Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 10:49:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472613.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_SRR3472613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472613_1.fastq.gz SRR3472613_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 10:49:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,833,832
Mapped reads	19,631,133 / 98.98%
Unmapped reads	202,699 / 1.02%
Mapped paired reads	19,631,133 / 98.98%
Mapped reads, first in pair	9,855,387 / 49.69%
Mapped reads, second in pair	9,775,746 / 49.29%
Mapped reads, both in pair	19,486,650 / 98.25%
Mapped reads, singletons	144,483 / 0.73%
Secondary alignments	0
Supplementary alignments	96,128 / 0.48%
Read min/max/mean length	30 / 101 / 99.68
Duplicated reads (estimated)	13,836,275 / 69.76%
Duplication rate	50.69%
Clipped reads	1,432,880 / 7.22%

2.2. ACGT Content

Number/percentage of A's	515,666,188 / 26.73%
Number/percentage of C's	451,205,099 / 23.39%
Number/percentage of T's	516,329,308 / 26.77%
Number/percentage of G's	445,409,329 / 23.09%
Number/percentage of N's	357,881 / 0.02%

GC Percentage	46.48%

2.3. Coverage

Mean	0.6232
Standard Deviation	26.4044

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	22,283.9
Standard Deviation	1,494,347.38
P25/Median/P75	151 / 208 / 280

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,972,816
Insertions	121,929
Mapped reads with at least one insertion	0.62%
Deletions	100,336
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.46%

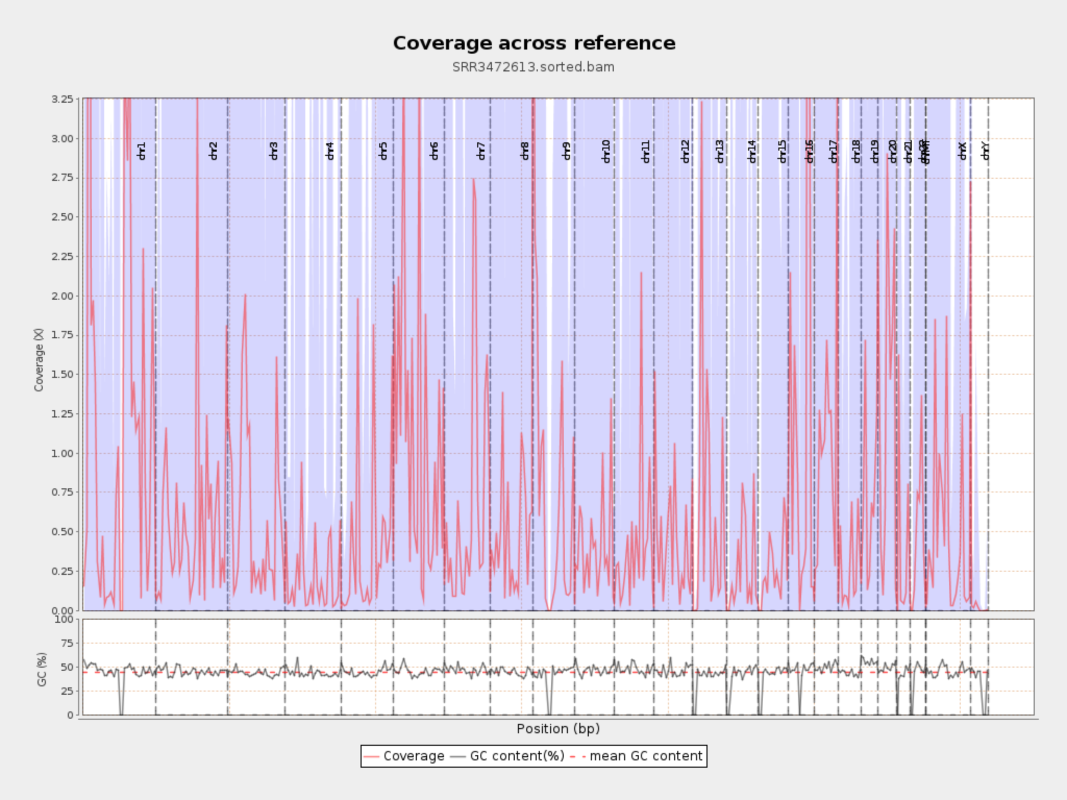
2.7. Chromosome stats

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

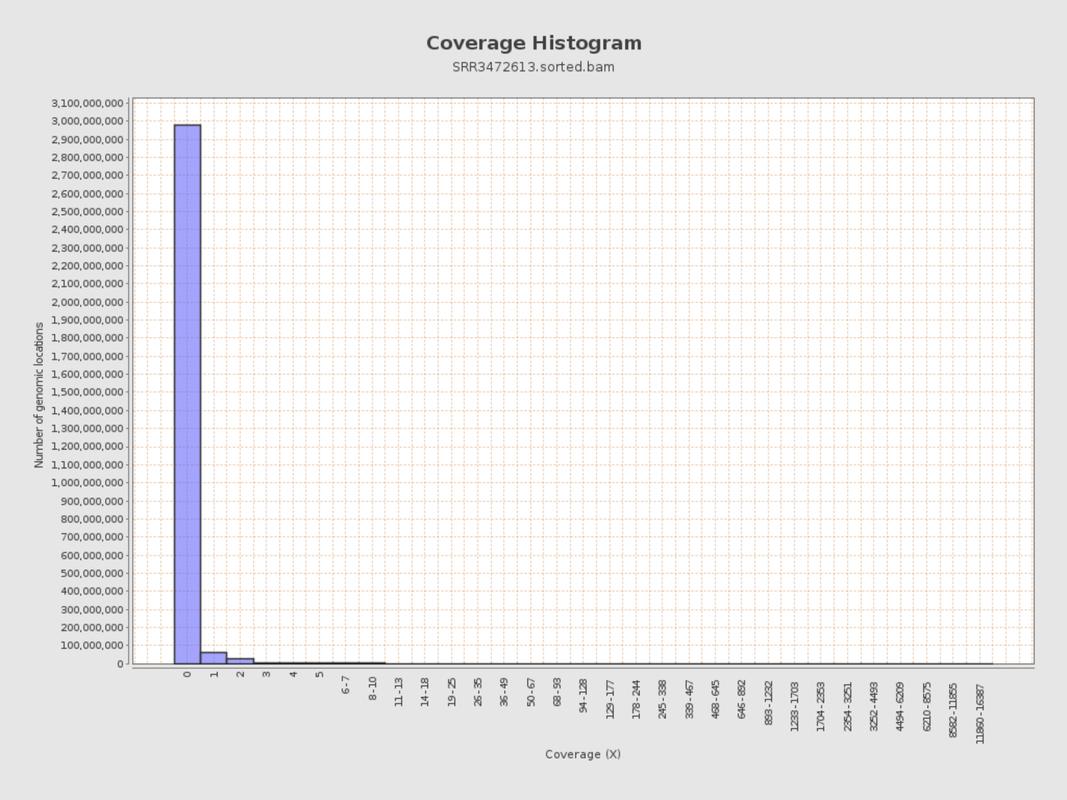
		bases	coverage	deviation
chr1	249250621	300420593	1.2053	49.8094
chr2	243199373	138403456	0.5691	24.1952
chr3	198022430	121187086	0.612	16.2965
chr4	191154276	41301039	0.2161	9.7795
chr5	180915260	77855007	0.4303	17.5705
chr6	171115067	195466722	1.1423	33.2639
chr7	159138663	110862026	0.6966	28.5694
chr8	146364022	70809541	0.4838	15.9865
chr9	141213431	96494732	0.6833	20.0557
chr10	135534747	57448828	0.4239	18.9345
chr11	135006516	56001487	0.4148	29.2452
chr12	133851895	61448334	0.4591	16.327
chr13	115169878	74101742	0.6434	25.3288
chr14	107349540	27382065	0.2551	12.2653
chr15	102531392	25832906	0.252	8.83
chr16	90354753	108898090	1.2052	53.073
chr17	81195210	84394864	1.0394	24.5504
chr18	78077248	20607610	0.2639	11.8213
chr19	59128983	45757320	0.7739	20.78
chr20	63025520	85047341	1.3494	37.3575
chr21	48129895	20806829	0.4323	26.8927
chr22	51304566	25652023	0.5	31.3302
chrMT	16571	3340	0.2016	0.5996
chrX	155270560	82071188	0.5286	17.255

chrY	59373566	947161	0.016	0.6927

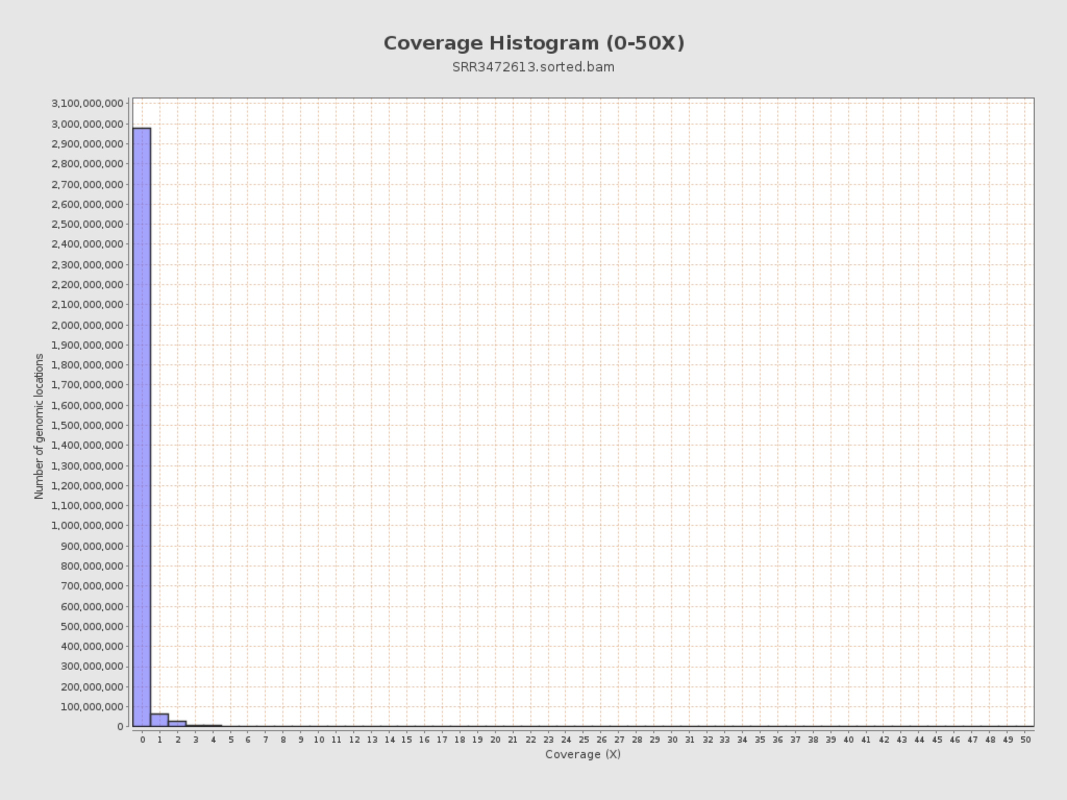
3. Results : Coverage across reference



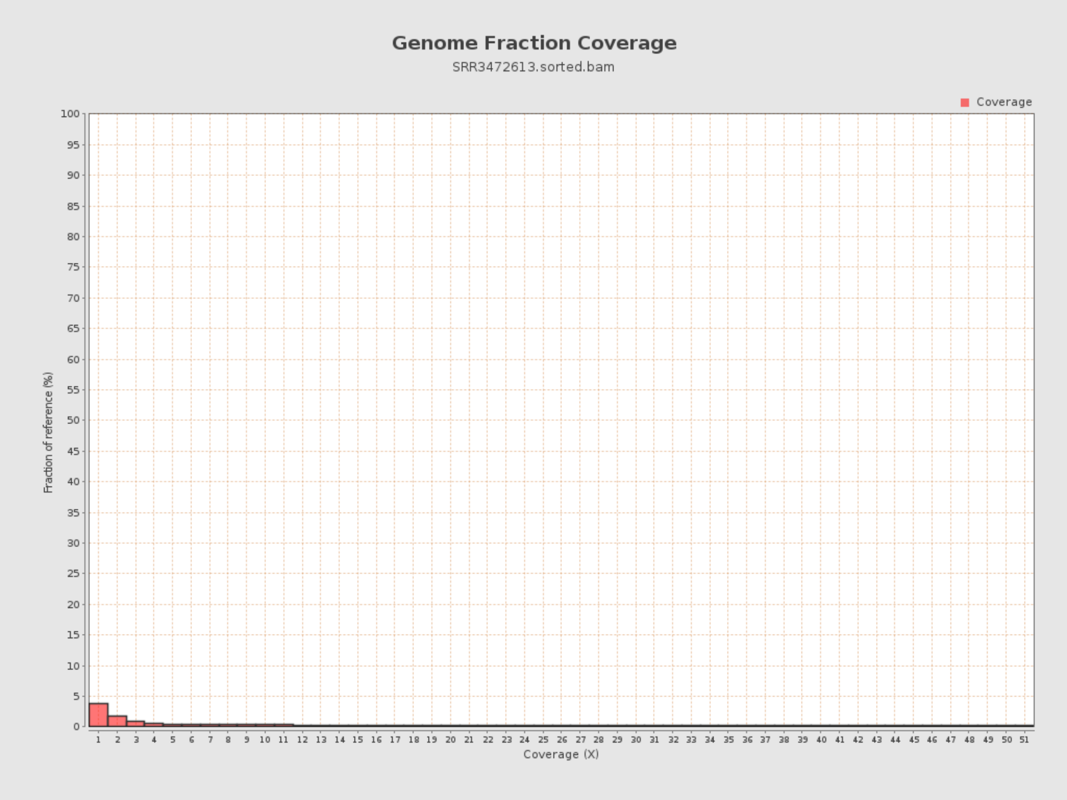
4. Results : Coverage Histogram



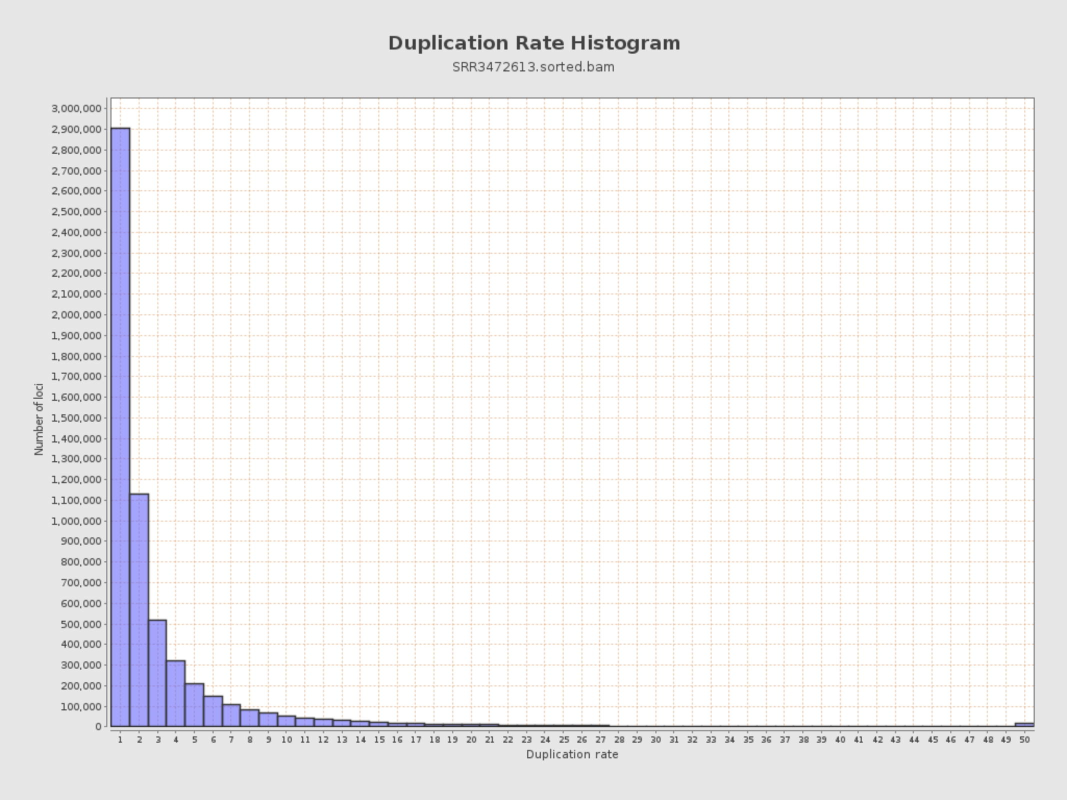
5. Results : Coverage Histogram (0-50X)



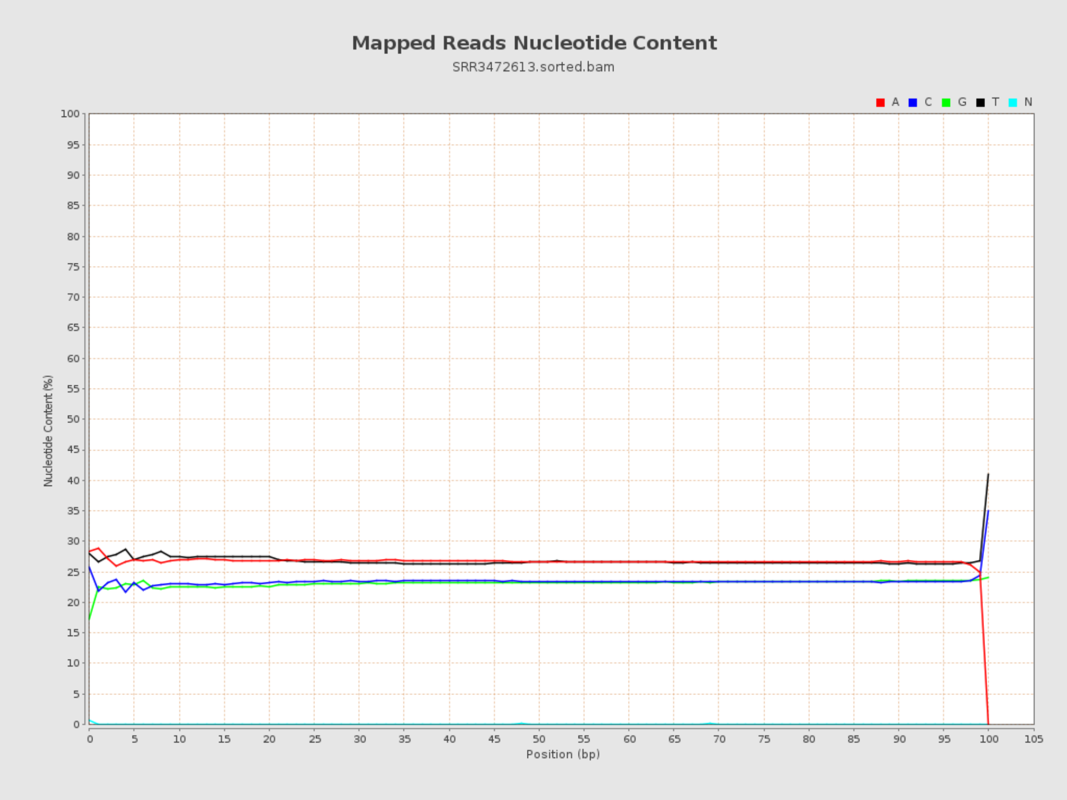
6. Results : Genome Fraction Coverage



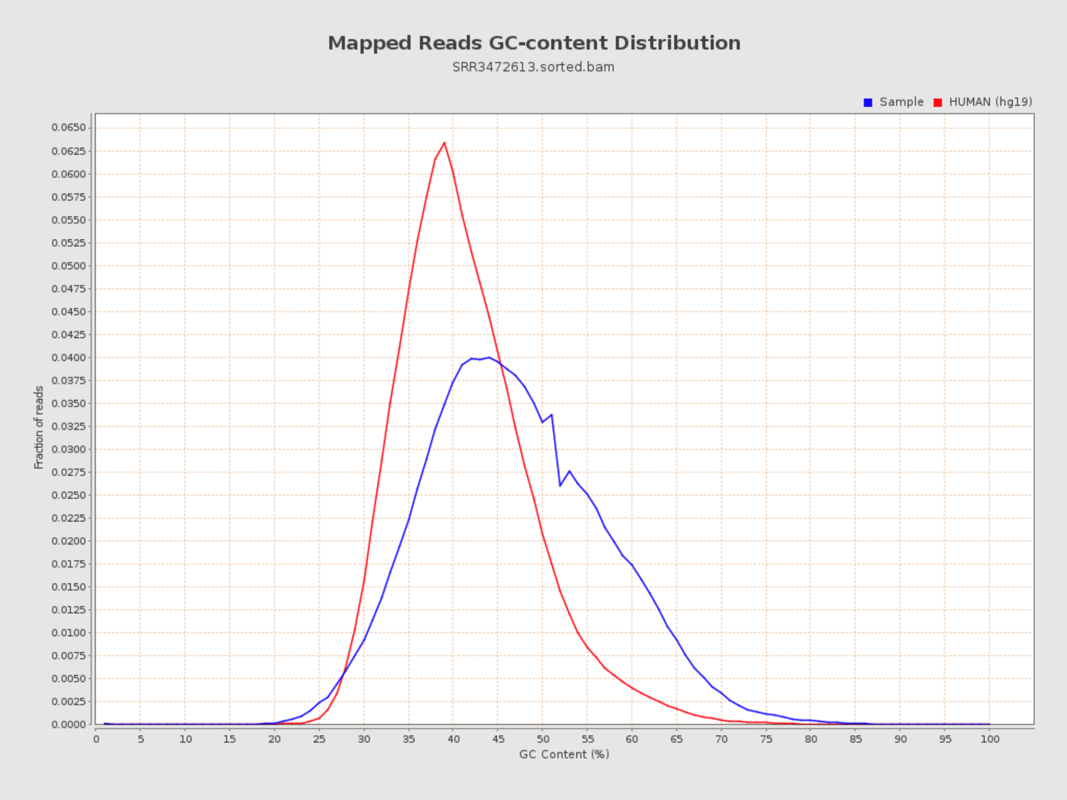
7. Results : Duplication Rate Histogram



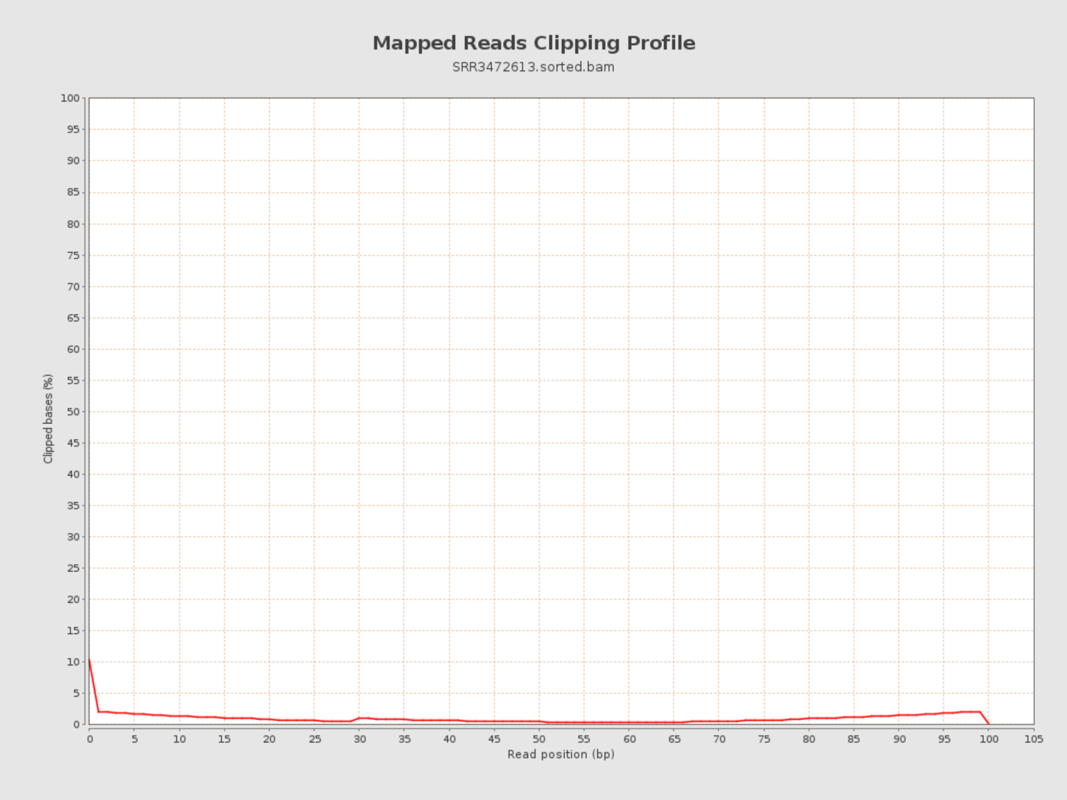
8. Results : Mapped Reads Nucleotide Content



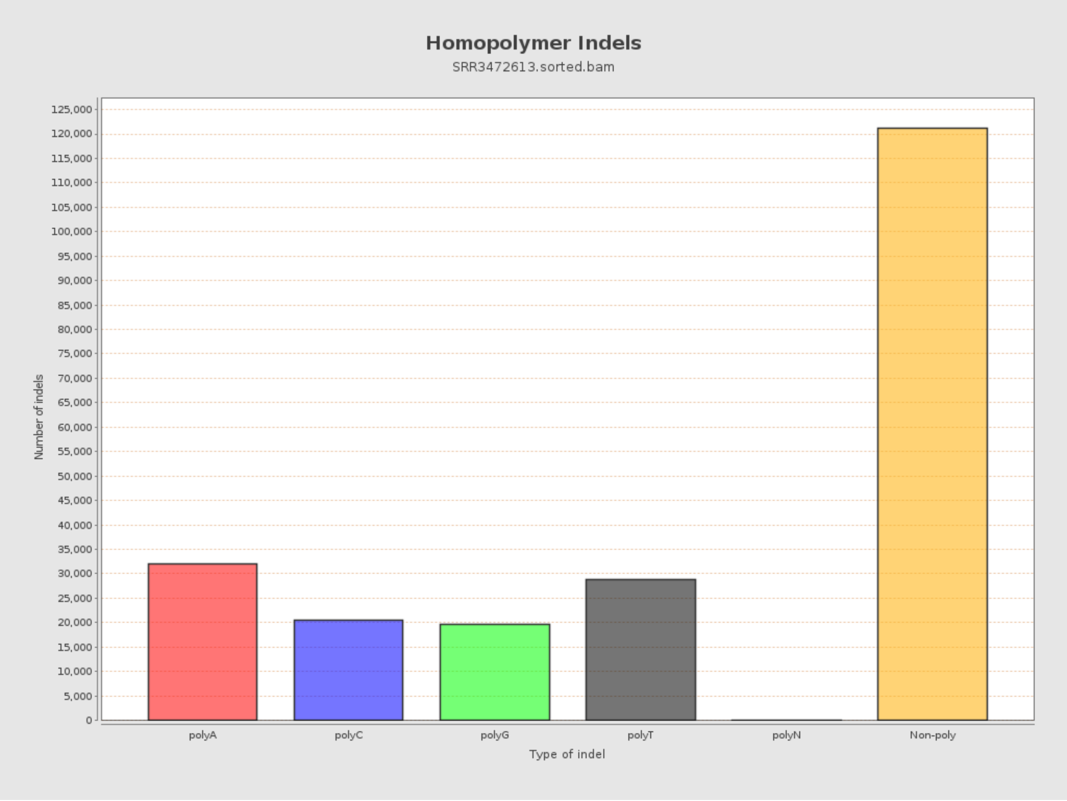
9. Results : Mapped Reads GC-content Distribution



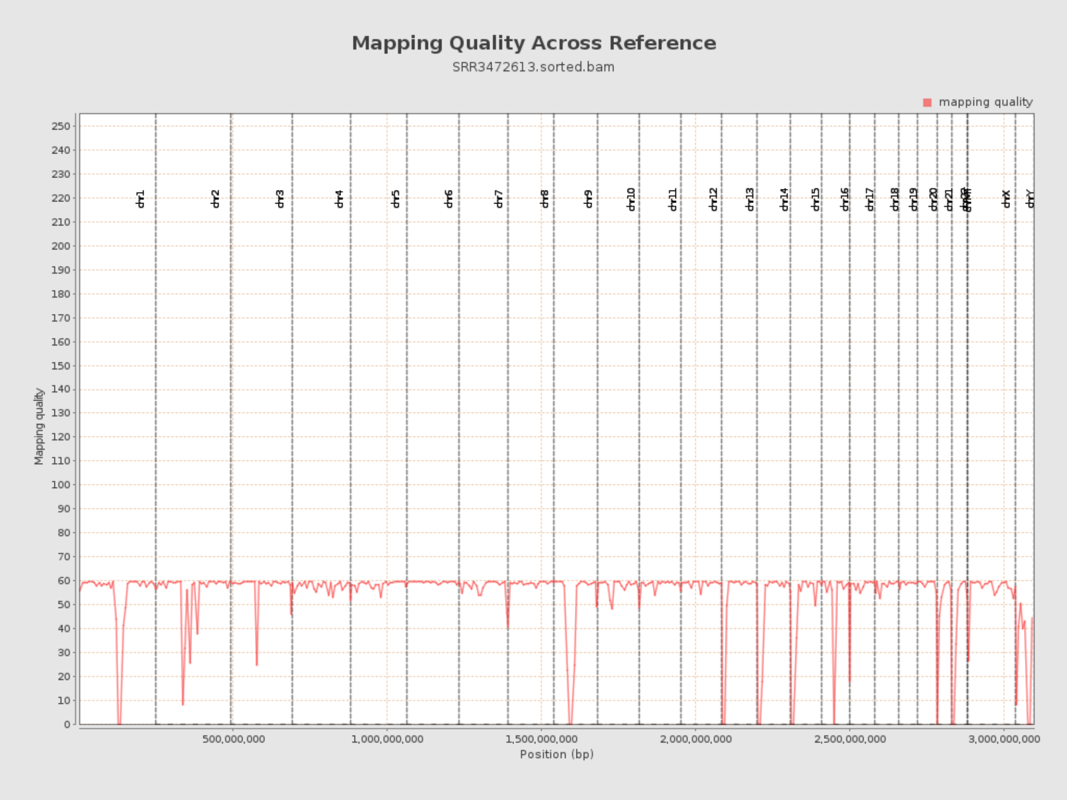
10. Results : Mapped Reads Clipping Profile



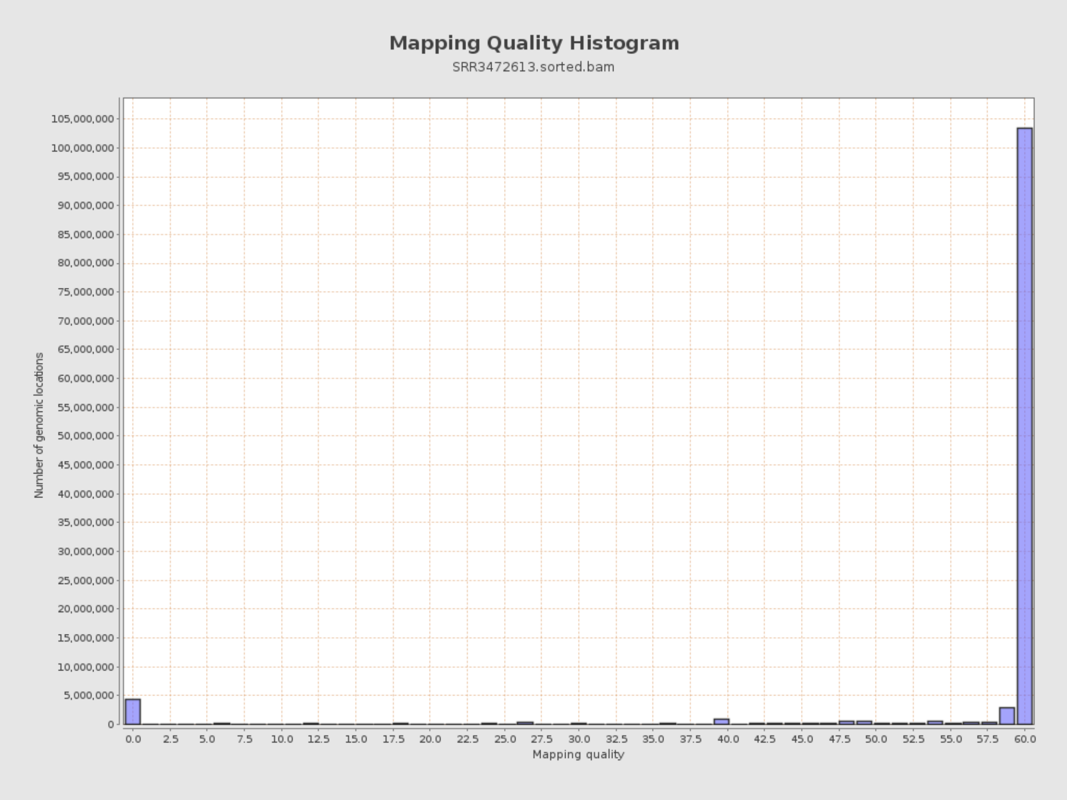
11. Results : Homopolymer Indels



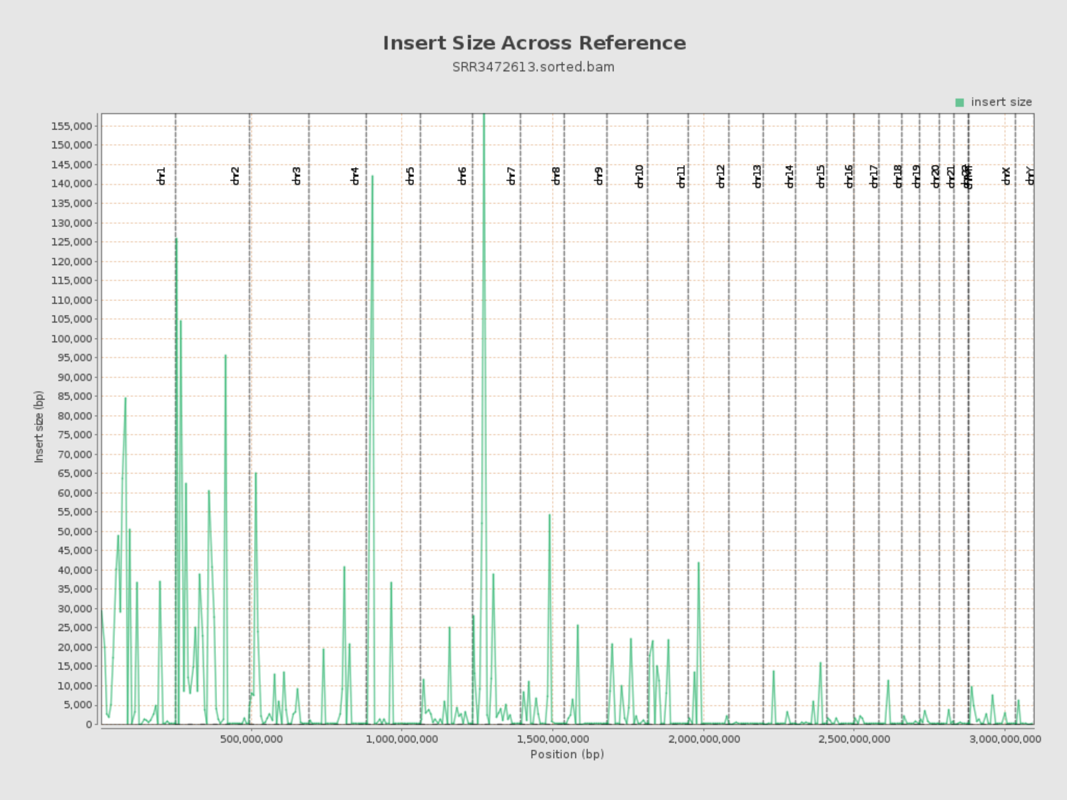
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram