

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:41:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173854.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_SRR10173854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173854_1.fastq.gz SRR10173854_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:41:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,909,322
Mapped reads	1,858,987 / 97.36%
Unmapped reads	50,335 / 2.64%
Mapped paired reads	1,858,987 / 97.36%
Mapped reads, first in pair	931,894 / 48.81%
Mapped reads, second in pair	927,093 / 48.56%
Mapped reads, both in pair	1,828,702 / 95.78%
Mapped reads, singletons	30,285 / 1.59%
Secondary alignments	0
Supplementary alignments	177,049 / 9.27%
Read min/max/mean length	30 / 133 / 127.27
Duplicated reads (estimated)	1,347,194 / 70.56%
Duplication rate	60.9%
Clipped reads	756,799 / 39.64%

2.2. ACGT Content

Number/percentage of A's	66,317,439 / 30.39%
Number/percentage of C's	42,248,983 / 19.36%
Number/percentage of T's	65,985,121 / 30.24%
Number/percentage of G's	43,672,937 / 20.01%
Number/percentage of N's	2,590 / 0%

GC Percentage	39.37%
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2.3. Coverage

Mean	0.0705
Standard Deviation	1.1686

2.4. Mapping Quality

Mean Mapping Quality	53.15
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2.5. Insert size

Mean	907,353.09
Standard Deviation	8,915,742.35
P25/Median/P75	134 / 186 / 262

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	2,217,053
Insertions	24,003
Mapped reads with at least one insertion	1.24%
Deletions	55,169
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.76%

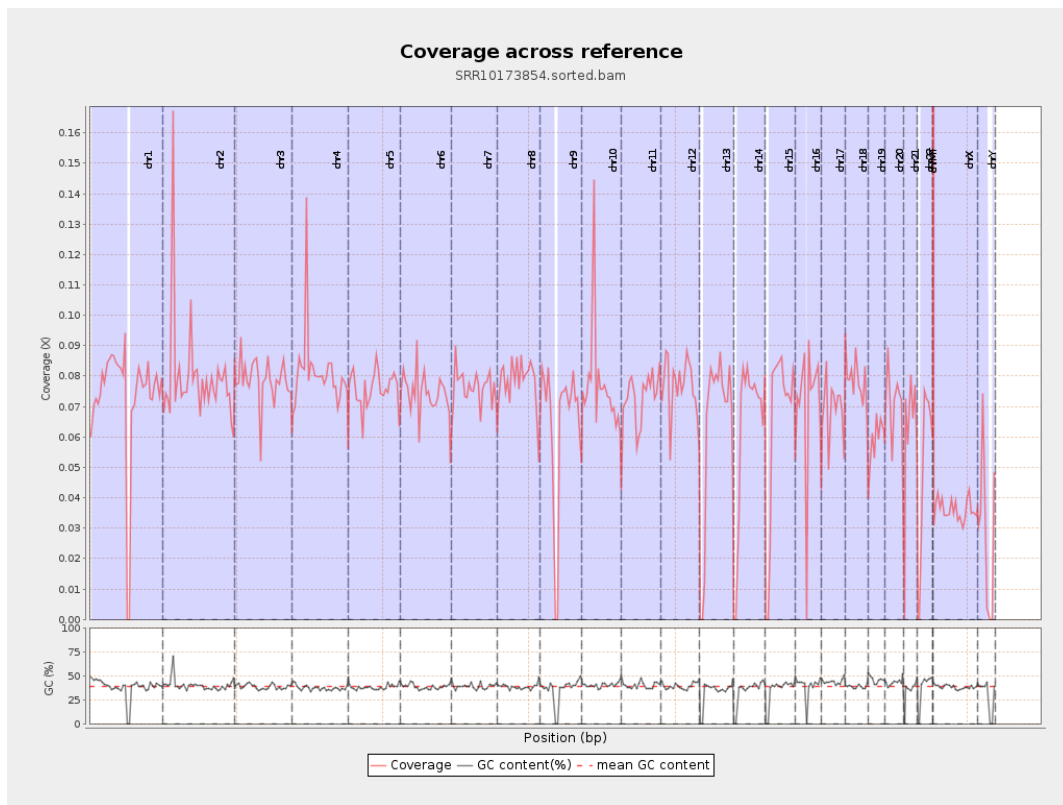
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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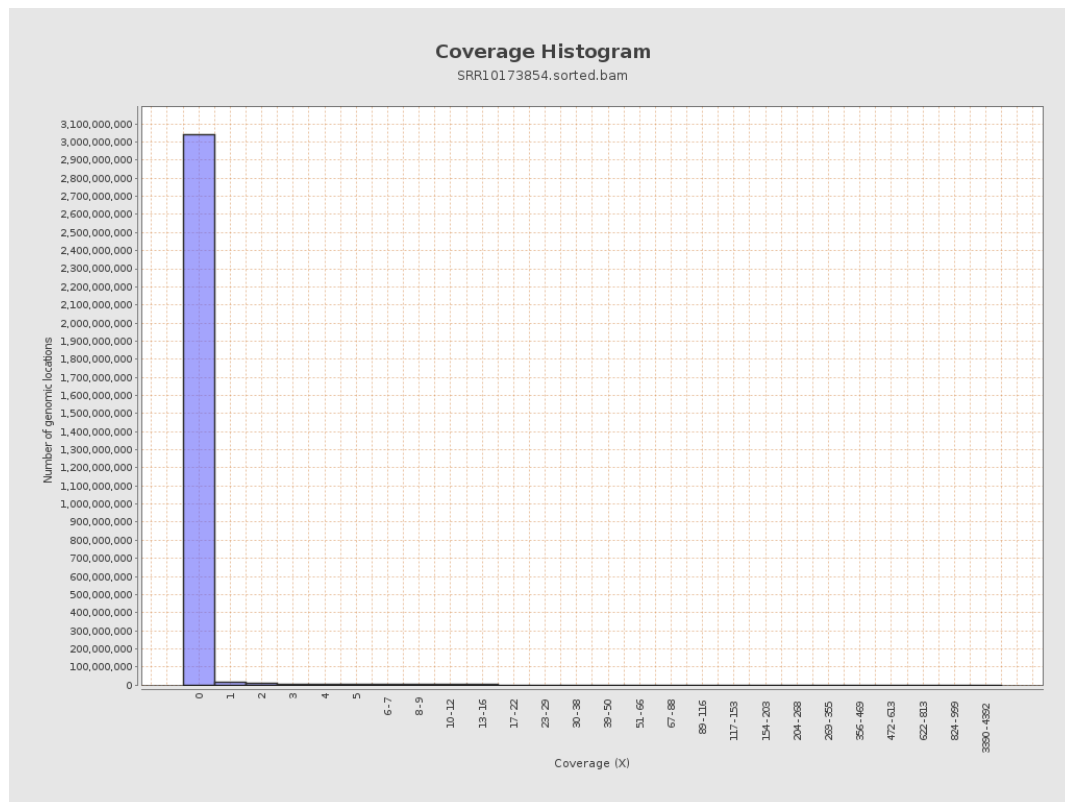
		bases	coverage	deviation
chr1	249250621	18309629	0.0735	0.8735
chr2	243199373	19279040	0.0793	3.1401
chr3	198022430	15582516	0.0787	0.7706
chr4	191154276	15523967	0.0812	0.9102
chr5	180915260	13693353	0.0757	0.7557
chr6	171115067	12740466	0.0745	0.7757
chr7	159138663	12097756	0.076	0.8466
chr8	146364022	11418400	0.078	0.9724
chr9	141213431	9134201	0.0647	0.7727
chr10	135534747	10394856	0.0767	1.0514
chr11	135006516	9832955	0.0728	0.7456
chr12	133851895	10298650	0.0769	0.7593
chr13	115169878	7347858	0.0638	0.7016
chr14	107349540	6774017	0.0631	0.6902
chr15	102531392	6589228	0.0643	0.689
chr16	90354753	6310955	0.0698	0.7543
chr17	81195210	5655976	0.0697	0.7305
chr18	78077248	6132337	0.0785	1.0241
chr19	59128983	3493208	0.0591	0.7037
chr20	63025520	4506391	0.0715	0.729
chr21	48129895	3002676	0.0624	0.7505
chr22	51304566	2542091	0.0495	0.6022
chrMT	16571	372984	22.5082	20.0225
chrX	155270560	5603120	0.0361	0.5186

chrY	59373566	1723710	0.029	0.5743
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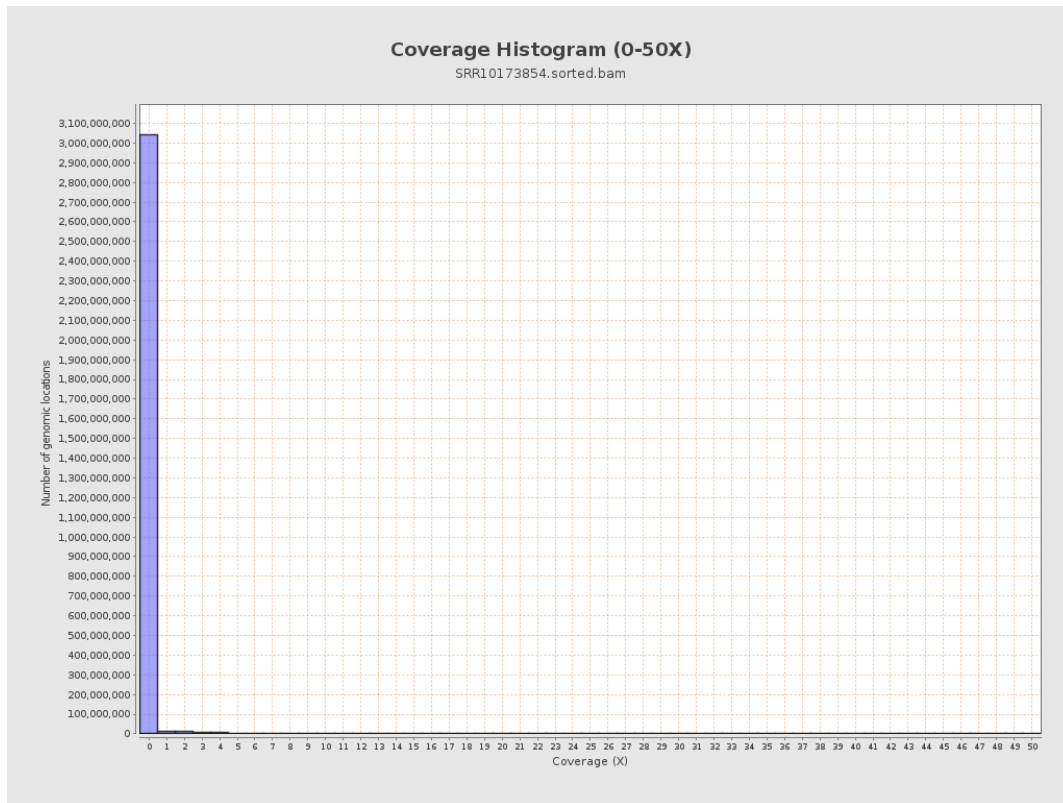
3. Results : Coverage across reference



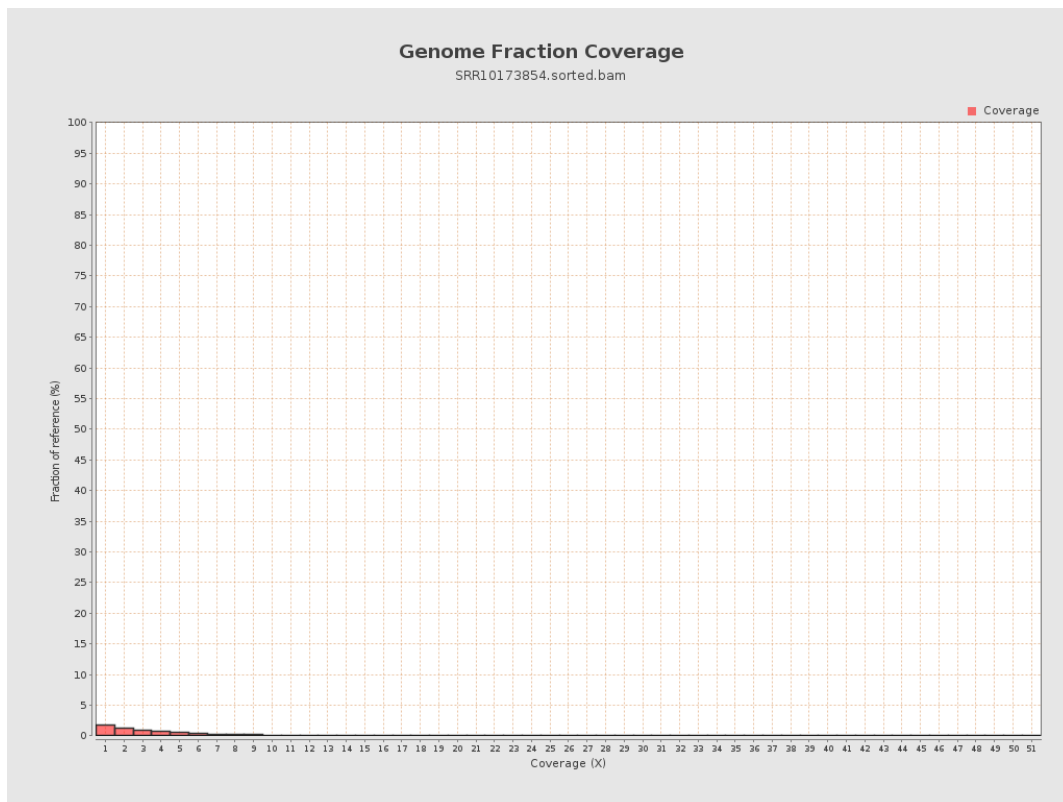
4. Results : Coverage Histogram



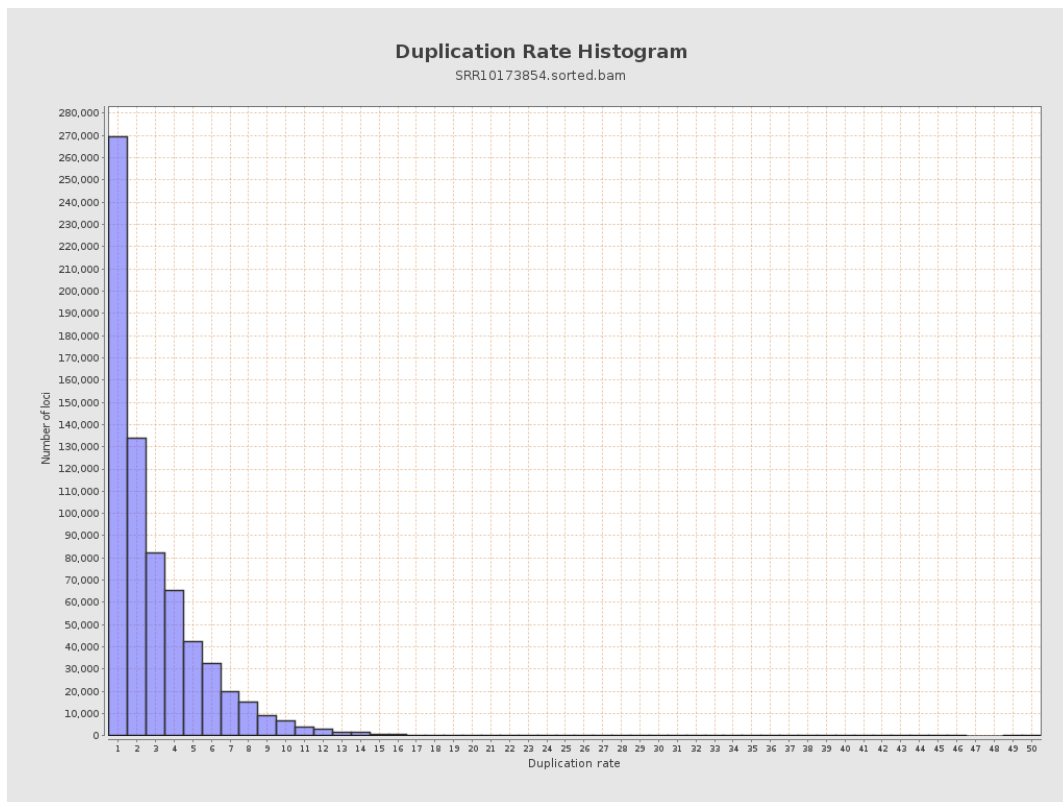
5. Results : Coverage Histogram (0-50X)



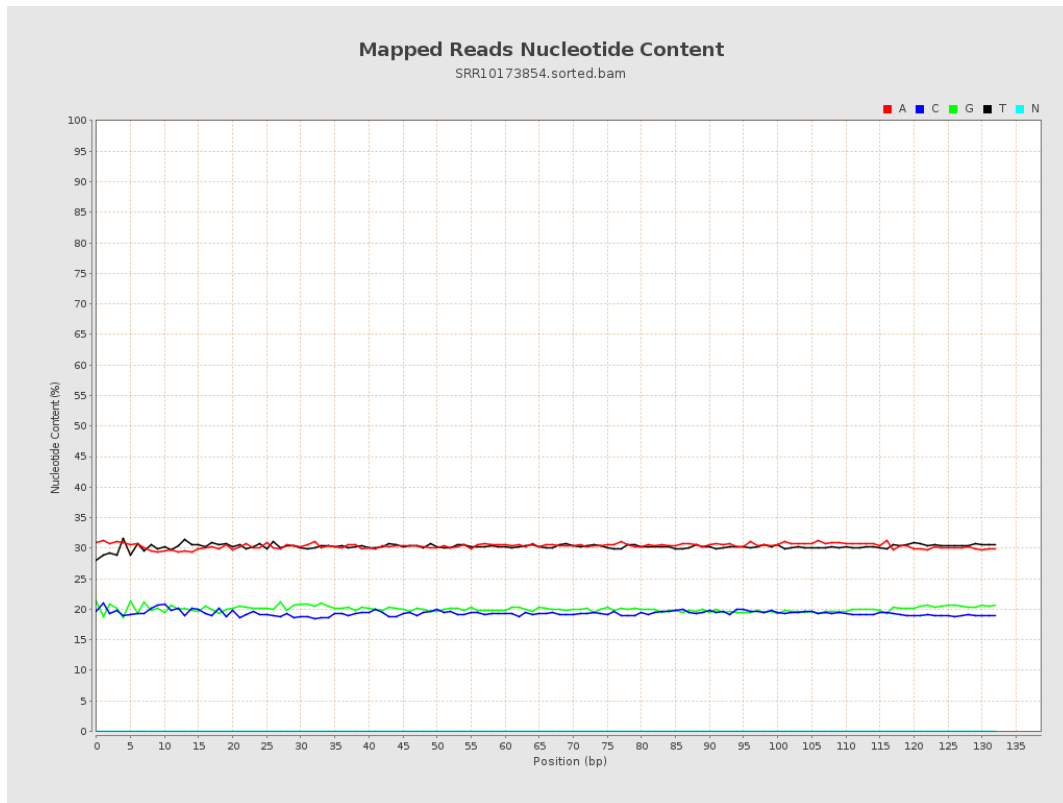
6. Results : Genome Fraction Coverage



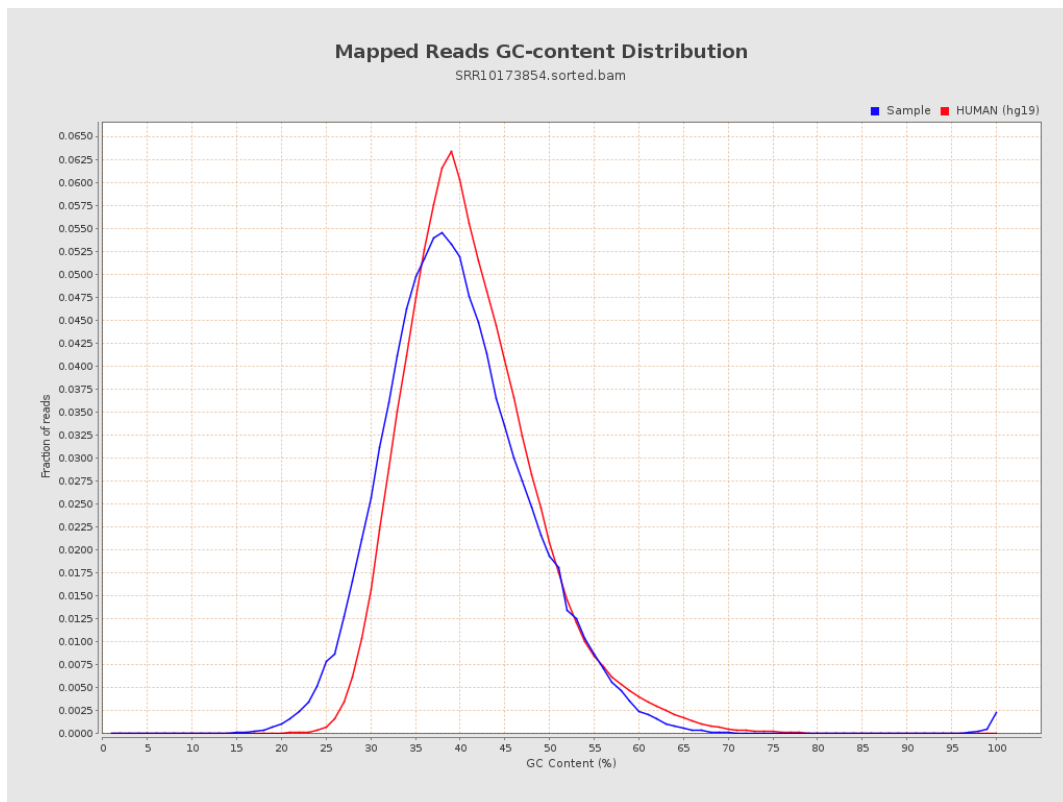
7. Results : Duplication Rate Histogram



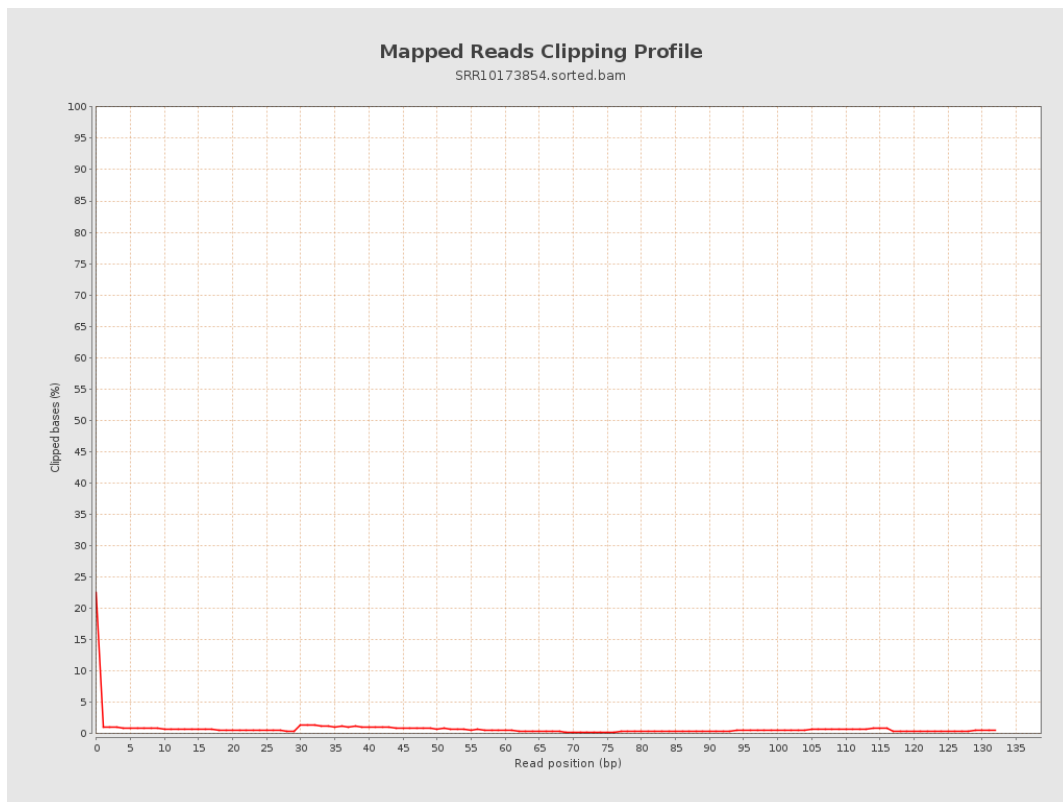
8. Results : Mapped Reads Nucleotide Content



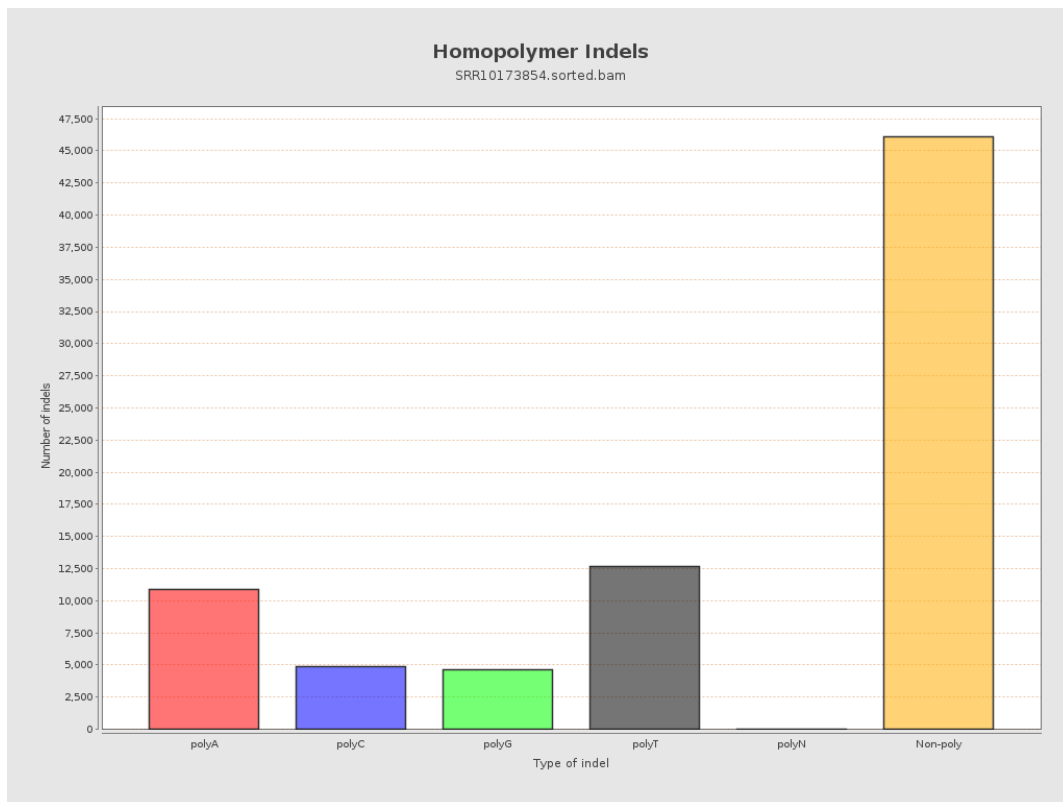
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



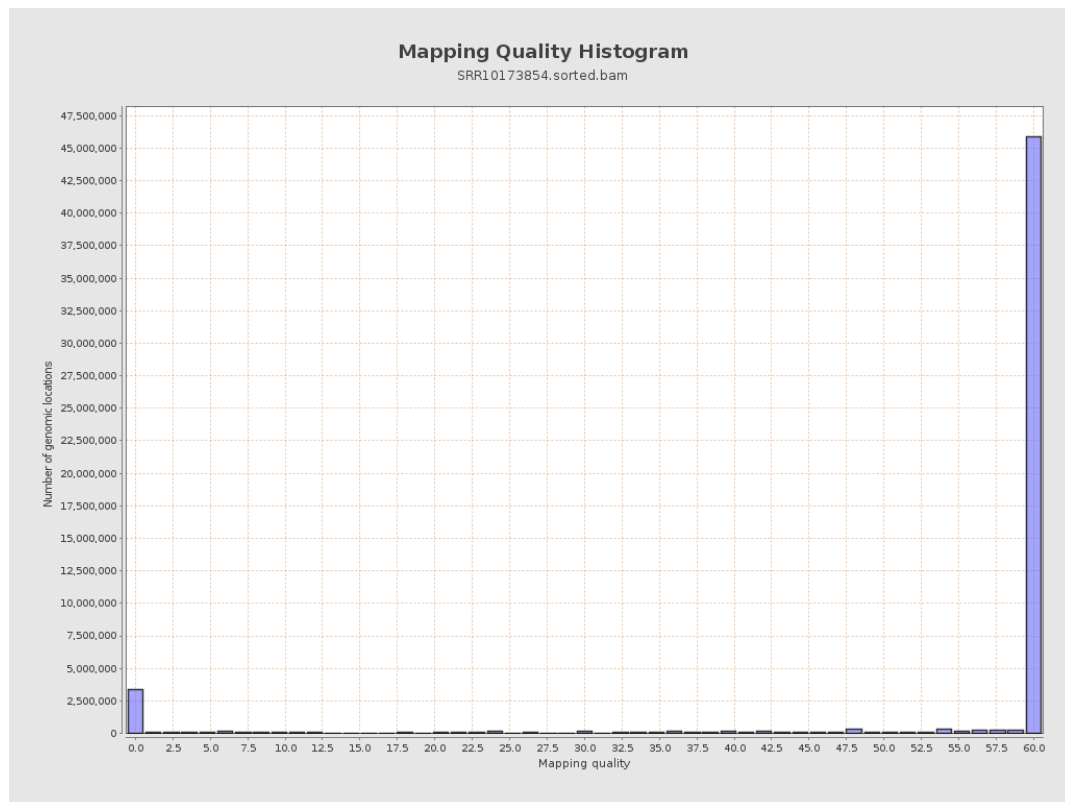
11. Results : Homopolymer Indels



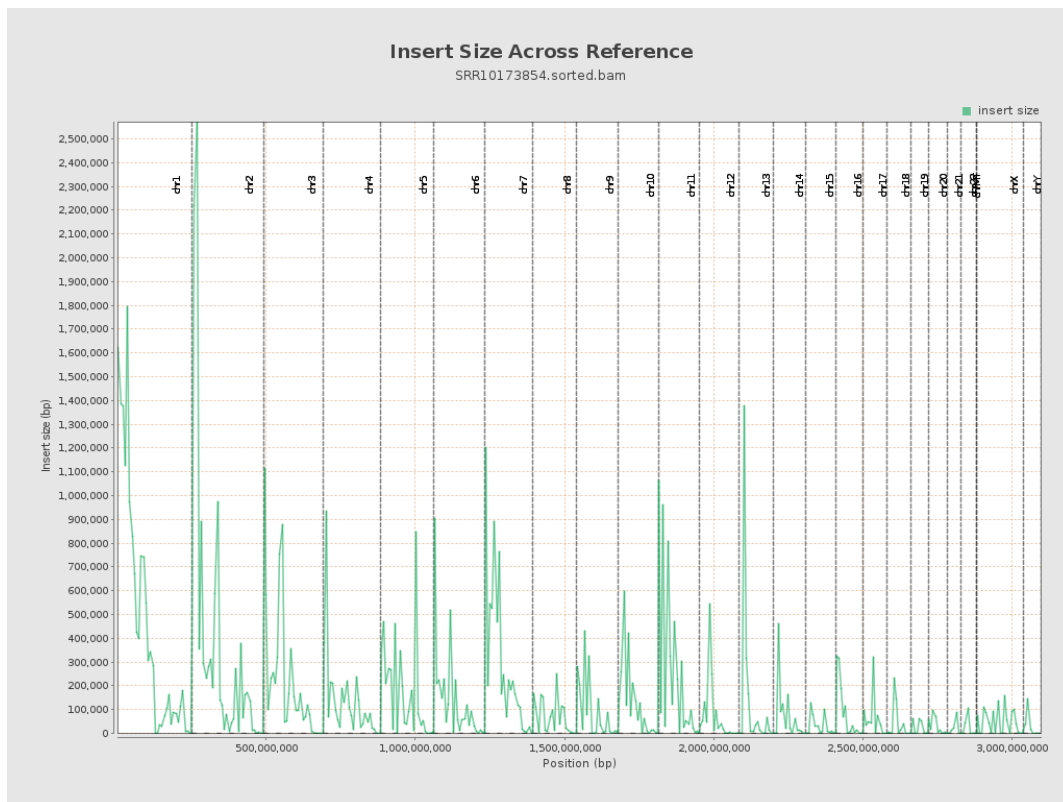
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

