

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 15:30:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264619.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_SRR1264619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264619_1.fastq.gz SRR1264619_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 15:30:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,787,448,744
Mapped reads	1,776,555,689 / 99.39%
Unmapped reads	10,893,055 / 0.61%
Mapped paired reads	1,776,555,689 / 99.39%
Mapped reads, first in pair	891,852,927 / 49.9%
Mapped reads, second in pair	884,702,762 / 49.5%
Mapped reads, both in pair	1,767,997,958 / 98.91%
Mapped reads, singletons	8,557,731 / 0.48%
Secondary alignments	0
Supplementary alignments	10,961,879 / 0.61%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	724,983,196 / 40.56%
Duplication rate	40.44%
Clipped reads	78,134,865 / 4.37%

2.2. ACGT Content

Number/percentage of A's	55,184,942,129 / 30.95%
Number/percentage of C's	33,816,907,324 / 18.97%
Number/percentage of T's	55,053,901,857 / 30.88%
Number/percentage of G's	34,220,771,845 / 19.19%
Number/percentage of N's	11,366,729 / 0.01%

GC Percentage	38.16%
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2.3. Coverage

Mean	57.6057
Standard Deviation	58.0608

2.4. Mapping Quality

Mean Mapping Quality	54.53
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2.5. Insert size

Mean	74,181.42
Standard Deviation	2,615,784.8
P25/Median/P75	308 / 339 / 375

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	798,935,624
Insertions	19,751,427
Mapped reads with at least one insertion	1.1%
Deletions	18,718,770
Mapped reads with at least one deletion	1.03%
Homopolymer indels	48.51%

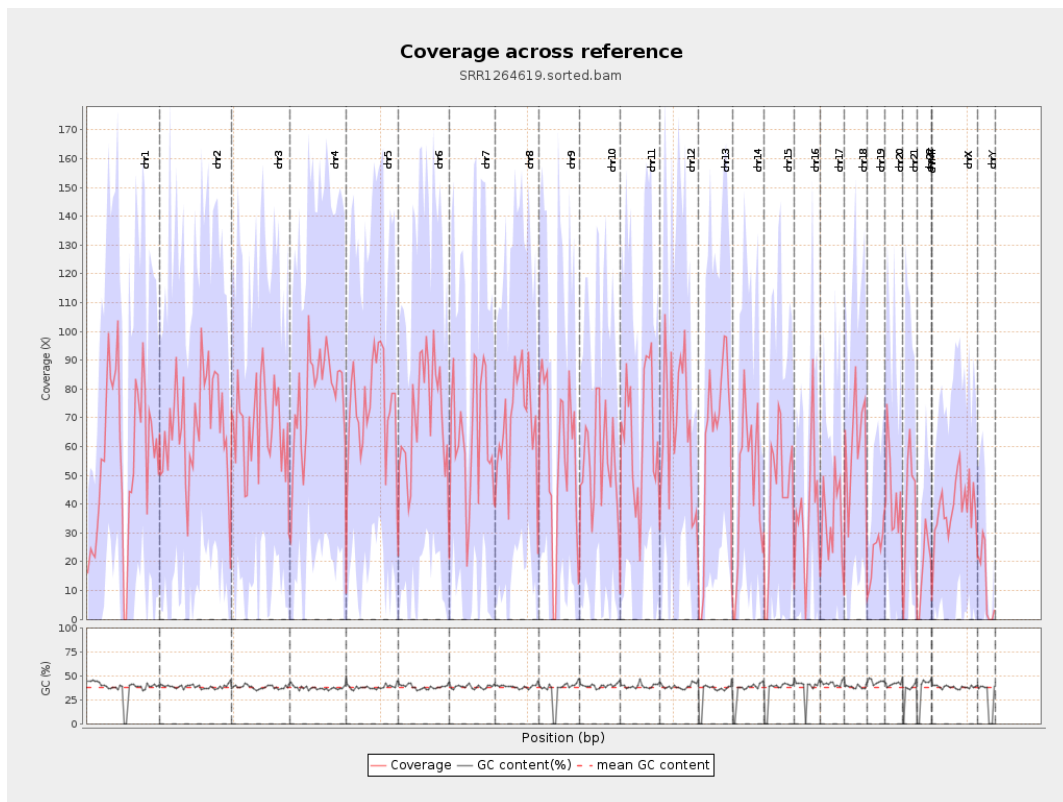
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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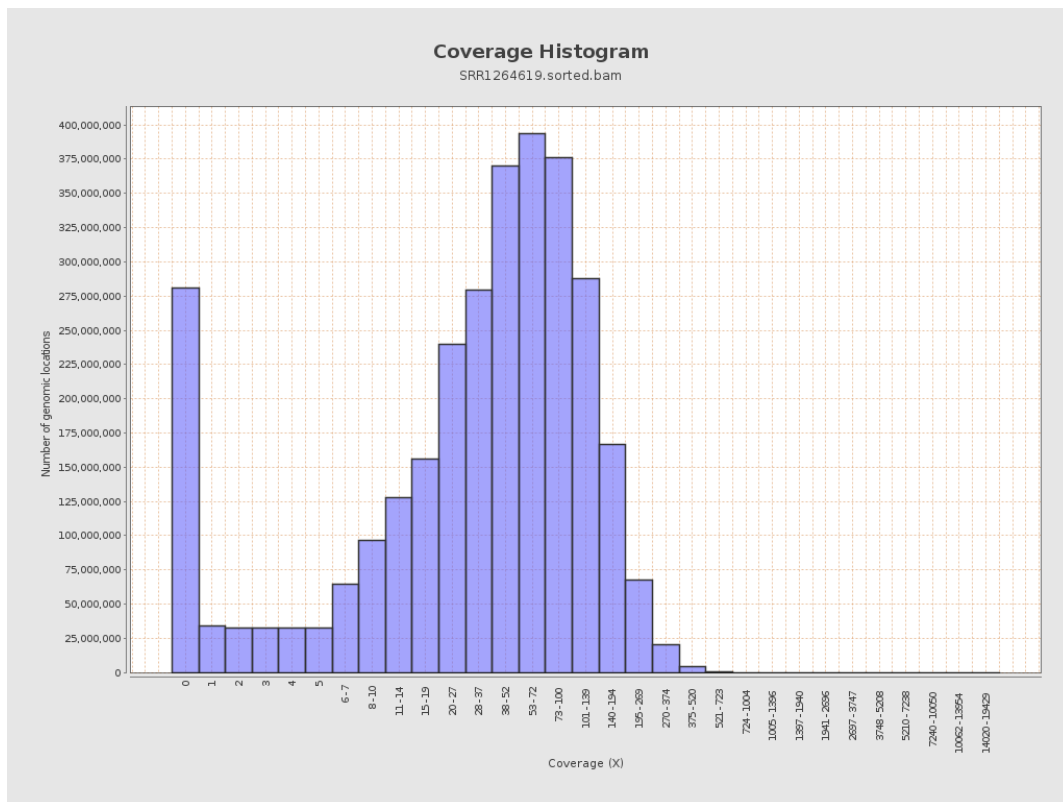
		bases	coverage	deviation
chr1	249250621	14036404336	56.3144	59.8296
chr2	243199373	16346097212	67.2127	59.8201
chr3	198022430	13261829503	66.9714	55.8256
chr4	191154276	14933027841	78.1203	62.632
chr5	180915260	13237095615	73.1674	59.0945
chr6	171115067	12203429241	71.3171	60.4674
chr7	159138663	10022030625	62.9767	60.0463
chr8	146364022	10157024267	69.3956	57.9865
chr9	141213431	7765401478	54.9905	62.8529
chr10	135534747	7464113397	55.0716	51.1471
chr11	135006516	8617022257	63.8267	59.9233
chr12	133851895	8896563092	66.4657	63.207
chr13	115169878	7217539799	62.6686	60.5402
chr14	107349540	5069954880	47.2285	53.1102
chr15	102531392	4539811545	44.2773	54.0558
chr16	90354753	3251061488	35.9811	44.4617
chr17	81195210	2717026919	33.4629	42.7946
chr18	78077248	4828817199	61.8467	52.9826
chr19	59128983	1332154377	22.5296	32.9092
chr20	63025520	2673201613	42.4146	56.1504
chr21	48129895	2011840857	41.8002	59.5852
chr22	51304566	903343664	17.6075	29.2932
chrMT	16571	105783	6.3836	8.9922
chrX	155270560	6094589096	39.2514	39.471

chrY	59373566	750040897	12.6326	27.2258
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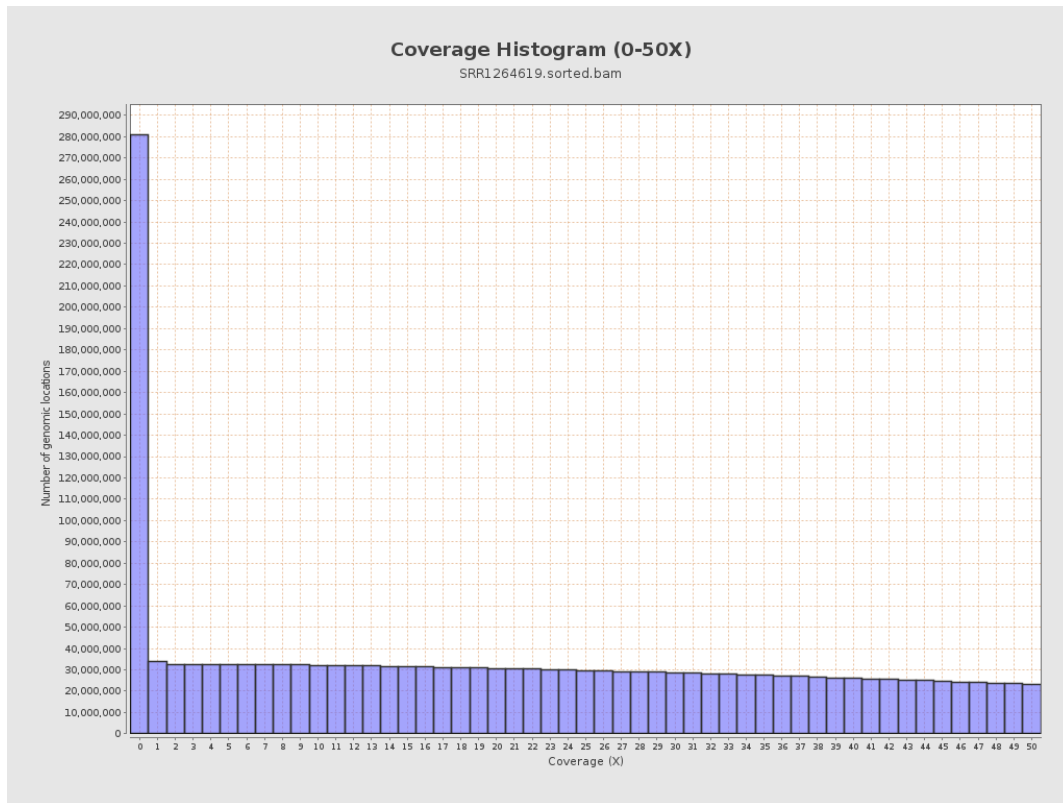
3. Results : Coverage across reference



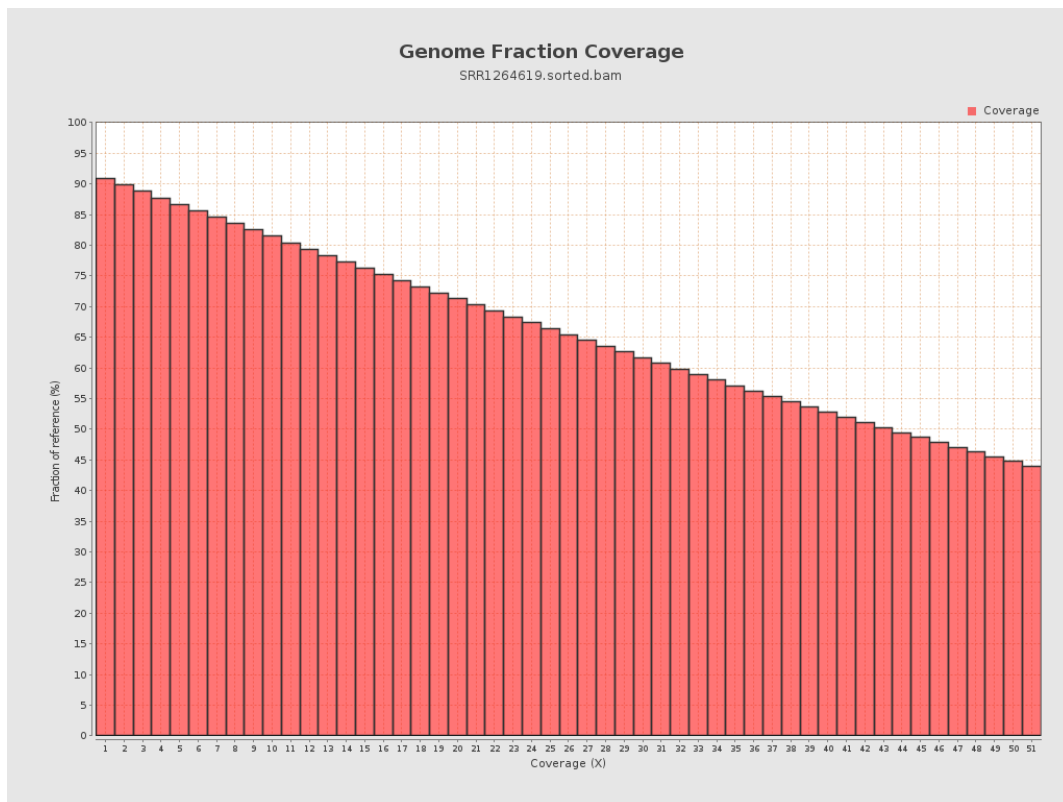
4. Results : Coverage Histogram



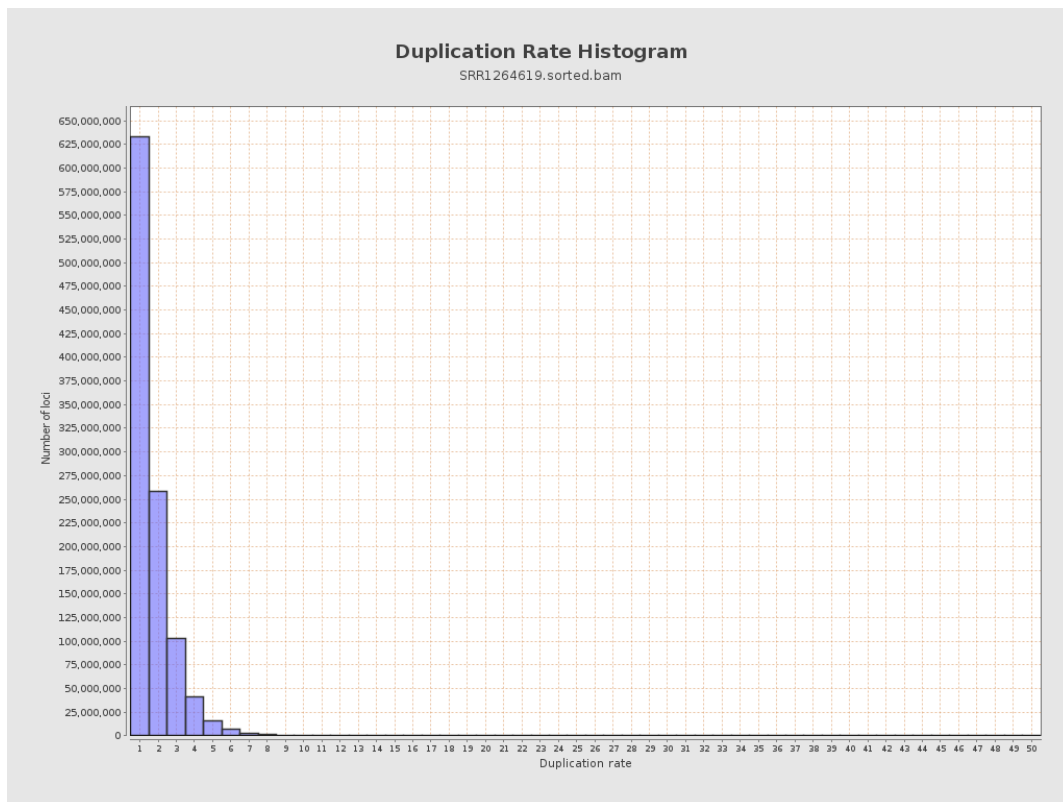
5. Results : Coverage Histogram (0-50X)



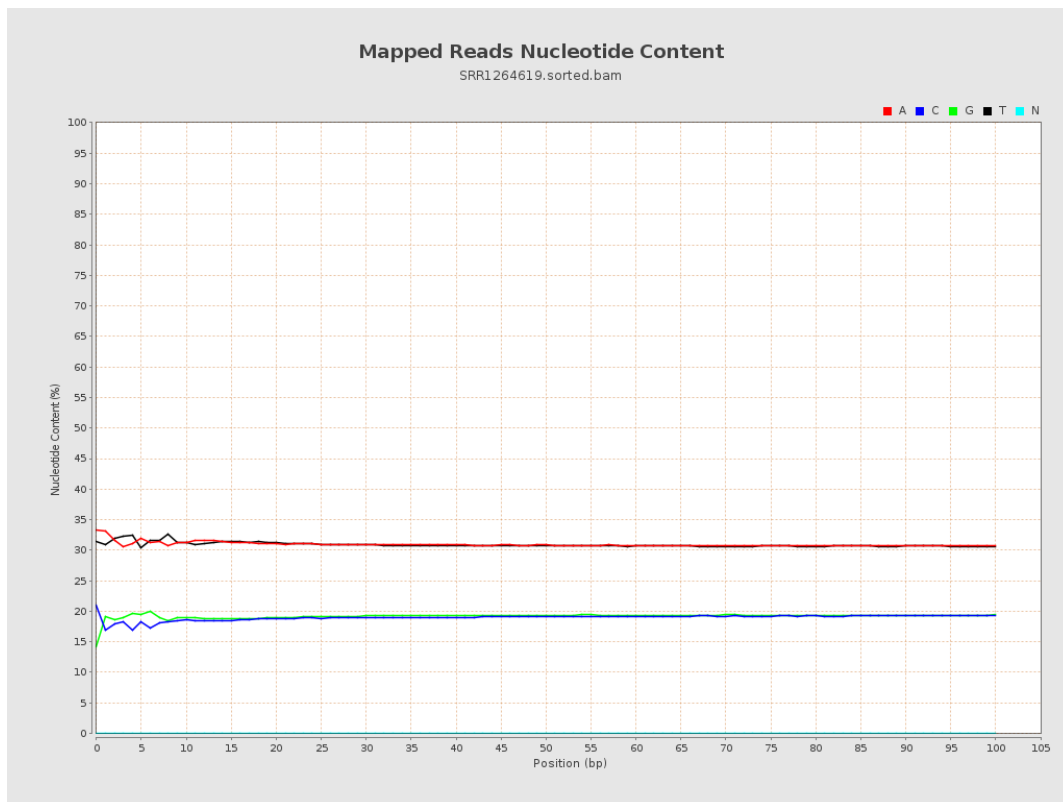
6. Results : Genome Fraction Coverage



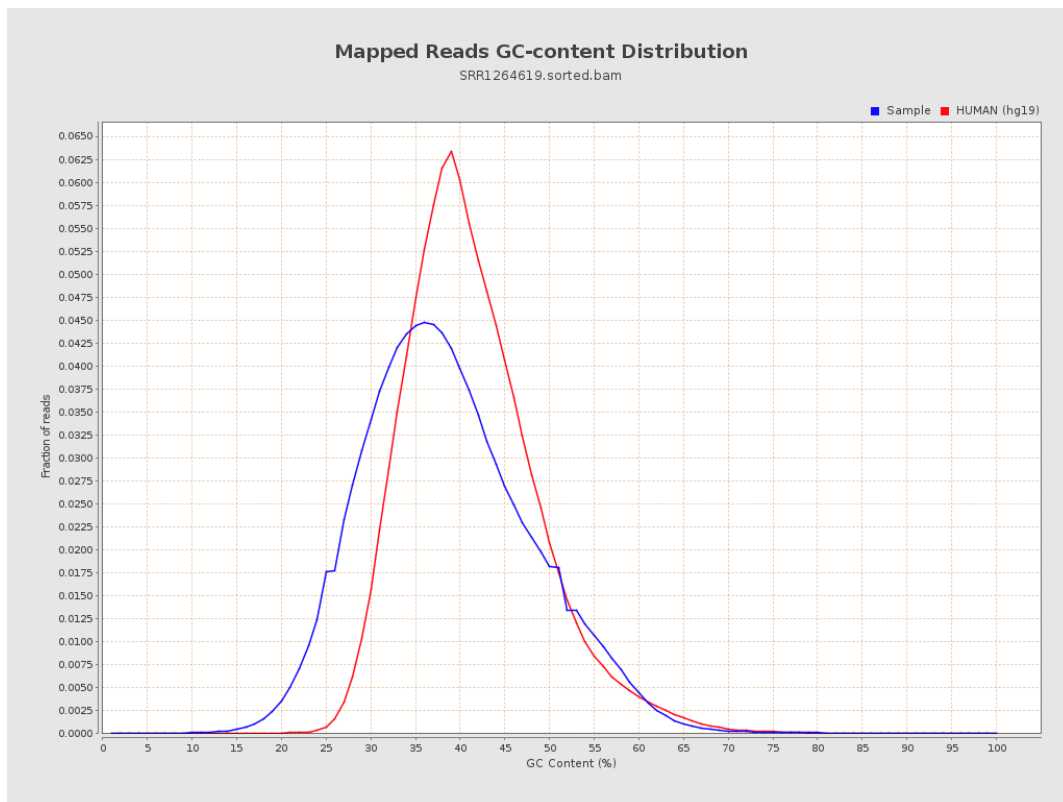
7. Results : Duplication Rate Histogram



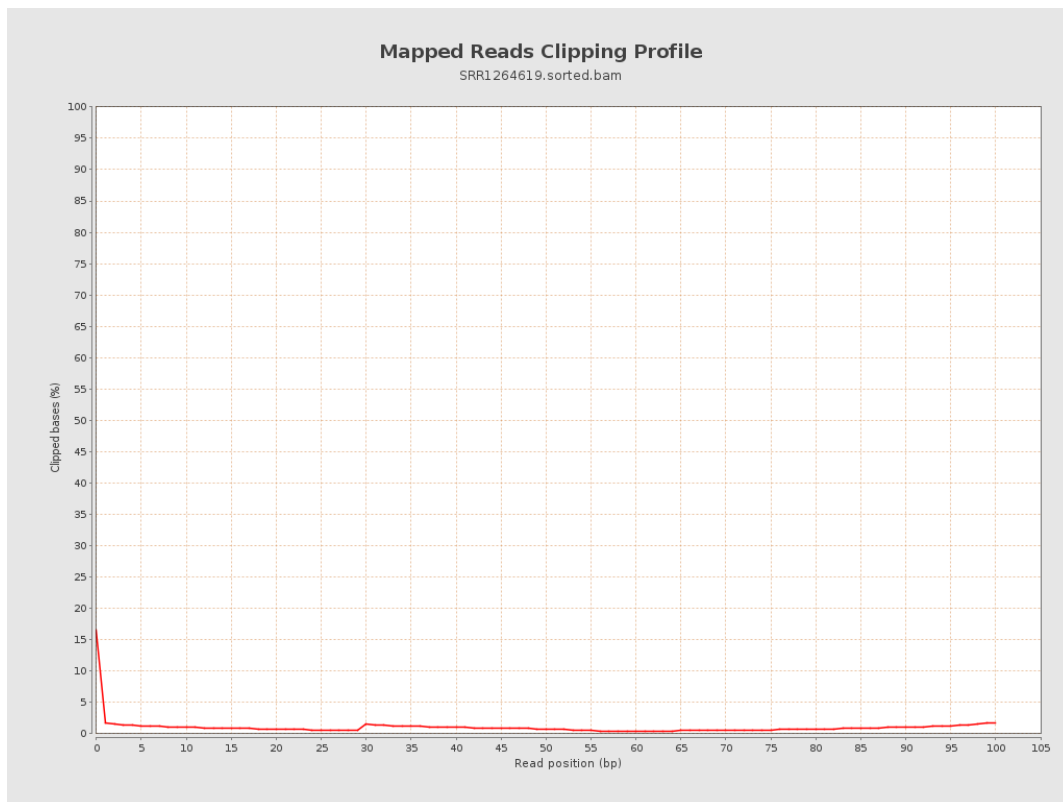
8. Results : Mapped Reads Nucleotide Content



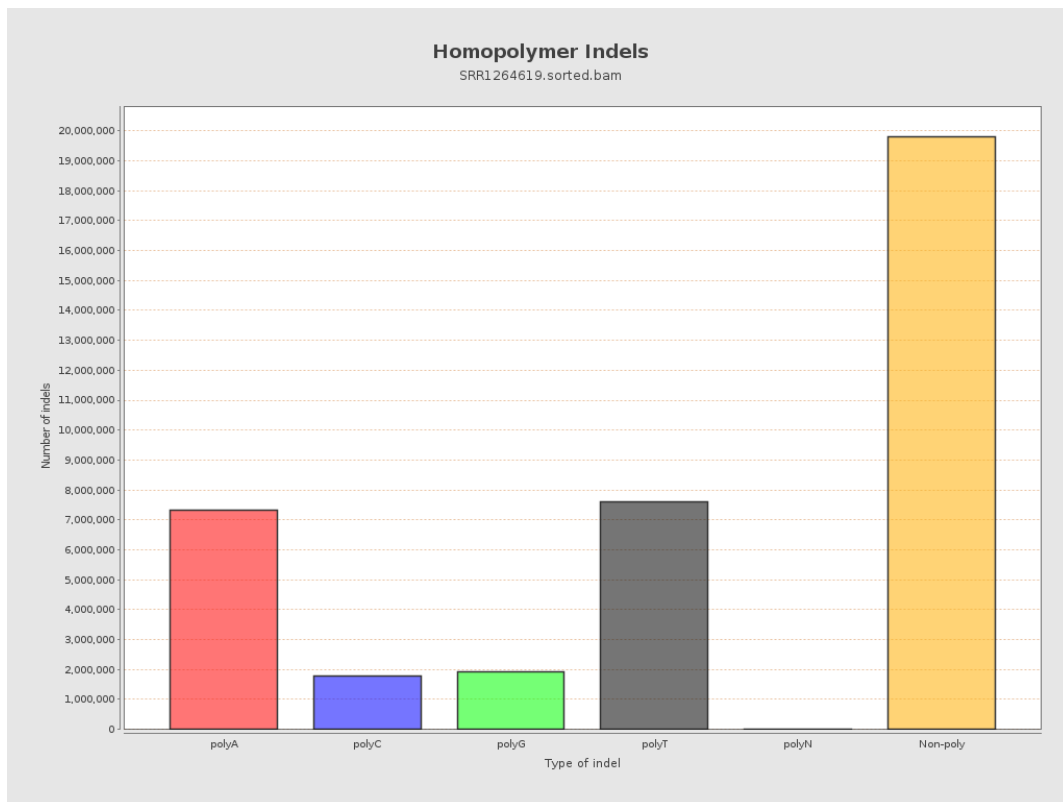
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



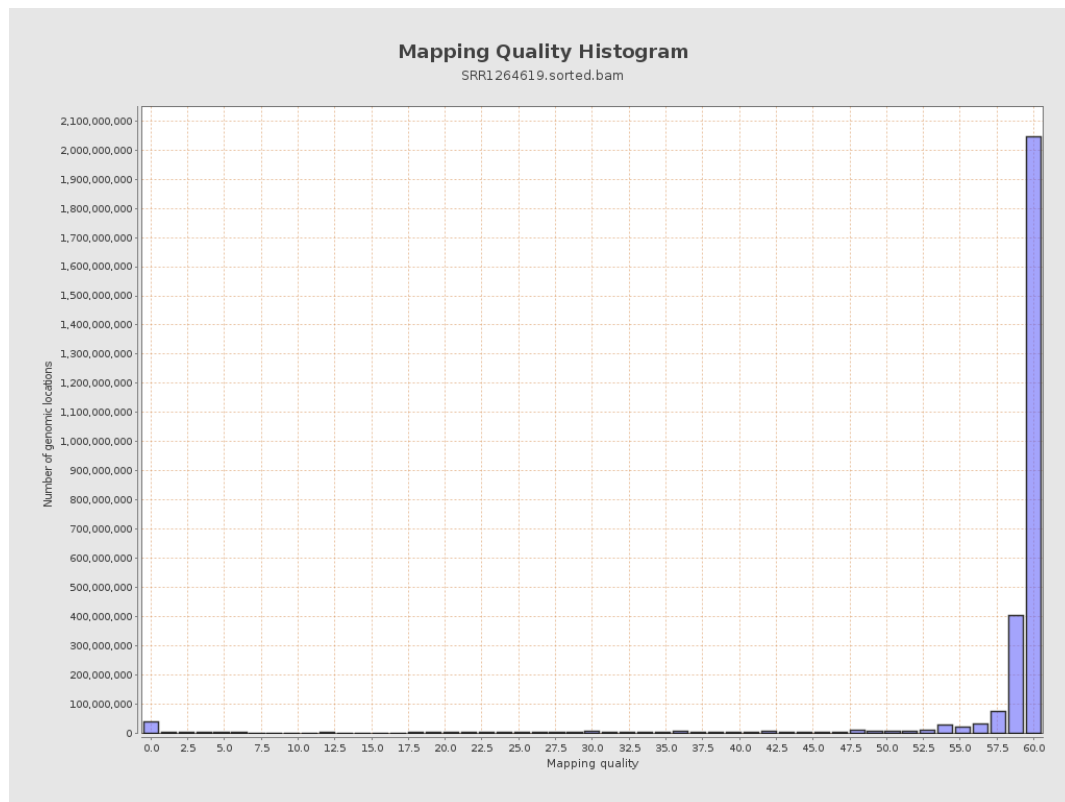
11. Results : Homopolymer Indels



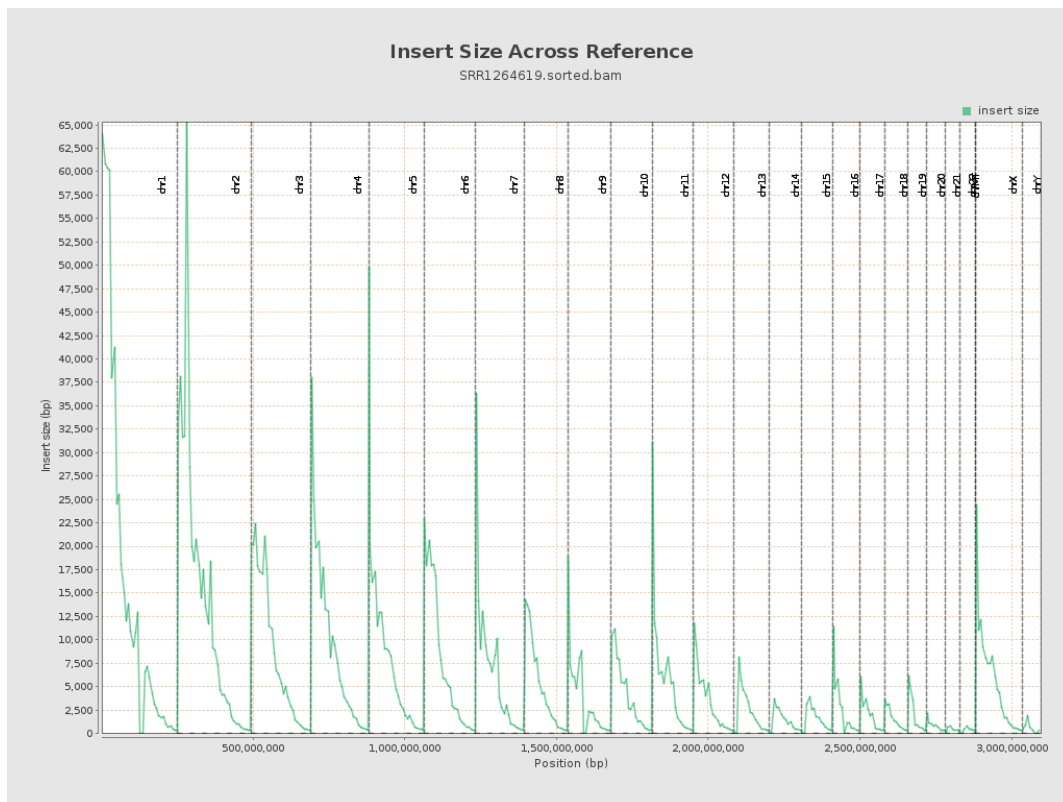
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

