

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:12:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173914.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_SRR10173914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173914_1.fastq.gz SRR10173914_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:11:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,599,928
Mapped reads	5,452,480 / 97.37%
Unmapped reads	147,448 / 2.63%
Mapped paired reads	5,452,480 / 97.37%
Mapped reads, first in pair	2,728,490 / 48.72%
Mapped reads, second in pair	2,723,990 / 48.64%
Mapped reads, both in pair	5,355,288 / 95.63%
Mapped reads, singletons	97,192 / 1.74%
Secondary alignments	0
Supplementary alignments	543,862 / 9.71%
Read min/max/mean length	30 / 133 / 128.18
Duplicated reads (estimated)	4,331,419 / 77.35%
Duplication rate	65.76%
Clipped reads	2,158,208 / 38.54%

2.2. ACGT Content

Number/percentage of A's	195,247,445 / 30.26%
Number/percentage of C's	125,552,723 / 19.46%
Number/percentage of T's	194,689,100 / 30.17%
Number/percentage of G's	129,760,677 / 20.11%
Number/percentage of N's	7,149 / 0%

GC Percentage	39.57%
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2.3. Coverage

Mean	0.2085
Standard Deviation	3.0692

2.4. Mapping Quality

Mean Mapping Quality	52.74
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2.5. Insert size

Mean	846,146
Standard Deviation	8,111,278.28
P25/Median/P75	145 / 201 / 289

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	6,554,056
Insertions	66,196
Mapped reads with at least one insertion	1.17%
Deletions	141,224
Mapped reads with at least one deletion	2.53%
Homopolymer indels	42.81%

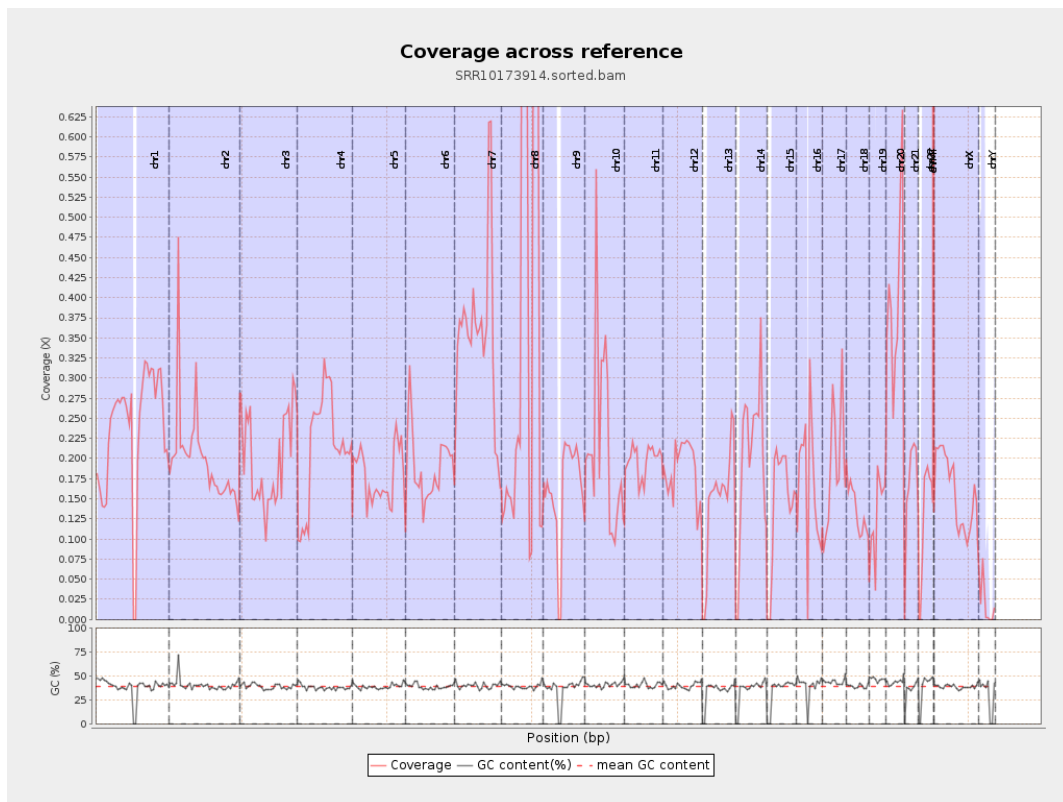
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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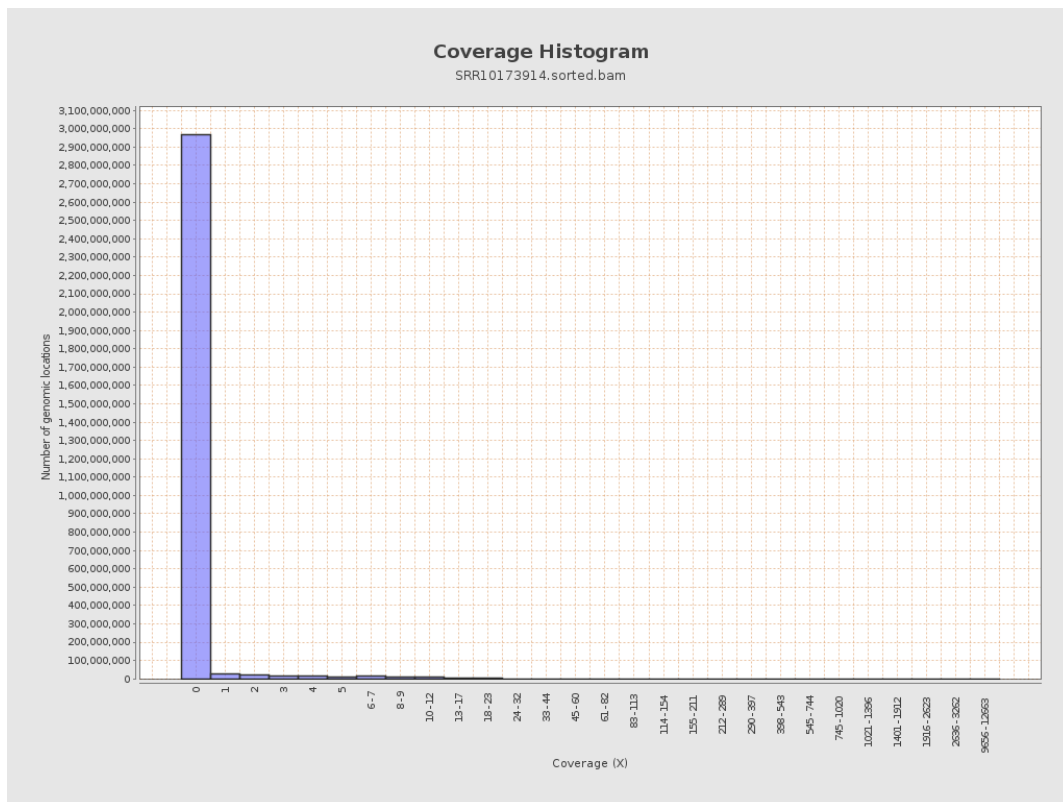
		bases	coverage	deviation
chr1	249250621	58704885	0.2355	1.7508
chr2	243199373	48408820	0.199	8.8641
chr3	198022430	39612887	0.2	1.3462
chr4	191154276	40713357	0.213	1.6428
chr5	180915260	32245540	0.1782	1.2581
chr6	171115067	32172548	0.188	1.3548
chr7	159138663	56965691	0.358	3.3676
chr8	146364022	64077502	0.4378	2.3506
chr9	141213431	22715757	0.1609	1.5944
chr10	135534747	29494647	0.2176	4.0114
chr11	135006516	26614594	0.1971	1.366
chr12	133851895	25146775	0.1879	1.2976
chr13	115169878	17044674	0.148	1.1585
chr14	107349540	21449421	0.1998	1.3398
chr15	102531392	14900501	0.1453	1.1209
chr16	90354753	14878852	0.1647	1.7301
chr17	81195210	15508327	0.191	1.3792
chr18	78077248	10591805	0.1357	2.026
chr19	59128983	7812218	0.1321	1.3399
chr20	63025520	25068463	0.3978	1.9131
chr21	48129895	8028784	0.1668	1.3109
chr22	51304566	6400220	0.1247	1.0081
chrMT	16571	1443143	87.0885	72.633
chrX	155270560	24491272	0.1577	1.1853

chrY	59373566	1115962	0.0188	0.8109
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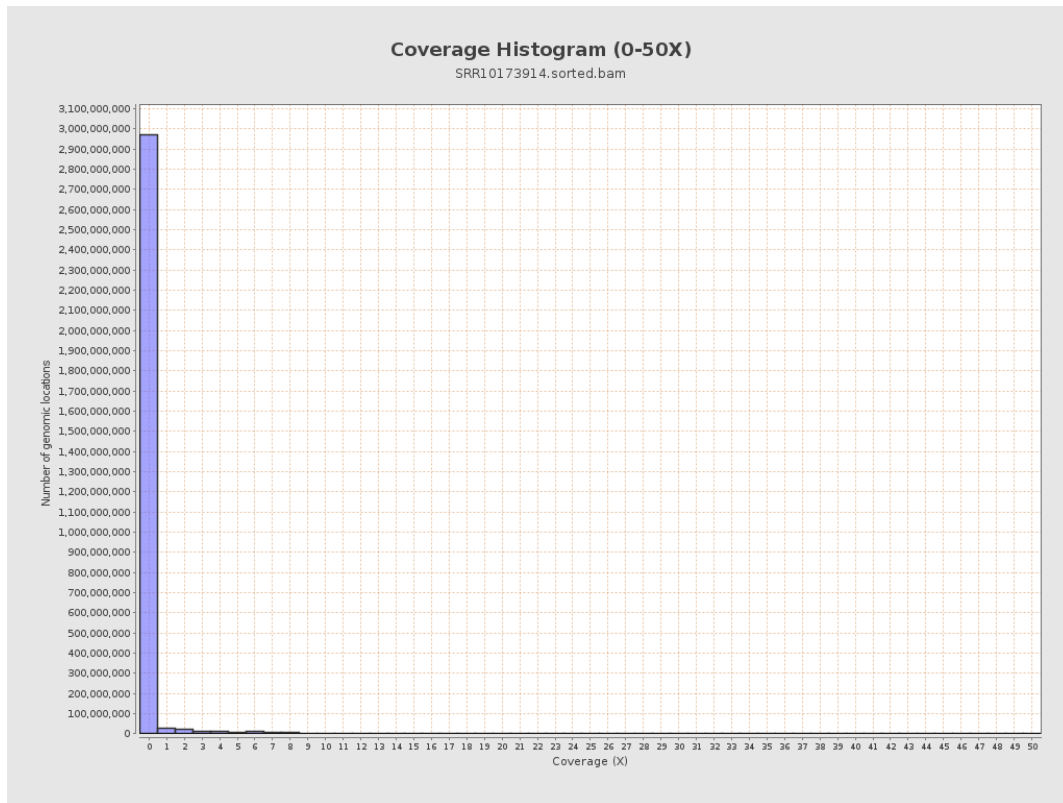
3. Results : Coverage across reference



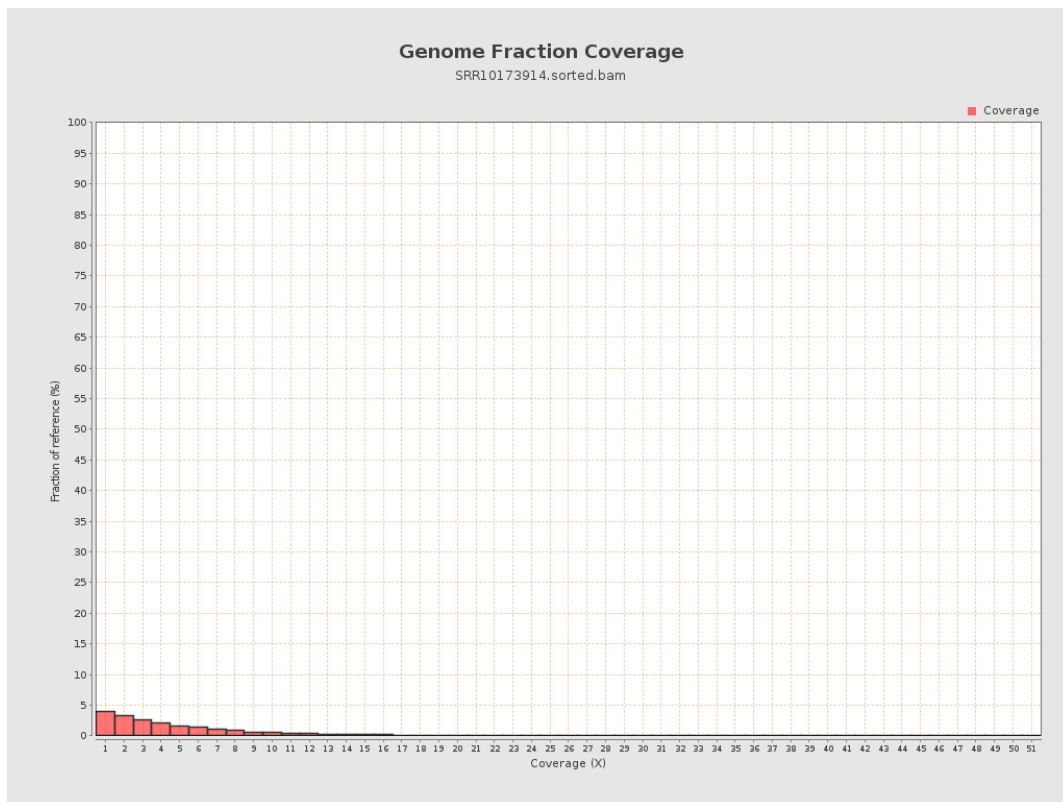
4. Results : Coverage Histogram



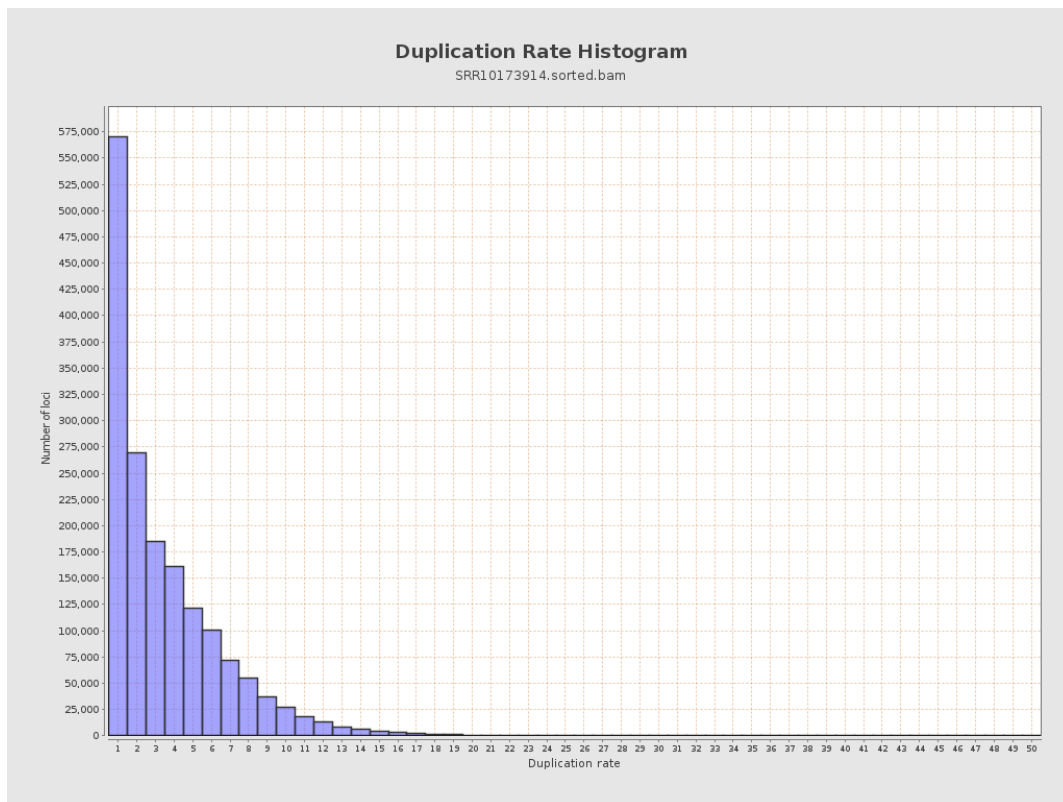
5. Results : Coverage Histogram (0-50X)



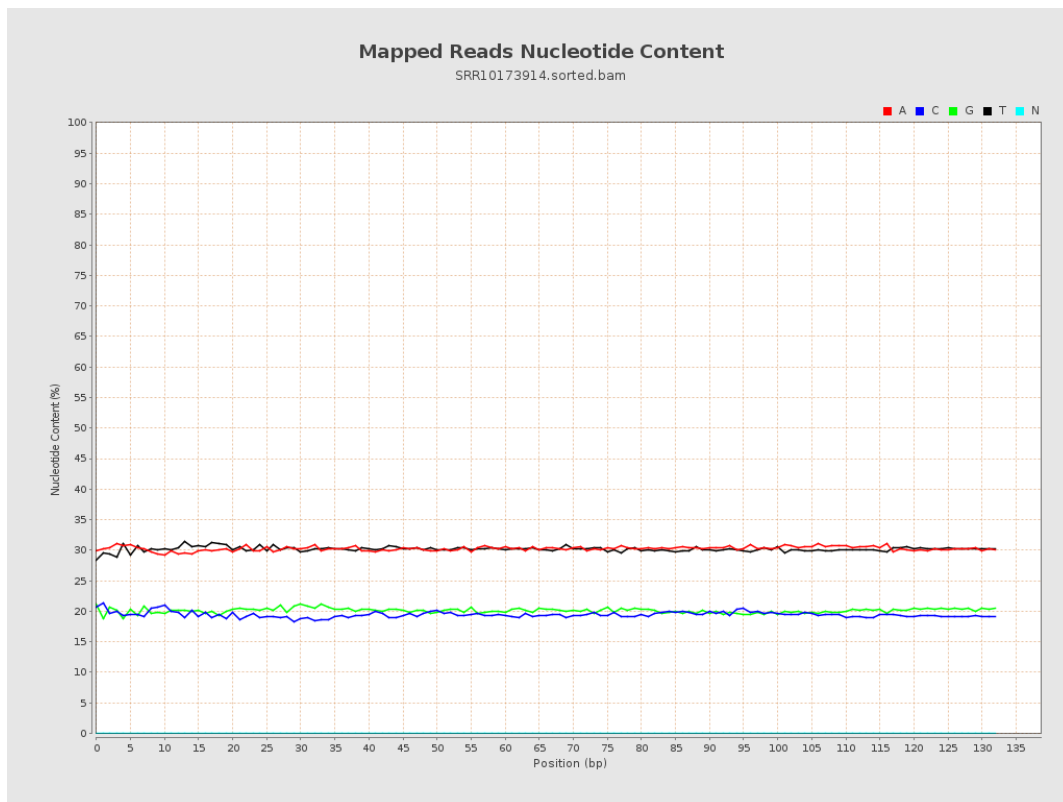
6. Results : Genome Fraction Coverage



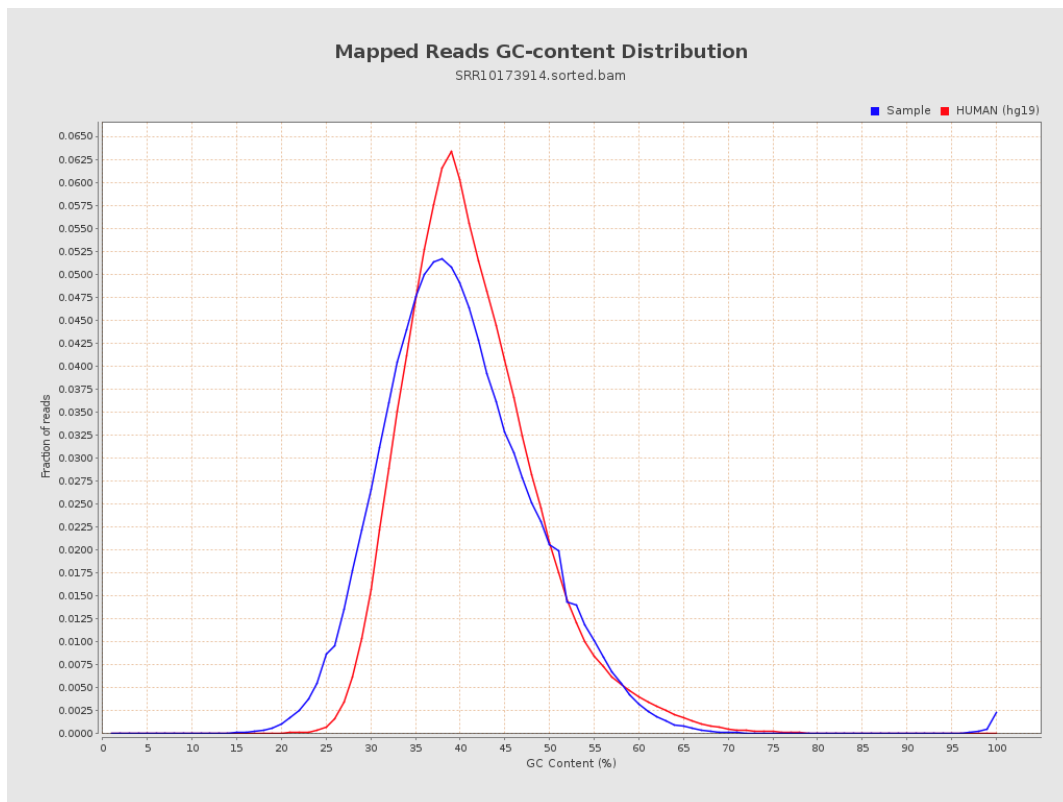
7. Results : Duplication Rate Histogram



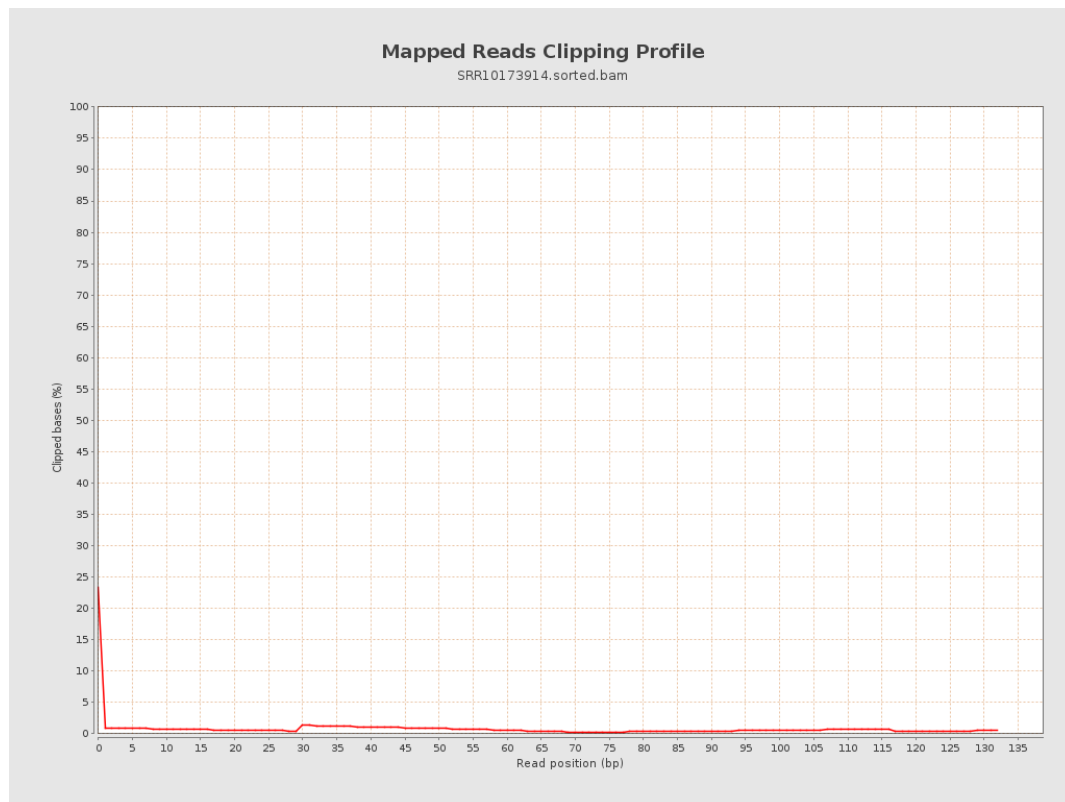
8. Results : Mapped Reads Nucleotide Content



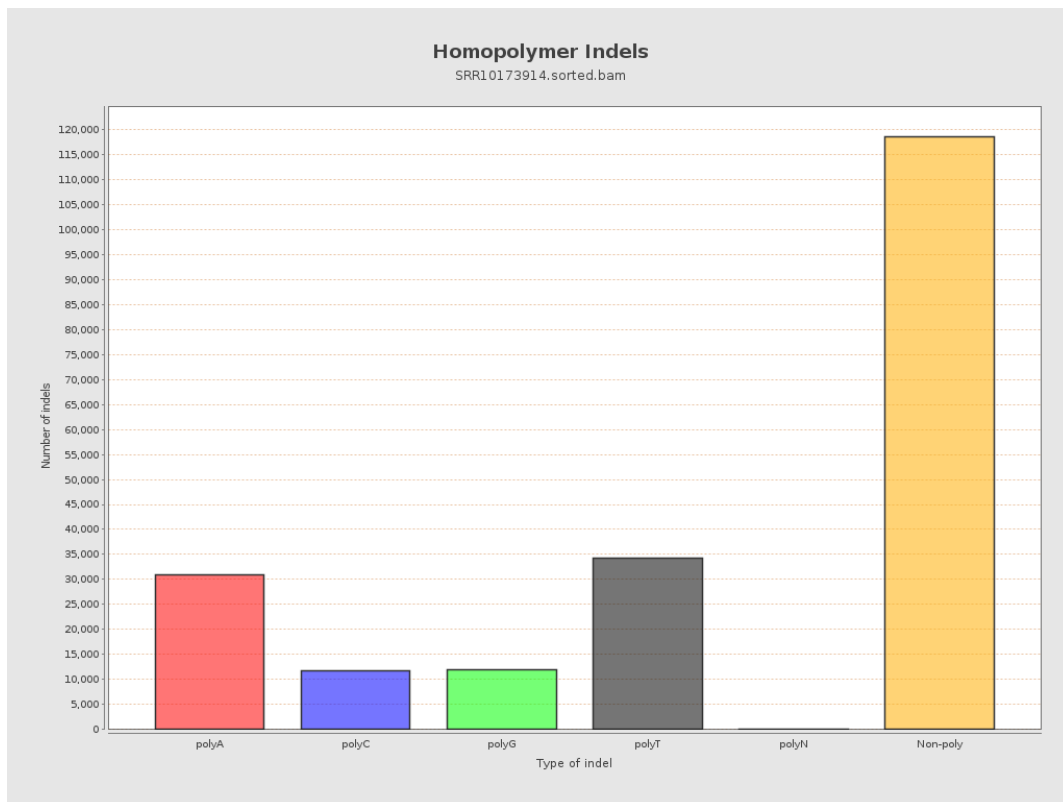
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



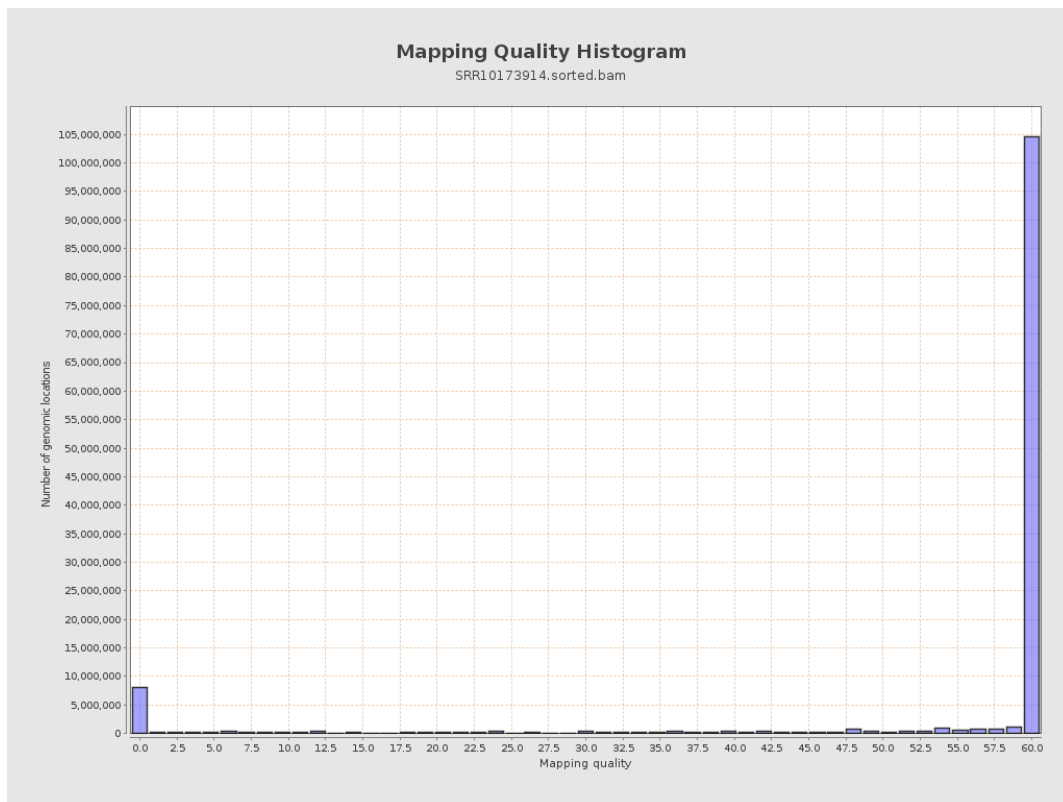
11. Results : Homopolymer Indels



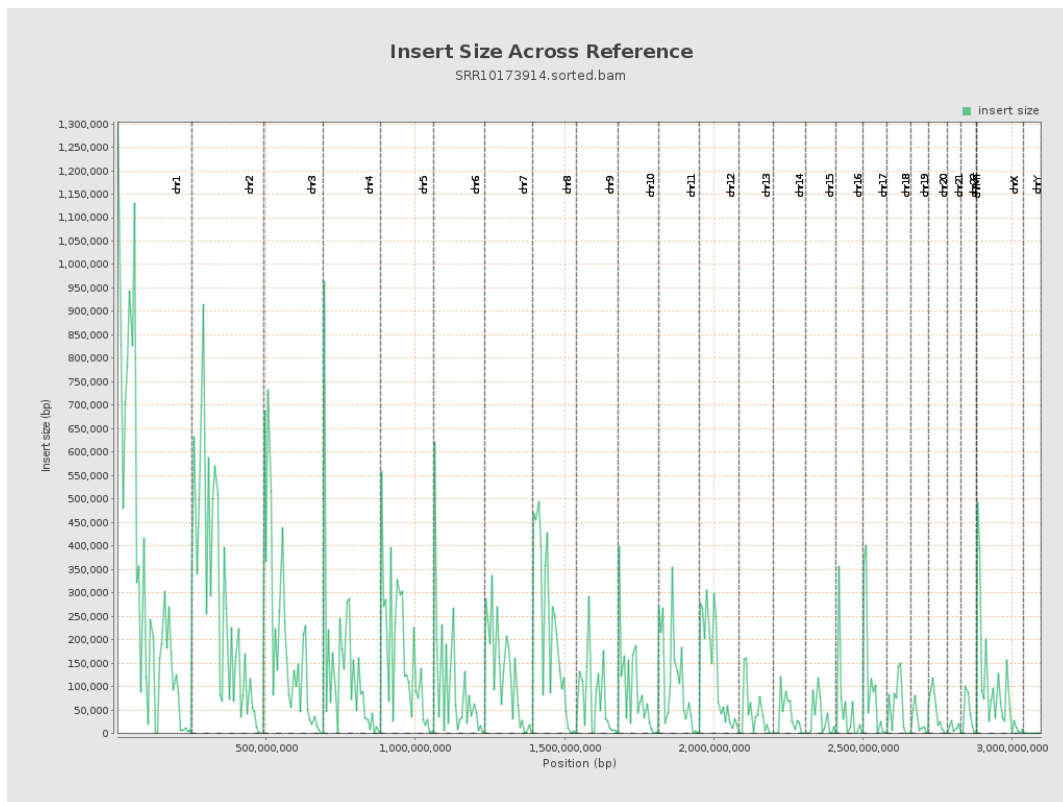
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

