Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 19:56:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472642.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_SRR3472642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472642_1.fastq.gz SRR3472642_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 19:56:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,025,204
Mapped reads	17,889,072 / 99.24%
Unmapped reads	136,132 / 0.76%
Mapped paired reads	17,889,072 / 99.24%
Mapped reads, first in pair	8,973,551 / 49.78%
Mapped reads, second in pair	8,915,521 / 49.46%
Mapped reads, both in pair	17,793,936 / 98.72%
Mapped reads, singletons	95,136 / 0.53%
Secondary alignments	0
Supplementary alignments	84,396 / 0.47%
Read min/max/mean length	30 / 101 / 99.72
Duplicated reads (estimated)	12,881,931 / 71.47%
Duplication rate	49.04%
Clipped reads	1,112,708 / 6.17%

2.2. ACGT Content

Number/percentage of A's	487,420,604 / 27.66%
Number/percentage of C's	395,304,820 / 22.43%
Number/percentage of T's	490,057,002 / 27.81%
Number/percentage of G's	389,346,173 / 22.09%
Number/percentage of N's	325,997 / 0.02%

GC Percentage	44.52%

2.3. Coverage

Mean	0.5694
Standard Deviation	33.9135

2.4. Mapping Quality

Mean Mapping Quality	54.8

2.5. Insert size

Mean	19,607.25
Standard Deviation	1,336,706.12
P25/Median/P75	156 / 213 / 286

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	10,274,098
Insertions	107,987
Mapped reads with at least one insertion	0.6%
Deletions	95,927
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.01%

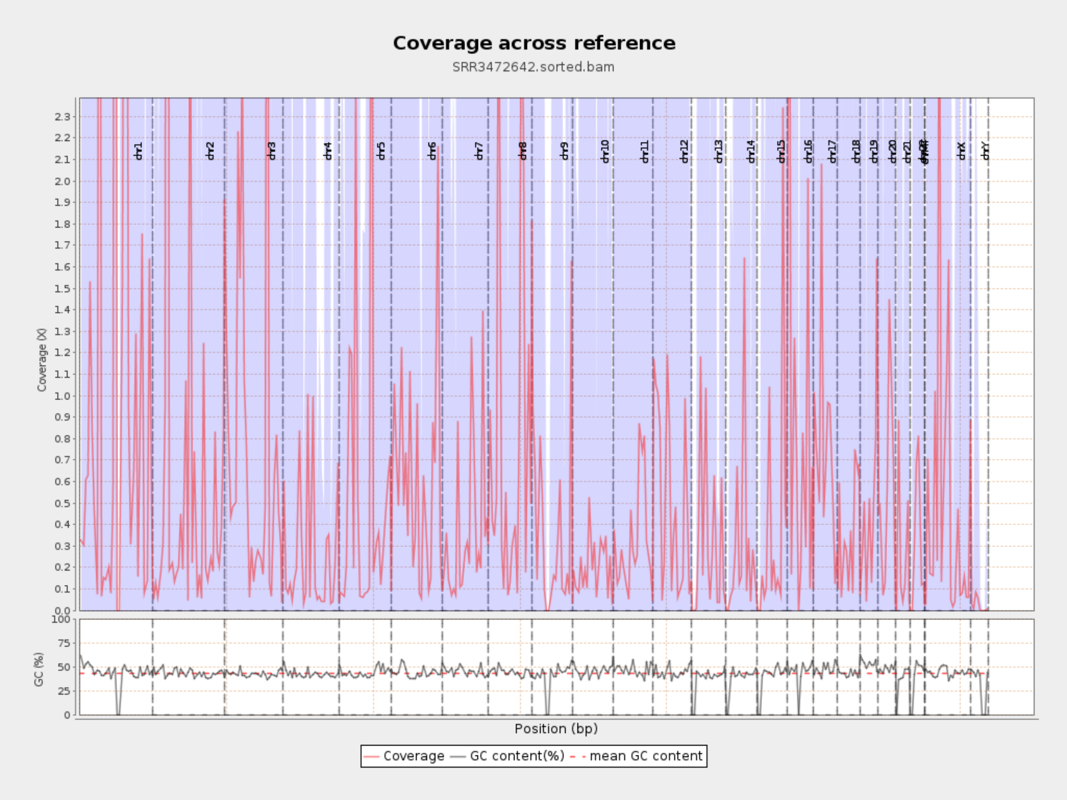
2.7. Chromosome stats

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

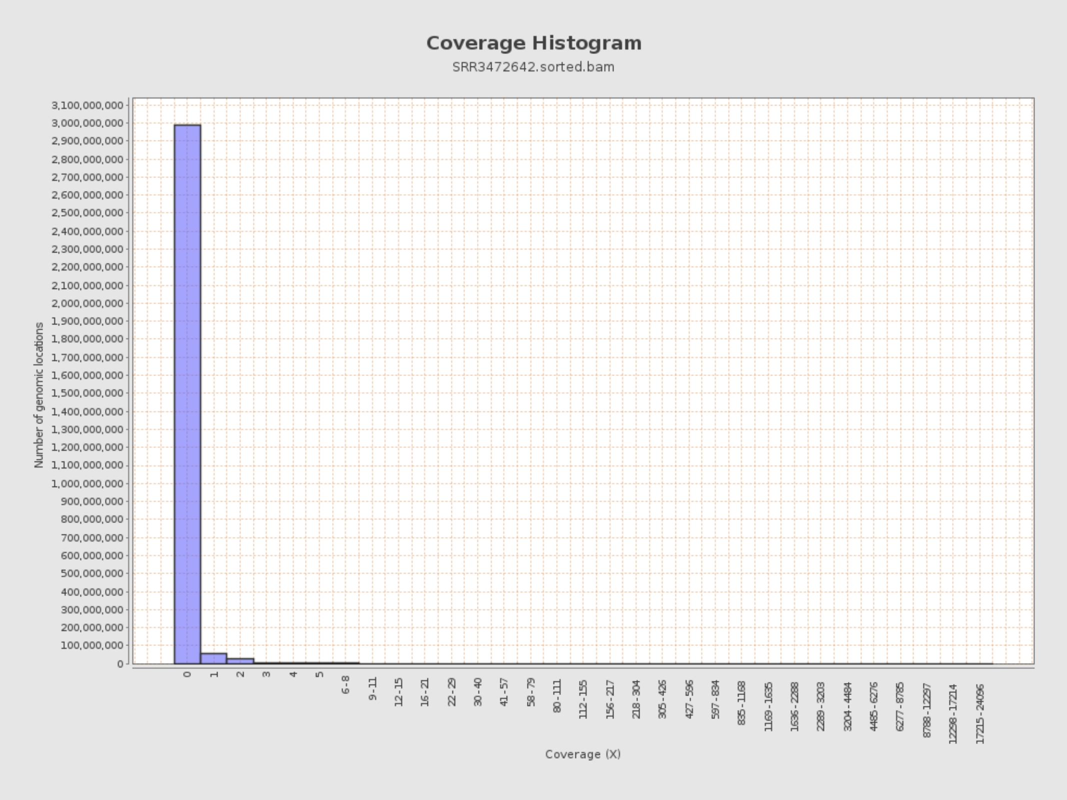
		bases	coverage	deviation
chr1	249250621	306283818	1.2288	57.5077
chr2	243199373	193540006	0.7958	76.2671
chr3	198022430	166881945	0.8427	35.1143
chr4	191154276	49745259	0.2602	12.1157
chr5	180915260	107499557	0.5942	30.7579
chr6	171115067	105054799	0.6139	21.2259
chr7	159138663	60928907	0.3829	19.6009
chr8	146364022	120147387	0.8209	35.2745
chr9	141213431	52584252	0.3724	16.76
chr10	135534747	27859179	0.2056	8.642
chr11	135006516	44704962	0.3311	12.5737
chr12	133851895	71325760	0.5329	22.5058
chr13	115169878	36826941	0.3198	13.8373
chr14	107349540	30210306	0.2814	13.3055
chr15	102531392	38620271	0.3767	15.8315
chr16	90354753	84930237	0.94	30.8899
chr17	81195210	62782159	0.7732	23.5629
chr18	78077248	28500573	0.365	13.3148
chr19	59128983	25057774	0.4238	11.0769
chr20	63025520	37278897	0.5915	20.0503
chr21	48129895	13182584	0.2739	16.9153
chr22	51304566	15752009	0.307	11.919
chrMT	16571	1792	0.1081	0.4472
chrX	155270560	81521544	0.525	31.3886

chrY	59373566	1454754	0.0245	1.1318

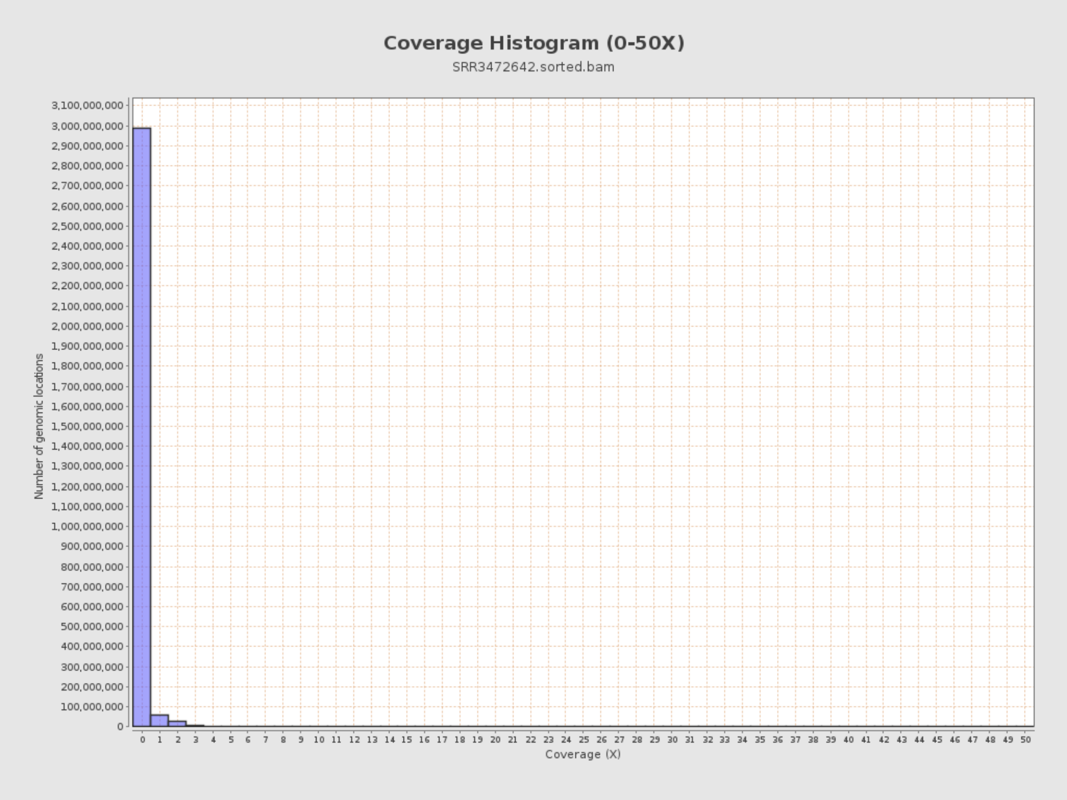
3. Results : Coverage across reference



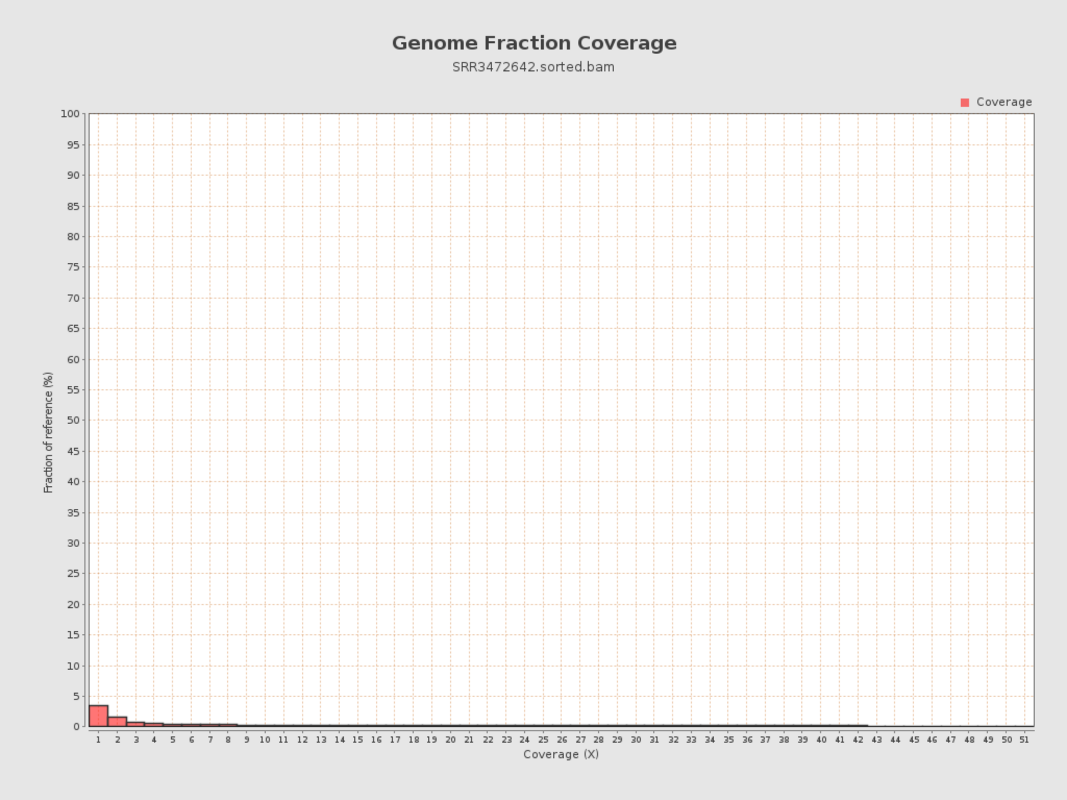
4. Results : Coverage Histogram



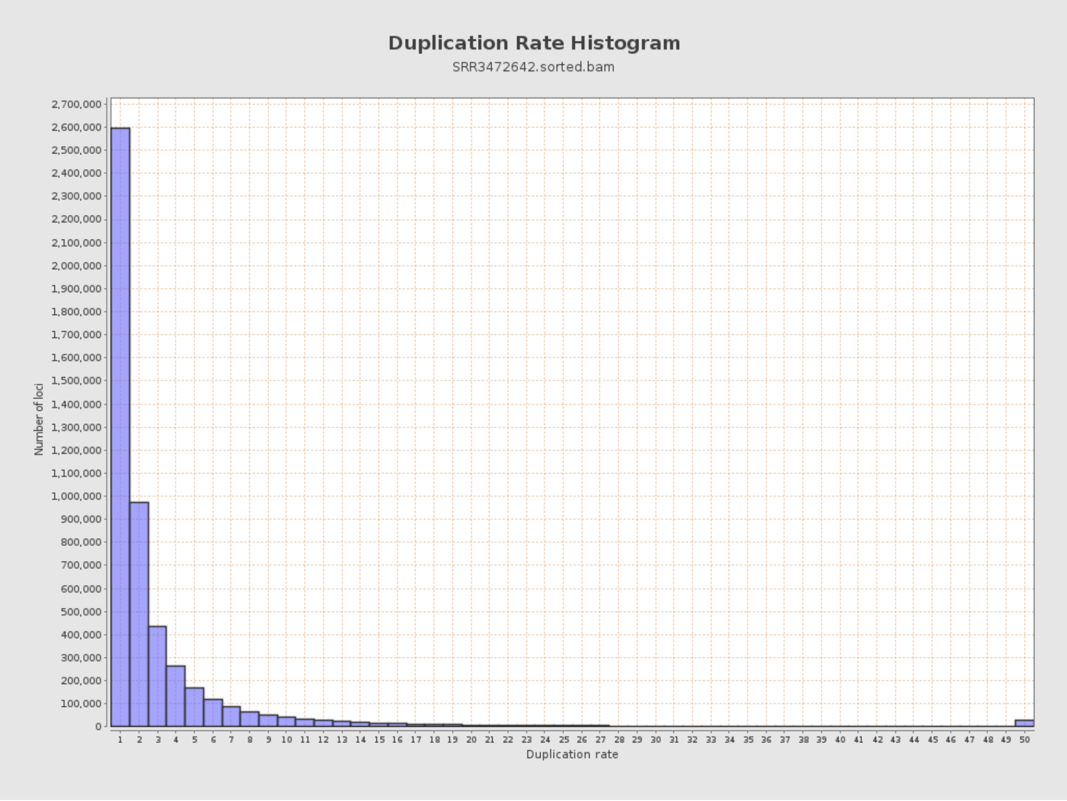
5. Results : Coverage Histogram (0-50X)



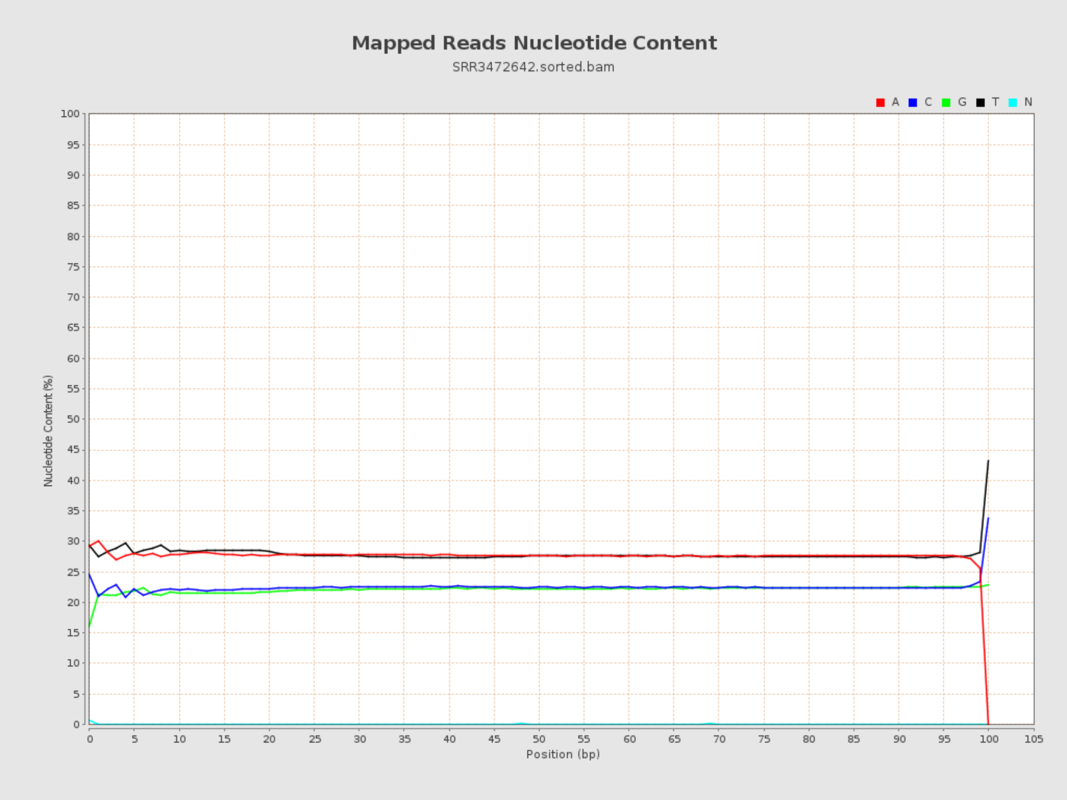
6. Results : Genome Fraction Coverage



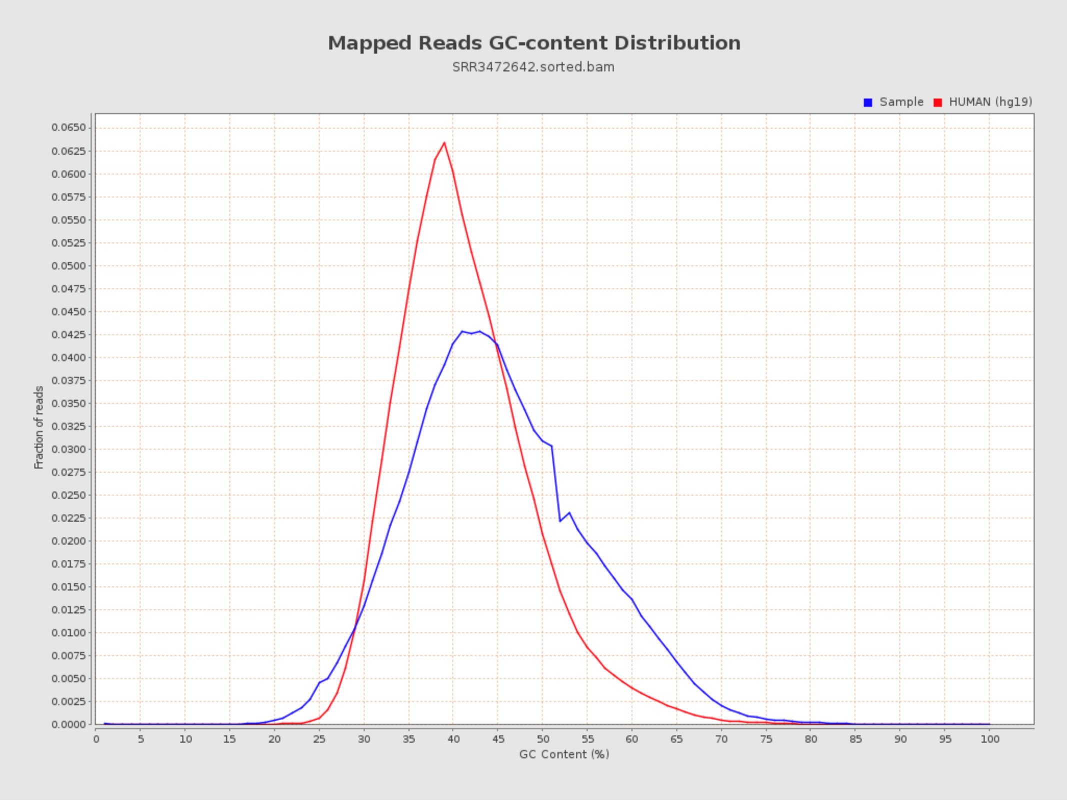
7. Results : Duplication Rate Histogram



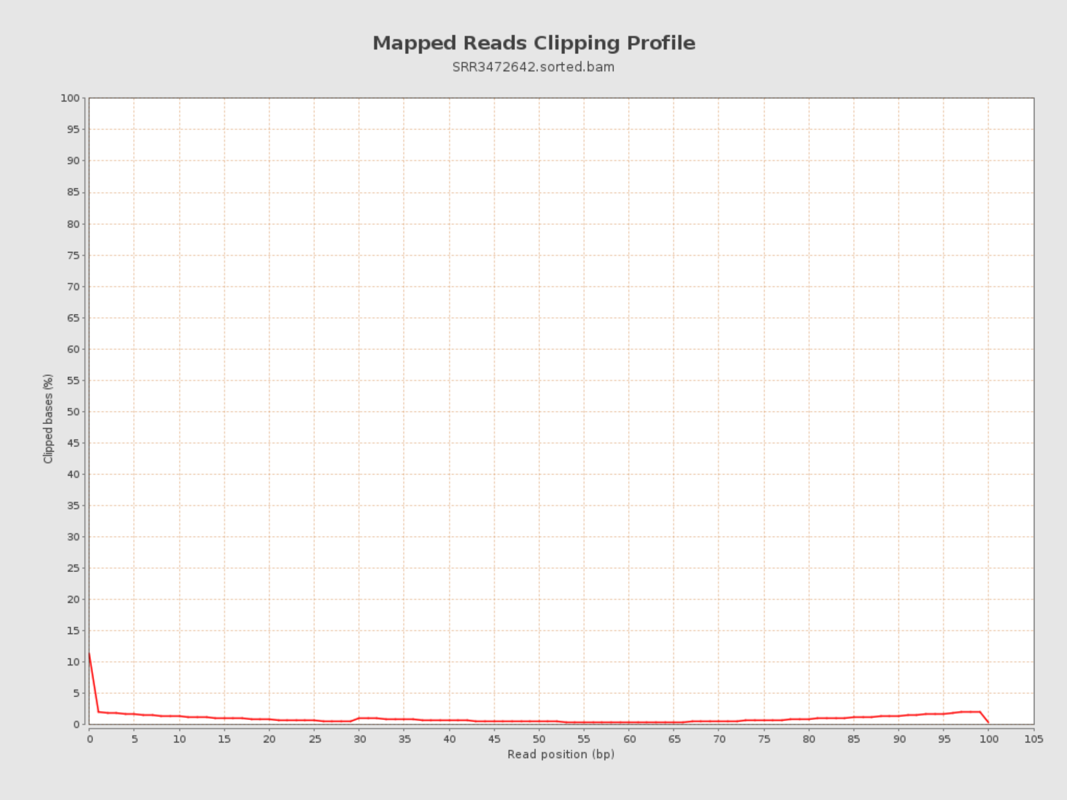
8. Results : Mapped Reads Nucleotide Content



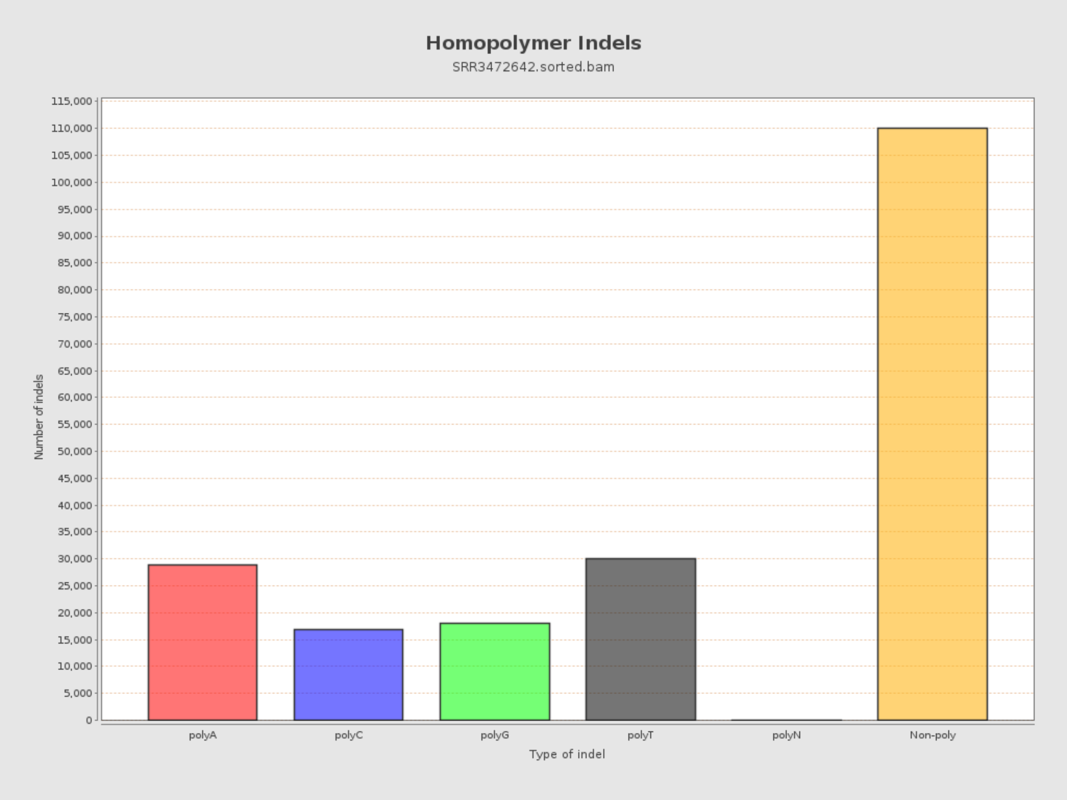
9. Results : Mapped Reads GC-content Distribution



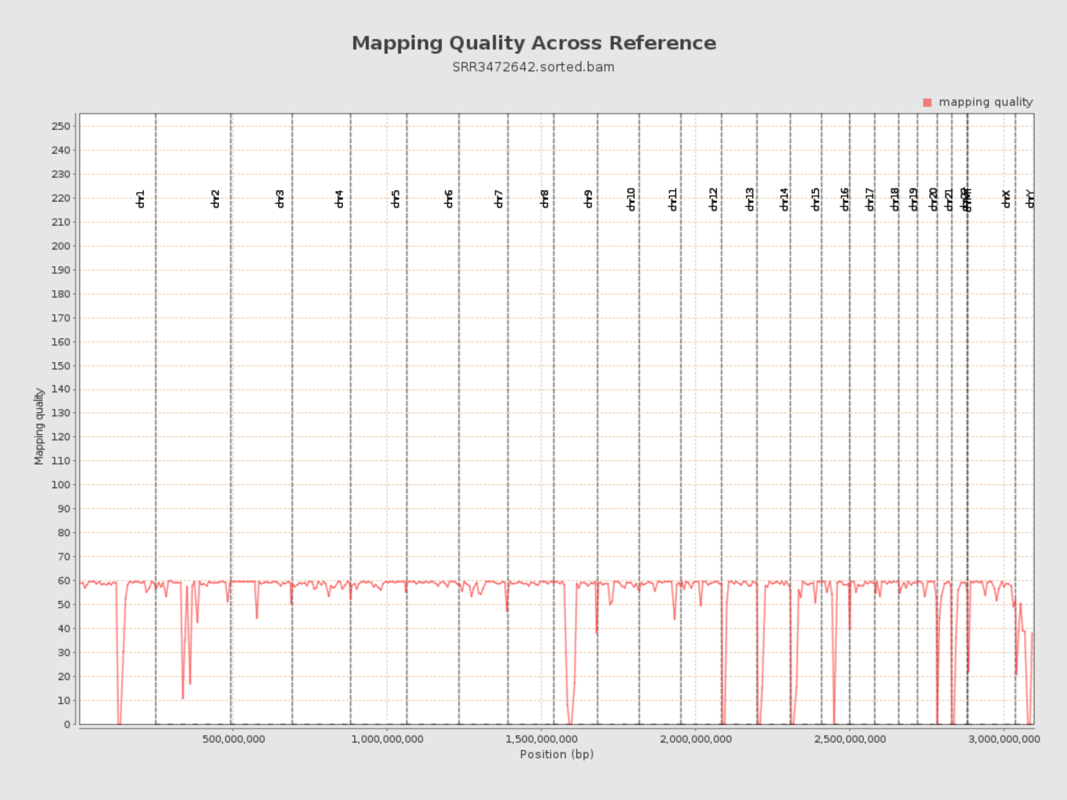
10. Results : Mapped Reads Clipping Profile



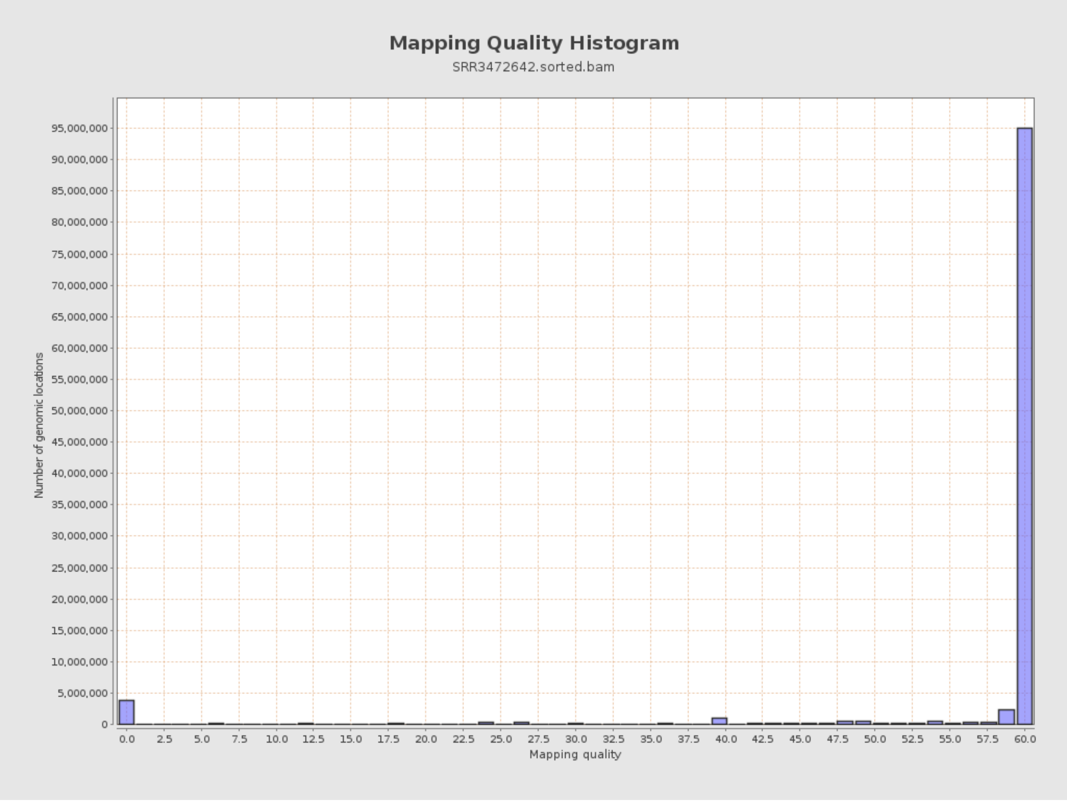
11. Results : Homopolymer Indels



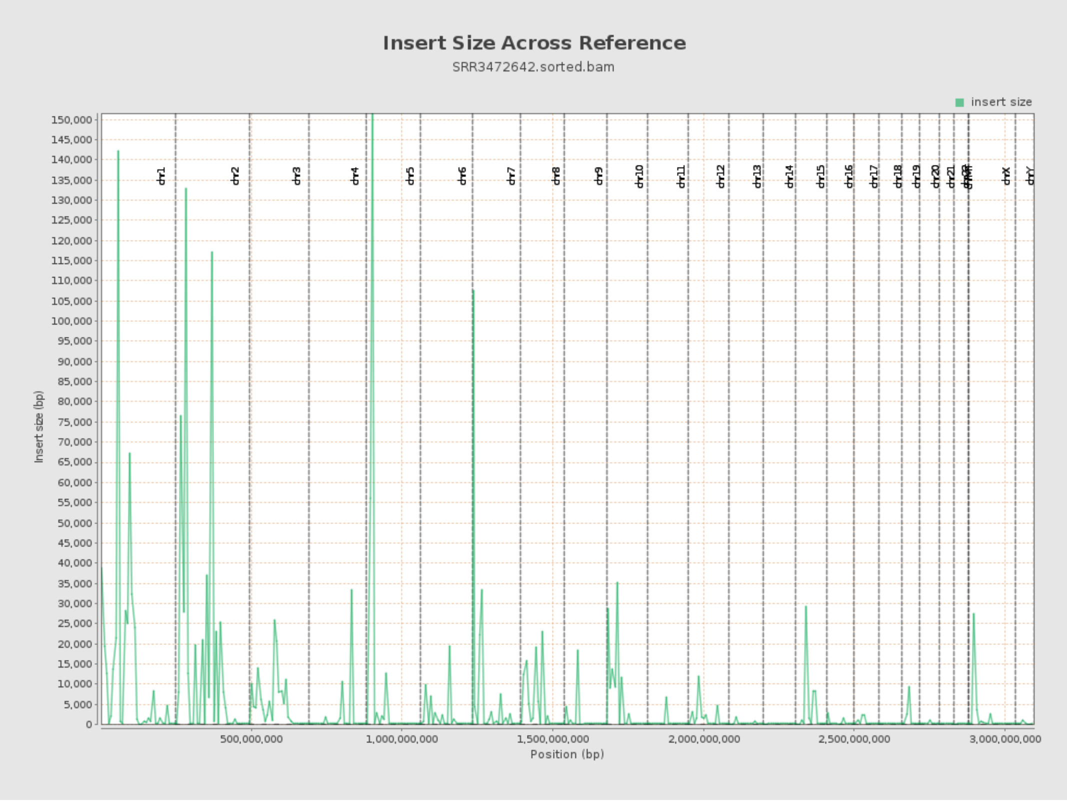
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram