Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 13:13:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472620.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_SRR3472620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472620_1.fastq.gz SRR3472620_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 13:13:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,337,722
Mapped reads	17,188,372 / 99.14%
Unmapped reads	149,350 / 0.86%
Mapped paired reads	17,188,372 / 99.14%
Mapped reads, first in pair	8,621,392 / 49.73%
Mapped reads, second in pair	8,566,980 / 49.41%
Mapped reads, both in pair	17,085,962 / 98.55%
Mapped reads, singletons	102,410 / 0.59%
Secondary alignments	0
Supplementary alignments	88,142 / 0.51%
Read min/max/mean length	30 / 101 / 99.87
Duplicated reads (estimated)	11,656,255 / 67.23%
Duplication rate	48.67%
Clipped reads	1,082,160 / 6.24%

2.2. ACGT Content

Number/percentage of A's	459,038,833 / 27.07%
Number/percentage of C's	391,048,601 / 23.06%
Number/percentage of T's	460,057,166 / 27.13%
Number/percentage of G's	385,322,601 / 22.72%
Number/percentage of N's	310,397 / 0.02%

GC Percentage	45.78%

2.3. Coverage

Mean	0.5479
Standard Deviation	22.5909

2.4. Mapping Quality

Mean Mapping Quality	54.81

2.5. Insert size

Mean	23,505.35
Standard Deviation	1,539,626.52
P25/Median/P75	166 / 227 / 301

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	10,711,839
Insertions	99,679
Mapped reads with at least one insertion	0.57%
Deletions	87,913
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.31%

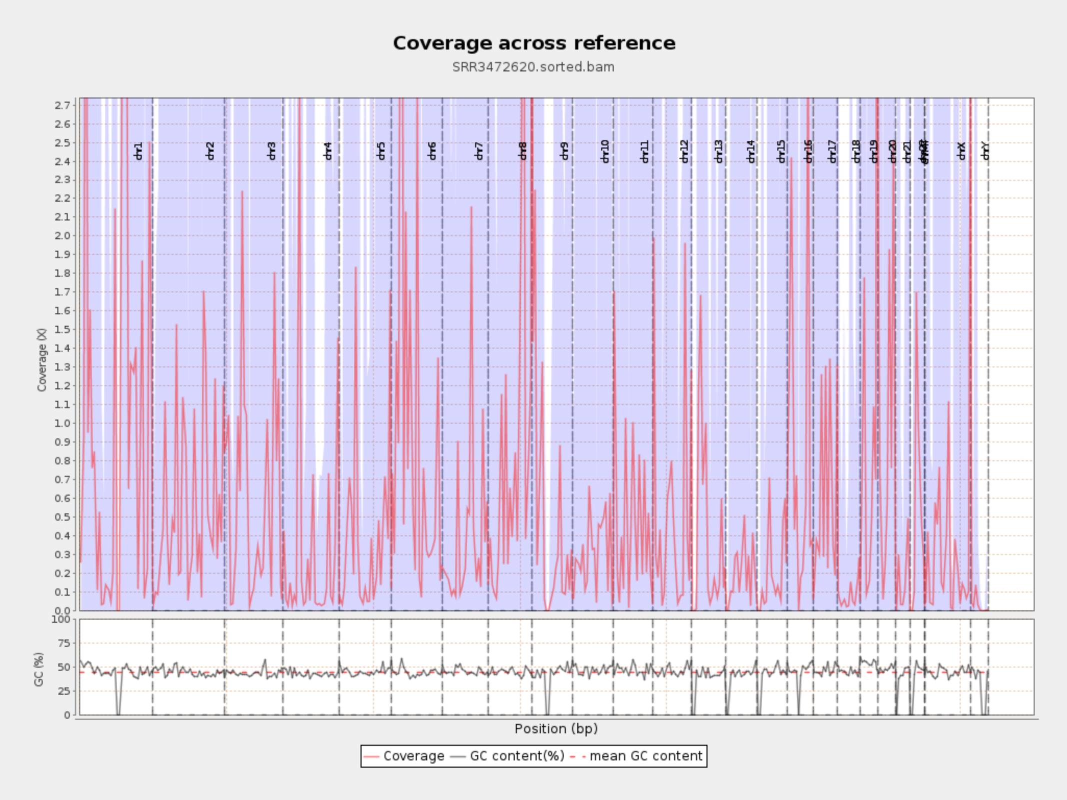
2.7. Chromosome stats

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

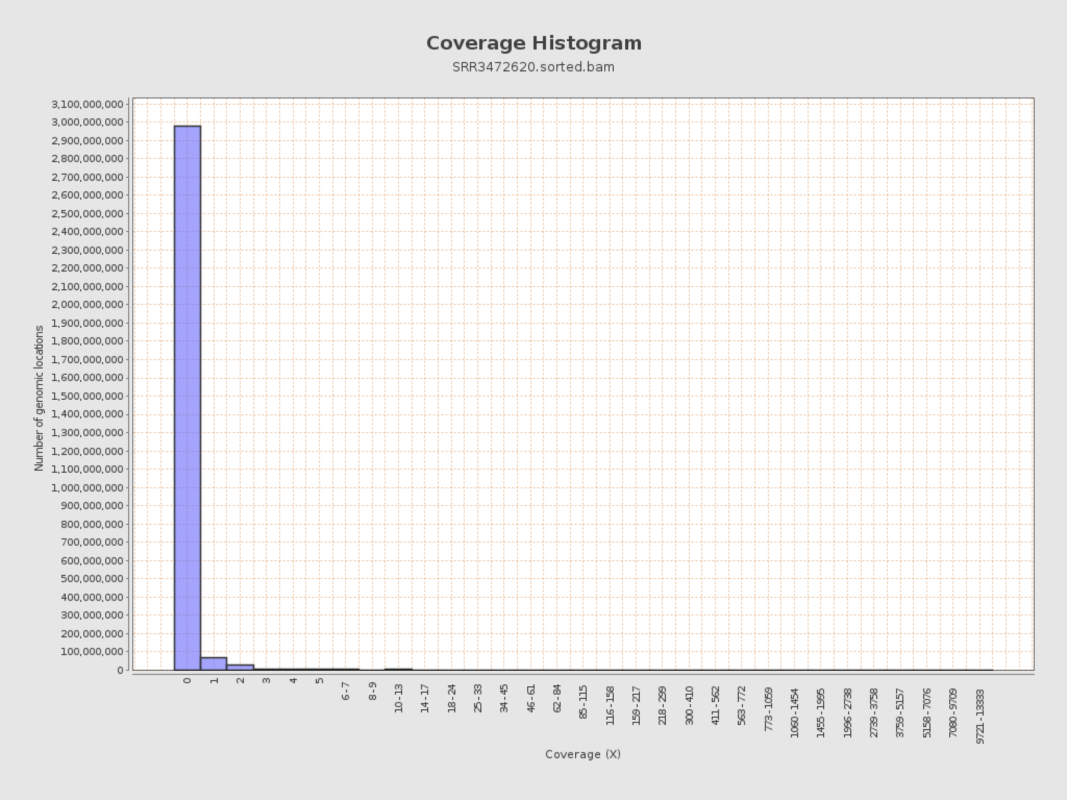
		bases	**coverage**	**deviation**
chr1	249250621	276875166	1.1108	37.7373
chr2	243199373	134358721	0.5525	21.6792
chr3	198022430	124670832	0.6296	21.0177
chr4	191154276	58824519	0.3077	18.0188
chr5	180915260	70612016	0.3903	16.3744
chr6	171115067	170123277	0.9942	37.2038
chr7	159138663	66097174	0.4153	15.8332
chr8	146364022	128603395	0.8787	33.0622
chr9	141213431	72216766	0.5114	14.2864
chr10	135534747	42790404	0.3157	11.9548
chr11	135006516	64356354	0.4767	20.4415
chr12	133851895	68525610	0.512	20.1406
chr13	115169878	45965703	0.3991	15.3675
chr14	107349540	20263541	0.1888	6.5955
chr15	102531392	20766630	0.2025	6.5793
chr16	90354753	78312071	0.8667	31.8896
chr17	81195210	50294245	0.6194	15.715
chr18	78077248	6499455	0.0832	3.2727
chr19	59128983	48528103	0.8207	24.9259
chr20	63025520	61315413	0.9729	32.9283
chr21	48129895	8572316	0.1781	7.1175
chr22	51304566	27303544	0.5322	24.7956
chrMT	16571	4395	0.2652	0.8566
chrX	155270560	48371292	0.3115	13.4984

chrY	59373566	1742141	0.0293	2.1102

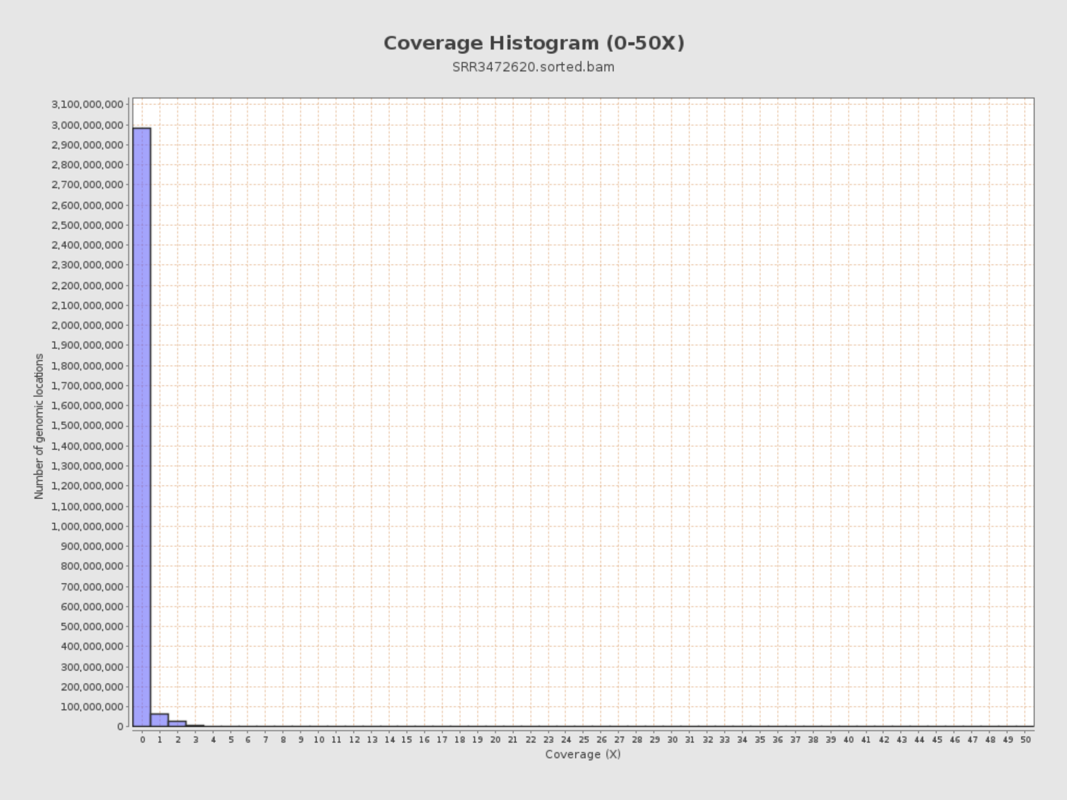
3. Results : Coverage across reference



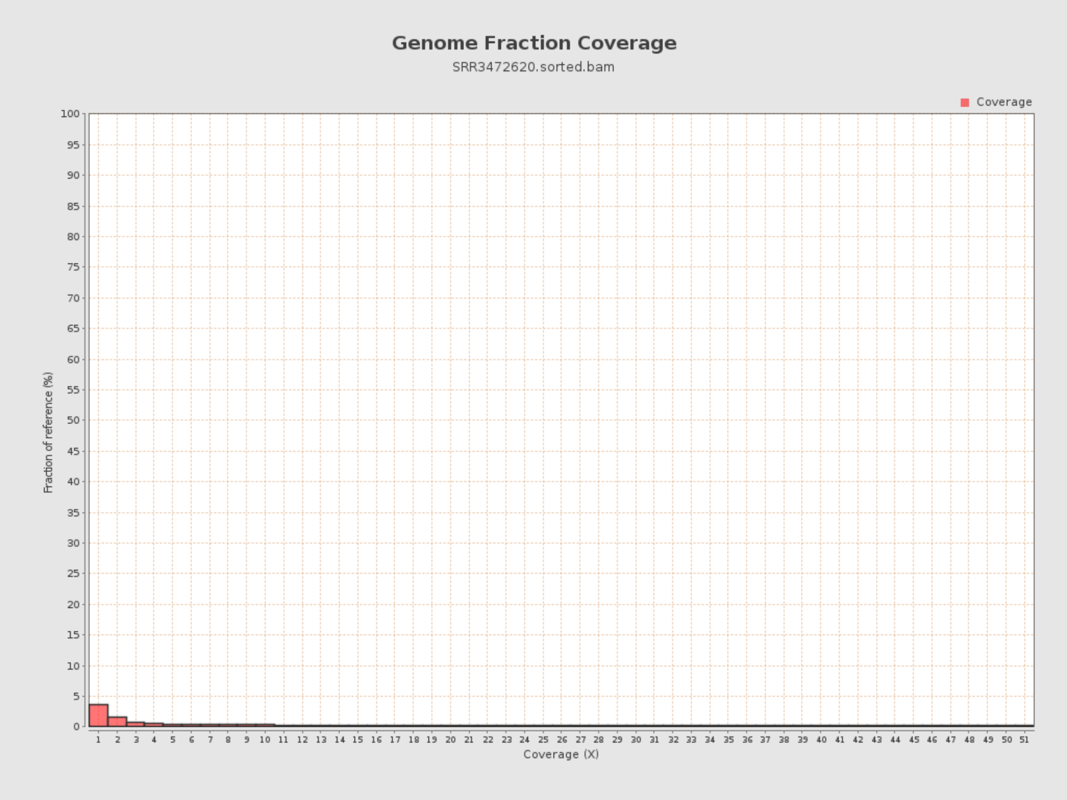
4. Results : Coverage Histogram



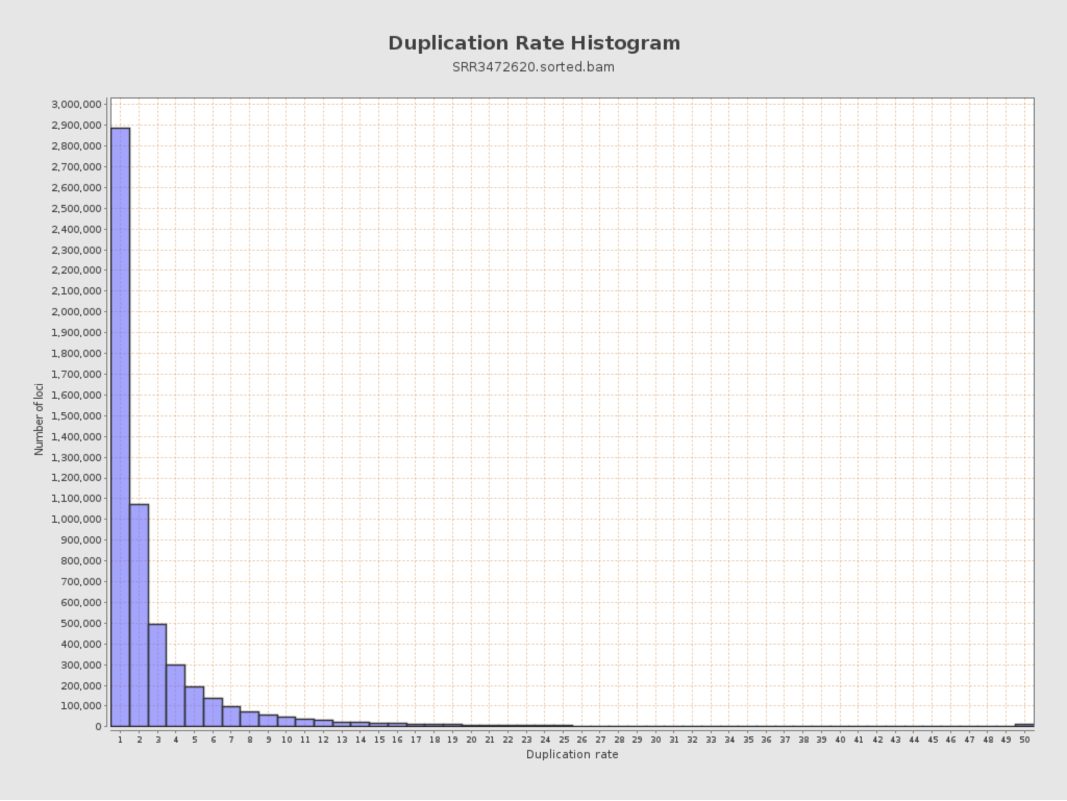
5. Results : Coverage Histogram (0-50X)



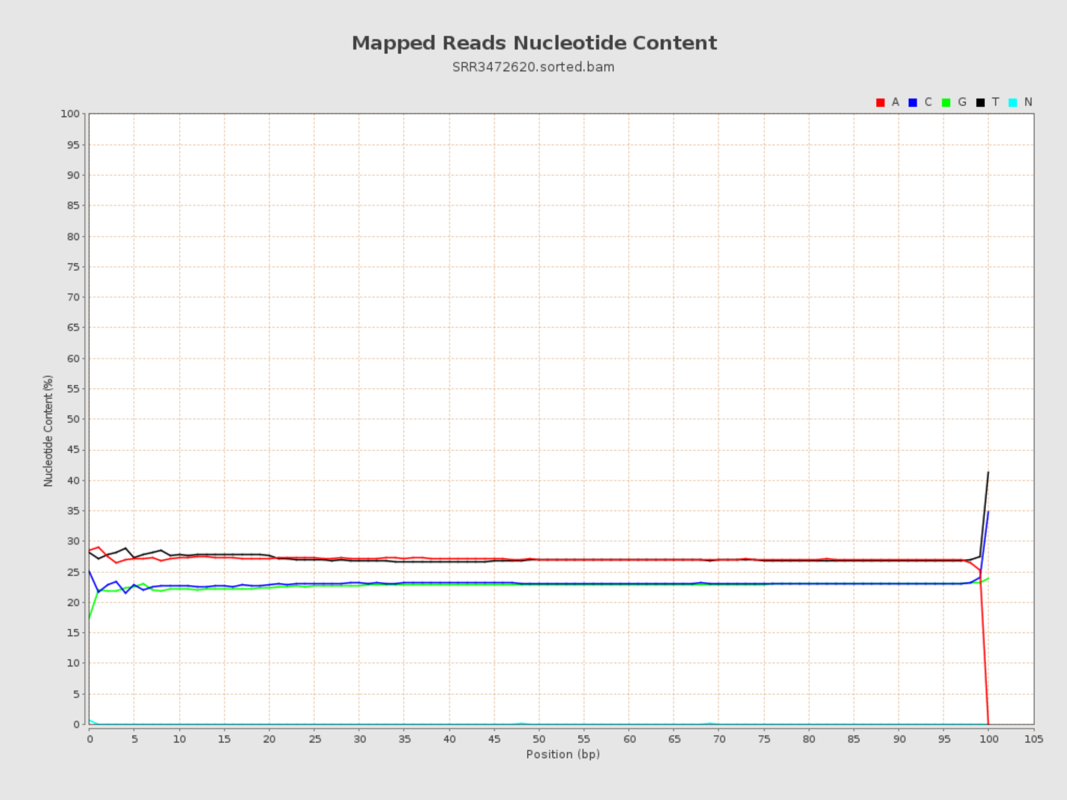
6. Results : Genome Fraction Coverage



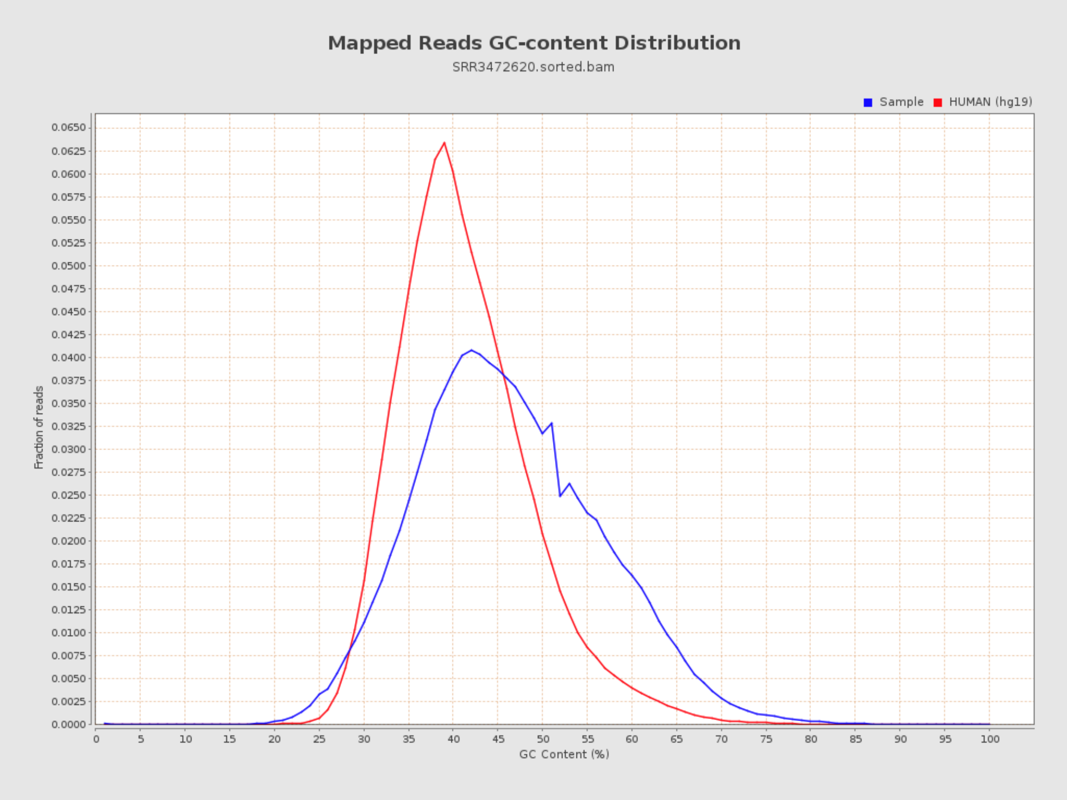
7. Results : Duplication Rate Histogram



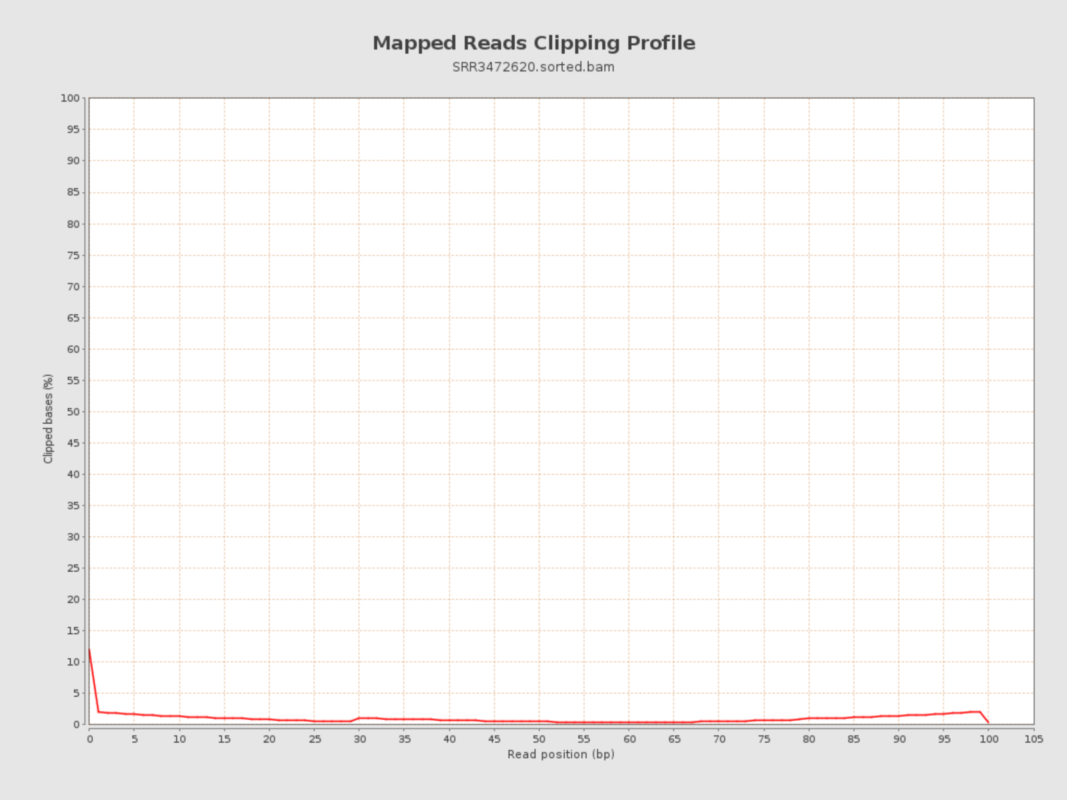
8. Results : Mapped Reads Nucleotide Content



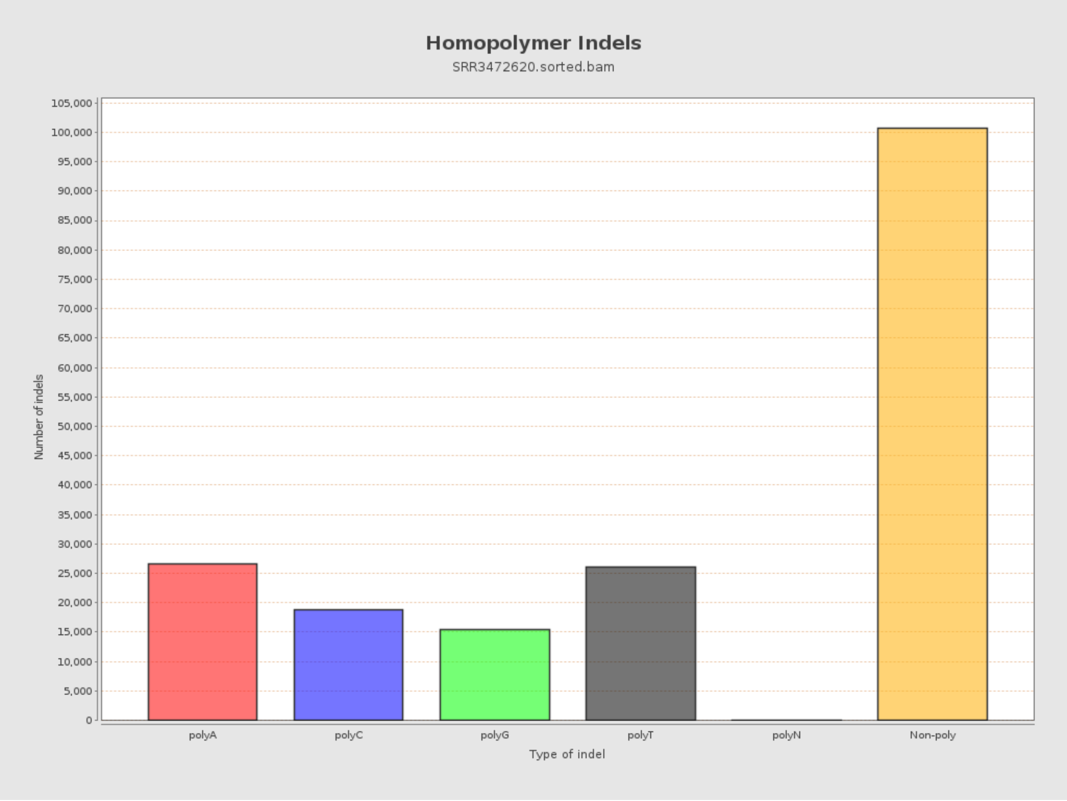
9. Results : Mapped Reads GC-content Distribution



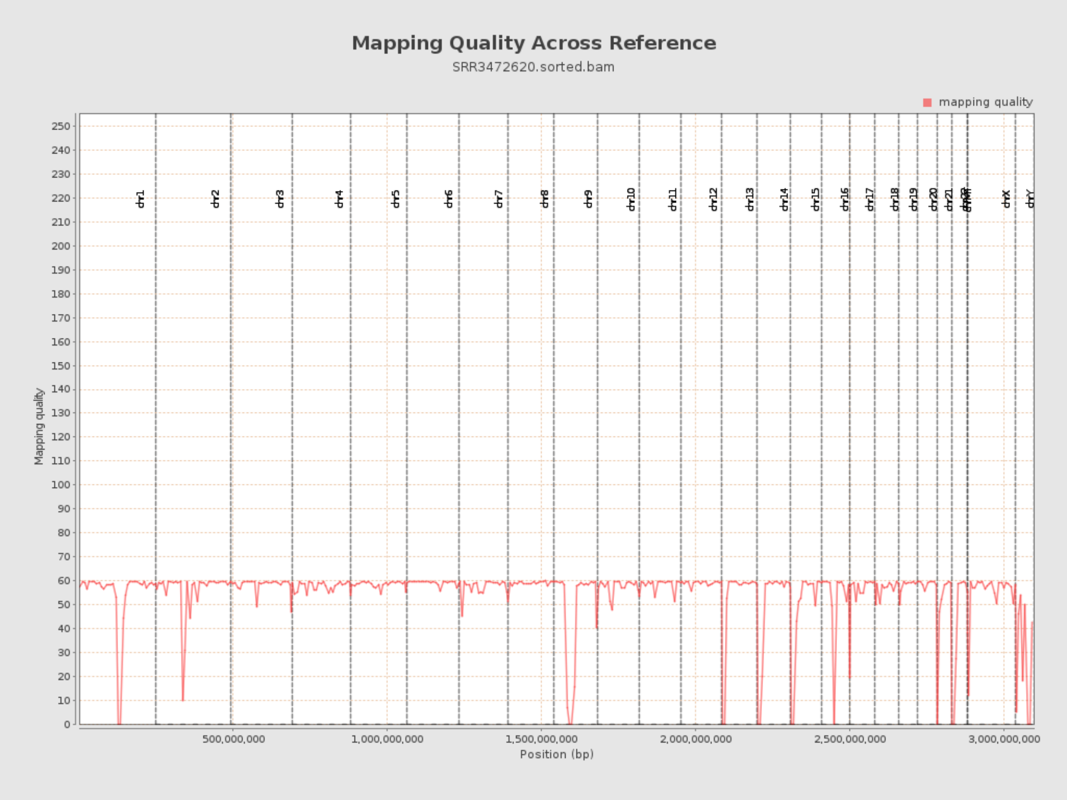
10. Results : Mapped Reads Clipping Profile



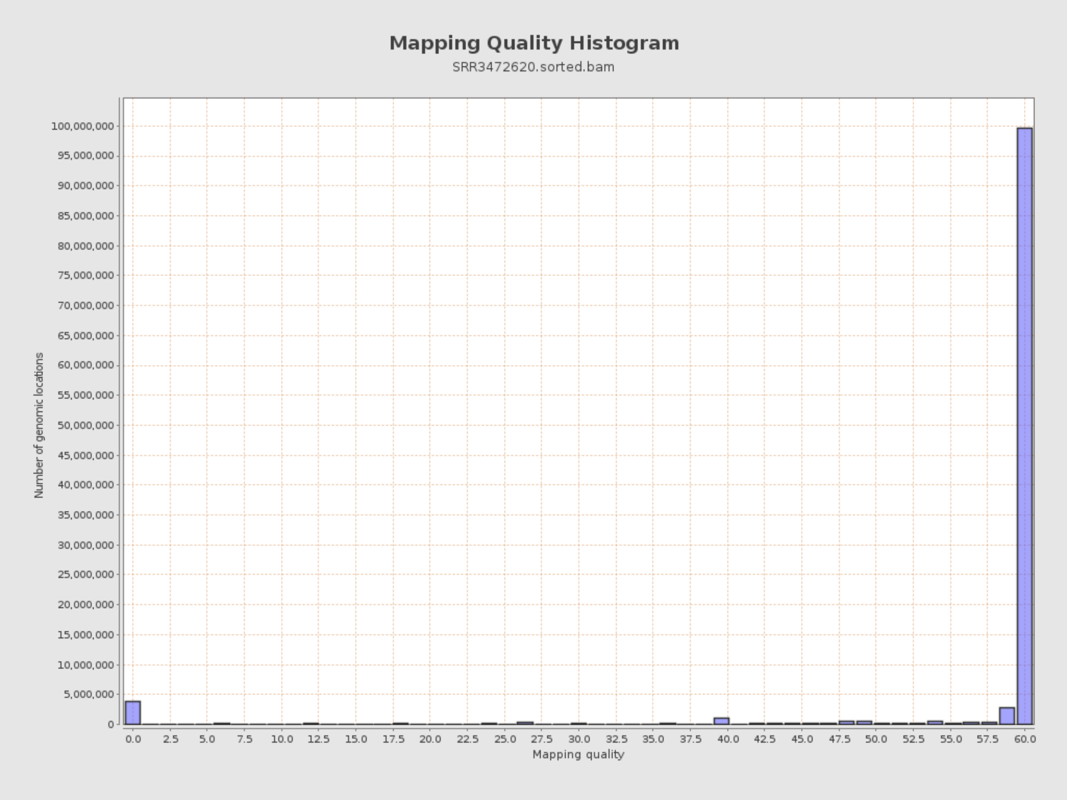
11. Results : Homopolymer Indels



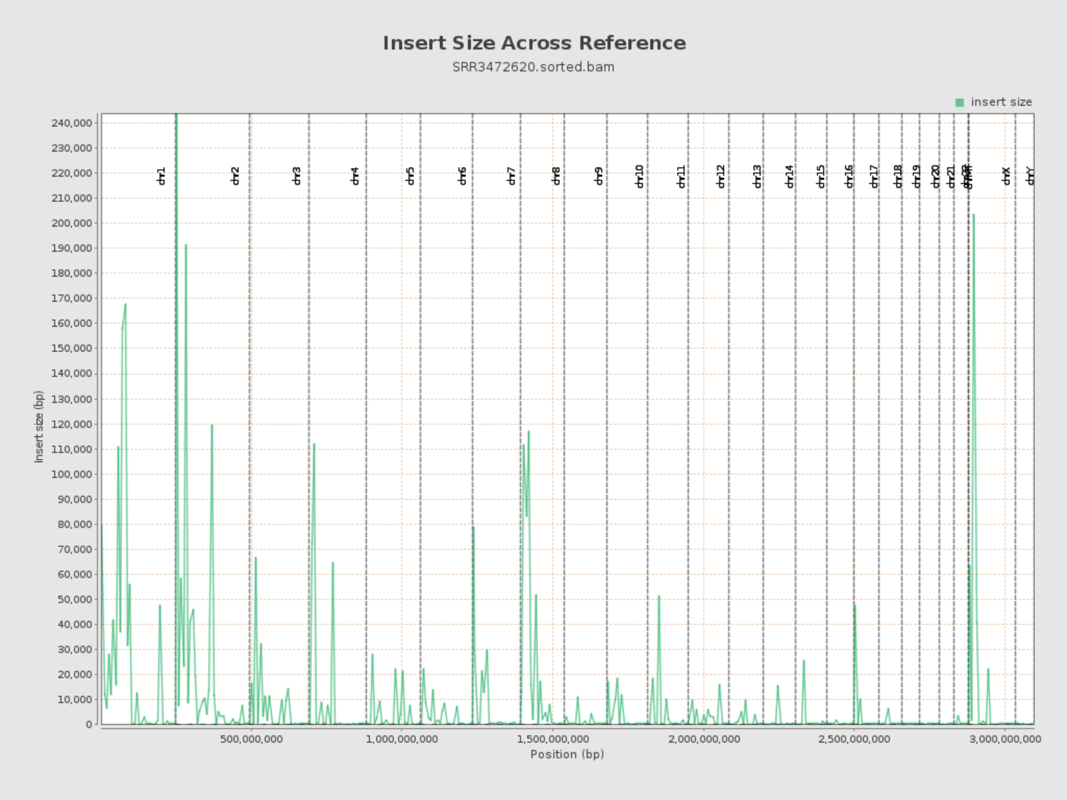
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram