Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:11:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472553.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_SRR3472553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472553_1.fastq.gz SRR3472553_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:11:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,068,346
Mapped reads	13,791,295 / 98.03%
Unmapped reads	277,051 / 1.97%
Mapped paired reads	13,791,295 / 98.03%
Mapped reads, first in pair	6,923,406 / 49.21%
Mapped reads, second in pair	6,867,889 / 48.82%
Mapped reads, both in pair	13,671,240 / 97.18%
Mapped reads, singletons	120,055 / 0.85%
Secondary alignments	0
Supplementary alignments	61,787 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	8,435,510 / 59.96%
Duplication rate	46.46%
Clipped reads	1,272,042 / 9.04%

2.2. ACGT Content

Number/percentage of A's	372,946,342 / 27.56%
Number/percentage of C's	305,713,415 / 22.6%
Number/percentage of T's	369,721,692 / 27.33%
Number/percentage of G's	304,407,787 / 22.5%
Number/percentage of N's	205,975 / 0.02%

GC Percentage	45.09%

2.3. Coverage

Mean	0.4371
Standard Deviation	15.4006

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	39,146.08
Standard Deviation	1,954,388.18
P25/Median/P75	170 / 242 / 330

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	8,431,176
Insertions	75,494
Mapped reads with at least one insertion	0.54%
Deletions	67,068
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.59%

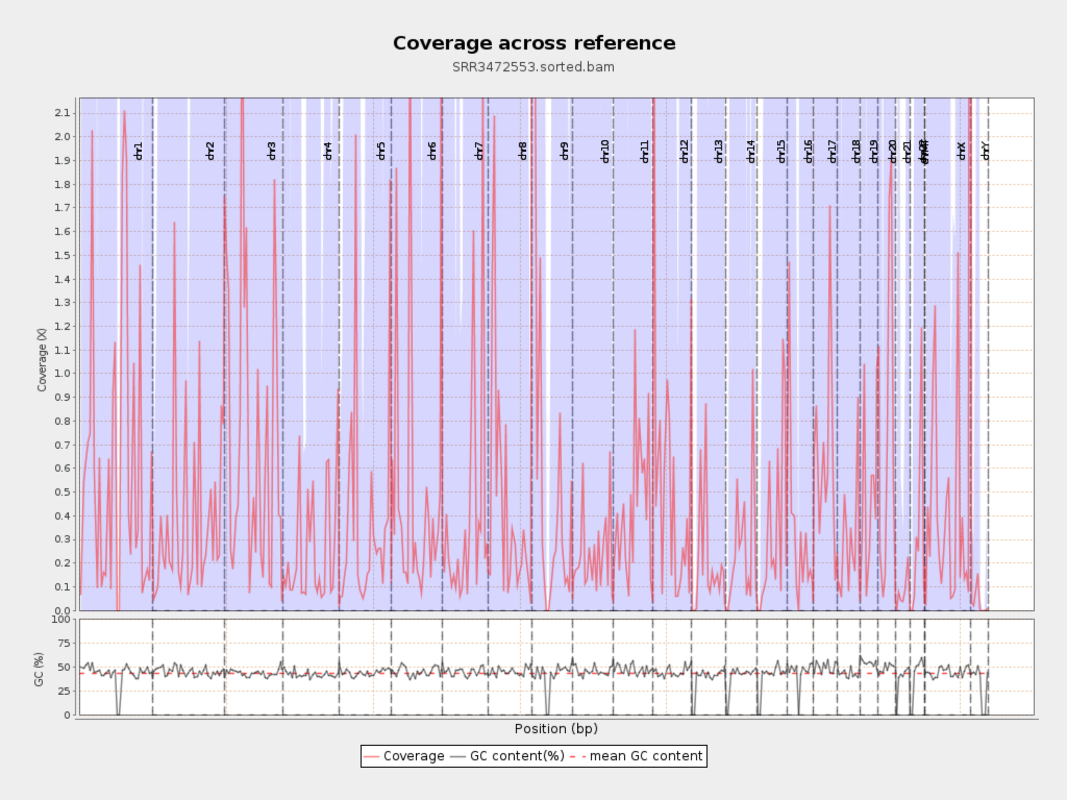
2.7. Chromosome stats

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

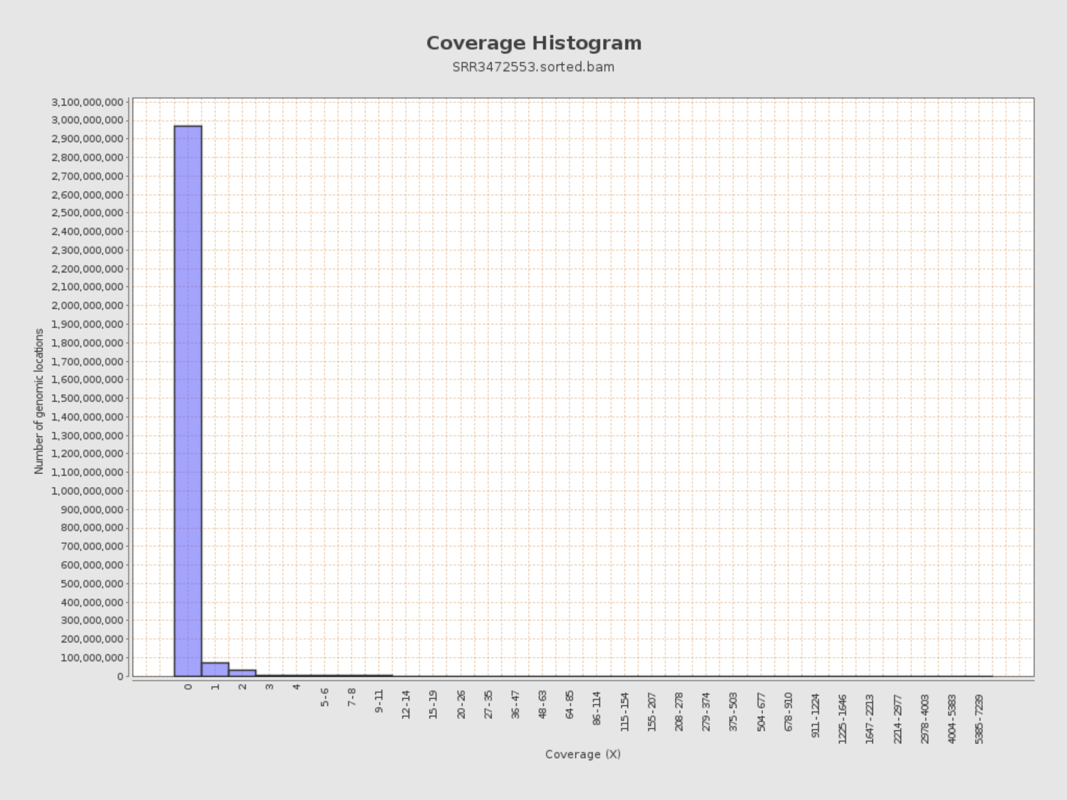
		bases	coverage	deviation
chr1	249250621	155793684	0.625	20.527
chr2	243199373	90445802	0.3719	11.8702
chr3	198022430	150753294	0.7613	18.1574
chr4	191154276	48748402	0.255	10.2558
chr5	180915260	72169868	0.3989	12.8689
chr6	171115067	85368517	0.4989	15.8895
chr7	159138663	65783070	0.4134	17.2368
chr8	146364022	66281850	0.4529	15.1982
chr9	141213431	82797352	0.5863	14.5257
chr10	135534747	33231635	0.2452	8.2396
chr11	135006516	59177931	0.4383	14.1399
chr12	133851895	72426777	0.5411	14.1844
chr13	115169878	23507333	0.2041	7.1257
chr14	107349540	26582447	0.2476	11.1395
chr15	102531392	34273260	0.3343	10.8238
chr16	90354753	30518155	0.3378	9.0905
chr17	81195210	51467686	0.6339	14.5245
chr18	78077248	22095804	0.283	10.4008
chr19	59128983	27058830	0.4576	13.4915
chr20	63025520	47949290	0.7608	34.2934
chr21	48129895	4069922	0.0846	3.0165
chr22	51304566	15102312	0.2944	11.2075
chrMT	16571	3144	0.1897	0.6974
chrX	155270560	85260031	0.5491	26.1306

chrY	59373566	2293878	0.0386	2.1511

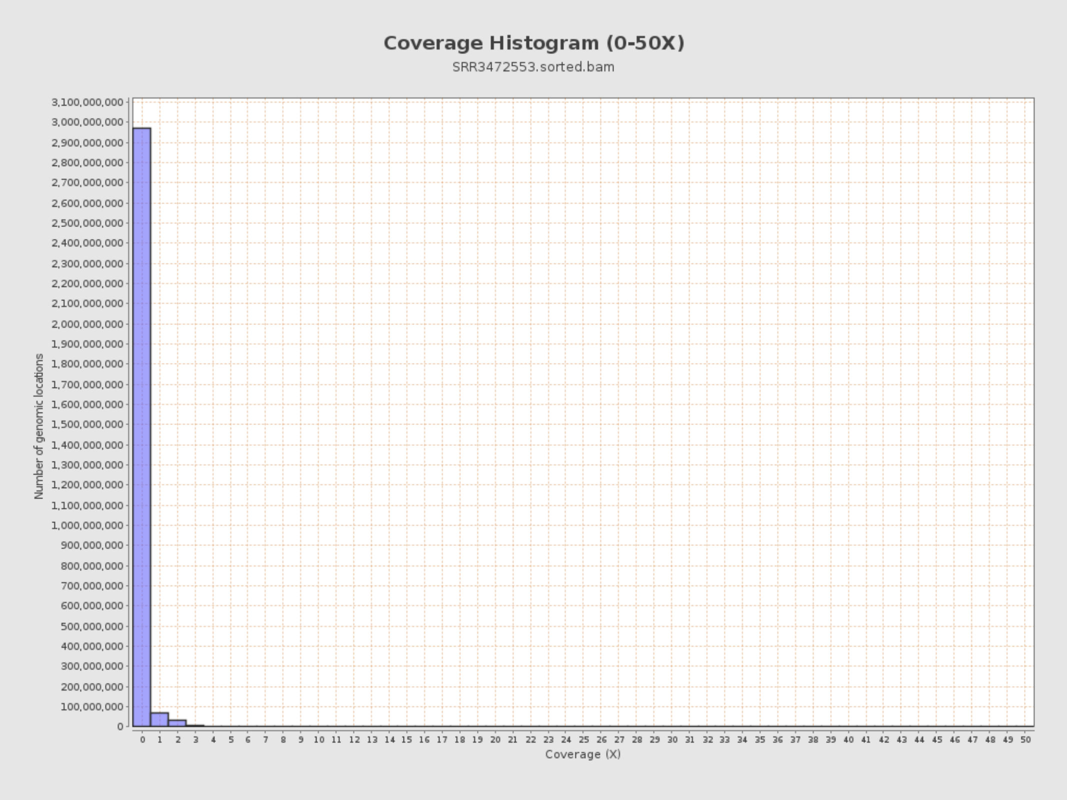
3. Results : Coverage across reference



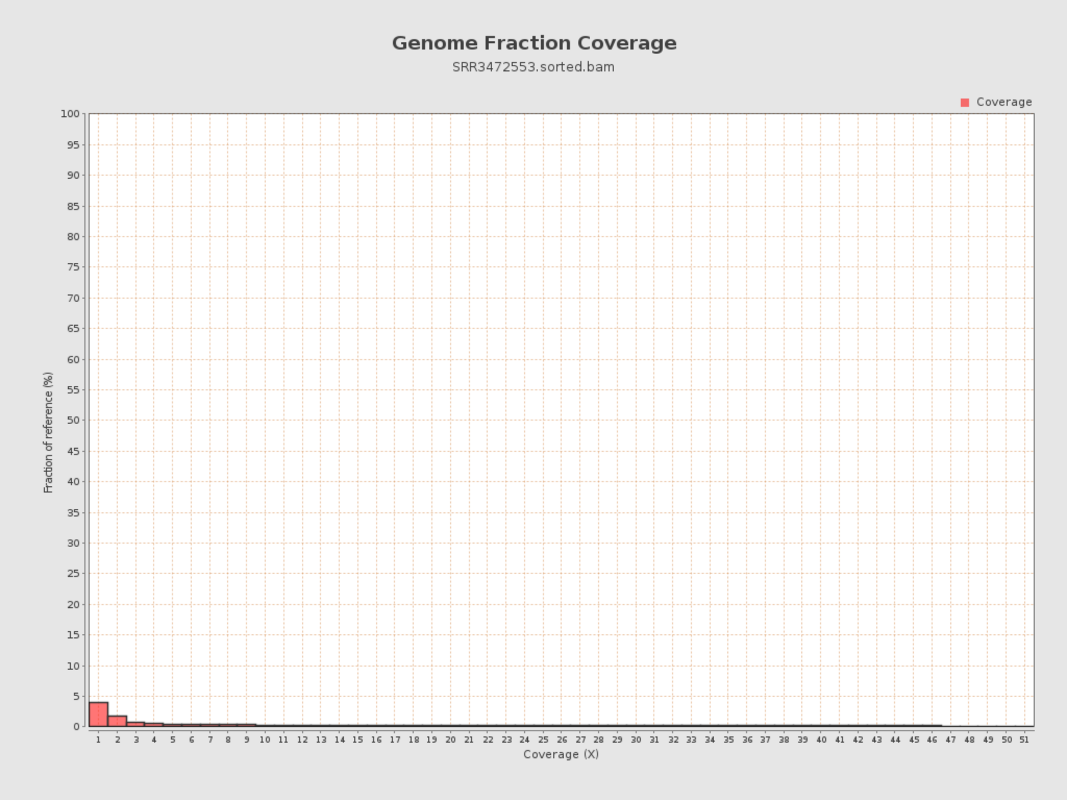
4. Results : Coverage Histogram



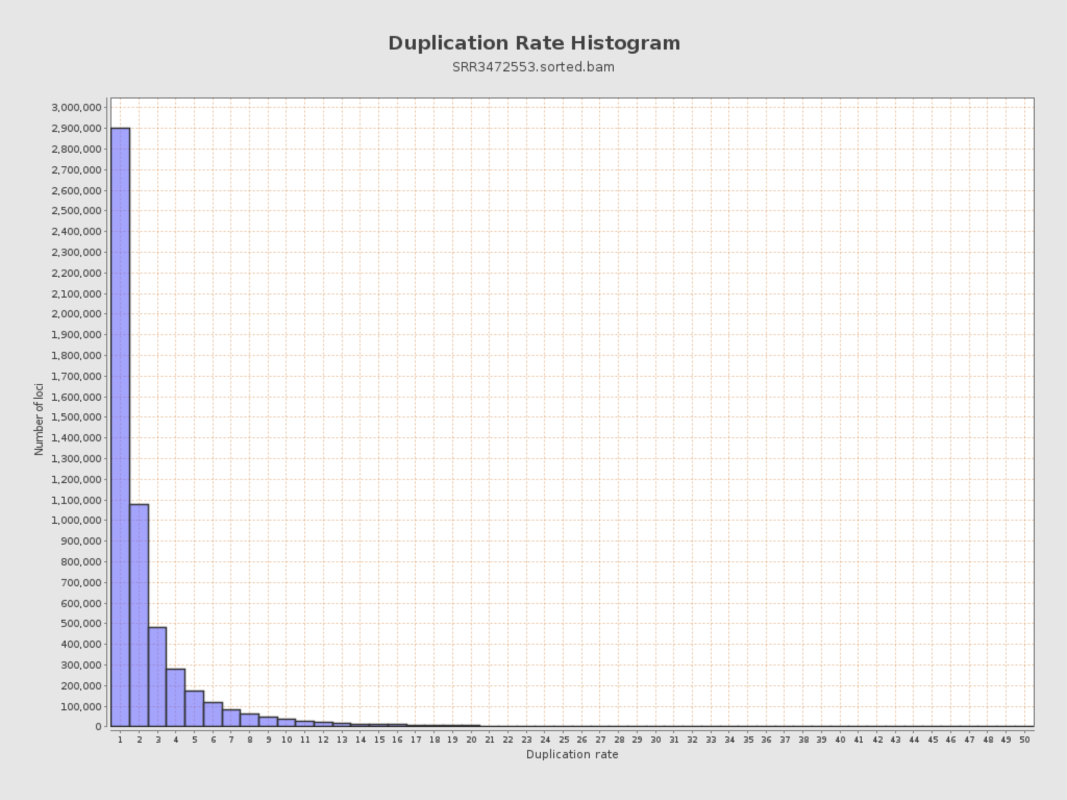
5. Results : Coverage Histogram (0-50X)



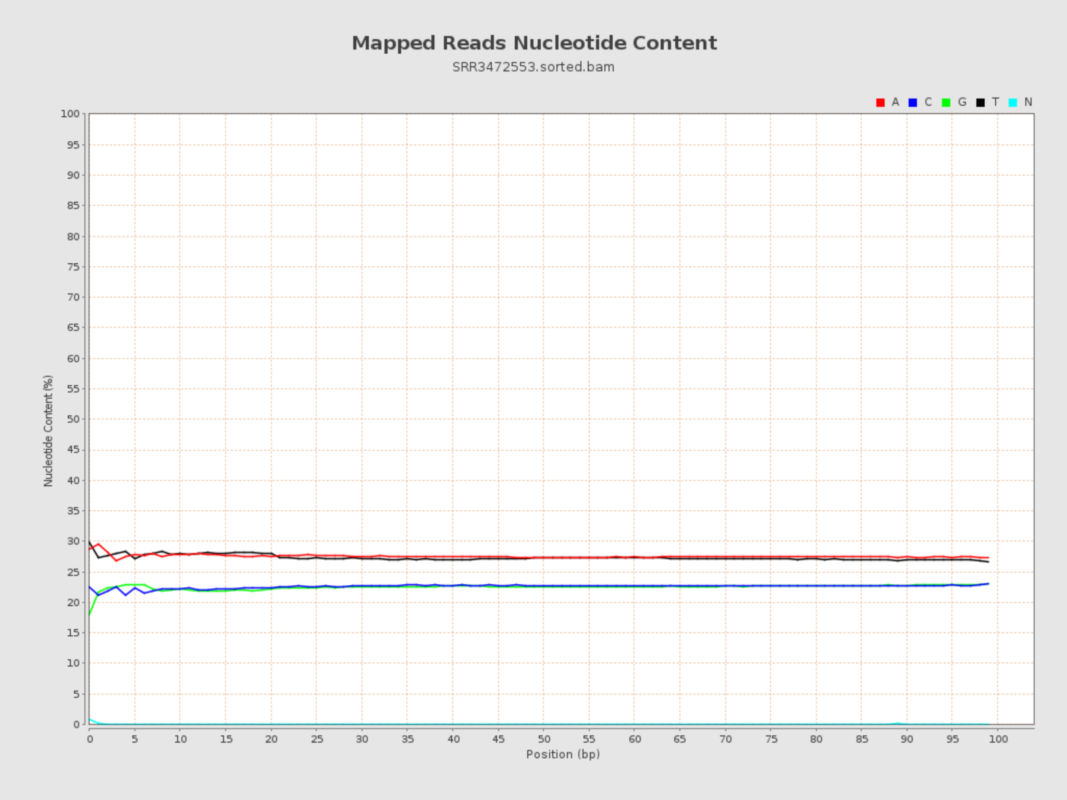
6. Results : Genome Fraction Coverage



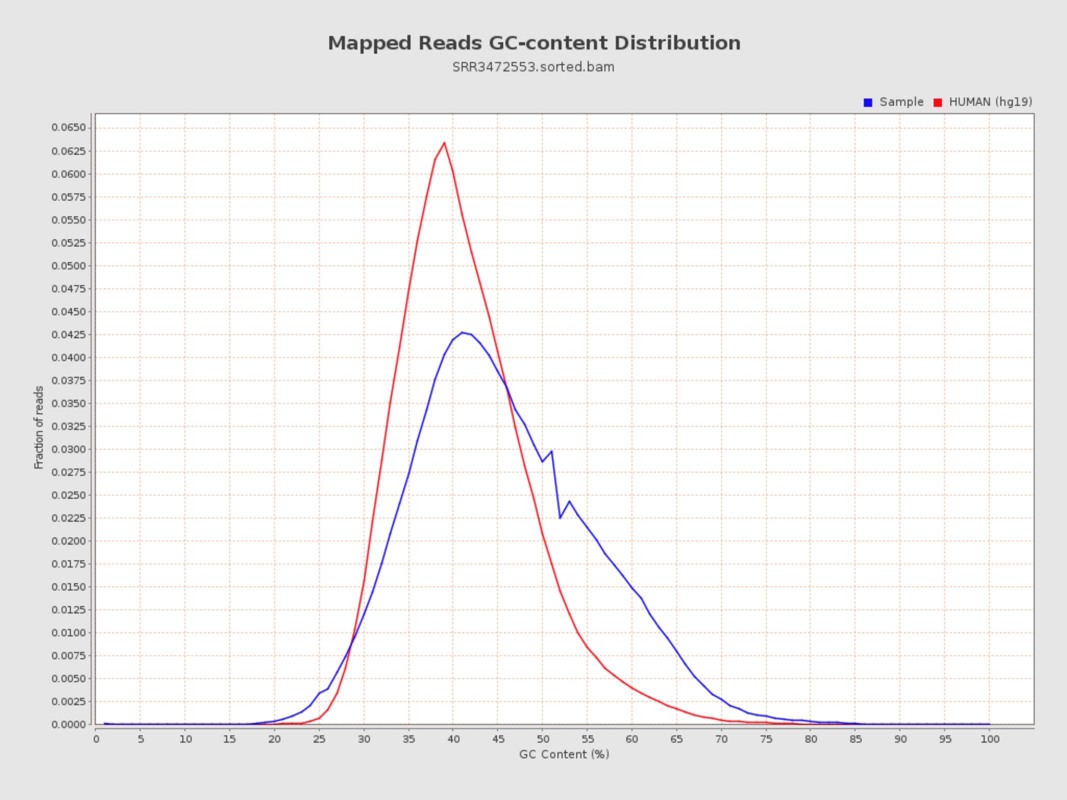
7. Results : Duplication Rate Histogram



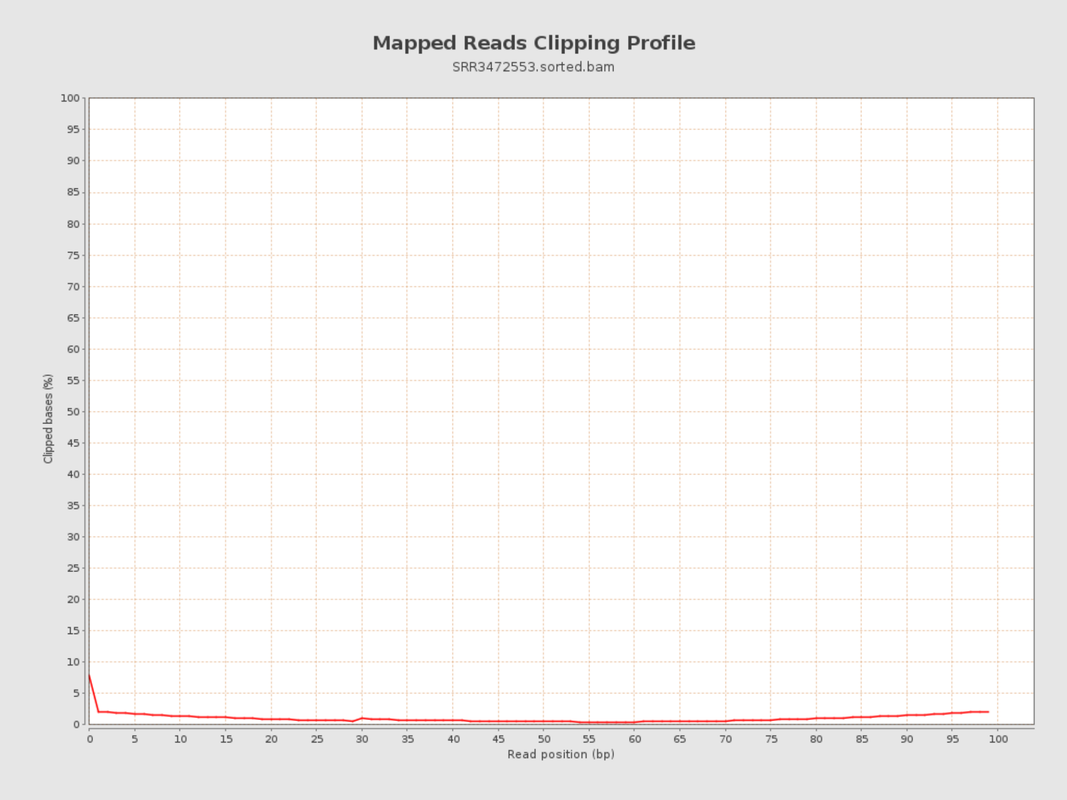
8. Results : Mapped Reads Nucleotide Content



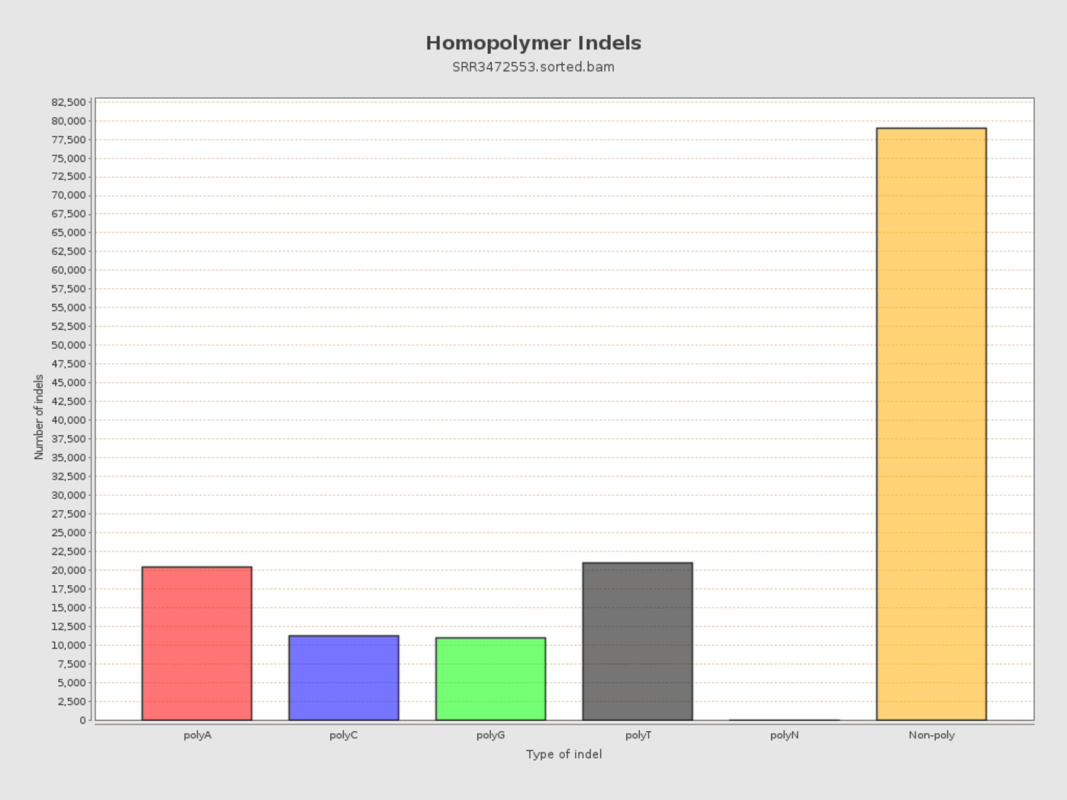
9. Results : Mapped Reads GC-content Distribution



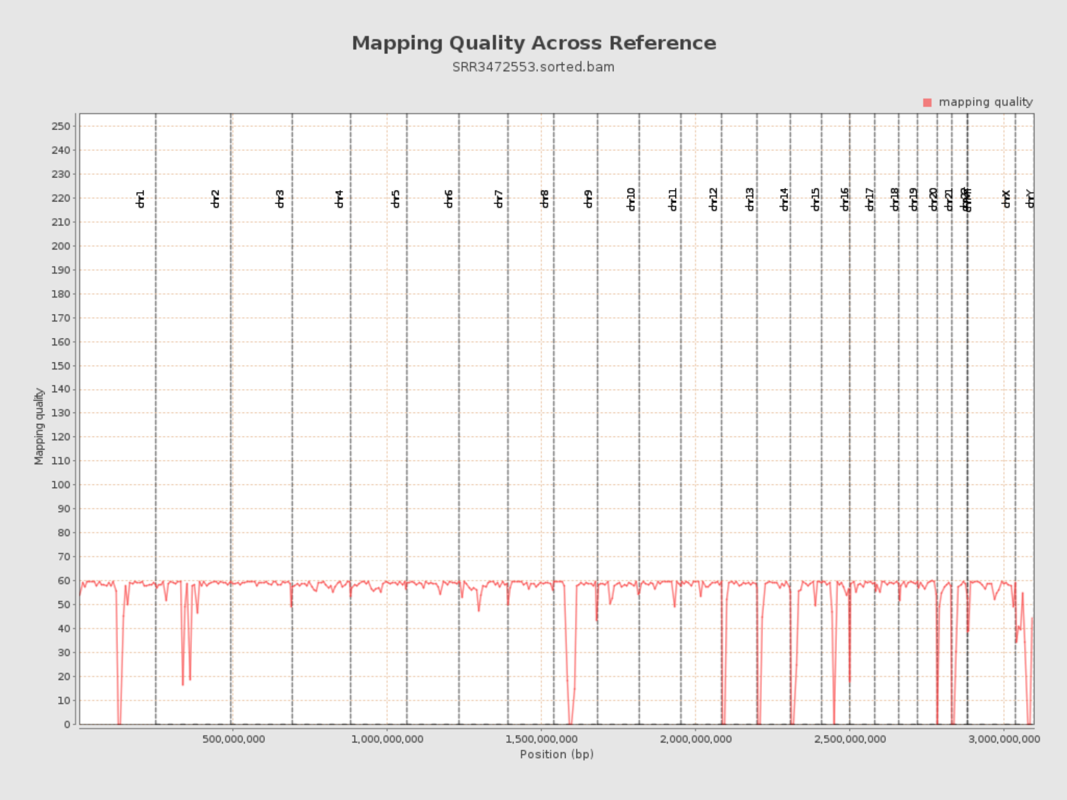
10. Results : Mapped Reads Clipping Profile



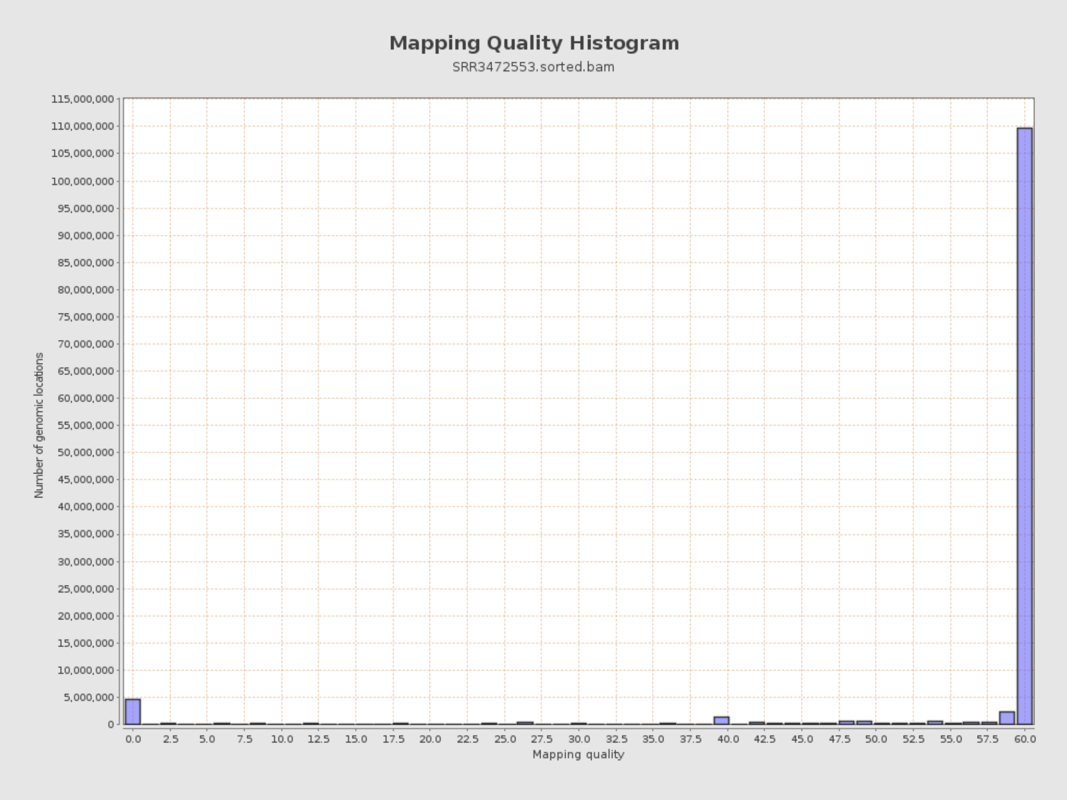
11. Results : Homopolymer Indels



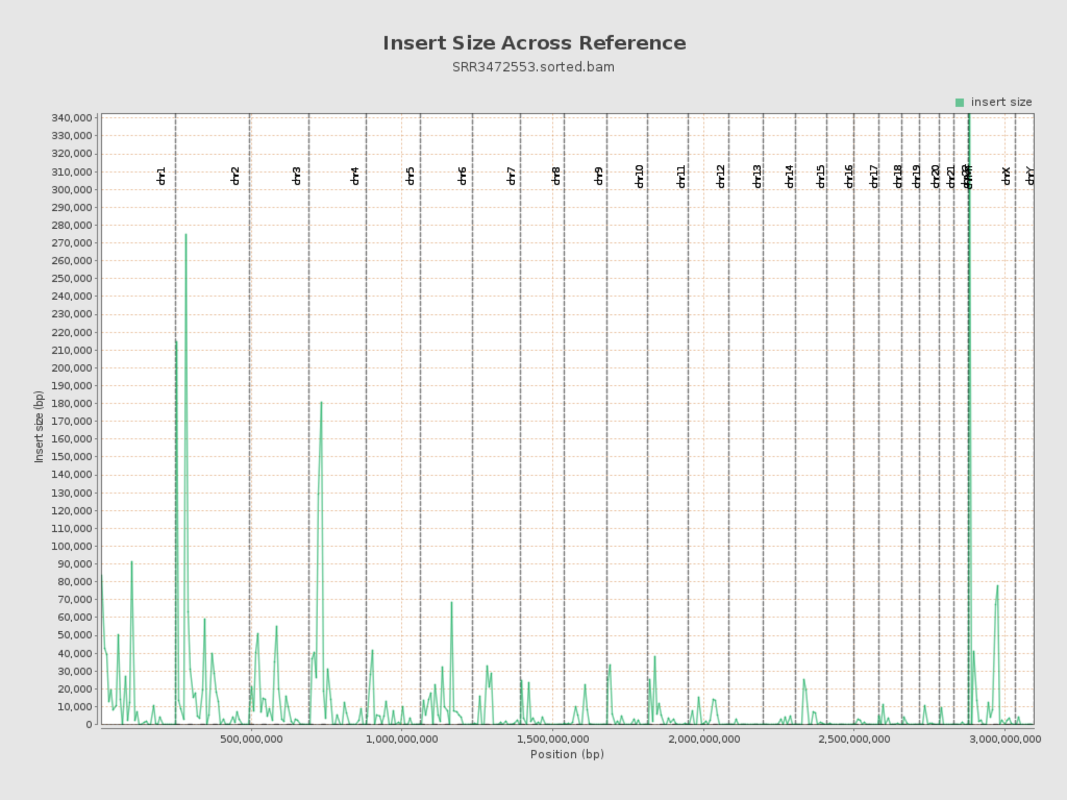
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram