Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 13:50:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472701.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_SRR3472701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472701_1.fastq.gz SRR3472701_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 13:50:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,739,244
Mapped reads	12,640,322 / 99.22%
Unmapped reads	98,922 / 0.78%
Mapped paired reads	12,640,322 / 99.22%
Mapped reads, first in pair	6,338,113 / 49.75%
Mapped reads, second in pair	6,302,209 / 49.47%
Mapped reads, both in pair	12,580,130 / 98.75%
Mapped reads, singletons	60,192 / 0.47%
Secondary alignments	0
Supplementary alignments	44,670 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	7,688,515 / 60.35%
Duplication rate	45.59%
Clipped reads	1,126,319 / 8.84%

2.2. ACGT Content

Number/percentage of A's	334,509,271 / 26.91%
Number/percentage of C's	289,030,937 / 23.26%
Number/percentage of T's	332,391,078 / 26.74%
Number/percentage of G's	286,694,043 / 23.07%
Number/percentage of N's	241,398 / 0.02%

GC Percentage	46.32%

2.3. Coverage

Mean	0.4015
Standard Deviation	16.0048

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	23,770.35
Standard Deviation	1,515,830.22
P25/Median/P75	161 / 227 / 307

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	7,209,562
Insertions	69,556
Mapped reads with at least one insertion	0.55%
Deletions	66,137
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.45%

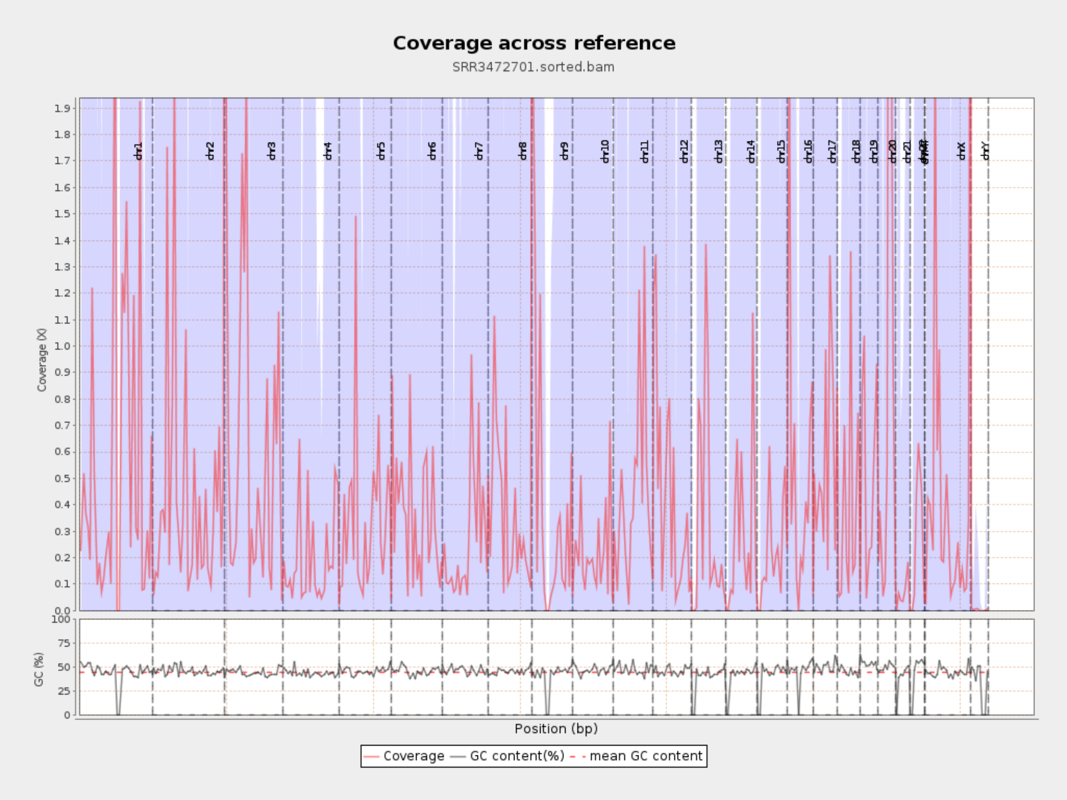
2.7. Chromosome stats

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

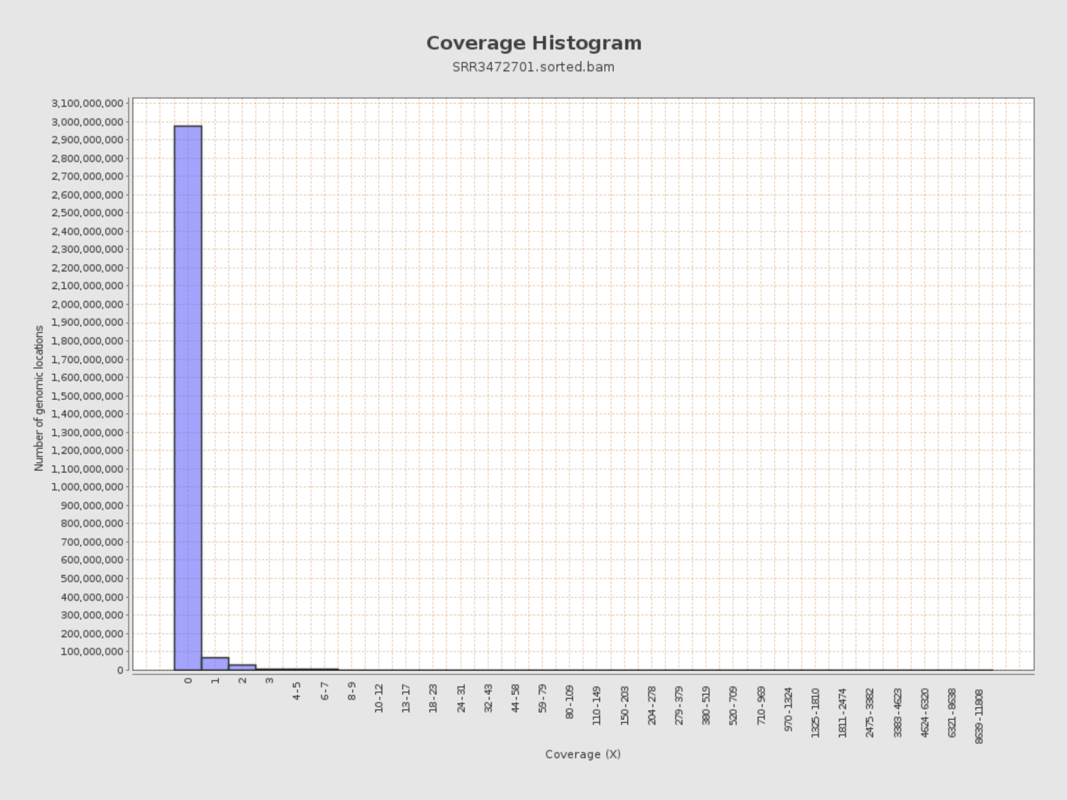
		bases	coverage	deviation
chr1	249250621	141651356	0.5683	23.4867
chr2	243199373	104124059	0.4281	16.4004
chr3	198022430	133954595	0.6765	15.8482
chr4	191154276	36281225	0.1898	6.8784
chr5	180915260	61842194	0.3418	11.613
chr6	171115067	60206005	0.3518	9.345
chr7	159138663	41888971	0.2632	8.4118
chr8	146364022	51688587	0.3532	10.6494
chr9	141213431	61585350	0.4361	11.8487
chr10	135534747	30885342	0.2279	8.922
chr11	135006516	60458738	0.4478	15.5313
chr12	133851895	58252421	0.4352	19.3333
chr13	115169878	37523009	0.3258	14.3419
chr14	107349540	29612071	0.2758	11.2009
chr15	102531392	22797866	0.2224	6.8289
chr16	90354753	48589435	0.5378	14.9516
chr17	81195210	46519727	0.5729	14.6383
chr18	78077248	30294395	0.388	14.9961
chr19	59128983	31020338	0.5246	13.7728
chr20	63025520	71514016	1.1347	57.3732
chr21	48129895	3395322	0.0705	2.5966
chr22	51304566	13269440	0.2586	8.5242
chrMT	16571	1253	0.0756	0.306
chrX	155270560	65425592	0.4214	14.1166

chrY	59373566	245467	0.0041	0.2644

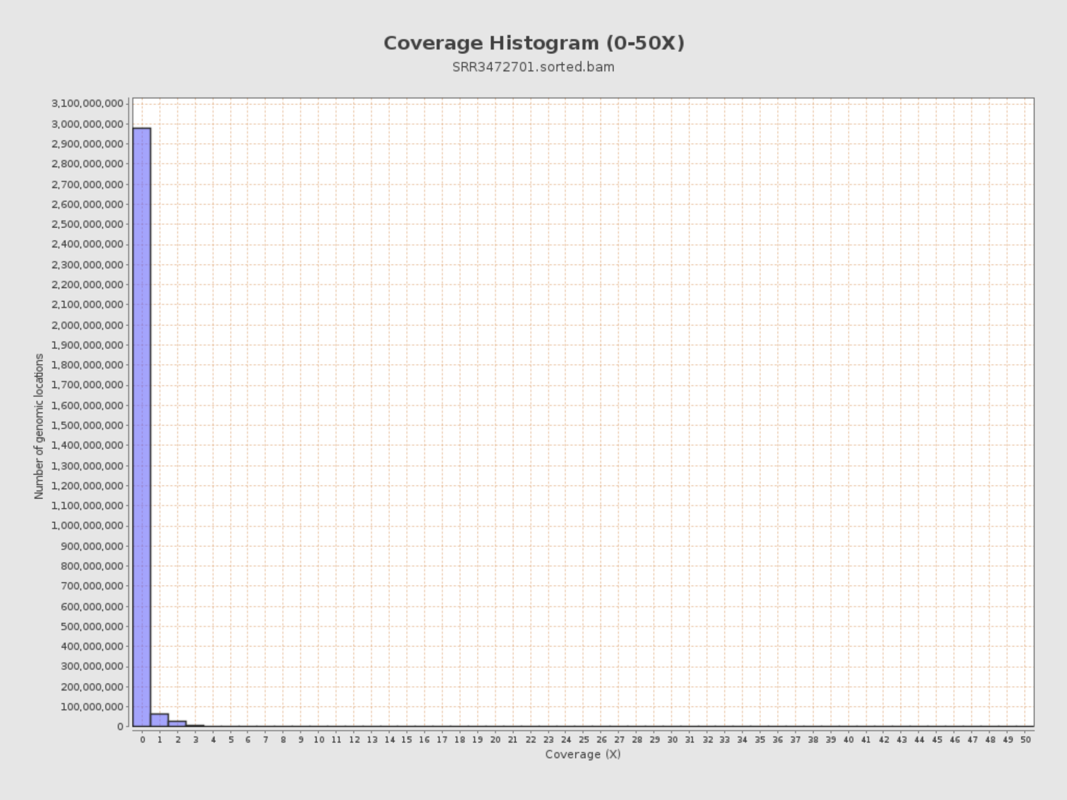
3. Results : Coverage across reference



