Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 05:22:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038431.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_SRR5038431 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038431_1.fastq.gz SRR5038431_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 05:22:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038431.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,532,914
Mapped reads	16,217,822 / 92.5%
Unmapped reads	1,315,092 / 7.5%
Mapped paired reads	16,217,822 / 92.5%
Mapped reads, first in pair	8,230,071 / 46.94%
Mapped reads, second in pair	7,987,751 / 45.56%
Mapped reads, both in pair	15,914,970 / 90.77%
Mapped reads, singletons	302,852 / 1.73%
Secondary alignments	0
Supplementary alignments	269,169 / 1.54%
Read min/max/mean length	30 / 150 / 150.77
Duplicated reads (estimated)	3,155,625 / 18%
Duplication rate	13.08%
Clipped reads	7,419,193 / 42.32%

2.2. ACGT Content

Number/percentage of A's	630,847,333 / 28.79%
Number/percentage of C's	431,905,324 / 19.71%
Number/percentage of T's	643,208,523 / 29.35%
Number/percentage of G's	485,130,169 / 22.14%
Number/percentage of N's	173,955 / 0.01%

GC Percentage	41.85%

2.3. Coverage

Mean	0.7083
Standard Deviation	10.6201

2.4. Mapping Quality

Mean Mapping Quality	53.5

2.5. Insert size

Mean	99,258.14
Standard Deviation	3,037,547.36
P25/Median/P75	209 / 262 / 330

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	29,479,766
Insertions	398,054
Mapped reads with at least one insertion	2.33%
Deletions	784,282
Mapped reads with at least one deletion	4.65%
Homopolymer indels	47.09%

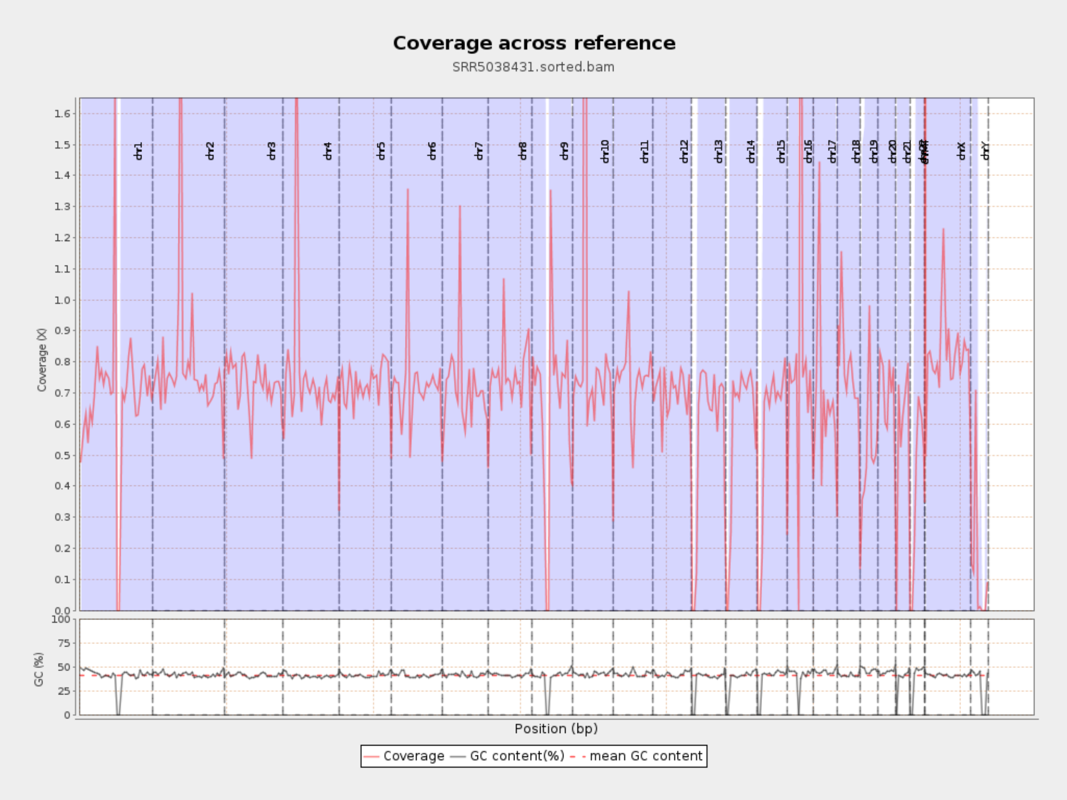
2.7. Chromosome stats

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

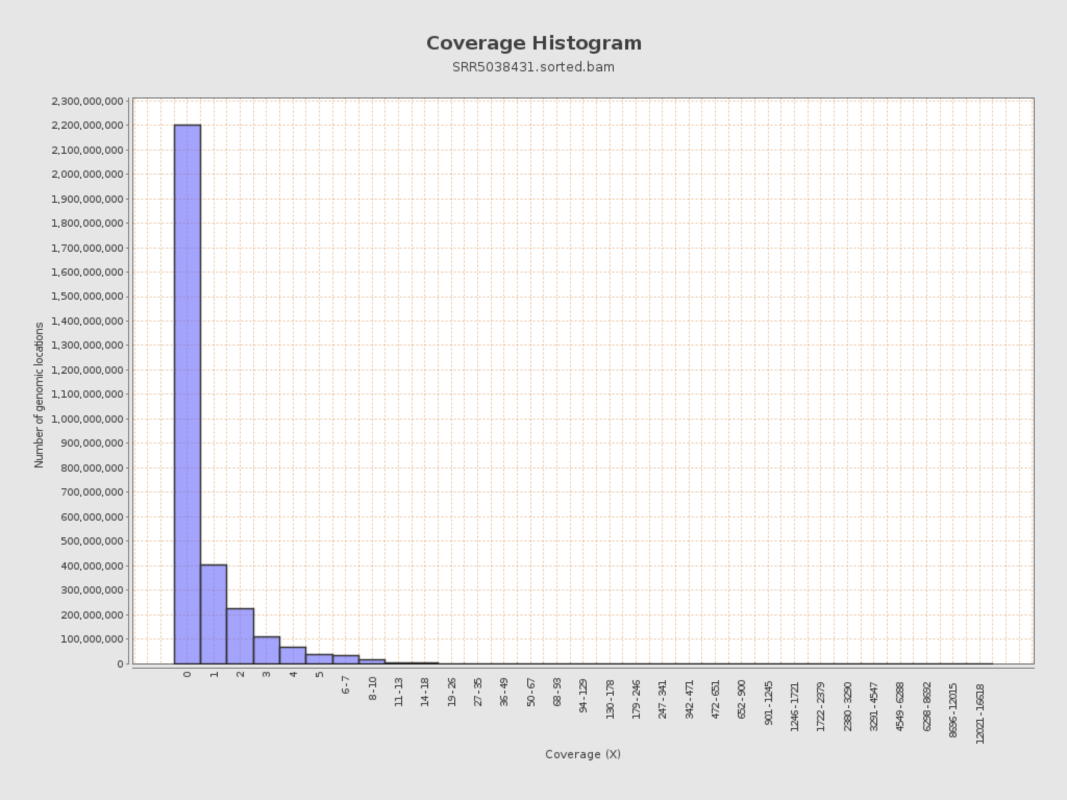
		bases	coverage	deviation
chr1	249250621	171856993	0.6895	16.6415
chr2	243199373	194855363	0.8012	9.85
chr3	198022430	145630223	0.7354	1.6355
chr4	191154276	145723803	0.7623	8.8204
chr5	180915260	131479812	0.7267	1.5334
chr6	171115067	125993750	0.7363	6.9091
chr7	159138663	114295433	0.7182	10.3203
chr8	146364022	110783199	0.7569	3.3332
chr9	141213431	91649382	0.649	16.2247
chr10	135534747	125338402	0.9248	28.6126
chr11	135006516	99404876	0.7363	6.9113
chr12	133851895	93483211	0.6984	1.6411
chr13	115169878	66910965	0.581	1.3345
chr14	107349540	62831942	0.5853	1.5018
chr15	102531392	58774954	0.5732	1.3404
chr16	90354753	76566678	0.8474	15.4082
chr17	81195210	54674925	0.6734	12.0889
chr18	78077248	61175666	0.7835	12.037
chr19	59128983	29753032	0.5032	7.521
chr20	63025520	44339654	0.7035	2.8056
chr21	48129895	28037766	0.5825	4.3393
chr22	51304566	20387433	0.3974	1.2031
chrMT	16571	3128796	188.8115	97.0009
chrX	155270560	127724781	0.8226	3.6647

chrY	59373566	8033673	0.1353	10.1024

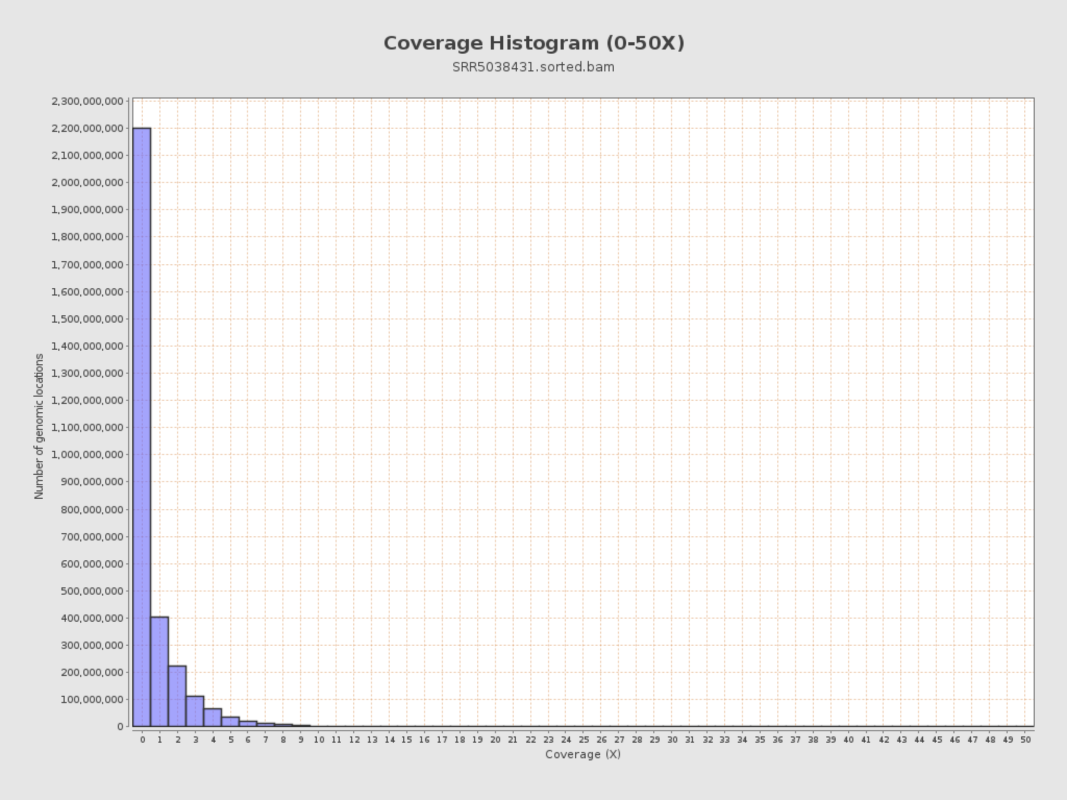
3. Results : Coverage across reference



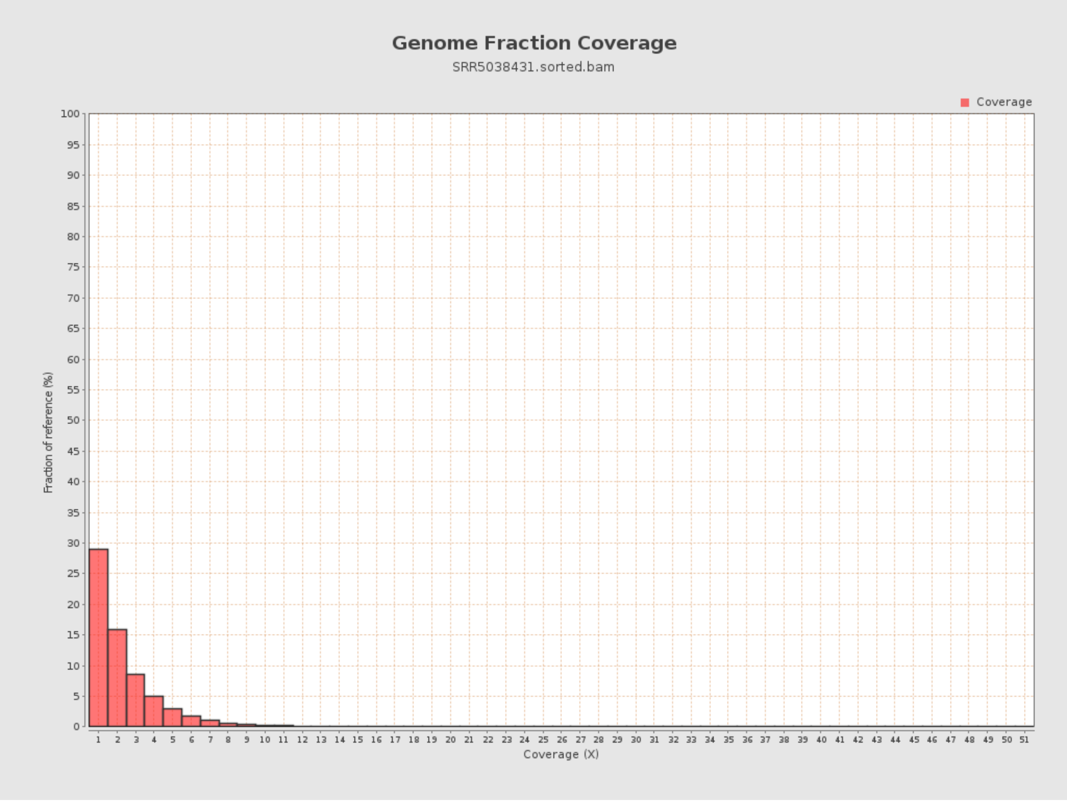
4. Results : Coverage Histogram



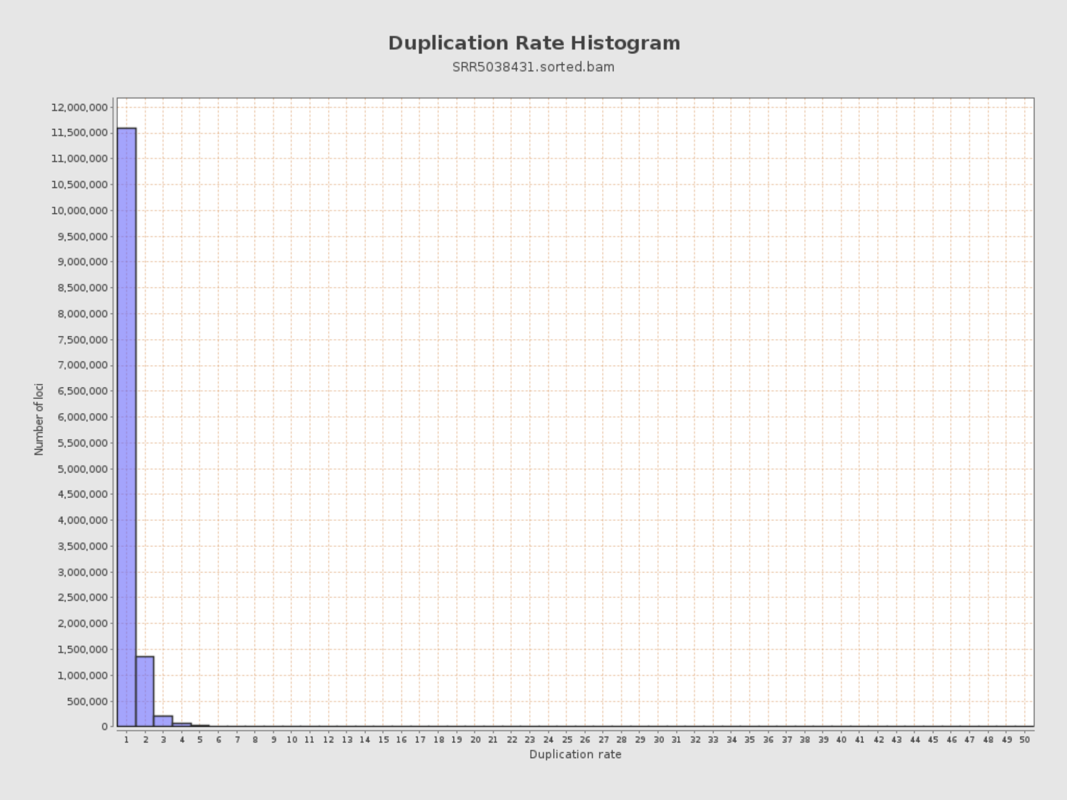
5. Results : Coverage Histogram (0-50X)



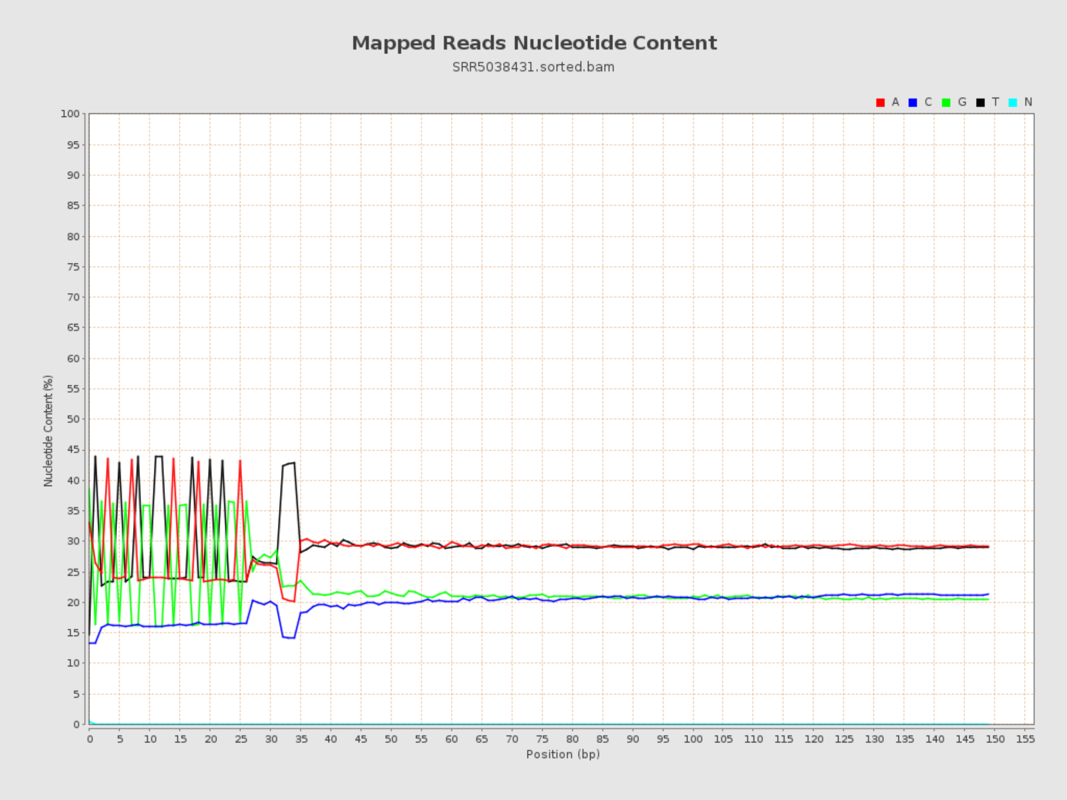
6. Results : Genome Fraction Coverage



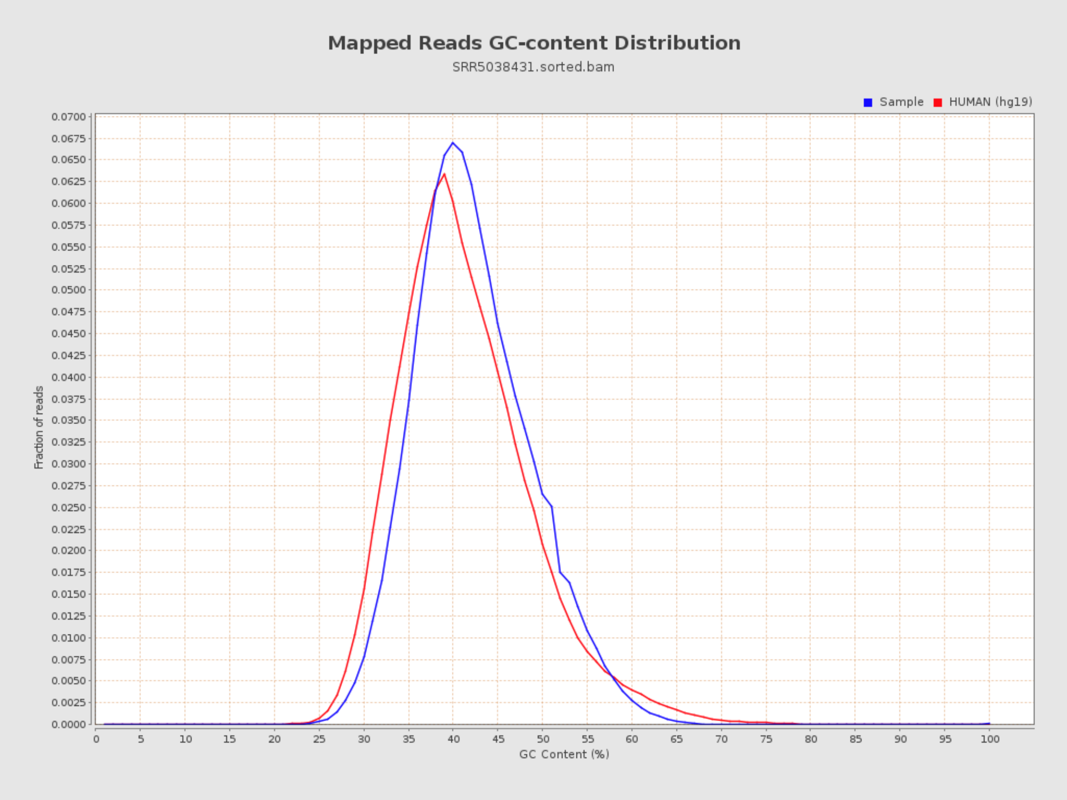
7. Results : Duplication Rate Histogram



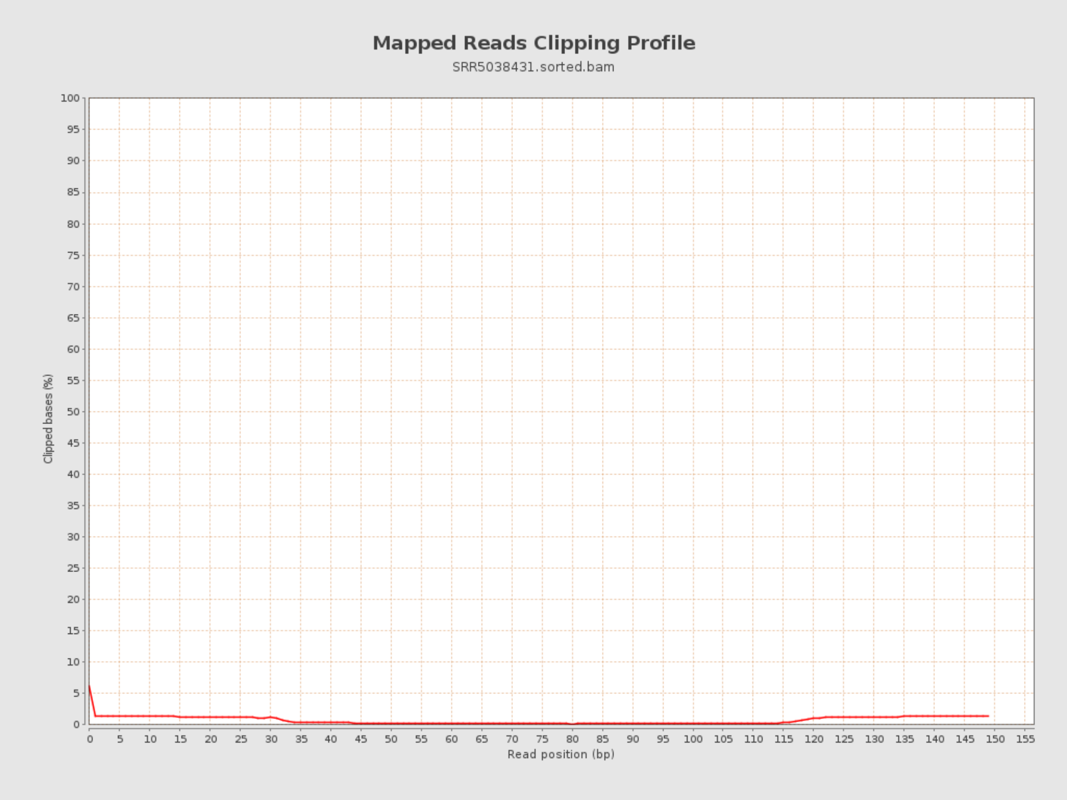
8. Results : Mapped Reads Nucleotide Content



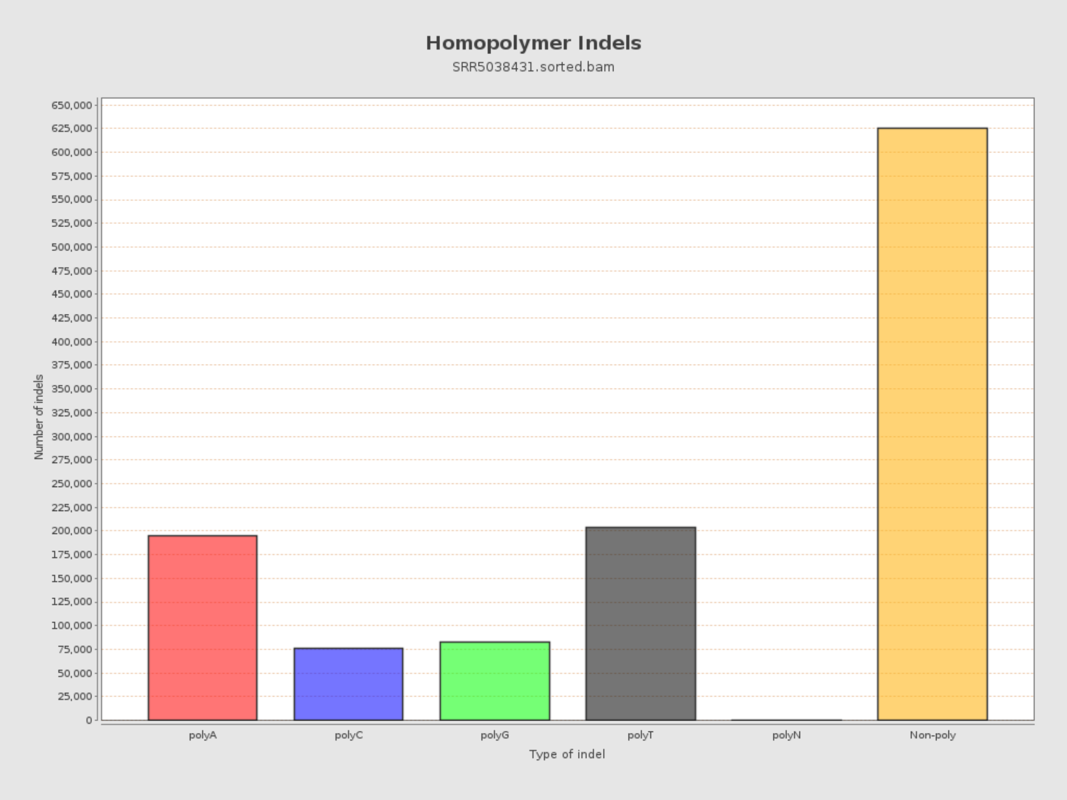
9. Results : Mapped Reads GC-content Distribution



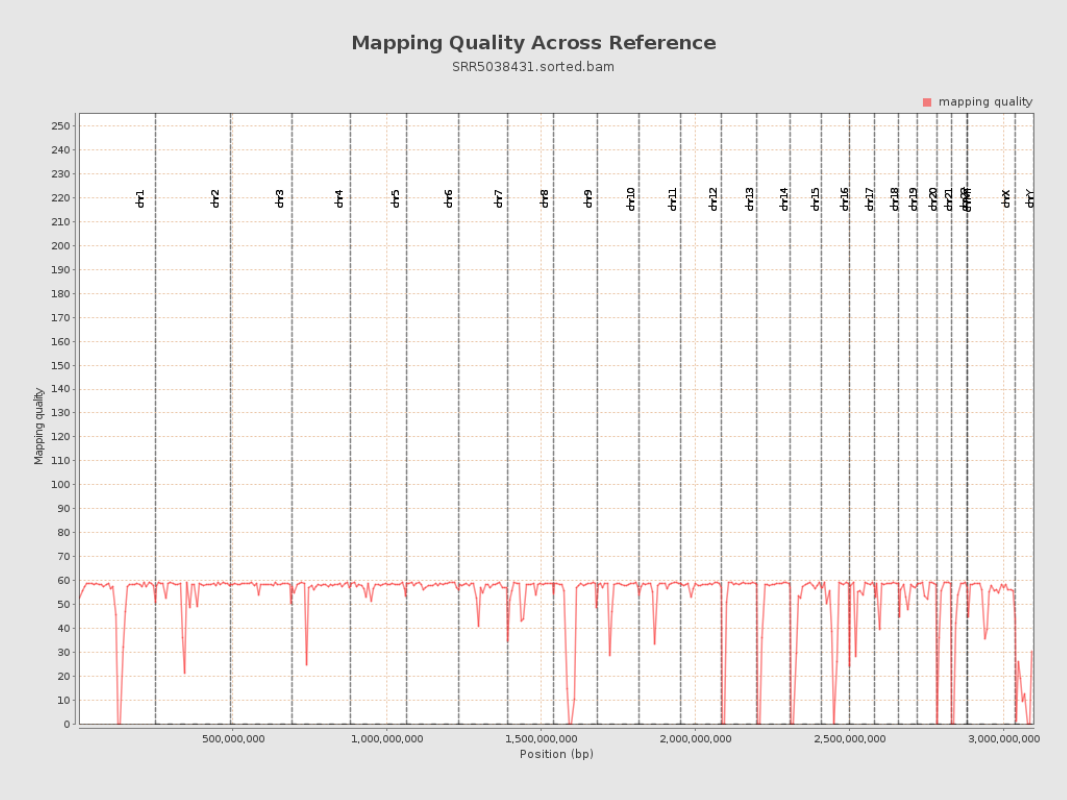
10. Results : Mapped Reads Clipping Profile



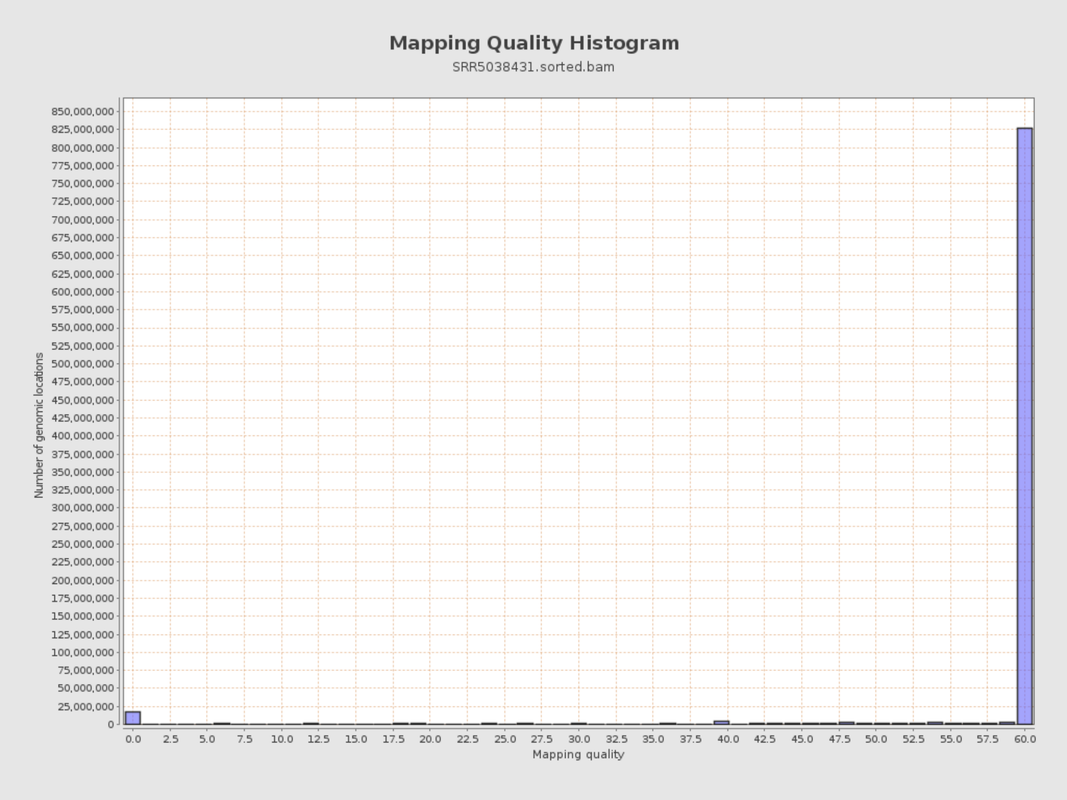
11. Results : Homopolymer Indels



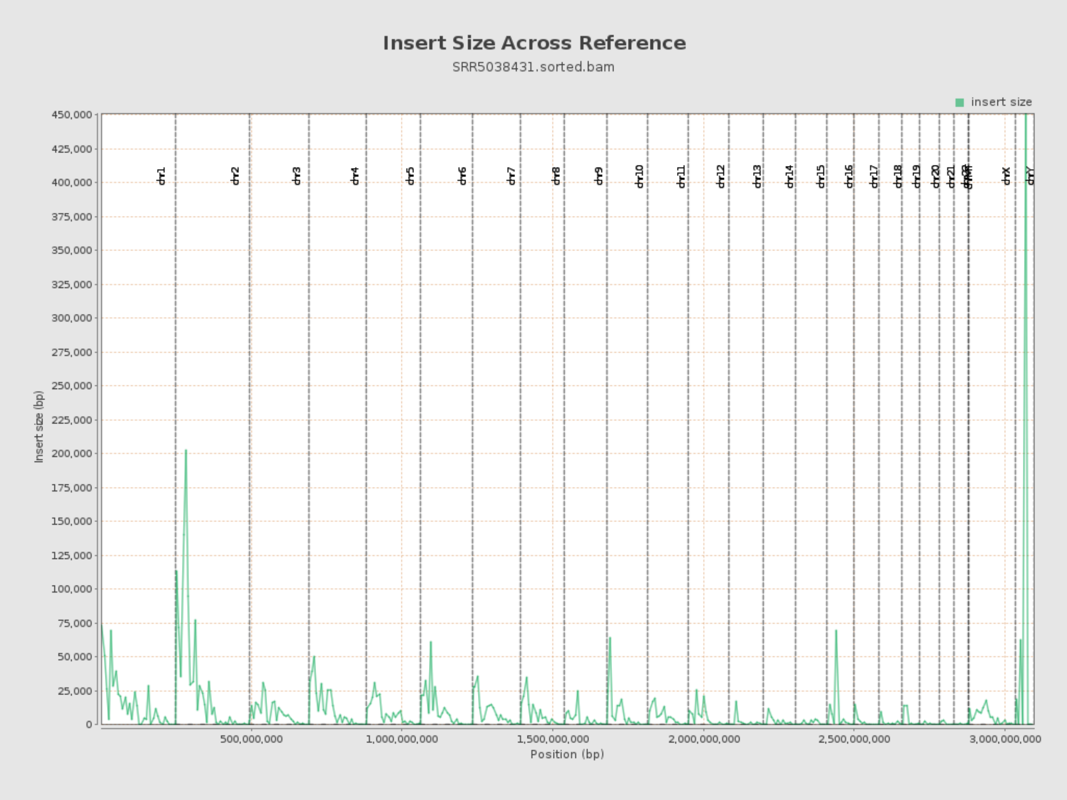
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram