Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 02:06:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038473.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_SRR5038473 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038473_1.fastq.gz SRR5038473_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 02:06:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038473.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,108,262
Mapped reads	13,895,315 / 98.49%
Unmapped reads	212,947 / 1.51%
Mapped paired reads	13,895,315 / 98.49%
Mapped reads, first in pair	7,020,501 / 49.76%
Mapped reads, second in pair	6,874,814 / 48.73%
Mapped reads, both in pair	13,734,944 / 97.35%
Mapped reads, singletons	160,371 / 1.14%
Secondary alignments	0
Supplementary alignments	122,768 / 0.87%
Read min/max/mean length	30 / 150 / 150.44
Duplicated reads (estimated)	1,444,625 / 10.24%
Duplication rate	7.44%
Clipped reads	1,544,461 / 10.95%

2.2. ACGT Content

Number/percentage of A's	594,864,041 / 29.15%
Number/percentage of C's	428,948,678 / 21.02%
Number/percentage of T's	589,685,659 / 28.9%
Number/percentage of G's	427,035,551 / 20.93%
Number/percentage of N's	45,161 / 0%

GC Percentage	41.95%

2.3. Coverage

Mean	0.6594
Standard Deviation	7.4449

2.4. Mapping Quality

Mean Mapping Quality	54.41

2.5. Insert size

Mean	72,798.05
Standard Deviation	2,676,670.64
P25/Median/P75	221 / 268 / 328

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	22,487,445
Insertions	257,511
Mapped reads with at least one insertion	1.74%
Deletions	271,303
Mapped reads with at least one deletion	1.86%
Homopolymer indels	43.67%

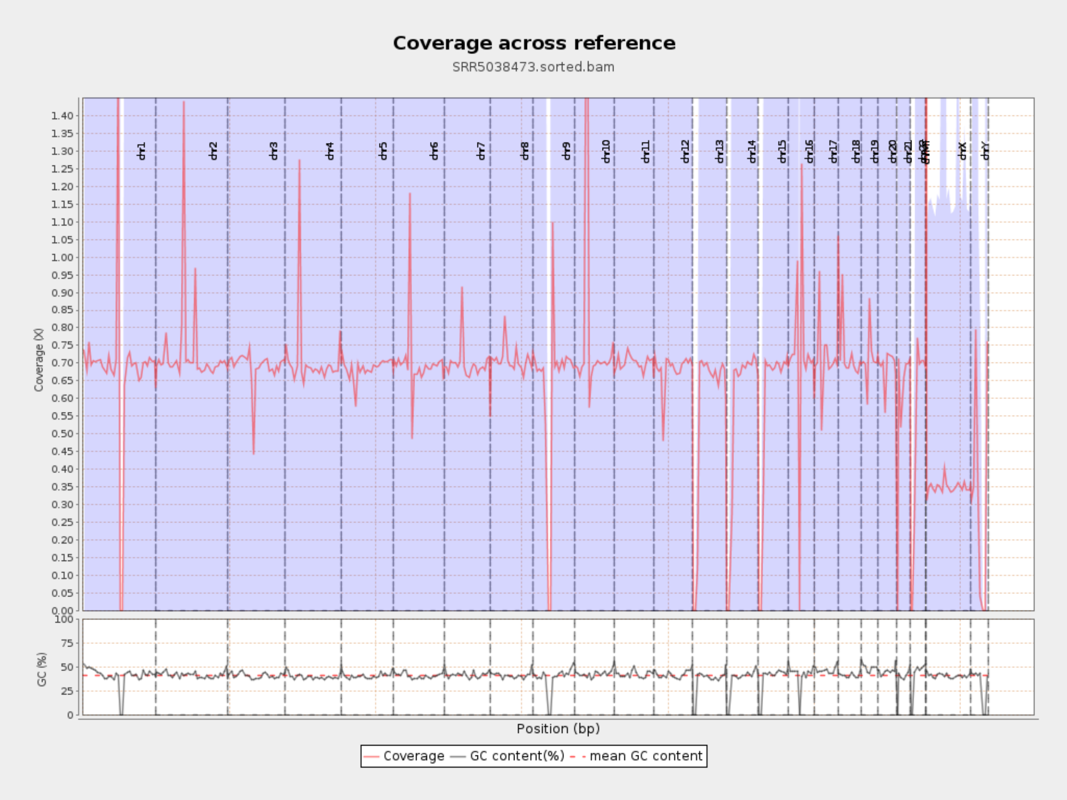
2.7. Chromosome stats

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

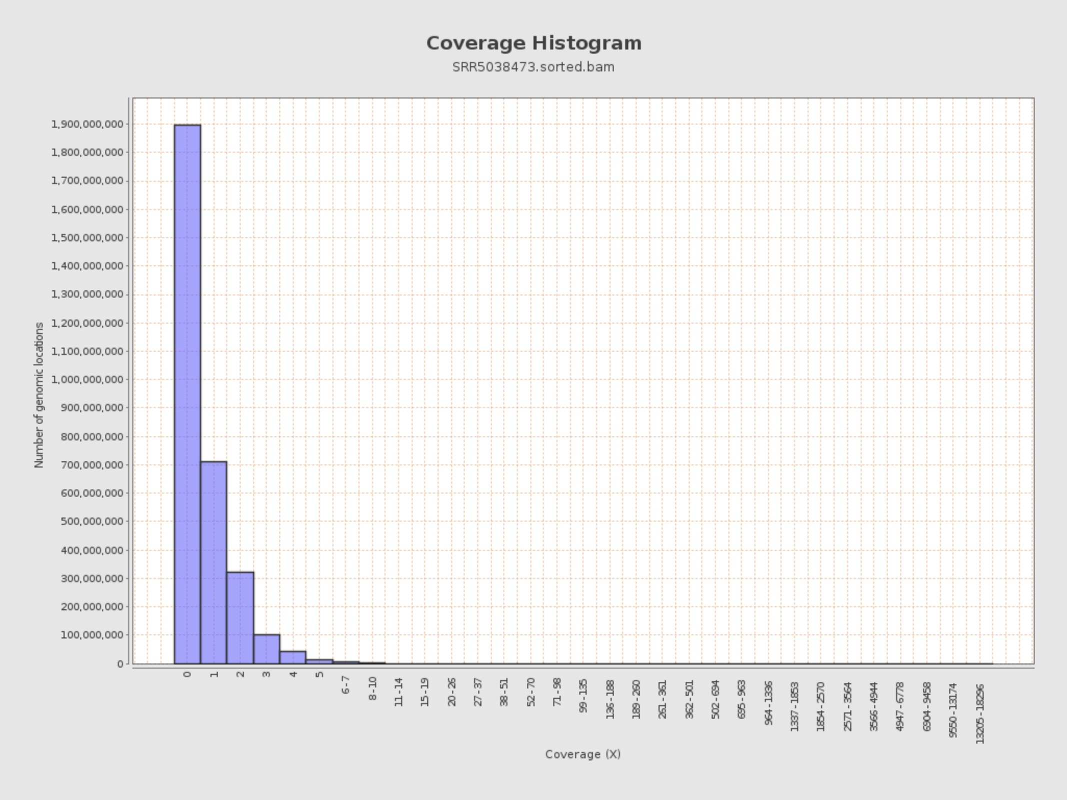
		bases	coverage	deviation
chr1	249250621	169885872	0.6816	18.8669
chr2	243199373	178233503	0.7329	5.4819
chr3	198022430	136544635	0.6895	1.0728
chr4	191154276	136010705	0.7115	5.3623
chr5	180915260	124011457	0.6855	1.1658
chr6	171115067	120381077	0.7035	5.6416
chr7	159138663	111487271	0.7006	5.3614
chr8	146364022	103741462	0.7088	5.6487
chr9	141213431	89238722	0.6319	10.14
chr10	135534747	104955098	0.7744	12.2714
chr11	135006516	94793586	0.7021	3.8451
chr12	133851895	91387421	0.6828	1.0934
chr13	115169878	65500825	0.5687	0.9844
chr14	107349540	61649781	0.5743	1.0416
chr15	102531392	58193713	0.5676	0.9769
chr16	90354753	65064144	0.7201	4.8743
chr17	81195210	57976448	0.714	3.7314
chr18	78077248	57505302	0.7365	8.7789
chr19	59128983	42292890	0.7153	8.6753
chr20	63025520	43508437	0.6903	2.055
chr21	48129895	28939582	0.6013	2.9598
chr22	51304566	25513653	0.4973	2.0898
chrMT	16571	738595	44.5715	9.6171
chrX	155270560	54271894	0.3495	1.2532

chrY	59373566	19507471	0.3286	6.5083

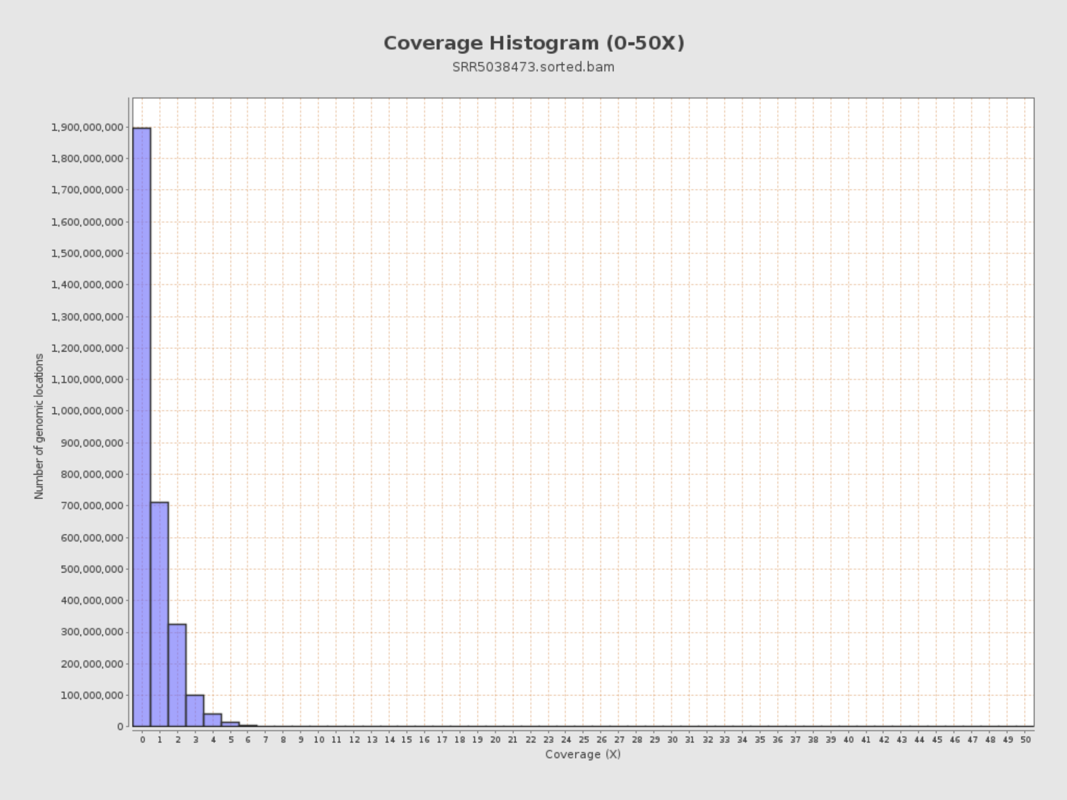
3. Results : Coverage across reference



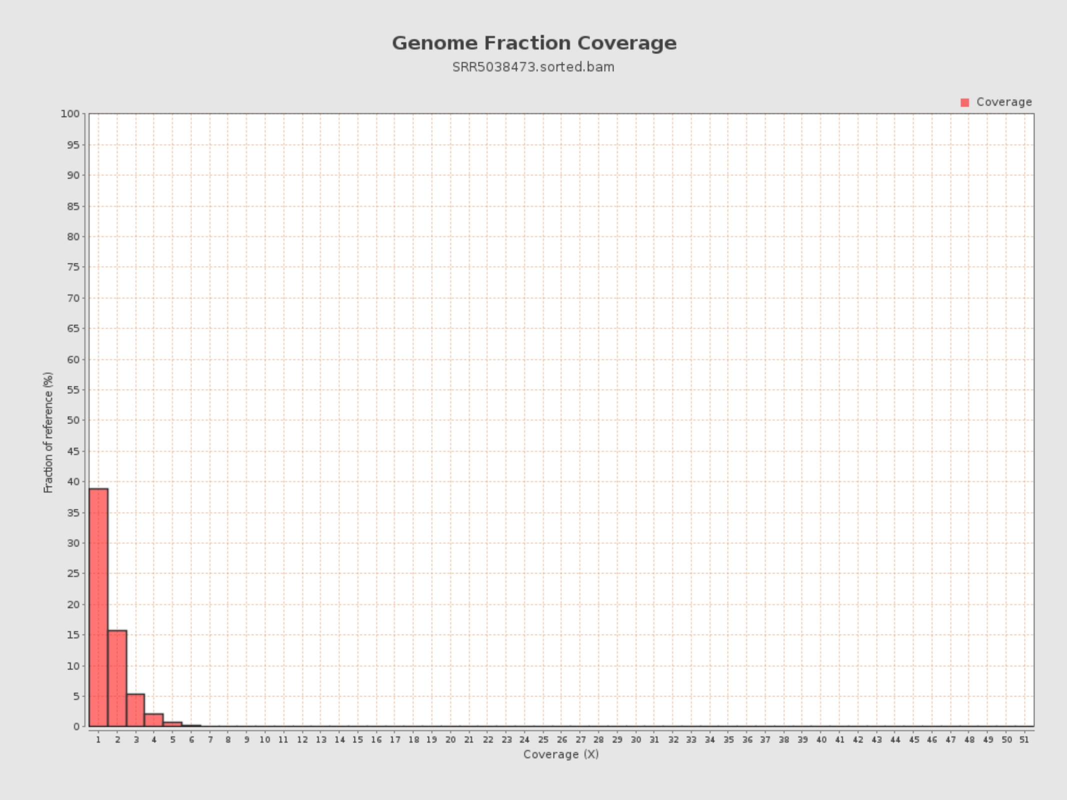
4. Results : Coverage Histogram



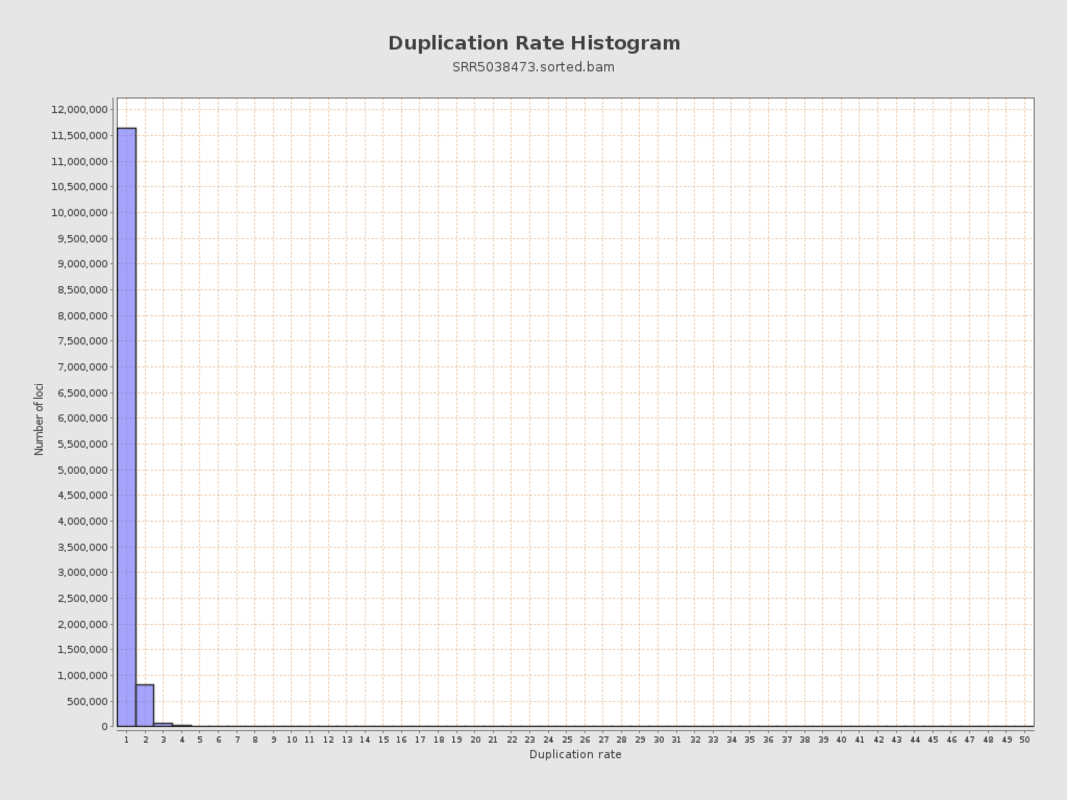
5. Results : Coverage Histogram (0-50X)



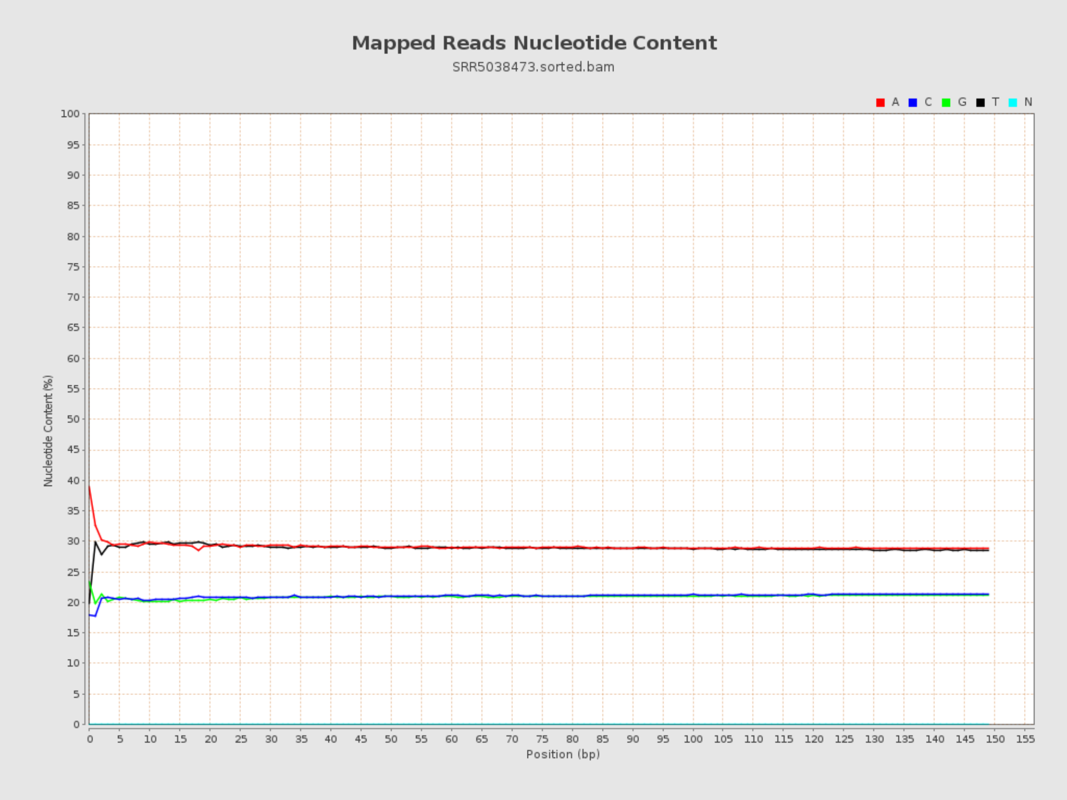
6. Results : Genome Fraction Coverage



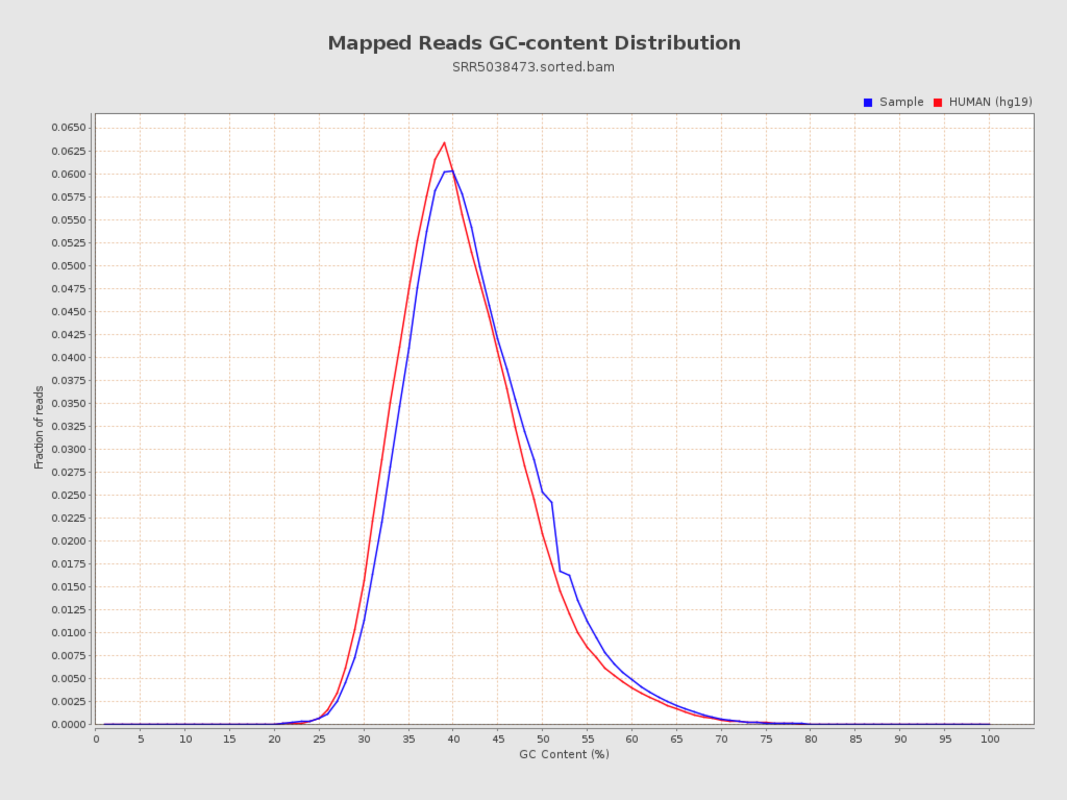
7. Results : Duplication Rate Histogram



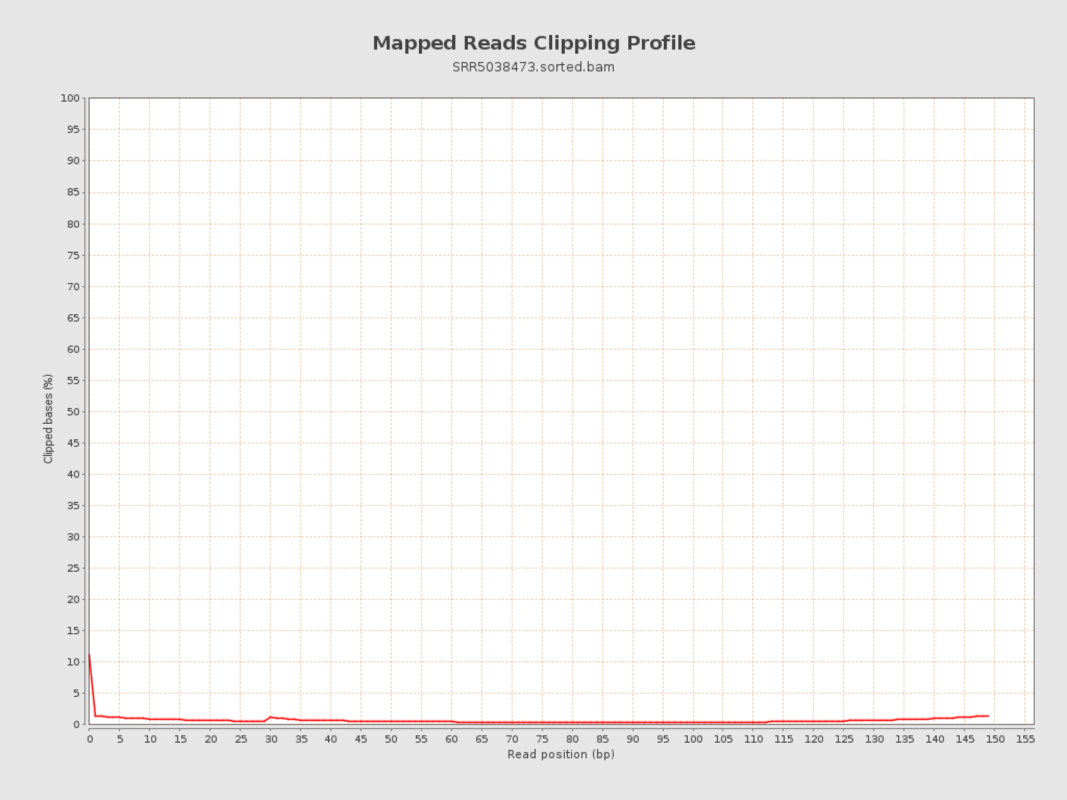
8. Results : Mapped Reads Nucleotide Content



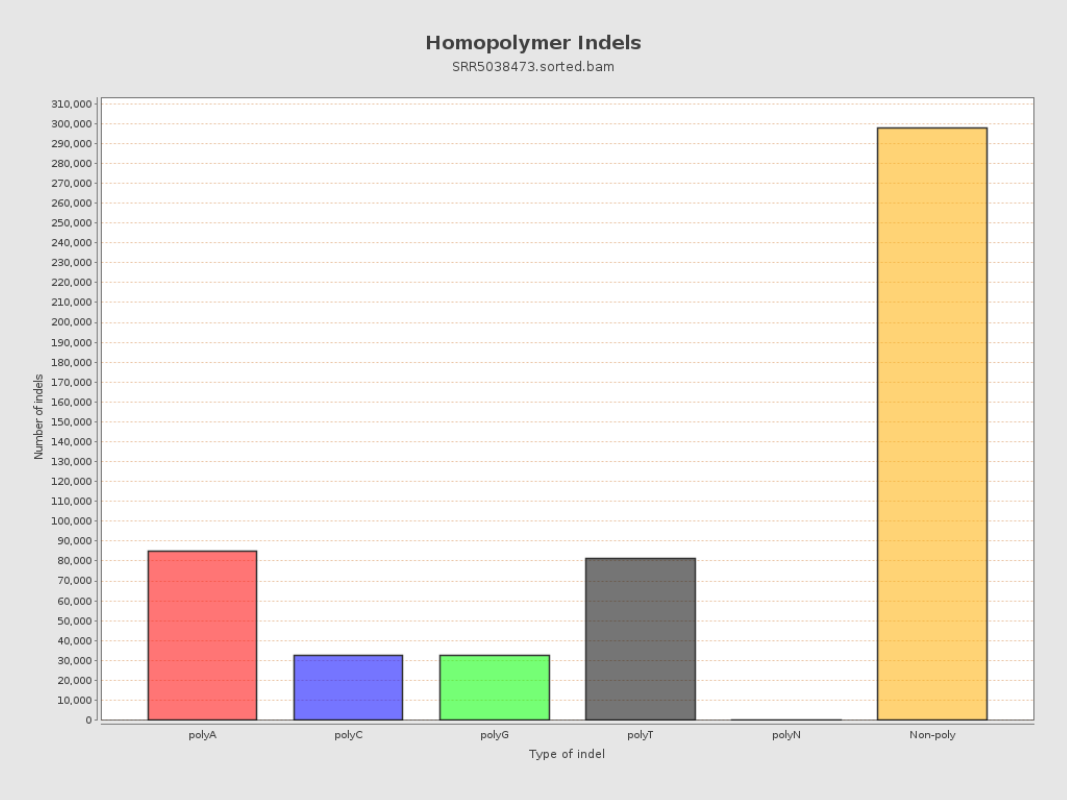
9. Results : Mapped Reads GC-content Distribution



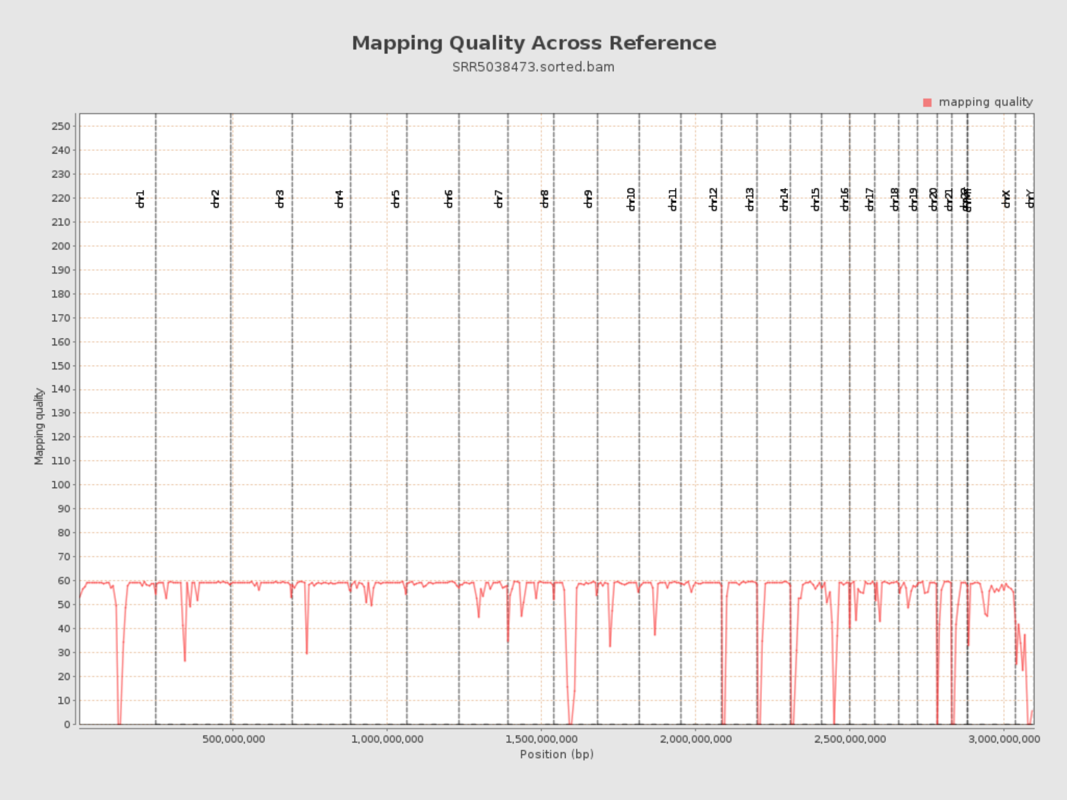
10. Results : Mapped Reads Clipping Profile



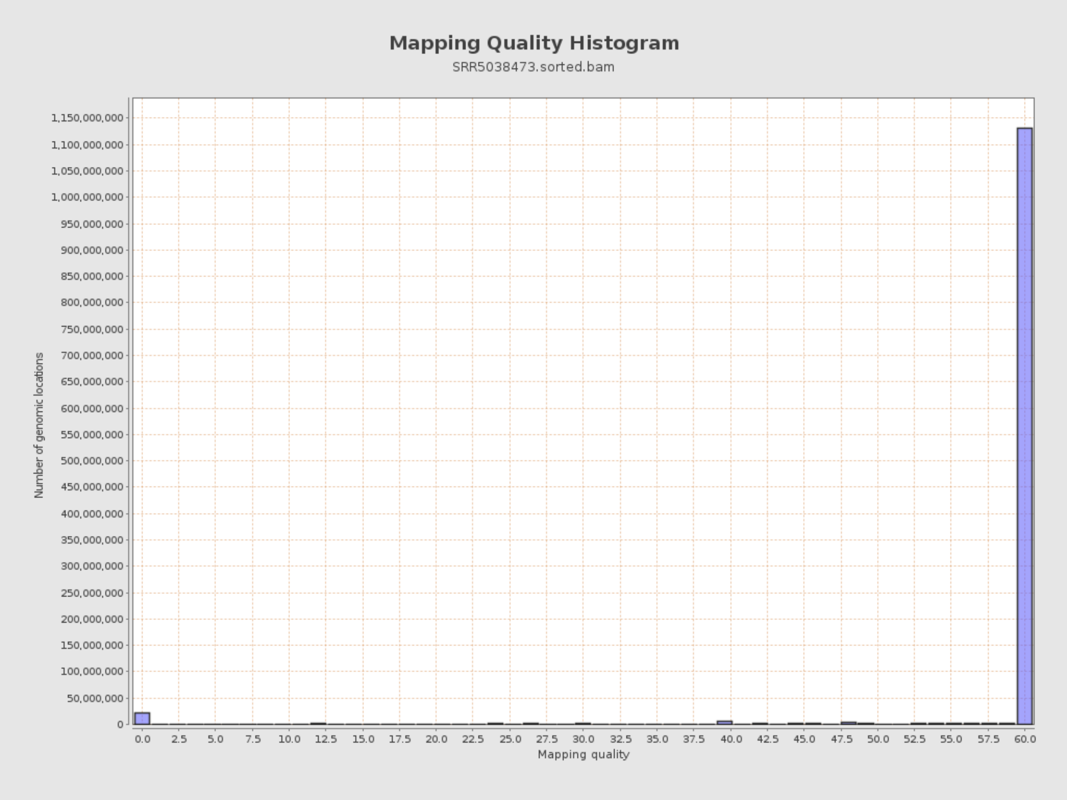
11. Results : Homopolymer Indels



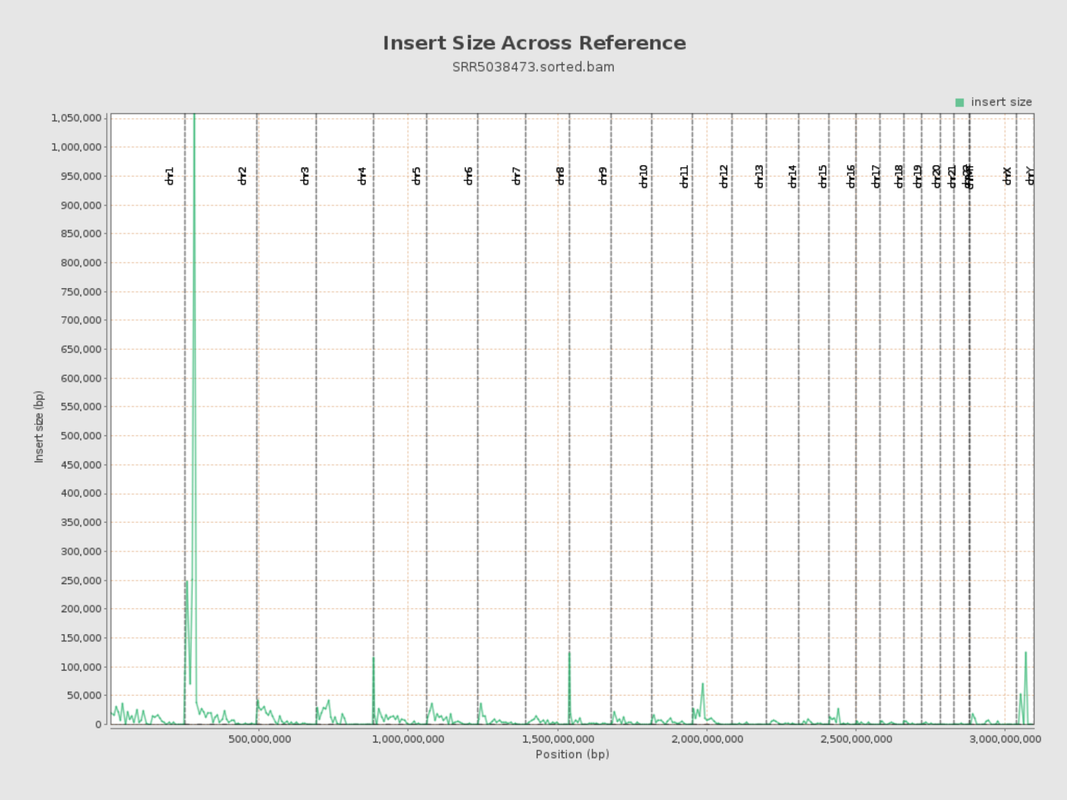
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram