Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 05:59:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124829.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_SRR3124829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124829_1.fastq.gz SRR3124829_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 05:59:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,978,148
Mapped reads	28,771,770 / 99.29%
Unmapped reads	206,378 / 0.71%
Mapped paired reads	28,771,770 / 99.29%
Mapped reads, first in pair	14,395,205 / 49.68%
Mapped reads, second in pair	14,376,565 / 49.61%
Mapped reads, both in pair	28,690,432 / 99.01%
Mapped reads, singletons	81,338 / 0.28%
Secondary alignments	0
Supplementary alignments	123,946 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	2,767,067 / 9.55%
Duplication rate	5.44%
Clipped reads	16,865,108 / 58.2%

2.2. ACGT Content

Number/percentage of A's	760,140,676 / 28.87%
Number/percentage of C's	514,673,794 / 19.55%
Number/percentage of T's	789,216,856 / 29.97%
Number/percentage of G's	568,901,342 / 21.61%
Number/percentage of N's	19,639 / 0%

GC Percentage	41.15%

2.3. Coverage

Mean	0.851
Standard Deviation	9.601

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	76,788.35
Standard Deviation	2,646,533.44
P25/Median/P75	138 / 171 / 216

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	18,739,981
Insertions	409,219
Mapped reads with at least one insertion	1.4%
Deletions	860,191
Mapped reads with at least one deletion	2.93%
Homopolymer indels	47.25%

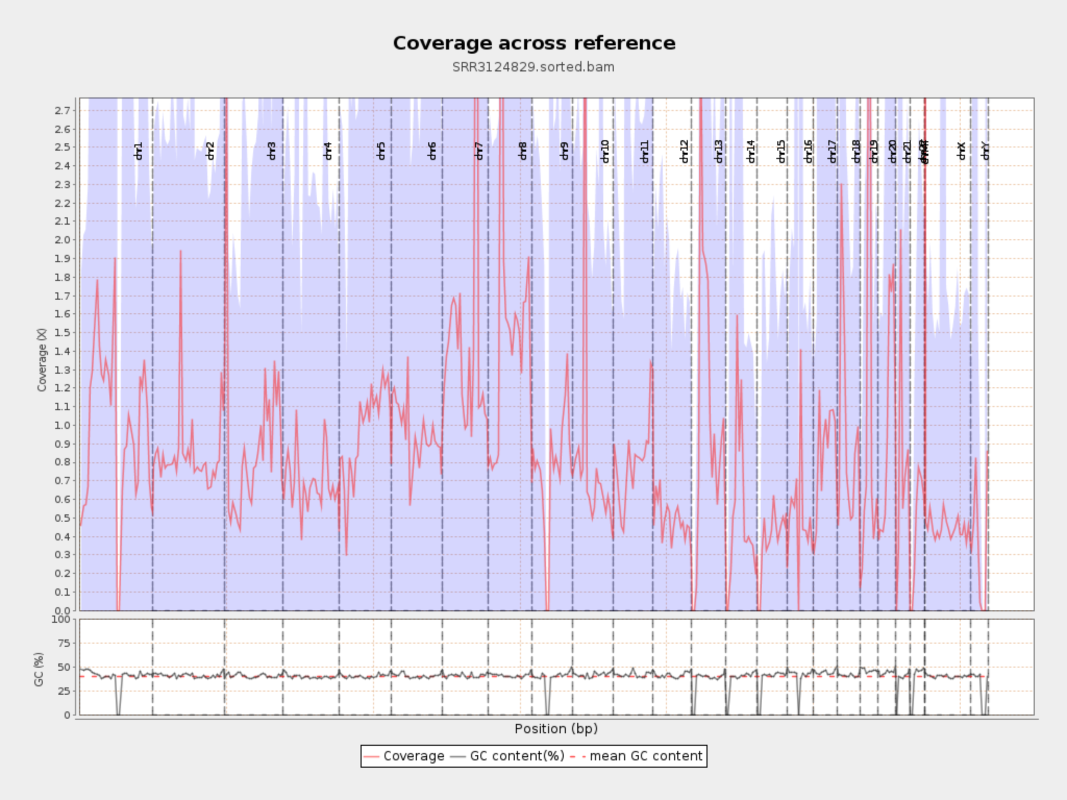
2.7. Chromosome stats

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

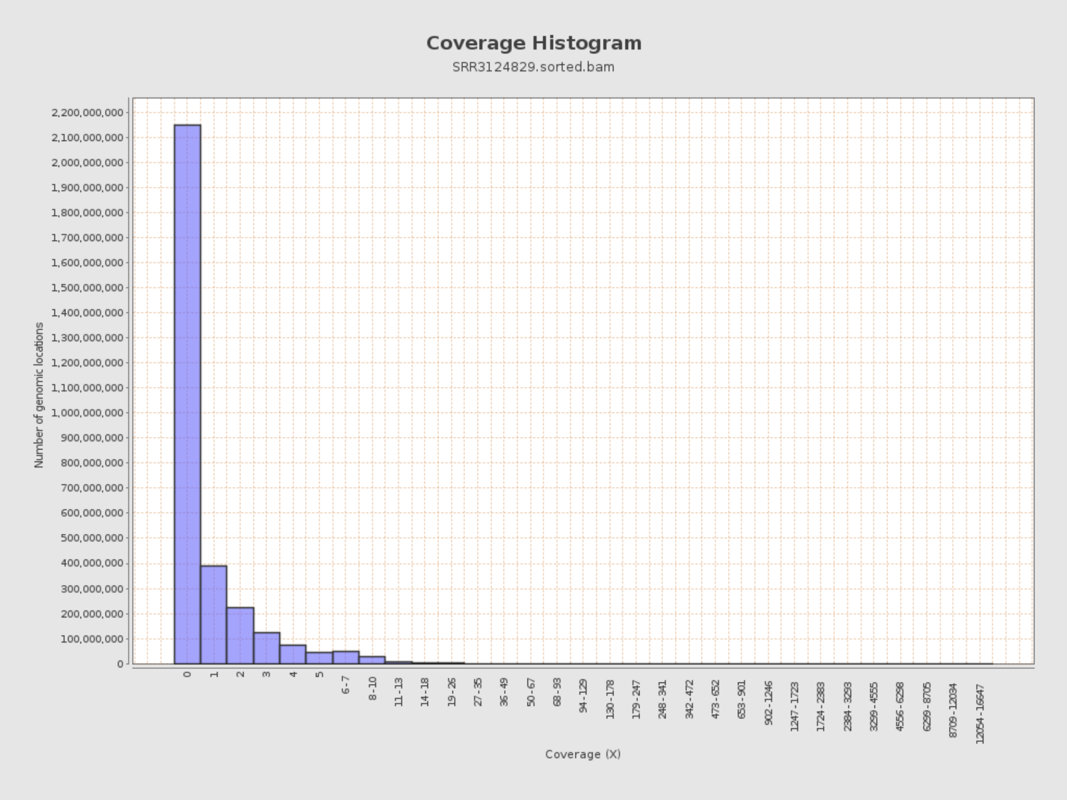
		bases	coverage	deviation
chr1	249250621	248160754	0.9956	15.8171
chr2	243199373	207278587	0.8523	7.6129
chr3	198022430	180506057	0.9115	2.4844
chr4	191154276	132452628	0.6929	3.9069
chr5	180915260	175303297	0.969	1.9244
chr6	171115067	163813202	0.9573	6.329
chr7	159138663	231700014	1.456	14.4365
chr8	146364022	223117859	1.5244	4.9225
chr9	141213431	106162247	0.7518	9.7373
chr10	135534747	113602809	0.8382	28.001
chr11	135006516	105195719	0.7792	5.9033
chr12	133851895	66053655	0.4935	1.3157
chr13	115169878	122071840	1.0599	2.3621
chr14	107349540	55062268	0.5129	1.8405
chr15	102531392	39250367	0.3828	1.1908
chr16	90354753	46707515	0.5169	6.748
chr17	81195210	68821134	0.8476	11.219
chr18	78077248	71598770	0.917	11.9881
chr19	59128983	60545841	1.024	8.627
chr20	63025520	65038984	1.0319	2.3797
chr21	48129895	37686639	0.783	2.5509
chr22	51304566	23270116	0.4536	1.2958
chrMT	16571	187685	11.3261	7.4451
chrX	155270560	68662303	0.4422	2.706

chrY	59373566	22122659	0.3726	6.711

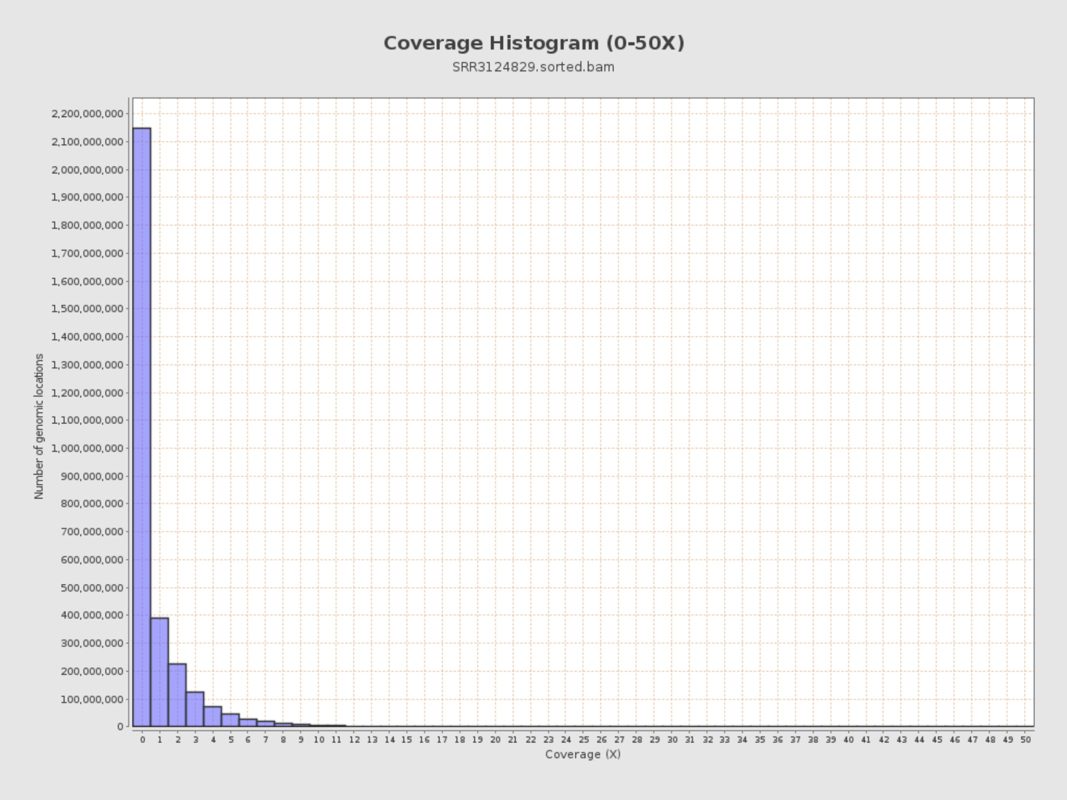
3. Results : Coverage across reference



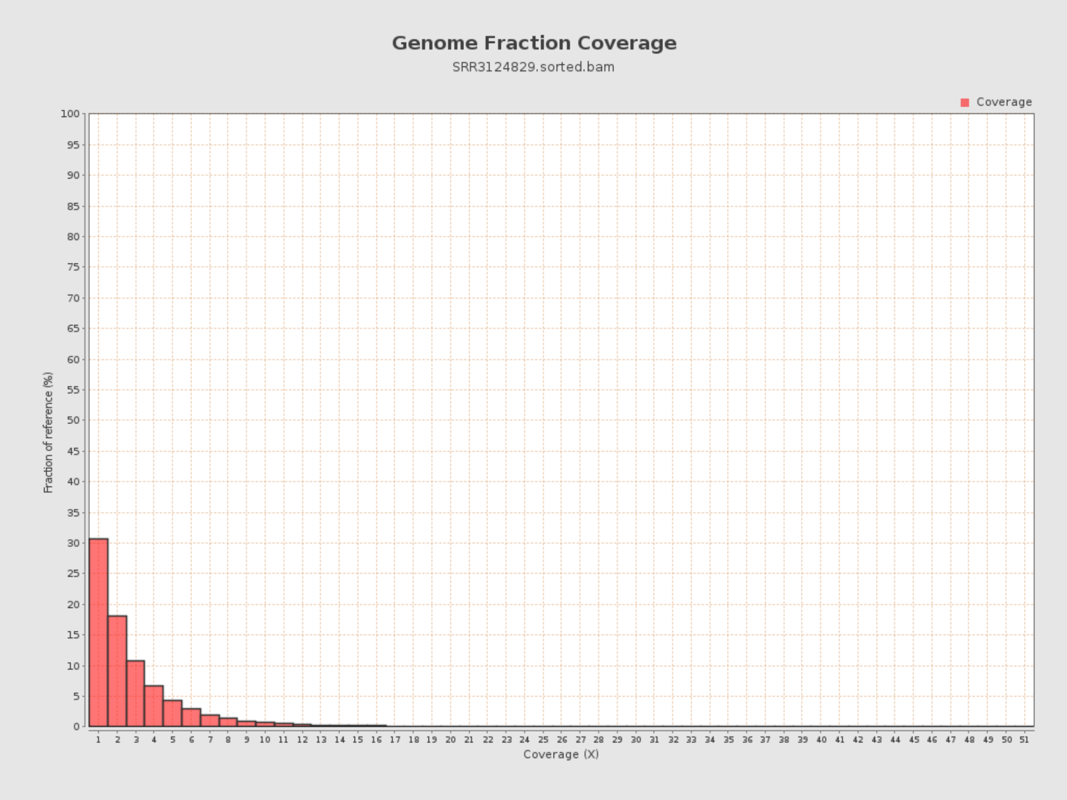
4. Results : Coverage Histogram



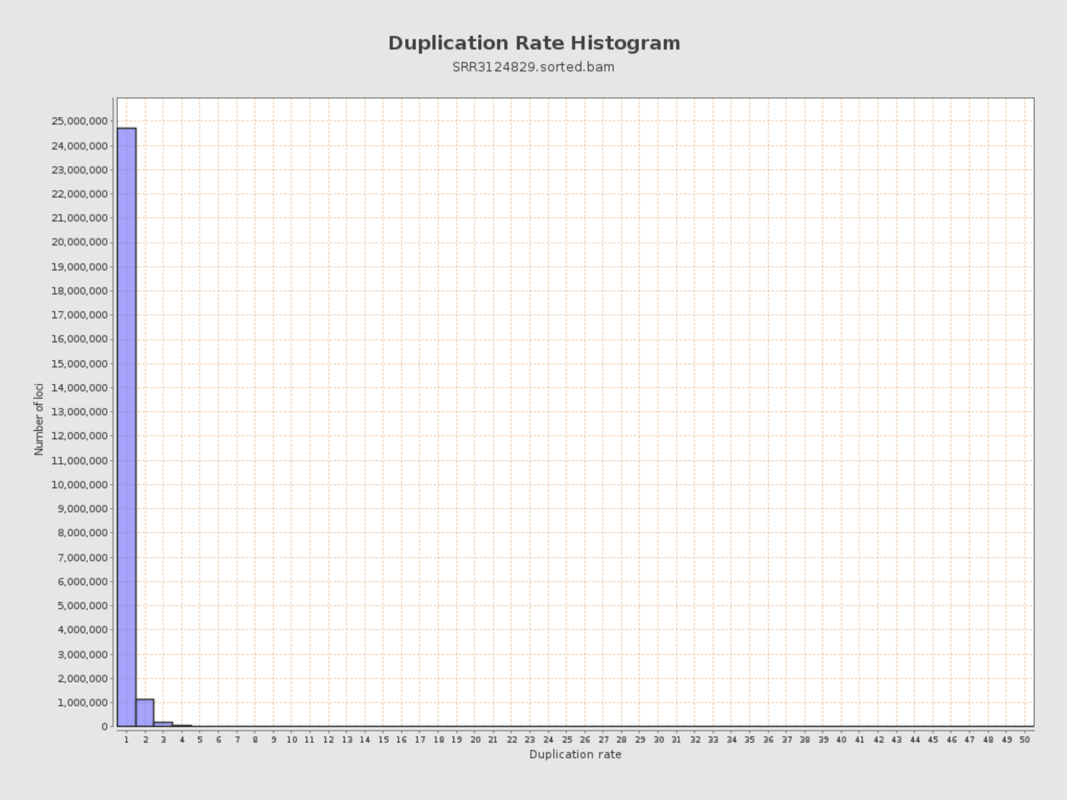
5. Results : Coverage Histogram (0-50X)



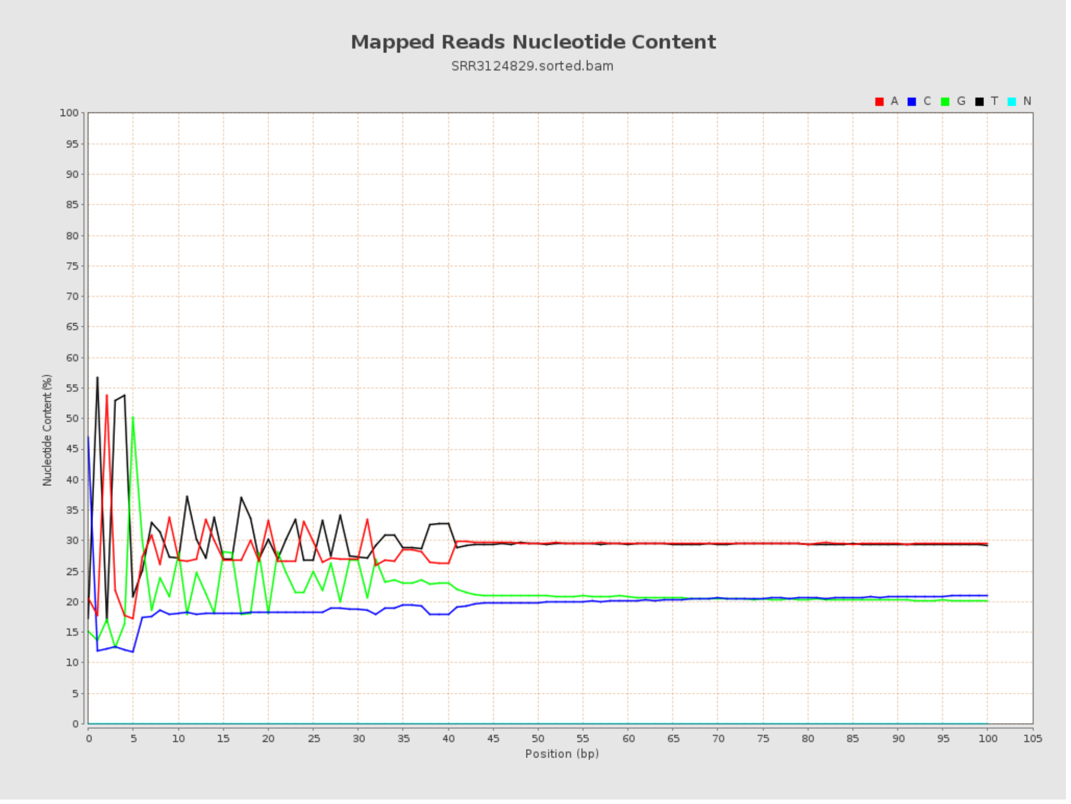
6. Results : Genome Fraction Coverage



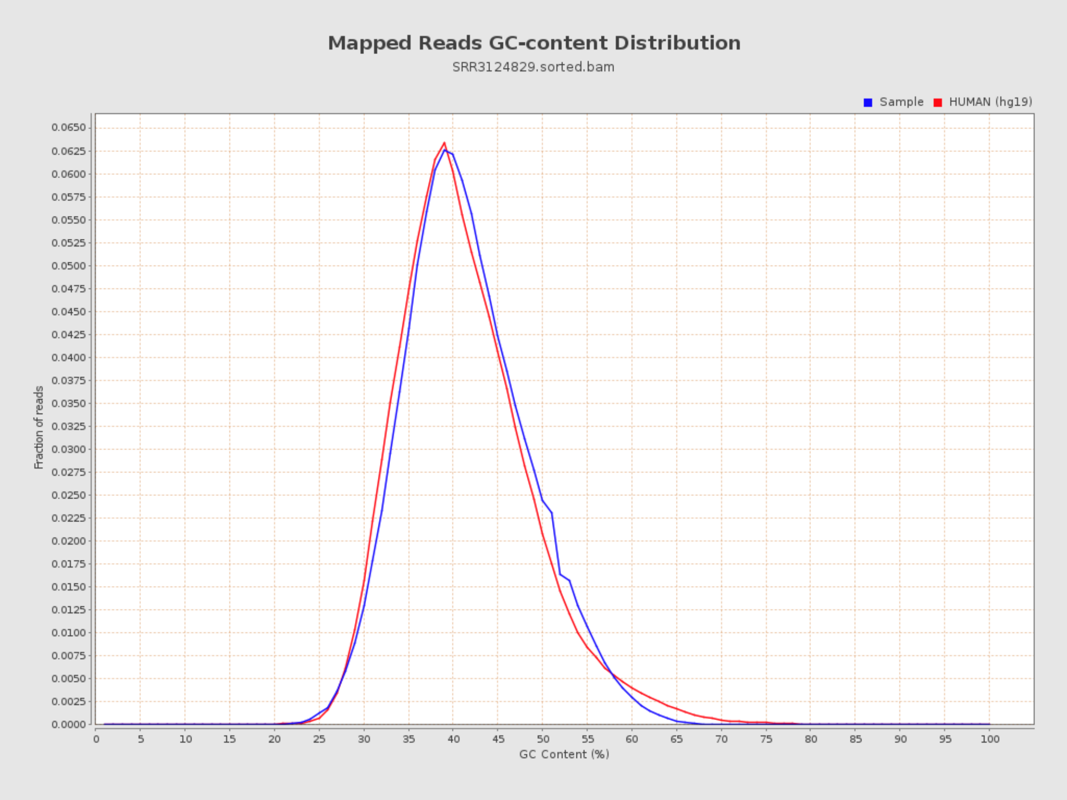
7. Results : Duplication Rate Histogram



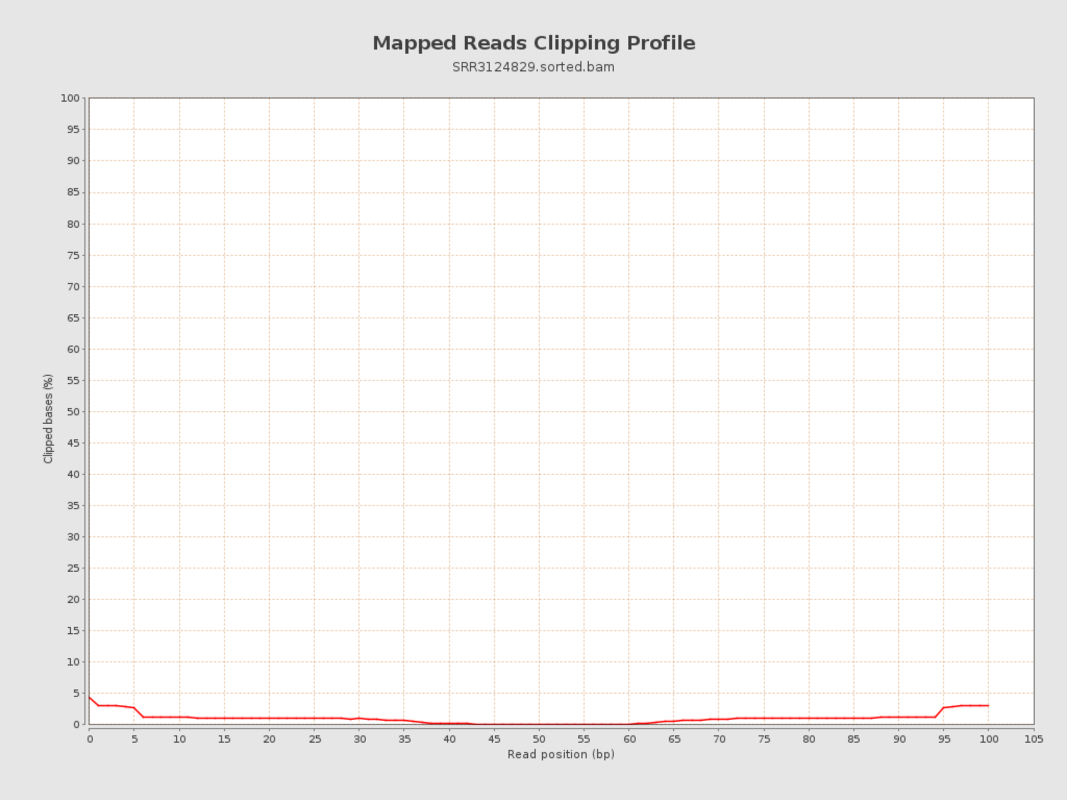
8. Results : Mapped Reads Nucleotide Content



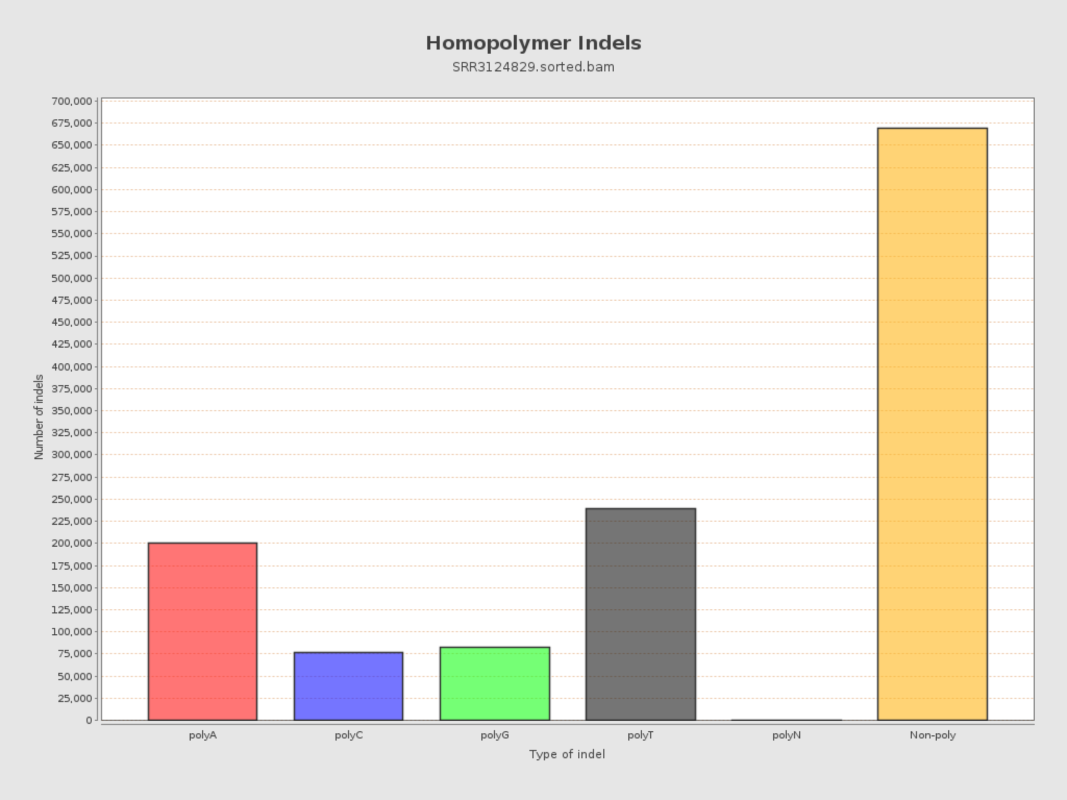
9. Results : Mapped Reads GC-content Distribution



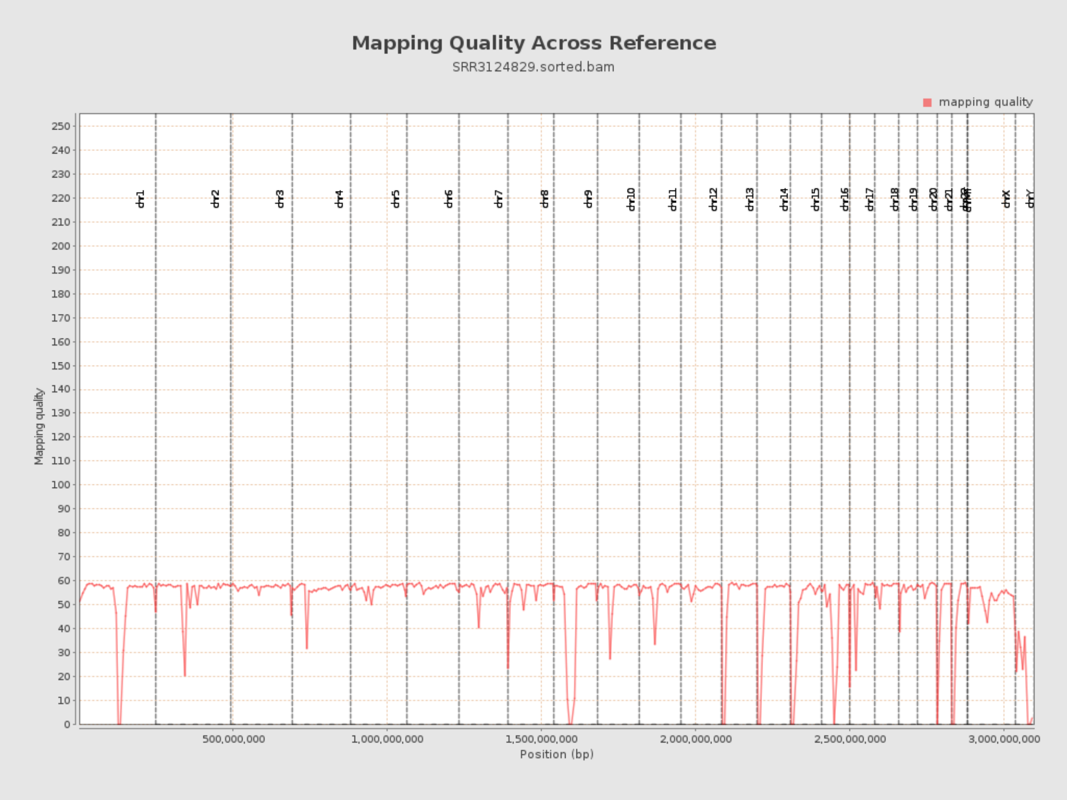
10. Results : Mapped Reads Clipping Profile



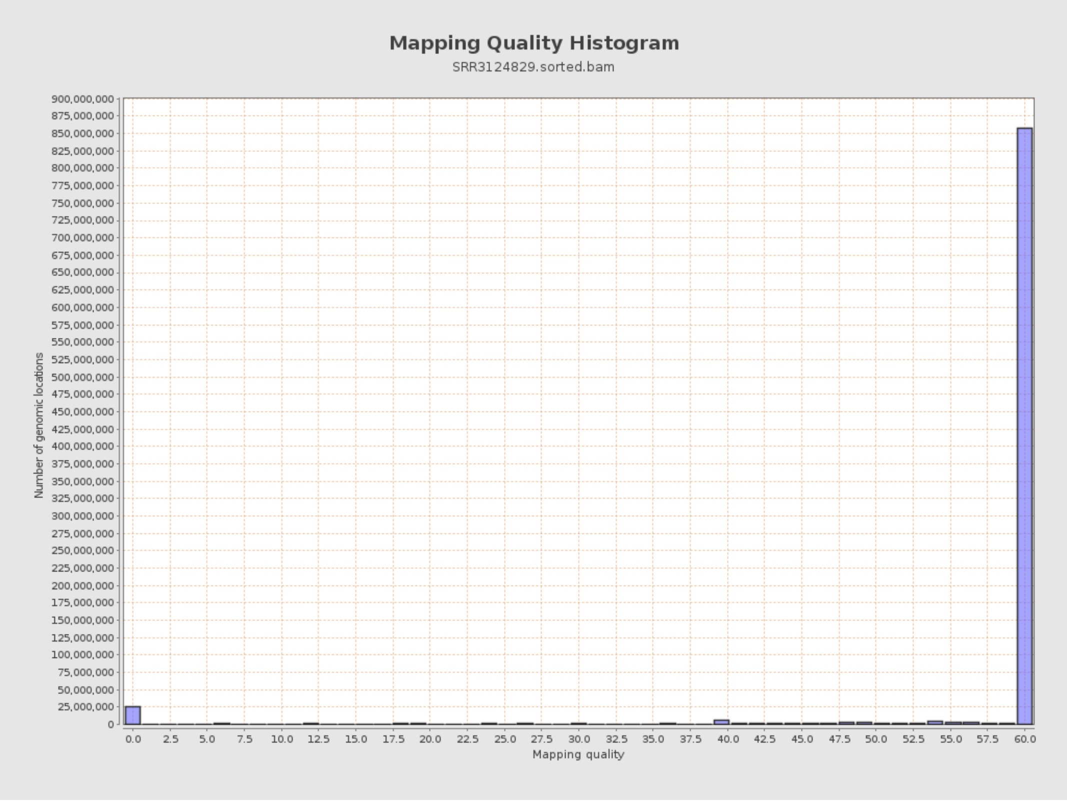
11. Results : Homopolymer Indels



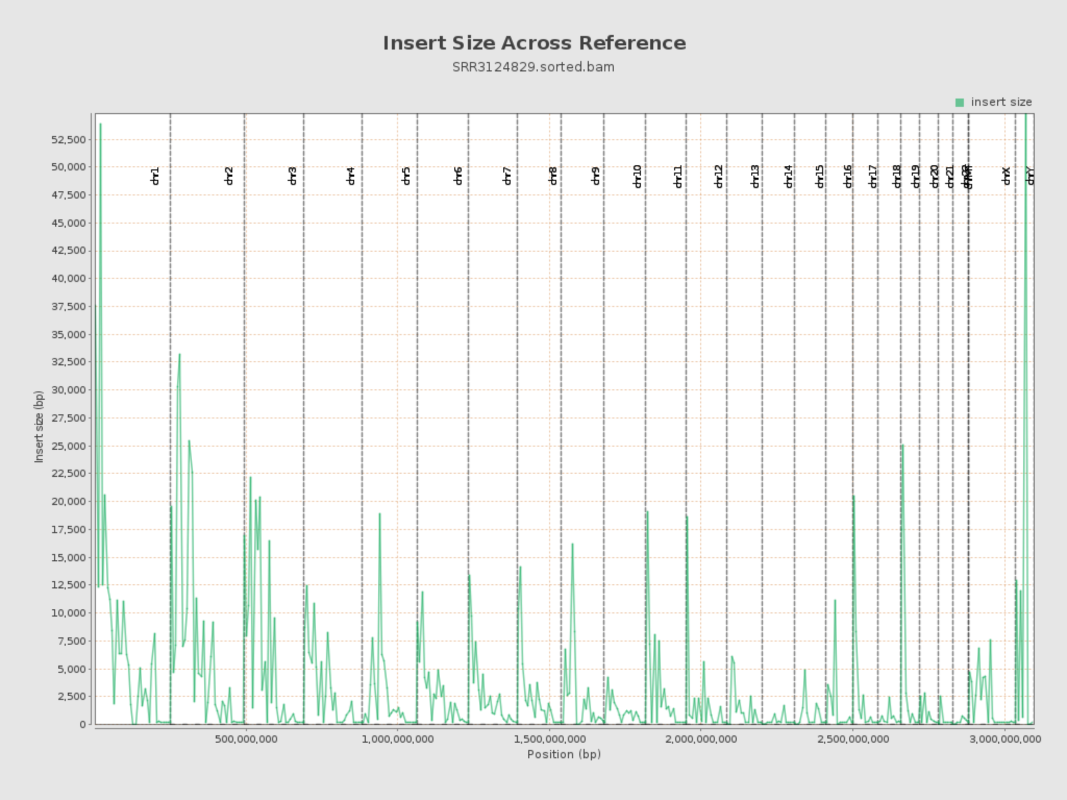
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram