Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 17:27:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472714.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_SRR3472714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472714_1.fastq.gz SRR3472714_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 17:27:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,268,014
Mapped reads	39,948,143 / 99.21%
Unmapped reads	319,871 / 0.79%
Mapped paired reads	39,948,143 / 99.21%
Mapped reads, first in pair	20,027,599 / 49.74%
Mapped reads, second in pair	19,920,544 / 49.47%
Mapped reads, both in pair	39,757,732 / 98.73%
Mapped reads, singletons	190,411 / 0.47%
Secondary alignments	0
Supplementary alignments	144,354 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	28,110,398 / 69.81%
Duplication rate	47.57%
Clipped reads	3,447,593 / 8.56%

2.2. ACGT Content

Number/percentage of A's	1,081,569,992 / 27.52%
Number/percentage of C's	888,956,002 / 22.62%
Number/percentage of T's	1,074,025,812 / 27.33%
Number/percentage of G's	884,862,538 / 22.51%
Number/percentage of N's	768,267 / 0.02%

GC Percentage	45.13%

2.3. Coverage

Mean	1.2697
Standard Deviation	37.9251

2.4. Mapping Quality

Mean Mapping Quality	55.26

2.5. Insert size

Mean	24,496.89
Standard Deviation	1,533,442.18
P25/Median/P75	164 / 229 / 310

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	22,939,190
Insertions	229,407
Mapped reads with at least one insertion	0.57%
Deletions	227,483
Mapped reads with at least one deletion	0.56%
Homopolymer indels	44.81%

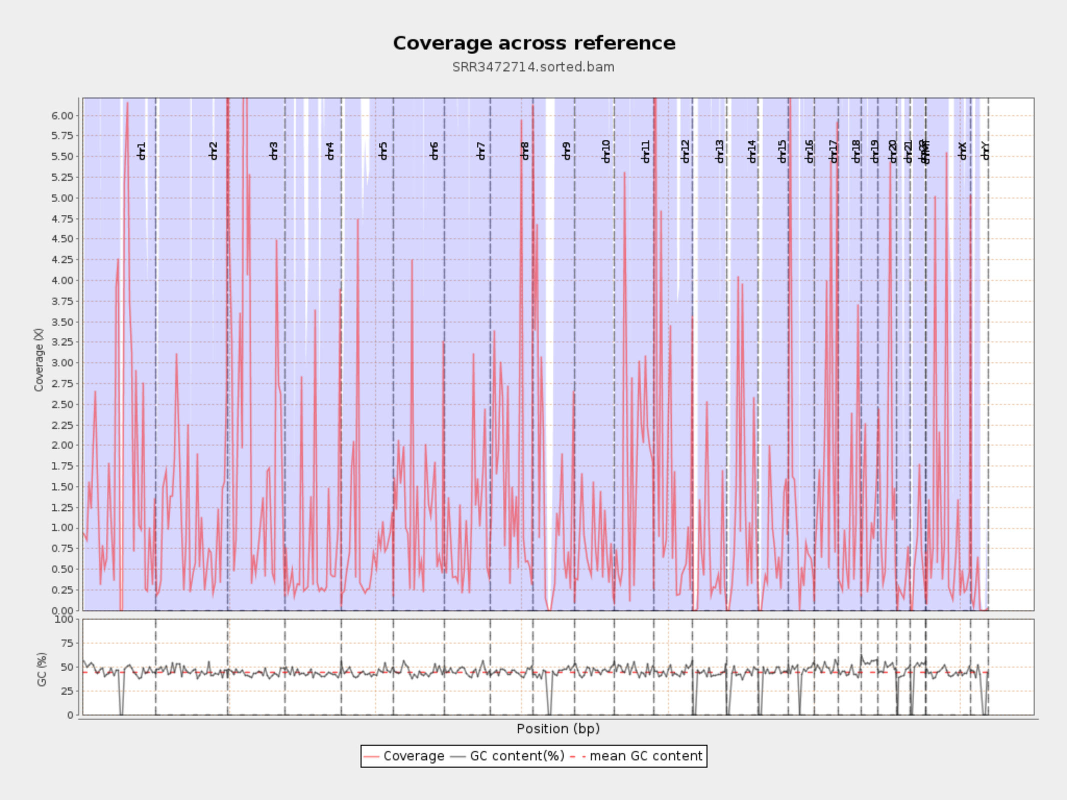
2.7. Chromosome stats

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

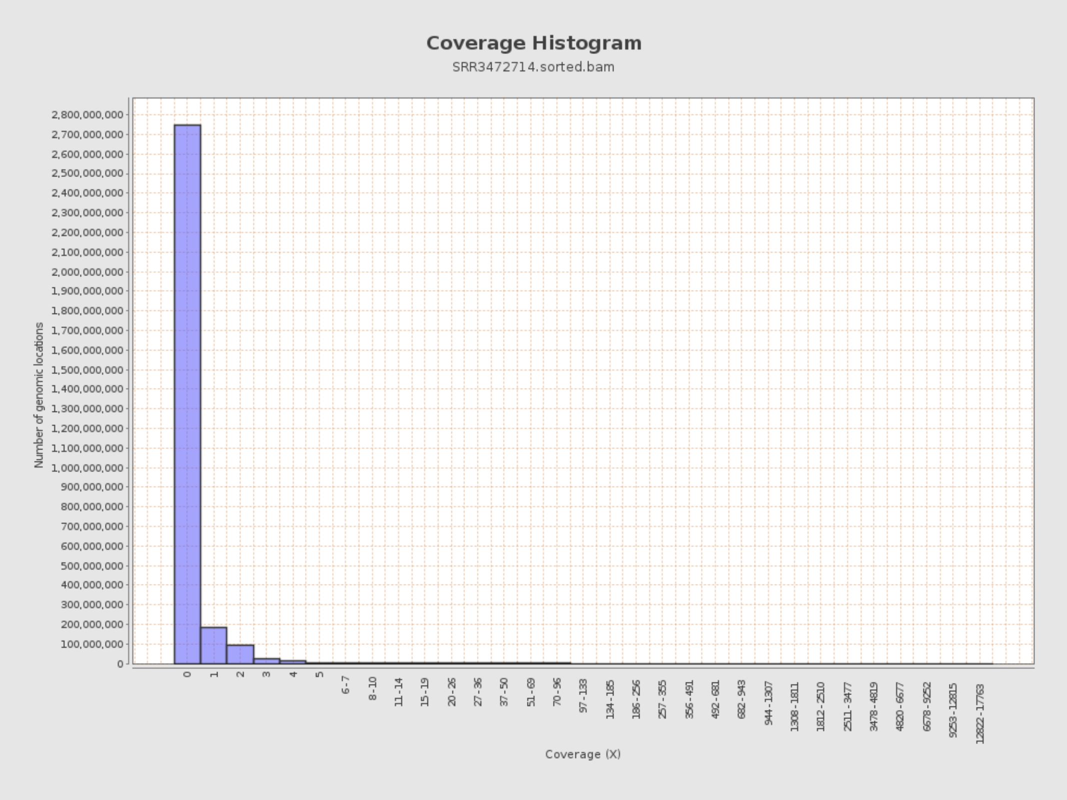
		bases	coverage	deviation
chr1	249250621	422185495	1.6938	51.7669
chr2	243199373	252413668	1.0379	35.3581
chr3	198022430	502769600	2.539	53.7804
chr4	191154276	155645749	0.8142	27.9631
chr5	180915260	154200029	0.8523	22.8288
chr6	171115067	217999224	1.274	34.9082
chr7	159138663	159530668	1.0025	29.0148
chr8	146364022	237009844	1.6193	47.0204
chr9	141213431	187517931	1.3279	31.9398
chr10	135534747	105770138	0.7804	23.9185
chr11	135006516	232421566	1.7216	55.4833
chr12	133851895	244401840	1.8259	51.939
chr13	115169878	73309634	0.6365	21.545
chr14	107349540	139301486	1.2976	48.796
chr15	102531392	72760090	0.7096	19.9181
chr16	90354753	113418033	1.2553	32.7051
chr17	81195210	172132851	2.12	37.9902
chr18	78077248	84102392	1.0772	33.2087
chr19	59128983	67305865	1.1383	22.4893
chr20	63025520	100583954	1.5959	45.4448
chr21	48129895	15333030	0.3186	10.2838
chr22	51304566	33878427	0.6603	19.2129
chrMT	16571	11866	0.7161	1.8979
chrX	155270560	178164888	1.1474	31.9829

chrY	59373566	8572416	0.1444	10.2546

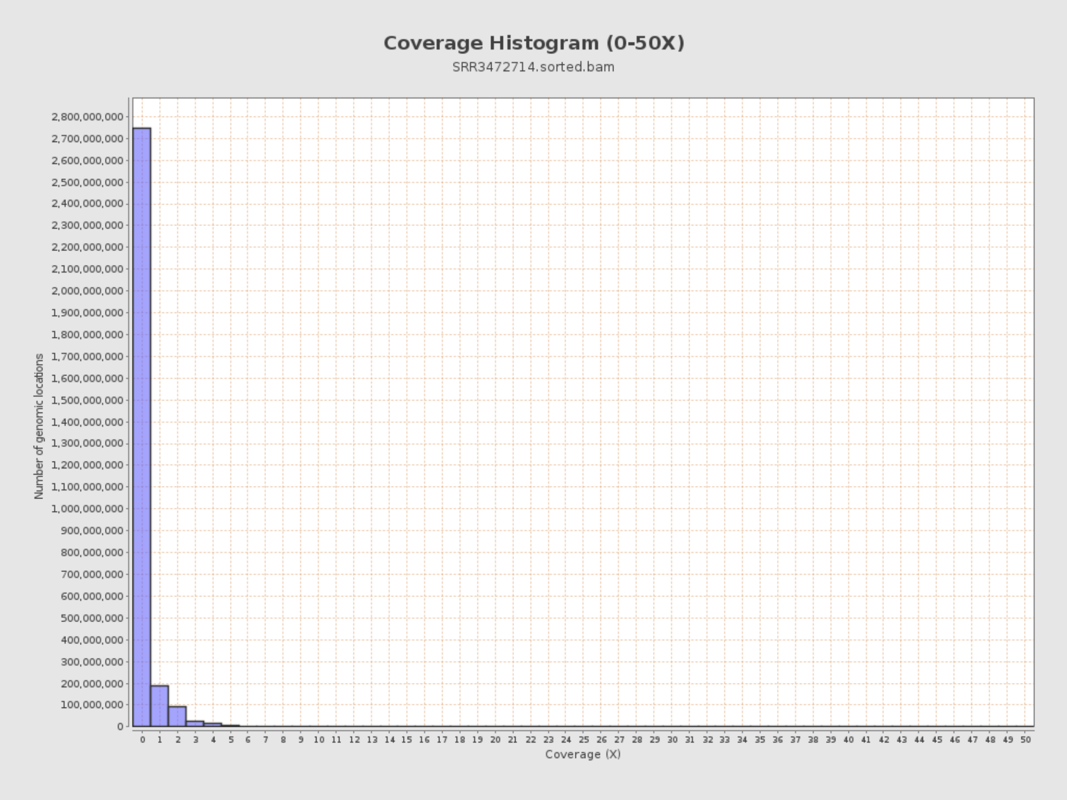
3. Results : Coverage across reference



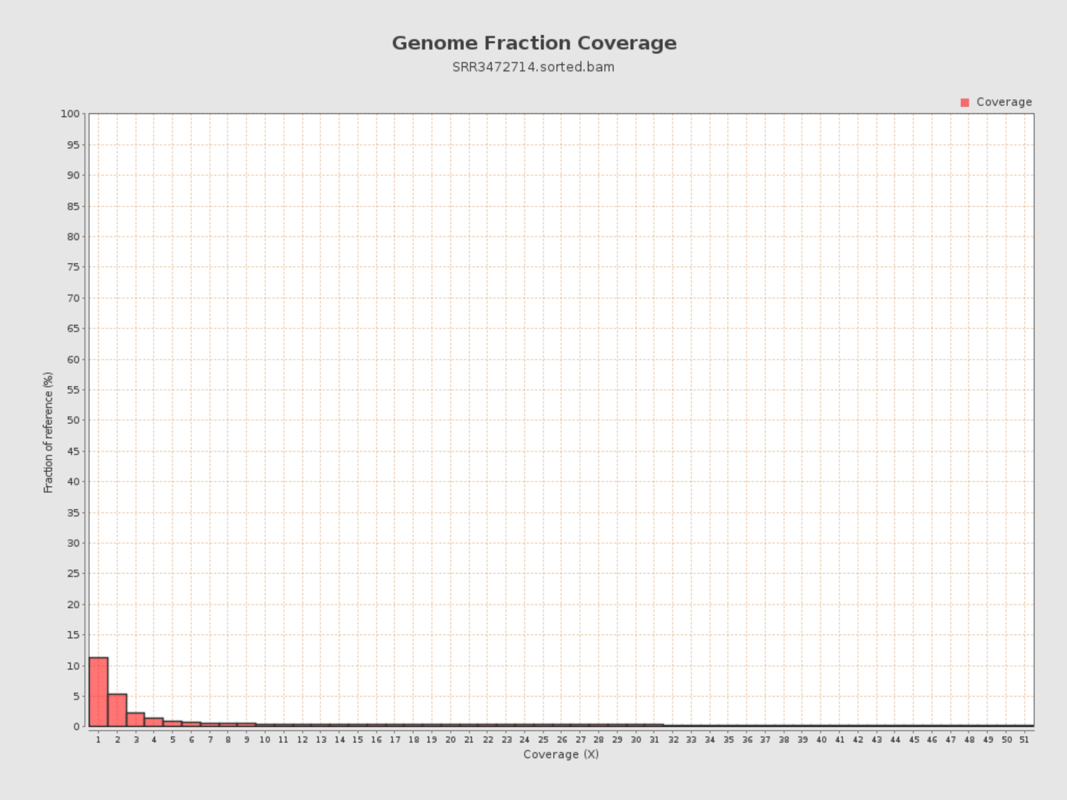
4. Results : Coverage Histogram



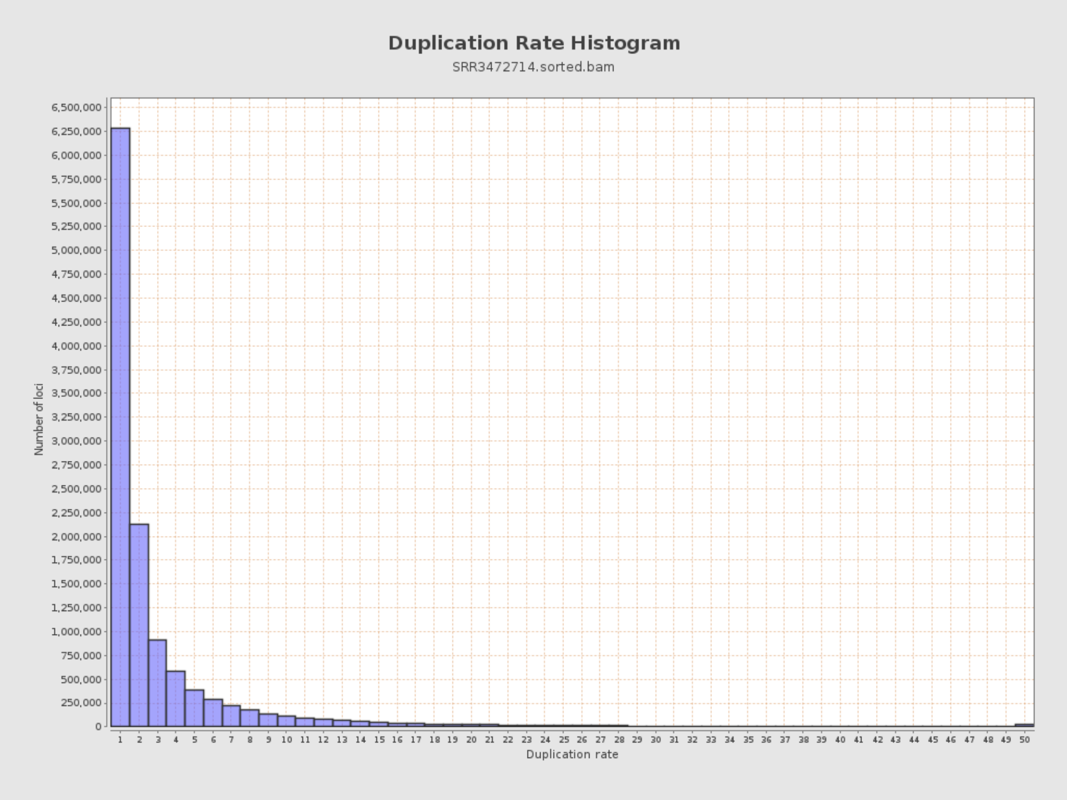
5. Results : Coverage Histogram (0-50X)



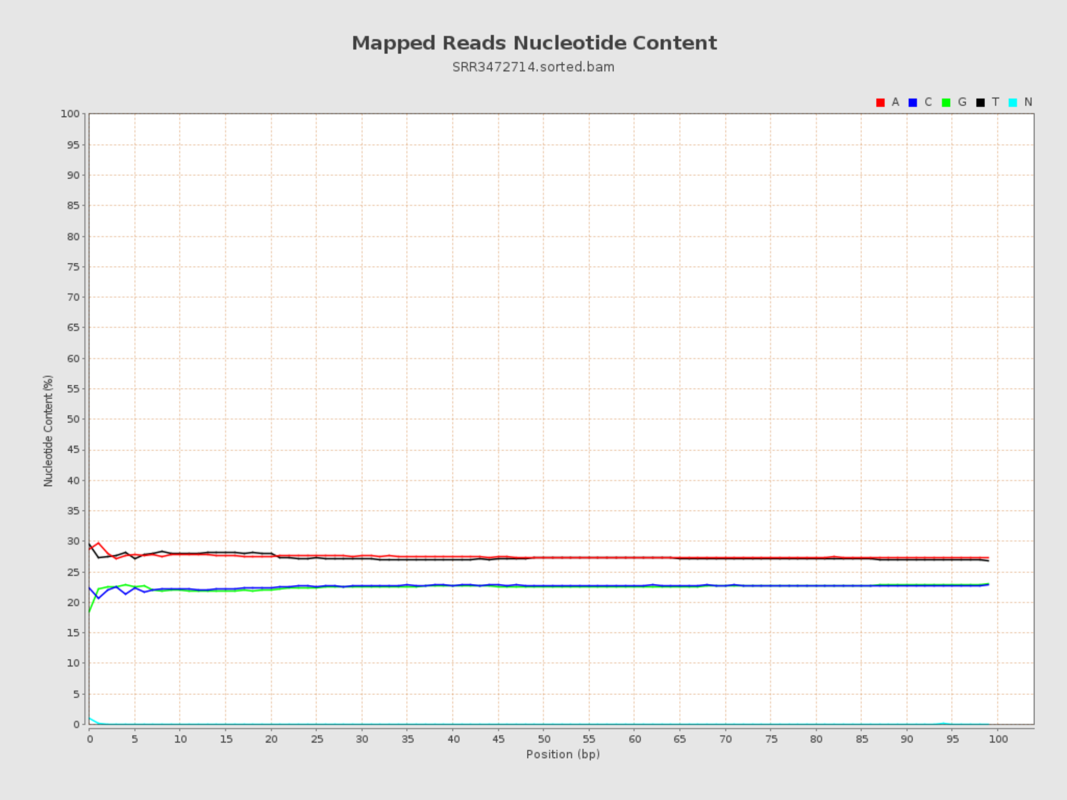
6. Results : Genome Fraction Coverage



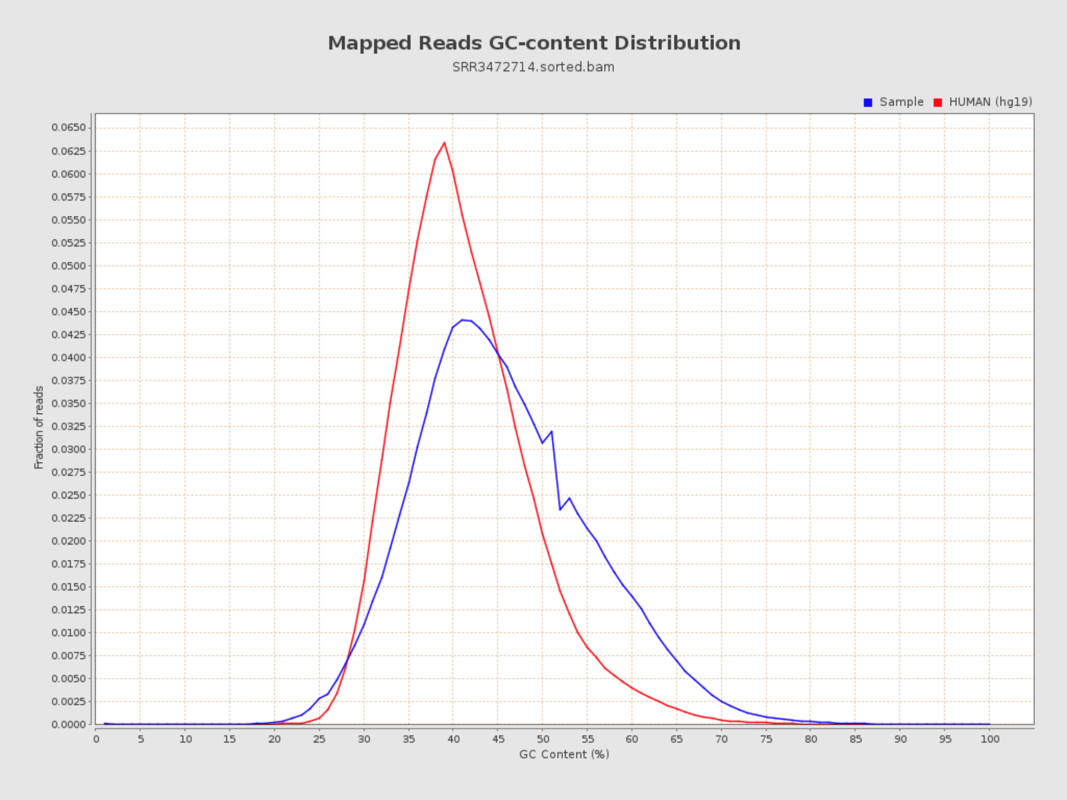
7. Results : Duplication Rate Histogram



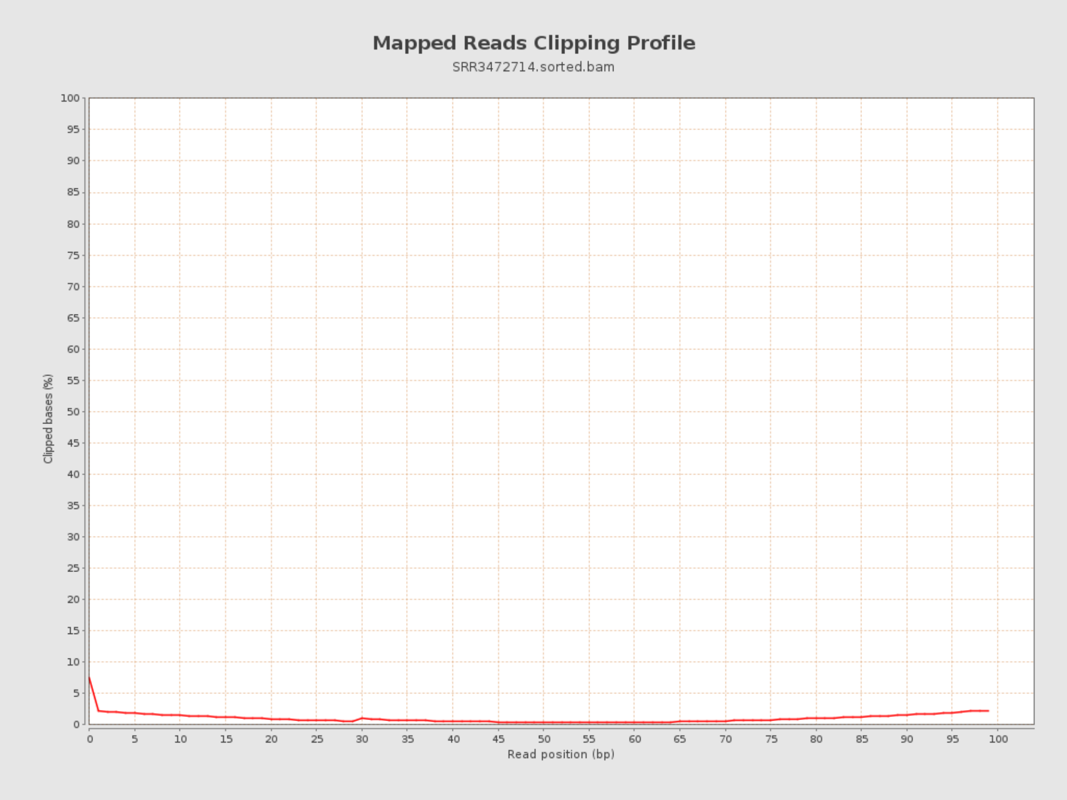
8. Results : Mapped Reads Nucleotide Content



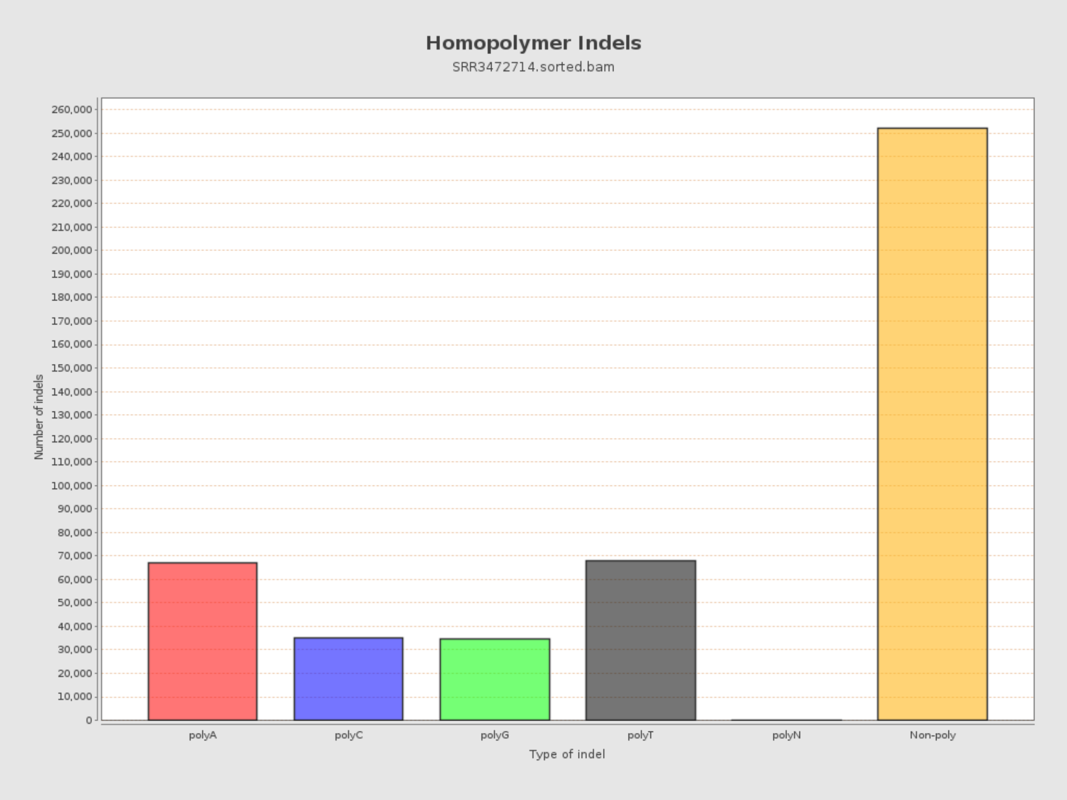
9. Results : Mapped Reads GC-content Distribution



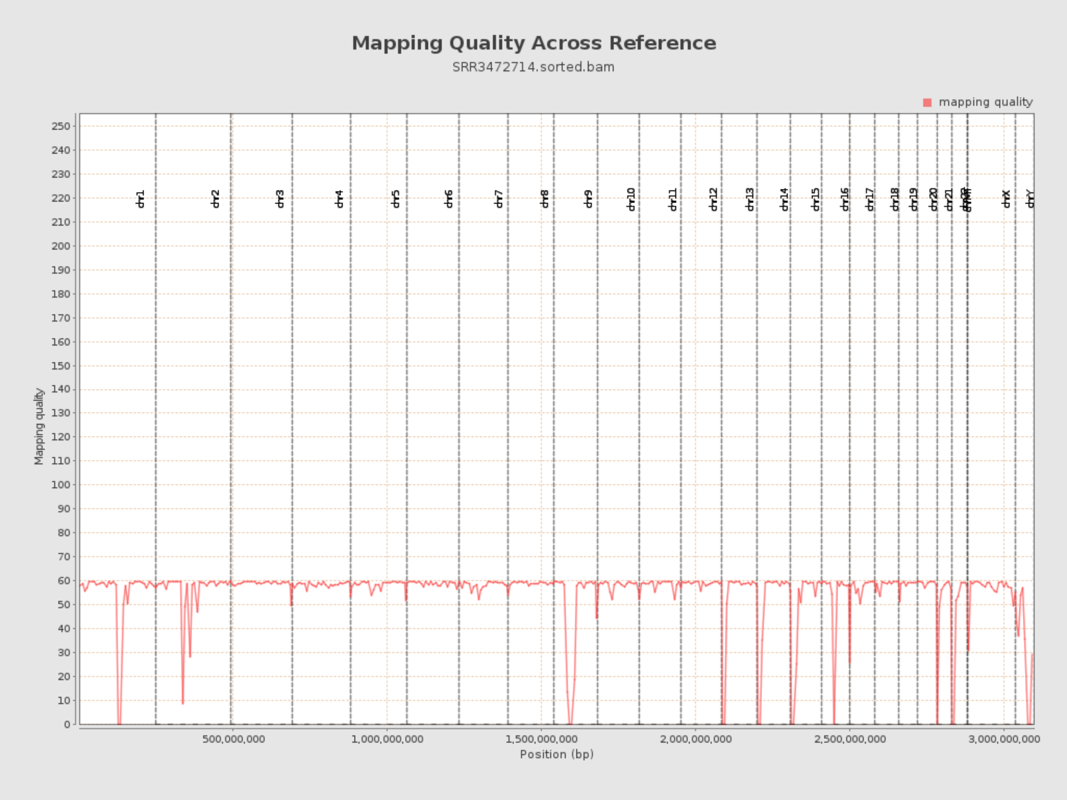
10. Results : Mapped Reads Clipping Profile



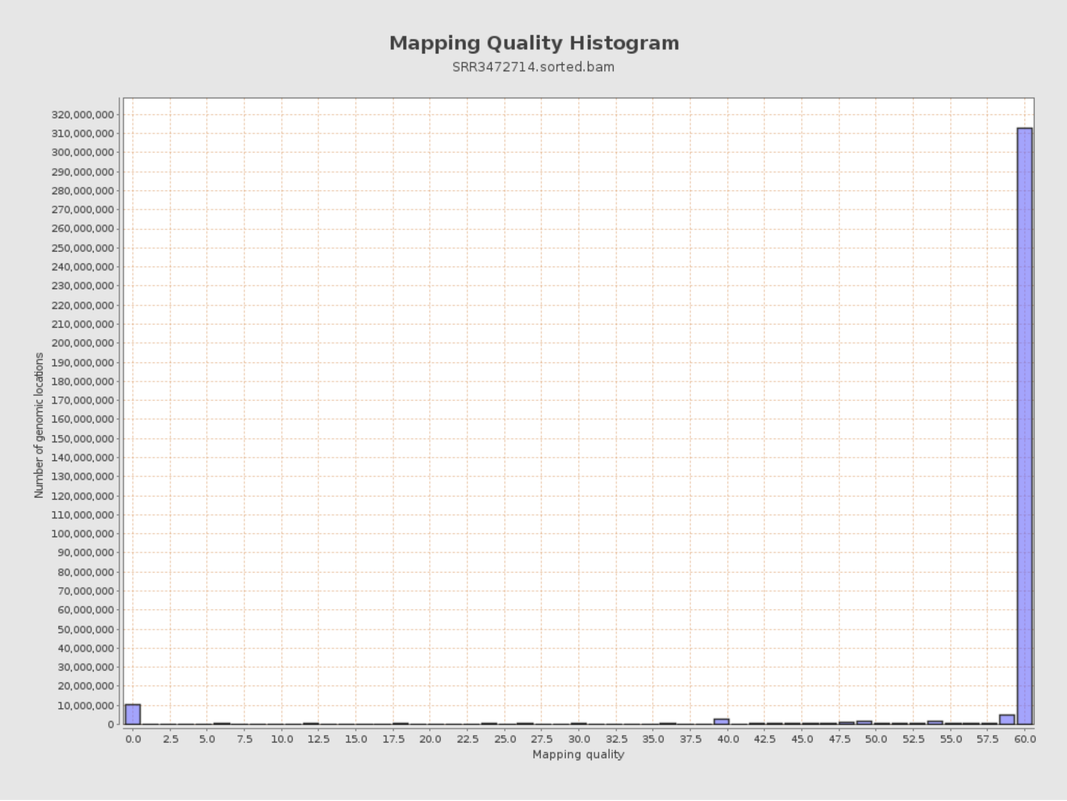
11. Results : Homopolymer Indels



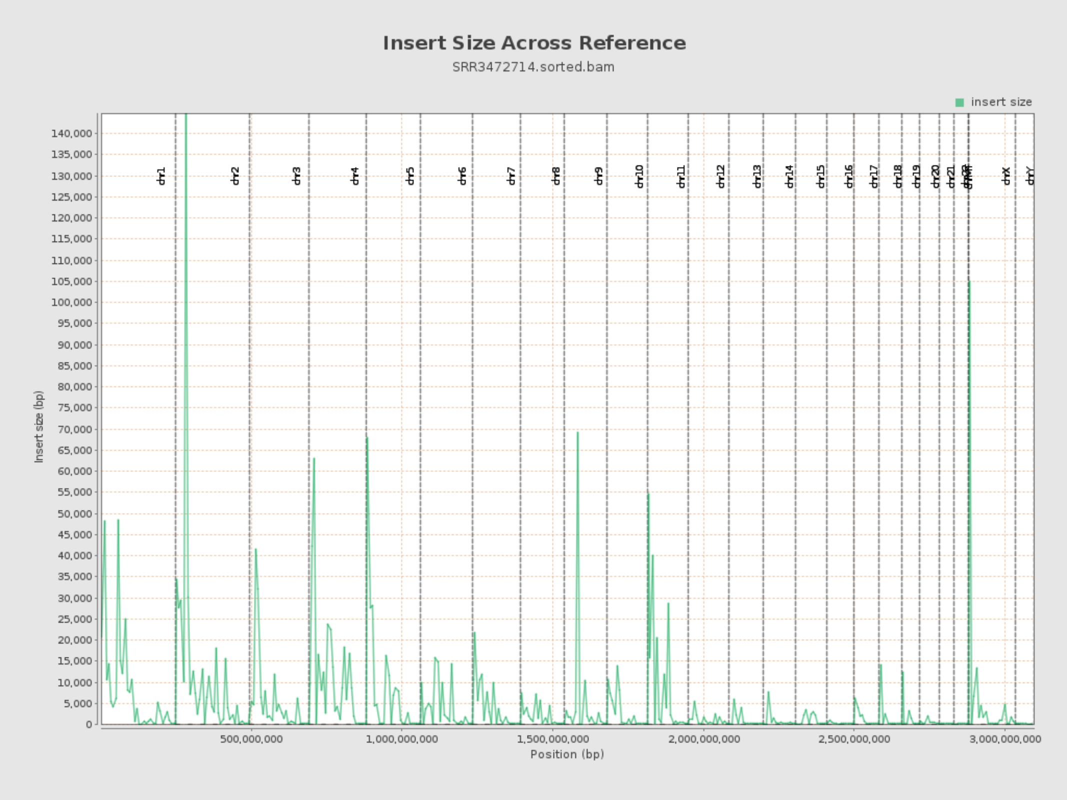
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram