Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472401.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_SRR3472401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472401_1.fastq.gz SRR3472401_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:55:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,625,970
Mapped reads	19,475,637 / 99.23%
Unmapped reads	150,333 / 0.77%
Mapped paired reads	19,475,637 / 99.23%
Mapped reads, first in pair	9,766,967 / 49.77%
Mapped reads, second in pair	9,708,670 / 49.47%
Mapped reads, both in pair	19,379,500 / 98.74%
Mapped reads, singletons	96,137 / 0.49%
Secondary alignments	0
Supplementary alignments	77,279 / 0.39%
Read min/max/mean length	30 / 100 / 99.44
Duplicated reads (estimated)	12,697,930 / 64.7%
Duplication rate	48.56%
Clipped reads	1,347,503 / 6.87%

2.2. ACGT Content

Number/percentage of A's	515,206,679 / 26.95%
Number/percentage of C's	441,685,309 / 23.11%
Number/percentage of T's	516,351,995 / 27.01%
Number/percentage of G's	438,154,408 / 22.92%
Number/percentage of N's	242,551 / 0.01%

GC Percentage	46.03%

2.3. Coverage

Mean	0.6176
Standard Deviation	19.9739

2.4. Mapping Quality

Mean Mapping Quality	55.08

2.5. Insert size

Mean	17,076.48
Standard Deviation	1,300,333.07
P25/Median/P75	156 / 216 / 290

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	10,303,309
Insertions	116,440
Mapped reads with at least one insertion	0.59%
Deletions	100,108
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.29%

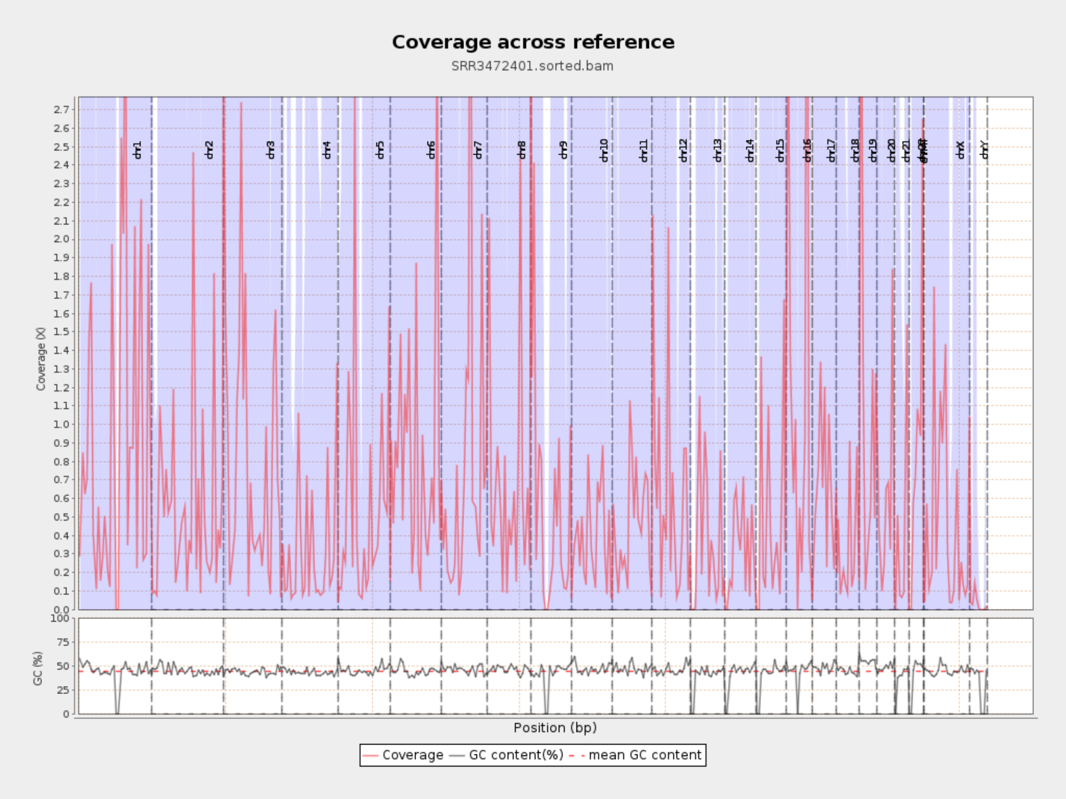
2.7. Chromosome stats

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

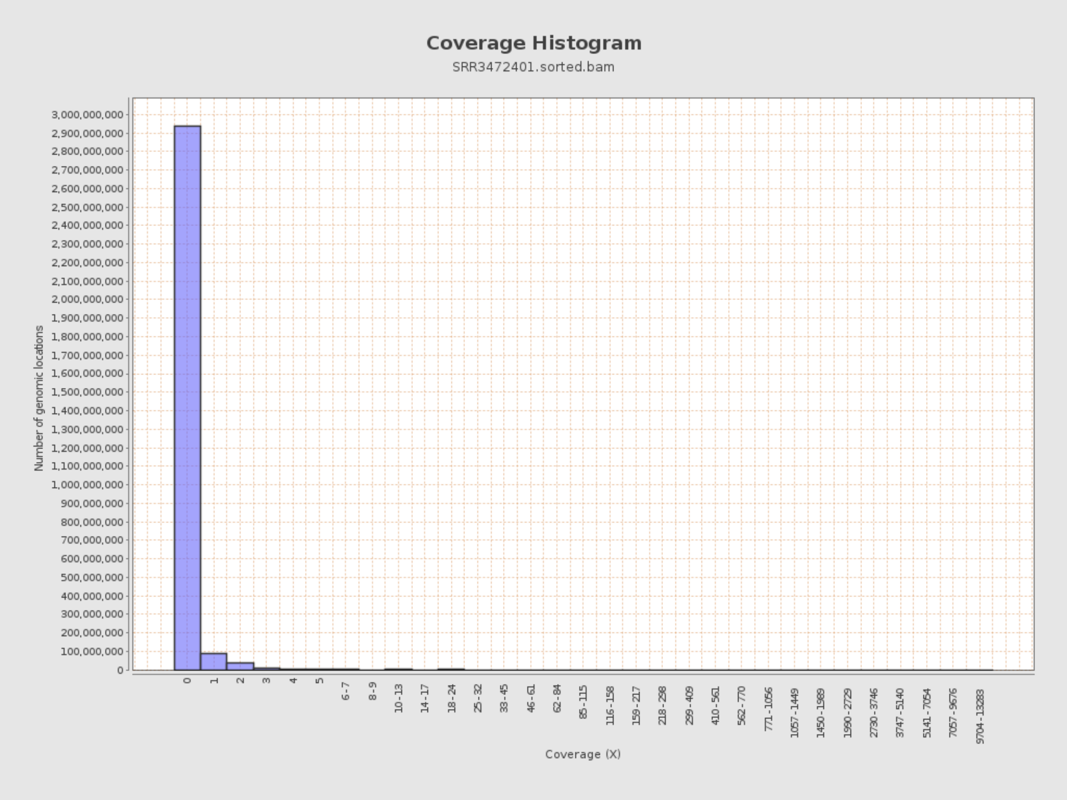
		bases	coverage	deviation
chr1	249250621	239437559	0.9606	26.8979
chr2	243199373	133080340	0.5472	17.0833
chr3	198022430	162986599	0.8231	19.3046
chr4	191154276	59971628	0.3137	11.4461
chr5	180915260	104616014	0.5783	16.9564
chr6	171115067	143036753	0.8359	20.0908
chr7	159138663	126491606	0.7949	25.9065
chr8	146364022	98148642	0.6706	18.114
chr9	141213431	79932879	0.566	13.9868
chr10	135534747	52056992	0.3841	13.769
chr11	135006516	64921825	0.4809	13.7853
chr12	133851895	88001235	0.6575	19.3218
chr13	115169878	42870728	0.3722	13.4682
chr14	107349540	33948781	0.3162	10.8194
chr15	102531392	50264940	0.4902	17.9921
chr16	90354753	109316887	1.2099	36.386
chr17	81195210	54474050	0.6709	13.7457
chr18	78077248	26809132	0.3434	11.5965
chr19	59128983	65133148	1.1015	46.8325
chr20	63025520	37753381	0.599	19.3818
chr21	48129895	18744802	0.3895	20.8217
chr22	51304566	46240153	0.9013	32.2479
chrMT	16571	7358	0.444	0.8406
chrX	155270560	71524976	0.4606	16.0245

chrY	59373566	2103729	0.0354	2.196

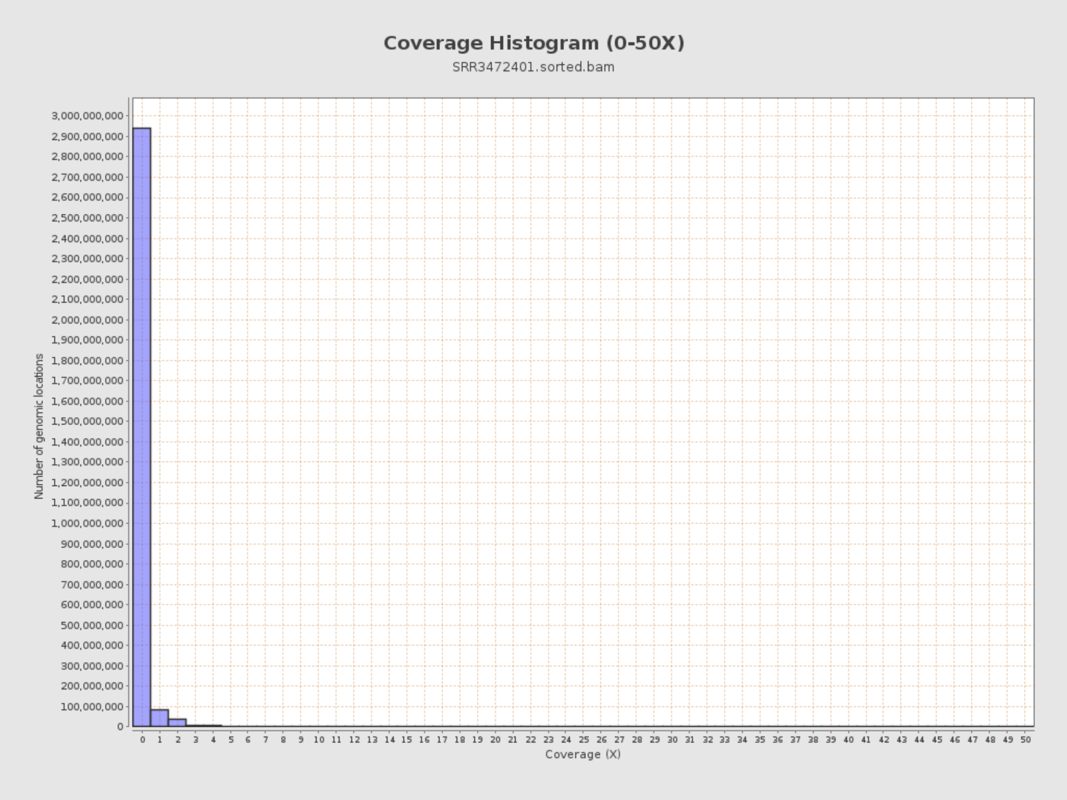
3. Results : Coverage across reference



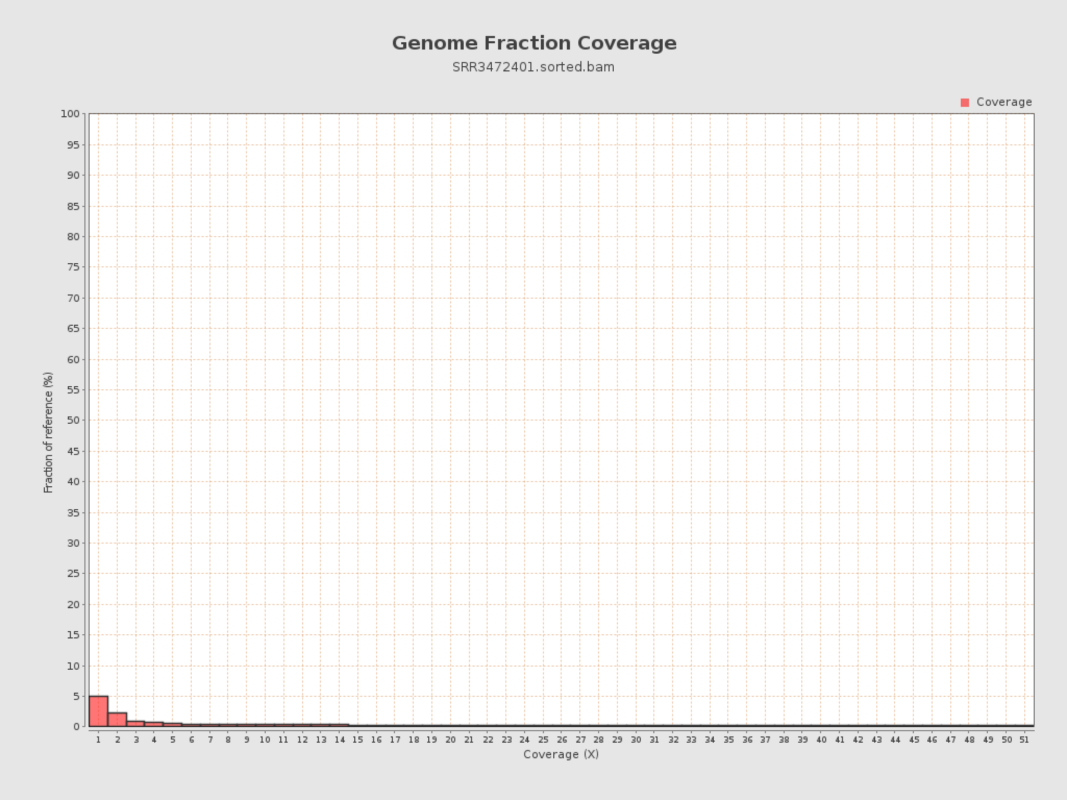
4. Results : Coverage Histogram



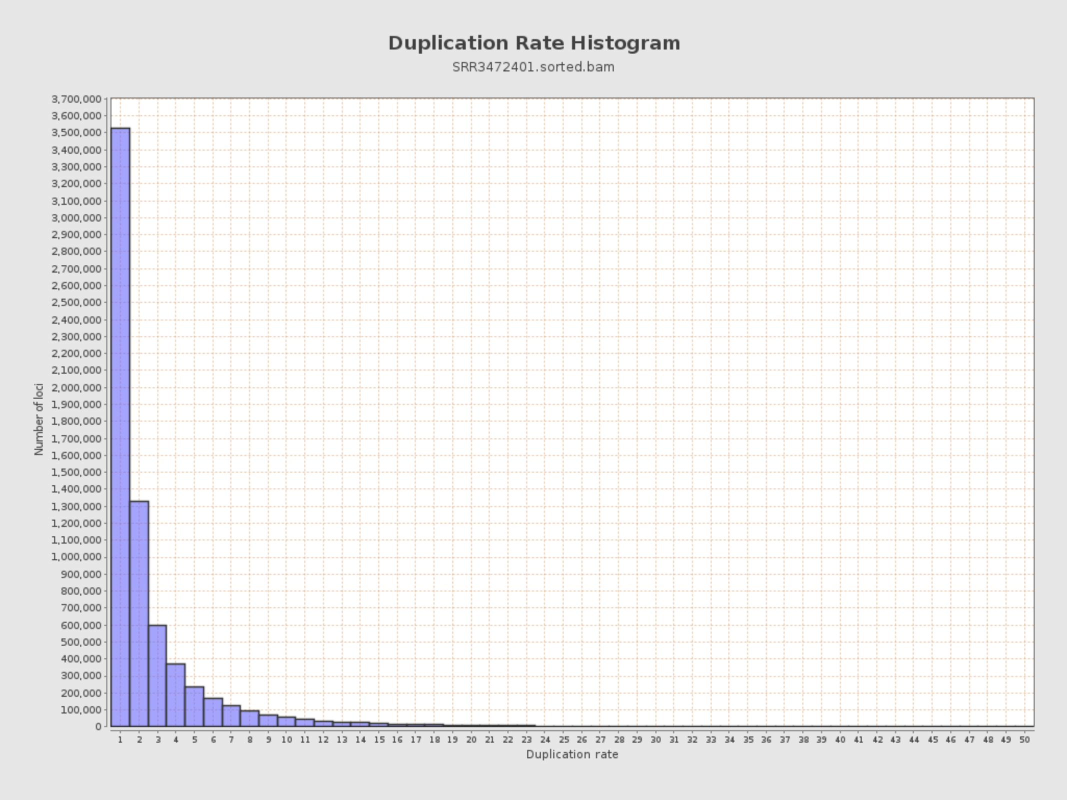
5. Results : Coverage Histogram (0-50X)



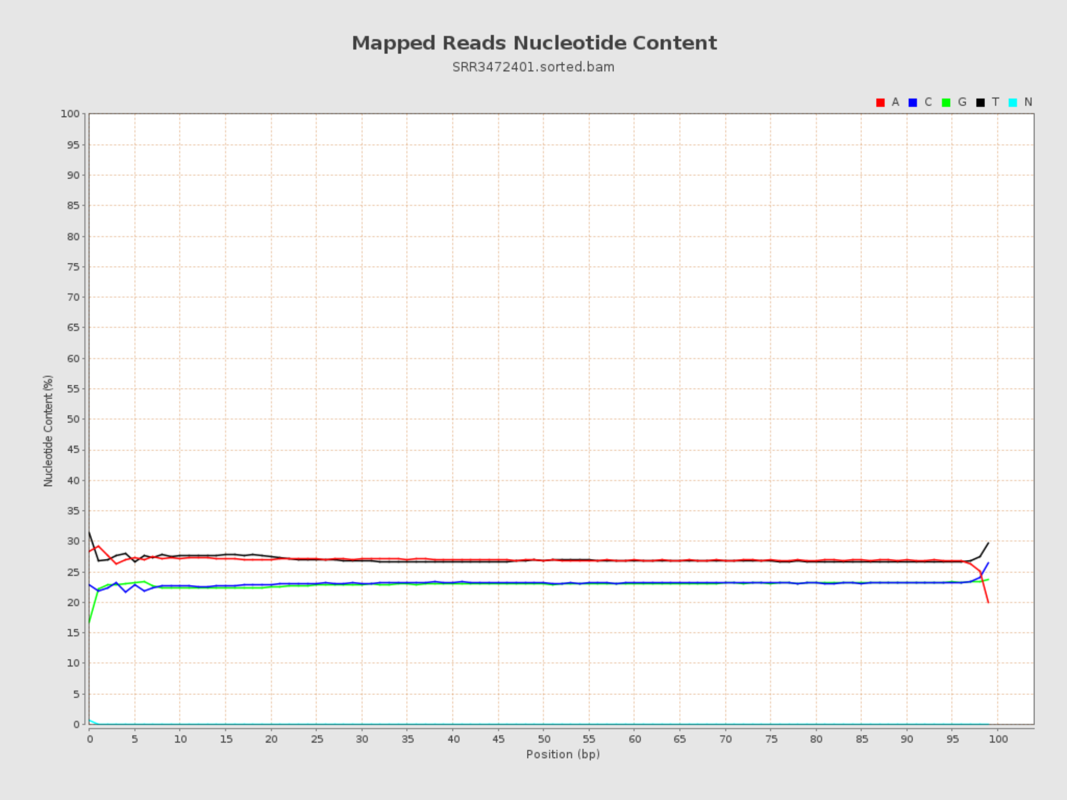
6. Results : Genome Fraction Coverage



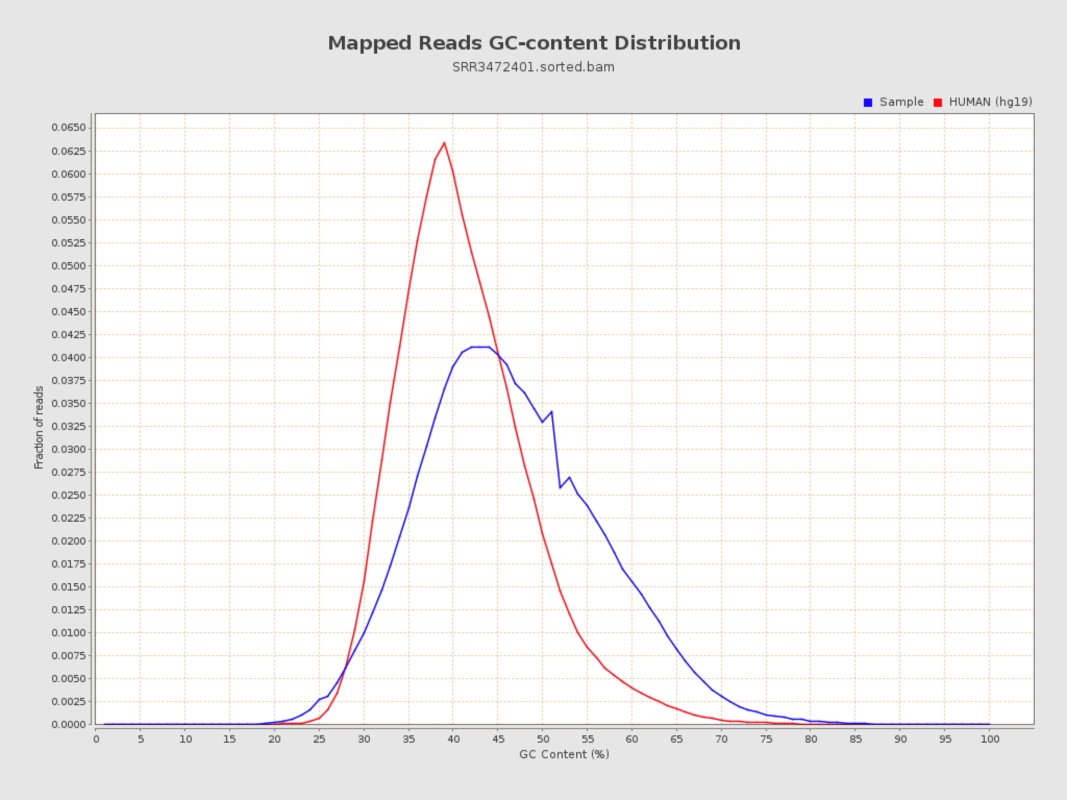
7. Results : Duplication Rate Histogram



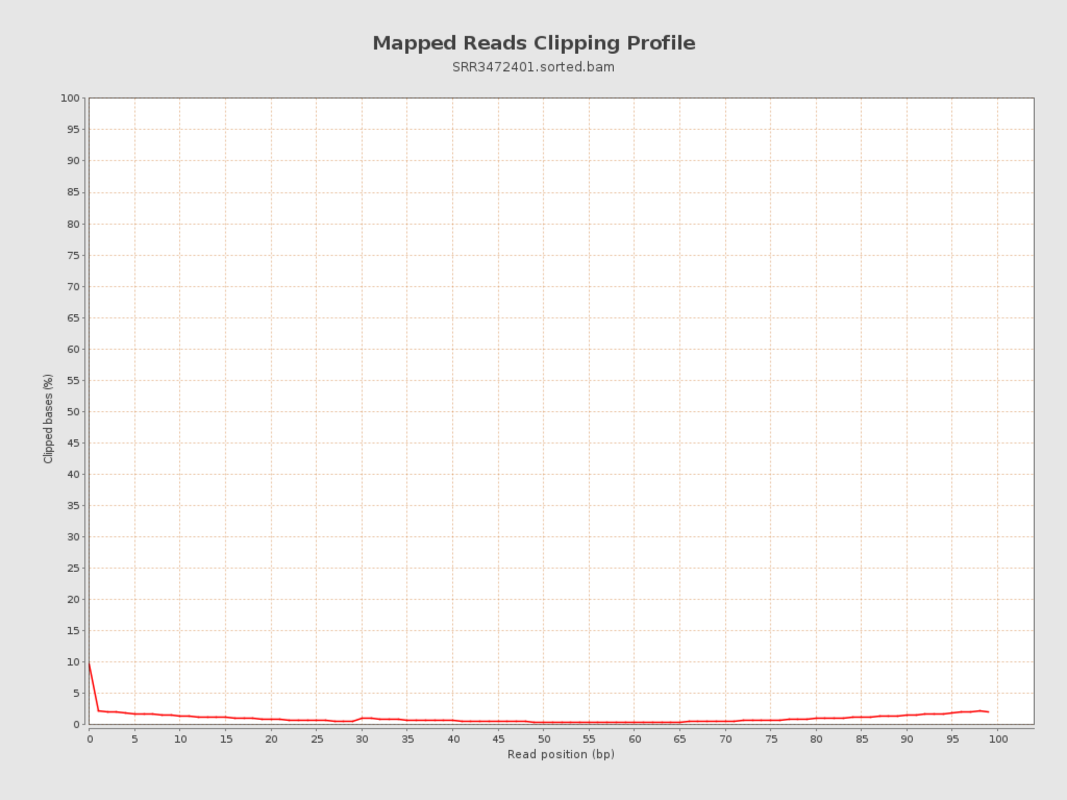
8. Results : Mapped Reads Nucleotide Content



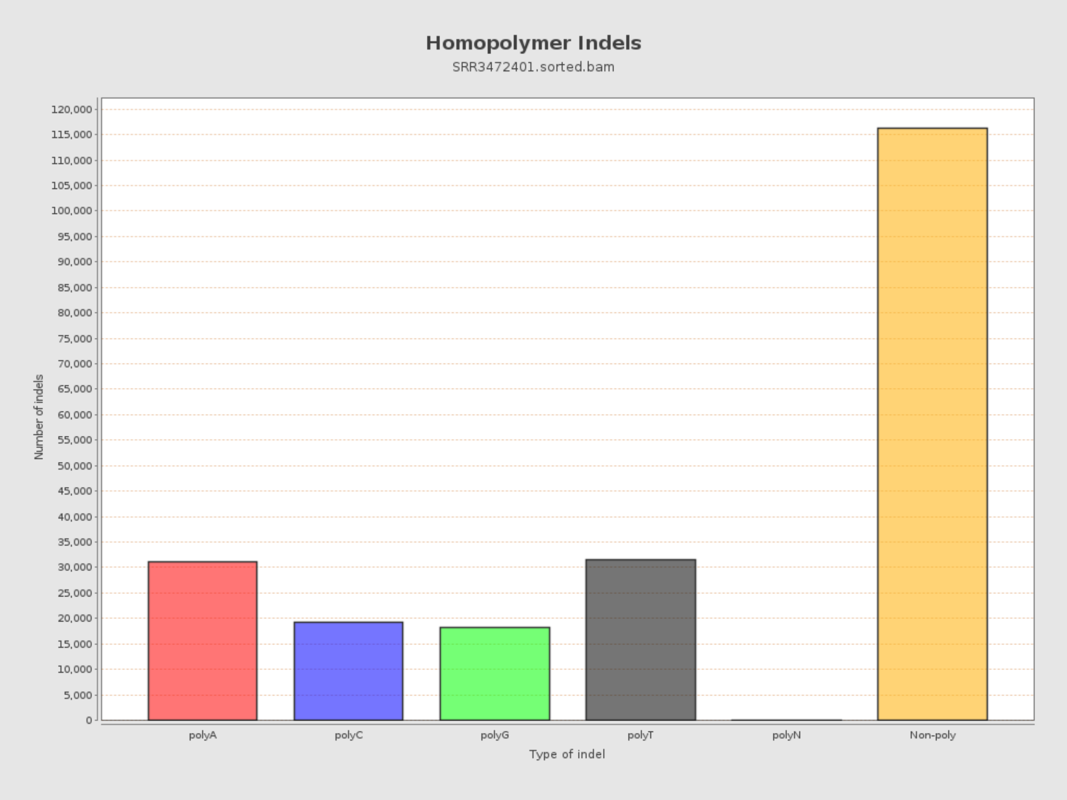
9. Results : Mapped Reads GC-content Distribution



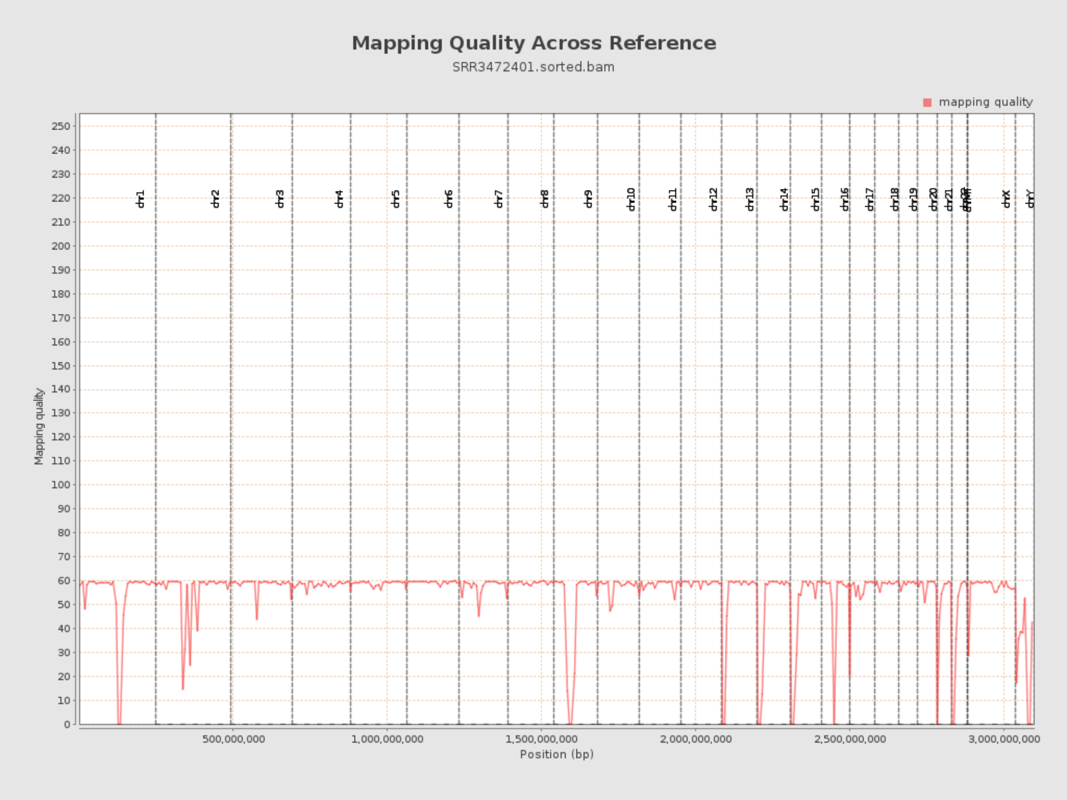
10. Results : Mapped Reads Clipping Profile



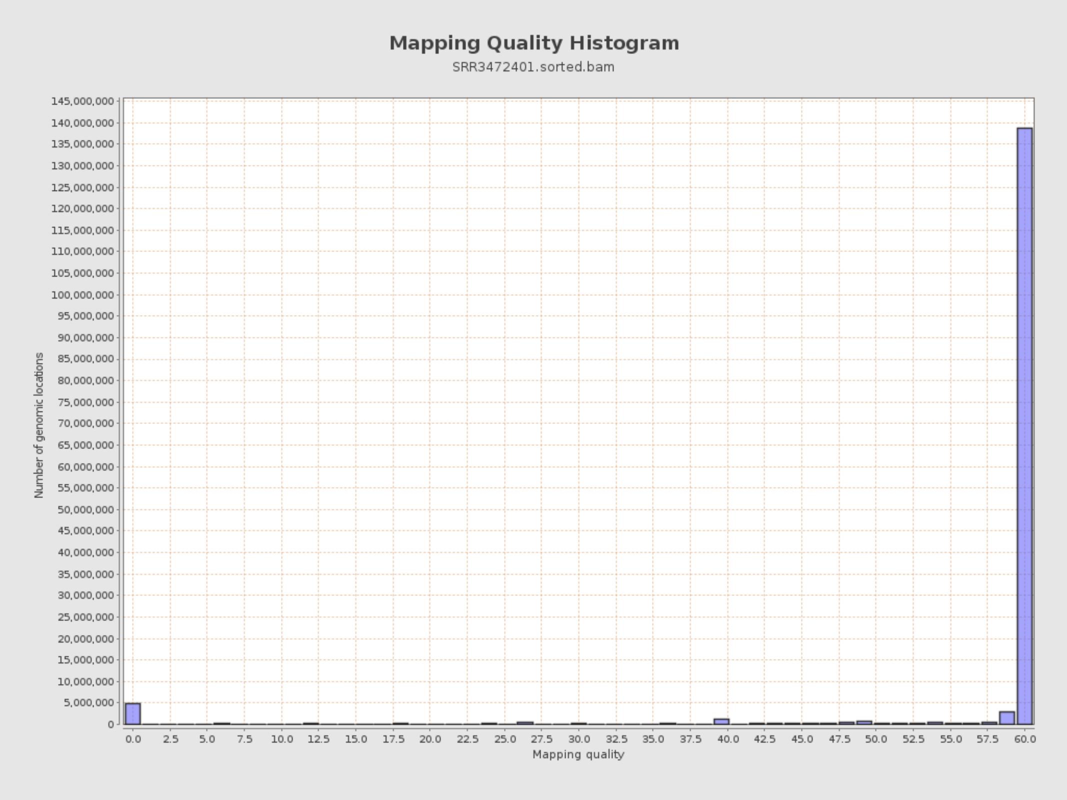
11. Results : Homopolymer Indels



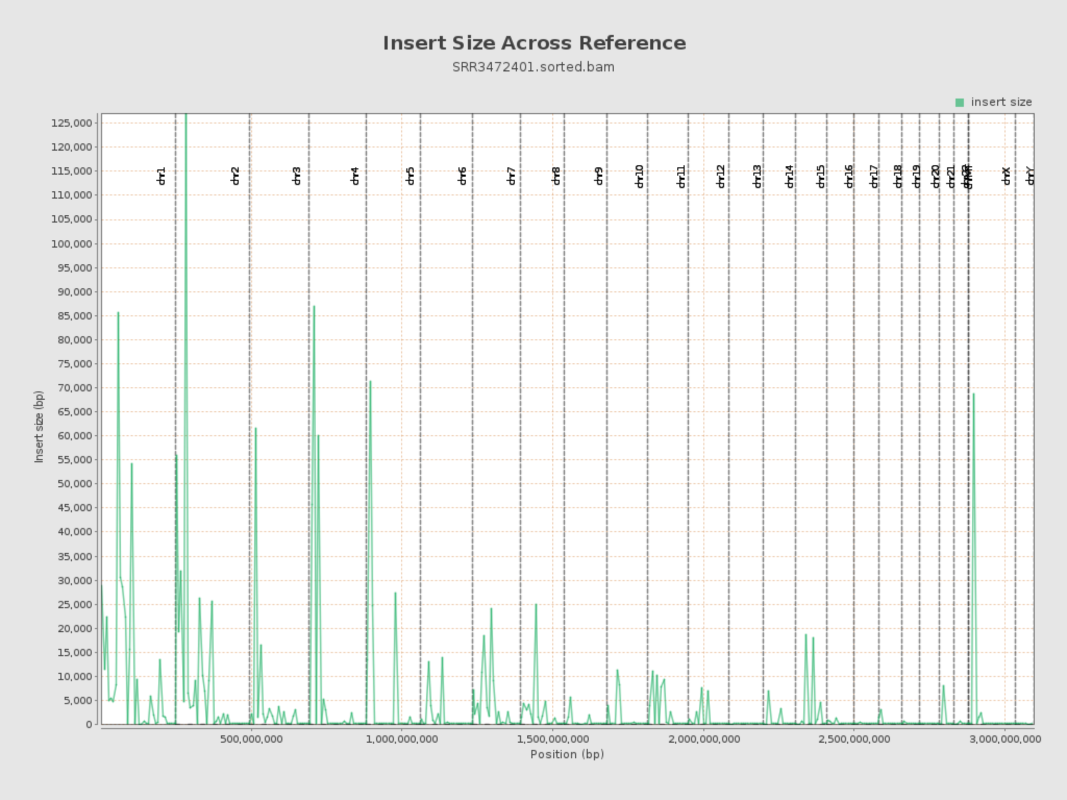
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram