Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006179.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_SRR1006179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006179_1.fastq.gz SRR1006179_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:36:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,686,328
Mapped reads	5,984,891 / 89.51%
Unmapped reads	701,437 / 10.49%
Mapped paired reads	5,984,891 / 89.51%
Mapped reads, first in pair	2,997,193 / 44.83%
Mapped reads, second in pair	2,987,698 / 44.68%
Mapped reads, both in pair	5,559,528 / 83.15%
Mapped reads, singletons	425,363 / 6.36%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	267,445 / 4%
Duplication rate	3.93%
Clipped reads	298,729 / 4.47%

2.2. ACGT Content

Number/percentage of A's	64,093,528 / 27.65%
Number/percentage of C's	50,280,604 / 21.69%
Number/percentage of T's	65,496,500 / 28.25%
Number/percentage of G's	51,954,234 / 22.41%
Number/percentage of N's	8,318 / 0%
GC Percentage	44.1%

2.3. Coverage

Mean	0.0749
Standard Deviation	0.4141

2.4. Mapping Quality

Mean Mapping Quality	48.34

2.5. Insert size

Mean	65,842.9
Standard Deviation	2,418,041.96
P25/Median/P75	98 / 132 / 185

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	660,140
Insertions	6,553
Mapped reads with at least one insertion	0.11%
Deletions	21,813
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.21%

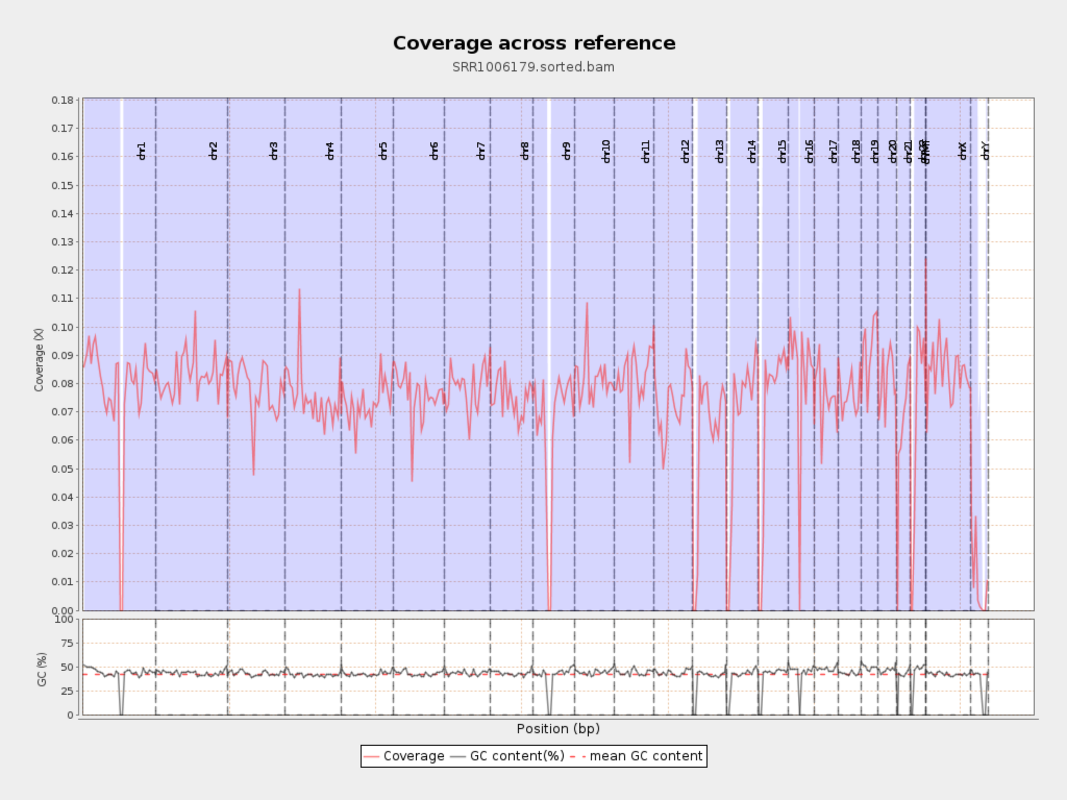
2.7. Chromosome stats

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

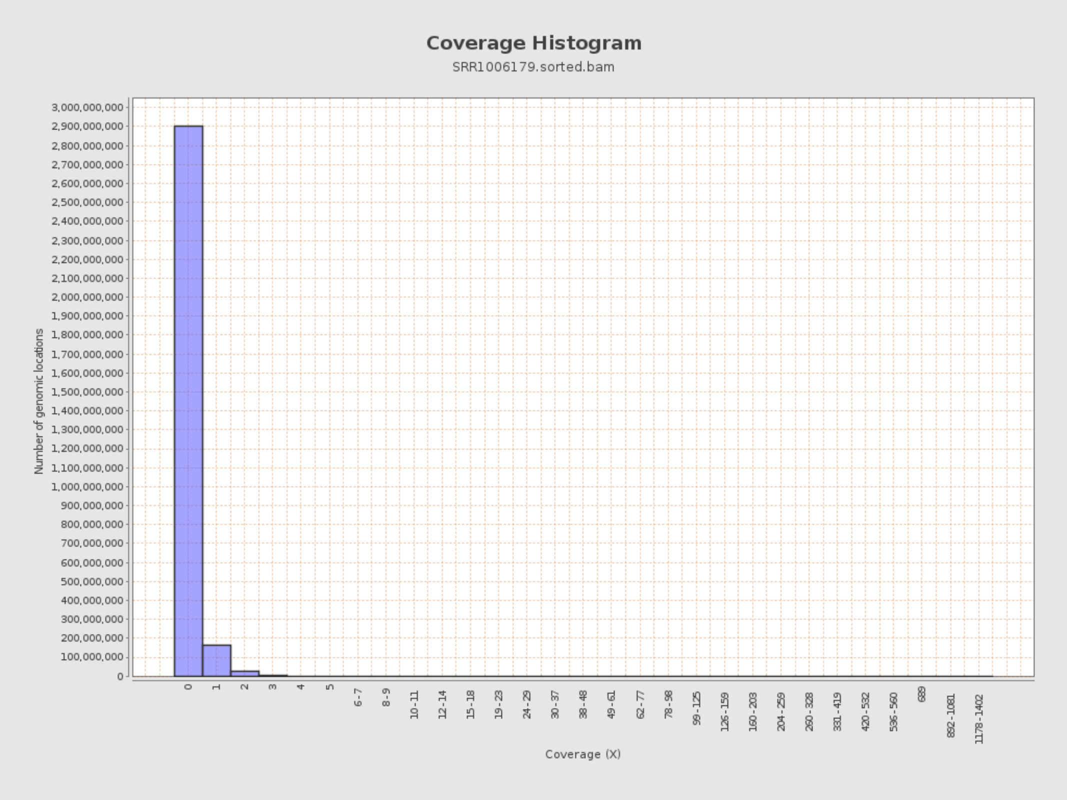
chr1	249250621	19362672	0.0777	0.5536
chr2	243199373	20187376	0.083	0.4005
chr3	198022430	15421144	0.0779	0.3211
chr4	191154276	14458614	0.0756	0.3588
chr5	180915260	13319927	0.0736	0.3134
chr6	171115067	12976846	0.0758	0.3525
chr7	159138663	12522052	0.0787	0.4713
chr8	146364022	11031078	0.0754	0.7585
chr9	141213431	9184365	0.065	0.3382
chr10	135534747	11043726	0.0815	0.4619
chr11	135006516	11102104	0.0822	0.3823
chr12	133851895	9857905	0.0736	0.3156
chr13	115169878	6950828	0.0604	0.2848
chr14	107349540	7158982	0.0667	0.3411
chr15	102531392	7039490	0.0687	0.3034
chr16	90354753	7438674	0.0823	0.3962
chr17	81195210	6203997	0.0764	0.3299
chr18	78077248	5934608	0.076	0.551
chr19	59128983	5452355	0.0922	0.4778
chr20	63025520	5106307	0.081	0.3409
chr21	48129895	3102974	0.0645	0.3443
chr22	51304566	3323194	0.0648	0.3077
chrMT	16571	2058	0.1242	0.4117
chrX	155270560	13091459	0.0843	0.3587

chrY	59373566	589422	0.0099	0.2615

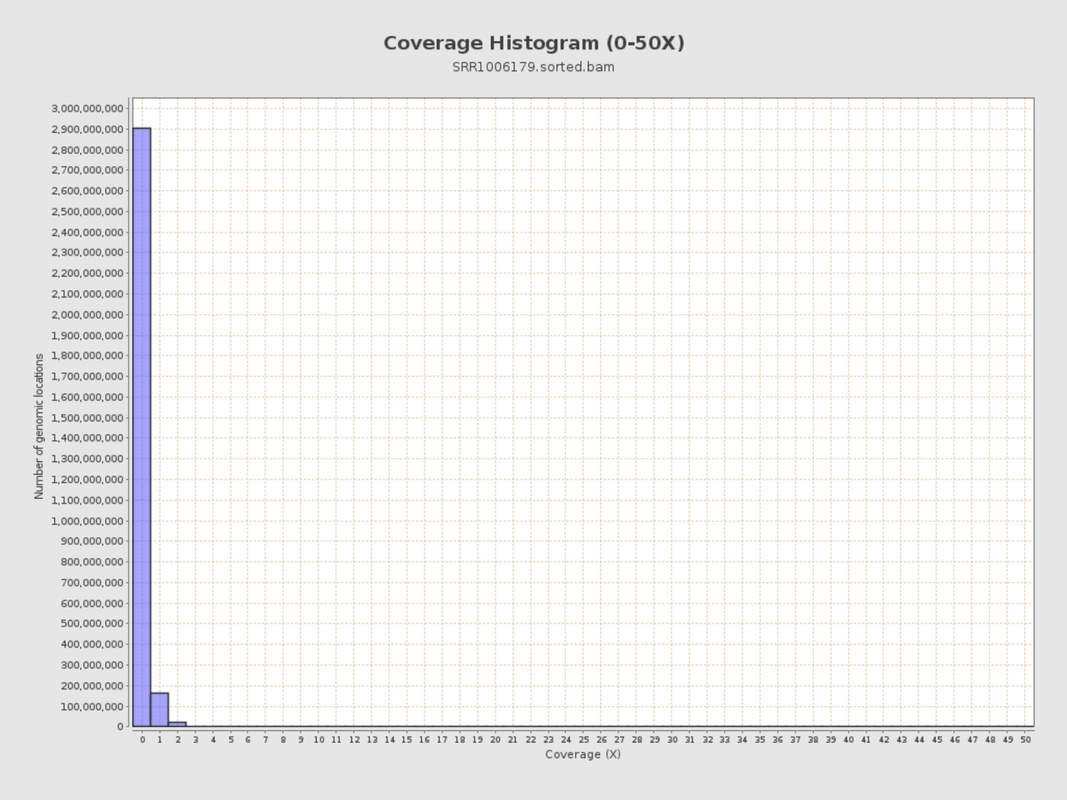
3. Results : Coverage across reference



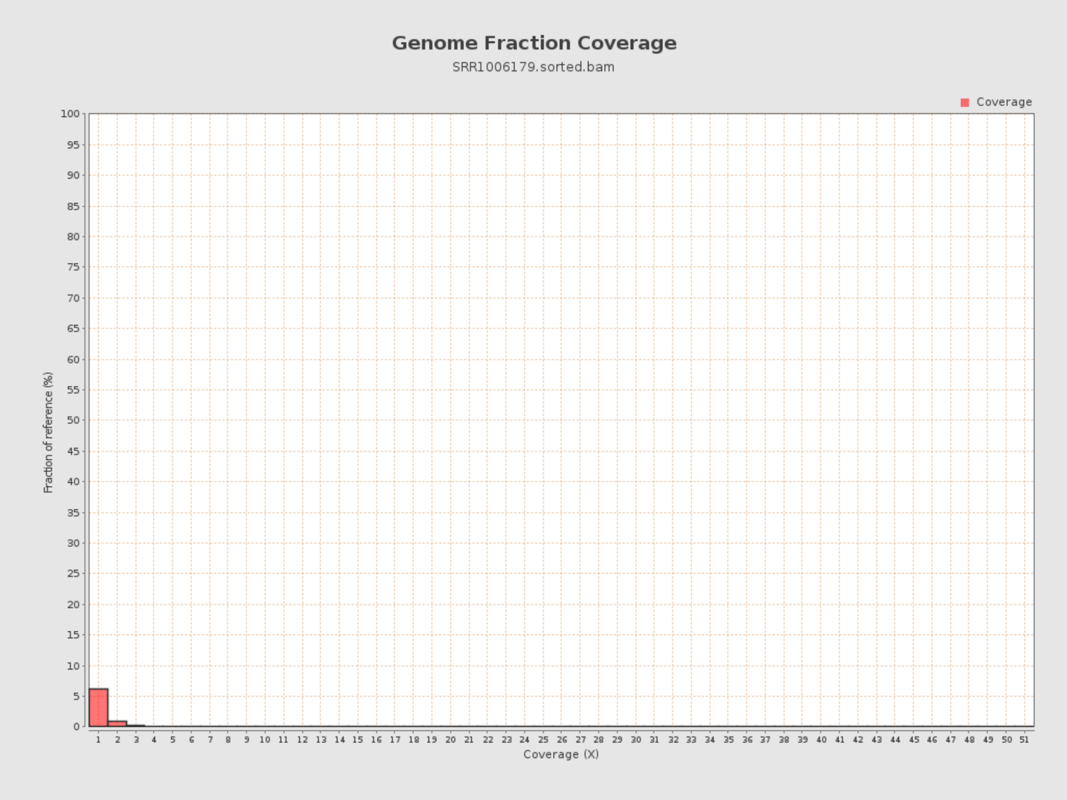
4. Results : Coverage Histogram



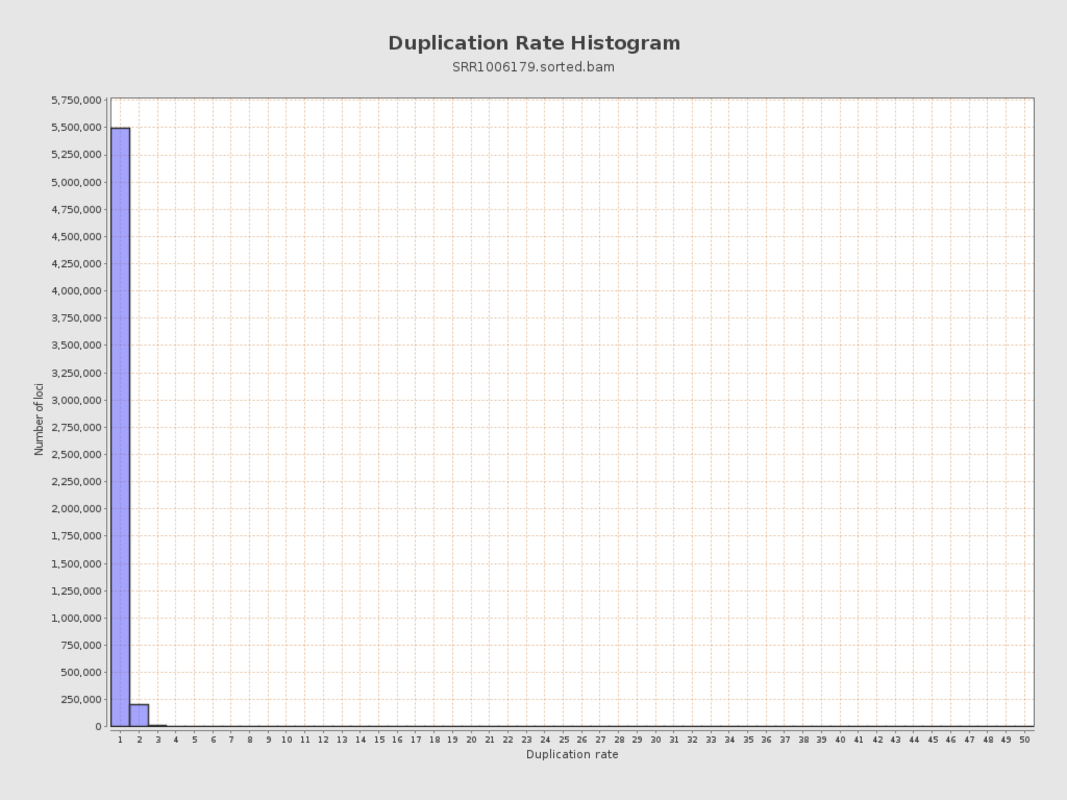
5. Results : Coverage Histogram (0-50X)



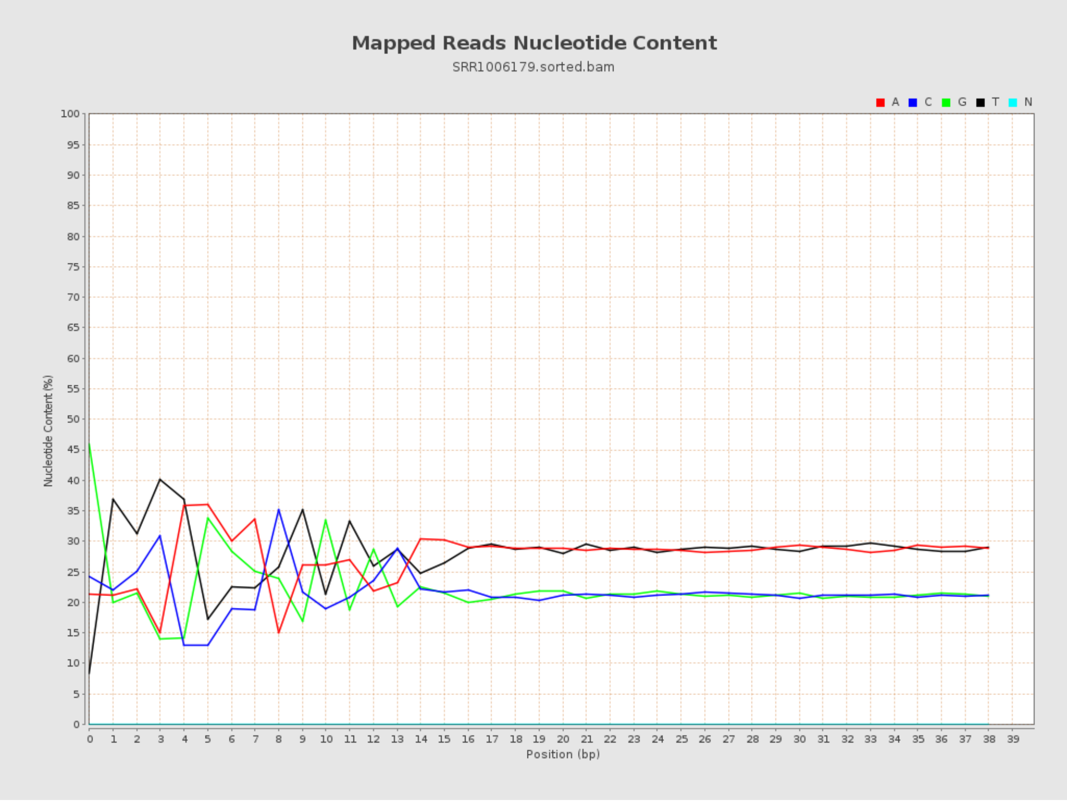
6. Results : Genome Fraction Coverage



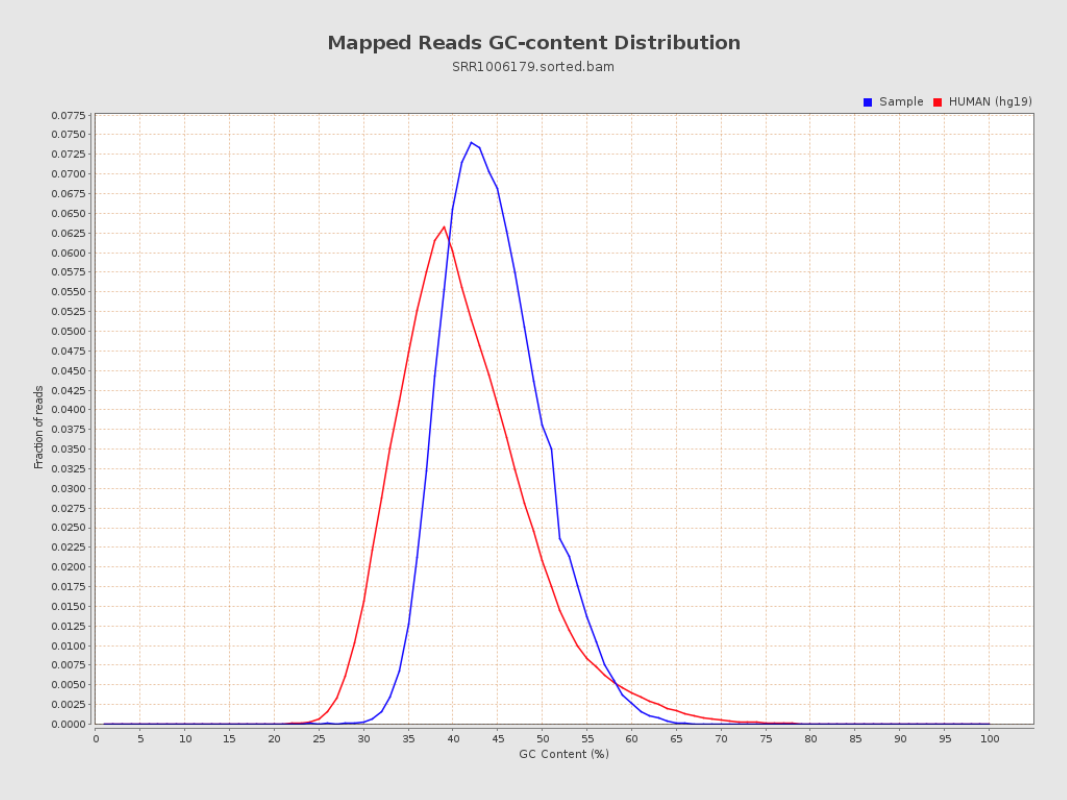
7. Results : Duplication Rate Histogram



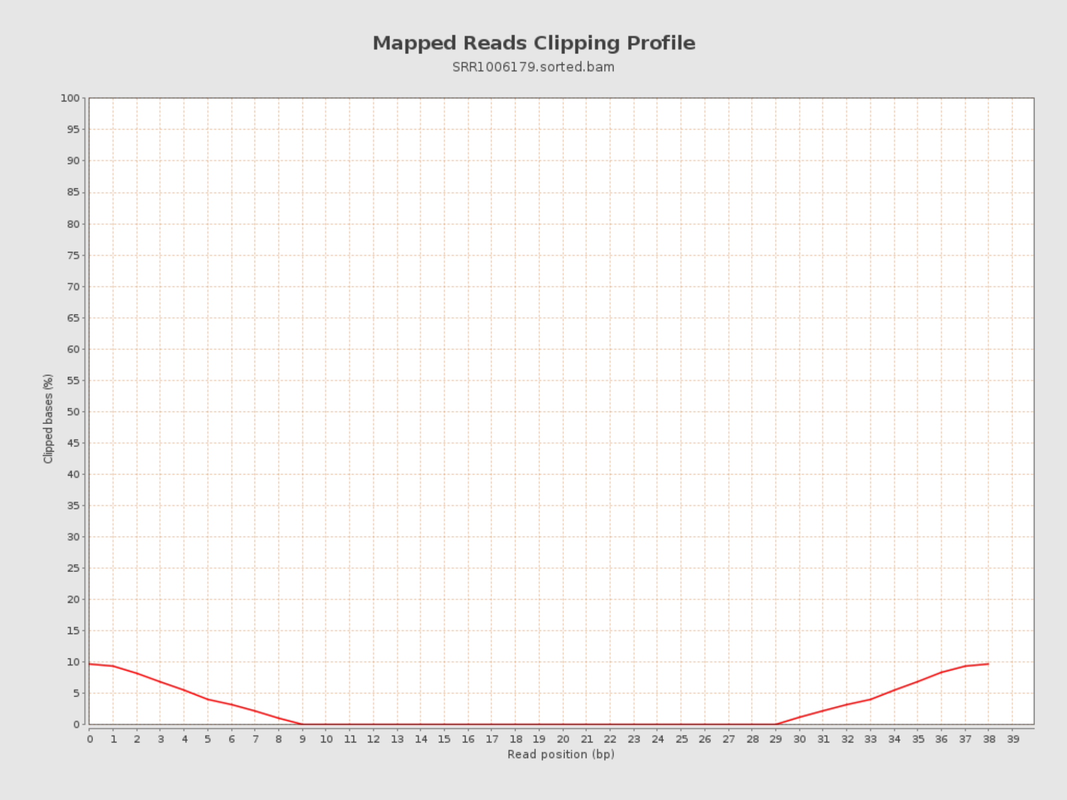
8. Results : Mapped Reads Nucleotide Content



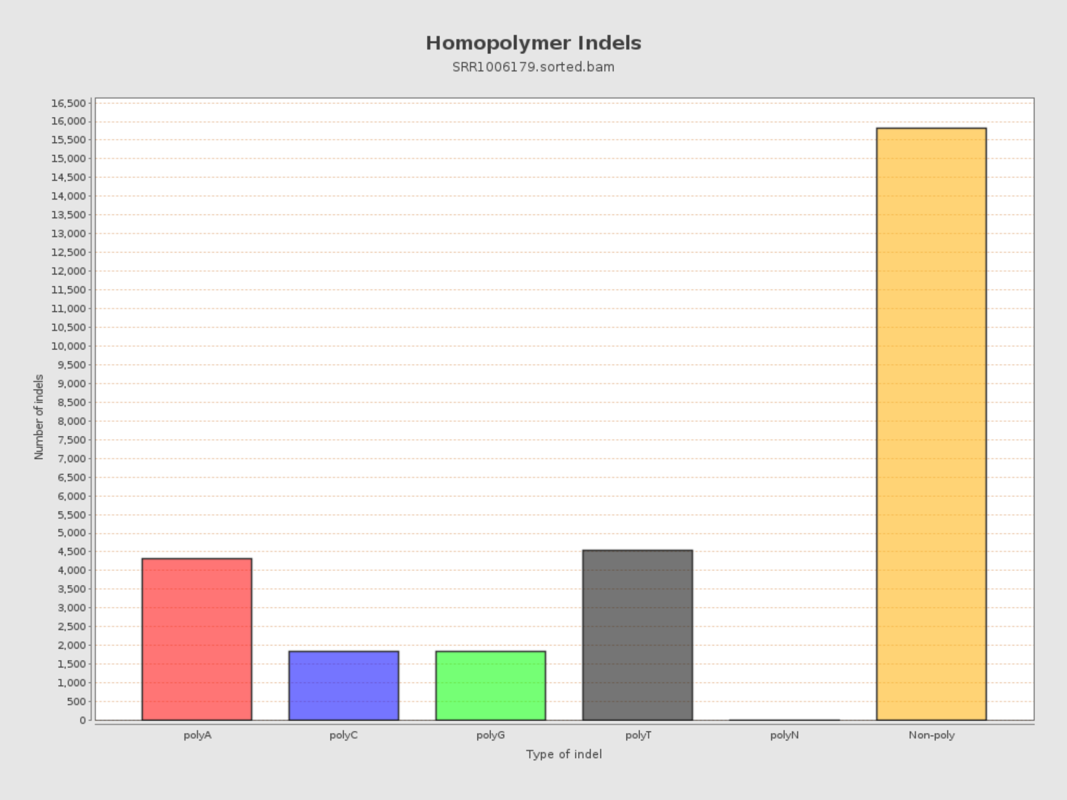
9. Results : Mapped Reads GC-content Distribution



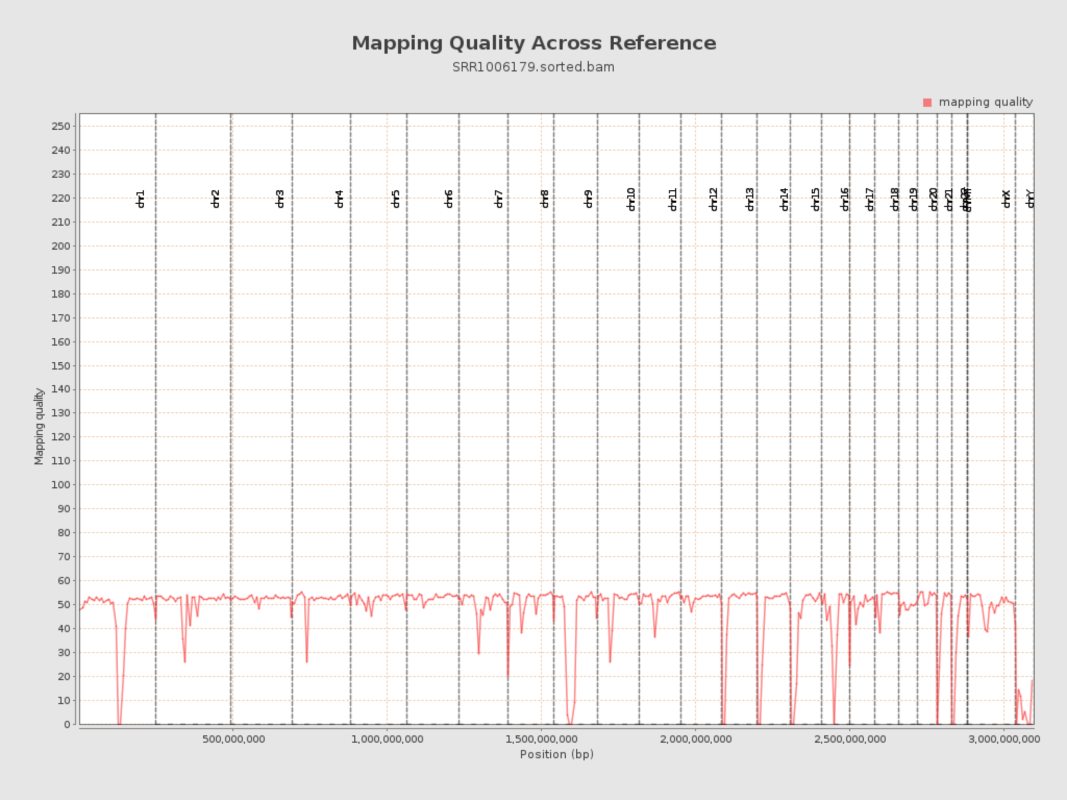
10. Results : Mapped Reads Clipping Profile



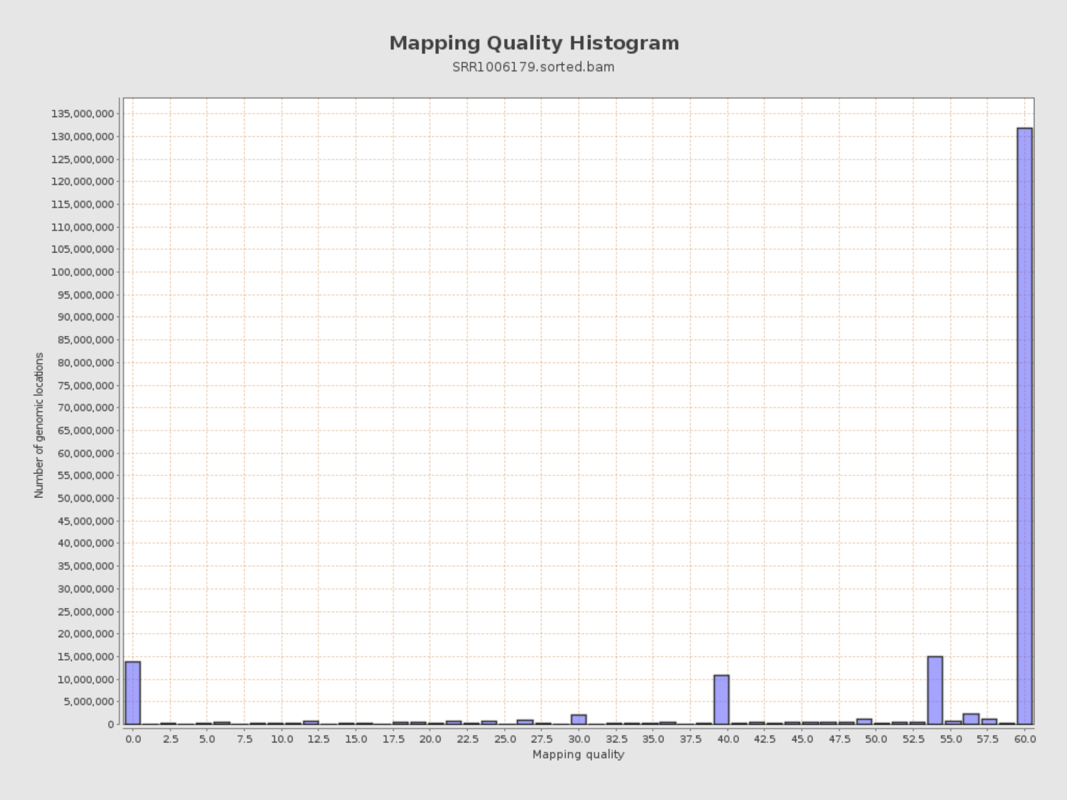
11. Results : Homopolymer Indels



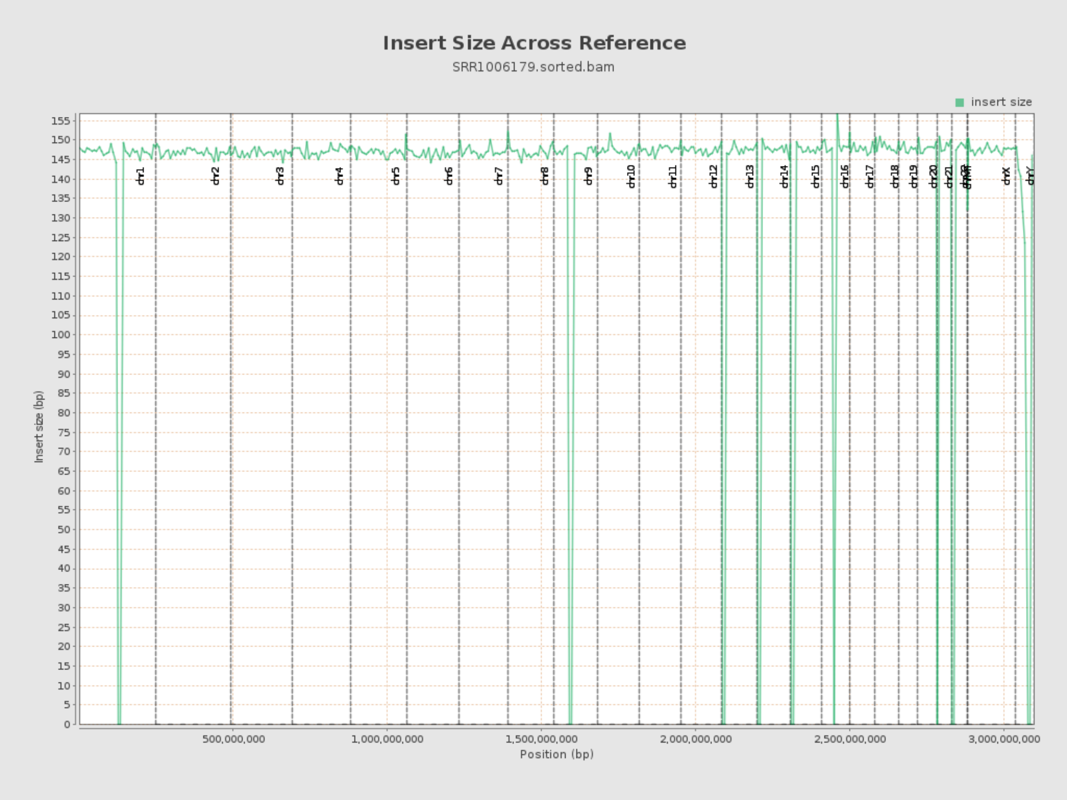
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram