

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:54:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174019.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_SRR10174019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174019_1.fastq.gz SRR10174019_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:54:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,432,338
Mapped reads	3,368,720 / 98.15%
Unmapped reads	63,618 / 1.85%
Mapped paired reads	3,368,720 / 98.15%
Mapped reads, first in pair	1,682,541 / 49.02%
Mapped reads, second in pair	1,686,179 / 49.13%
Mapped reads, both in pair	3,328,176 / 96.97%
Mapped reads, singletons	40,544 / 1.18%
Secondary alignments	0
Supplementary alignments	303,549 / 8.84%
Read min/max/mean length	30 / 133 / 127.65
Duplicated reads (estimated)	2,556,921 / 74.5%
Duplication rate	64.36%
Clipped reads	1,154,006 / 33.62%

2.2. ACGT Content

Number/percentage of A's	123,239,454 / 30.64%
Number/percentage of C's	77,206,463 / 19.2%
Number/percentage of T's	122,678,965 / 30.5%
Number/percentage of G's	79,090,723 / 19.66%
Number/percentage of N's	4,975 / 0%

GC Percentage	38.86%
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2.3. Coverage

Mean	0.13
Standard Deviation	1.9215

2.4. Mapping Quality

Mean Mapping Quality	52.97
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2.5. Insert size

Mean	695,468.48
Standard Deviation	7,673,839.12
P25/Median/P75	143 / 193 / 265

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	3,658,534
Insertions	41,331
Mapped reads with at least one insertion	1.18%
Deletions	72,110
Mapped reads with at least one deletion	2.08%
Homopolymer indels	44.24%

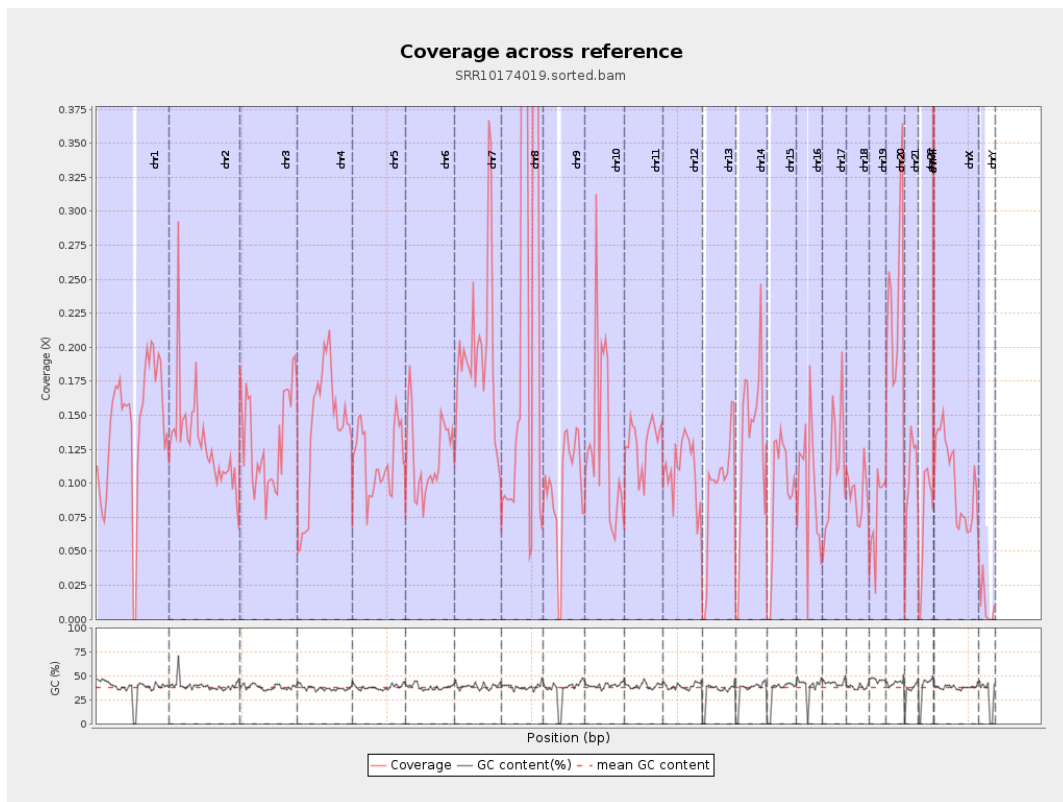
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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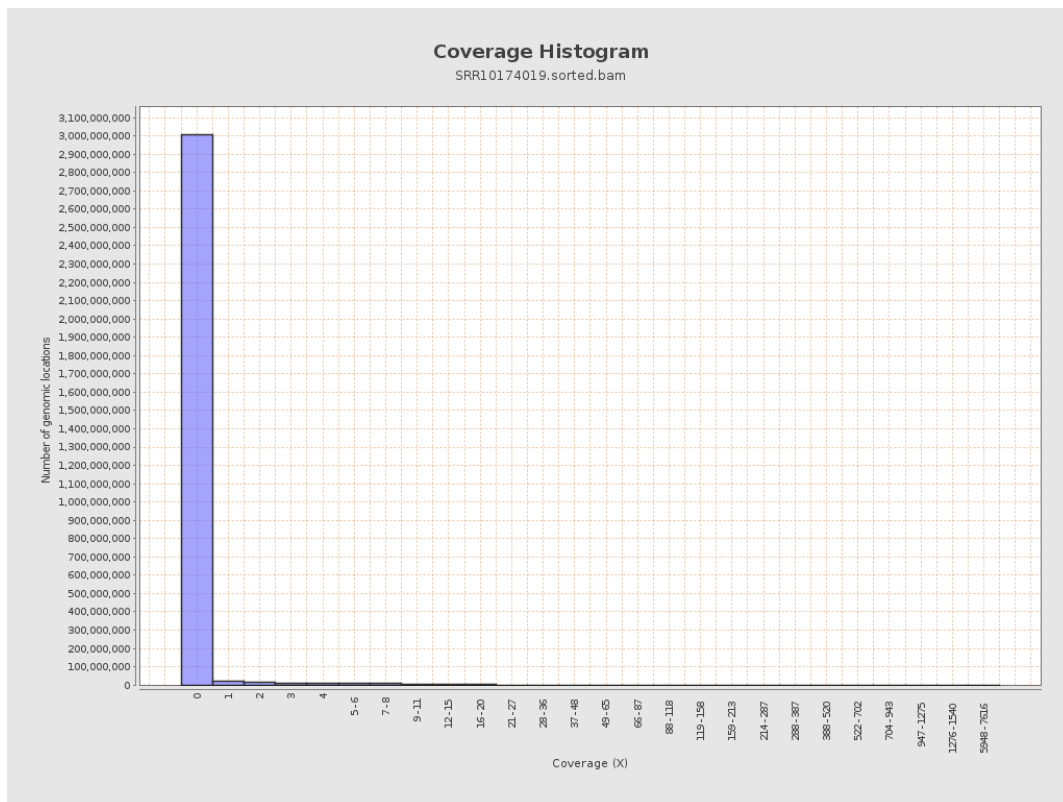
		bases	coverage	deviation
chr1	249250621	35287202	0.1416	1.1653
chr2	243199373	31564313	0.1298	5.3817
chr3	198022430	26391505	0.1333	1.0592
chr4	191154276	26510769	0.1387	1.1797
chr5	180915260	21231558	0.1174	0.9781
chr6	171115067	20302612	0.1186	1.0121
chr7	159138663	31326275	0.1968	1.9672
chr8	146364022	40977111	0.28	1.7931
chr9	141213431	13903195	0.0985	0.9867
chr10	135534747	17825317	0.1315	2.2645
chr11	135006516	17531969	0.1299	1.0303
chr12	133851895	14816315	0.1107	0.9537
chr13	115169878	11021123	0.0957	0.8993
chr14	107349540	13871761	0.1292	1.0309
chr15	102531392	9527914	0.0929	0.8667
chr16	90354753	8670165	0.096	1.114
chr17	81195210	9079638	0.1118	1.0025
chr18	78077248	7260083	0.093	1.0758
chr19	59128983	4539487	0.0768	0.8918
chr20	63025520	14944990	0.2371	1.3915
chr21	48129895	4853948	0.1009	0.942
chr22	51304566	3679299	0.0717	0.729
chrMT	16571	792376	47.817	45.7111
chrX	155270560	15870582	0.1022	0.9122

chrY	59373566	630158	0.0106	0.43
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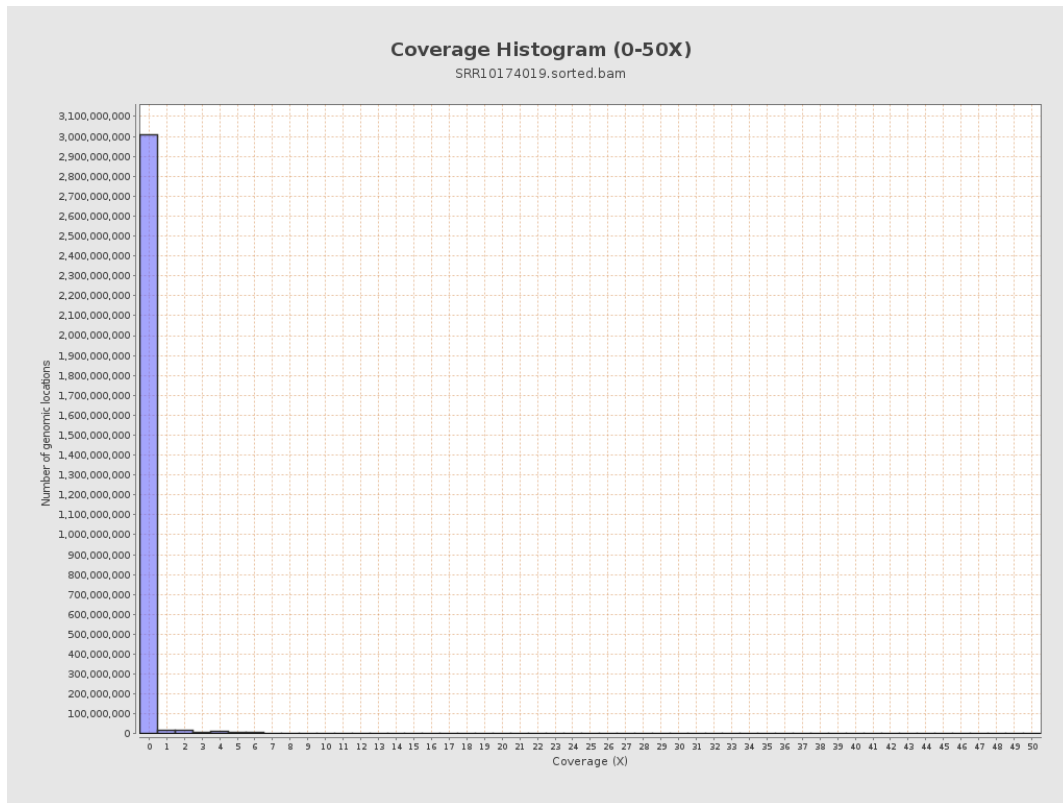
3. Results : Coverage across reference



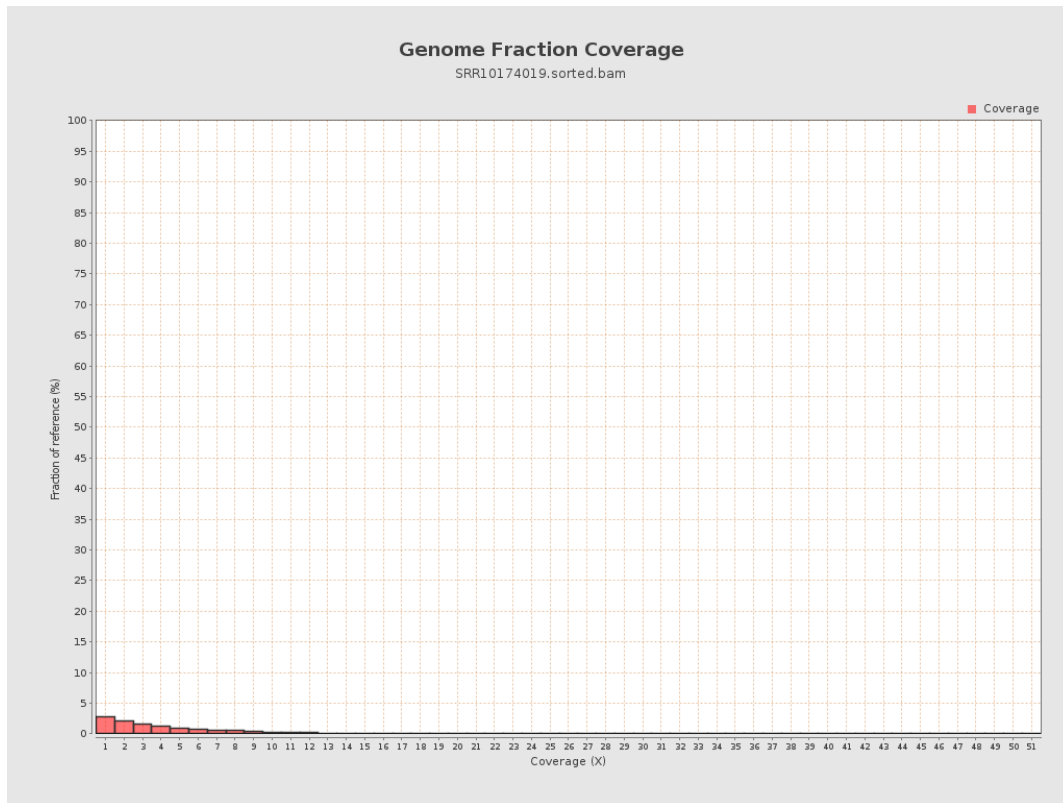
4. Results : Coverage Histogram



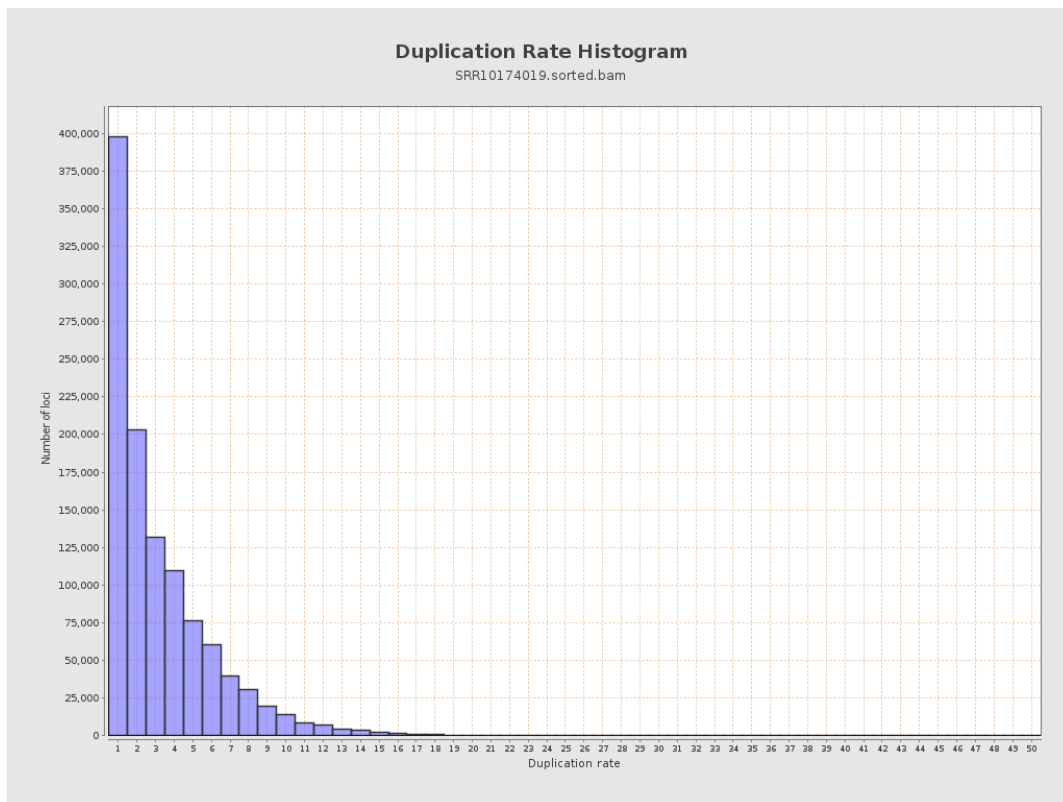
5. Results : Coverage Histogram (0-50X)



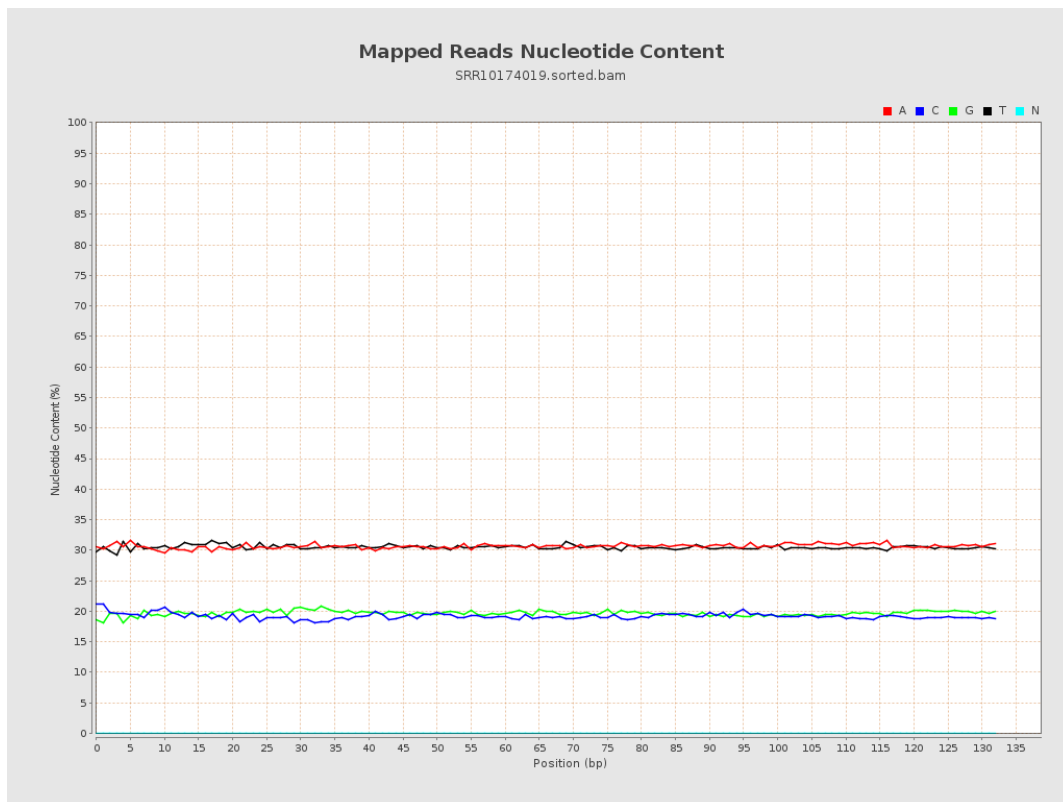
6. Results : Genome Fraction Coverage



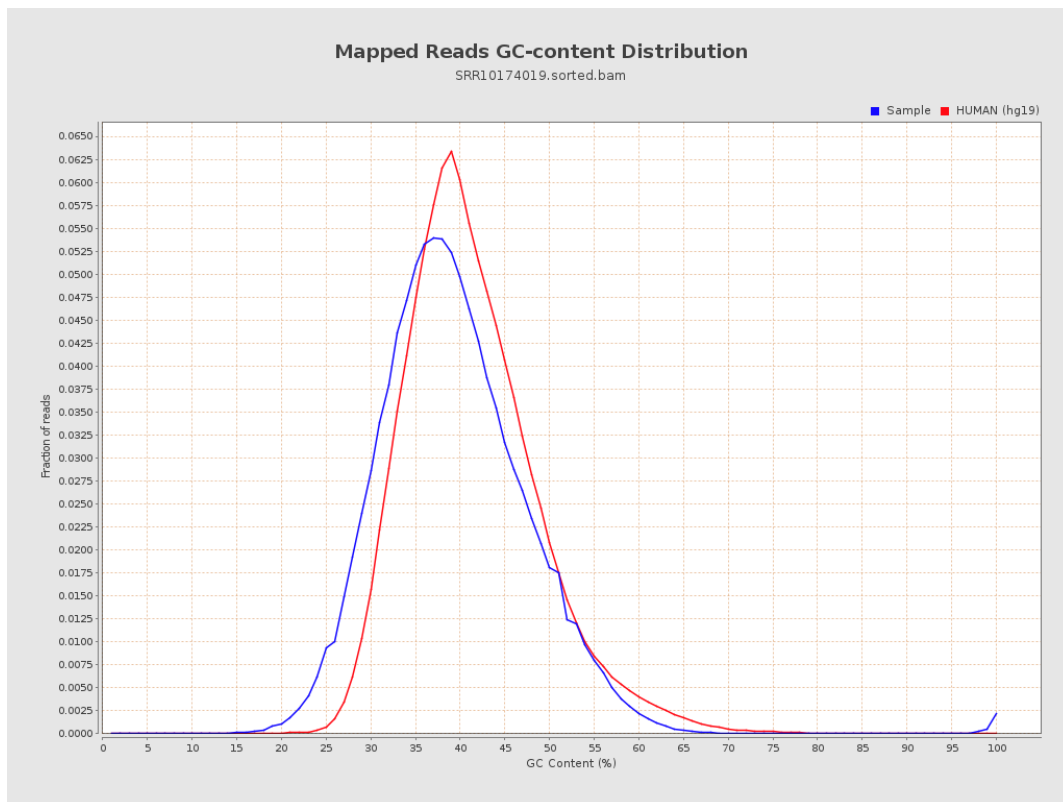
7. Results : Duplication Rate Histogram



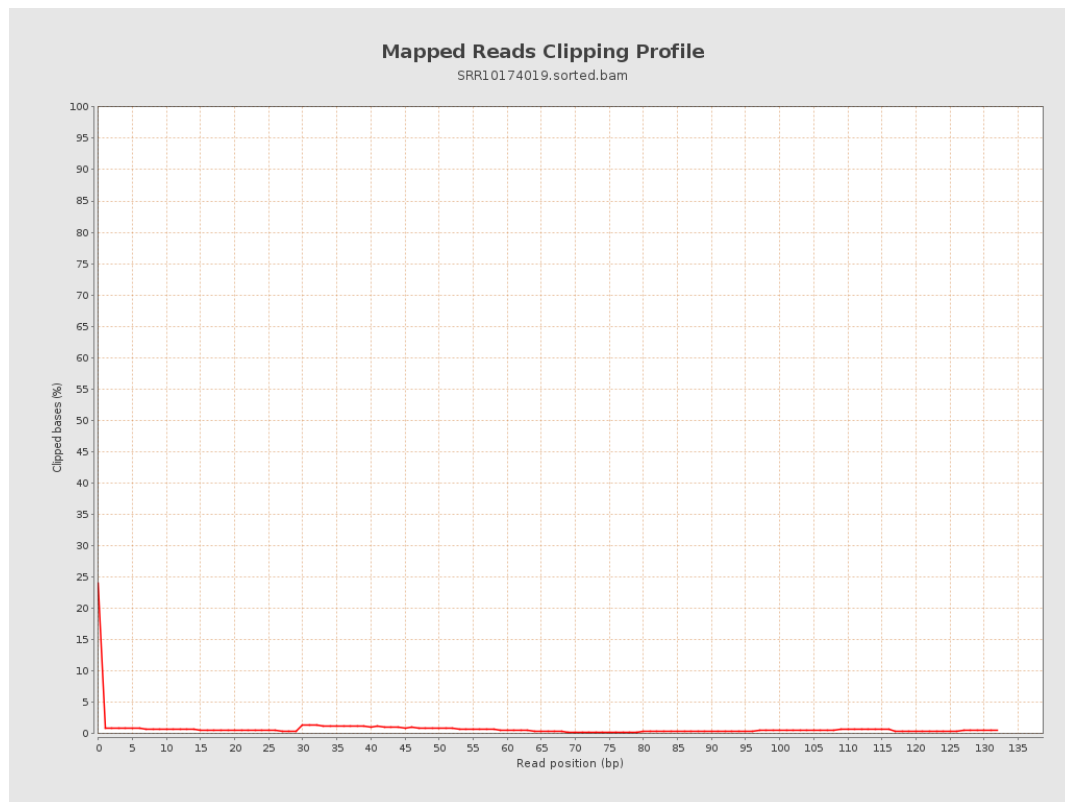
8. Results : Mapped Reads Nucleotide Content



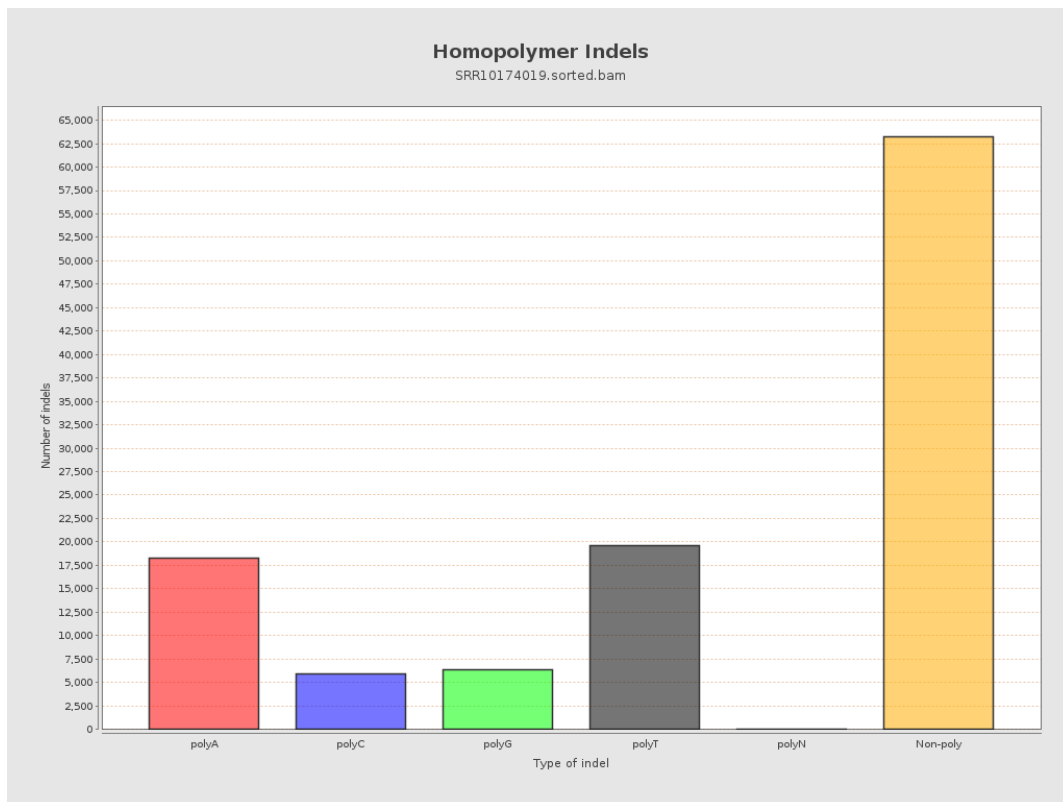
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



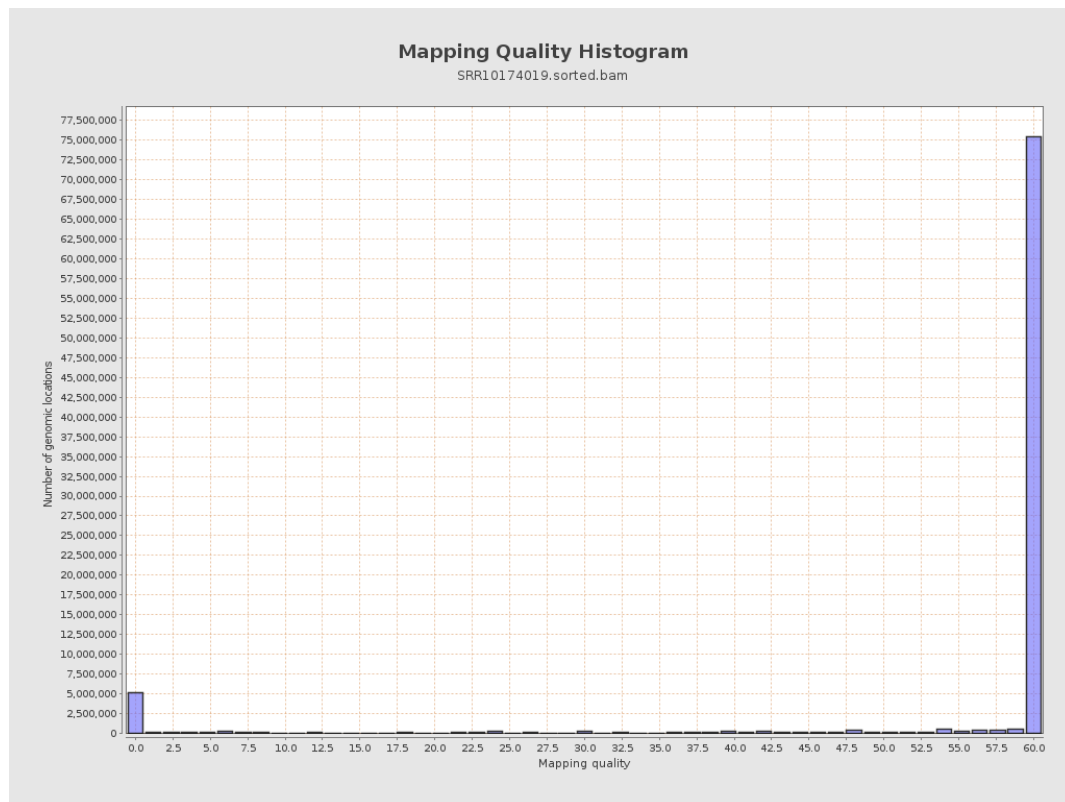
11. Results : Homopolymer Indels



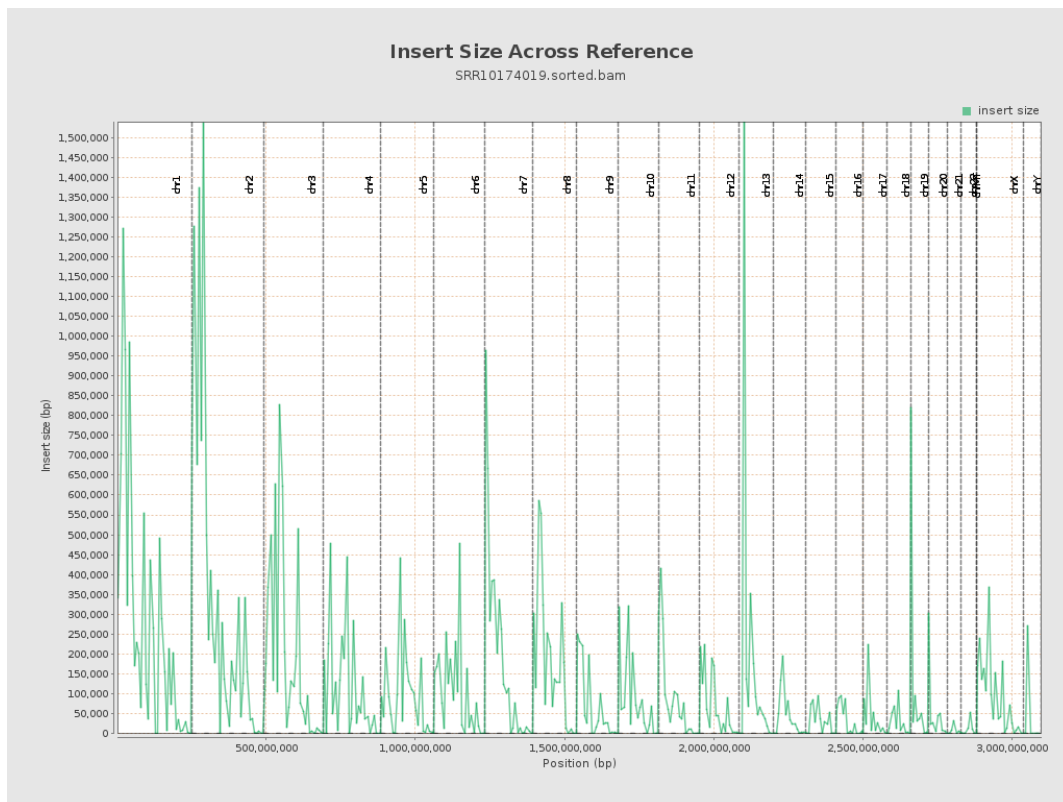
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

