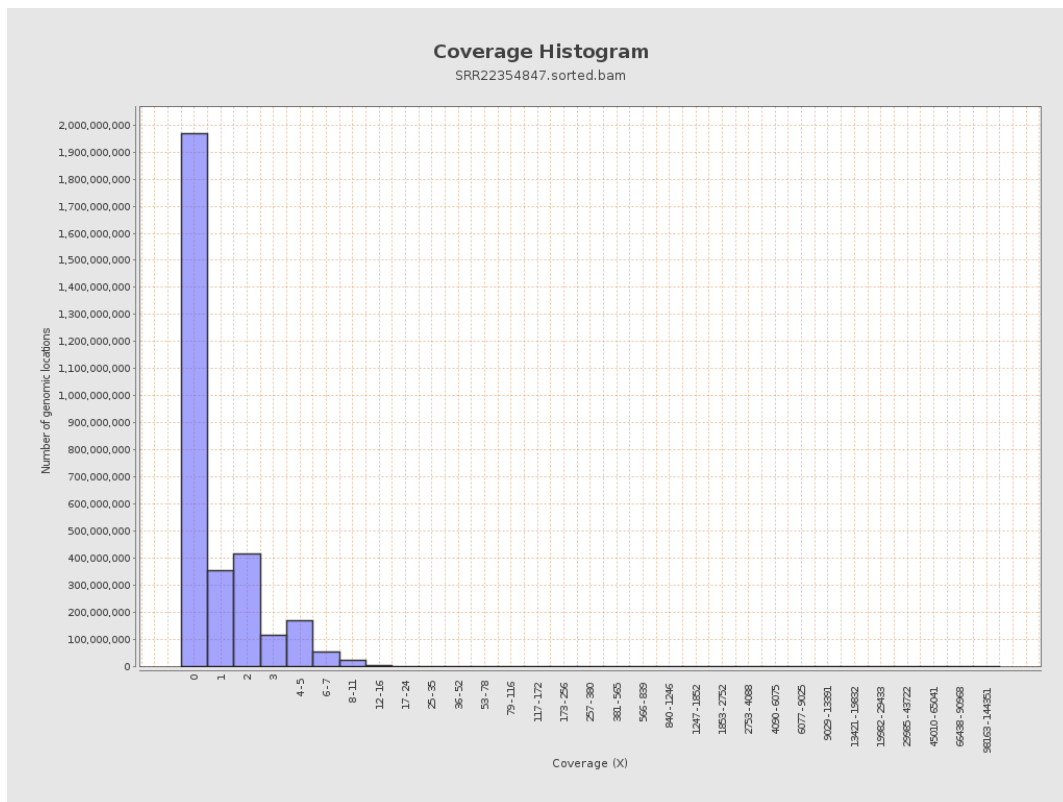
		bases	coverage	deviation
chr1	249250621	242816027	0.9742	26.2168
chr2	243199373	267102937	1.0983	76.9895
chr3	198022430	192870199	0.974	2.156
chr4	191154276	196745286	1.0292	13.5607
chr5	180915260	174615024	0.9652	1.7389
chr6	171115067	166681474	0.9741	3.8876
chr7	159138663	161200854	1.013	15.2254
chr8	146364022	144797079	0.9893	3.6061
chr9	141213431	126736654	0.8975	14.0693
chr10	135534747	166594536	1.2292	33.6152
chr11	135006516	135832832	1.0061	4.8874
chr12	133851895	130165232	0.9725	1.8565
chr13	115169878	89487775	0.777	1.4979
chr14	107349540	88561053	0.825	3.6982
chr15	102531392	84826604	0.8273	1.5416
chr16	90354753	93978344	1.0401	5.9931
chr17	81195210	85729934	1.0558	6.0602
chr18	78077248	80163539	1.0267	12.2386
chr19	59128983	62636172	1.0593	12.9219
chr20	63025520	63740692	1.0113	4.4958
chr21	48129895	40799837	0.8477	7.2617
chr22	51304566	38180814	0.7442	2.9603
chrMT	16571	13819065	833.9307	171.6037
chrX	155270560	79011738	0.5089	2.1355

chrY	59373566	36202956	0.6097	17.3005
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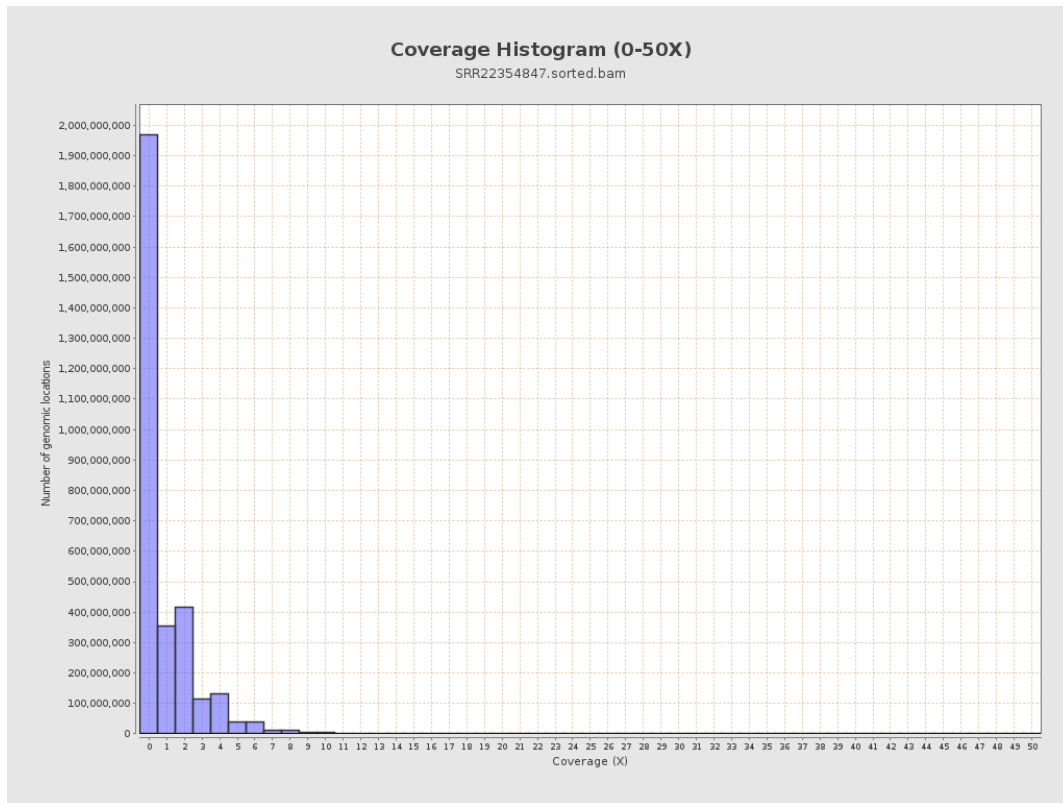
3. Results : Coverage across reference



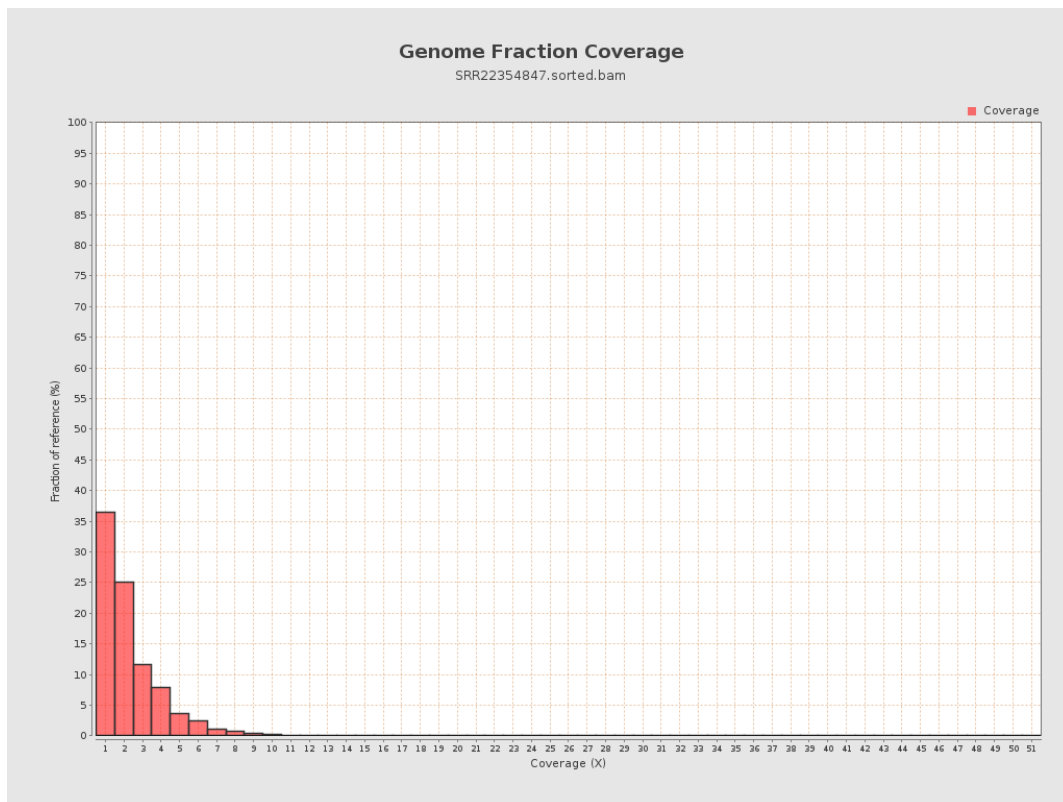
4. Results : Coverage Histogram



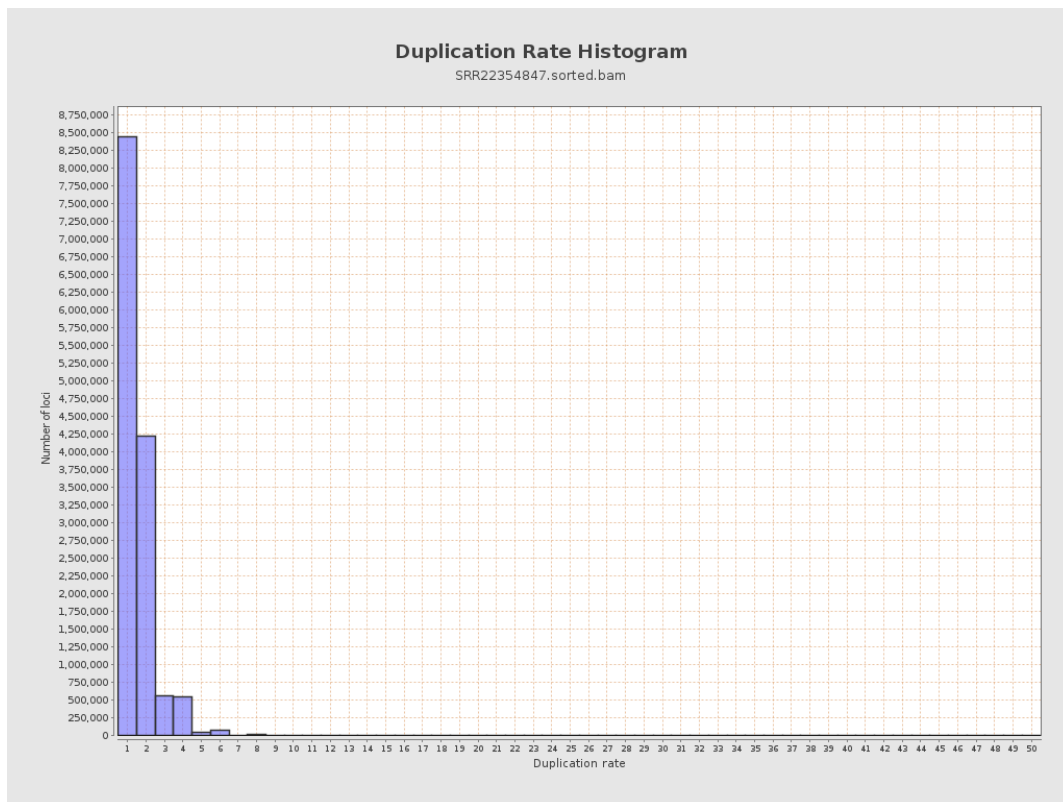
5. Results : Coverage Histogram (0-50X)



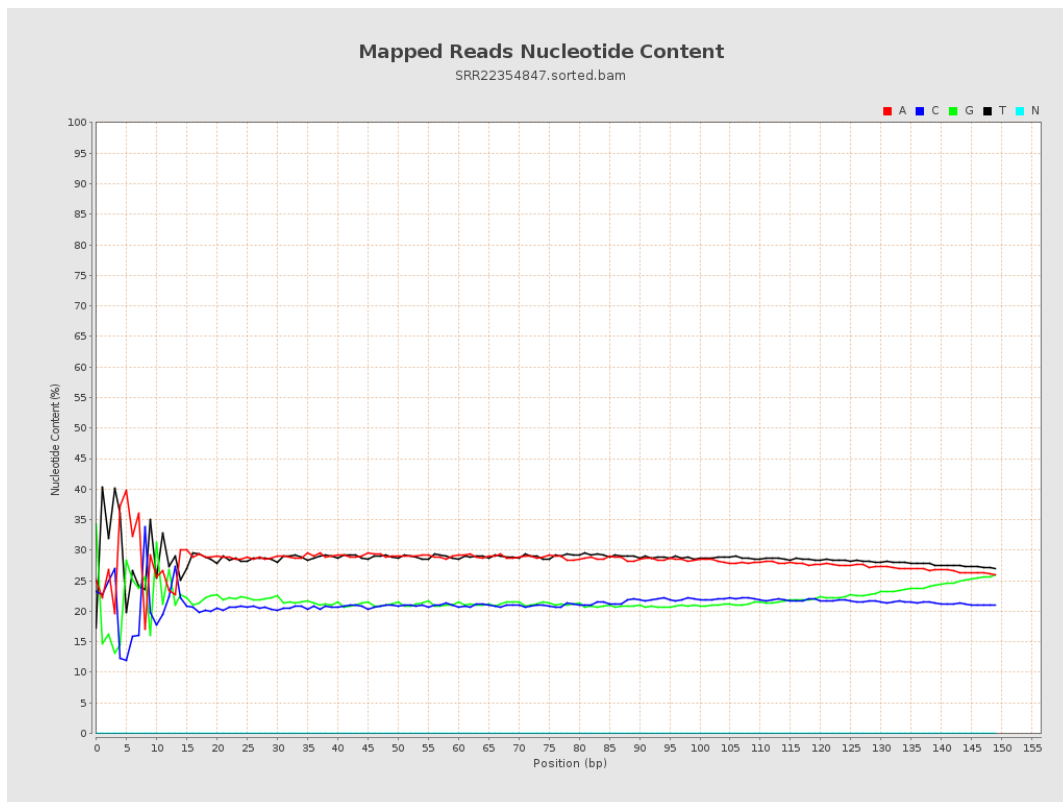
6. Results : Genome Fraction Coverage



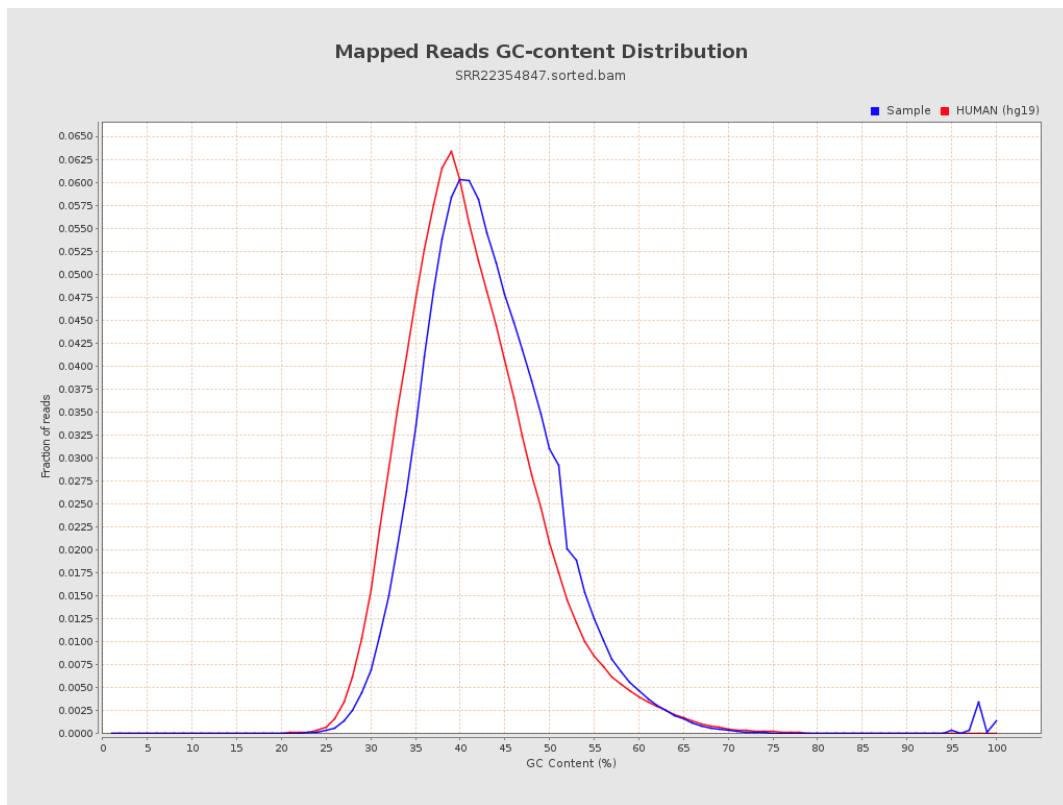
7. Results : Duplication Rate Histogram



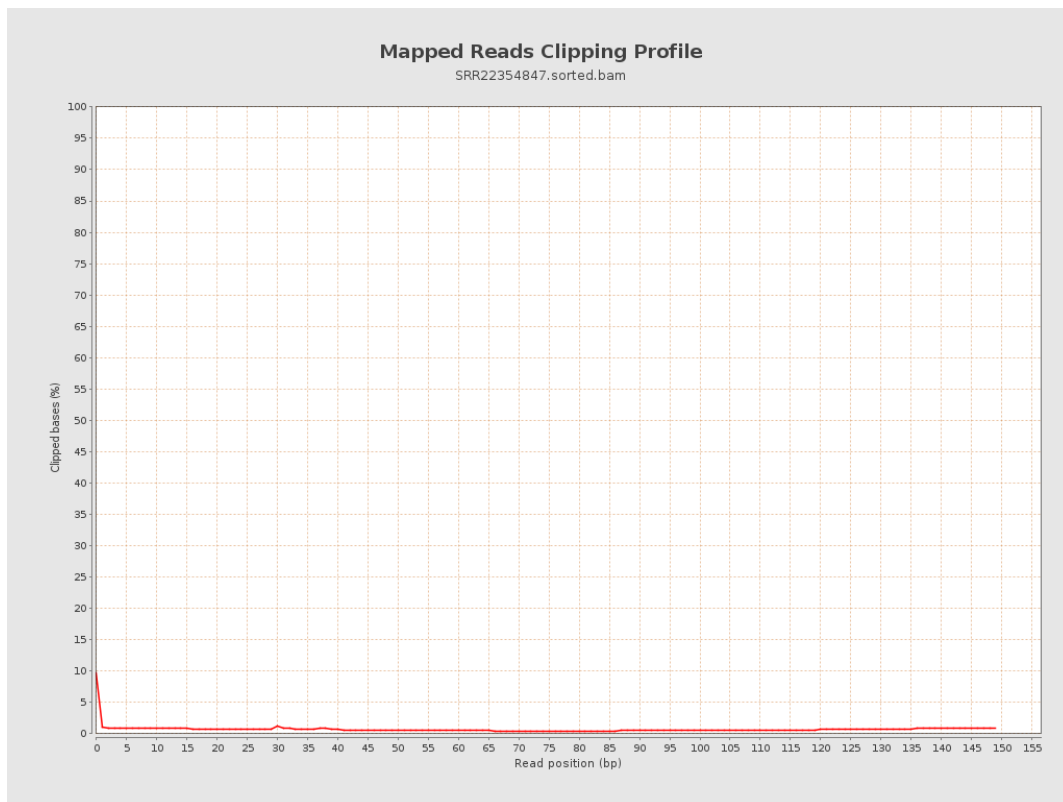
8. Results : Mapped Reads Nucleotide Content



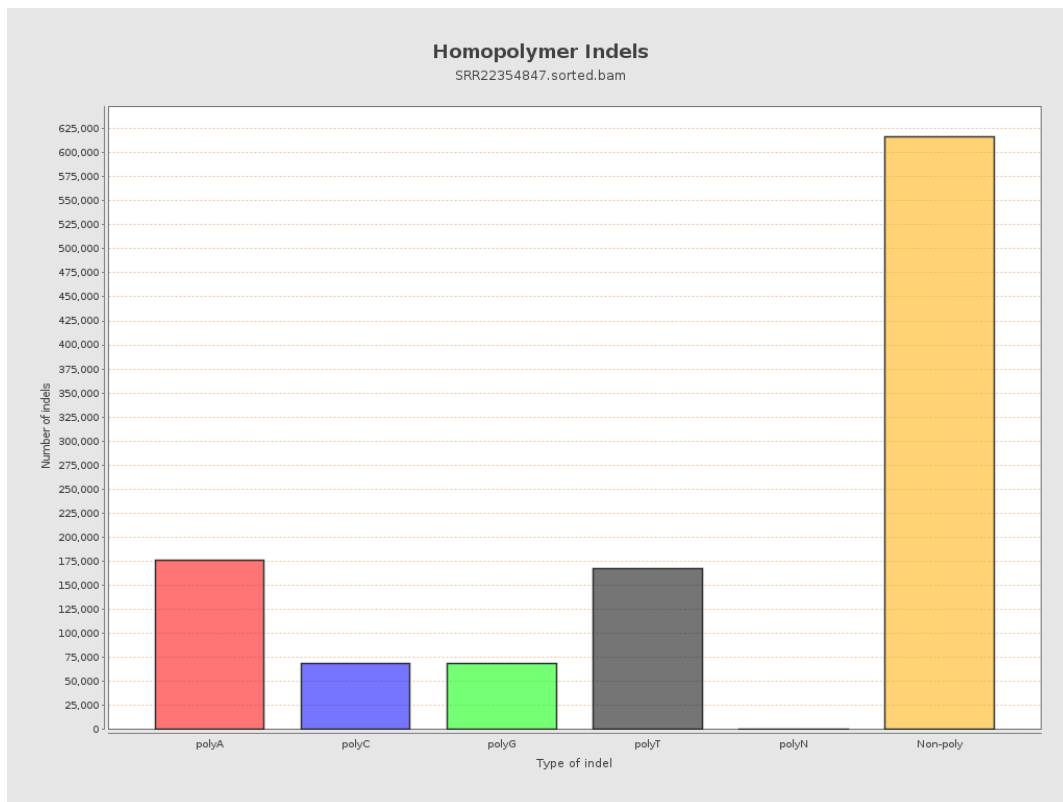
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



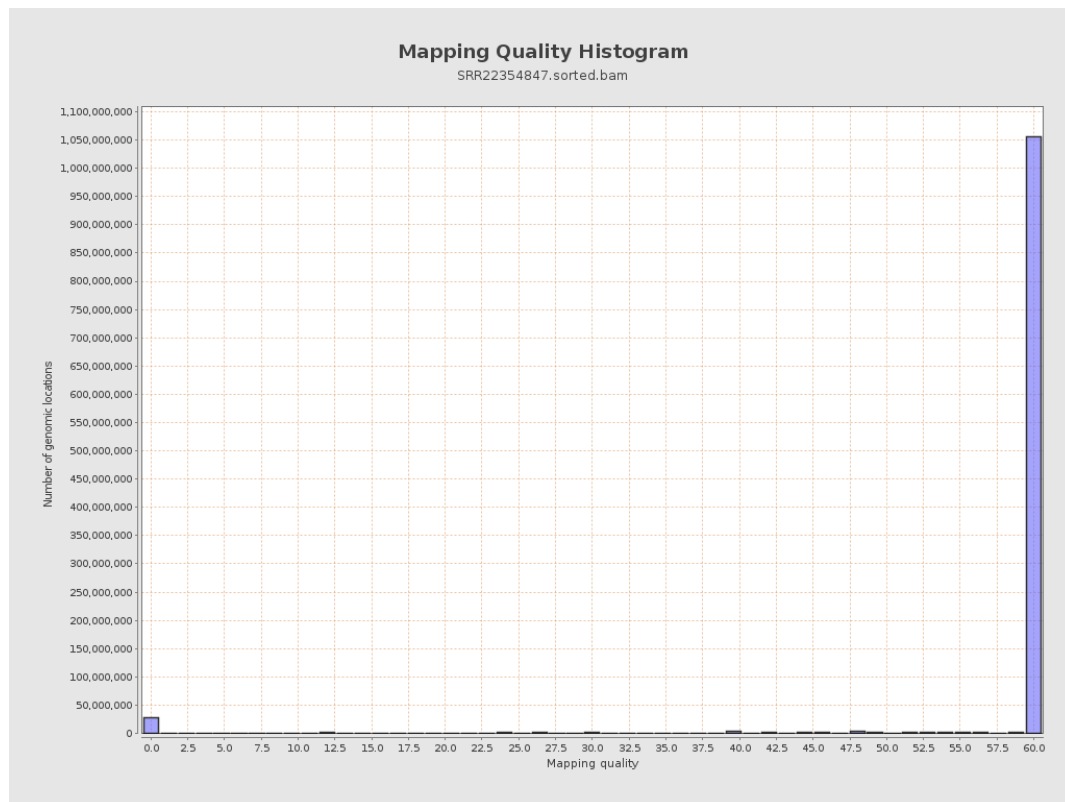
11. Results : Homopolymer Indels



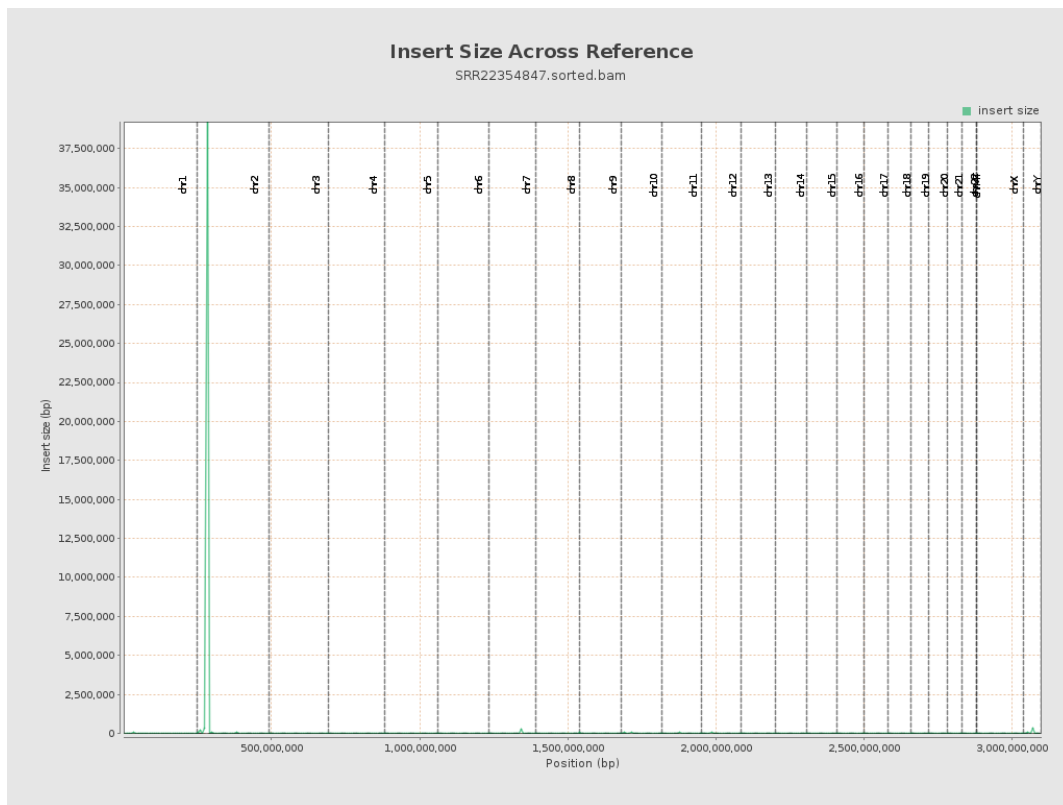
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

