Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 05:16:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063593.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_SRR6063593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063593_1.fastq.gz SRR6063593_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 05:16:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	127,571,644
Mapped reads	127,036,016 / 99.58%
Unmapped reads	535,628 / 0.42%
Mapped paired reads	127,036,016 / 99.58%
Mapped reads, first in pair	63,725,498 / 49.95%
Mapped reads, second in pair	63,310,518 / 49.63%
Mapped reads, both in pair	126,577,754 / 99.22%
Mapped reads, singletons	458,262 / 0.36%
Secondary alignments	0
Supplementary alignments	215,606 / 0.17%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	74,524,207 / 58.42%
Duplication rate	53.63%
Clipped reads	6,656,388 / 5.22%

2.2. ACGT Content

Number/percentage of A's	3,632,189,731 / 28.87%
Number/percentage of C's	2,648,916,685 / 21.06%
Number/percentage of T's	3,681,872,922 / 29.27%
Number/percentage of G's	2,616,833,838 / 20.8%
Number/percentage of N's	888,678 / 0.01%

GC Percentage	41.86%

2.3. Coverage

Mean	4.0645
Standard Deviation	31.2568

2.4. Mapping Quality

Mean Mapping Quality	53.65

2.5. Insert size

Mean	21,175.74
Standard Deviation	1,436,744.62
P25/Median/P75	172 / 233 / 317

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	45,793,063
Insertions	594,786
Mapped reads with at least one insertion	0.46%
Deletions	738,777
Mapped reads with at least one deletion	0.57%
Homopolymer indels	47.6%

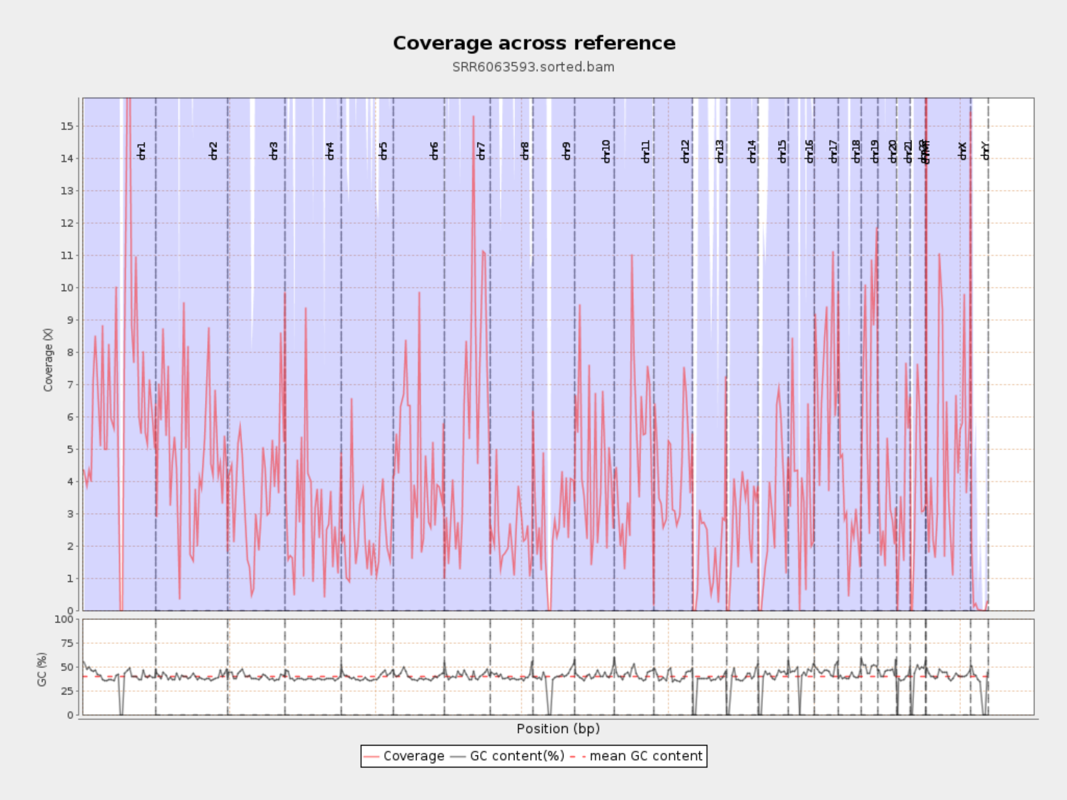
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

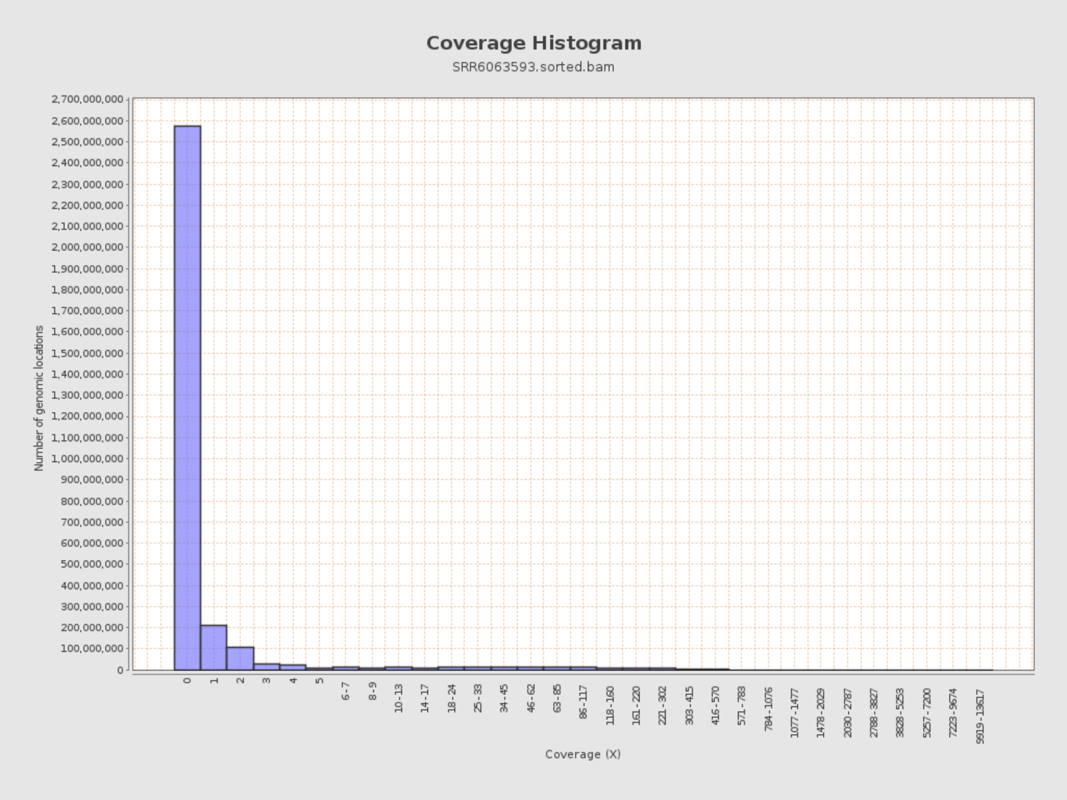
		bases	coverage	deviation
chr1	249250621	1681646796	6.7468	44.8482
chr2	243199373	1215388756	4.9975	36.6559
chr3	198022430	732927341	3.7012	27.5723
chr4	191154276	551331520	2.8842	23.8708
chr5	180915260	435350474	2.4064	18.5833
chr6	171115067	776517315	4.538	34.3564
chr7	159138663	930216601	5.8453	44.6488
chr8	146364022	335169772	2.29	18.8671
chr9	141213431	369638399	2.6176	20.4107
chr10	135534747	610235015	4.5024	33.3185
chr11	135006516	645900279	4.7842	31.2856
chr12	133851895	583644231	4.3604	29.0705
chr13	115169878	197811375	1.7176	15.7675
chr14	107349540	287378274	2.677	20.0735
chr15	102531392	295833431	2.8853	22.7524
chr16	90354753	326263935	3.6109	27.4224
chr17	81195210	590723108	7.2753	36.8339
chr18	78077248	244290163	3.1288	27.5933
chr19	59128983	460683101	7.7912	35.4574
chr20	63025520	176936307	2.8074	18.6561
chr21	48129895	184383642	3.831	33.4803
chr22	51304566	177231415	3.4545	24.2014
chrMT	16571	2568865	155.0217	418.8433
chrX	155270560	754812559	4.8613	43.2806

chrY	59373566	15591214	0.2626	7.775

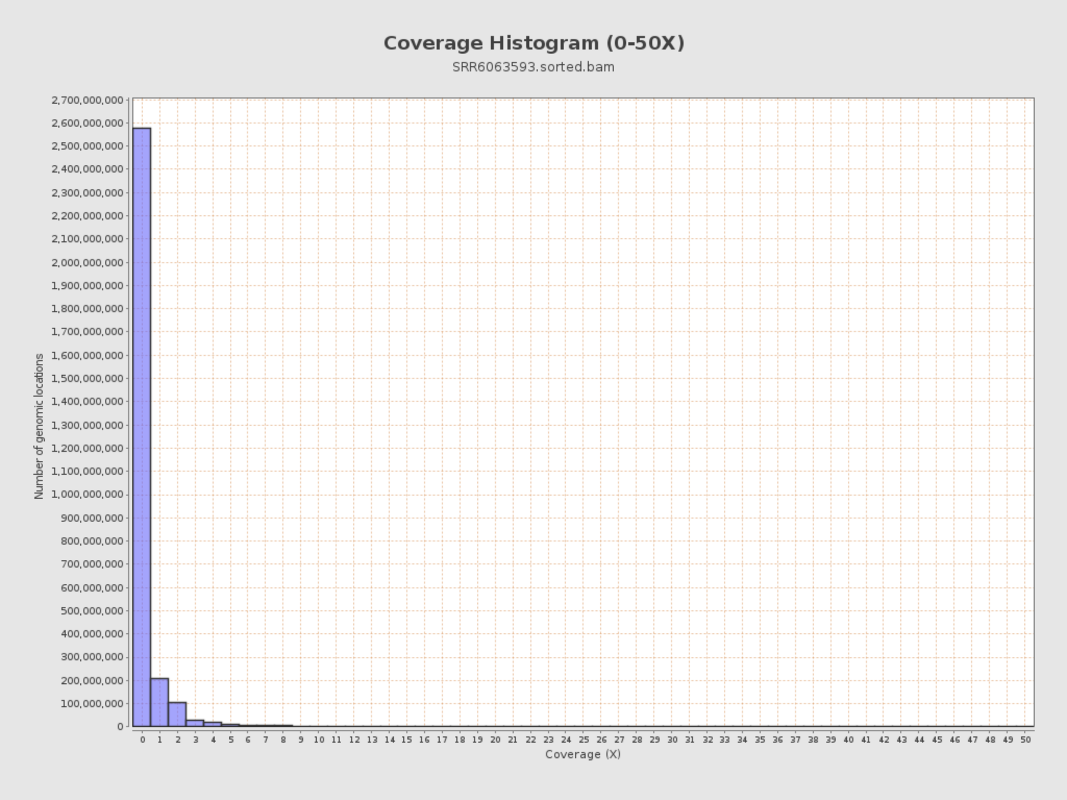
3. Results : Coverage across reference



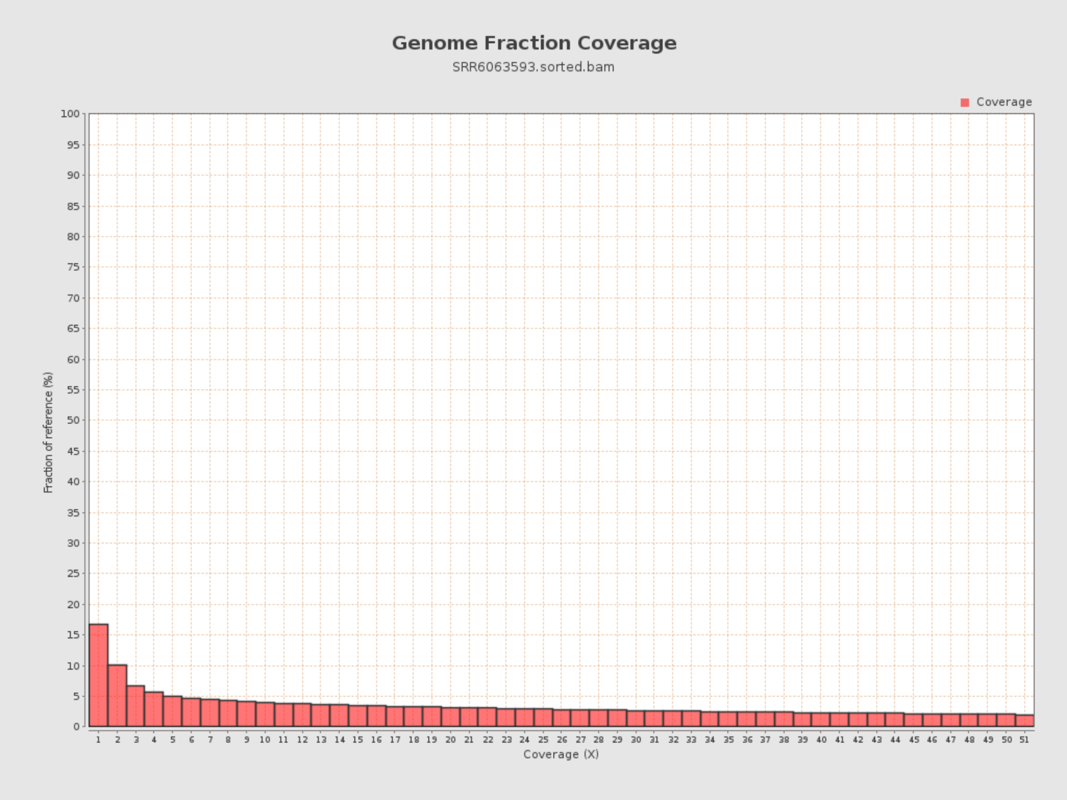
4. Results : Coverage Histogram



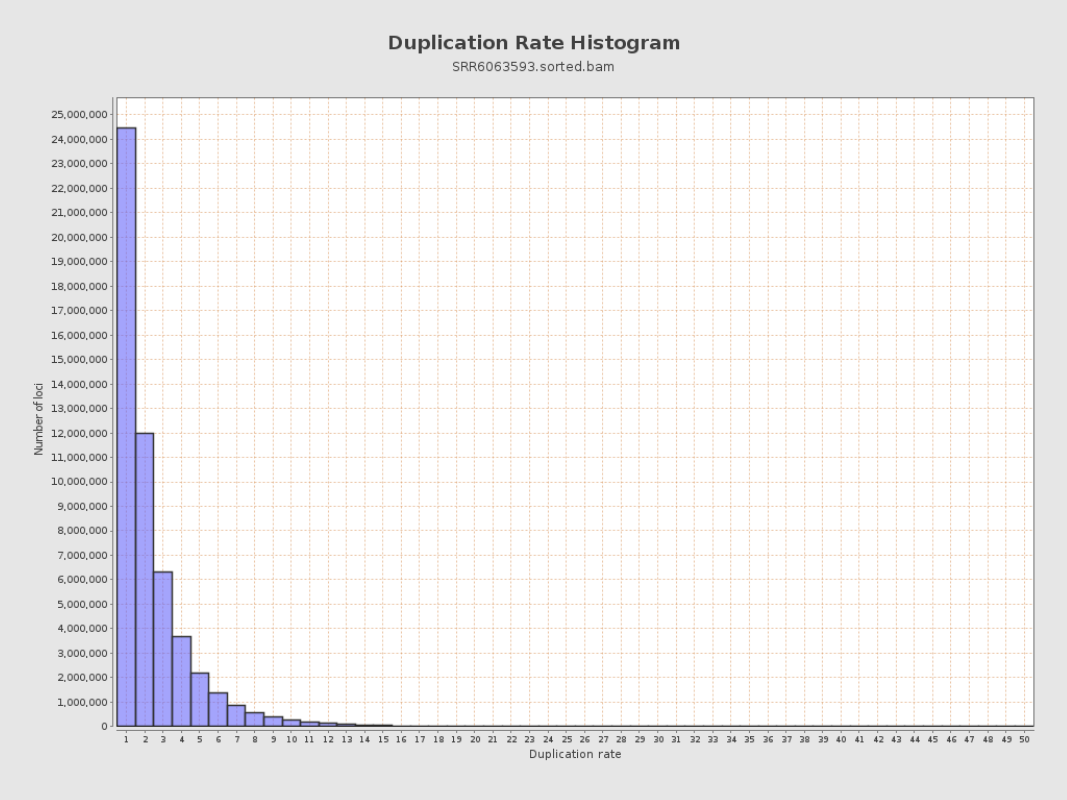
5. Results : Coverage Histogram (0-50X)



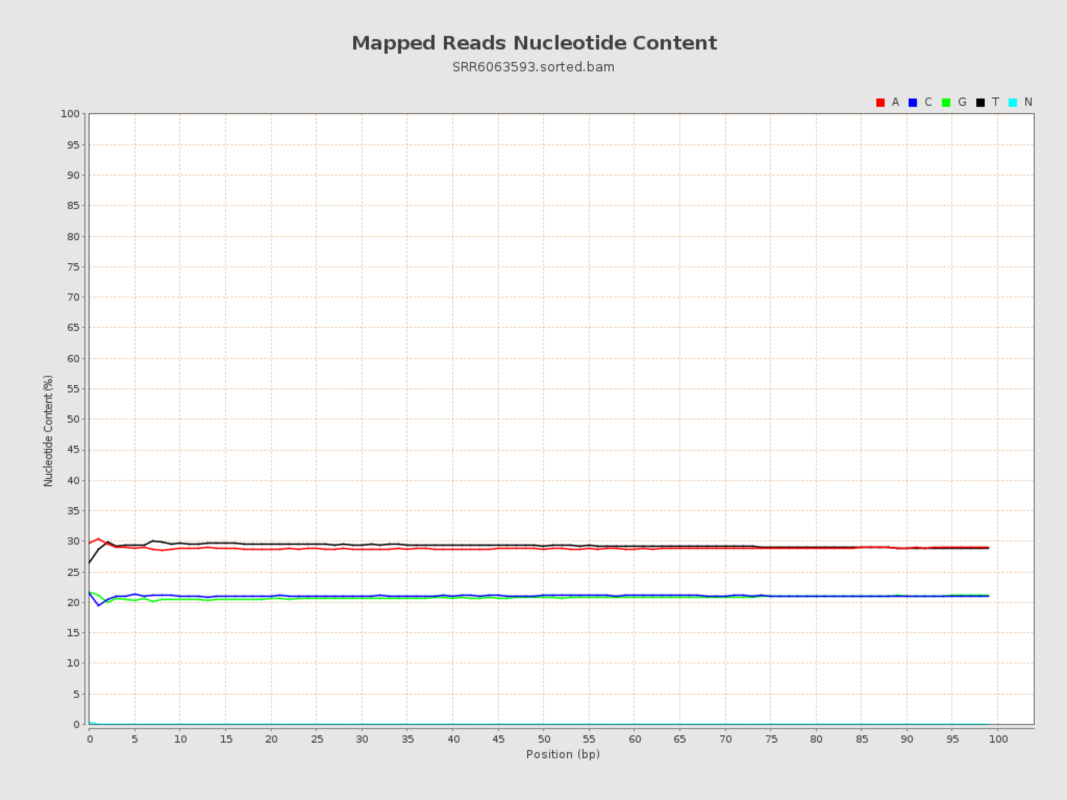
6. Results : Genome Fraction Coverage



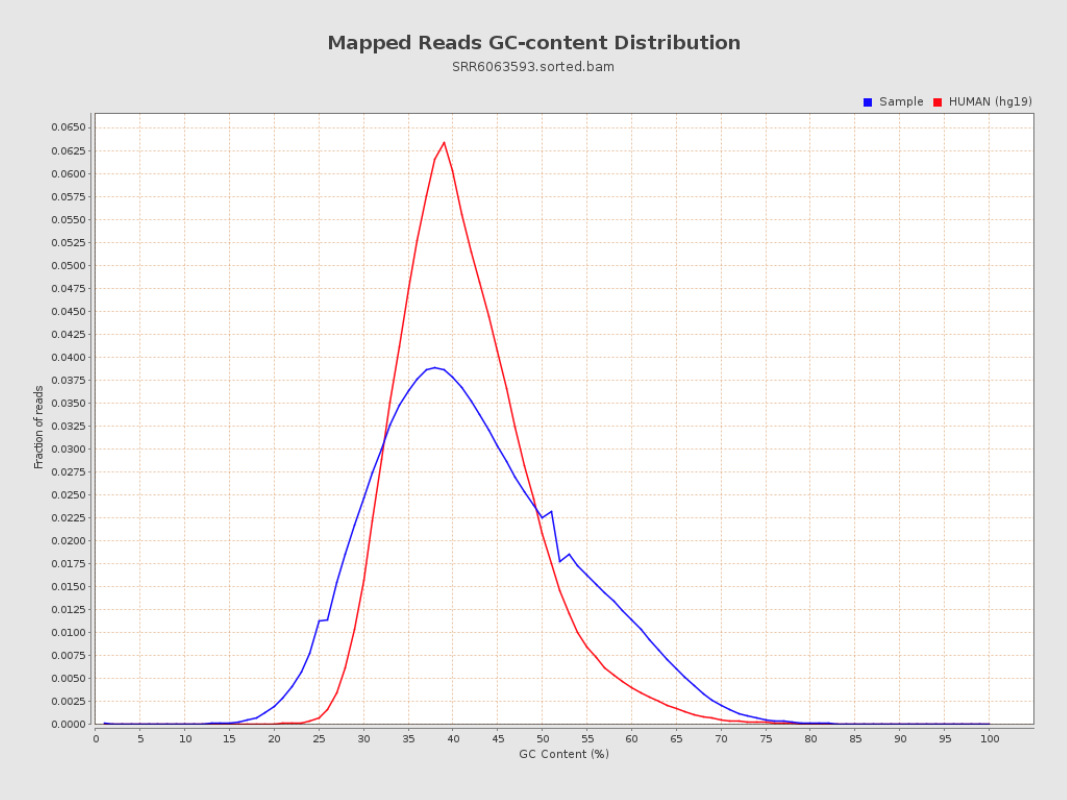
7. Results : Duplication Rate Histogram



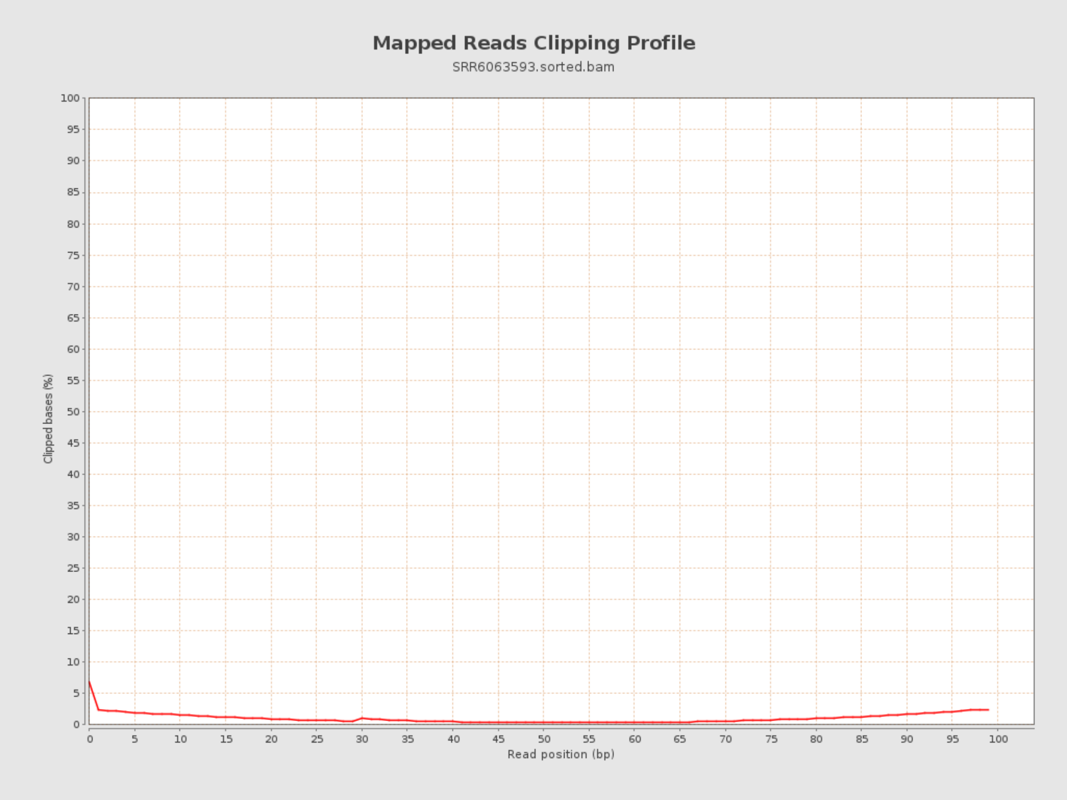
8. Results : Mapped Reads Nucleotide Content



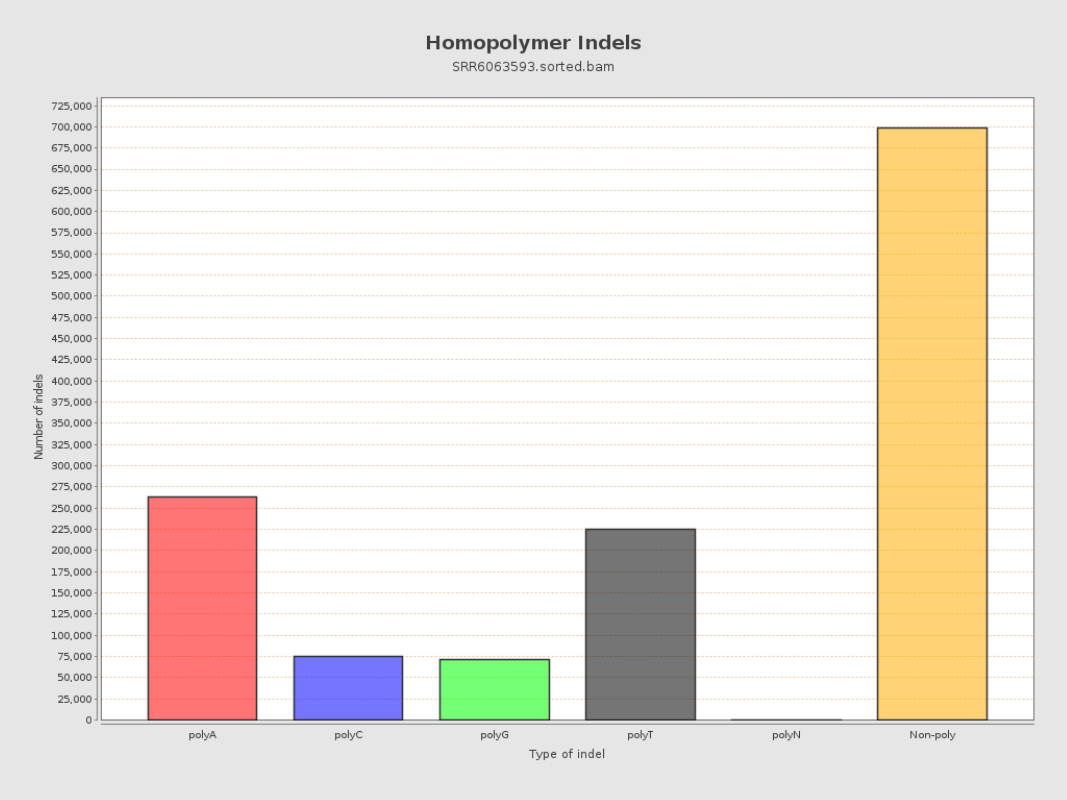
9. Results : Mapped Reads GC-content Distribution



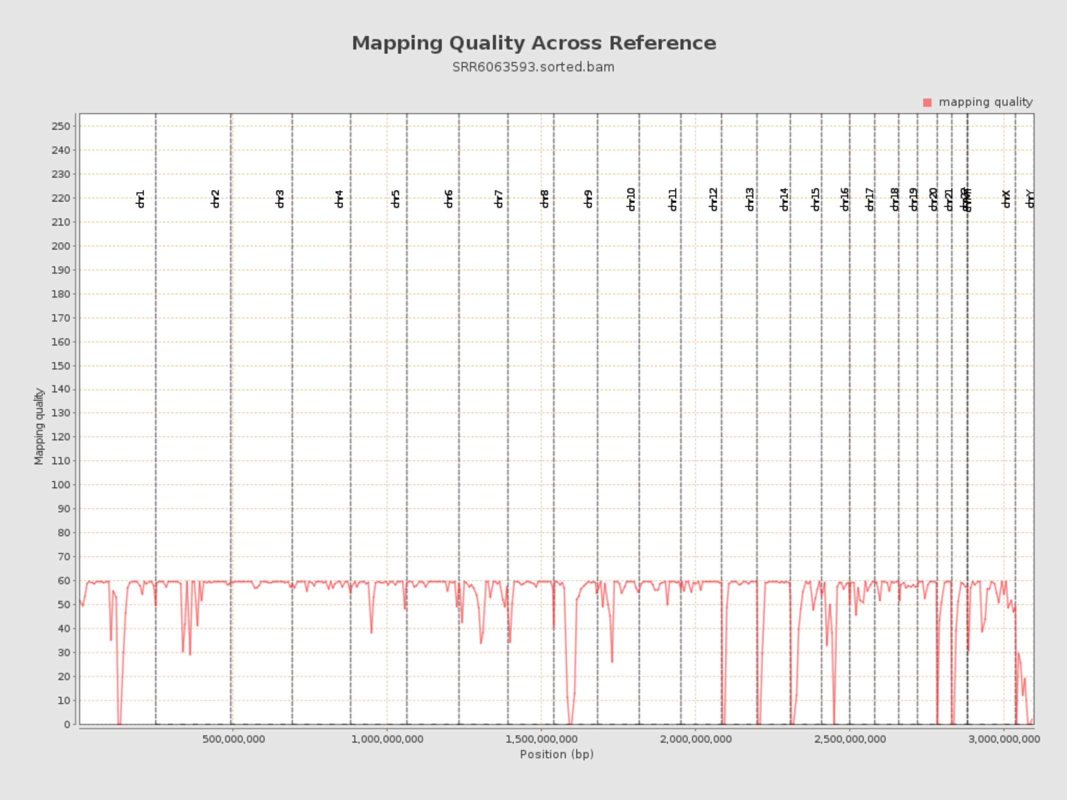
10. Results : Mapped Reads Clipping Profile



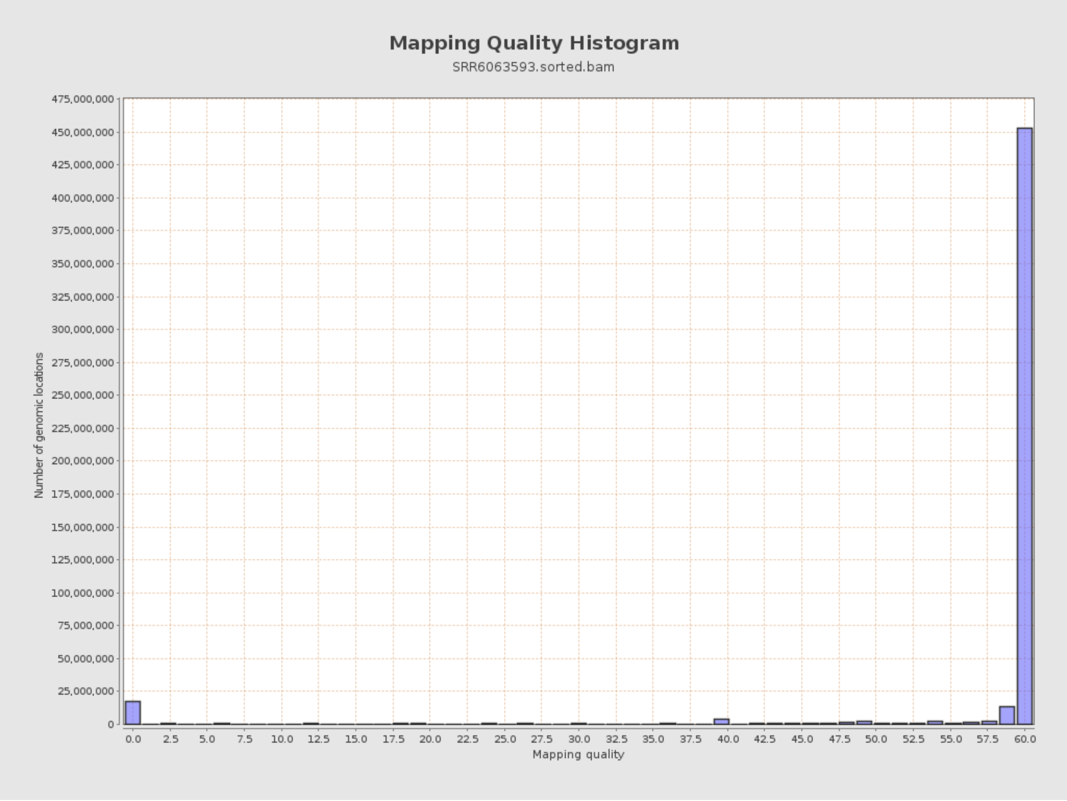
11. Results : Homopolymer Indels



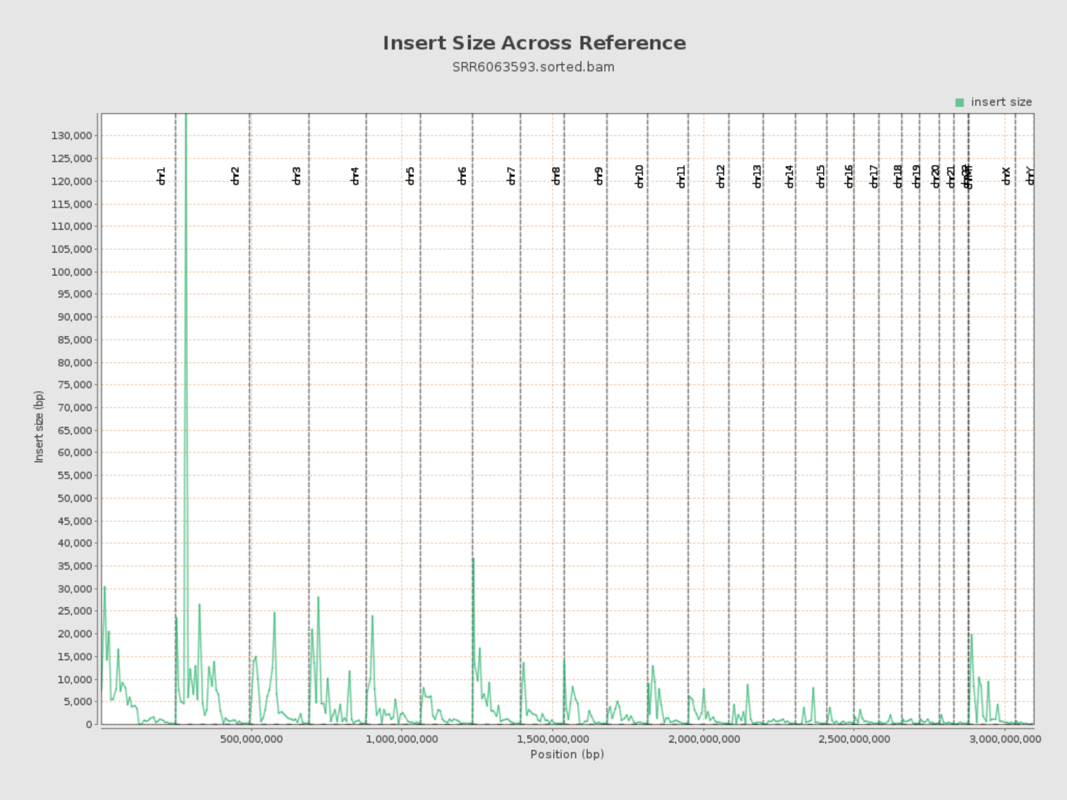
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram