Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:24:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006363.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_SRR1006363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006363_1.fastq.gz SRR1006363_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:24:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,977,774
Mapped reads	3,937,156 / 79.09%
Unmapped reads	1,040,618 / 20.91%
Mapped paired reads	3,937,156 / 79.09%
Mapped reads, first in pair	1,989,747 / 39.97%
Mapped reads, second in pair	1,947,409 / 39.12%
Mapped reads, both in pair	3,574,362 / 71.81%
Mapped reads, singletons	362,794 / 7.29%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	310,710 / 6.24%
Duplication rate	7.45%
Clipped reads	270,247 / 5.43%

2.2. ACGT Content

Number/percentage of A's	42,642,441 / 28.03%
Number/percentage of C's	32,579,465 / 21.41%
Number/percentage of T's	43,498,714 / 28.59%
Number/percentage of G's	33,415,920 / 21.96%
Number/percentage of N's	6,303 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0492
Standard Deviation	0.3671

2.4. Mapping Quality

Mean Mapping Quality	47.97

2.5. Insert size

Mean	77,448.57
Standard Deviation	2,613,397.23
P25/Median/P75	106 / 139 / 190

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	621,103
Insertions	4,350
Mapped reads with at least one insertion	0.11%
Deletions	17,460
Mapped reads with at least one deletion	0.44%
Homopolymer indels	41.55%

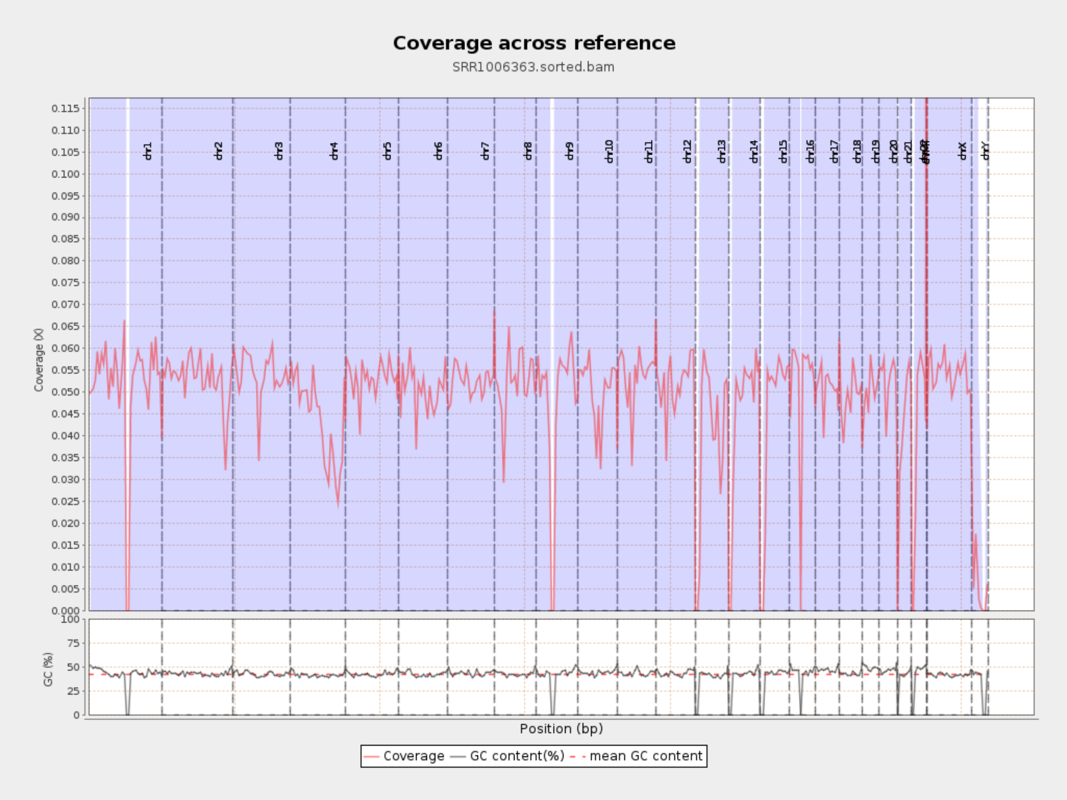
2.7. Chromosome stats

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

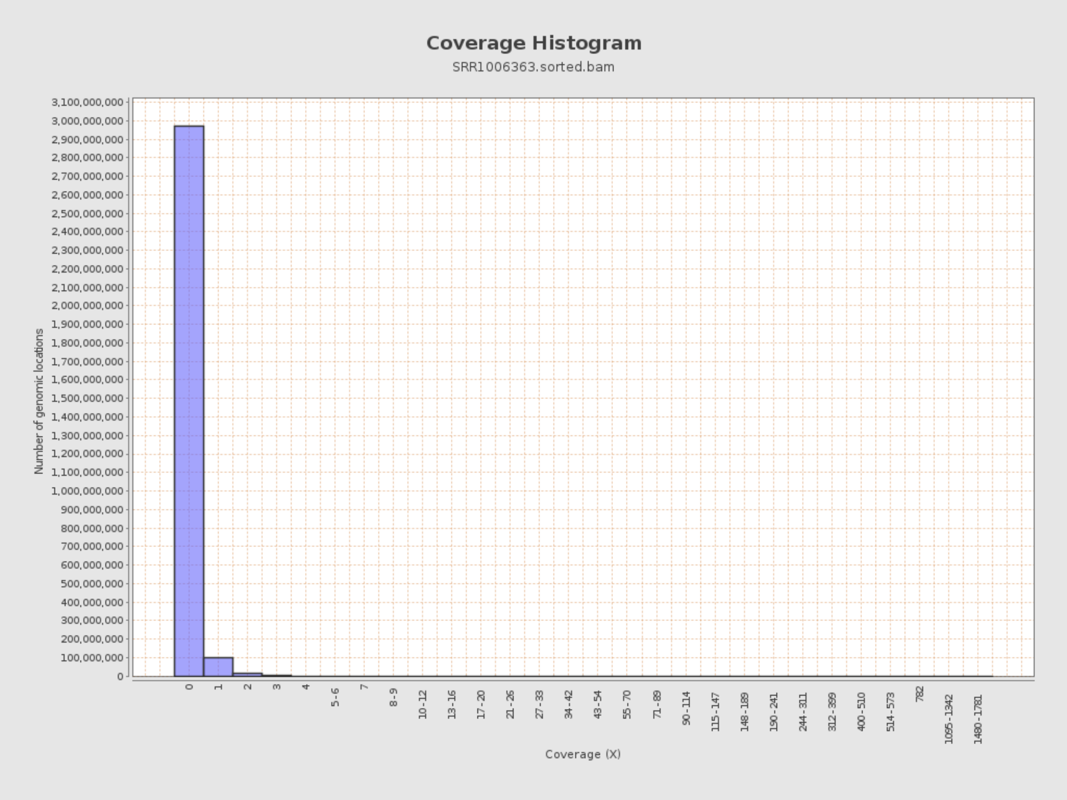
chr1	249250621	12844861	0.0515	0.5108
chr2	243199373	12883083	0.053	0.3119
chr3	198022430	10725703	0.0542	0.2743
chr4	191154276	8318954	0.0435	0.2494
chr5	180915260	9621435	0.0532	0.287
chr6	171115067	8695474	0.0508	0.2778
chr7	159138663	8333854	0.0524	0.3747
chr8	146364022	7656384	0.0523	0.9049
chr9	141213431	6704856	0.0475	0.2796
chr10	135534747	6817385	0.0503	0.312
chr11	135006516	7239034	0.0536	0.3035
chr12	133851895	6938203	0.0518	0.2709
chr13	115169878	4483312	0.0389	0.2345
chr14	107349540	4753927	0.0443	0.3293
chr15	102531392	4490546	0.0438	0.2481
chr16	90354753	4655093	0.0515	0.3014
chr17	81195210	4140275	0.051	0.2763
chr18	78077248	3850481	0.0493	0.3988
chr19	59128983	2974985	0.0503	0.3747
chr20	63025520	3321172	0.0527	0.2775
chr21	48129895	1983156	0.0412	0.2487
chr22	51304566	1968828	0.0384	0.2355
chrMT	16571	16166	0.9756	1.3181
chrX	155270560	8412191	0.0542	0.2906

chrY	59373566	337661	0.0057	0.1569

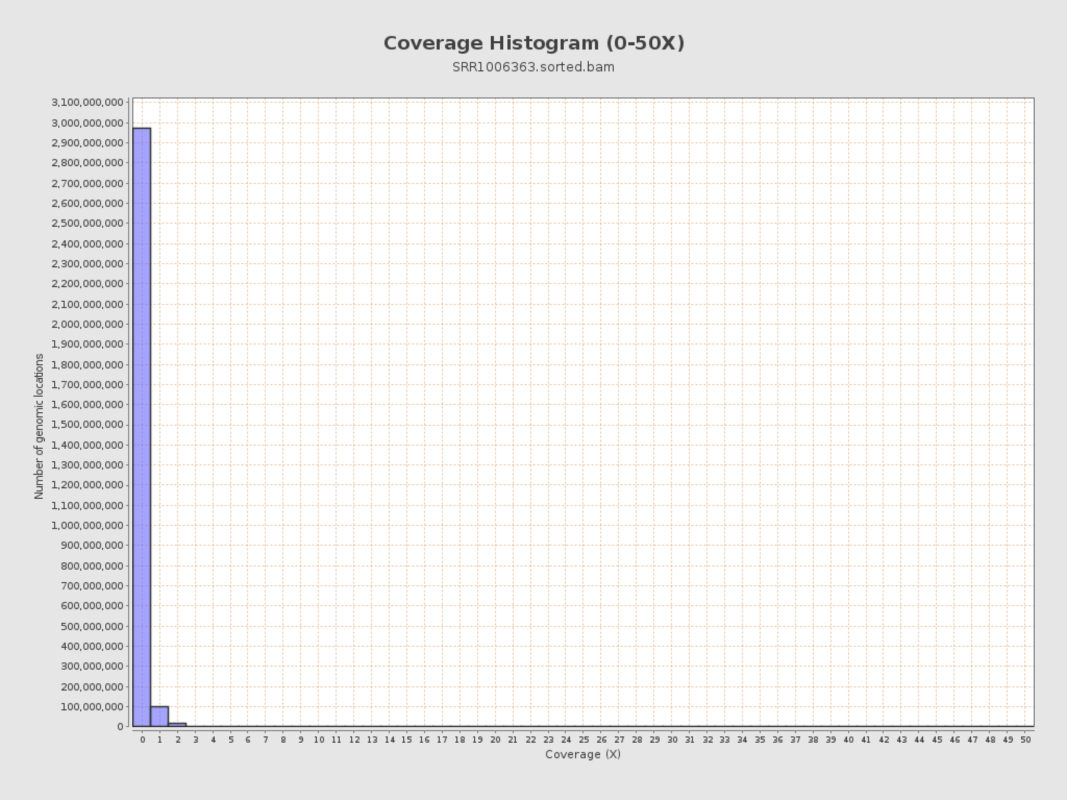
3. Results : Coverage across reference



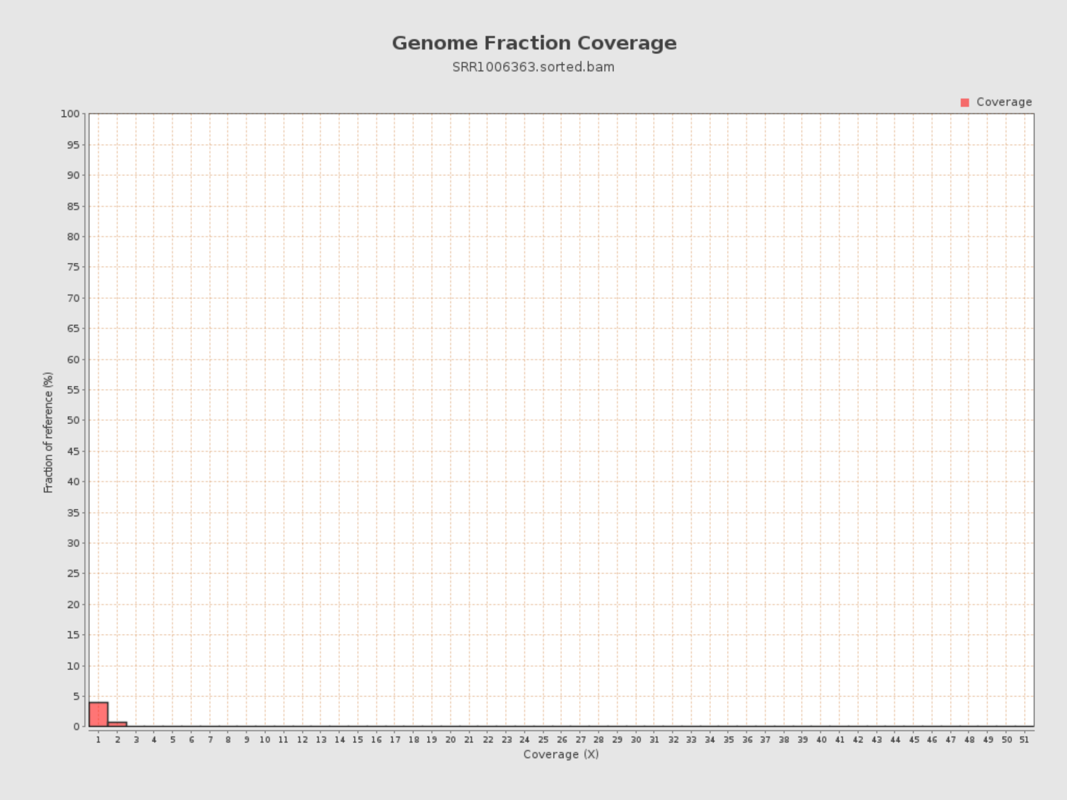
4. Results : Coverage Histogram



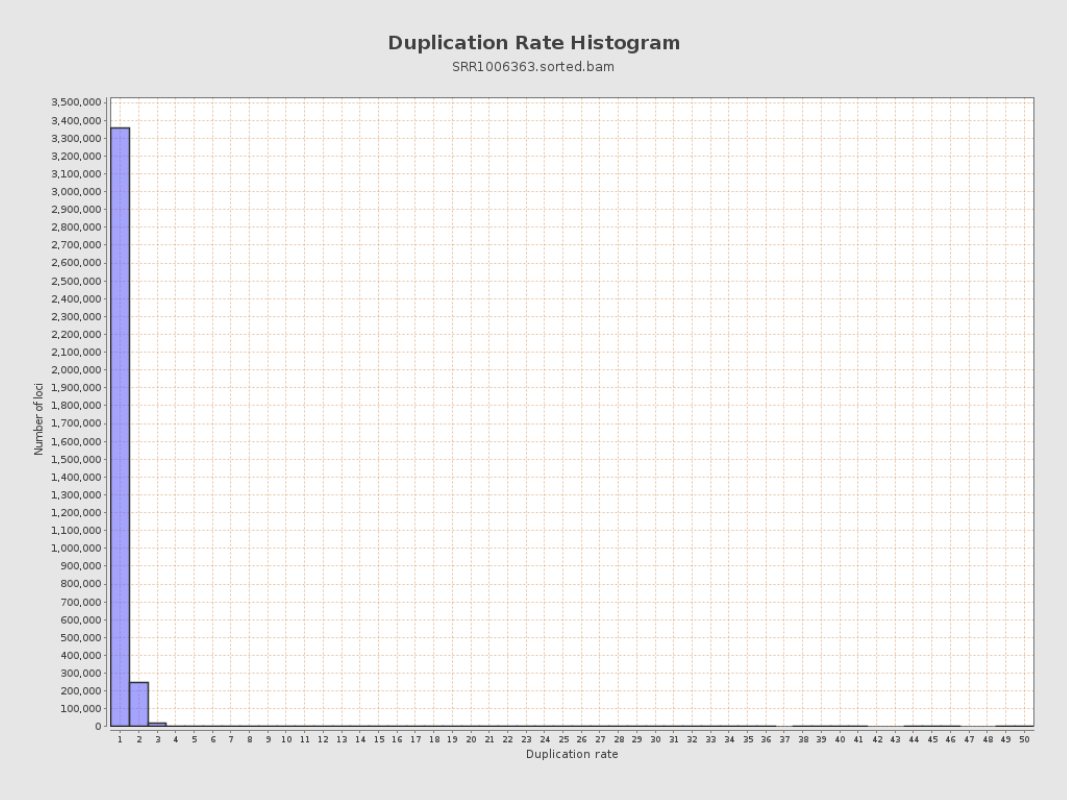
5. Results : Coverage Histogram (0-50X)



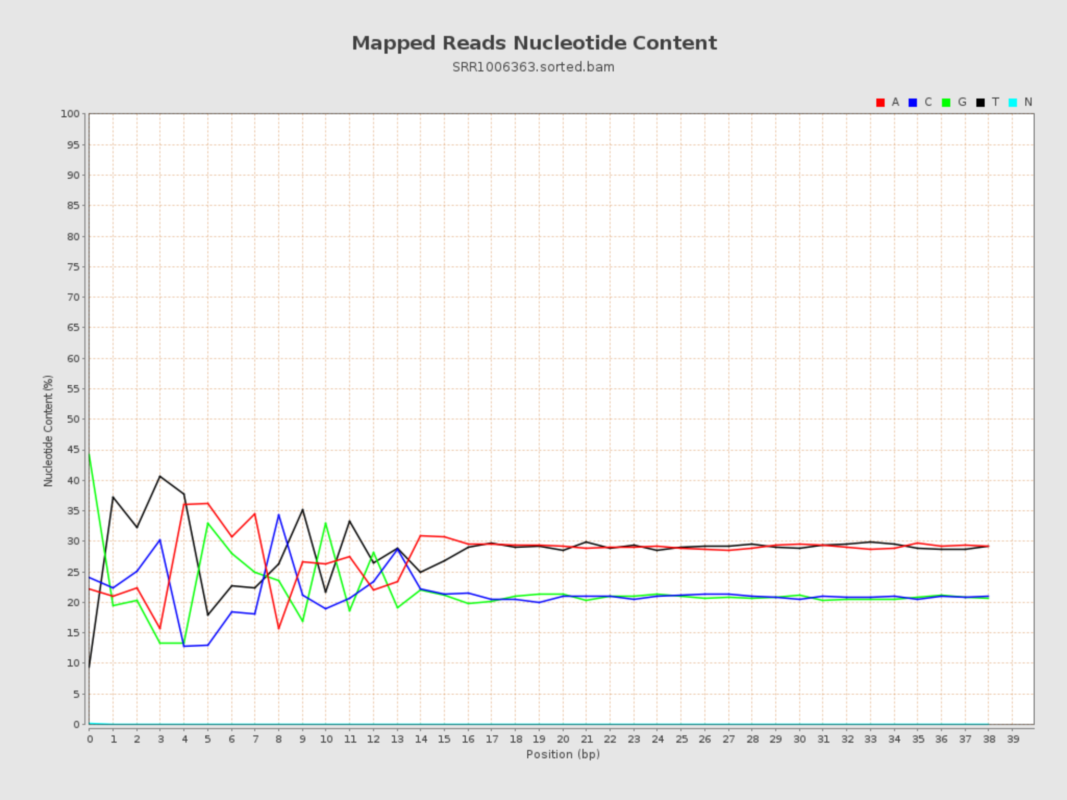
6. Results : Genome Fraction Coverage



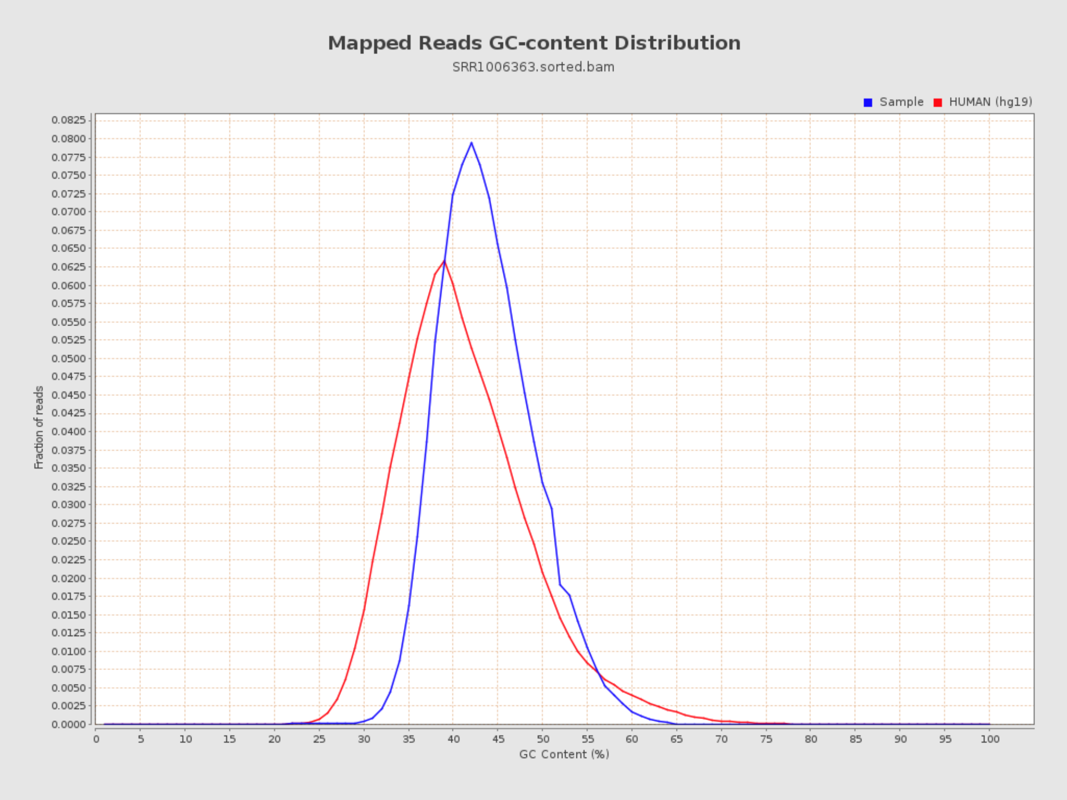
7. Results : Duplication Rate Histogram



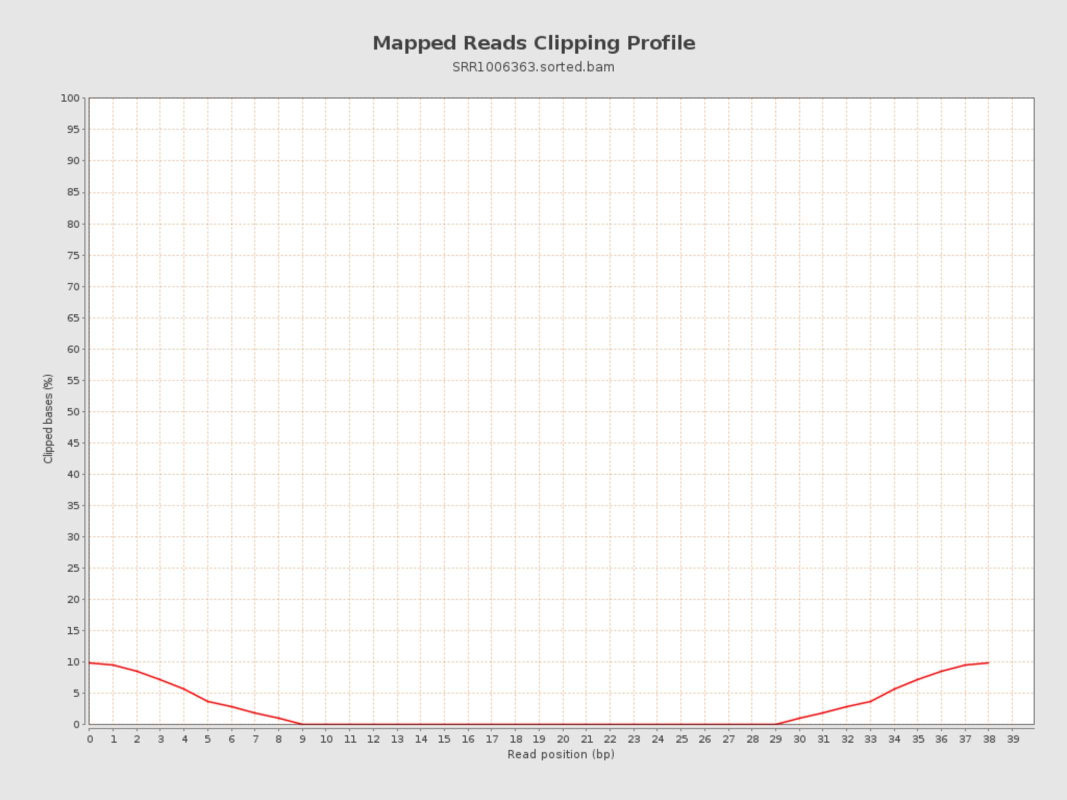
8. Results : Mapped Reads Nucleotide Content



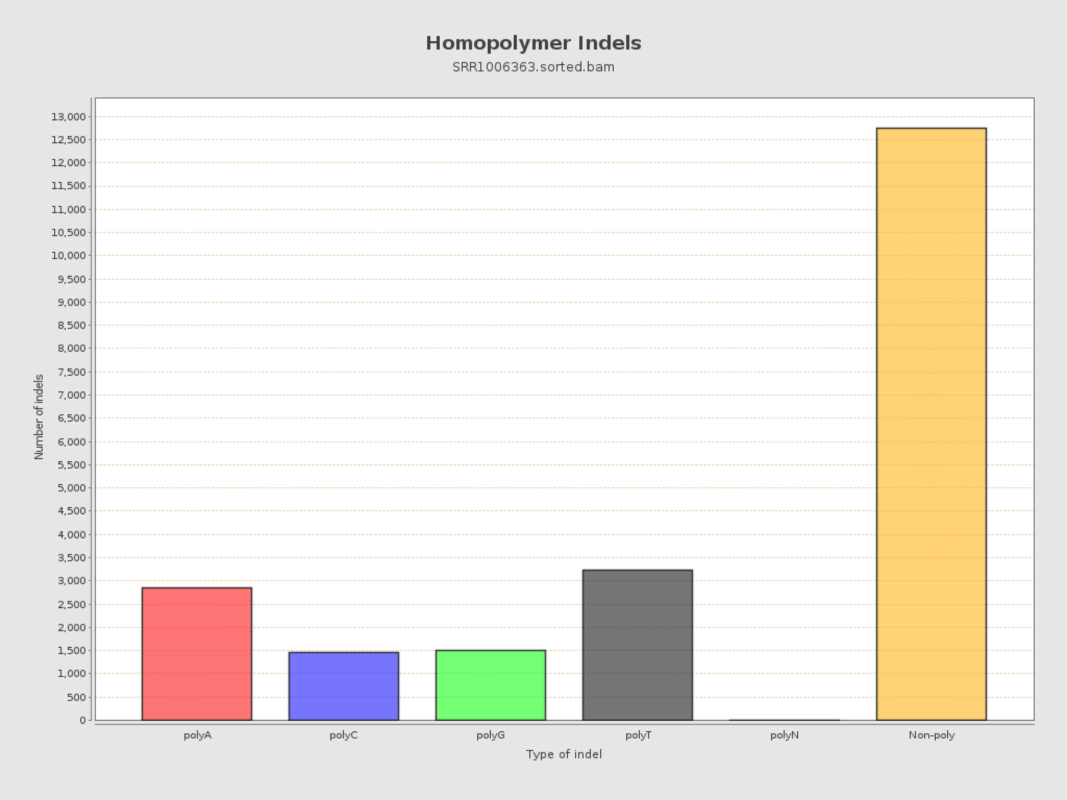
9. Results : Mapped Reads GC-content Distribution



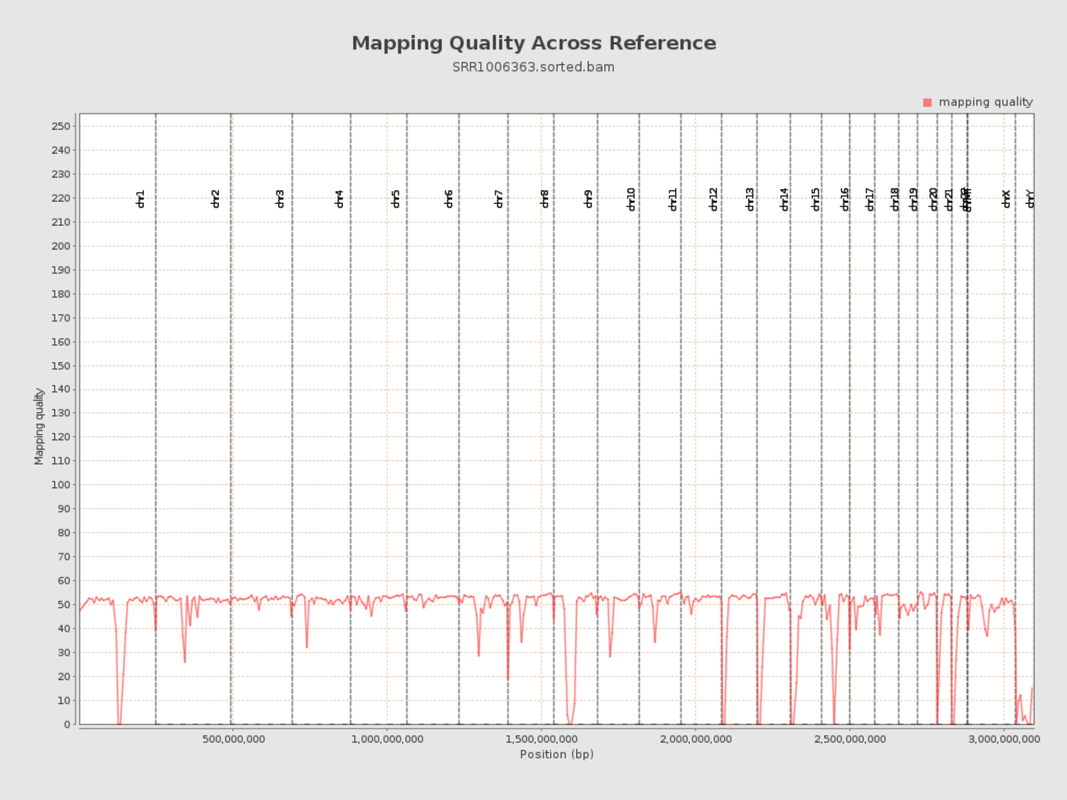
10. Results : Mapped Reads Clipping Profile



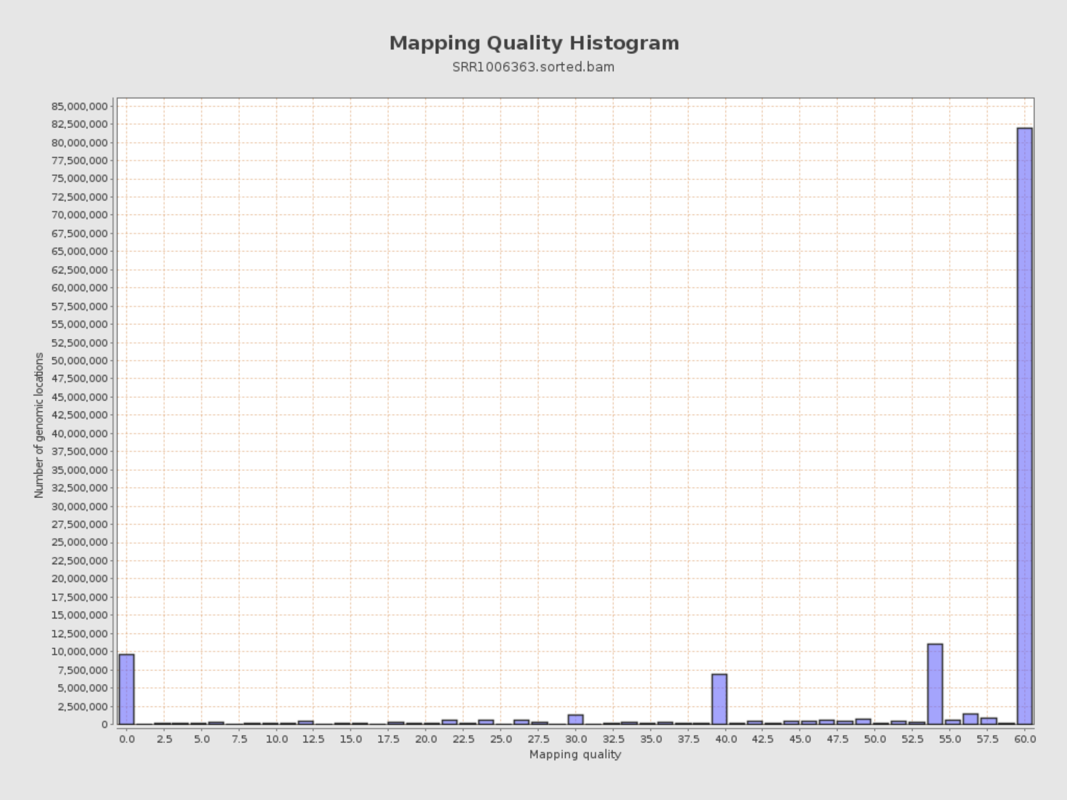
11. Results : Homopolymer Indels



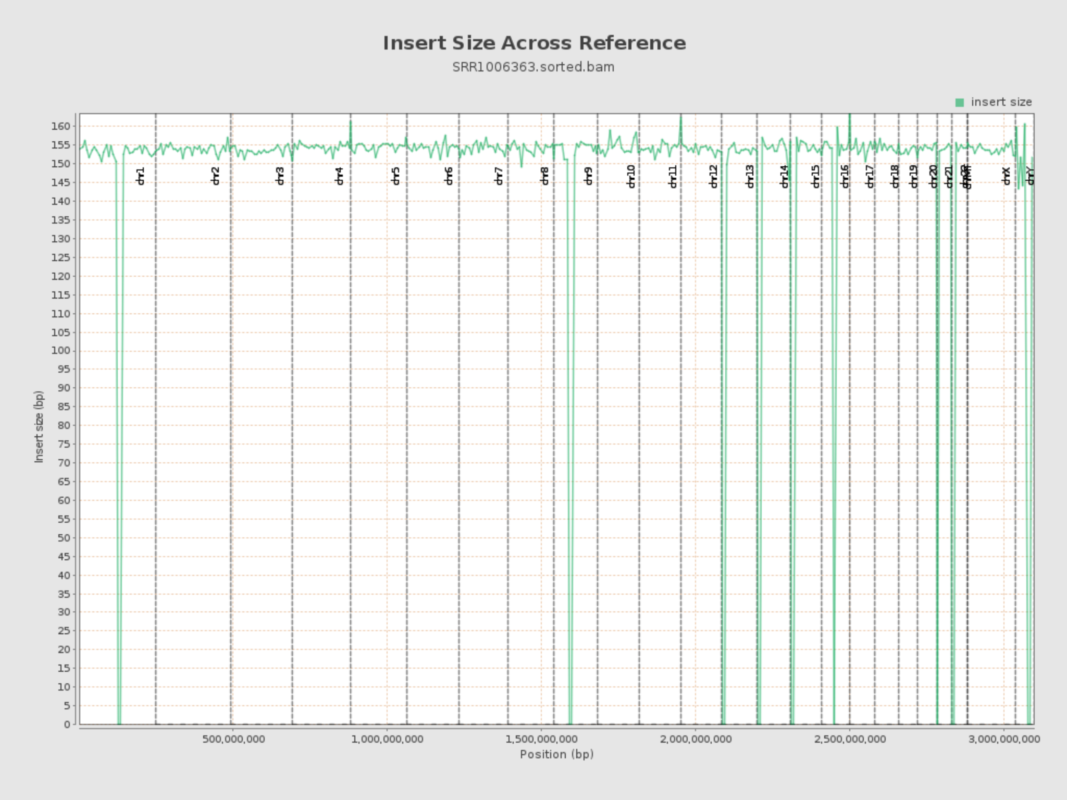
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram