Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 15:46:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038450.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_SRR5038450 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038450_1.fastq.gz SRR5038450_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 15:46:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038450.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,570,926
Mapped reads	15,964,619 / 96.34%
Unmapped reads	606,307 / 3.66%
Mapped paired reads	15,964,619 / 96.34%
Mapped reads, first in pair	8,032,664 / 48.47%
Mapped reads, second in pair	7,931,955 / 47.87%
Mapped reads, both in pair	15,844,582 / 95.62%
Mapped reads, singletons	120,037 / 0.72%
Secondary alignments	0
Supplementary alignments	166,592 / 1.01%
Read min/max/mean length	30 / 150 / 150.52
Duplicated reads (estimated)	1,555,233 / 9.39%
Duplication rate	7.51%
Clipped reads	1,551,306 / 9.36%

2.2. ACGT Content

Number/percentage of A's	674,290,539 / 28.69%
Number/percentage of C's	503,224,764 / 21.41%
Number/percentage of T's	669,174,683 / 28.47%
Number/percentage of G's	503,660,362 / 21.43%
Number/percentage of N's	221,459 / 0.01%

GC Percentage	42.84%

2.3. Coverage

Mean	0.7596
Standard Deviation	7.0065

2.4. Mapping Quality

Mean Mapping Quality	54.34

2.5. Insert size

Mean	105,929.4
Standard Deviation	3,250,603.06
P25/Median/P75	236 / 288 / 356

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	20,520,459
Insertions	276,978
Mapped reads with at least one insertion	1.64%
Deletions	297,746
Mapped reads with at least one deletion	1.78%
Homopolymer indels	44.37%

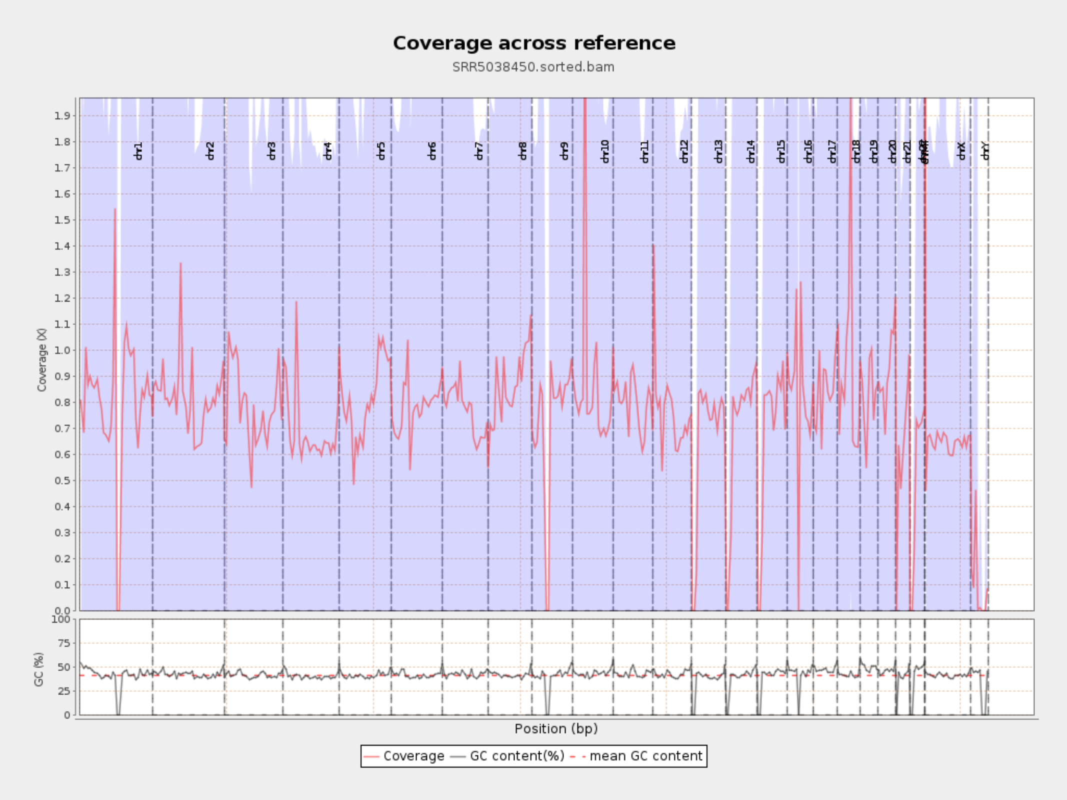
2.7. Chromosome stats

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

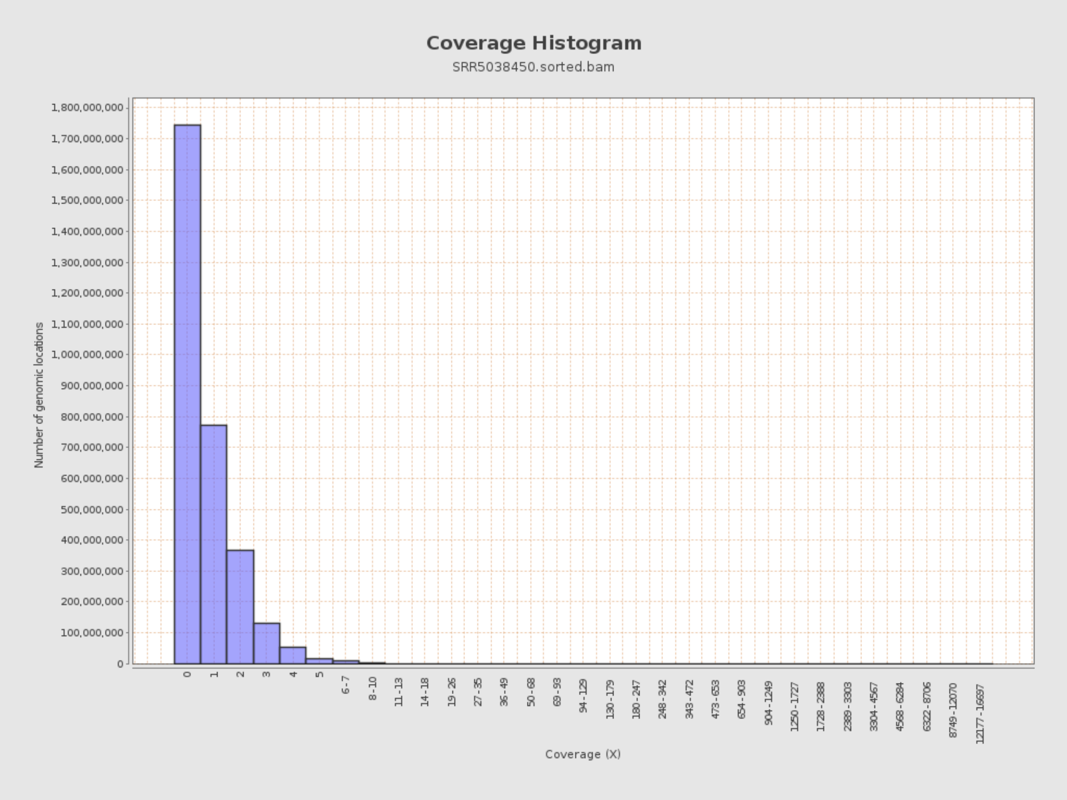
		bases	coverage	deviation
chr1	249250621	200698130	0.8052	17.0829
chr2	243199373	199670095	0.821	5.9718
chr3	198022430	155255460	0.784	1.1639
chr4	191154276	131305896	0.6869	5.084
chr5	180915260	147002723	0.8126	1.1412
chr6	171115067	133633201	0.781	3.1482
chr7	159138663	122793647	0.7716	5.5455
chr8	146364022	127383677	0.8703	4.2545
chr9	141213431	100068988	0.7086	7.8307
chr10	135534747	119790035	0.8838	15.5737
chr11	135006516	108647575	0.8048	2.9566
chr12	133851895	102419305	0.7652	1.2769
chr13	115169878	75193325	0.6529	1.0248
chr14	107349540	73341849	0.6832	1.0967
chr15	102531392	67472050	0.6581	1.0416
chr16	90354753	74221040	0.8214	4.2871
chr17	81195210	68595137	0.8448	3.8602
chr18	78077248	72878160	0.9334	6.5842
chr19	59128983	48641335	0.8226	7.0137
chr20	63025520	57582324	0.9136	2.008
chr21	48129895	30273684	0.629	2.8152
chr22	51304566	25864397	0.5041	0.9356
chrMT	16571	3539546	213.5988	28.2518
chrX	155270560	99326407	0.6397	1.6029

chrY	59373566	5792181	0.0976	5.0789

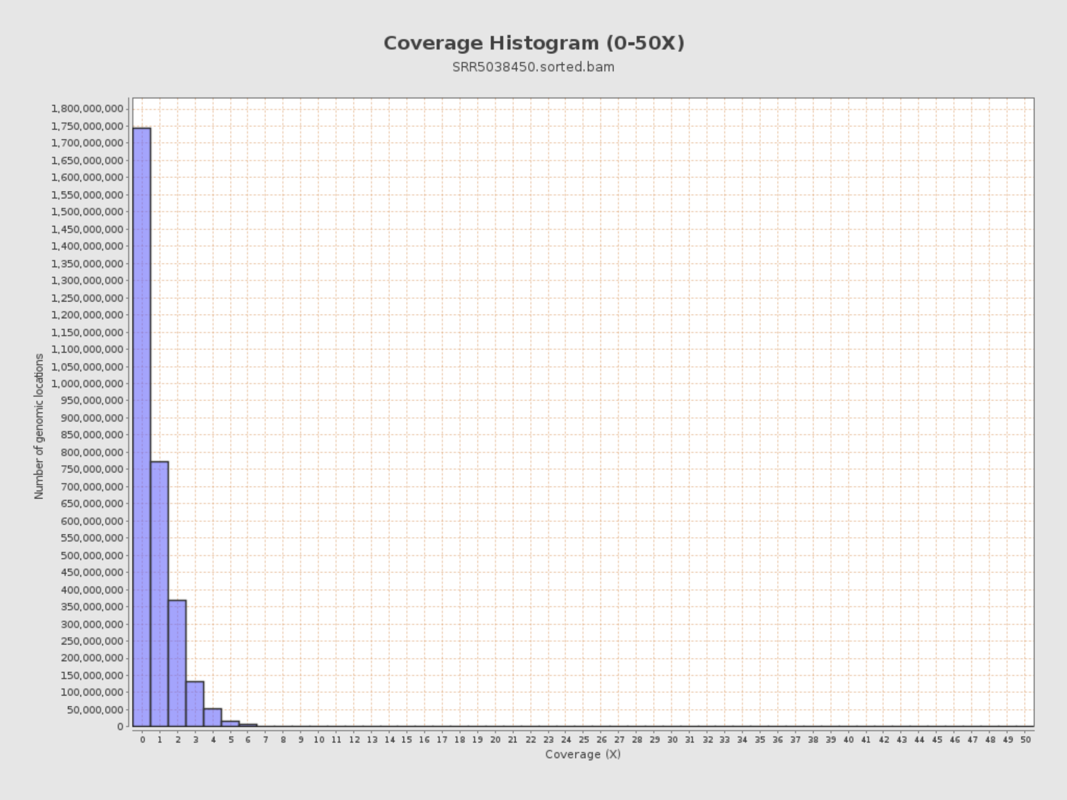
3. Results : Coverage across reference



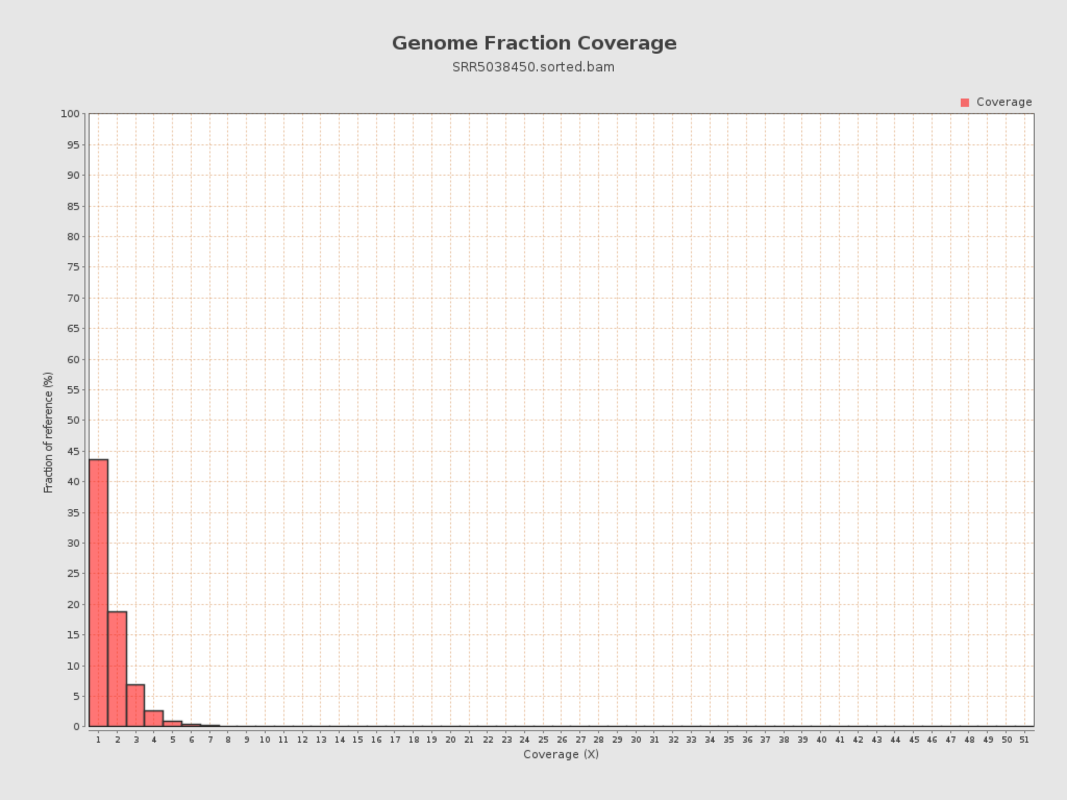
4. Results : Coverage Histogram



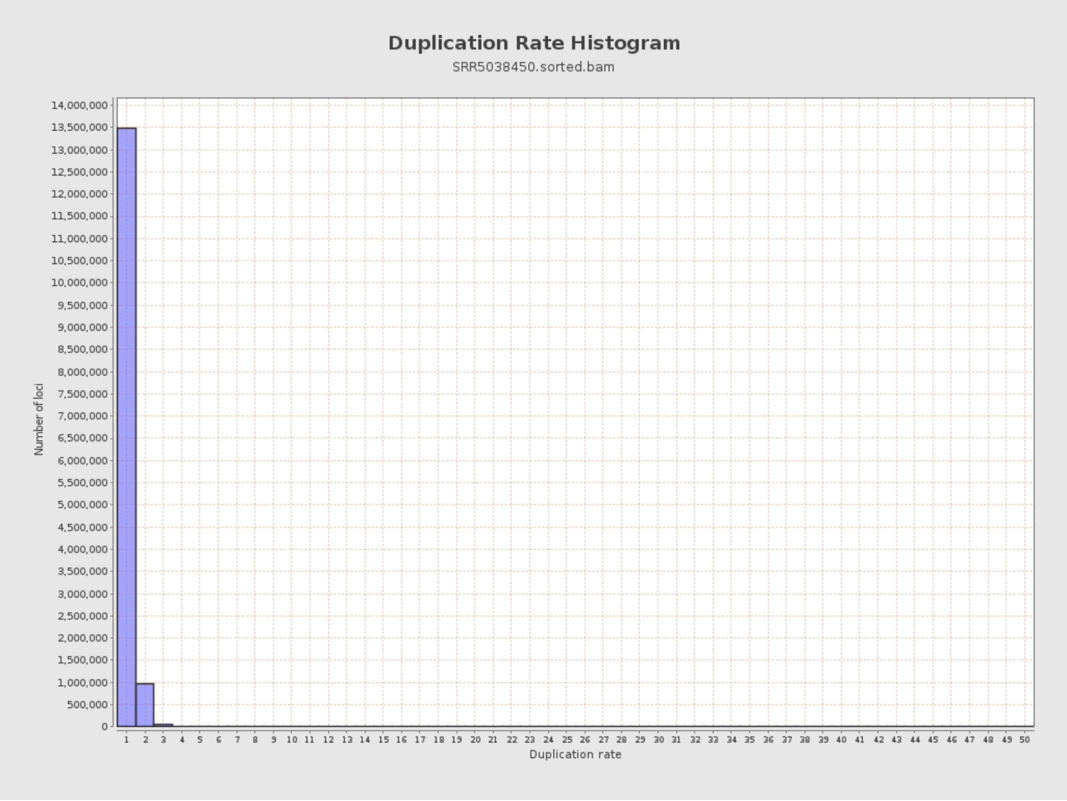
5. Results : Coverage Histogram (0-50X)



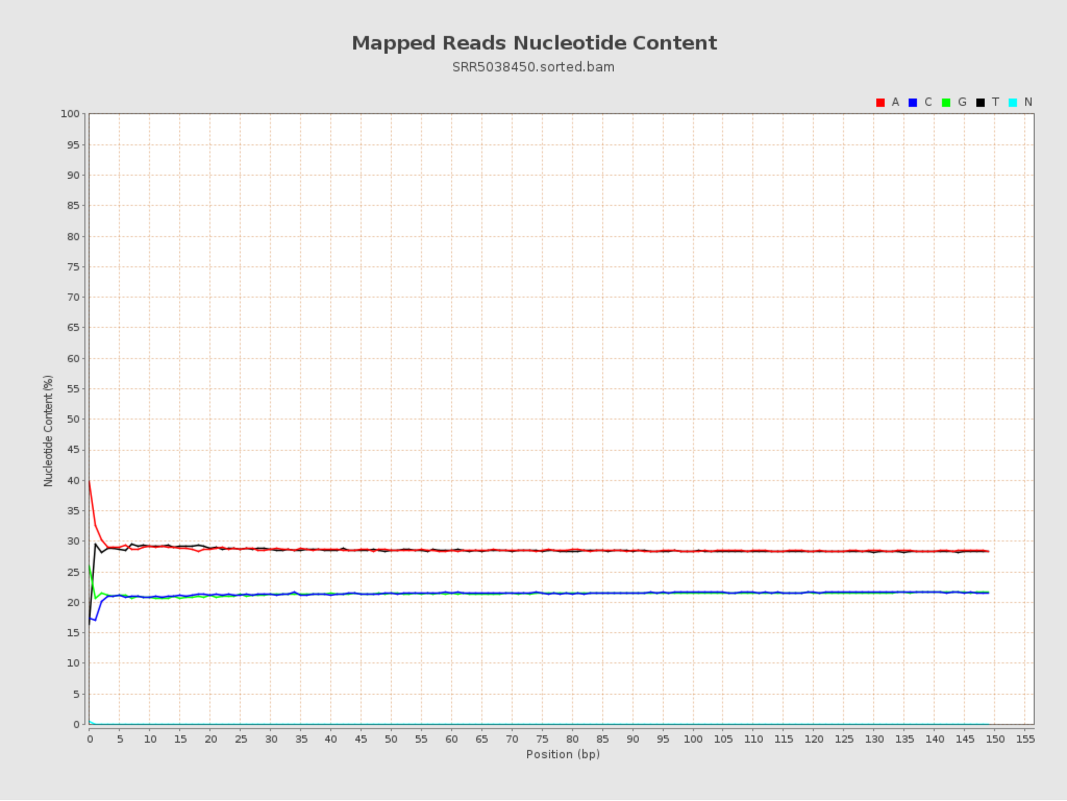
6. Results : Genome Fraction Coverage



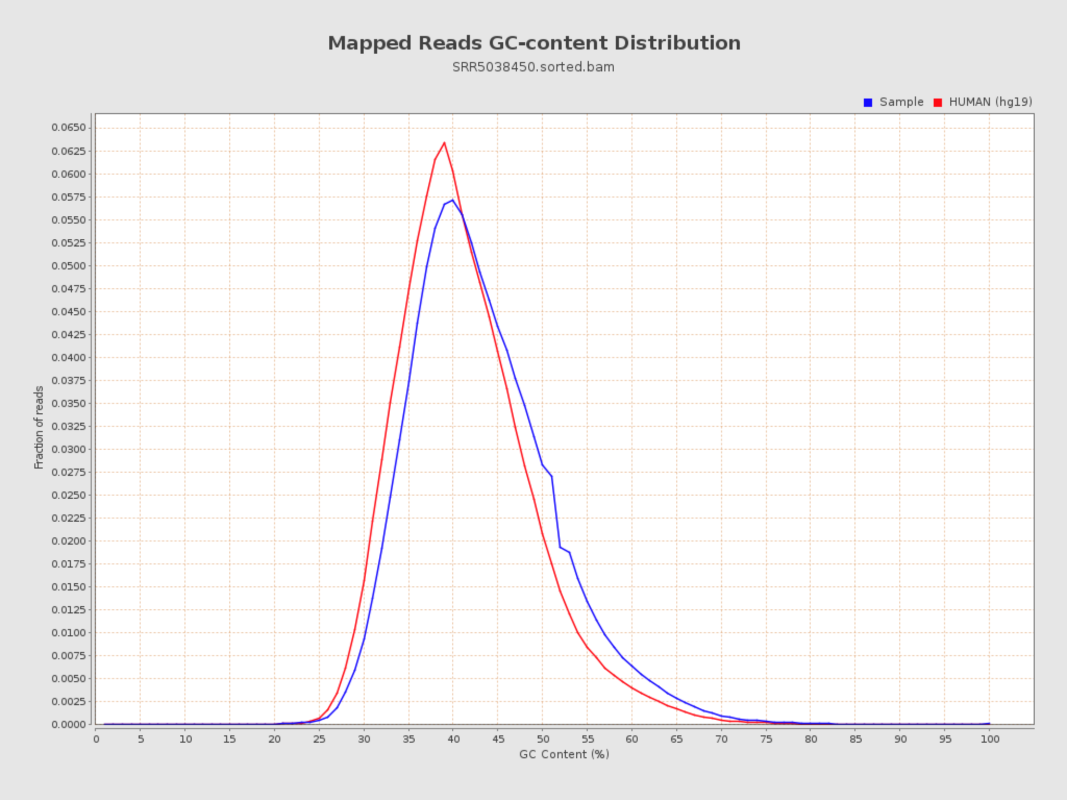
7. Results : Duplication Rate Histogram



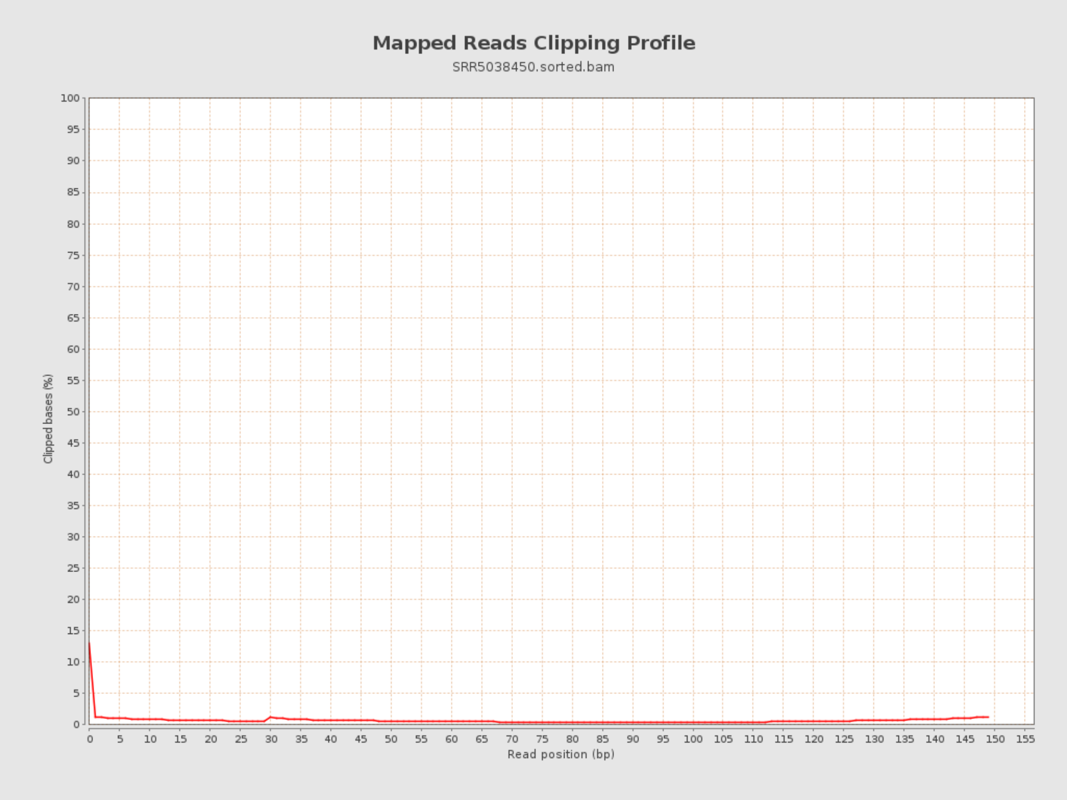
8. Results : Mapped Reads Nucleotide Content



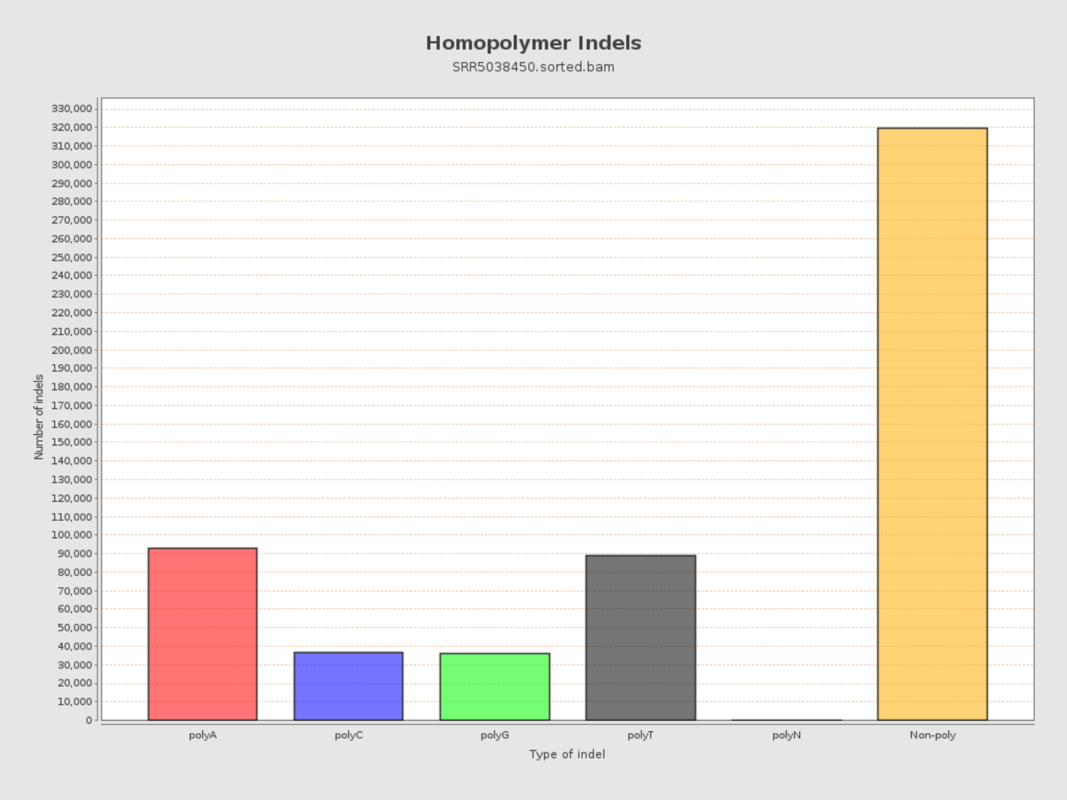
9. Results : Mapped Reads GC-content Distribution



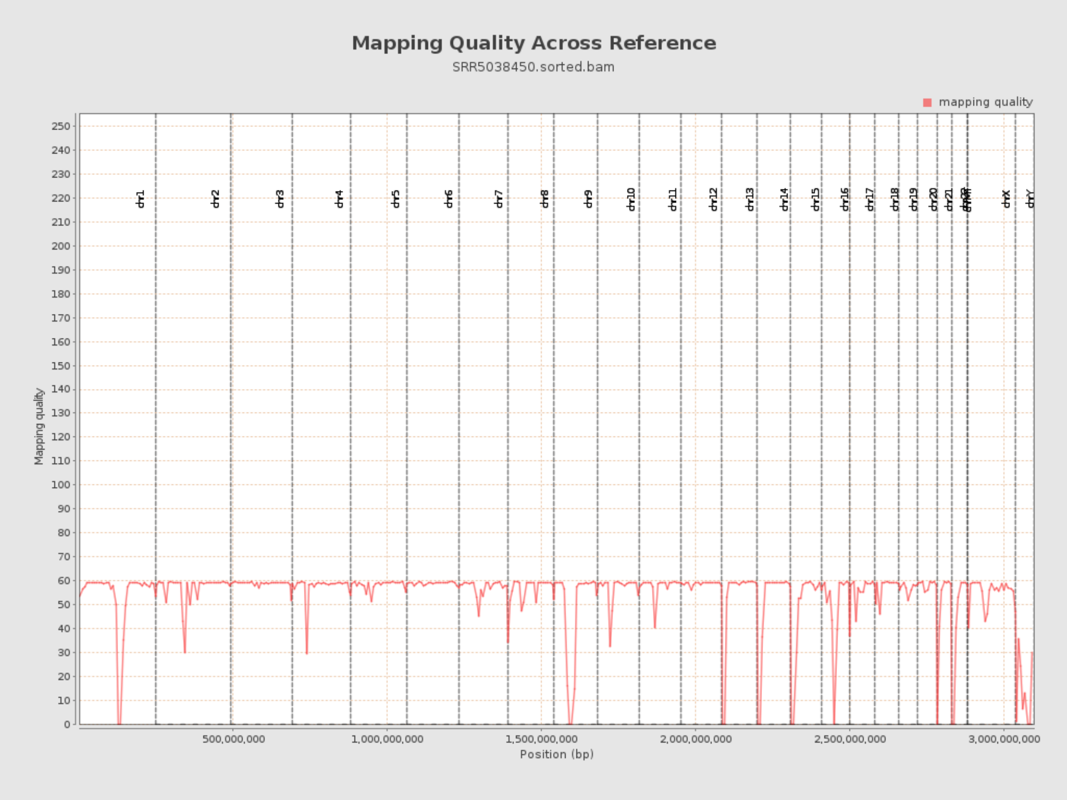
10. Results : Mapped Reads Clipping Profile



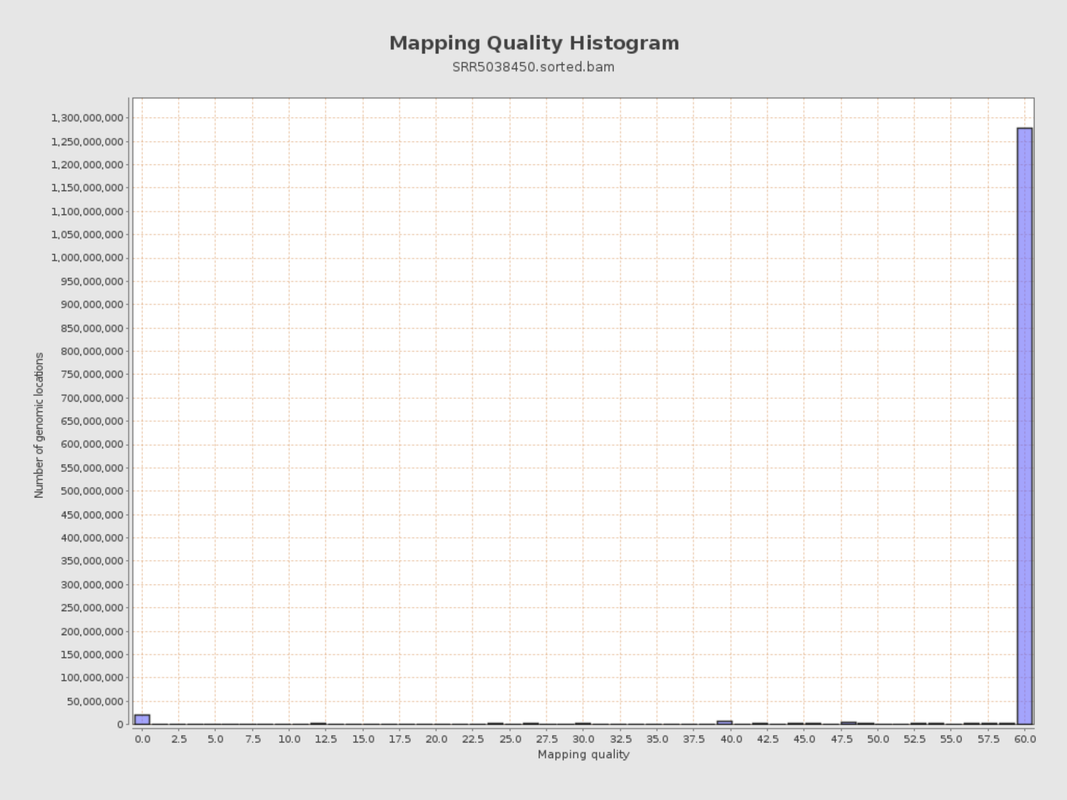
11. Results : Homopolymer Indels



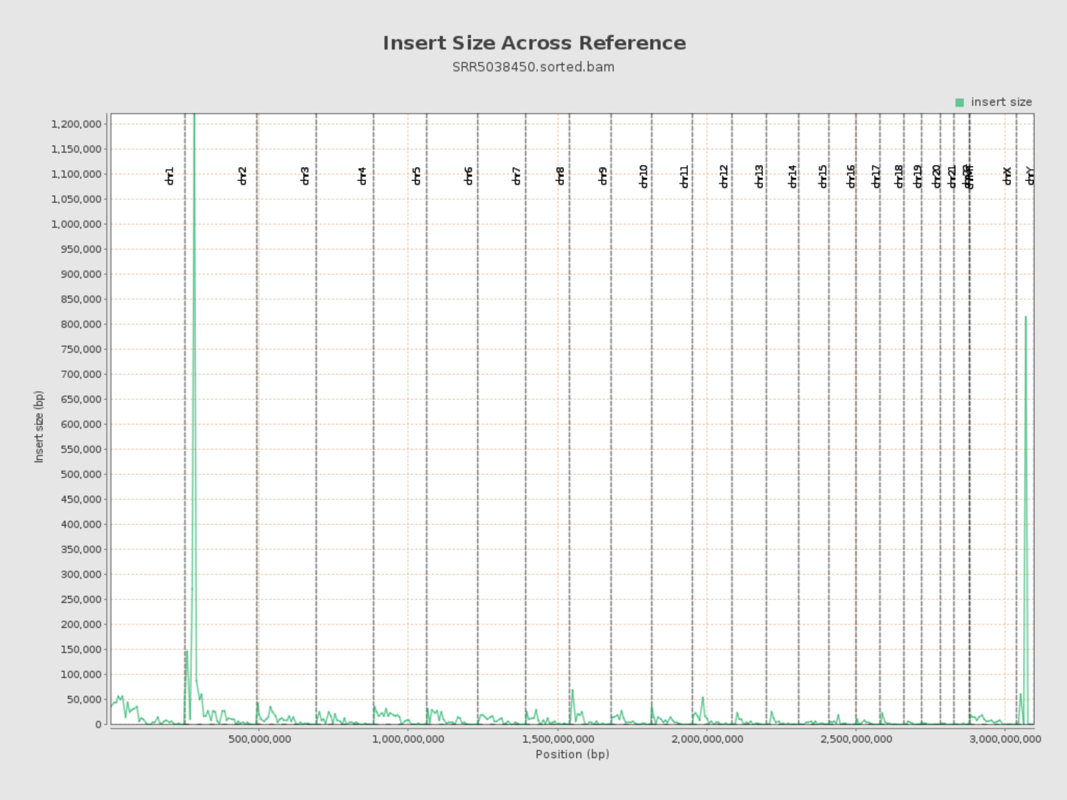
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram