Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 13:26:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472774.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_SRR3472774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472774_1.fastq.gz SRR3472774_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 13:26:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,952,916
Mapped reads	17,745,972 / 98.85%
Unmapped reads	206,944 / 1.15%
Mapped paired reads	17,745,972 / 98.85%
Mapped reads, first in pair	8,915,428 / 49.66%
Mapped reads, second in pair	8,830,544 / 49.19%
Mapped reads, both in pair	17,619,368 / 98.14%
Mapped reads, singletons	126,604 / 0.71%
Secondary alignments	0
Supplementary alignments	61,774 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,188,212 / 62.32%
Duplication rate	47.18%
Clipped reads	1,329,057 / 7.4%

2.2. ACGT Content

Number/percentage of A's	485,328,879 / 27.74%
Number/percentage of C's	392,127,298 / 22.42%
Number/percentage of T's	482,483,908 / 27.58%
Number/percentage of G's	389,107,211 / 22.24%
Number/percentage of N's	332,382 / 0.02%

GC Percentage	44.66%

2.3. Coverage

Mean	0.5652
Standard Deviation	18.1623

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	23,391.84
Standard Deviation	1,515,997.82
P25/Median/P75	187 / 264 / 356

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	11,908,137
Insertions	109,477
Mapped reads with at least one insertion	0.61%
Deletions	96,784
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.01%

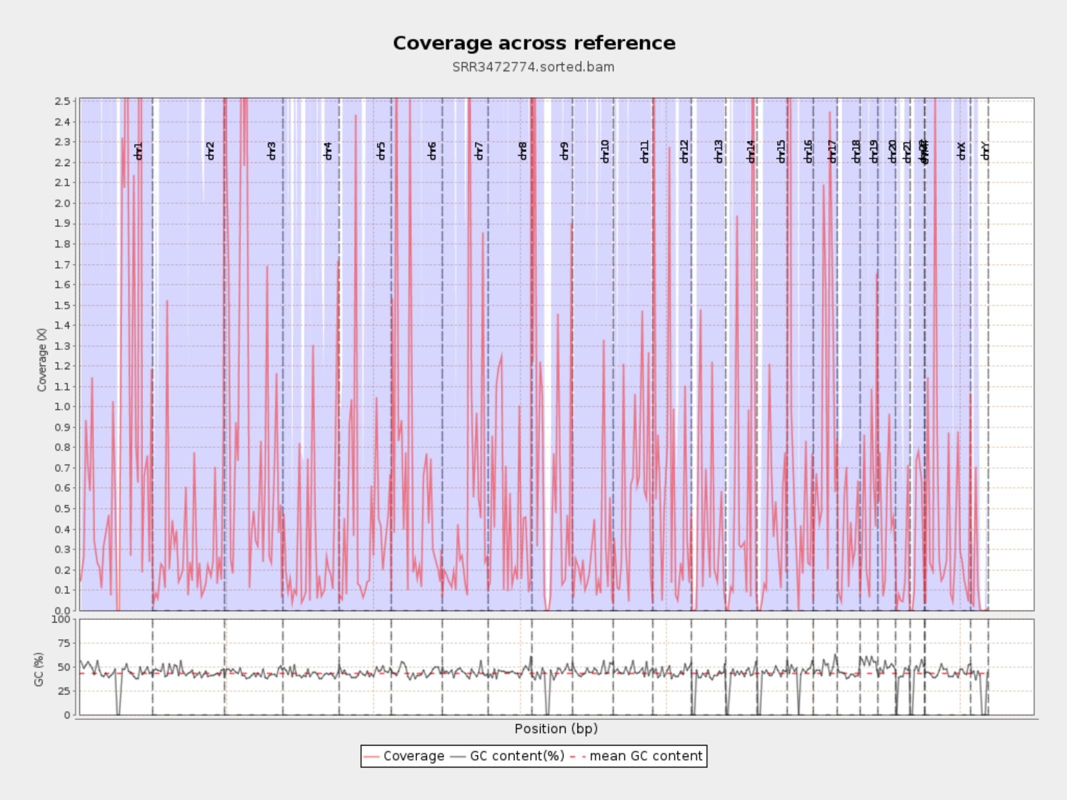
2.7. Chromosome stats

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

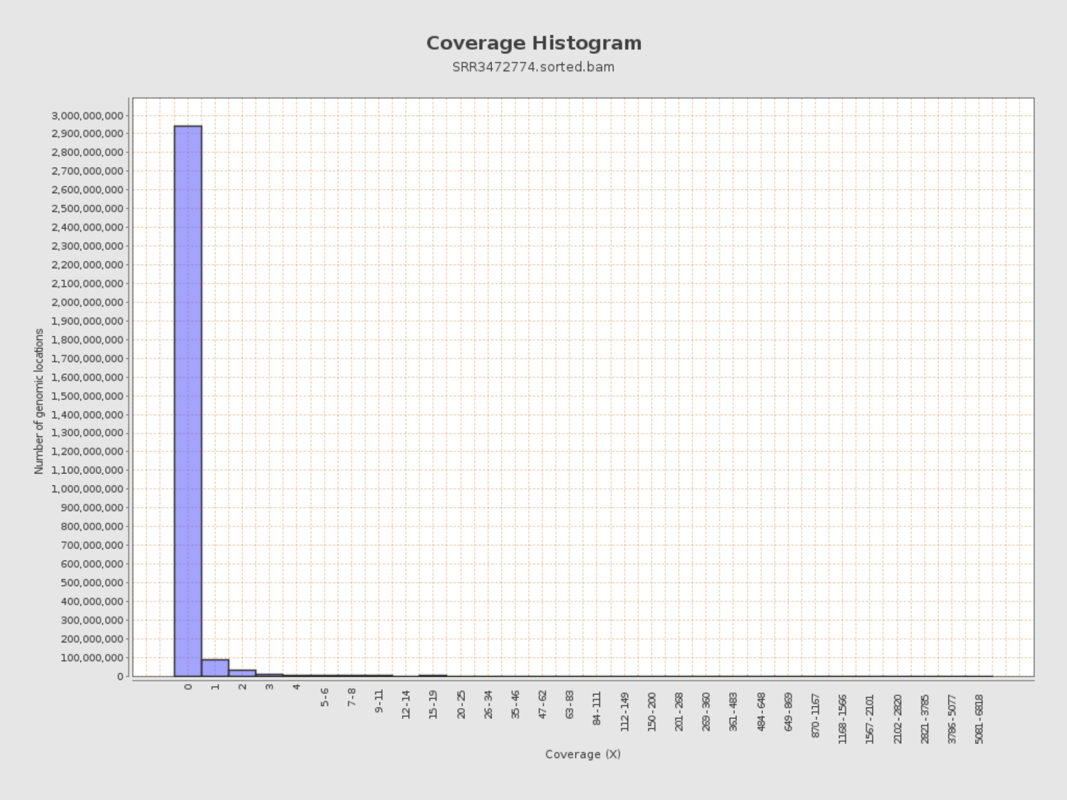
		bases	coverage	deviation
chr1	249250621	234347228	0.9402	29.4616
chr2	243199373	70169859	0.2885	10.7351
chr3	198022430	203593689	1.0281	22.5034
chr4	191154276	61737819	0.323	13.7177
chr5	180915260	82091563	0.4538	13.071
chr6	171115067	112228824	0.6559	18.6866
chr7	159138663	88138770	0.5538	20.6298
chr8	146364022	71456444	0.4882	14.662
chr9	141213431	113335918	0.8026	19.2638
chr10	135534747	36861593	0.272	11.0859
chr11	135006516	77981280	0.5776	18.7538
chr12	133851895	90732497	0.6779	18.253
chr13	115169878	49719397	0.4317	16.8692
chr14	107349540	65741683	0.6124	25.686
chr15	102531392	38559891	0.3761	12.6474
chr16	90354753	76714918	0.849	20.167
chr17	81195210	83495168	1.0283	24.5947
chr18	78077248	25863728	0.3313	11.1512
chr19	59128983	31470721	0.5322	14.6834
chr20	63025520	30684568	0.4869	18.8943
chr21	48129895	8255475	0.1715	7.9274
chr22	51304566	18833642	0.3671	11.1527
chrMT	16571	10714	0.6466	1.6736
chrX	155270560	70724054	0.4555	13.2204

chrY	59373566	6874036	0.1158	5.8089

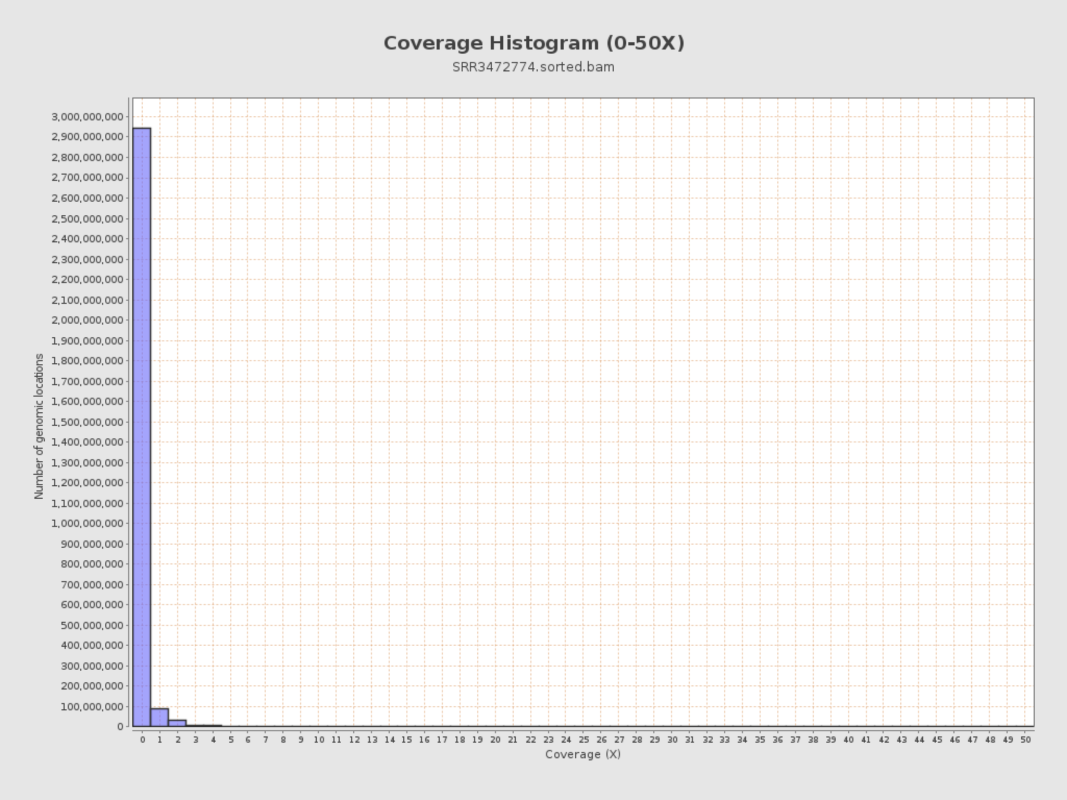
3. Results : Coverage across reference



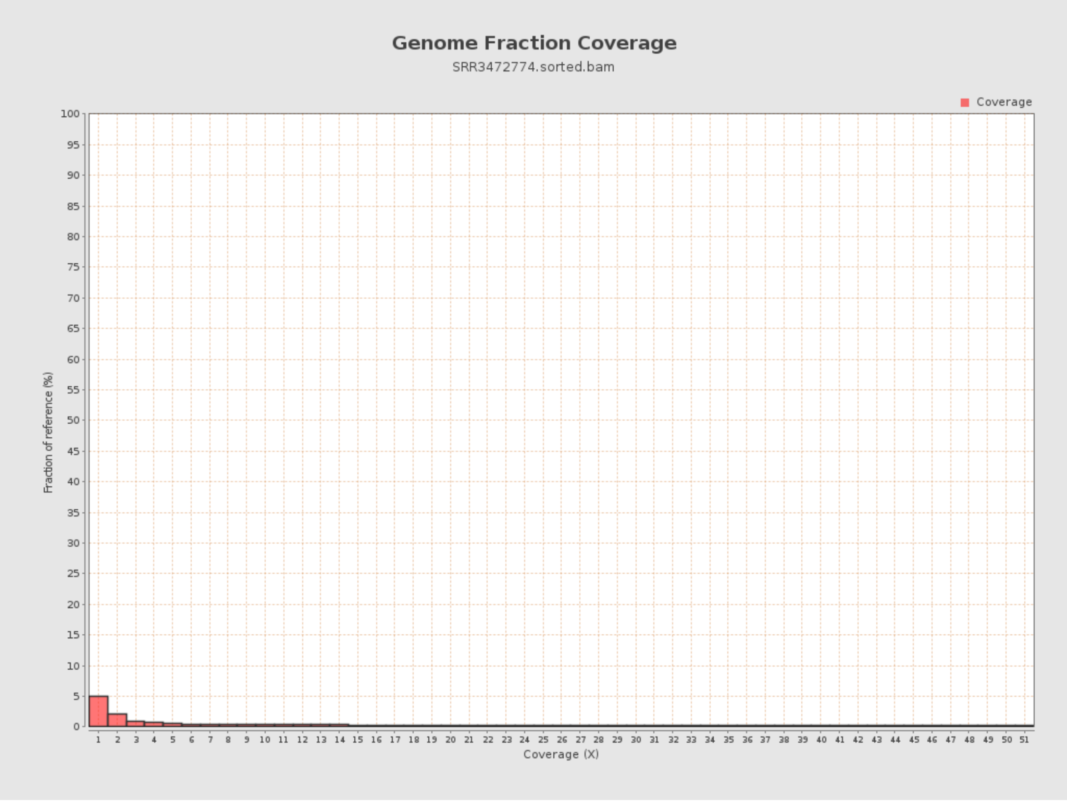
4. Results : Coverage Histogram



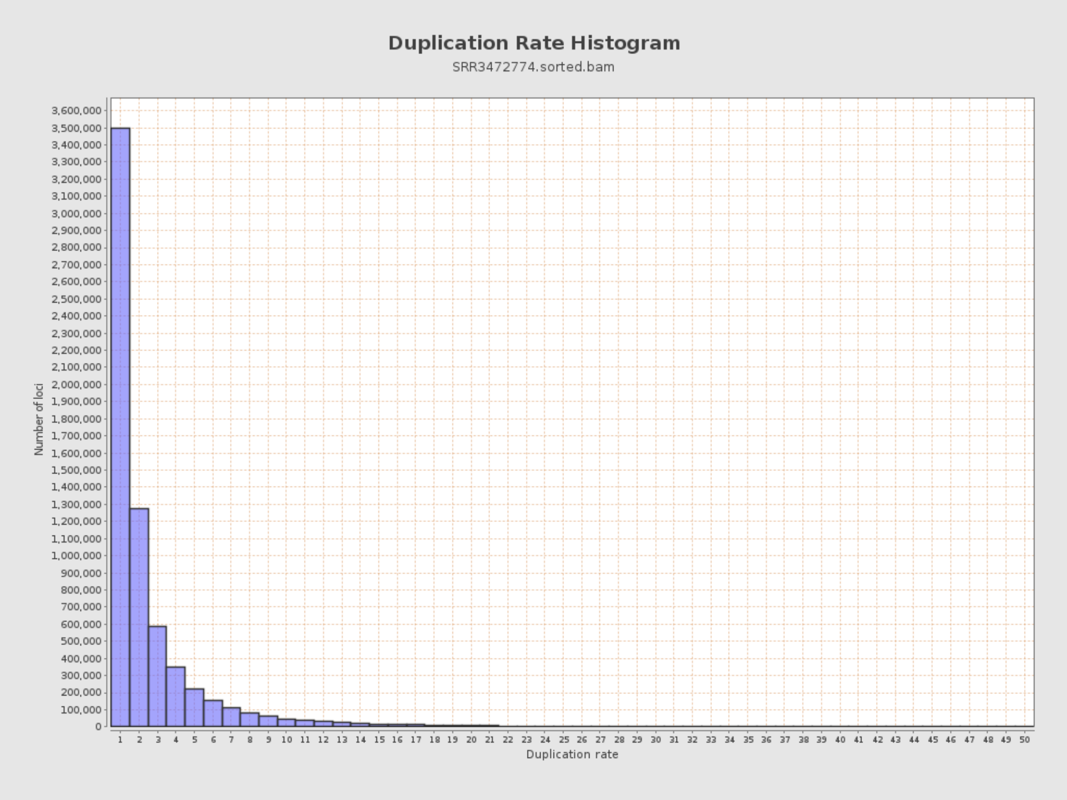
5. Results : Coverage Histogram (0-50X)



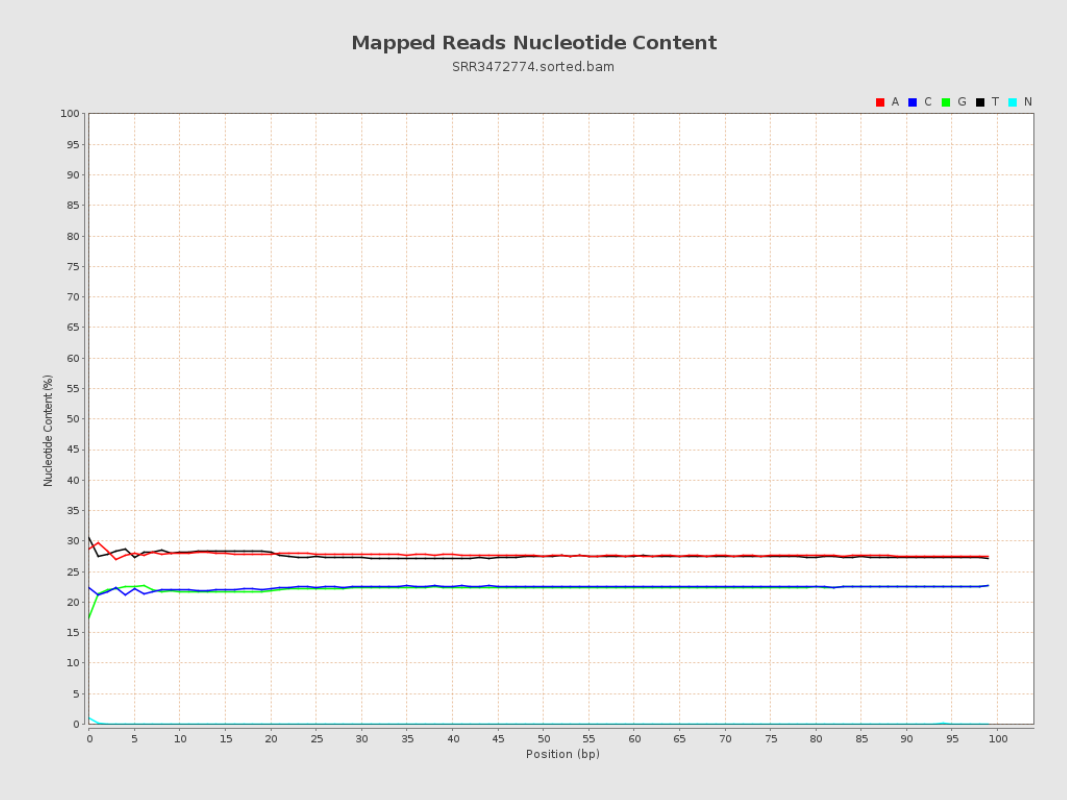
6. Results : Genome Fraction Coverage



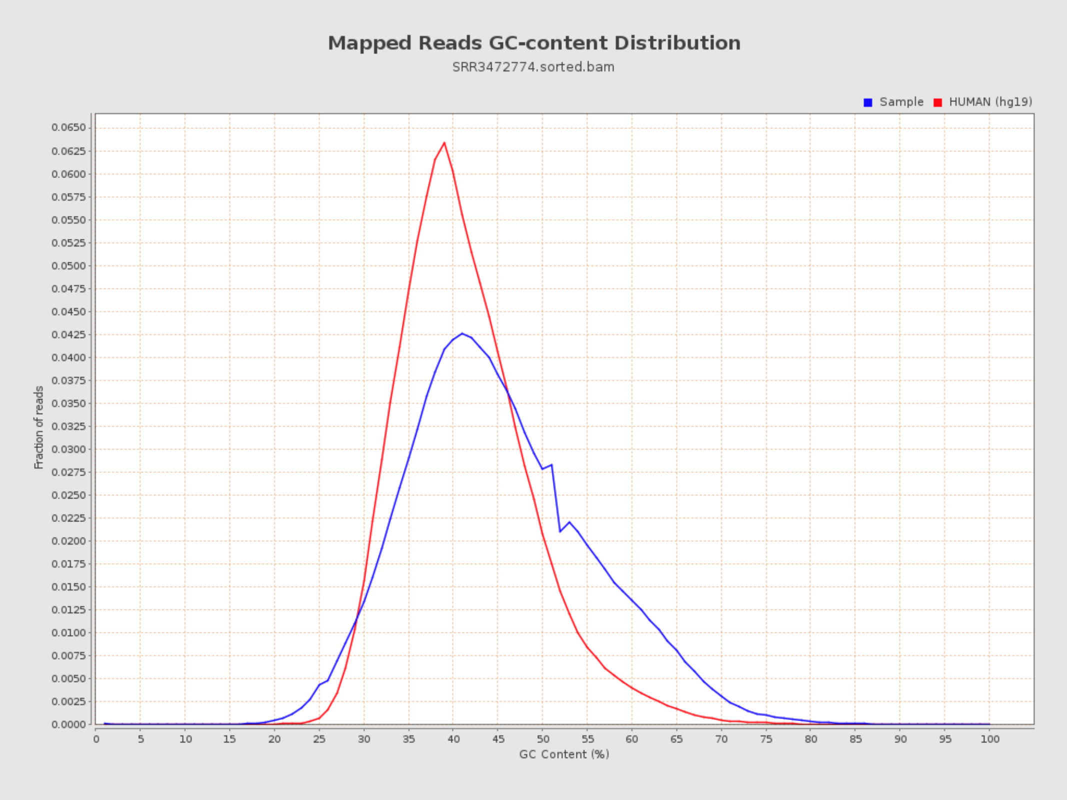
7. Results : Duplication Rate Histogram



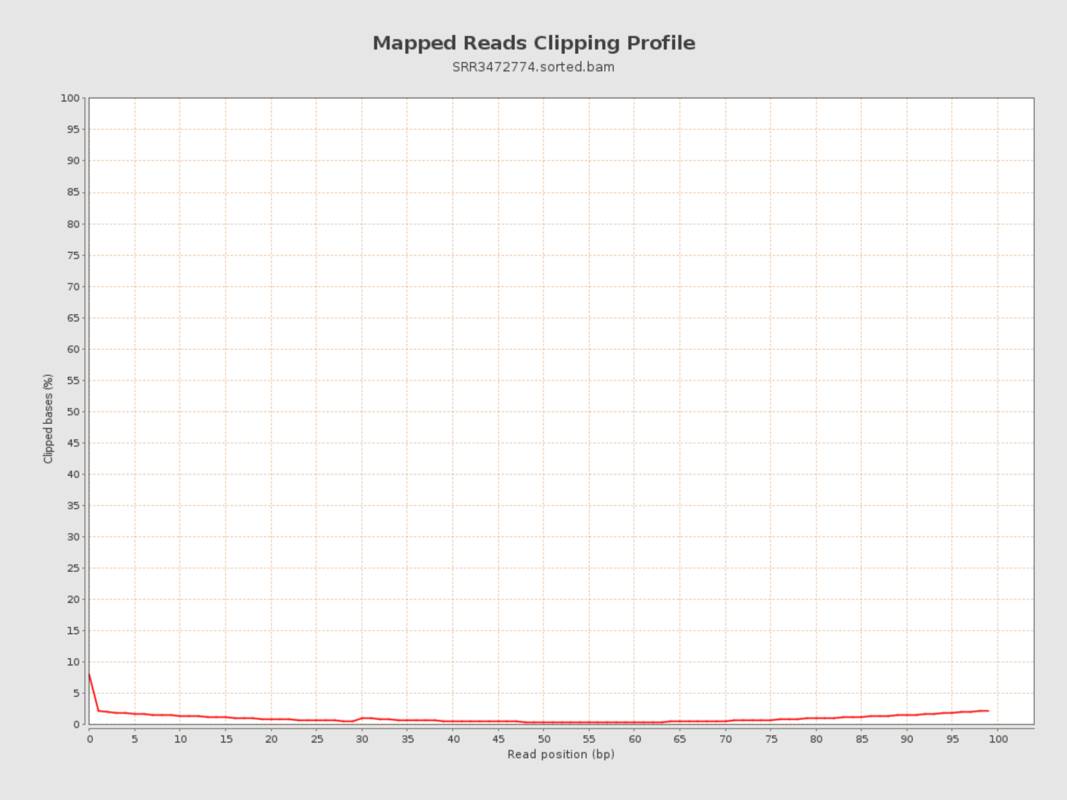
8. Results : Mapped Reads Nucleotide Content



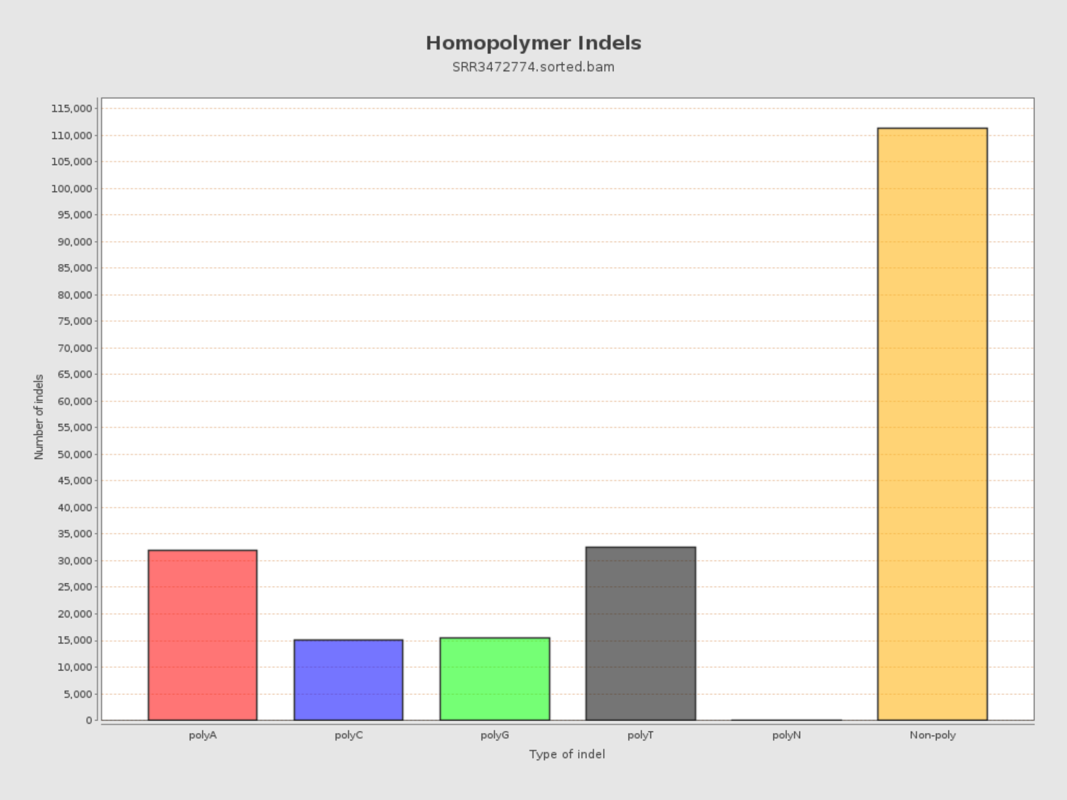
9. Results : Mapped Reads GC-content Distribution



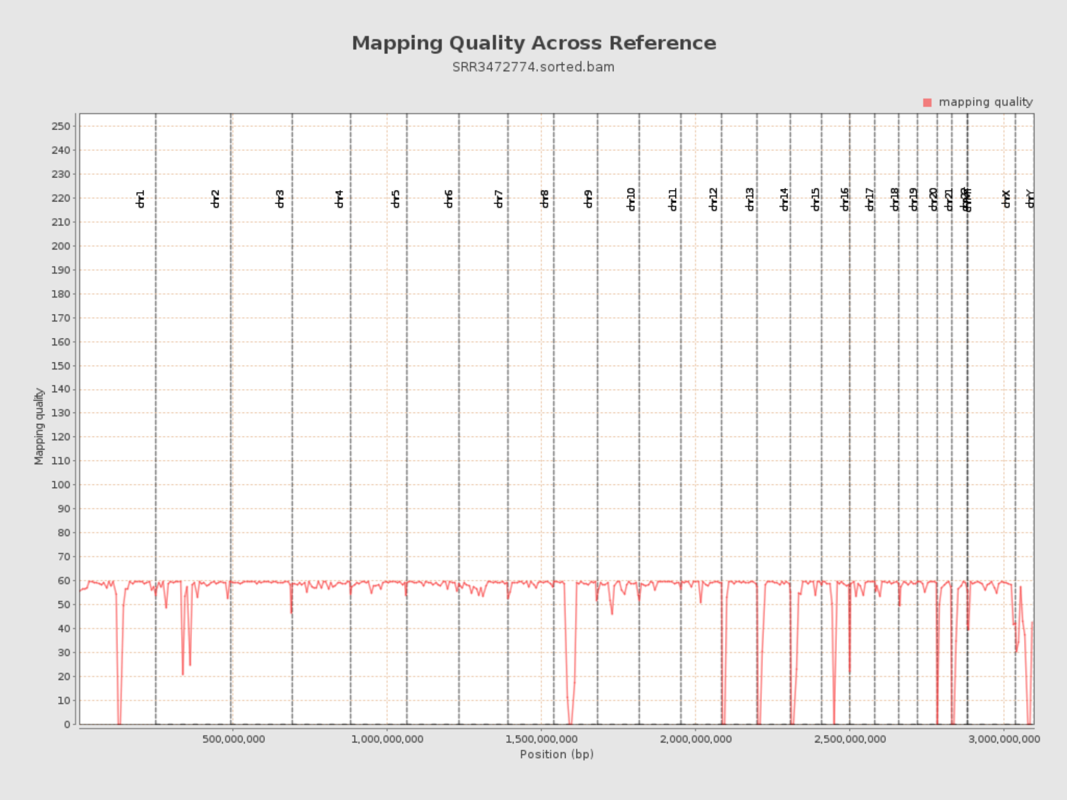
10. Results : Mapped Reads Clipping Profile



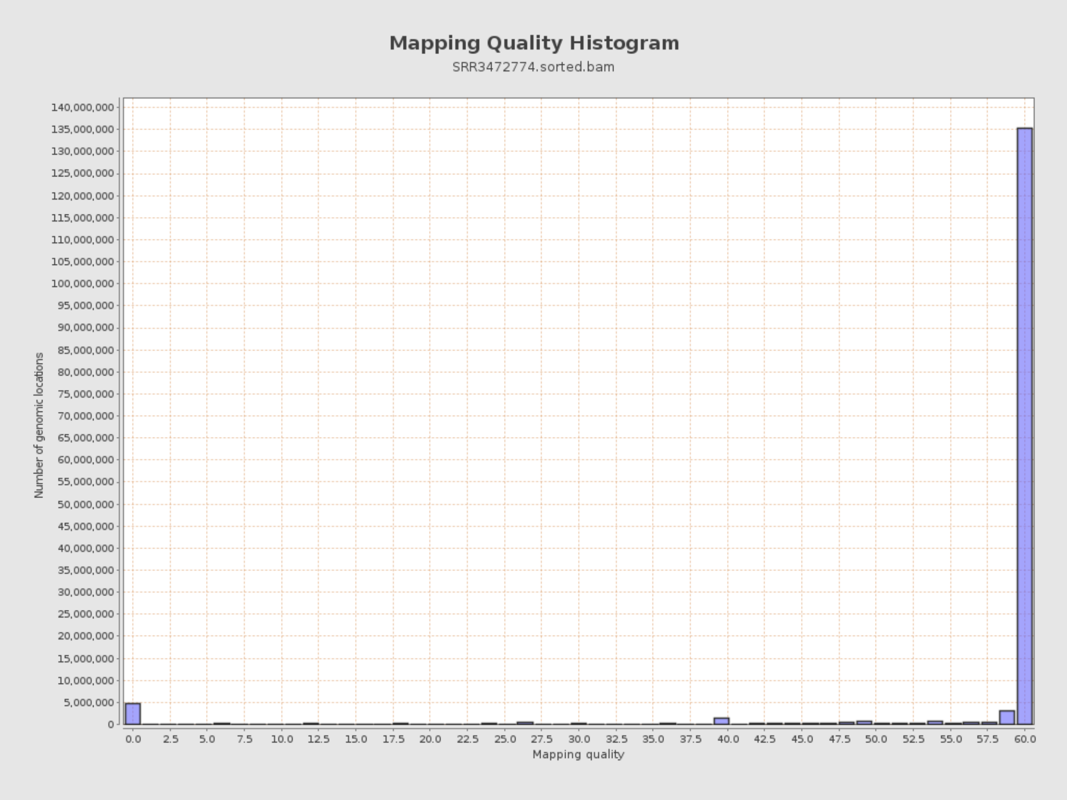
11. Results : Homopolymer Indels



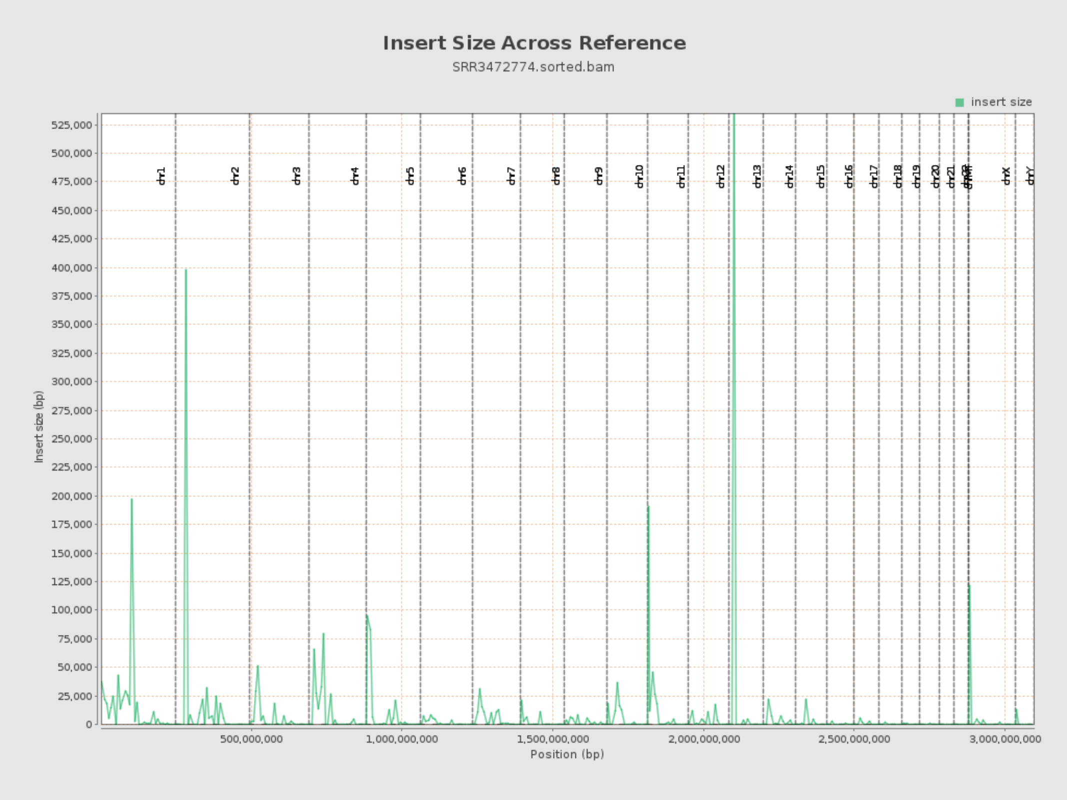
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram