Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:42:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472515.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_SRR3472515 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472515_1.fastq.gz SRR3472515_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:42:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472515.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,748,238
Mapped reads	16,549,842 / 98.82%
Unmapped reads	198,396 / 1.18%
Mapped paired reads	16,549,842 / 98.82%
Mapped reads, first in pair	8,302,851 / 49.57%
Mapped reads, second in pair	8,246,991 / 49.24%
Mapped reads, both in pair	16,445,410 / 98.19%
Mapped reads, singletons	104,432 / 0.62%
Secondary alignments	0
Supplementary alignments	68,337 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,165,100 / 60.69%
Duplication rate	46.29%
Clipped reads	1,525,688 / 9.11%

2.2. ACGT Content

Number/percentage of A's	450,669,184 / 27.73%
Number/percentage of C's	364,790,436 / 22.44%
Number/percentage of T's	448,200,848 / 27.58%
Number/percentage of G's	361,457,294 / 22.24%
Number/percentage of N's	252,479 / 0.02%

GC Percentage	44.68%

2.3. Coverage

Mean	0.5251
Standard Deviation	17.0968

2.4. Mapping Quality

Mean Mapping Quality	55.2

2.5. Insert size

Mean	29,699.01
Standard Deviation	1,663,090.05
P25/Median/P75	164 / 232 / 316

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,799,475
Insertions	86,392
Mapped reads with at least one insertion	0.52%
Deletions	78,737
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.24%

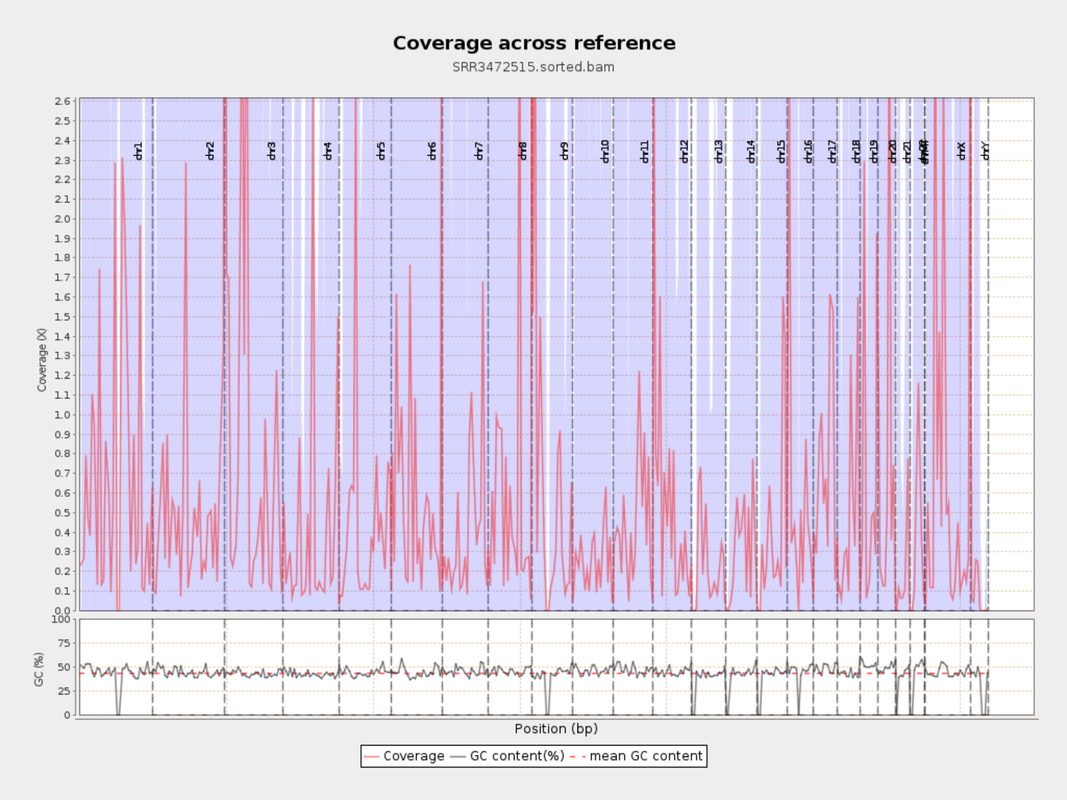
2.7. Chromosome stats

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

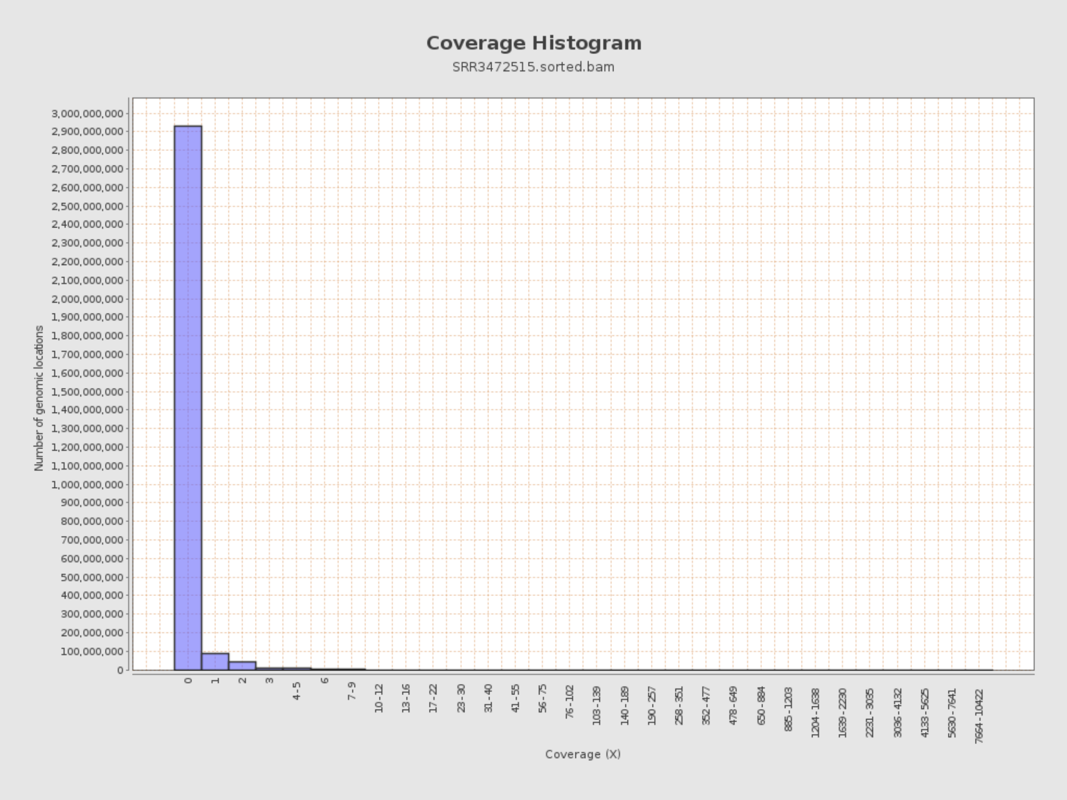
		bases	coverage	deviation
chr1	249250621	175017796	0.7022	24.0863
chr2	243199373	118248155	0.4862	15.2593
chr3	198022430	186217200	0.9404	19.536
chr4	191154276	75947160	0.3973	16.0585
chr5	180915260	80168163	0.4431	13.4103
chr6	171115067	98534589	0.5758	16.0904
chr7	159138663	66192008	0.4159	12.4966
chr8	146364022	82965912	0.5668	20.9208
chr9	141213431	94990789	0.6727	16.0767
chr10	135534747	34960236	0.2579	7.7383
chr11	135006516	61192223	0.4533	13.0169
chr12	133851895	79294558	0.5924	20.709
chr13	115169878	27470886	0.2385	8.0065
chr14	107349540	32935423	0.3068	10.7081
chr15	102531392	42300990	0.4126	13.4448
chr16	90354753	51001751	0.5645	17.1426
chr17	81195210	58956312	0.7261	17.0091
chr18	78077248	38678244	0.4954	17.1157
chr19	59128983	35885783	0.6069	18.1654
chr20	63025520	48088736	0.763	24.0725
chr21	48129895	9161462	0.1903	7.7373
chr22	51304566	18399013	0.3586	12.7187
chrMT	16571	945	0.057	0.3087
chrX	155270560	104227746	0.6713	26.4729

chrY	59373566	4724400	0.0796	3.7726

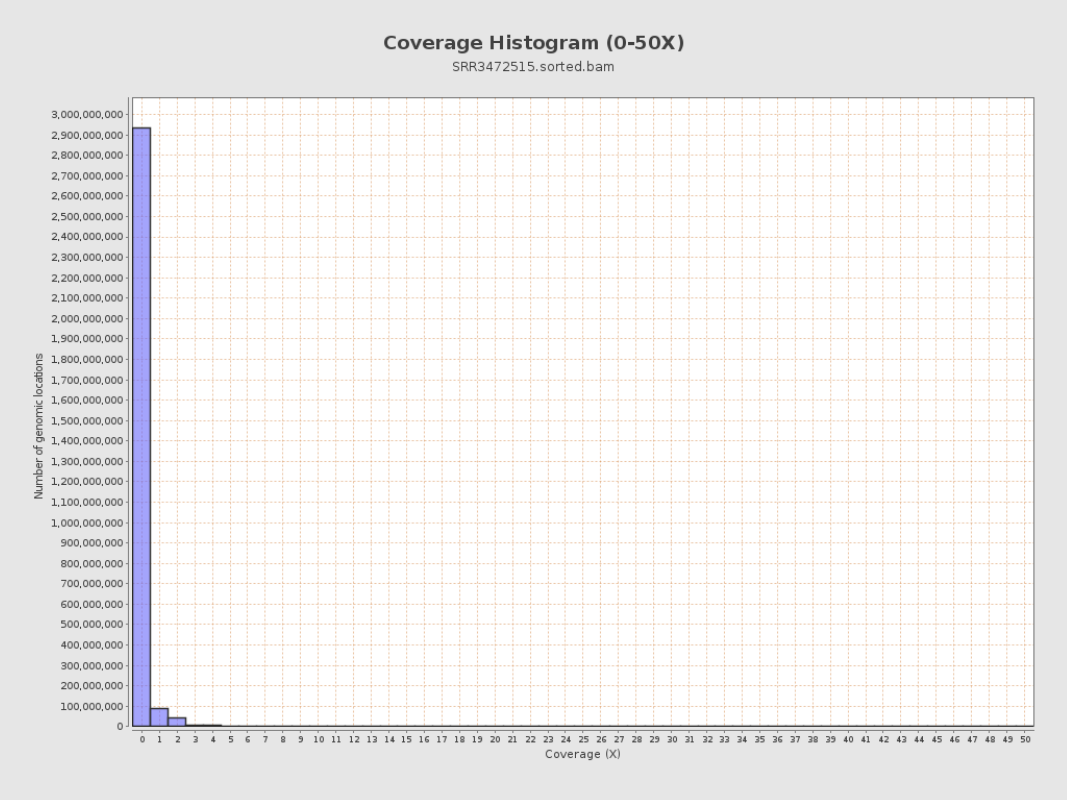
3. Results : Coverage across reference



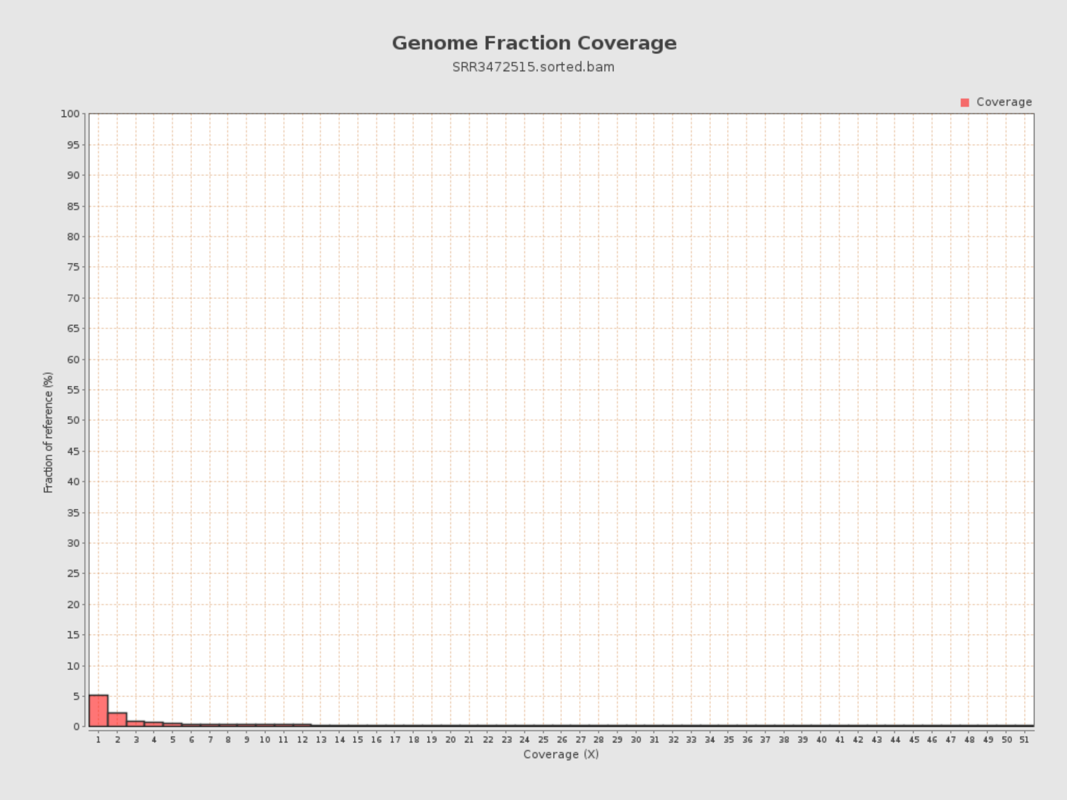
4. Results : Coverage Histogram



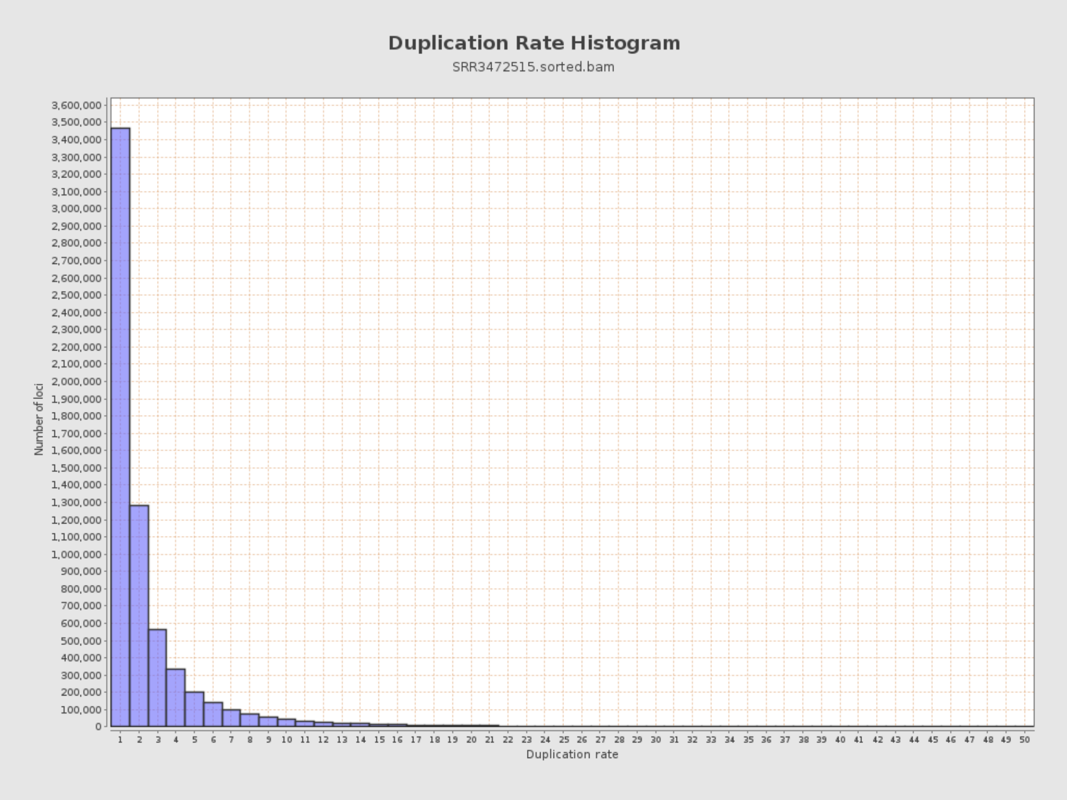
5. Results : Coverage Histogram (0-50X)



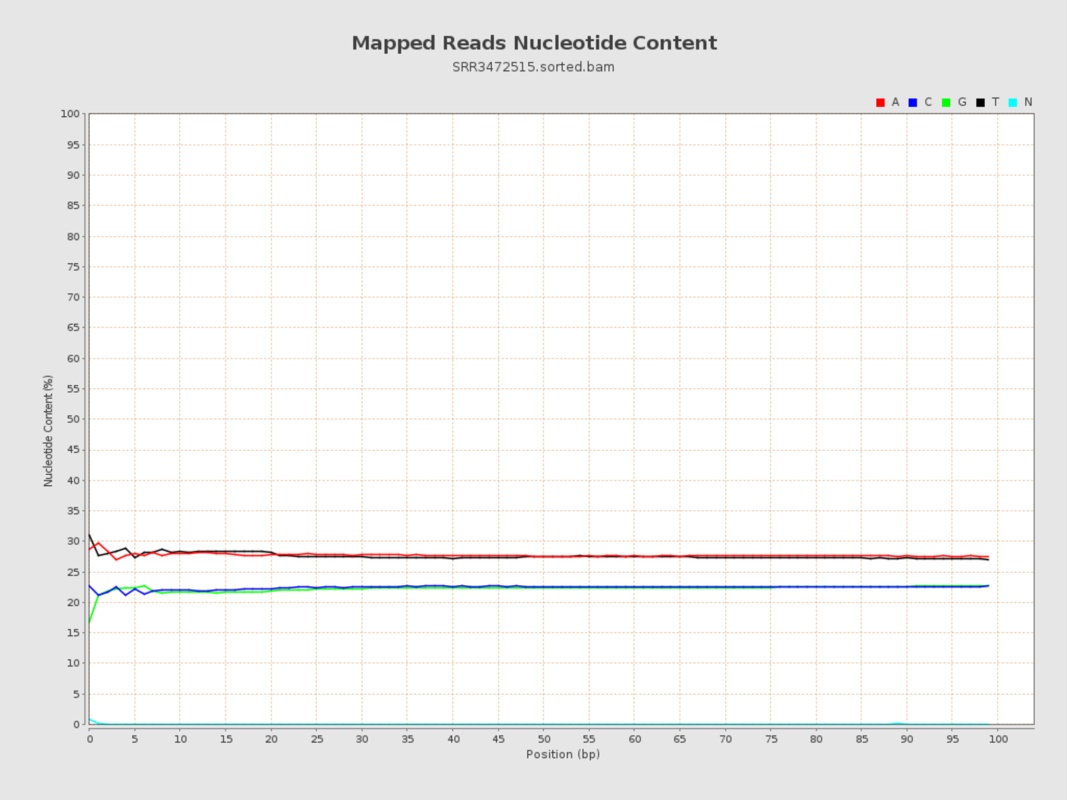
6. Results : Genome Fraction Coverage



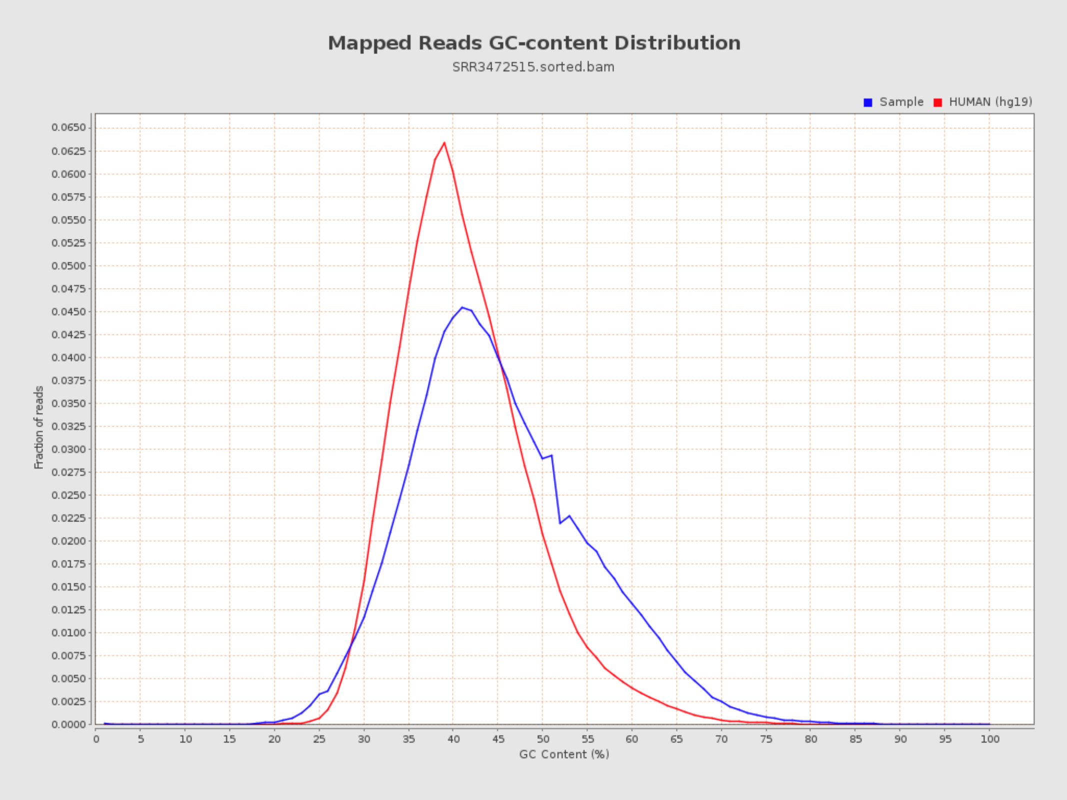
7. Results : Duplication Rate Histogram



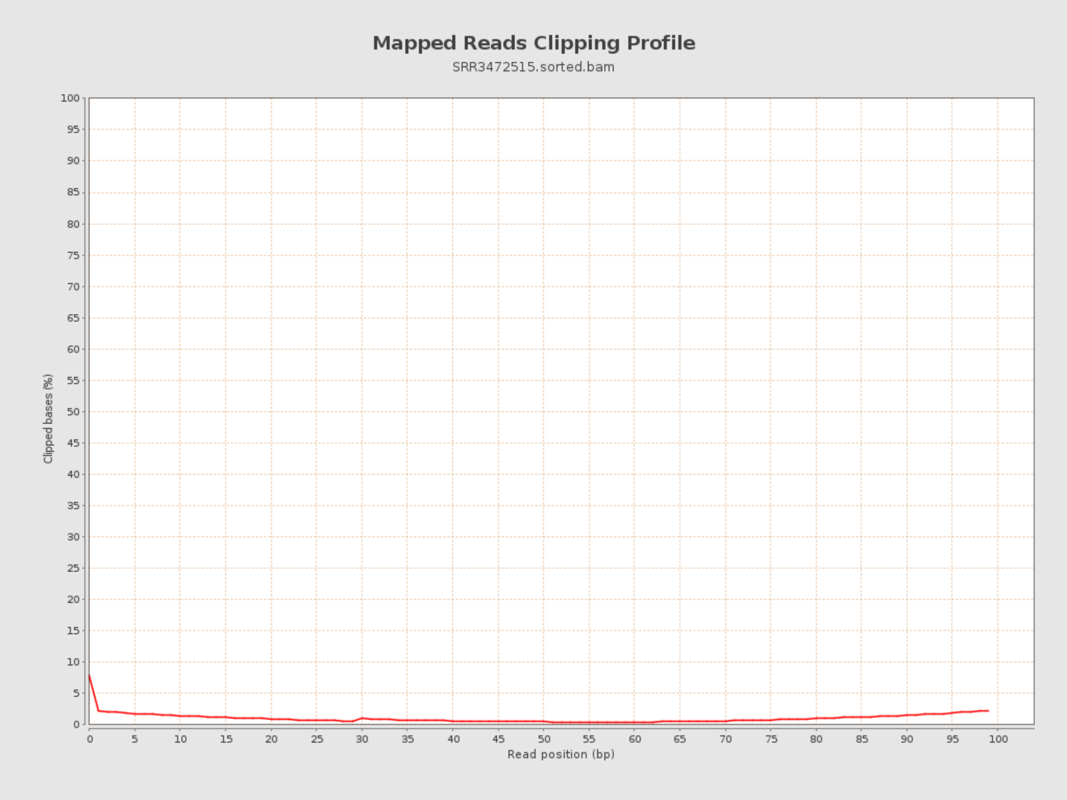
8. Results : Mapped Reads Nucleotide Content



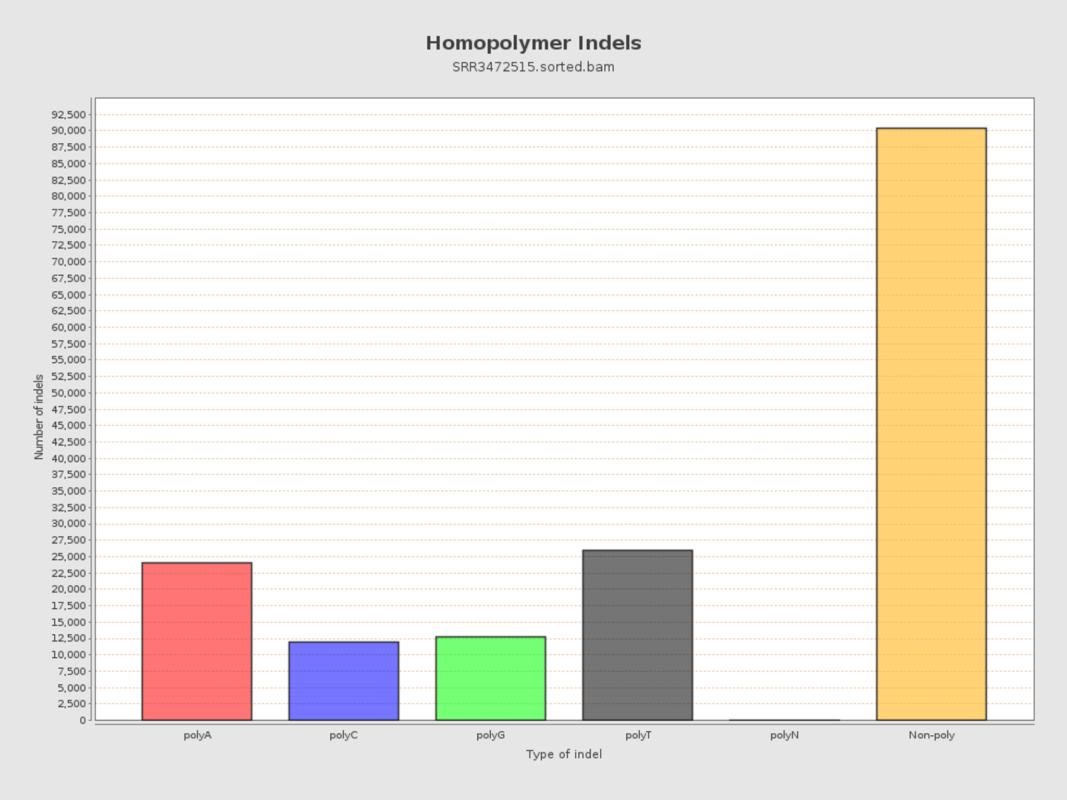
9. Results : Mapped Reads GC-content Distribution



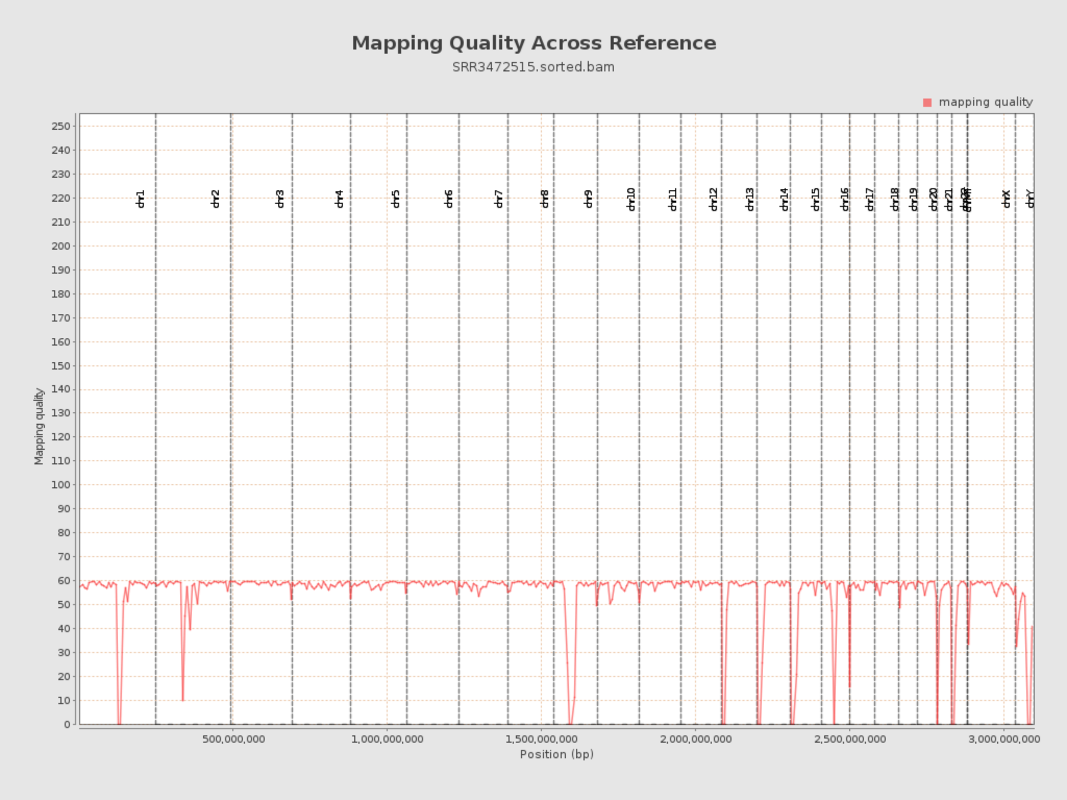
10. Results : Mapped Reads Clipping Profile



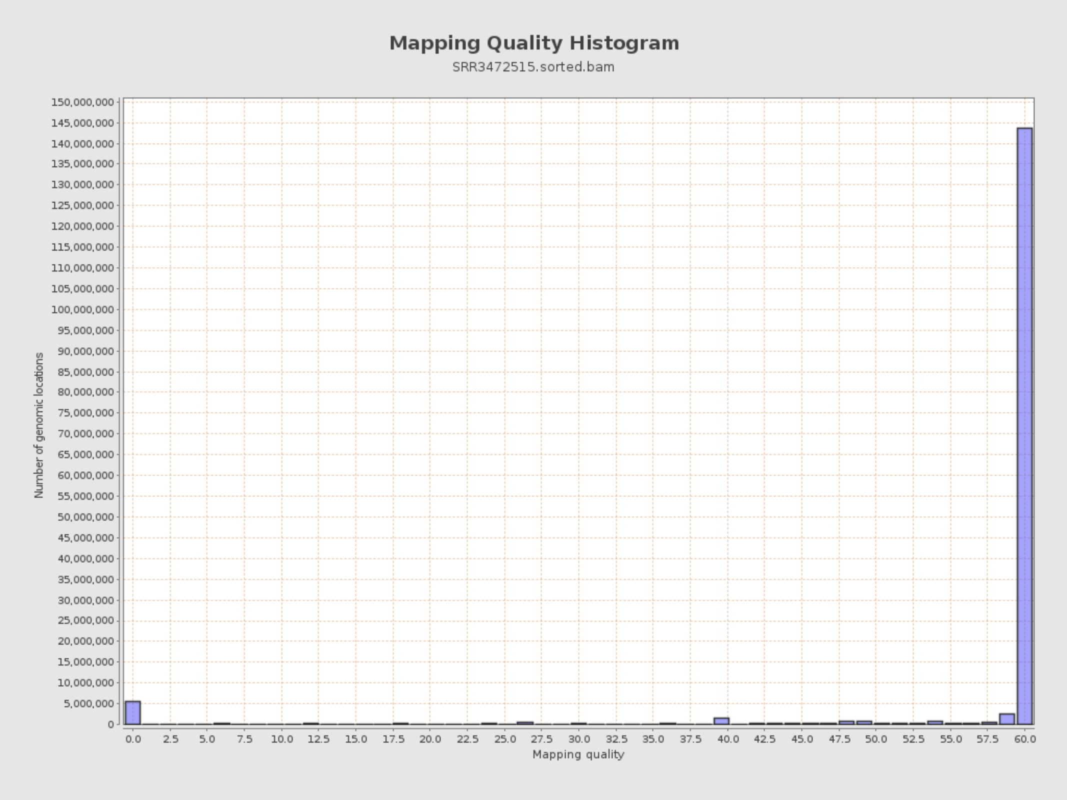
11. Results : Homopolymer Indels



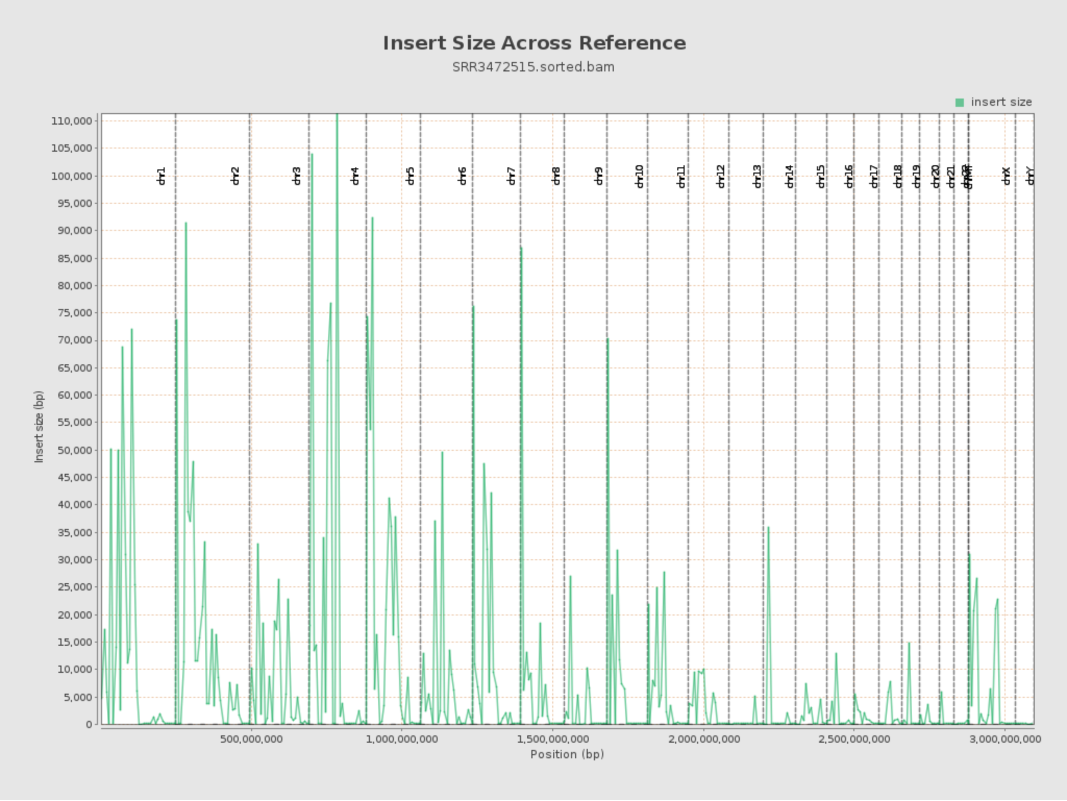
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram