

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:53:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173840.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_SRR10173840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173840_1.fastq.gz SRR10173840_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:53:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,932,788
Mapped reads	4,809,671 / 97.5%
Unmapped reads	123,117 / 2.5%
Mapped paired reads	4,809,671 / 97.5%
Mapped reads, first in pair	2,406,758 / 48.79%
Mapped reads, second in pair	2,402,913 / 48.71%
Mapped reads, both in pair	4,726,872 / 95.83%
Mapped reads, singletons	82,799 / 1.68%
Secondary alignments	0
Supplementary alignments	446,119 / 9.04%
Read min/max/mean length	30 / 133 / 127.8
Duplicated reads (estimated)	3,693,051 / 74.87%
Duplication rate	64.74%
Clipped reads	1,866,763 / 37.84%

2.2. ACGT Content

Number/percentage of A's	172,208,327 / 30.28%
Number/percentage of C's	110,498,440 / 19.43%
Number/percentage of T's	172,012,586 / 30.24%
Number/percentage of G's	114,034,387 / 20.05%
Number/percentage of N's	6,669 / 0%

GC Percentage	39.48%
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2.3. Coverage

Mean	0.1838
Standard Deviation	2.7123

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	810,219.33
Standard Deviation	8,143,607.98
P25/Median/P75	144 / 198 / 277

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	5,596,442
Insertions	58,240
Mapped reads with at least one insertion	1.17%
Deletions	117,502
Mapped reads with at least one deletion	2.38%
Homopolymer indels	43.74%

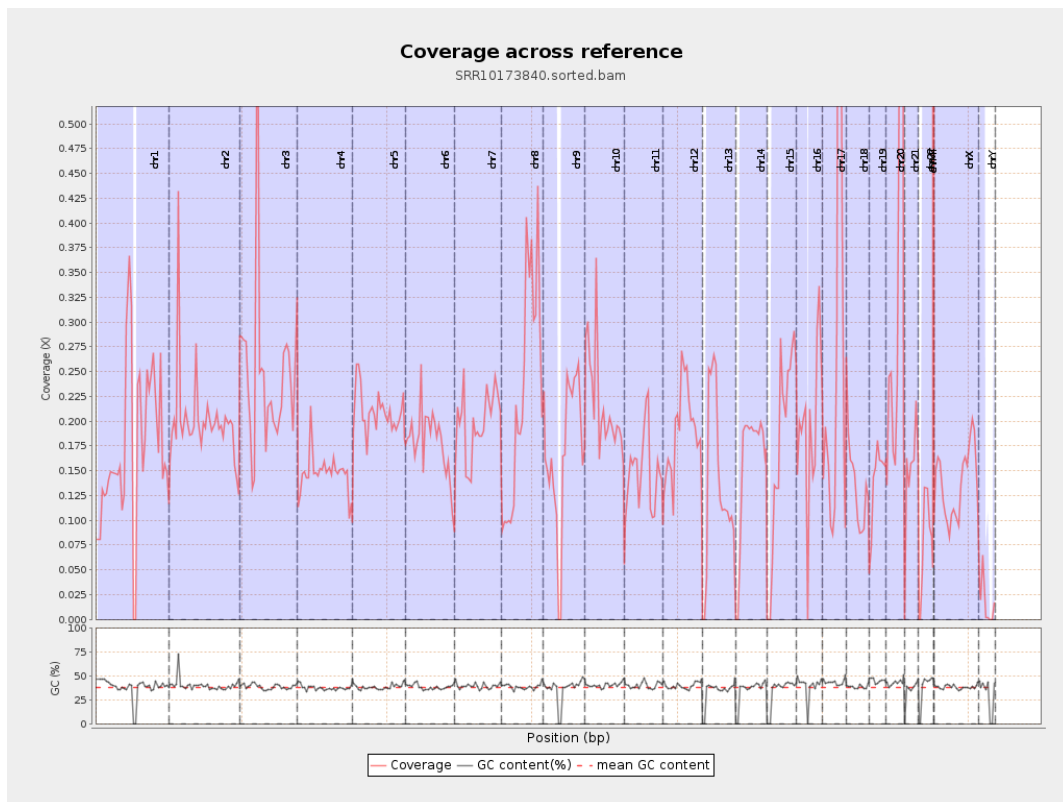
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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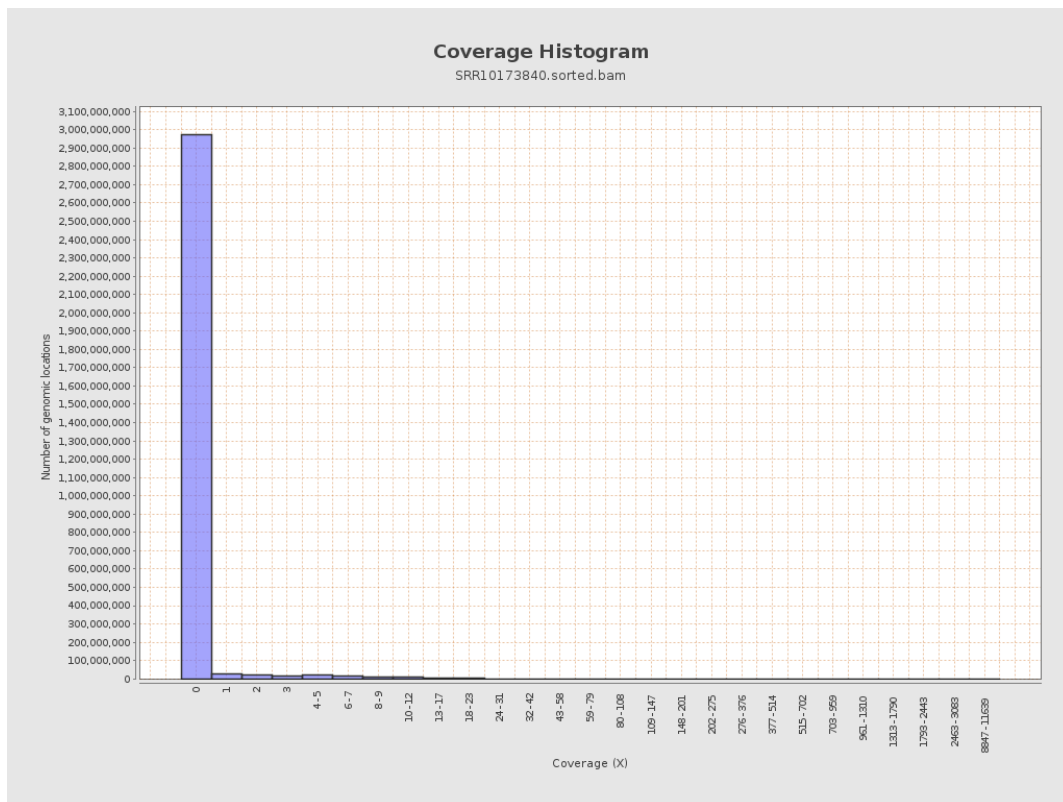
		bases	coverage	deviation
chr1	249250621	43332968	0.1739	1.9272
chr2	243199373	48802103	0.2007	8.1449
chr3	198022430	48420576	0.2445	1.4515
chr4	191154276	28113002	0.1471	1.2765
chr5	180915260	37871786	0.2093	1.3197
chr6	171115067	30469867	0.1781	1.4081
chr7	159138663	31754092	0.1995	1.8073
chr8	146364022	33334959	0.2278	1.7908
chr9	141213431	23638120	0.1674	1.4221
chr10	135534747	29559346	0.2181	2.251
chr11	135006516	20128256	0.1491	1.1225
chr12	133851895	25423897	0.1899	1.2562
chr13	115169878	15322759	0.133	1.0572
chr14	107349540	16835573	0.1568	1.1427
chr15	102531392	18098202	0.1765	1.2017
chr16	90354753	17876840	0.1979	1.5528
chr17	81195210	22183932	0.2732	1.6461
chr18	78077248	10492598	0.1344	1.9244
chr19	59128983	8410477	0.1422	1.3264
chr20	63025520	24131131	0.3829	1.9387
chr21	48129895	7273624	0.1511	1.1696
chr22	51304566	3899417	0.076	0.765
chrMT	16571	1443266	87.0959	66.7247
chrX	155270560	21253284	0.1369	1.0631

chrY	59373566	974356	0.0164	0.6545
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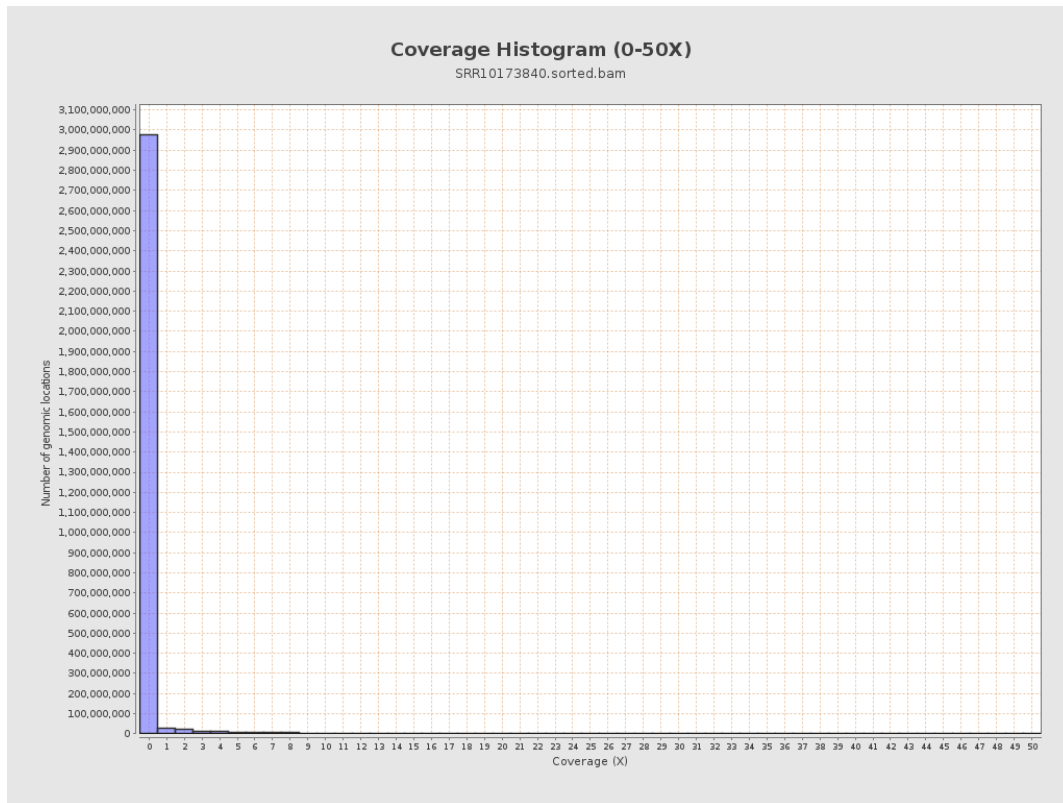
3. Results : Coverage across reference



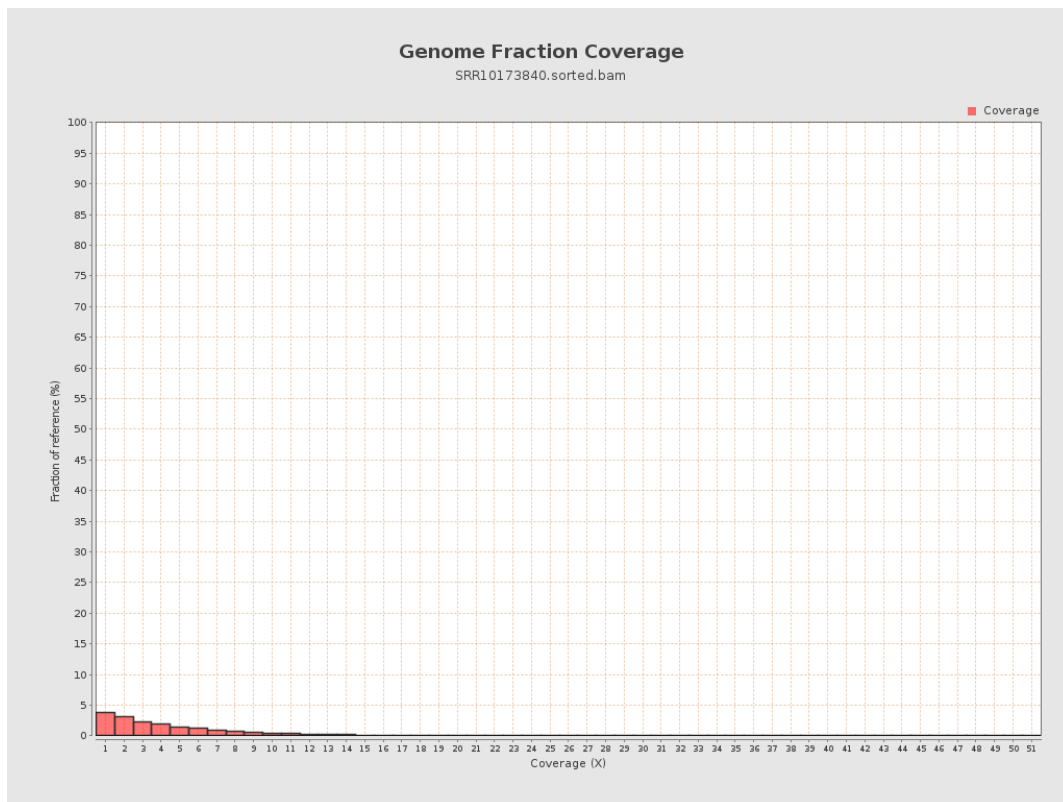
4. Results : Coverage Histogram



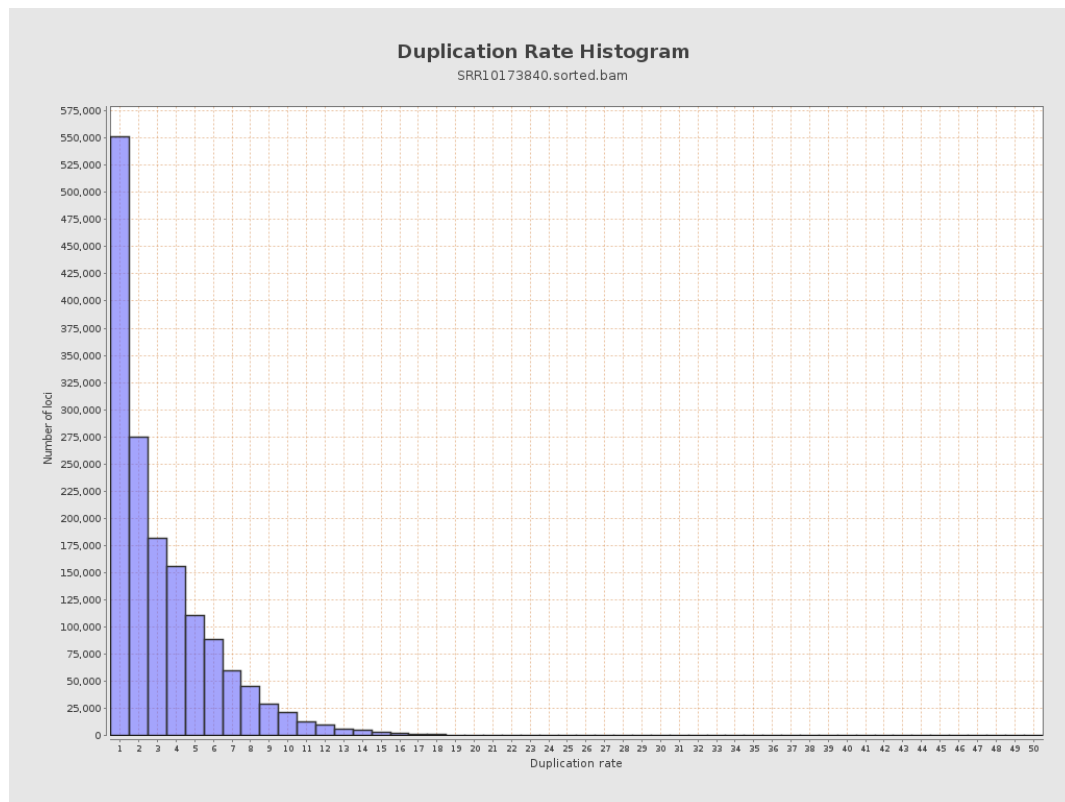
5. Results : Coverage Histogram (0-50X)



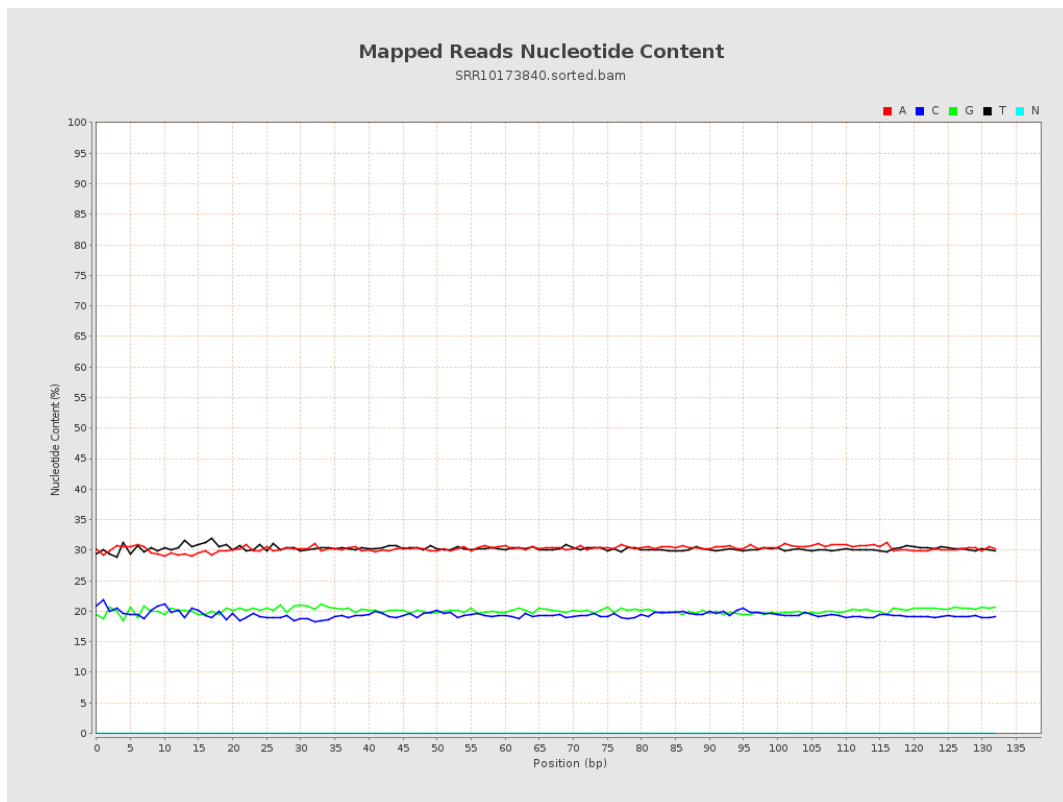
6. Results : Genome Fraction Coverage



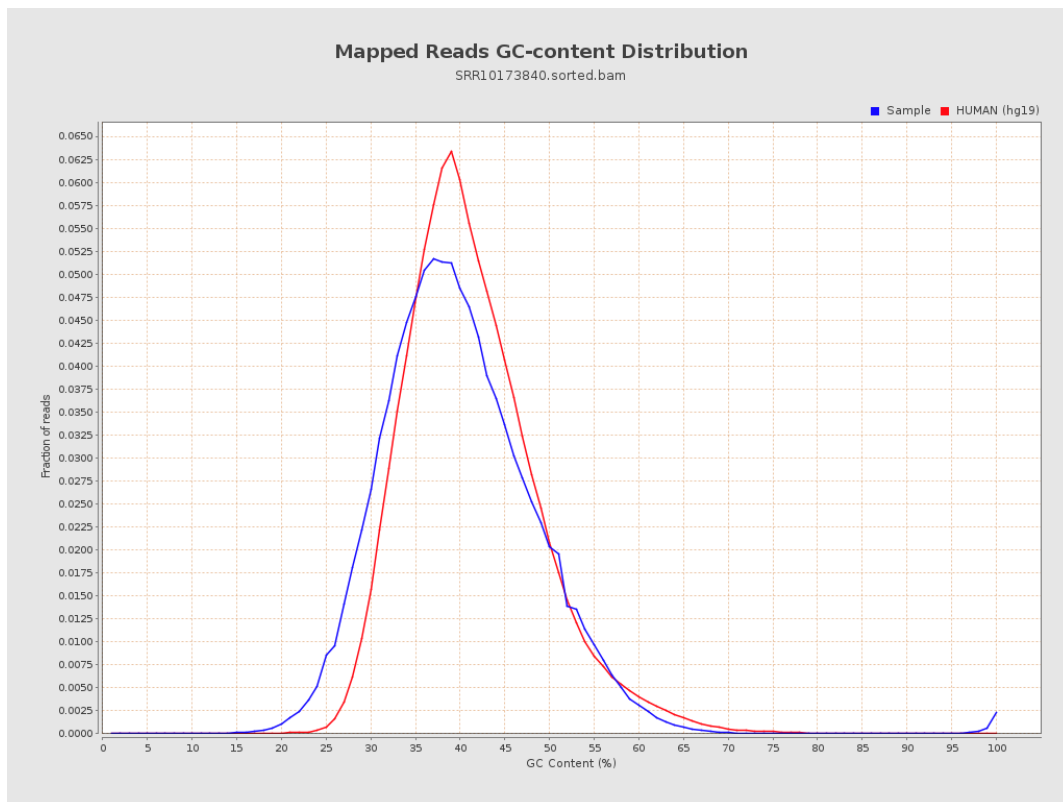
7. Results : Duplication Rate Histogram



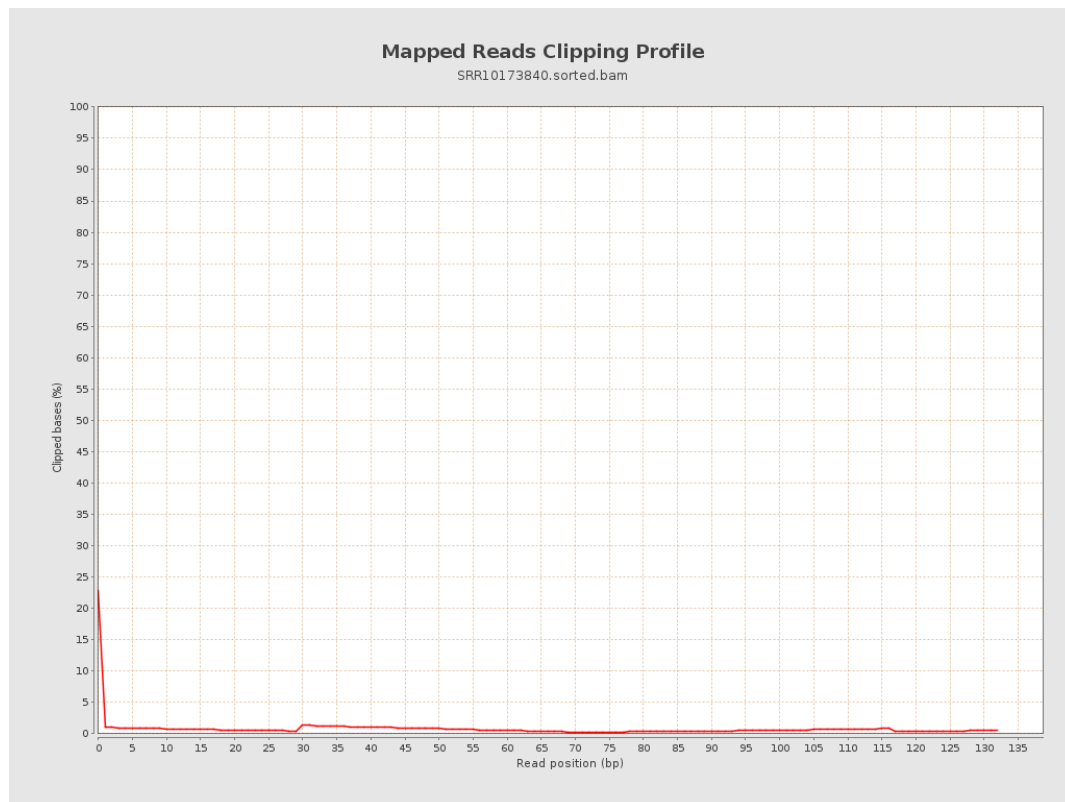
8. Results : Mapped Reads Nucleotide Content



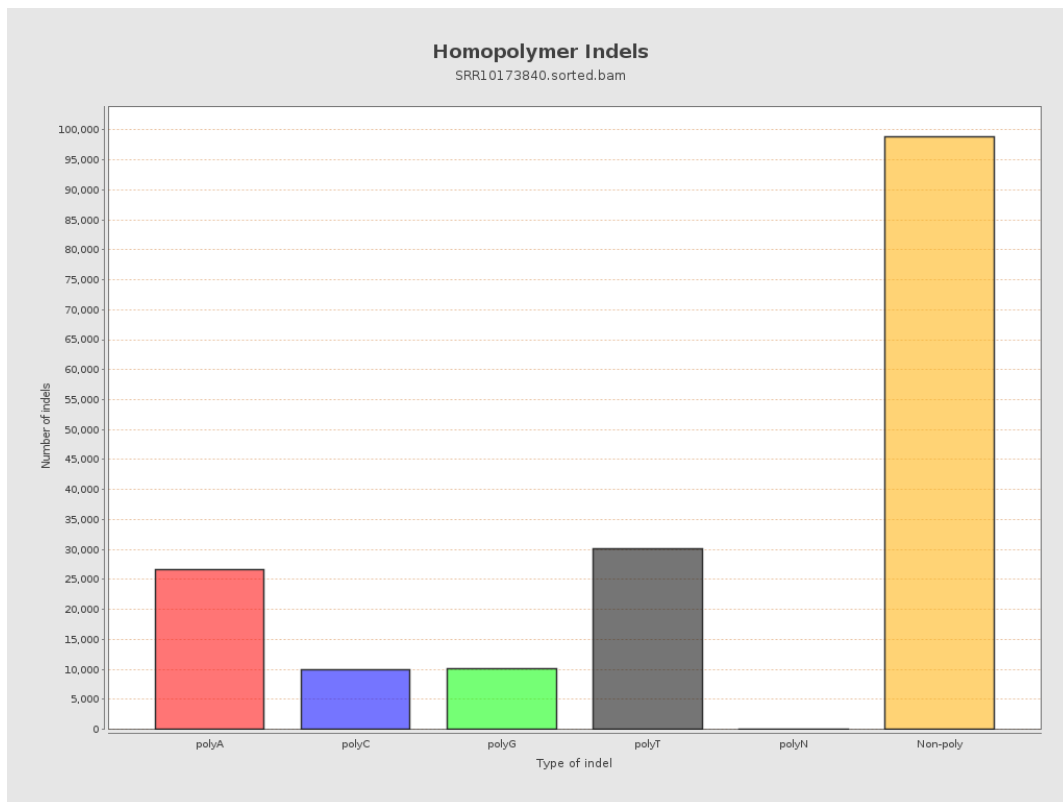
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



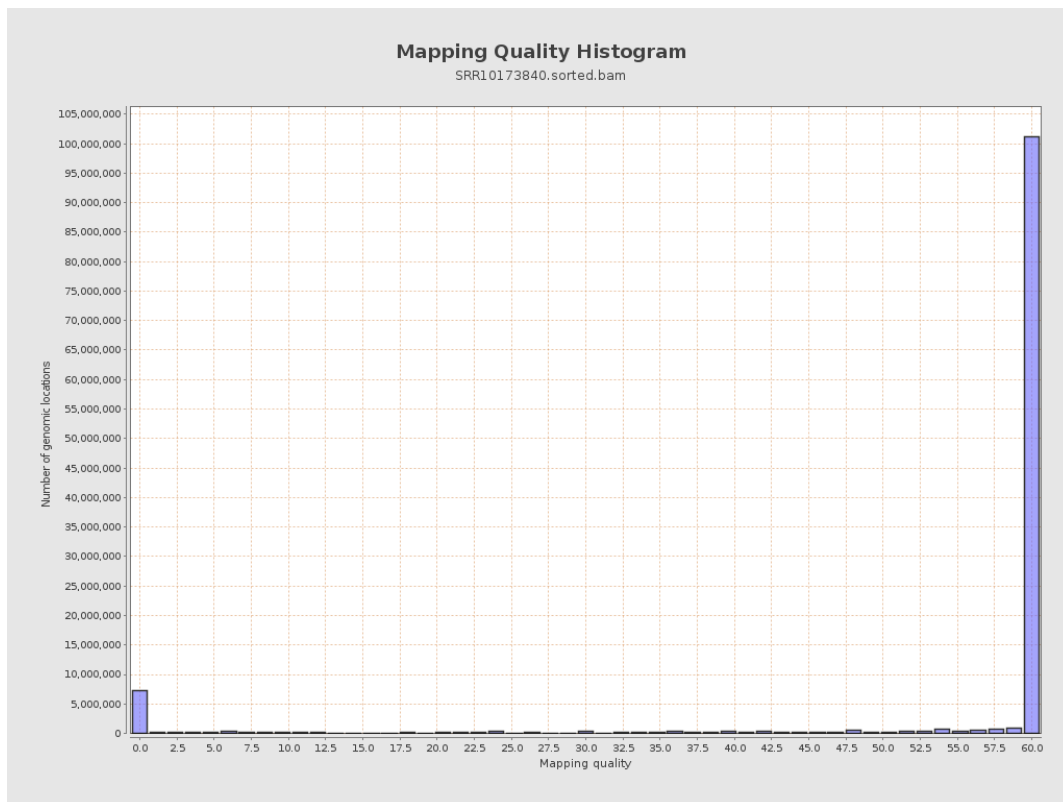
11. Results : Homopolymer Indels



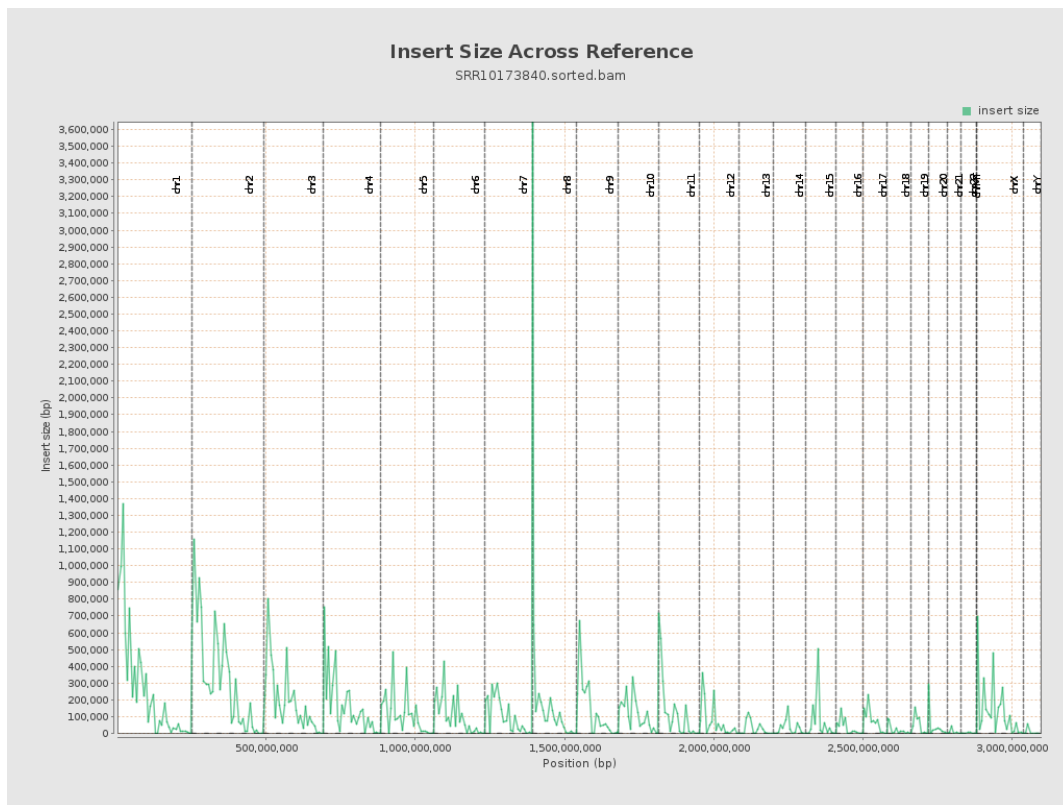
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

