

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:36:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354849.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_SRR22354849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354849_1.fastq.gz SRR22354849_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:36:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,331,876
Mapped reads	15,174,391 / 98.97%
Unmapped reads	157,485 / 1.03%
Mapped paired reads	15,174,391 / 98.97%
Mapped reads, first in pair	7,594,676 / 49.54%
Mapped reads, second in pair	7,579,715 / 49.44%
Mapped reads, both in pair	15,146,762 / 98.79%
Mapped reads, singletons	27,629 / 0.18%
Secondary alignments	0
Supplementary alignments	483,374 / 3.15%
Read min/max/mean length	30 / 150 / 151.16
Duplicated reads (estimated)	11,685,306 / 76.22%
Duplication rate	75.02%
Clipped reads	8,036,467 / 52.42%

2.2. ACGT Content

Number/percentage of A's	545,867,980 / 28.74%
Number/percentage of C's	391,502,602 / 20.62%
Number/percentage of T's	557,557,401 / 29.36%
Number/percentage of G's	404,174,910 / 21.28%
Number/percentage of N's	4,930 / 0%

GC Percentage	41.9%
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2.3. Coverage

Mean	0.6137
Standard Deviation	23.4211

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	314,928.05
Standard Deviation	6,482,955.31
P25/Median/P75	102 / 154 / 229

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	12,193,273
Insertions	287,262
Mapped reads with at least one insertion	1.79%
Deletions	313,160
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.25%

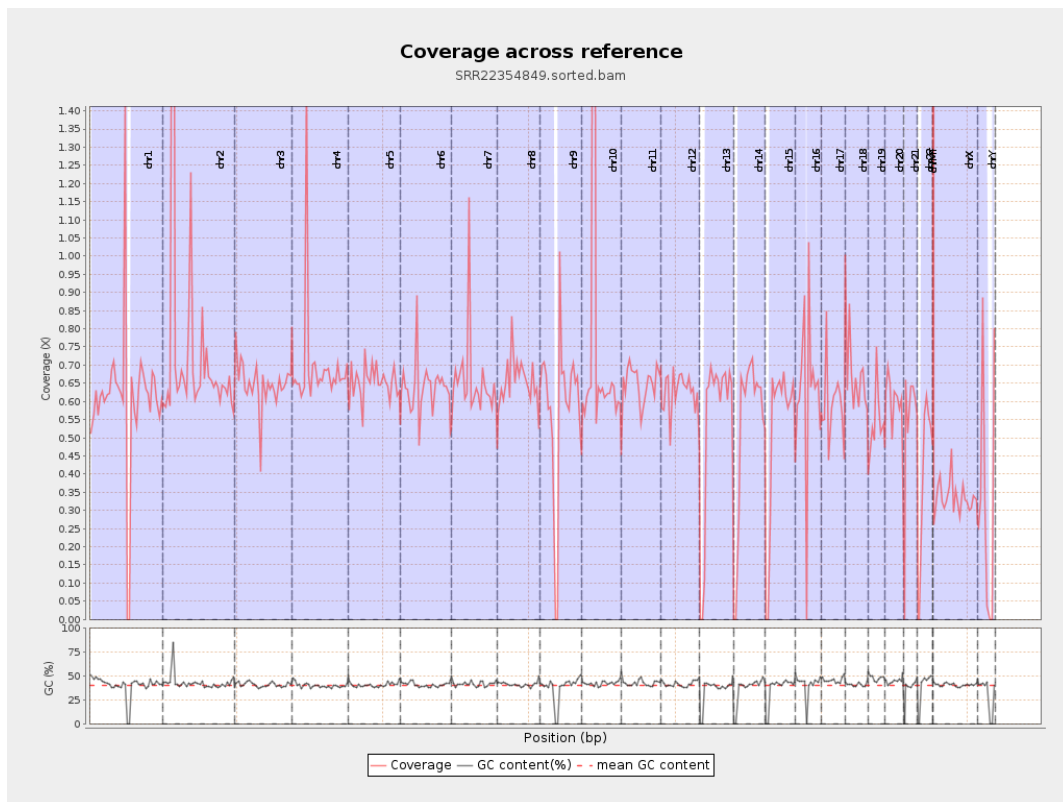
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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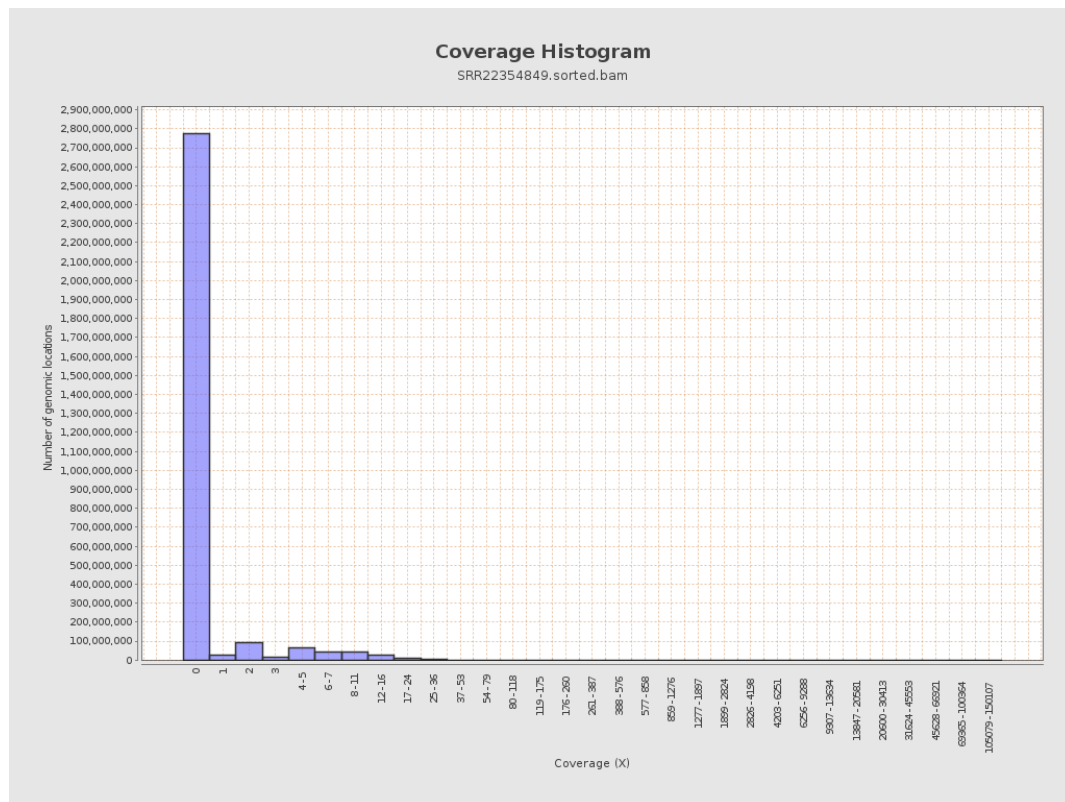
		bases	coverage	deviation
chr1	249250621	151587762	0.6082	18.7743
chr2	243199373	179601653	0.7385	78.132
chr3	198022430	128320931	0.648	2.7646
chr4	191154276	133310656	0.6974	6.4964
chr5	180915260	117649156	0.6503	2.5292
chr6	171115067	109456326	0.6397	3.5407
chr7	159138663	104132475	0.6544	11.8821
chr8	146364022	95821278	0.6547	3.6423
chr9	141213431	82206119	0.5821	9.4364
chr10	135534747	100018247	0.738	18.3473
chr11	135006516	87591006	0.6488	4.4386
chr12	133851895	83608845	0.6246	2.4913
chr13	115169878	62326267	0.5412	2.2928
chr14	107349540	57936771	0.5397	4.4213
chr15	102531392	52864603	0.5156	2.2148
chr16	90354753	56156502	0.6215	4.4324
chr17	81195210	48454476	0.5968	4.3825
chr18	78077248	52686310	0.6748	8.2438
chr19	59128983	32217520	0.5449	9.2719
chr20	63025520	38023641	0.6033	3.0774
chr21	48129895	26506143	0.5507	3.9029
chr22	51304566	20396358	0.3976	2.2709
chrMT	16571	7453725	449.8054	101.925
chrX	155270560	51864675	0.334	2.2079

chrY	59373566	19733823	0.3324	8.0297
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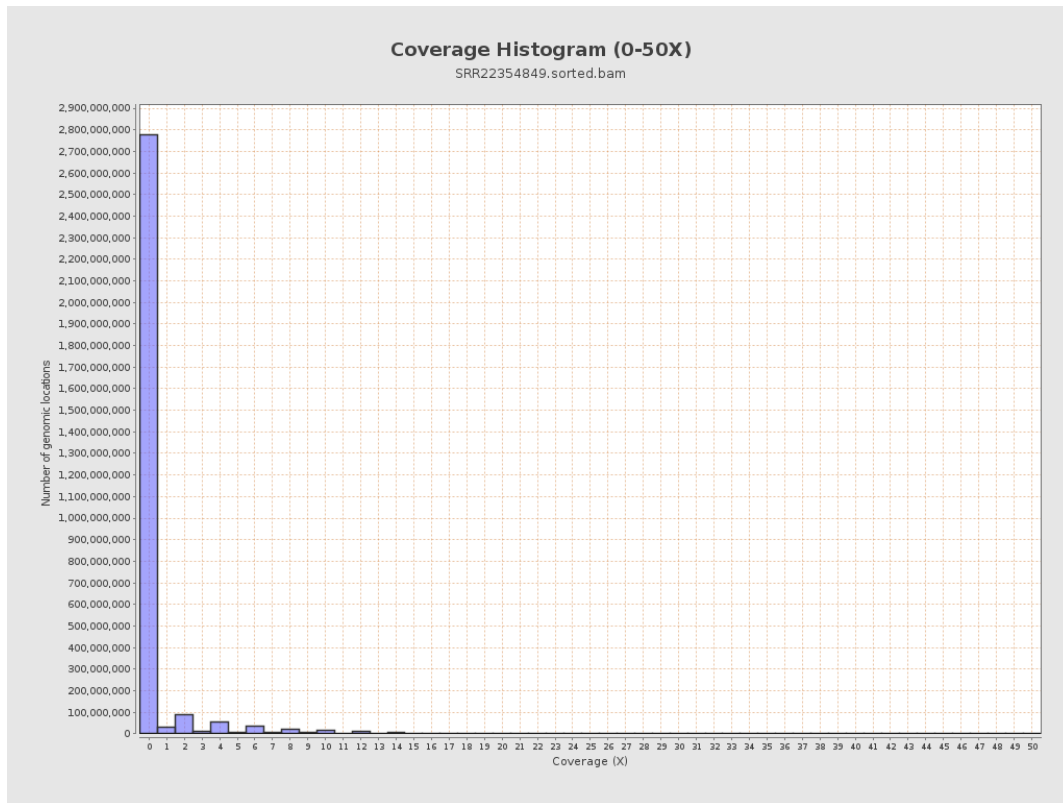
3. Results : Coverage across reference



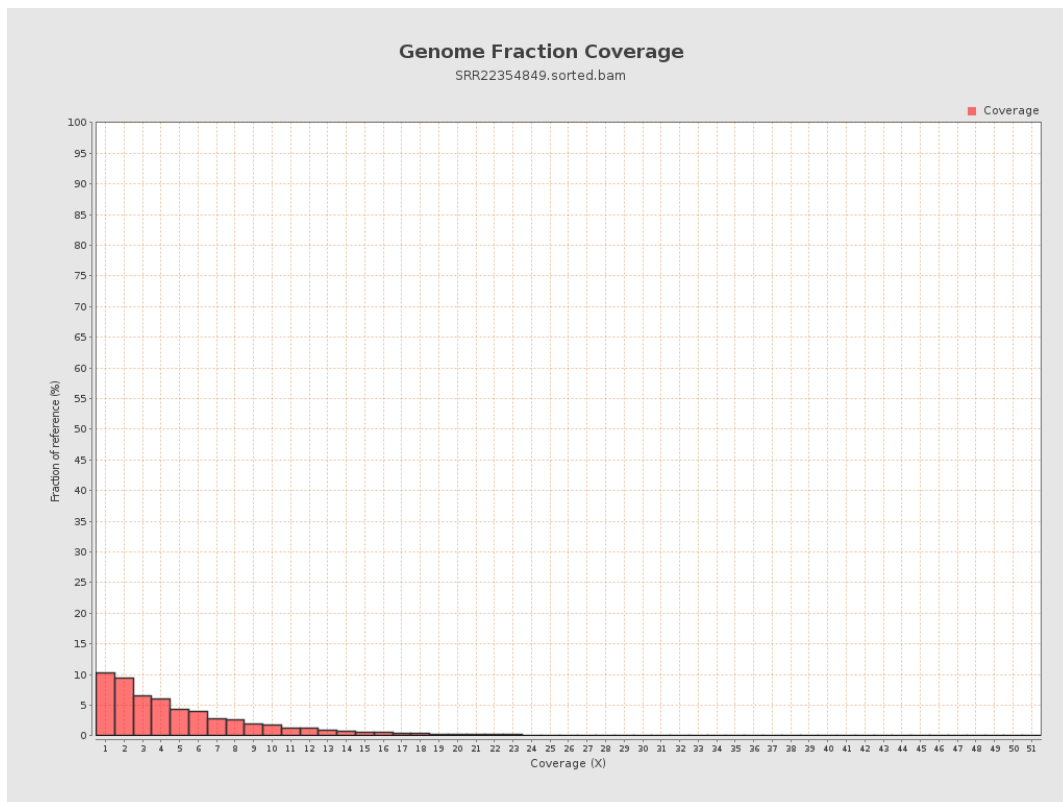
4. Results : Coverage Histogram



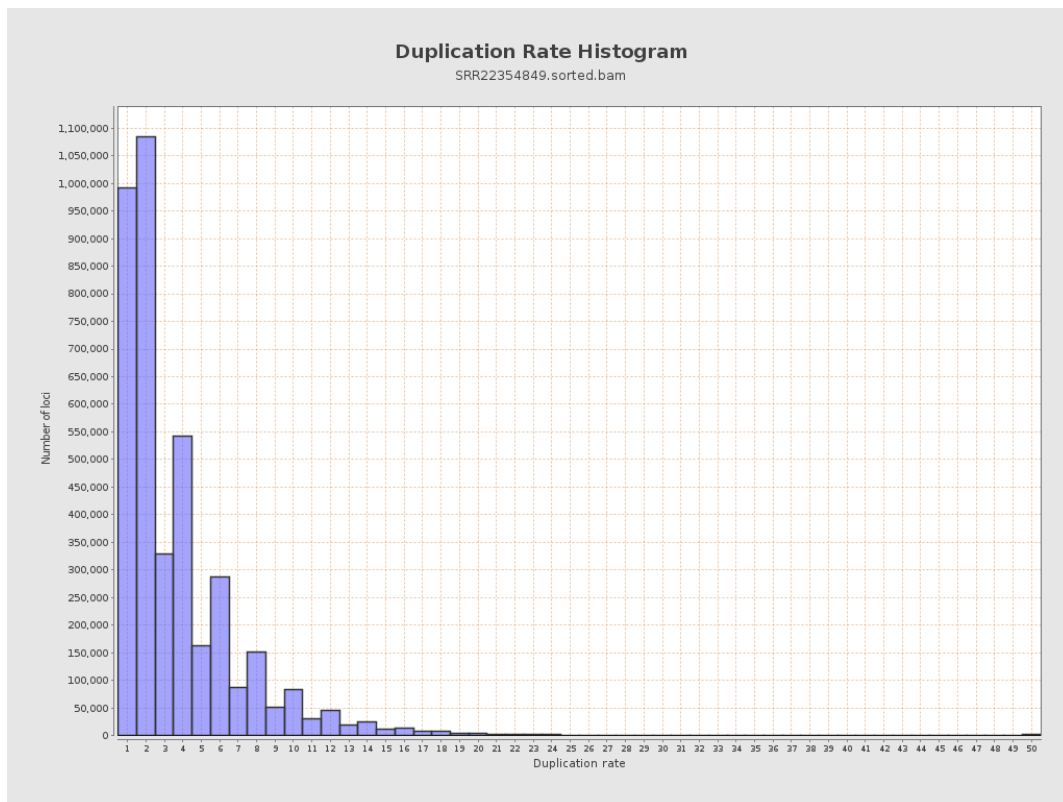
5. Results : Coverage Histogram (0-50X)



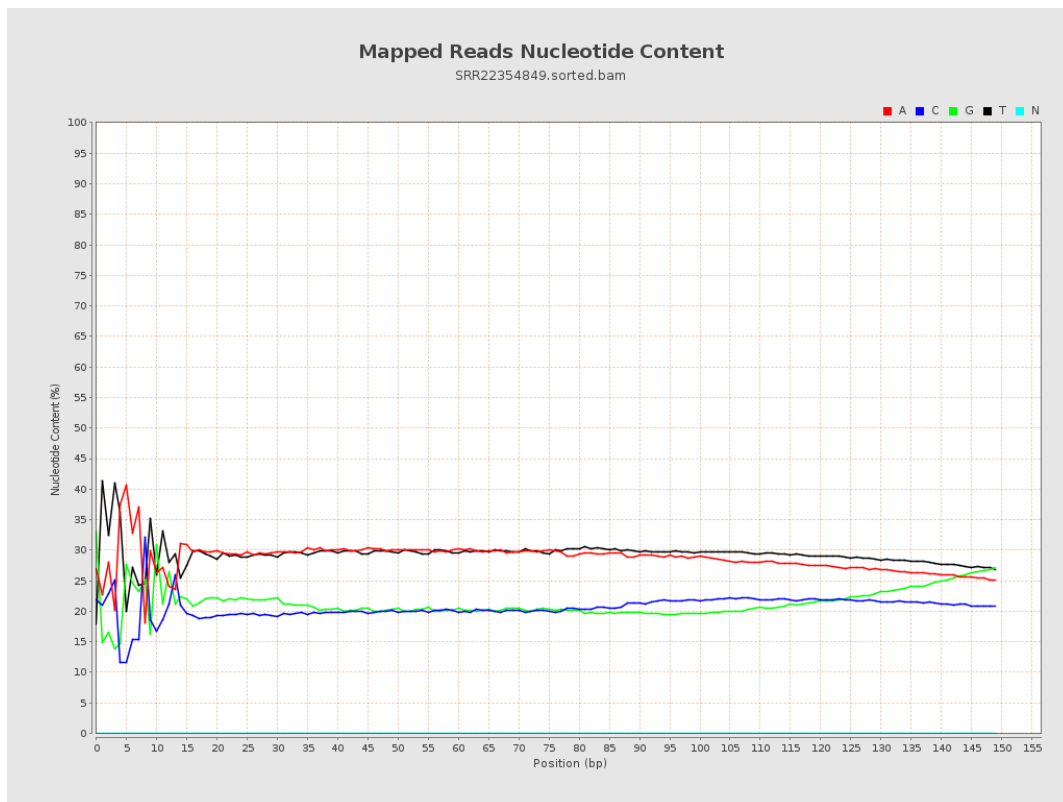
6. Results : Genome Fraction Coverage



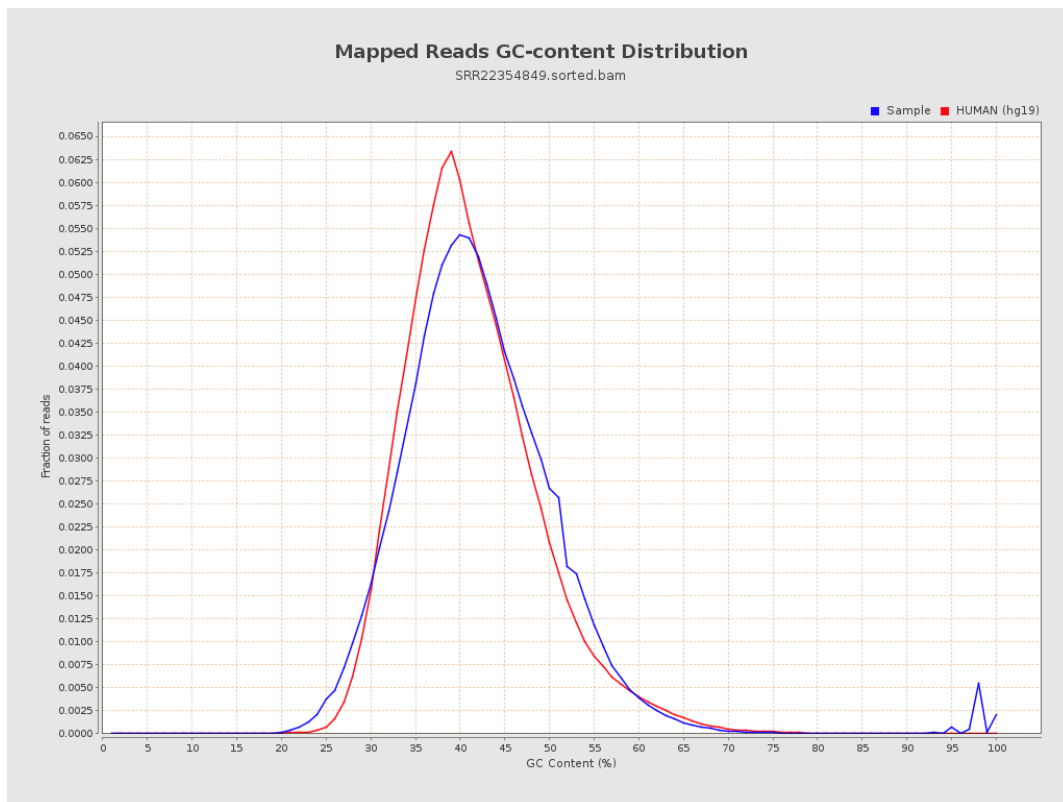
7. Results : Duplication Rate Histogram



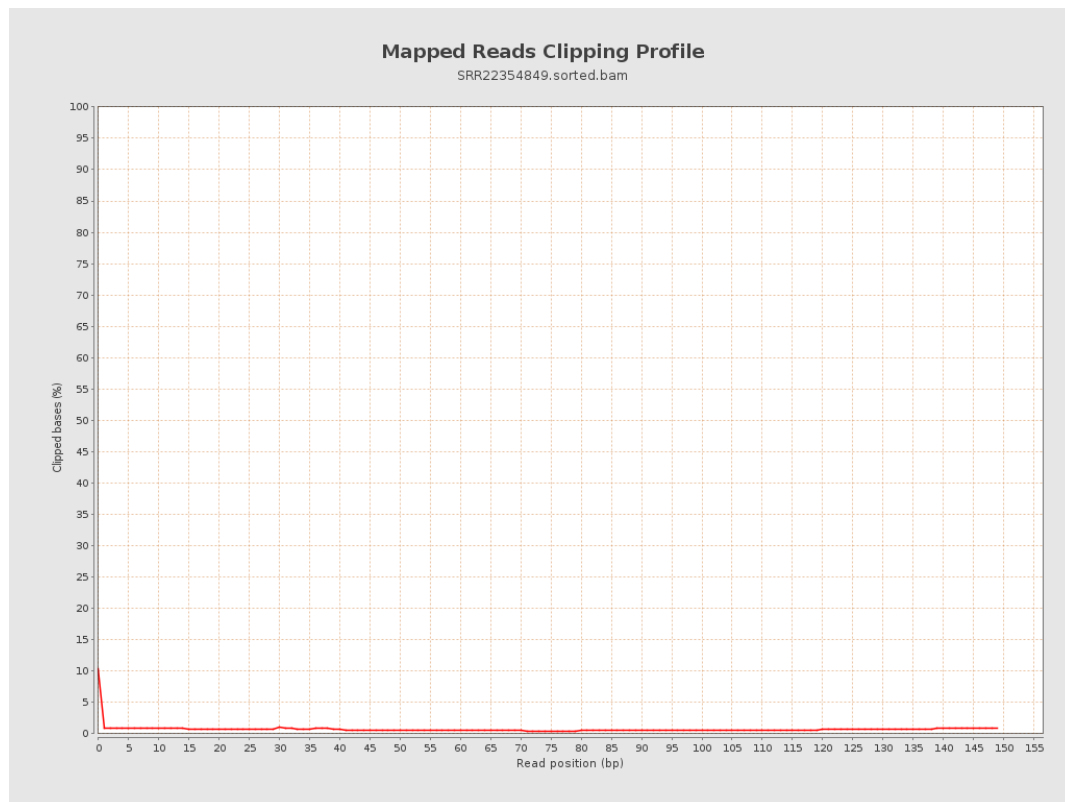
8. Results : Mapped Reads Nucleotide Content



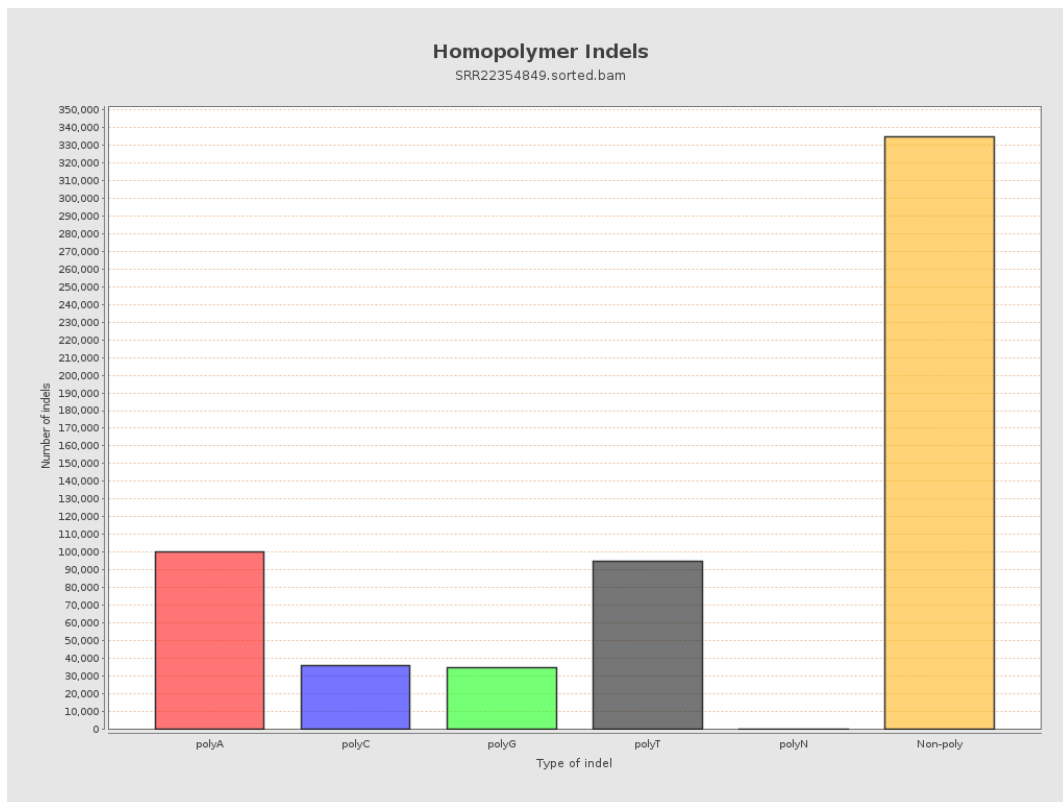
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



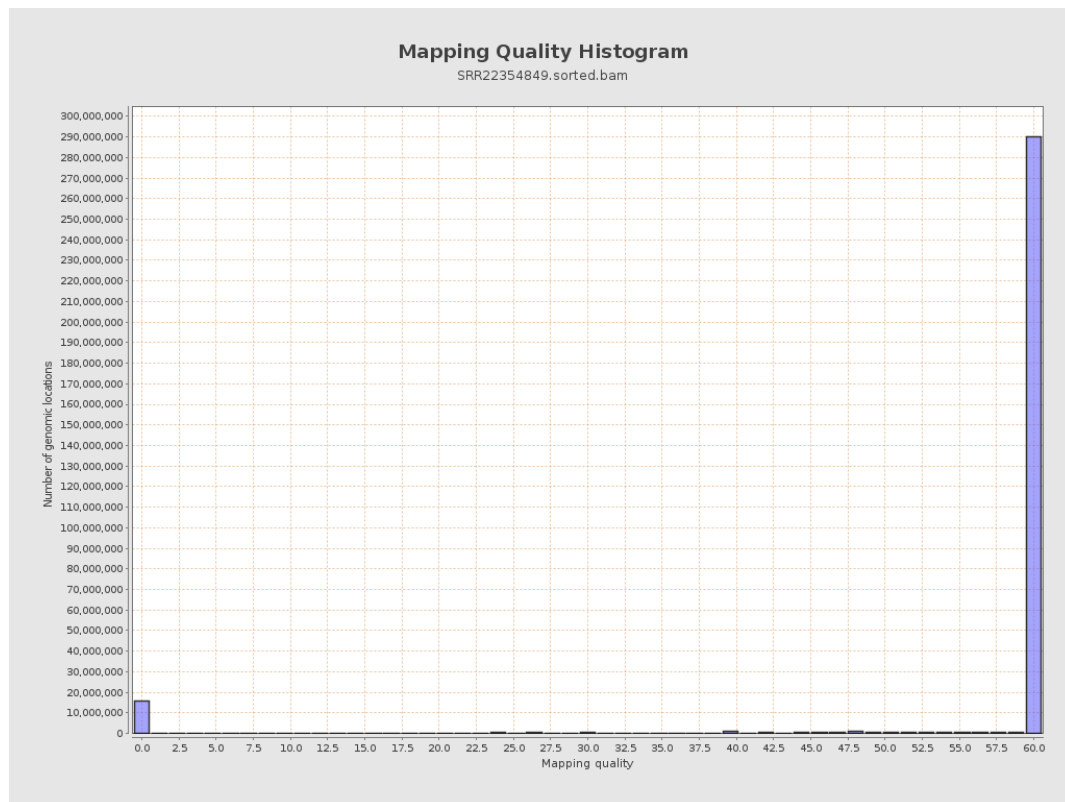
11. Results : Homopolymer Indels



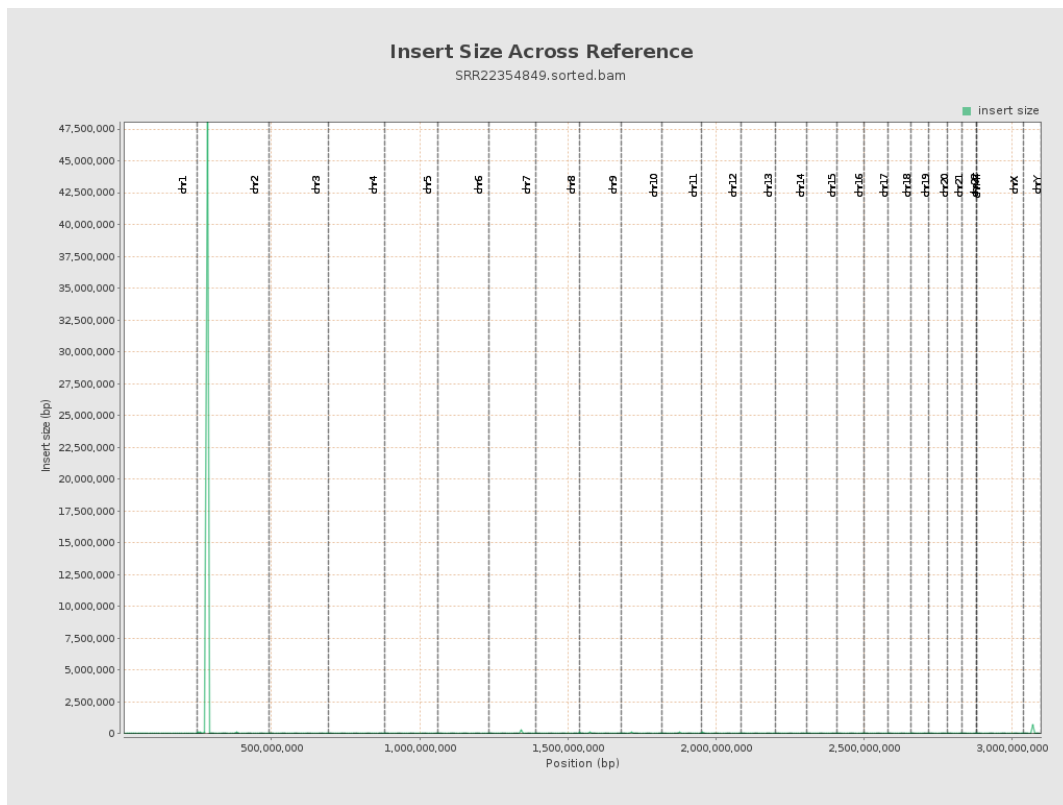
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

