Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 10:21:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038439.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_SRR5038439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038439_1.fastq.gz SRR5038439_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 10:21:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038439.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,266,762
Mapped reads	11,030,304 / 97.9%
Unmapped reads	236,458 / 2.1%
Mapped paired reads	11,030,304 / 97.9%
Mapped reads, first in pair	5,569,757 / 49.44%
Mapped reads, second in pair	5,460,547 / 48.47%
Mapped reads, both in pair	10,907,538 / 96.81%
Mapped reads, singletons	122,766 / 1.09%
Secondary alignments	0
Supplementary alignments	212,955 / 1.89%
Read min/max/mean length	30 / 150 / 150.98
Duplicated reads (estimated)	1,579,809 / 14.02%
Duplication rate	7.74%
Clipped reads	2,910,940 / 25.84%

2.2. ACGT Content

Number/percentage of A's	456,282,080 / 29.1%
Number/percentage of C's	319,877,099 / 20.4%
Number/percentage of T's	456,955,610 / 29.15%
Number/percentage of G's	334,698,495 / 21.35%
Number/percentage of N's	33,963 / 0%

GC Percentage	41.75%

2.3. Coverage

Mean	0.5068
Standard Deviation	9.3655

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	89,067.58
Standard Deviation	2,844,128.34
P25/Median/P75	224 / 264 / 316

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	22,025,828
Insertions	279,853
Mapped reads with at least one insertion	2.39%
Deletions	521,403
Mapped reads with at least one deletion	4.54%
Homopolymer indels	46.72%

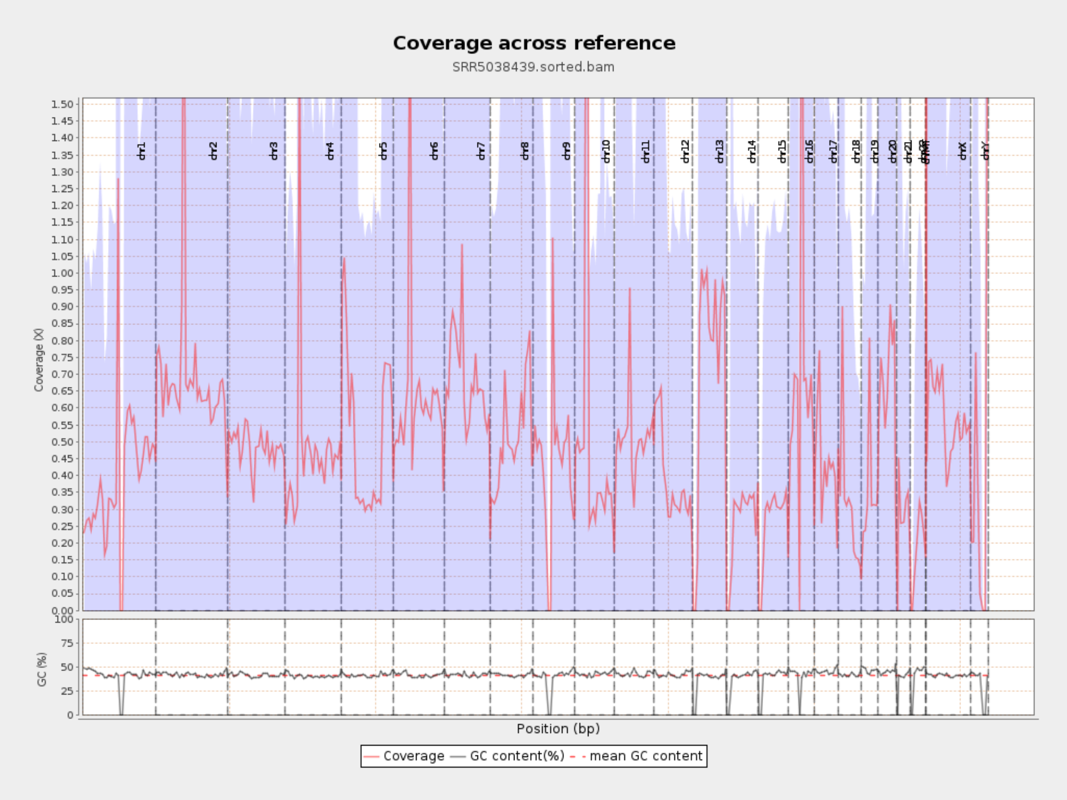
2.7. Chromosome stats

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

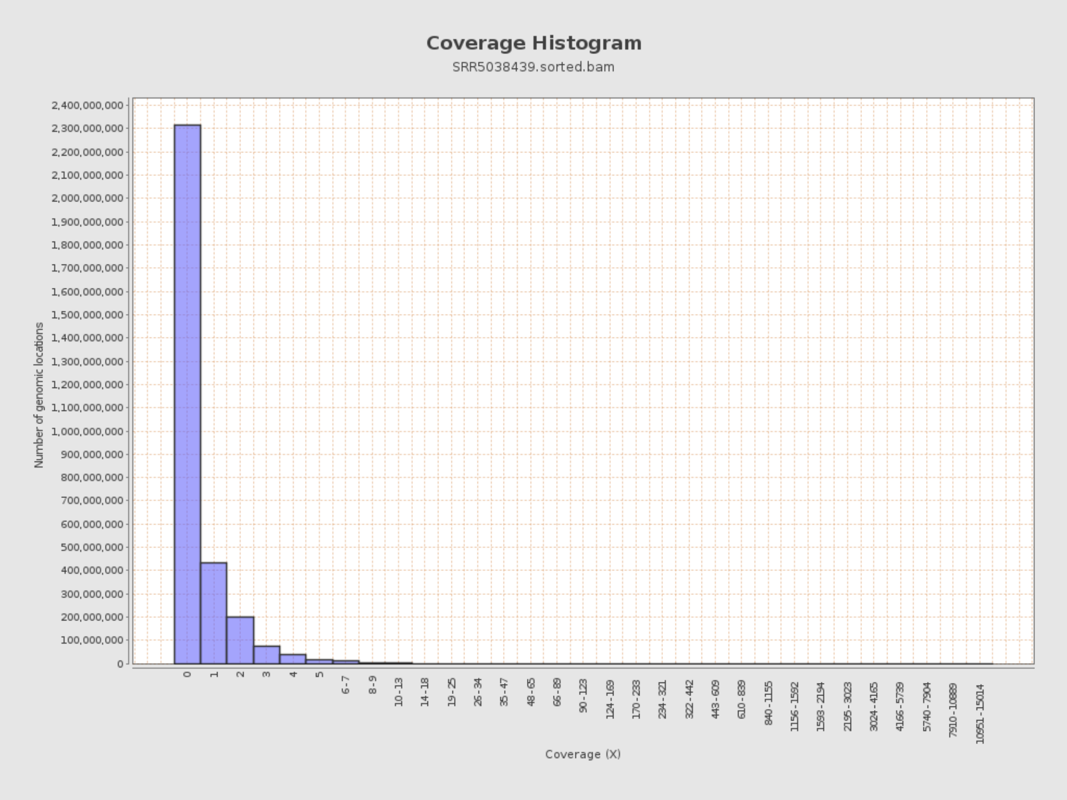
		bases	coverage	deviation
chr1	249250621	97741672	0.3921	15.5477
chr2	243199373	172297222	0.7085	9.1373
chr3	198022430	95334271	0.4814	1.0894
chr4	191154276	91478766	0.4786	8.6484
chr5	180915260	94510688	0.5224	1.214
chr6	171115067	110508047	0.6458	15.3896
chr7	159138663	108864814	0.6841	8.2736
chr8	146364022	75564854	0.5163	2.2253
chr9	141213431	62499145	0.4426	13.26
chr10	135534747	68815074	0.5077	18.7568
chr11	135006516	68809086	0.5097	7.2383
chr12	133851895	52556678	0.3926	0.979
chr13	115169878	85115233	0.739	1.403
chr14	107349540	28193685	0.2626	0.8944
chr15	102531392	26592069	0.2594	0.7232
chr16	90354753	63873534	0.7069	12.3171
chr17	81195210	36358269	0.4478	7.4747
chr18	78077248	25609928	0.328	11.2665
chr19	59128983	20616935	0.3487	8.3642
chr20	63025520	44098474	0.6997	2.823
chr21	48129895	13655762	0.2837	3.4081
chr22	51304566	9331087	0.1819	0.6492
chrMT	16571	3691365	222.7605	150.1471
chrX	155270560	88390026	0.5693	1.991

chrY	59373566	24446344	0.4117	12.1083

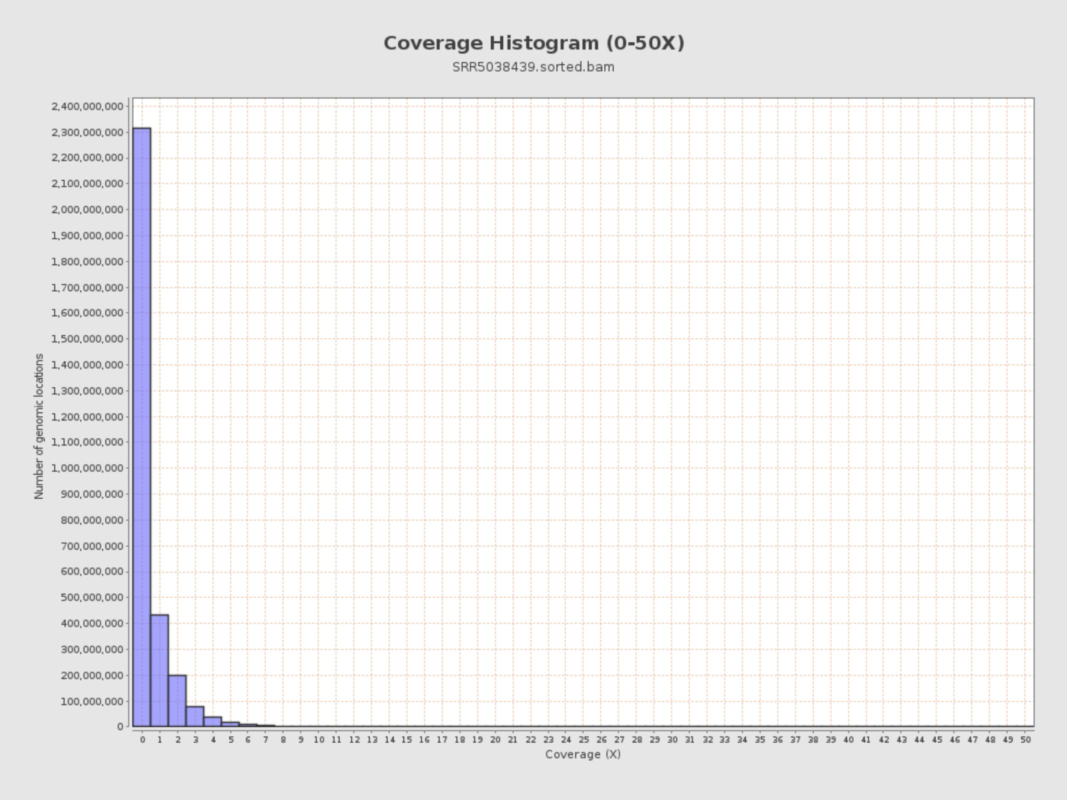
3. Results : Coverage across reference



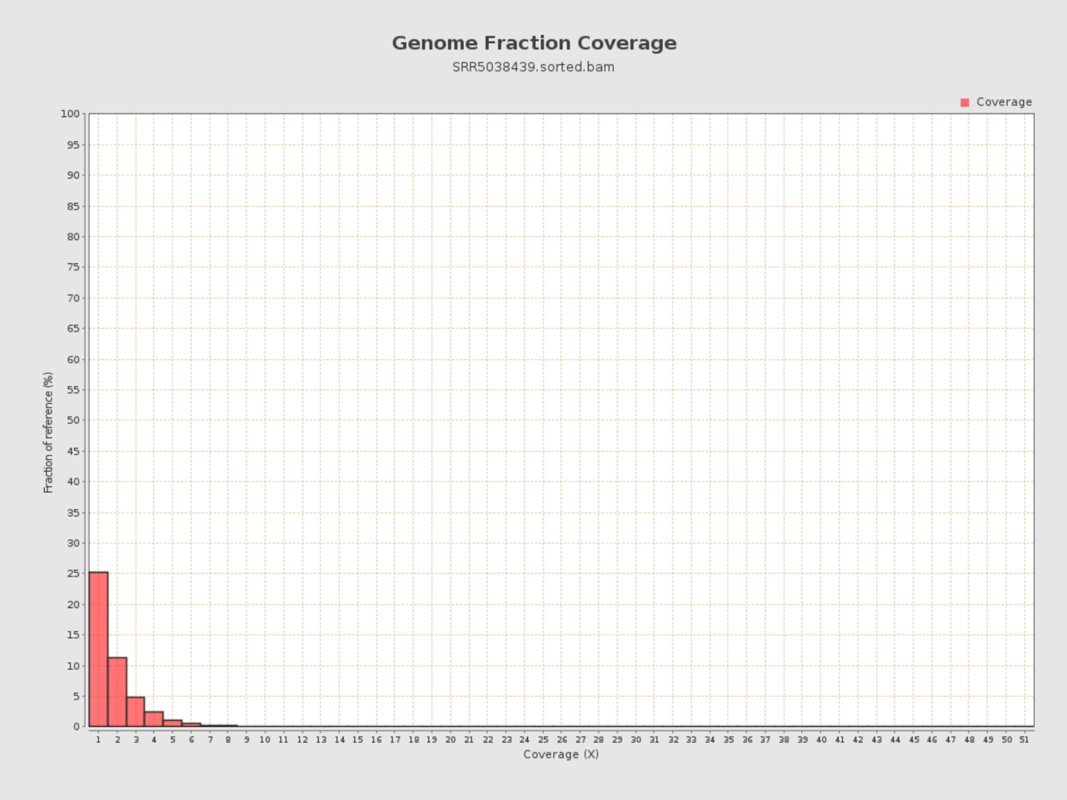
4. Results : Coverage Histogram



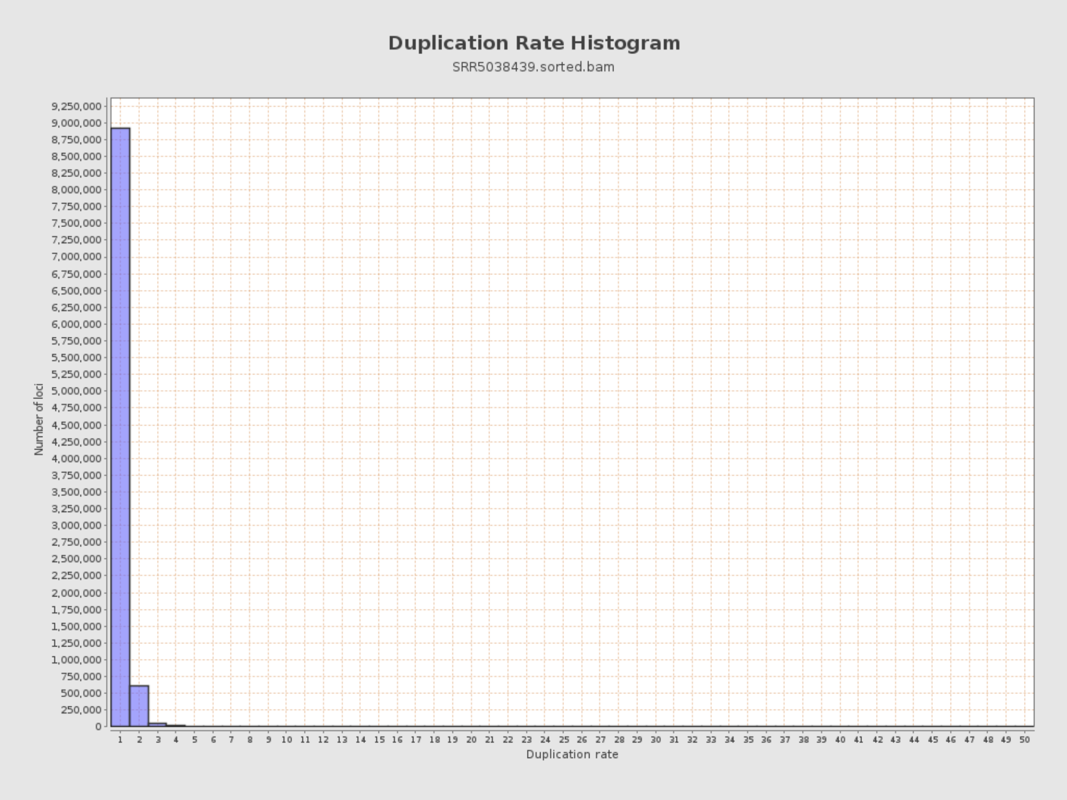
5. Results : Coverage Histogram (0-50X)



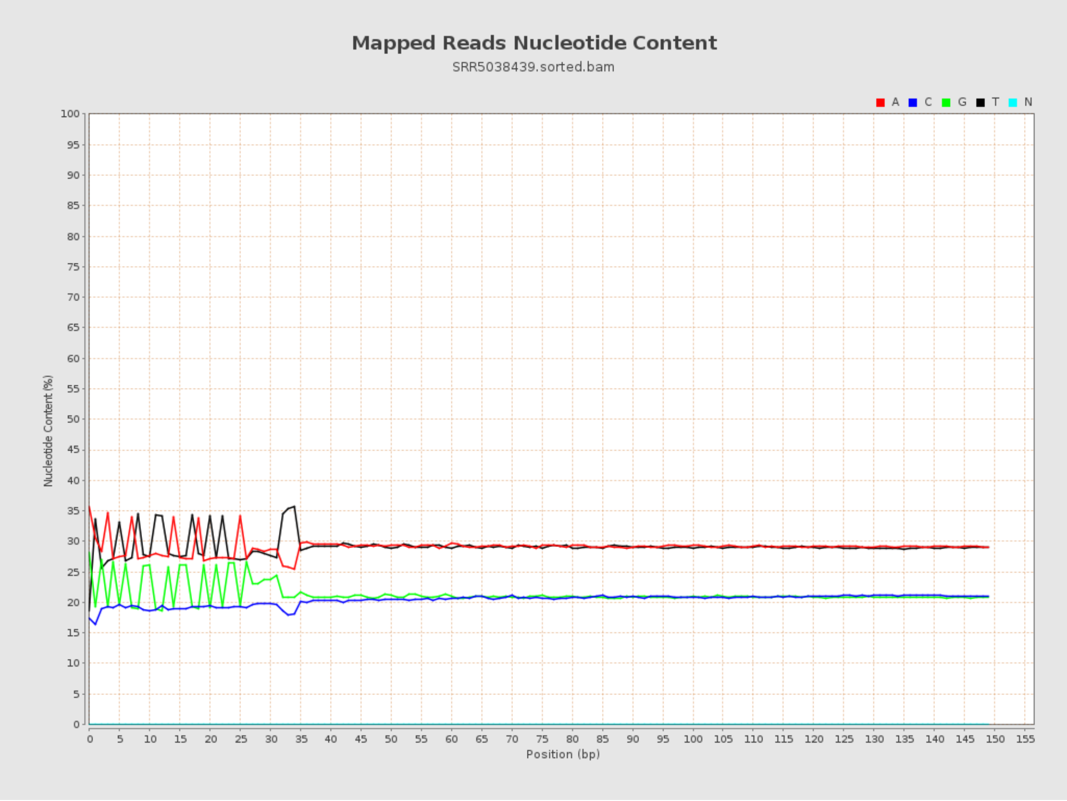
6. Results : Genome Fraction Coverage



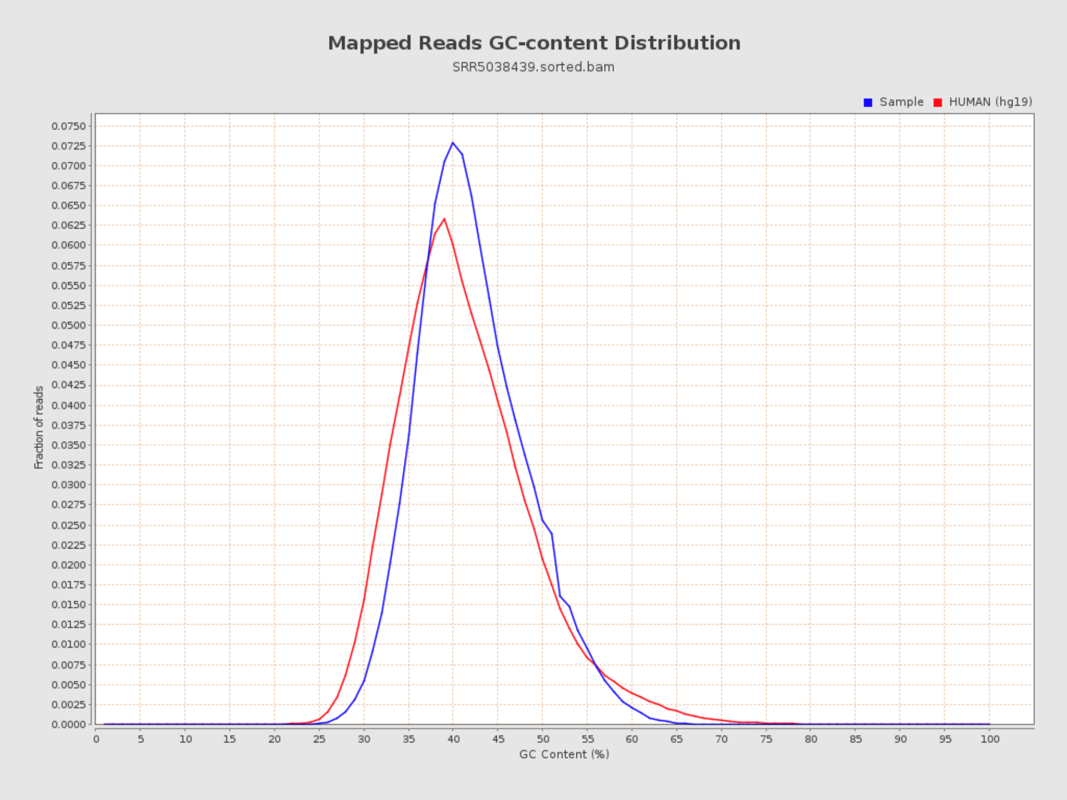
7. Results : Duplication Rate Histogram



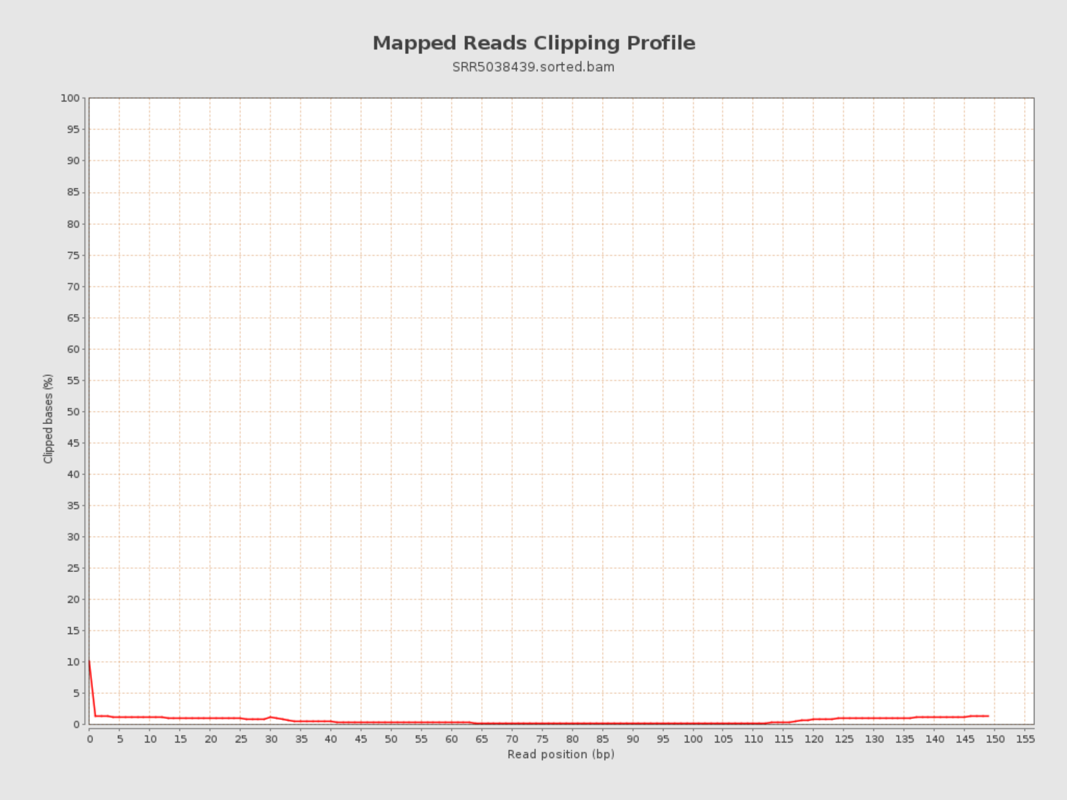
8. Results : Mapped Reads Nucleotide Content



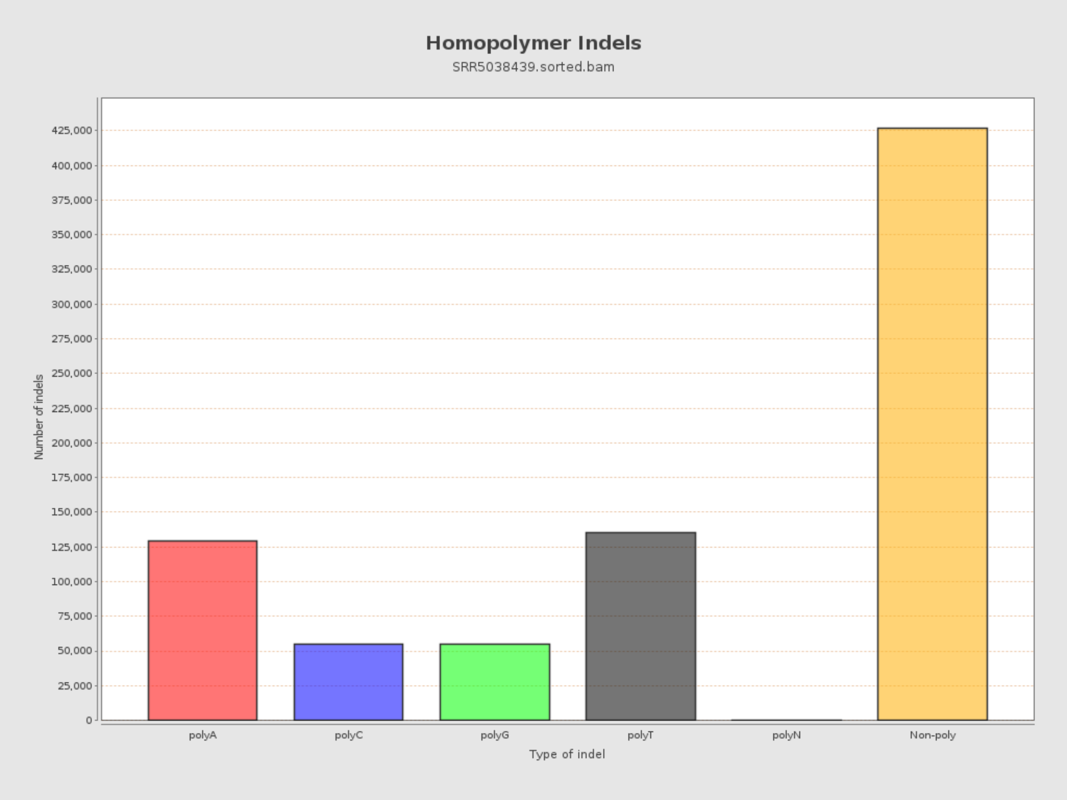
9. Results : Mapped Reads GC-content Distribution



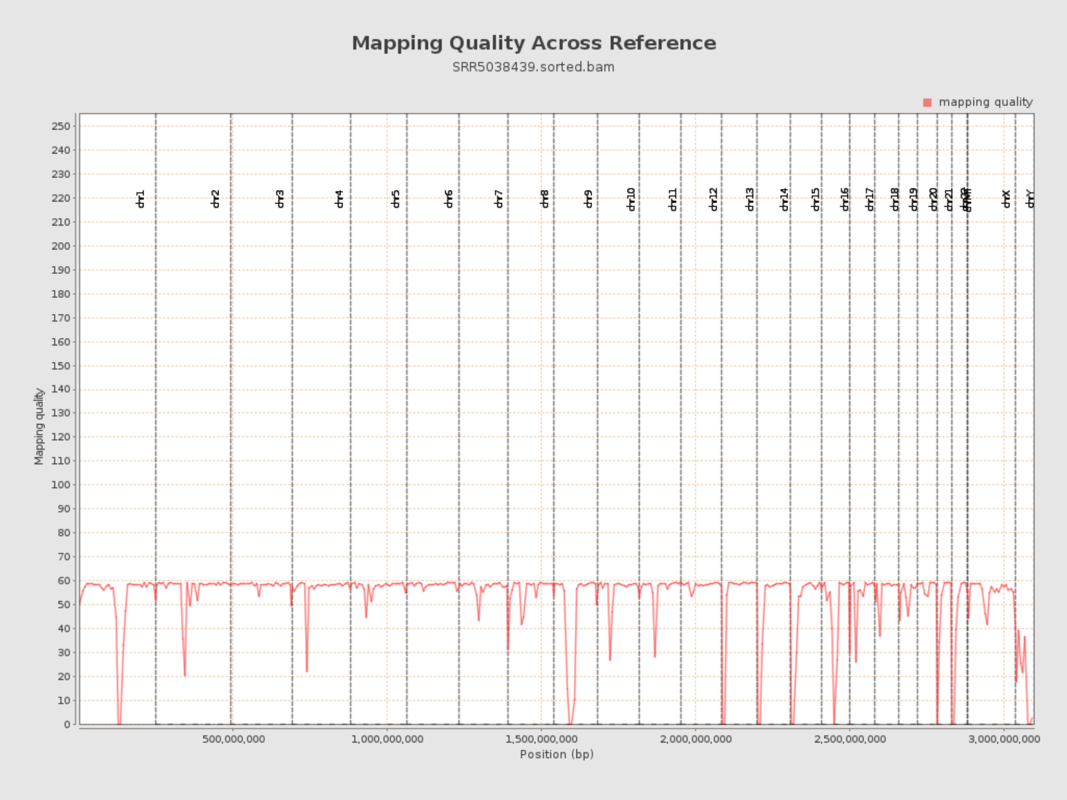
10. Results : Mapped Reads Clipping Profile



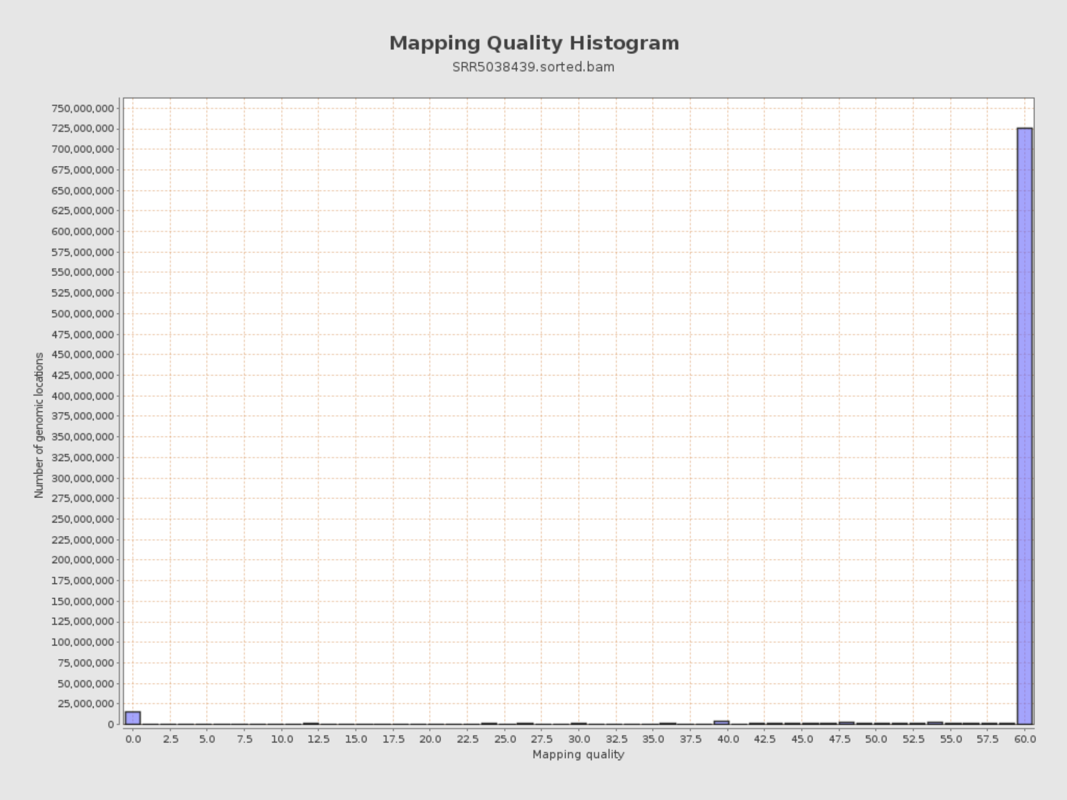
11. Results : Homopolymer Indels



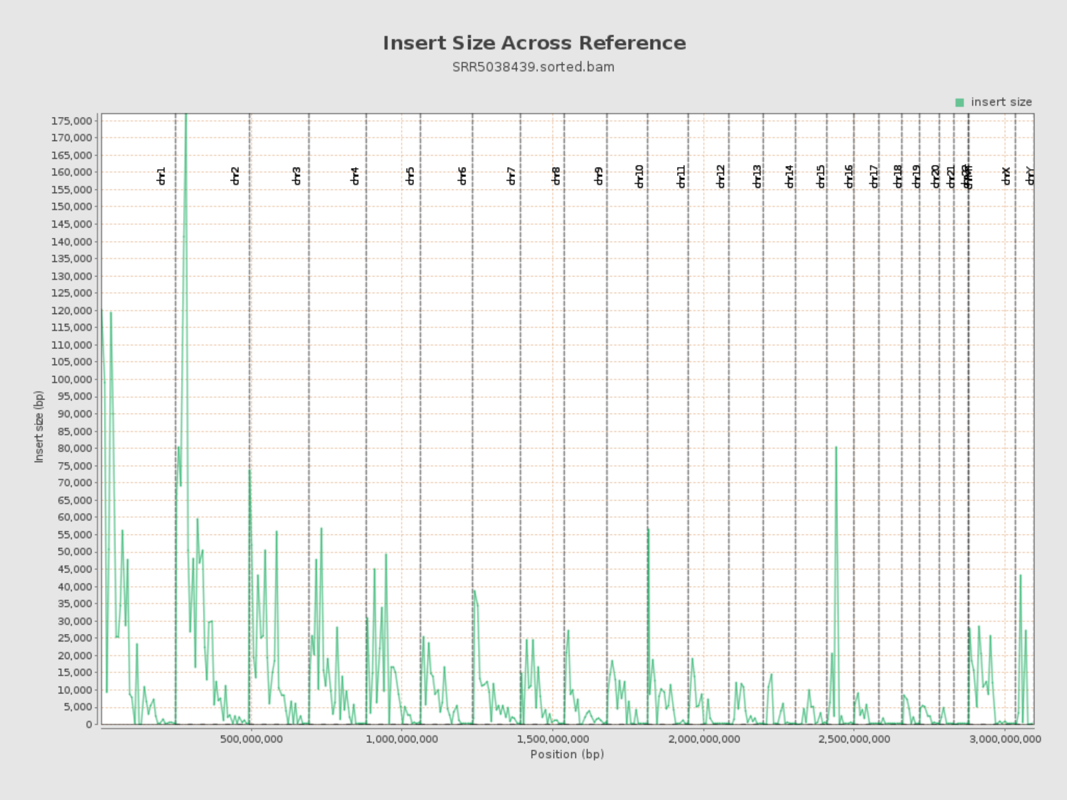
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram