Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 23:56:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671999.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_SRR21671999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671999_1.fastq.gz SRR21671999_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 23:56:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	335,285,616
Mapped reads	333,045,864 / 99.33%
Unmapped reads	2,239,752 / 0.67%
Mapped paired reads	333,045,864 / 99.33%
Mapped reads, first in pair	166,594,419 / 49.69%
Mapped reads, second in pair	166,451,445 / 49.64%
Mapped reads, both in pair	332,478,200 / 99.16%
Mapped reads, singletons	567,664 / 0.17%
Secondary alignments	0
Supplementary alignments	1,121,121 / 0.33%
Read min/max/mean length	15 / 150 / 149.66
Duplicated reads (estimated)	100,783,646 / 30.06%
Duplication rate	27.24%
Clipped reads	14,182,630 / 4.23%

2.2. ACGT Content

Number/percentage of A's	15,240,894,778 / 30.83%
Number/percentage of C's	9,514,409,417 / 19.25%
Number/percentage of T's	15,126,539,503 / 30.6%
Number/percentage of G's	9,550,464,534 / 19.32%
Number/percentage of N's	257,693 / 0%

GC Percentage	38.57%

2.3. Coverage

Mean	15.9742
Standard Deviation	220.7576

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	16,575.8
Standard Deviation	1,162,202.55
P25/Median/P75	294 / 338 / 389

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	304,333,222
Insertions	5,895,705
Mapped reads with at least one insertion	1.69%
Deletions	7,049,199
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.28%

2.7. Chromosome stats

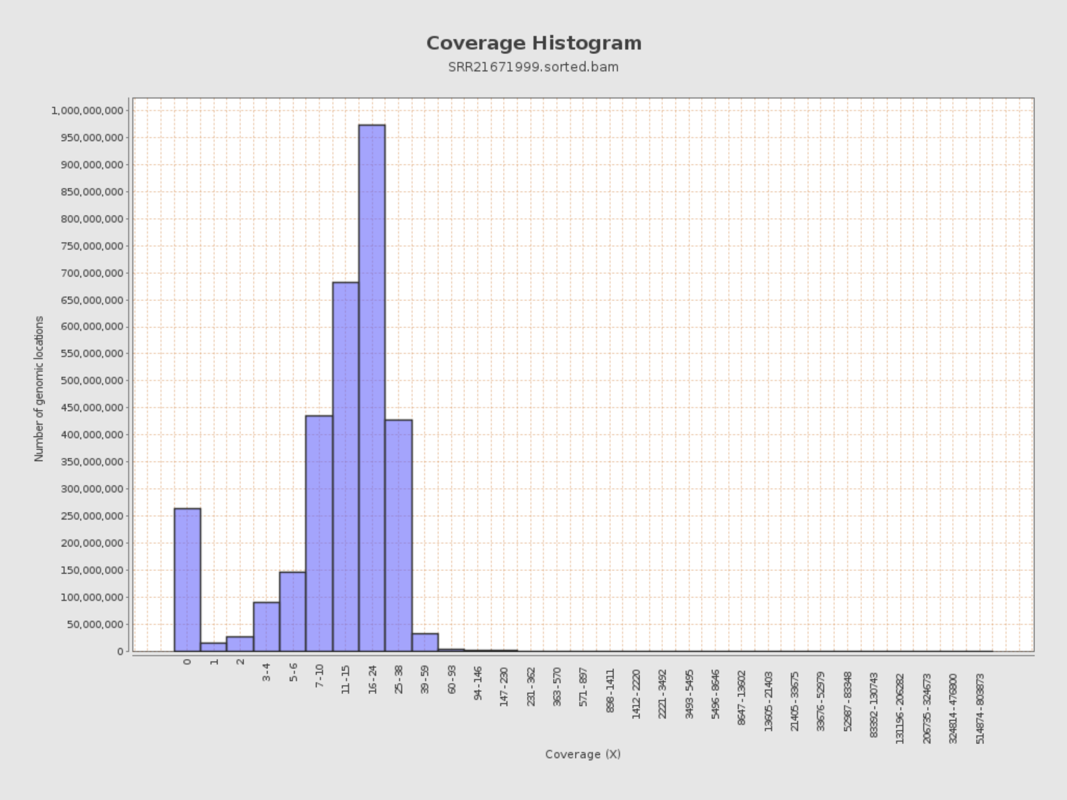
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	3717137114	14.9133	367.2861
chr2	243199373	4507968080	18.5361	96.2729
chr3	198022430	3651217386	18.4384	10.0348
chr4	191154276	3876965818	20.2819	60.9723
chr5	180915260	3334099906	18.4291	13.0841
chr6	171115067	3199777581	18.6996	45.763
chr7	159138663	2765496698	17.3779	128.8044
chr8	146364022	2749704020	18.7867	649.0467
chr9	141213431	1980993286	14.0284	264.4948
chr10	135534747	2418705933	17.8457	343.4194
chr11	135006516	2129995287	15.777	83.8471
chr12	133851895	2228175560	16.6466	13.699
chr13	115169878	1854656255	16.1037	10.6314
chr14	107349540	1459793865	13.5985	11.789
chr15	102531392	1162035652	11.3335	9.3327
chr16	90354753	1043392412	11.5477	63.7459
chr17	81195210	924571218	11.387	60.2108
chr18	78077248	1380628111	17.6828	190.9665
chr19	59128983	577828146	9.7723	168.4852
chr20	63025520	755317234	11.9843	24.6493
chr21	48129895	629683928	13.083	29.7477
chr22	51304566	309366965	6.03	16.0495
chrMT	16571	527410749	31,827.3338	3,538.5756
chrX	155270560	2183215448	14.0607	29.6305

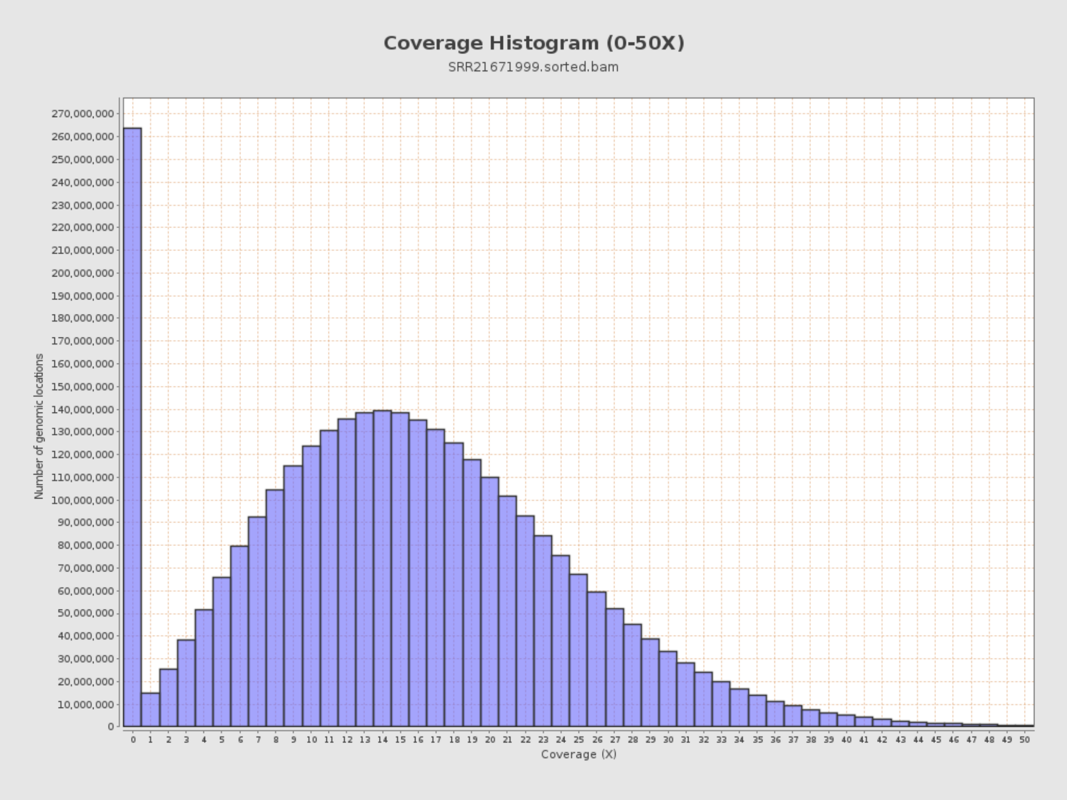
chrY	59373566	83144521	1.4004	66.6733

3. Results : Coverage across reference

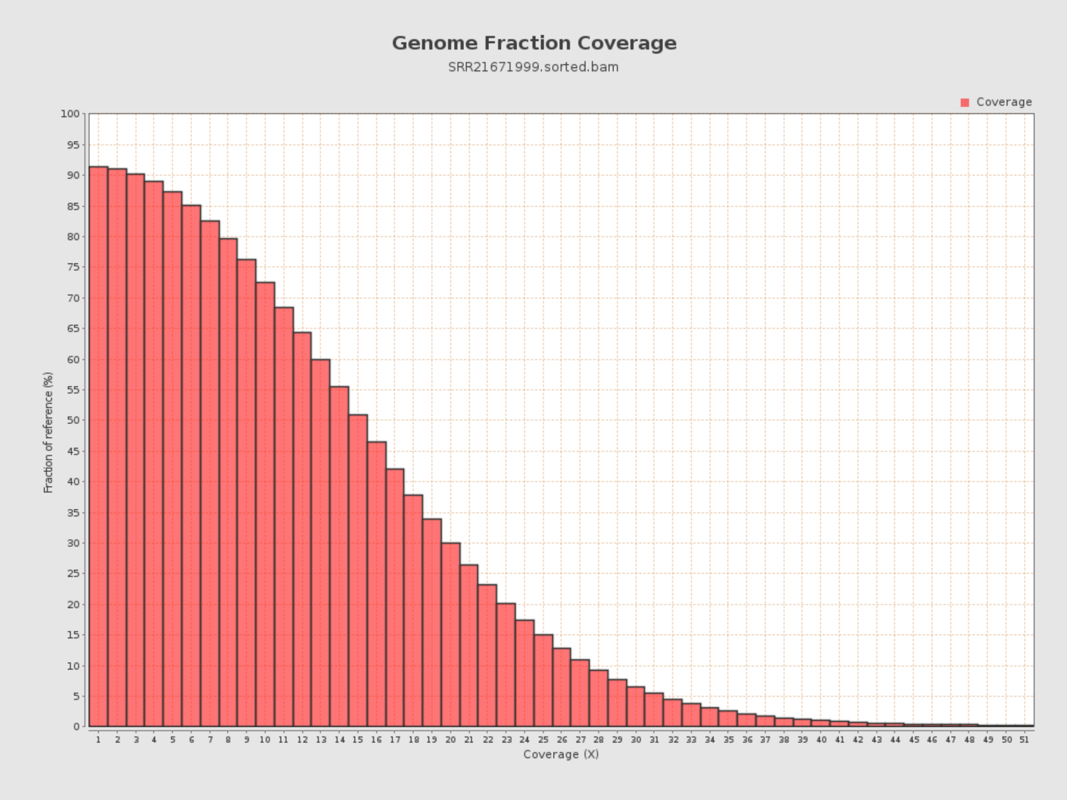
4. Results : Coverage Histogram



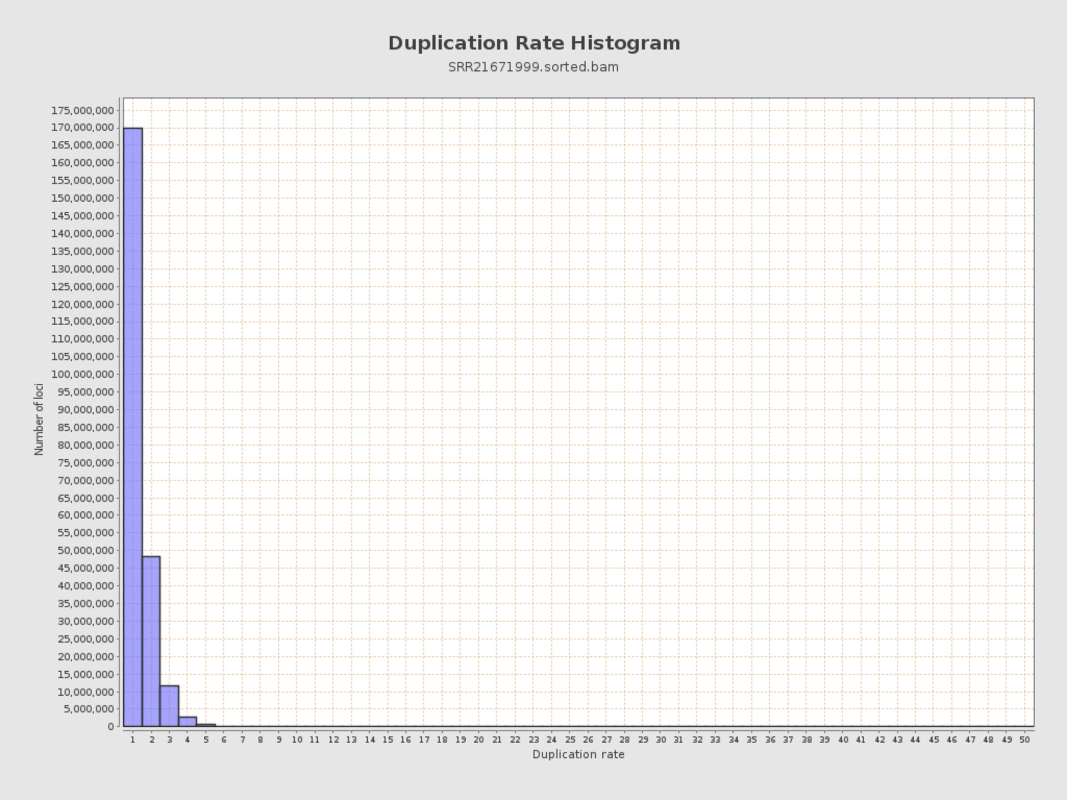
5. Results : Coverage Histogram (0-50X)



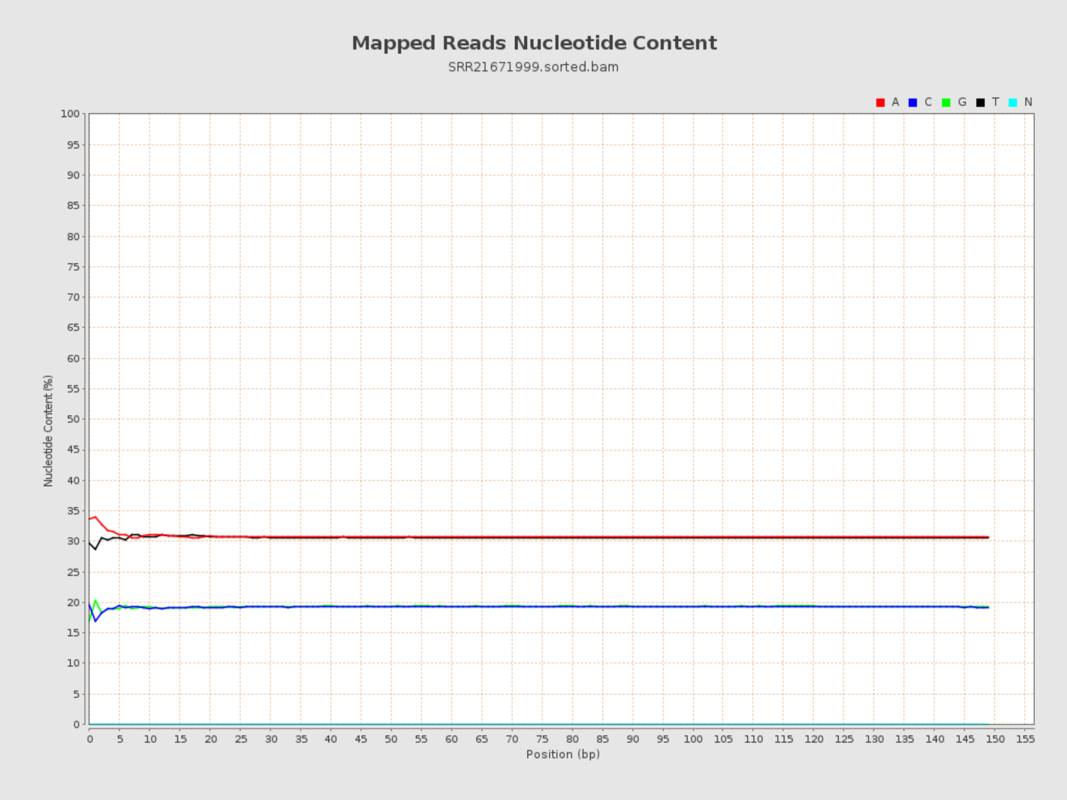
6. Results : Genome Fraction Coverage



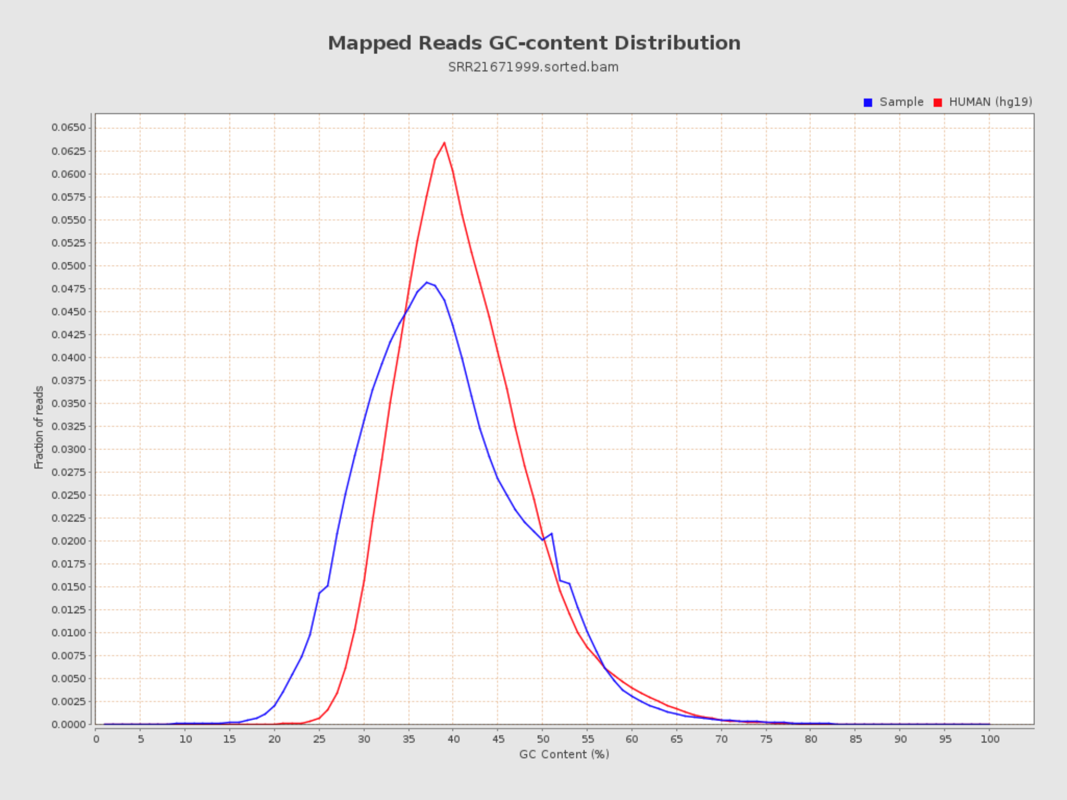
7. Results : Duplication Rate Histogram



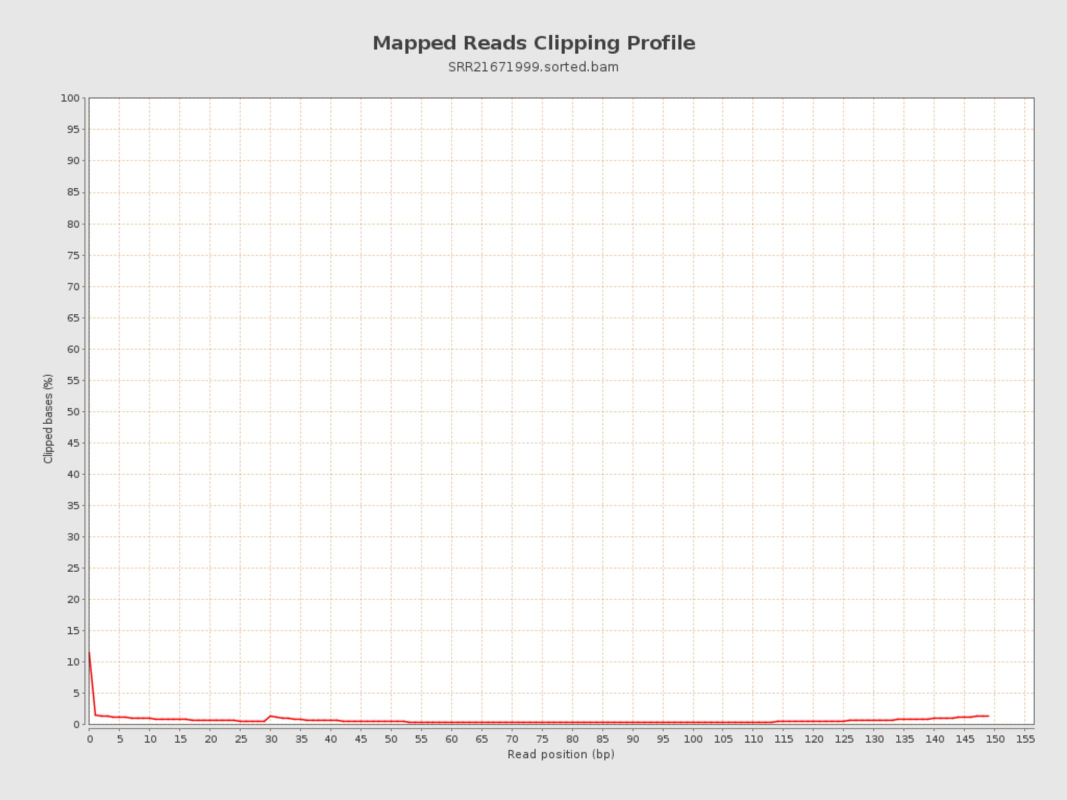
8. Results : Mapped Reads Nucleotide Content



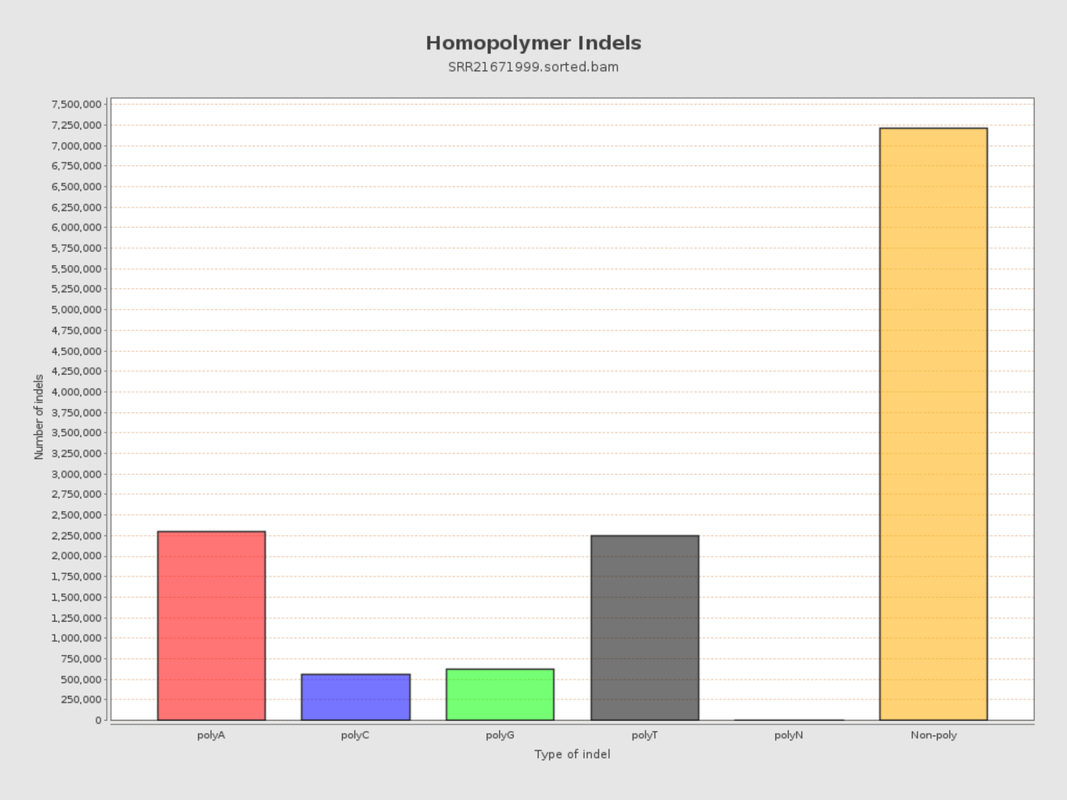
9. Results : Mapped Reads GC-content Distribution



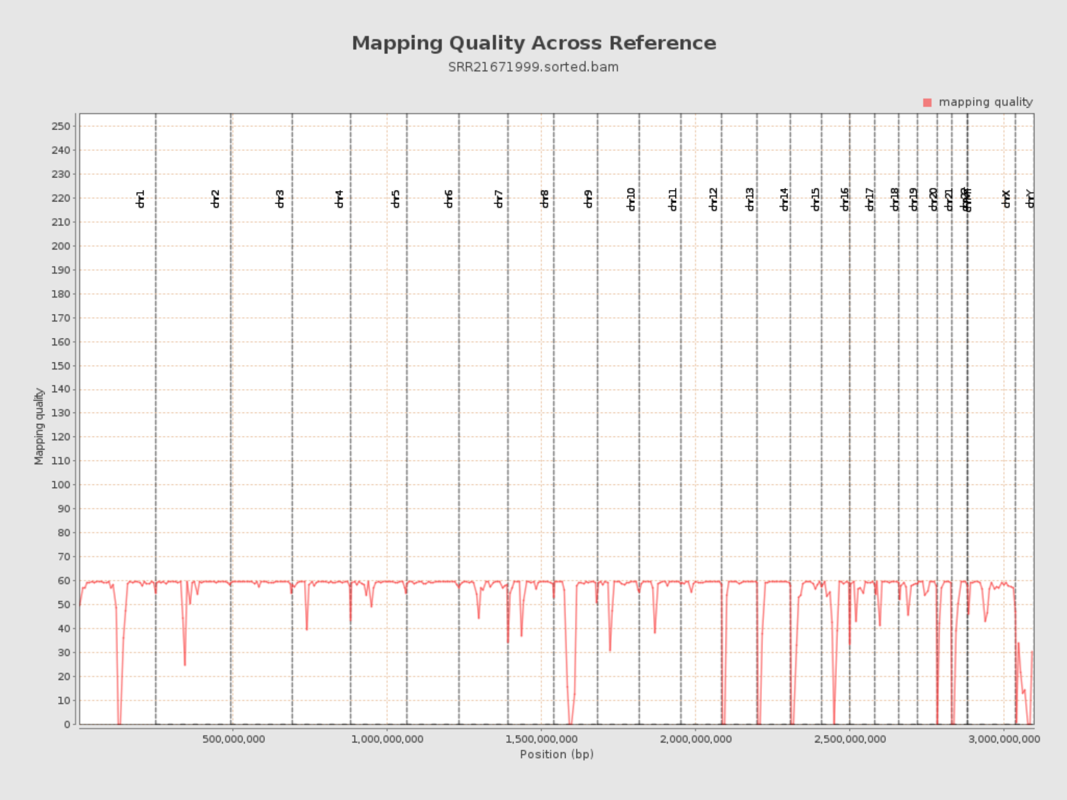
10. Results : Mapped Reads Clipping Profile



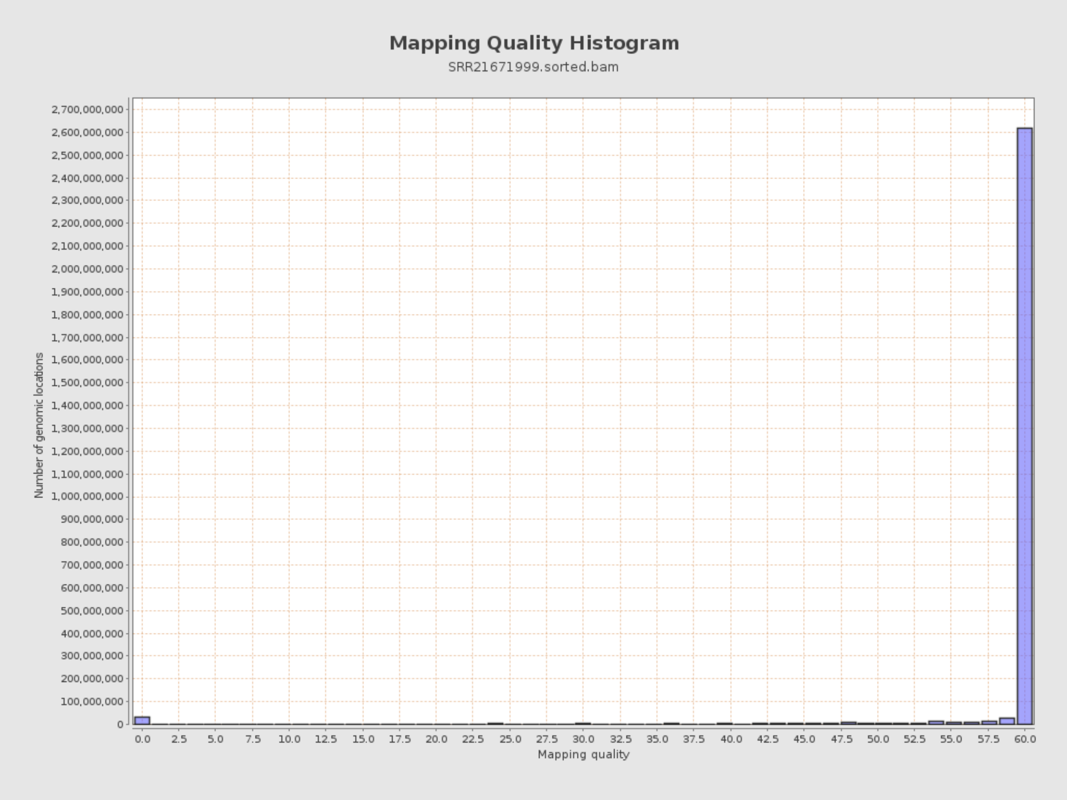
11. Results : Homopolymer Indels



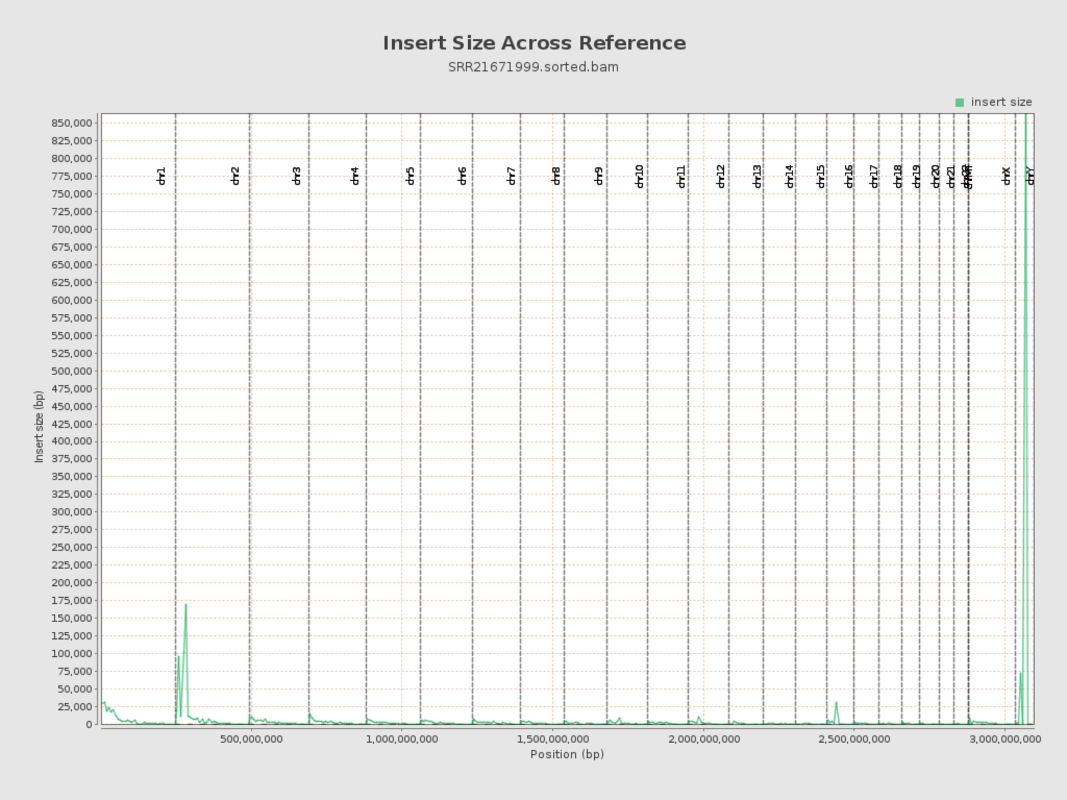
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram