

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:16:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173844.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_SRR10173844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173844_1.fastq.gz SRR10173844_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:16:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,556,928
Mapped reads	1,517,124 / 97.44%
Unmapped reads	39,804 / 2.56%
Mapped paired reads	1,517,124 / 97.44%
Mapped reads, first in pair	758,967 / 48.75%
Mapped reads, second in pair	758,157 / 48.7%
Mapped reads, both in pair	1,491,578 / 95.8%
Mapped reads, singletons	25,546 / 1.64%
Secondary alignments	0
Supplementary alignments	142,213 / 9.13%
Read min/max/mean length	30 / 133 / 128.05
Duplicated reads (estimated)	1,170,428 / 75.18%
Duplication rate	64.13%
Clipped reads	576,221 / 37.01%

2.2. ACGT Content

Number/percentage of A's	54,066,360 / 30.04%
Number/percentage of C's	35,416,493 / 19.68%
Number/percentage of T's	53,821,221 / 29.91%
Number/percentage of G's	36,655,291 / 20.37%
Number/percentage of N's	2,155 / 0%

GC Percentage	40.05%
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2.3. Coverage

Mean	0.0582
Standard Deviation	1.0152

2.4. Mapping Quality

Mean Mapping Quality	53.07
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2.5. Insert size

Mean	1,060,268.07
Standard Deviation	9,483,433.78
P25/Median/P75	148 / 203 / 285

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	1,884,460
Insertions	20,695
Mapped reads with at least one insertion	1.31%
Deletions	40,268
Mapped reads with at least one deletion	2.59%
Homopolymer indels	42.1%

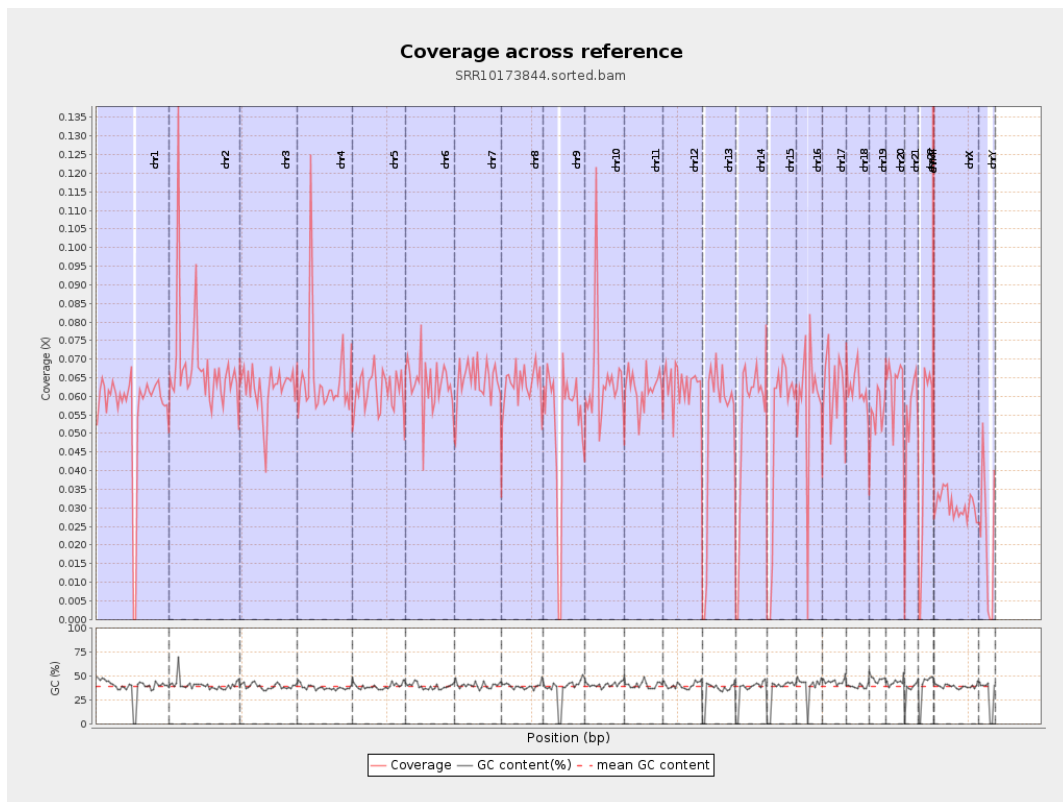
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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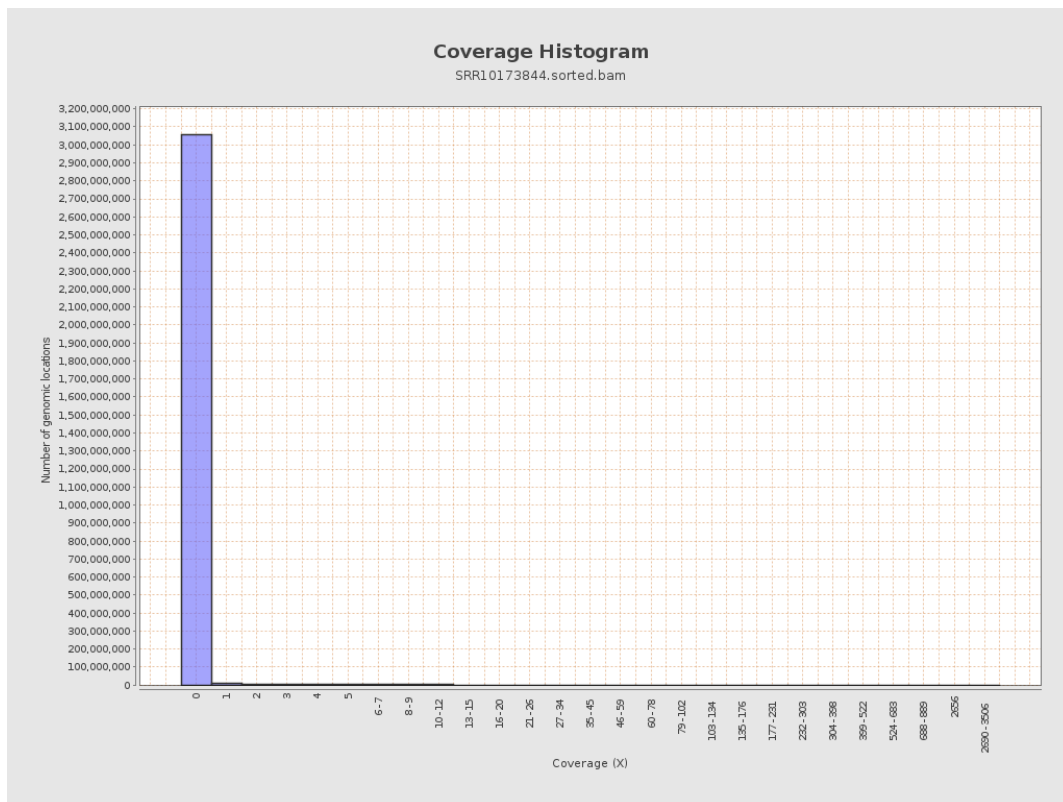
		bases	coverage	deviation
chr1	249250621	14125951	0.0567	0.8247
chr2	243199373	16554094	0.0681	2.5329
chr3	198022430	12275440	0.062	0.7238
chr4	191154276	12284201	0.0643	0.8562
chr5	180915260	11130328	0.0615	0.7211
chr6	171115067	10812964	0.0632	0.7542
chr7	159138663	10262700	0.0645	0.8224
chr8	146364022	9256304	0.0632	0.8457
chr9	141213431	7461173	0.0528	0.7754
chr10	135534747	8741320	0.0645	0.9231
chr11	135006516	8366172	0.062	0.7236
chr12	133851895	8447996	0.0631	0.7254
chr13	115169878	5955702	0.0517	0.6661
chr14	107349540	5656713	0.0527	0.6573
chr15	102531392	5198432	0.0507	0.6462
chr16	90354753	5312841	0.0588	0.7286
chr17	81195210	4996935	0.0615	0.734
chr18	78077248	4861767	0.0623	0.9843
chr19	59128983	3301271	0.0558	0.7033
chr20	63025520	3969262	0.063	0.7179
chr21	48129895	2541808	0.0528	0.6968
chr22	51304566	2270139	0.0442	0.5976
chrMT	16571	266457	16.0797	14.9011
chrX	155270560	4757123	0.0306	0.504

chrY	59373566	1253040	0.0211	0.4703
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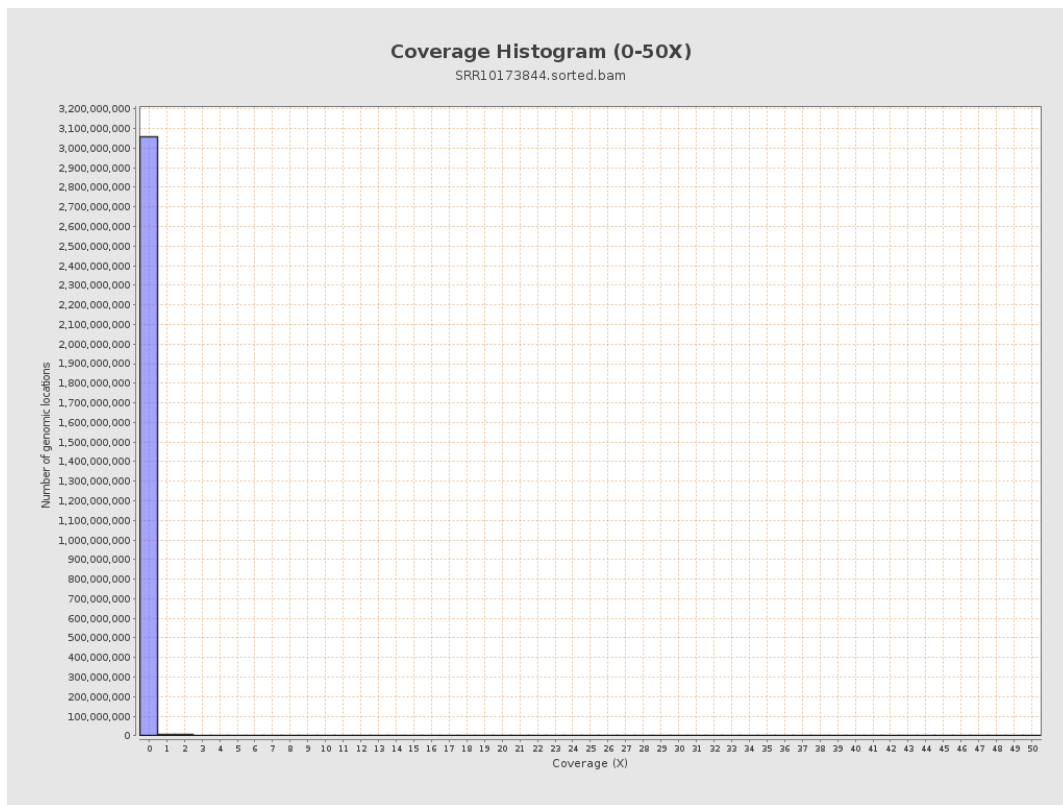
3. Results : Coverage across reference



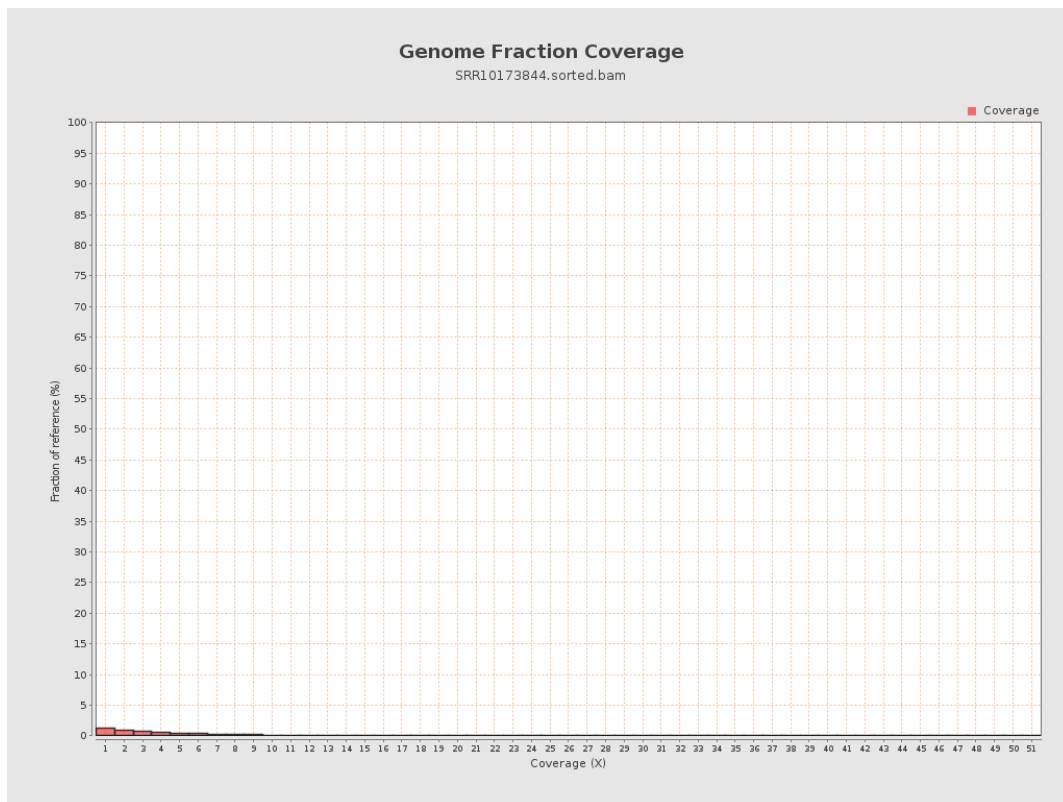
4. Results : Coverage Histogram



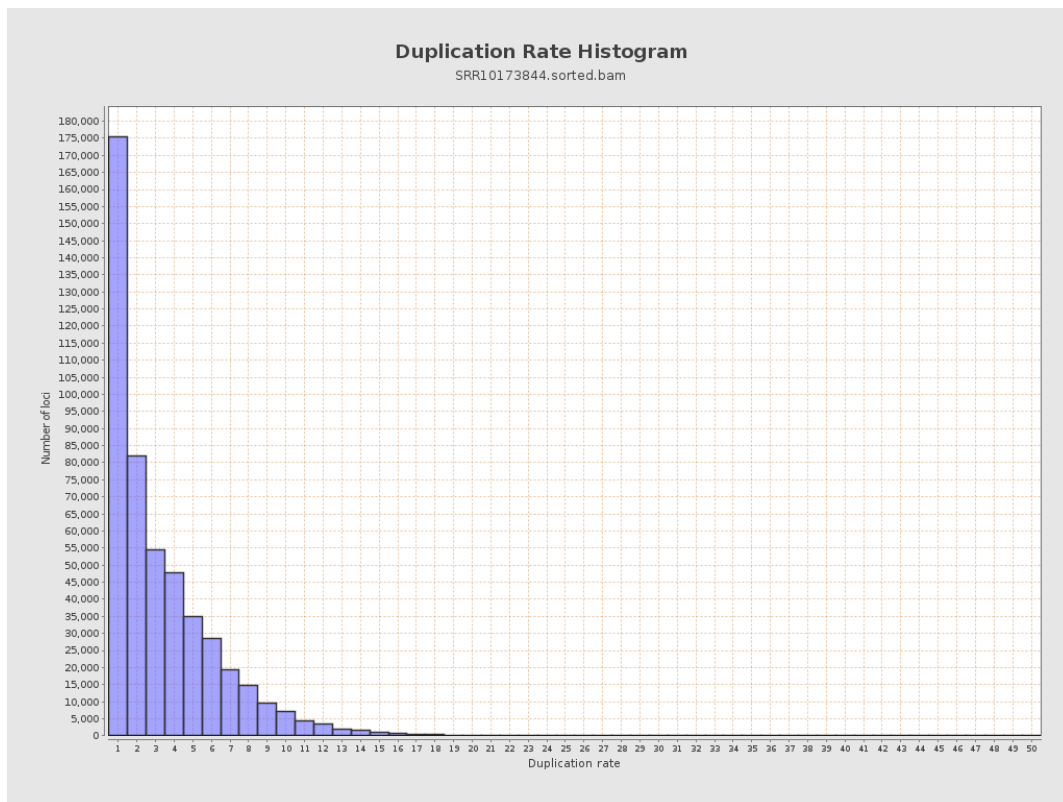
5. Results : Coverage Histogram (0-50X)



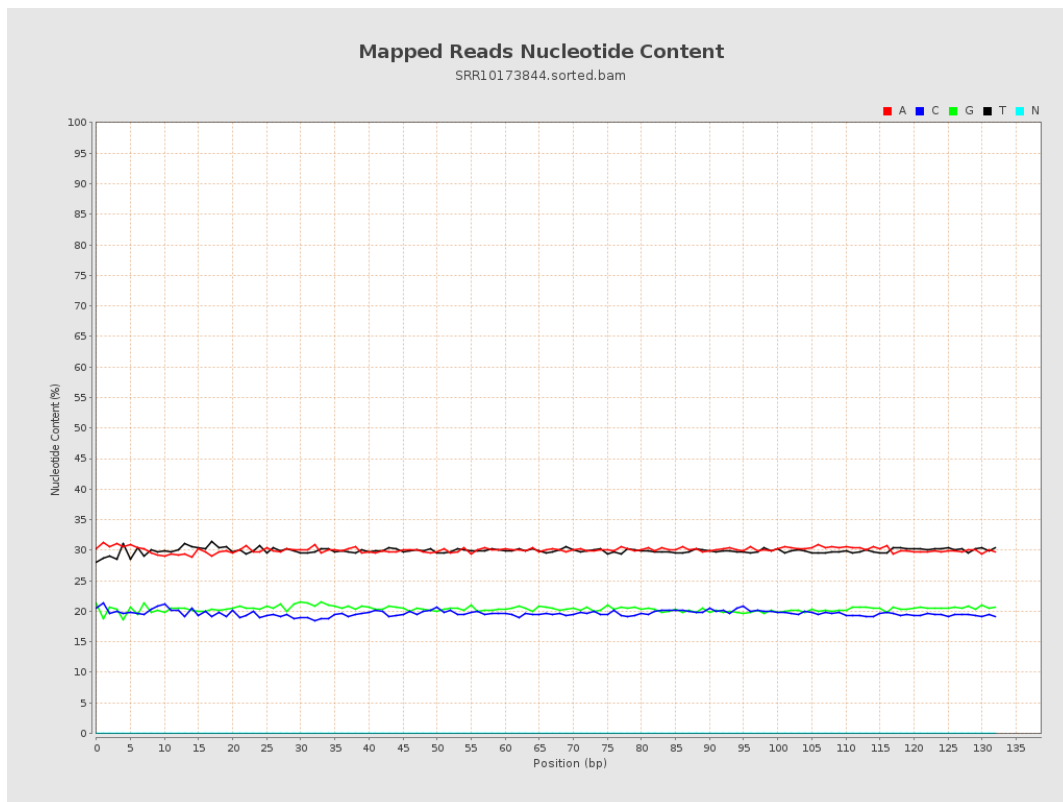
6. Results : Genome Fraction Coverage



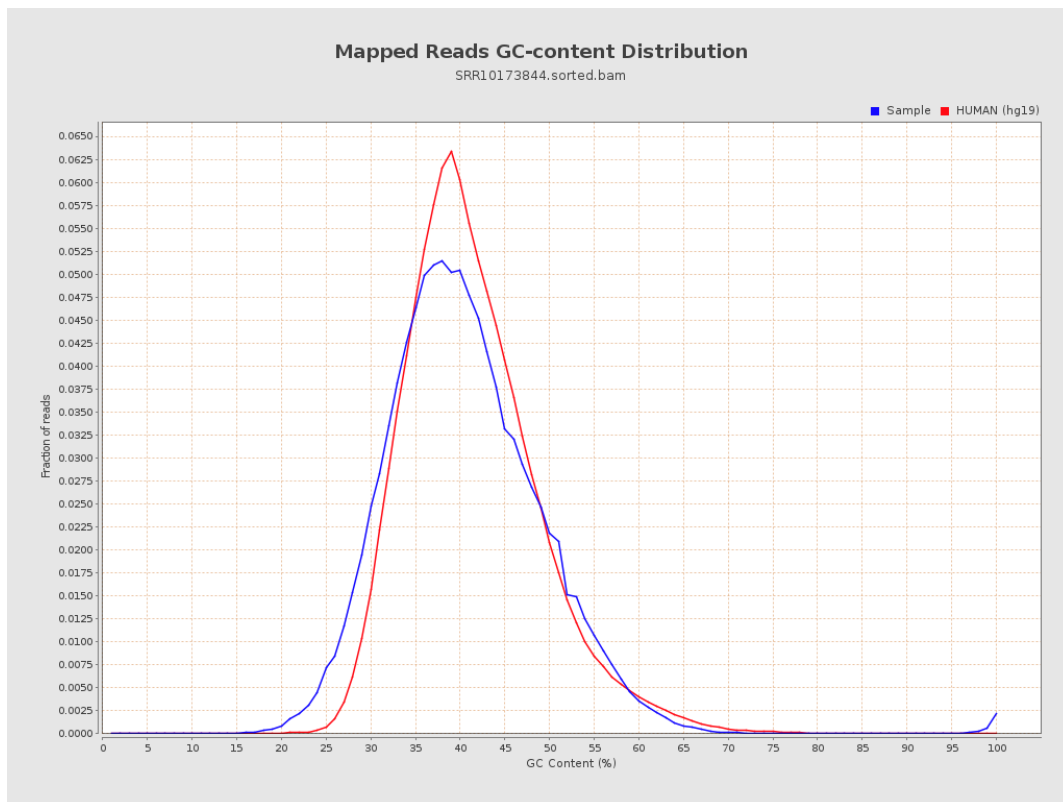
7. Results : Duplication Rate Histogram



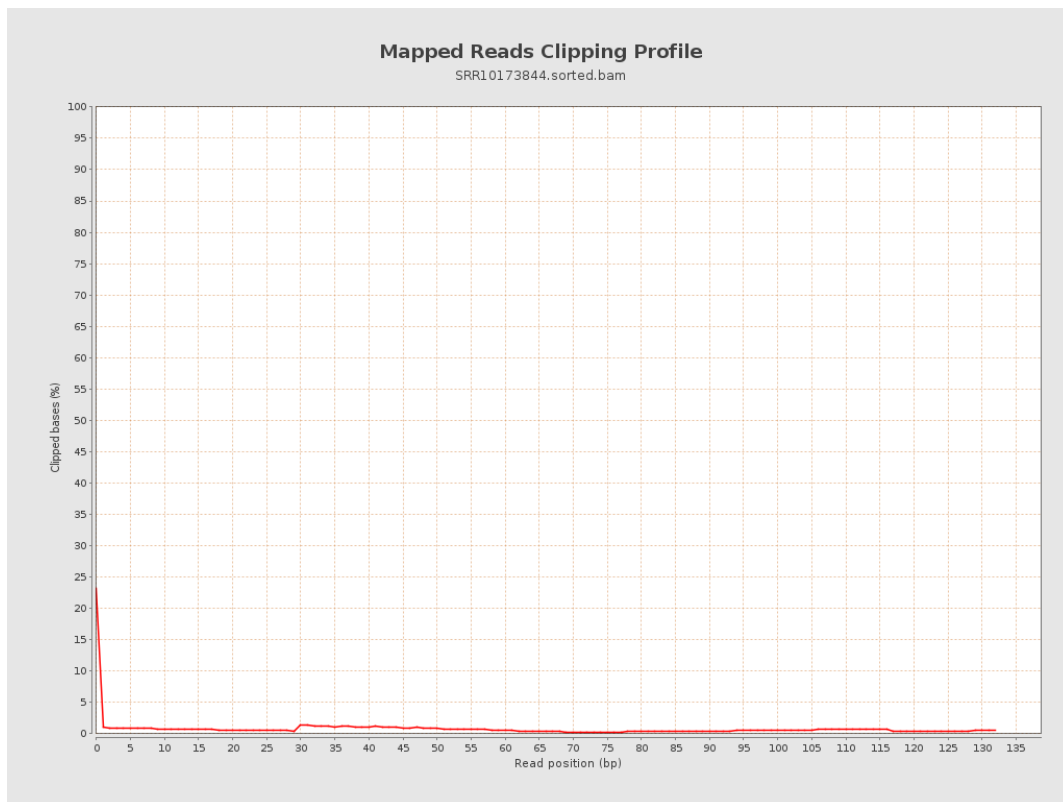
8. Results : Mapped Reads Nucleotide Content



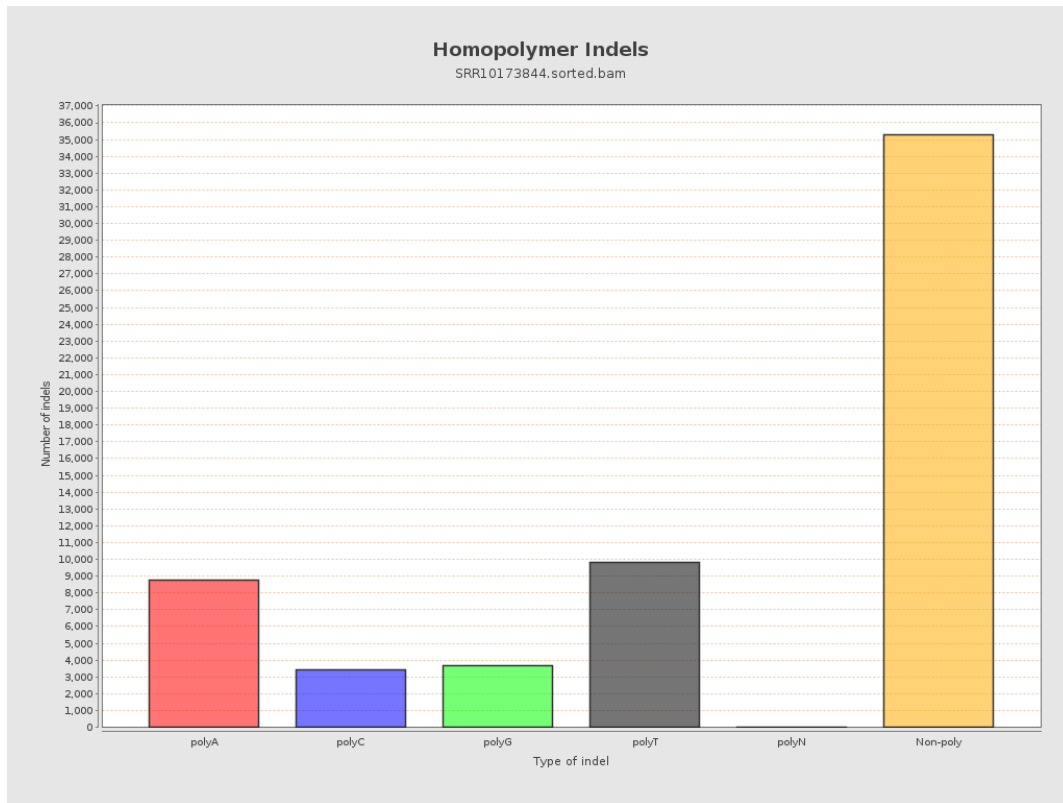
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



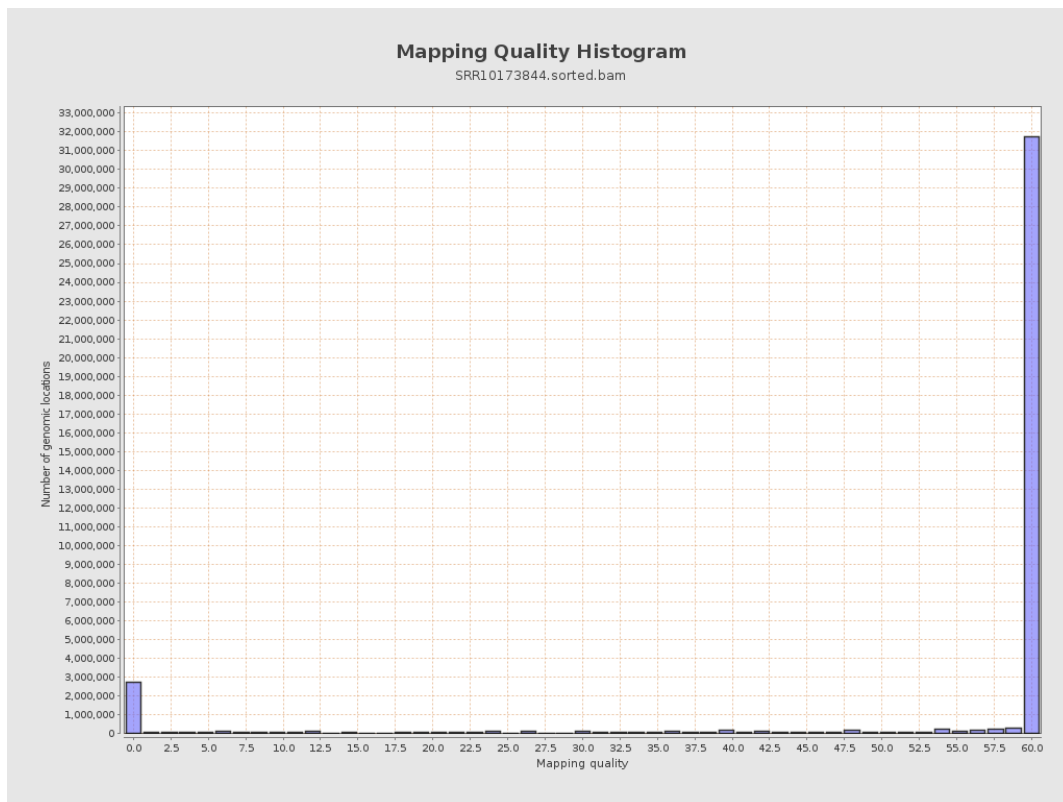
11. Results : Homopolymer Indels



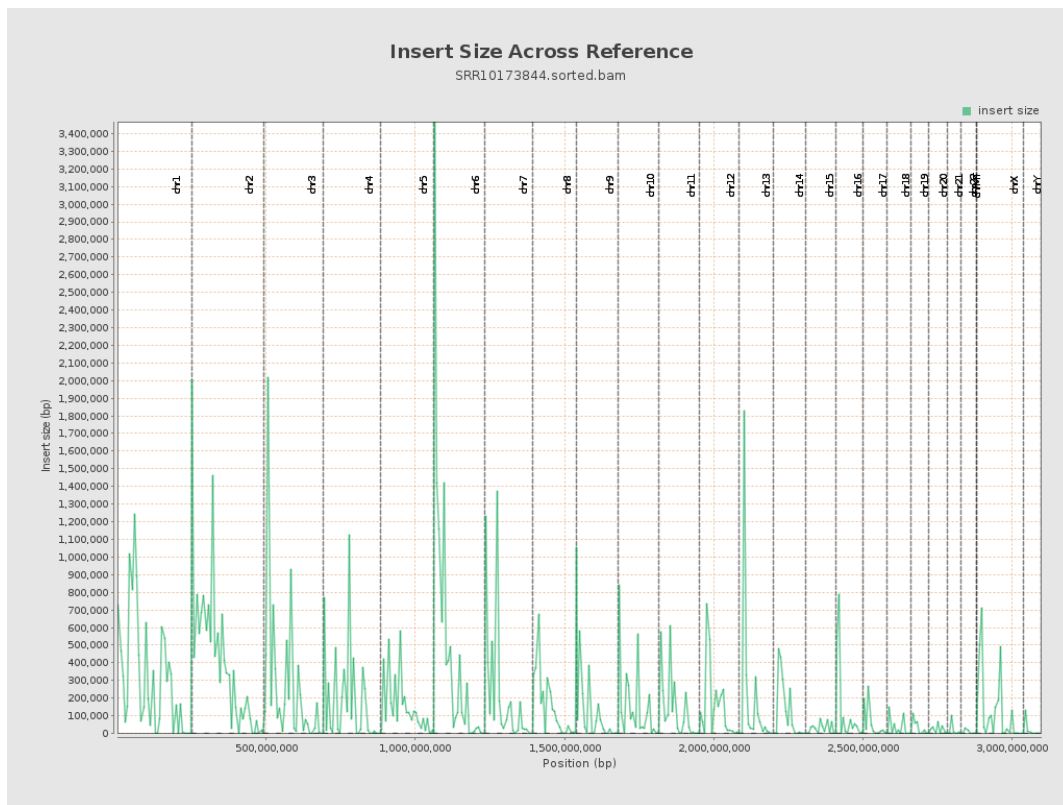
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

