

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2025/02/12 19:02:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16362019.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_SRR16362019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16362019_1.fastq.gz SRR16362019_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 12 19:02:14 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16362019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,180,347,088
Mapped reads	2,149,537,308 / 98.59%
Unmapped reads	30,809,780 / 1.41%
Mapped paired reads	2,149,537,308 / 98.59%
Mapped reads, first in pair	1,076,641,466 / 49.38%
Mapped reads, second in pair	1,072,895,842 / 49.21%
Mapped reads, both in pair	2,134,694,382 / 97.91%
Mapped reads, singletons	14,842,926 / 0.68%
Secondary alignments	0
Supplementary alignments	86,319,000 / 3.96%
Read min/max/mean length	30 / 150 / 151.96
Duplicated reads (estimated)	1,061,375,812 / 48.68%
Duplication rate	45.11%
Clipped reads	1,363,579,689 / 62.54%

2.2. ACGT Content

Number/percentage of A's	86,395,910,276 / 28.88%
Number/percentage of C's	62,450,146,518 / 20.88%
Number/percentage of T's	85,657,886,188 / 28.63%
Number/percentage of G's	64,643,135,442 / 21.61%
Number/percentage of N's	5,590,465 / 0%

GC Percentage	42.48%
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2.3. Coverage

Mean	96.7288
Standard Deviation	1,594.4582

2.4. Mapping Quality

Mean Mapping Quality	53.97
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2.5. Insert size

Mean	87,951.22
Standard Deviation	2,951,531.54
P25/Median/P75	203 / 269 / 380

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	2,317,663,662
Insertions	52,047,432
Mapped reads with at least one insertion	2.3%
Deletions	176,361,313
Mapped reads with at least one deletion	7.84%
Homopolymer indels	45.41%

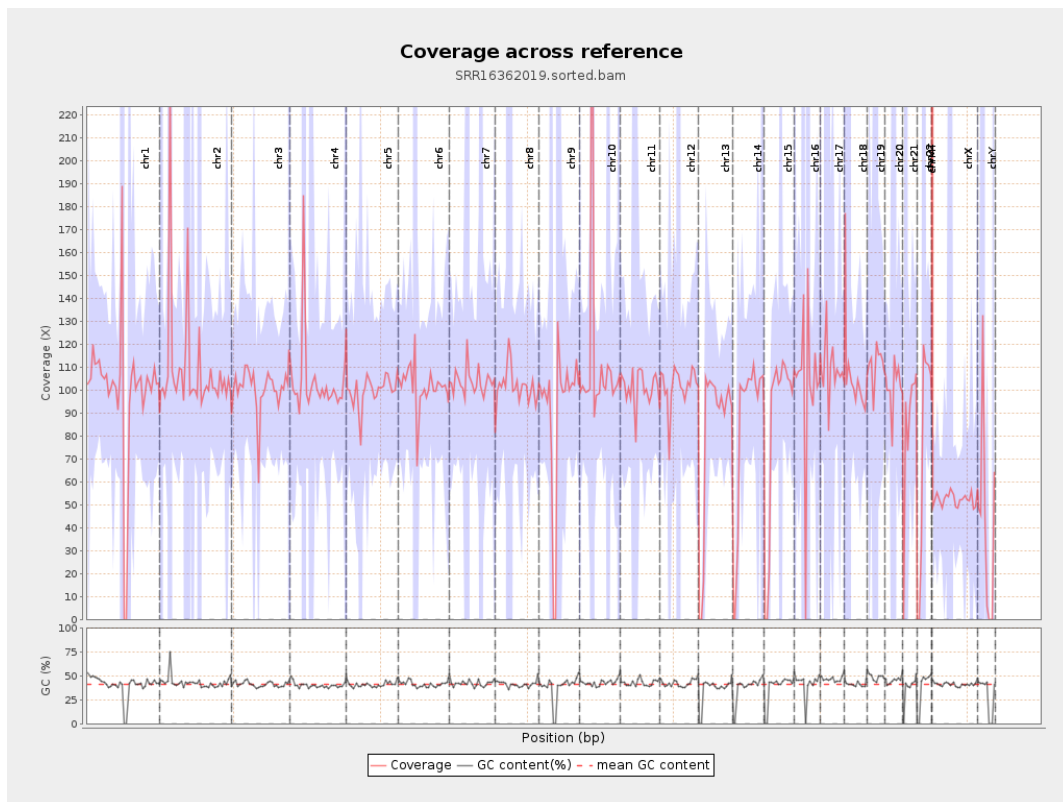
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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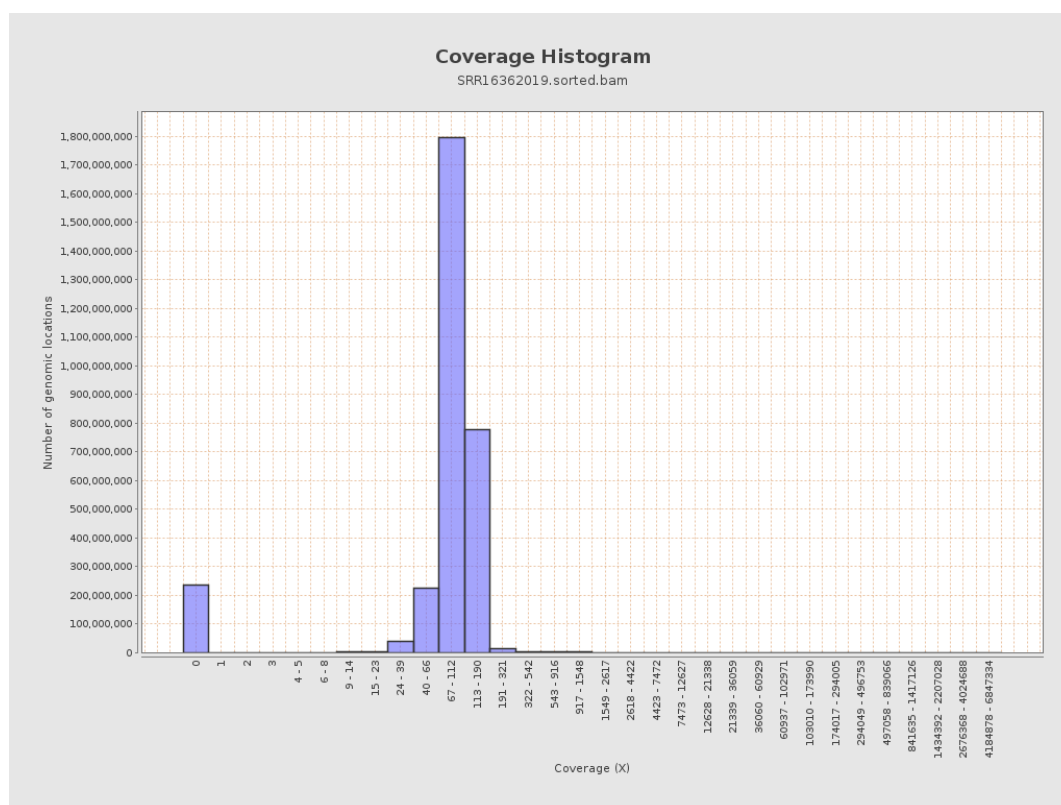
		bases	coverage	deviation
chr1	249250621	24987963288	100.2524	2,109.7963
chr2	243199373	26625153834	109.4787	4,697.0316
chr3	198022430	19925104275	100.6204	86.7845
chr4	191154276	19699129564	103.0536	821.7675
chr5	180915260	18079494426	99.9335	69.006
chr6	171115067	17366469223	101.49	322.3962
chr7	159138663	16514150275	103.7721	642.2346
chr8	146364022	14976260479	102.322	1,249.6485
chr9	141213431	12838286859	90.9141	1,021.6243
chr10	135534747	15474176459	114.1713	1,906.4914
chr11	135006516	13681649053	101.3407	281.1621
chr12	133851895	13619022453	101.747	262.5699
chr13	115169878	9450585176	82.0578	51.8734
chr14	107349540	9120316608	84.9591	102.9676
chr15	102531392	8605772138	83.933	85.9324
chr16	90354753	9355103137	103.5375	513.2427
chr17	81195210	8813887658	108.5518	412.4501
chr18	78077248	8111747864	103.8939	966.1005
chr19	59128983	6587919850	111.4161	1,204.4217
chr20	63025520	6390340567	101.3929	237.6263
chr21	48129895	4137720743	85.9699	422.4726
chr22	51304566	3925352669	76.5108	295.9448
chrMT	16571	506606095	30,571.8481	4,134.7547
chrX	155270560	8121012296	52.3023	128.9874

chrY	59373566	2529594435	42.6047	986.5969
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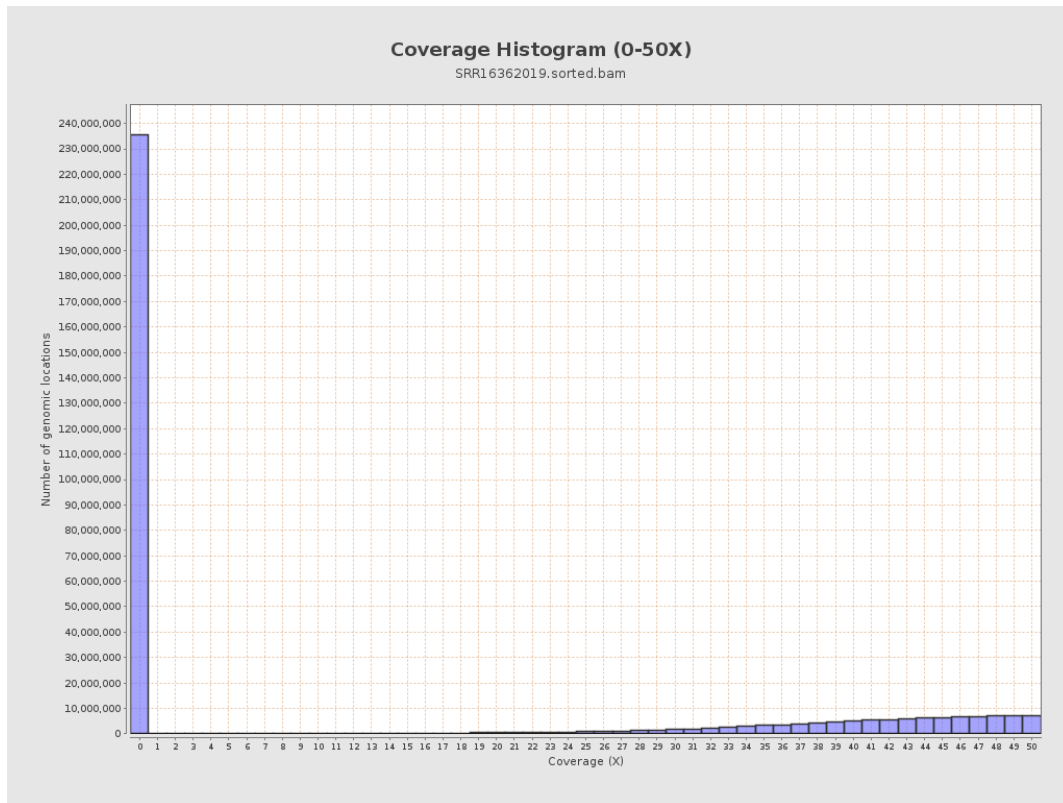
3. Results : Coverage across reference



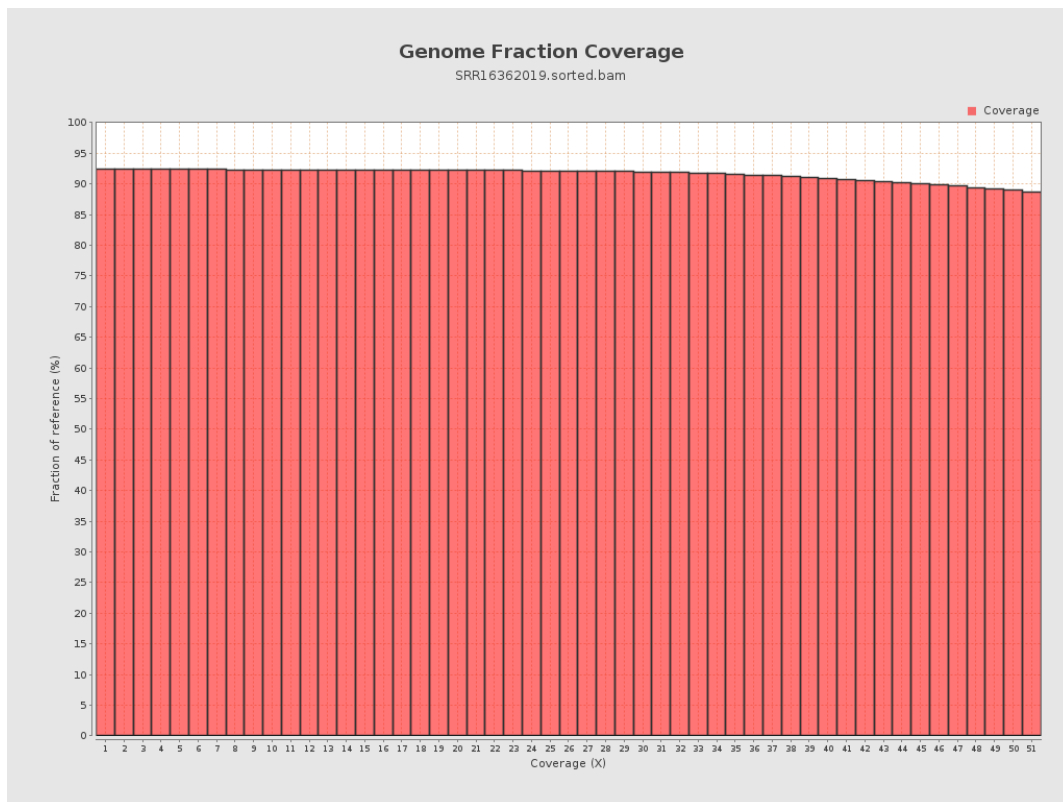
4. Results : Coverage Histogram



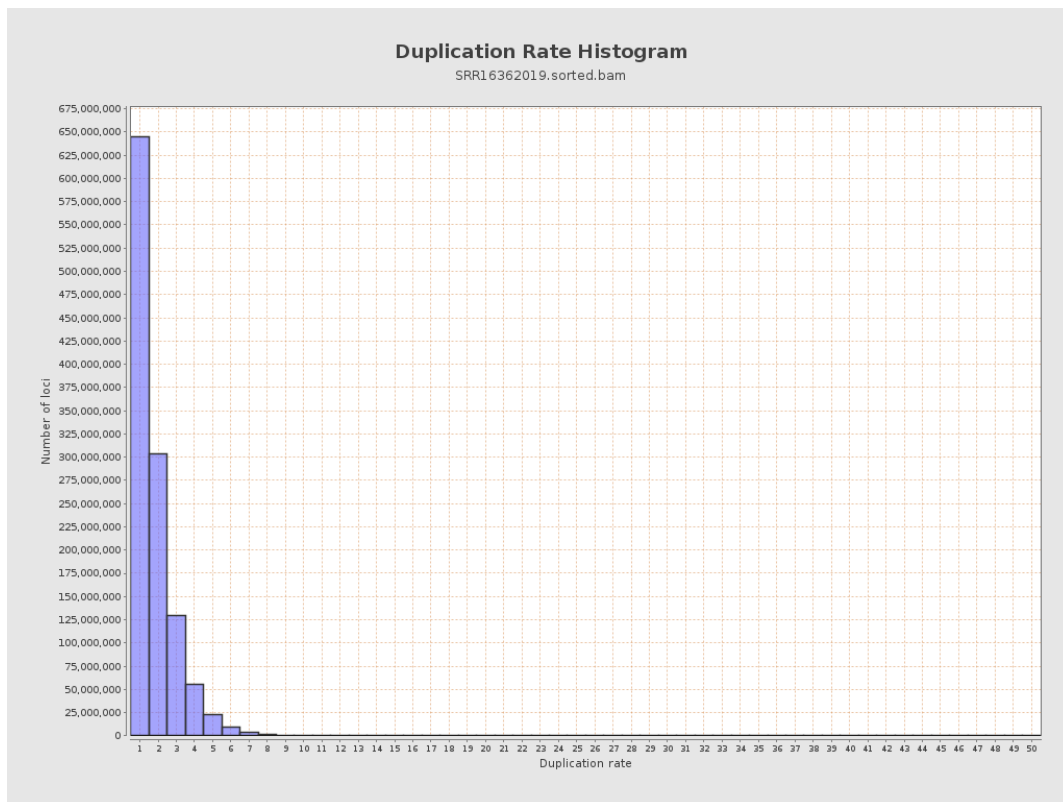
5. Results : Coverage Histogram (0-50X)



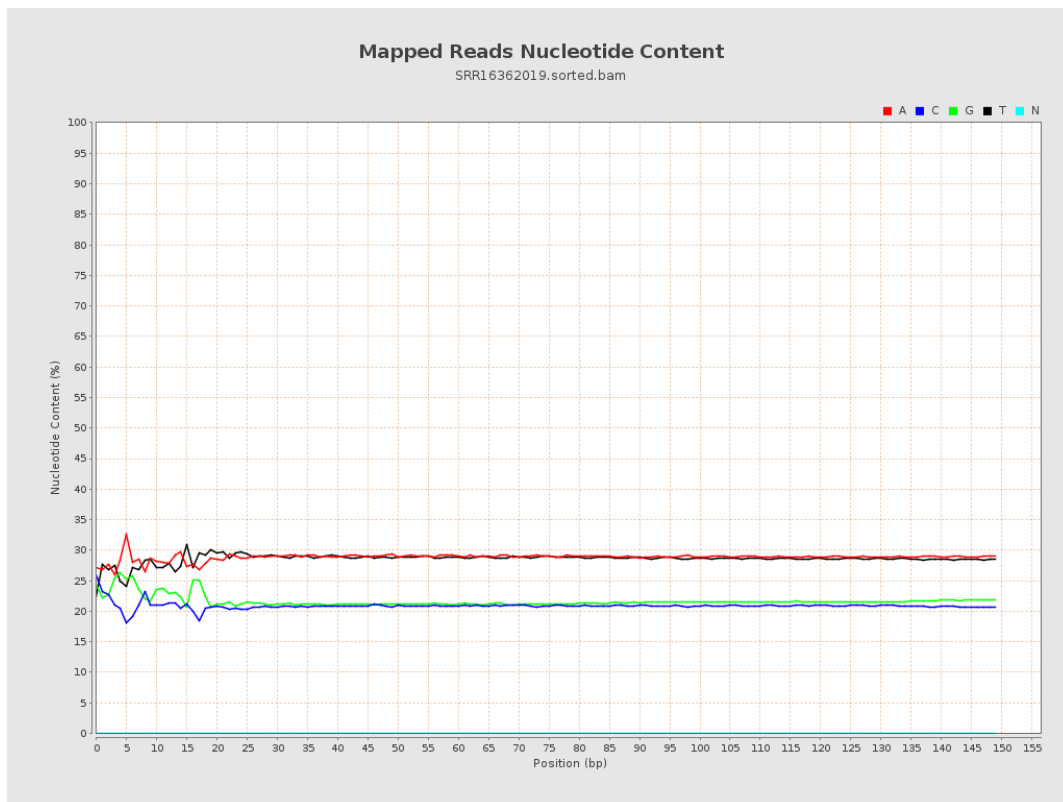
6. Results : Genome Fraction Coverage



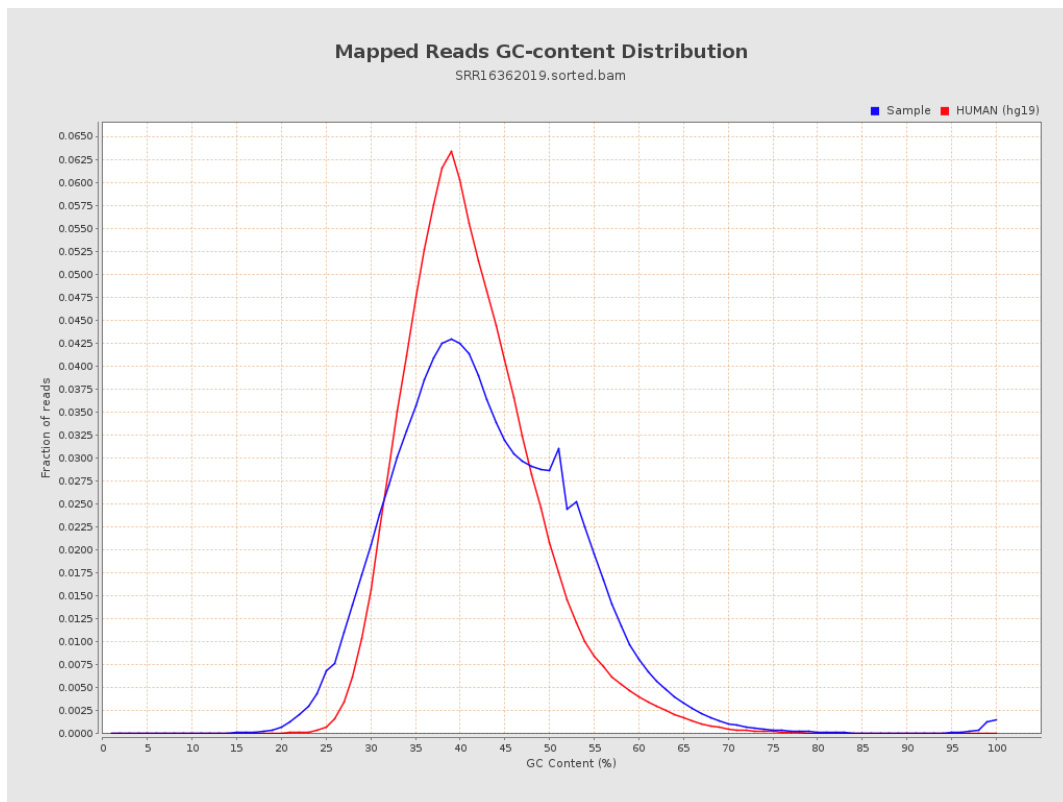
7. Results : Duplication Rate Histogram



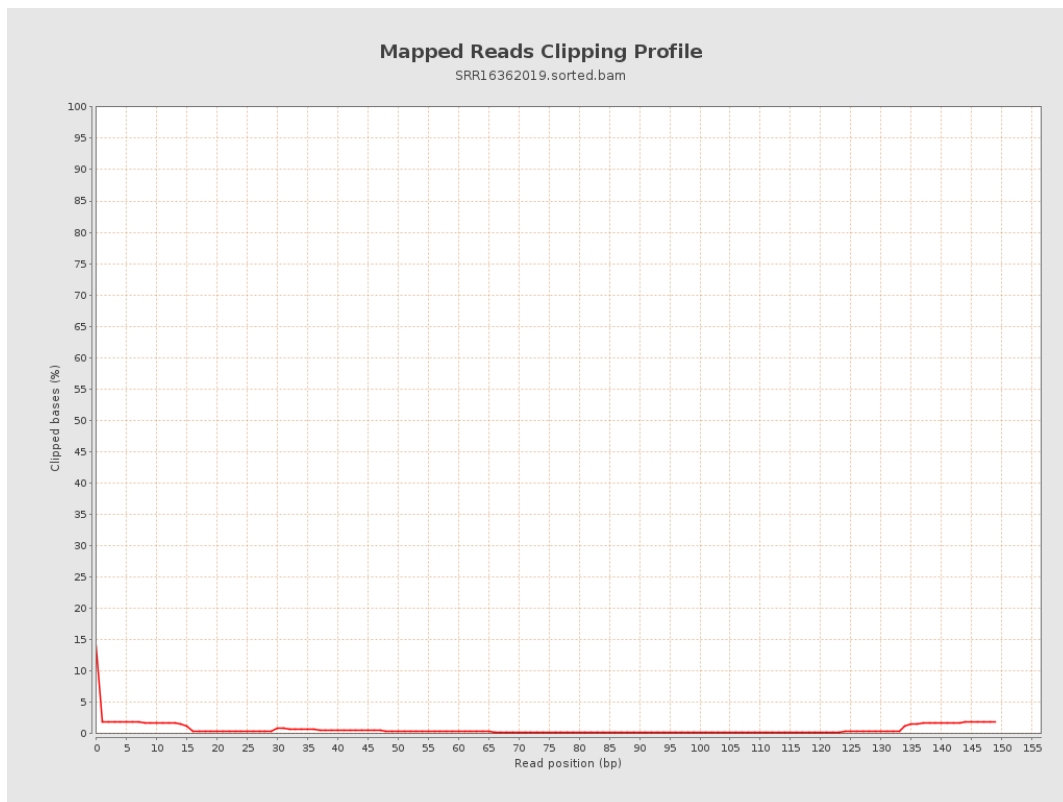
8. Results : Mapped Reads Nucleotide Content



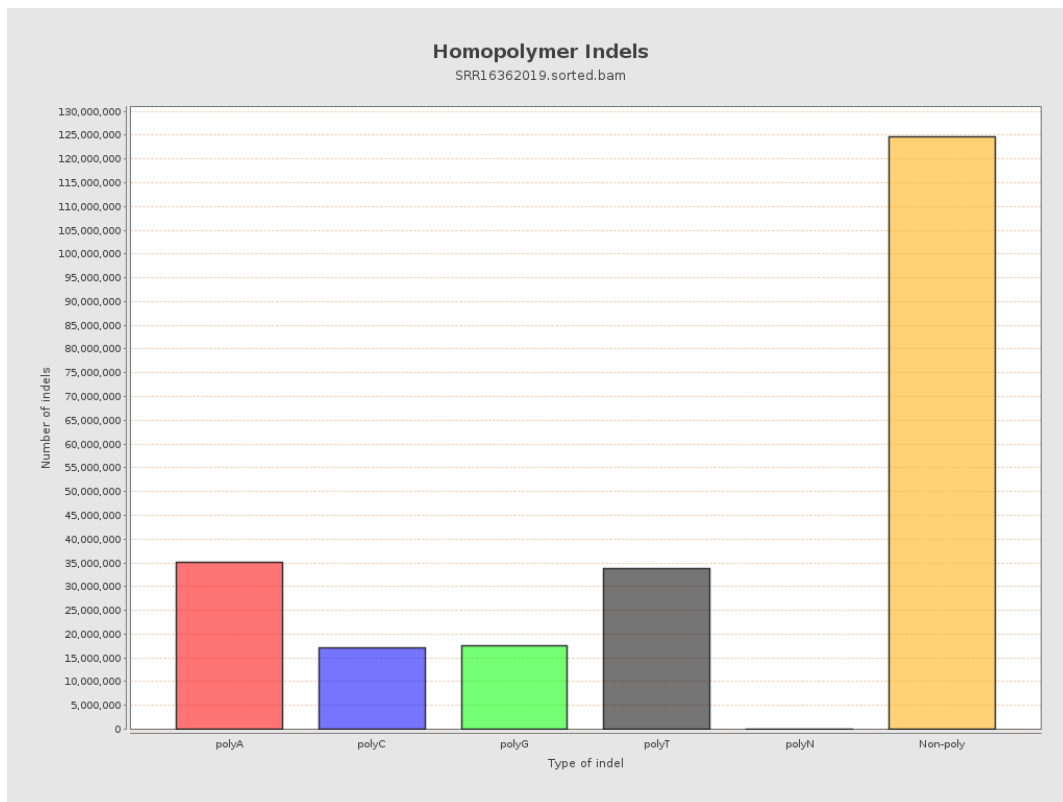
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



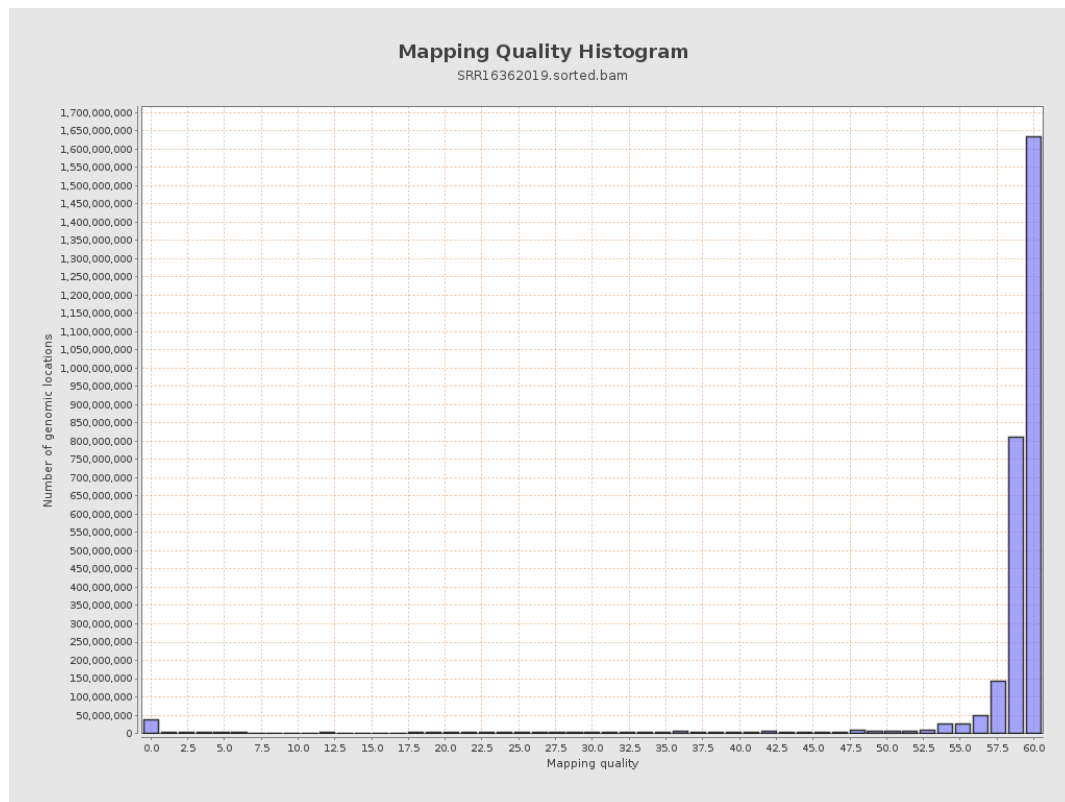
11. Results : Homopolymer Indels



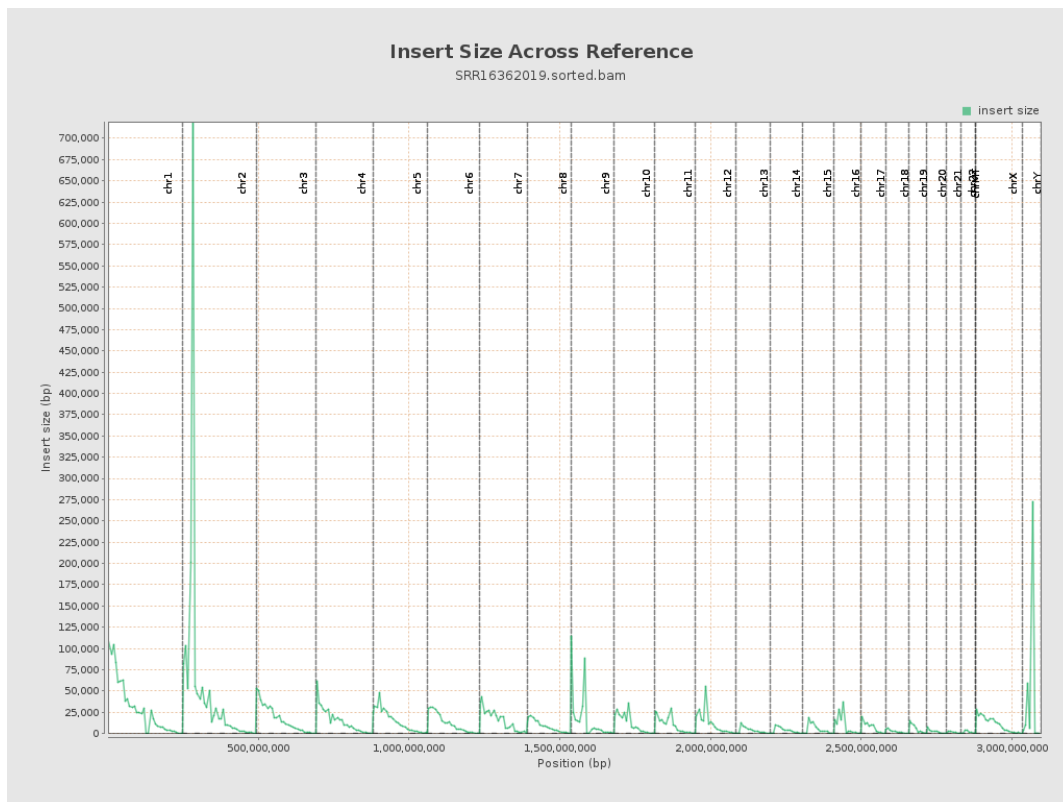
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

