Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 23:50:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672008.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_SRR21672008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672008_1.fastq.gz SRR21672008_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 23:50:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,789,502
Mapped reads	161,118,315 / 98.97%
Unmapped reads	1,671,187 / 1.03%
Mapped paired reads	161,118,315 / 98.97%
Mapped reads, first in pair	80,539,458 / 49.47%
Mapped reads, second in pair	80,578,857 / 49.5%
Mapped reads, both in pair	160,448,500 / 98.56%
Mapped reads, singletons	669,815 / 0.41%
Secondary alignments	0
Supplementary alignments	1,085,669 / 0.67%
Read min/max/mean length	15 / 150 / 150.07
Duplicated reads (estimated)	68,846,636 / 42.29%
Duplication rate	31.83%
Clipped reads	79,746,847 / 48.99%

2.2. ACGT Content

Number/percentage of A's	5,595,367,389 / 25.35%
Number/percentage of C's	4,799,270,256 / 21.74%
Number/percentage of T's	5,999,380,657 / 27.18%
Number/percentage of G's	5,678,828,860 / 25.73%
Number/percentage of N's	187,796 / 0%

GC Percentage	47.47%

2.3. Coverage

Mean	7.1344
Standard Deviation	59.9049

2.4. Mapping Quality

Mean Mapping Quality	54.09

2.5. Insert size

Mean	118,940.67
Standard Deviation	3,457,762.48
P25/Median/P75	256 / 307 / 358

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	209,808,950
Insertions	3,305,516
Mapped reads with at least one insertion	1.95%
Deletions	6,685,186
Mapped reads with at least one deletion	4.02%
Homopolymer indels	45.94%

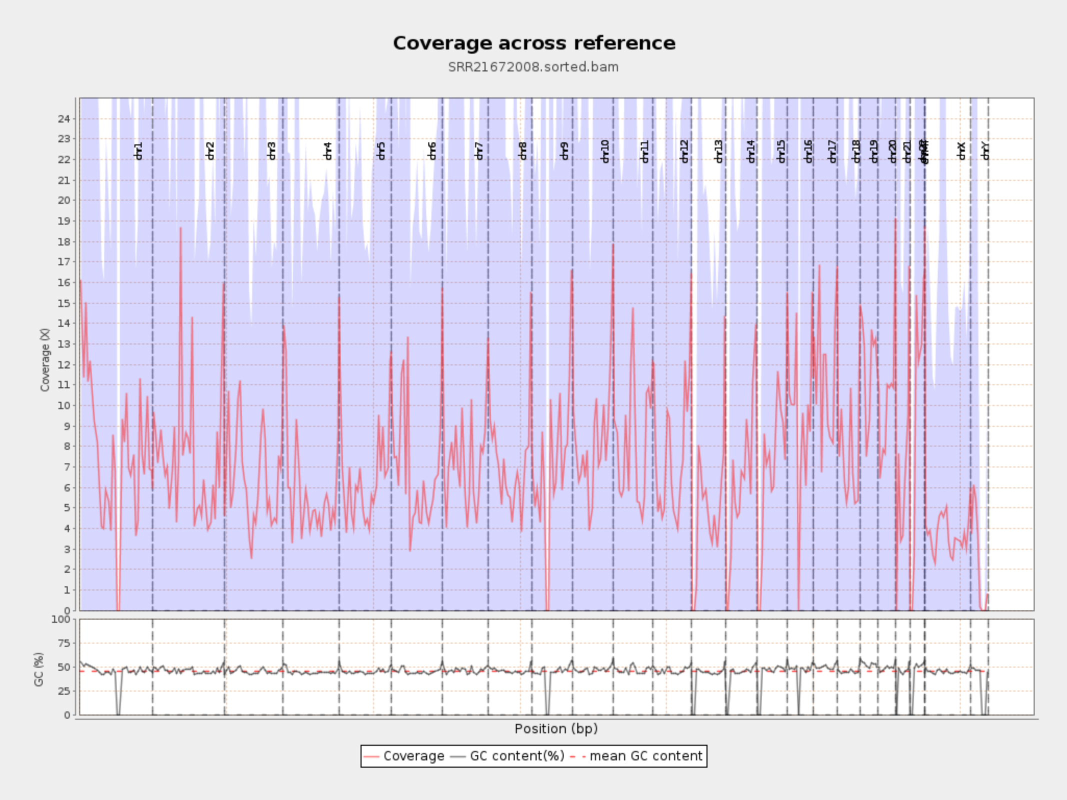
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

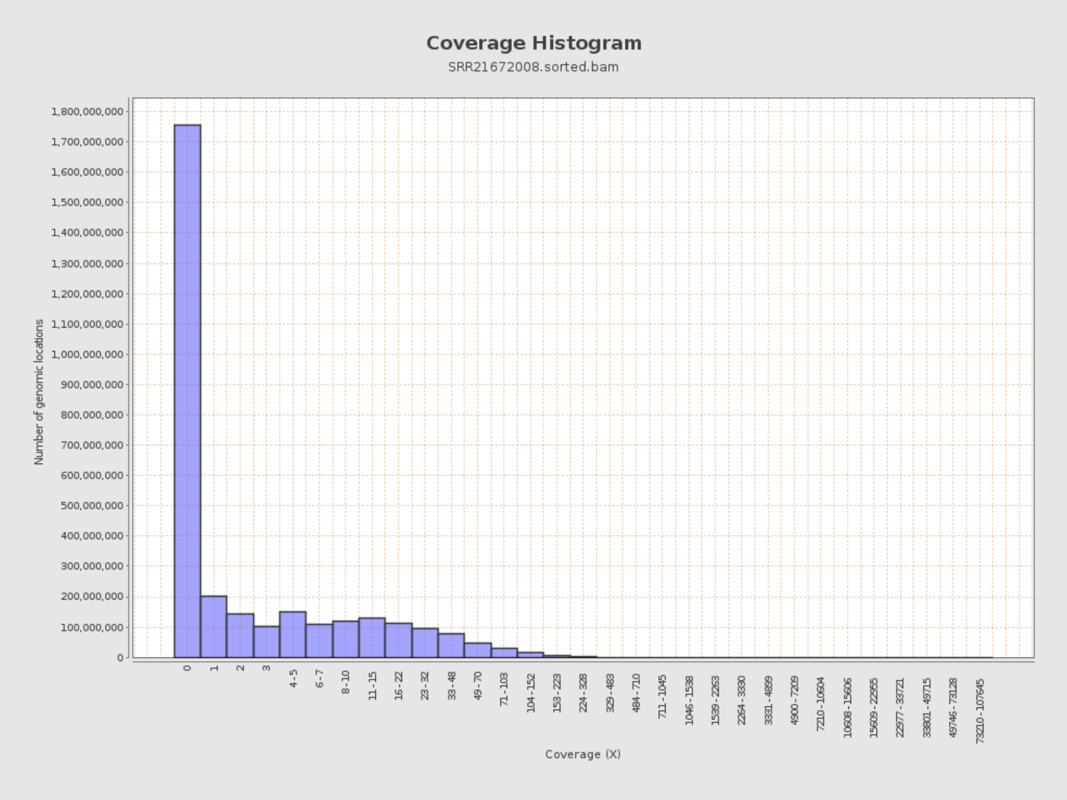
		bases	coverage	deviation
chr1	249250621	1912024141	7.6711	54.8722
chr2	243199373	1831399149	7.5304	106.2524
chr3	198022430	1287157611	6.5001	18.0903
chr4	191154276	1105429227	5.7829	30.6303
chr5	180915260	1182565234	6.5366	19.5539
chr6	171115067	1155375431	6.752	124.7564
chr7	159138663	1169355073	7.348	31.7895
chr8	146364022	1039123106	7.0996	23.3061
chr9	141213431	1011187655	7.1607	92.699
chr10	135534747	1102494404	8.1344	22.8165
chr11	135006516	1133678055	8.3972	49.795
chr12	133851895	1005255149	7.5102	21.1066
chr13	115169878	538665576	4.6771	15.424
chr14	107349540	671594536	6.2561	20.1916
chr15	102531392	686217932	6.6928	19.6572
chr16	90354753	869783064	9.6263	60.84
chr17	81195210	931956584	11.478	97.0898
chr18	78077248	573636863	7.347	103.0823
chr19	59128983	717540291	12.1352	33.9148
chr20	63025520	631800008	10.0245	25.6739
chr21	48129895	319313970	6.6344	88.6425
chr22	51304566	494103213	9.6308	32.1047
chrMT	16571	310382	18.7304	65.2497
chrX	155270560	570508524	3.6743	19.6821

chrY	59373566	145372797	2.4484	33.6723

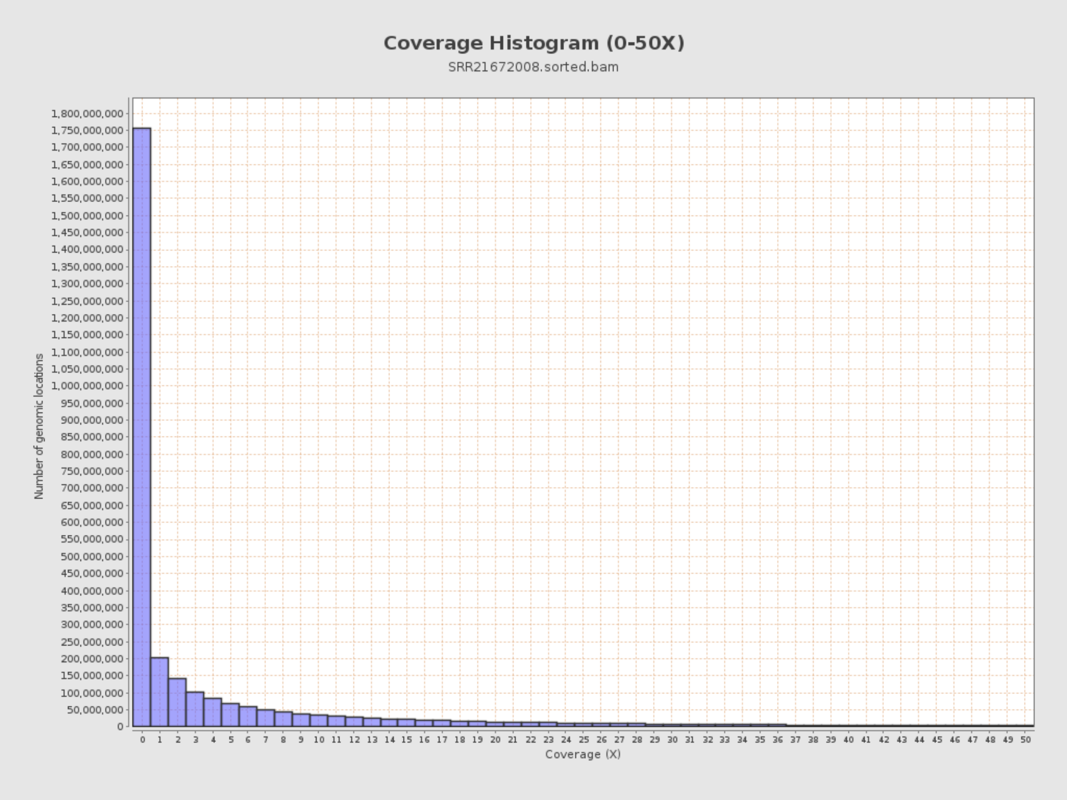
3. Results : Coverage across reference



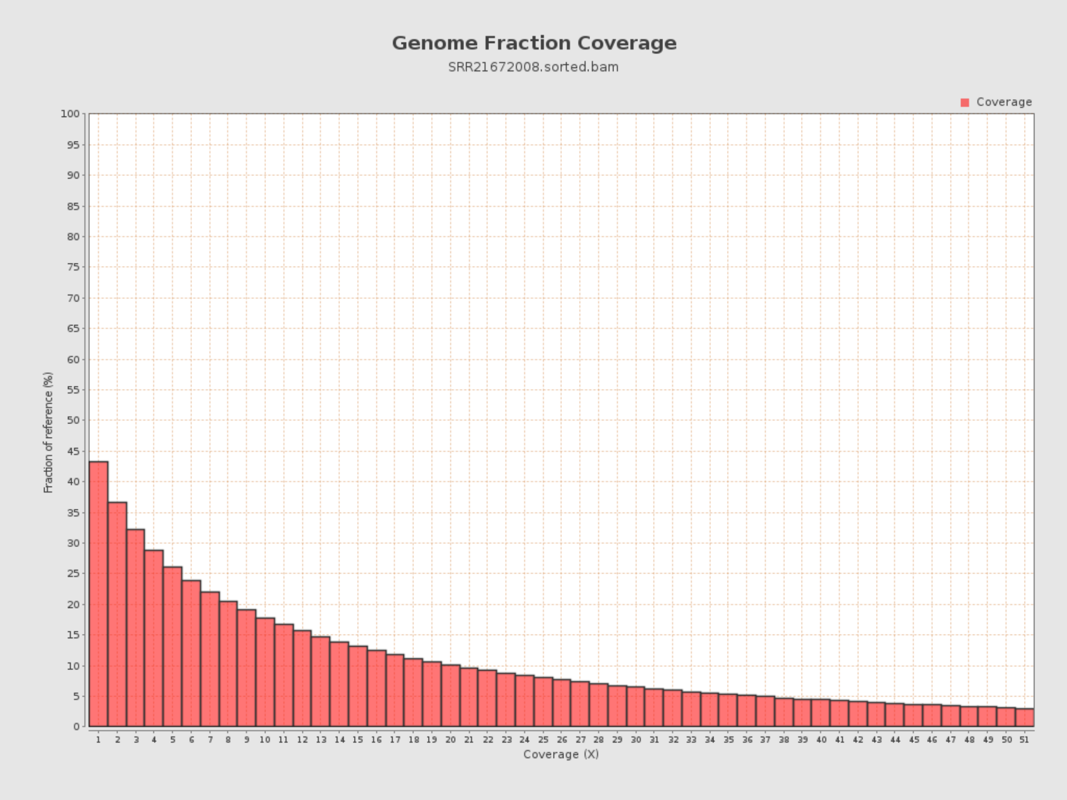
4. Results : Coverage Histogram



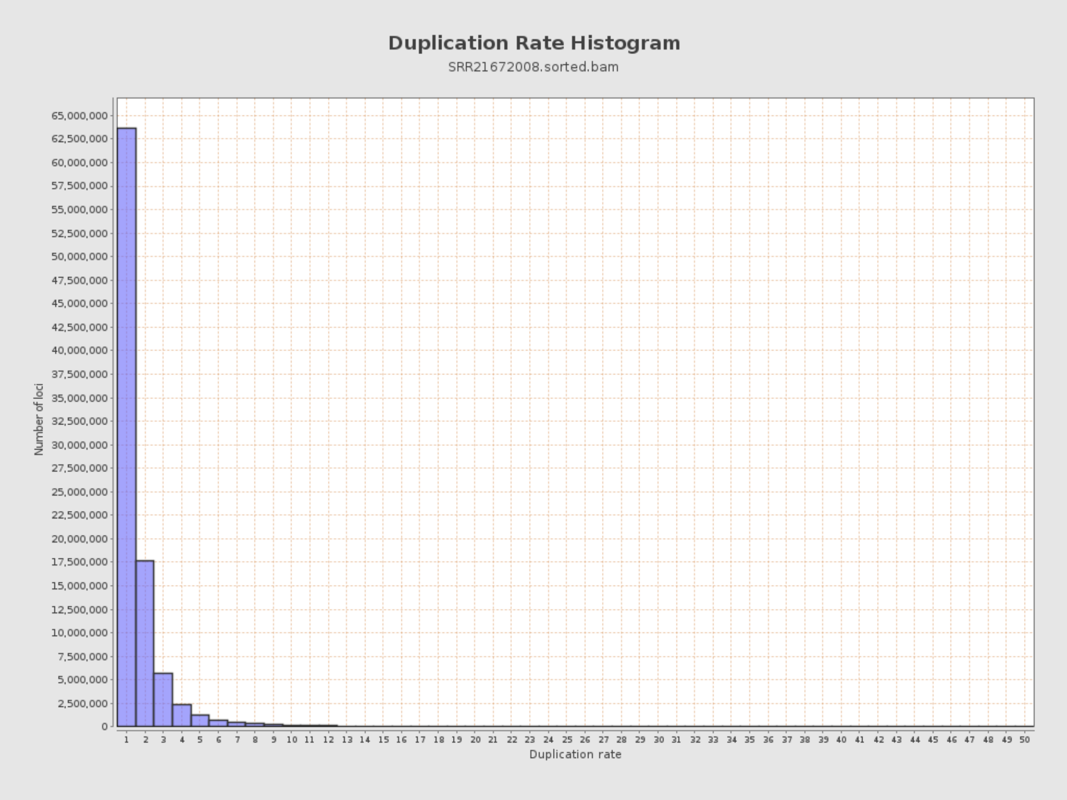
5. Results : Coverage Histogram (0-50X)



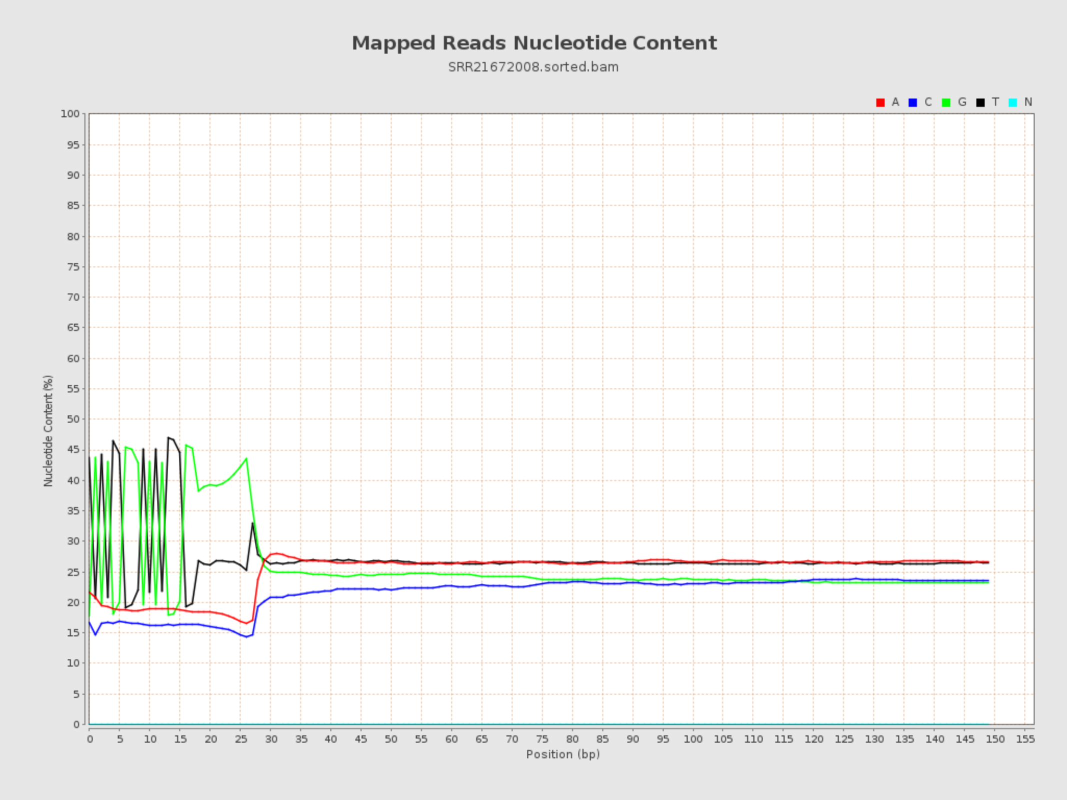
6. Results : Genome Fraction Coverage



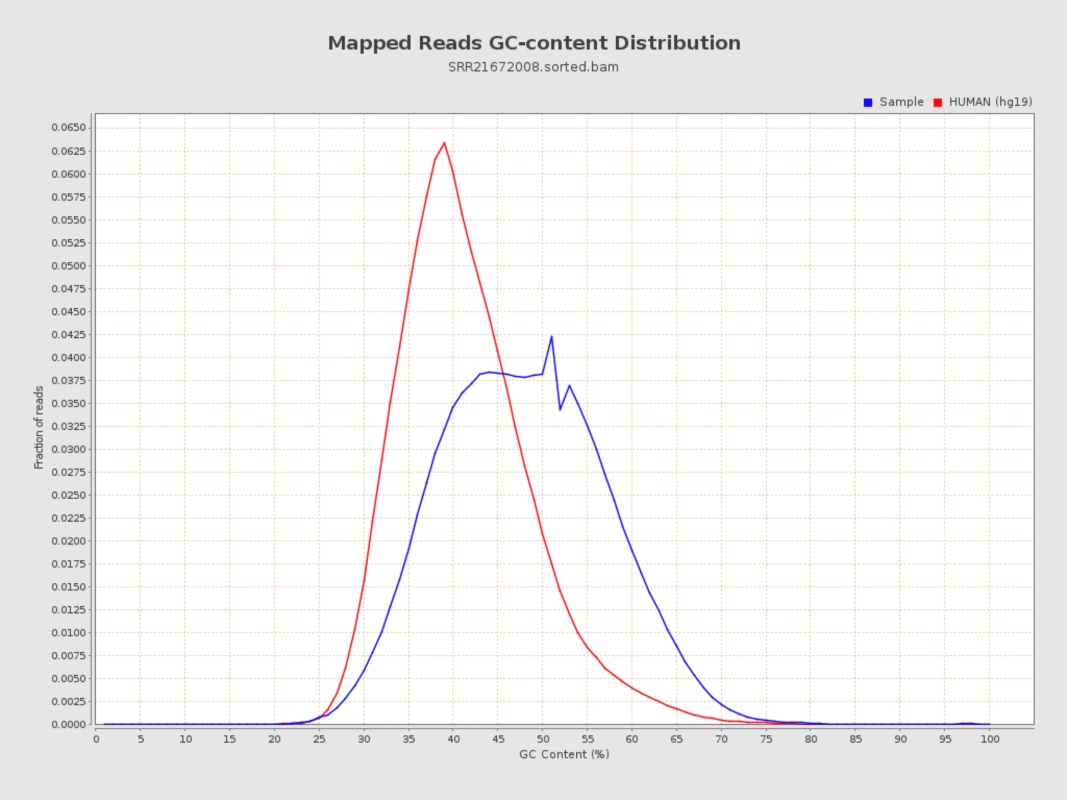
7. Results : Duplication Rate Histogram



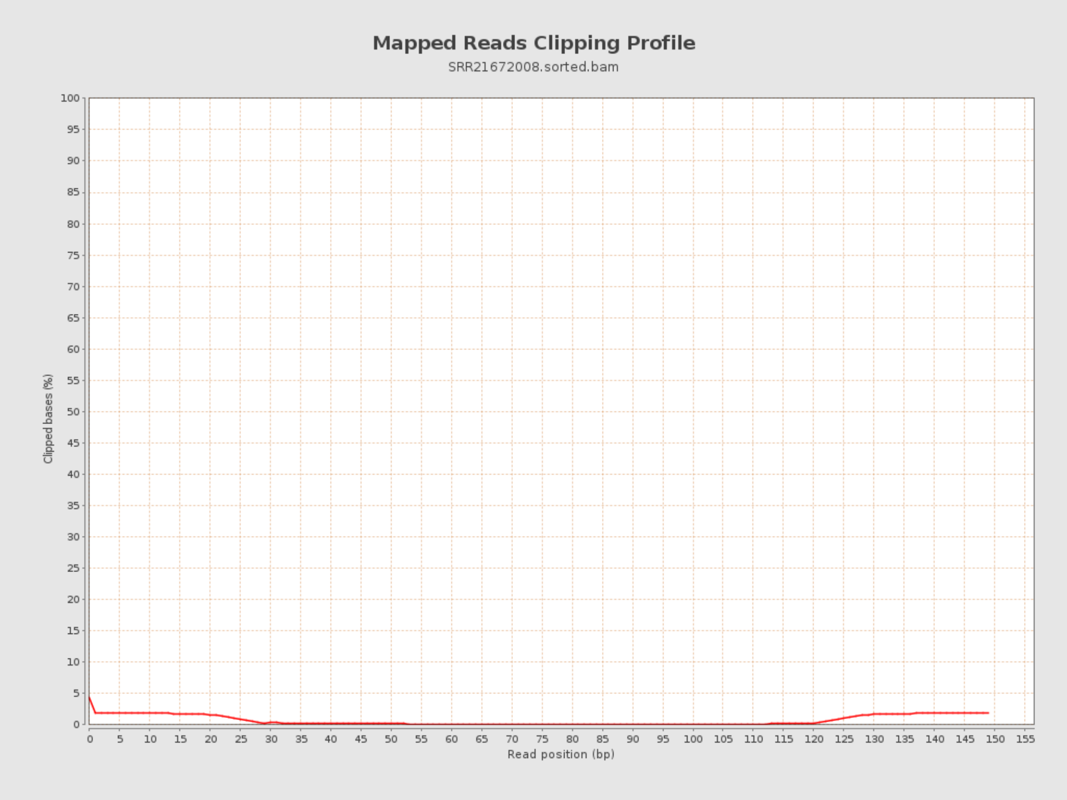
8. Results : Mapped Reads Nucleotide Content



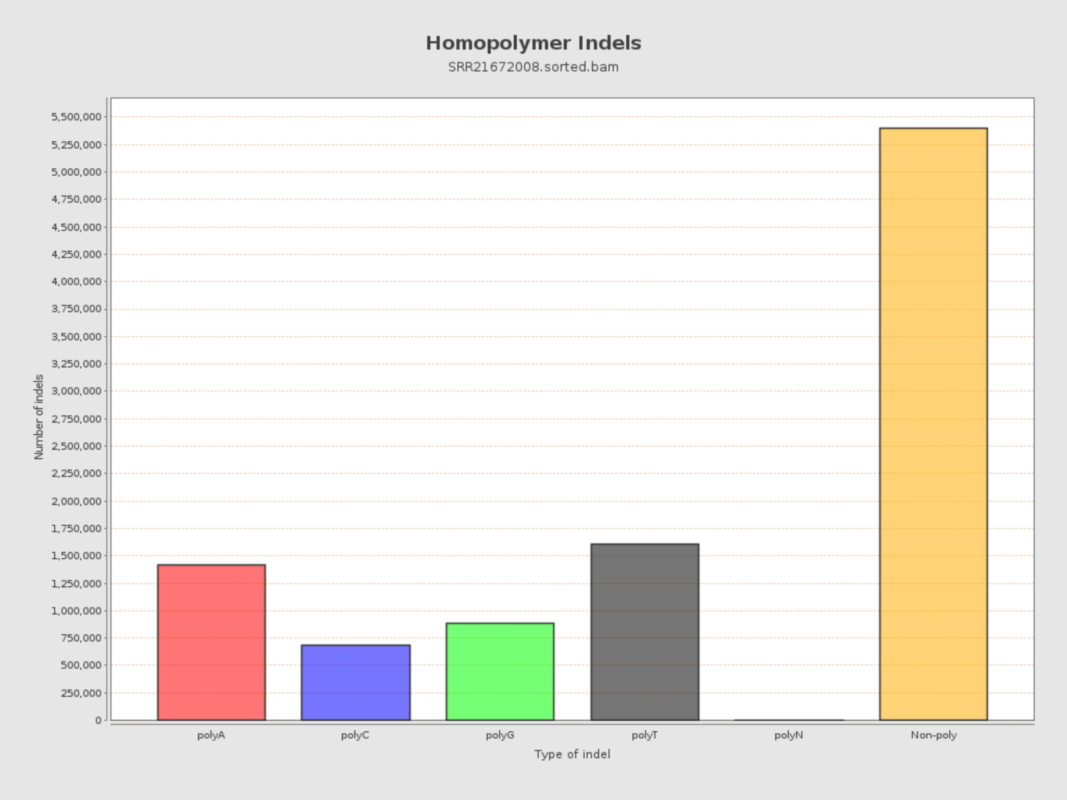
9. Results : Mapped Reads GC-content Distribution



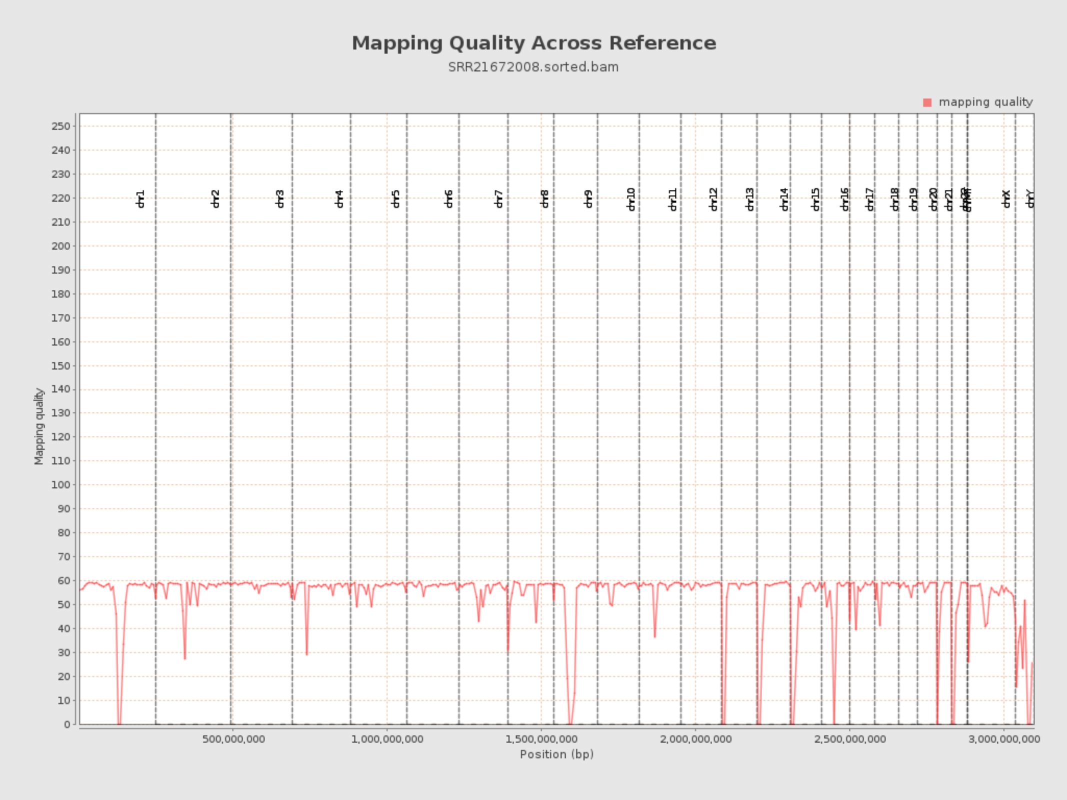
10. Results : Mapped Reads Clipping Profile



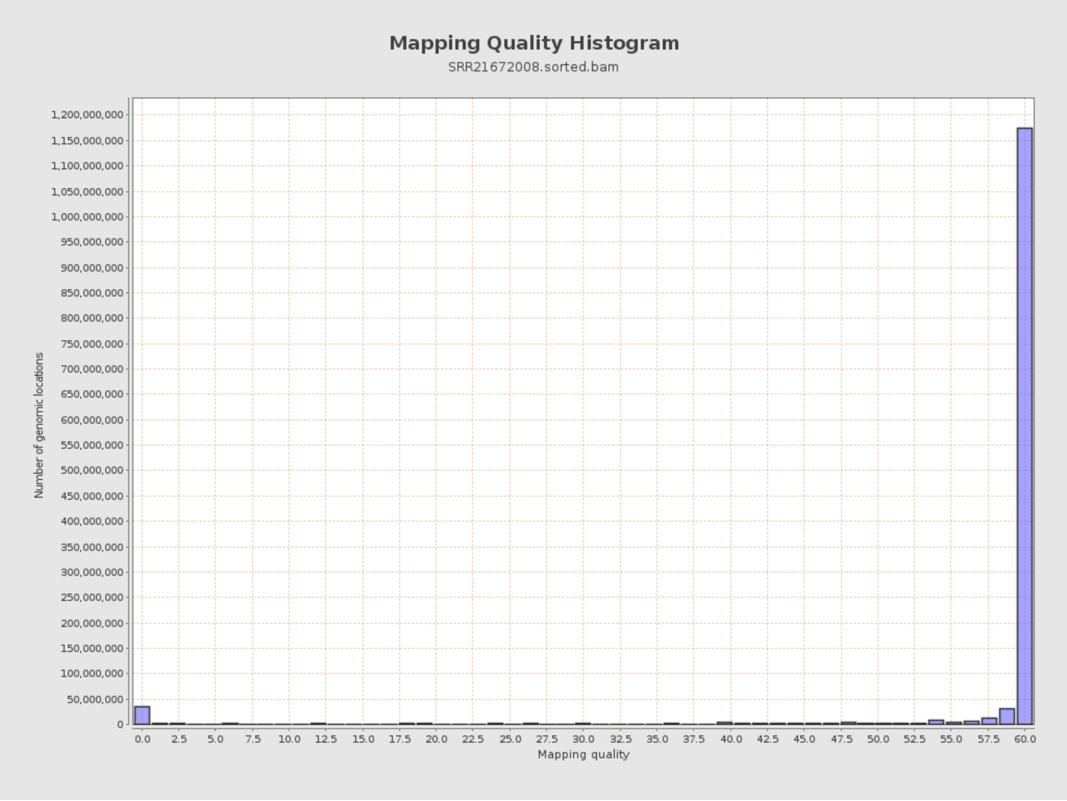
11. Results : Homopolymer Indels



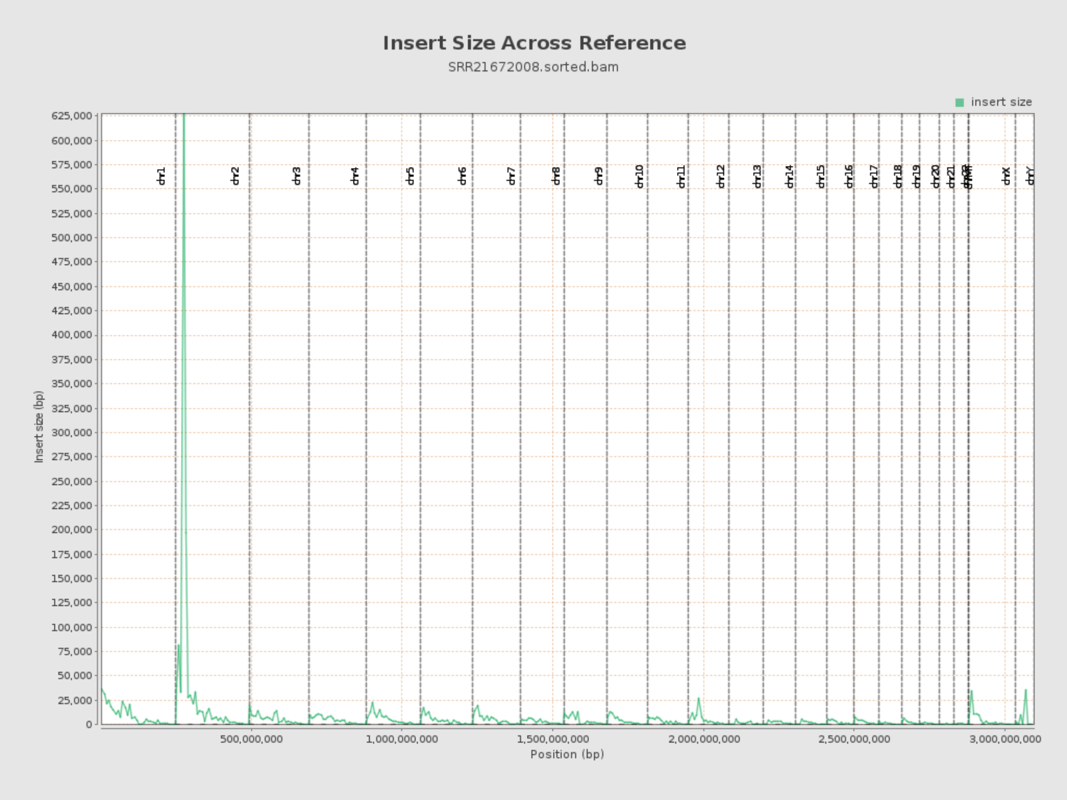
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram