Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 22:17:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046546.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_SRR2046546 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046546_1.fastq.gz SRR2046546_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 22:17:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046546.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,996,024
Mapped reads	7,967,630 / 99.64%
Unmapped reads	28,394 / 0.36%
Mapped paired reads	7,967,630 / 99.64%
Mapped reads, first in pair	3,987,625 / 49.87%
Mapped reads, second in pair	3,980,005 / 49.77%
Mapped reads, both in pair	7,948,080 / 99.4%
Mapped reads, singletons	19,550 / 0.24%
Secondary alignments	0
Supplementary alignments	38,265 / 0.48%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	5,873,985 / 73.46%
Duplication rate	37.69%
Clipped reads	1,274,195 / 15.94%

2.2. ACGT Content

Number/percentage of A's	230,715,648 / 29.72%
Number/percentage of C's	157,699,275 / 20.31%
Number/percentage of T's	231,757,438 / 29.85%
Number/percentage of G's	156,082,080 / 20.11%
Number/percentage of N's	66,171 / 0.01%

GC Percentage	40.42%

2.3. Coverage

Mean	0.2508
Standard Deviation	22.4878

2.4. Mapping Quality

Mean Mapping Quality	52.41

2.5. Insert size

Mean	19,102.18
Standard Deviation	1,441,819.91
P25/Median/P75	113 / 140 / 171

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	2,868,376
Insertions	65,200
Mapped reads with at least one insertion	0.8%
Deletions	76,861
Mapped reads with at least one deletion	0.93%
Homopolymer indels	49.45%

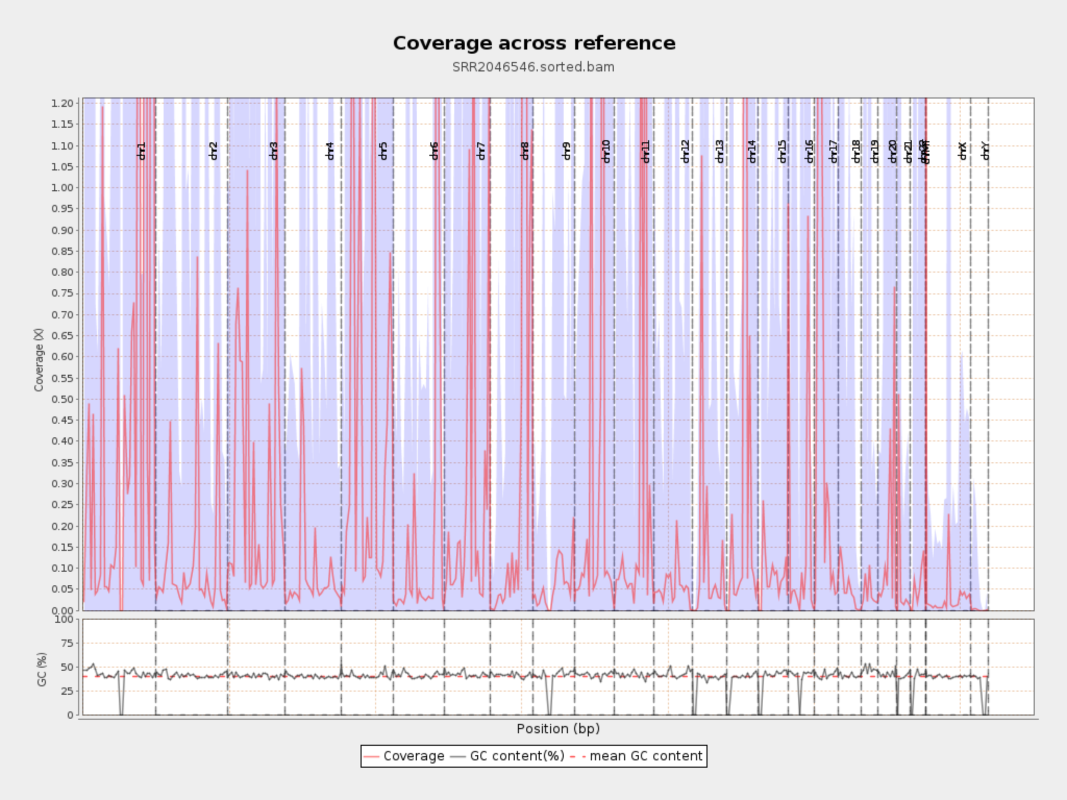
2.7. Chromosome stats

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

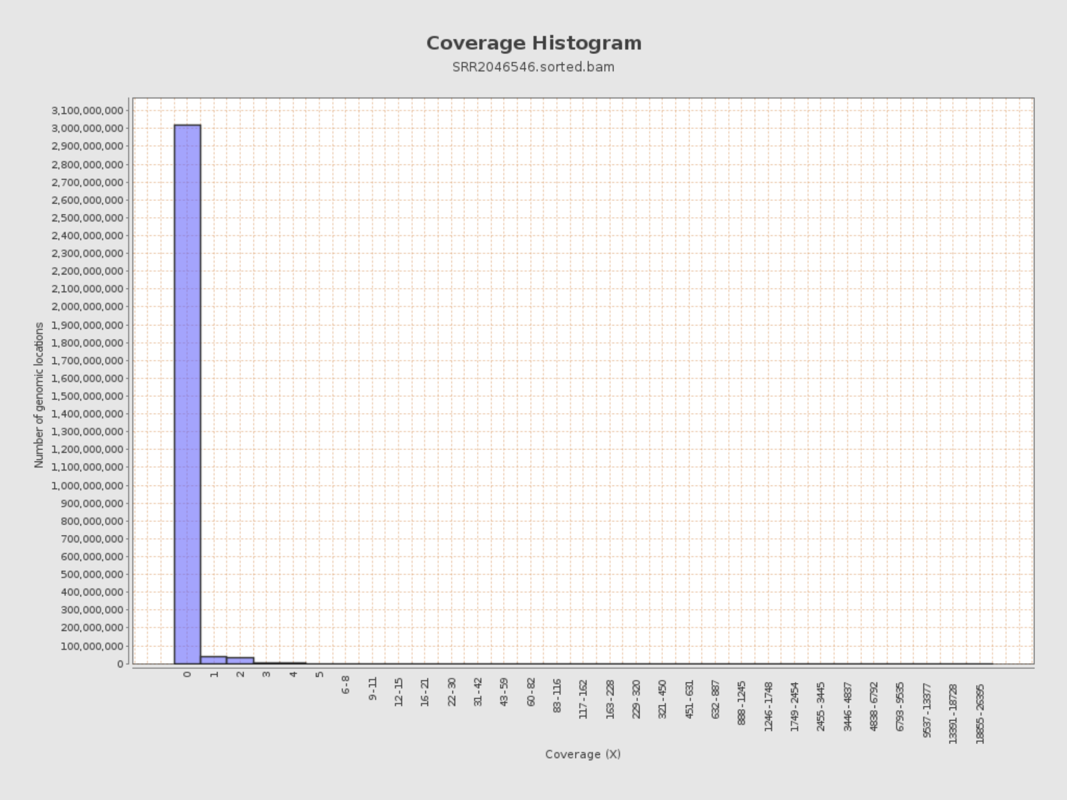
		bases	coverage	deviation
chr1	249250621	166905492	0.6696	49.2053
chr2	243199373	28008324	0.1152	7.382
chr3	198022430	60877480	0.3074	19.7805
chr4	191154276	17564913	0.0919	4.2933
chr5	180915260	81963240	0.453	26.4987
chr6	171115067	39097668	0.2285	24.5545
chr7	159138663	49007757	0.308	19.7885
chr8	146364022	76016486	0.5194	30.1901
chr9	141213431	8716829	0.0617	3.299
chr10	135534747	43413400	0.3203	32.4262
chr11	135006516	42920634	0.3179	20.6934
chr12	133851895	7681832	0.0574	2.8162
chr13	115169878	14873907	0.1291	8.1946
chr14	107349540	41052378	0.3824	26.6512
chr15	102531392	8689614	0.0848	2.9869
chr16	90354753	14920790	0.1651	12.3394
chr17	81195210	44236111	0.5448	37.7404
chr18	78077248	4125413	0.0528	2.8337
chr19	59128983	2502870	0.0423	2.1557
chr20	63025520	11651572	0.1849	15.4387
chr21	48129895	4619929	0.096	11.7868
chr22	51304566	3012308	0.0587	4.4288
chrMT	16571	38284	2.3103	2.1894
chrX	155270560	4520063	0.0291	2.3743

chrY	59373566	110444	0.0019	0.1501

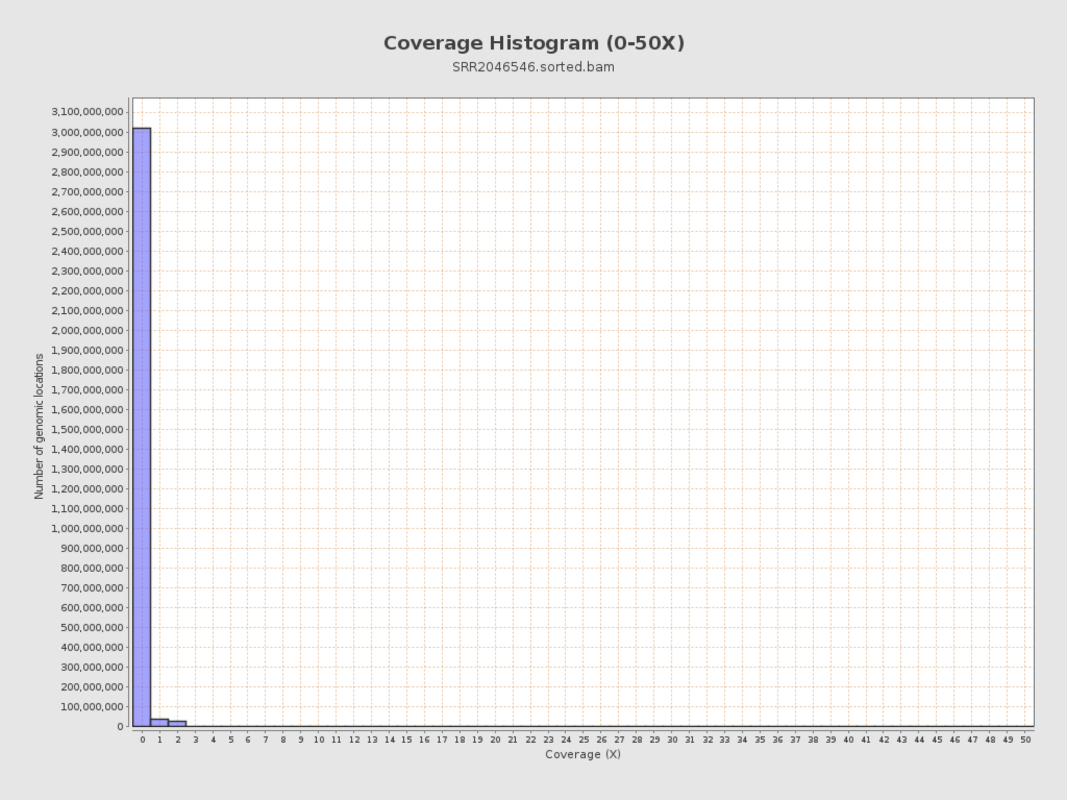
3. Results : Coverage across reference



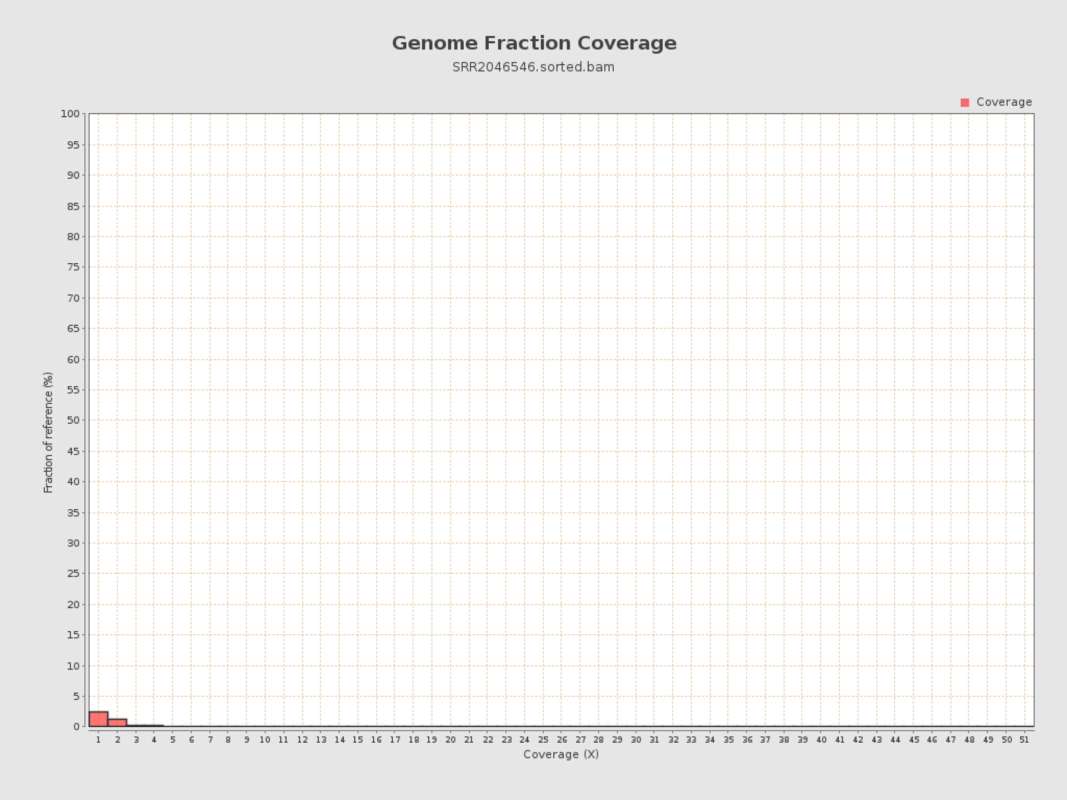
4. Results : Coverage Histogram



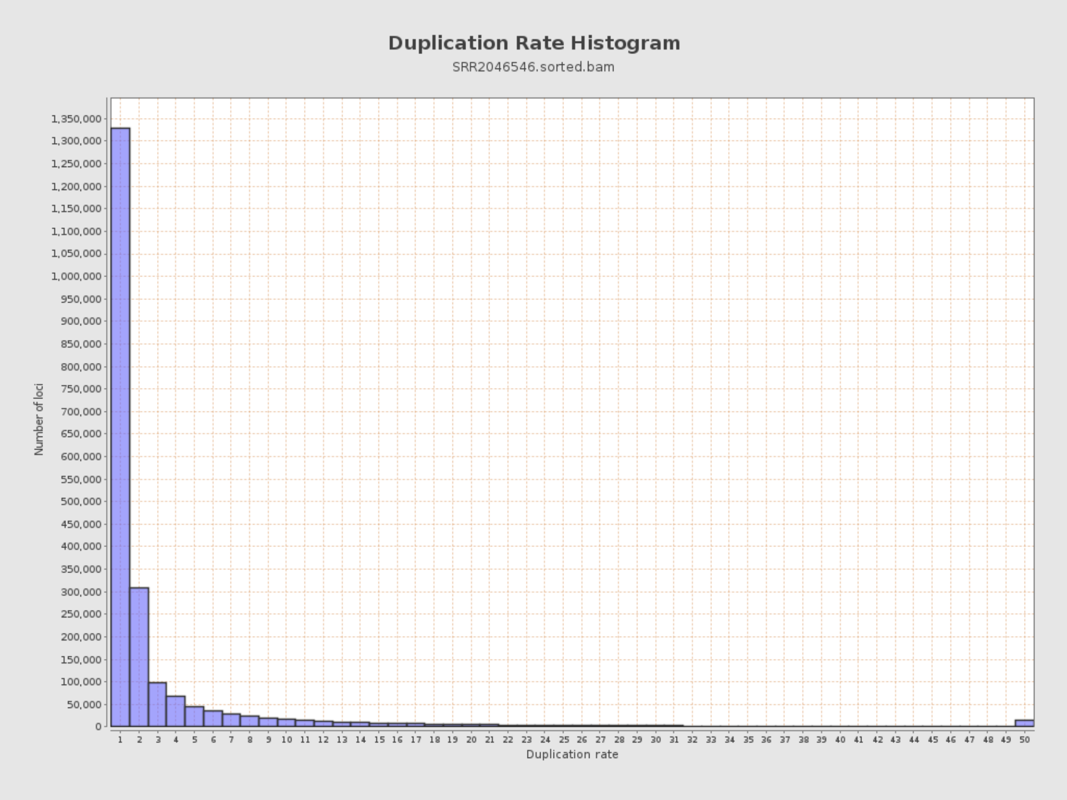
5. Results : Coverage Histogram (0-50X)



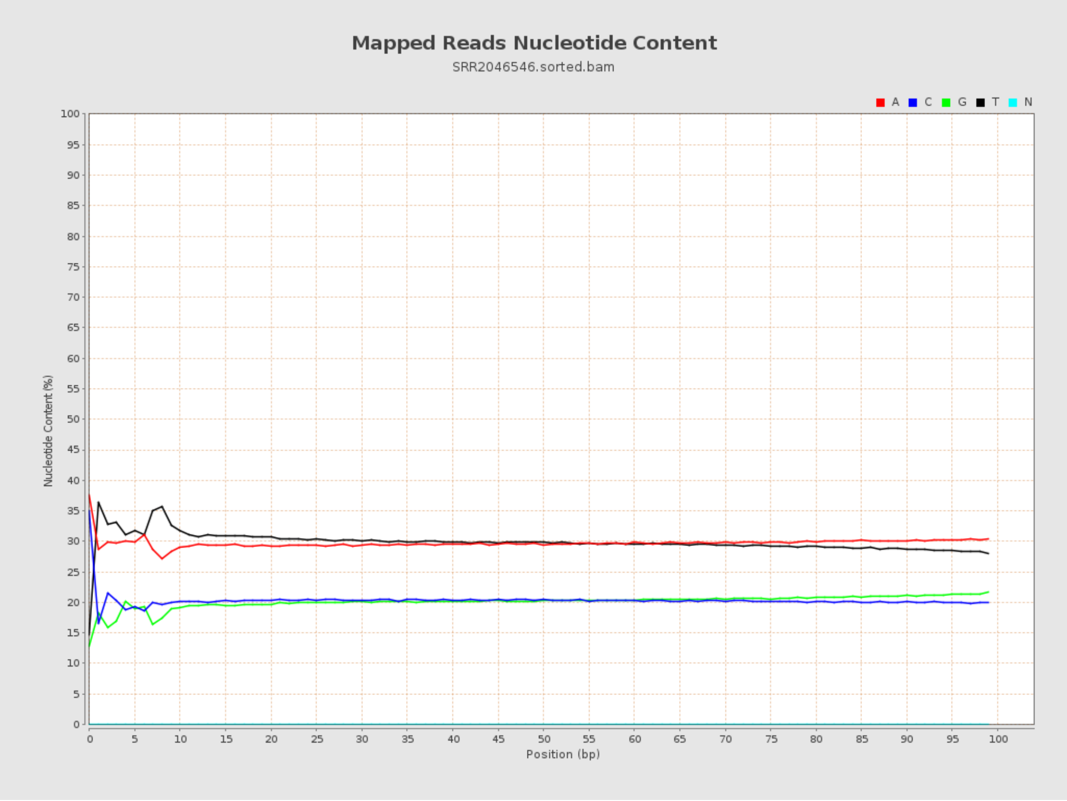
6. Results : Genome Fraction Coverage



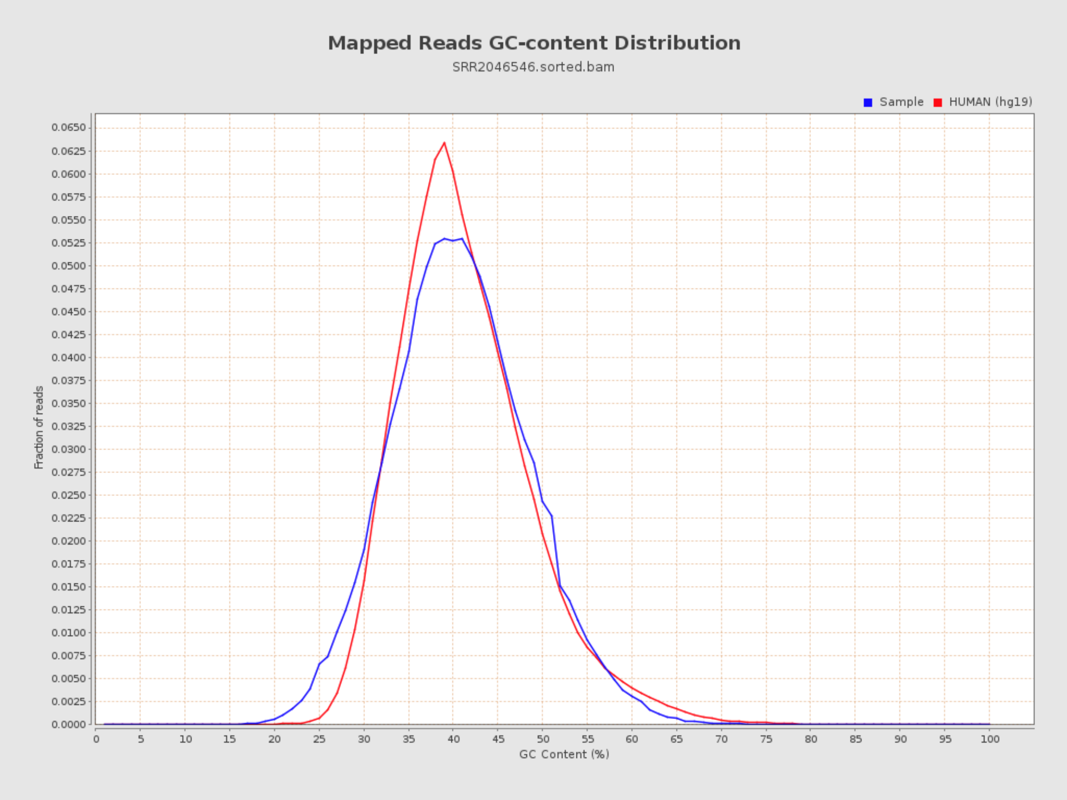
7. Results : Duplication Rate Histogram



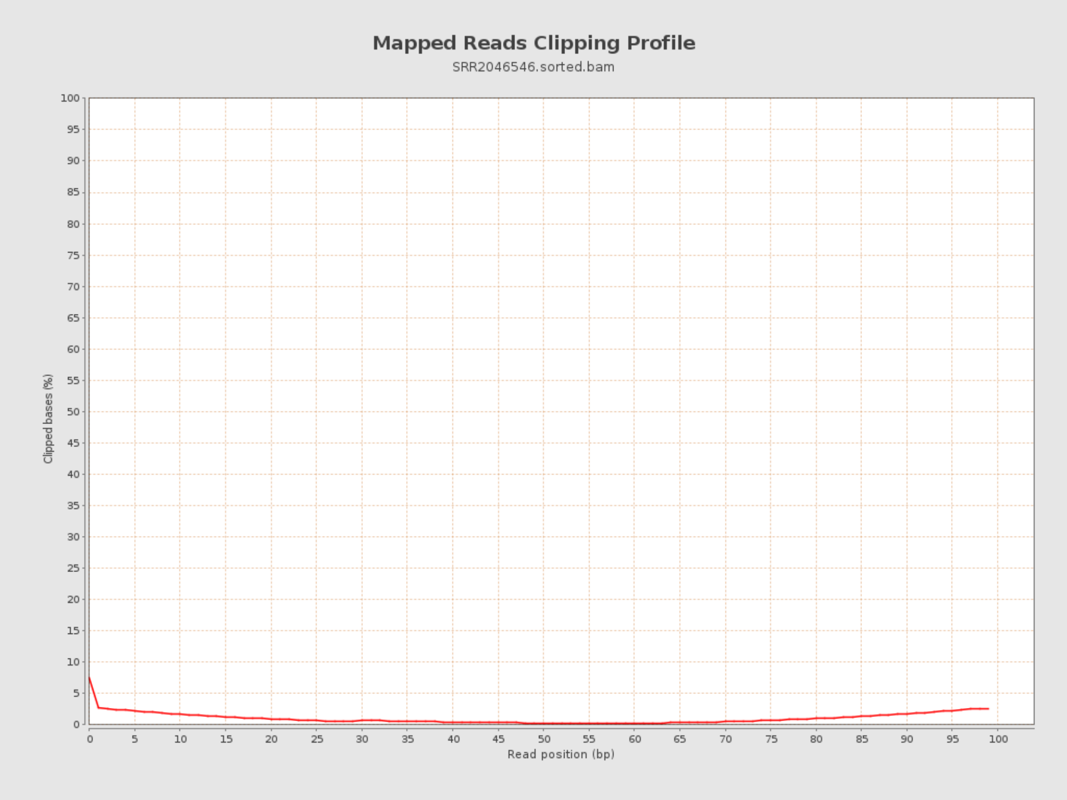
8. Results : Mapped Reads Nucleotide Content



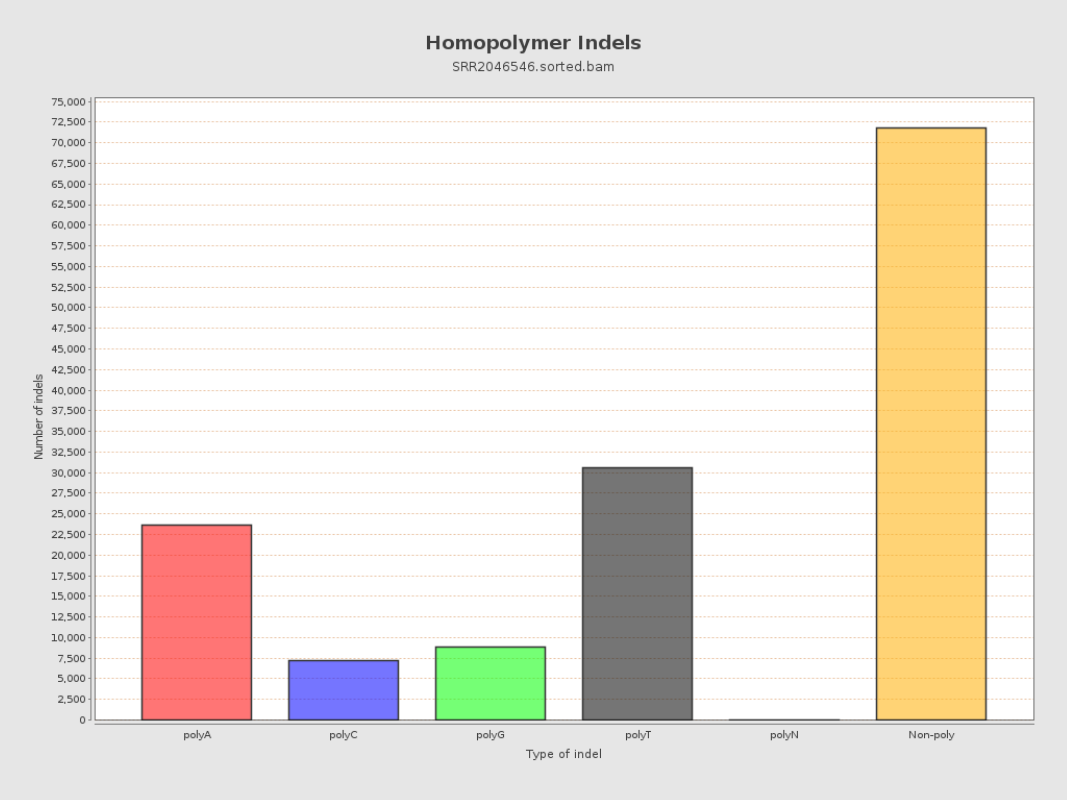
9. Results : Mapped Reads GC-content Distribution



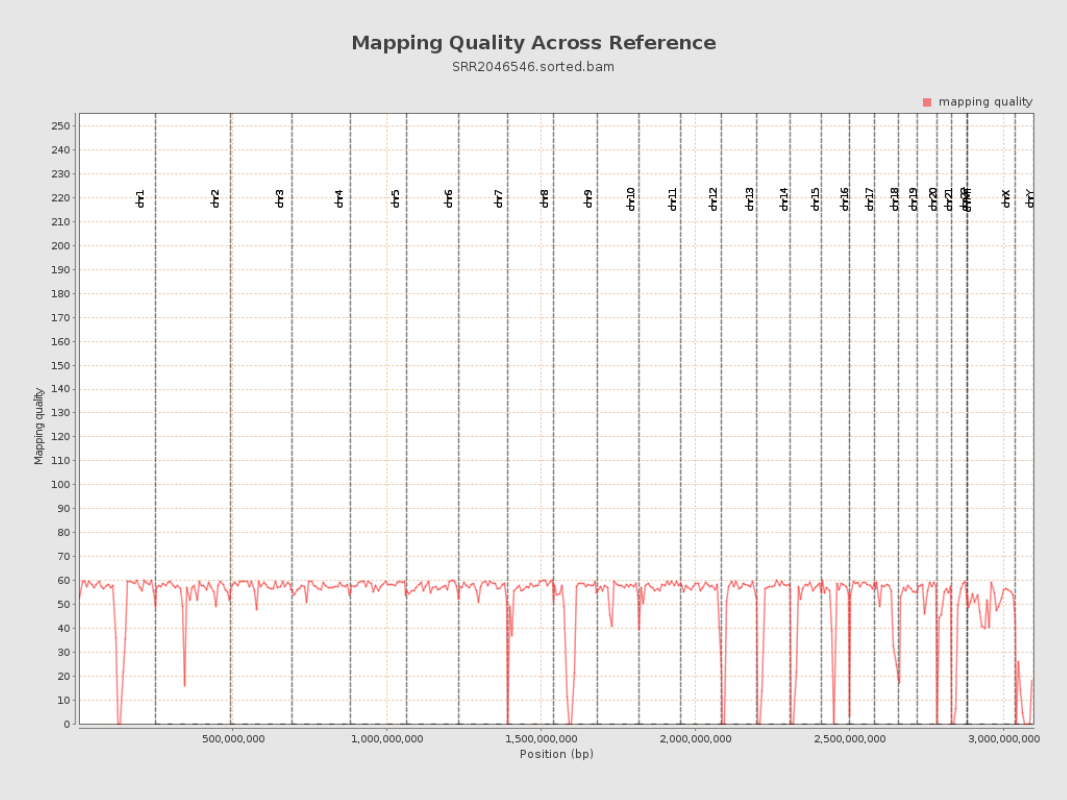
10. Results : Mapped Reads Clipping Profile



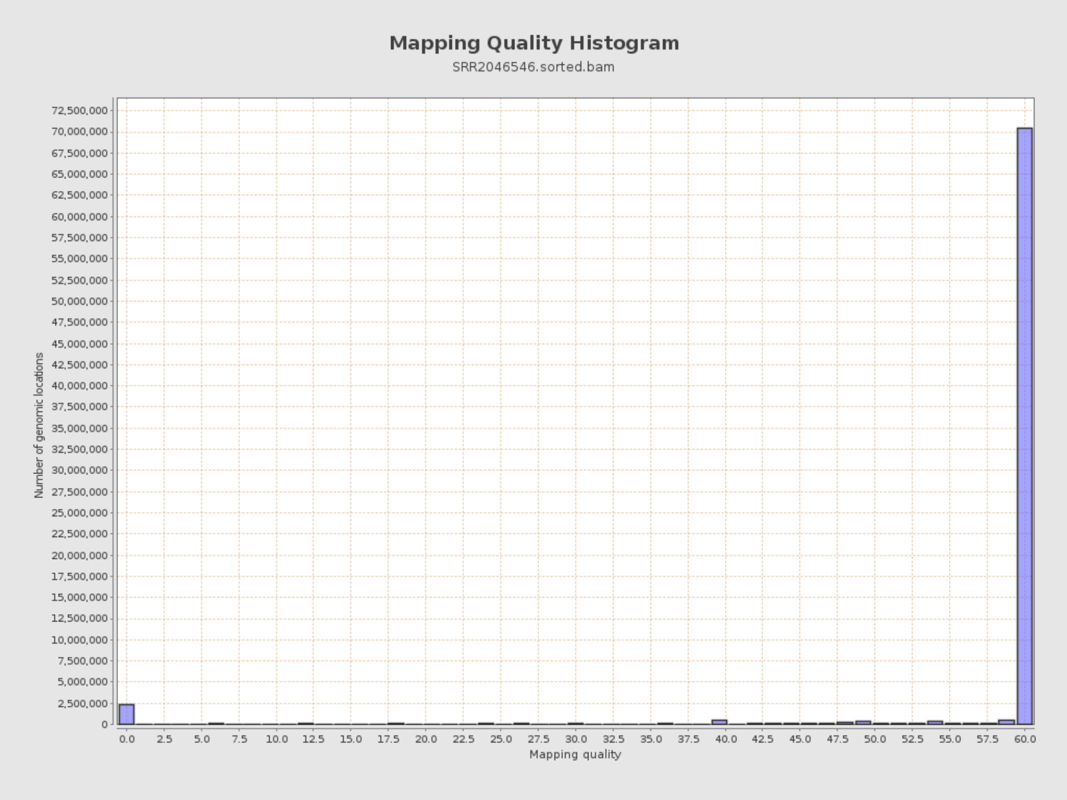
11. Results : Homopolymer Indels



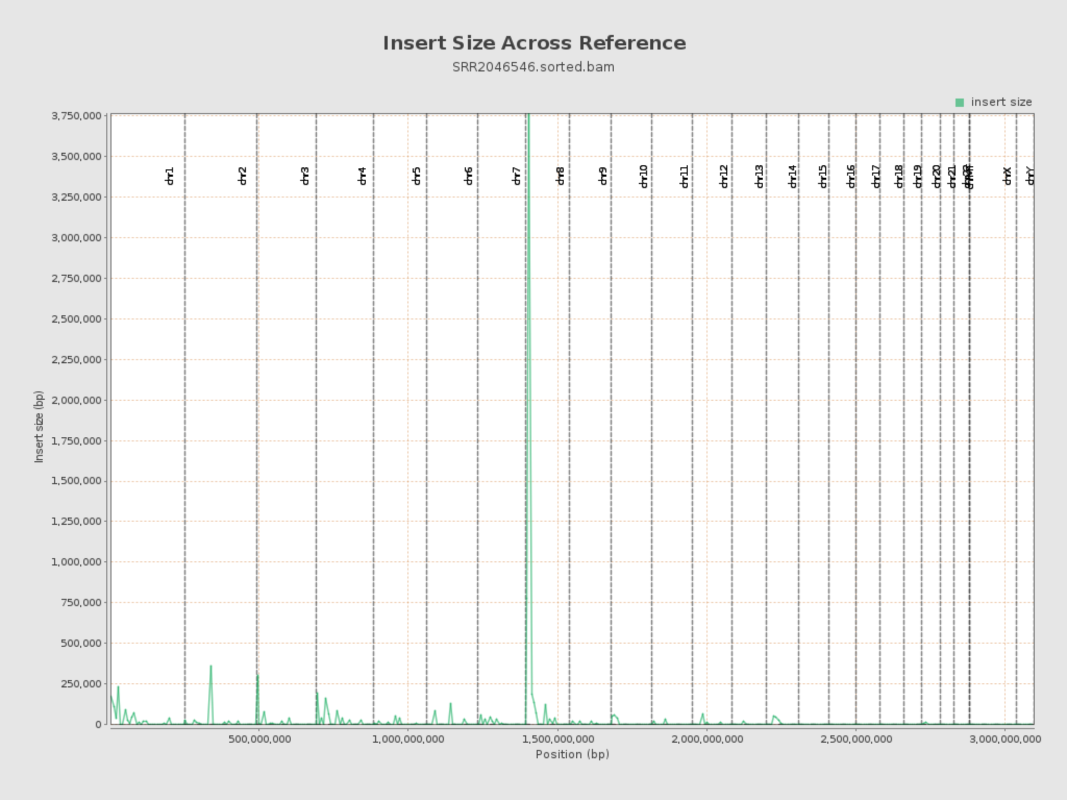
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram