Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 21:57:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472728.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_SRR3472728 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472728_1.fastq.gz SRR3472728_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 21:57:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472728.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,925,114
Mapped reads	14,799,999 / 99.16%
Unmapped reads	125,115 / 0.84%
Mapped paired reads	14,799,999 / 99.16%
Mapped reads, first in pair	7,422,499 / 49.73%
Mapped reads, second in pair	7,377,500 / 49.43%
Mapped reads, both in pair	14,724,282 / 98.65%
Mapped reads, singletons	75,717 / 0.51%
Secondary alignments	0
Supplementary alignments	51,201 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	9,171,119 / 61.45%
Duplication rate	47.26%
Clipped reads	1,072,993 / 7.19%

2.2. ACGT Content

Number/percentage of A's	398,882,949 / 27.31%
Number/percentage of C's	333,370,289 / 22.83%
Number/percentage of T's	396,966,632 / 27.18%
Number/percentage of G's	331,025,687 / 22.66%
Number/percentage of N's	283,641 / 0.02%

GC Percentage	45.49%

2.3. Coverage

Mean	0.4719
Standard Deviation	16.1586

2.4. Mapping Quality

Mean Mapping Quality	55.32

2.5. Insert size

Mean	23,005.99
Standard Deviation	1,472,638.43
P25/Median/P75	177 / 242 / 321

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	8,903,281
Insertions	80,263
Mapped reads with at least one insertion	0.54%
Deletions	82,037
Mapped reads with at least one deletion	0.54%
Homopolymer indels	44.9%

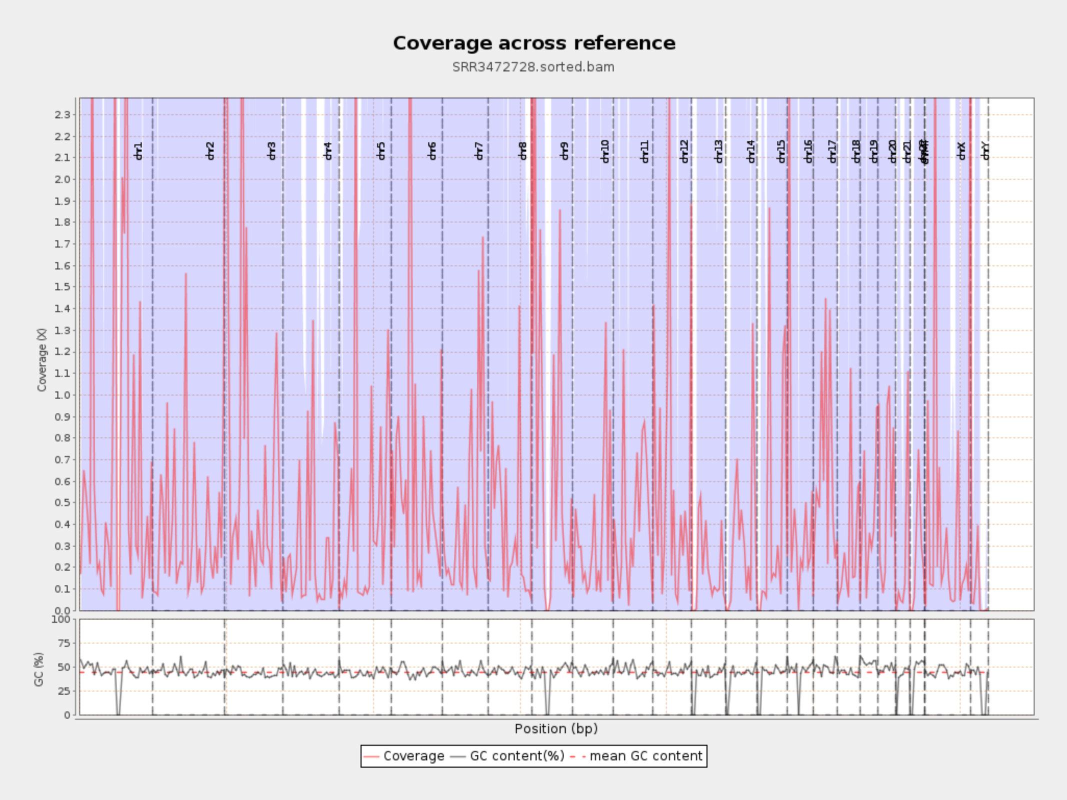
2.7. Chromosome stats

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

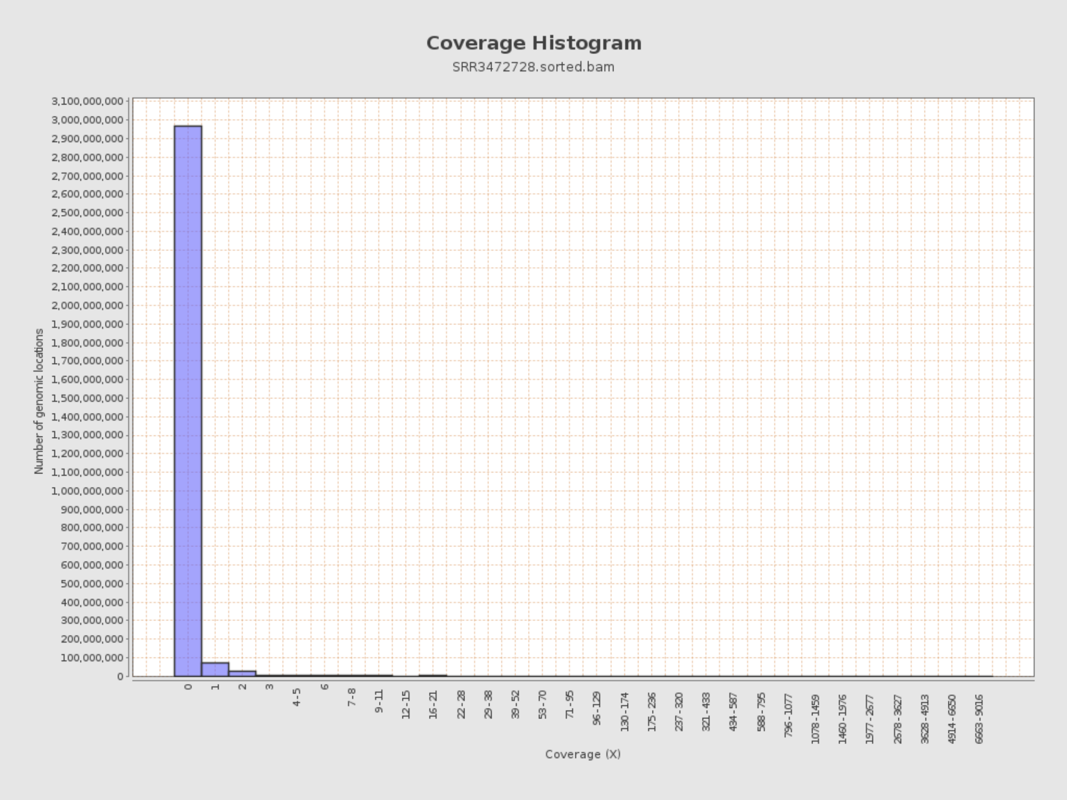
		bases	coverage	deviation
chr1	249250621	182638079	0.7327	27.0761
chr2	243199373	87792524	0.361	10.8271
chr3	198022430	154431702	0.7799	18.2275
chr4	191154276	56359318	0.2948	11.235
chr5	180915260	83495531	0.4615	16.1657
chr6	171115067	103476948	0.6047	18.577
chr7	159138663	73299399	0.4606	18.0448
chr8	146364022	56248001	0.3843	12.141
chr9	141213431	102460026	0.7256	20.9661
chr10	135534747	46499246	0.3431	14.1882
chr11	135006516	59850739	0.4433	14.6133
chr12	133851895	77272839	0.5773	15.5574
chr13	115169878	21801735	0.1893	6.7487
chr14	107349540	36235115	0.3375	10.4491
chr15	102531392	44036024	0.4295	24.1171
chr16	90354753	43714977	0.4838	12.3823
chr17	81195210	54392564	0.6699	14.7187
chr18	78077248	23674460	0.3032	10.9845
chr19	59128983	24289981	0.4108	9.5231
chr20	63025520	34041505	0.5401	15.546
chr21	48129895	11435198	0.2376	11.7943
chr22	51304566	13090573	0.2552	8.1698
chrMT	16571	843	0.0509	0.2211
chrX	155270560	65489872	0.4218	13.1629

chrY	59373566	4710267	0.0793	5.2574

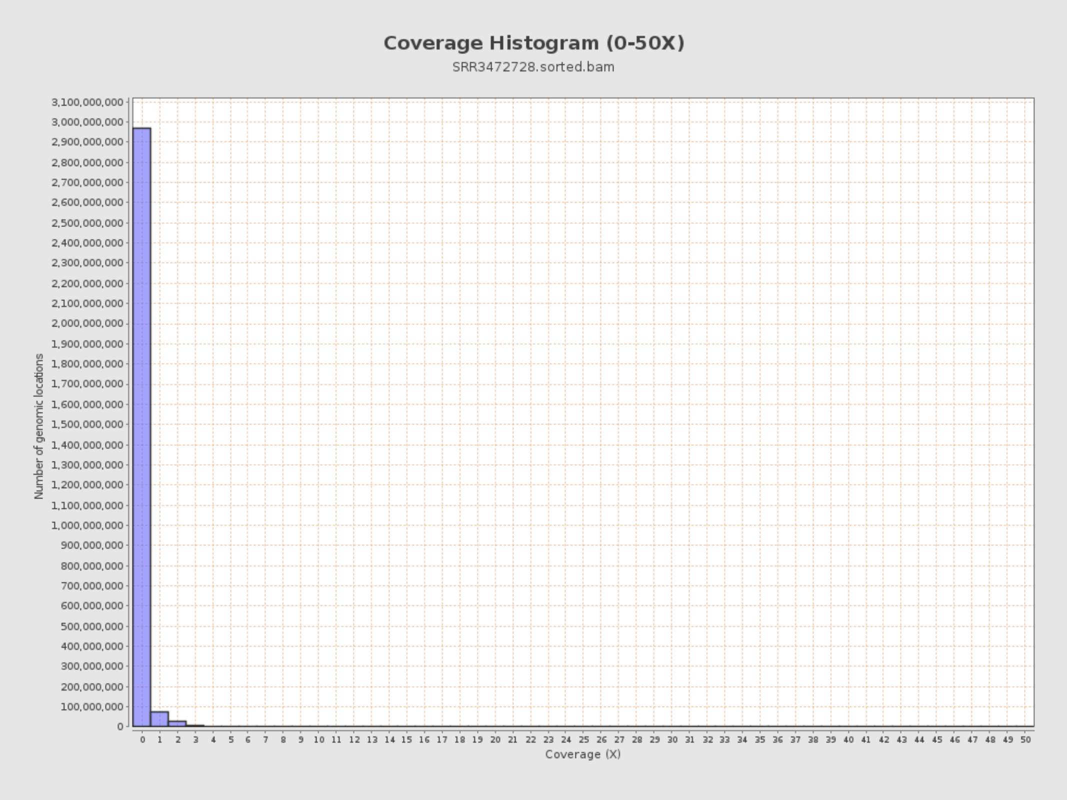
3. Results : Coverage across reference



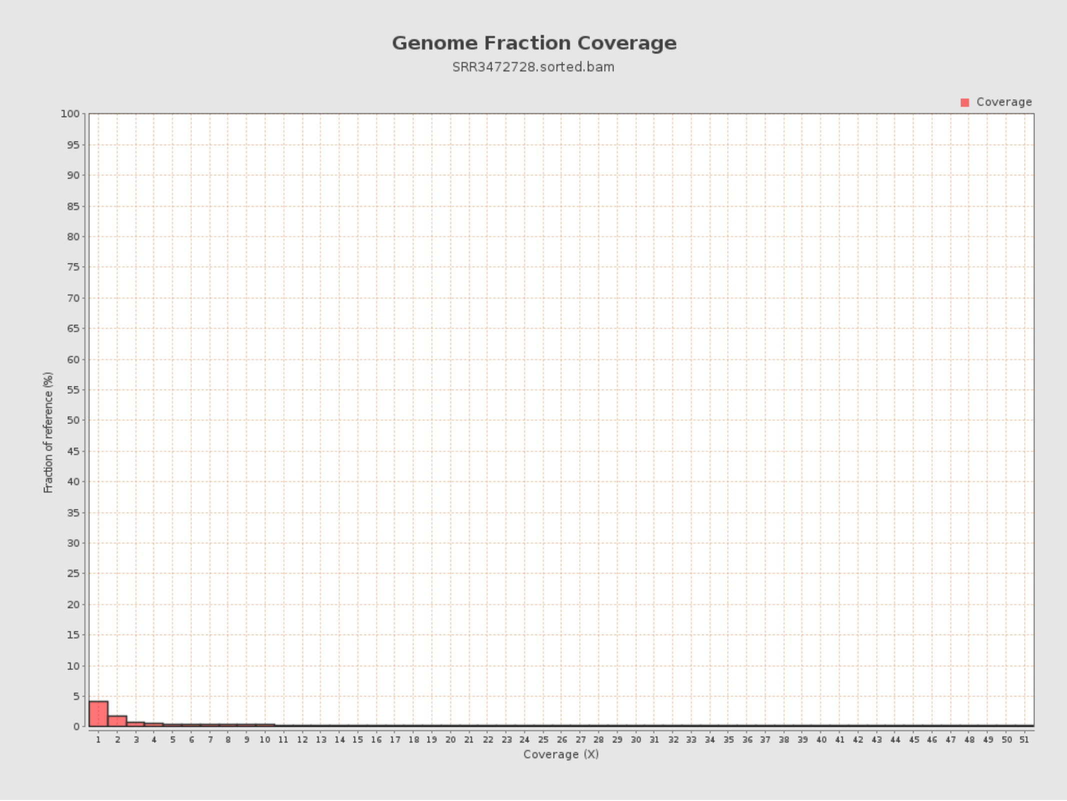
4. Results : Coverage Histogram



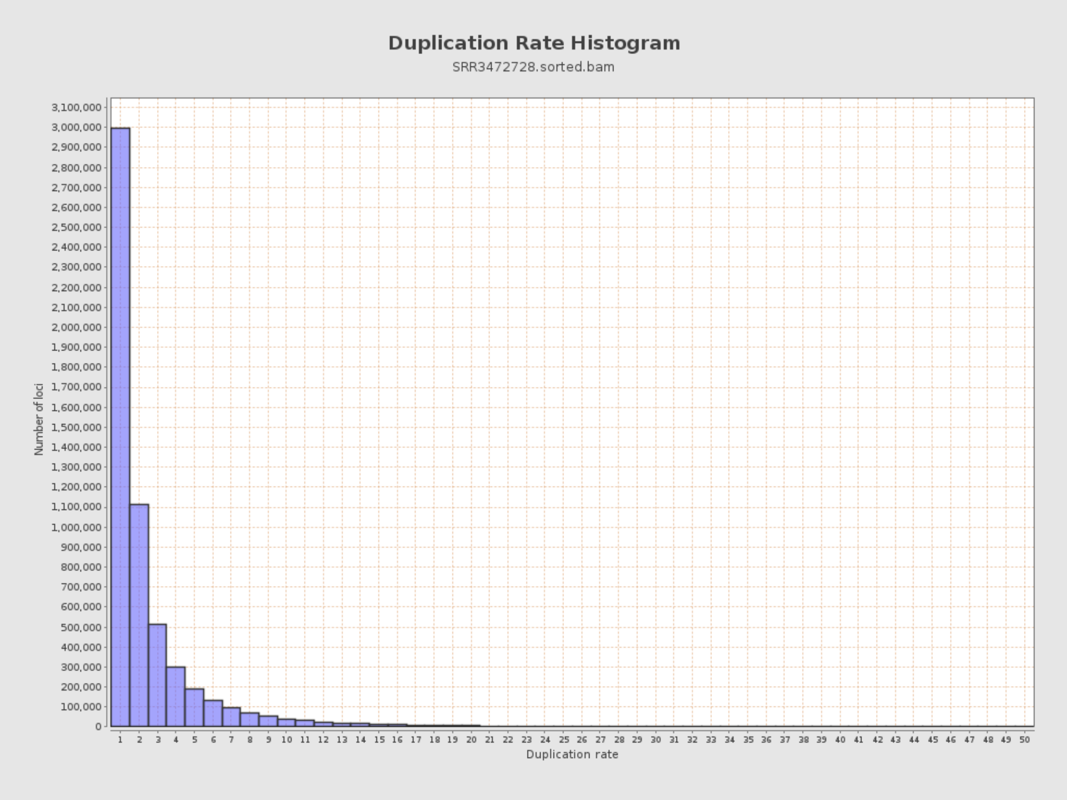
5. Results : Coverage Histogram (0-50X)



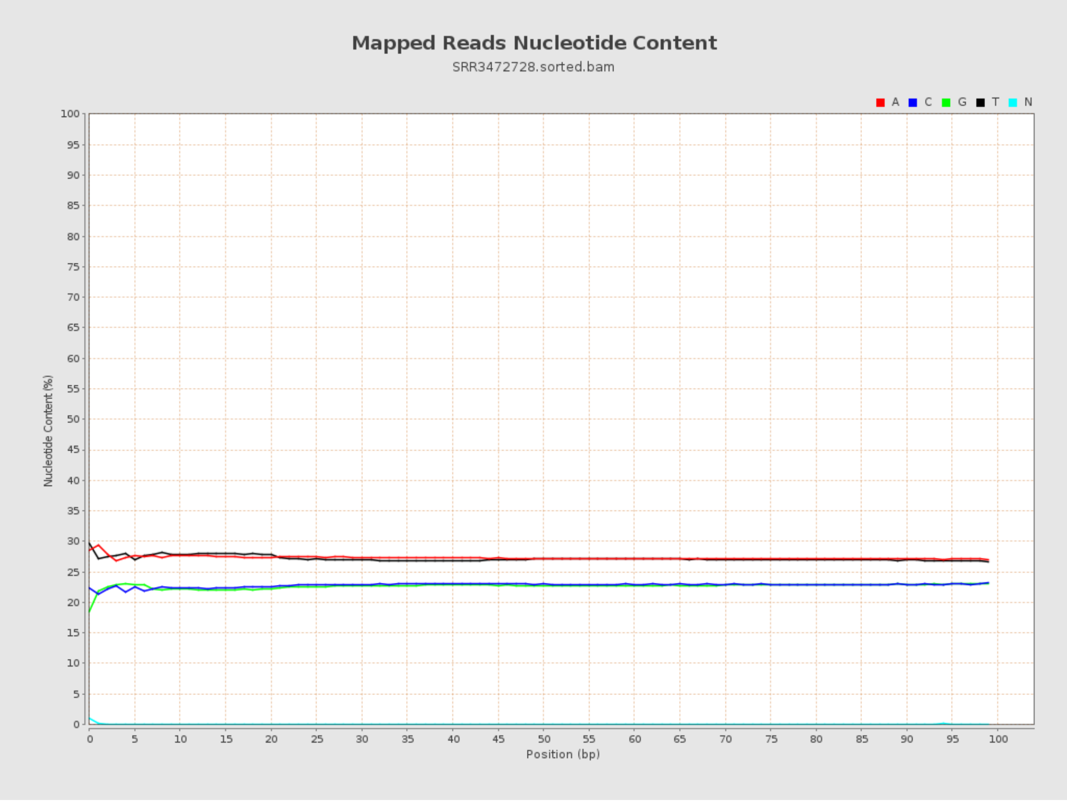
6. Results : Genome Fraction Coverage



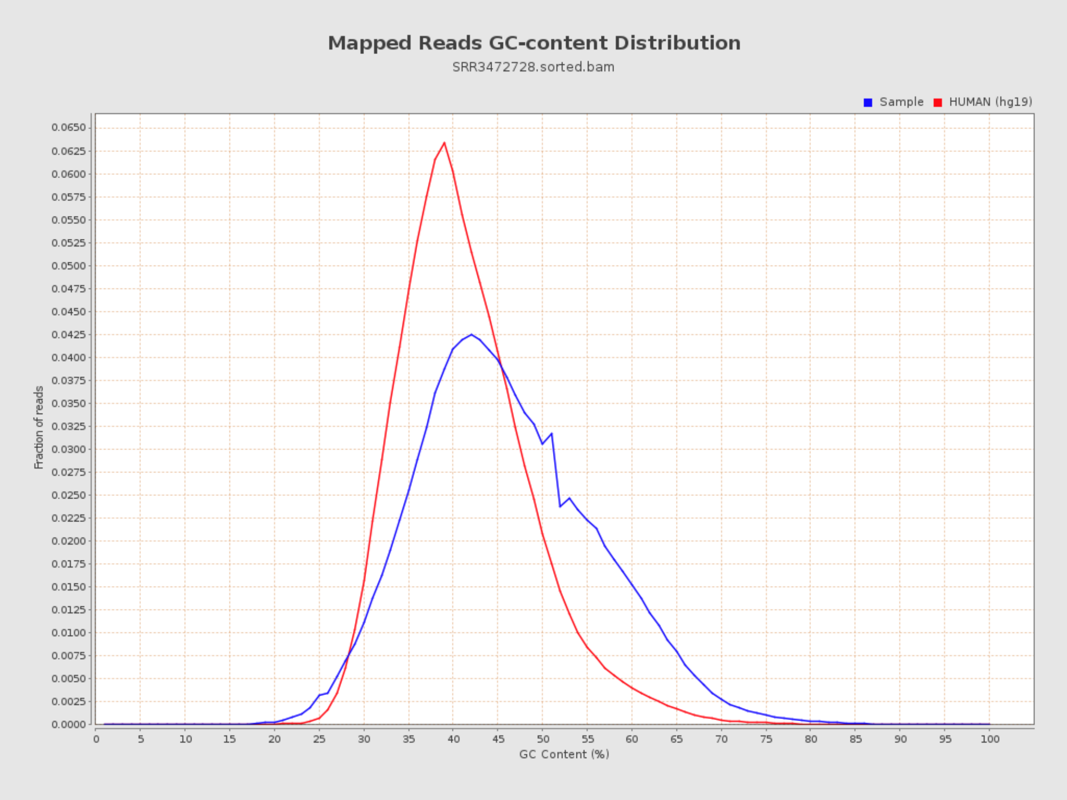
7. Results : Duplication Rate Histogram



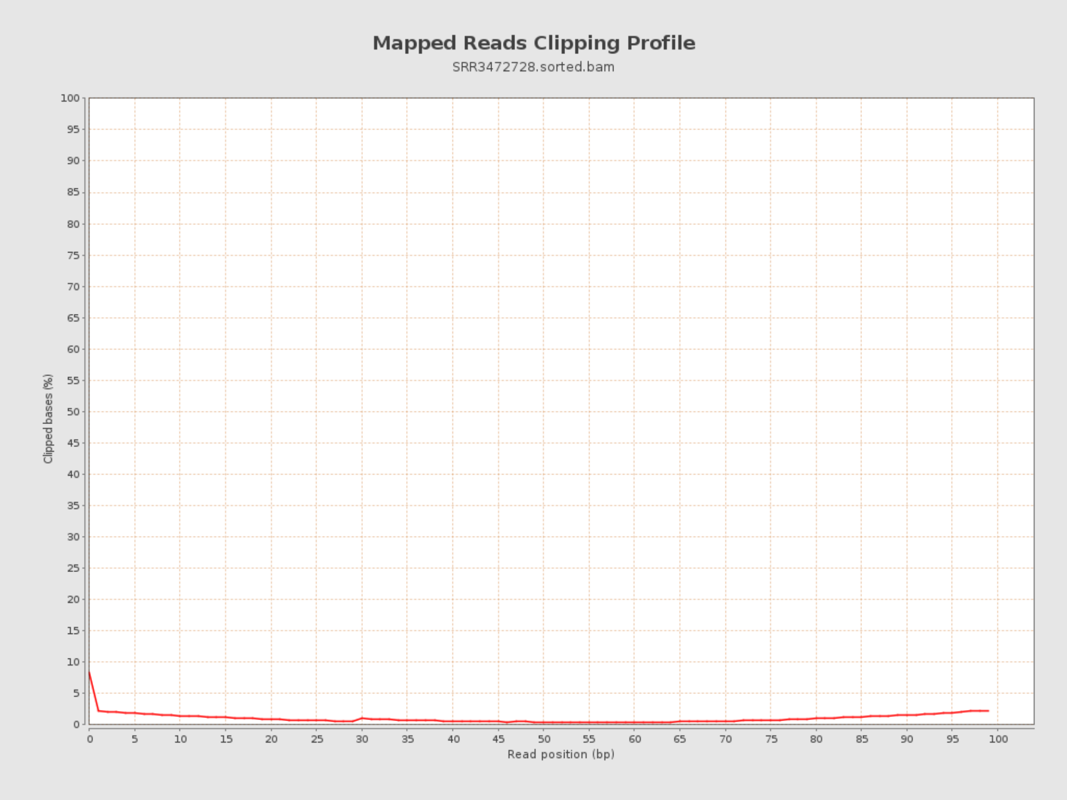
8. Results : Mapped Reads Nucleotide Content



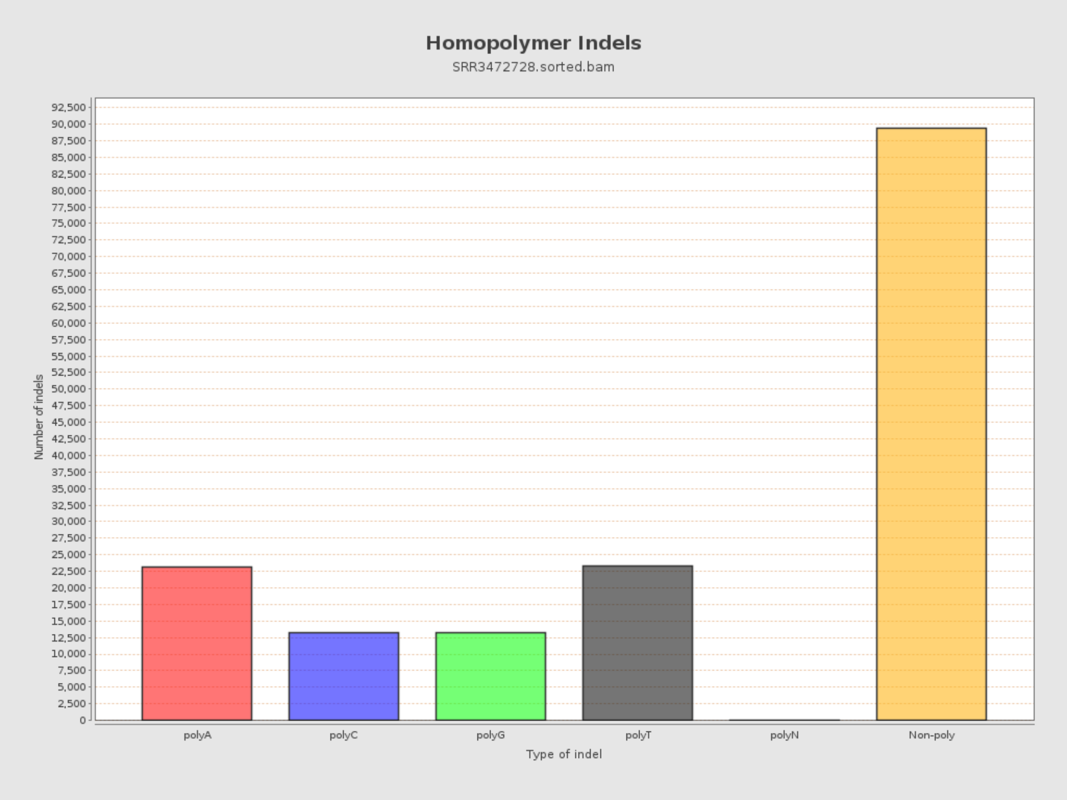
9. Results : Mapped Reads GC-content Distribution



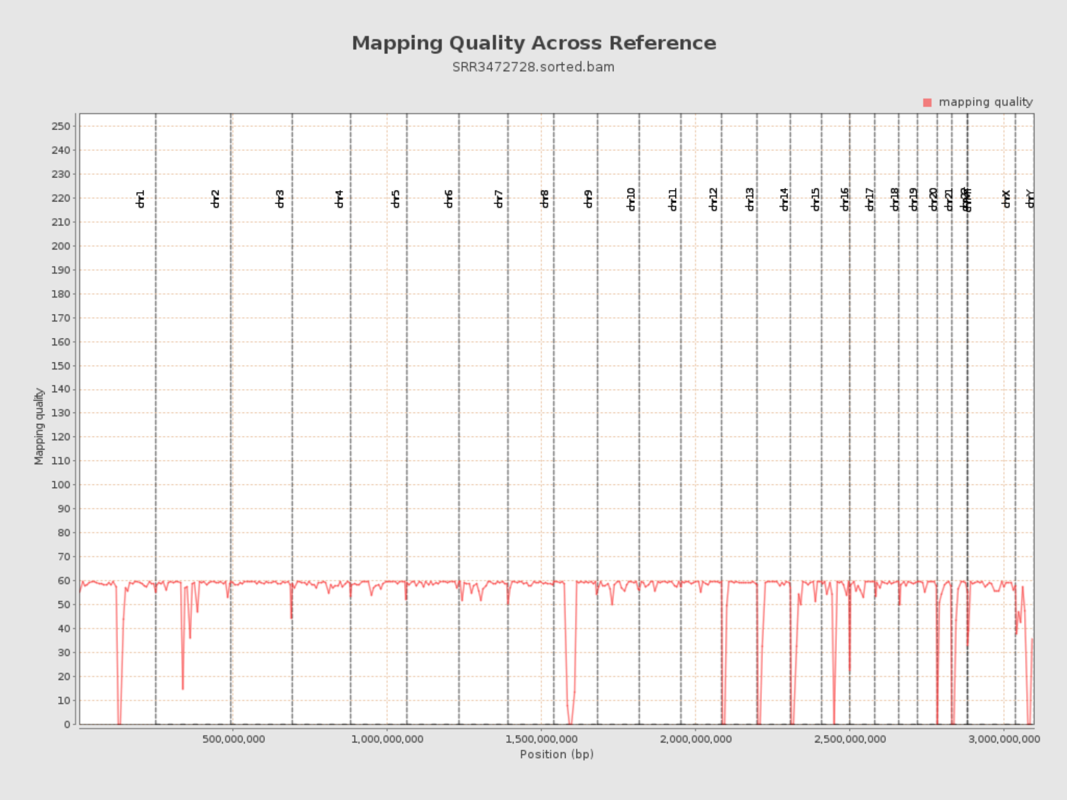
10. Results : Mapped Reads Clipping Profile



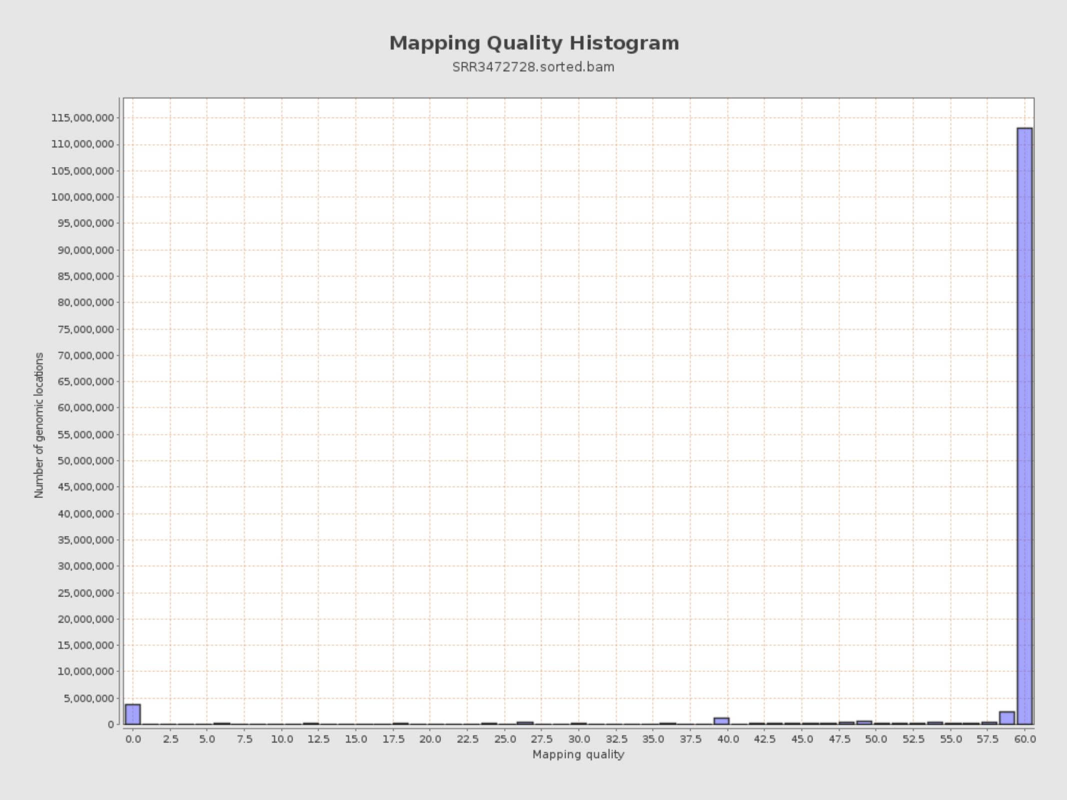
11. Results : Homopolymer Indels



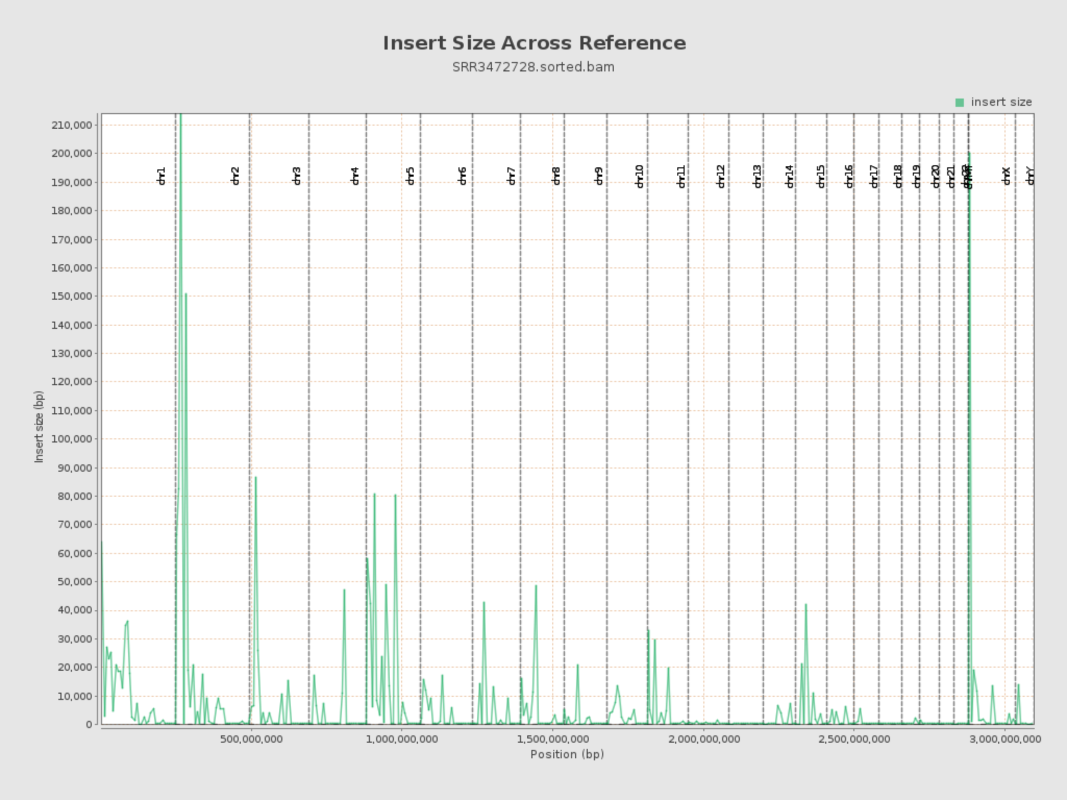
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram