Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 10:51:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038390.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_SRR5038390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038390_1.fastq.gz SRR5038390_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 10:51:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,422,782
Mapped reads	14,656,844 / 95.03%
Unmapped reads	765,938 / 4.97%
Mapped paired reads	14,656,844 / 95.03%
Mapped reads, first in pair	7,425,336 / 48.15%
Mapped reads, second in pair	7,231,508 / 46.89%
Mapped reads, both in pair	14,441,038 / 93.63%
Mapped reads, singletons	215,806 / 1.4%
Secondary alignments	0
Supplementary alignments	247,692 / 1.61%
Read min/max/mean length	30 / 150 / 150.84
Duplicated reads (estimated)	2,437,433 / 15.8%
Duplication rate	10.06%
Clipped reads	3,175,038 / 20.59%

2.2. ACGT Content

Number/percentage of A's	622,453,754 / 29.53%
Number/percentage of C's	428,628,041 / 20.33%
Number/percentage of T's	620,330,032 / 29.42%
Number/percentage of G's	436,739,177 / 20.72%
Number/percentage of N's	46,473 / 0%

GC Percentage	41.05%

2.3. Coverage

Mean	0.6815
Standard Deviation	11.7769

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	76,229.02
Standard Deviation	2,615,191.21
P25/Median/P75	198 / 241 / 296

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	31,176,427
Insertions	367,064
Mapped reads with at least one insertion	2.36%
Deletions	700,006
Mapped reads with at least one deletion	4.59%
Homopolymer indels	46.45%

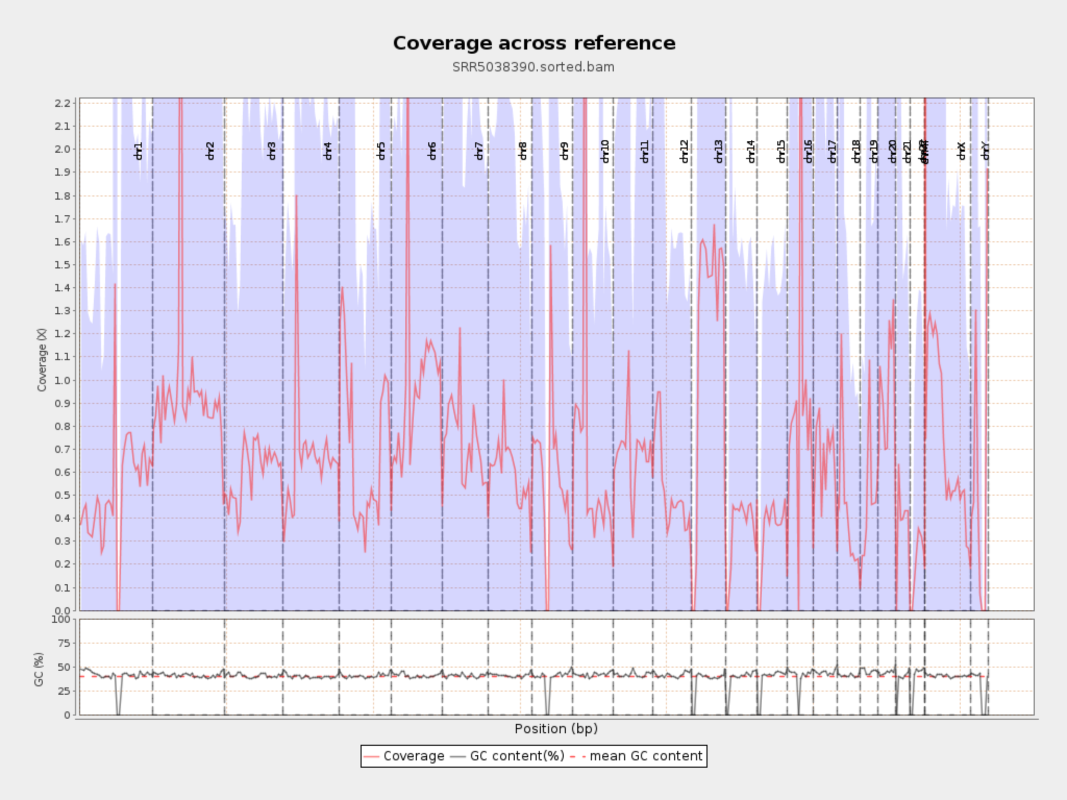
2.7. Chromosome stats

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

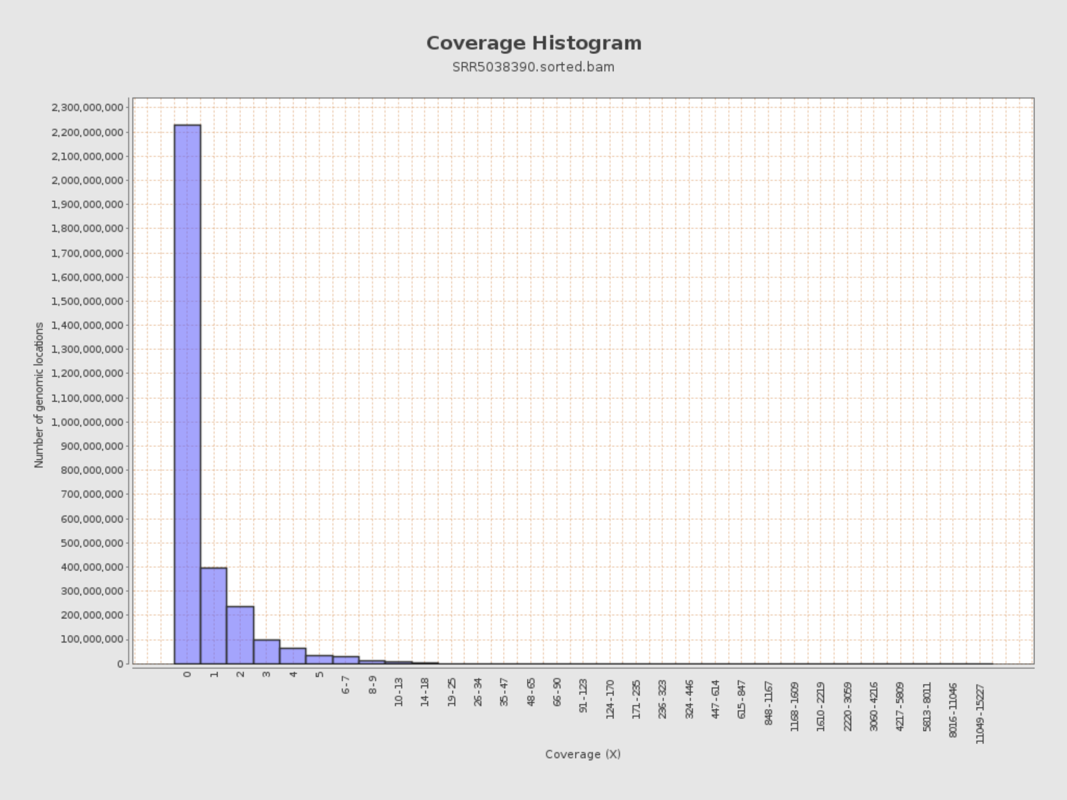
		bases	coverage	deviation
chr1	249250621	129861587	0.521	15.9998
chr2	243199373	239895592	0.9864	16.8167
chr3	198022430	119750025	0.6047	1.4039
chr4	191154276	126061098	0.6595	8.2554
chr5	180915260	127760089	0.7062	1.6285
chr6	171115067	169659446	0.9915	18.2315
chr7	159138663	116464911	0.7318	9.8605
chr8	146364022	88479979	0.6045	3.4536
chr9	141213431	80006760	0.5666	18.9536
chr10	135534747	98471235	0.7265	23.9849
chr11	135006516	90908189	0.6734	7.4494
chr12	133851895	71012209	0.5305	1.3093
chr13	115169878	142140470	1.2342	2.2027
chr14	107349540	37643948	0.3507	1.2357
chr15	102531392	34854627	0.3399	0.9411
chr16	90354753	84193584	0.9318	17.2859
chr17	81195210	52482952	0.6464	8.3334
chr18	78077248	32509285	0.4164	15.263
chr19	59128983	26996576	0.4566	8.7246
chr20	63025520	60377283	0.958	3.051
chr21	48129895	18633809	0.3872	4.186
chr22	51304566	10411013	0.2029	0.8161
chrMT	16571	1258725	75.9595	49.2854
chrX	155270560	114717605	0.7388	2.454

chrY	59373566	35068093	0.5906	15.1021

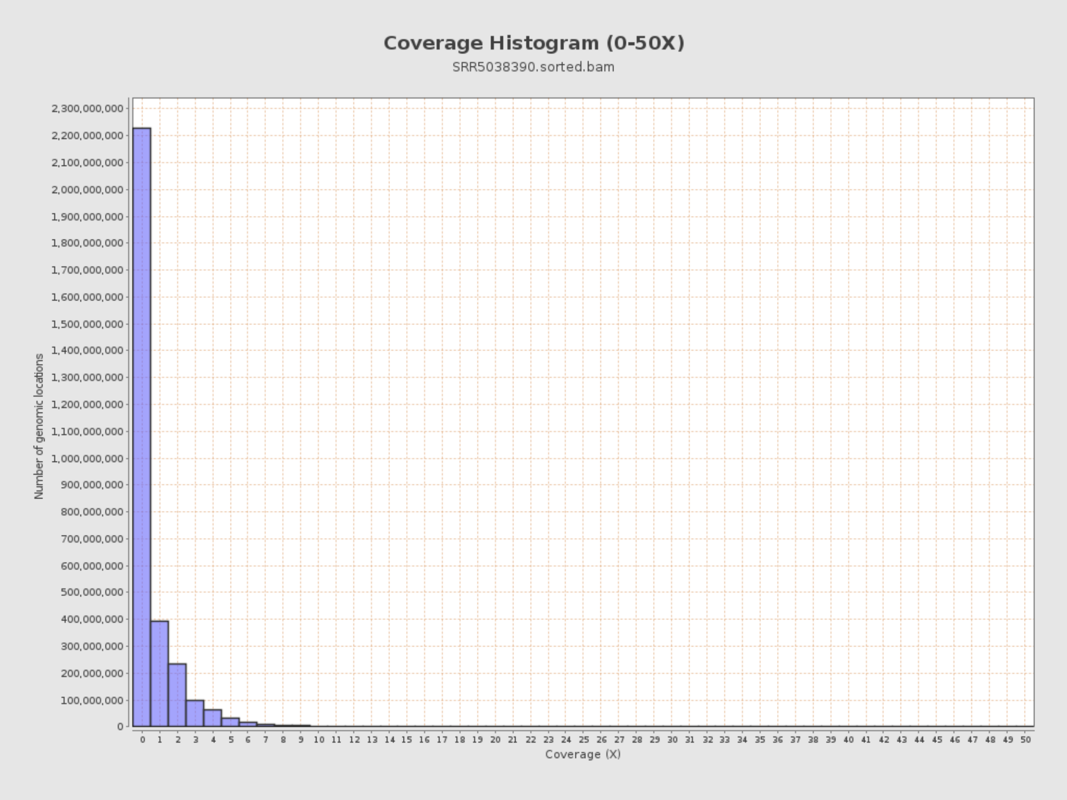
3. Results : Coverage across reference



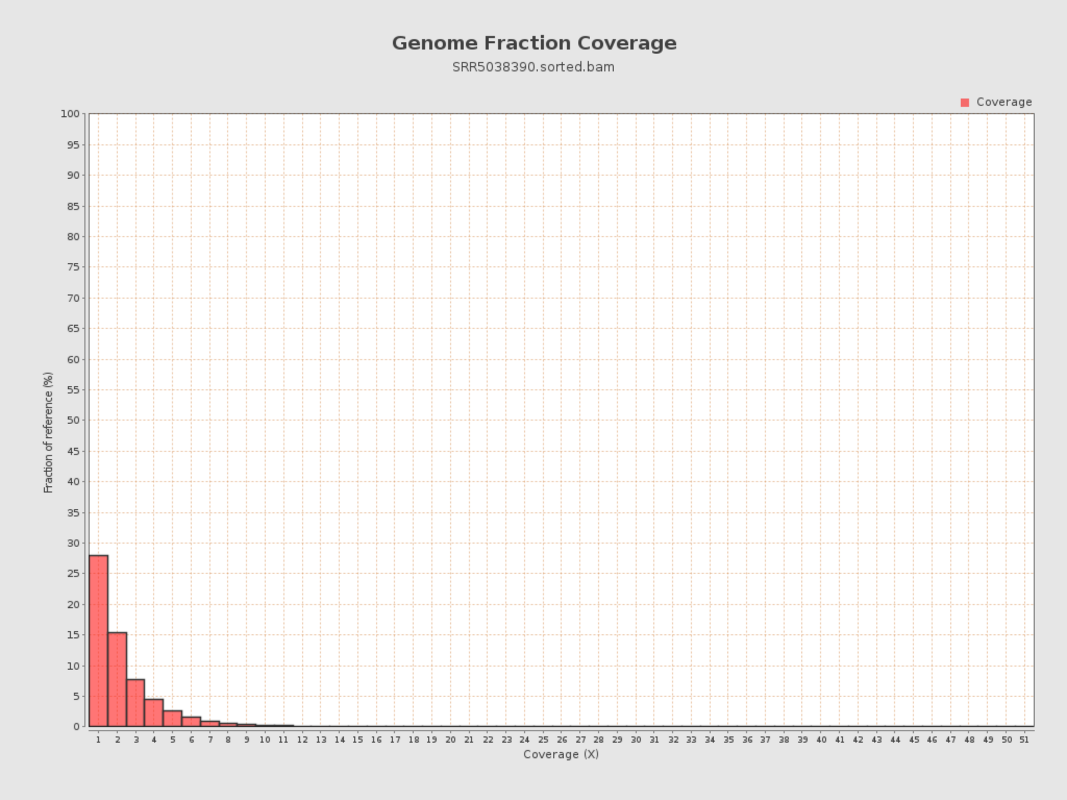
4. Results : Coverage Histogram



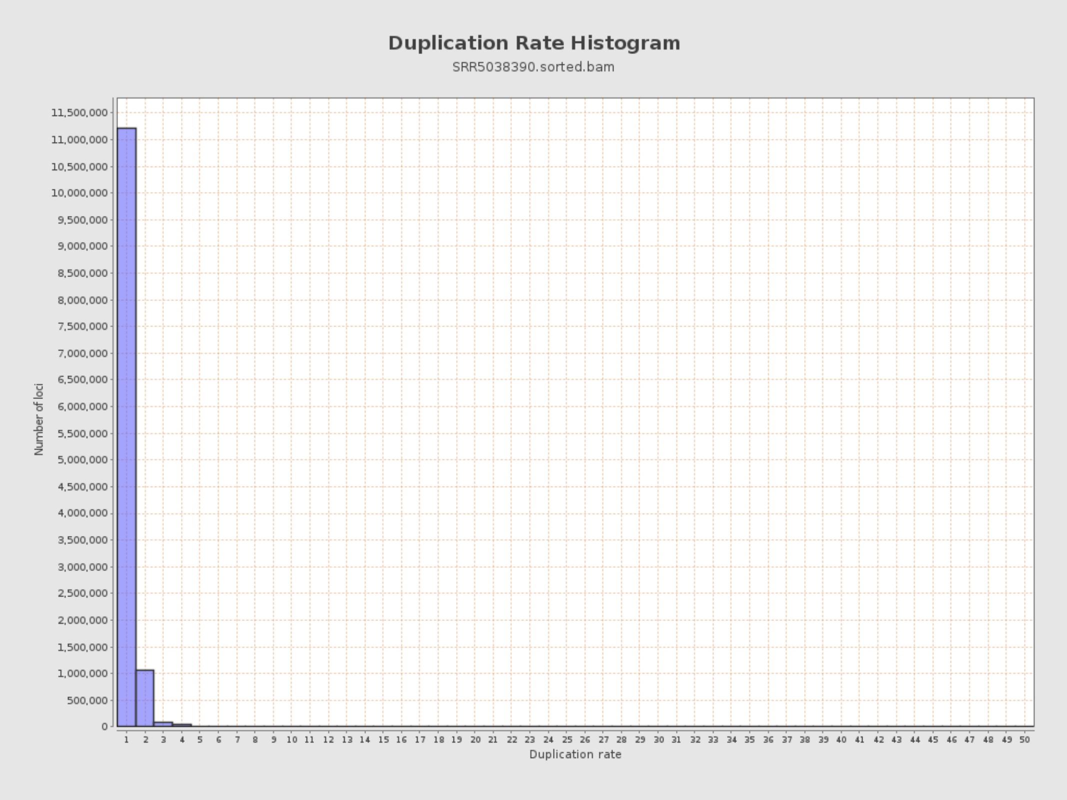
5. Results : Coverage Histogram (0-50X)



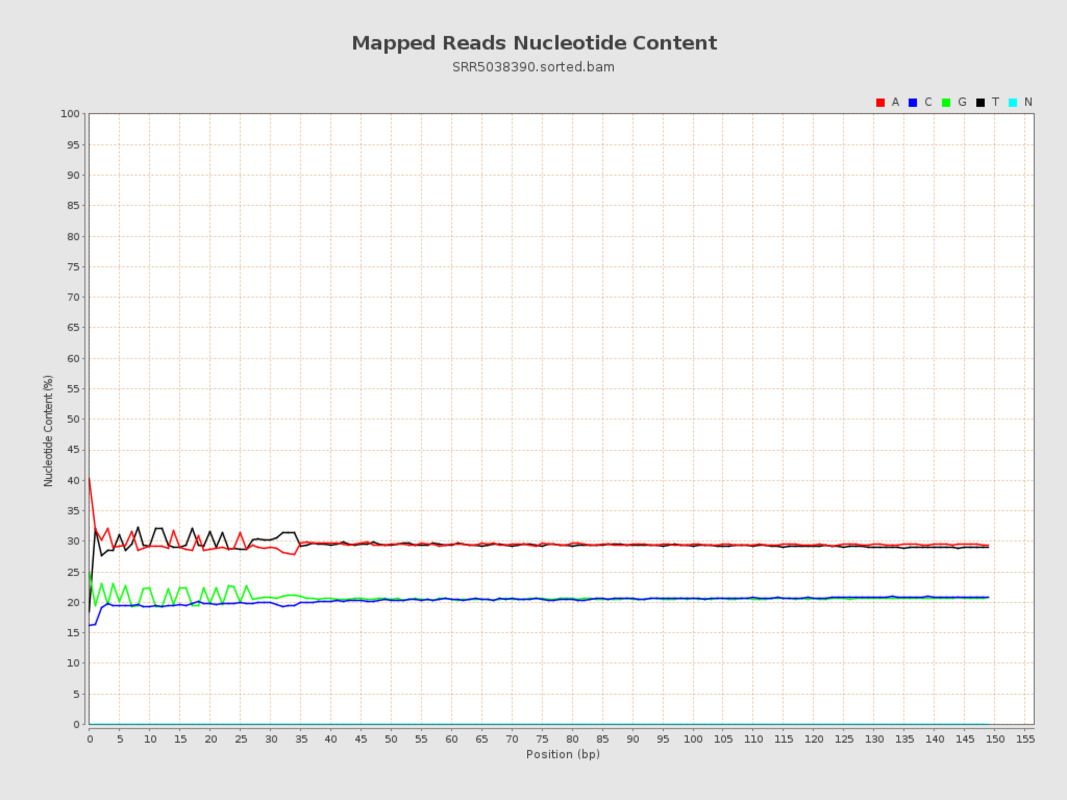
6. Results : Genome Fraction Coverage



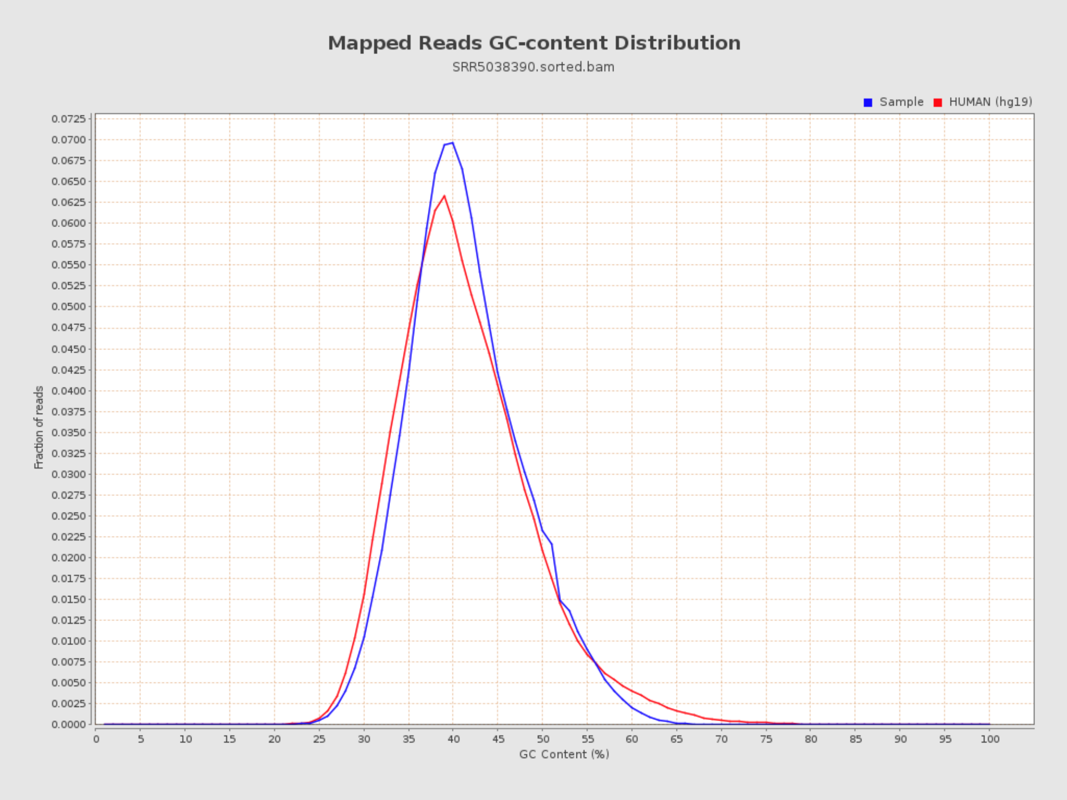
7. Results : Duplication Rate Histogram



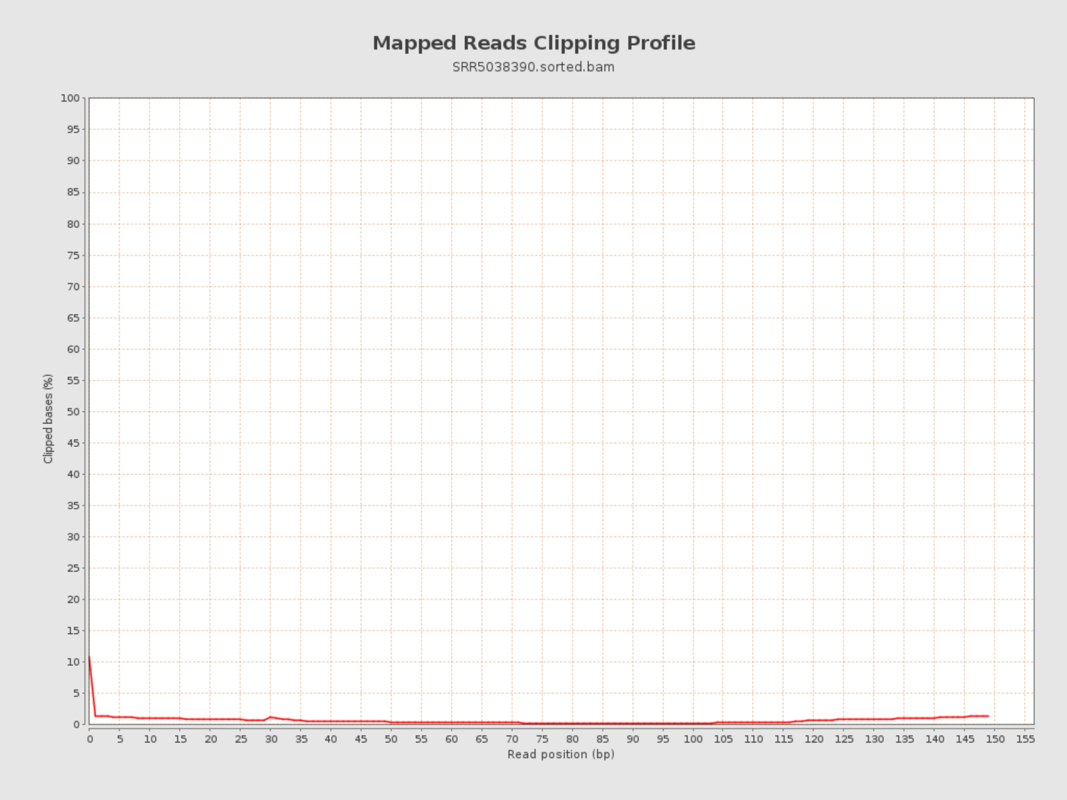
8. Results : Mapped Reads Nucleotide Content



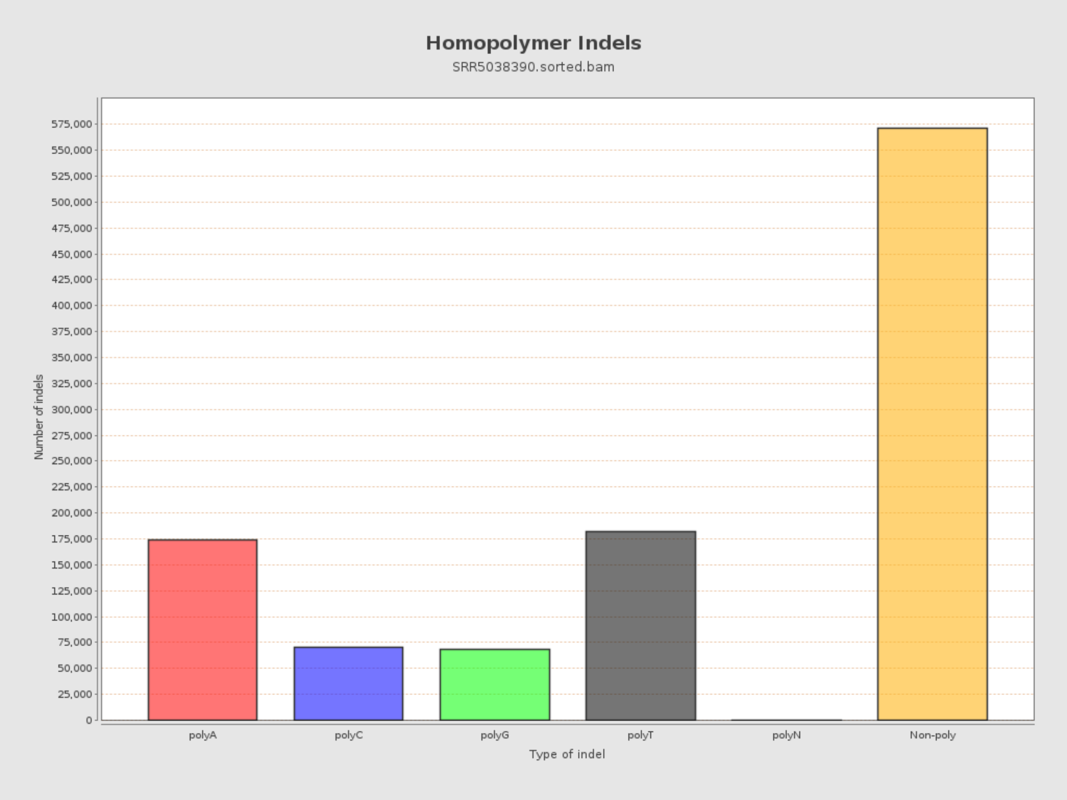
9. Results : Mapped Reads GC-content Distribution



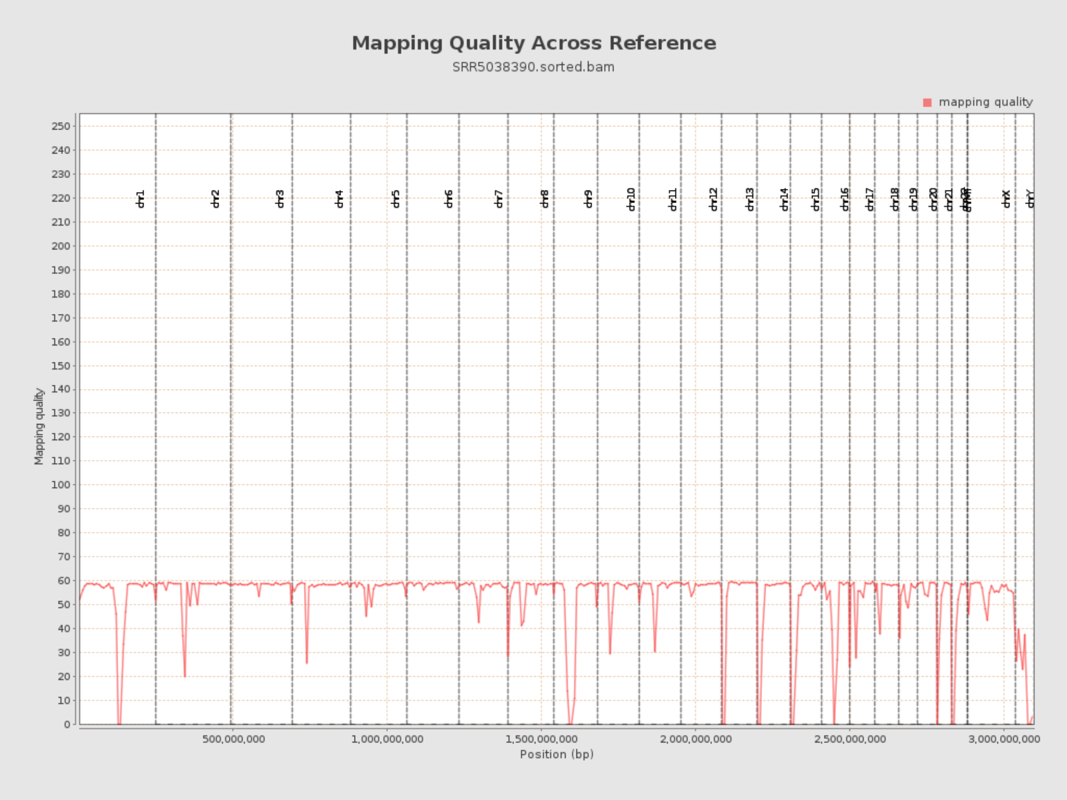
10. Results : Mapped Reads Clipping Profile



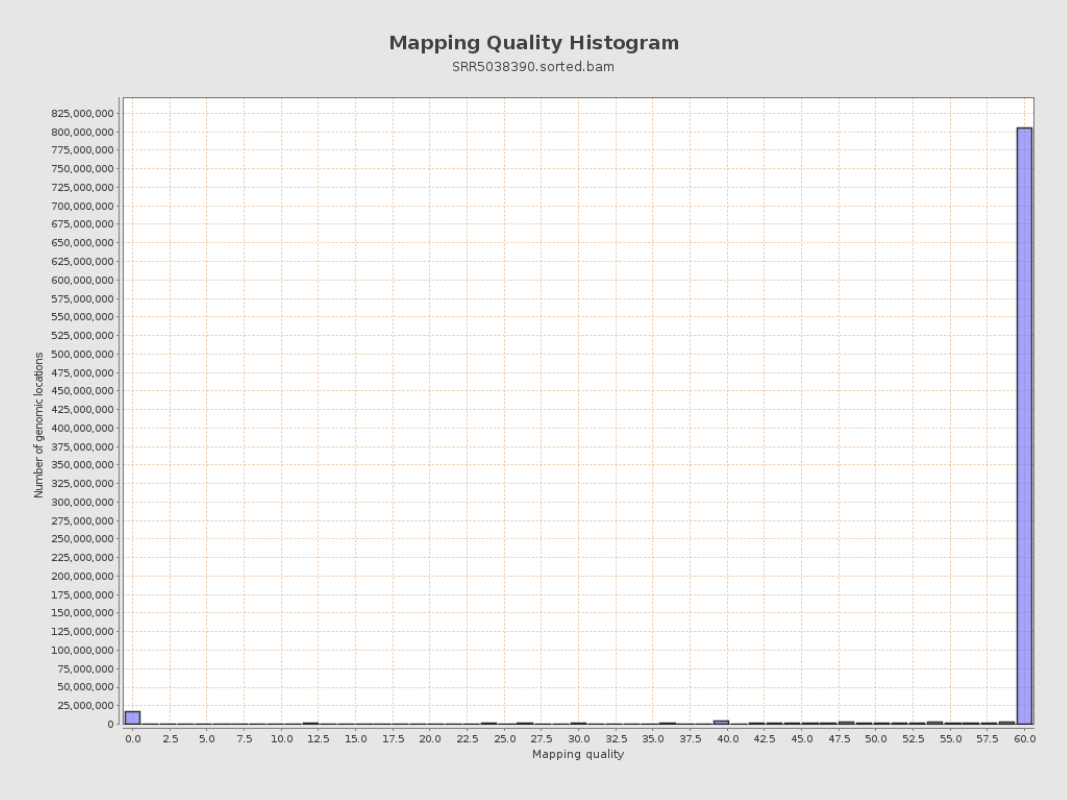
11. Results : Homopolymer Indels



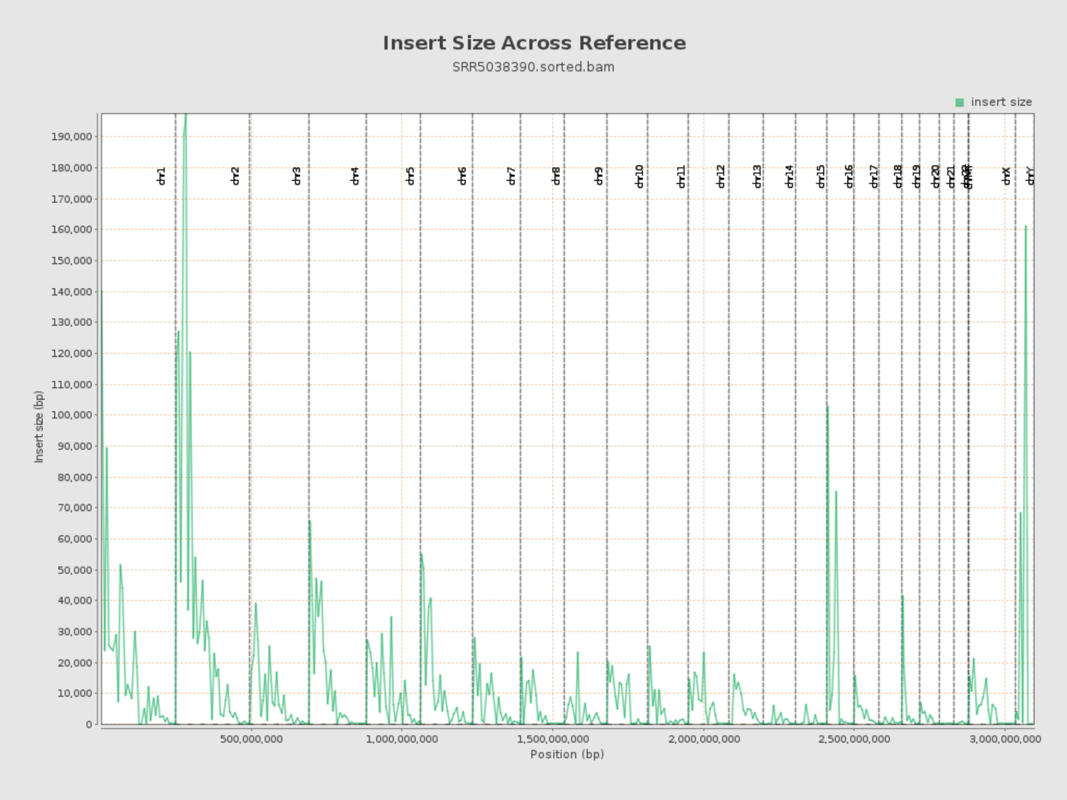
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram