Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:45:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006408.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_SRR1006408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006408_1.fastq.gz SRR1006408_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:45:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,280,186
Mapped reads	6,493,910 / 89.2%
Unmapped reads	786,276 / 10.8%
Mapped paired reads	6,493,910 / 89.2%
Mapped reads, first in pair	3,271,163 / 44.93%
Mapped reads, second in pair	3,222,747 / 44.27%
Mapped reads, both in pair	5,997,828 / 82.39%
Mapped reads, singletons	496,082 / 6.81%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	210,777 / 2.9%
Duplication rate	2.73%
Clipped reads	327,682 / 4.5%

2.2. ACGT Content

Number/percentage of A's	70,164,660 / 27.89%
Number/percentage of C's	54,074,151 / 21.5%
Number/percentage of T's	71,364,528 / 28.37%
Number/percentage of G's	55,940,859 / 22.24%
Number/percentage of N's	10,613 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0813
Standard Deviation	0.4267

2.4. Mapping Quality

Mean Mapping Quality	48.45

2.5. Insert size

Mean	64,894.41
Standard Deviation	2,435,312.78
P25/Median/P75	105 / 156 / 209

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	845,220
Insertions	6,971
Mapped reads with at least one insertion	0.11%
Deletions	22,358
Mapped reads with at least one deletion	0.34%
Homopolymer indels	45.05%

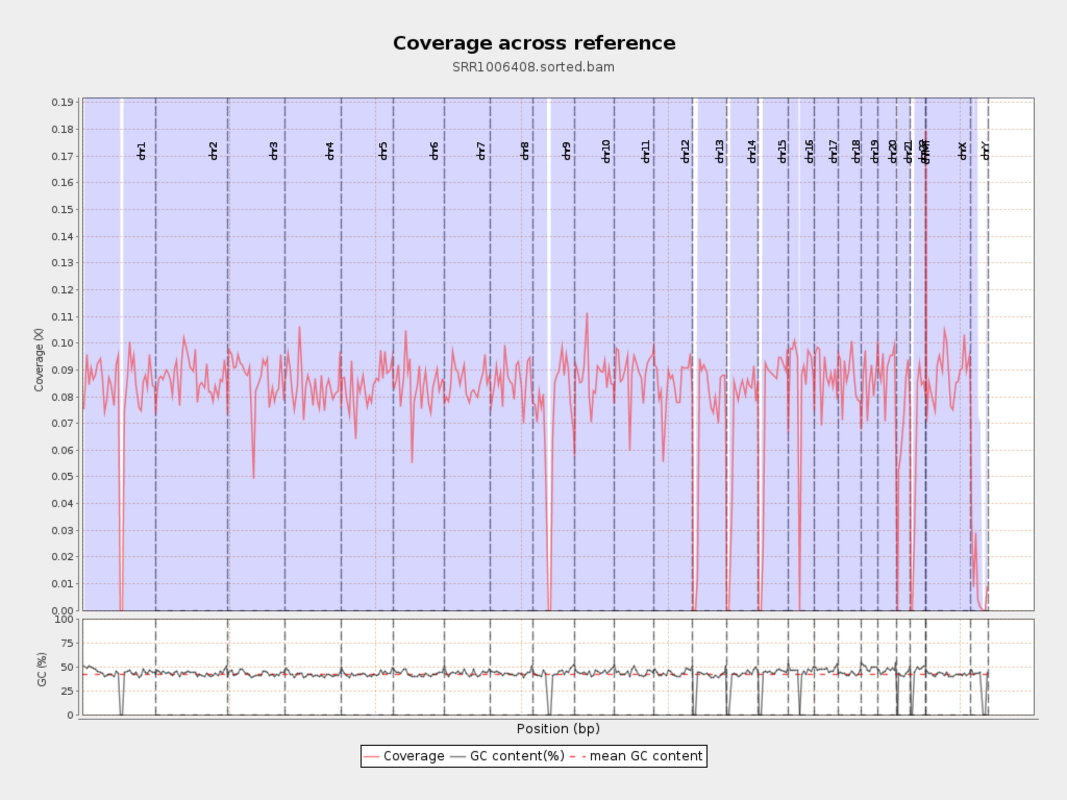
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

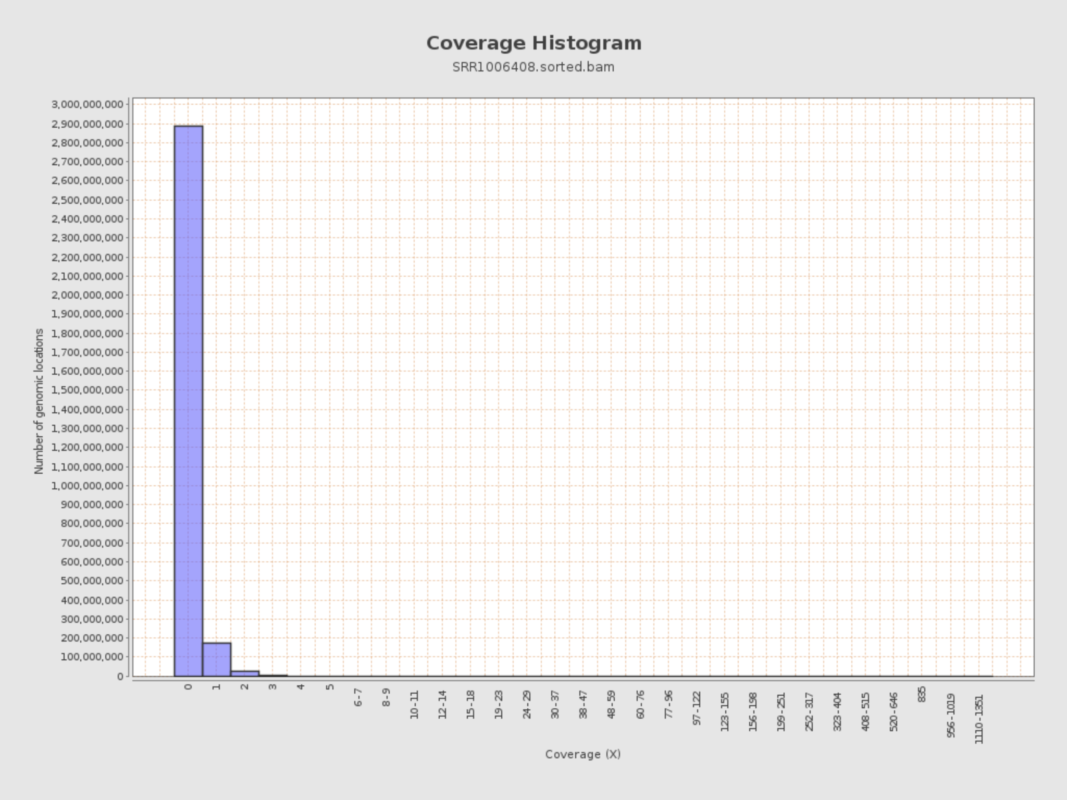
chr1	249250621	20142999	0.0808	0.5736
chr2	243199373	21269200	0.0875	0.4219
chr3	198022430	17045972	0.0861	0.3382
chr4	191154276	16136454	0.0844	0.3625
chr5	180915260	15303678	0.0846	0.336
chr6	171115067	14421683	0.0843	0.3765
chr7	159138663	13554249	0.0852	0.4871
chr8	146364022	12568253	0.0859	0.7488
chr9	141213431	10082931	0.0714	0.363
chr10	135534747	11874063	0.0876	0.4577
chr11	135006516	11999455	0.0889	0.407
chr12	133851895	11330468	0.0846	0.3404
chr13	115169878	8062383	0.07	0.3062
chr14	107349540	7501685	0.0699	0.3288
chr15	102531392	7490233	0.0731	0.3138
chr16	90354753	7594824	0.0841	0.4003
chr17	81195210	7191962	0.0886	0.3694
chr18	78077248	6782880	0.0869	0.5898
chr19	59128983	5098297	0.0862	0.463
chr20	63025520	5656804	0.0898	0.356
chr21	48129895	3203168	0.0666	0.3447
chr22	51304566	3055013	0.0595	0.2936
chrMT	16571	2979	0.1798	0.5905
chrX	155270560	13634546	0.0878	0.3778

chrY	59373566	579910	0.0098	0.2067

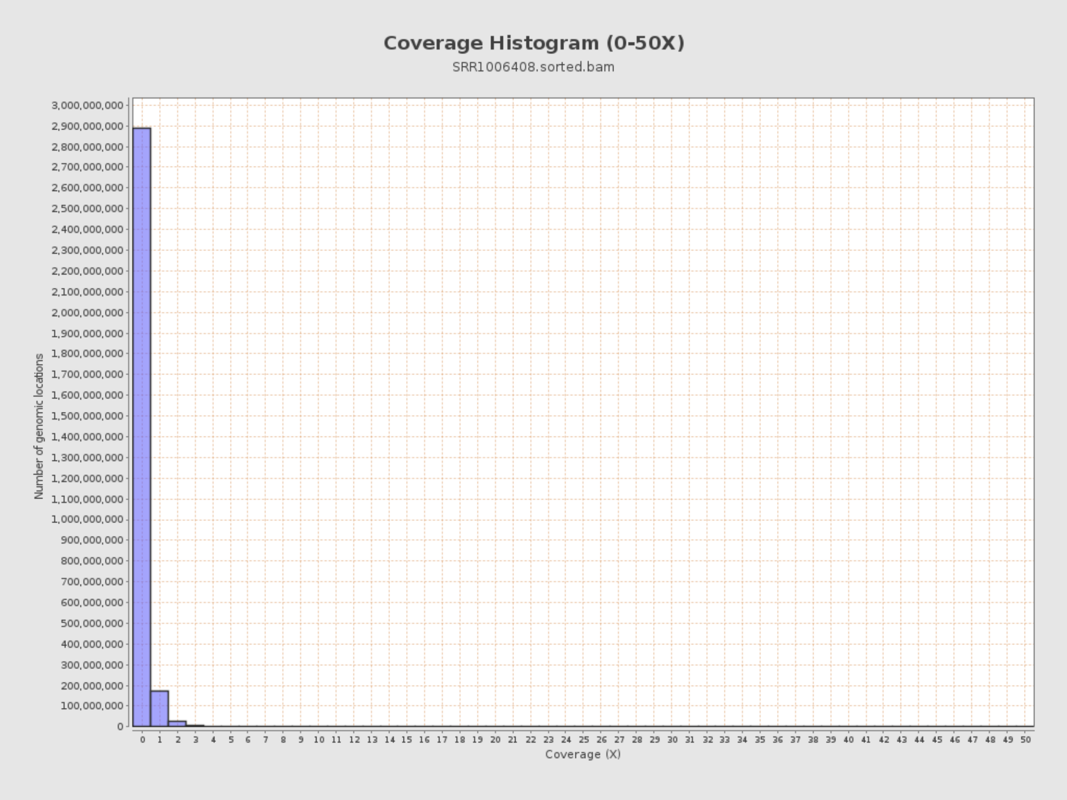
3. Results : Coverage across reference



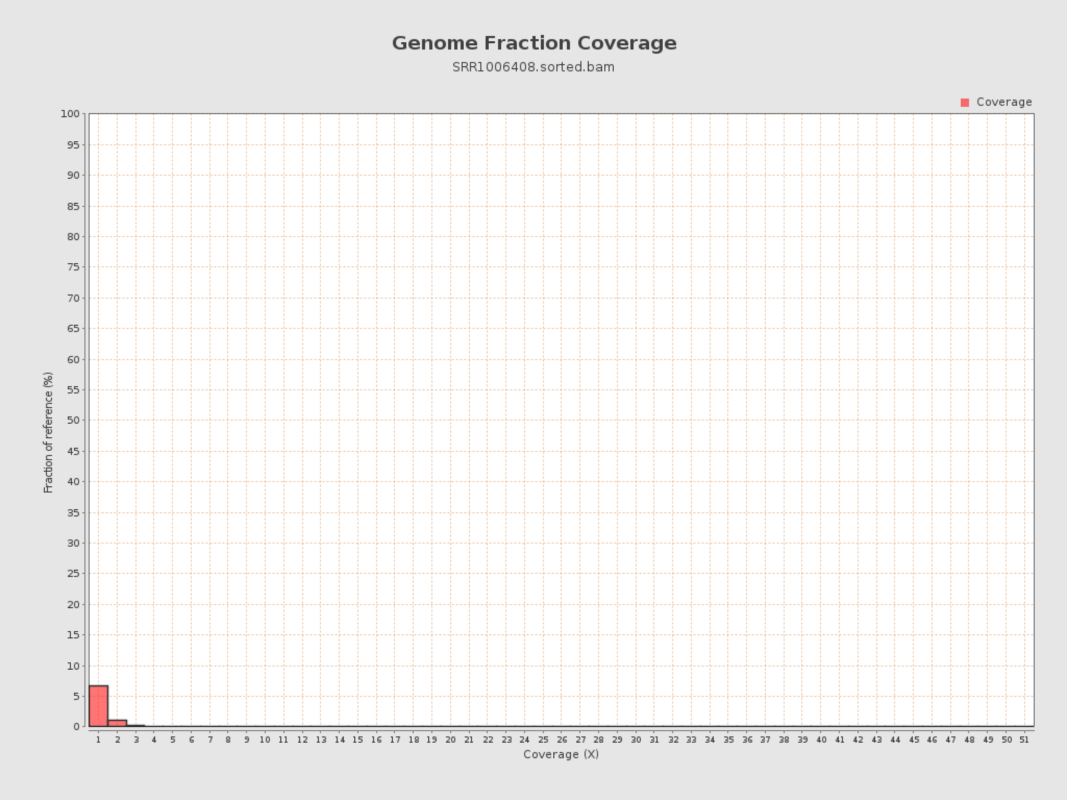
4. Results : Coverage Histogram



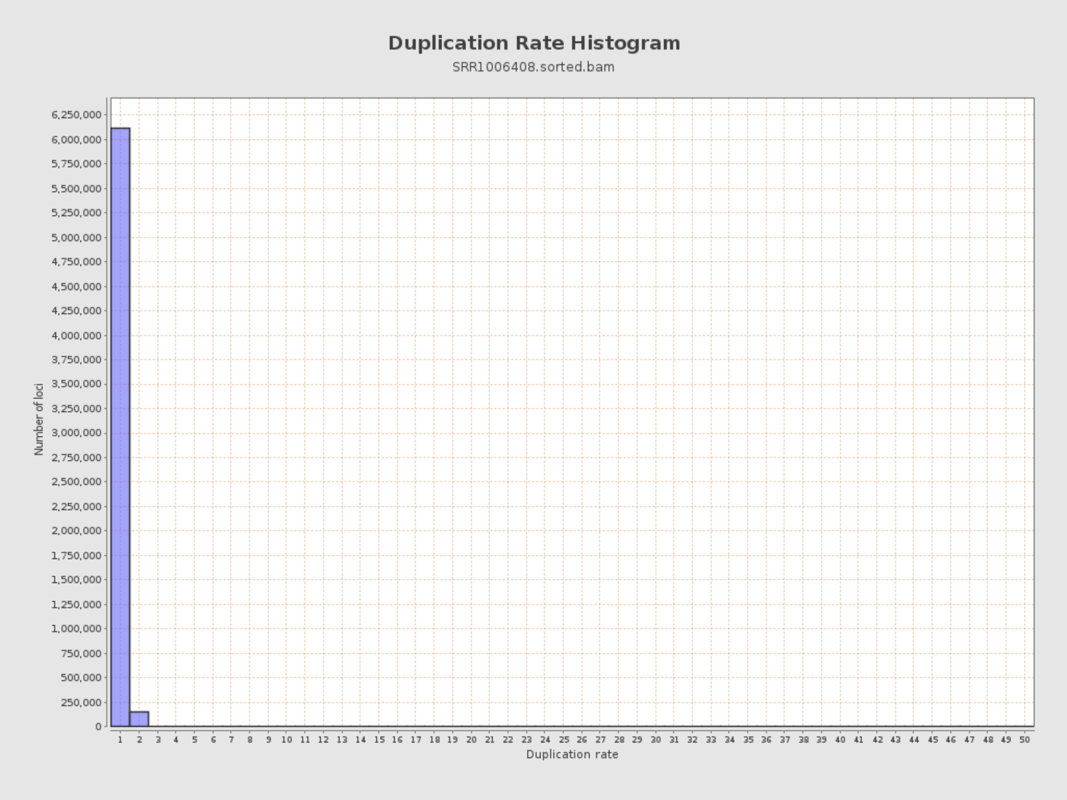
5. Results : Coverage Histogram (0-50X)



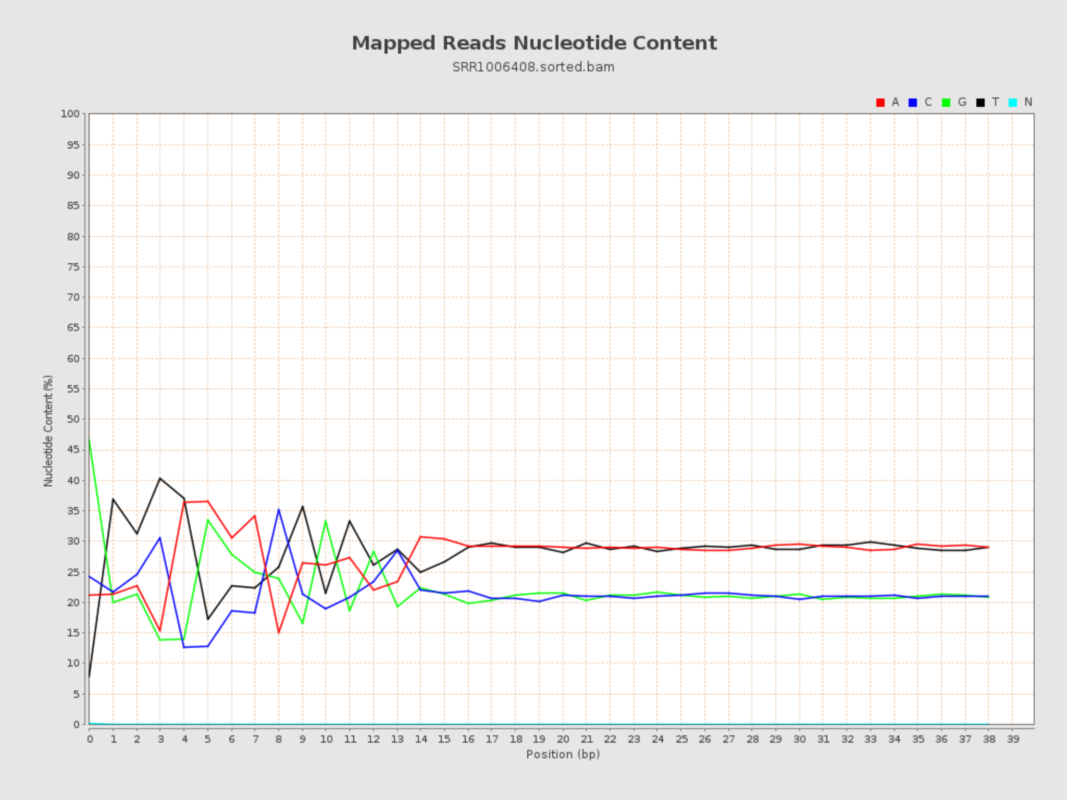
6. Results : Genome Fraction Coverage



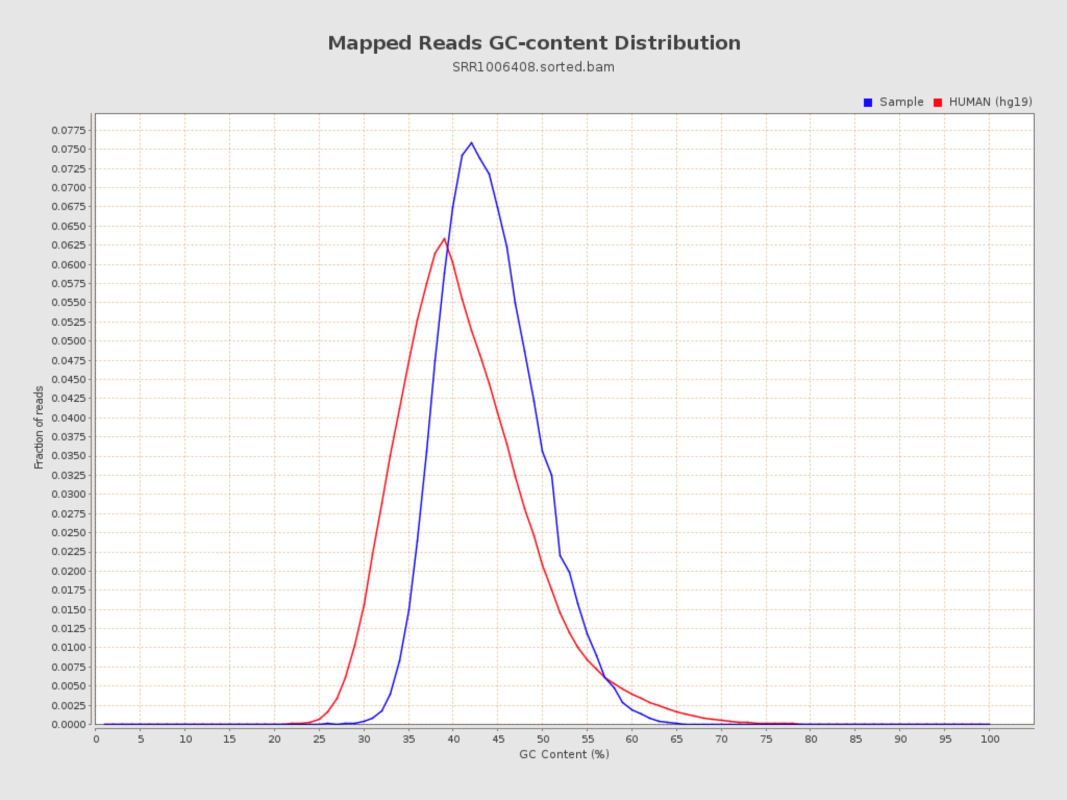
7. Results : Duplication Rate Histogram



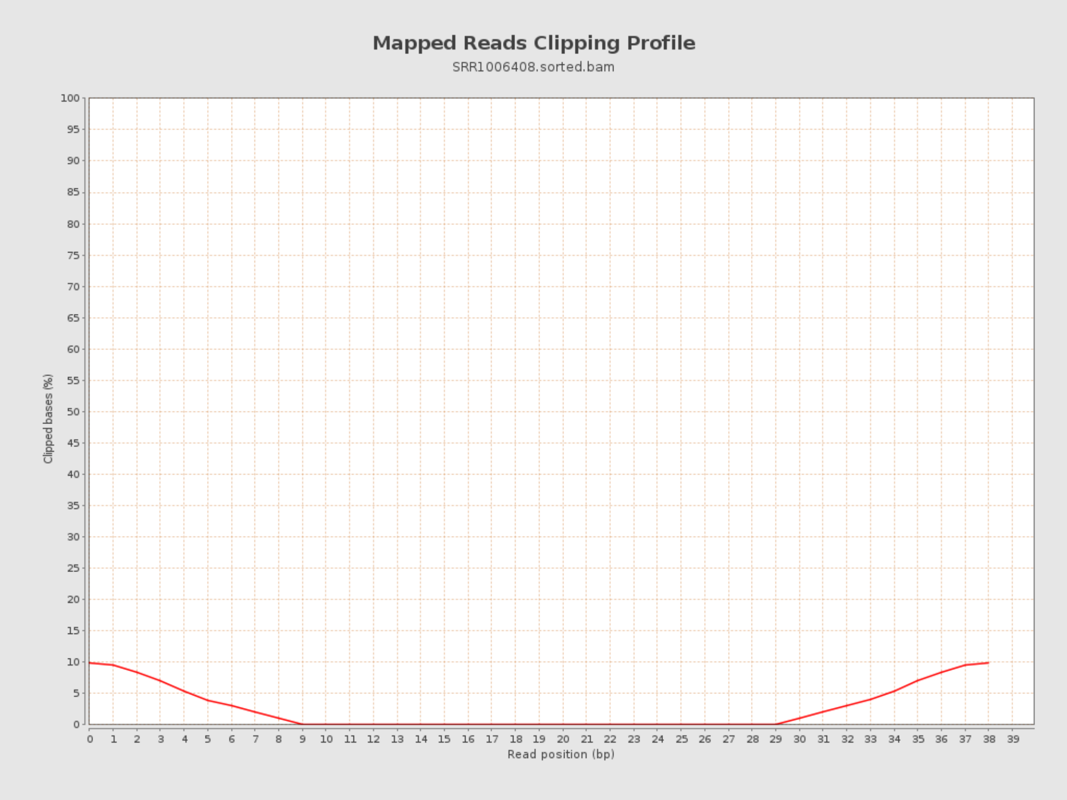
8. Results : Mapped Reads Nucleotide Content



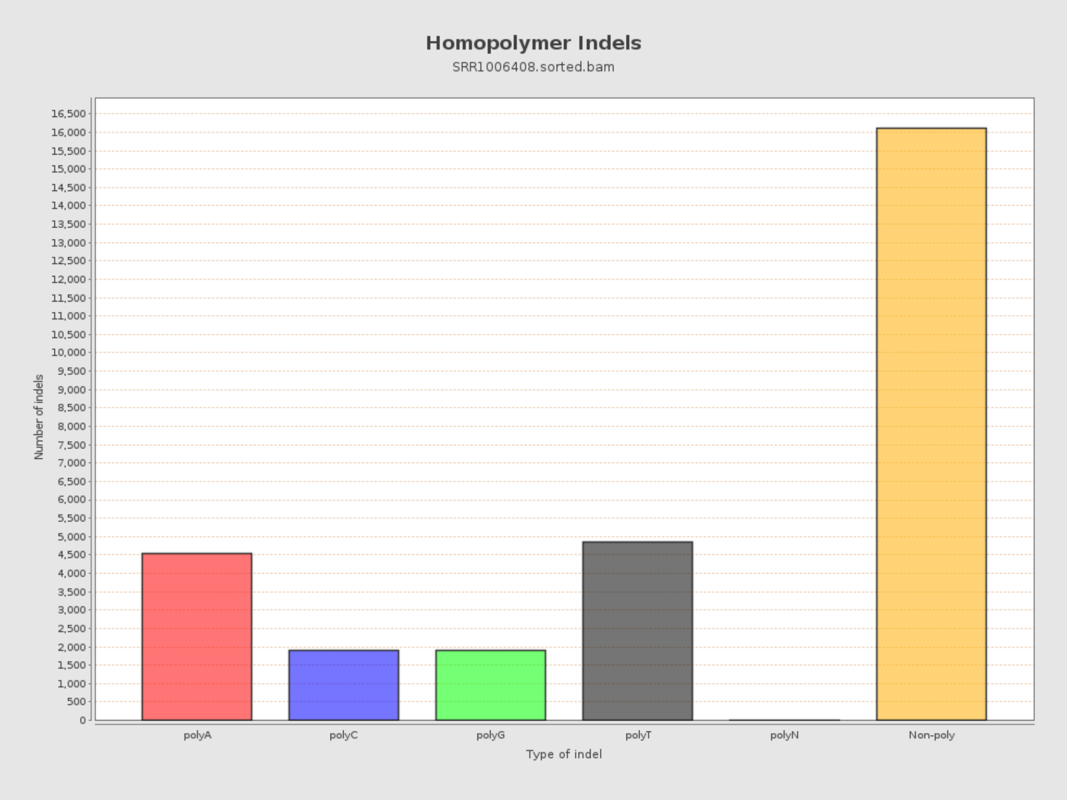
9. Results : Mapped Reads GC-content Distribution



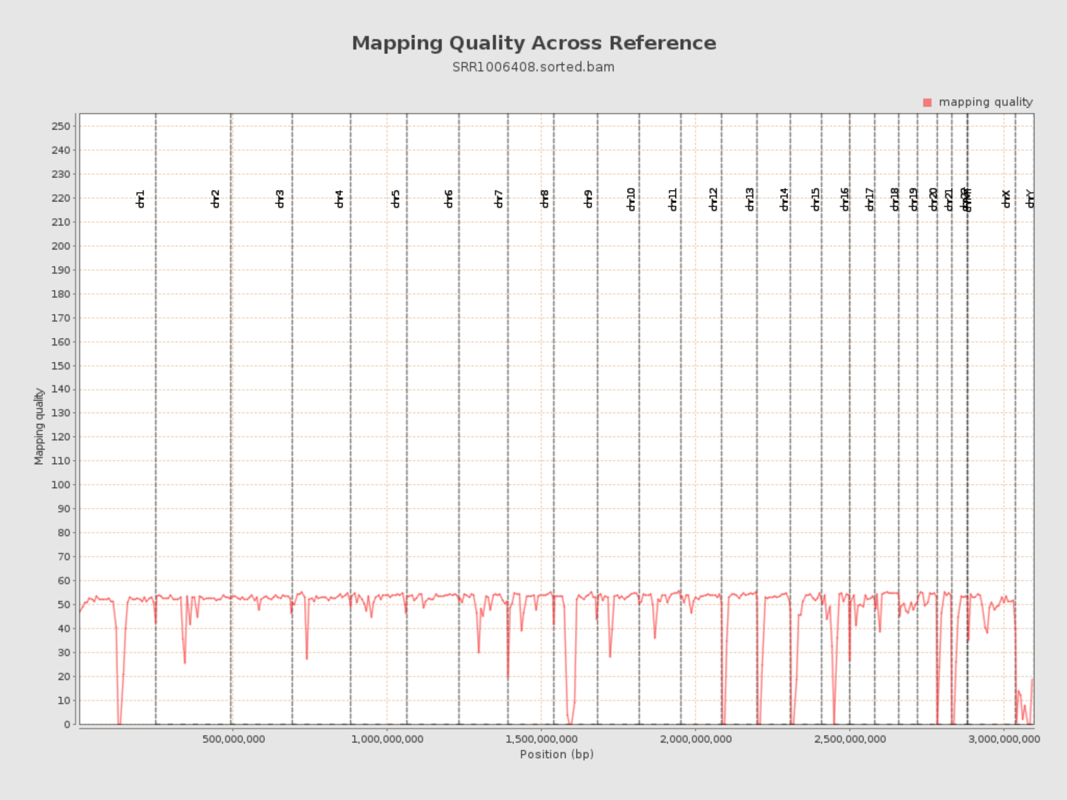
10. Results : Mapped Reads Clipping Profile



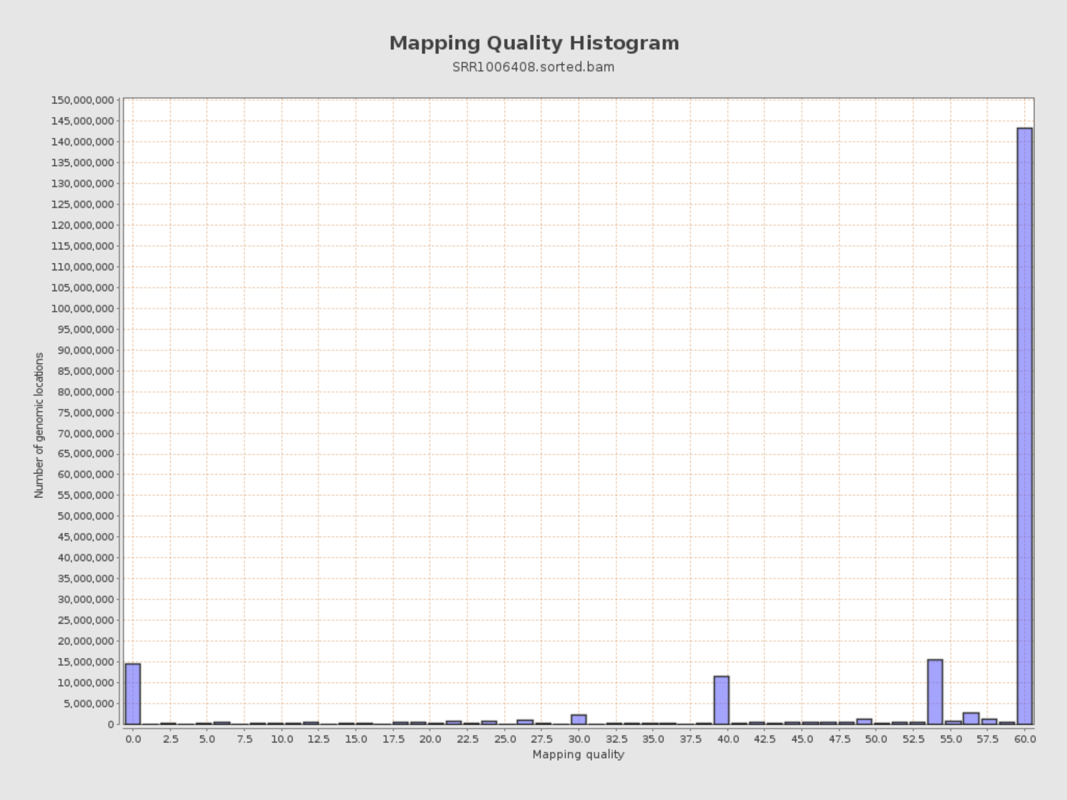
11. Results : Homopolymer Indels



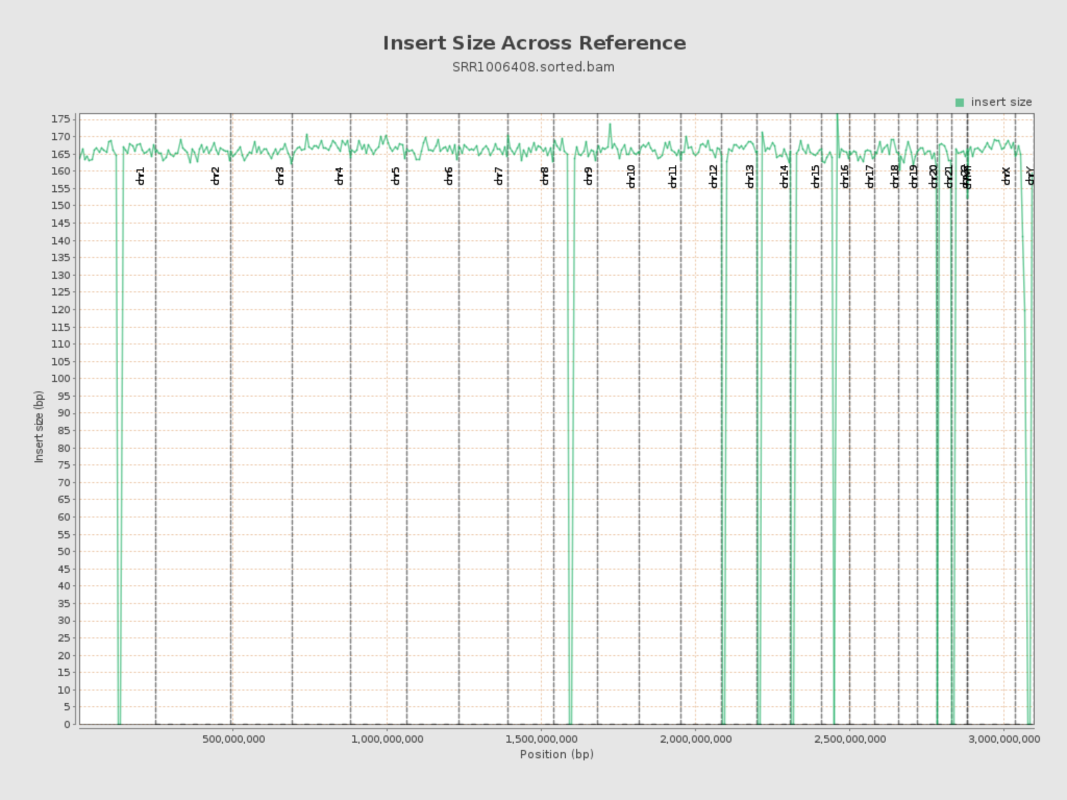
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram