Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:35:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006194.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_SRR1006194 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006194_1.fastq.gz SRR1006194_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:35:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006194.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,981,672
Mapped reads	2,599,323 / 87.18%
Unmapped reads	382,349 / 12.82%
Mapped paired reads	2,599,323 / 87.18%
Mapped reads, first in pair	1,302,388 / 43.68%
Mapped reads, second in pair	1,296,935 / 43.5%
Mapped reads, both in pair	2,407,984 / 80.76%
Mapped reads, singletons	191,339 / 6.42%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	67,904 / 2.28%
Duplication rate	2.26%
Clipped reads	157,988 / 5.3%

2.2. ACGT Content

Number/percentage of A's	27,634,548 / 27.48%
Number/percentage of C's	21,913,862 / 21.79%
Number/percentage of T's	28,235,695 / 28.08%
Number/percentage of G's	22,770,013 / 22.64%
Number/percentage of N's	4,805 / 0%
GC Percentage	44.44%

2.3. Coverage

Mean	0.0325
Standard Deviation	0.2319

2.4. Mapping Quality

Mean Mapping Quality	47.84

2.5. Insert size

Mean	50,441.48
Standard Deviation	2,097,956.57
P25/Median/P75	72 / 113 / 156

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	294,431
Insertions	3,319
Mapped reads with at least one insertion	0.13%
Deletions	10,133
Mapped reads with at least one deletion	0.39%
Homopolymer indels	44.19%

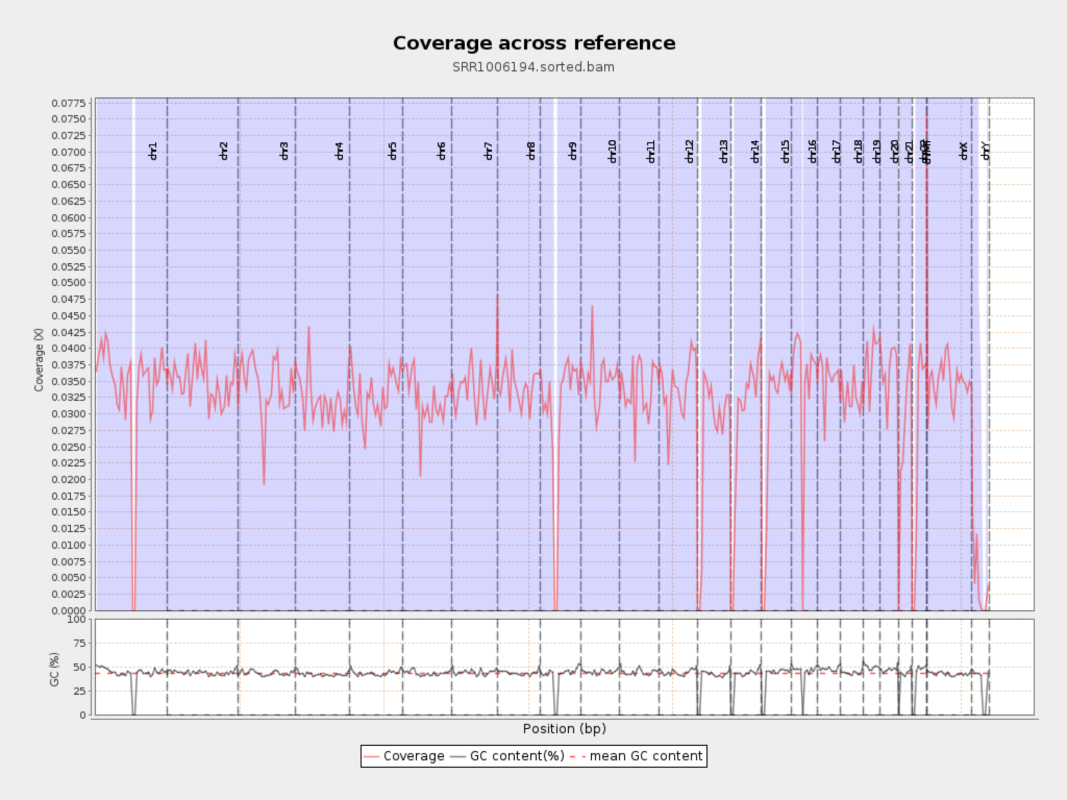
2.7. Chromosome stats

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

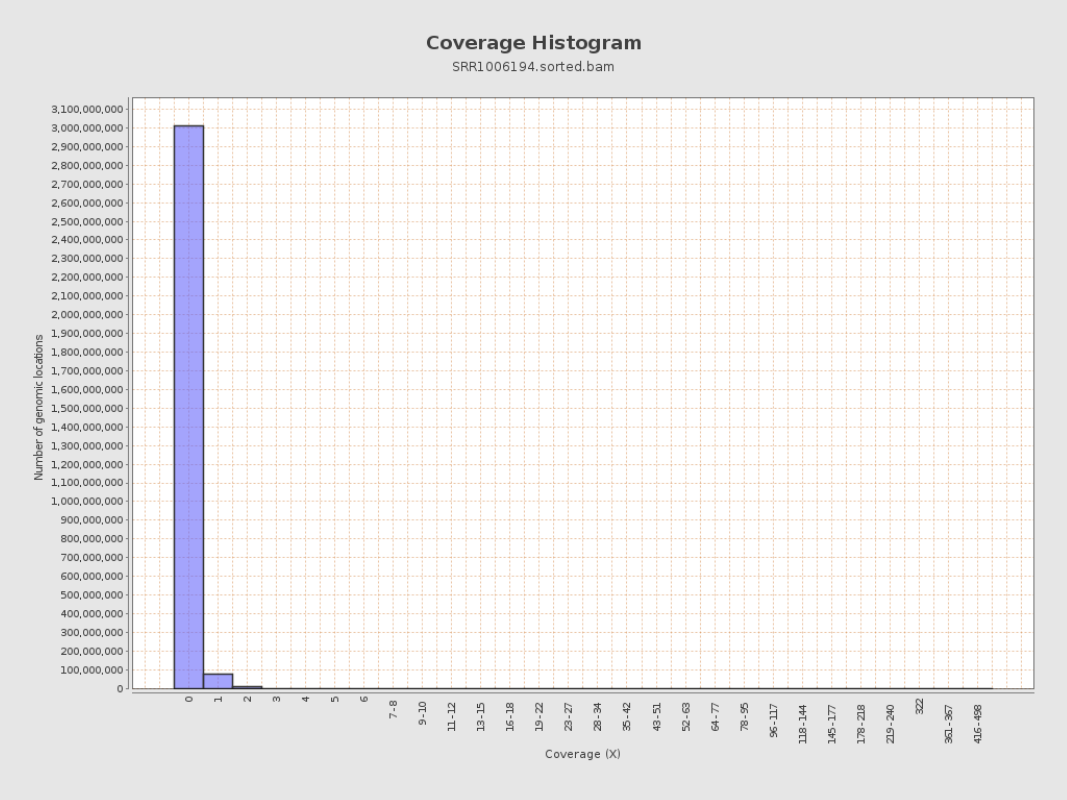
chr1	249250621	8443076	0.0339	0.2779
chr2	243199373	8527466	0.0351	0.2333
chr3	198022430	6785143	0.0343	0.207
chr4	191154276	6167676	0.0323	0.2105
chr5	180915260	5978352	0.033	0.2032
chr6	171115067	5526919	0.0323	0.2106
chr7	159138663	5405535	0.034	0.26
chr8	146364022	5019306	0.0343	0.3231
chr9	141213431	4218049	0.0299	0.2109
chr10	135534747	4817120	0.0355	0.2458
chr11	135006516	4572303	0.0339	0.2266
chr12	133851895	4567009	0.0341	0.2071
chr13	115169878	3038157	0.0264	0.1813
chr14	107349540	3097872	0.0289	0.2793
chr15	102531392	2923112	0.0285	0.1894
chr16	90354753	3140575	0.0348	0.2224
chr17	81195210	2897145	0.0357	0.2176
chr18	78077248	2561589	0.0328	0.2784
chr19	59128983	2266767	0.0383	0.2528
chr20	63025520	2299661	0.0365	0.2172
chr21	48129895	1318690	0.0274	0.2039
chr22	51304566	1332242	0.026	0.1927
chrMT	16571	1257	0.0759	0.3812
chrX	155270560	5424809	0.0349	0.2158

chrY	59373566	242637	0.0041	0.1007

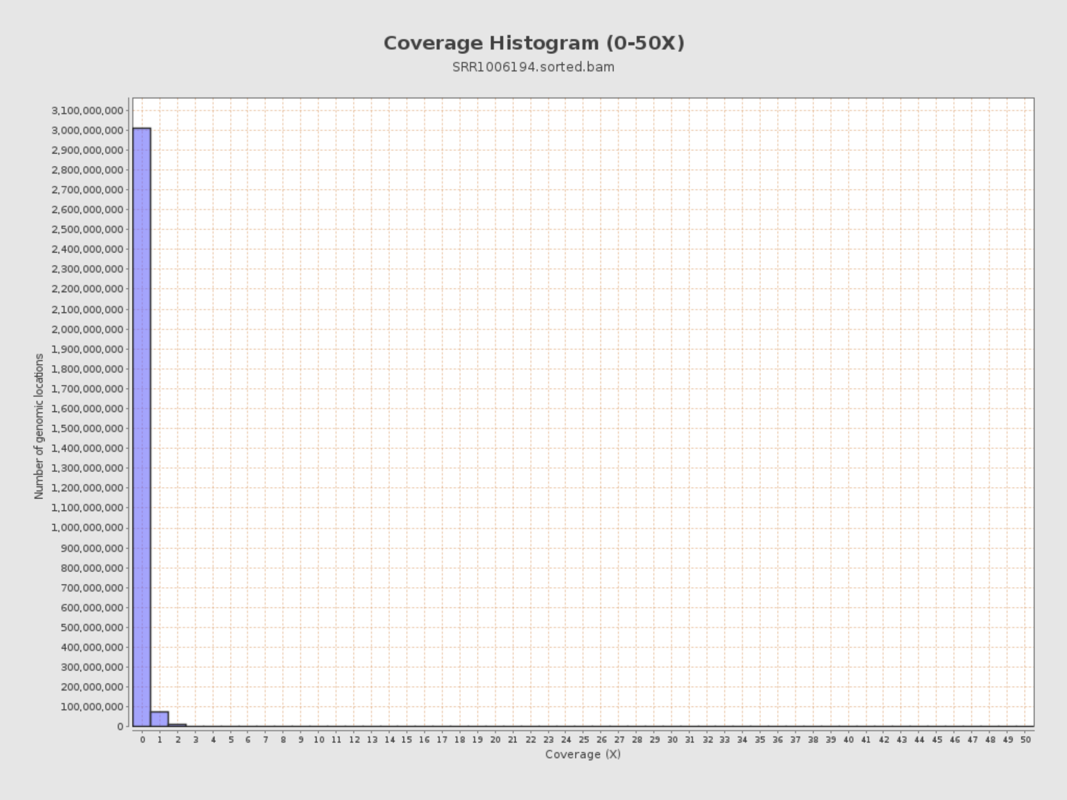
3. Results : Coverage across reference



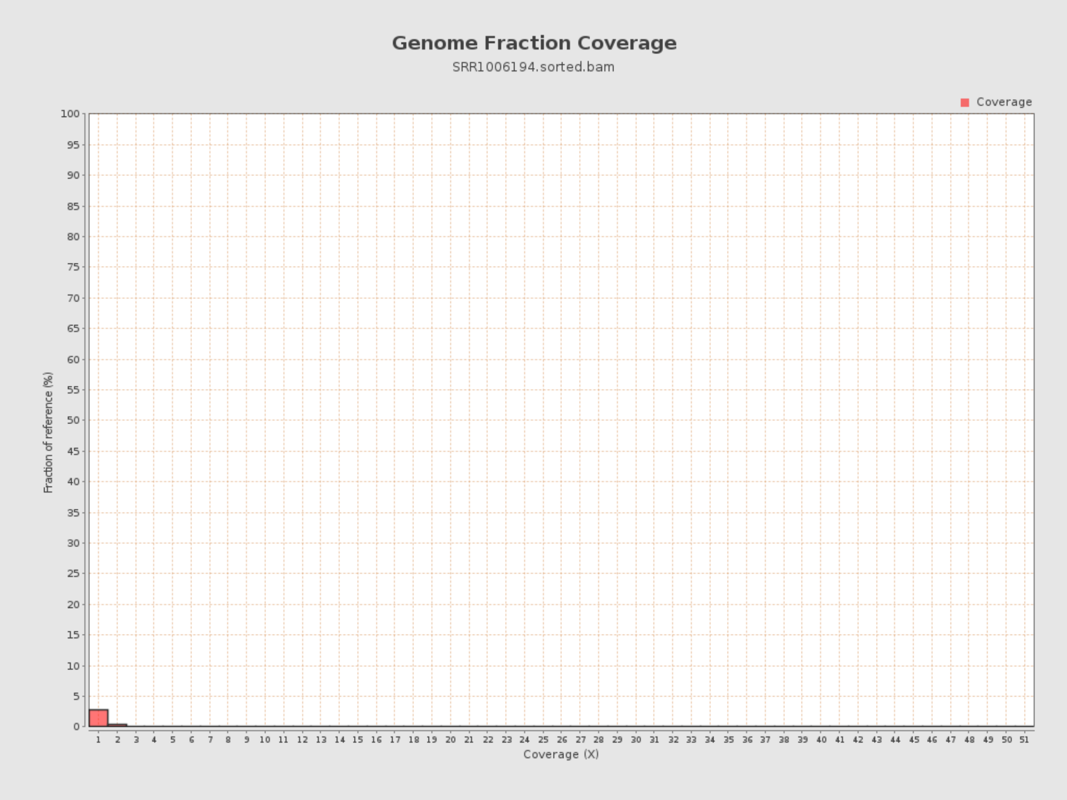
4. Results : Coverage Histogram



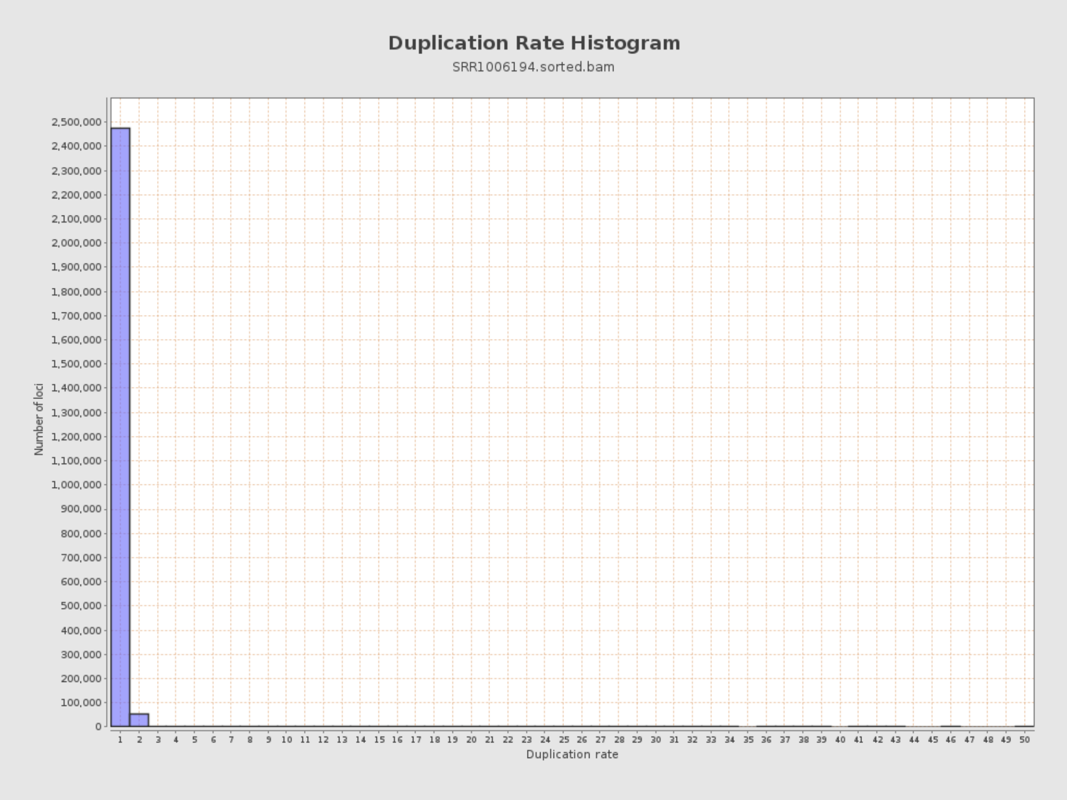
5. Results : Coverage Histogram (0-50X)



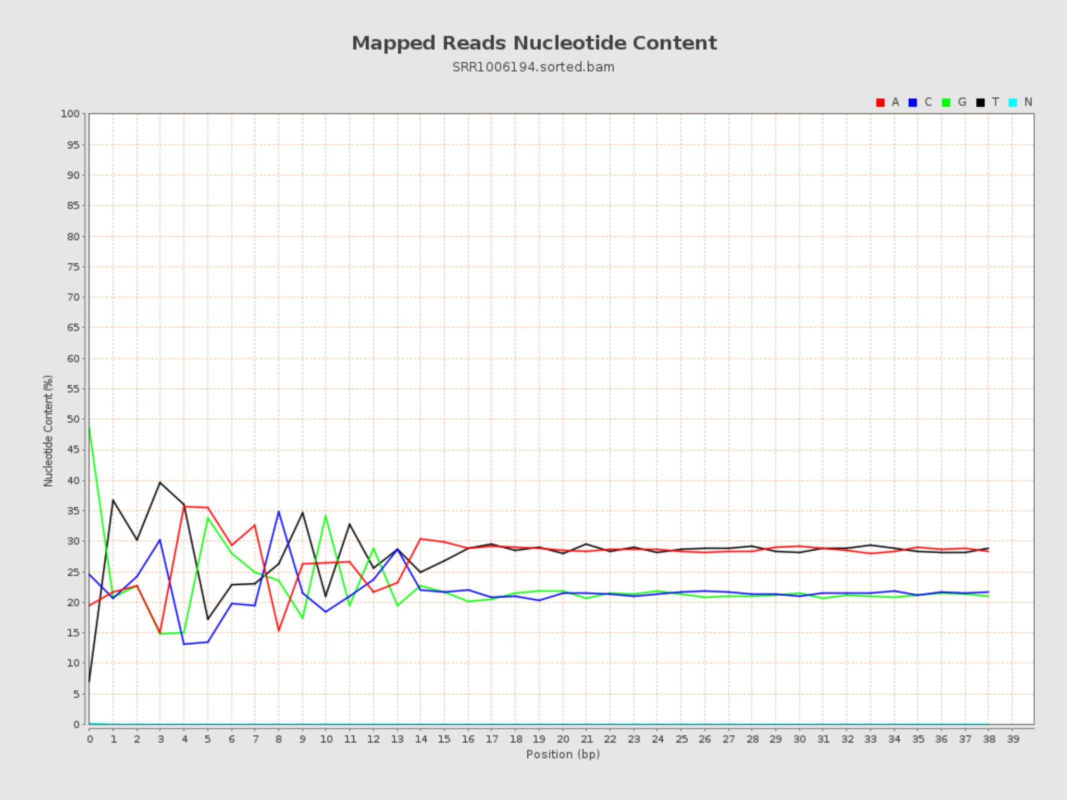
6. Results : Genome Fraction Coverage



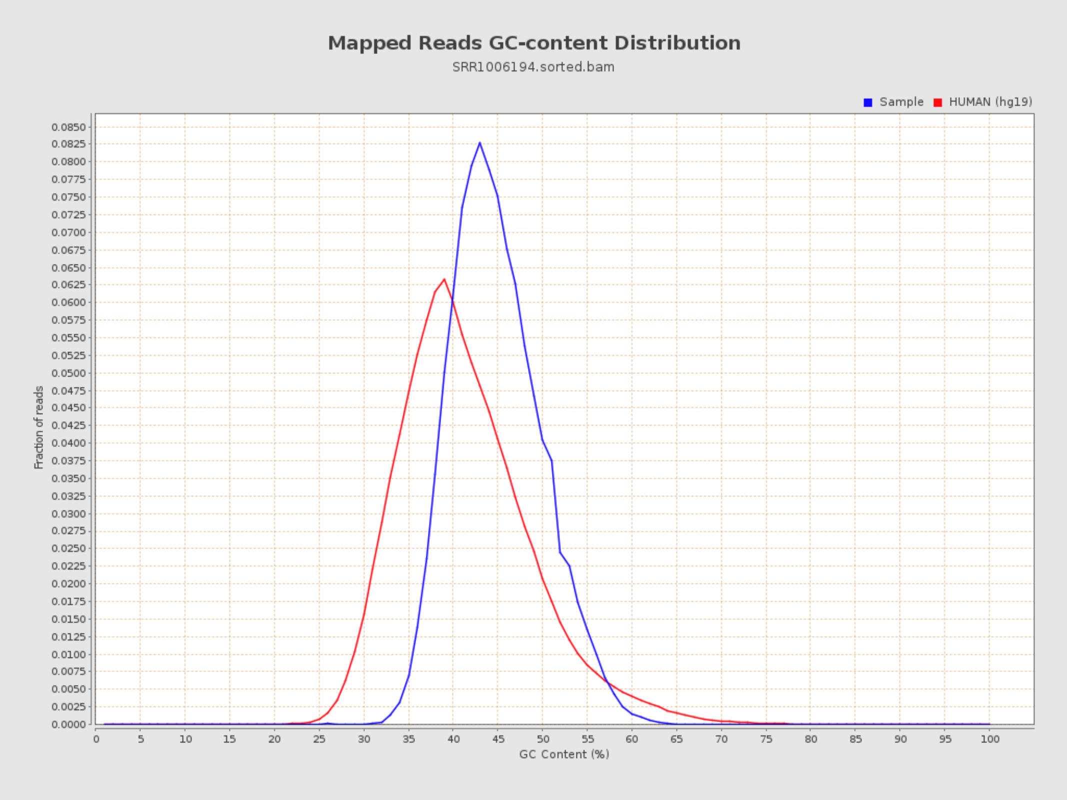
7. Results : Duplication Rate Histogram



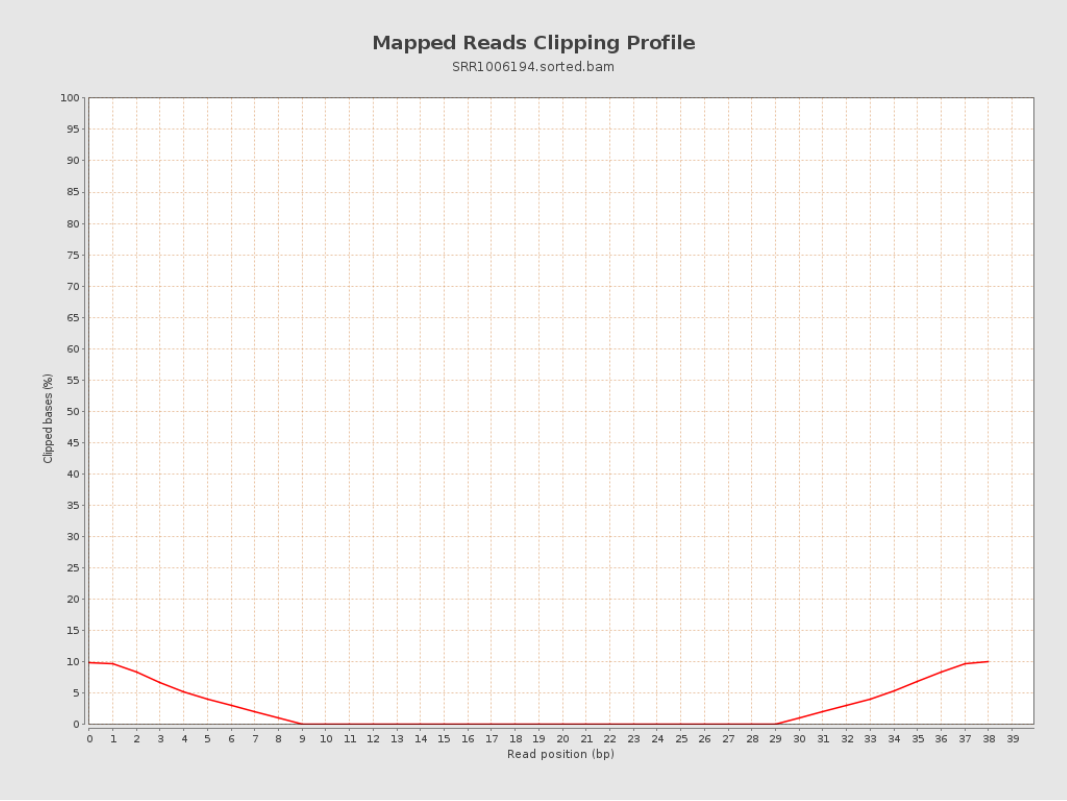
8. Results : Mapped Reads Nucleotide Content



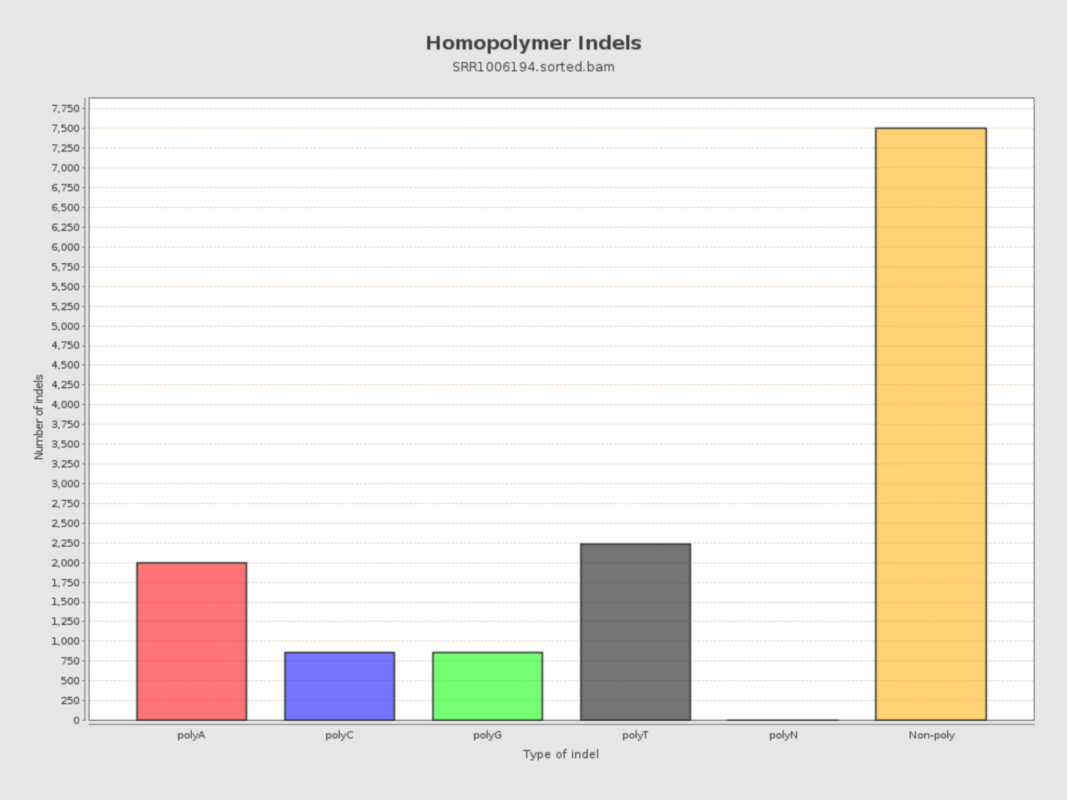
9. Results : Mapped Reads GC-content Distribution



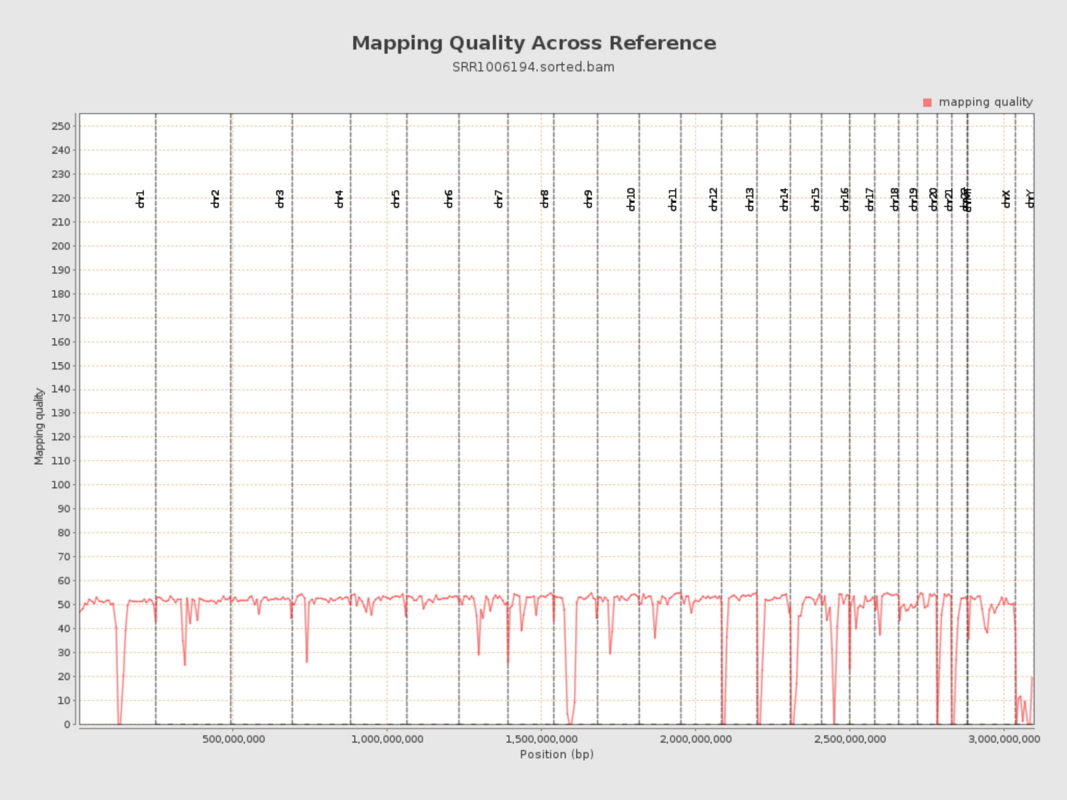
10. Results : Mapped Reads Clipping Profile



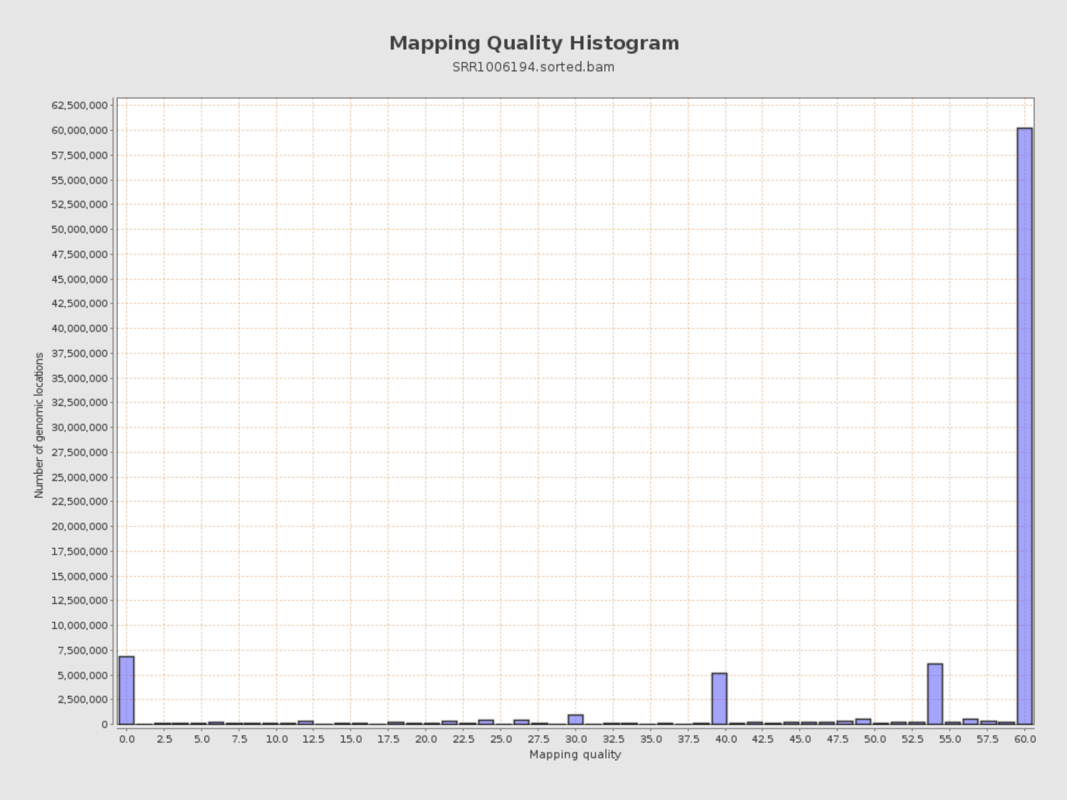
11. Results : Homopolymer Indels



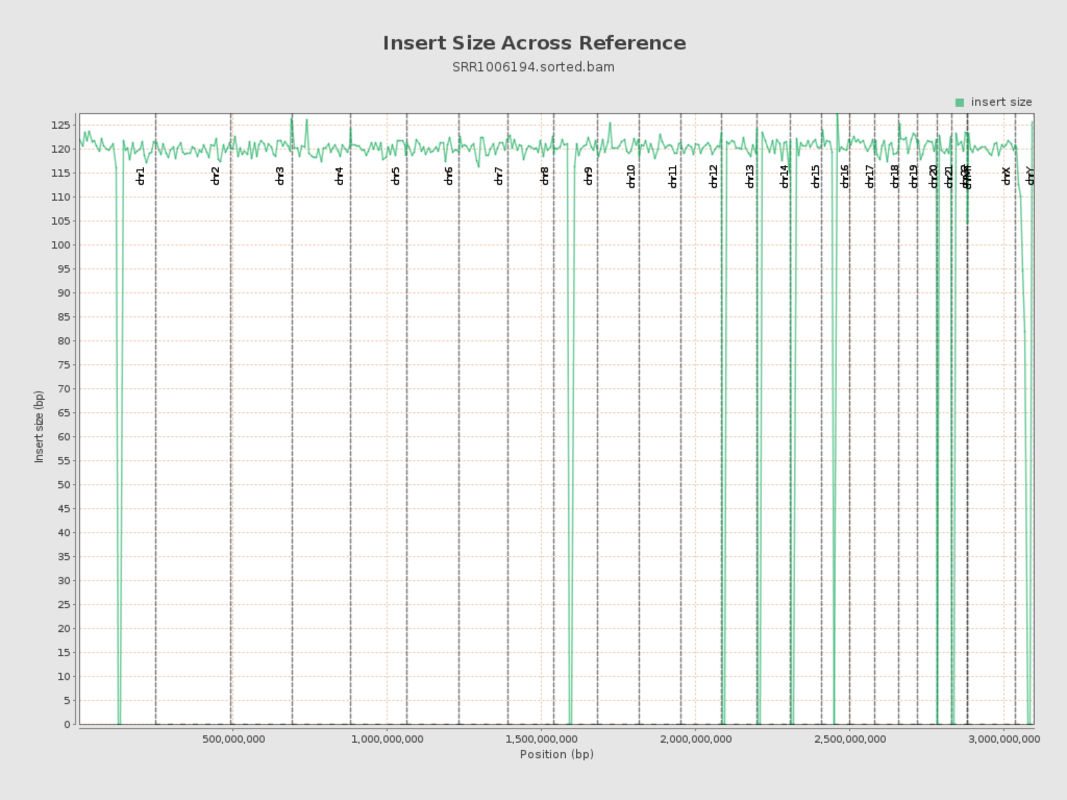
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram