Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 15:35:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472627.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_SRR3472627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472627_1.fastq.gz SRR3472627_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 15:35:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,922,114
Mapped reads	17,806,749 / 99.36%
Unmapped reads	115,365 / 0.64%
Mapped paired reads	17,806,749 / 99.36%
Mapped reads, first in pair	8,922,263 / 49.78%
Mapped reads, second in pair	8,884,486 / 49.57%
Mapped reads, both in pair	17,730,896 / 98.93%
Mapped reads, singletons	75,853 / 0.42%
Secondary alignments	0
Supplementary alignments	81,164 / 0.45%
Read min/max/mean length	30 / 101 / 99.74
Duplicated reads (estimated)	11,984,110 / 66.87%
Duplication rate	50.49%
Clipped reads	1,203,892 / 6.72%

2.2. ACGT Content

Number/percentage of A's	470,310,373 / 26.83%
Number/percentage of C's	408,004,865 / 23.28%
Number/percentage of T's	470,327,617 / 26.83%
Number/percentage of G's	403,913,915 / 23.04%
Number/percentage of N's	320,498 / 0.02%

GC Percentage	46.32%

2.3. Coverage

Mean	0.5663
Standard Deviation	20.7517

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	18,919.53
Standard Deviation	1,325,291.49
P25/Median/P75	154 / 211 / 283

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,320,692
Insertions	103,230
Mapped reads with at least one insertion	0.57%
Deletions	90,005
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.22%

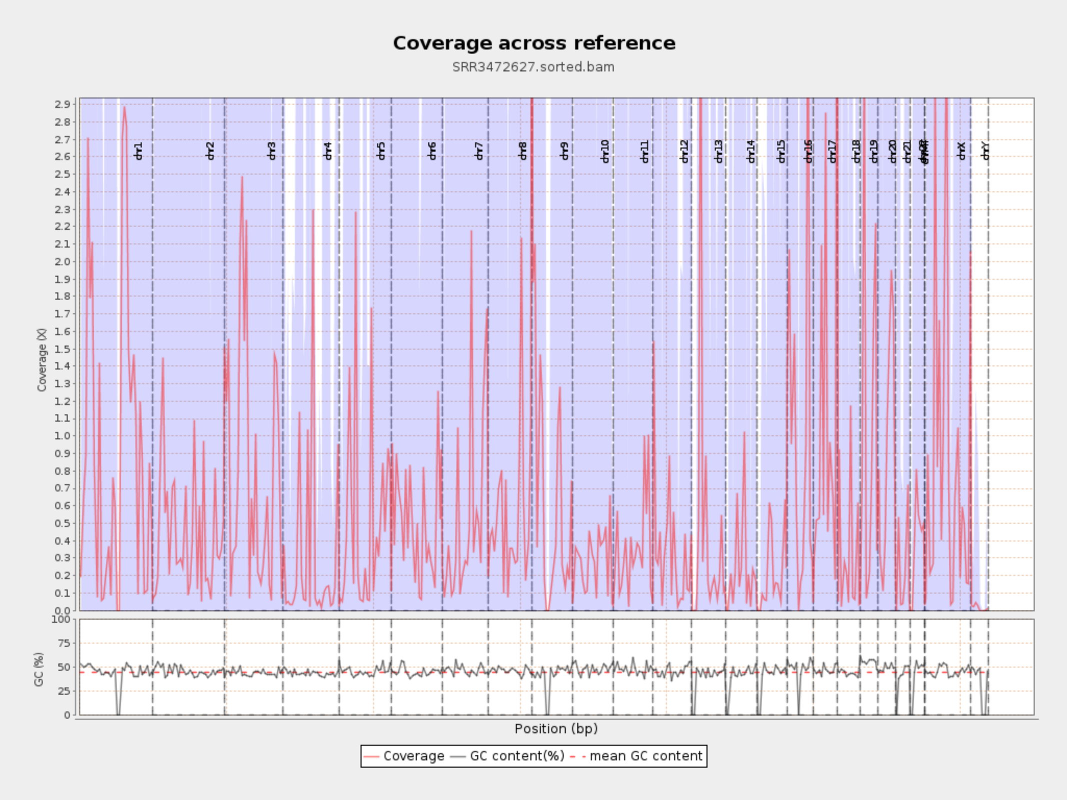
2.7. Chromosome stats

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

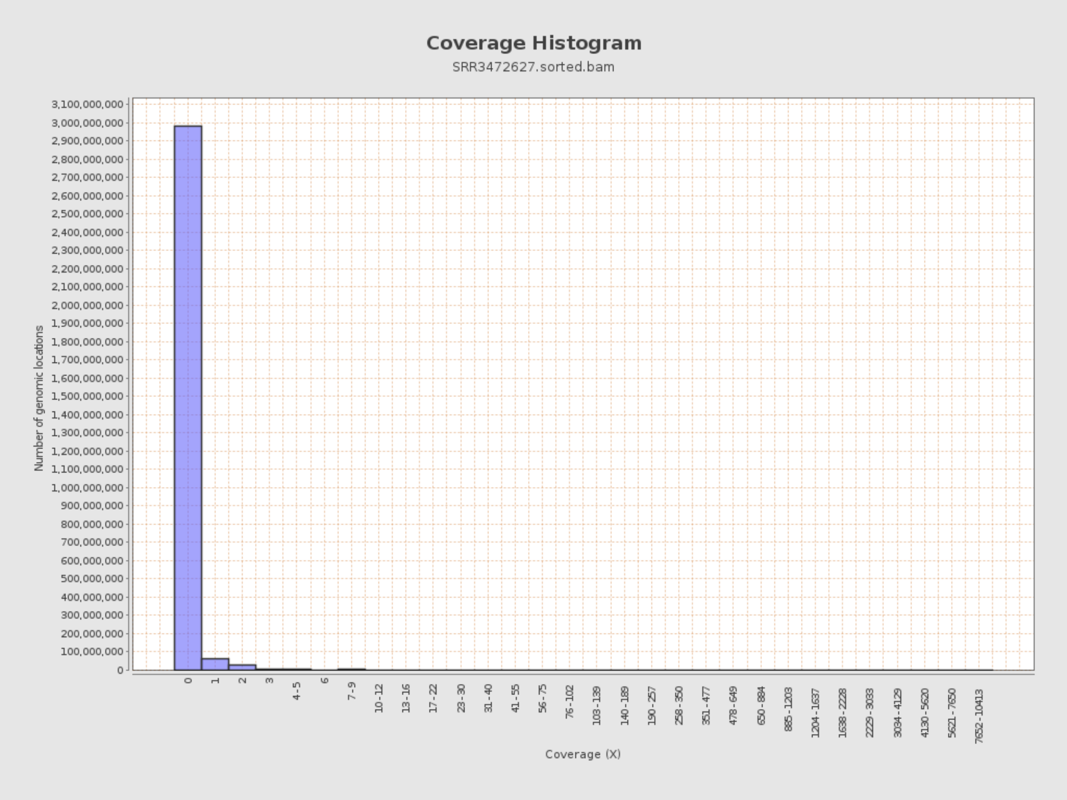
		bases	coverage	deviation
chr1	249250621	233991382	0.9388	29.9602
chr2	243199373	107157741	0.4406	15.6728
chr3	198022430	166900807	0.8428	22.408
chr4	191154276	54901445	0.2872	23.948
chr5	180915260	93171751	0.515	20.621
chr6	171115067	84626319	0.4946	13.4835
chr7	159138663	91085359	0.5724	21.5272
chr8	146364022	82331458	0.5625	18.5833
chr9	141213431	96968829	0.6867	16.8368
chr10	135534747	39510092	0.2915	10.894
chr11	135006516	49006279	0.363	13.805
chr12	133851895	46978598	0.351	9.6331
chr13	115169878	53884837	0.4679	23.7868
chr14	107349540	24891591	0.2319	10.1298
chr15	102531392	22489543	0.2193	9.1446
chr16	90354753	92460531	1.0233	31.1437
chr17	81195210	89827568	1.1063	34.4584
chr18	78077248	26870861	0.3442	17.5977
chr19	59128983	70865729	1.1985	30.8105
chr20	63025520	60523697	0.9603	26.7594
chr21	48129895	11975304	0.2488	11.5306
chr22	51304566	20745718	0.4044	14.2328
chrMT	16571	581	0.0351	0.2324
chrX	155270560	131015954	0.8438	25.7166

chrY	59373566	909803	0.0153	0.6153

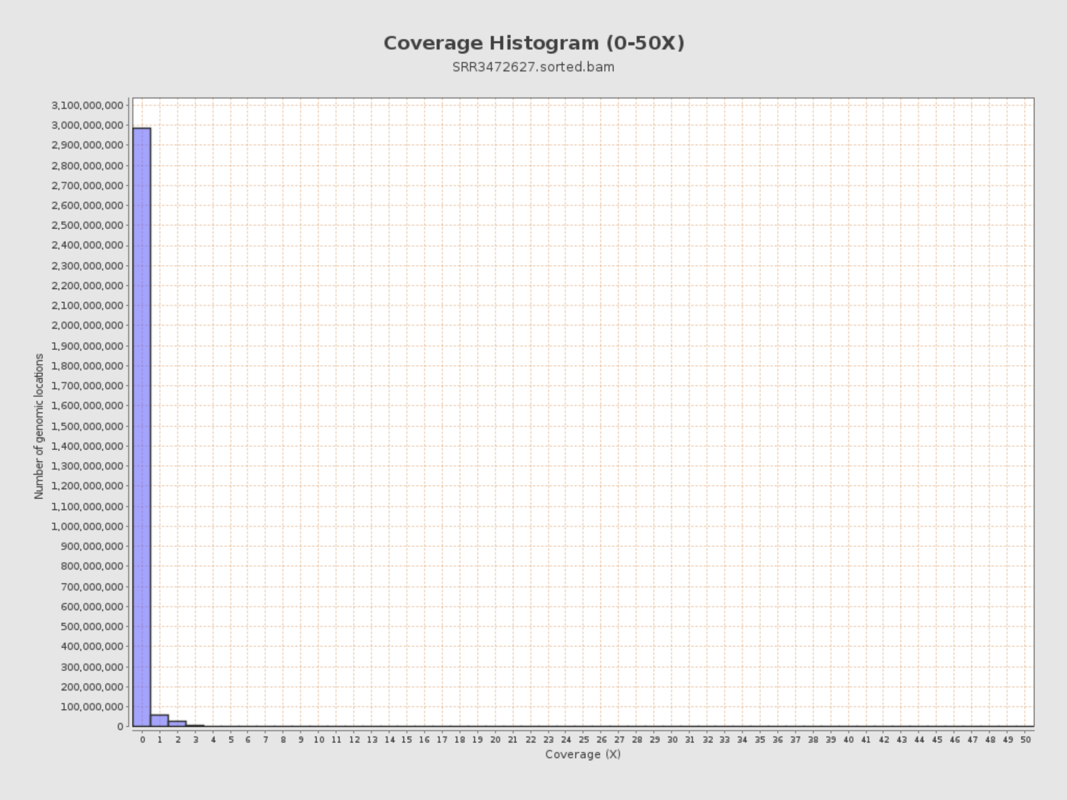
3. Results : Coverage across reference



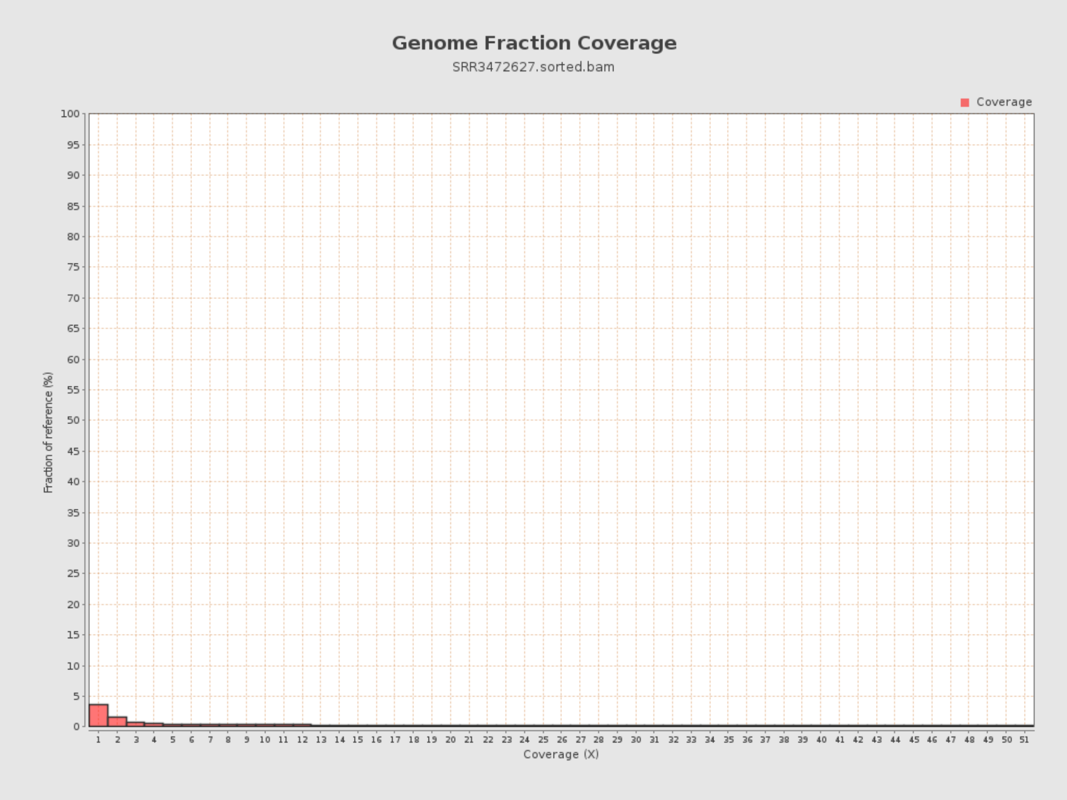
4. Results : Coverage Histogram



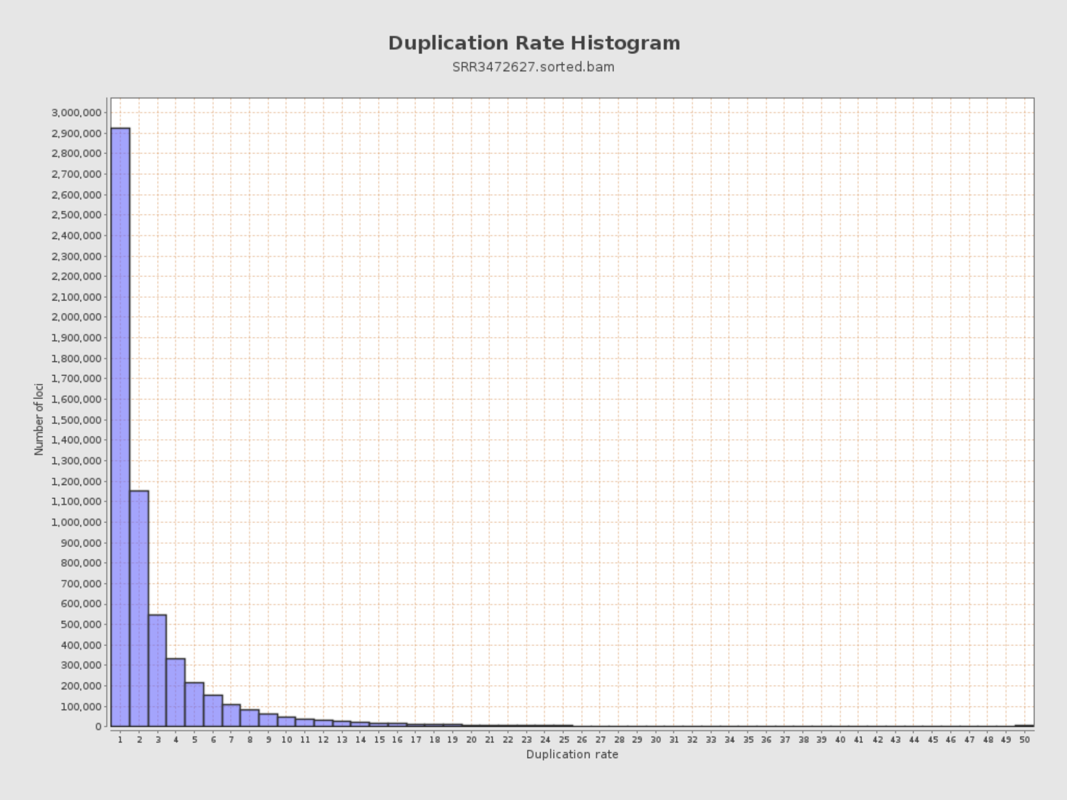
5. Results : Coverage Histogram (0-50X)



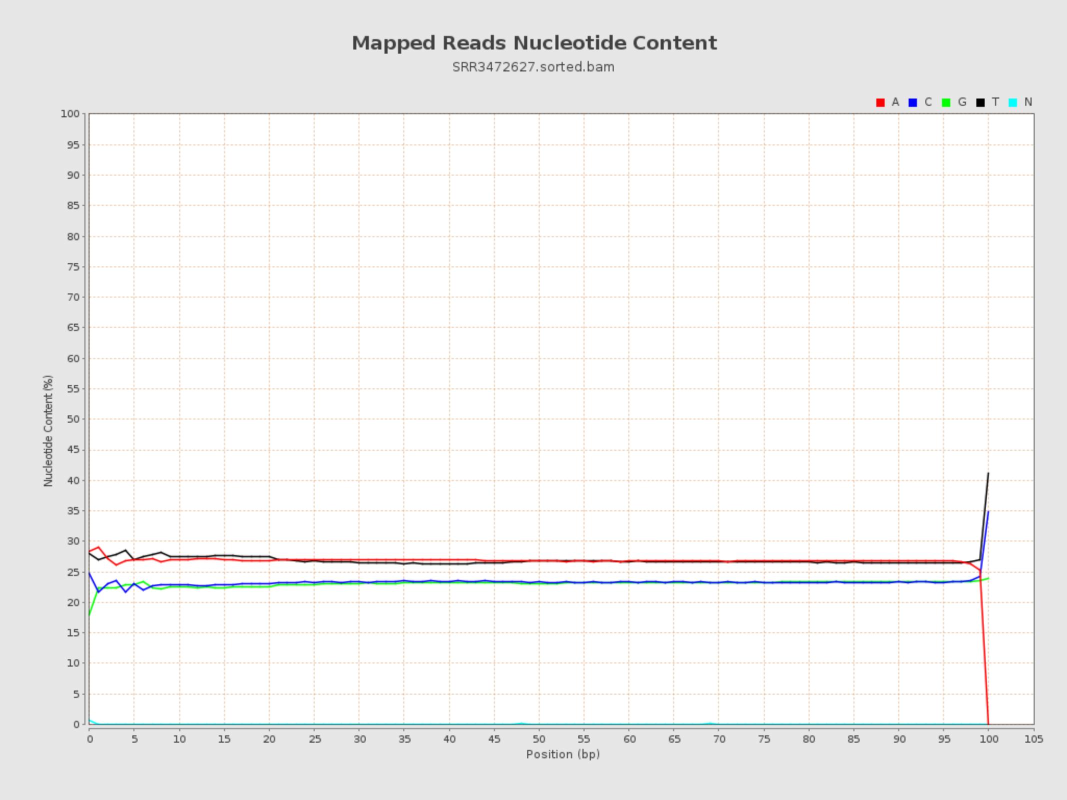
6. Results : Genome Fraction Coverage



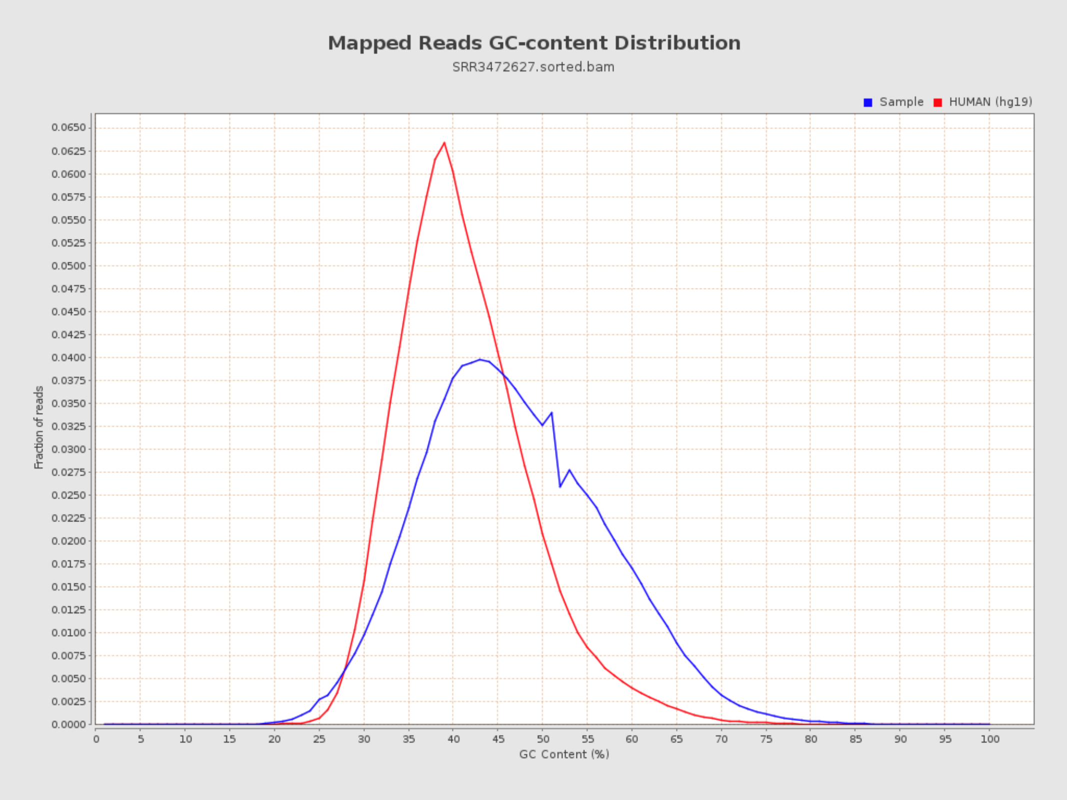
7. Results : Duplication Rate Histogram



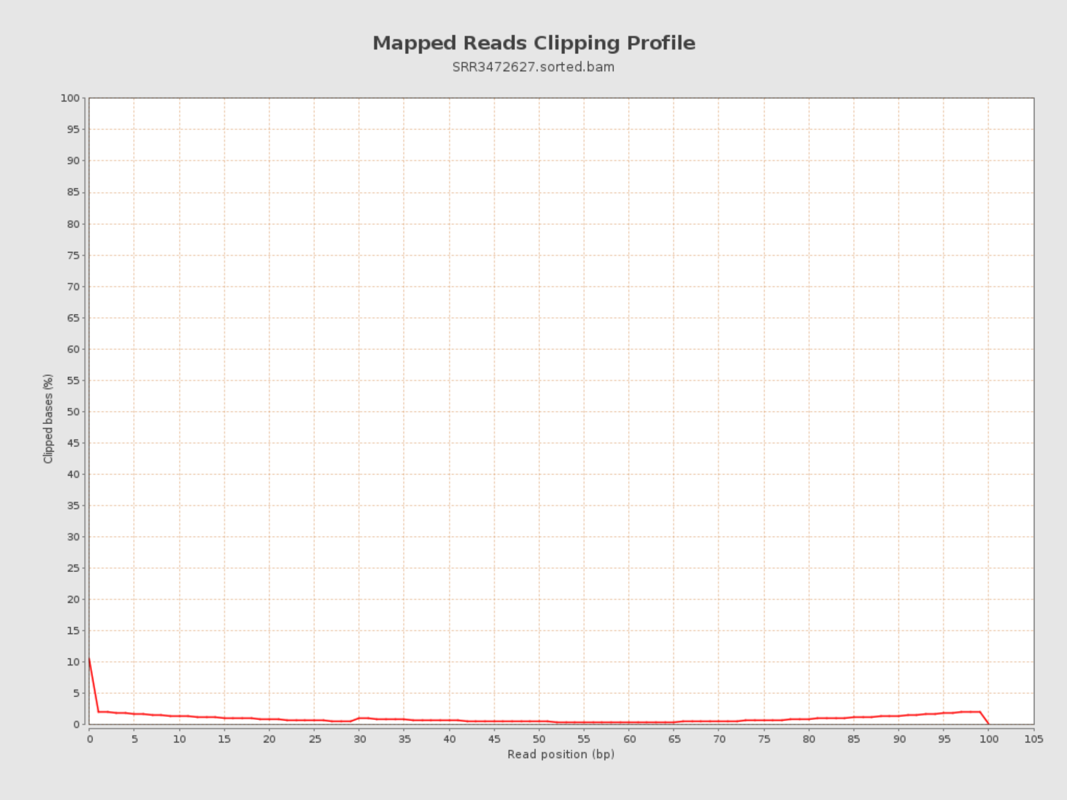
8. Results : Mapped Reads Nucleotide Content



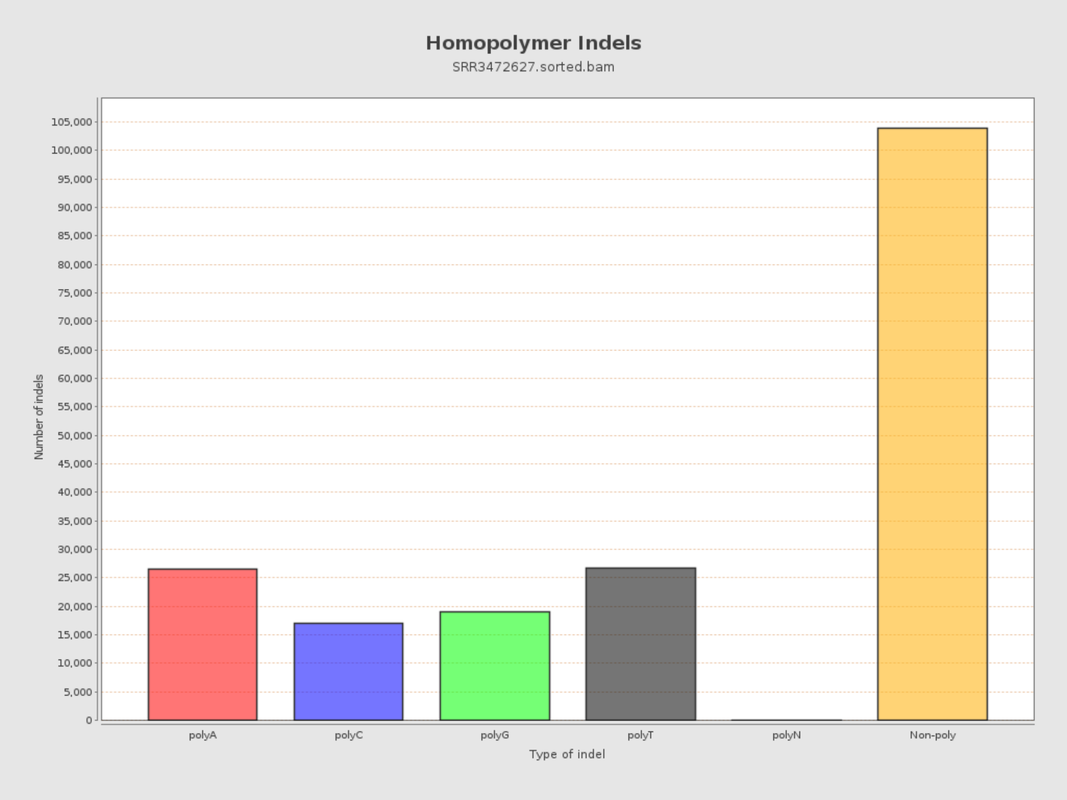
9. Results : Mapped Reads GC-content Distribution



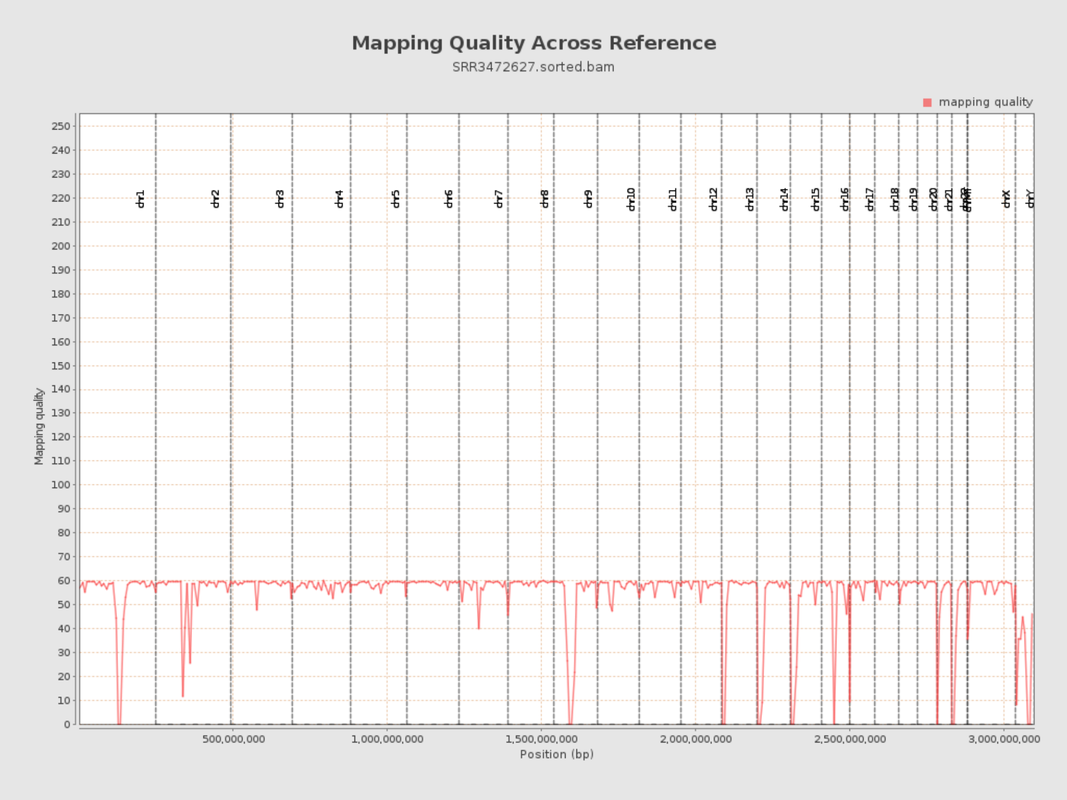
10. Results : Mapped Reads Clipping Profile



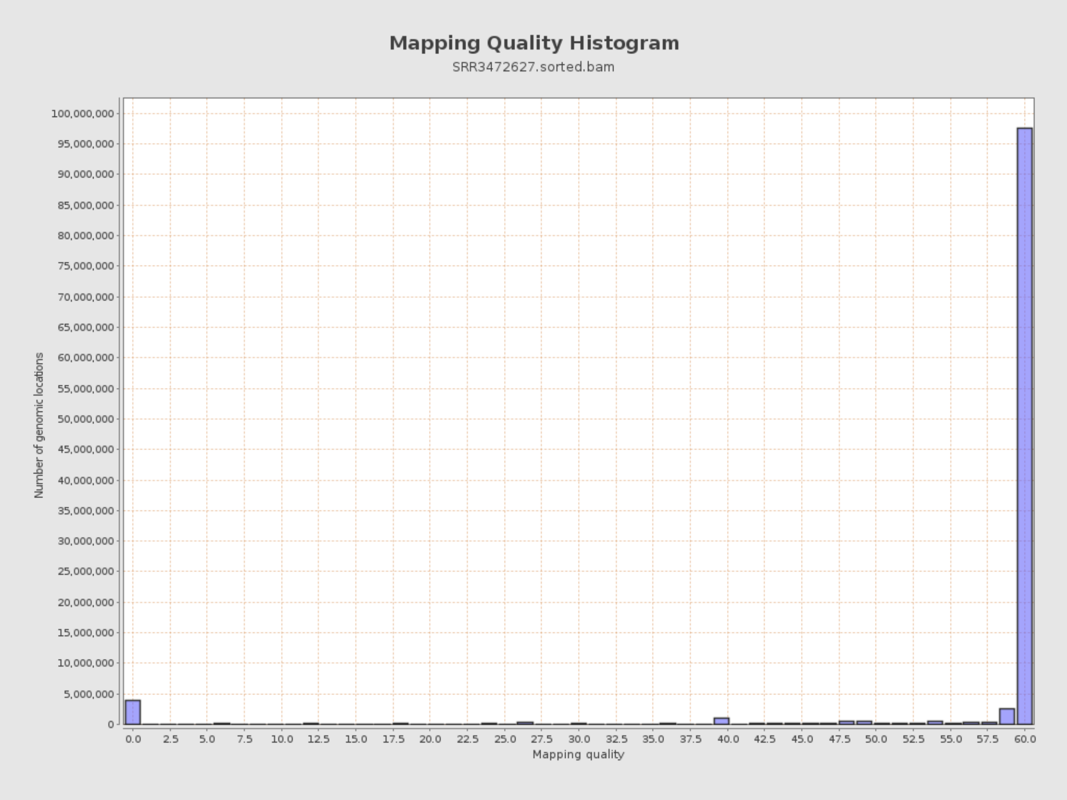
11. Results : Homopolymer Indels



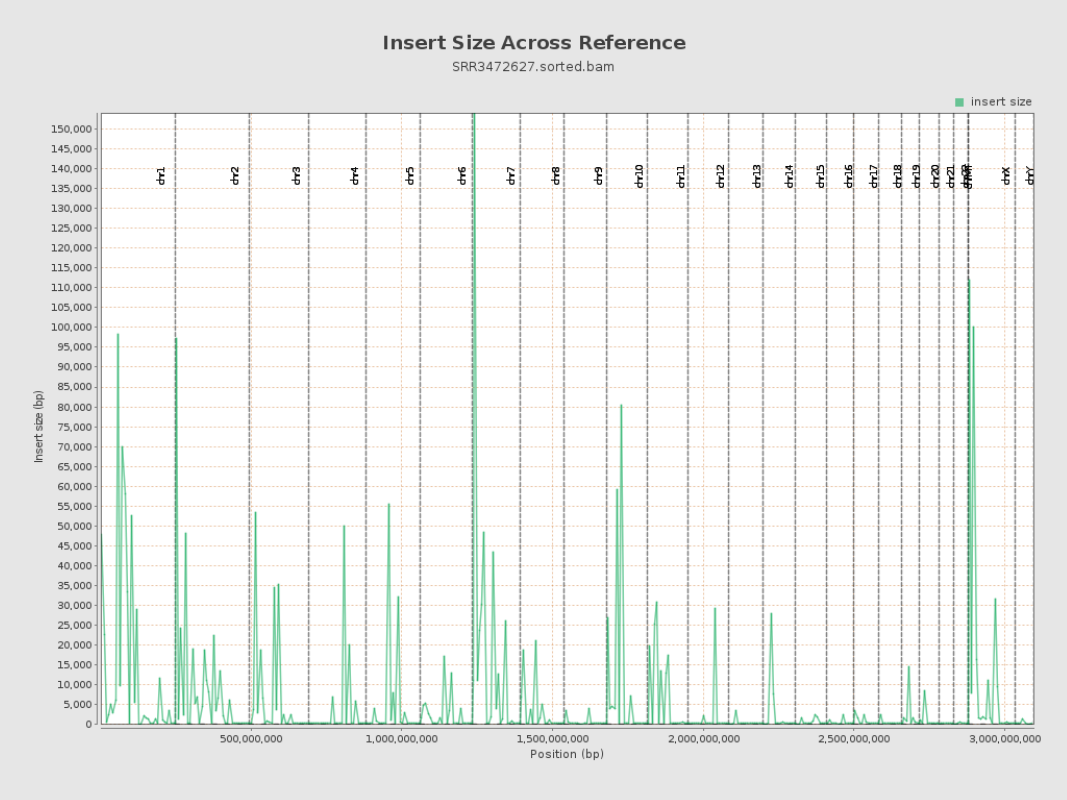
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram