Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 14:33:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472777.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_SRR3472777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472777_1.fastq.gz SRR3472777_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 14:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,660,872
Mapped reads	18,379,041 / 98.49%
Unmapped reads	281,831 / 1.51%
Mapped paired reads	18,379,041 / 98.49%
Mapped reads, first in pair	9,248,372 / 49.56%
Mapped reads, second in pair	9,130,669 / 48.93%
Mapped reads, both in pair	18,211,076 / 97.59%
Mapped reads, singletons	167,965 / 0.9%
Secondary alignments	0
Supplementary alignments	64,735 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,631,137 / 62.33%
Duplication rate	47.5%
Clipped reads	1,485,570 / 7.96%

2.2. ACGT Content

Number/percentage of A's	508,348,374 / 28.12%
Number/percentage of C's	398,672,868 / 22.05%
Number/percentage of T's	505,298,349 / 27.95%
Number/percentage of G's	395,359,711 / 21.87%
Number/percentage of N's	344,320 / 0.02%

GC Percentage	43.92%

2.3. Coverage

Mean	0.5841
Standard Deviation	20.132

2.4. Mapping Quality

Mean Mapping Quality	55.24

2.5. Insert size

Mean	25,373.19
Standard Deviation	1,556,267.76
P25/Median/P75	186 / 263 / 357

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	12,462,198
Insertions	109,635
Mapped reads with at least one insertion	0.59%
Deletions	104,435
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.42%

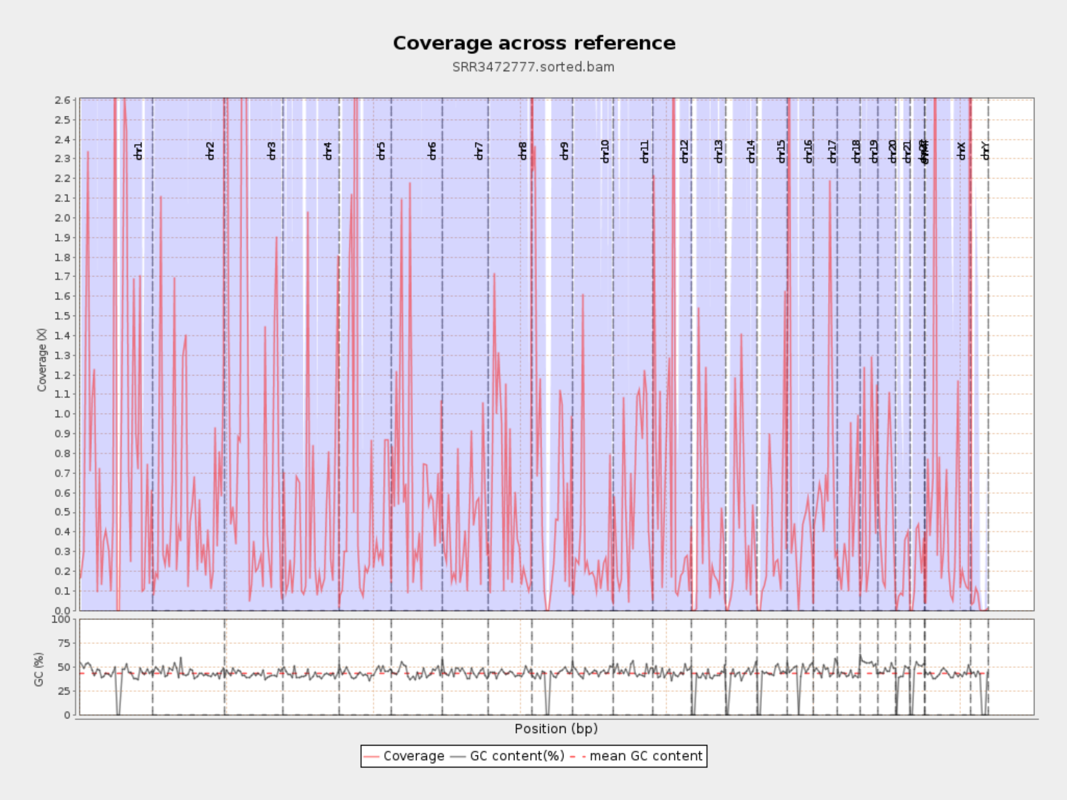
2.7. Chromosome stats

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

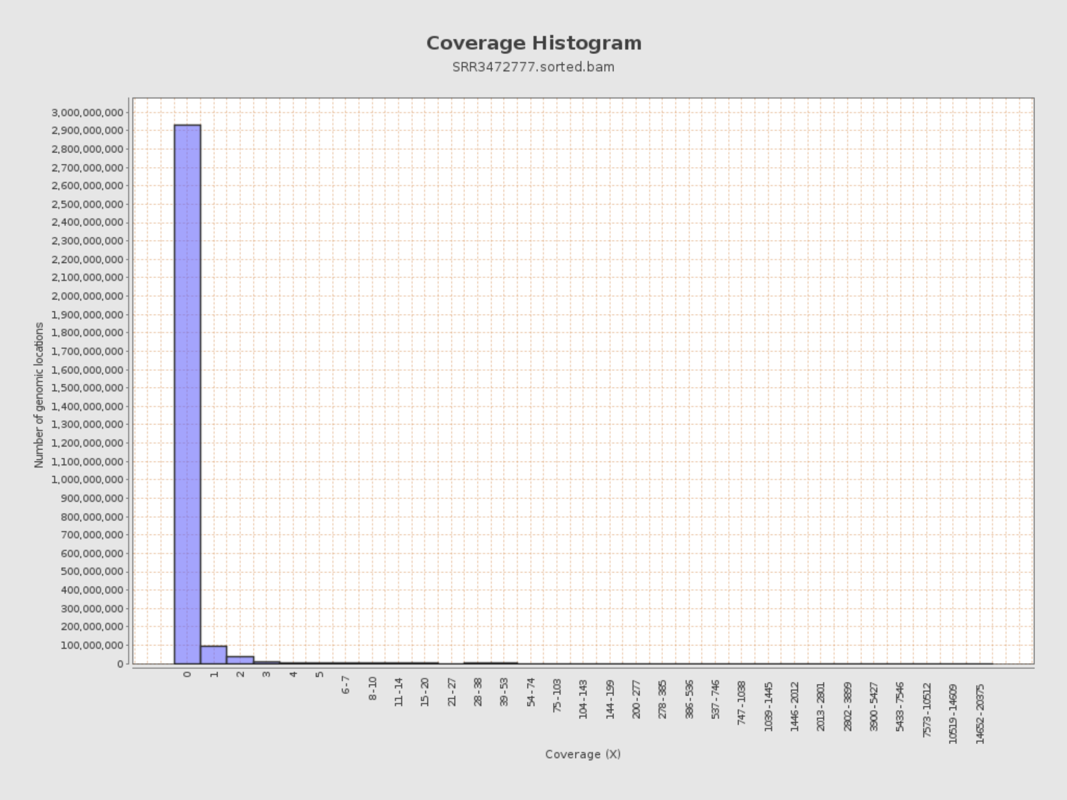
		bases	**coverage**	**deviation**
chr1	249250621	214364162	0.86	37.2213
chr2	243199373	132224763	0.5437	25.1309
chr3	198022430	211165817	1.0664	24.6748
chr4	191154276	84919819	0.4442	17.5749
chr5	180915260	128657599	0.7111	22.1155
chr6	171115067	113322959	0.6623	16.4639
chr7	159138663	66869142	0.4202	10.7151
chr8	146364022	79977088	0.5464	14.9532
chr9	141213431	98566018	0.698	19.1817
chr10	135534747	42958002	0.317	12.5594
chr11	135006516	80938144	0.5995	19.1593
chr12	133851895	97153067	0.7258	25.0973
chr13	115169878	46714302	0.4056	15.2413
chr14	107349540	45037732	0.4195	14.4024
chr15	102531392	40779223	0.3977	11.786
chr16	90354753	54625589	0.6046	13.6364
chr17	81195210	56299261	0.6934	15.4026
chr18	78077248	31375185	0.4018	12.7691
chr19	59128983	35952407	0.608	15.3936
chr20	63025520	31953330	0.507	14.7222
chr21	48129895	8812560	0.1831	7.0127
chr22	51304566	11773185	0.2295	6.6732
chrMT	16571	6685	0.4034	1.125
chrX	155270560	91689758	0.5905	15.7482

chrY	59373566	2137751	0.036	1.0009

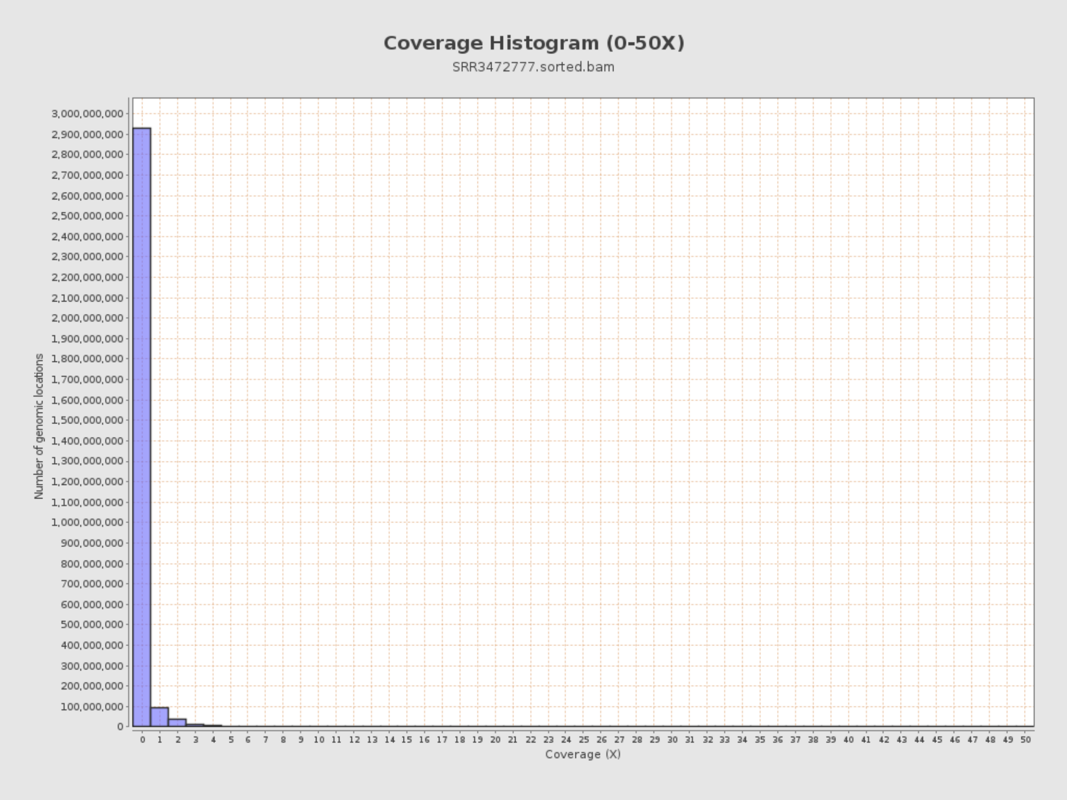
3. Results : Coverage across reference



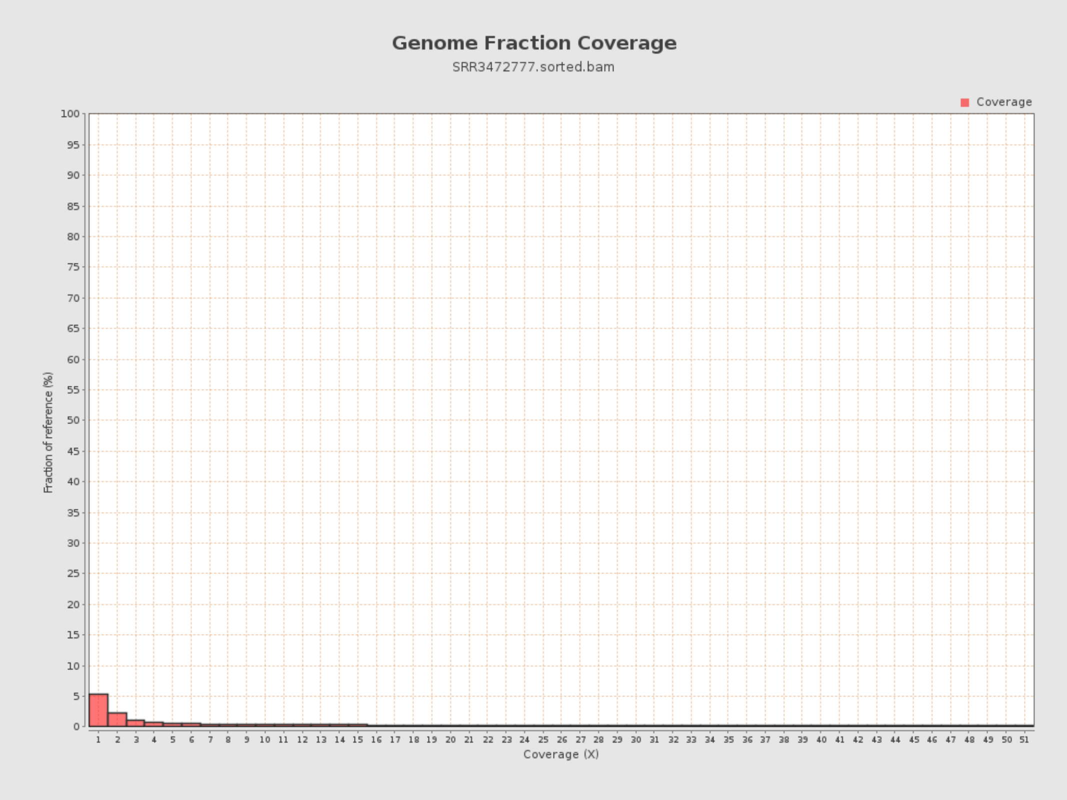
4. Results : Coverage Histogram



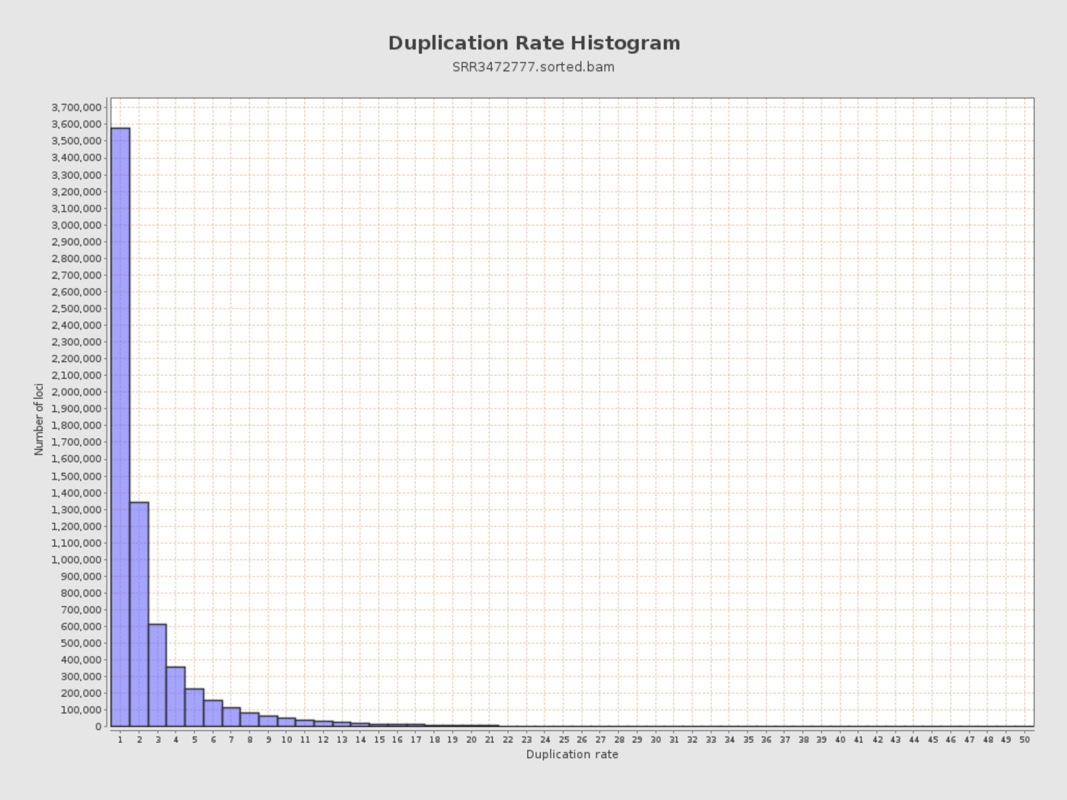
5. Results : Coverage Histogram (0-50X)



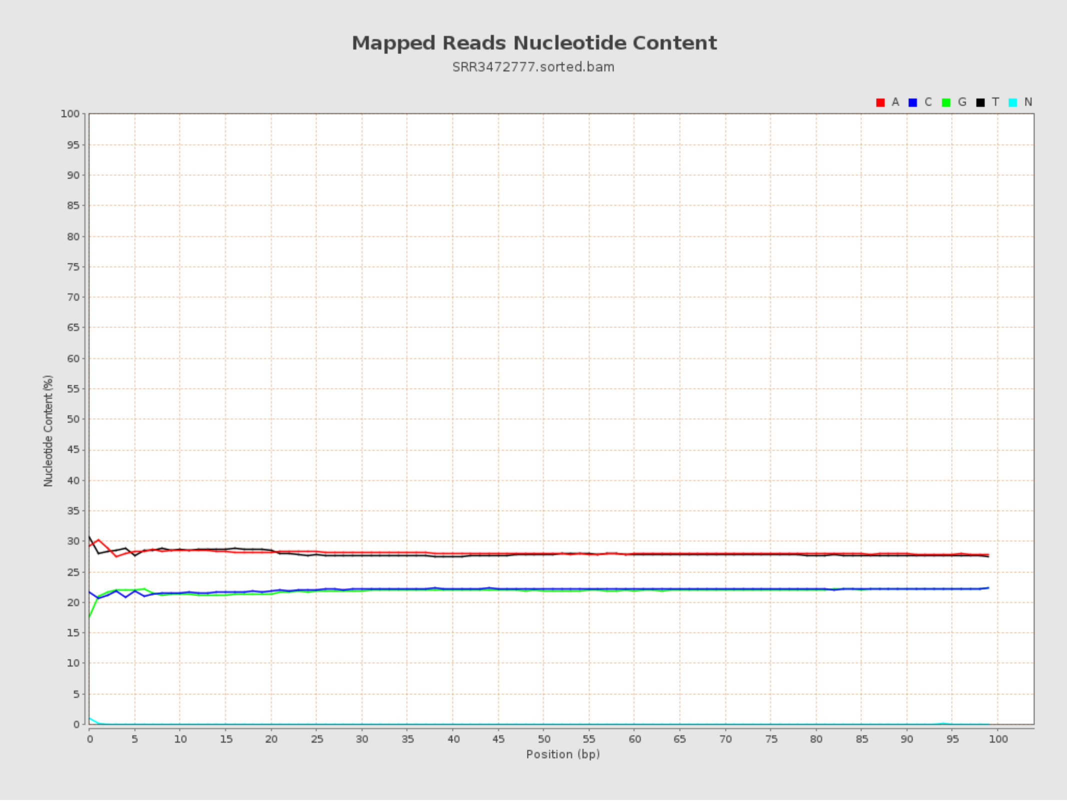
6. Results : Genome Fraction Coverage



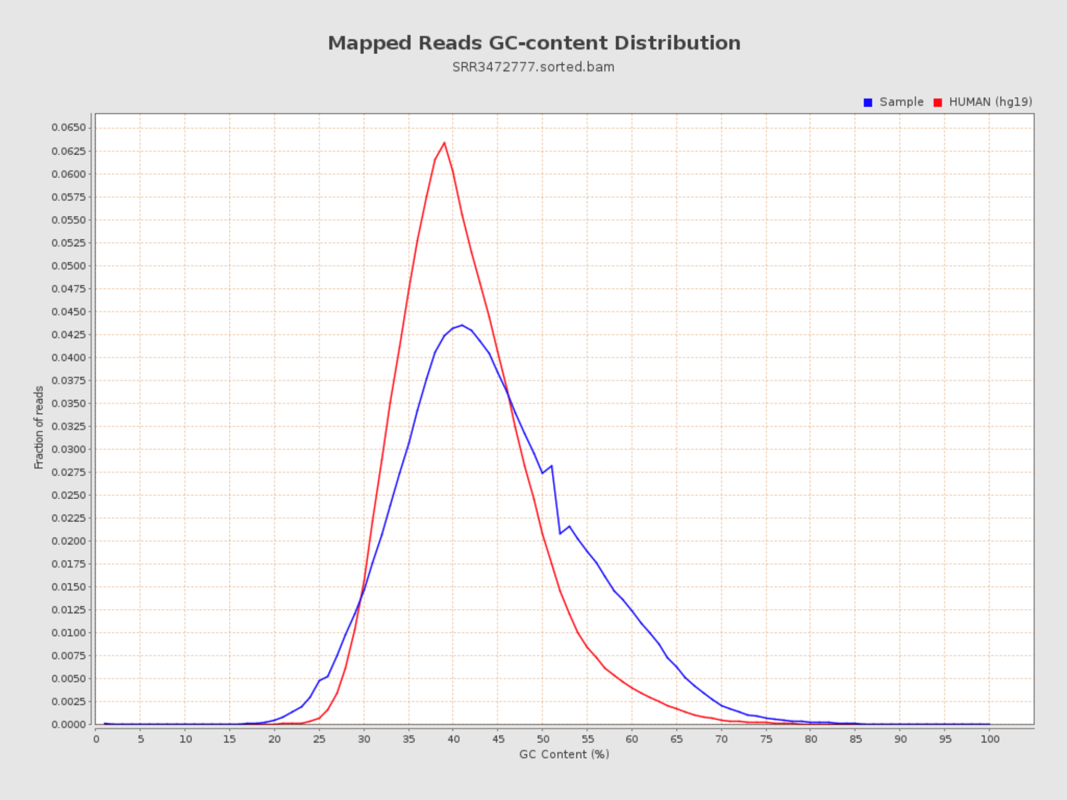
7. Results : Duplication Rate Histogram



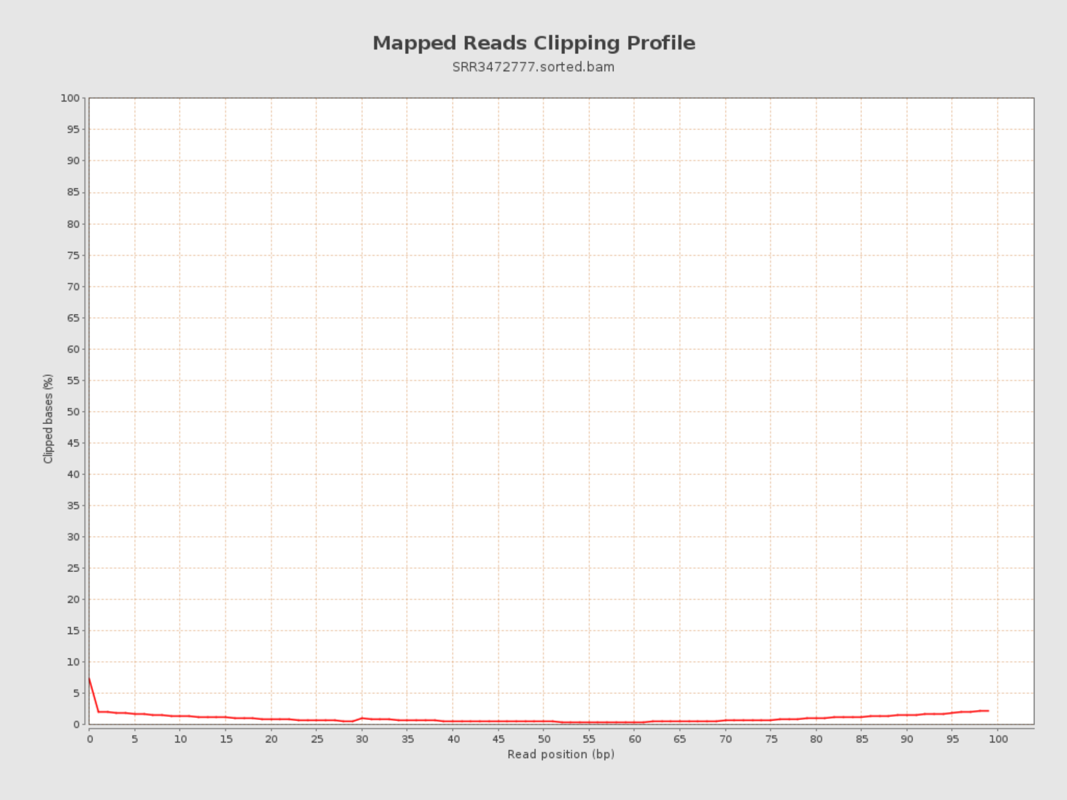
8. Results : Mapped Reads Nucleotide Content



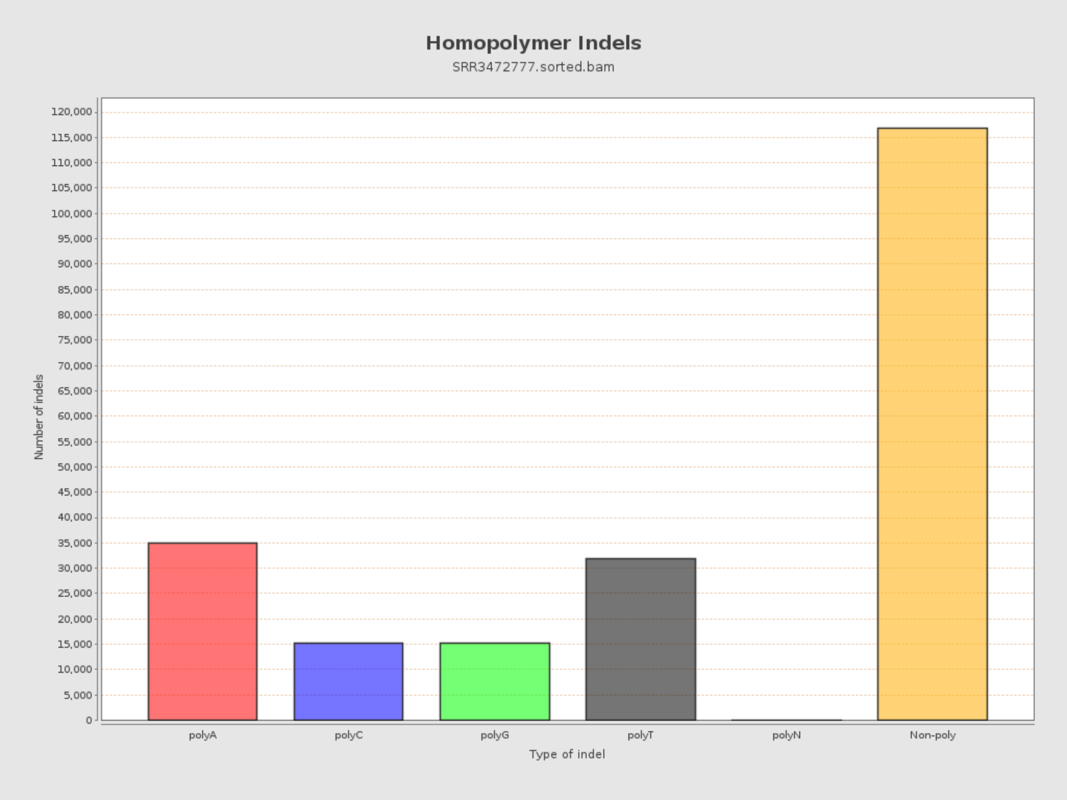
9. Results : Mapped Reads GC-content Distribution



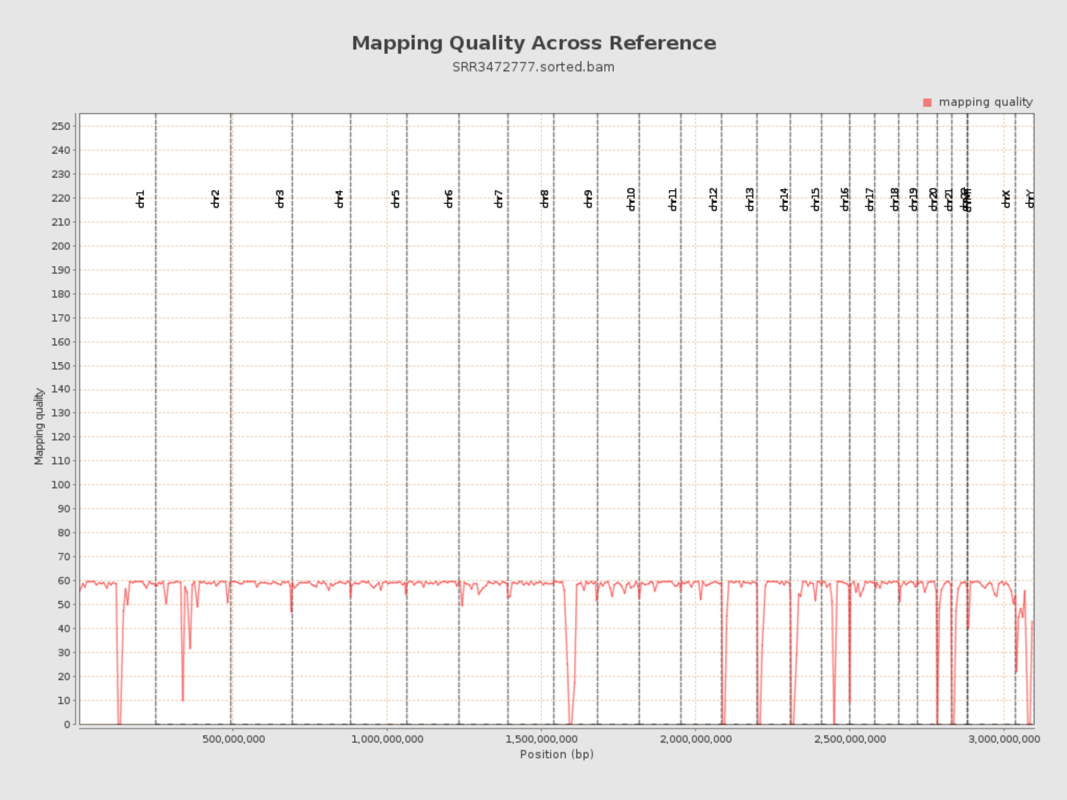
10. Results : Mapped Reads Clipping Profile



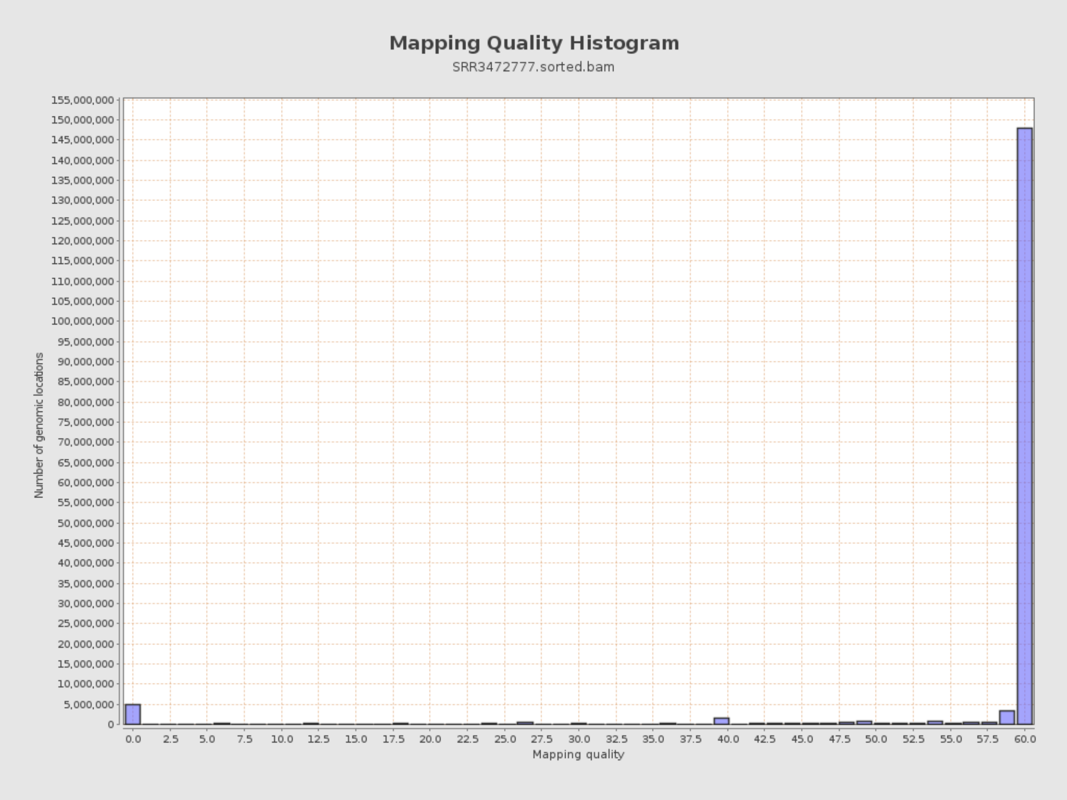
11. Results : Homopolymer Indels



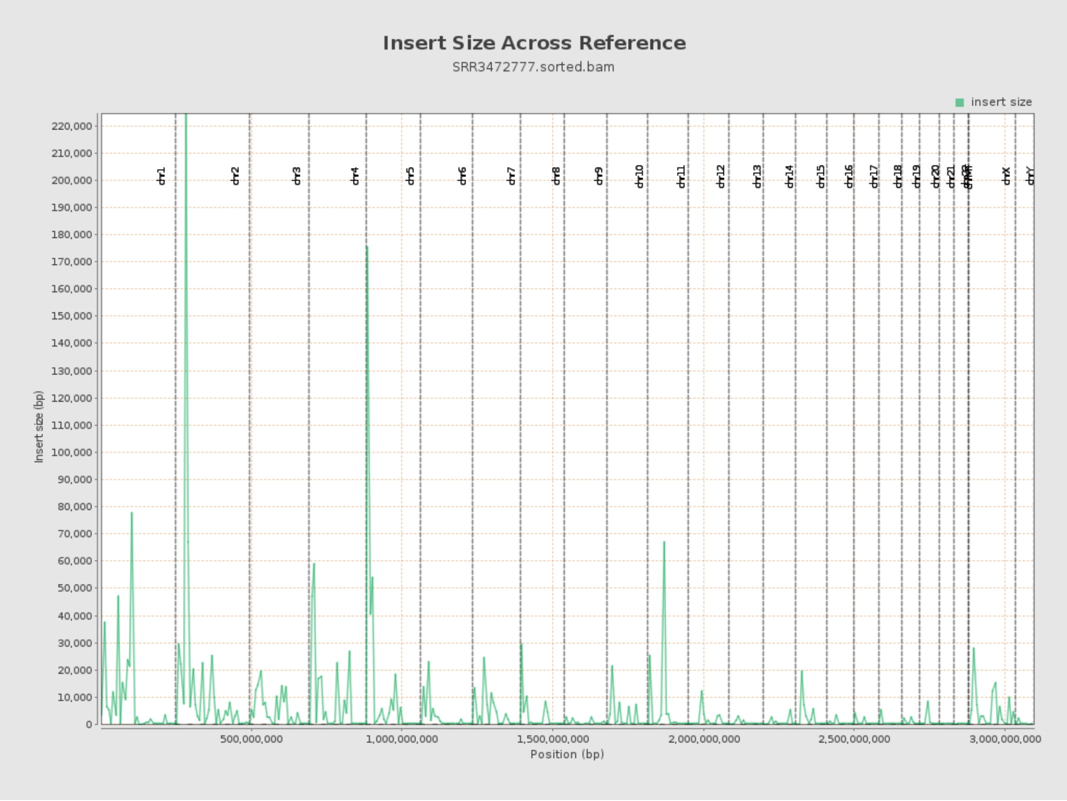
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram