Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 07:02:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472682.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_SRR3472682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472682_1.fastq.gz SRR3472682_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 07:02:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,589,830
Mapped reads	15,461,694 / 99.18%
Unmapped reads	128,136 / 0.82%
Mapped paired reads	15,461,694 / 99.18%
Mapped reads, first in pair	7,750,812 / 49.72%
Mapped reads, second in pair	7,710,882 / 49.46%
Mapped reads, both in pair	15,382,714 / 98.67%
Mapped reads, singletons	78,980 / 0.51%
Secondary alignments	0
Supplementary alignments	91,480 / 0.59%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	10,551,571 / 67.68%
Duplication rate	47.73%
Clipped reads	1,173,623 / 7.53%

2.2. ACGT Content

Number/percentage of A's	401,556,211 / 26.43%
Number/percentage of C's	360,362,968 / 23.72%
Number/percentage of T's	401,528,434 / 26.43%
Number/percentage of G's	355,388,736 / 23.39%
Number/percentage of N's	285,527 / 0.02%

GC Percentage	47.12%

2.3. Coverage

Mean	0.4908
Standard Deviation	22.5499

2.4. Mapping Quality

Mean Mapping Quality	55

2.5. Insert size

Mean	19,812.98
Standard Deviation	1,389,604.29
P25/Median/P75	152 / 209 / 280

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	8,904,426
Insertions	97,892
Mapped reads with at least one insertion	0.63%
Deletions	78,437
Mapped reads with at least one deletion	0.5%
Homopolymer indels	48.49%

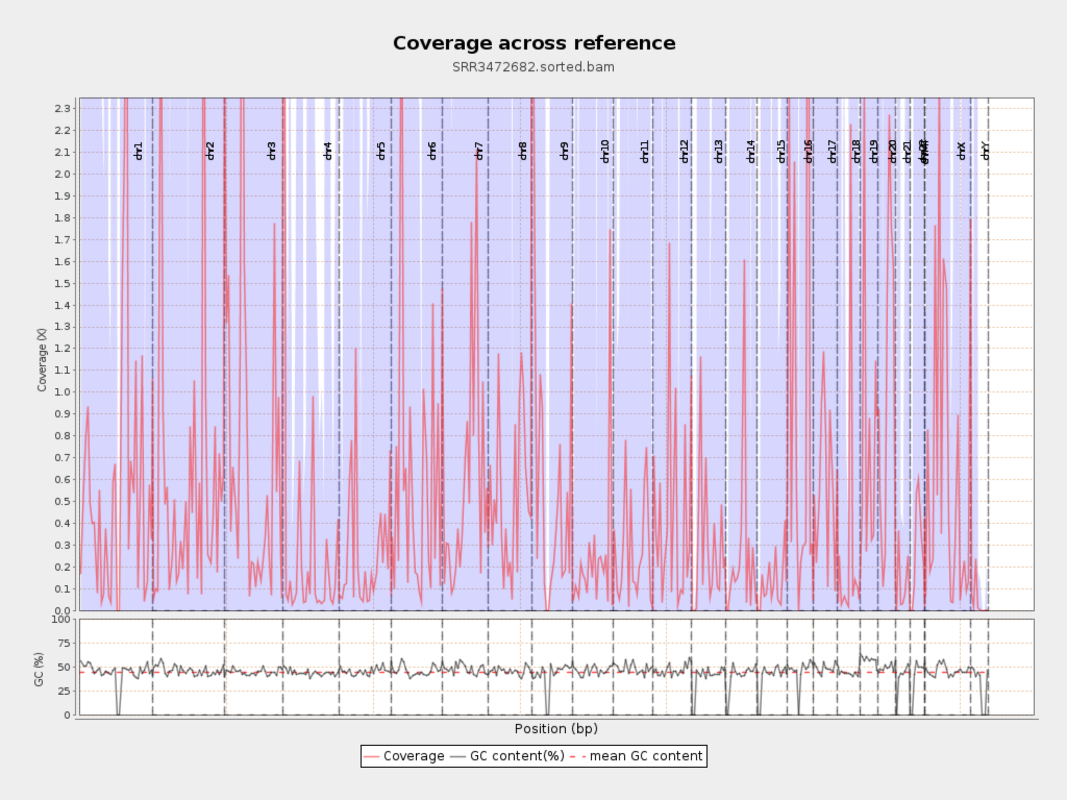
2.7. Chromosome stats

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

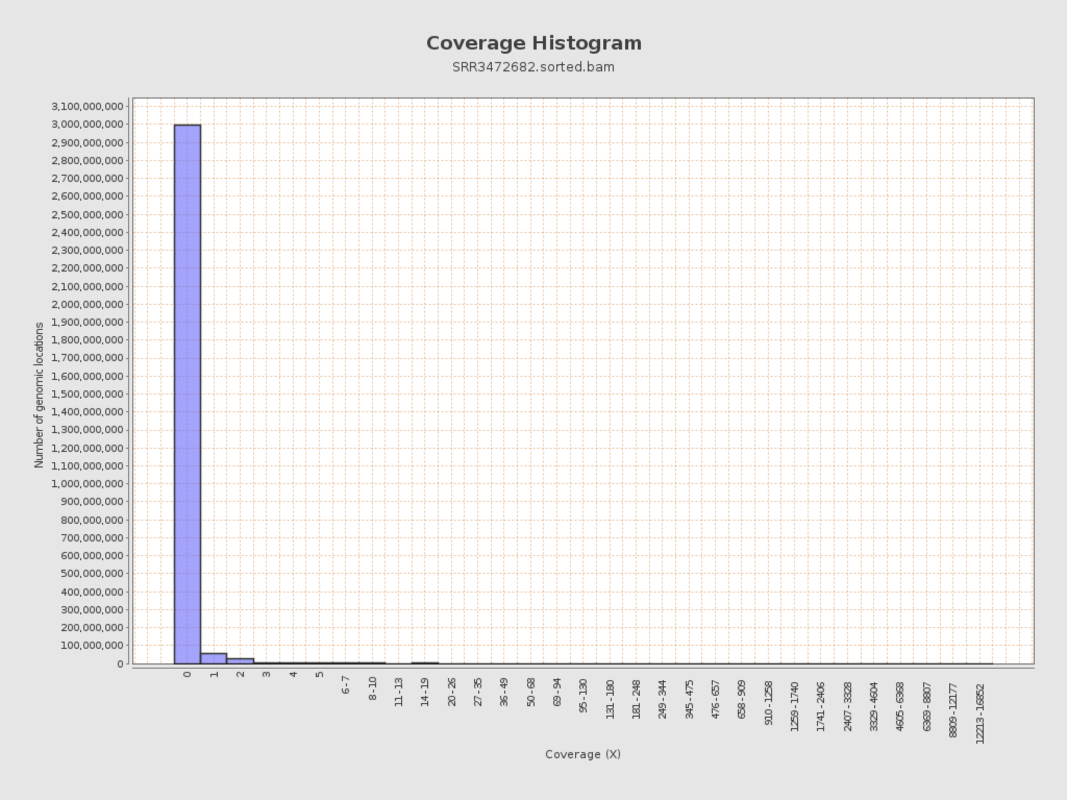
		bases	coverage	deviation
chr1	249250621	149485784	0.5997	23.1333
chr2	243199373	147056657	0.6047	27.8913
chr3	198022430	150512660	0.7601	26.8986
chr4	191154276	58406507	0.3055	23.5762
chr5	180915260	49371986	0.2729	15.0783
chr6	171115067	98522161	0.5758	26.8015
chr7	159138663	97449185	0.6124	26.793
chr8	146364022	77301805	0.5281	18.6511
chr9	141213431	92691729	0.6564	21.8307
chr10	135534747	34131347	0.2518	13.9066
chr11	135006516	38126587	0.2824	14.8906
chr12	133851895	58805107	0.4393	17.9416
chr13	115169878	33060982	0.2871	10.235
chr14	107349540	27082414	0.2523	13.3734
chr15	102531392	13496832	0.1316	6.5109
chr16	90354753	88894931	0.9838	38.5936
chr17	81195210	48137106	0.5929	17.8874
chr18	78077248	23118701	0.2961	36.6715
chr19	59128983	47533018	0.8039	20.5731
chr20	63025520	67040163	1.0637	32.4387
chr21	48129895	6377620	0.1325	6.8547
chr22	51304566	13874226	0.2704	8.8412
chrMT	16571	7132	0.4304	0.8496
chrX	155270560	96283525	0.6201	26.1052

chrY	59373566	2535669	0.0427	5.1212

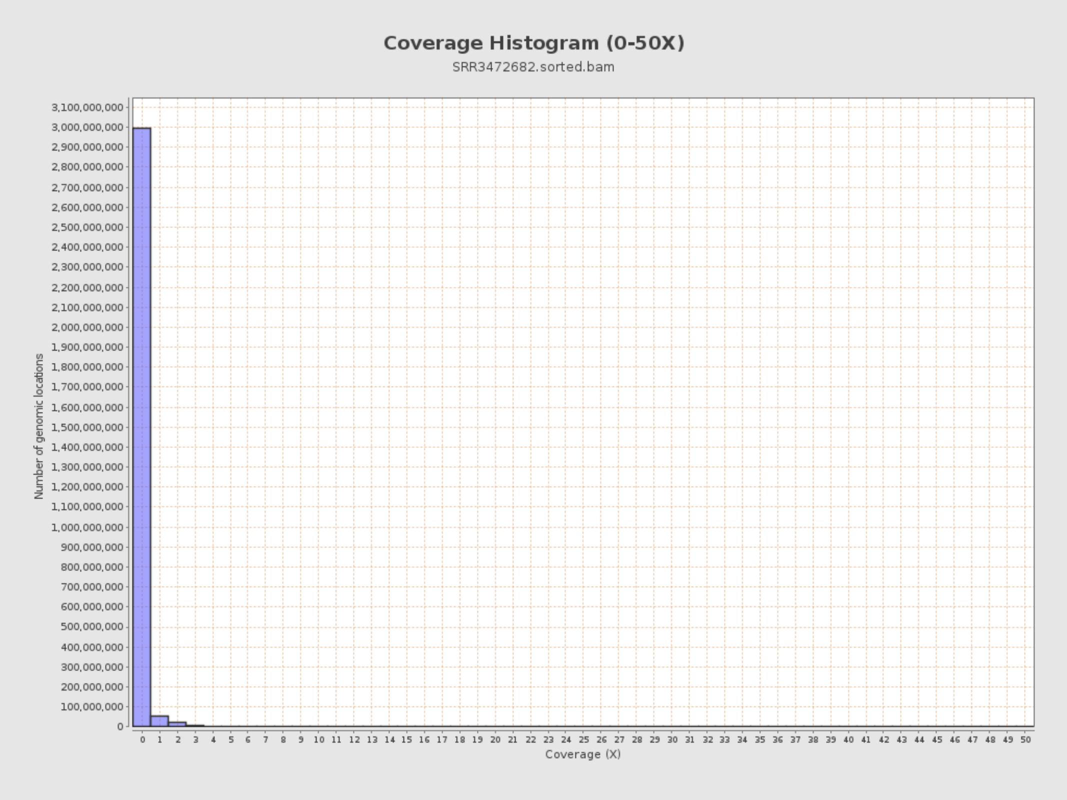
3. Results : Coverage across reference



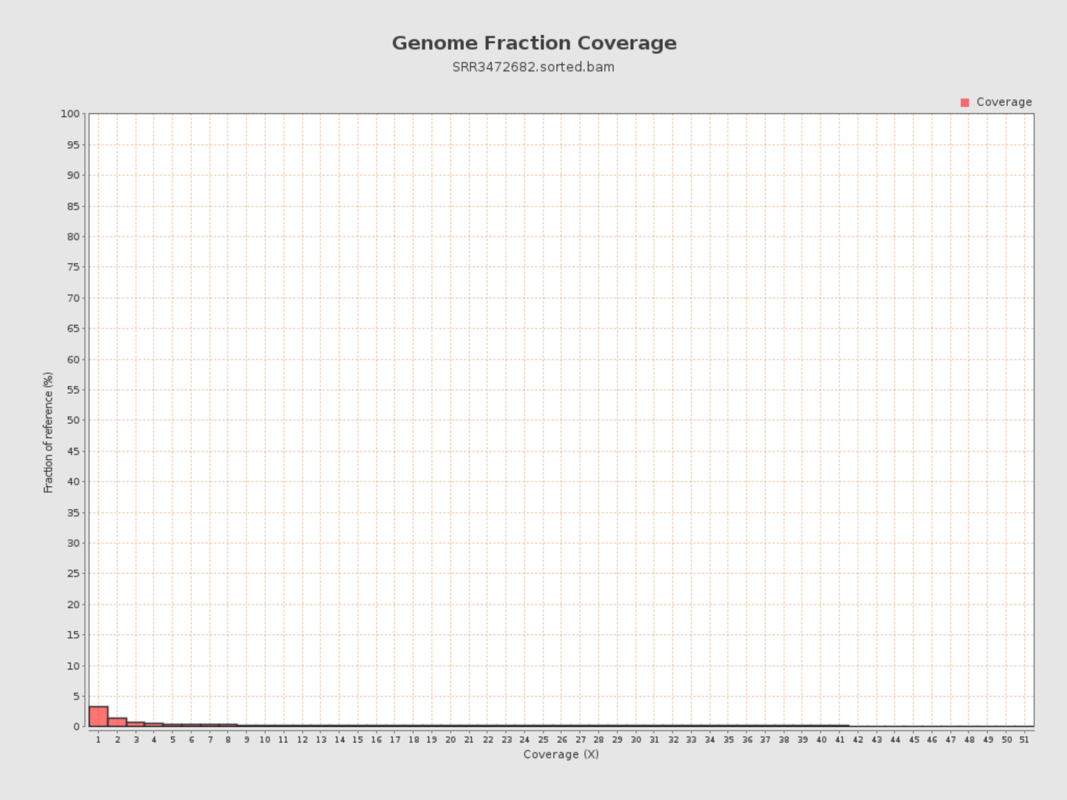
4. Results : Coverage Histogram



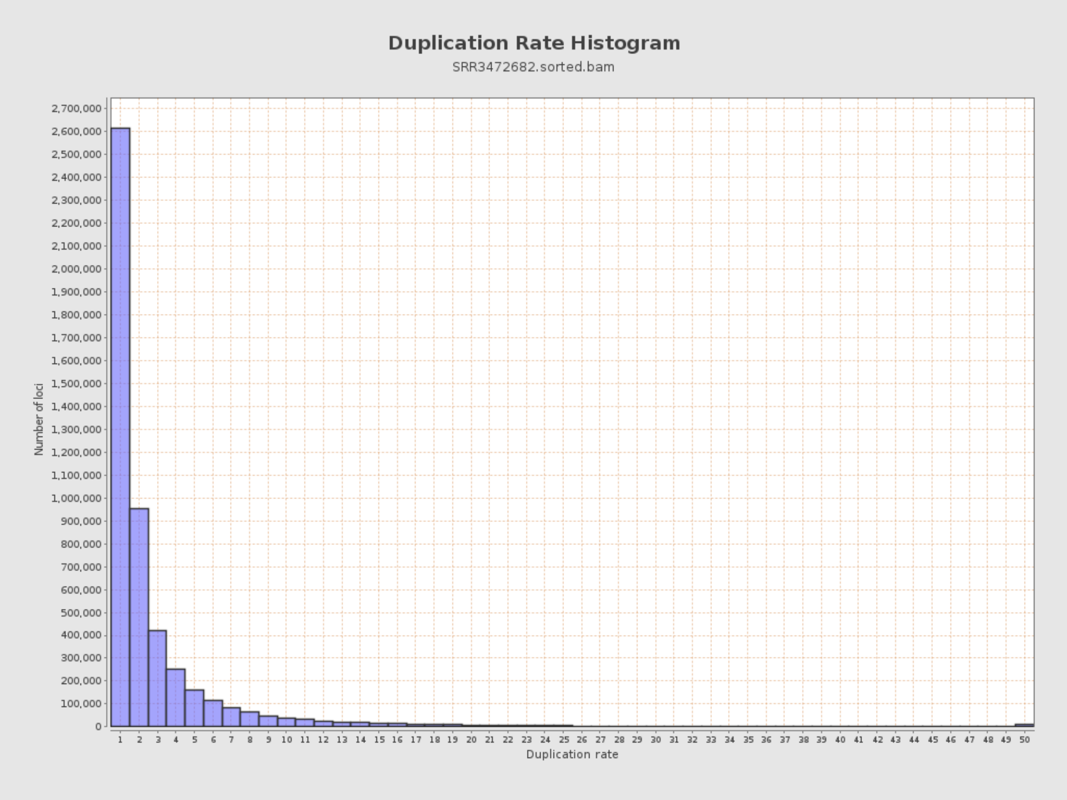
5. Results : Coverage Histogram (0-50X)



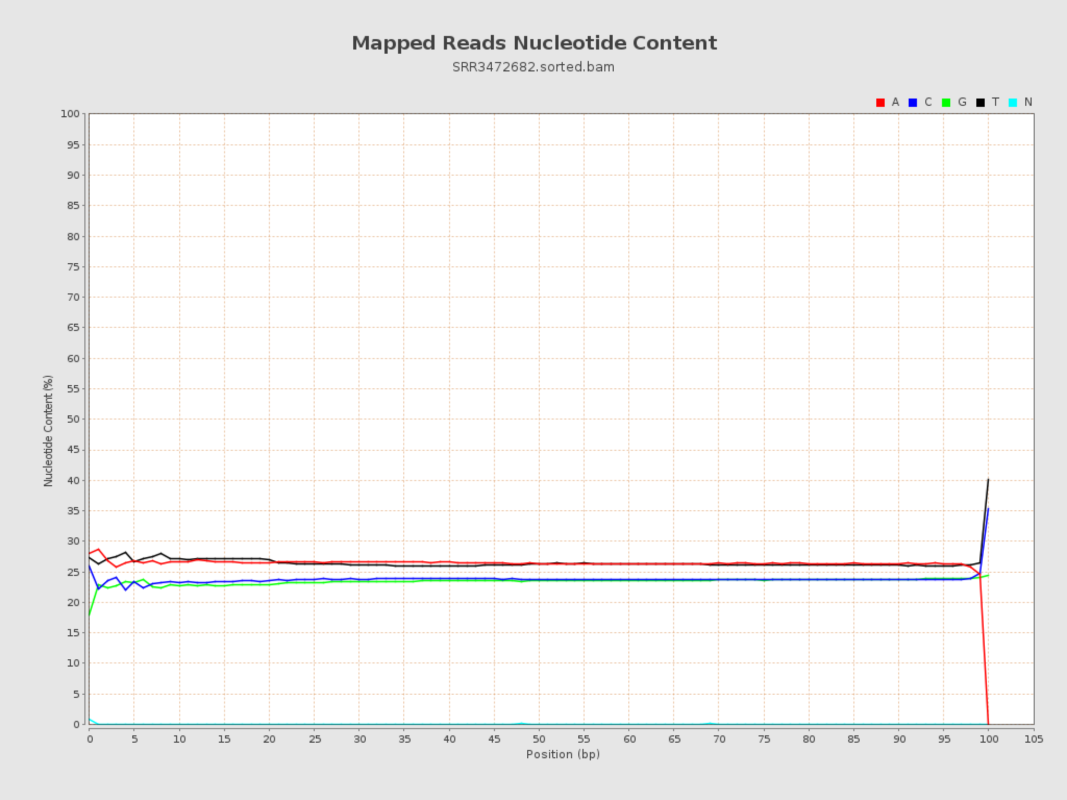
6. Results : Genome Fraction Coverage



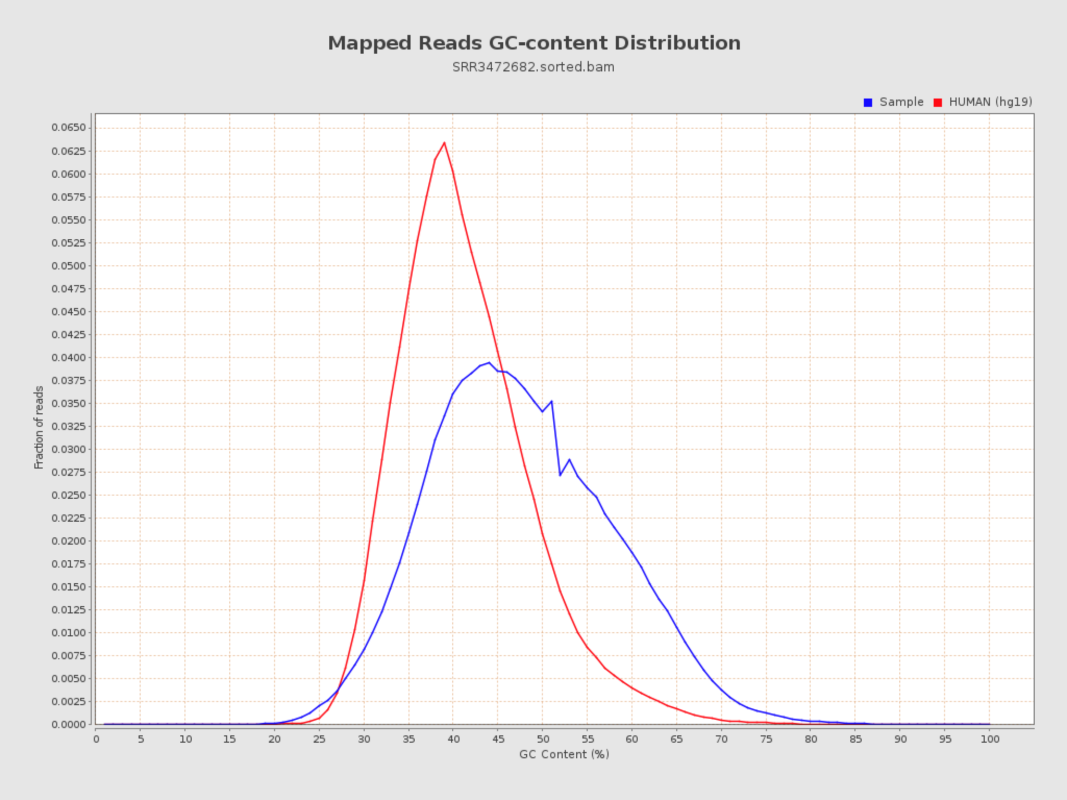
7. Results : Duplication Rate Histogram



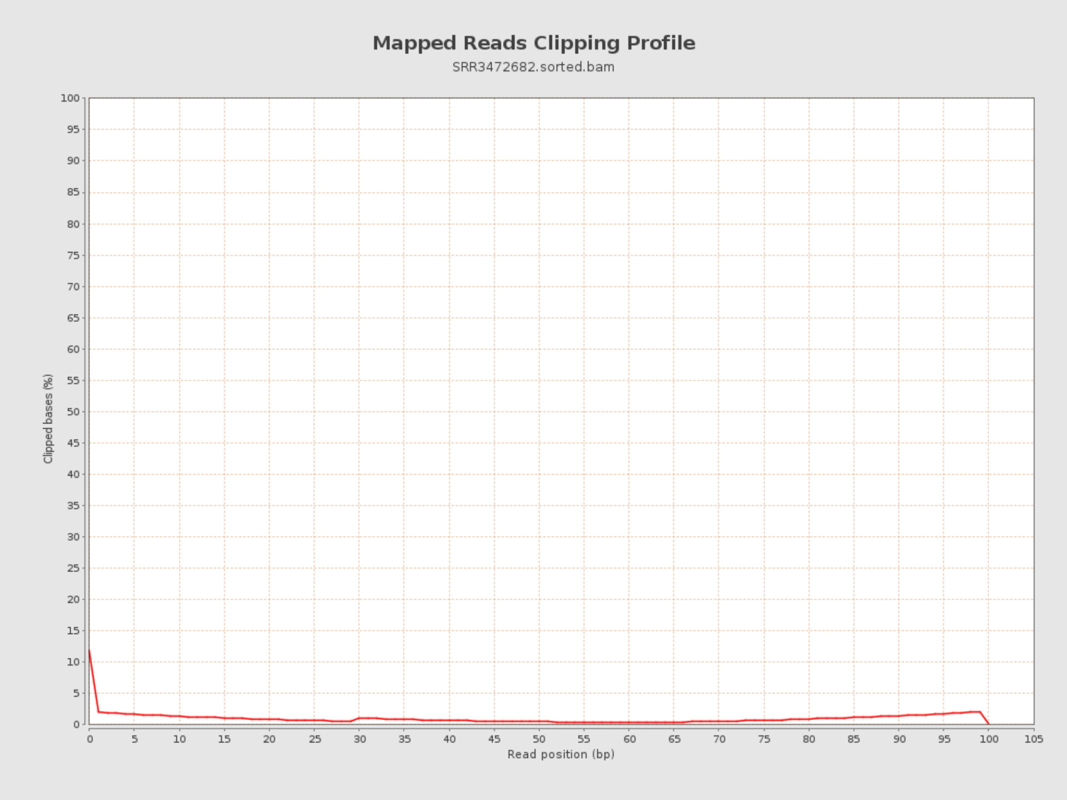
8. Results : Mapped Reads Nucleotide Content



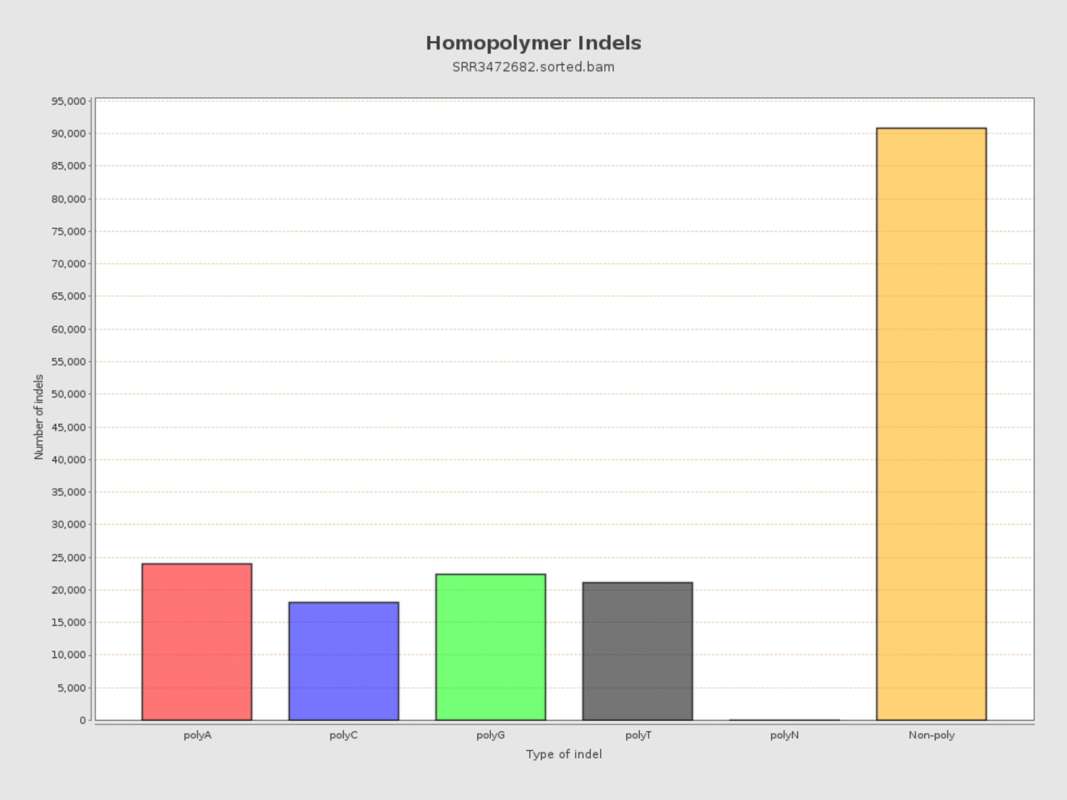
9. Results : Mapped Reads GC-content Distribution



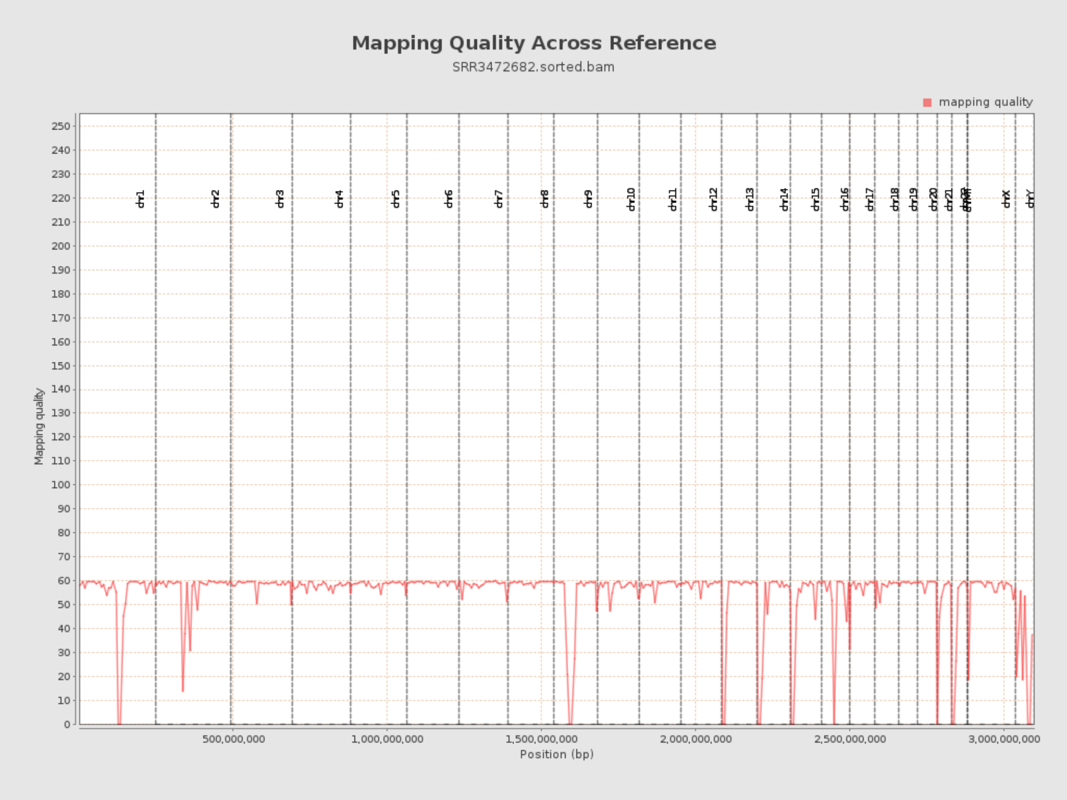
10. Results : Mapped Reads Clipping Profile



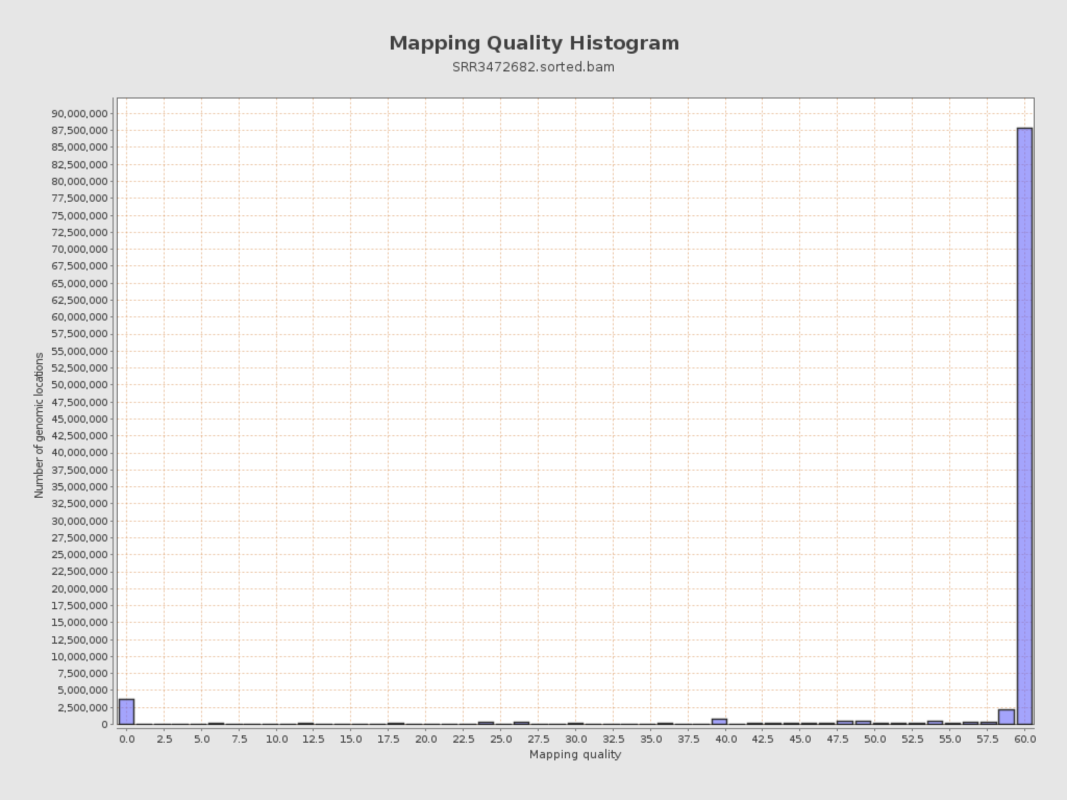
11. Results : Homopolymer Indels



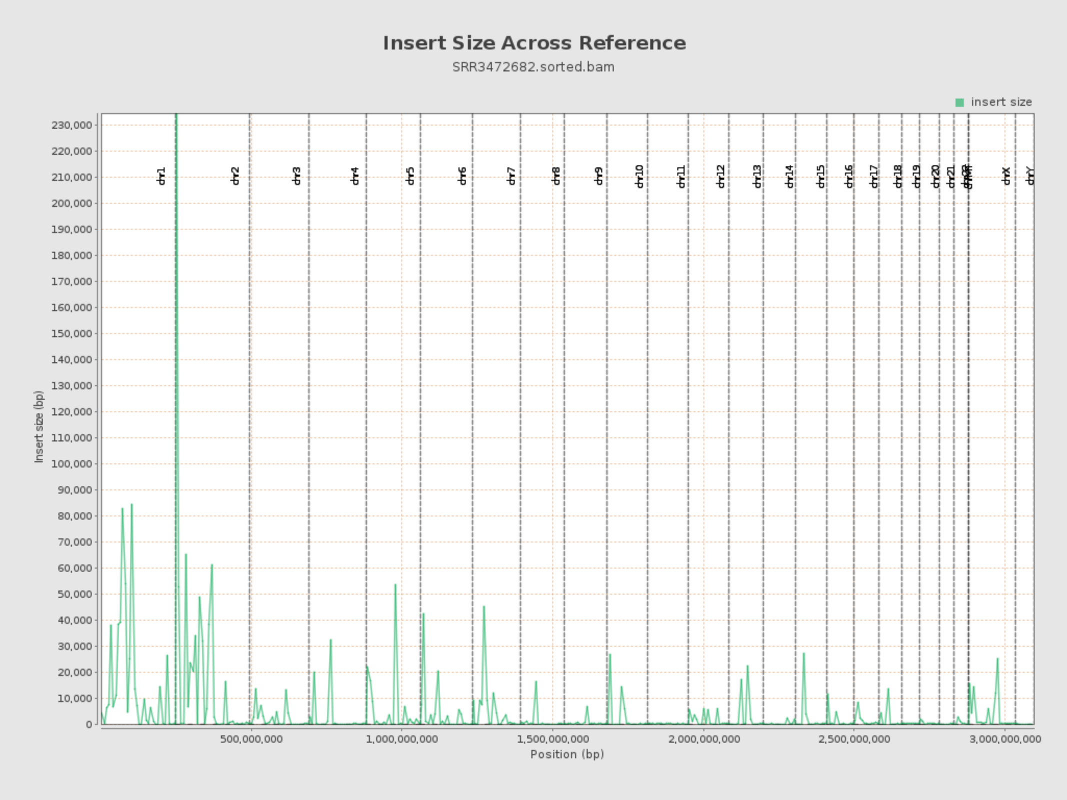
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram