

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 05:59:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617419.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_SRR617419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617419_1.fastq.gz SRR617419_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 05:59:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,305,443 / 94.7%
Unmapped reads	1,694,557 / 5.3%
Mapped paired reads	30,305,443 / 94.7%
Mapped reads, first in pair	15,331,113 / 47.91%
Mapped reads, second in pair	14,974,330 / 46.79%
Mapped reads, both in pair	29,705,800 / 92.83%
Mapped reads, singletons	599,643 / 1.87%
Secondary alignments	0
Supplementary alignments	501,291 / 1.57%
Read min/max/mean length	30 / 100 / 100.64
Duplicated reads (estimated)	1,447,853 / 4.52%
Duplication rate	4.26%
Clipped reads	3,067,162 / 9.58%

2.2. ACGT Content

Number/percentage of A's	888,941,986 / 29.76%
Number/percentage of C's	601,886,046 / 20.15%
Number/percentage of T's	882,525,043 / 29.55%
Number/percentage of G's	613,012,882 / 20.53%
Number/percentage of N's	218,031 / 0.01%

GC Percentage	40.68%
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2.3. Coverage

Mean	0.965
Standard Deviation	2.9746

2.4. Mapping Quality

Mean Mapping Quality	53.9
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2.5. Insert size

Mean	60,414.37
Standard Deviation	2,358,857.46
P25/Median/P75	173 / 214 / 281

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	24,160,433
Insertions	248,202
Mapped reads with at least one insertion	0.81%
Deletions	295,912
Mapped reads with at least one deletion	0.96%
Homopolymer indels	45.15%

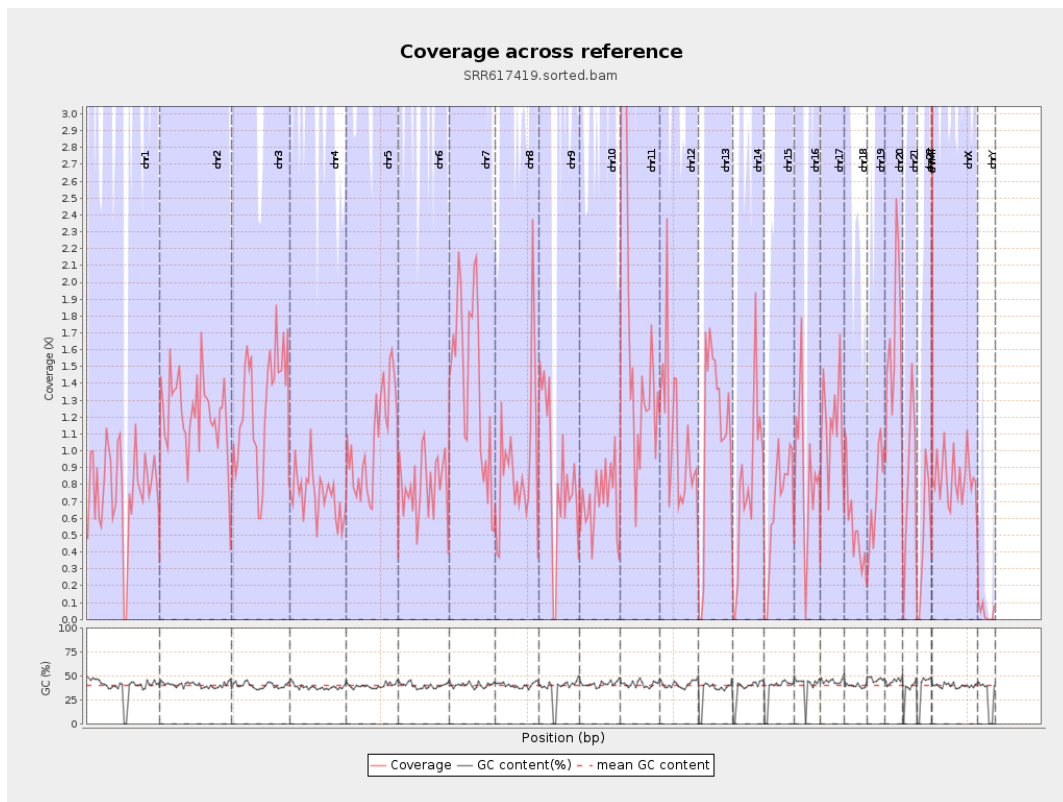
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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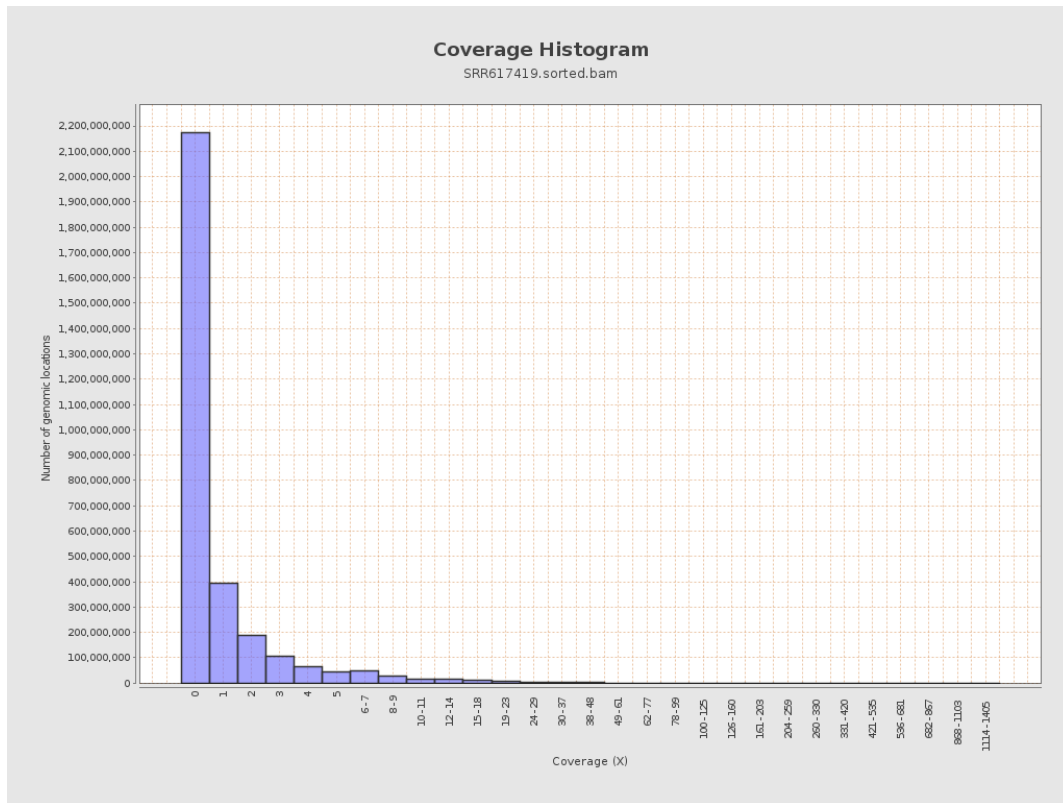
		bases	coverage	deviation
chr1	249250621	192625108	0.7728	2.7974
chr2	243199373	297827691	1.2246	3.1652
chr3	198022430	251597313	1.2705	3.4695
chr4	191154276	142583988	0.7459	2.2916
chr5	180915260	190685946	1.054	2.8957
chr6	171115067	136508706	0.7978	2.6247
chr7	159138663	223099158	1.4019	3.2777
chr8	146364022	131804151	0.9005	3.2968
chr9	141213431	119286601	0.8447	2.6356
chr10	135534747	95801073	0.7068	2.462
chr11	135006516	221905609	1.6437	3.8848
chr12	133851895	142411150	1.0639	2.8454
chr13	115169878	128909674	1.1193	2.7975
chr14	107349540	86915571	0.8097	2.951
chr15	102531392	68795574	0.671	2.4157
chr16	90354753	75870012	0.8397	3.3908
chr17	81195210	93023850	1.1457	3.7953
chr18	78077248	42643820	0.5462	2.0234
chr19	59128983	43506471	0.7358	2.4
chr20	63025520	102970696	1.6338	4.8501
chr21	48129895	40668168	0.845	2.5285
chr22	51304566	24517038	0.4779	2.1344
chrMT	16571	188210	11.3578	6.2611
chrX	155270560	130689503	0.8417	2.5975

chrY	59373566	2421602	0.0408	0.6541
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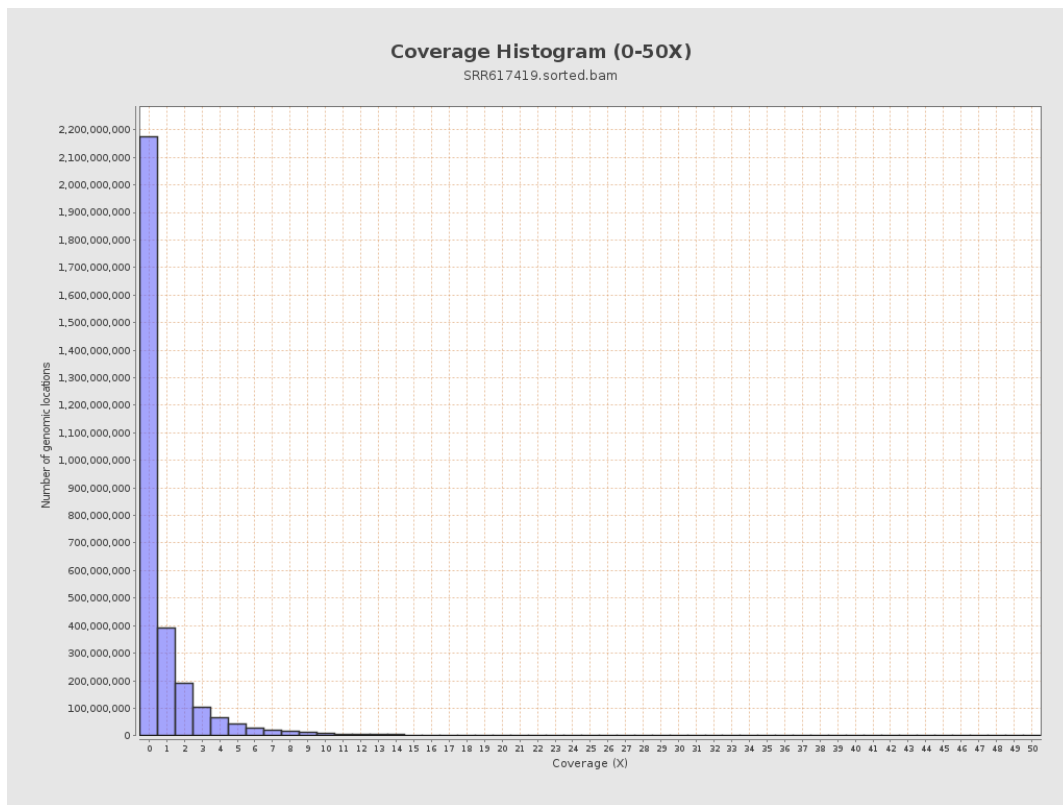
3. Results : Coverage across reference



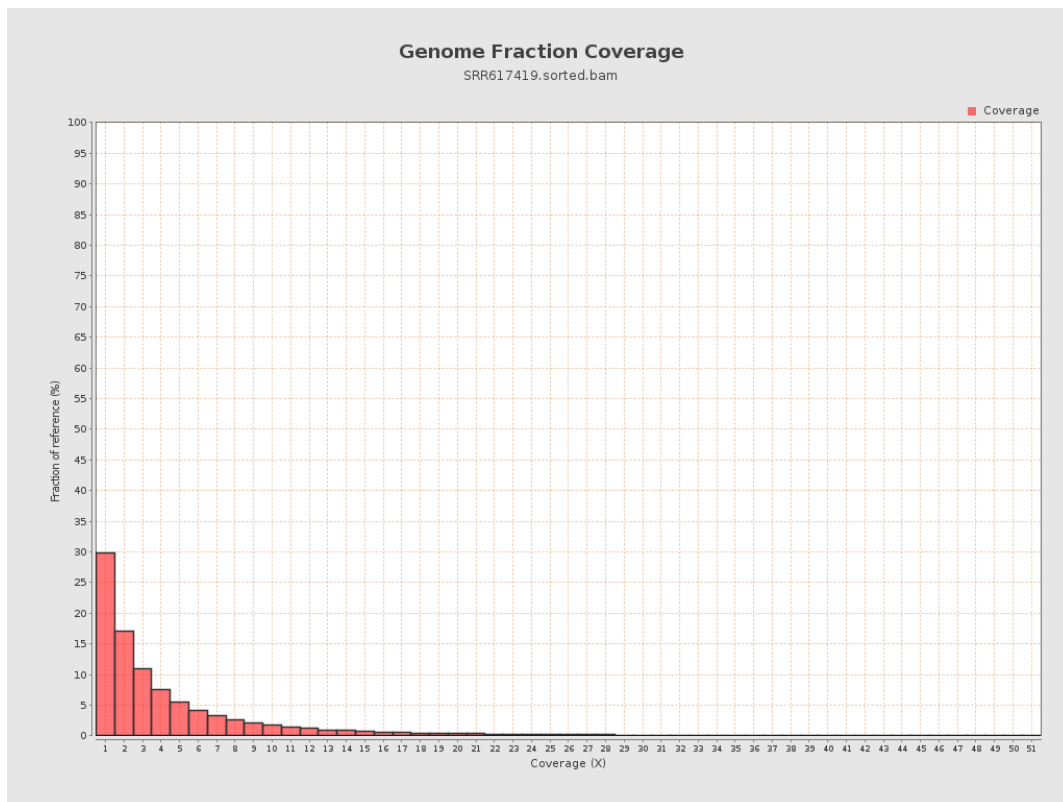
4. Results : Coverage Histogram



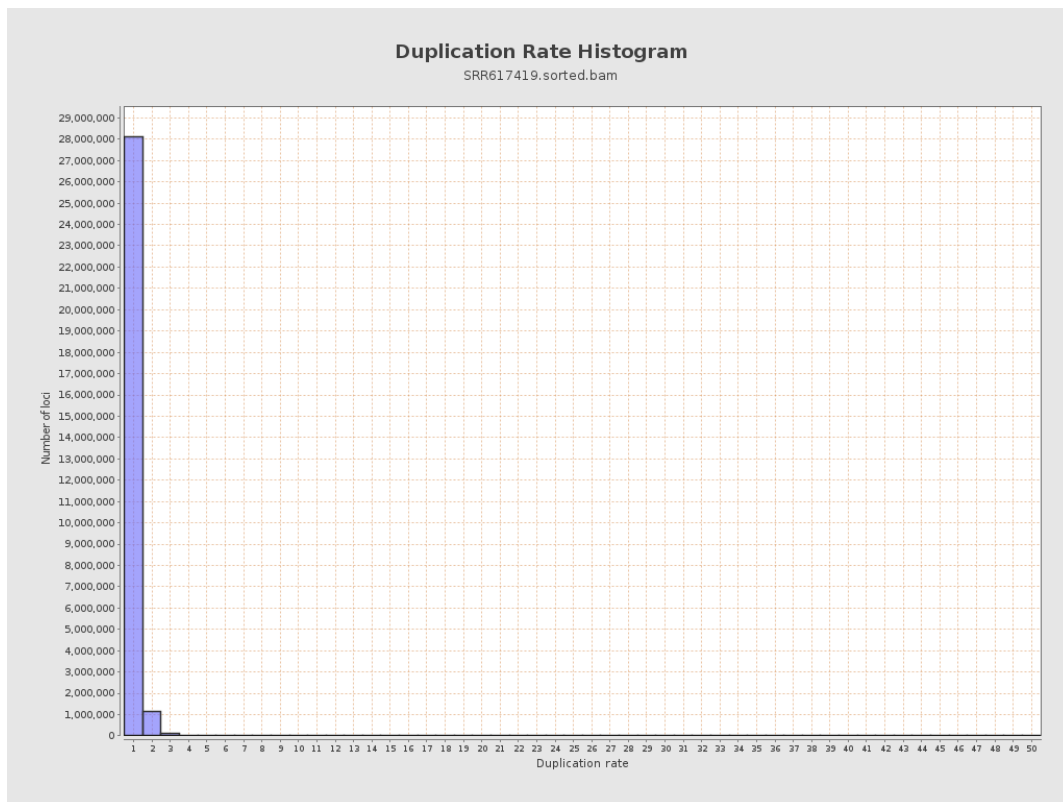
5. Results : Coverage Histogram (0-50X)



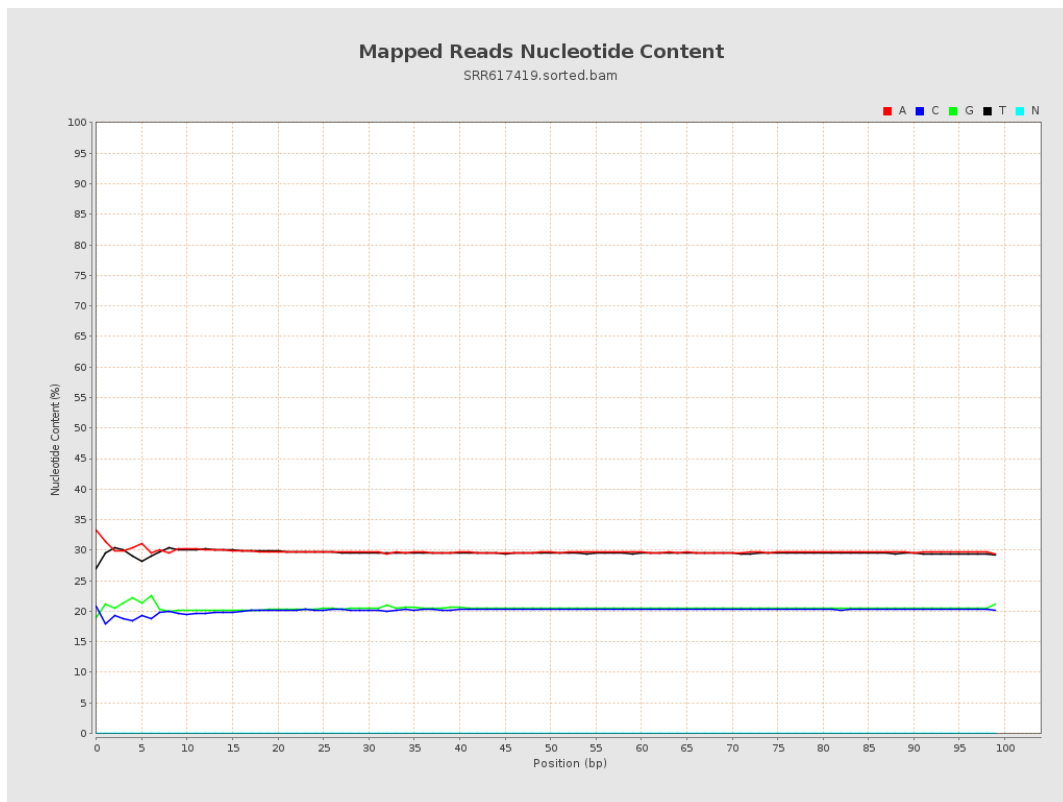
6. Results : Genome Fraction Coverage



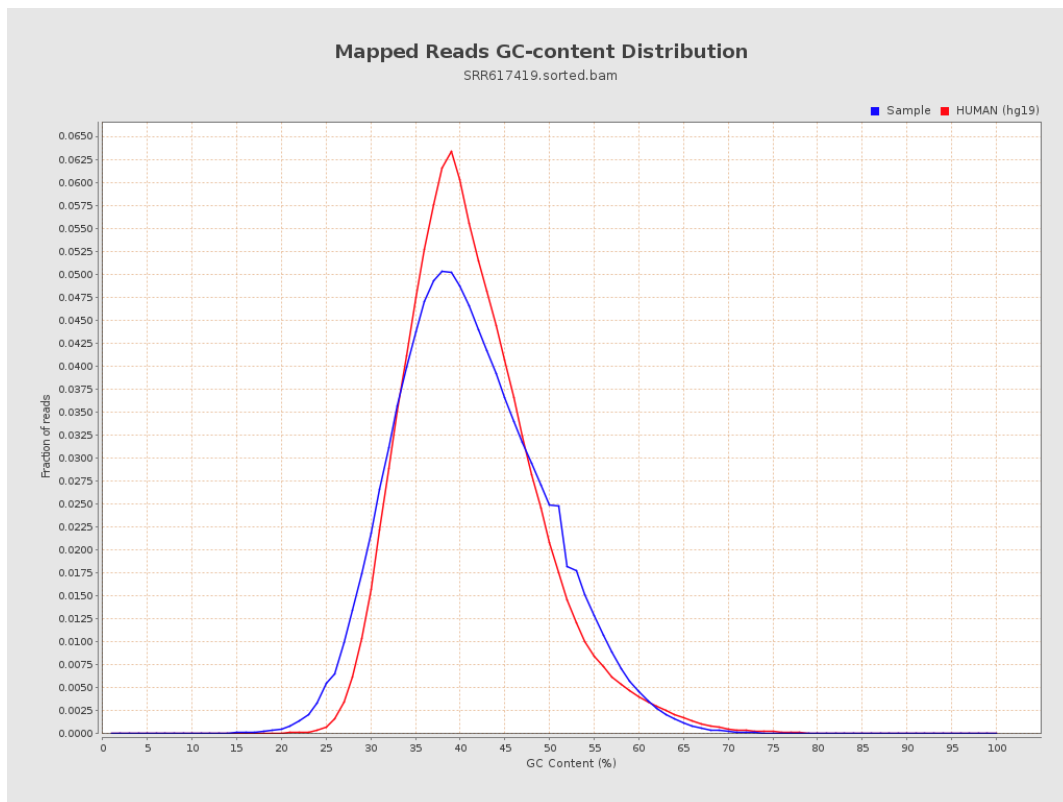
7. Results : Duplication Rate Histogram



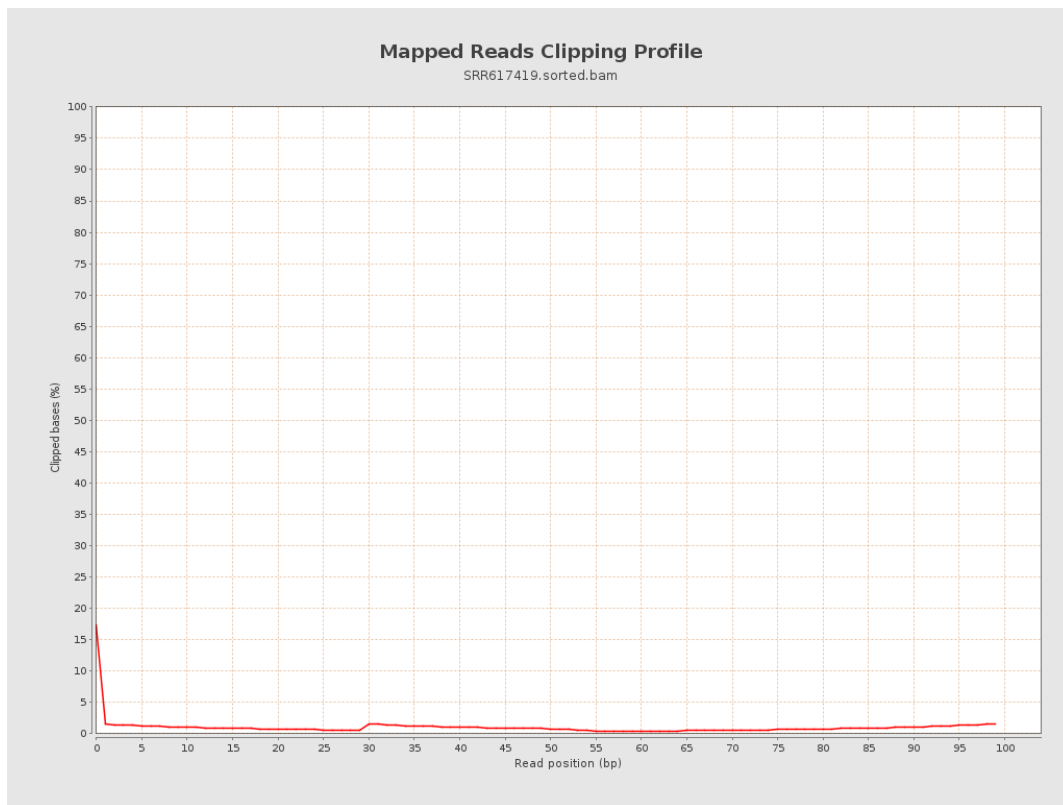
8. Results : Mapped Reads Nucleotide Content



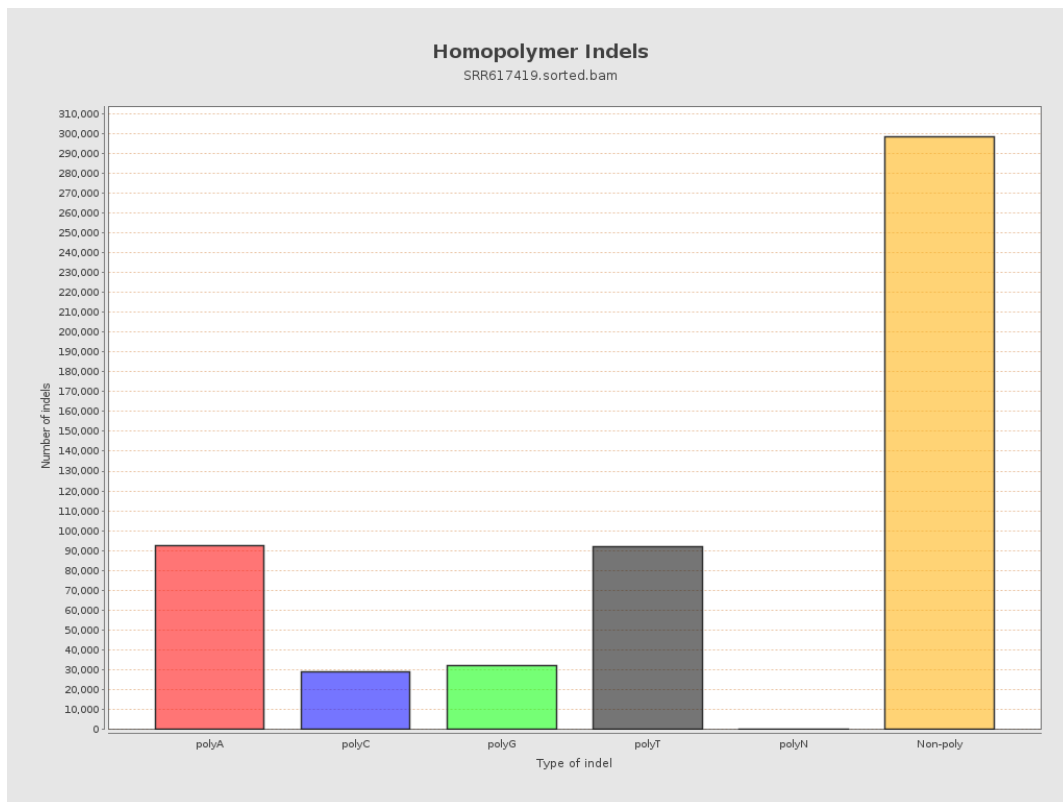
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



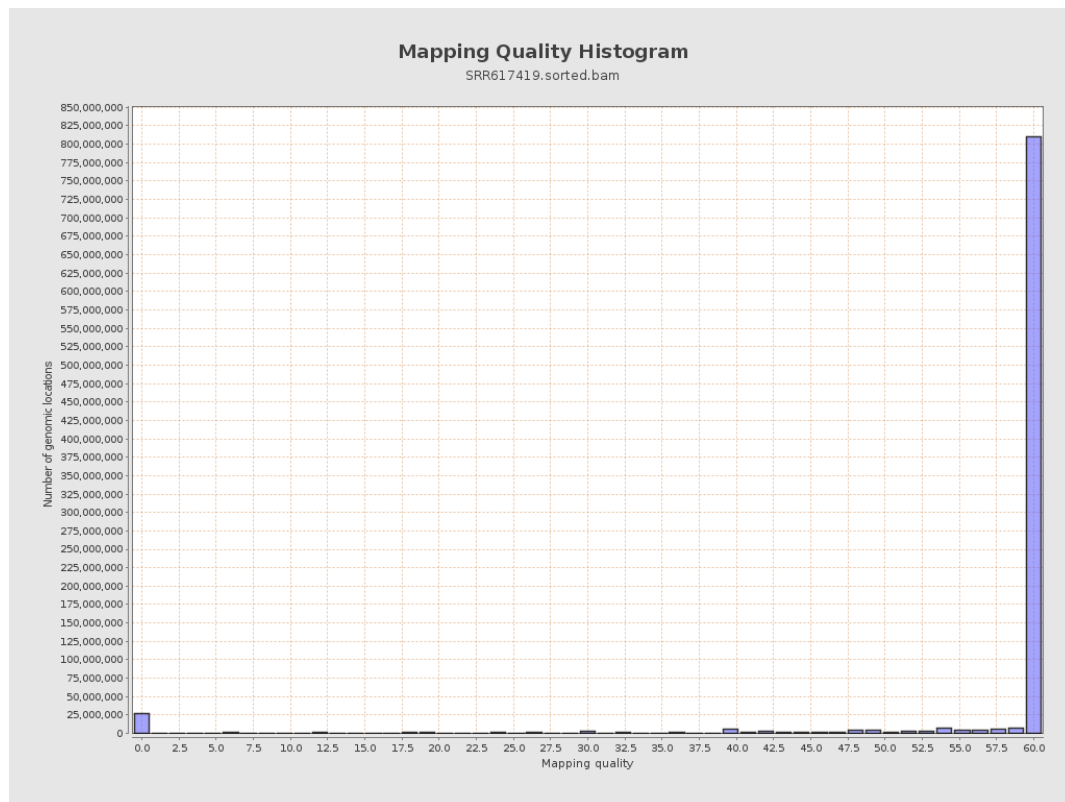
11. Results : Homopolymer Indels



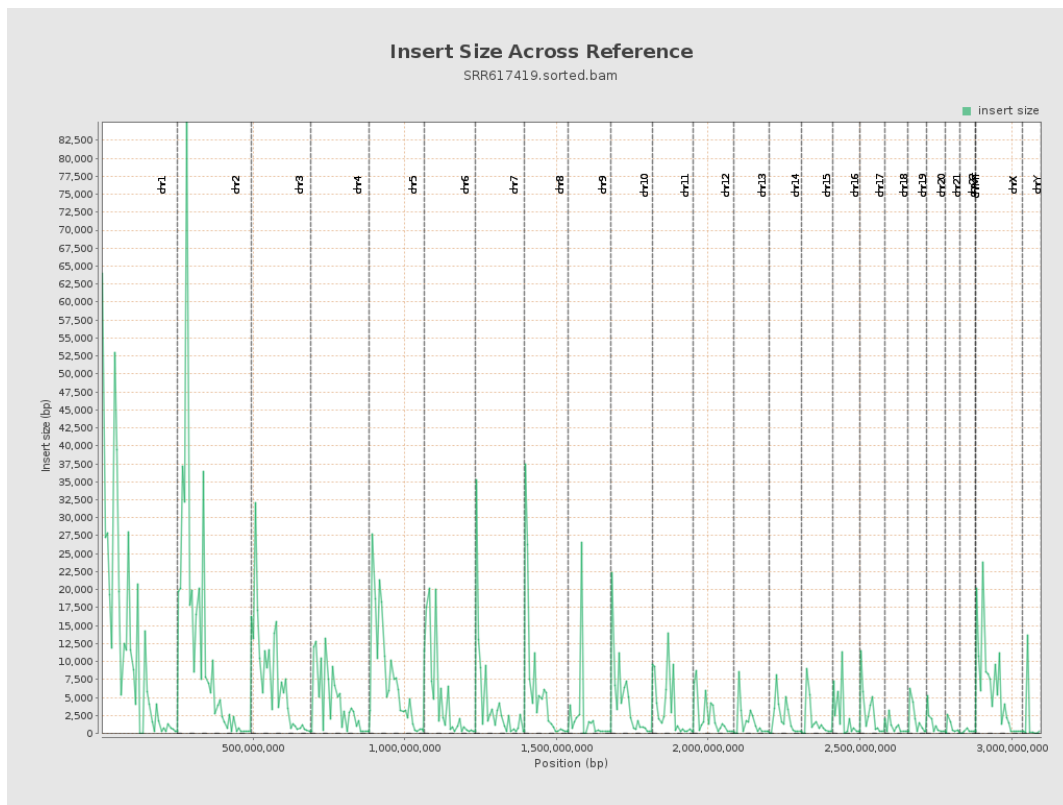
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

