Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 00:04:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472659.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_SRR3472659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472659_1.fastq.gz SRR3472659_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 00:04:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,099,560
Mapped reads	41,768,002 / 99.21%
Unmapped reads	331,558 / 0.79%
Mapped paired reads	41,768,002 / 99.21%
Mapped reads, first in pair	20,944,128 / 49.75%
Mapped reads, second in pair	20,823,874 / 49.46%
Mapped reads, both in pair	41,542,282 / 98.68%
Mapped reads, singletons	225,720 / 0.54%
Secondary alignments	0
Supplementary alignments	265,631 / 0.63%
Read min/max/mean length	30 / 101 / 99.87
Duplicated reads (estimated)	31,975,059 / 75.95%
Duplication rate	50.94%
Clipped reads	2,956,421 / 7.02%

2.2. ACGT Content

Number/percentage of A's	1,108,173,400 / 26.94%
Number/percentage of C's	953,430,897 / 23.18%
Number/percentage of T's	1,110,623,029 / 27%
Number/percentage of G's	940,931,223 / 22.87%
Number/percentage of N's	792,803 / 0.02%

GC Percentage	46.05%

2.3. Coverage

Mean	1.3291
Standard Deviation	51.8603

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	22,773.77
Standard Deviation	1,494,483.91
P25/Median/P75	166 / 228 / 301

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	25,792,671
Insertions	297,620
Mapped reads with at least one insertion	0.71%
Deletions	233,158
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.21%

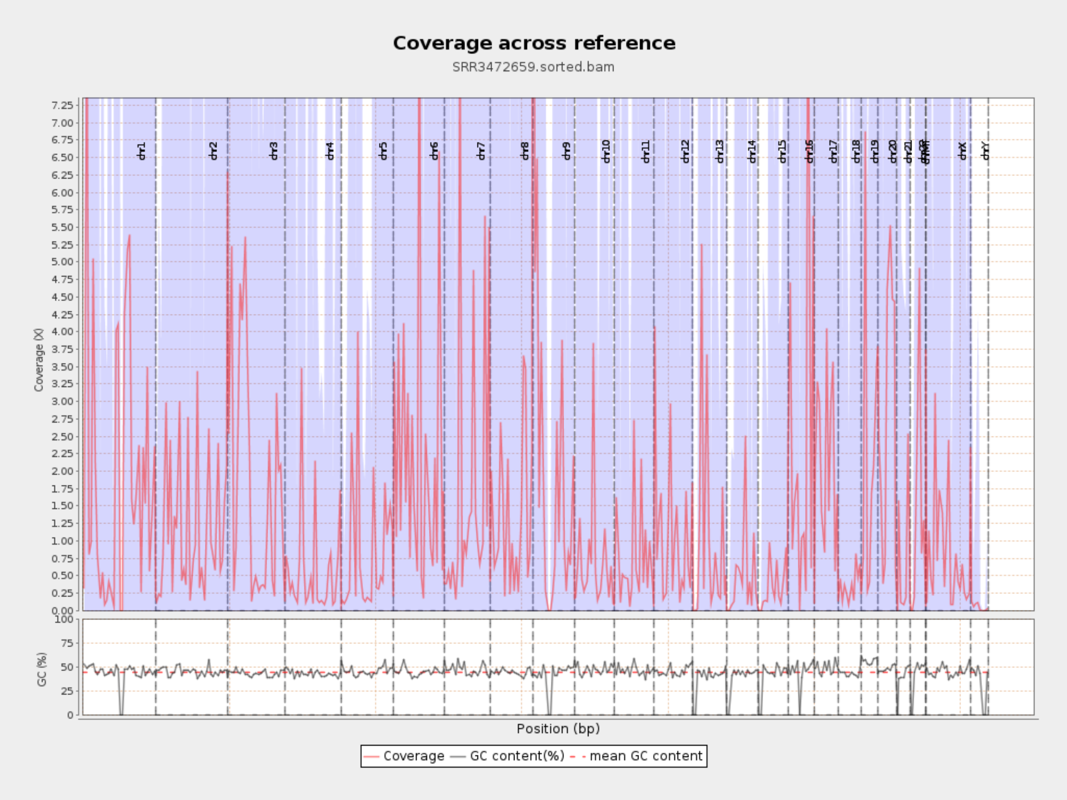
2.7. Chromosome stats

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

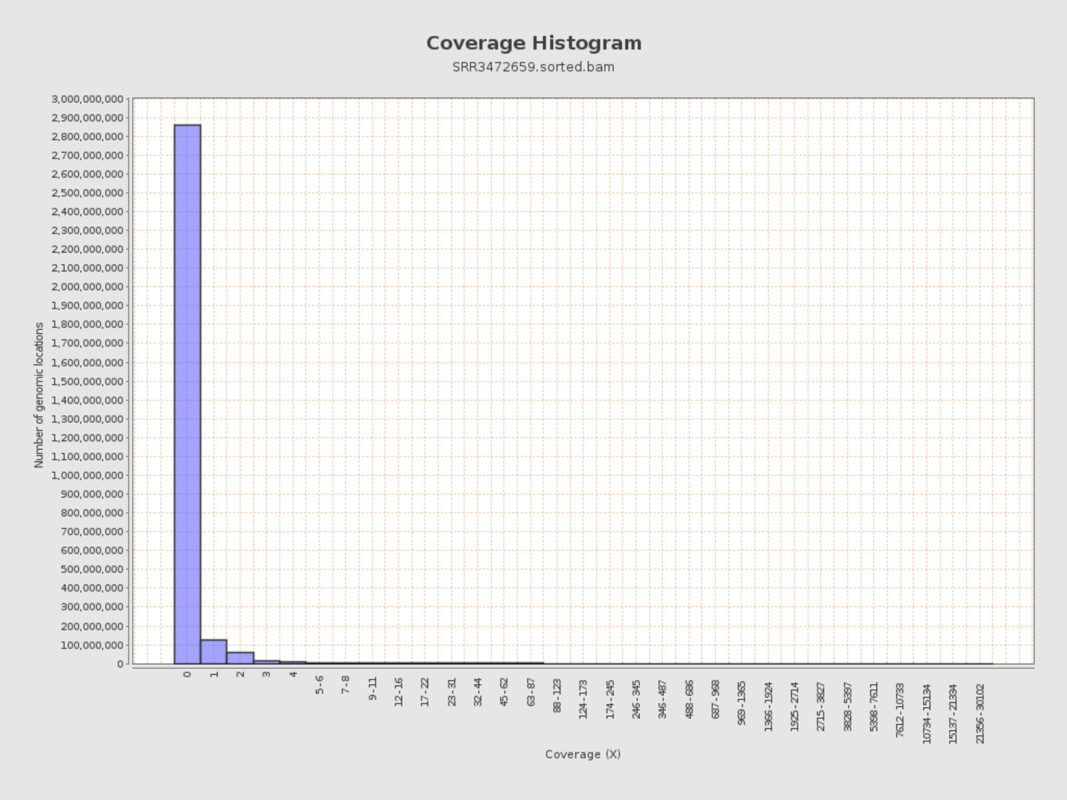
		bases	coverage	deviation
chr1	249250621	483103693	1.9382	78.7378
chr2	243199373	285001156	1.1719	49.3995
chr3	198022430	374895852	1.8932	53.657
chr4	191154276	115722506	0.6054	31.3793
chr5	180915260	152122993	0.8409	27.8614
chr6	171115067	385942744	2.2555	66.5075
chr7	159138663	290768993	1.8271	77.7795
chr8	146364022	198242978	1.3545	45.3928
chr9	141213431	266830809	1.8896	45.6258
chr10	135534747	101574600	0.7494	46.9511
chr11	135006516	104997193	0.7777	33.1612
chr12	133851895	148651009	1.1106	29.9134
chr13	115169878	119304315	1.0359	39.0132
chr14	107349540	53090529	0.4946	21.3946
chr15	102531392	34448847	0.336	16.111
chr16	90354753	226736459	2.5094	89.0939
chr17	81195210	186067227	2.2916	64.9459
chr18	78077248	27794936	0.356	14.1928
chr19	59128983	129277311	2.1864	61.5051
chr20	63025520	184712875	2.9308	82.1027
chr21	48129895	35612185	0.7399	42.6912
chr22	51304566	77232074	1.5054	68.4937
chrMT	16571	62130	3.7493	2.7801
chrX	155270560	129407651	0.8334	25.5089

chrY	59373566	2956025	0.0498	2.1122

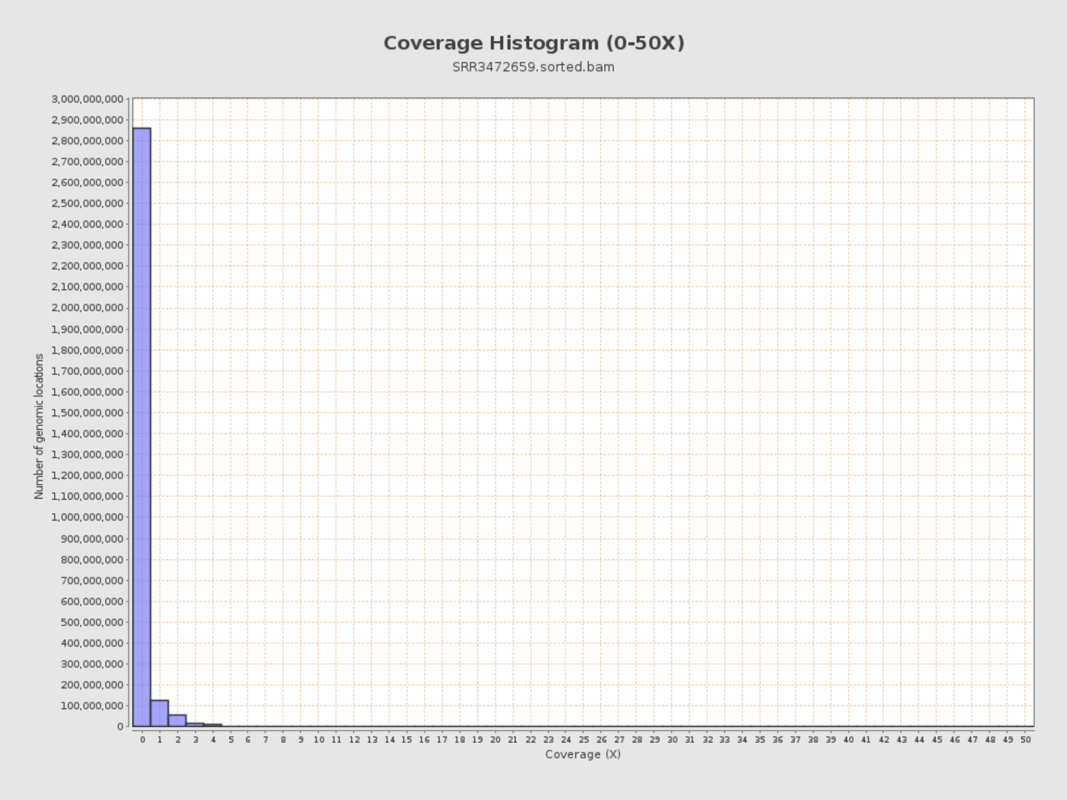
3. Results : Coverage across reference



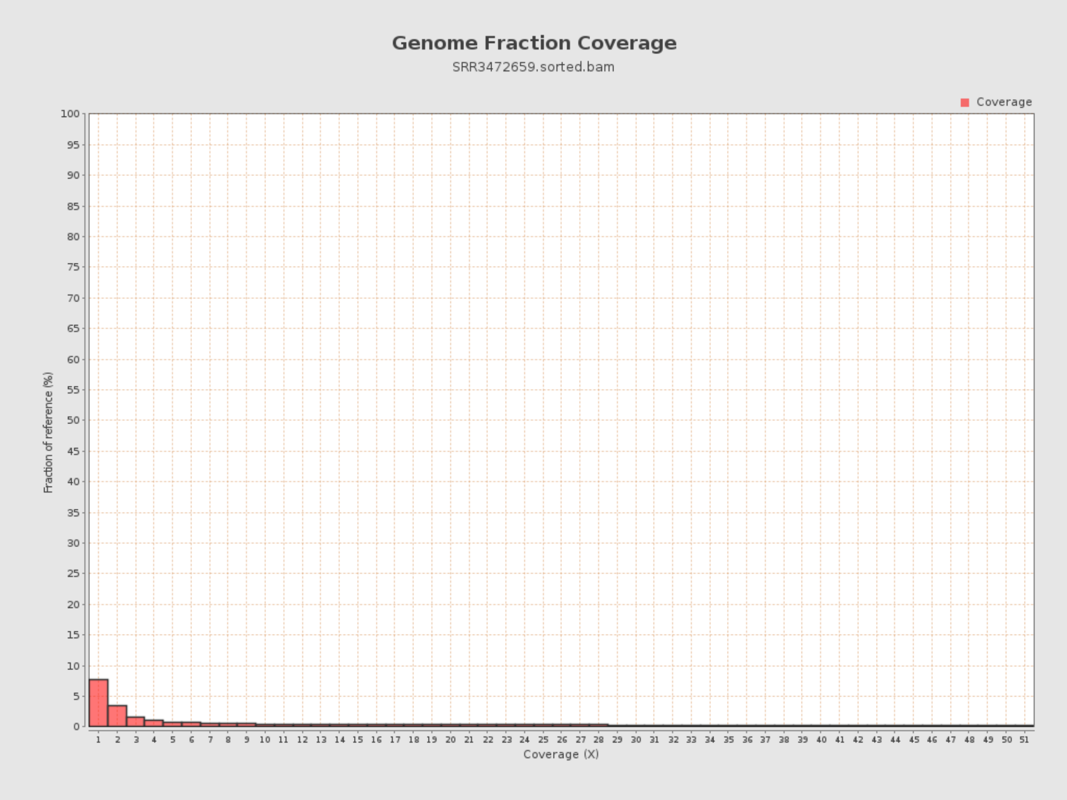
4. Results : Coverage Histogram



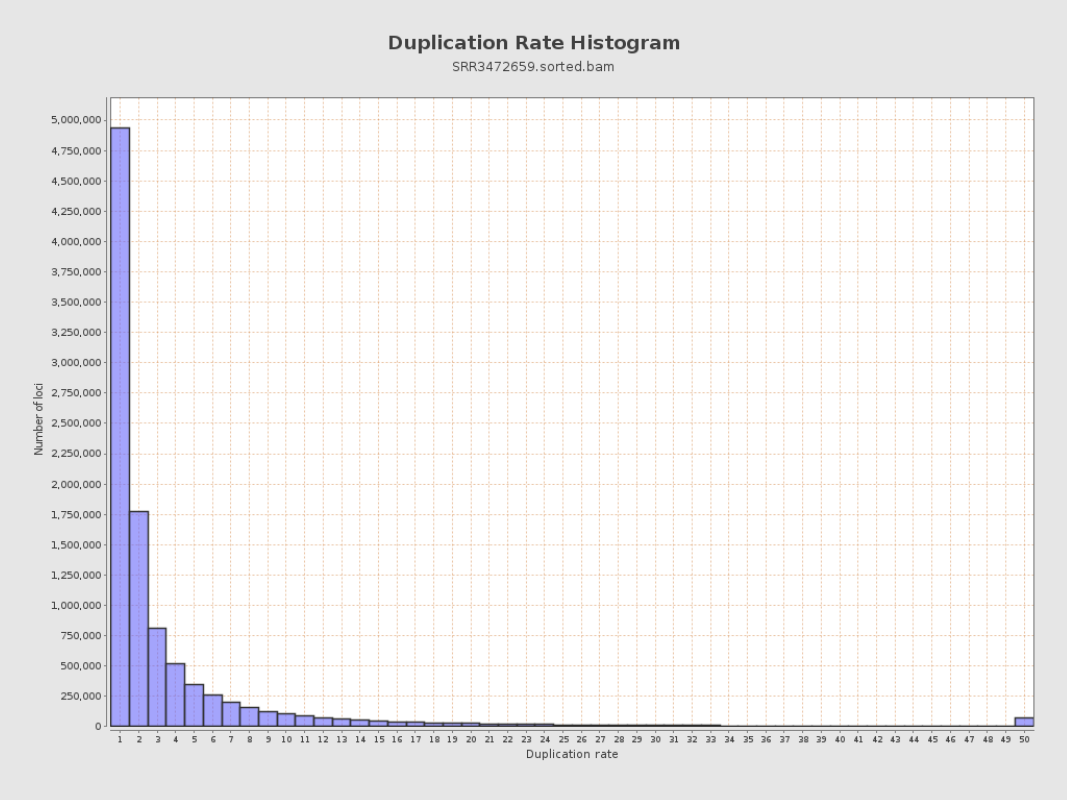
5. Results : Coverage Histogram (0-50X)



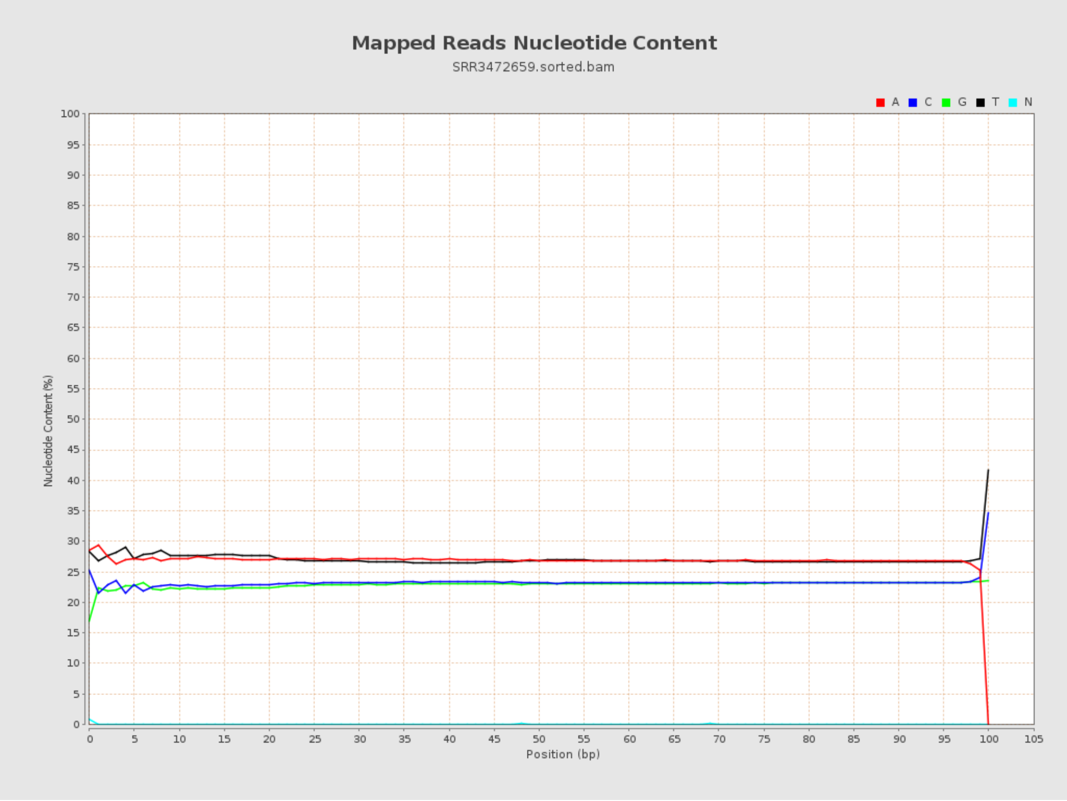
6. Results : Genome Fraction Coverage



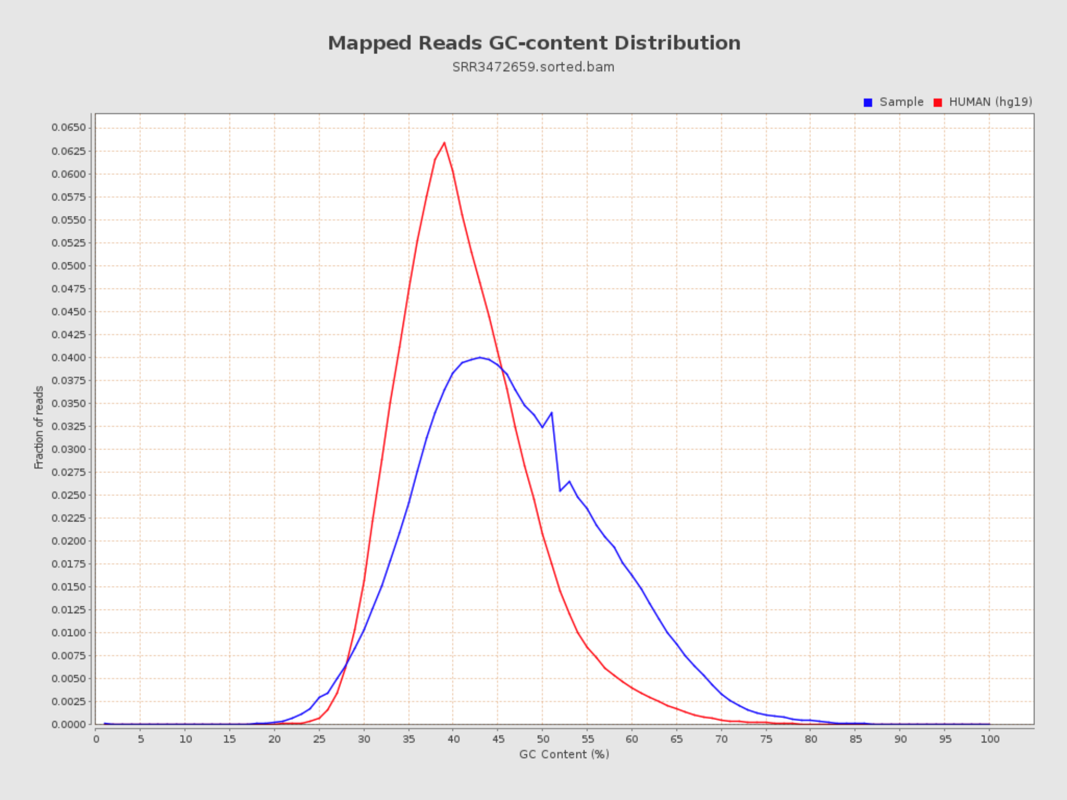
7. Results : Duplication Rate Histogram



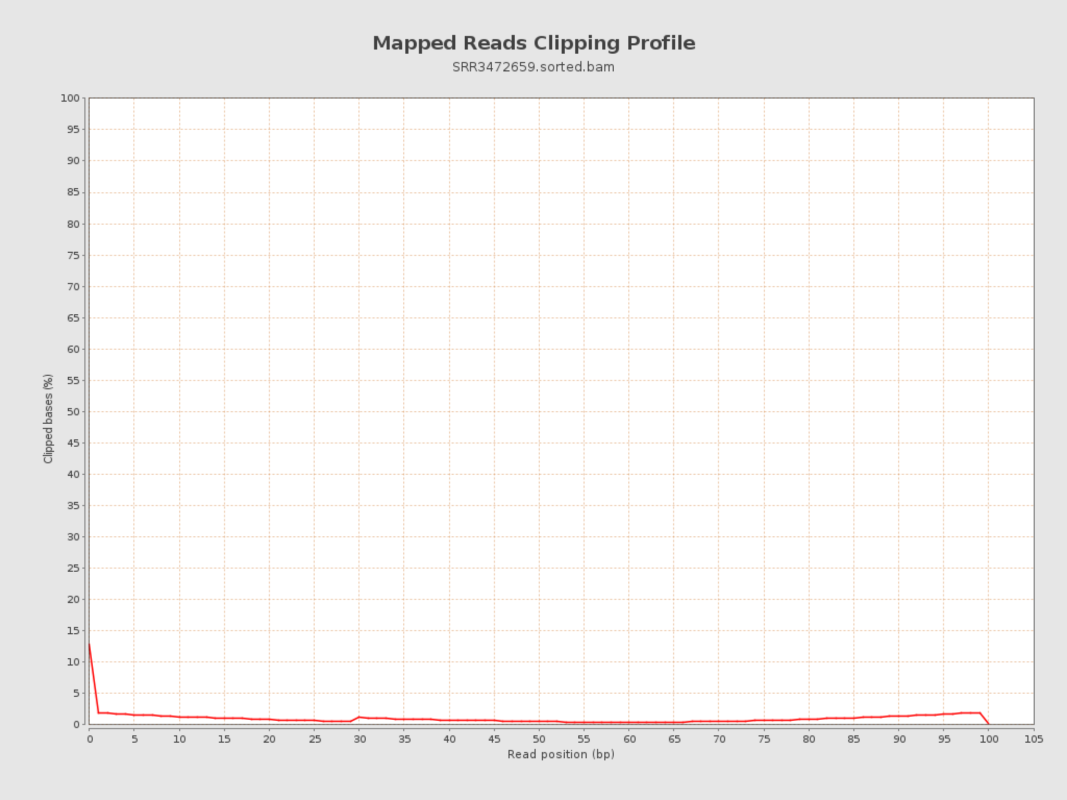
8. Results : Mapped Reads Nucleotide Content



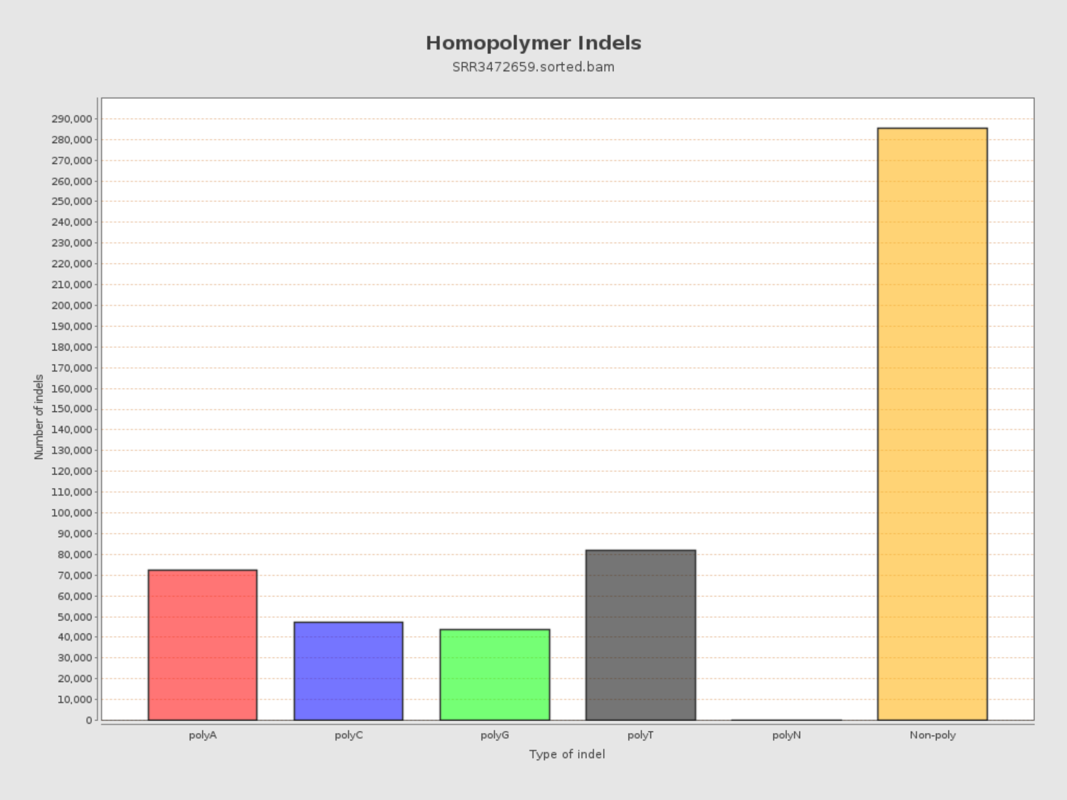
9. Results : Mapped Reads GC-content Distribution



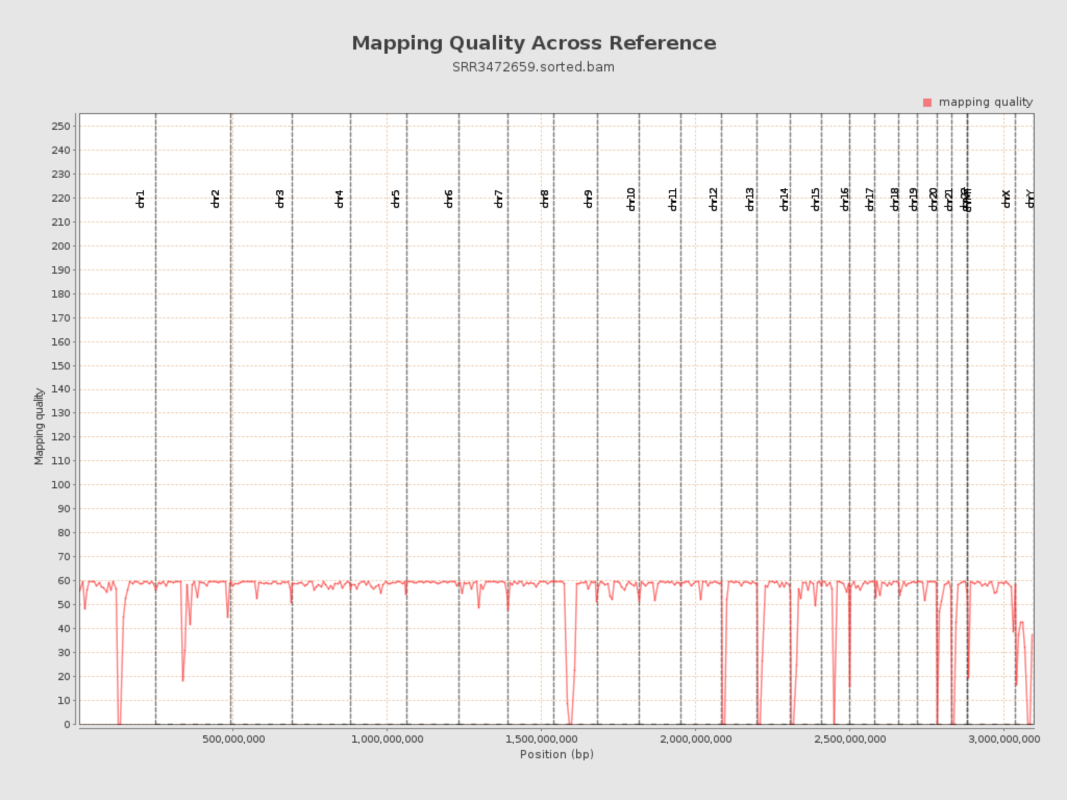
10. Results : Mapped Reads Clipping Profile



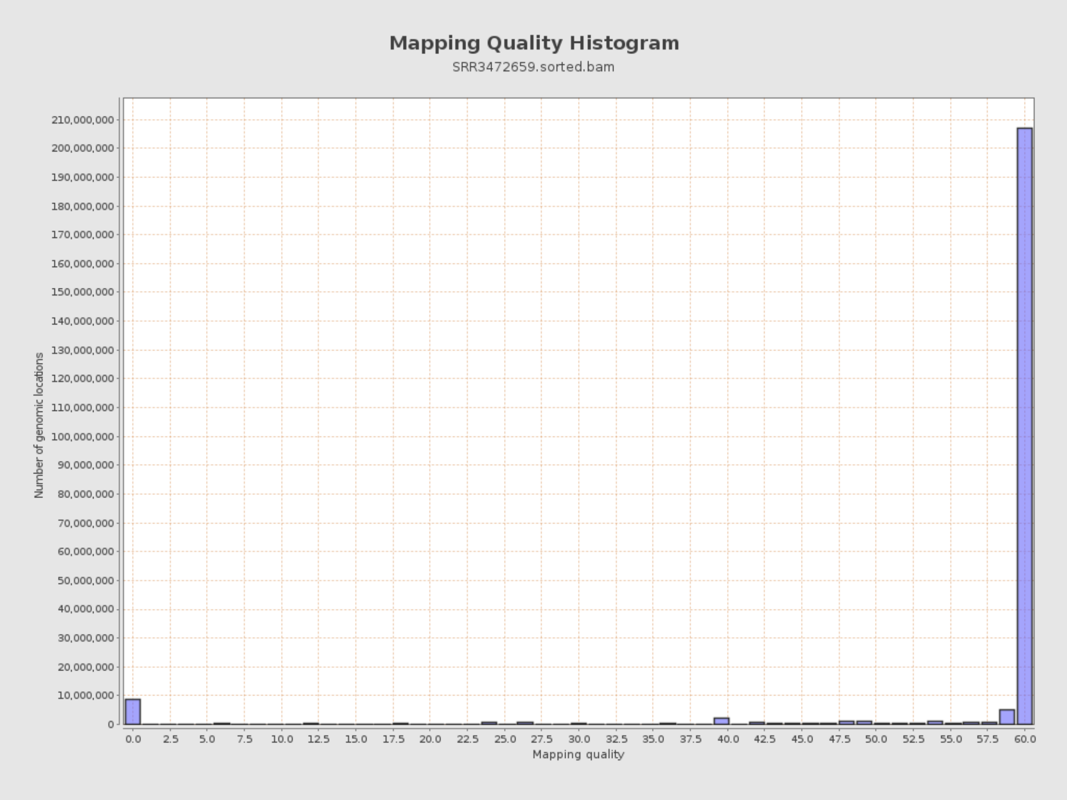
11. Results : Homopolymer Indels



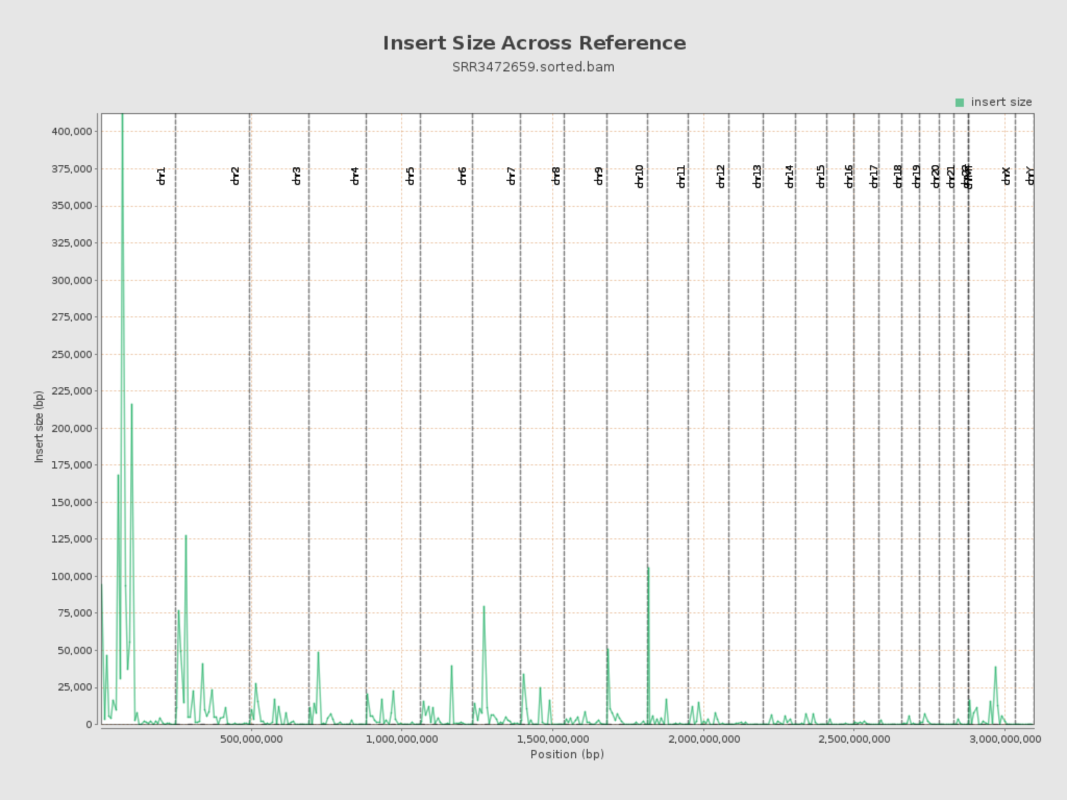
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram