

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:20:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174001.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_SRR10174001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174001_1.fastq.gz SRR10174001_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:20:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,245,412
Mapped reads	6,087,428 / 97.47%
Unmapped reads	157,984 / 2.53%
Mapped paired reads	6,087,428 / 97.47%
Mapped reads, first in pair	3,045,399 / 48.76%
Mapped reads, second in pair	3,042,029 / 48.71%
Mapped reads, both in pair	5,981,290 / 95.77%
Mapped reads, singletons	106,138 / 1.7%
Secondary alignments	0
Supplementary alignments	632,763 / 10.13%
Read min/max/mean length	30 / 133 / 128.25
Duplicated reads (estimated)	4,704,481 / 75.33%
Duplication rate	64.32%
Clipped reads	2,471,151 / 39.57%

2.2. ACGT Content

Number/percentage of A's	217,418,717 / 30.22%
Number/percentage of C's	140,093,158 / 19.47%
Number/percentage of T's	216,761,814 / 30.13%
Number/percentage of G's	145,118,724 / 20.17%
Number/percentage of N's	9,302 / 0%

GC Percentage	39.65%
---------------	--------

2.3. Coverage

Mean	0.2325
Standard Deviation	3.2986

2.4. Mapping Quality

Mean Mapping Quality	52.74
----------------------	-------

2.5. Insert size

Mean	931,094.71
Standard Deviation	8,367,740.45
P25/Median/P75	143 / 201 / 290

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	7,230,317
Insertions	78,025
Mapped reads with at least one insertion	1.24%
Deletions	163,922
Mapped reads with at least one deletion	2.62%
Homopolymer indels	42.9%

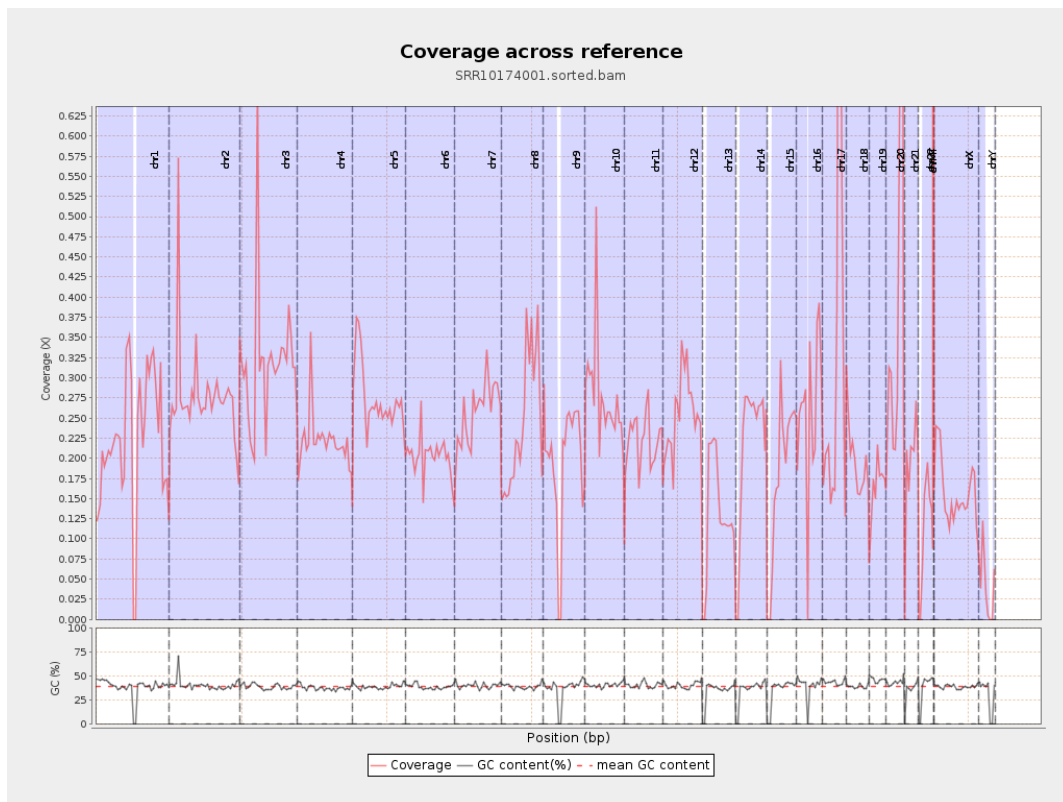
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

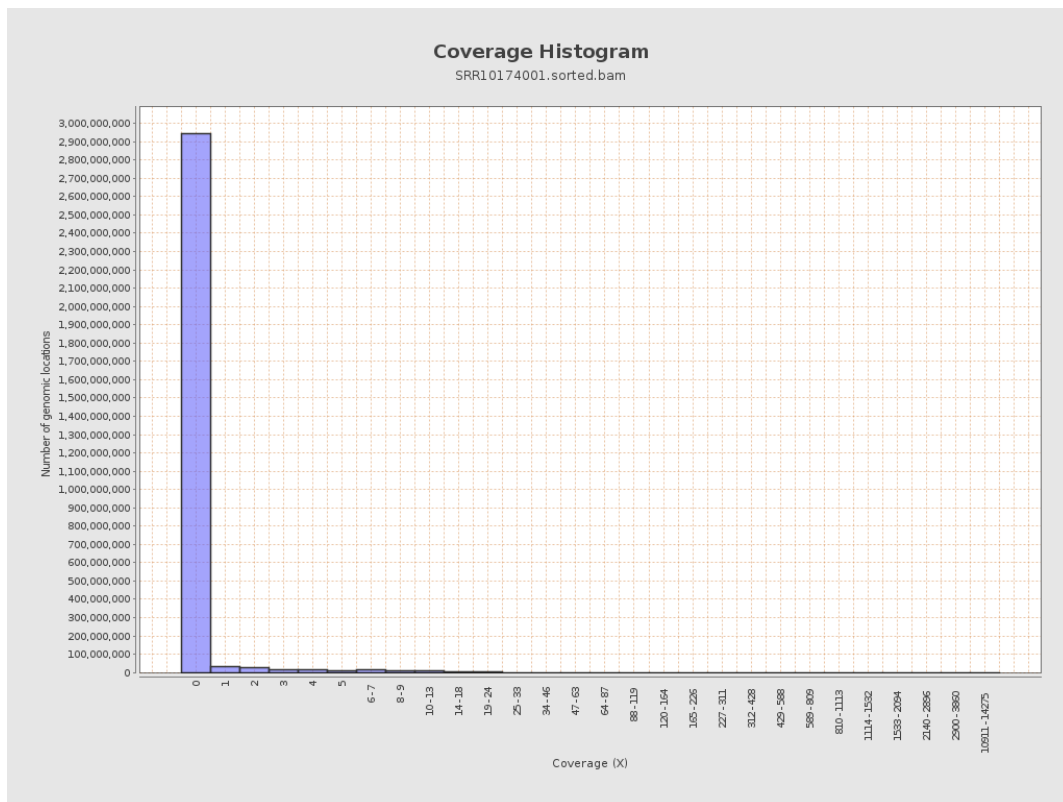
		bases	coverage	deviation
chr1	249250621	55686934	0.2234	2.1228
chr2	243199373	67256916	0.2766	10.0233
chr3	198022430	62732775	0.3168	1.6452
chr4	191154276	42155483	0.2205	1.766
chr5	180915260	49542117	0.2738	1.5044
chr6	171115067	34571651	0.202	1.5098
chr7	159138663	41376094	0.26	2.1064
chr8	146364022	35739142	0.2442	2.1287
chr9	141213431	27383371	0.1939	1.7243
chr10	135534747	37505853	0.2767	2.9553
chr11	135006516	29930222	0.2217	1.3882
chr12	133851895	34054967	0.2544	1.4561
chr13	115169878	14910080	0.1295	1.0378
chr14	107349540	23216543	0.2163	1.3453
chr15	102531392	18465161	0.1801	1.2125
chr16	90354753	23438467	0.2594	2.0611
chr17	81195210	26591037	0.3275	1.8198
chr18	78077248	15362947	0.1968	2.2179
chr19	59128983	9791552	0.1656	1.6965
chr20	63025520	26535697	0.421	2.0267
chr21	48129895	9222476	0.1916	1.4308
chr22	51304566	5604785	0.1092	0.9256
chrMT	16571	1838332	110.9367	85.7504
chrX	155270560	24562641	0.1582	1.1434

chrY	59373566	2338721	0.0394	1.0224
------	----------	---------	--------	--------

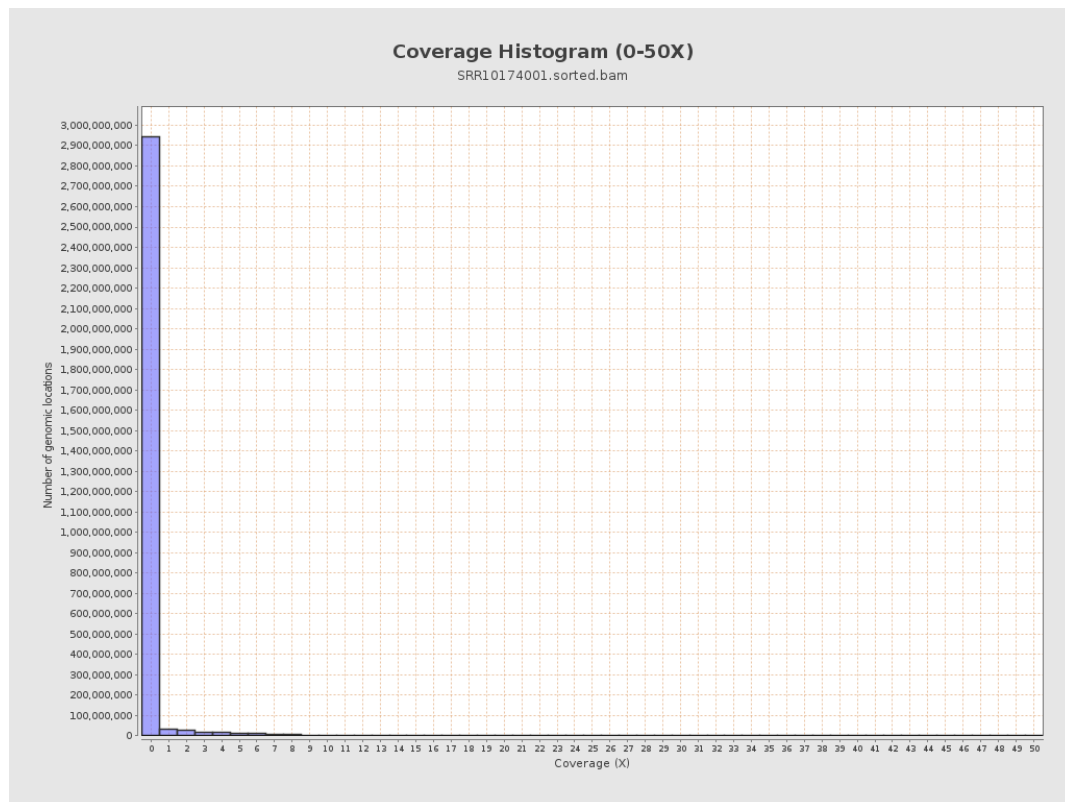
3. Results : Coverage across reference



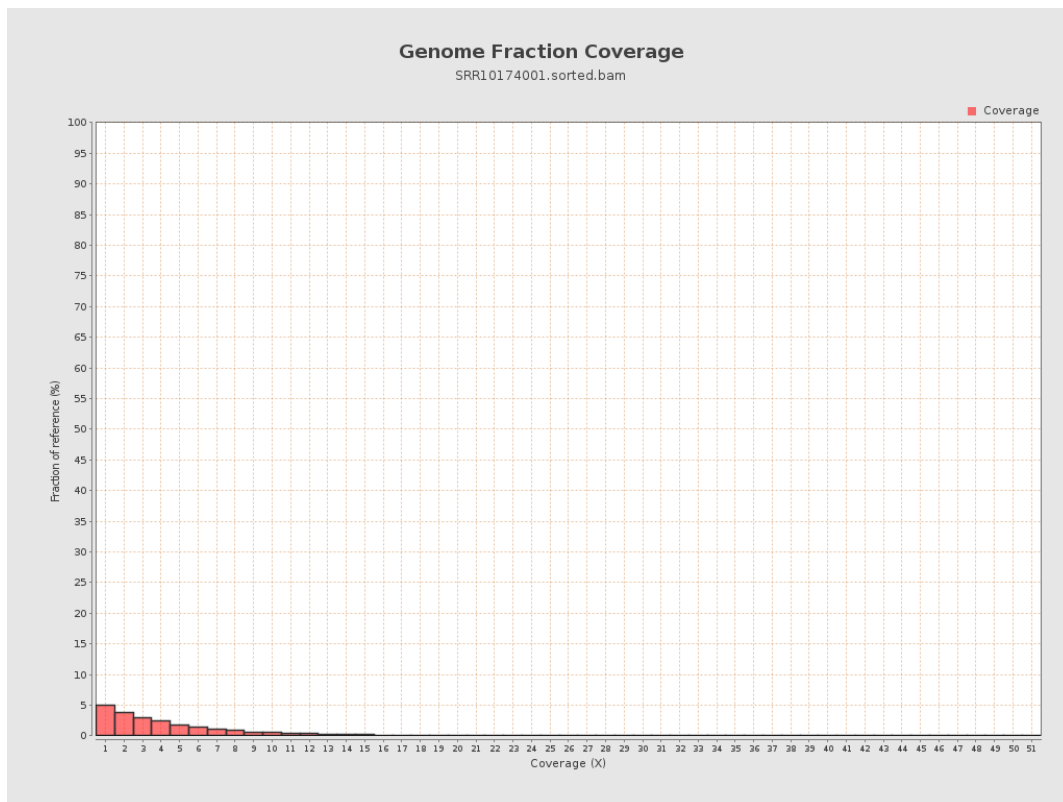
4. Results : Coverage Histogram



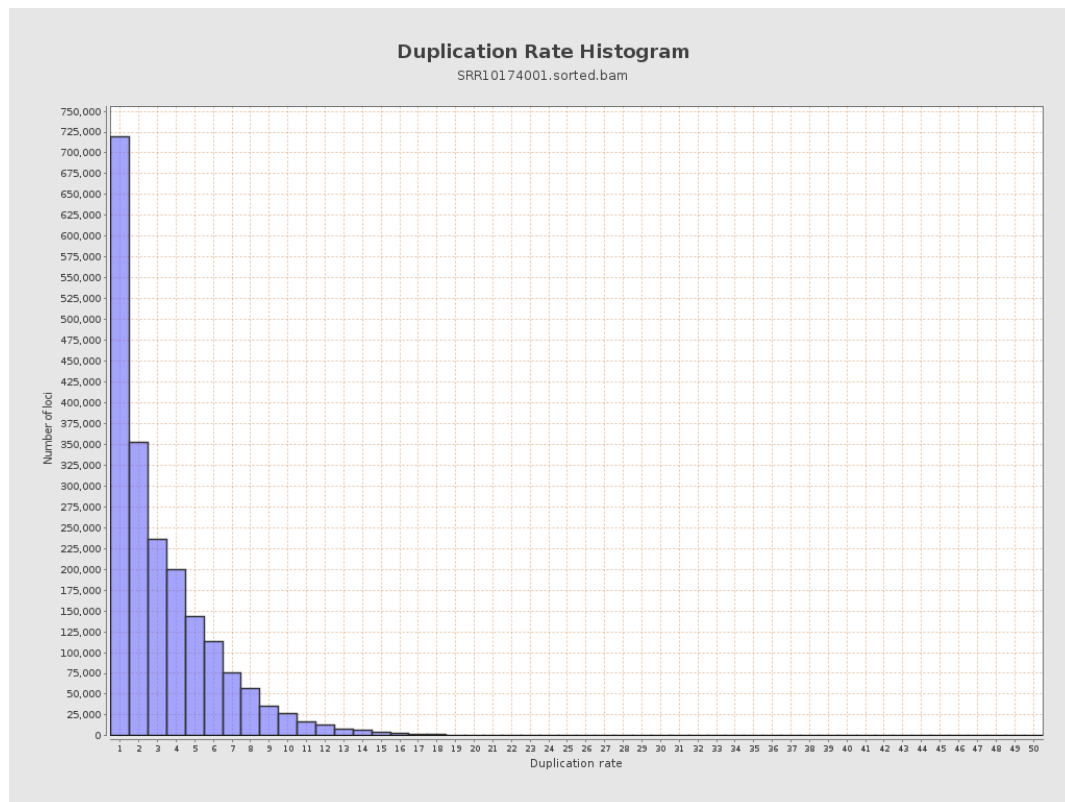
5. Results : Coverage Histogram (0-50X)



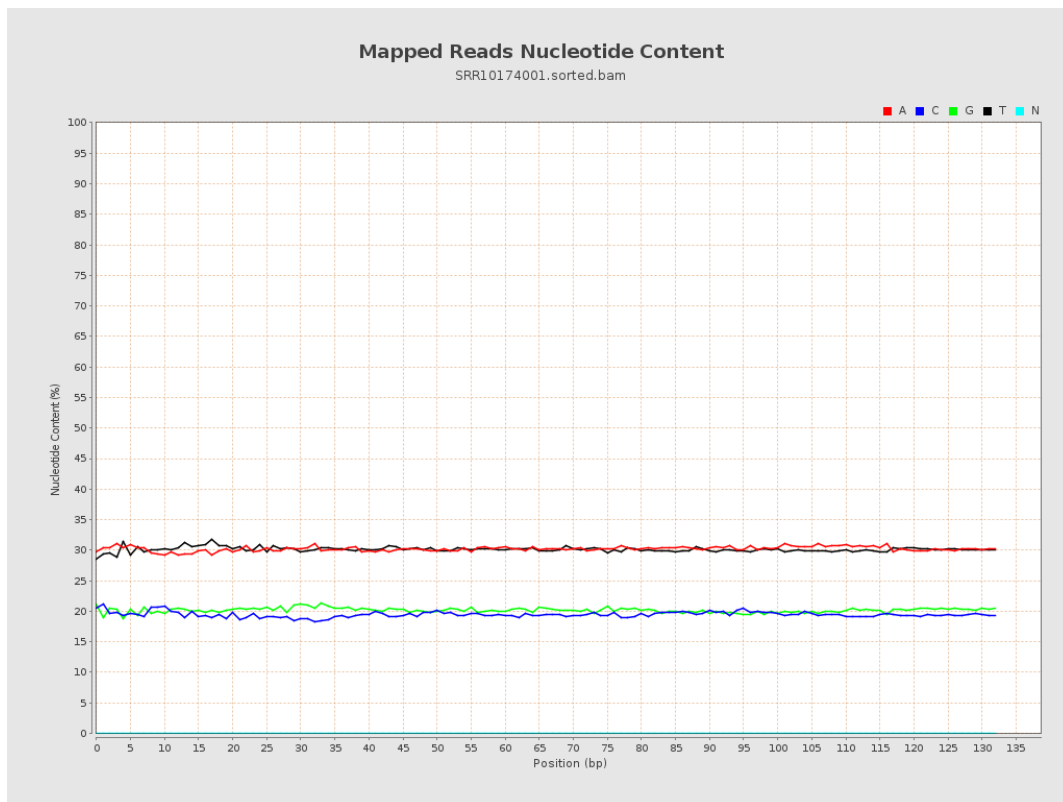
6. Results : Genome Fraction Coverage



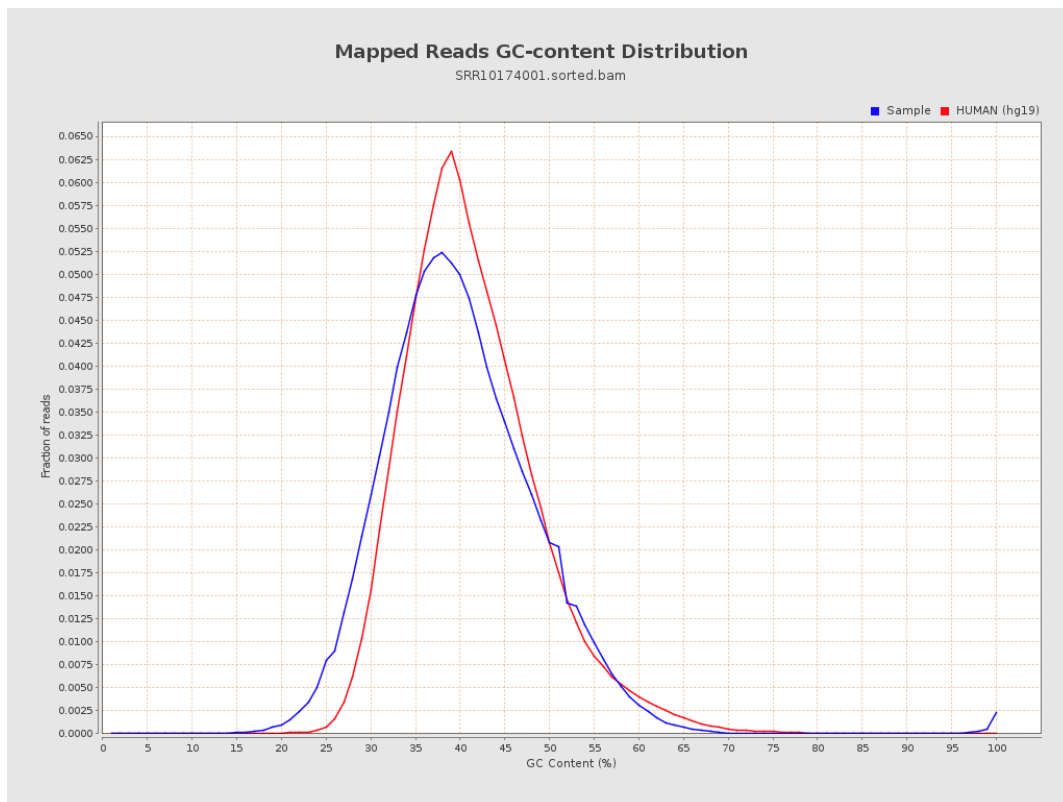
7. Results : Duplication Rate Histogram



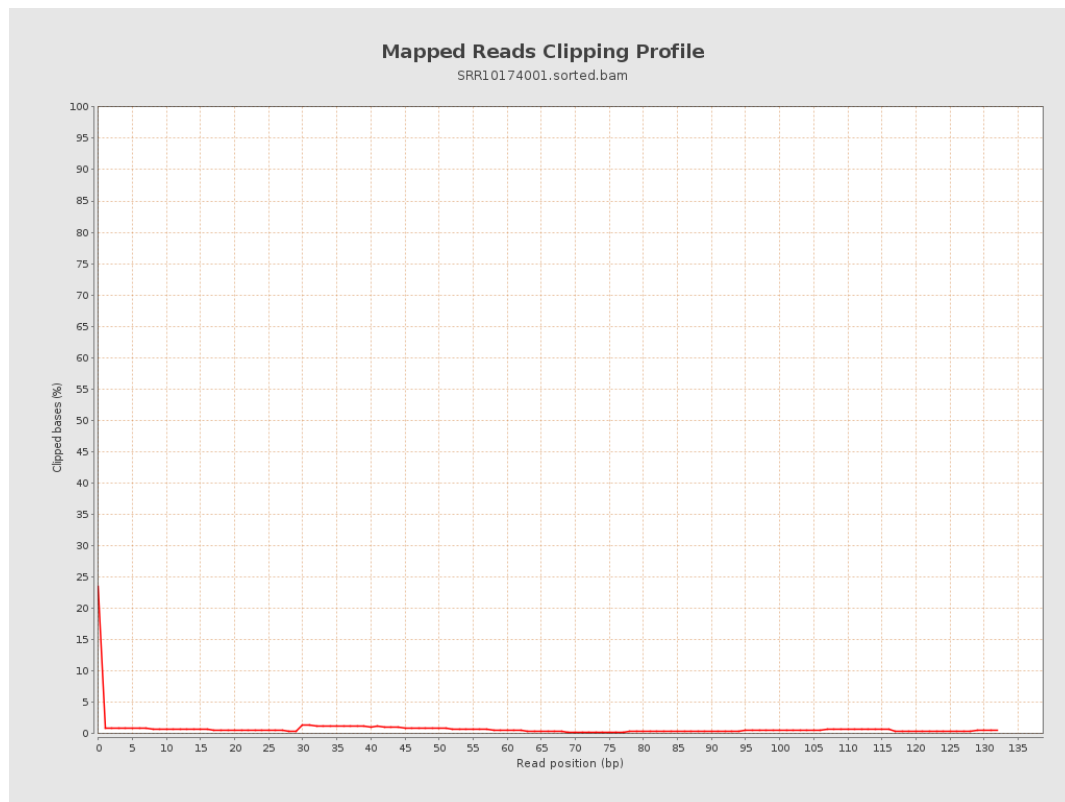
8. Results : Mapped Reads Nucleotide Content



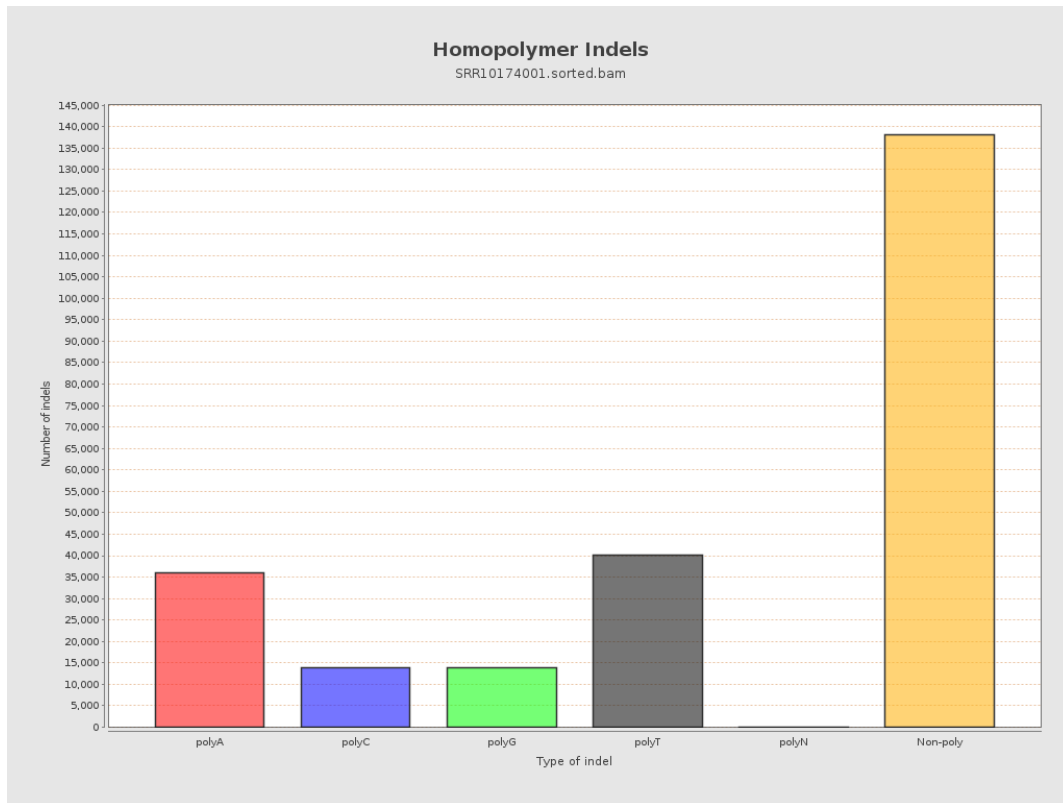
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



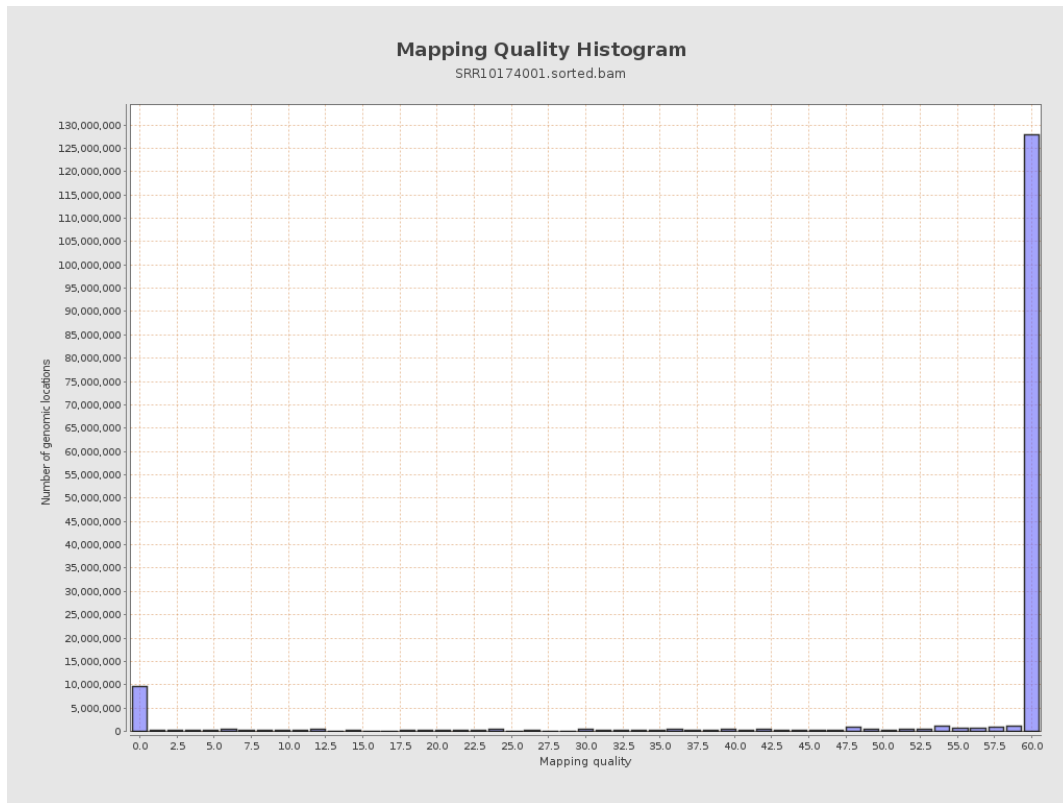
11. Results : Homopolymer Indels



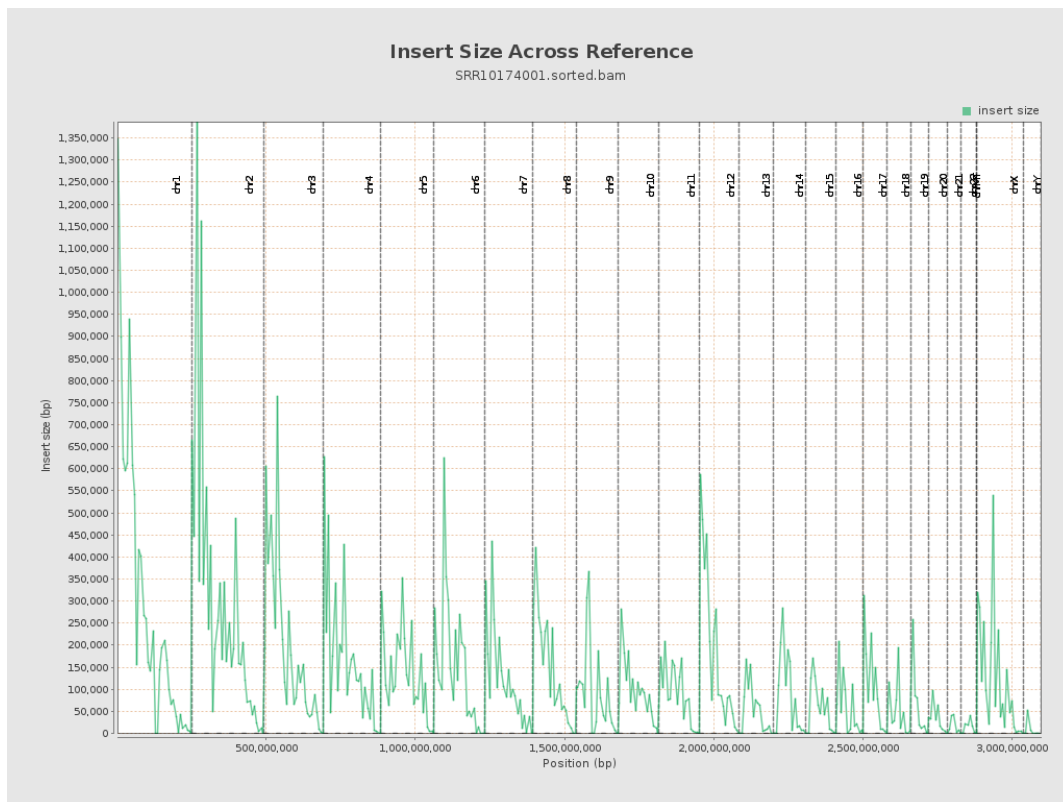
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

