Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 13:50:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438258.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_SRR8438258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438258_1.fastq.gz SRR8438258_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 13:50:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	795,555,712
Mapped reads	791,315,274 / 99.47%
Unmapped reads	4,240,438 / 0.53%
Mapped paired reads	791,315,274 / 99.47%
Mapped reads, first in pair	395,946,177 / 49.77%
Mapped reads, second in pair	395,369,097 / 49.7%
Mapped reads, both in pair	788,636,222 / 99.13%
Mapped reads, singletons	2,679,052 / 0.34%
Secondary alignments	0
Supplementary alignments	21,389,618 / 2.69%
Read min/max/mean length	30 / 149 / 143.21
Duplicated reads (estimated)	336,327,076 / 42.28%
Duplication rate	37.49%
Clipped reads	109,605,187 / 13.78%

2.2. ACGT Content

Number/percentage of A's	34,525,586,764 / 30.81%
Number/percentage of C's	21,165,175,052 / 18.89%
Number/percentage of T's	32,522,388,832 / 29.03%
Number/percentage of G's	23,828,574,973 / 21.27%
Number/percentage of N's	205,690 / 0%

GC Percentage	40.16%

2.3. Coverage

Mean	36.2044
Standard Deviation	109.517

2.4. Mapping Quality

Mean Mapping Quality	54.26

2.5. Insert size

Mean	107,086.39
Standard Deviation	3,155,936.67
P25/Median/P75	383 / 456 / 573

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	629,661,965
Insertions	14,916,622
Mapped reads with at least one insertion	1.84%
Deletions	13,203,981
Mapped reads with at least one deletion	1.62%
Homopolymer indels	48.05%

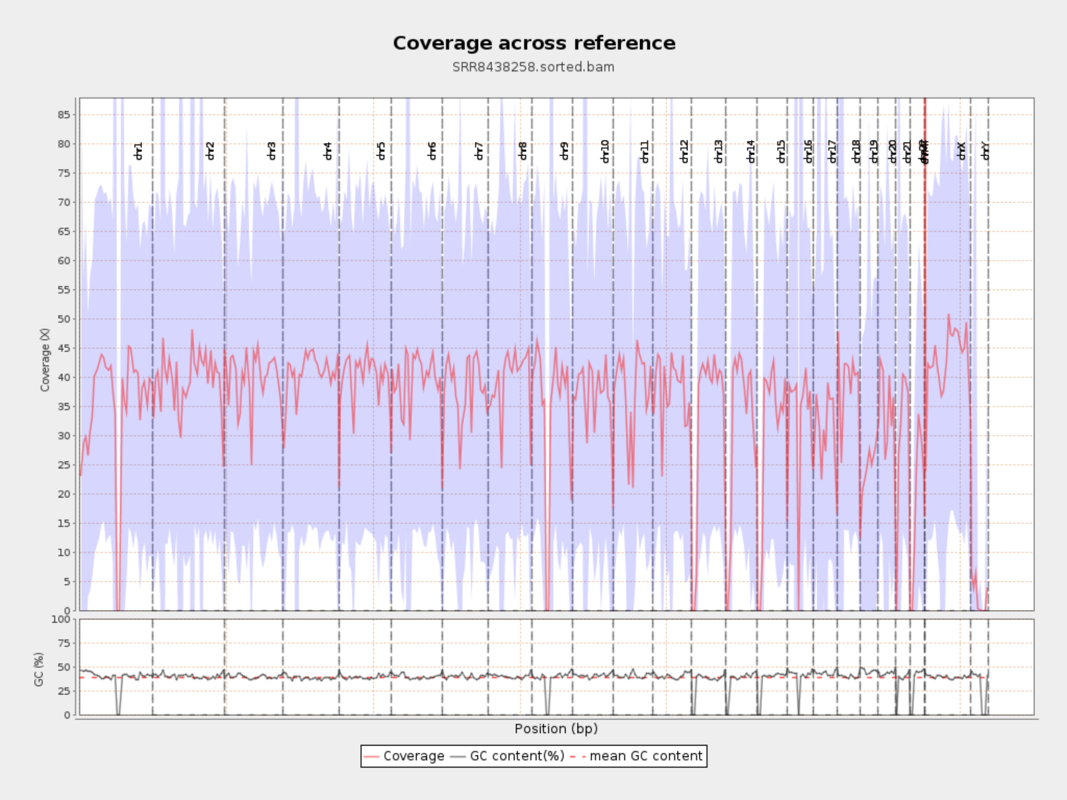
2.7. Chromosome stats

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

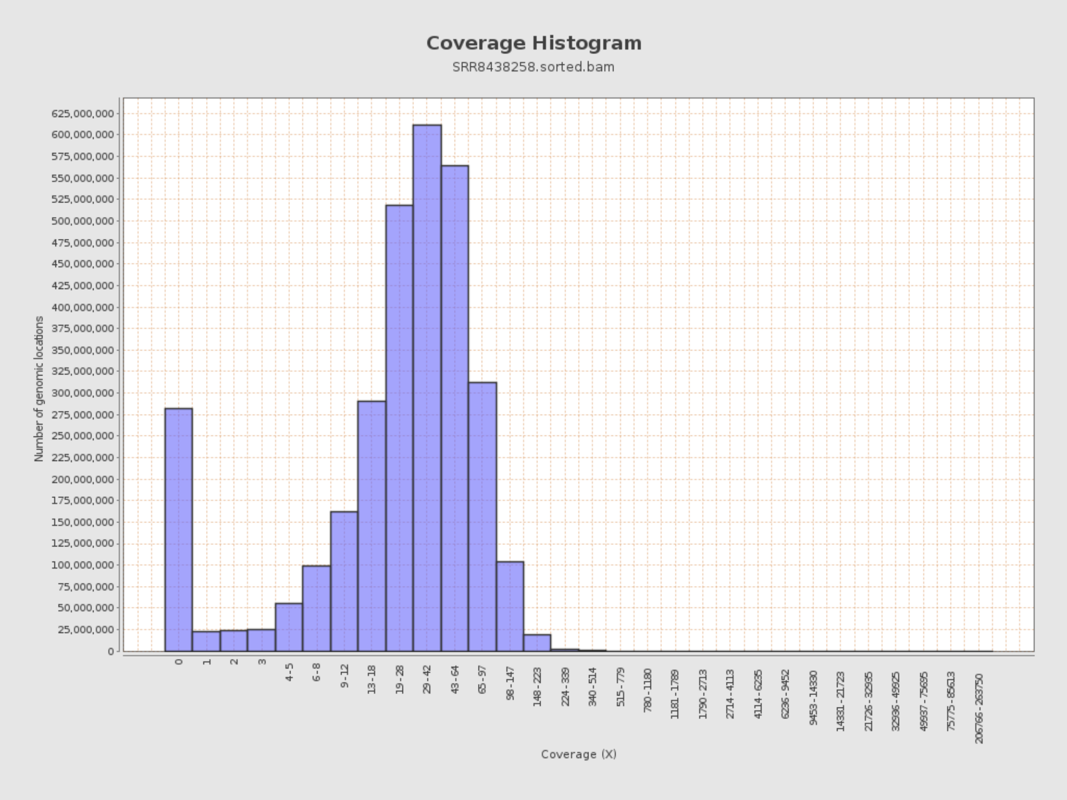
		bases	coverage	deviation
chr1	249250621	8768719346	35.1803	45.5059
chr2	243199373	9614548624	39.5336	198.5419
chr3	198022430	7867800981	39.7319	29.4025
chr4	191154276	7787688814	40.7403	38.6569
chr5	180915260	7241461865	40.0268	29.8341
chr6	171115067	6835543124	39.9471	40.1154
chr7	159138663	5994378888	37.6676	32.2598
chr8	146364022	5794037798	39.5865	34.1679
chr9	141213431	4785897174	33.8912	56.8642
chr10	135534747	5068879271	37.3991	82.6143
chr11	135006516	5065814488	37.5227	32.7396
chr12	133851895	5039779116	37.6519	31.1218
chr13	115169878	3854136655	33.4648	30.0634
chr14	107349540	3392746646	31.6047	31.0151
chr15	102531392	3081340801	30.0527	30.1171
chr16	90354753	2900242663	32.0984	91.2572
chr17	81195210	2484429459	30.5982	52.3548
chr18	78077248	3068771028	39.3043	69.1213
chr19	59128983	1440595196	24.3636	32.5748
chr20	63025520	2142254721	33.9903	34.3824
chr21	48129895	1482612459	30.8044	48.6261
chr22	51304566	968794479	18.8832	26.3739
chrMT	16571	564258015	34,050.9333	12,626.7414
chrX	155270560	6685307396	43.0559	33.3801

chrY	59373566	147795307	2.4892	39.5558

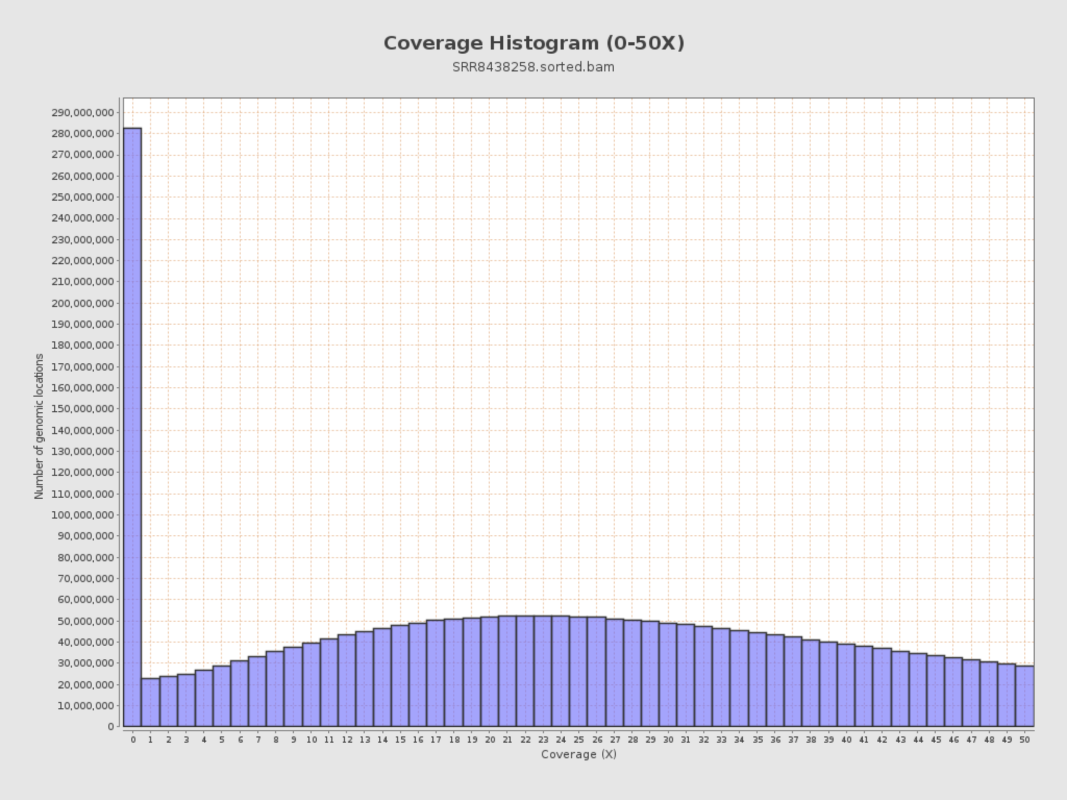
3. Results : Coverage across reference



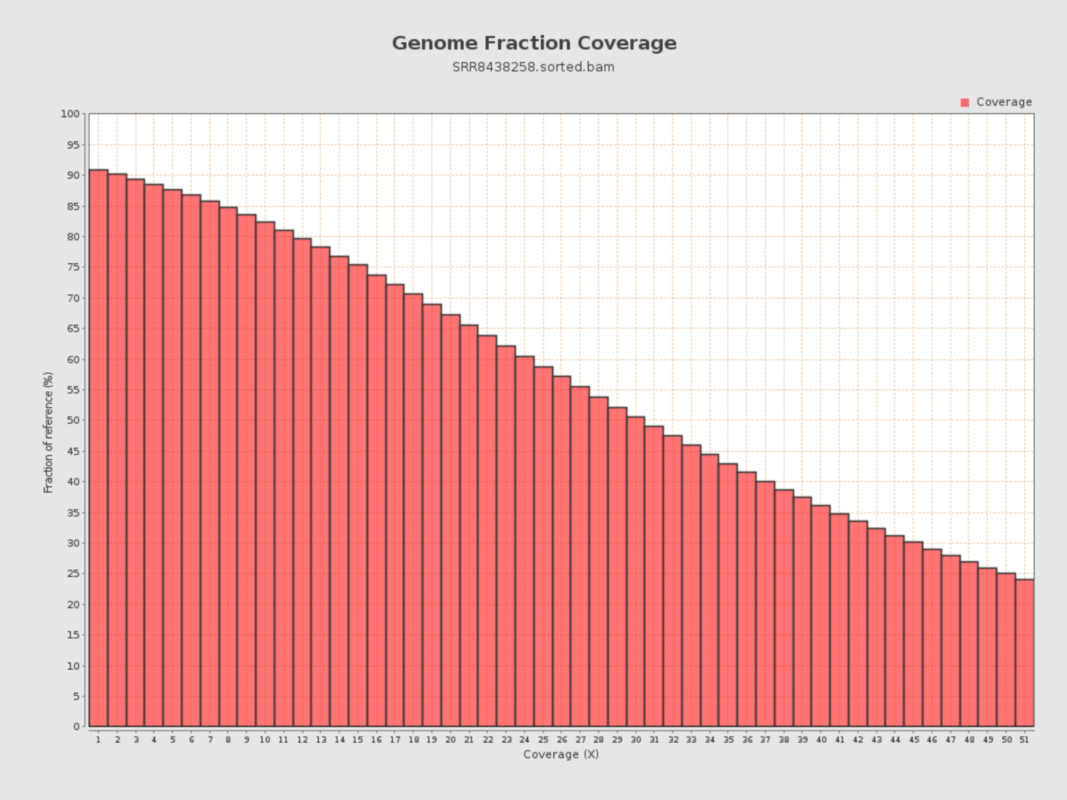
4. Results : Coverage Histogram



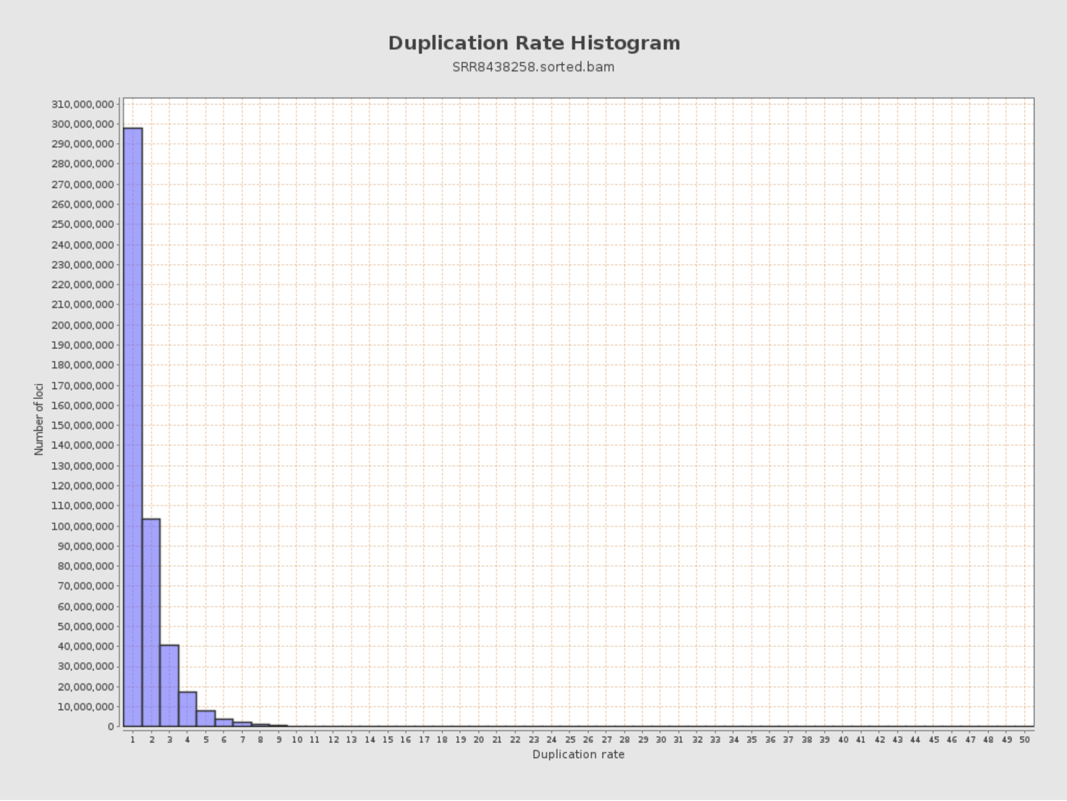
5. Results : Coverage Histogram (0-50X)



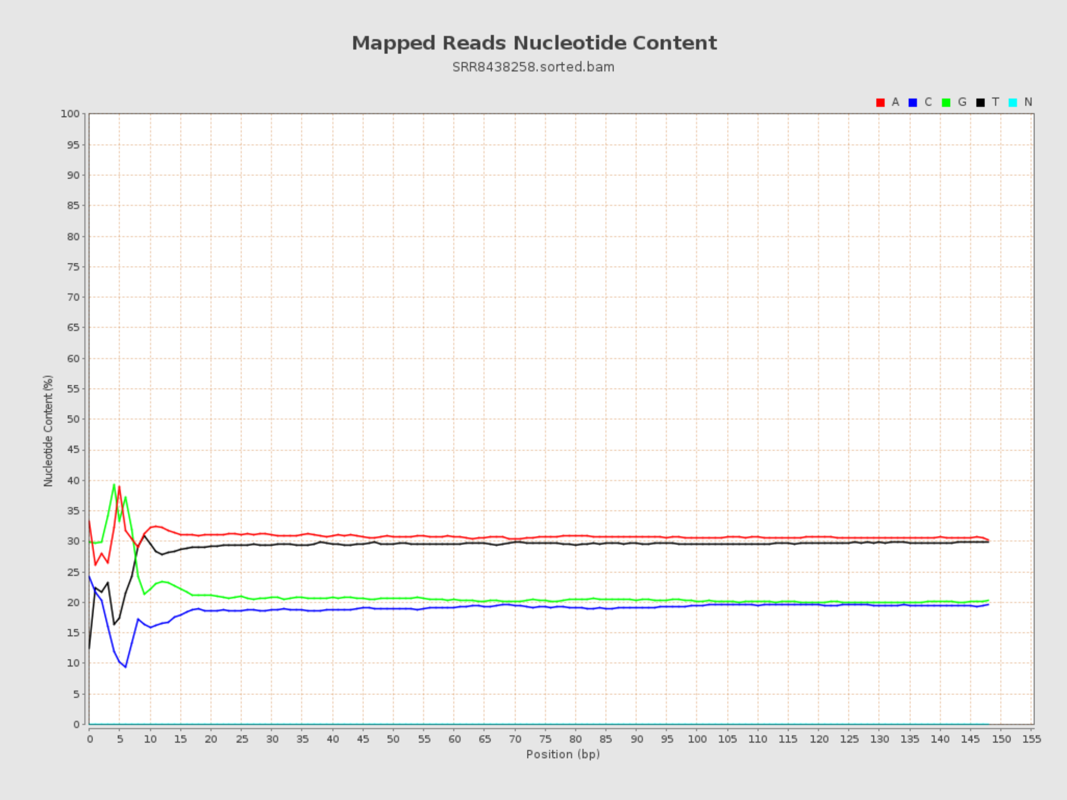
6. Results : Genome Fraction Coverage



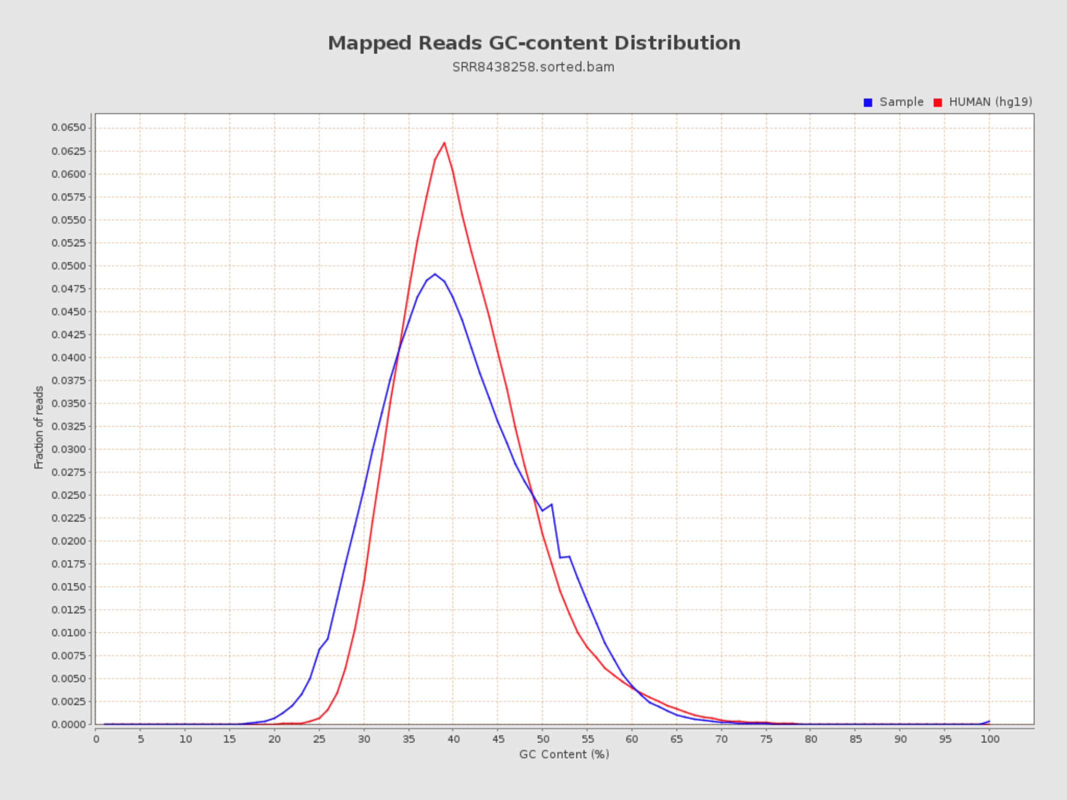
7. Results : Duplication Rate Histogram



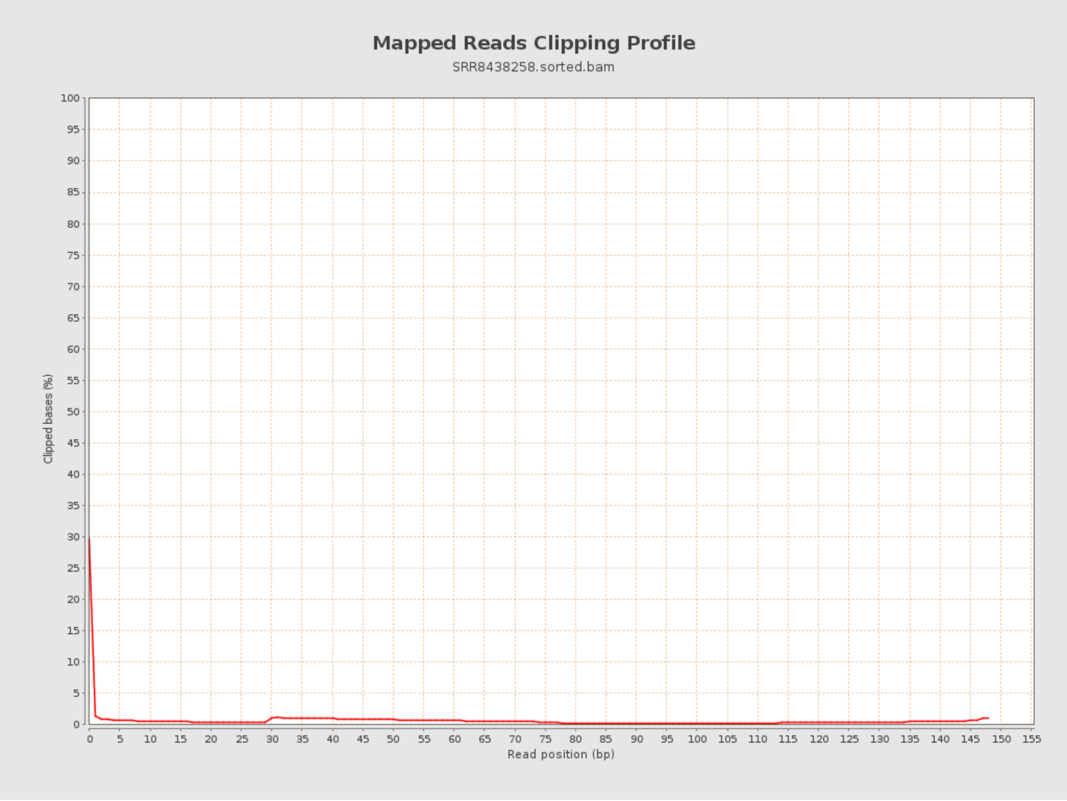
8. Results : Mapped Reads Nucleotide Content



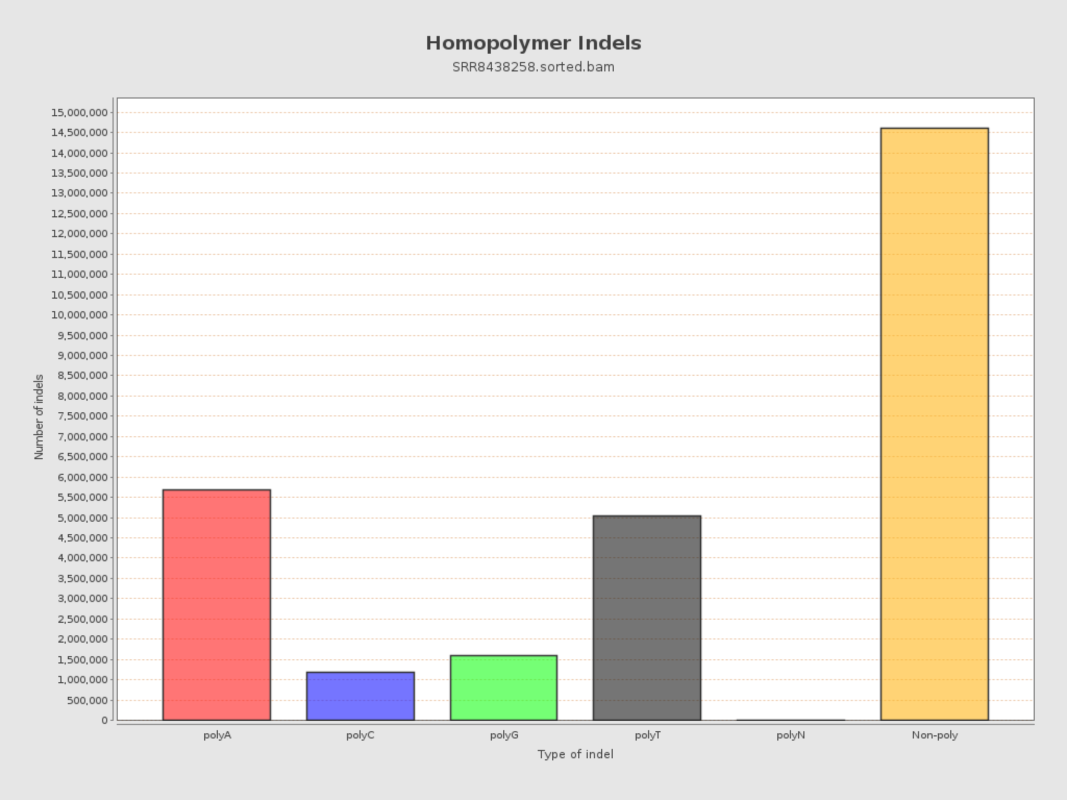
9. Results : Mapped Reads GC-content Distribution



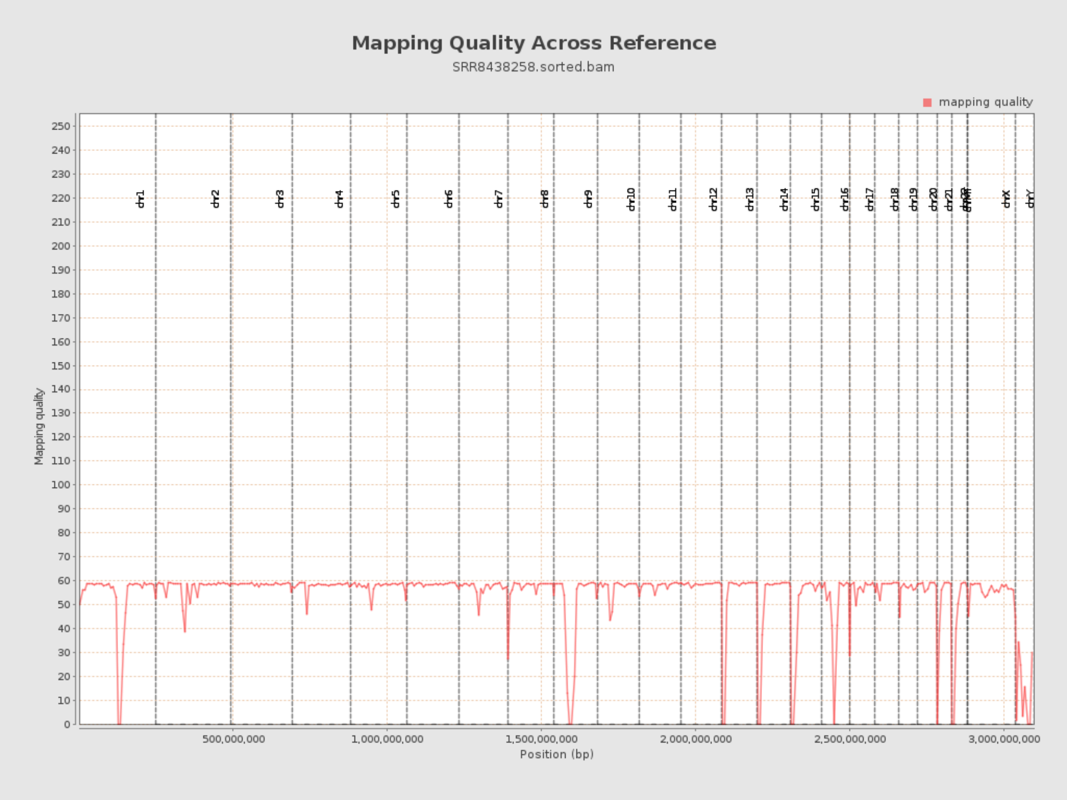
10. Results : Mapped Reads Clipping Profile



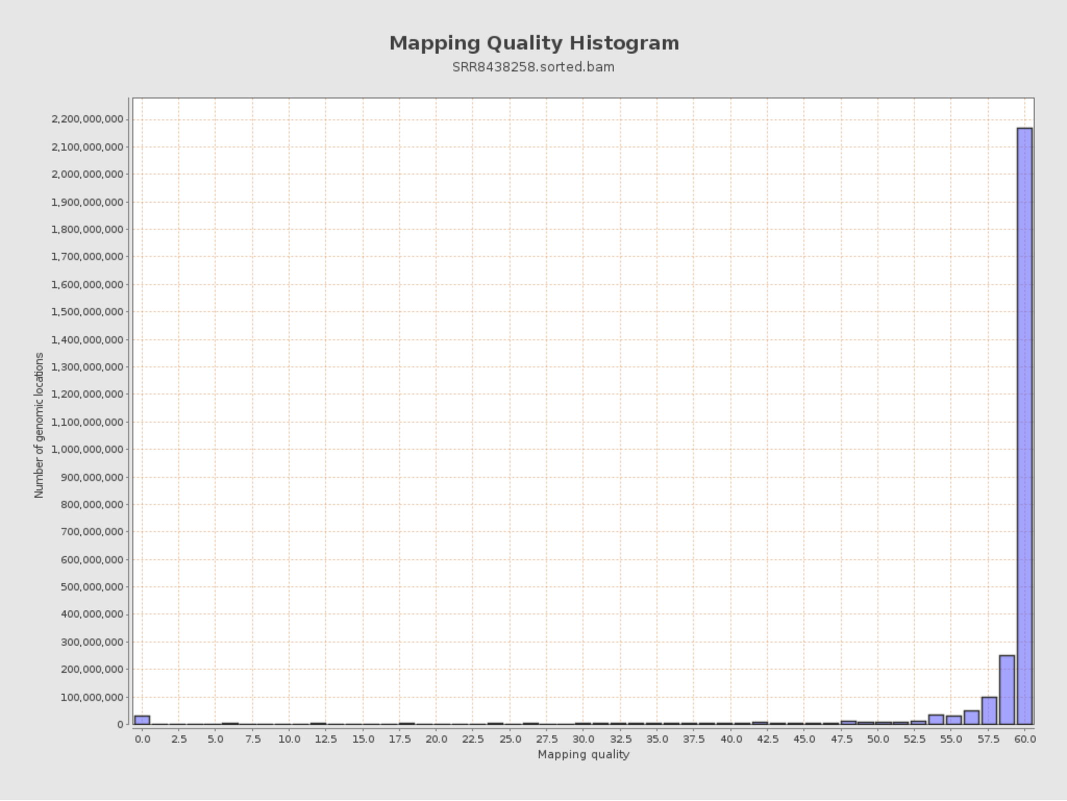
11. Results : Homopolymer Indels



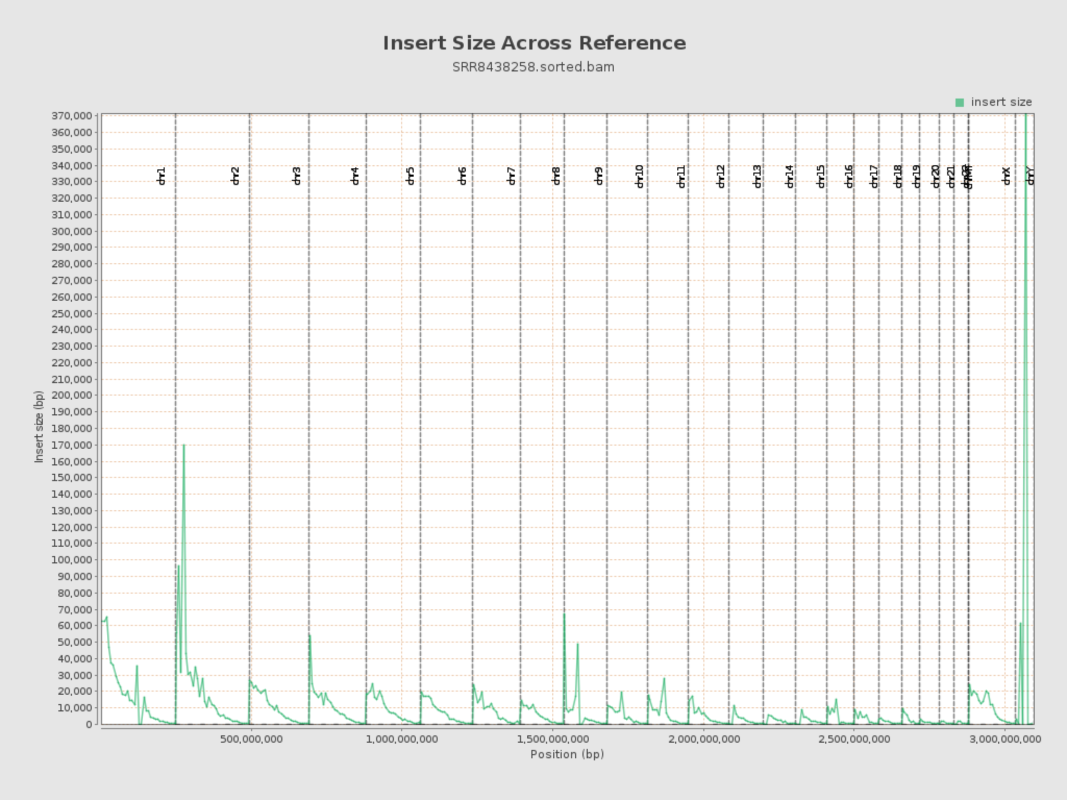
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram