Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:25:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472406.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_SRR3472406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472406_1.fastq.gz SRR3472406_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:25:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,674,906
Mapped reads	18,516,451 / 99.15%
Unmapped reads	158,455 / 0.85%
Mapped paired reads	18,516,451 / 99.15%
Mapped reads, first in pair	9,286,193 / 49.73%
Mapped reads, second in pair	9,230,258 / 49.43%
Mapped reads, both in pair	18,420,474 / 98.64%
Mapped reads, singletons	95,977 / 0.51%
Secondary alignments	0
Supplementary alignments	98,539 / 0.53%
Read min/max/mean length	30 / 100 / 99.46
Duplicated reads (estimated)	13,526,324 / 72.43%
Duplication rate	45.12%
Clipped reads	1,364,397 / 7.31%

2.2. ACGT Content

Number/percentage of A's	491,816,167 / 27.08%
Number/percentage of C's	417,494,979 / 22.99%
Number/percentage of T's	492,738,300 / 27.13%
Number/percentage of G's	413,690,653 / 22.78%
Number/percentage of N's	221,158 / 0.01%

GC Percentage	45.77%

2.3. Coverage

Mean	0.5867
Standard Deviation	36.1867

2.4. Mapping Quality

Mean Mapping Quality	54.14

2.5. Insert size

Mean	15,797.32
Standard Deviation	1,135,373.08
P25/Median/P75	154 / 214 / 287

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	9,646,345
Insertions	106,876
Mapped reads with at least one insertion	0.57%
Deletions	90,173
Mapped reads with at least one deletion	0.48%
Homopolymer indels	49.06%

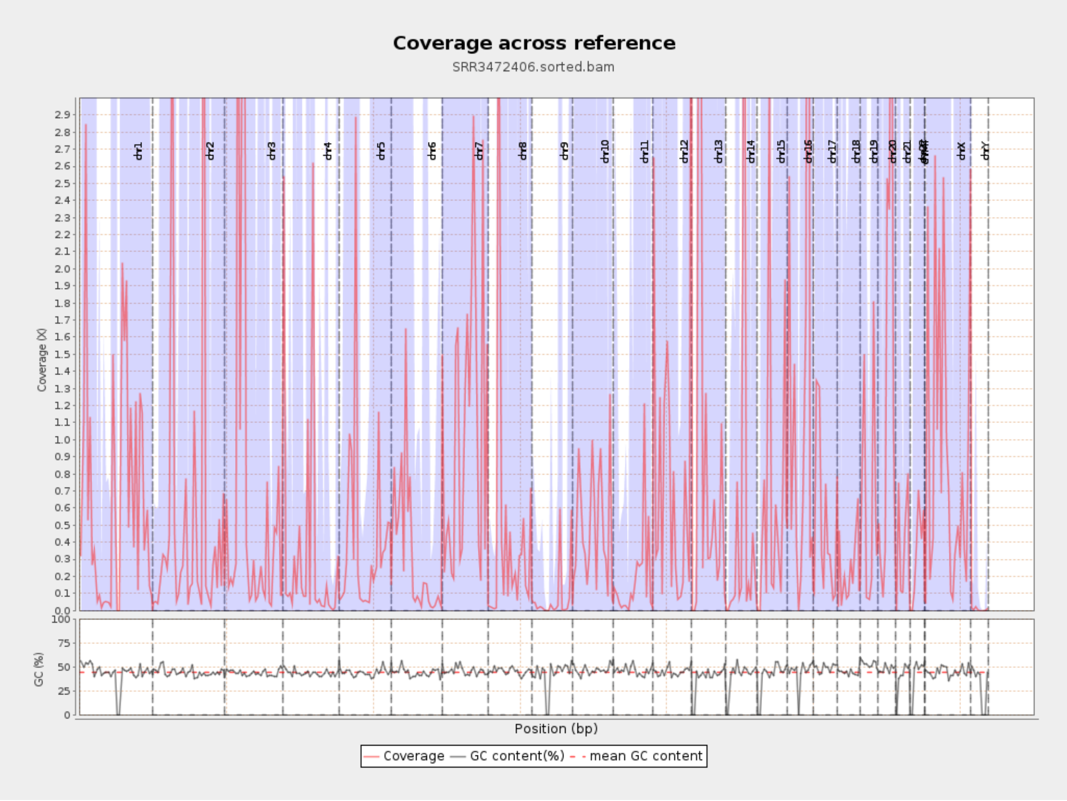
2.7. Chromosome stats

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

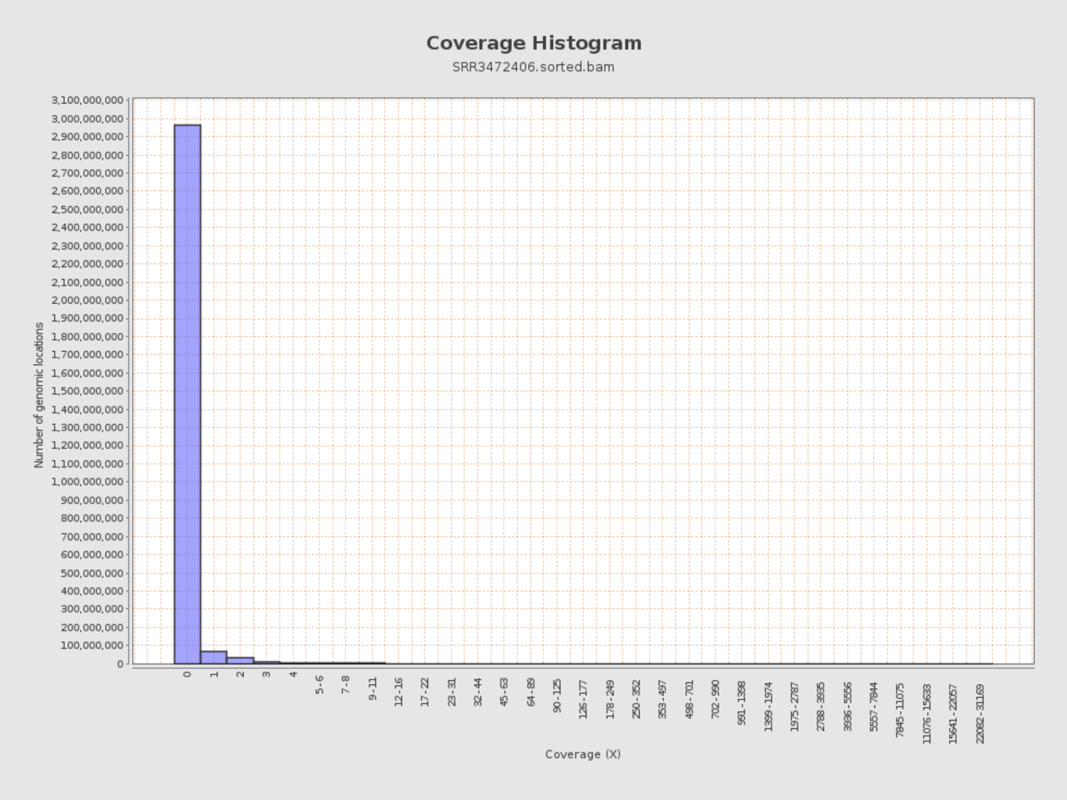
		bases	coverage	deviation
chr1	249250621	167177051	0.6707	31.6904
chr2	243199373	132335798	0.5441	47.3894
chr3	198022430	150873307	0.7619	57.2278
chr4	191154276	62259910	0.3257	21.2116
chr5	180915260	77833233	0.4302	20.1757
chr6	171115067	55552326	0.3246	17.0288
chr7	159138663	169874023	1.0675	45.8412
chr8	146364022	65144475	0.4451	25.7307
chr9	141213431	11811443	0.0836	5.6317
chr10	135534747	67682985	0.4994	23.5517
chr11	135006516	26264653	0.1945	13.8905
chr12	133851895	102605972	0.7666	28.222
chr13	115169878	107250836	0.9312	49.9692
chr14	107349540	52504764	0.4891	39.6529
chr15	102531392	68507033	0.6682	30.9025
chr16	90354753	128288302	1.4198	57.2595
chr17	81195210	40223746	0.4954	40.1804
chr18	78077248	18897505	0.242	10.2651
chr19	59128983	40176211	0.6795	21.2756
chr20	63025520	92967022	1.4751	84.6009
chr21	48129895	18247553	0.3791	18.412
chr22	51304566	17099556	0.3333	11.7163
chrMT	16571	8747	0.5278	0.9362
chrX	155270560	142191168	0.9158	41.2691

chrY	59373566	405608	0.0068	0.5639

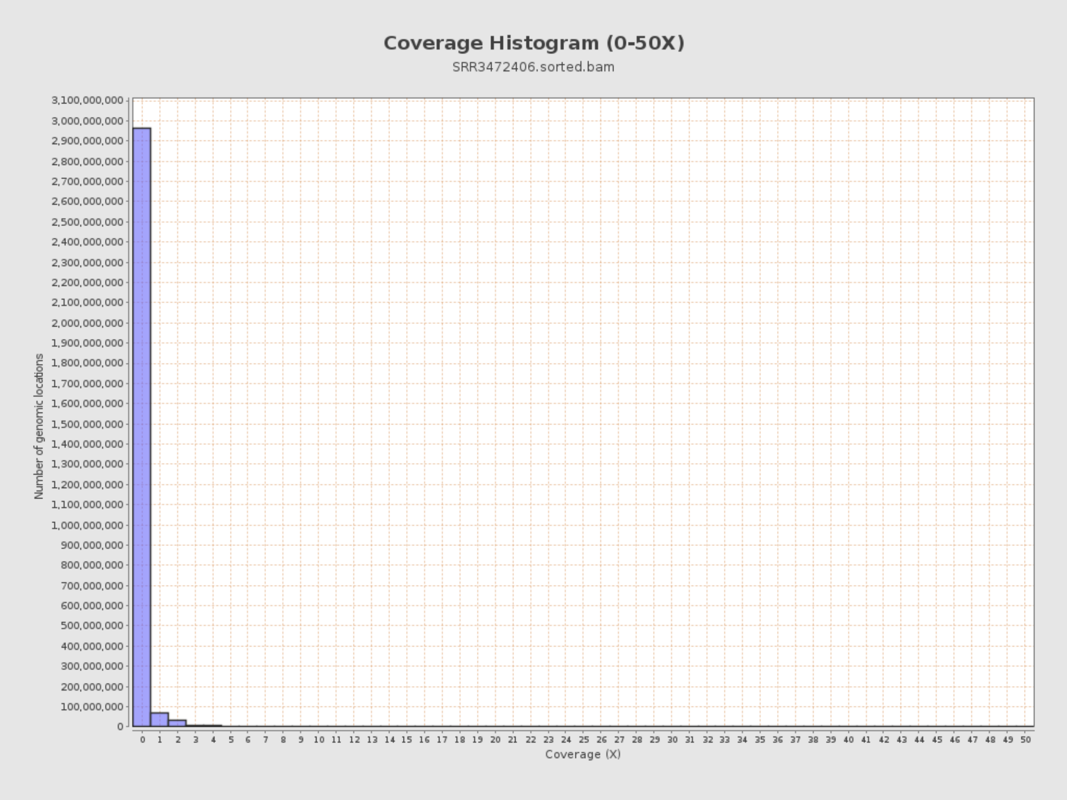
3. Results : Coverage across reference



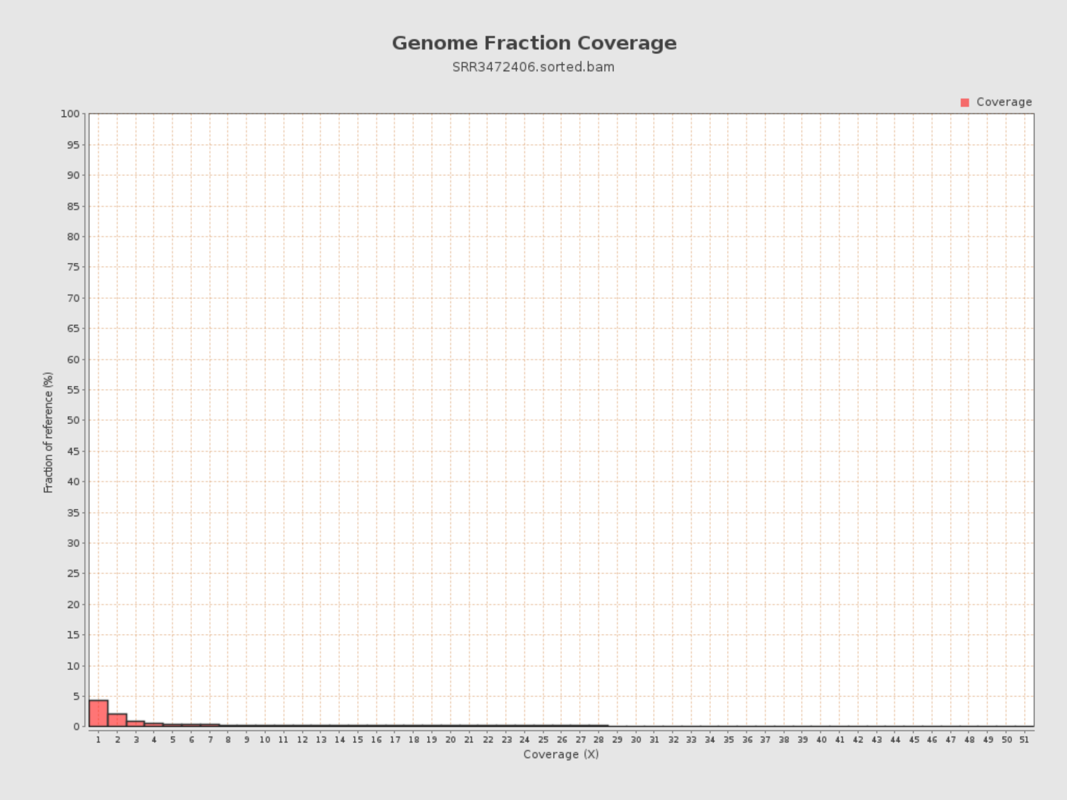
4. Results : Coverage Histogram



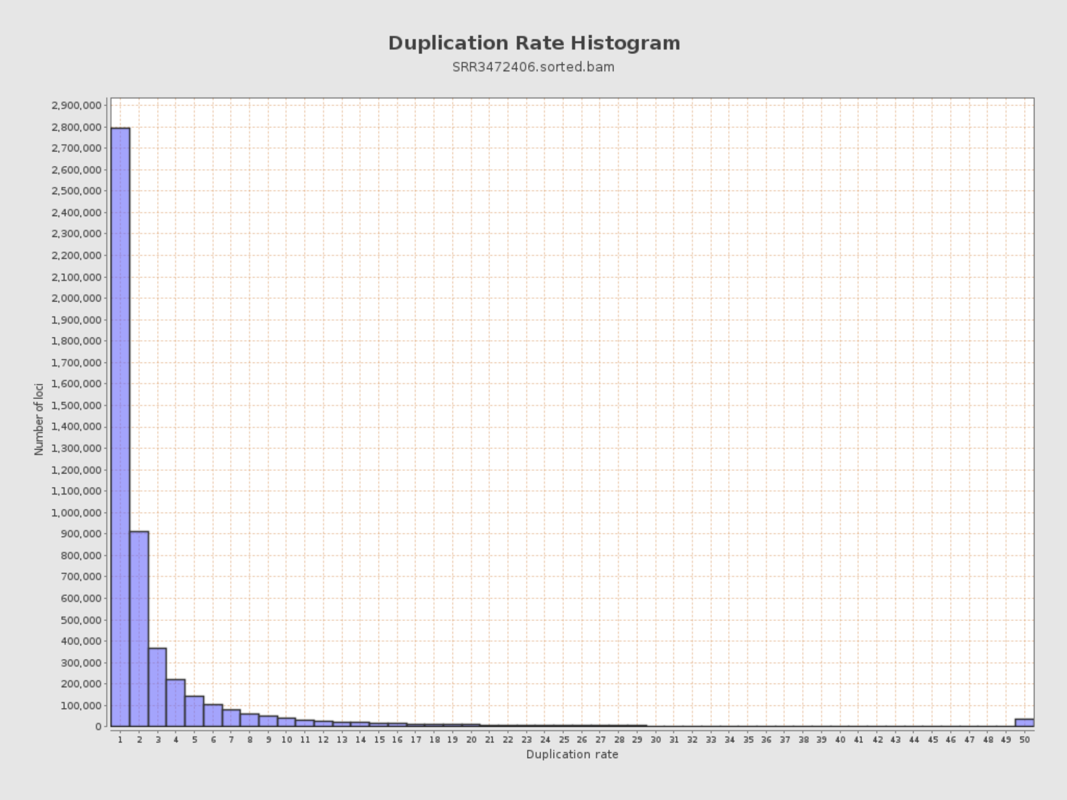
5. Results : Coverage Histogram (0-50X)



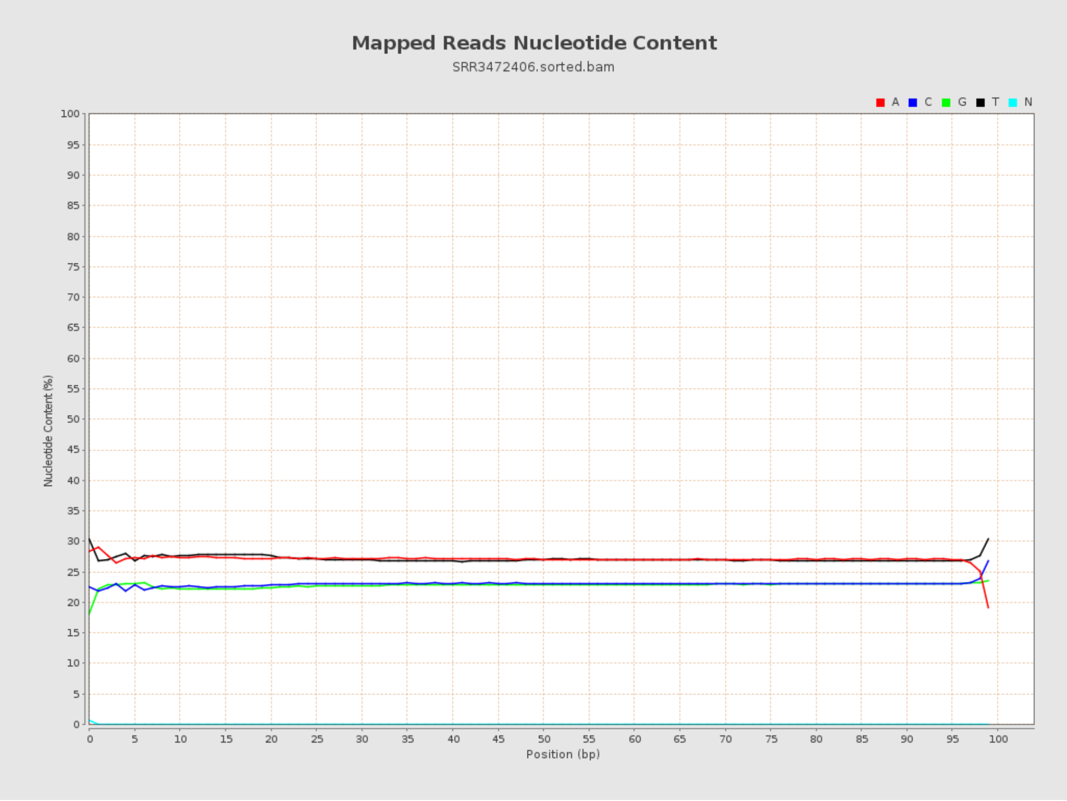
6. Results : Genome Fraction Coverage



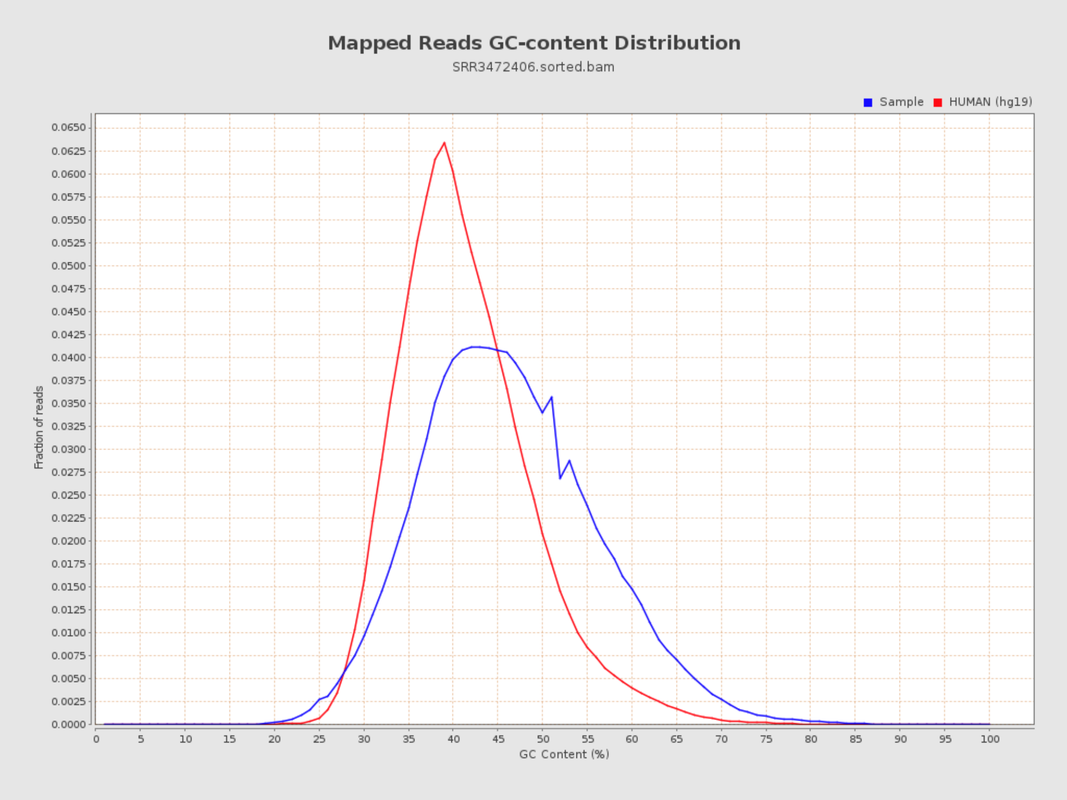
7. Results : Duplication Rate Histogram



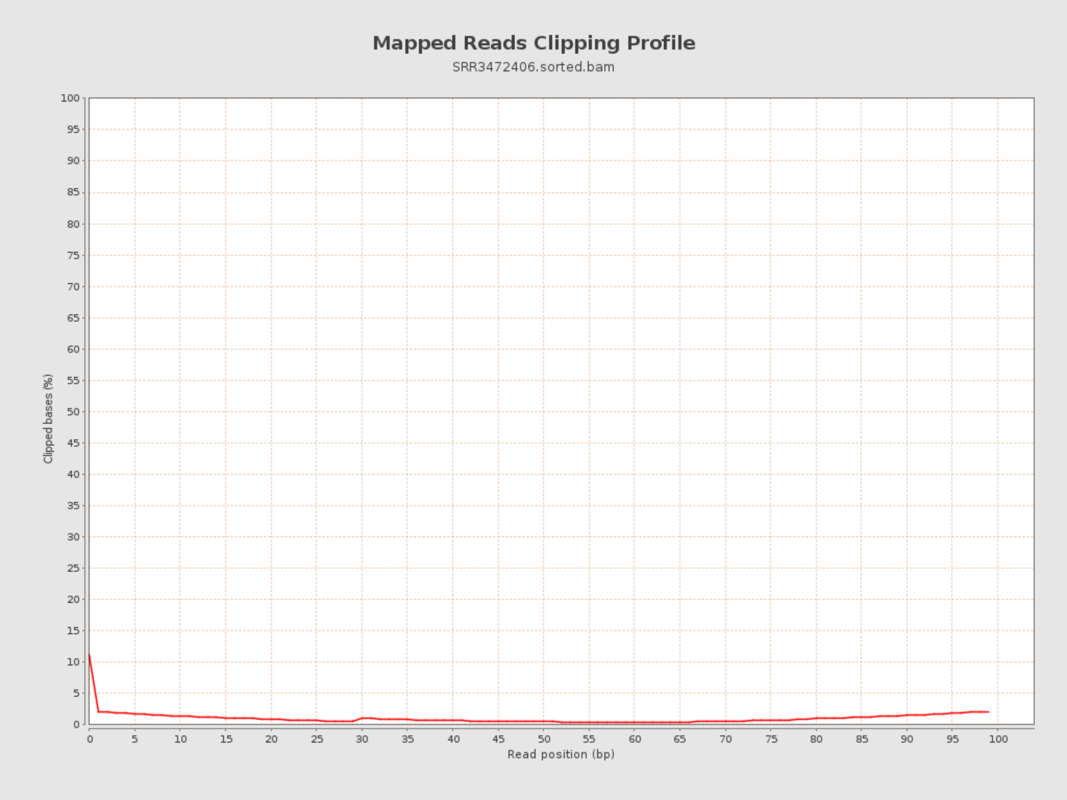
8. Results : Mapped Reads Nucleotide Content



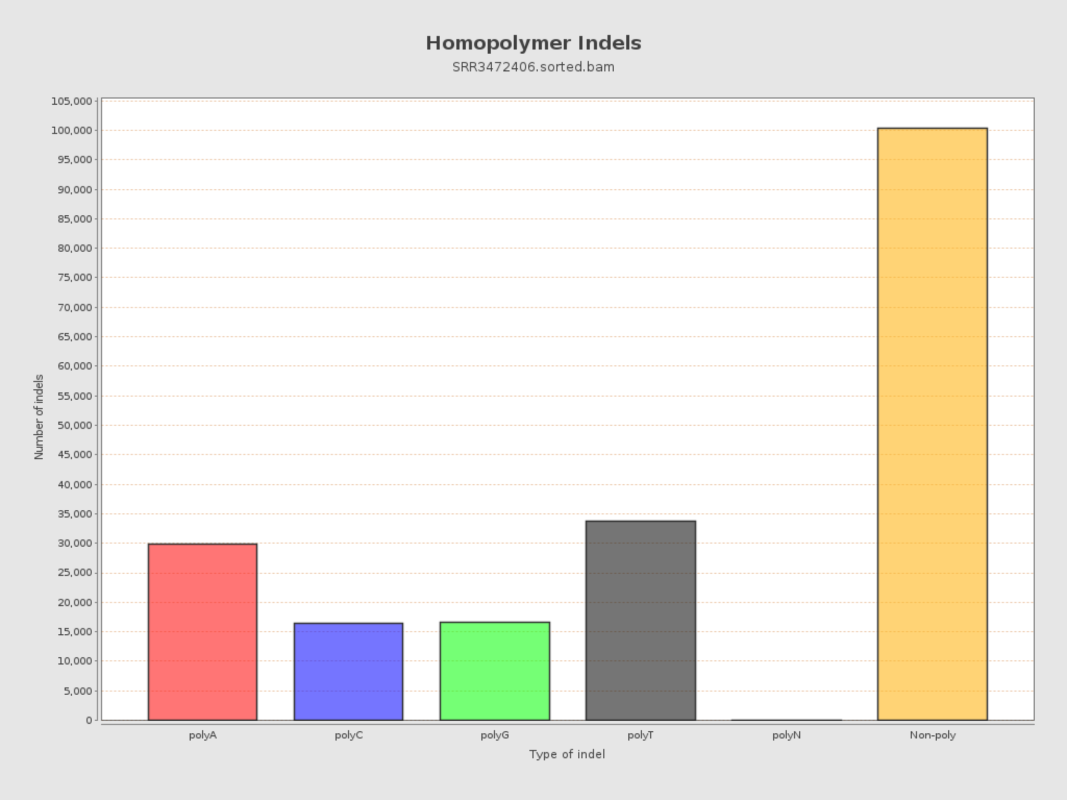
9. Results : Mapped Reads GC-content Distribution



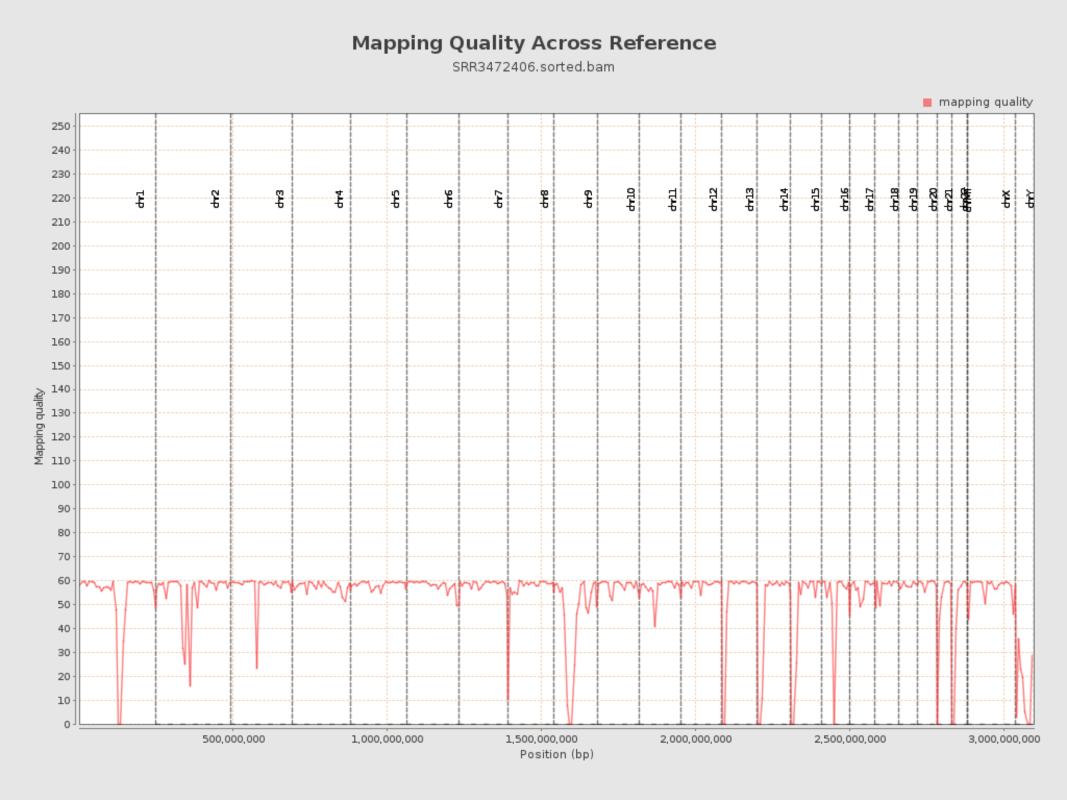
10. Results : Mapped Reads Clipping Profile



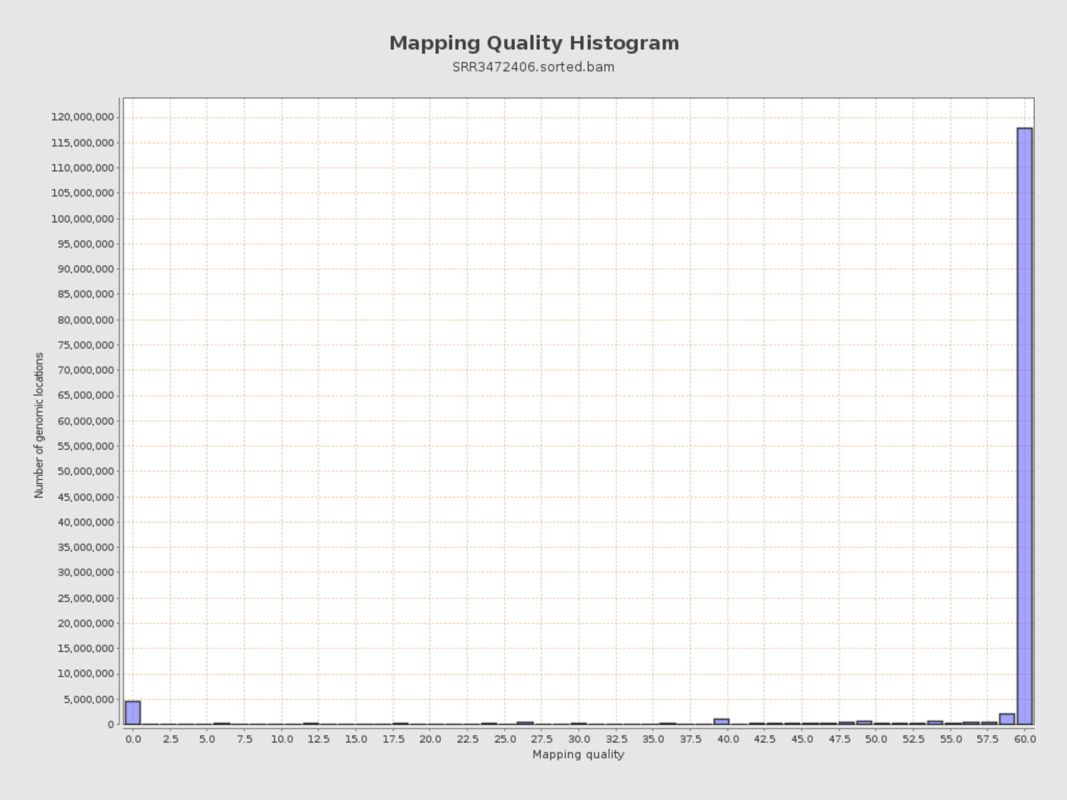
11. Results : Homopolymer Indels



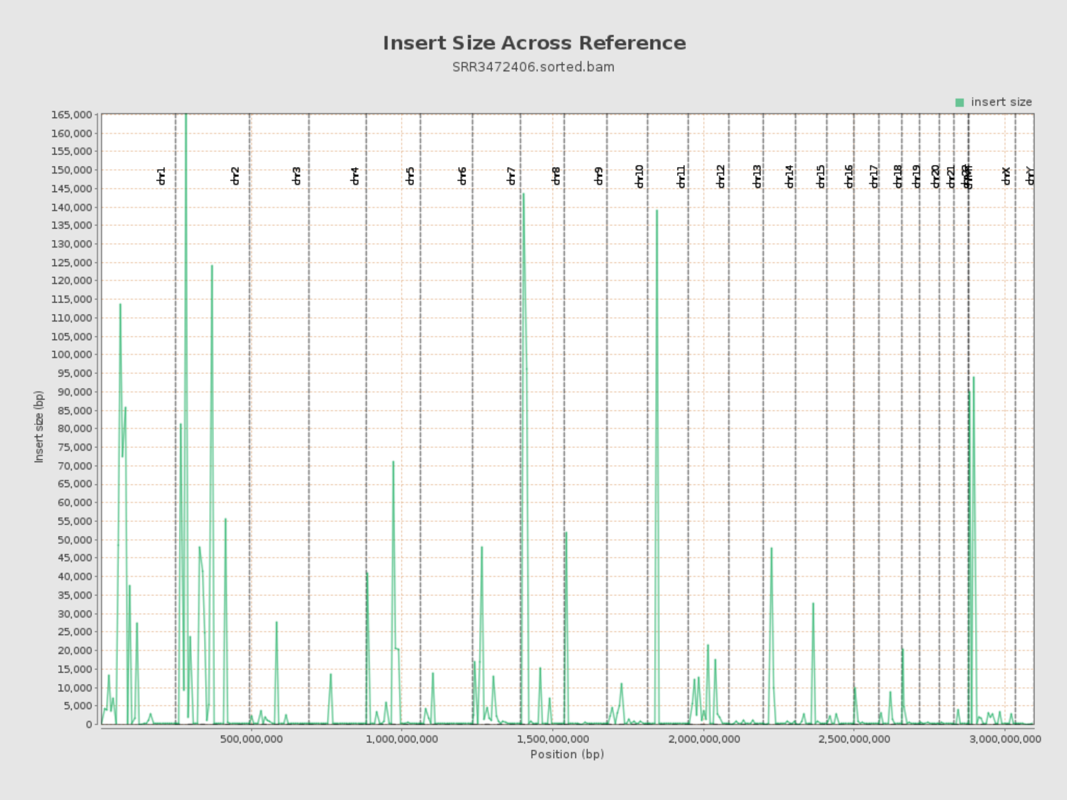
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram