Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:57:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006394.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_SRR1006394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006394_1.fastq.gz SRR1006394_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:56:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,051,058
Mapped reads	11,569,884 / 88.65%
Unmapped reads	1,481,174 / 11.35%
Mapped paired reads	11,569,884 / 88.65%
Mapped reads, first in pair	5,864,357 / 44.93%
Mapped reads, second in pair	5,705,527 / 43.72%
Mapped reads, both in pair	10,623,576 / 81.4%
Mapped reads, singletons	946,308 / 7.25%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	772,330 / 5.92%
Duplication rate	5.93%
Clipped reads	623,416 / 4.78%

2.2. ACGT Content

Number/percentage of A's	125,508,469 / 28.02%
Number/percentage of C's	96,027,720 / 21.43%
Number/percentage of T's	127,041,548 / 28.36%
Number/percentage of G's	99,405,799 / 22.19%
Number/percentage of N's	18,876 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.1447
Standard Deviation	0.7489

2.4. Mapping Quality

Mean Mapping Quality	48.32

2.5. Insert size

Mean	72,831.93
Standard Deviation	2,573,582.03
P25/Median/P75	102 / 134 / 184

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	1,644,085
Insertions	11,660
Mapped reads with at least one insertion	0.1%
Deletions	41,015
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.95%

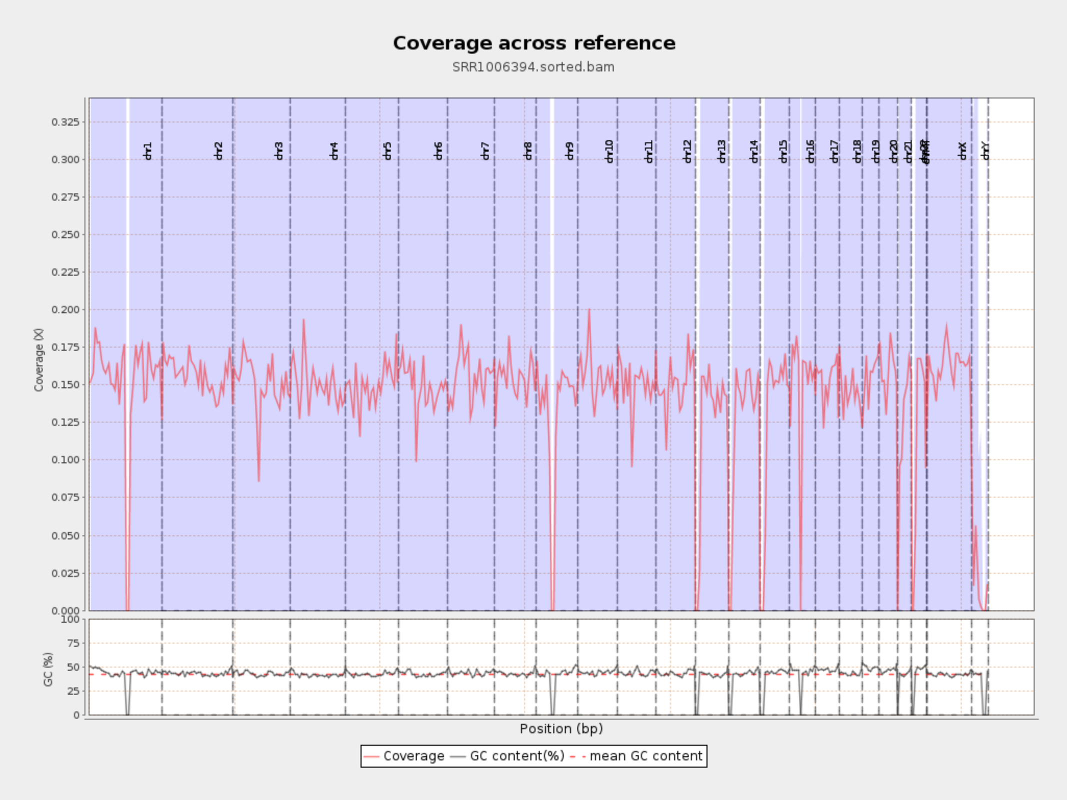
2.7. Chromosome stats

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

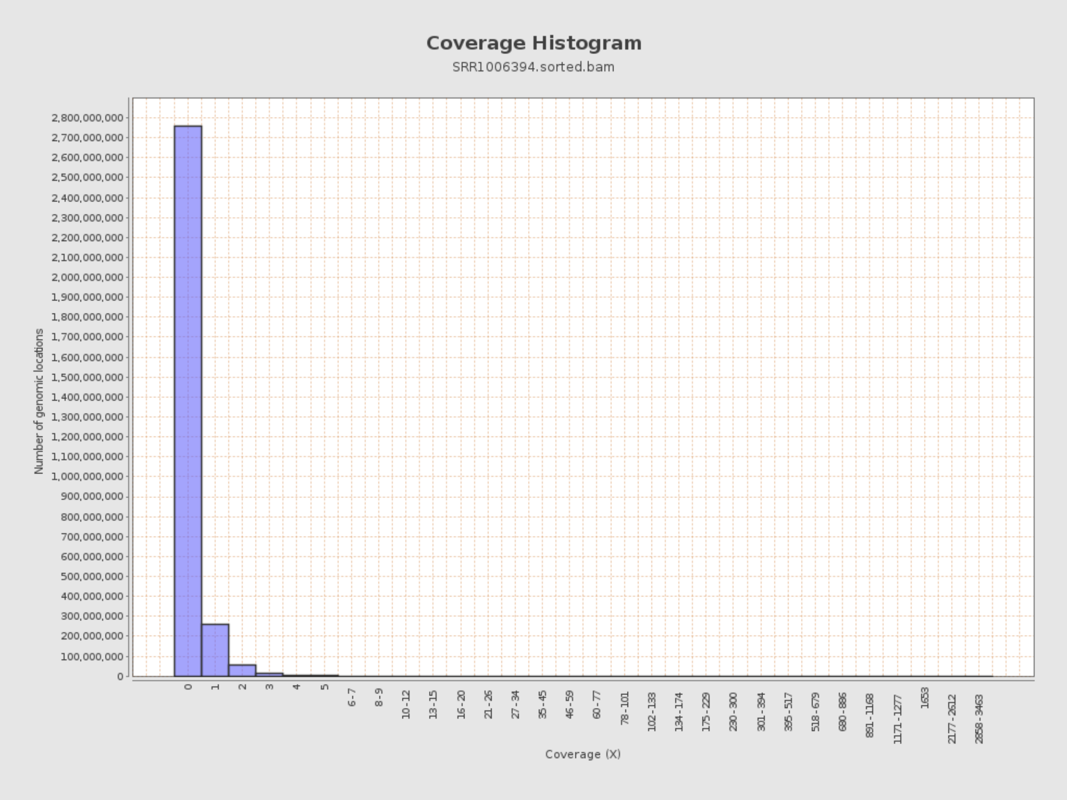
chr1	249250621	37573572	0.1507	1.1144
chr2	243199373	38293858	0.1575	0.6504
chr3	198022430	29875126	0.1509	0.4835
chr4	191154276	28646810	0.1499	0.5537
chr5	180915260	27079635	0.1497	0.4822
chr6	171115067	25541884	0.1493	0.5591
chr7	159138663	24699488	0.1552	0.9294
chr8	146364022	22573253	0.1542	1.7607
chr9	141213431	18022371	0.1276	0.542
chr10	135534747	21130965	0.1559	0.7431
chr11	135006516	20272857	0.1502	0.6316
chr12	133851895	20099103	0.1502	0.4907
chr13	115169878	13919339	0.1209	0.4304
chr14	107349540	13289037	0.1238	0.4999
chr15	102531392	12959262	0.1264	0.443
chr16	90354753	13467471	0.1491	0.6088
chr17	81195210	12403031	0.1528	0.5274
chr18	78077248	11388671	0.1459	0.9266
chr19	59128983	9208820	0.1557	0.8101
chr20	63025520	10010450	0.1588	0.5364
chr21	48129895	5859731	0.1217	0.5082
chr22	51304566	5590025	0.109	0.4248
chrMT	16571	2834	0.171	0.6238
chrX	155270560	25097245	0.1616	0.5585

chrY	59373566	1052503	0.0177	0.4096

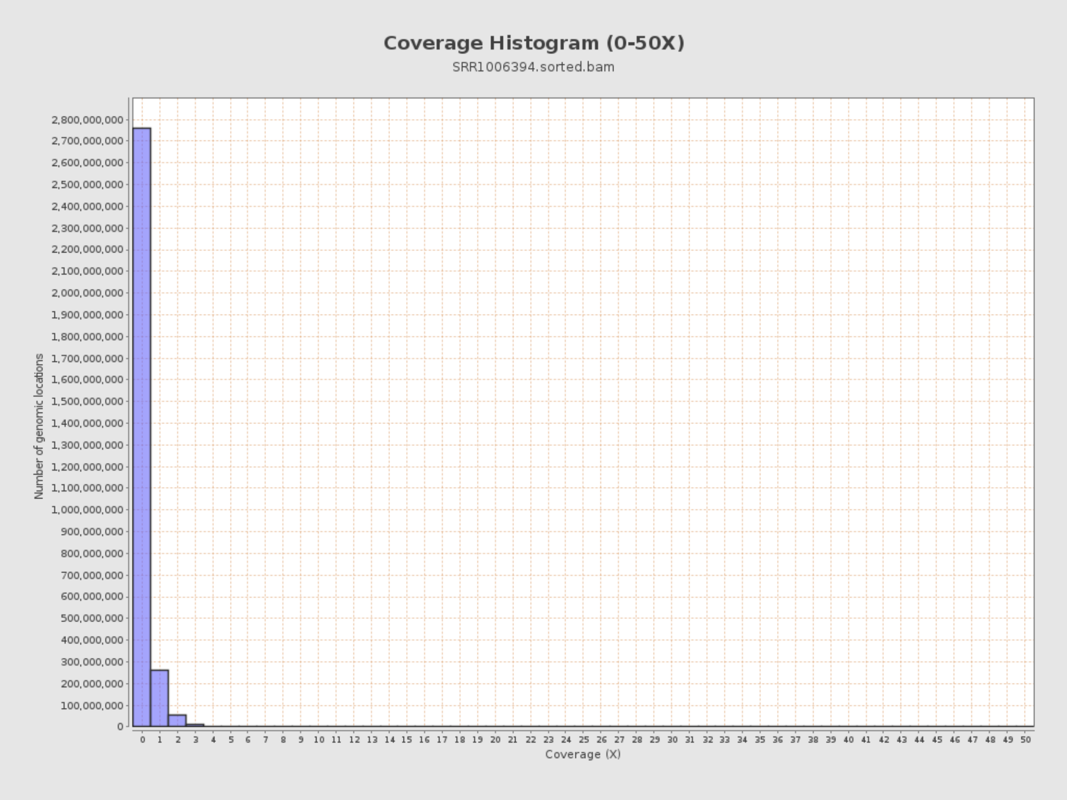
3. Results : Coverage across reference



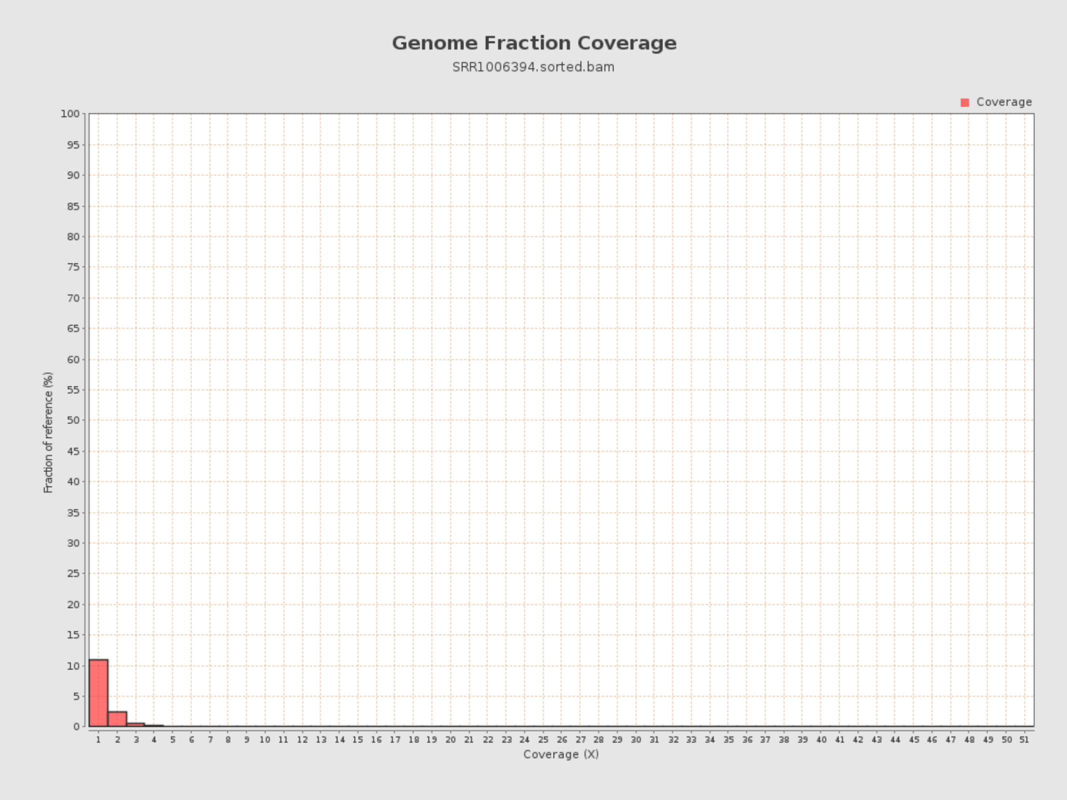
4. Results : Coverage Histogram



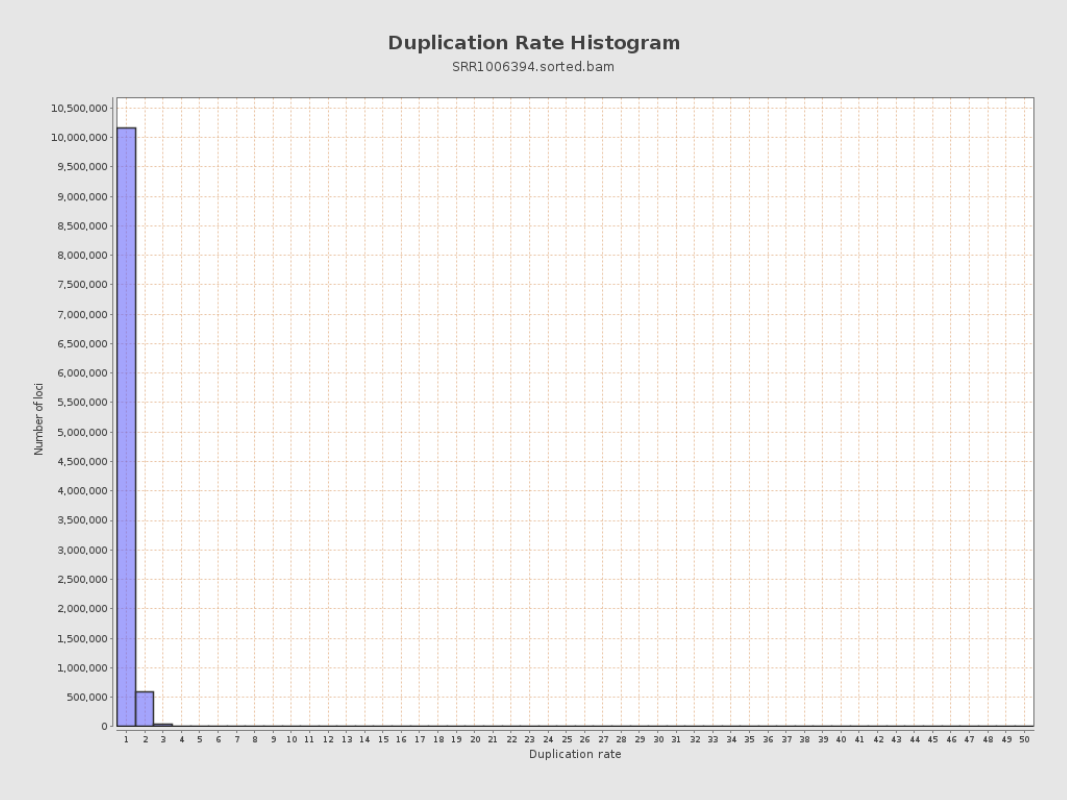
5. Results : Coverage Histogram (0-50X)



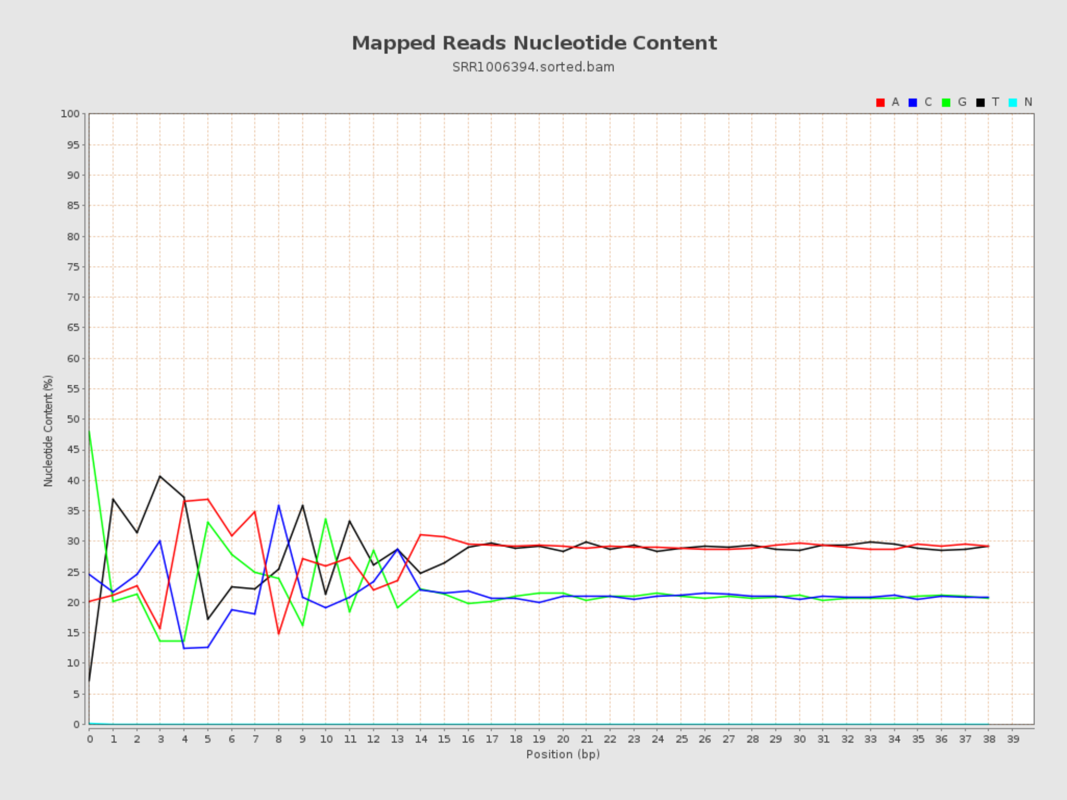
6. Results : Genome Fraction Coverage



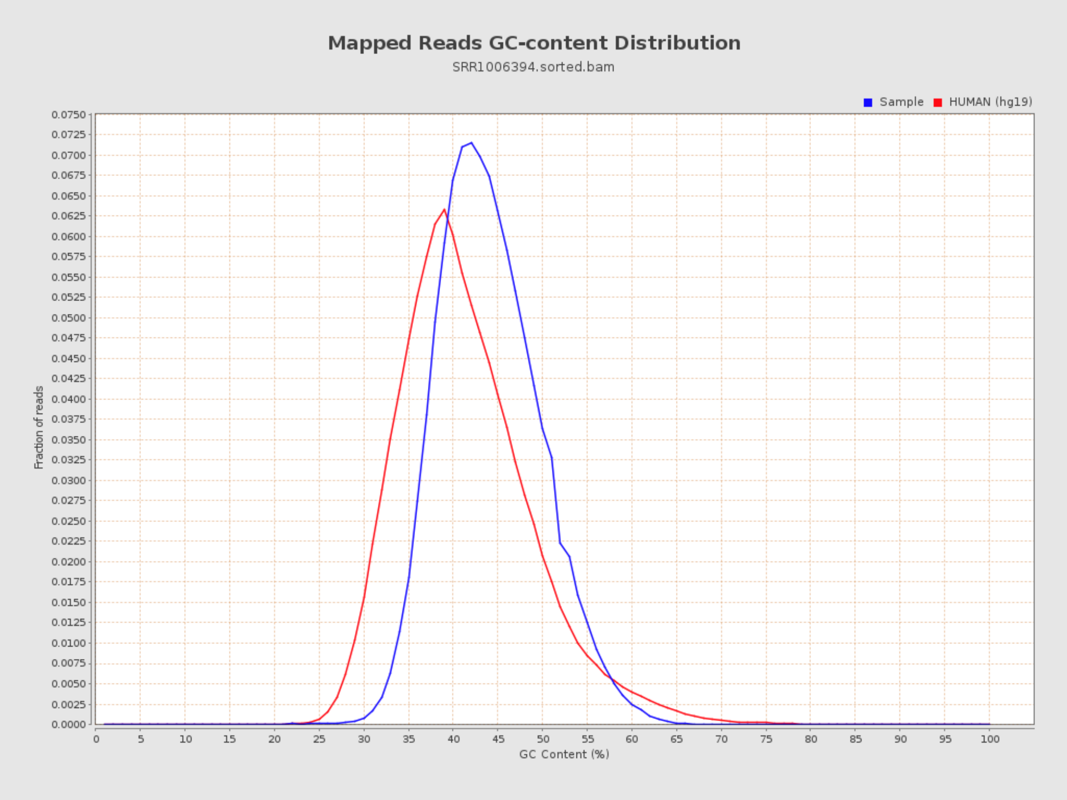
7. Results : Duplication Rate Histogram



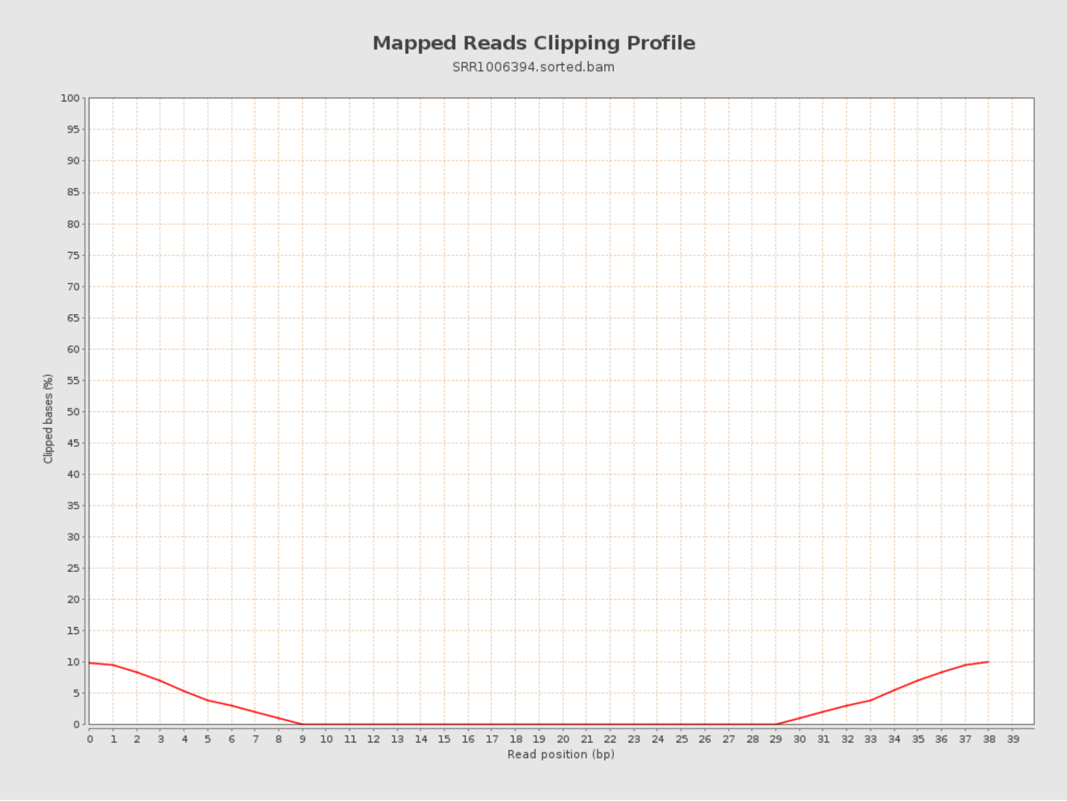
8. Results : Mapped Reads Nucleotide Content



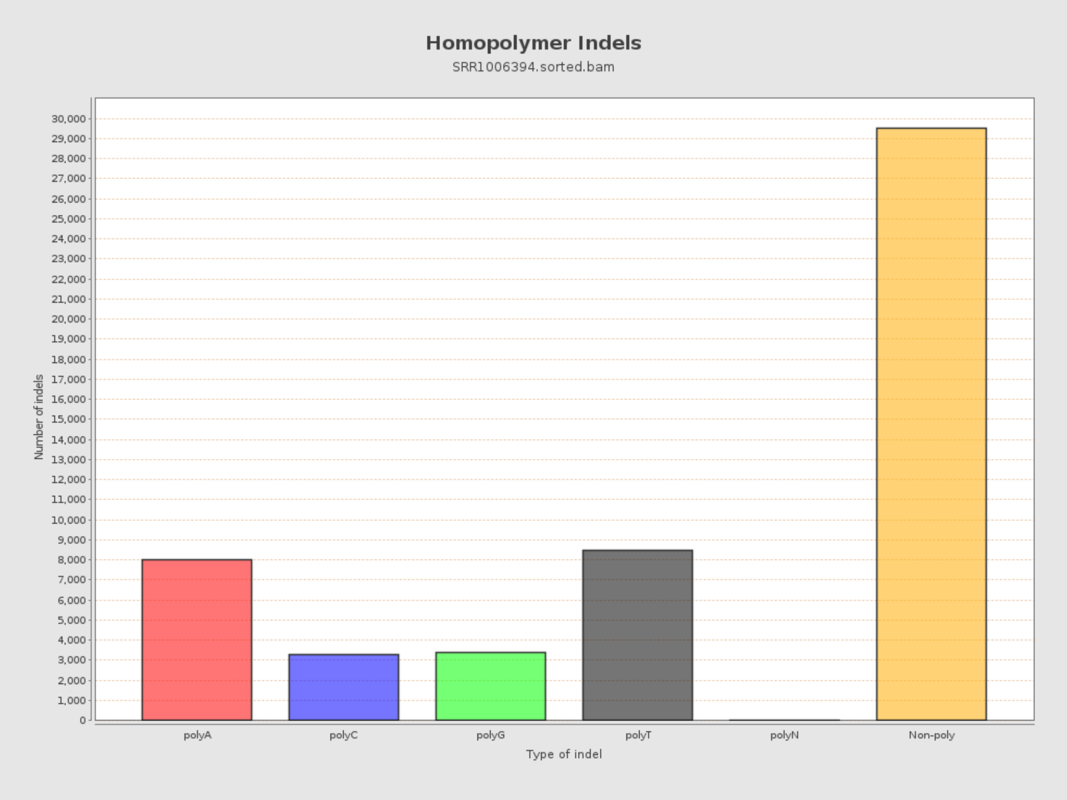
9. Results : Mapped Reads GC-content Distribution



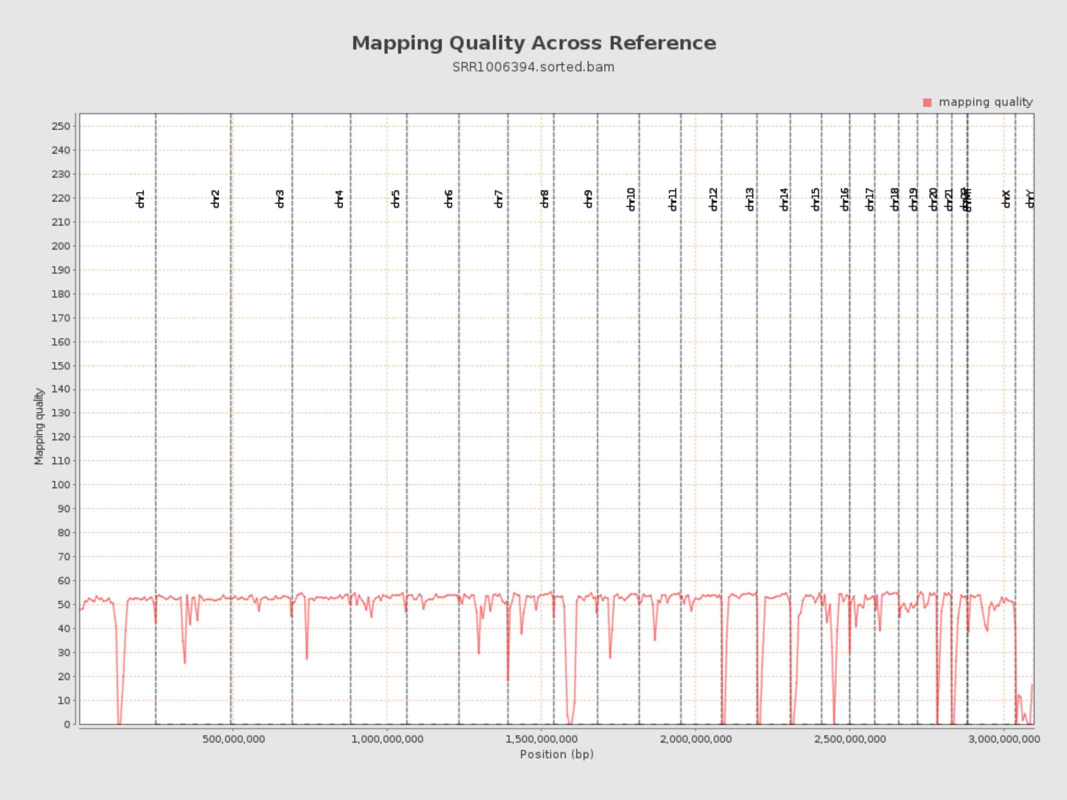
10. Results : Mapped Reads Clipping Profile



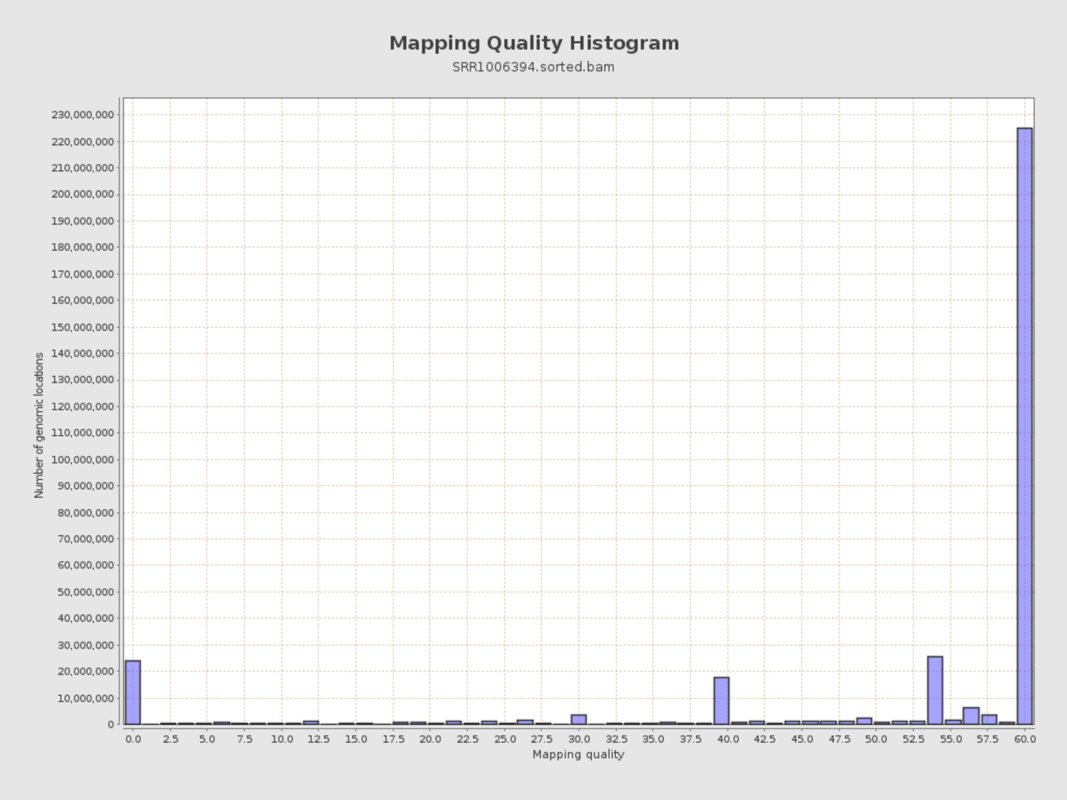
11. Results : Homopolymer Indels



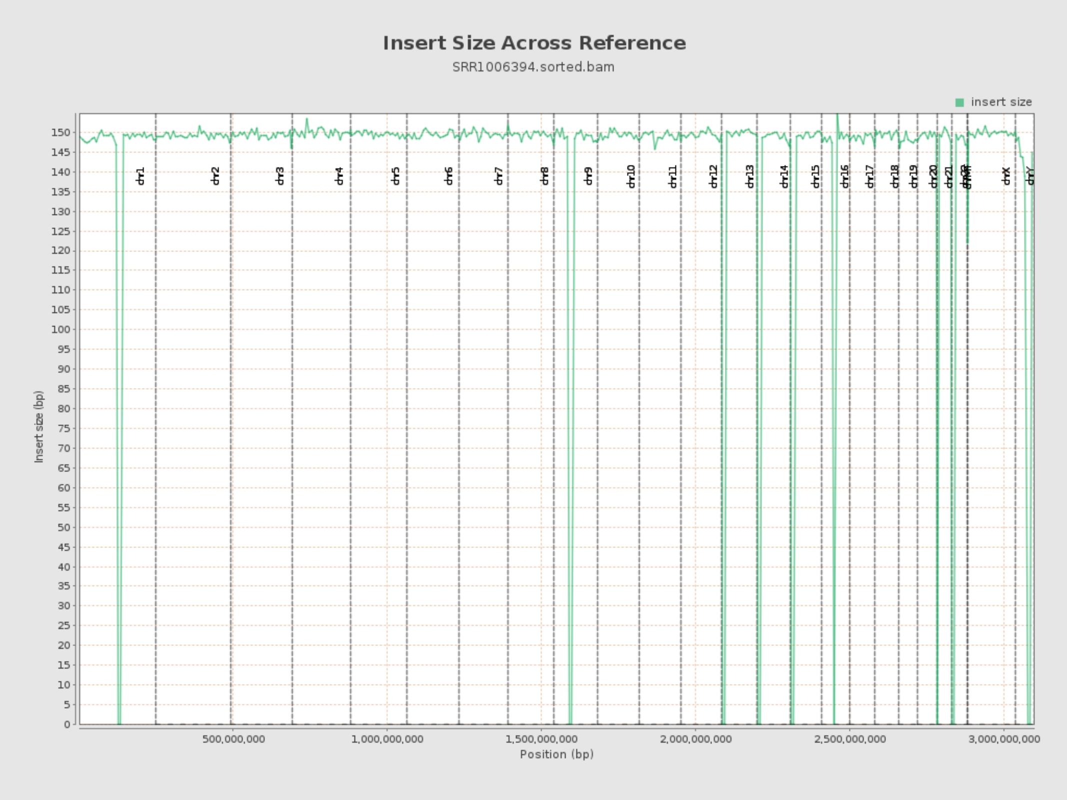
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram