Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 01:40:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672004.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_SRR21672004 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672004_1.fastq.gz SRR21672004_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 01:40:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672004.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	220,558,222
Mapped reads	219,223,887 / 99.4%
Unmapped reads	1,334,335 / 0.6%
Mapped paired reads	219,223,887 / 99.4%
Mapped reads, first in pair	109,624,014 / 49.7%
Mapped reads, second in pair	109,599,873 / 49.69%
Mapped reads, both in pair	218,833,598 / 99.22%
Mapped reads, singletons	390,289 / 0.18%
Secondary alignments	0
Supplementary alignments	884,235 / 0.4%
Read min/max/mean length	15 / 150 / 149.61
Duplicated reads (estimated)	60,727,368 / 27.53%
Duplication rate	25.11%
Clipped reads	9,922,009 / 4.5%

2.2. ACGT Content

Number/percentage of A's	9,485,796,163 / 29.19%
Number/percentage of C's	6,777,898,887 / 20.86%
Number/percentage of T's	9,437,843,193 / 29.04%
Number/percentage of G's	6,797,325,303 / 20.92%
Number/percentage of N's	142,003 / 0%

GC Percentage	41.77%

2.3. Coverage

Mean	10.5024
Standard Deviation	105.7071

2.4. Mapping Quality

Mean Mapping Quality	54.57

2.5. Insert size

Mean	37,968.75
Standard Deviation	1,850,289.3
P25/Median/P75	319 / 369 / 421

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	192,067,164
Insertions	4,476,362
Mapped reads with at least one insertion	1.93%
Deletions	4,742,950
Mapped reads with at least one deletion	2.08%
Homopolymer indels	45.95%

2.7. Chromosome stats

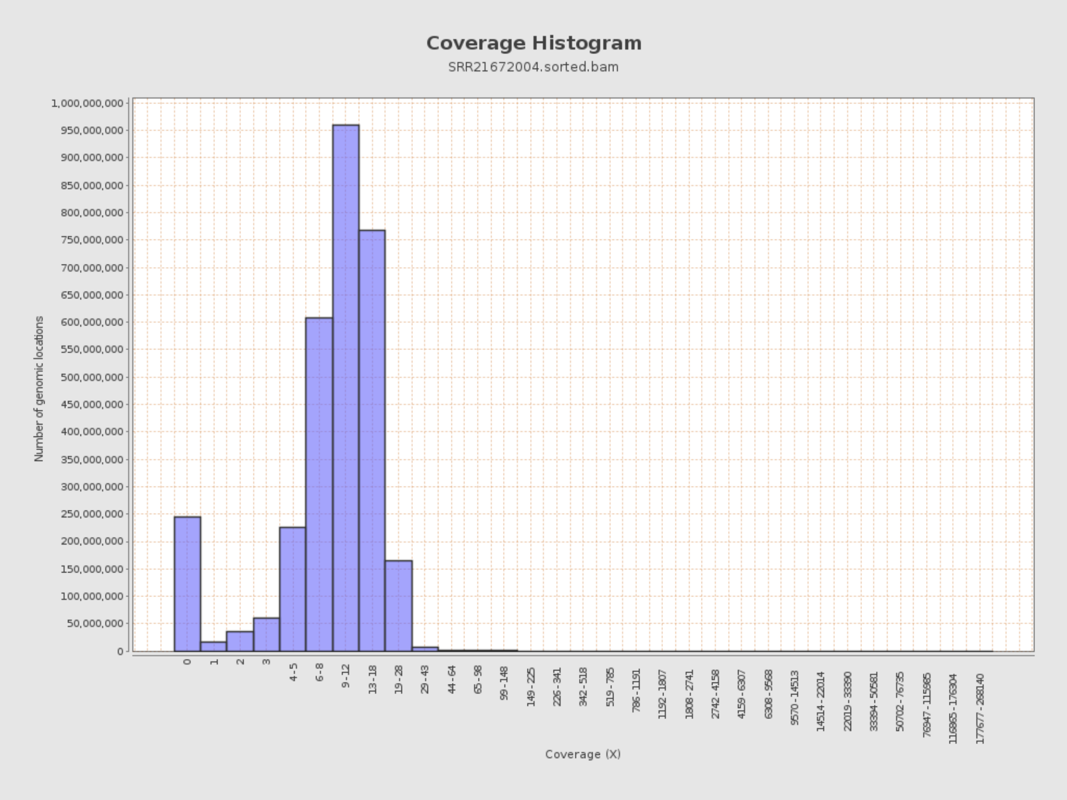
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	2720207735	10.9135	280.228
chr2	243199373	2809279668	11.5513	68.254
chr3	198022430	2147635336	10.8454	7.5739
chr4	191154276	2109816338	11.0372	60.155
chr5	180915260	1955897533	10.8111	9.6668
chr6	171115067	1880883544	10.9919	58.1102
chr7	159138663	1779014687	11.179	72.2424
chr8	146364022	1637774186	11.1897	68.8791
chr9	141213431	1427250626	10.107	159.2478
chr10	135534747	1639347456	12.0954	137.2054
chr11	135006516	1514918754	11.2211	52.0483
chr12	133851895	1451724618	10.8458	8.7518
chr13	115169878	1029437690	8.9384	6.9415
chr14	107349540	995044060	9.2692	8.7027
chr15	102531392	926988146	9.041	6.5716
chr16	90354753	1051685437	11.6395	60.7151
chr17	81195210	968266006	11.9252	66.9328
chr18	78077248	934068445	11.9634	169.7835
chr19	59128983	703413575	11.8963	119.2462
chr20	63025520	712359229	11.3027	25.4739
chr21	48129895	465573797	9.6733	40.2237
chr22	51304566	444498398	8.6639	40.9057
chrMT	16571	33424765	2,017.0638	280.5737
chrX	155270560	863611149	5.562	20.764

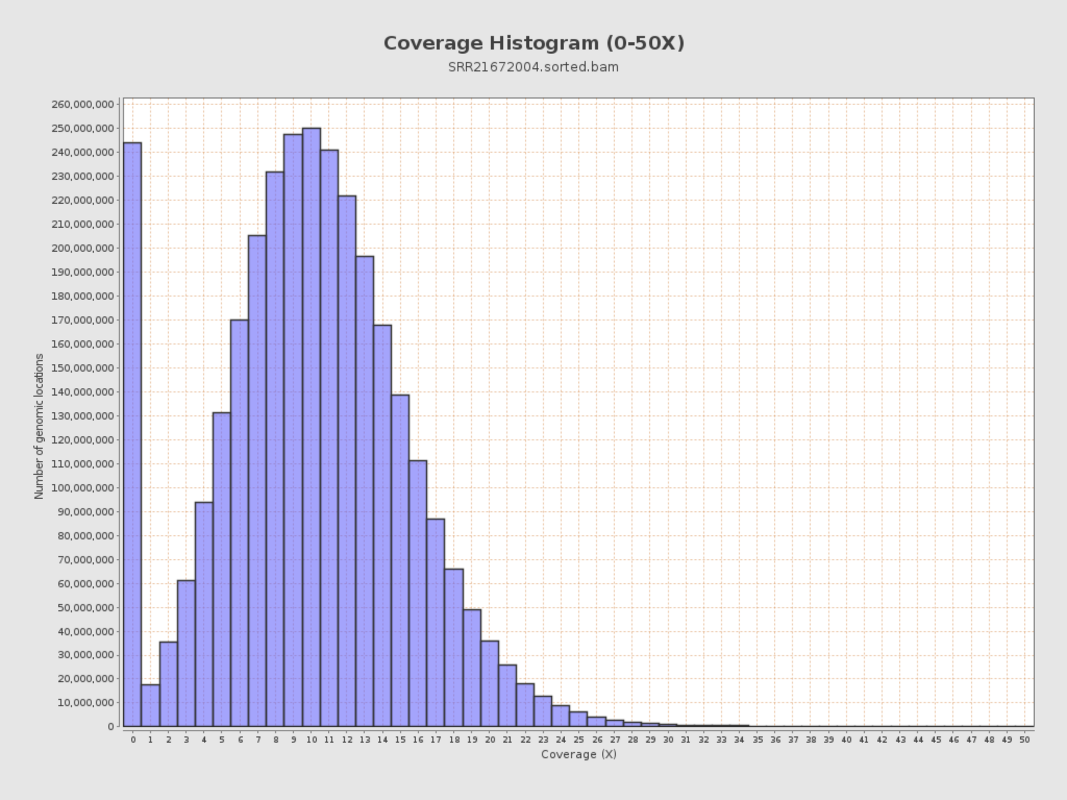
chrY	59373566	309972730	5.2207	82.0705

3. Results : Coverage across reference

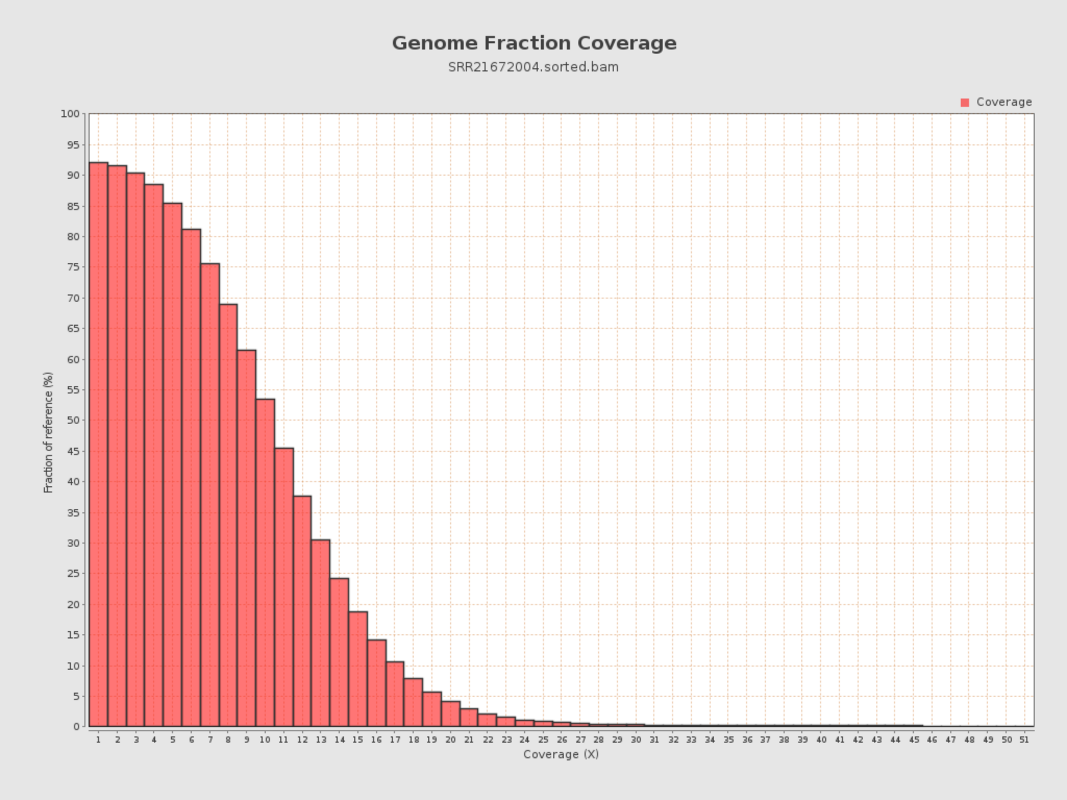
4. Results : Coverage Histogram



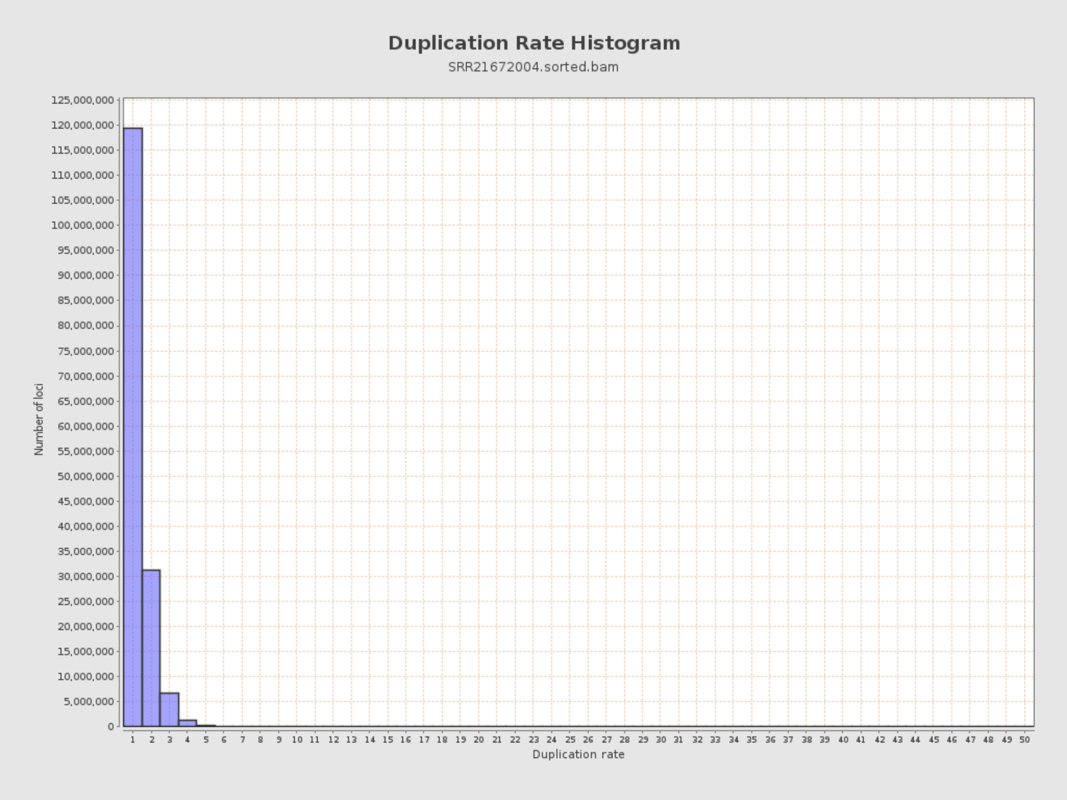
5. Results : Coverage Histogram (0-50X)



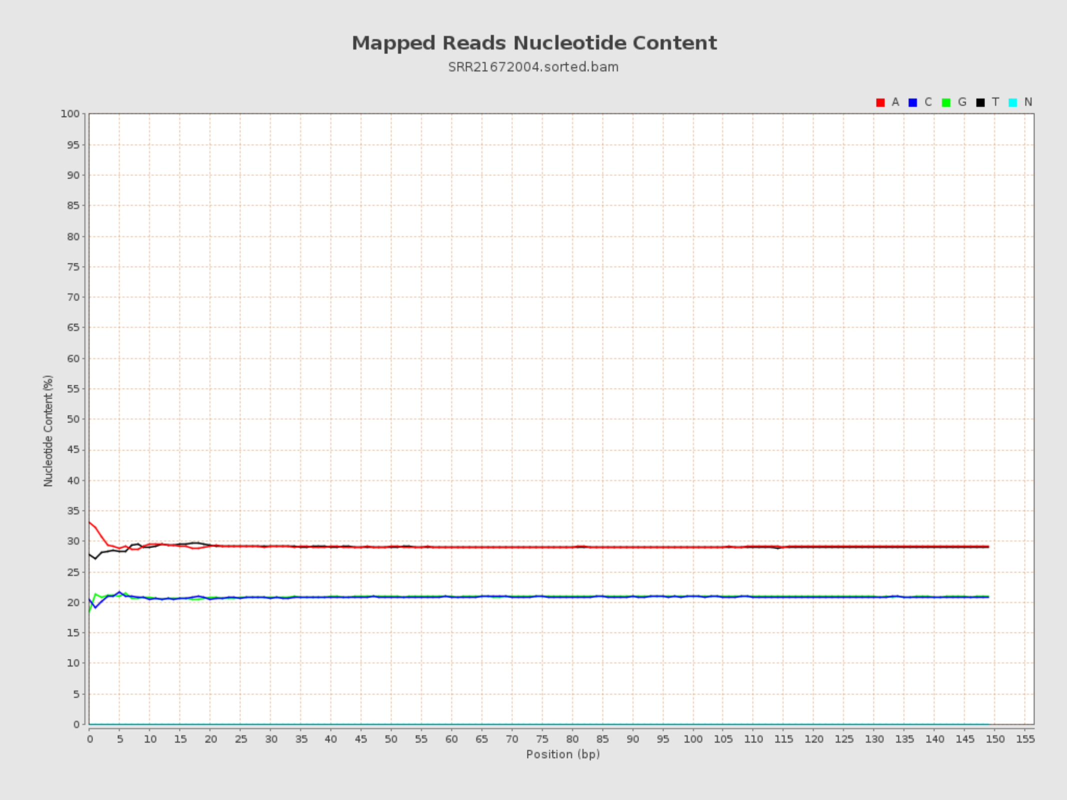
6. Results : Genome Fraction Coverage



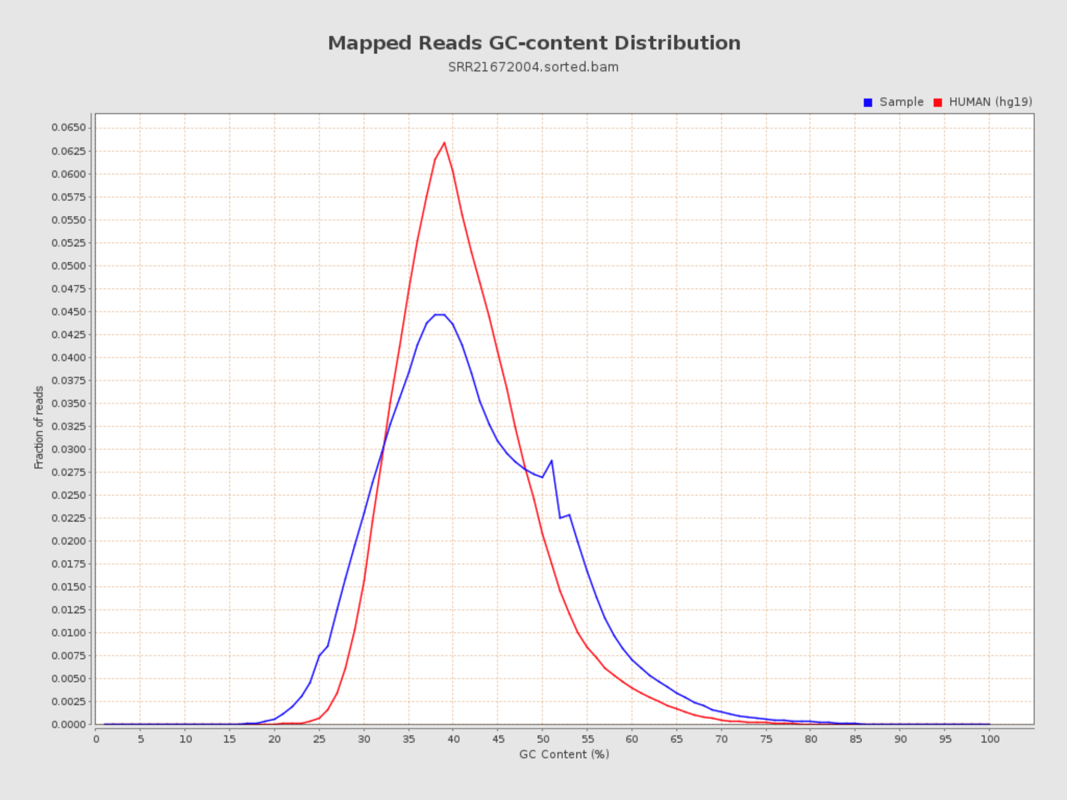
7. Results : Duplication Rate Histogram



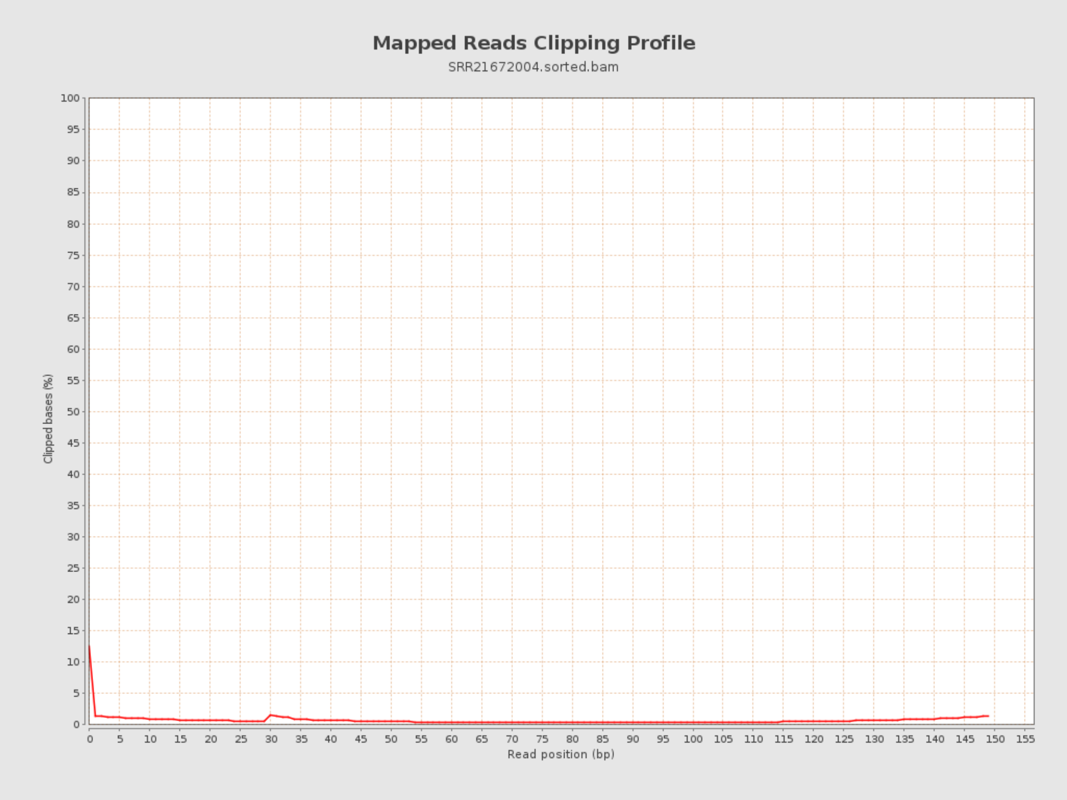
8. Results : Mapped Reads Nucleotide Content



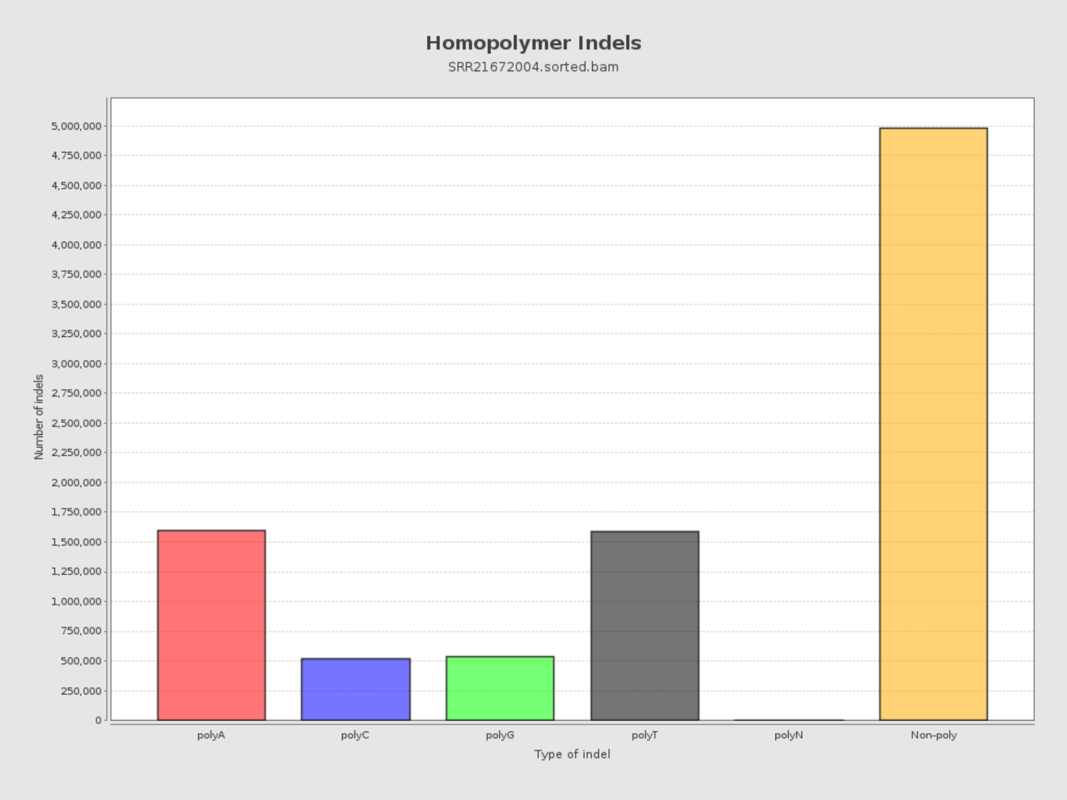
9. Results : Mapped Reads GC-content Distribution



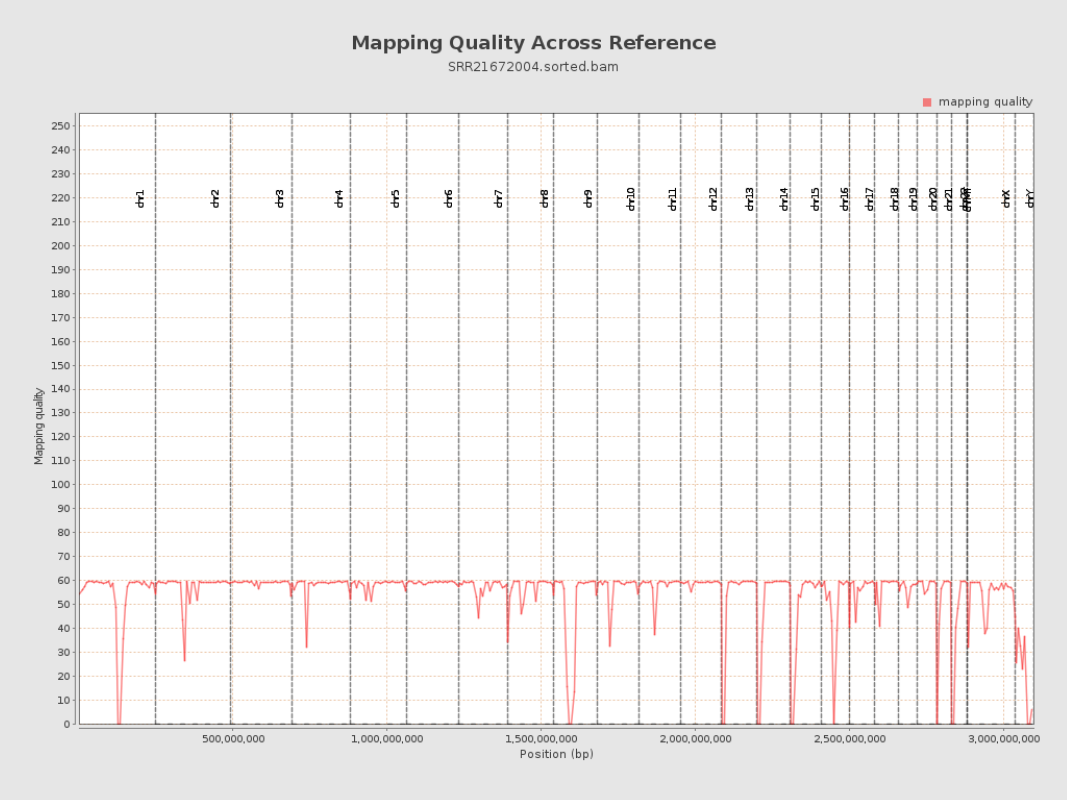
10. Results : Mapped Reads Clipping Profile



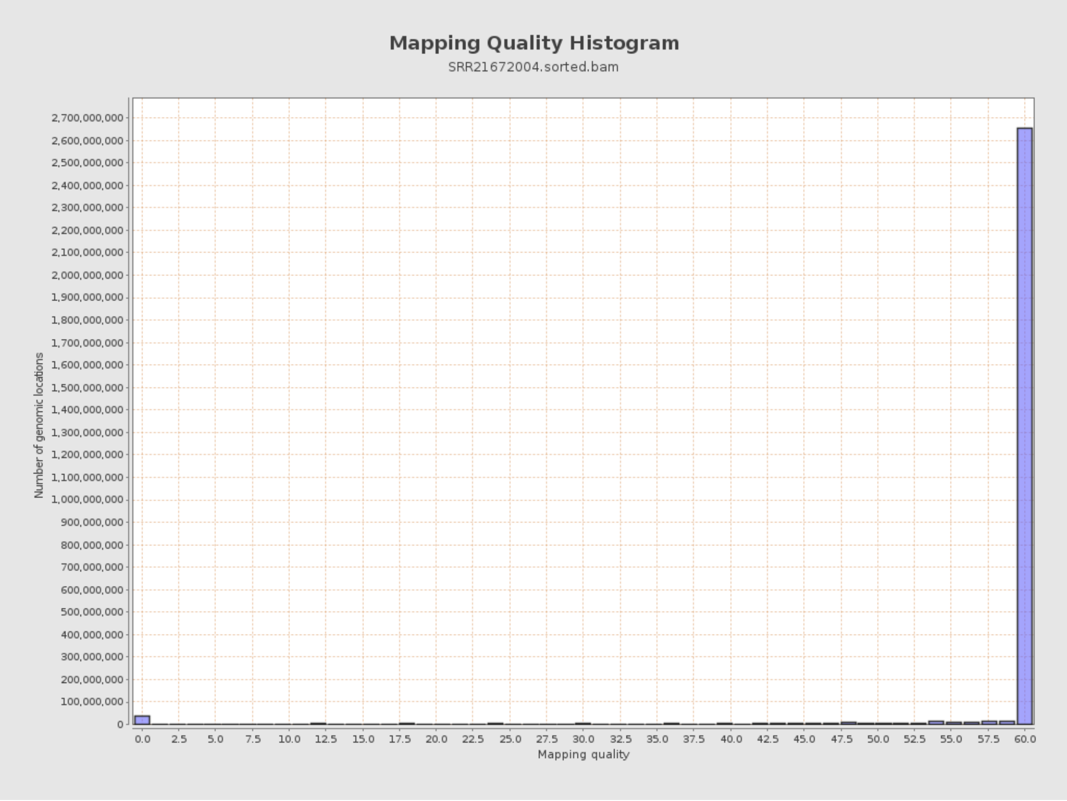
11. Results : Homopolymer Indels



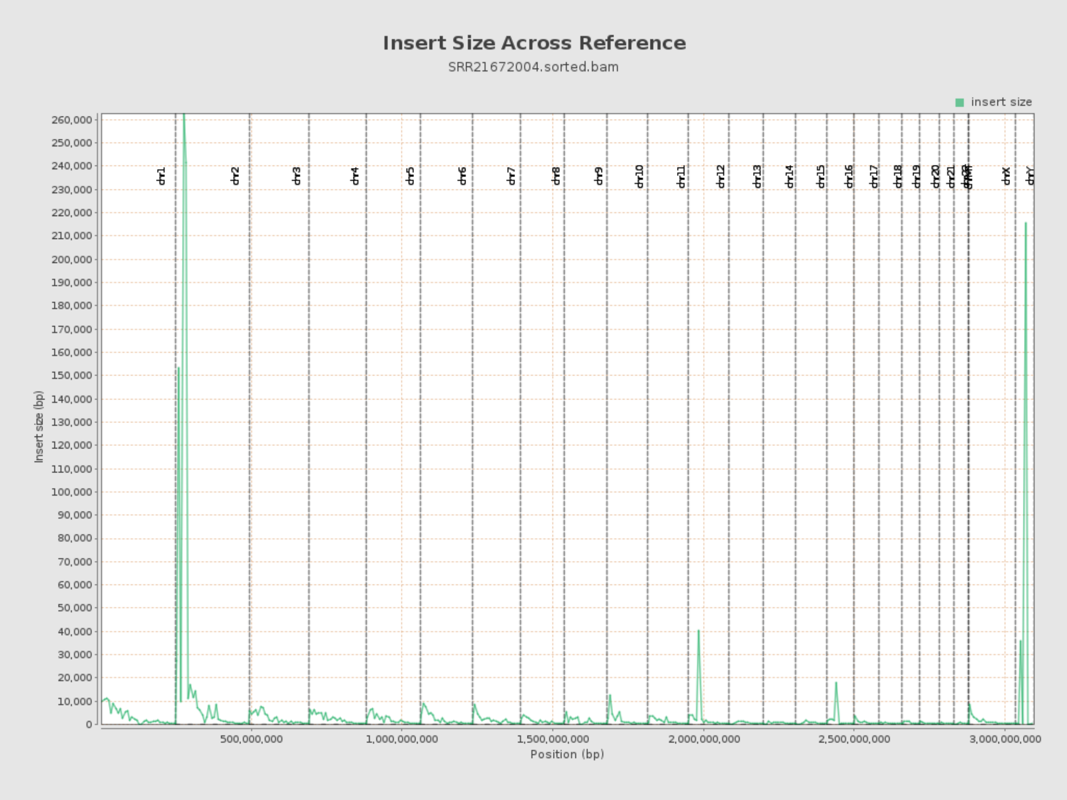
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram