Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/12 06:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438263.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_SRR8438263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438263_1.fastq.gz SRR8438263_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 12 06:27:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	599,171,020
Mapped reads	597,241,380 / 99.68%
Unmapped reads	1,929,640 / 0.32%
Mapped paired reads	597,241,380 / 99.68%
Mapped reads, first in pair	298,723,100 / 49.86%
Mapped reads, second in pair	298,518,280 / 49.82%
Mapped reads, both in pair	595,873,434 / 99.45%
Mapped reads, singletons	1,367,946 / 0.23%
Secondary alignments	0
Supplementary alignments	9,868,261 / 1.65%
Read min/max/mean length	28 / 151 / 145.36
Duplicated reads (estimated)	251,622,998 / 42%
Duplication rate	39.27%
Clipped reads	108,352,779 / 18.08%

2.2. ACGT Content

Number/percentage of A's	25,887,025,046 / 30.09%
Number/percentage of C's	17,303,627,765 / 20.11%
Number/percentage of T's	24,691,151,510 / 28.7%
Number/percentage of G's	18,146,011,054 / 21.09%
Number/percentage of N's	528,985 / 0%

GC Percentage	41.21%

2.3. Coverage

Mean	27.7975
Standard Deviation	97.0742

2.4. Mapping Quality

Mean Mapping Quality	55.09

2.5. Insert size

Mean	42,994.15
Standard Deviation	2,017,345.38
P25/Median/P75	187 / 243 / 335

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	437,179,059
Insertions	10,968,567
Mapped reads with at least one insertion	1.81%
Deletions	9,824,761
Mapped reads with at least one deletion	1.62%
Homopolymer indels	48.57%

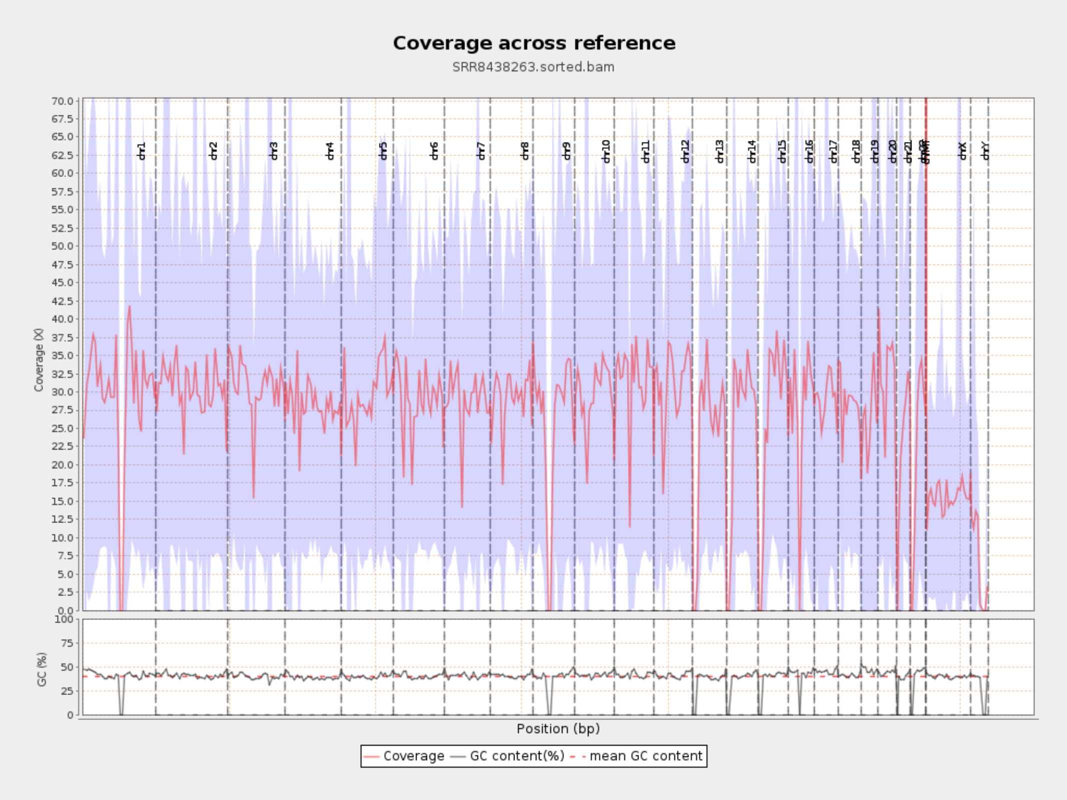
2.7. Chromosome stats

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

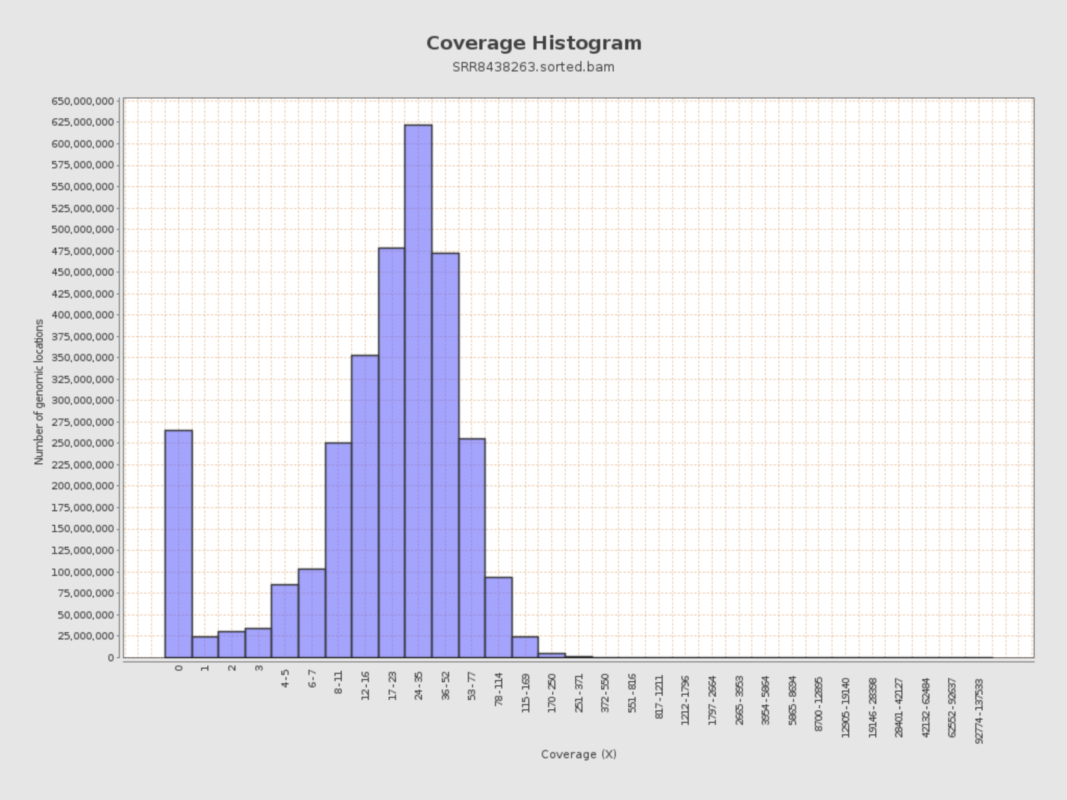
		bases	coverage	deviation
chr1	249250621	7380990578	29.6127	30.6228
chr2	243199373	7450153044	30.6339	113.4104
chr3	198022430	6086496816	30.7364	154.0587
chr4	191154276	5396985006	28.2337	27.1777
chr5	180915260	5363941312	29.6489	35.2727
chr6	171115067	4982311514	29.1167	24.5405
chr7	159138663	4599539243	28.9027	26.3578
chr8	146364022	4269172571	29.1682	23.2888
chr9	141213431	3646134943	25.82	29.3988
chr10	135534747	4070649913	30.034	37.6111
chr11	135006516	4255014734	31.5171	26.7279
chr12	133851895	4201188031	31.3868	26.3927
chr13	115169878	2753885086	23.9115	22.5341
chr14	107349540	2782142198	25.9167	28.1008
chr15	102531392	2660026225	25.9435	27.5562
chr16	90354753	2469308221	27.329	45.6418
chr17	81195210	2392107830	29.4612	35.6458
chr18	78077248	2224567375	28.4919	23.0785
chr19	59128983	1554724562	26.2938	210.9893
chr20	63025520	2033914589	32.2713	30.0401
chr21	48129895	1083240884	22.5066	79.0527
chr22	51304566	1097773266	21.3972	28.1841
chrMT	16571	482750989	29,132.2786	11,302.919
chrX	155270560	2424636347	15.6156	27.1085

chrY	59373566	391040728	6.5861	22.2161

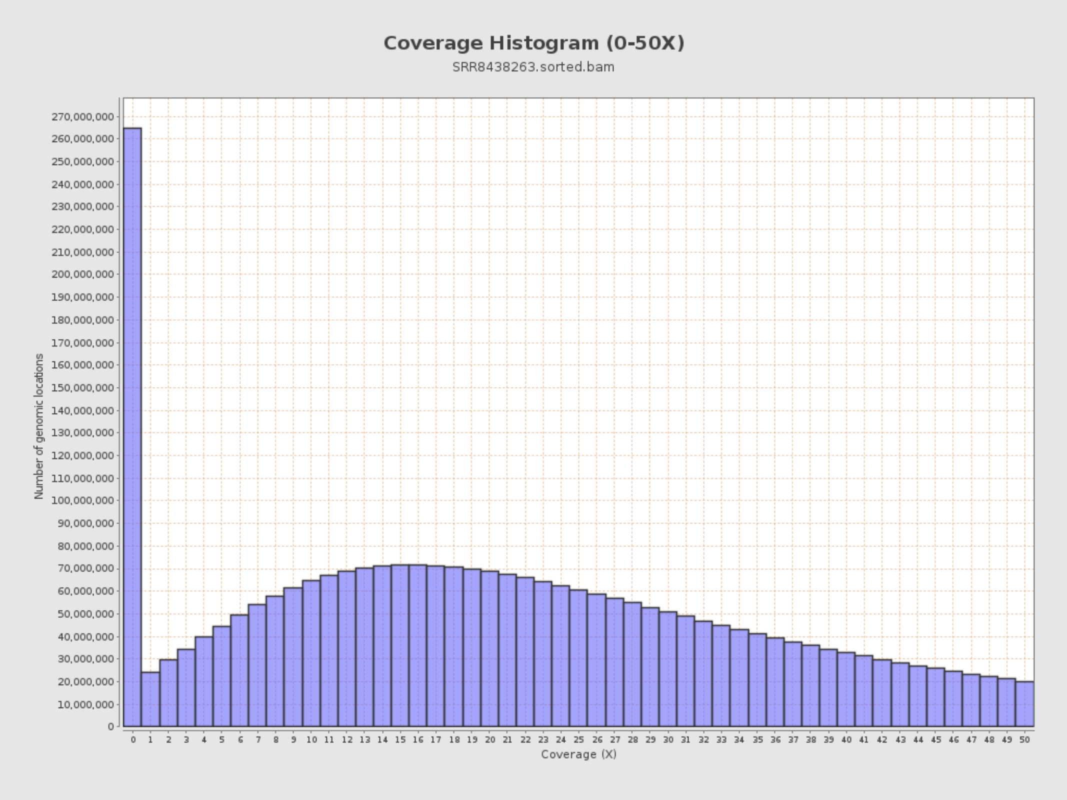
3. Results : Coverage across reference



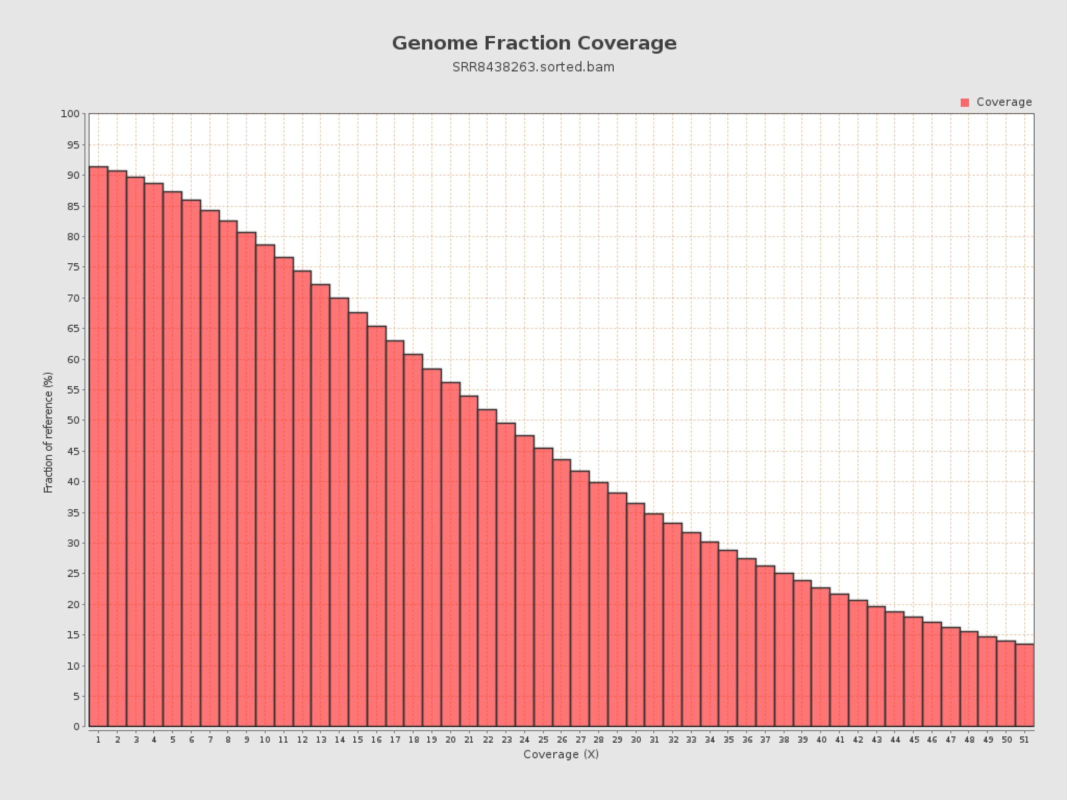
4. Results : Coverage Histogram



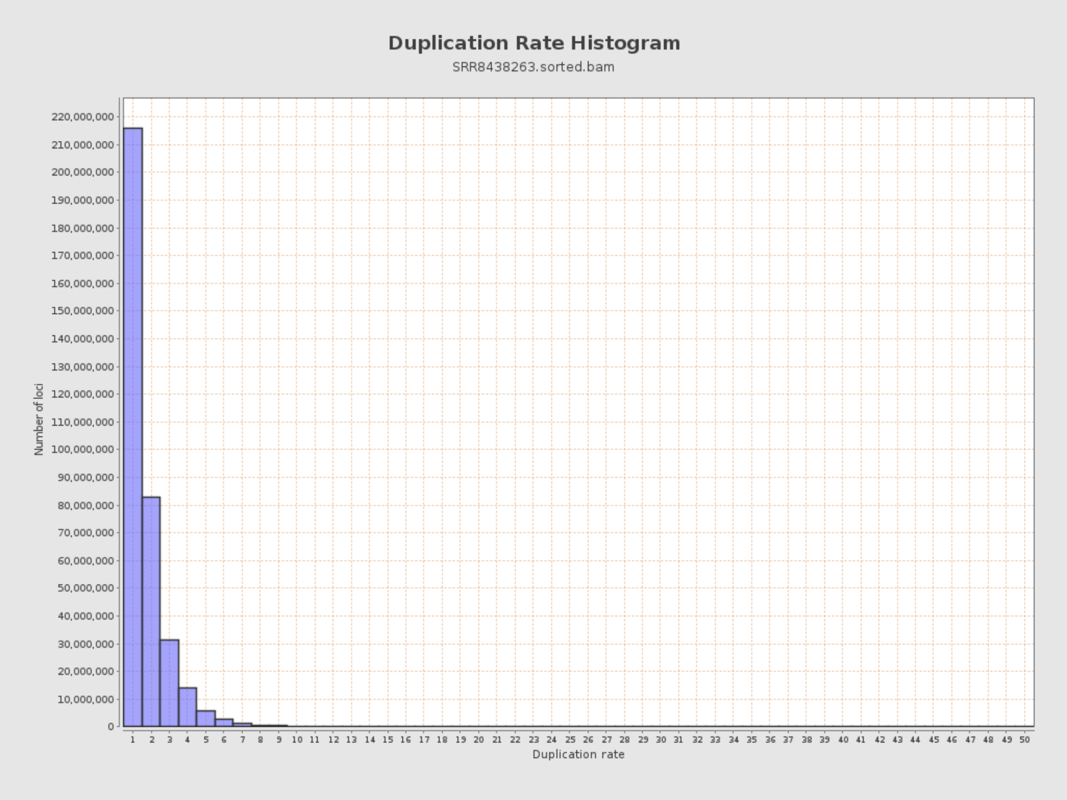
5. Results : Coverage Histogram (0-50X)



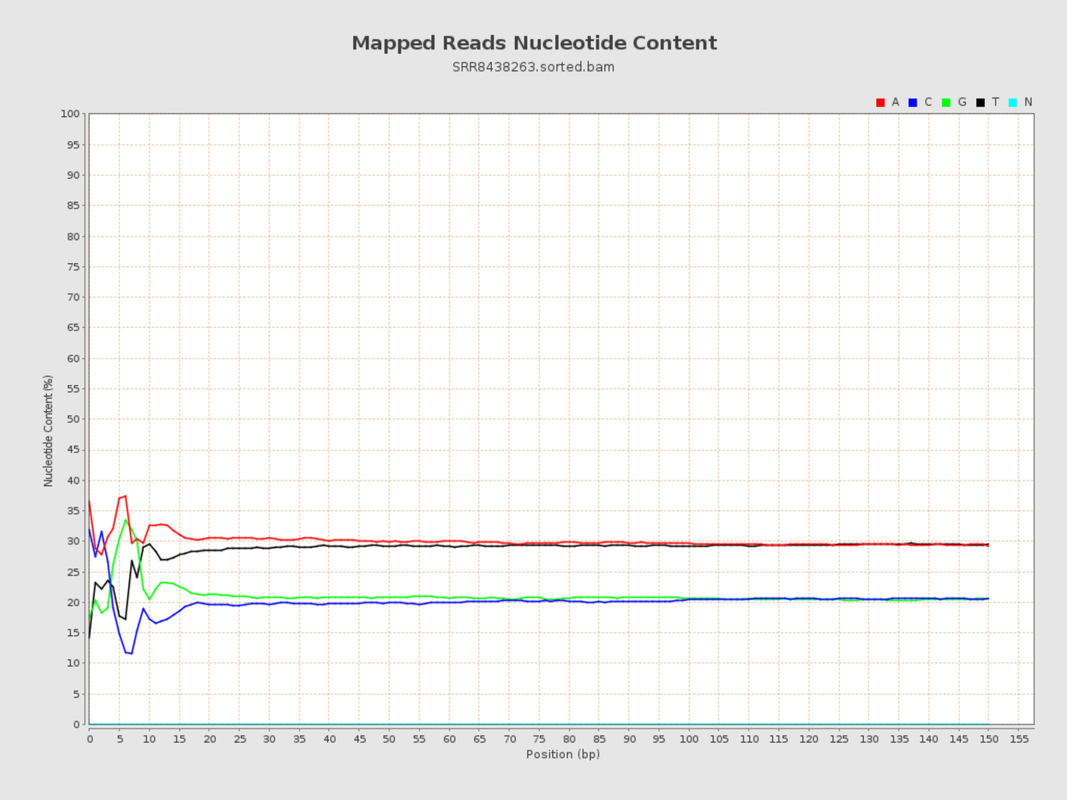
6. Results : Genome Fraction Coverage



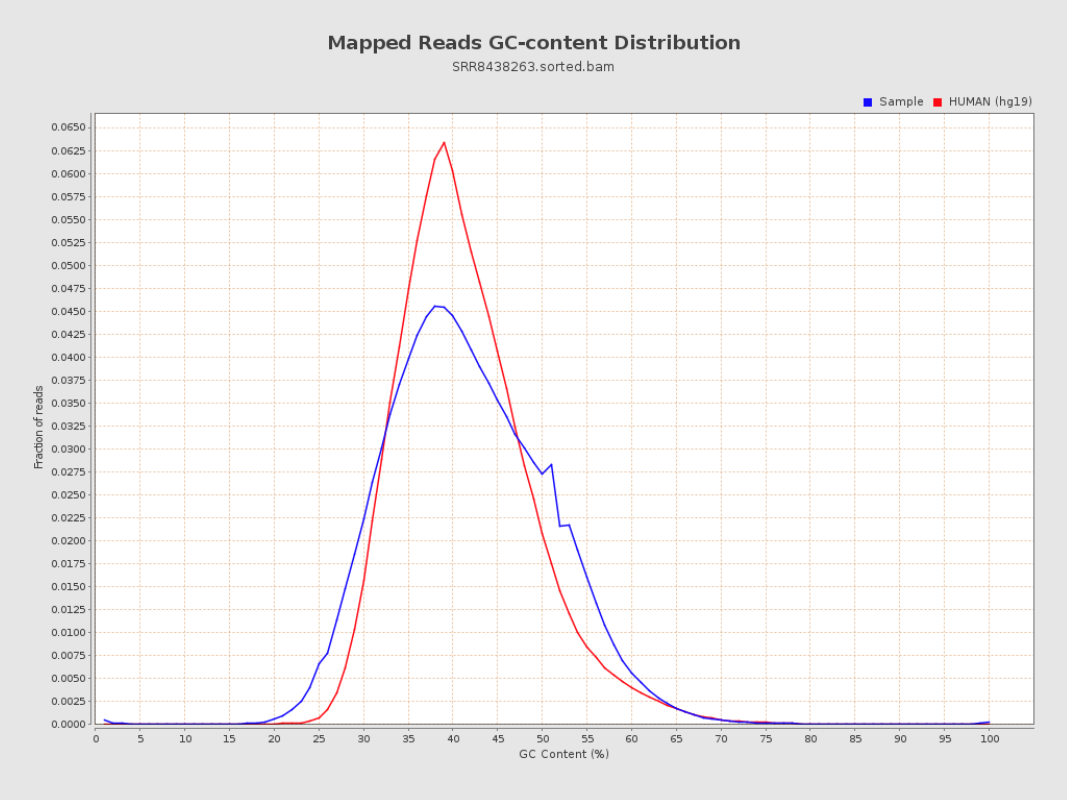
7. Results : Duplication Rate Histogram



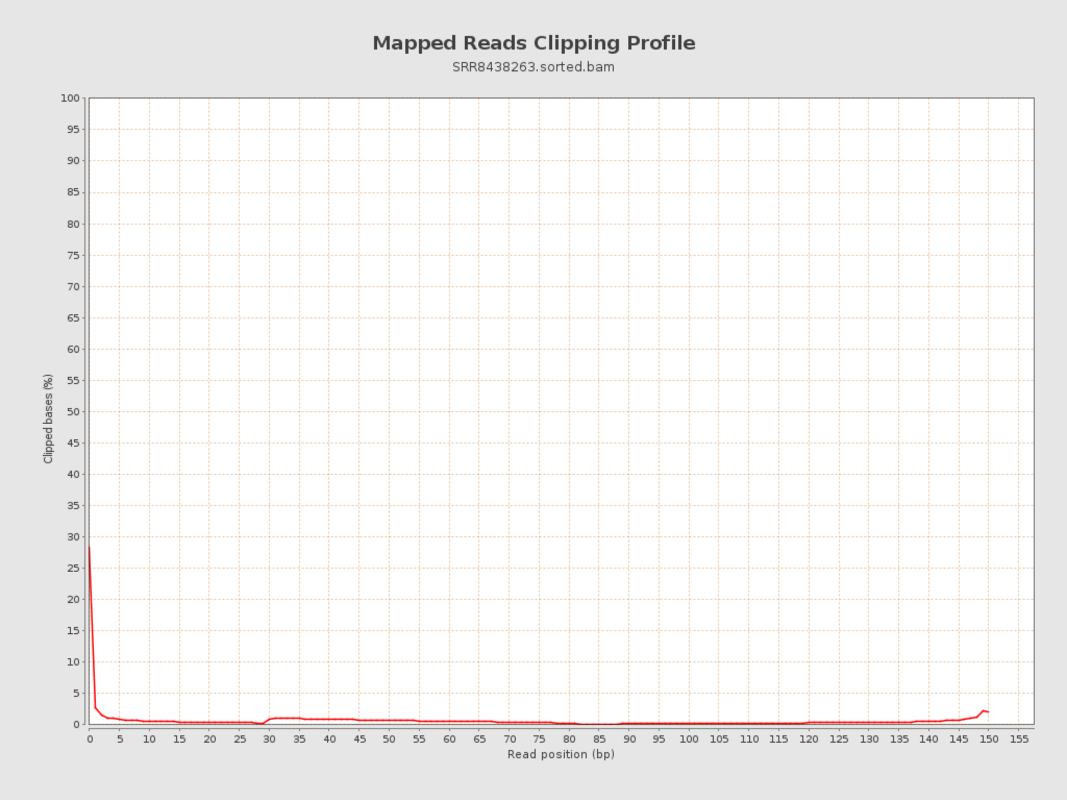
8. Results : Mapped Reads Nucleotide Content



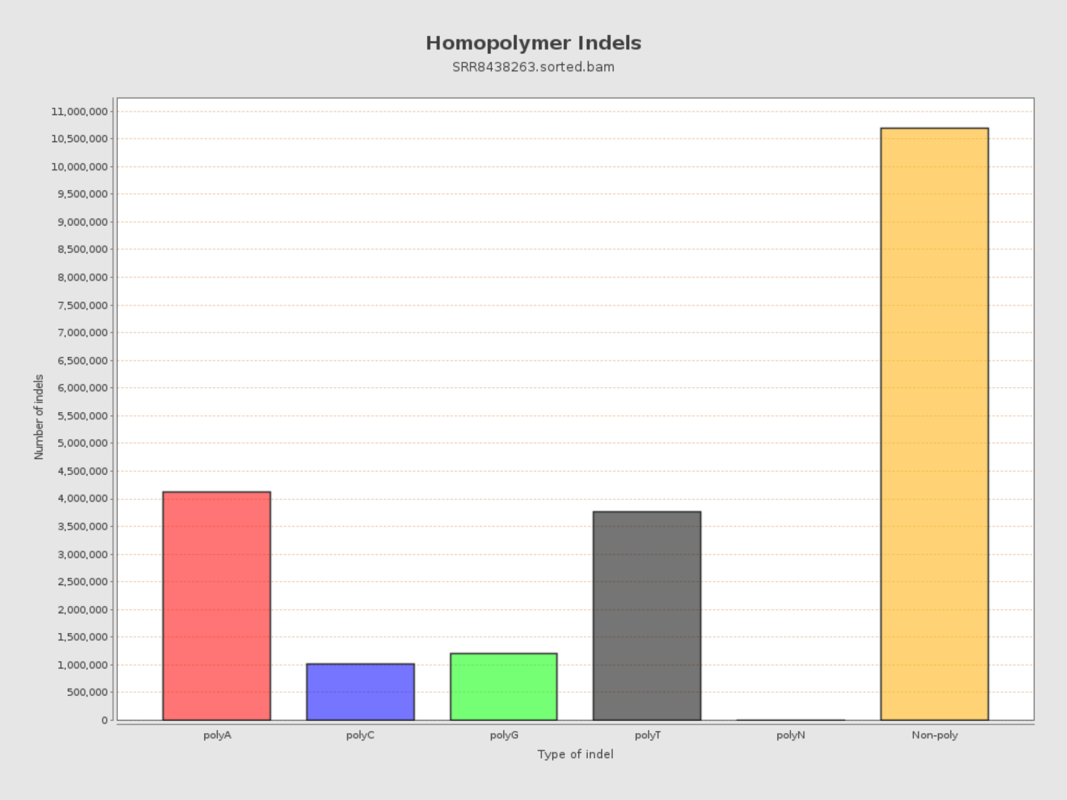
9. Results : Mapped Reads GC-content Distribution



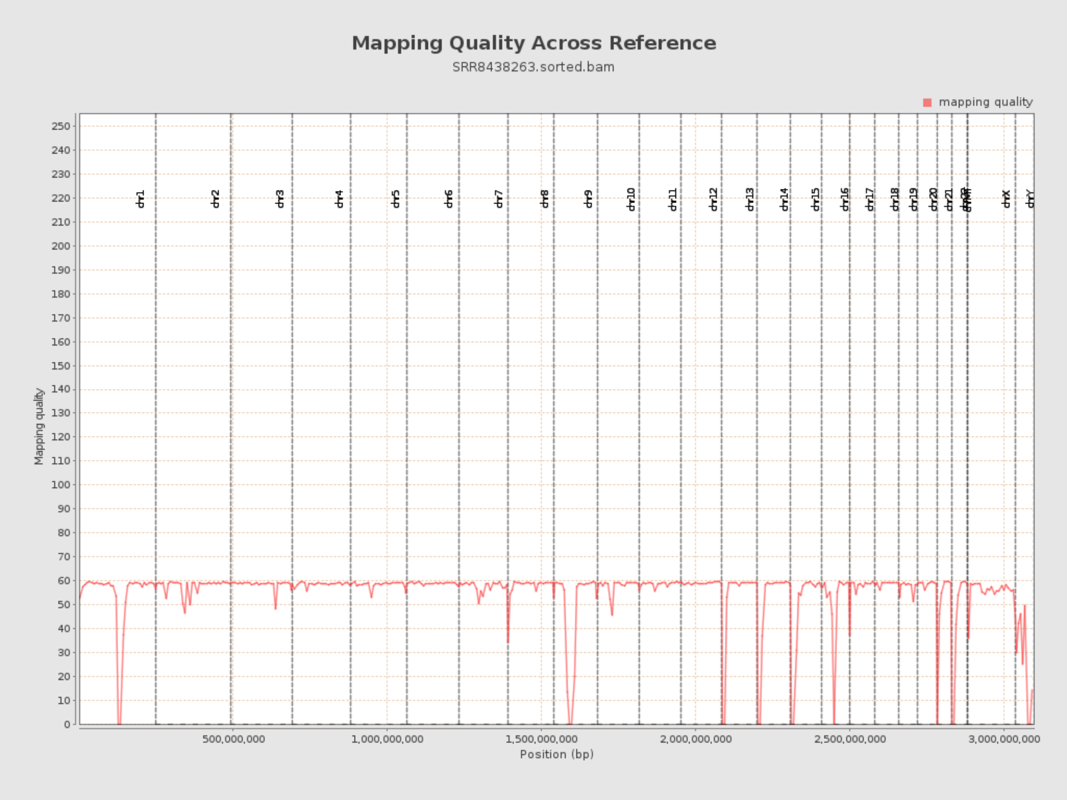
10. Results : Mapped Reads Clipping Profile



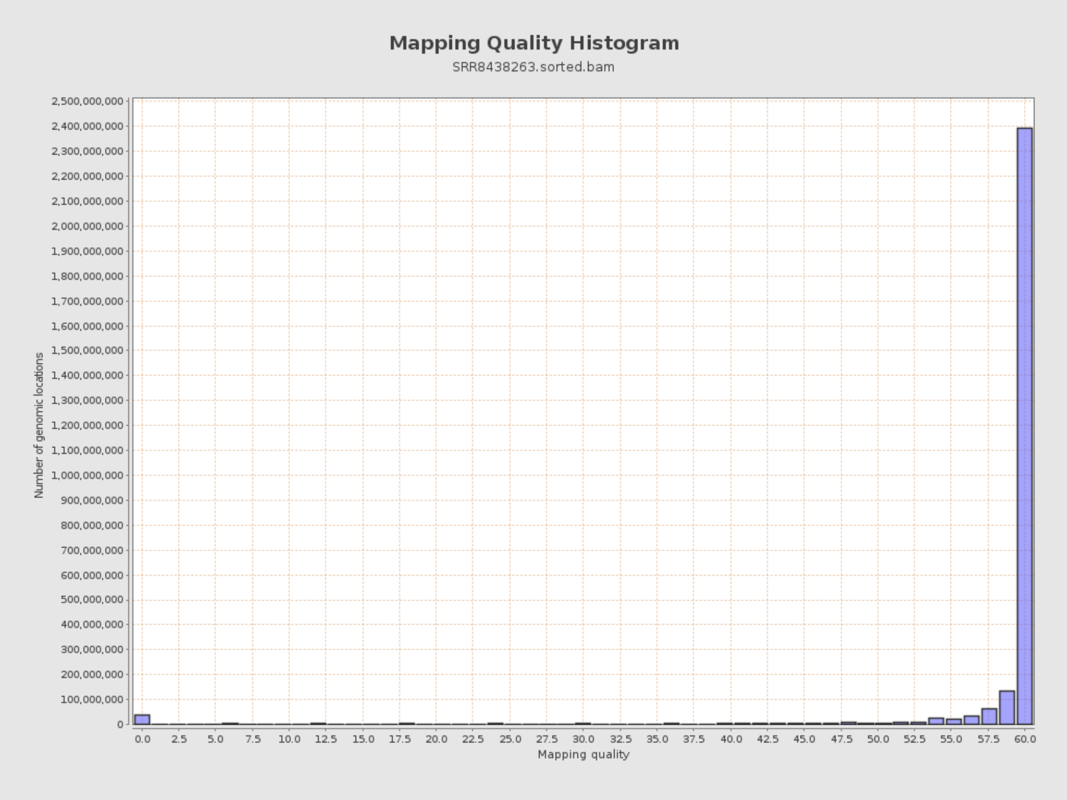
11. Results : Homopolymer Indels



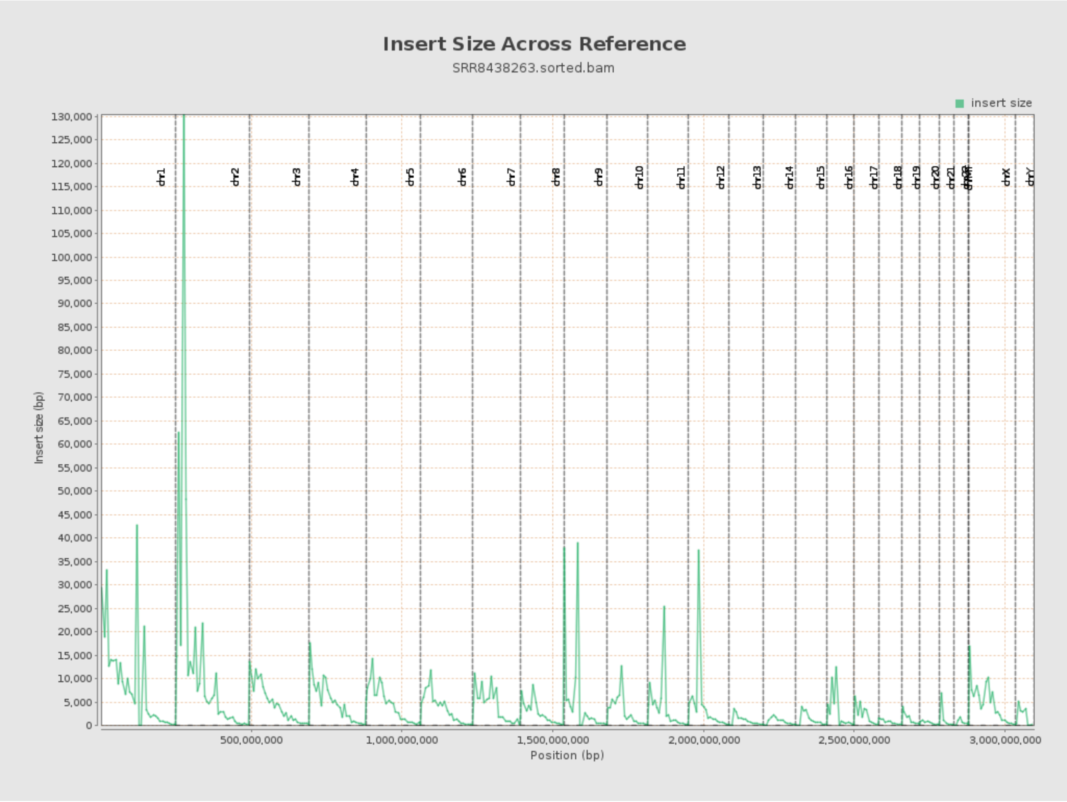
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram