Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:57:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006410.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_SRR1006410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006410_1.fastq.gz SRR1006410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:57:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,563,710
Mapped reads	5,734,879 / 87.37%
Unmapped reads	828,831 / 12.63%
Mapped paired reads	5,734,879 / 87.37%
Mapped reads, first in pair	2,896,684 / 44.13%
Mapped reads, second in pair	2,838,195 / 43.24%
Mapped reads, both in pair	5,204,032 / 79.28%
Mapped reads, singletons	530,847 / 8.09%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	203,714 / 3.1%
Duplication rate	3%
Clipped reads	323,425 / 4.93%

2.2. ACGT Content

Number/percentage of A's	62,494,355 / 28.16%
Number/percentage of C's	46,951,201 / 21.15%
Number/percentage of T's	63,711,536 / 28.71%
Number/percentage of G's	48,779,047 / 21.98%
Number/percentage of N's	9,148 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0717
Standard Deviation	0.4312

2.4. Mapping Quality

Mean Mapping Quality	48.12

2.5. Insert size

Mean	82,793.36
Standard Deviation	2,733,474.74
P25/Median/P75	112 / 147 / 204

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	765,512
Insertions	6,112
Mapped reads with at least one insertion	0.11%
Deletions	22,628
Mapped reads with at least one deletion	0.39%
Homopolymer indels	43.84%

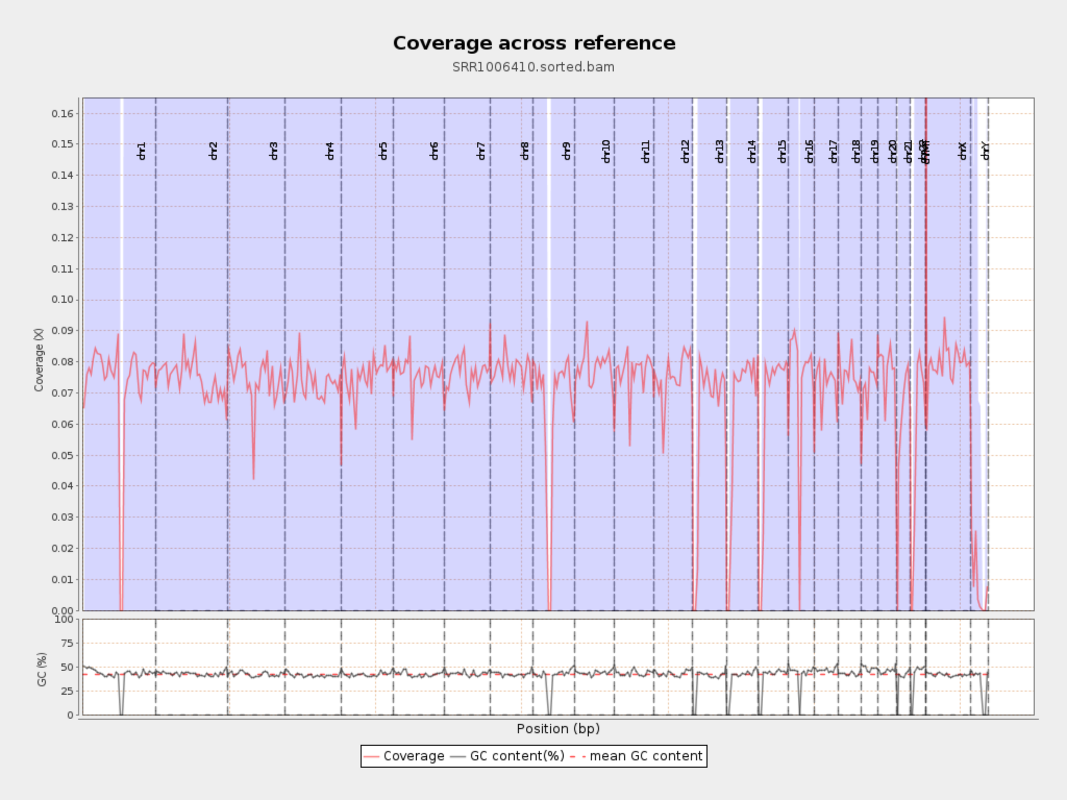
2.7. Chromosome stats

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

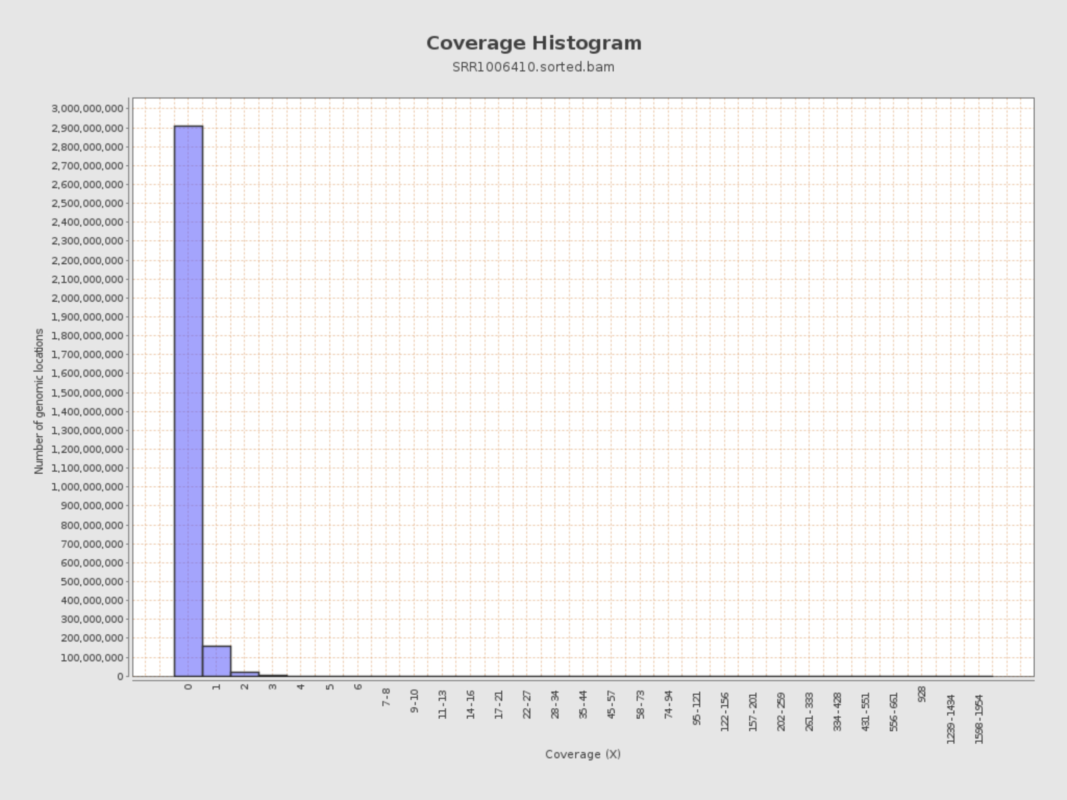
chr1	249250621	18120990	0.0727	0.5702
chr2	243199373	18225344	0.0749	0.3867
chr3	198022430	14712877	0.0743	0.3124
chr4	191154276	14070270	0.0736	0.3283
chr5	180915260	13707748	0.0758	0.3158
chr6	171115067	13057523	0.0763	0.3494
chr7	159138663	12134256	0.0762	0.4818
chr8	146364022	11357390	0.0776	1.005
chr9	141213431	9094251	0.0644	0.342
chr10	135534747	10635242	0.0785	0.396
chr11	135006516	10305537	0.0763	0.3848
chr12	133851895	10095485	0.0754	0.3177
chr13	115169878	7075148	0.0614	0.2822
chr14	107349540	6854114	0.0638	0.3211
chr15	102531392	6416868	0.0626	0.2872
chr16	90354753	6603449	0.0731	0.3522
chr17	81195210	5990248	0.0738	0.335
chr18	78077248	5928831	0.0759	0.5705
chr19	59128983	4265807	0.0721	0.4465
chr20	63025520	4861267	0.0771	0.3274
chr21	48129895	2881443	0.0599	0.308
chr22	51304566	2743111	0.0535	0.2733
chrMT	16571	6228	0.3758	0.7731
chrX	155270560	12344794	0.0795	0.355

chrY	59373566	487813	0.0082	0.1852

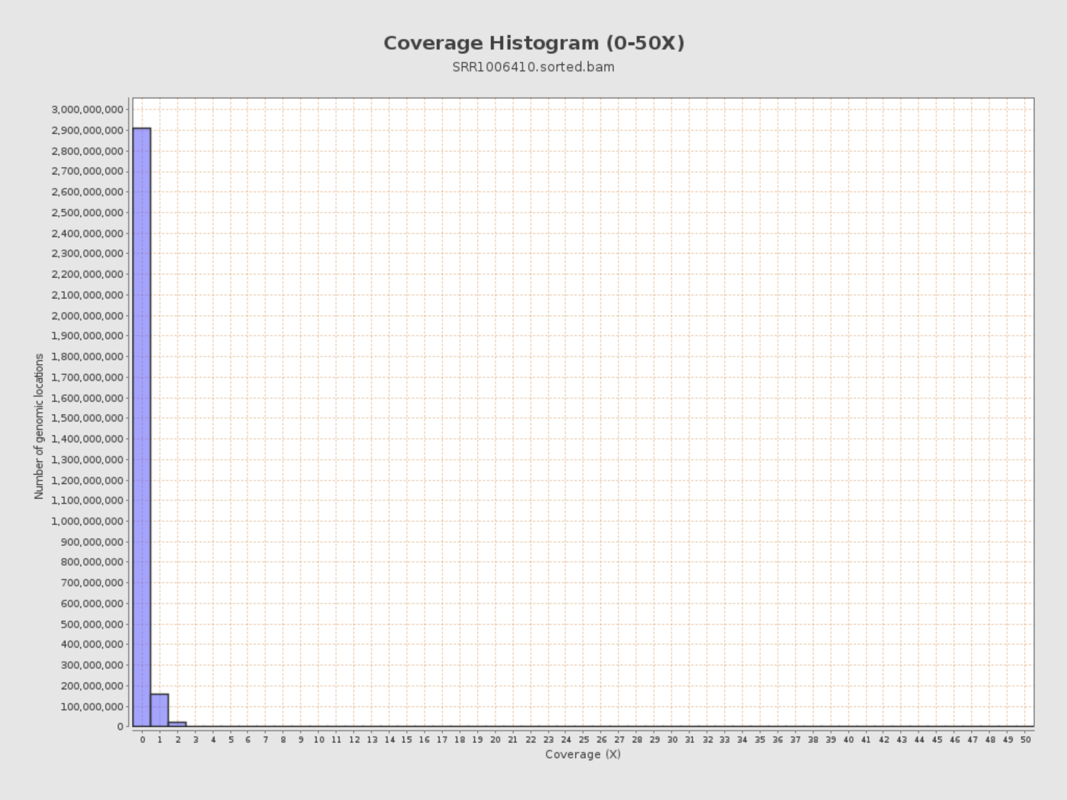
3. Results : Coverage across reference



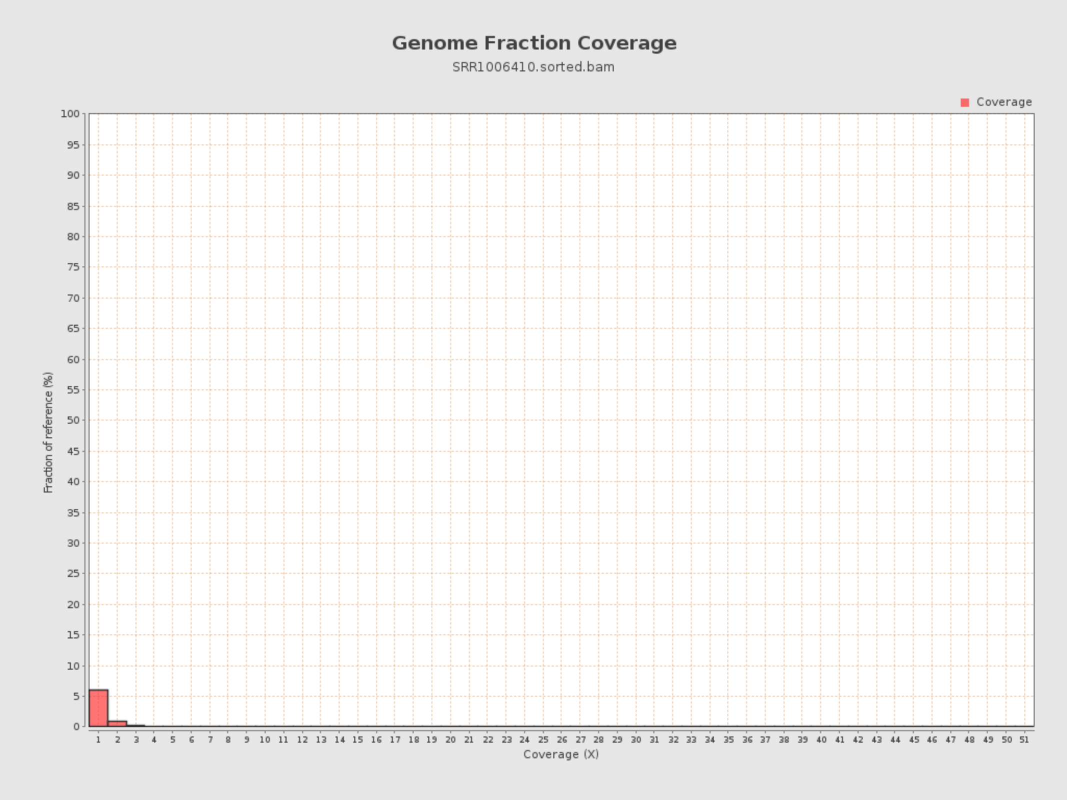
4. Results : Coverage Histogram



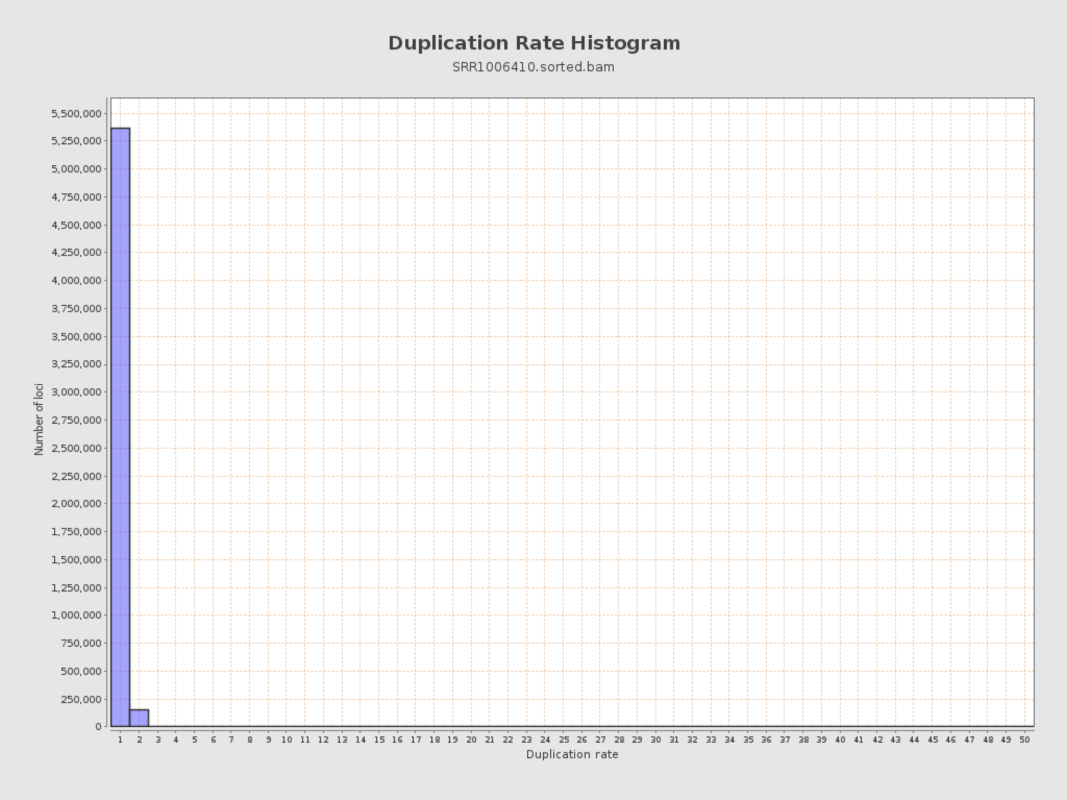
5. Results : Coverage Histogram (0-50X)



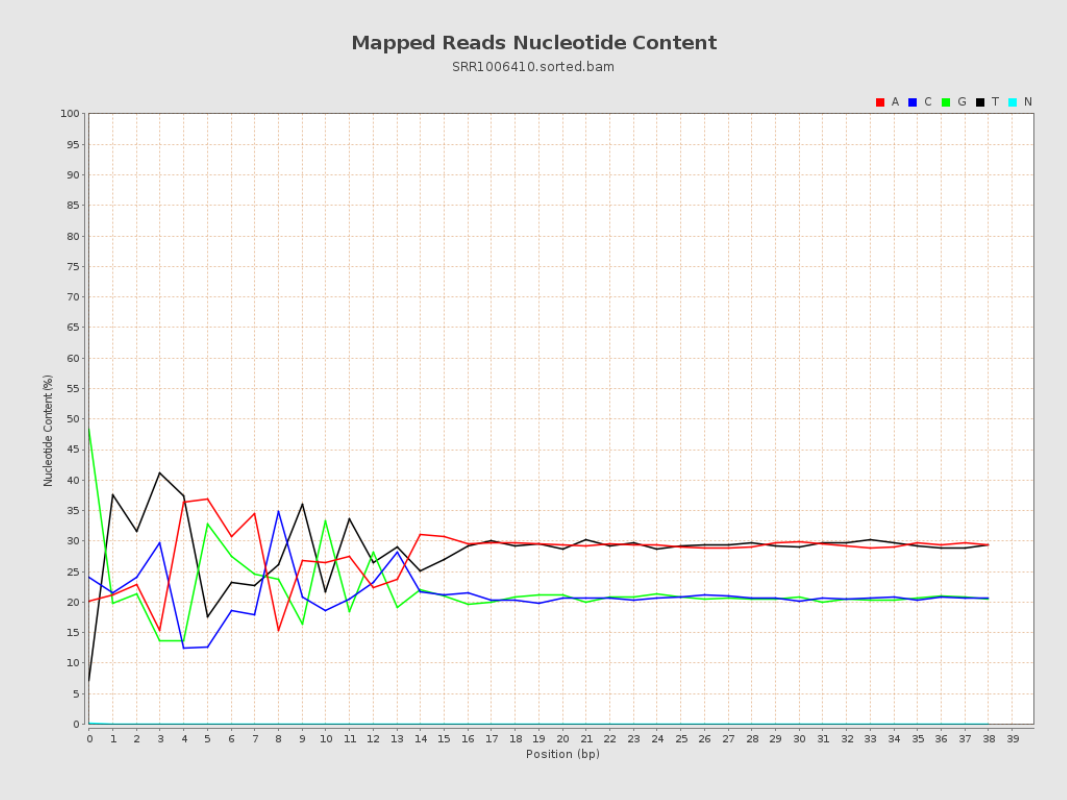
6. Results : Genome Fraction Coverage



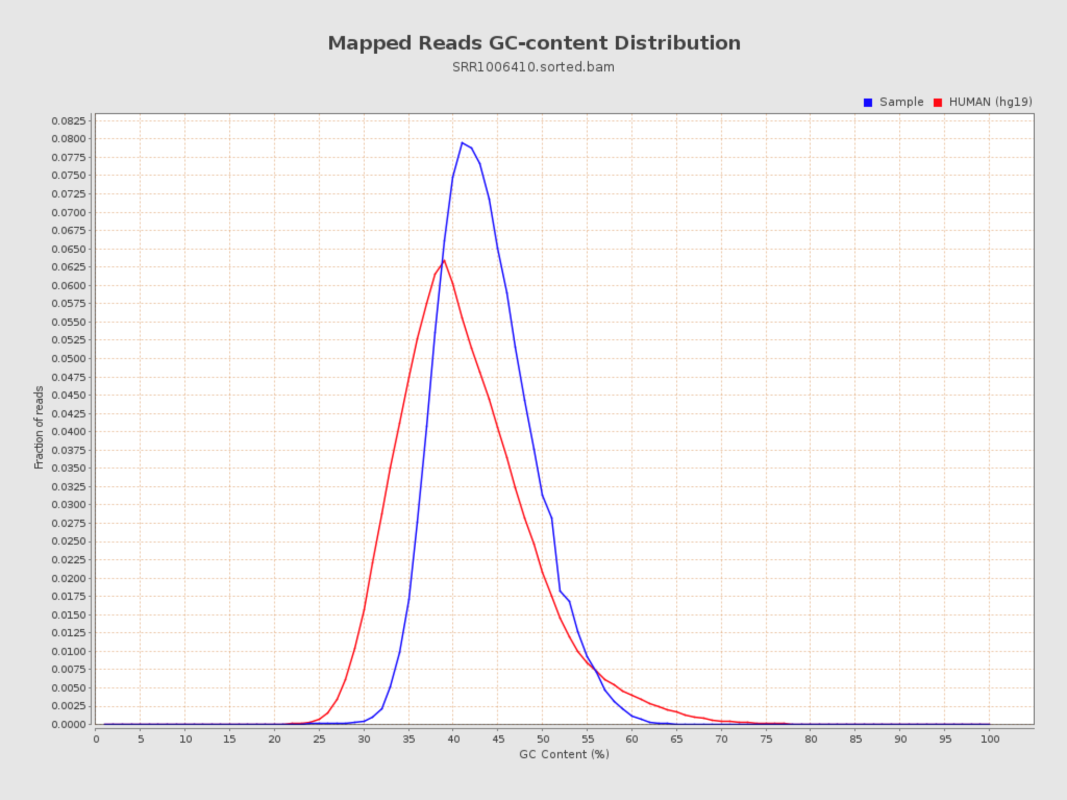
7. Results : Duplication Rate Histogram



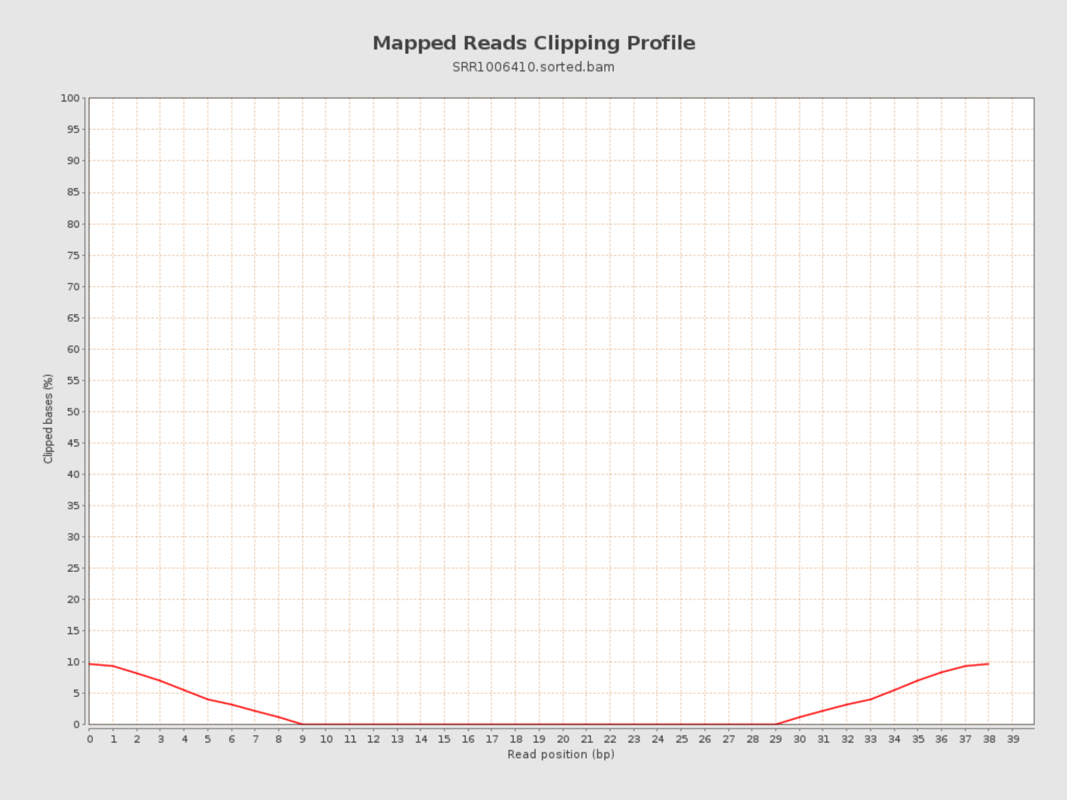
8. Results : Mapped Reads Nucleotide Content



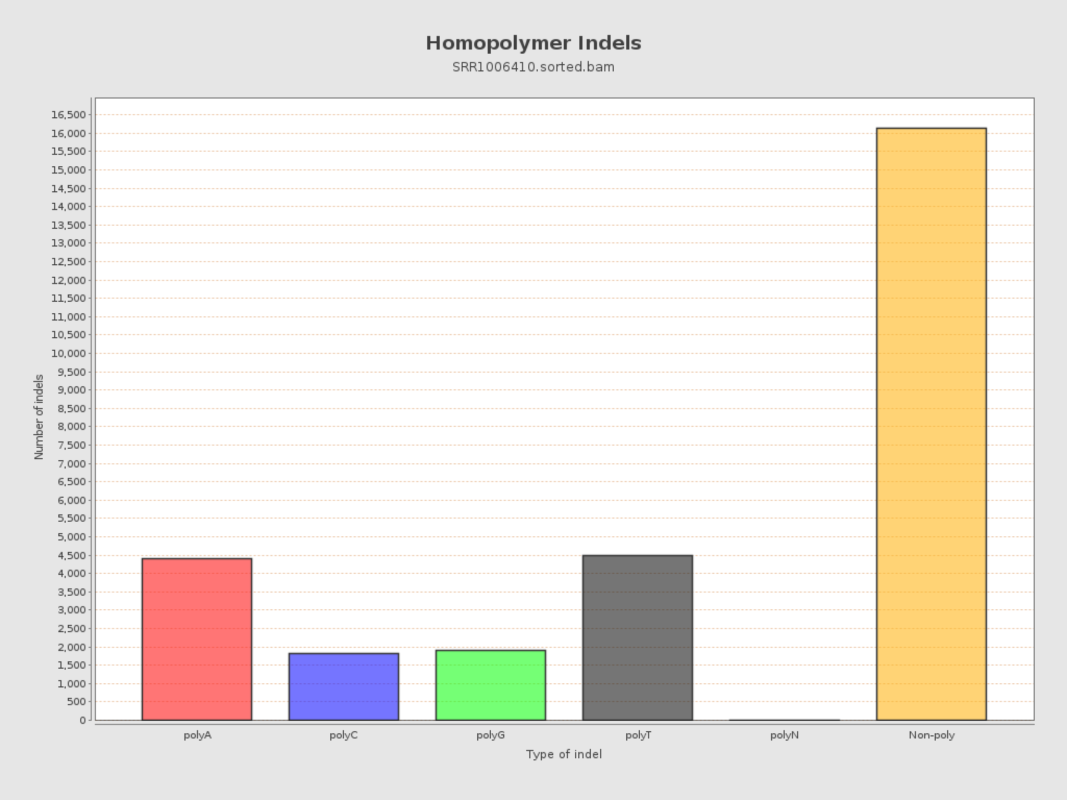
9. Results : Mapped Reads GC-content Distribution



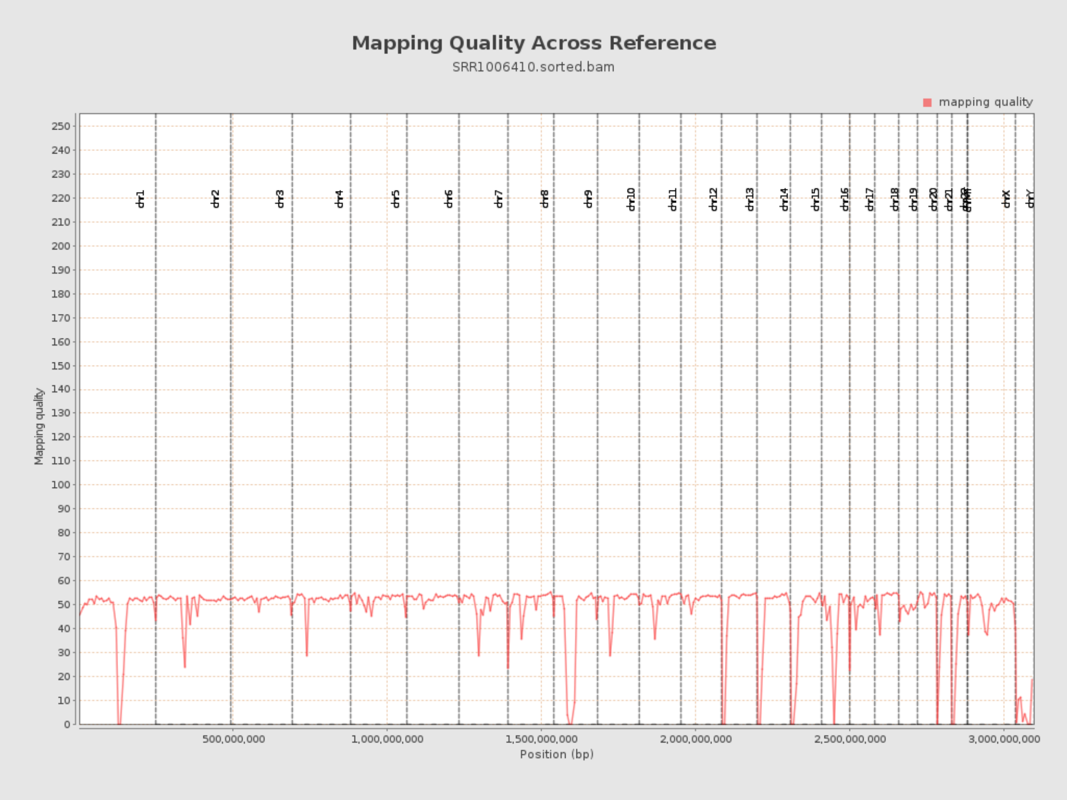
10. Results : Mapped Reads Clipping Profile



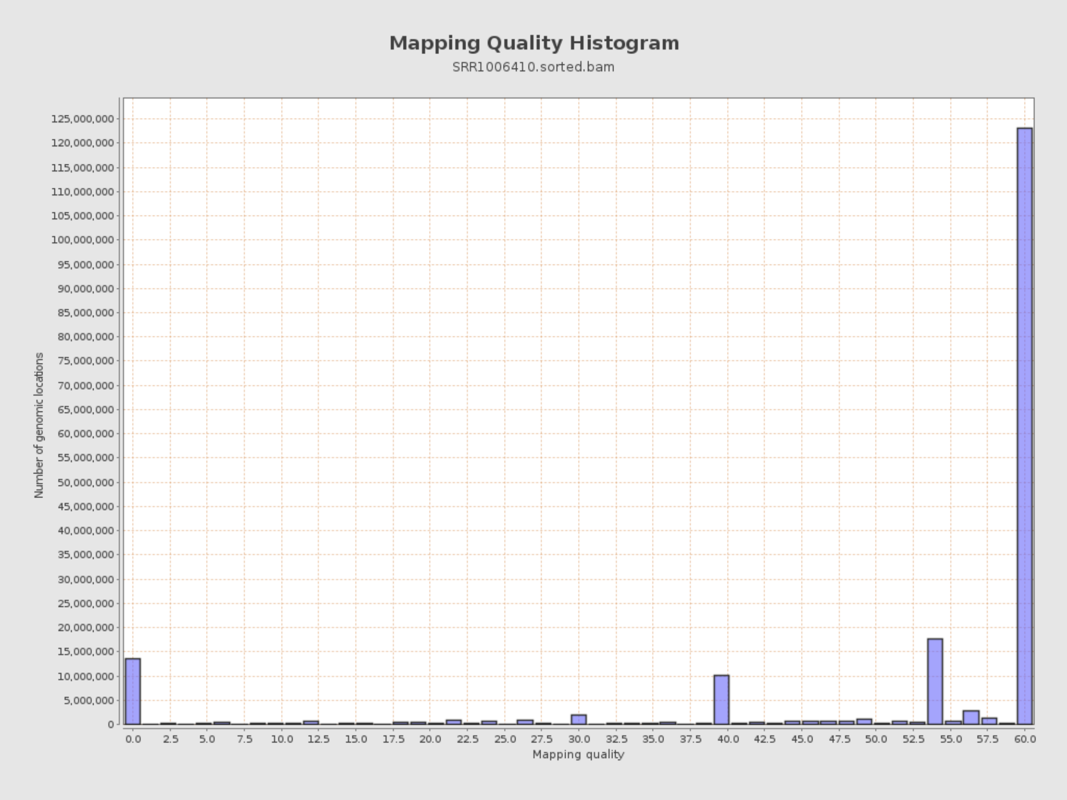
11. Results : Homopolymer Indels



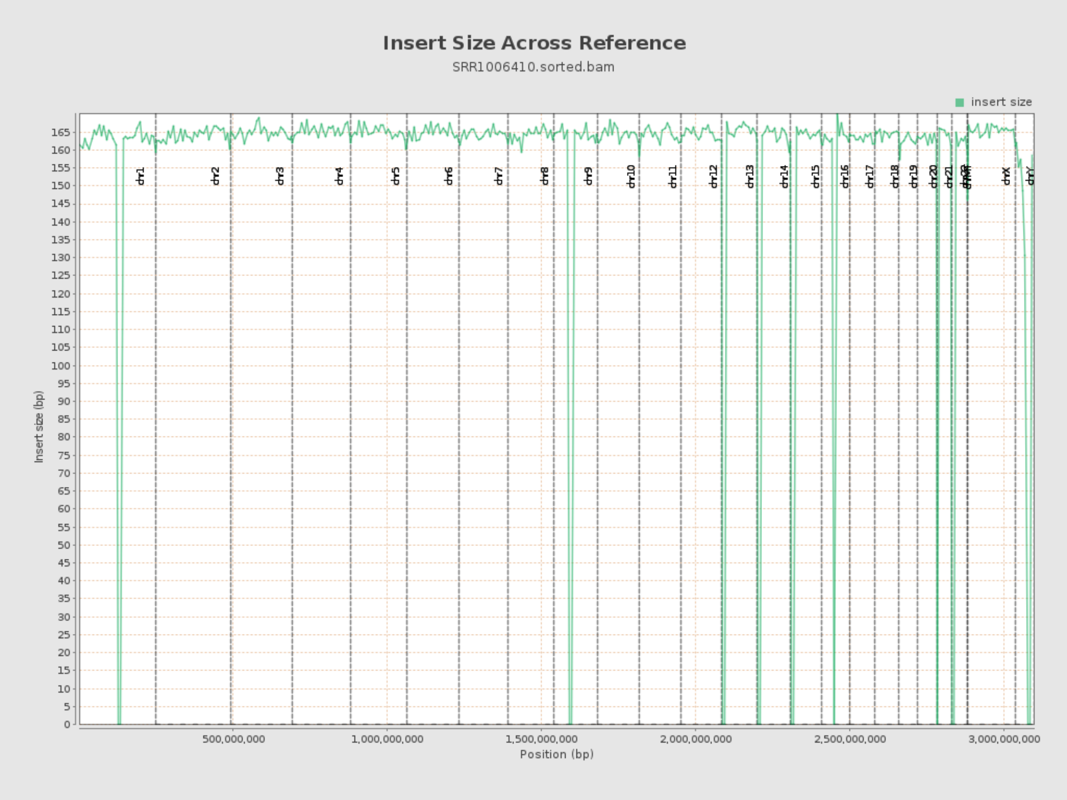
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram