Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 02:42:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472582.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_SRR3472582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472582_1.fastq.gz SRR3472582_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 02:42:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,866,736
Mapped reads	9,735,337 / 89.59%
Unmapped reads	1,131,399 / 10.41%
Mapped paired reads	9,735,337 / 89.59%
Mapped reads, first in pair	4,912,850 / 45.21%
Mapped reads, second in pair	4,822,487 / 44.38%
Mapped reads, both in pair	9,483,228 / 87.27%
Mapped reads, singletons	252,109 / 2.32%
Secondary alignments	0
Supplementary alignments	286,981 / 2.64%
Read min/max/mean length	30 / 100 / 101.03
Duplicated reads (estimated)	1,653,698 / 15.22%
Duplication rate	13.94%
Clipped reads	7,545,404 / 69.44%

2.2. ACGT Content

Number/percentage of A's	201,925,269 / 25.61%
Number/percentage of C's	156,686,859 / 19.88%
Number/percentage of T's	236,003,699 / 29.94%
Number/percentage of G's	193,180,445 / 24.51%
Number/percentage of N's	524,960 / 0.07%

GC Percentage	44.38%

2.3. Coverage

Mean	0.2548
Standard Deviation	3.1482

2.4. Mapping Quality

Mean Mapping Quality	50.29

2.5. Insert size

Mean	219,934.15
Standard Deviation	4,511,219.82
P25/Median/P75	91 / 128 / 174

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	9,642,828
Insertions	76,596
Mapped reads with at least one insertion	0.77%
Deletions	176,375
Mapped reads with at least one deletion	1.77%
Homopolymer indels	41.98%

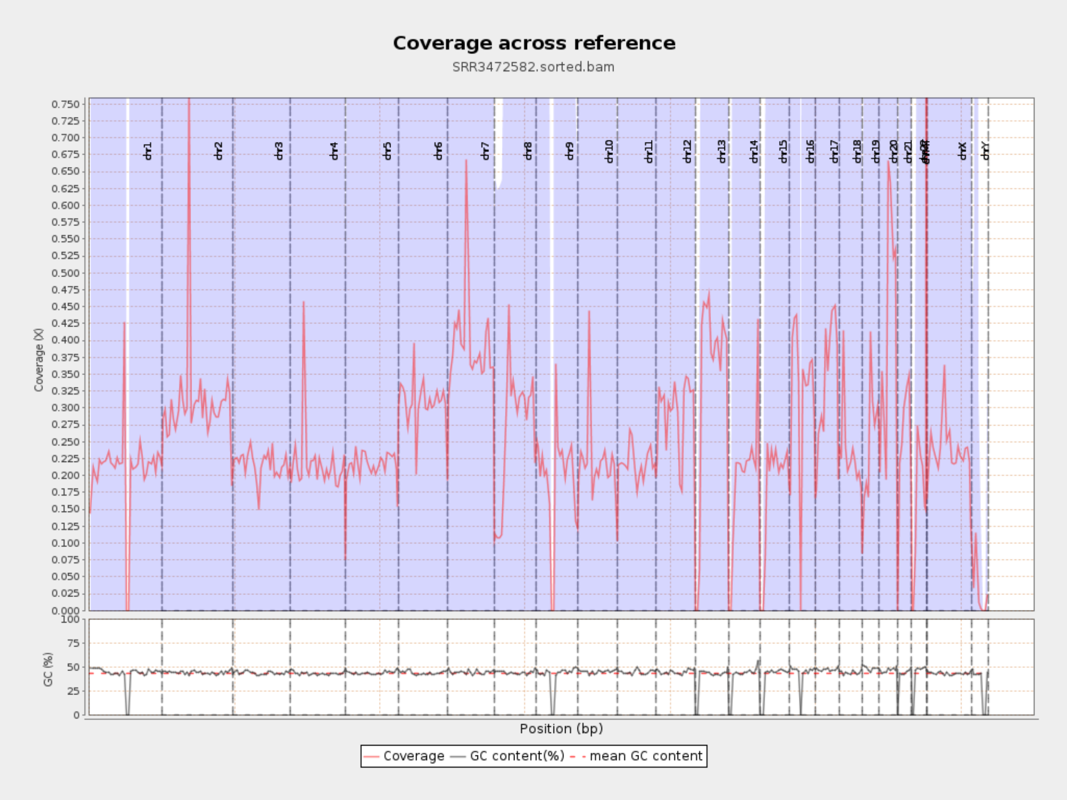
2.7. Chromosome stats

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

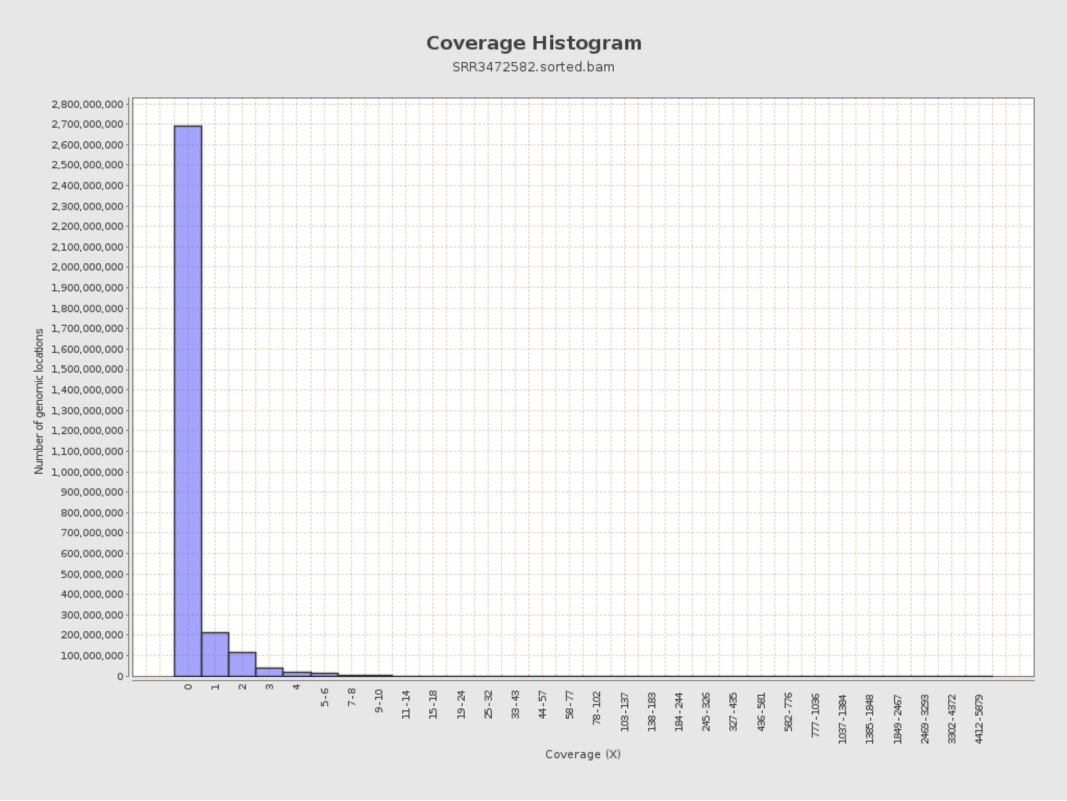
		bases	coverage	deviation
chr1	249250621	51977227	0.2085	3.7592
chr2	243199373	76077777	0.3128	4.1963
chr3	198022430	42756043	0.2159	0.7379
chr4	191154276	41894216	0.2192	1.4954
chr5	180915260	39247822	0.2169	0.8105
chr6	171115067	52754409	0.3083	1.5522
chr7	159138663	64088105	0.4027	4.9177
chr8	146364022	39340724	0.2688	2.5602
chr9	141213431	27698975	0.1961	3.1576
chr10	135534747	30146523	0.2224	2.4825
chr11	135006516	29129071	0.2158	2.0984
chr12	133851895	38935456	0.2909	0.9152
chr13	115169878	39170968	0.3401	0.995
chr14	107349540	21256806	0.198	9.5666
chr15	102531392	18499437	0.1804	0.6958
chr16	90354753	29254426	0.3238	1.4857
chr17	81195210	27515257	0.3389	2.4574
chr18	78077248	18547653	0.2376	5.3673
chr19	59128983	14950787	0.2529	2.6279
chr20	63025520	26652173	0.4229	2.0879
chr21	48129895	12104317	0.2515	1.1036
chr22	51304566	7697923	0.15	0.634
chrMT	16571	54020	3.2599	3.9716
chrX	155270560	37108663	0.239	1.3012

chrY	59373566	1790690	0.0302	1.2

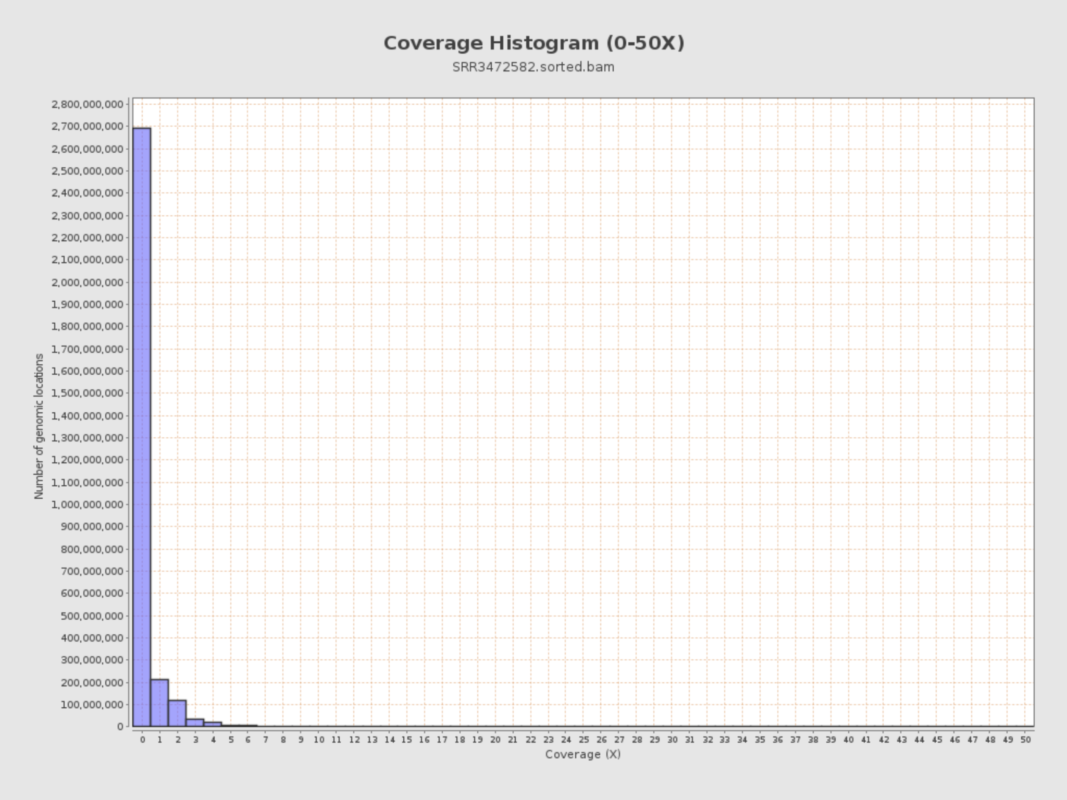
3. Results : Coverage across reference



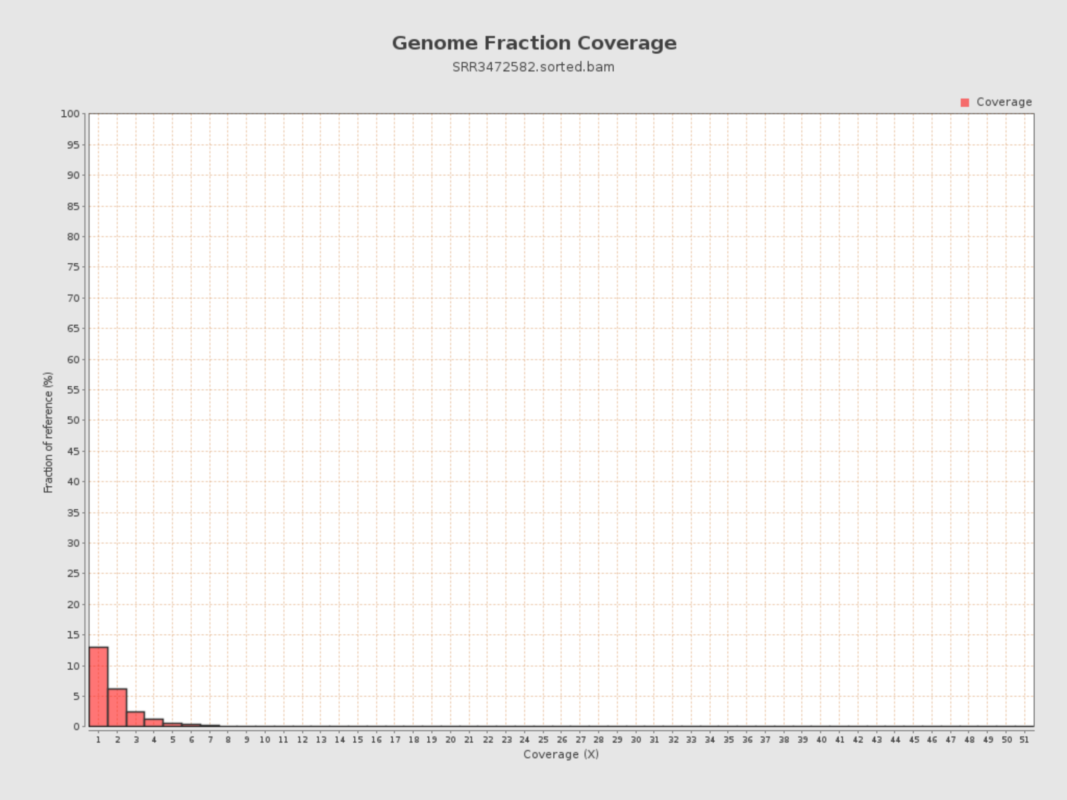
4. Results : Coverage Histogram



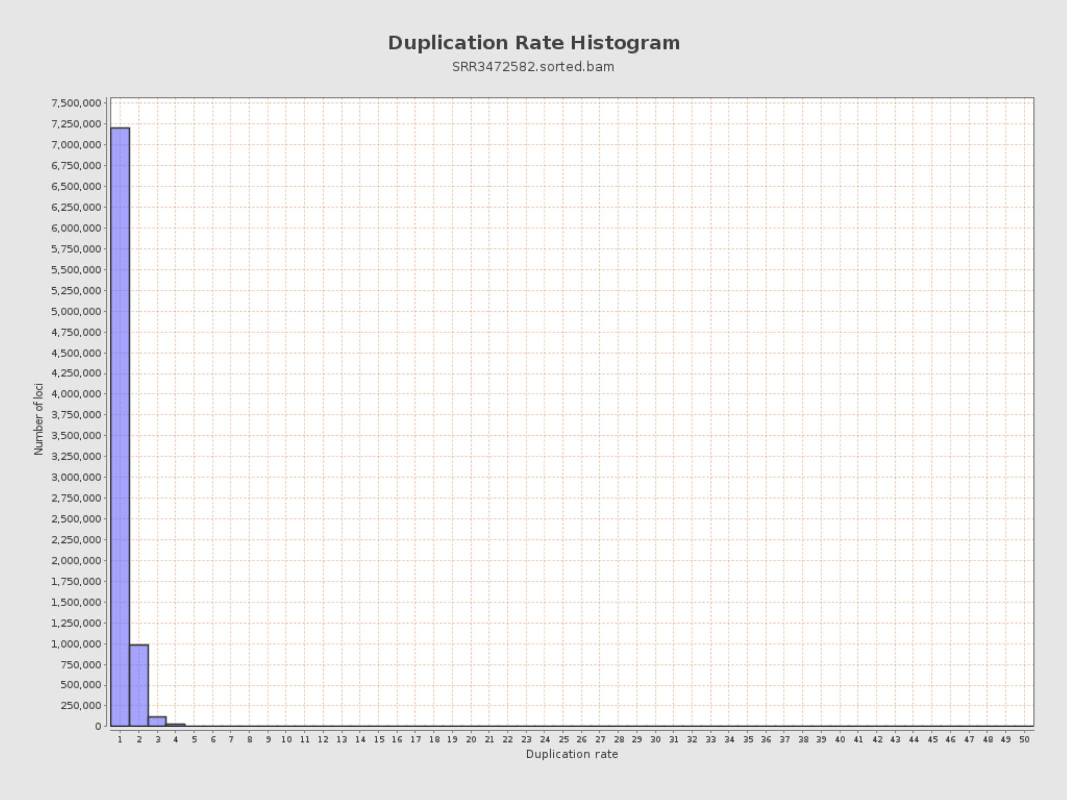
5. Results : Coverage Histogram (0-50X)



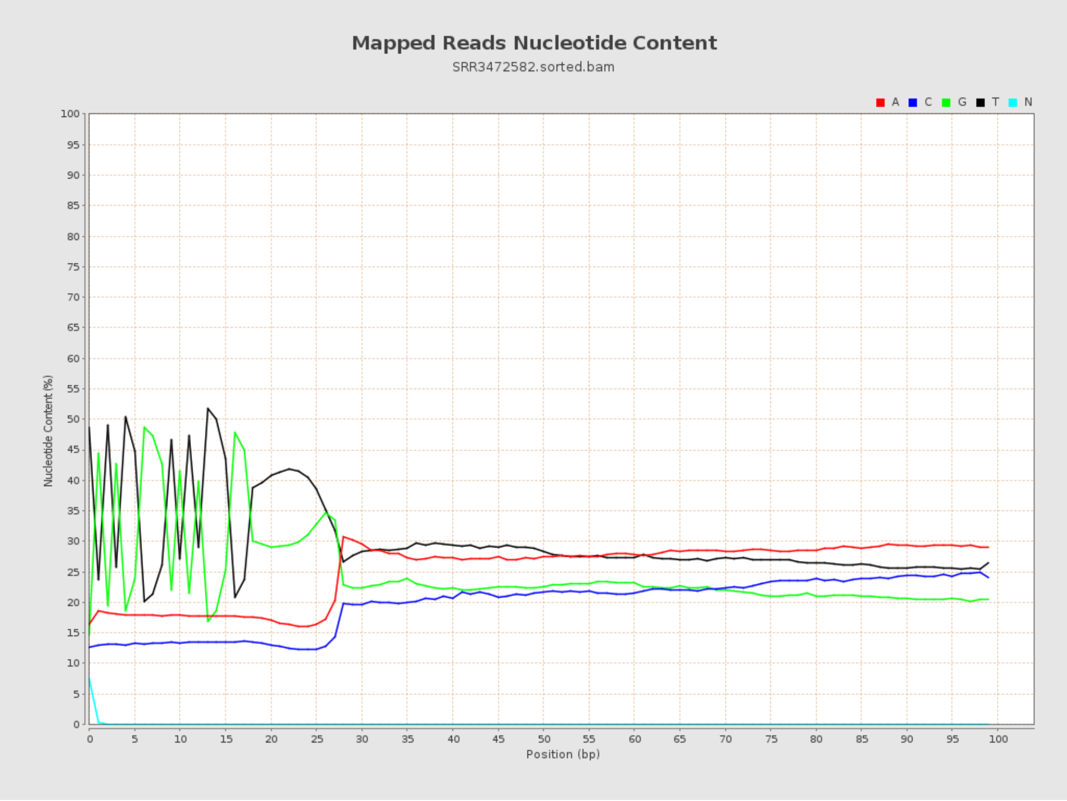
6. Results : Genome Fraction Coverage



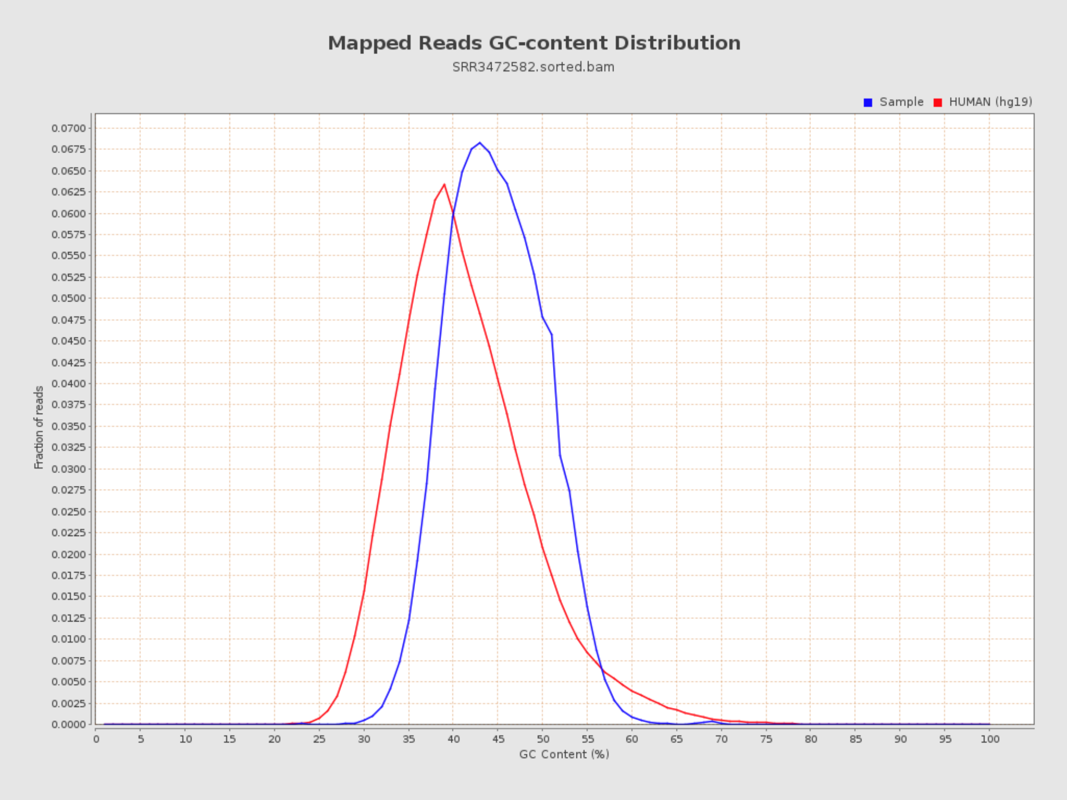
7. Results : Duplication Rate Histogram



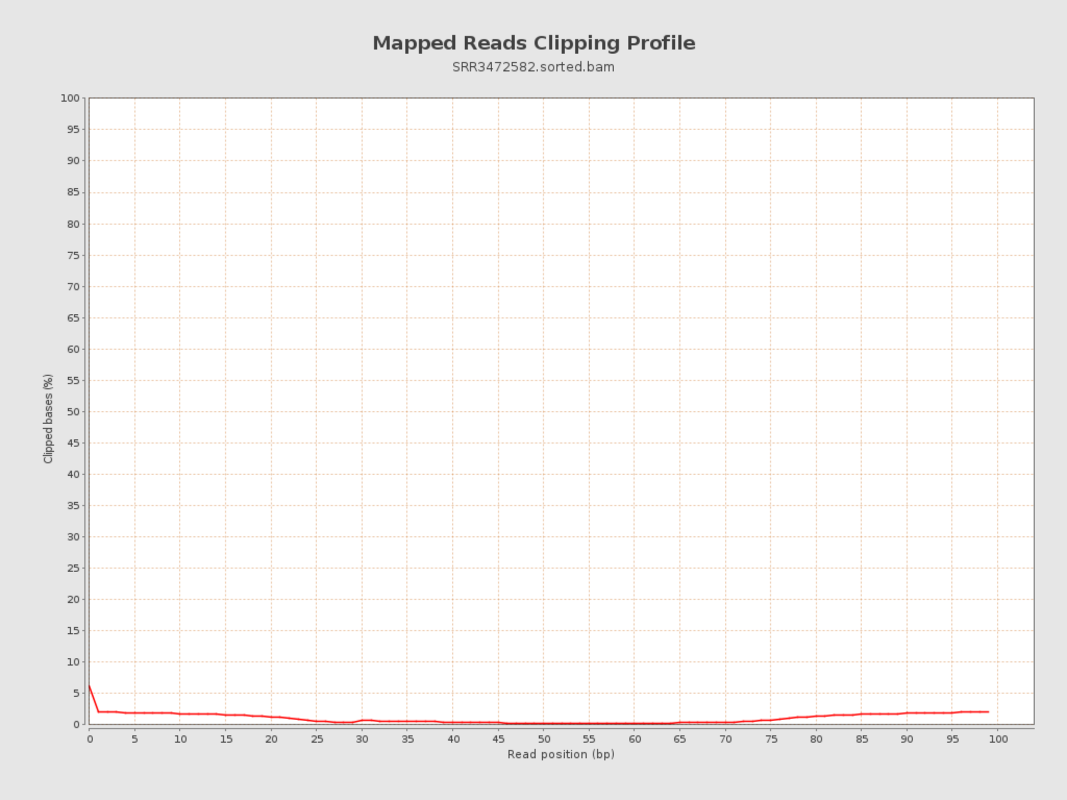
8. Results : Mapped Reads Nucleotide Content



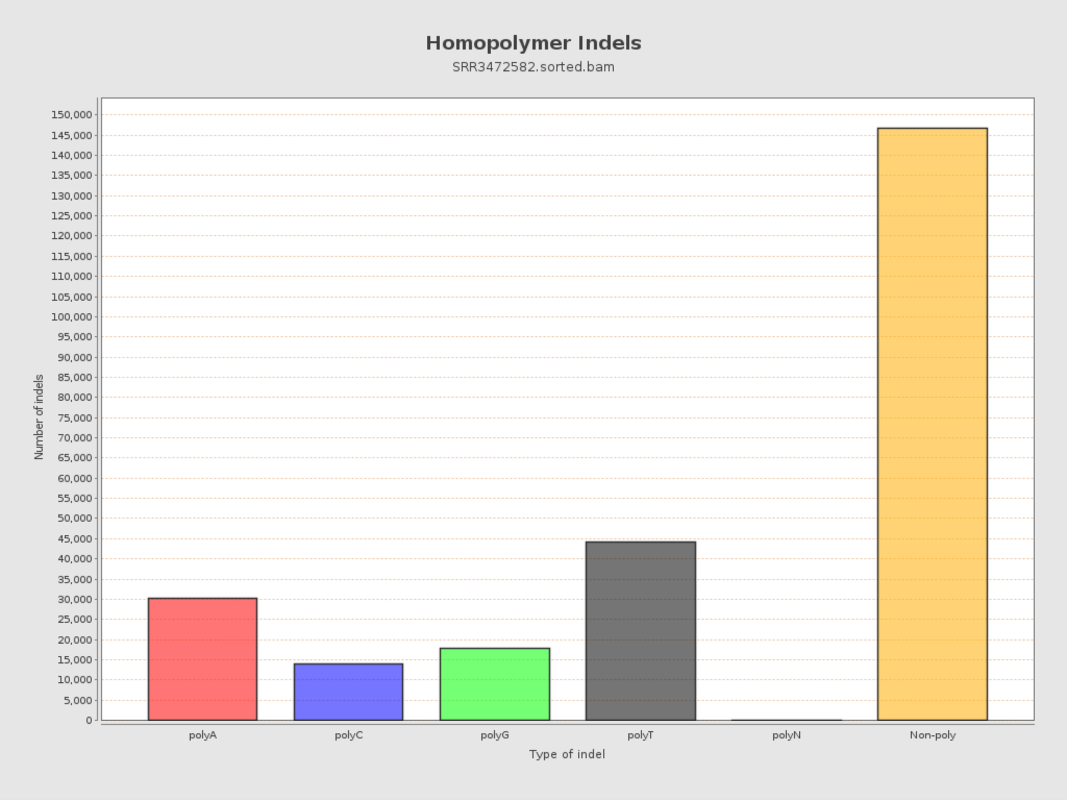
9. Results : Mapped Reads GC-content Distribution



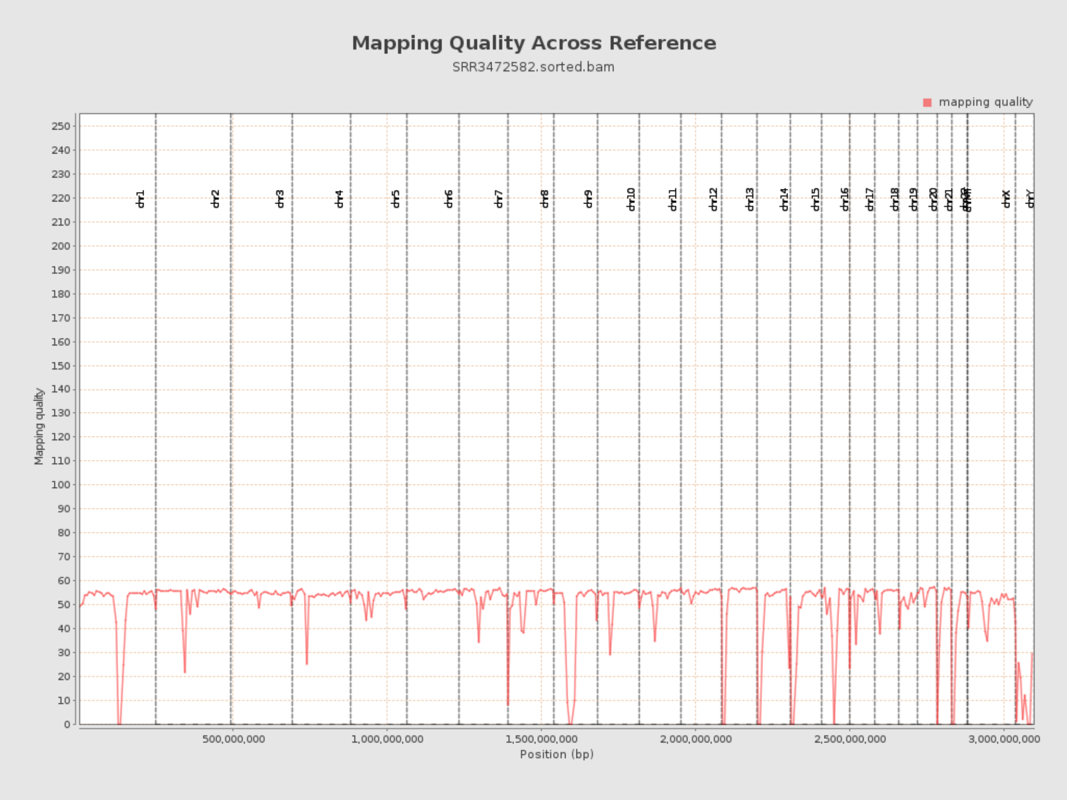
10. Results : Mapped Reads Clipping Profile



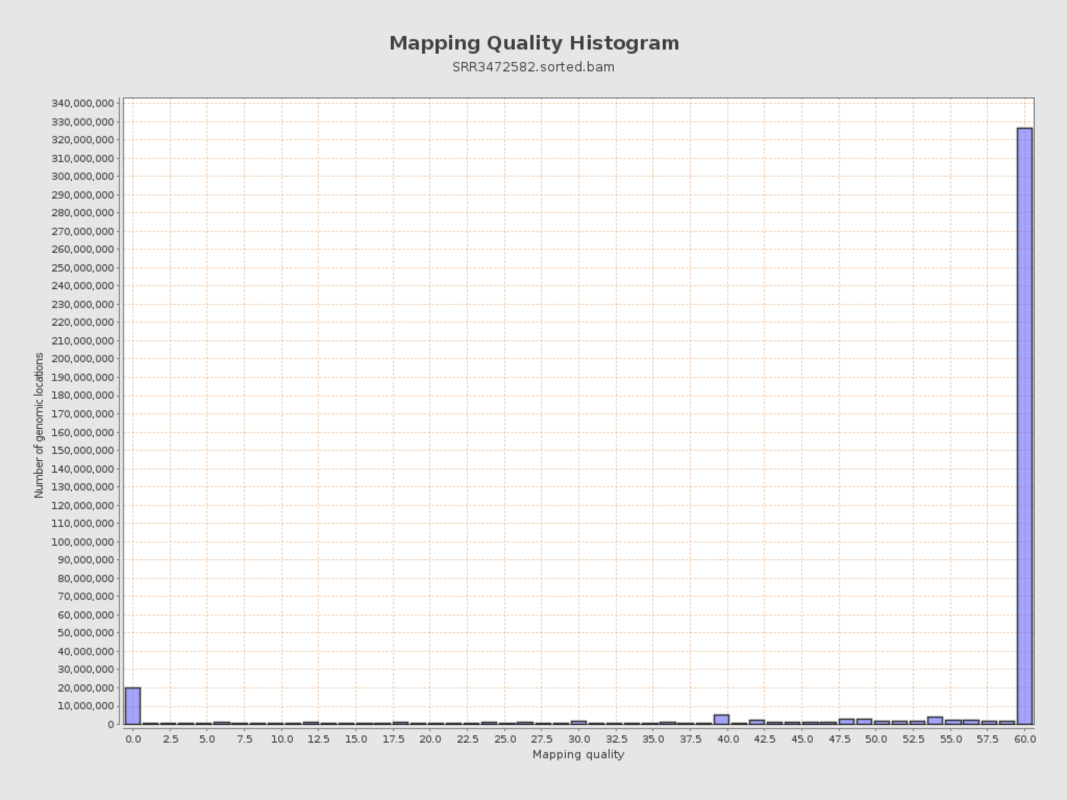
11. Results : Homopolymer Indels



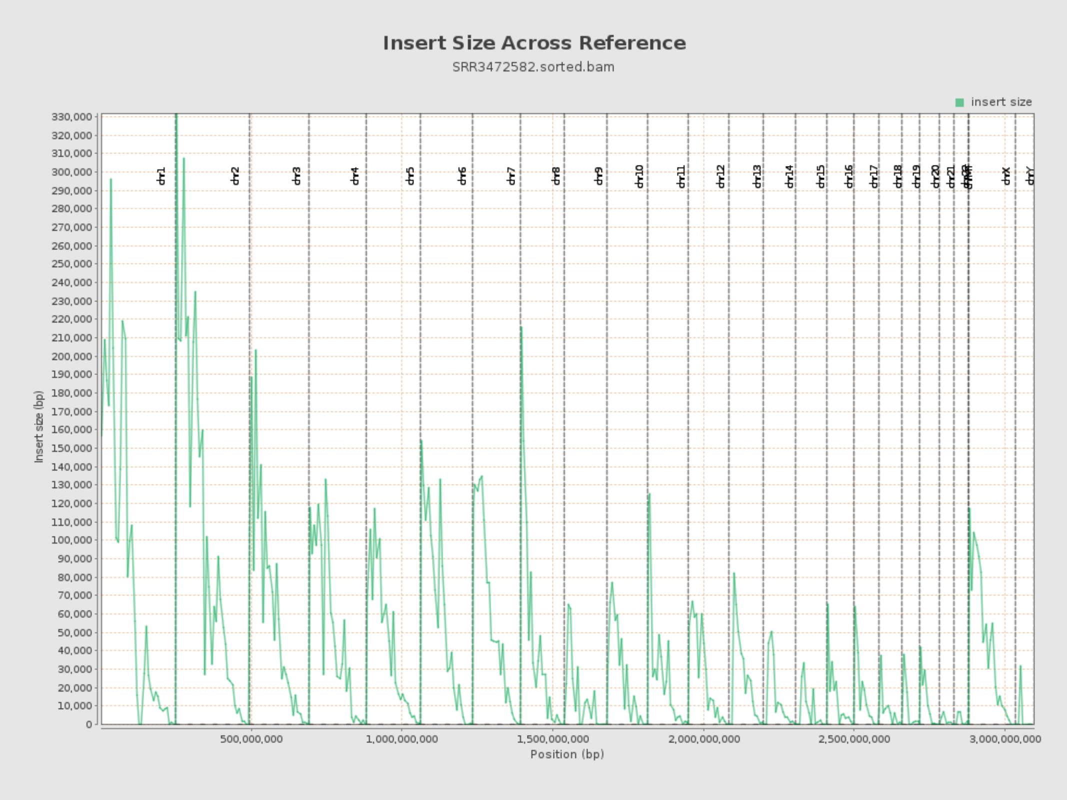
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram