

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 22:16:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264618.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_SRR1264618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264618_1.fastq.gz SRR1264618_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 22:16:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,085,673,012
Mapped reads	1,080,944,839 / 99.56%
Unmapped reads	4,728,173 / 0.44%
Mapped paired reads	1,080,944,839 / 99.56%
Mapped reads, first in pair	541,656,825 / 49.89%
Mapped reads, second in pair	539,288,014 / 49.67%
Mapped reads, both in pair	1,077,555,784 / 99.25%
Mapped reads, singletons	3,389,055 / 0.31%
Secondary alignments	0
Supplementary alignments	11,641,336 / 1.07%
Read min/max/mean length	30 / 100 / 100.44
Duplicated reads (estimated)	357,137,562 / 32.9%
Duplication rate	32.62%
Clipped reads	70,612,503 / 6.5%

2.2. ACGT Content

Number/percentage of A's	33,060,718,185 / 30.82%
Number/percentage of C's	20,454,395,582 / 19.07%
Number/percentage of T's	32,968,906,749 / 30.73%
Number/percentage of G's	20,747,898,711 / 19.34%
Number/percentage of N's	54,029,197 / 0.05%

GC Percentage	38.4%
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2.3. Coverage

Mean	34.6646
Standard Deviation	34.4324

2.4. Mapping Quality

Mean Mapping Quality	54.37
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2.5. Insert size

Mean	139,569.44
Standard Deviation	3,592,175.29
P25/Median/P75	270 / 304 / 341

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	398,933,554
Insertions	11,508,666
Mapped reads with at least one insertion	1.05%
Deletions	11,159,772
Mapped reads with at least one deletion	1.01%
Homopolymer indels	47.26%

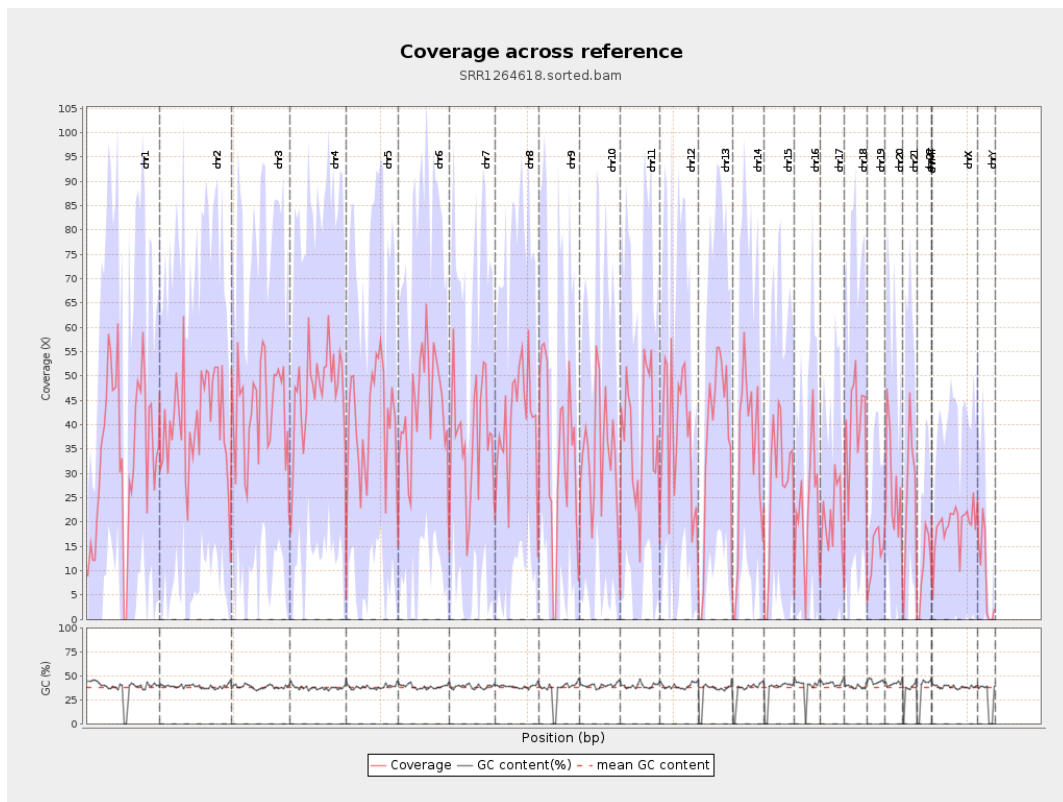
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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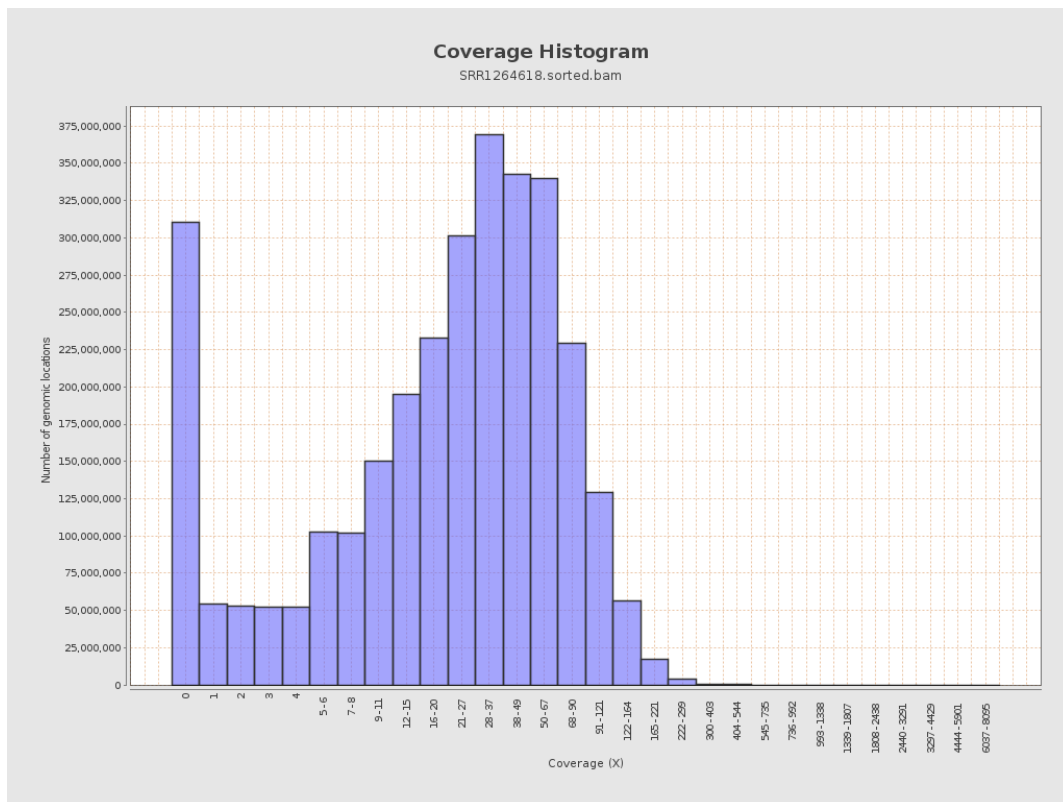
		bases	coverage	deviation
chr1	249250621	8499634578	34.1008	36.2922
chr2	243199373	9777467590	40.2035	34.4085
chr3	198022430	8564495294	43.2501	35.1888
chr4	191154276	9007957147	47.124	35.9352
chr5	180915260	7254473540	40.0987	34.5438
chr6	171115067	7616606465	44.5116	36.1577
chr7	159138663	5914680133	37.1668	34.3424
chr8	146364022	6038459599	41.2564	34.8798
chr9	141213431	4602610501	32.5933	36.8628
chr10	135534747	4591079847	33.8738	31.3513
chr11	135006516	5146185293	38.1181	35.5905
chr12	133851895	5019198594	37.4982	34.5028
chr13	115169878	4265627912	37.0377	34.9481
chr14	107349540	3550111995	33.0706	35.1123
chr15	102531392	2835950679	27.6593	32.0048
chr16	90354753	1984450699	21.9629	27.1122
chr17	81195210	1648961143	20.3086	24.4112
chr18	78077248	3159211159	40.4626	34.1463
chr19	59128983	801756135	13.5594	19.2019
chr20	63025520	1685660702	26.7457	33.2881
chr21	48129895	1296273473	26.9328	33.8611
chr22	51304566	541669411	10.5579	17.7025
chrMT	16571	353603	21.3387	8.0159
chrX	155270560	2992108510	19.2703	21.3473

chrY	59373566	516000397	8.6907	18.1249
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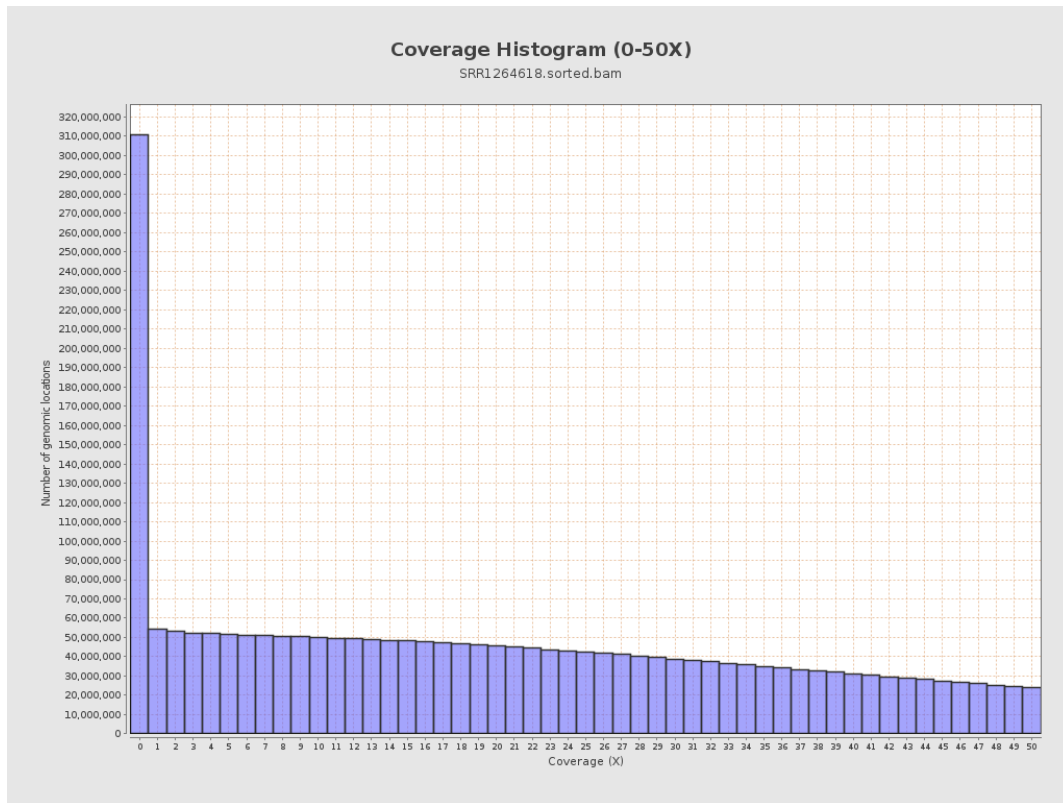
3. Results : Coverage across reference



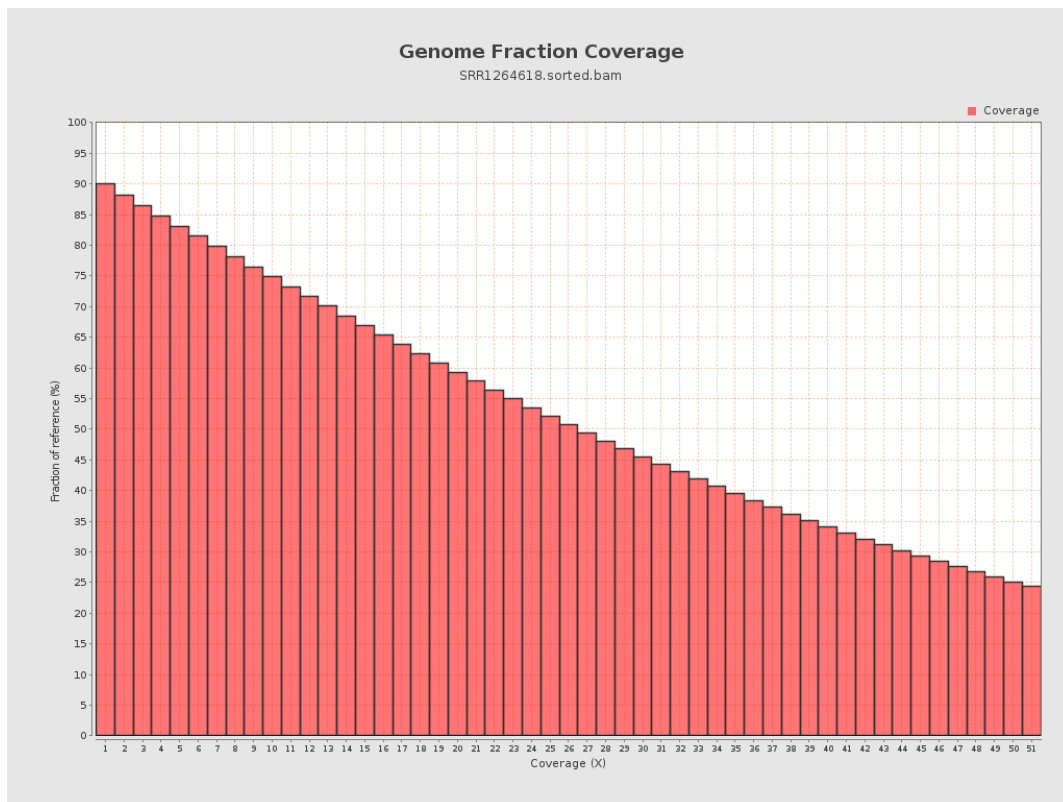
4. Results : Coverage Histogram



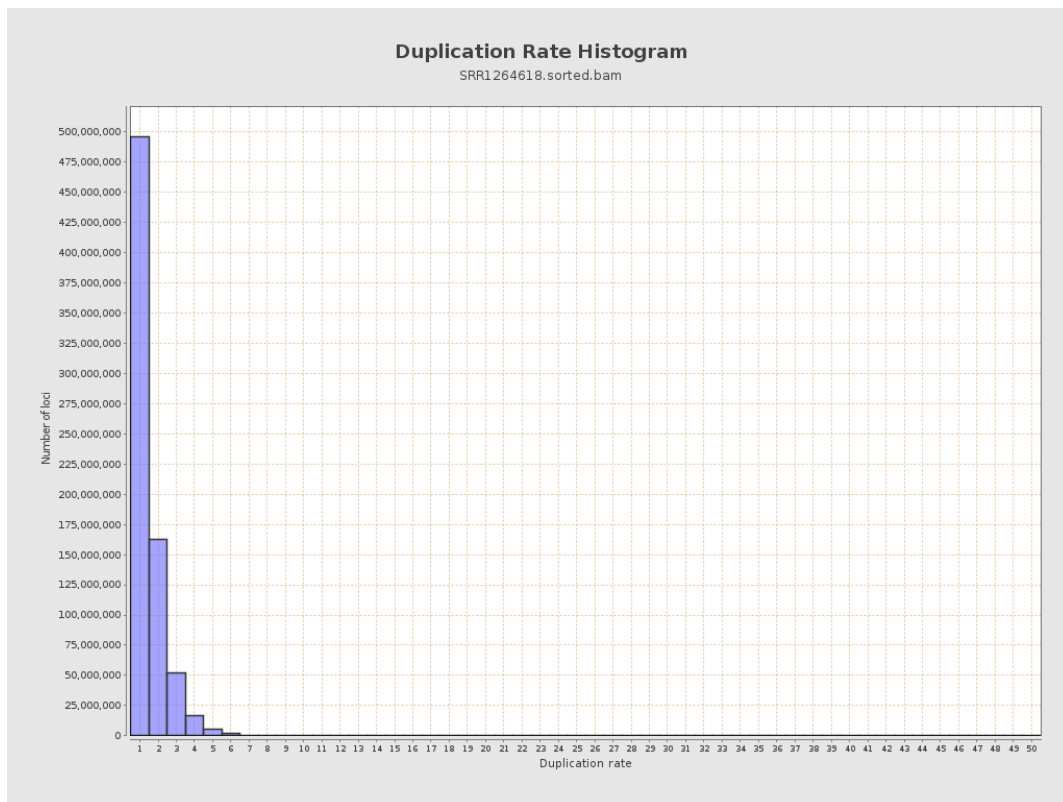
5. Results : Coverage Histogram (0-50X)



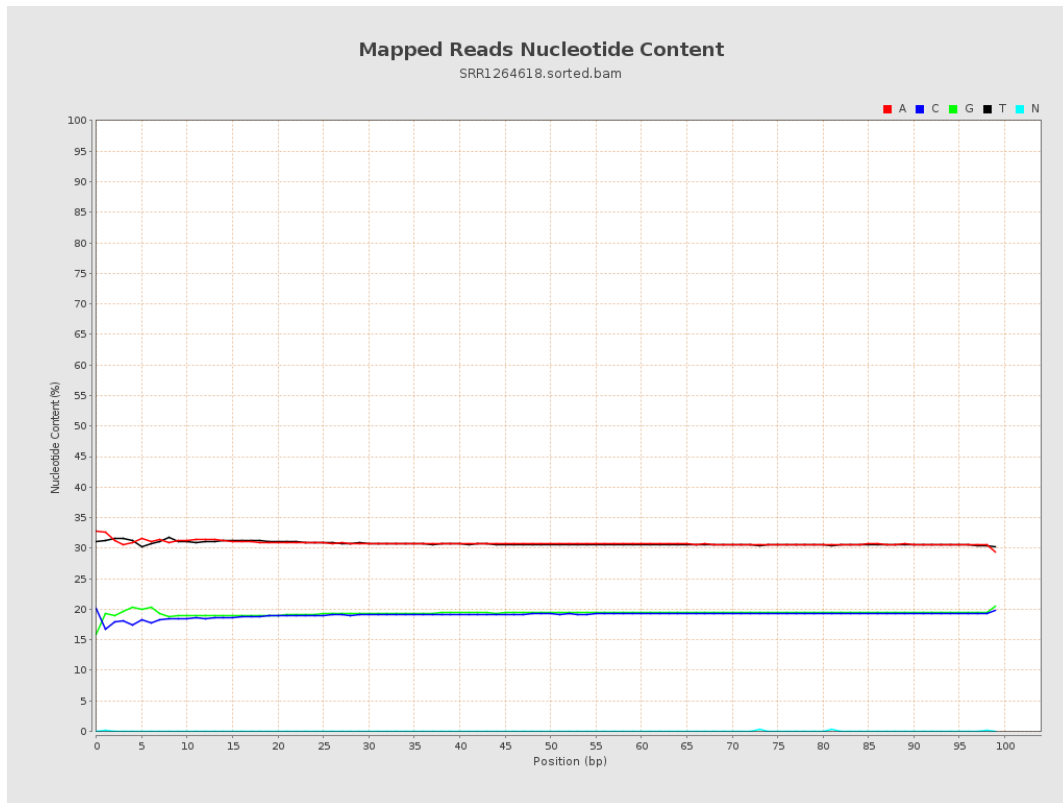
6. Results : Genome Fraction Coverage



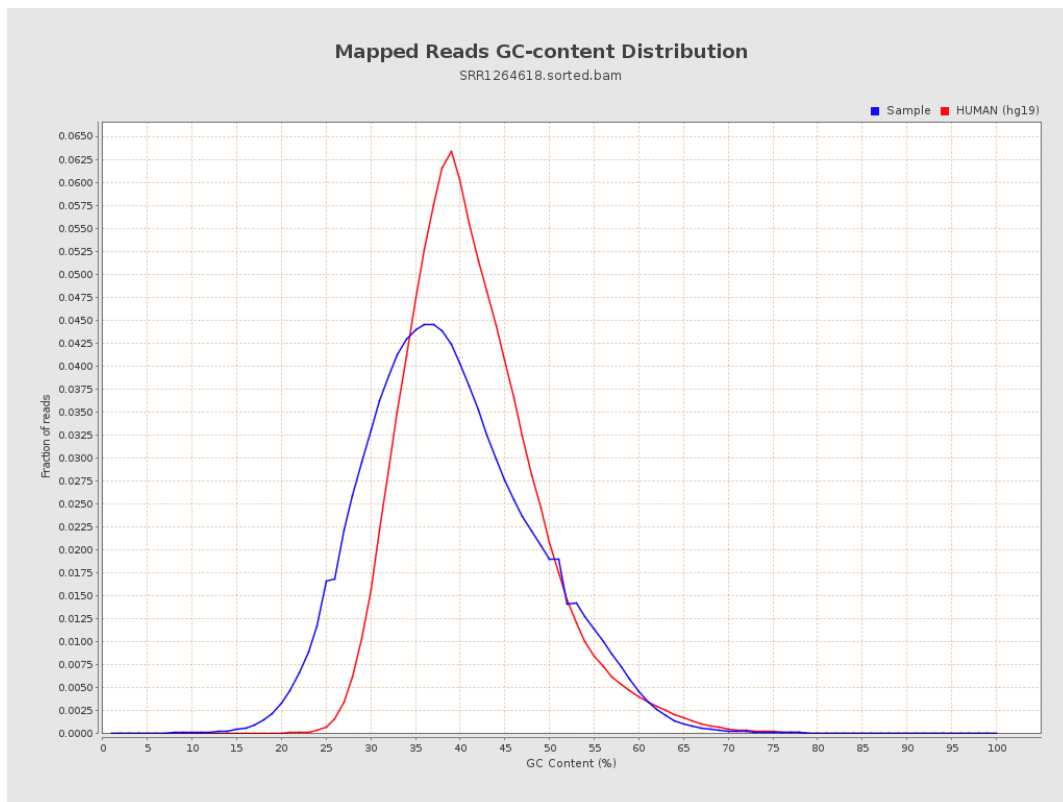
7. Results : Duplication Rate Histogram



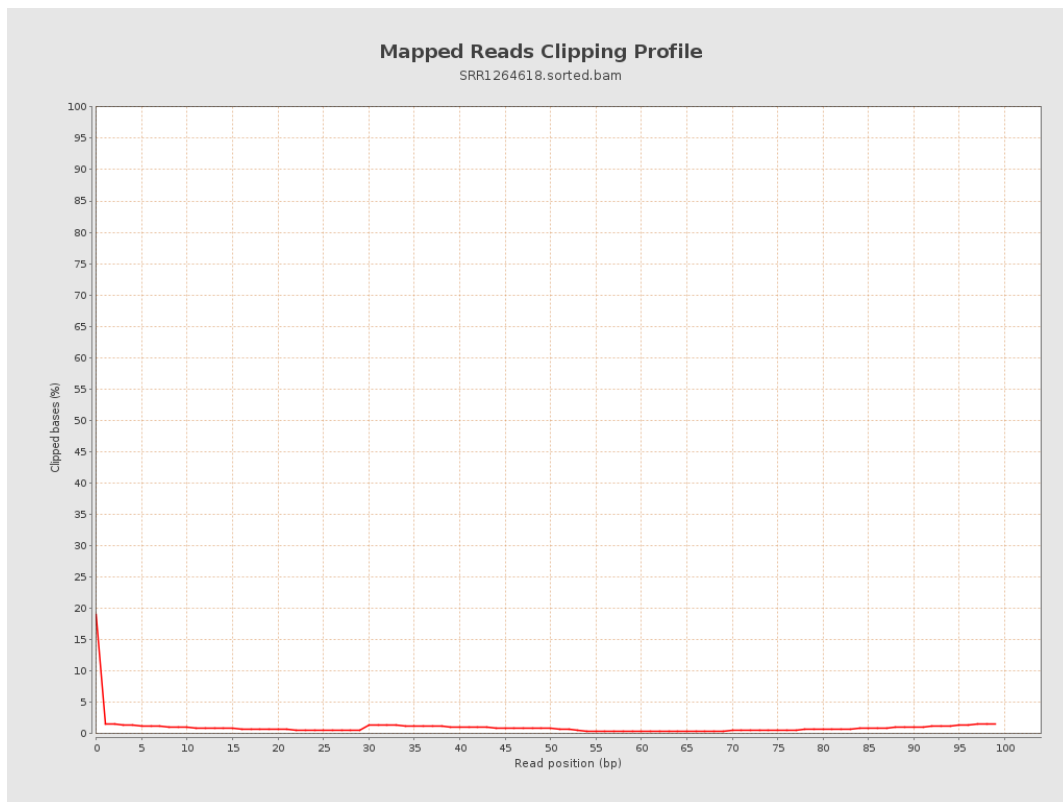
8. Results : Mapped Reads Nucleotide Content



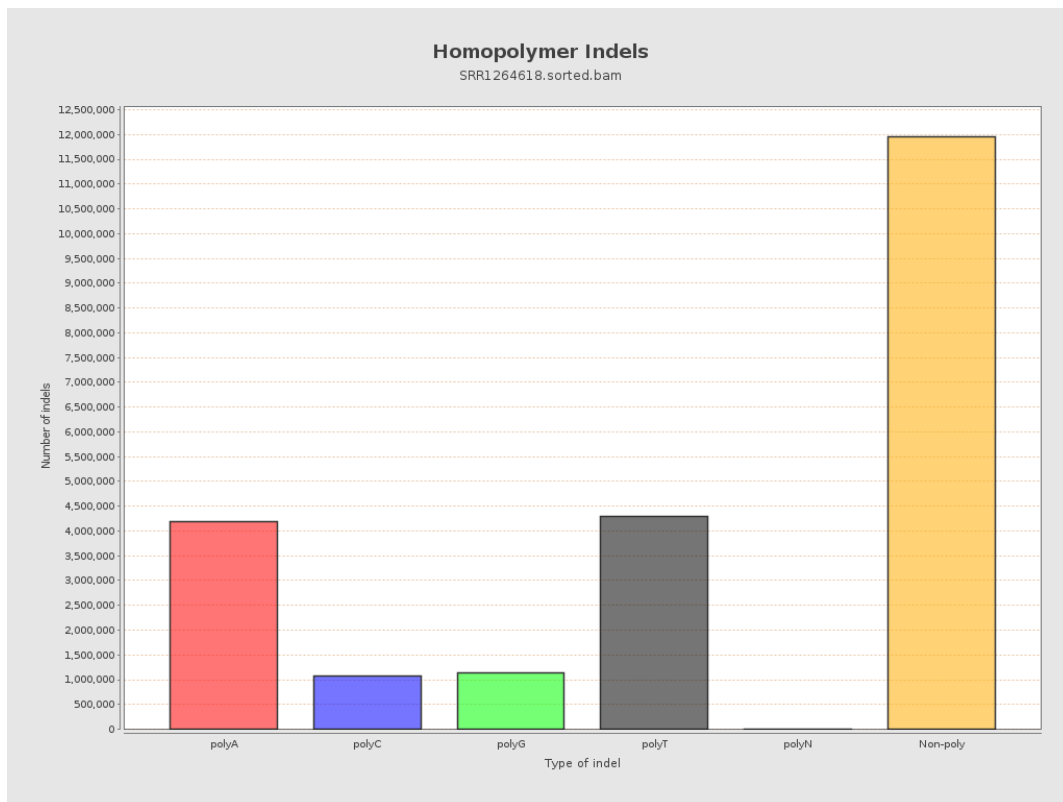
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



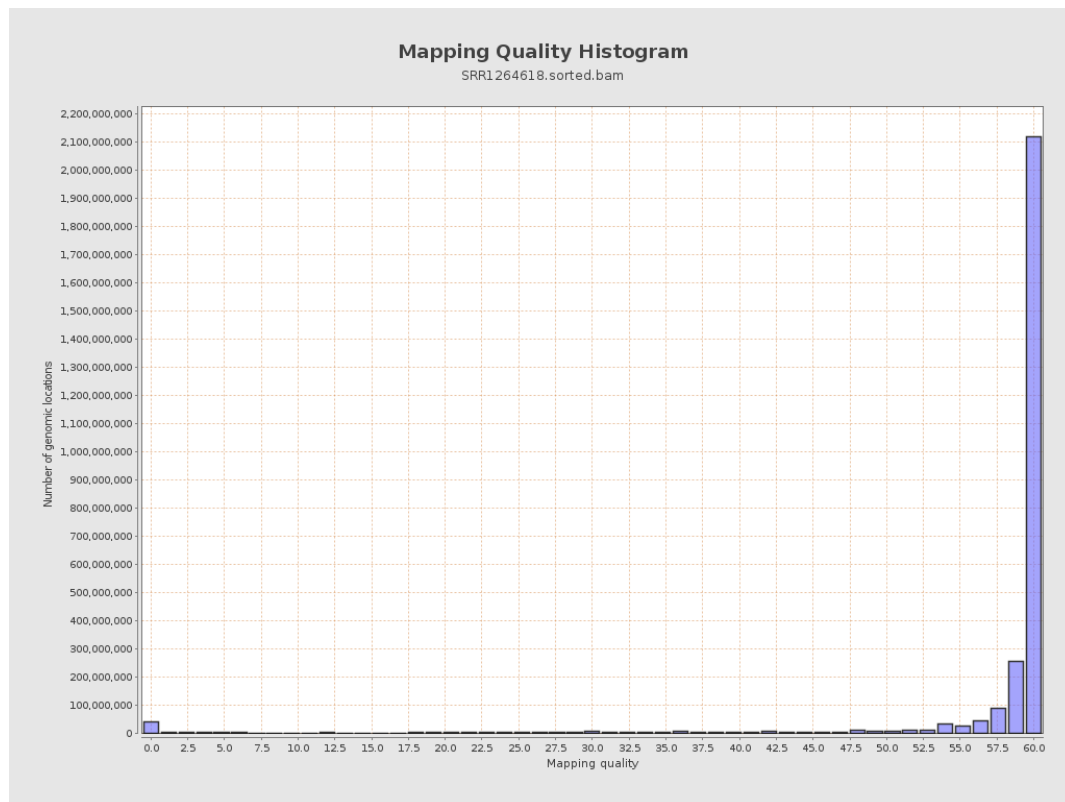
11. Results : Homopolymer Indels



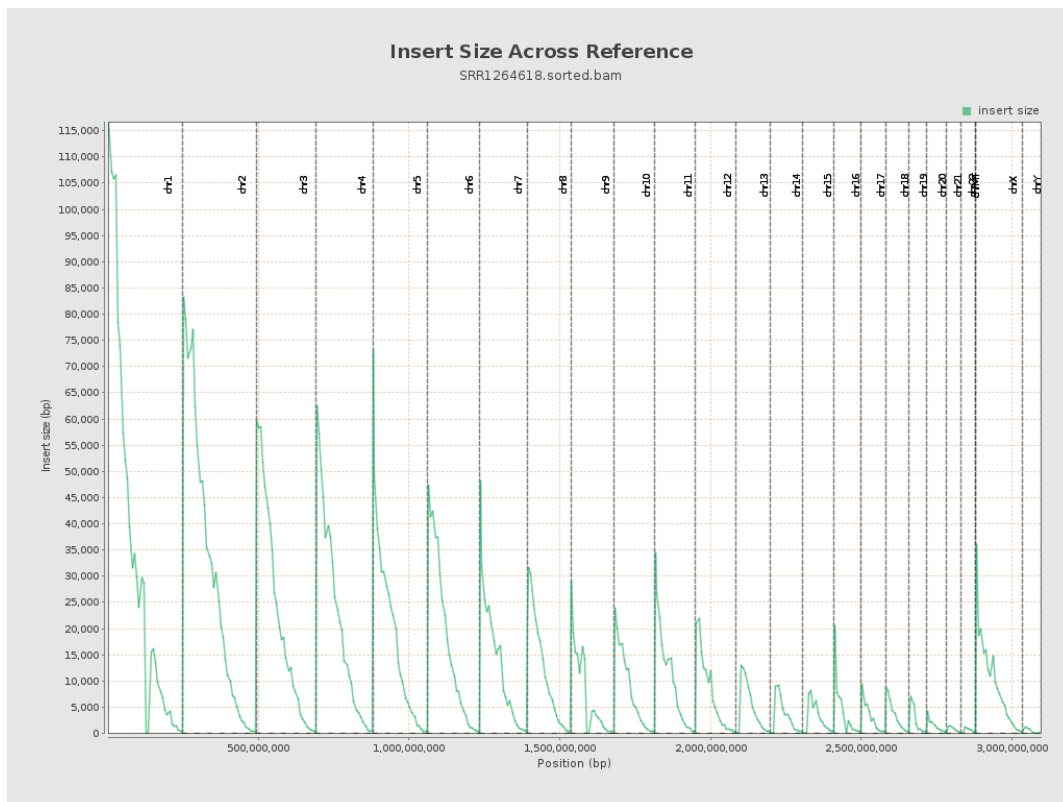
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

