Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 06:01:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472679.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_SRR3472679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472679_1.fastq.gz SRR3472679_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 06:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,979,008
Mapped reads	19,801,820 / 99.11%
Unmapped reads	177,188 / 0.89%
Mapped paired reads	19,801,820 / 99.11%
Mapped reads, first in pair	9,934,108 / 49.72%
Mapped reads, second in pair	9,867,712 / 49.39%
Mapped reads, both in pair	19,683,702 / 98.52%
Mapped reads, singletons	118,118 / 0.59%
Secondary alignments	0
Supplementary alignments	118,721 / 0.59%
Read min/max/mean length	30 / 101 / 99.84
Duplicated reads (estimated)	14,076,209 / 70.45%
Duplication rate	49.29%
Clipped reads	1,410,032 / 7.06%

2.2. ACGT Content

Number/percentage of A's	523,126,694 / 26.83%
Number/percentage of C's	454,778,197 / 23.32%
Number/percentage of T's	523,256,721 / 26.83%
Number/percentage of G's	448,463,738 / 23%
Number/percentage of N's	371,187 / 0.02%

GC Percentage	46.32%

2.3. Coverage

Mean	0.63
Standard Deviation	30.5441

2.4. Mapping Quality

Mean Mapping Quality	54.59

2.5. Insert size

Mean	21,897.54
Standard Deviation	1,472,044.82
P25/Median/P75	164 / 225 / 297

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	12,454,431
Insertions	125,709
Mapped reads with at least one insertion	0.63%
Deletions	109,052
Mapped reads with at least one deletion	0.54%
Homopolymer indels	45.06%

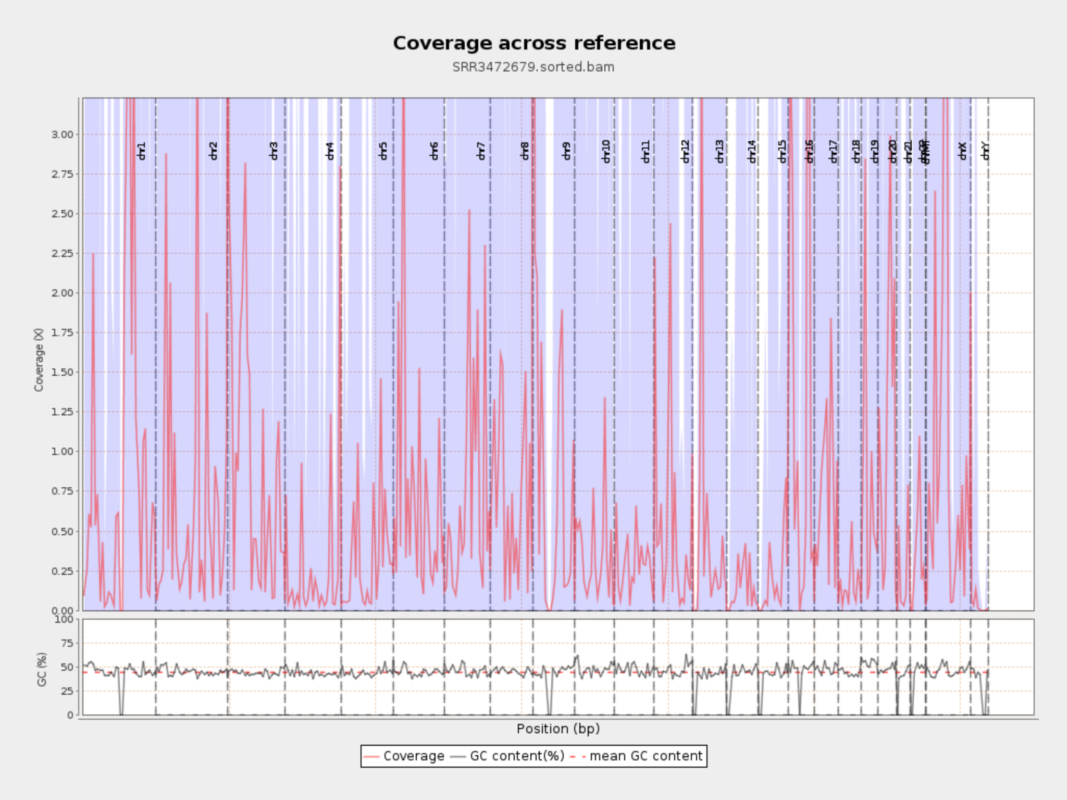
2.7. Chromosome stats

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

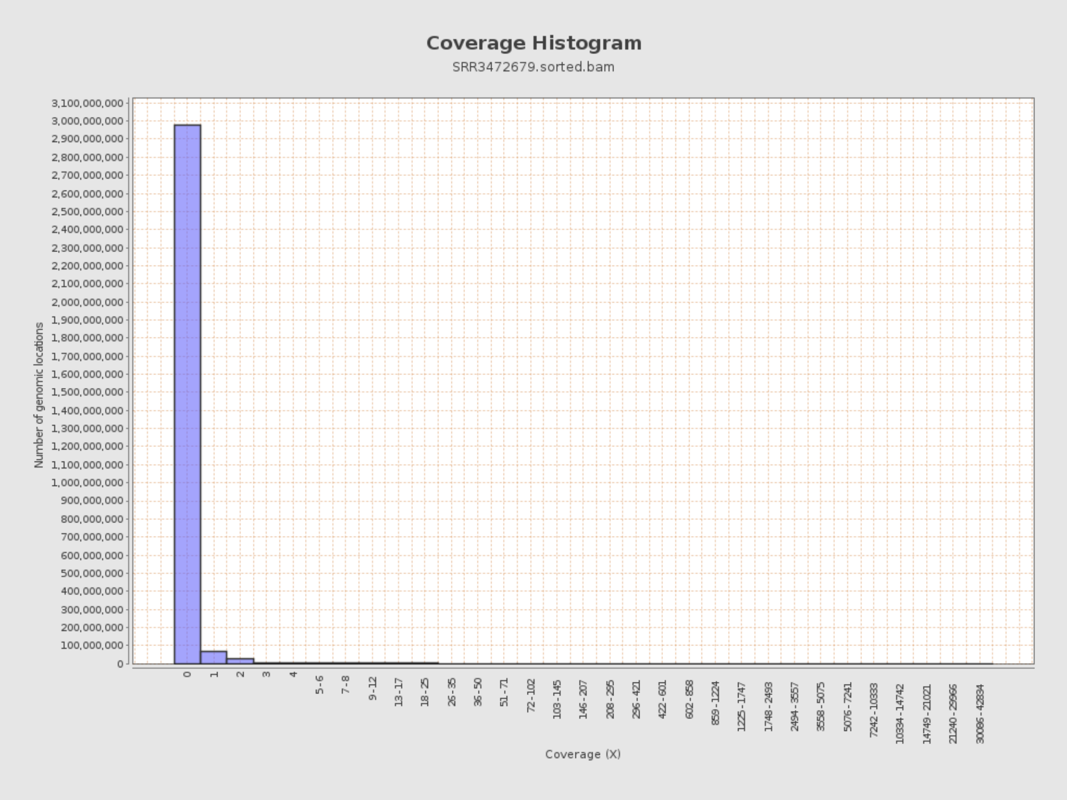
		bases	coverage	deviation
chr1	249250621	215791888	0.8658	36.1254
chr2	243199373	162884722	0.6698	33.6365
chr3	198022430	191296273	0.966	27.211
chr4	191154276	56261605	0.2943	19.6298
chr5	180915260	61165171	0.3381	21.386
chr6	171115067	128426271	0.7505	27.246
chr7	159138663	118533951	0.7448	32.2485
chr8	146364022	107061738	0.7315	23.8016
chr9	141213431	117354685	0.831	25.9629
chr10	135534747	51870658	0.3827	16.9734
chr11	135006516	38837832	0.2877	15.3754
chr12	133851895	78077473	0.5833	22.9718
chr13	115169878	57517325	0.4994	19.1235
chr14	107349540	15633412	0.1456	7.2414
chr15	102531392	20722521	0.2021	20.0379
chr16	90354753	125642636	1.3905	55.2342
chr17	81195210	64329477	0.7923	18.9258
chr18	78077248	12507785	0.1602	9.1826
chr19	59128983	47643491	0.8058	26.5001
chr20	63025520	77973606	1.2372	34.0616
chr21	48129895	12018140	0.2497	14.5377
chr22	51304566	18685257	0.3642	15.8466
chrMT	16571	2879	0.1737	0.4692
chrX	155270560	168226432	1.0834	73.2881

chrY	59373566	1815181	0.0306	1.7131

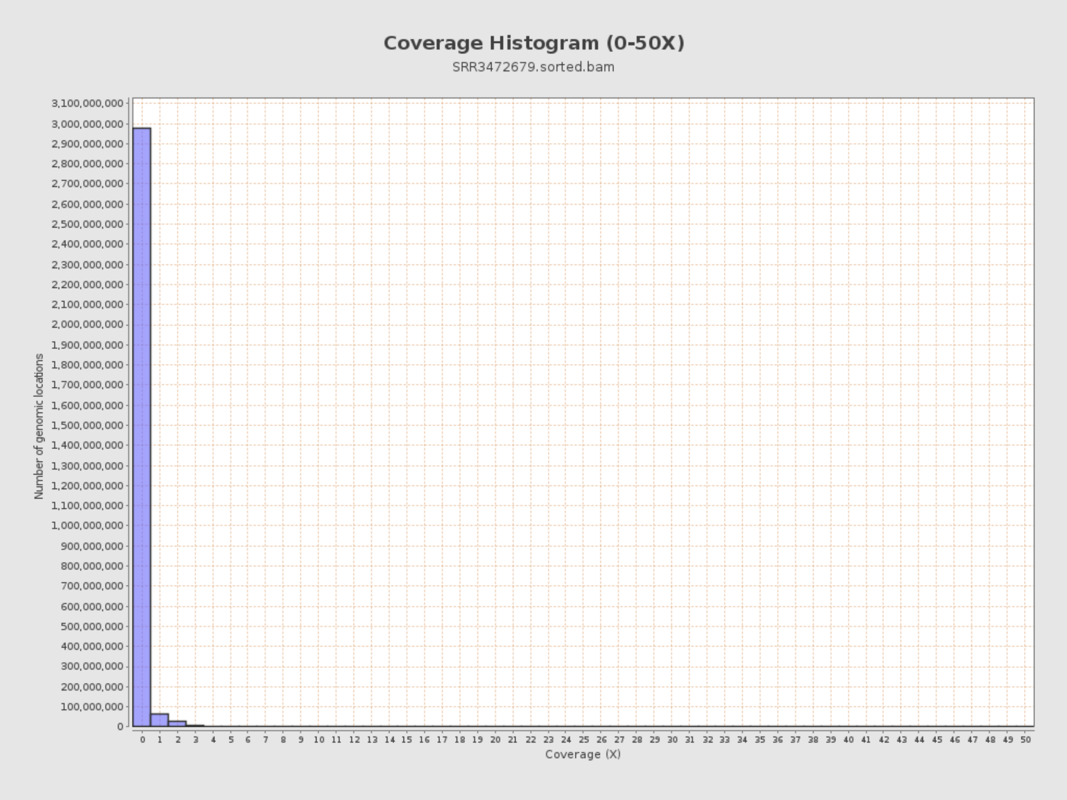
3. Results : Coverage across reference



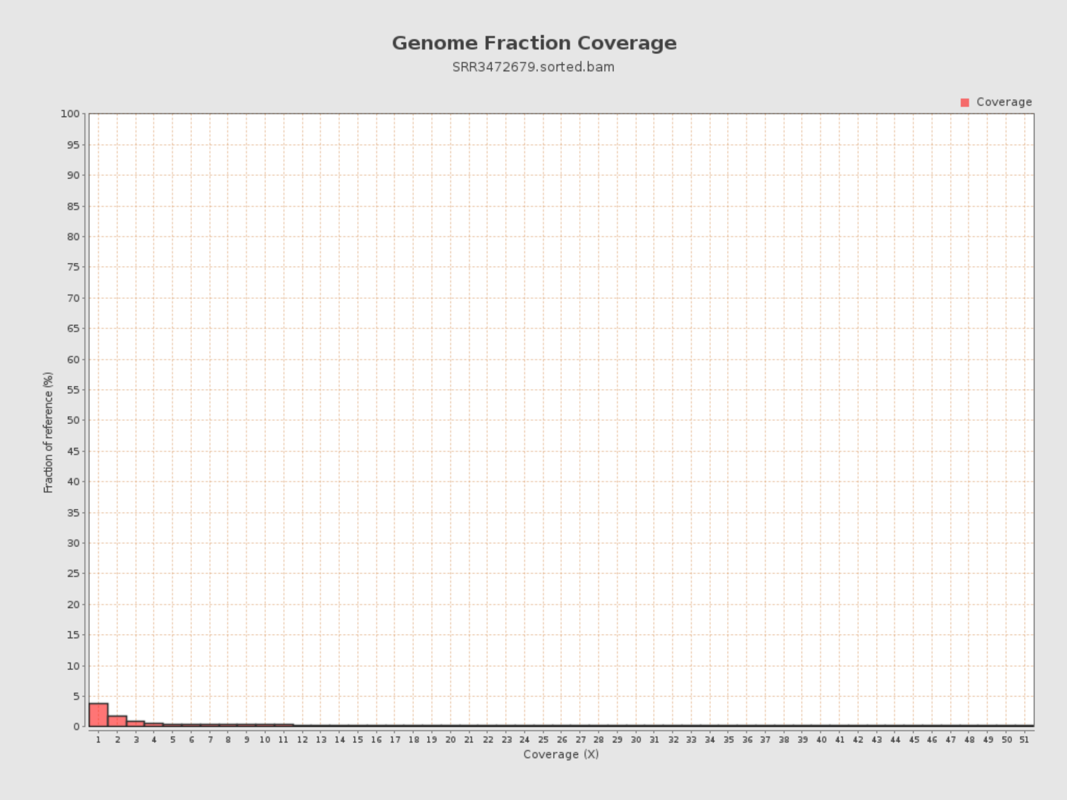
4. Results : Coverage Histogram



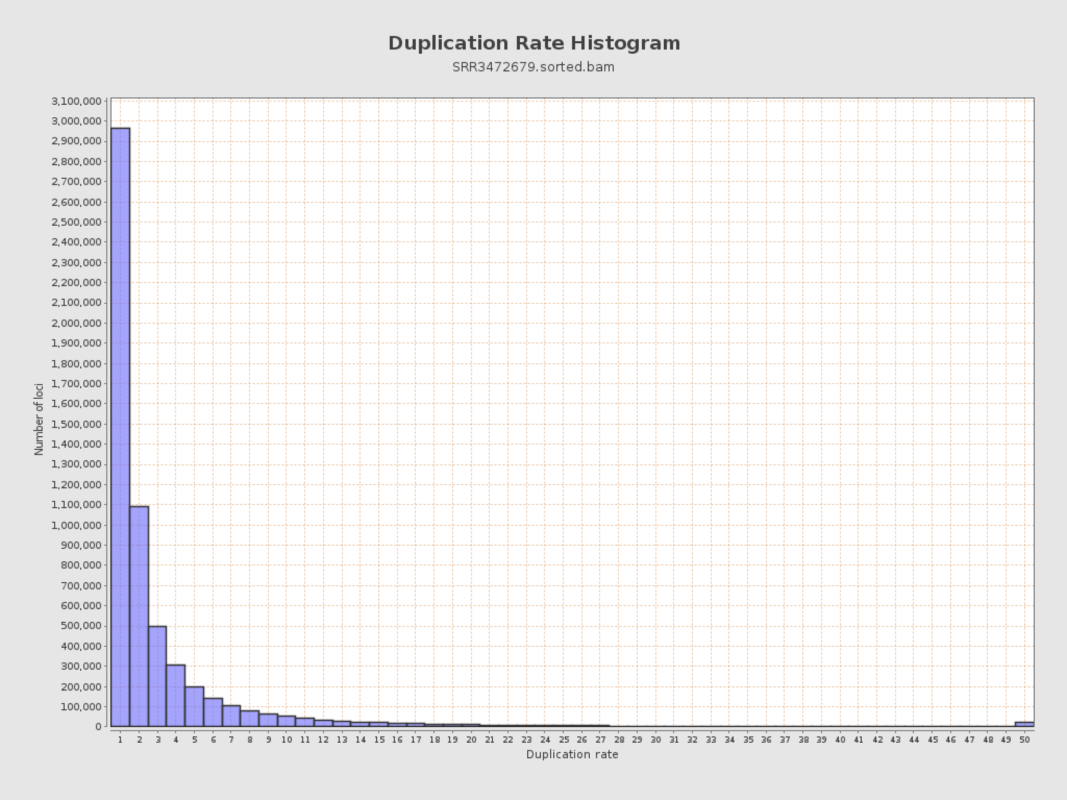
5. Results : Coverage Histogram (0-50X)



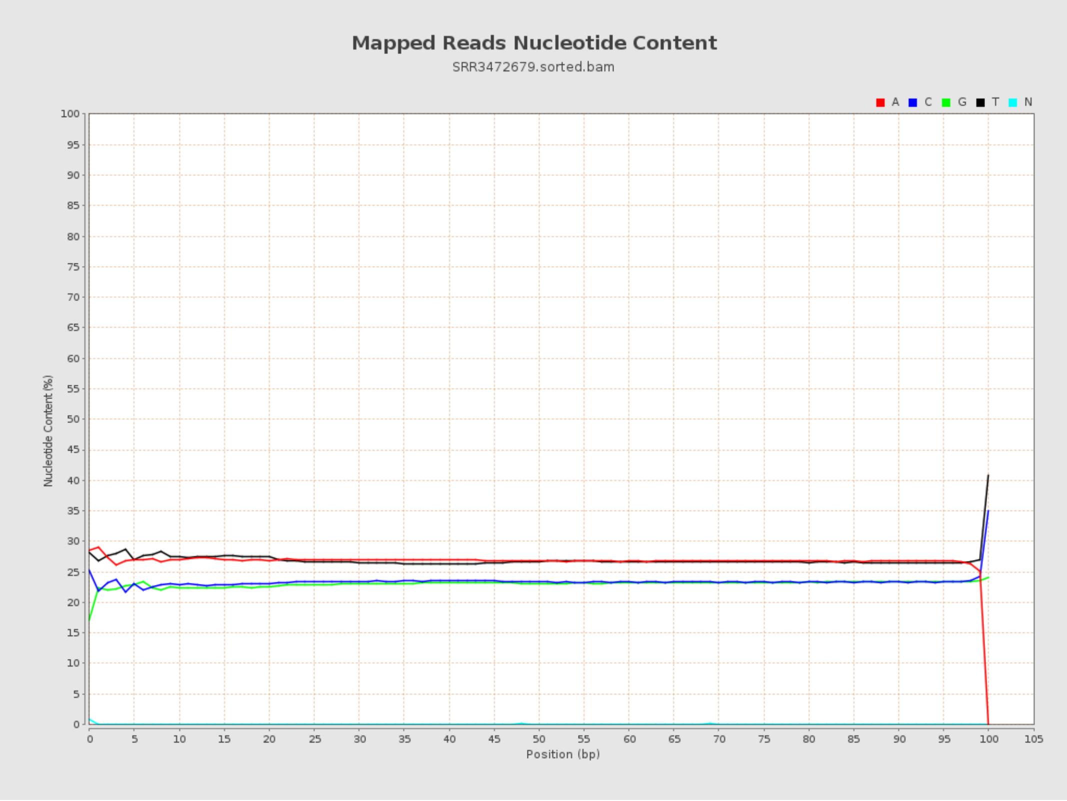
6. Results : Genome Fraction Coverage



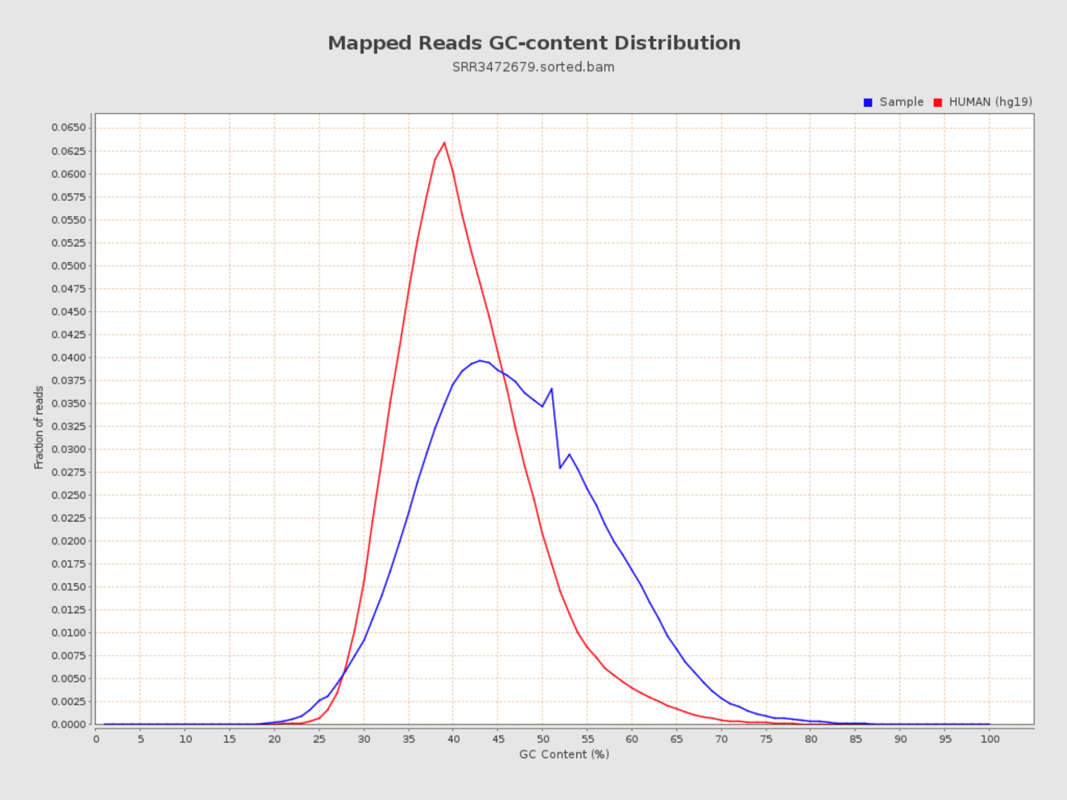
7. Results : Duplication Rate Histogram



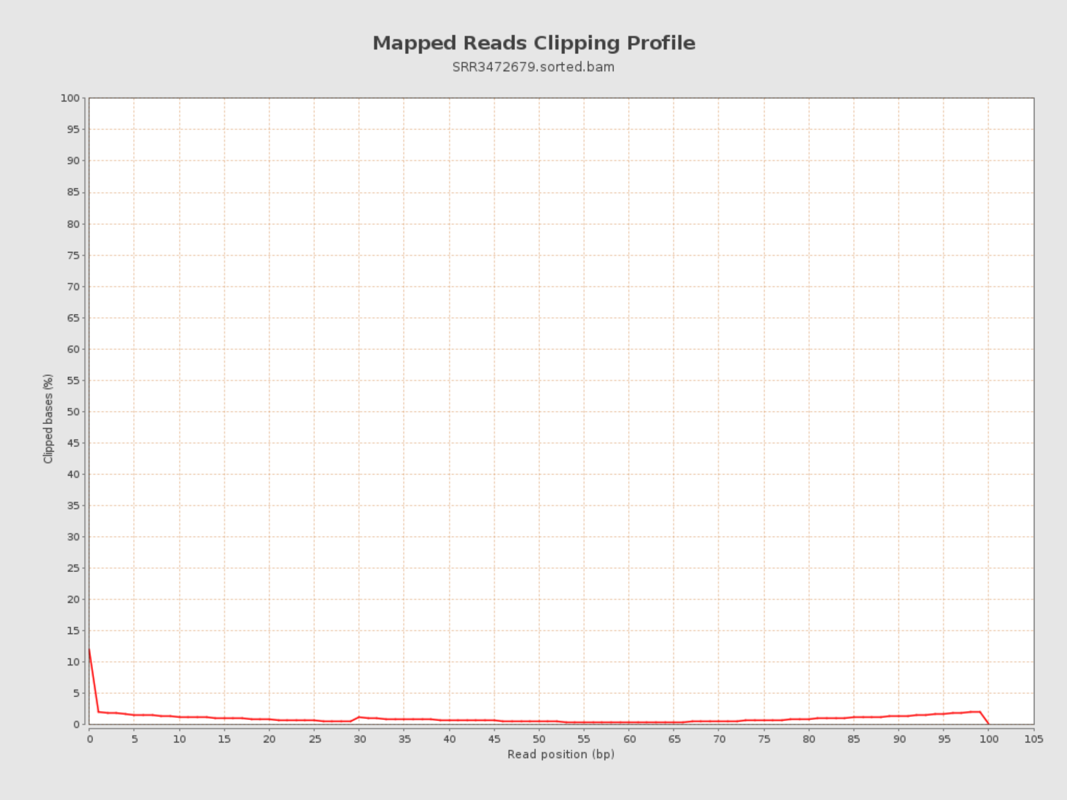
8. Results : Mapped Reads Nucleotide Content



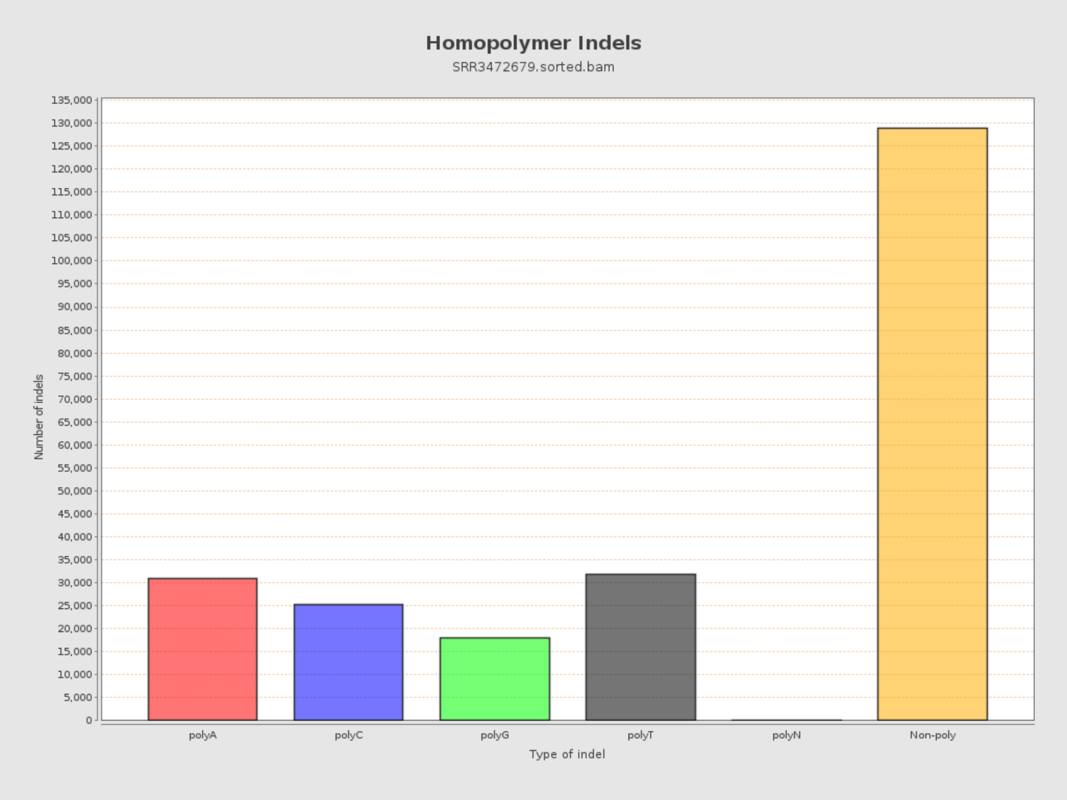
9. Results : Mapped Reads GC-content Distribution



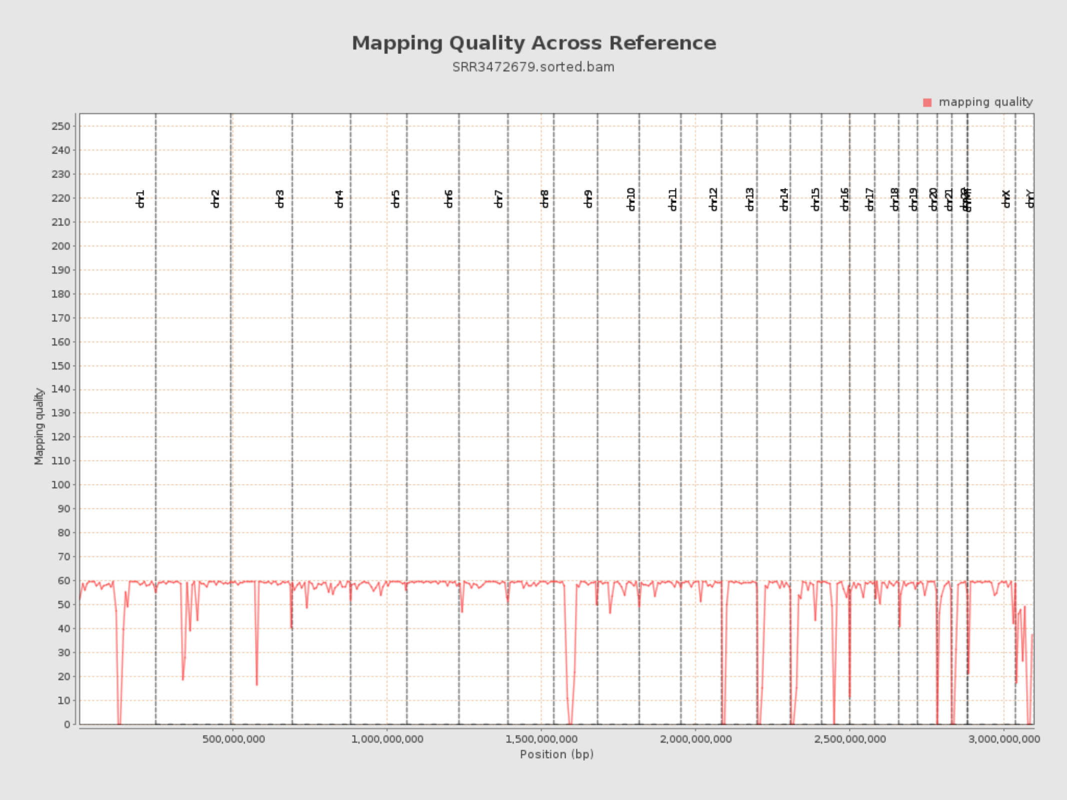
10. Results : Mapped Reads Clipping Profile



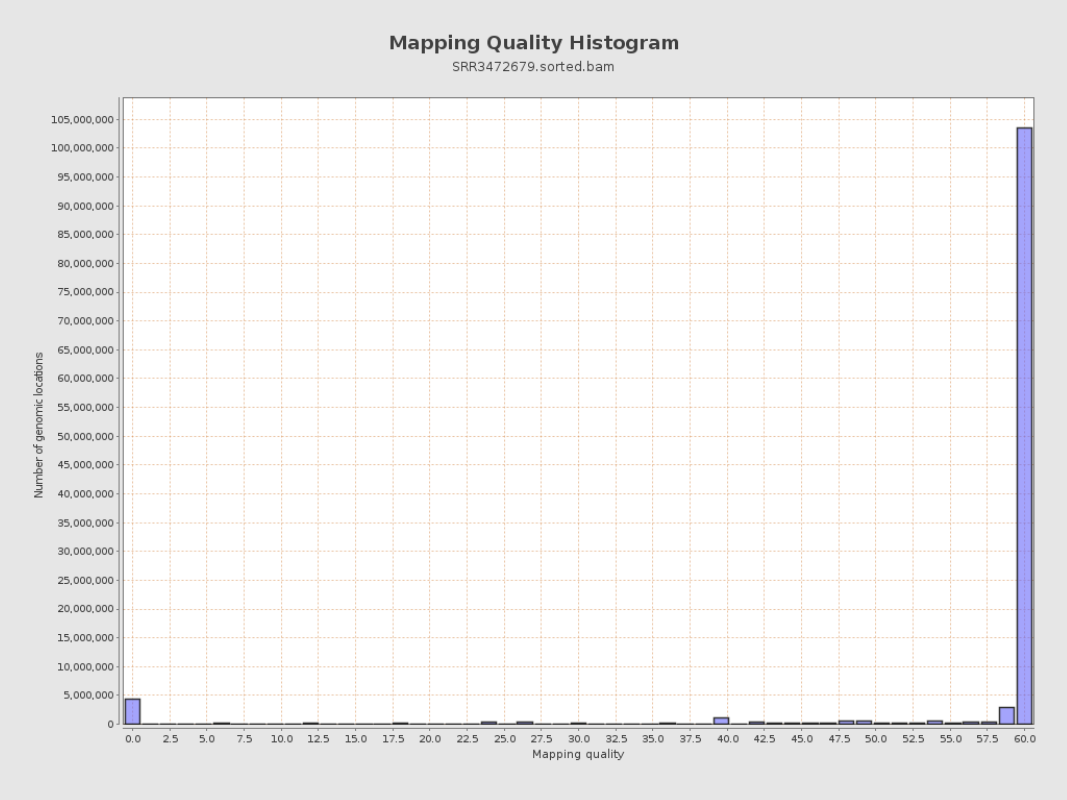
11. Results : Homopolymer Indels



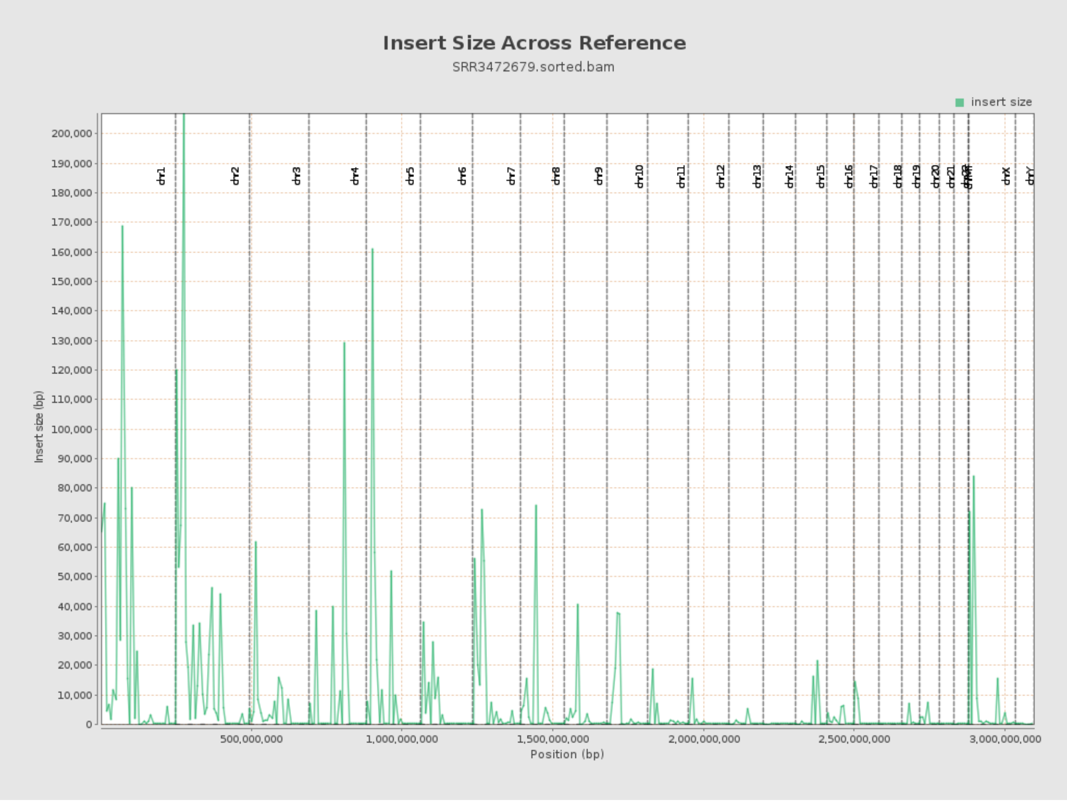
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram