

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 18:08:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671992.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_SRR21671992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671992_1.fastq.gz SRR21671992_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 18:08:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	418,210,598
Mapped reads	402,961,623 / 96.35%
Unmapped reads	15,248,975 / 3.65%
Mapped paired reads	402,961,623 / 96.35%
Mapped reads, first in pair	202,112,221 / 48.33%
Mapped reads, second in pair	200,849,402 / 48.03%
Mapped reads, both in pair	399,188,664 / 95.45%
Mapped reads, singletons	3,772,959 / 0.9%
Secondary alignments	0
Supplementary alignments	5,781,313 / 1.38%
Read min/max/mean length	15 / 150 / 149.78
Duplicated reads (estimated)	213,449,130 / 51.04%
Duplication rate	36.53%
Clipped reads	236,008,064 / 56.43%

2.2. ACGT Content

Number/percentage of A's	14,346,043,000 / 26.47%
Number/percentage of C's	10,900,279,560 / 20.11%
Number/percentage of T's	15,764,343,640 / 29.09%
Number/percentage of G's	13,184,492,261 / 24.33%
Number/percentage of N's	71,349 / 0%

GC Percentage	44.44%
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2.3. Coverage

Mean	17.5164
Standard Deviation	284.5282

2.4. Mapping Quality

Mean Mapping Quality	53.59
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2.5. Insert size

Mean	168,578.13
Standard Deviation	4,074,009.09
P25/Median/P75	266 / 314 / 361

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	663,994,428
Insertions	8,664,966
Mapped reads with at least one insertion	2.05%
Deletions	15,714,368
Mapped reads with at least one deletion	3.77%
Homopolymer indels	46.28%

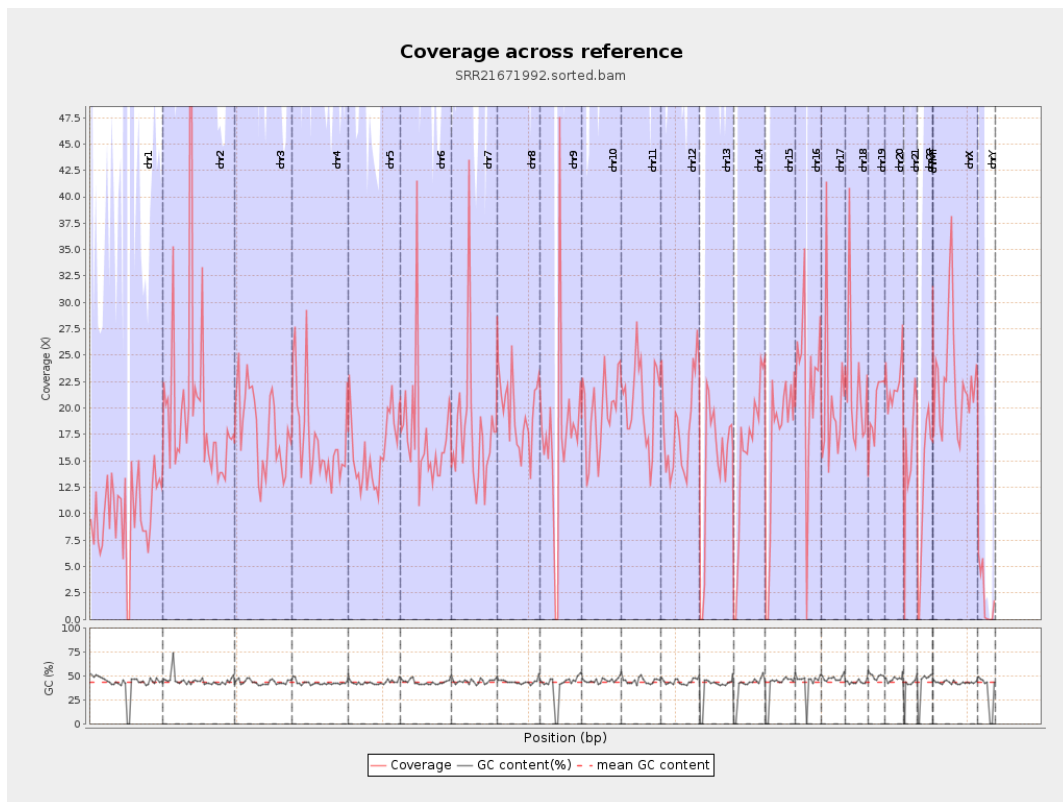
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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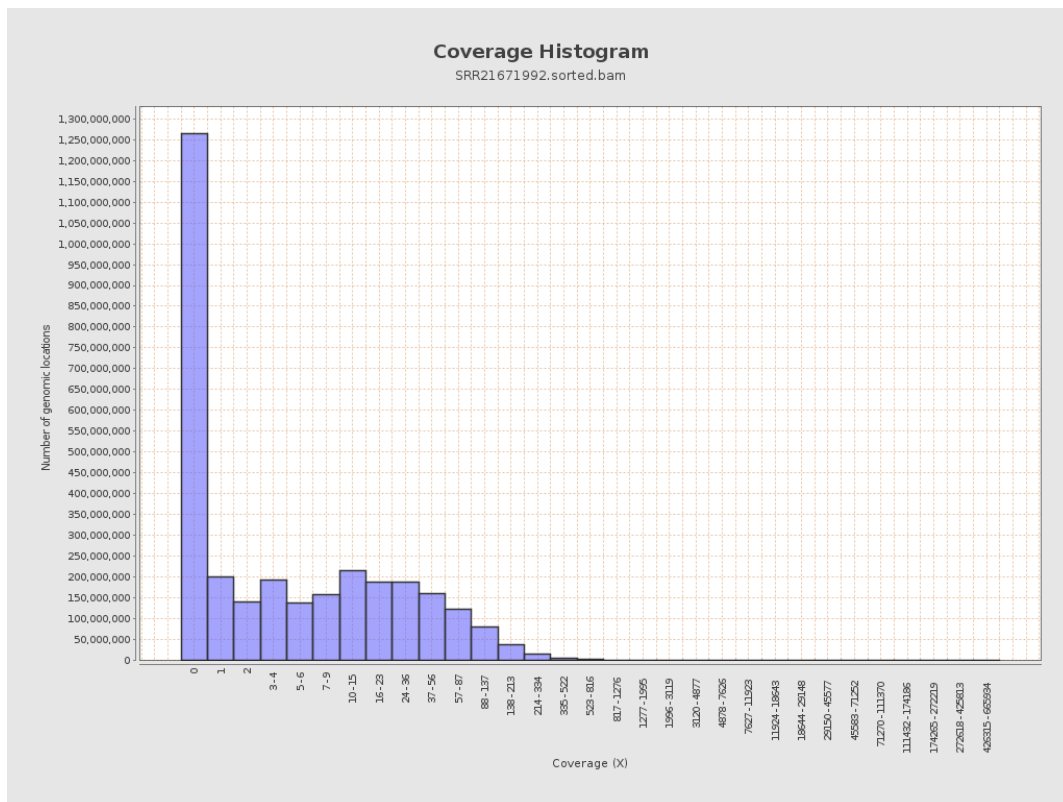
		bases	coverage	deviation
chr1	249250621	2469625516	9.9082	128.1286
chr2	243199373	4938767028	20.3075	657.0166
chr3	198022430	3542622737	17.89	40.1938
chr4	191154276	3281027257	17.1643	77.9601
chr5	180915260	2912282309	16.0975	41.4924
chr6	171115067	2983989252	17.4385	351.995
chr7	159138663	2835417139	17.8173	450.6787
chr8	146364022	2856683346	19.5177	90.5837
chr9	141213431	2451537729	17.3605	495.7774
chr10	135534747	2627497315	19.3862	88.8995
chr11	135006516	2787169210	20.6447	233.4744
chr12	133851895	2445271593	18.2685	43.9794
chr13	115169878	1689578748	14.6703	36.8272
chr14	107349540	1700119251	15.8372	180.5927
chr15	102531392	1678505248	16.3706	38.7158
chr16	90354753	2020372195	22.3604	154.508
chr17	81195210	1663647765	20.4895	326.0172
chr18	78077248	1706351961	21.8547	509.667
chr19	59128983	1186476907	20.0659	87.1565
chr20	63025520	1402769478	22.2572	50.1586
chr21	48129895	767795297	15.9526	107.3982
chr22	51304566	644108262	12.5546	31.9471
chrMT	16571	522517	31.532	88.9386
chrX	155270560	3508115786	22.5936	182.2685

chrY	59373566	125192867	2.1086	74.0408
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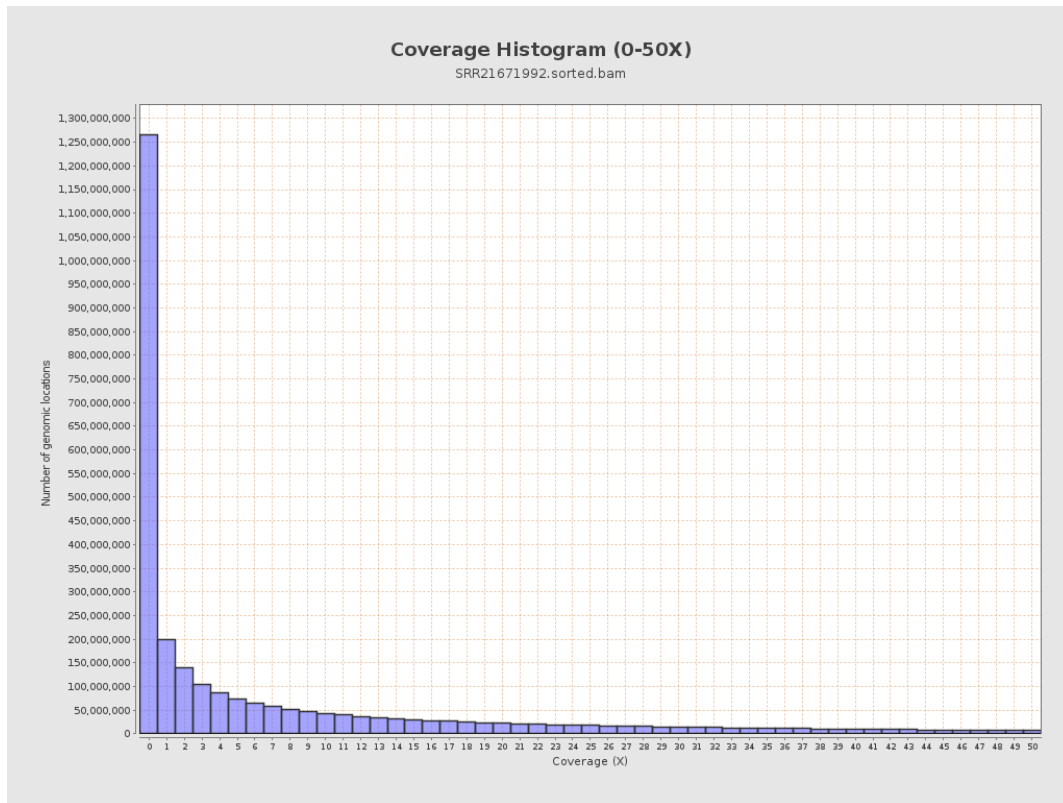
3. Results : Coverage across reference



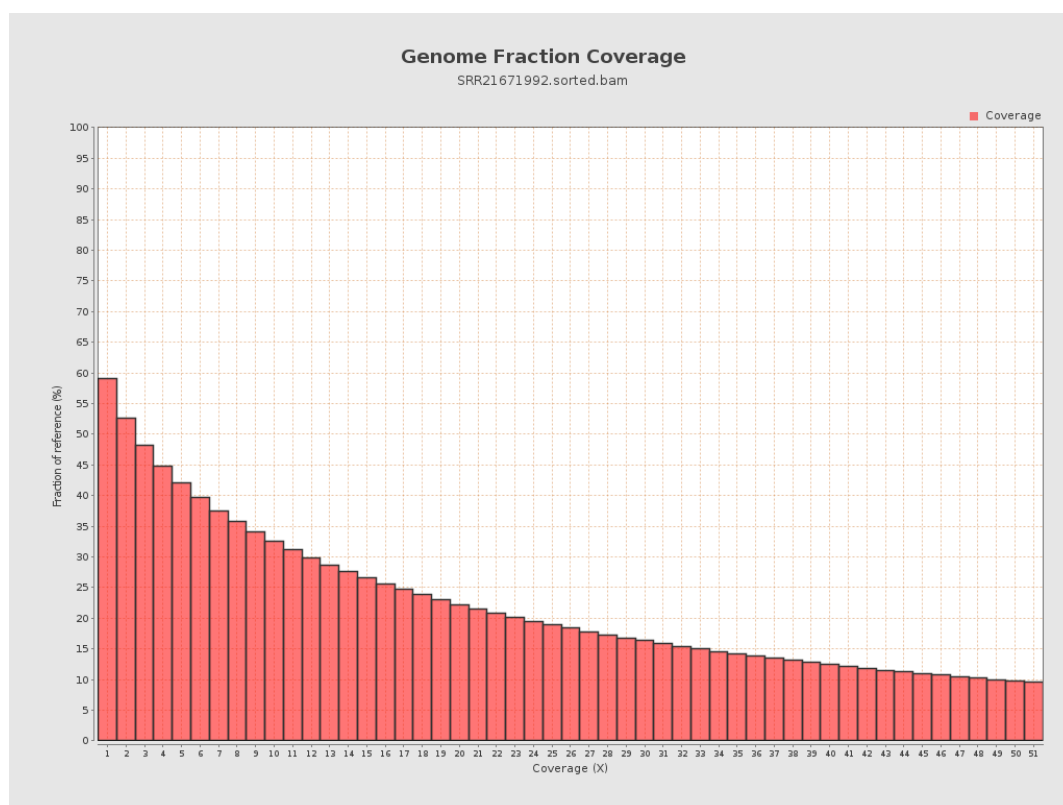
4. Results : Coverage Histogram



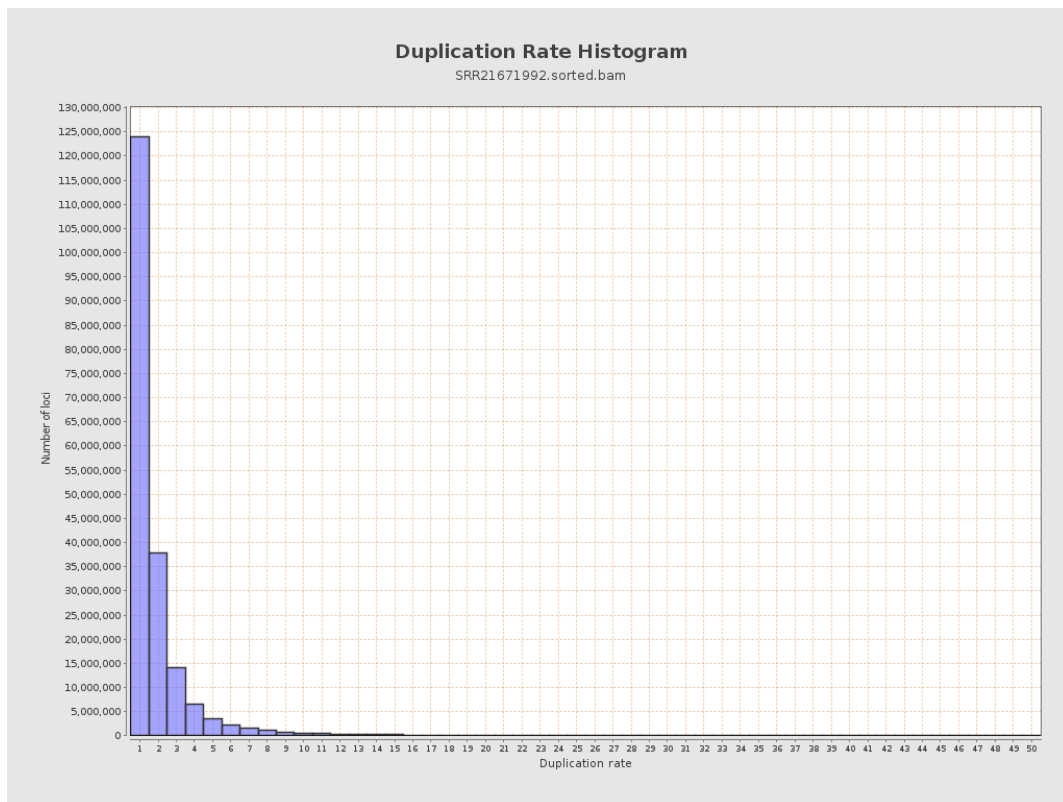
5. Results : Coverage Histogram (0-50X)



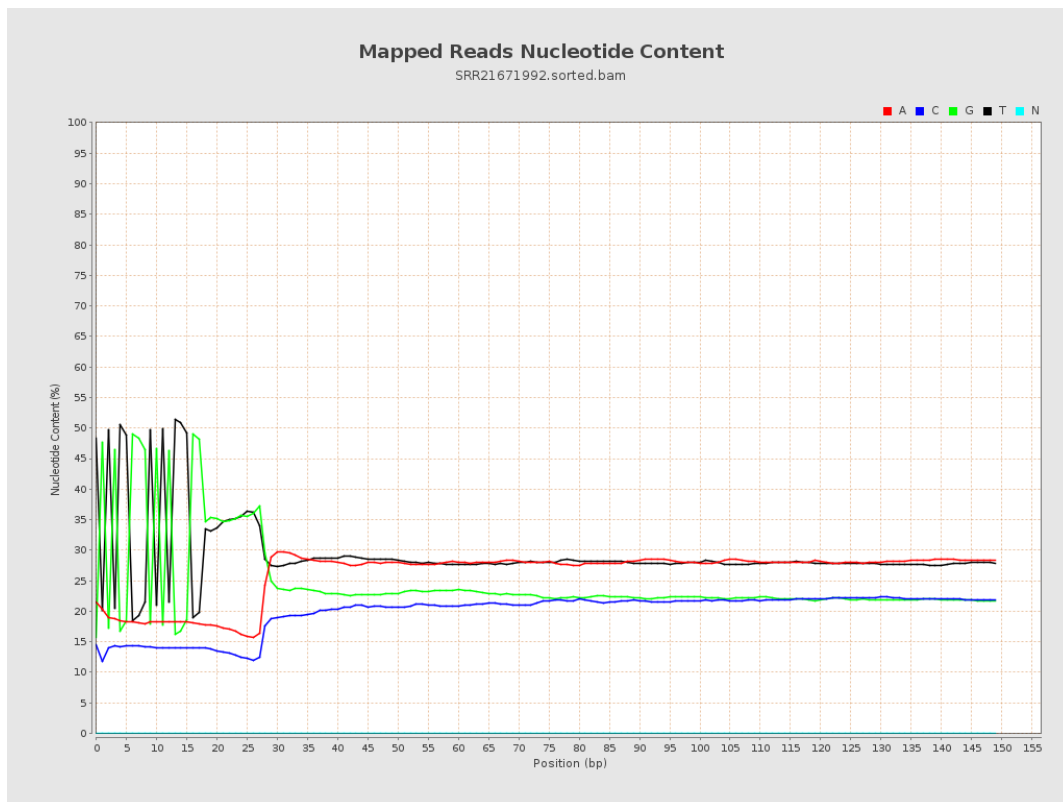
6. Results : Genome Fraction Coverage



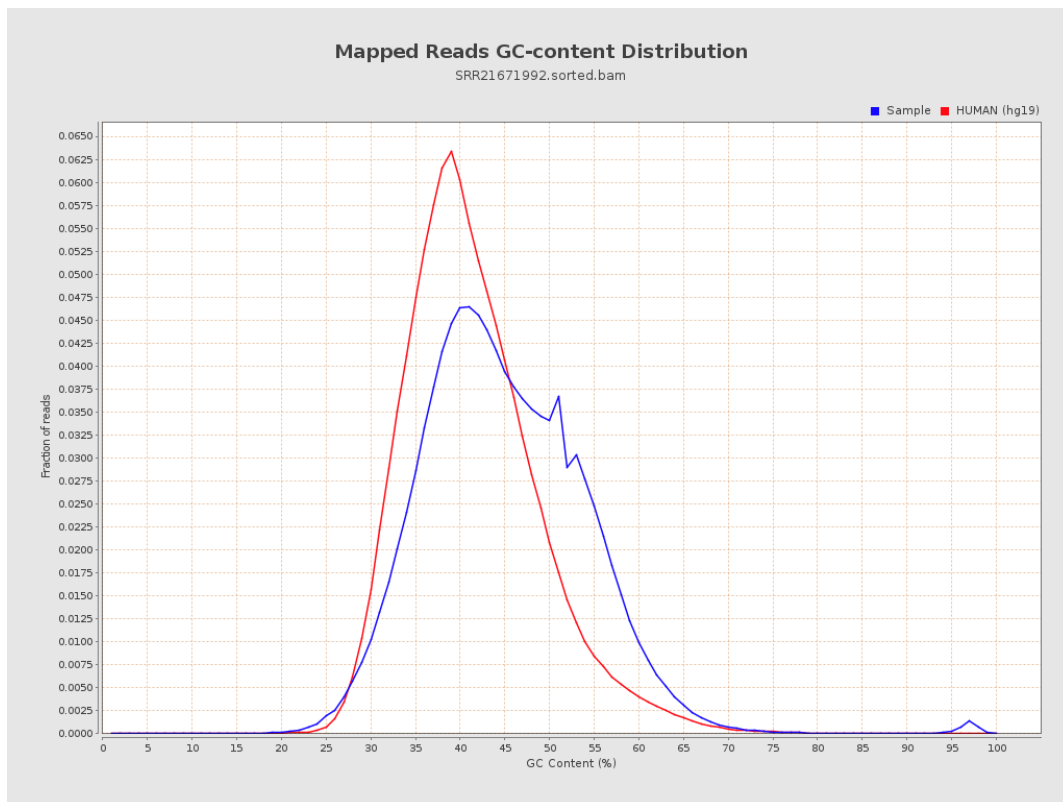
7. Results : Duplication Rate Histogram



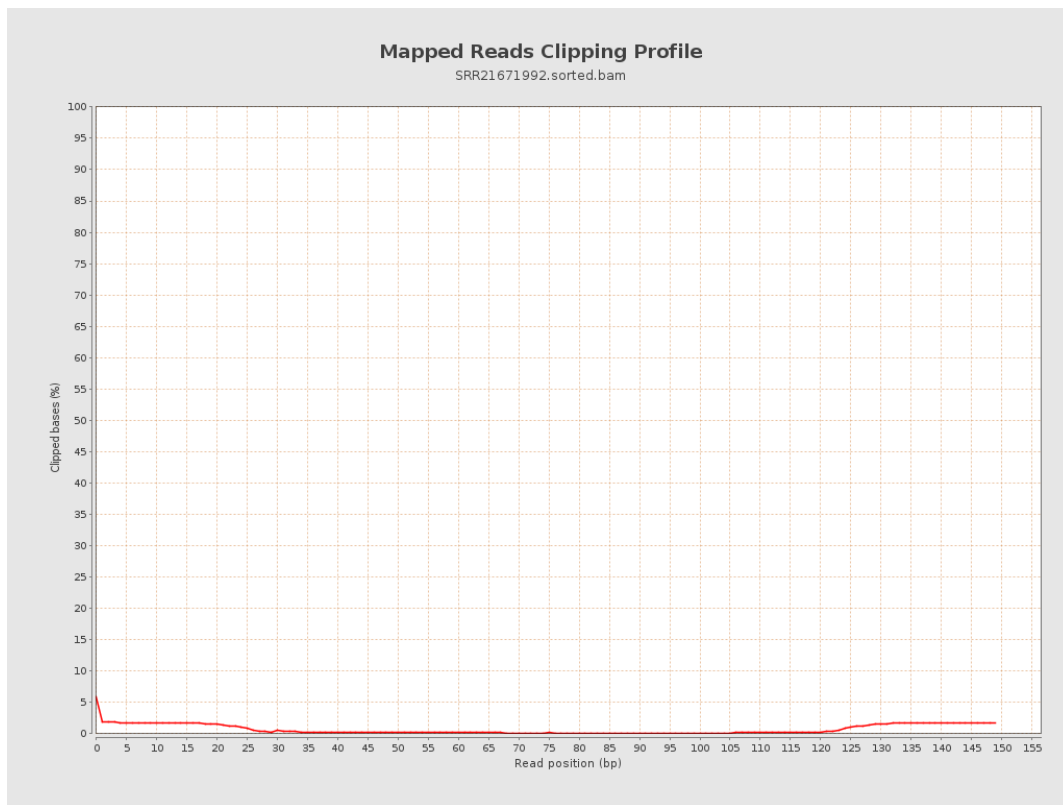
8. Results : Mapped Reads Nucleotide Content



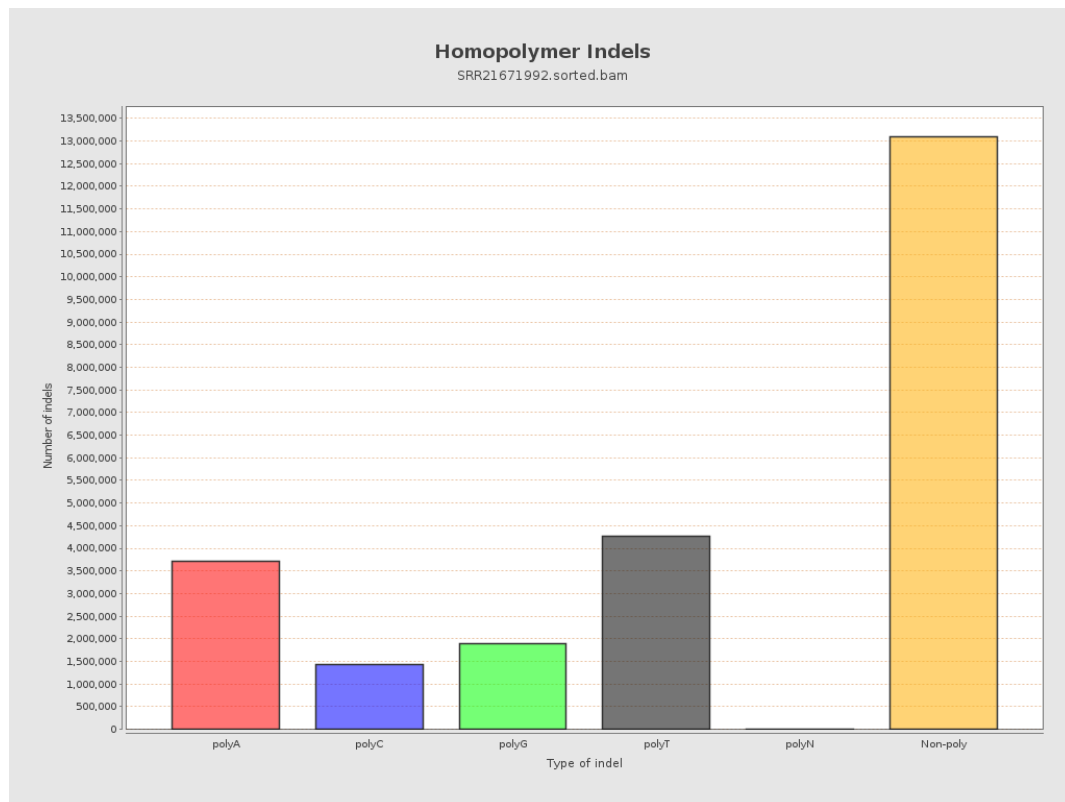
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



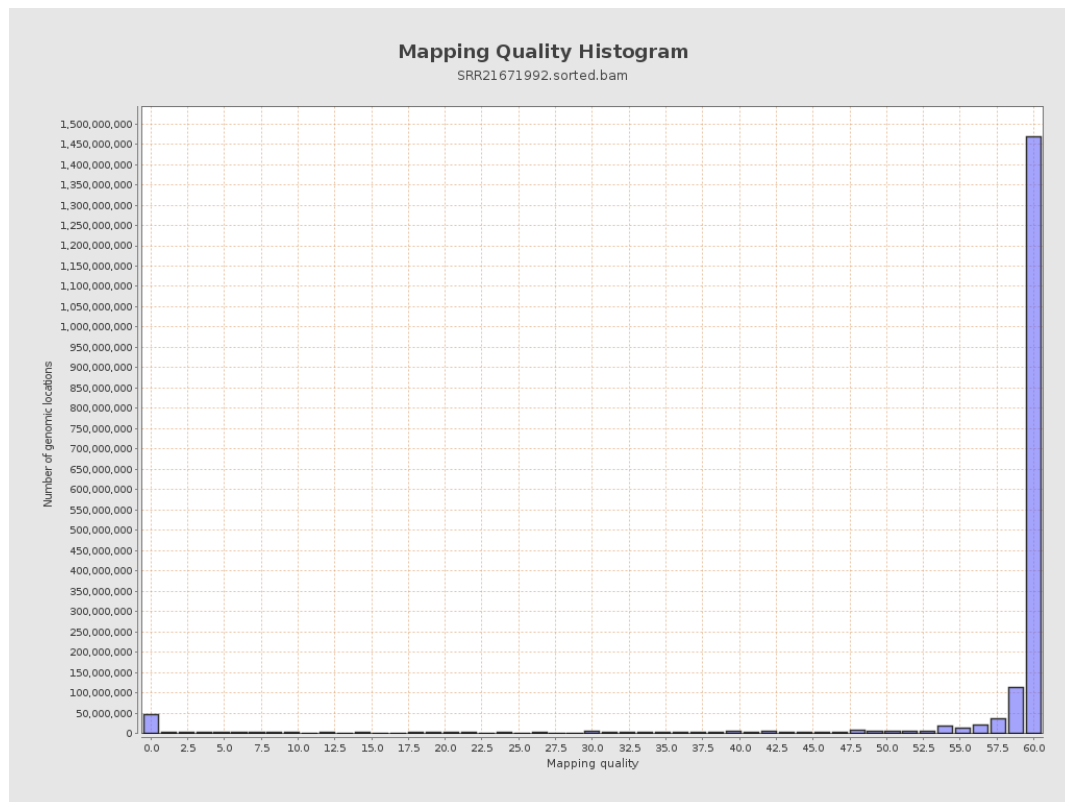
11. Results : Homopolymer Indels



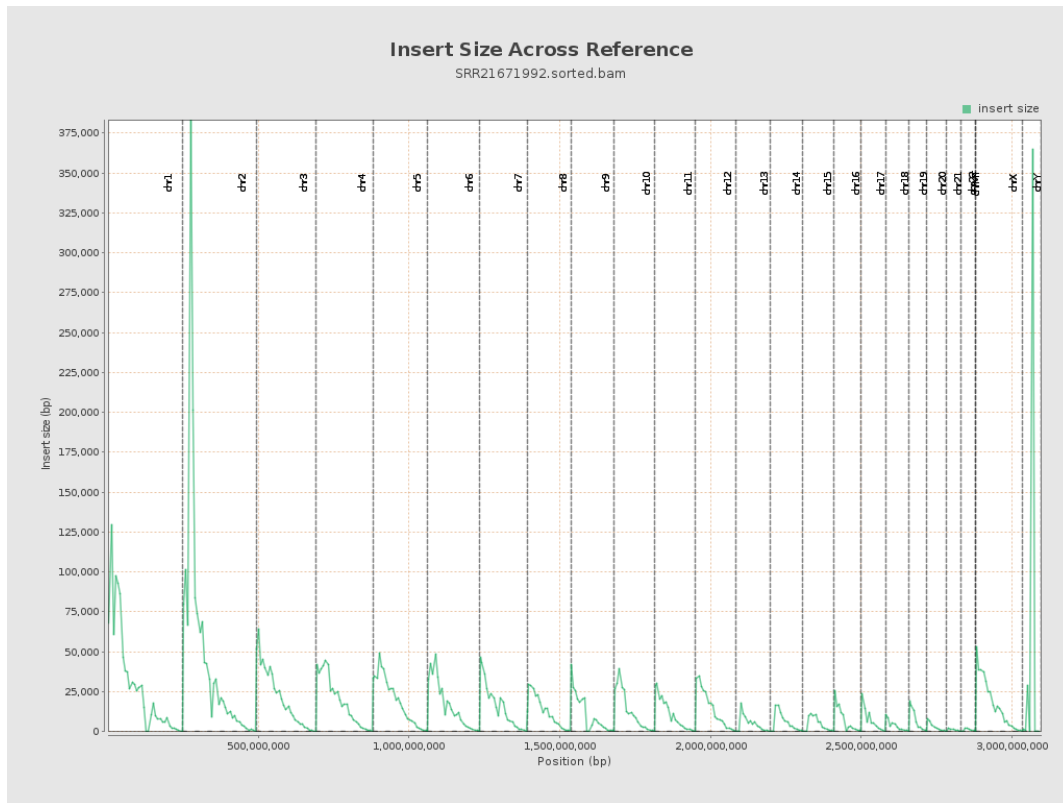
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