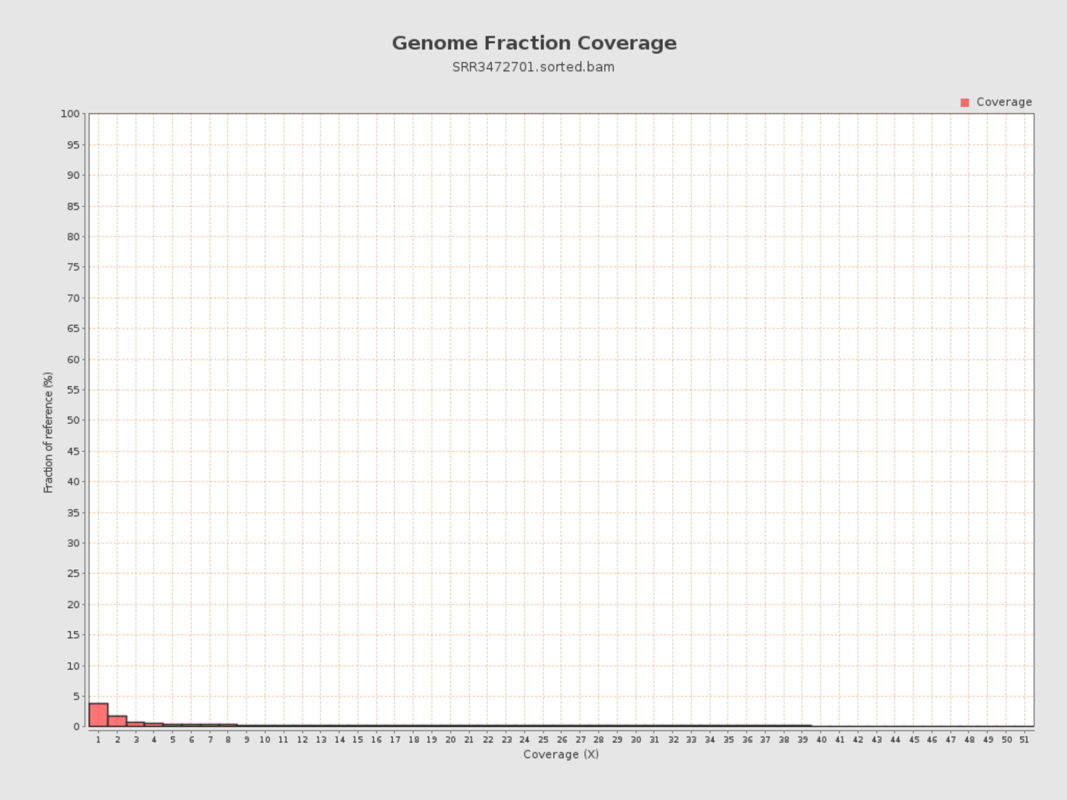
4. Results : Coverage Histogram



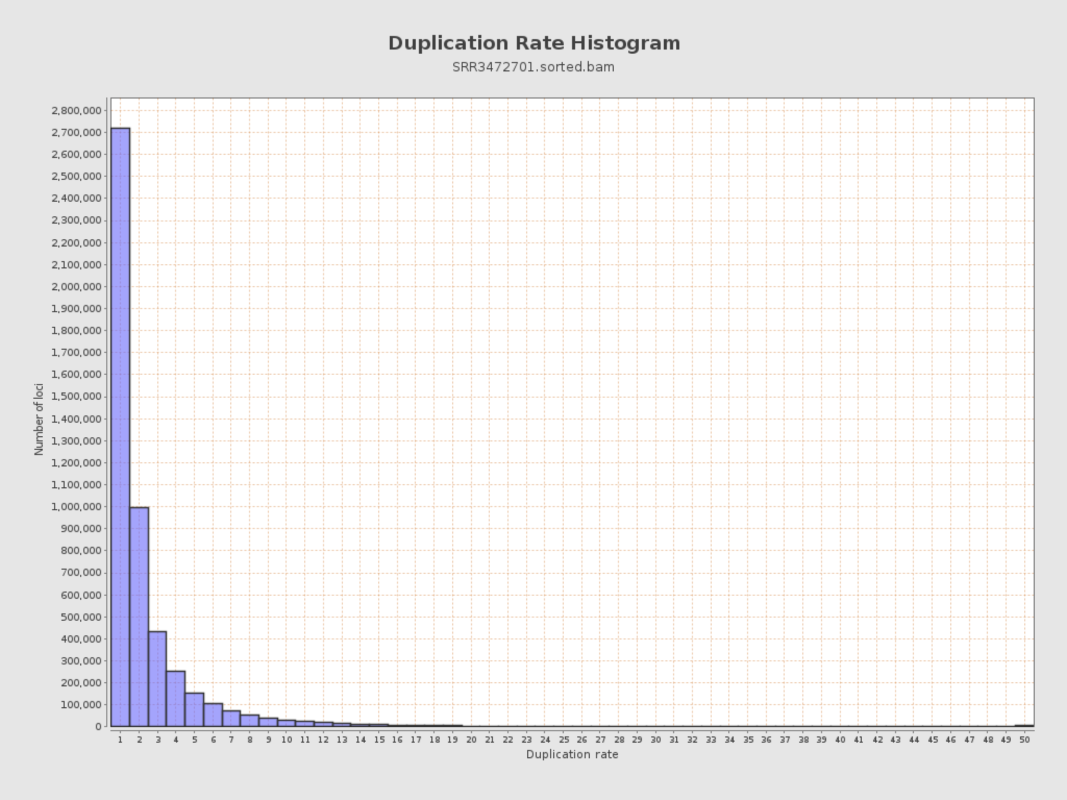
5. Results : Coverage Histogram (0-50X)



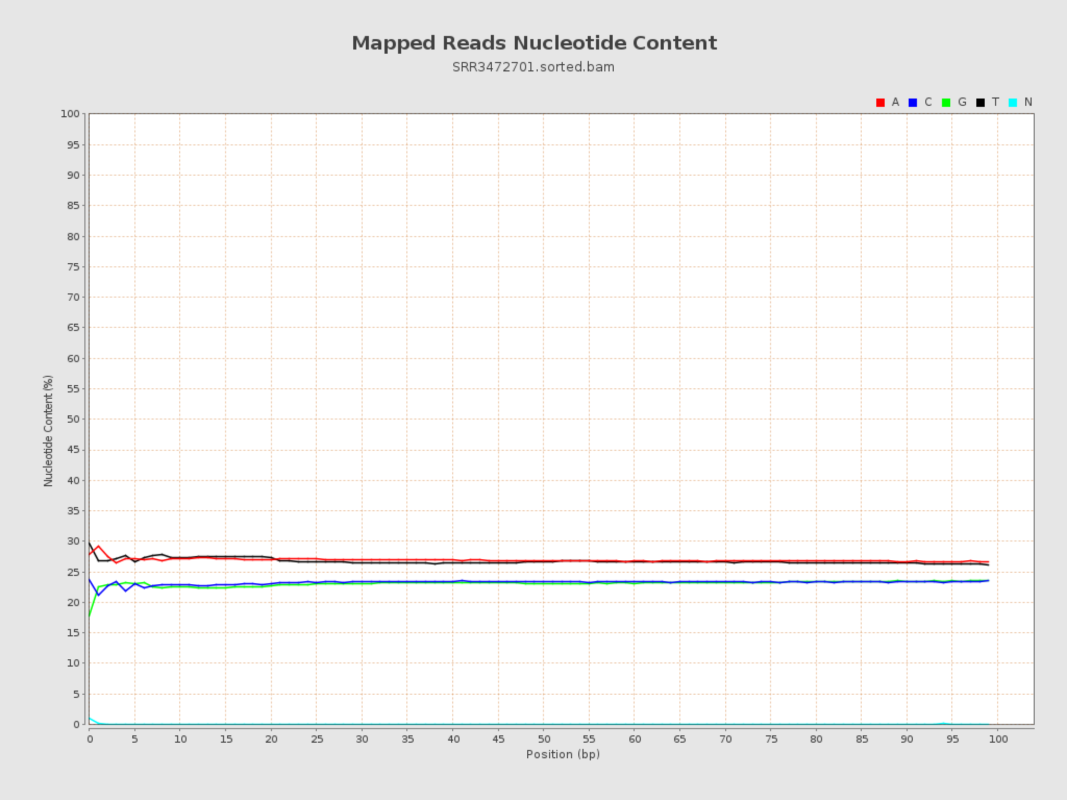
6. Results : Genome Fraction Coverage



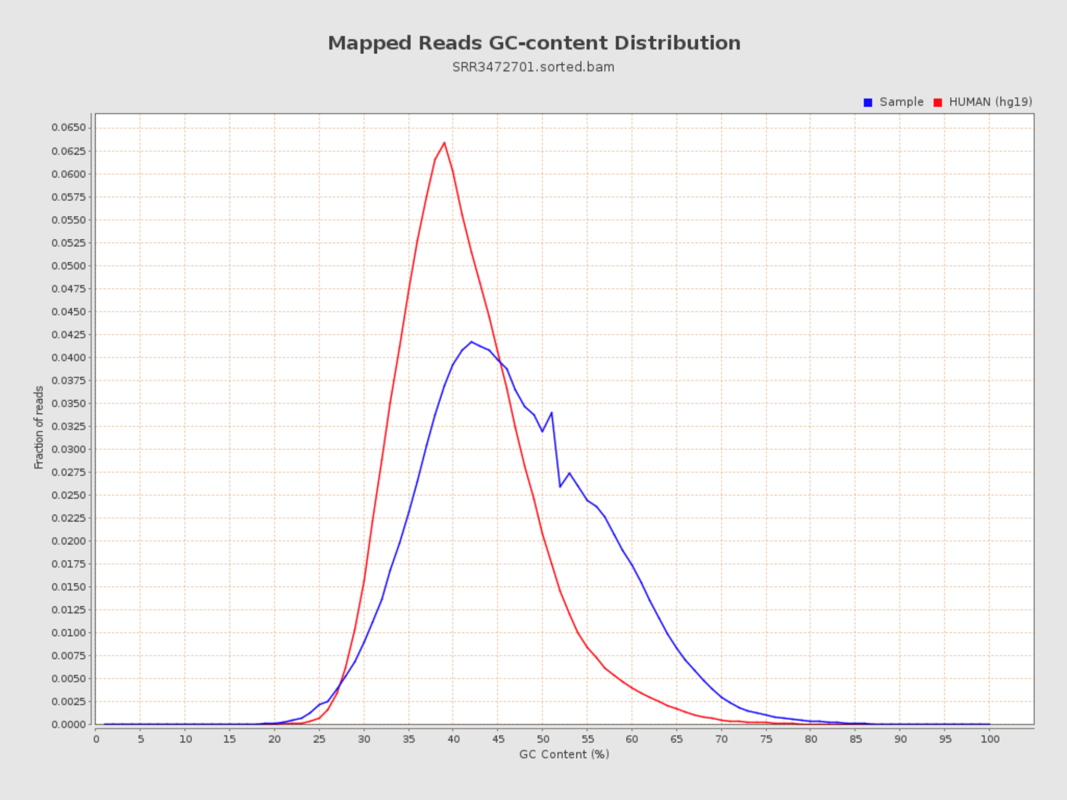
7. Results : Duplication Rate Histogram



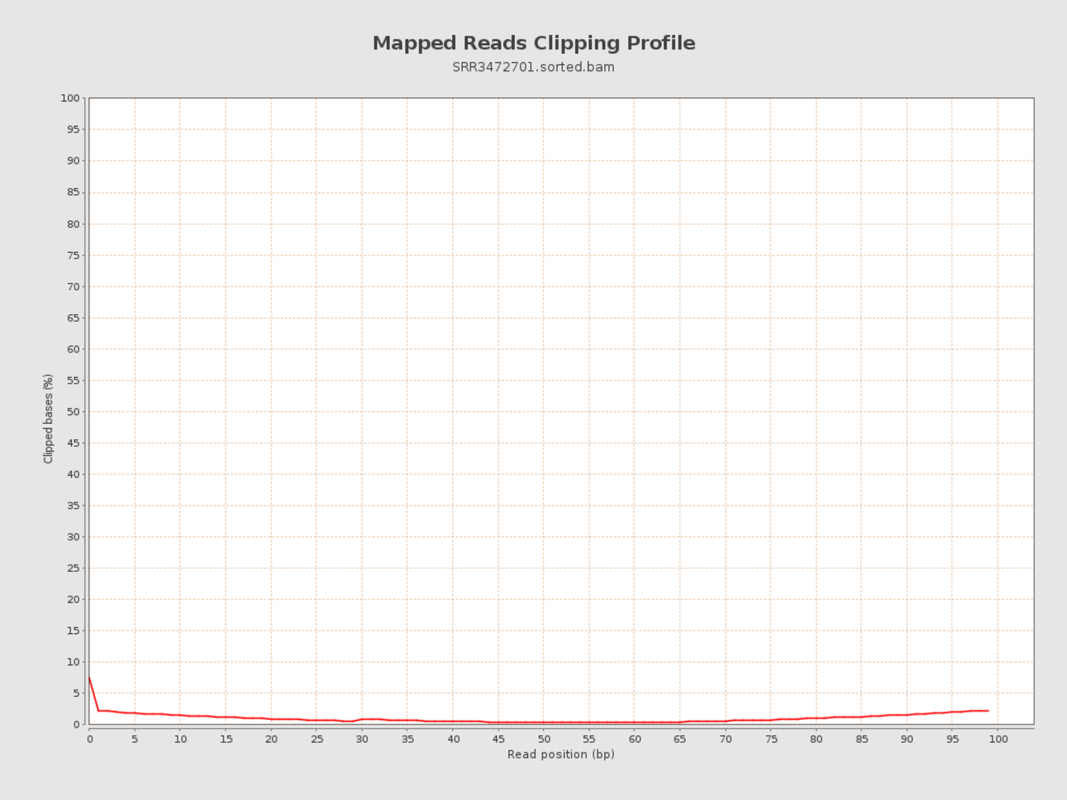
8. Results : Mapped Reads Nucleotide Content



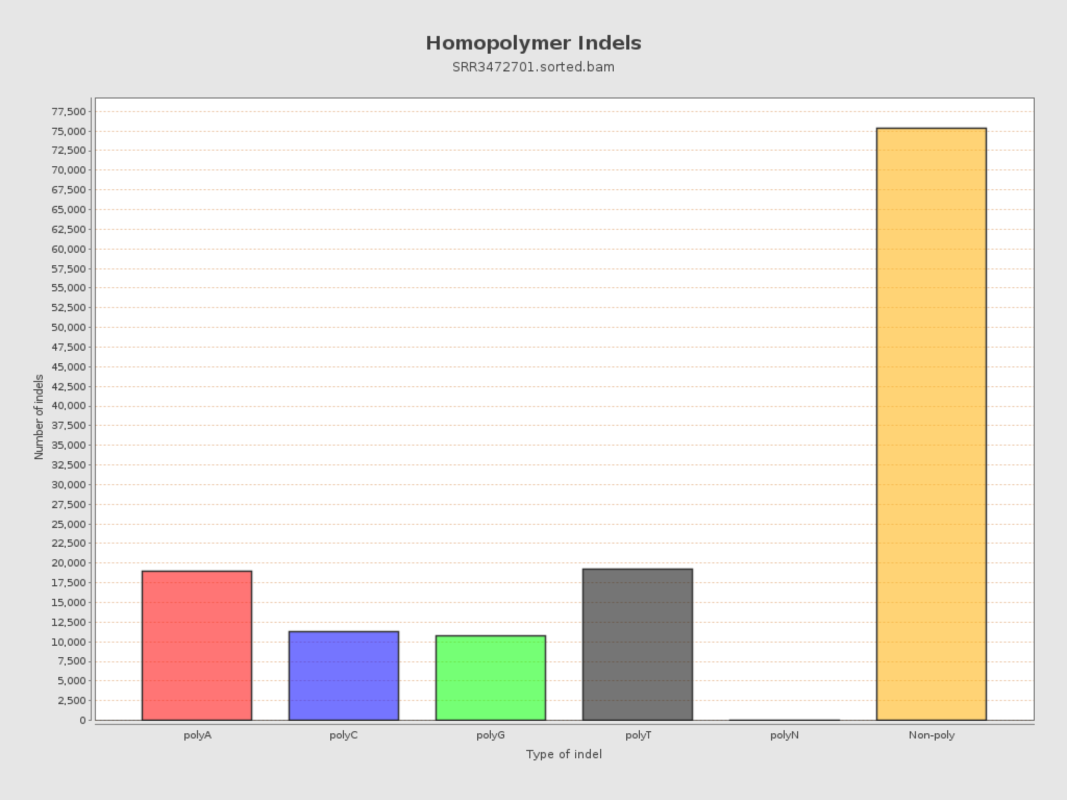
9. Results : Mapped Reads GC-content Distribution



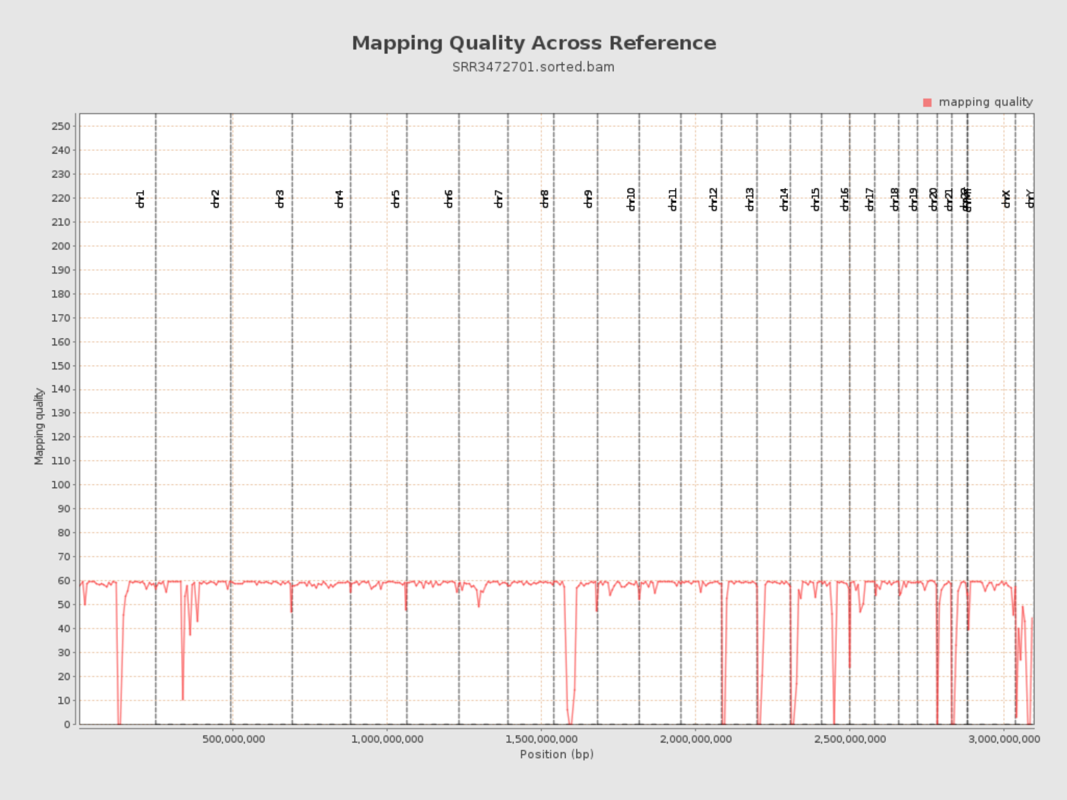
10. Results : Mapped Reads Clipping Profile



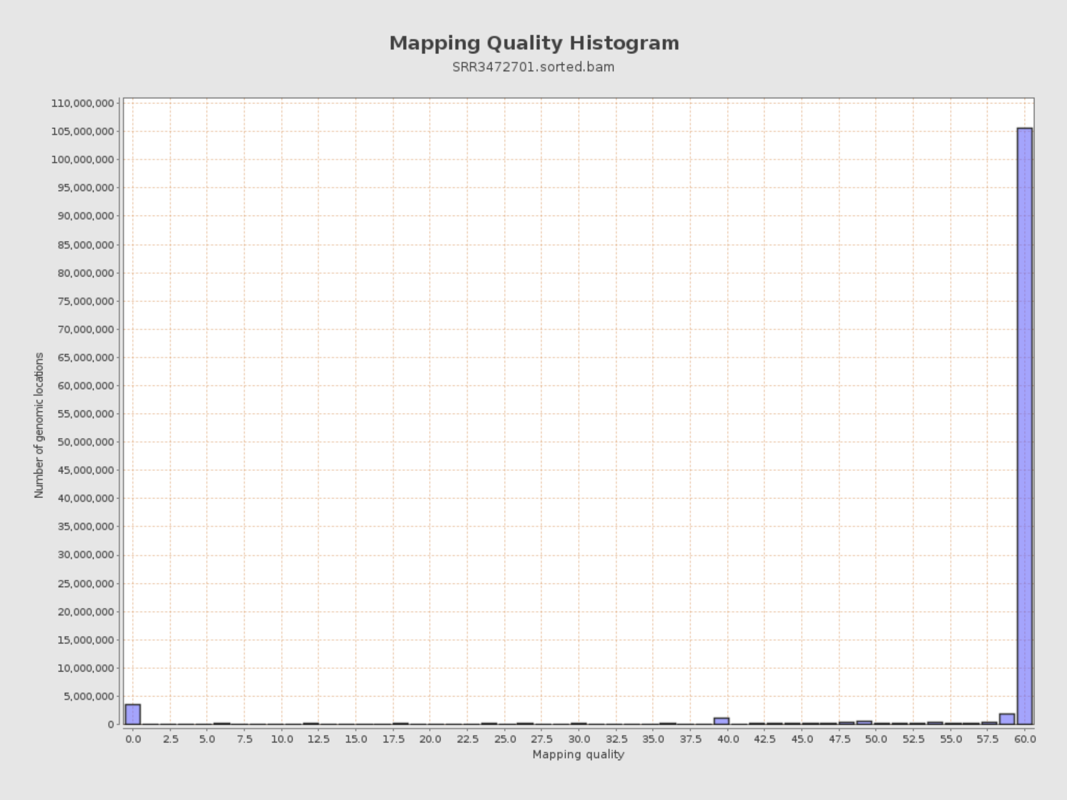
11. Results : Homopolymer Indels



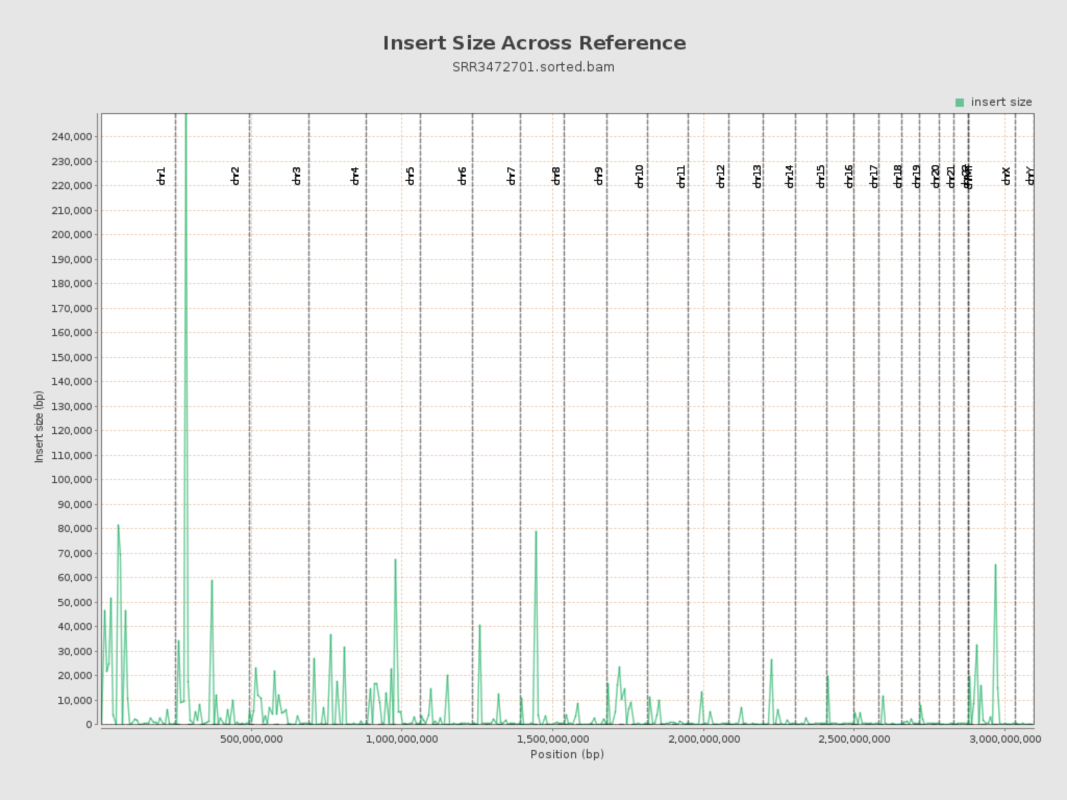
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram