Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 14:46:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472705.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_SRR3472705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472705_1.fastq.gz SRR3472705_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 14:46:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,187,568
Mapped reads	18,051,414 / 99.25%
Unmapped reads	136,154 / 0.75%
Mapped paired reads	18,051,414 / 99.25%
Mapped reads, first in pair	9,048,475 / 49.75%
Mapped reads, second in pair	9,002,939 / 49.5%
Mapped reads, both in pair	17,968,256 / 98.79%
Mapped reads, singletons	83,158 / 0.46%
Secondary alignments	0
Supplementary alignments	114,879 / 0.63%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	13,746,612 / 75.58%
Duplication rate	44.06%
Clipped reads	1,663,543 / 9.15%

2.2. ACGT Content

Number/percentage of A's	477,776,048 / 26.89%
Number/percentage of C's	412,880,390 / 23.24%
Number/percentage of T's	476,323,002 / 26.81%
Number/percentage of G's	409,349,102 / 23.04%
Number/percentage of N's	348,116 / 0.02%

GC Percentage	46.28%

2.3. Coverage

Mean	0.574
Standard Deviation	42.9811

2.4. Mapping Quality

Mean Mapping Quality	54.92

2.5. Insert size

Mean	23,496.73
Standard Deviation	1,475,741.16
P25/Median/P75	160 / 221 / 299

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,208,809
Insertions	108,864
Mapped reads with at least one insertion	0.6%
Deletions	106,618
Mapped reads with at least one deletion	0.57%
Homopolymer indels	43.94%

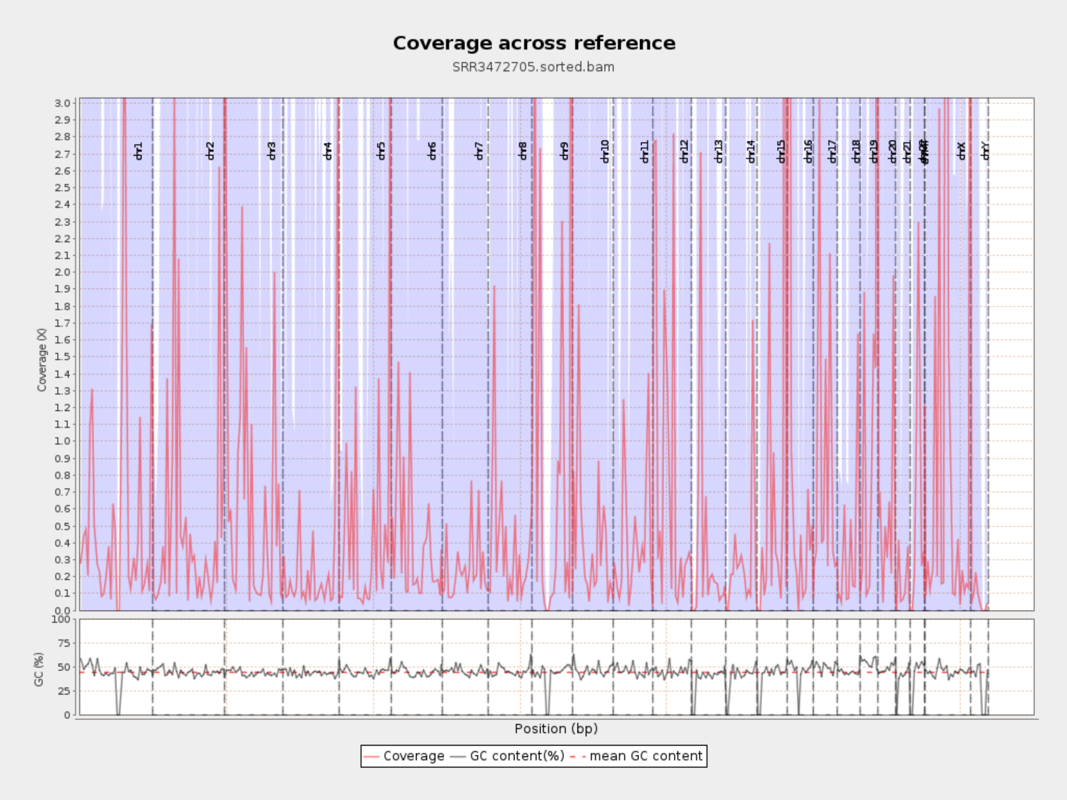
2.7. Chromosome stats

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

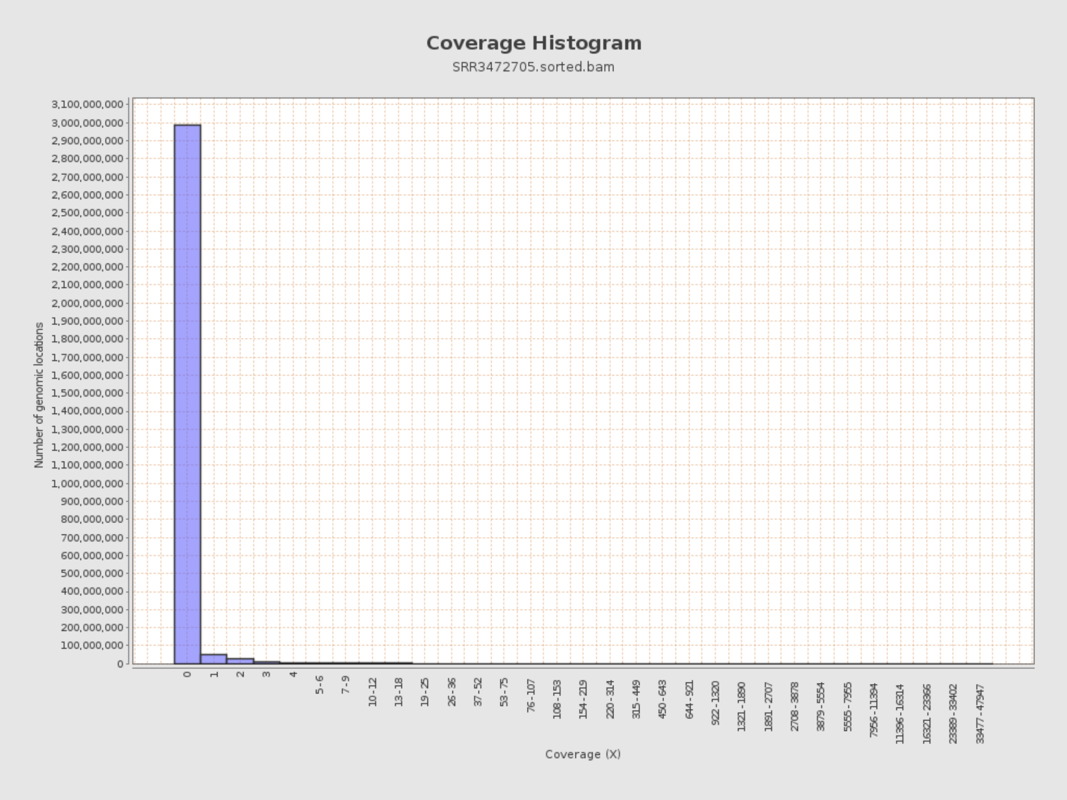
		bases	coverage	deviation
chr1	249250621	147013776	0.5898	32.258
chr2	243199373	127401141	0.5239	39.7913
chr3	198022430	140094971	0.7075	43.9908
chr4	191154276	54831688	0.2868	29.4096
chr5	180915260	90157034	0.4983	34.5317
chr6	171115067	68560547	0.4007	21.763
chr7	159138663	40120358	0.2521	13.8454
chr8	146364022	57911227	0.3957	20.3243
chr9	141213431	160114106	1.1338	72.1268
chr10	135534747	57163339	0.4218	41.1921
chr11	135006516	58587534	0.434	27.0307
chr12	133851895	113318746	0.8466	51.3244
chr13	115169878	42199605	0.3664	49.7584
chr14	107349540	31685434	0.2952	17.0495
chr15	102531392	109155552	1.0646	108.3379
chr16	90354753	82615220	0.9143	50.231
chr17	81195210	70275044	0.8655	35.0649
chr18	78077248	29567526	0.3787	37.3161
chr19	59128983	62672436	1.0599	44.686
chr20	63025520	37357471	0.5927	31.7387
chr21	48129895	8284369	0.1721	13.989
chr22	51304566	32244967	0.6285	38.4977
chrMT	16571	20188	1.2183	1.38
chrX	155270560	151356150	0.9748	56.6151

chrY	59373566	4215587	0.071	4.3271

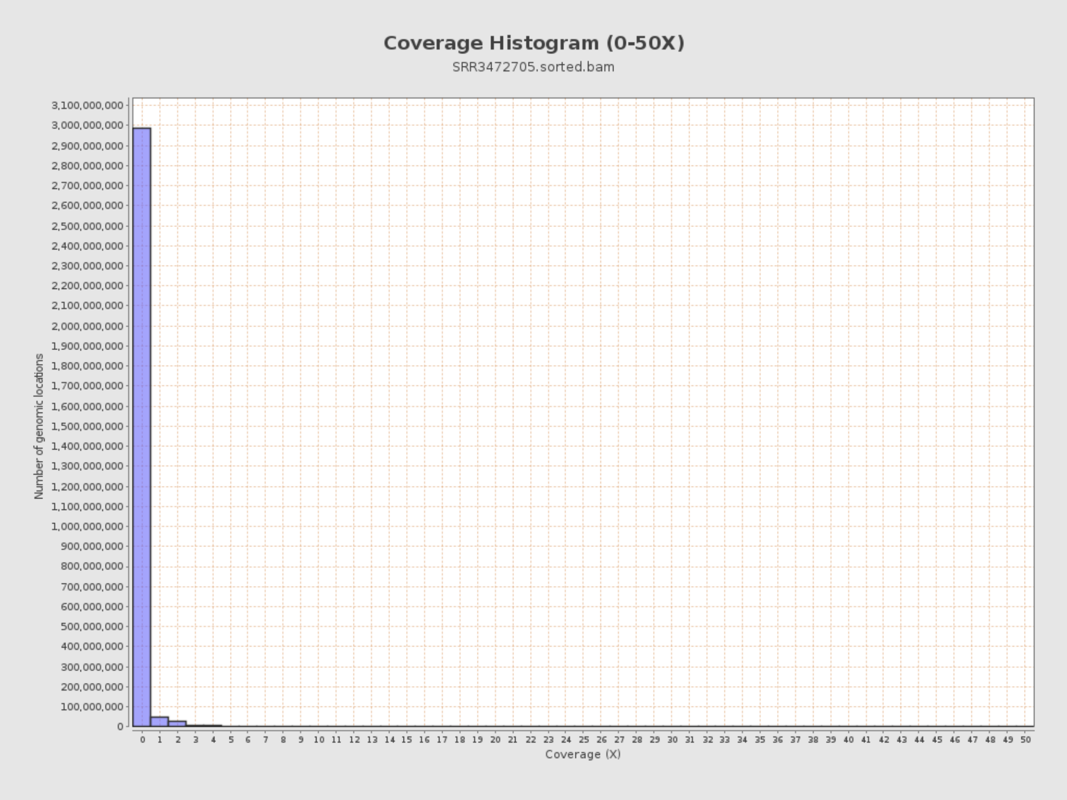
3. Results : Coverage across reference



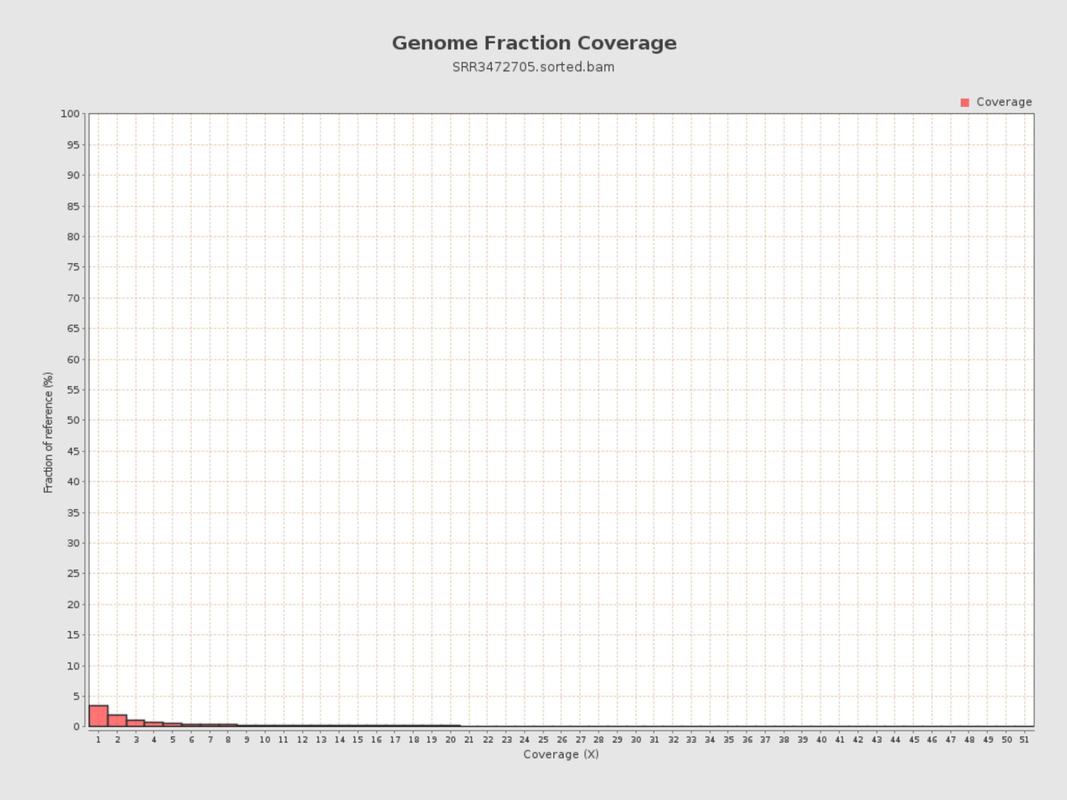
4. Results : Coverage Histogram



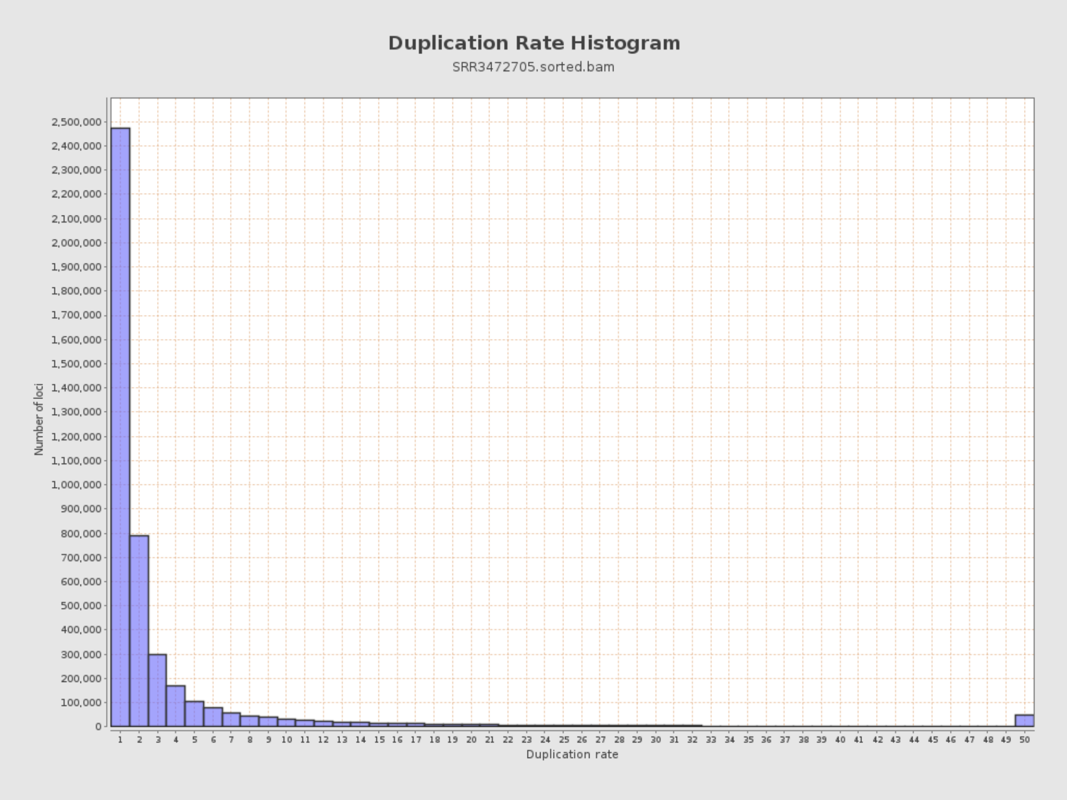
5. Results : Coverage Histogram (0-50X)



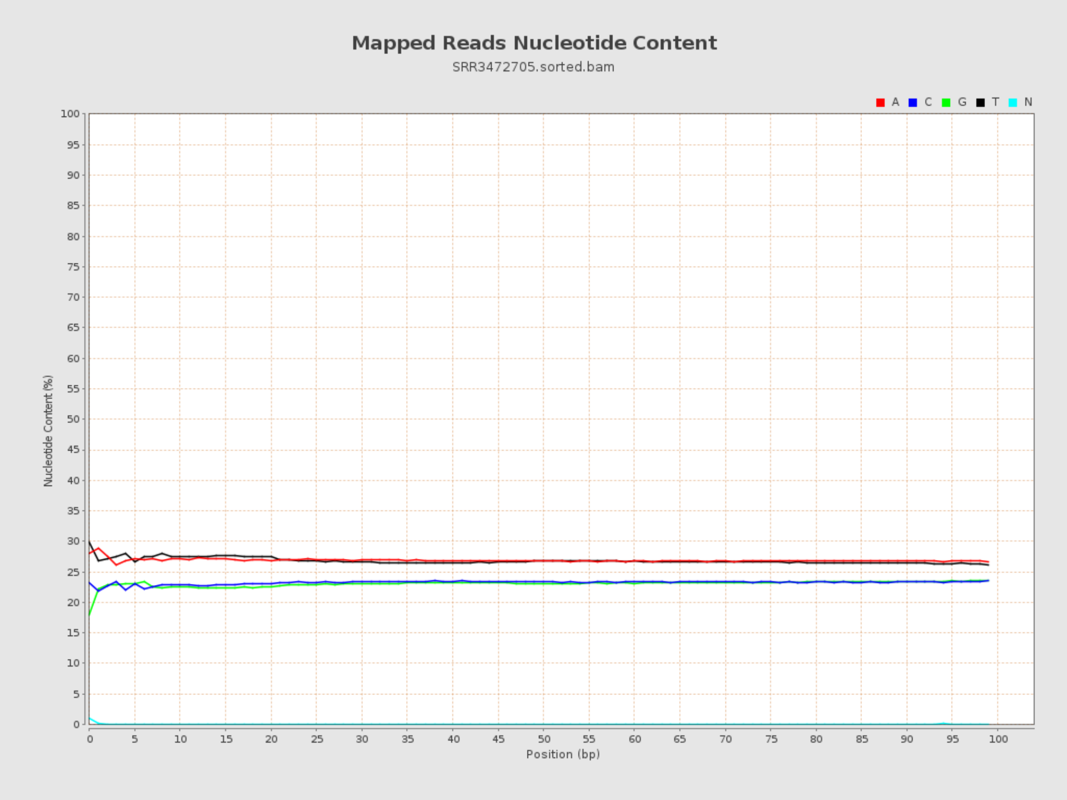
6. Results : Genome Fraction Coverage



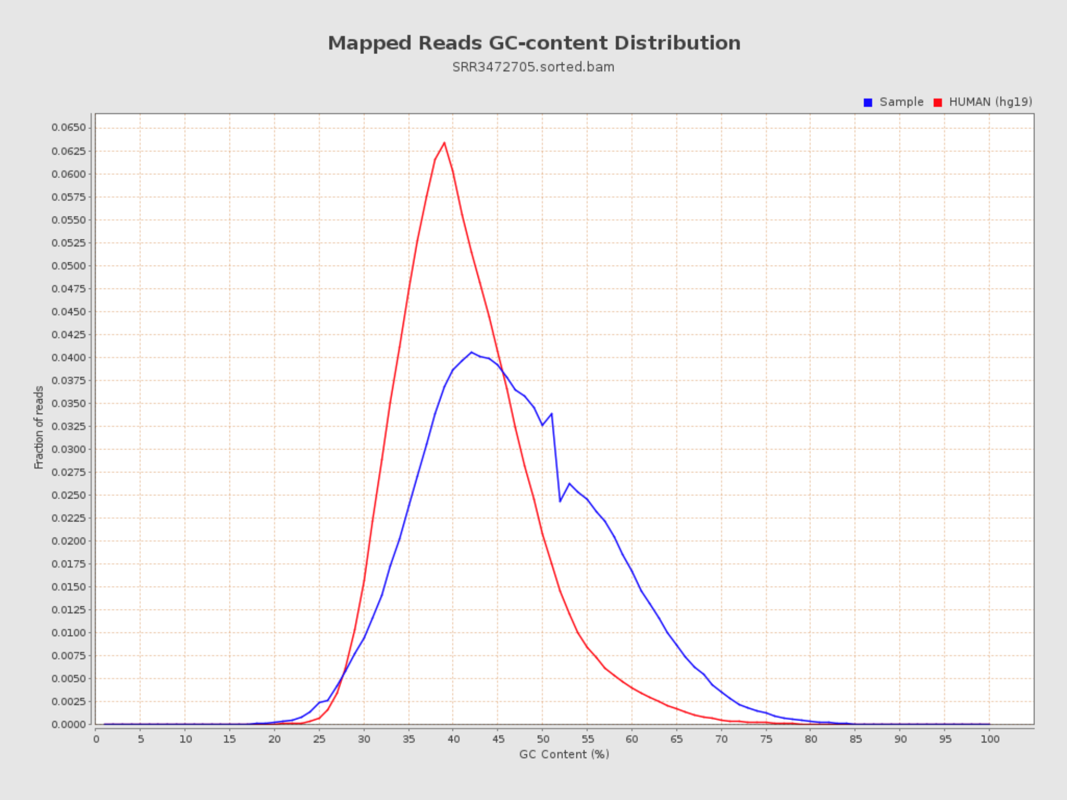
7. Results : Duplication Rate Histogram



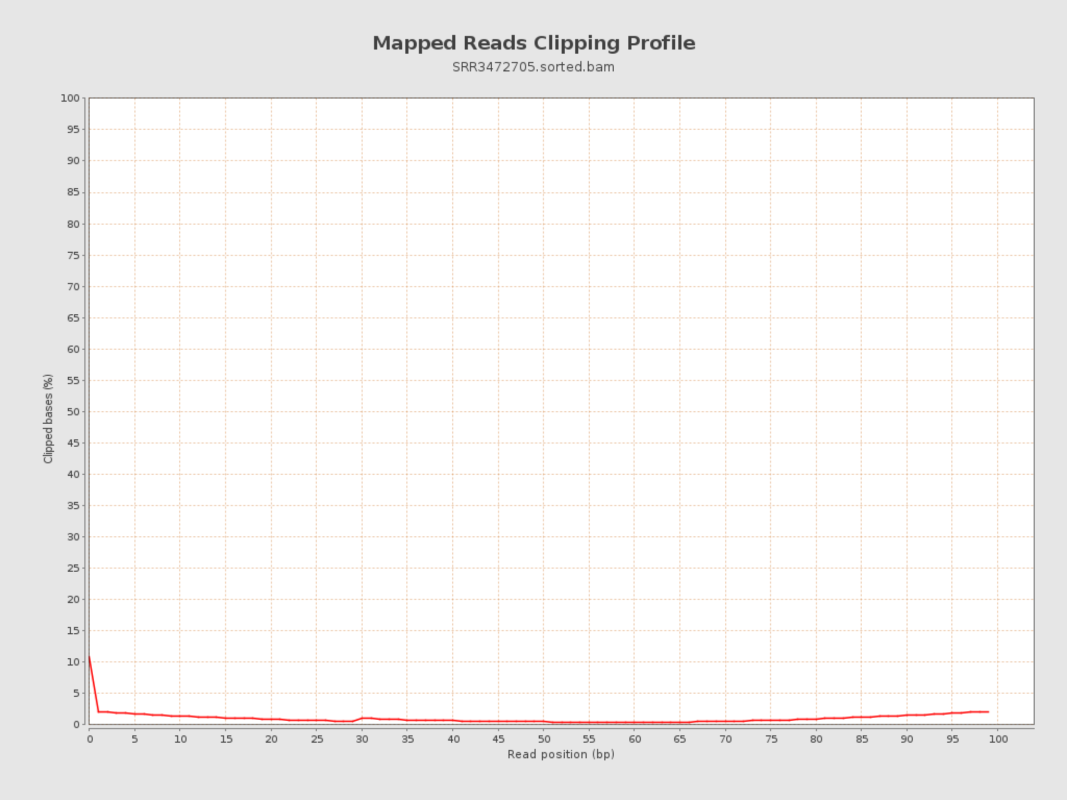
8. Results : Mapped Reads Nucleotide Content



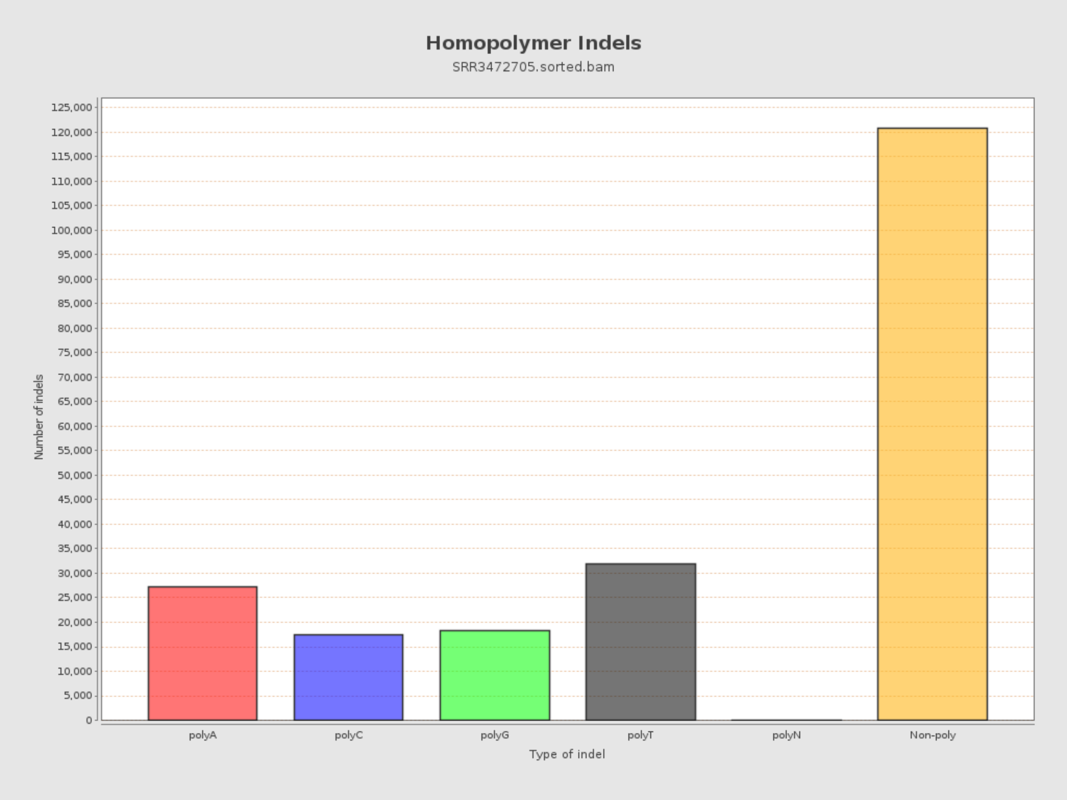
9. Results : Mapped Reads GC-content Distribution



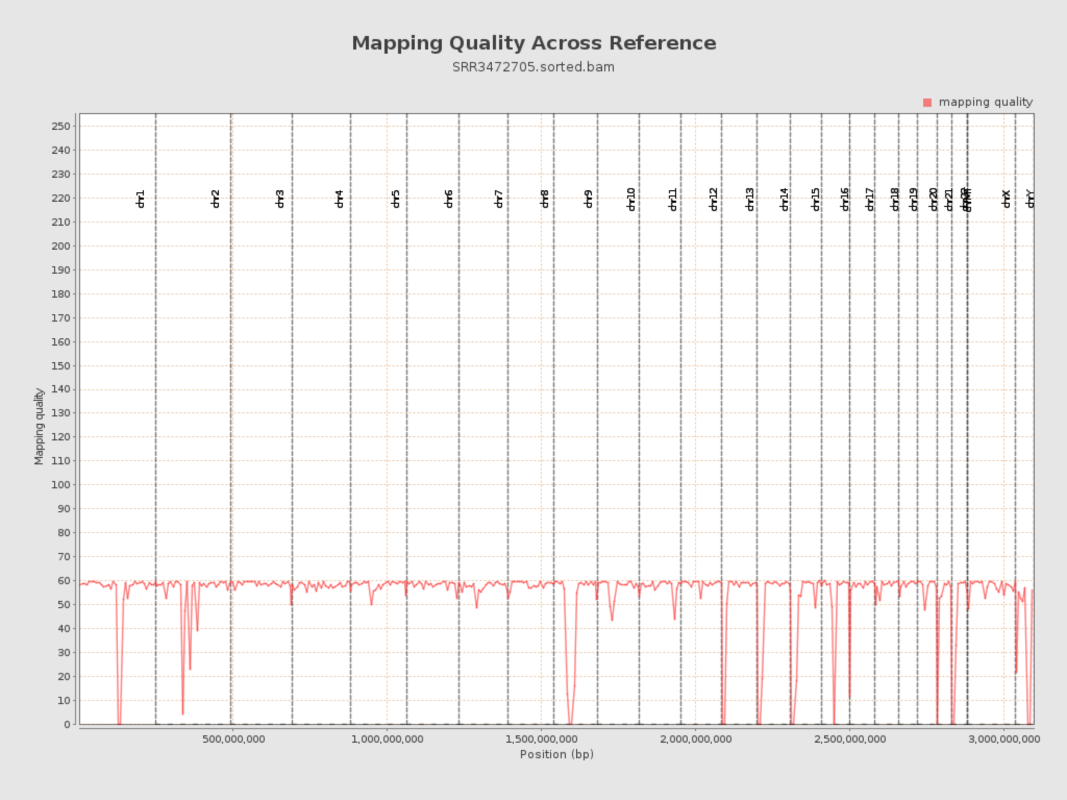
10. Results : Mapped Reads Clipping Profile



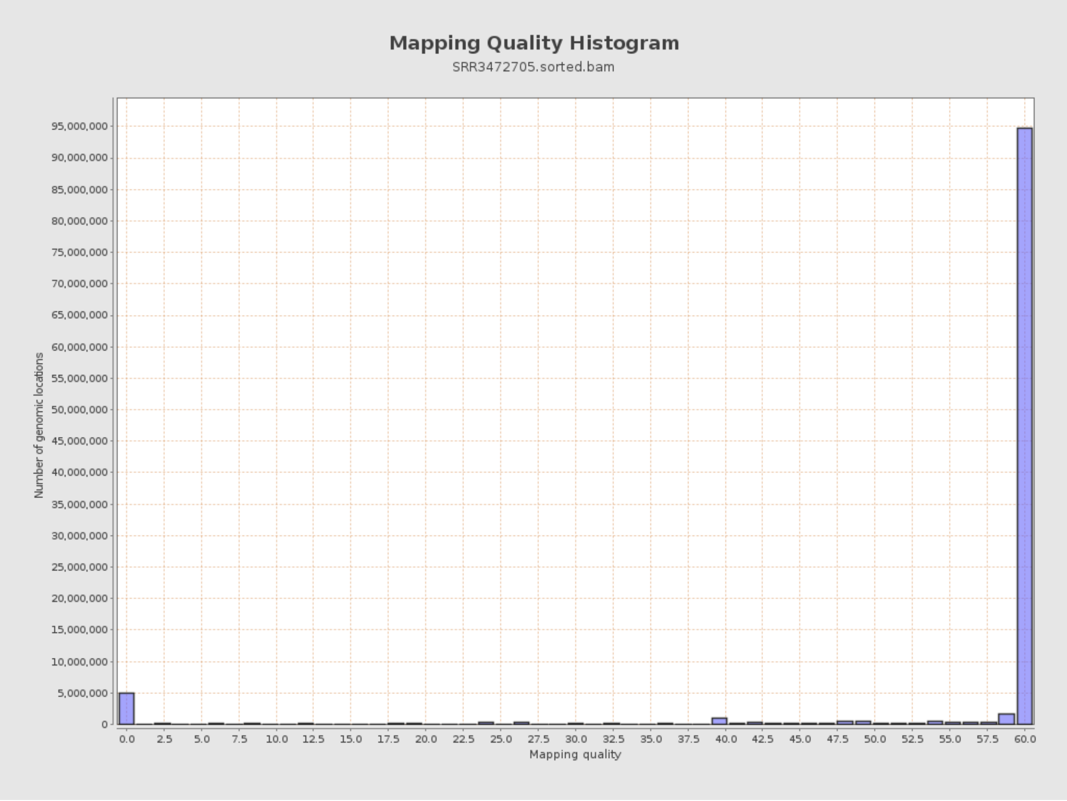
11. Results : Homopolymer Indels



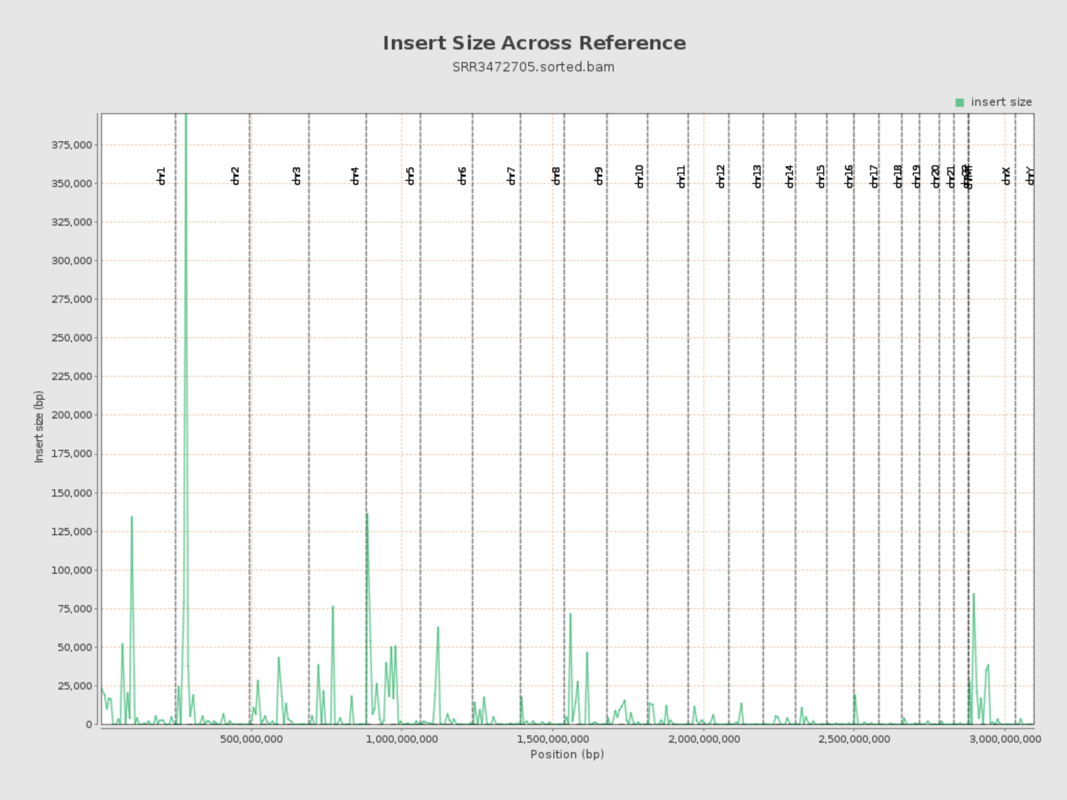
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram