

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:58:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173841.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_SRR10173841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173841_1.fastq.gz SRR10173841_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:58:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,133,470
Mapped reads	2,081,173 / 97.55%
Unmapped reads	52,297 / 2.45%
Mapped paired reads	2,081,173 / 97.55%
Mapped reads, first in pair	1,040,513 / 48.77%
Mapped reads, second in pair	1,040,660 / 48.78%
Mapped reads, both in pair	2,046,540 / 95.93%
Mapped reads, singletons	34,633 / 1.62%
Secondary alignments	0
Supplementary alignments	196,780 / 9.22%
Read min/max/mean length	30 / 133 / 127.7
Duplicated reads (estimated)	1,604,259 / 75.19%
Duplication rate	64.73%
Clipped reads	800,521 / 37.52%

2.2. ACGT Content

Number/percentage of A's	74,111,948 / 30.13%
Number/percentage of C's	48,262,696 / 19.62%
Number/percentage of T's	73,848,687 / 30.02%
Number/percentage of G's	49,746,390 / 20.22%
Number/percentage of N's	3,399 / 0%

GC Percentage	39.85%
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2.3. Coverage

Mean	0.0795
Standard Deviation	1.355

2.4. Mapping Quality

Mean Mapping Quality	52.84
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2.5. Insert size

Mean	864,818.11
Standard Deviation	8,678,904.49
P25/Median/P75	144 / 202 / 289

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	2,504,413
Insertions	24,387
Mapped reads with at least one insertion	1.14%
Deletions	49,719
Mapped reads with at least one deletion	2.33%
Homopolymer indels	43.38%

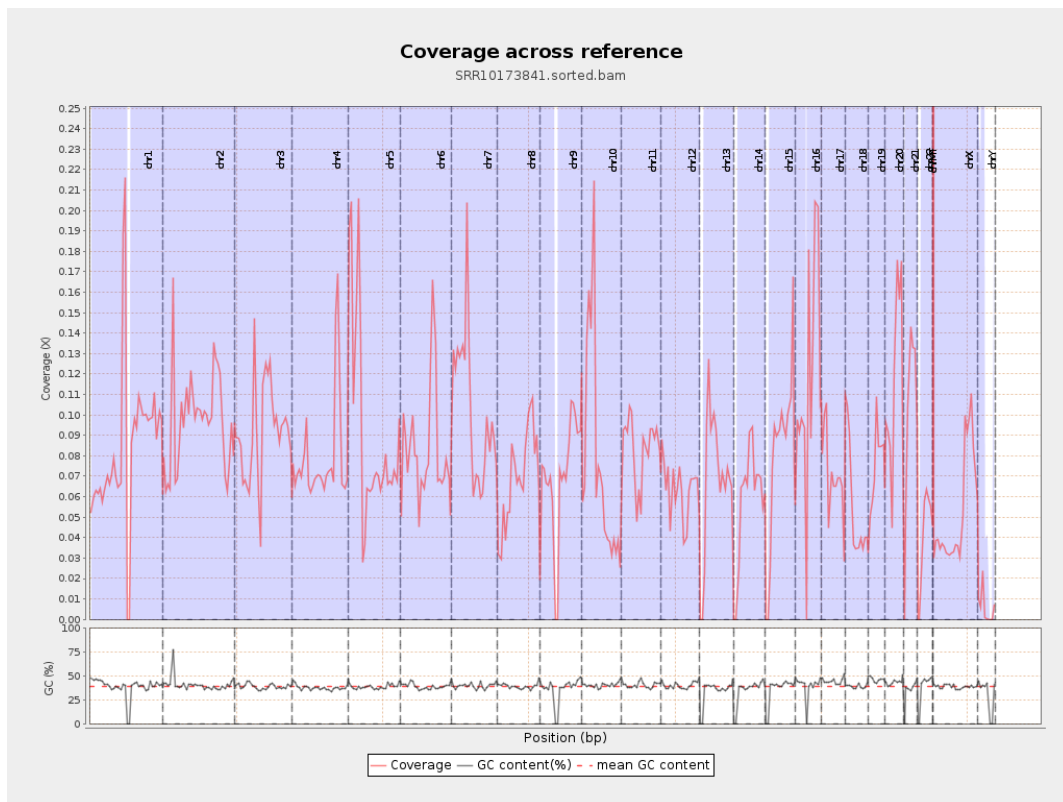
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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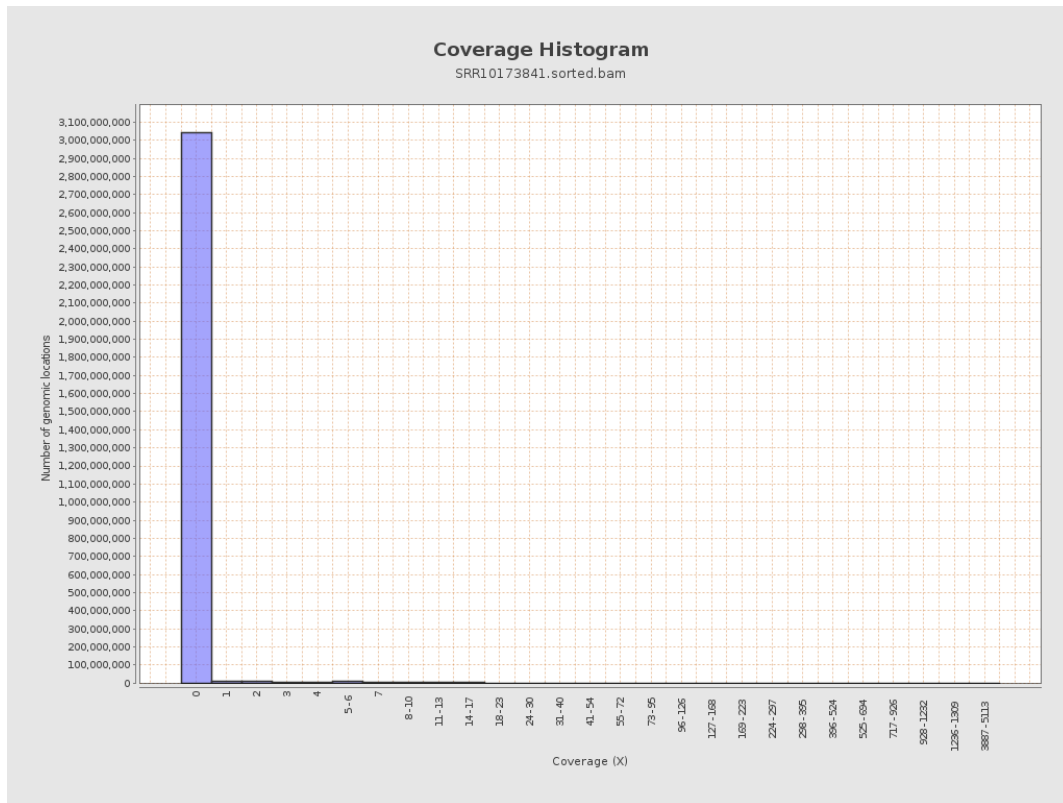
		bases	coverage	deviation
chr1	249250621	21019459	0.0843	1.0761
chr2	243199373	23623394	0.0971	3.6435
chr3	198022430	18108161	0.0914	0.8721
chr4	191154276	15186205	0.0794	0.8801
chr5	180915260	16665299	0.0921	0.8749
chr6	171115067	14245174	0.0832	0.8452
chr7	159138663	16217829	0.1019	1.2467
chr8	146364022	10199058	0.0697	0.8175
chr9	141213431	9991986	0.0708	0.8503
chr10	135534747	10211899	0.0753	1.4276
chr11	135006516	11197238	0.0829	0.8194
chr12	133851895	8591477	0.0642	0.7216
chr13	115169878	7929170	0.0688	0.7472
chr14	107349540	6291781	0.0586	0.6907
chr15	102531392	8256399	0.0805	0.8007
chr16	90354753	10364970	0.1147	1.14
chr17	81195210	5805624	0.0715	0.8006
chr18	78077248	4294642	0.055	0.9554
chr19	59128983	4405318	0.0745	1.0592
chr20	63025520	7448549	0.1182	0.9712
chr21	48129895	4831855	0.1004	0.9225
chr22	51304566	2087278	0.0407	0.5539
chrMT	16571	581433	35.0874	38.8903
chrX	155270560	8196513	0.0528	0.6575

chrY	59373566	349067	0.0059	0.2961
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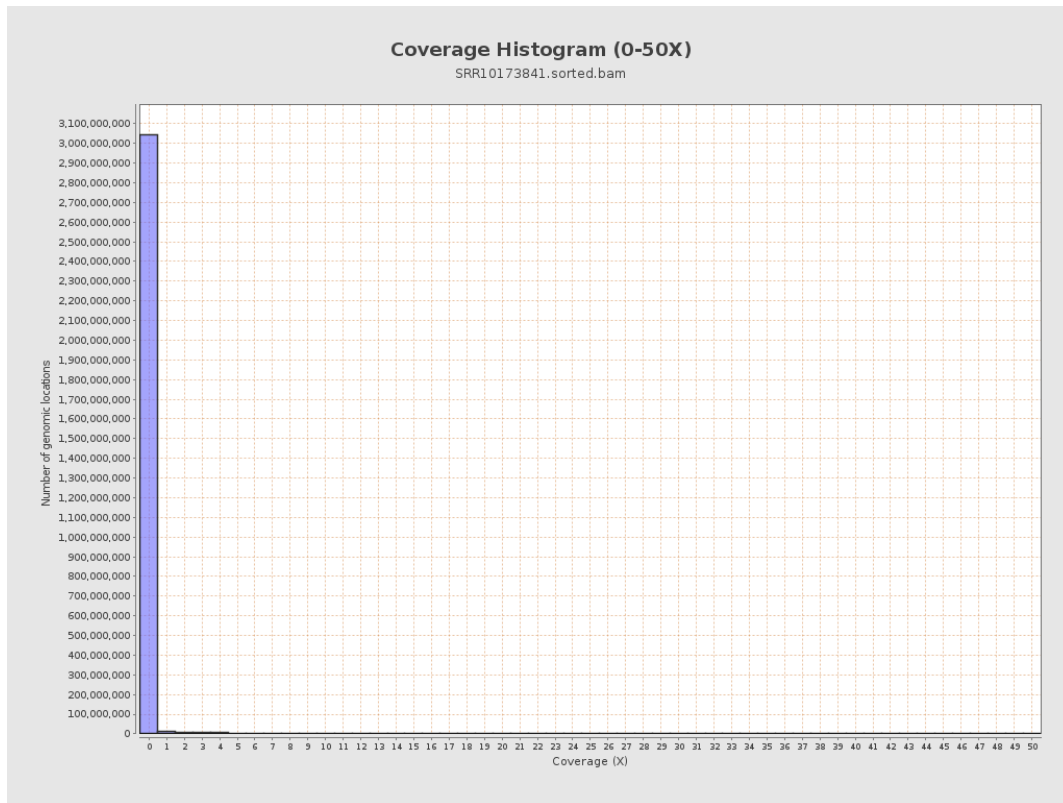
3. Results : Coverage across reference



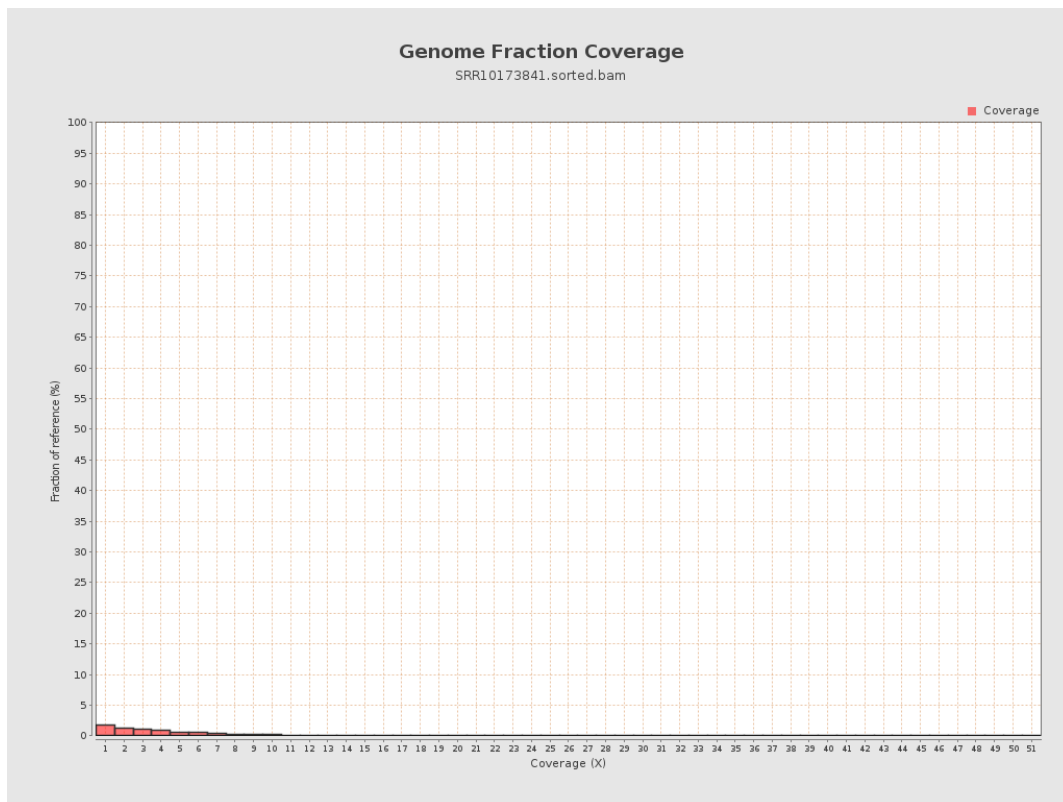
4. Results : Coverage Histogram



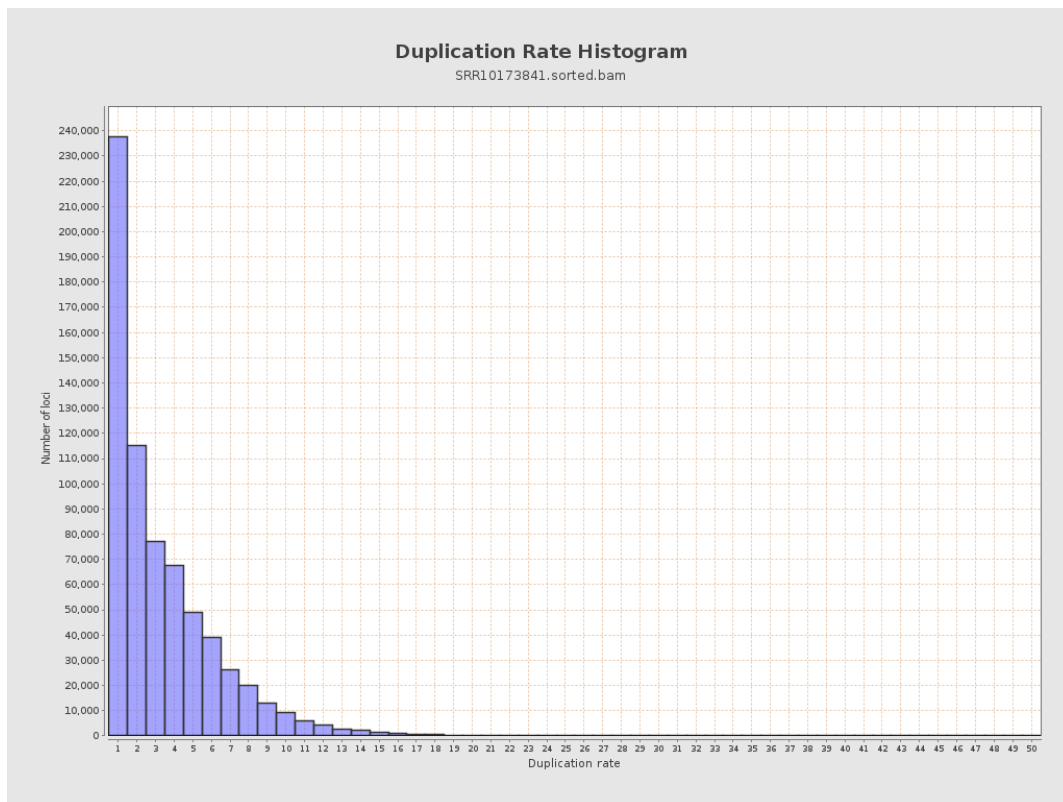
5. Results : Coverage Histogram (0-50X)



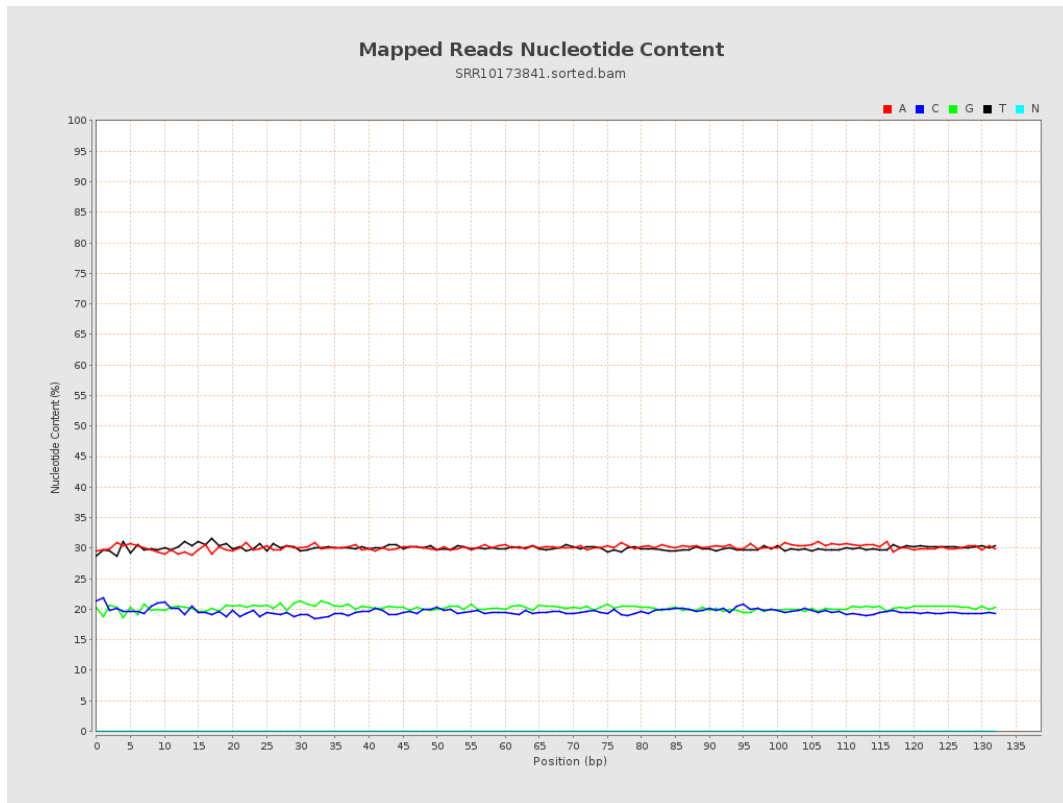
6. Results : Genome Fraction Coverage



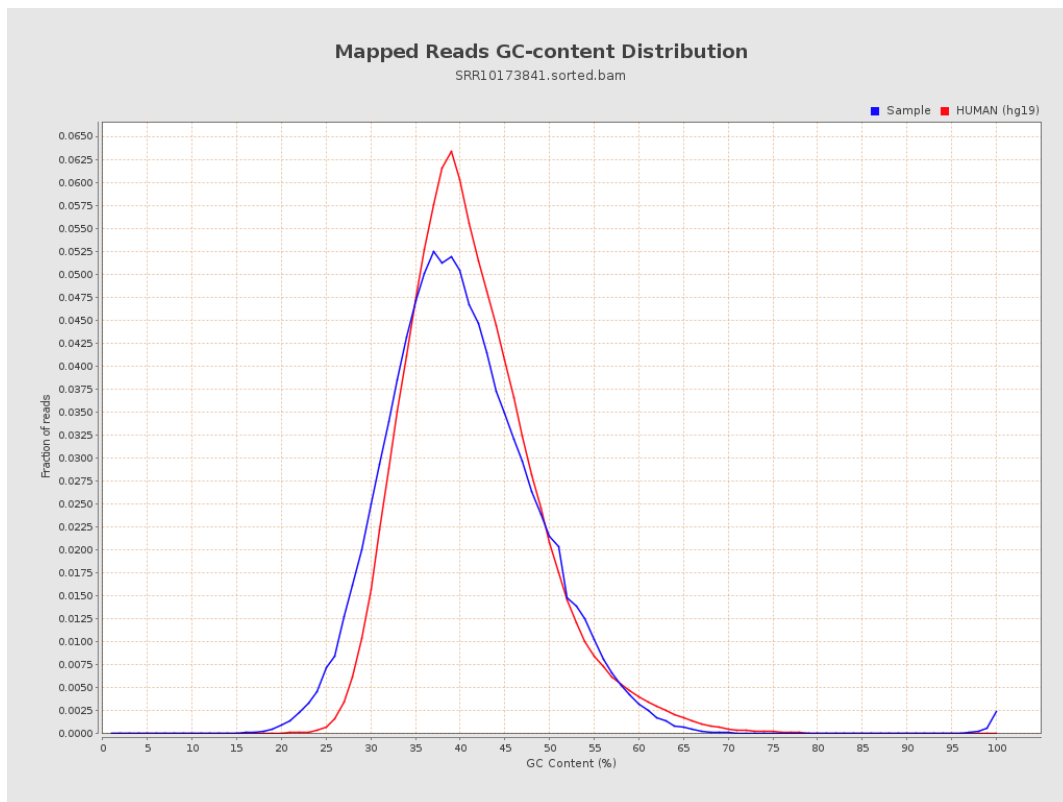
7. Results : Duplication Rate Histogram



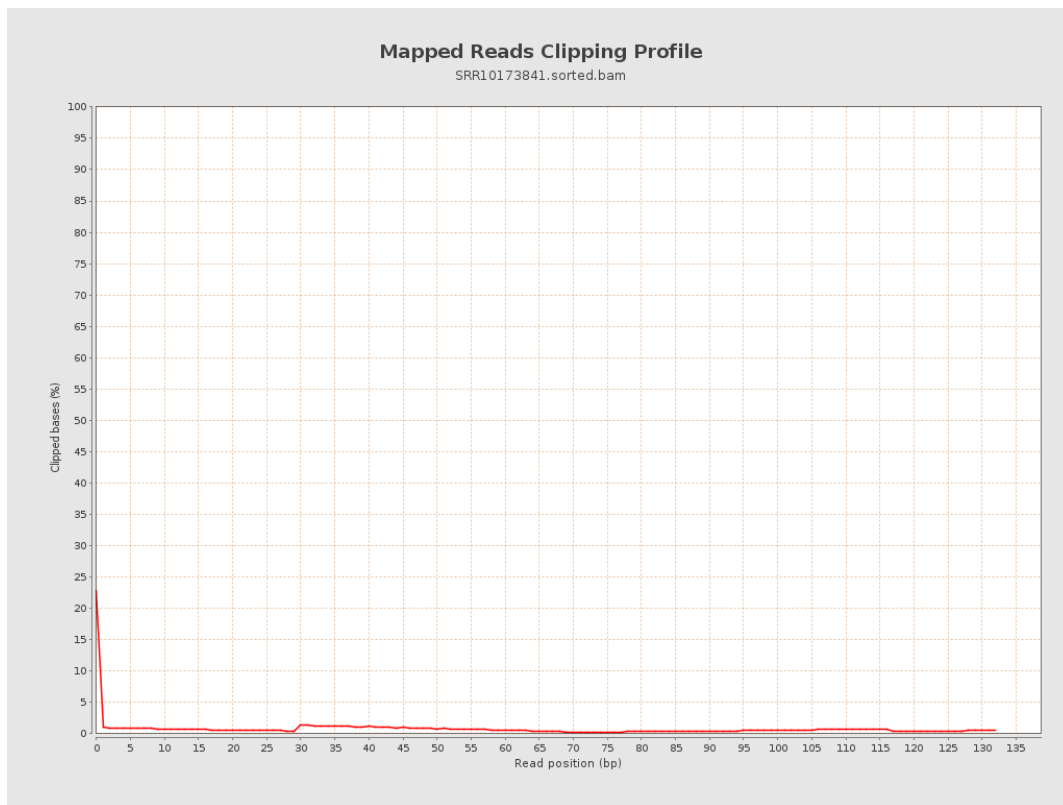
8. Results : Mapped Reads Nucleotide Content



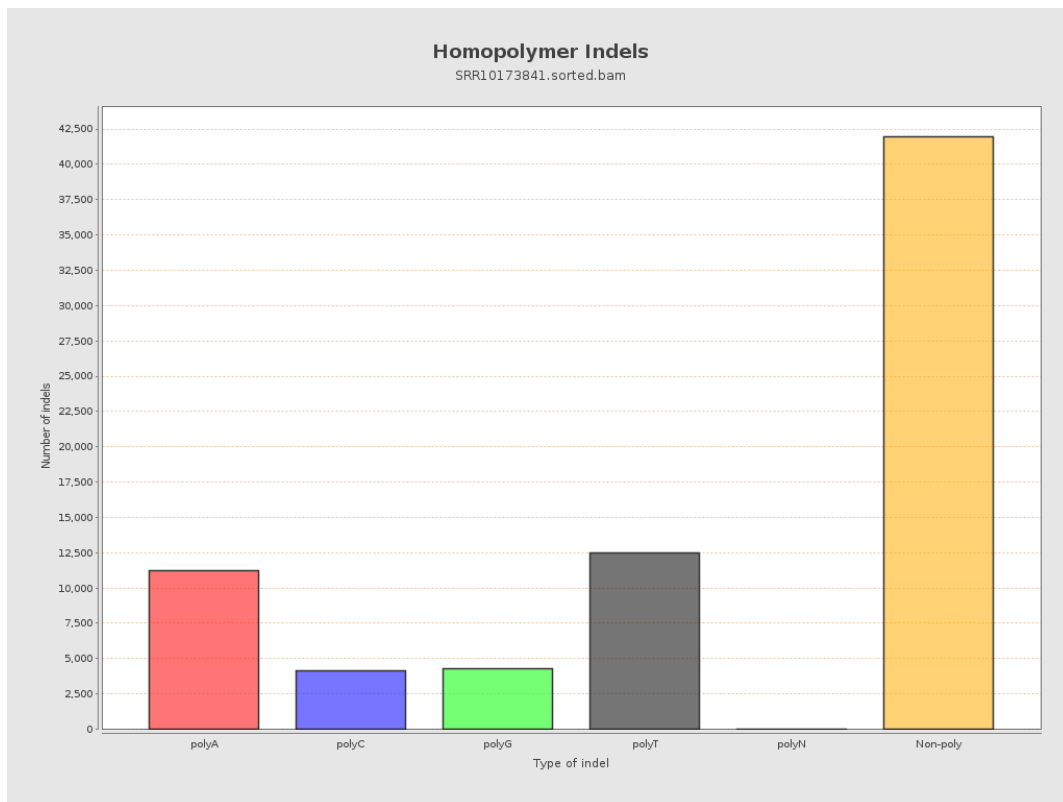
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



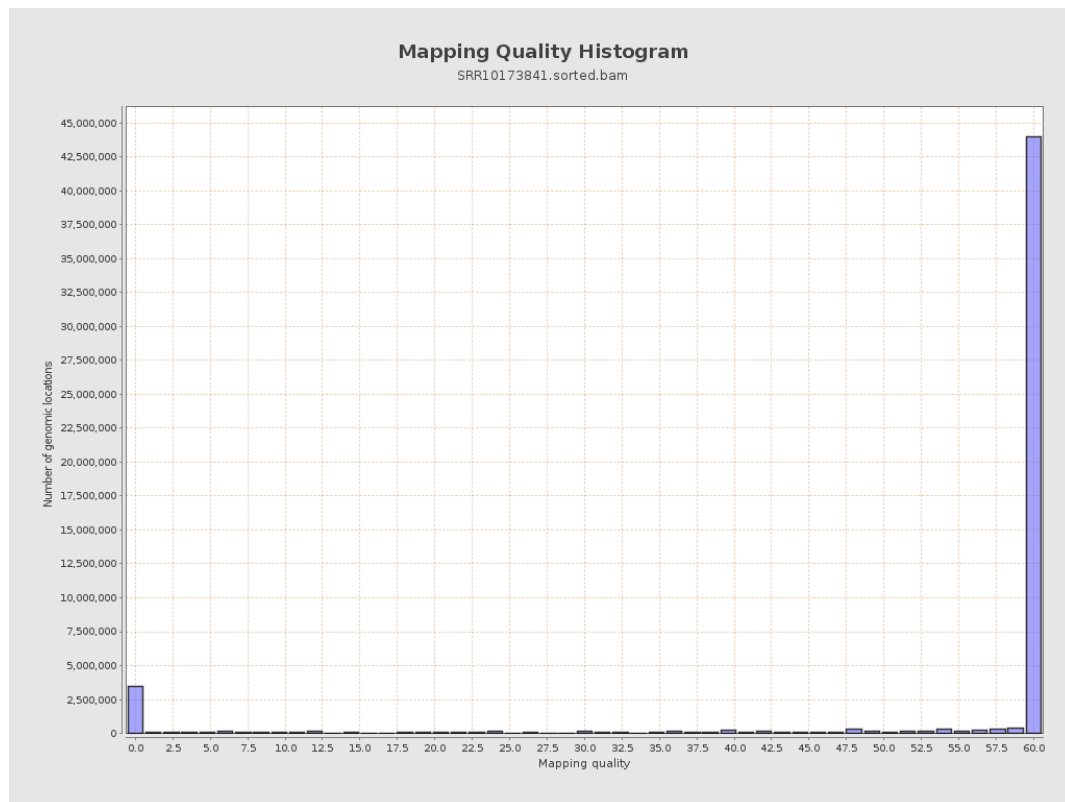
11. Results : Homopolymer Indels



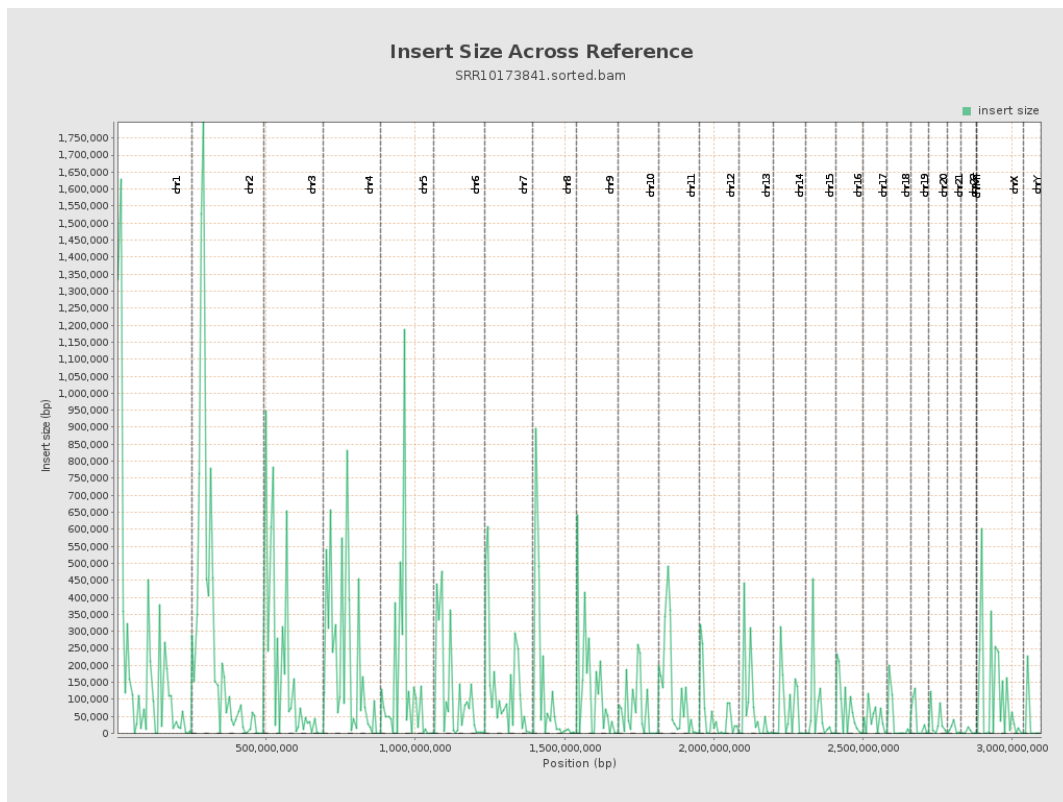
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

