Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 01:57:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438252.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_SRR8438252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438252_1.fastq.gz SRR8438252_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 01:57:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	787,729,130
Mapped reads	783,272,873 / 99.43%
Unmapped reads	4,456,257 / 0.57%
Mapped paired reads	783,272,873 / 99.43%
Mapped reads, first in pair	391,985,990 / 49.76%
Mapped reads, second in pair	391,286,883 / 49.67%
Mapped reads, both in pair	780,481,608 / 99.08%
Mapped reads, singletons	2,791,265 / 0.35%
Secondary alignments	0
Supplementary alignments	21,233,256 / 2.7%
Read min/max/mean length	30 / 149 / 142.94
Duplicated reads (estimated)	335,540,317 / 42.6%
Duplication rate	37.78%
Clipped reads	109,820,023 / 13.94%

2.2. ACGT Content

Number/percentage of A's	34,072,881,211 / 30.78%
Number/percentage of C's	20,930,199,869 / 18.91%
Number/percentage of T's	32,091,985,284 / 28.99%
Number/percentage of G's	23,595,183,800 / 21.32%
Number/percentage of N's	204,556 / 0%

GC Percentage	40.23%

2.3. Coverage

Mean	35.7677
Standard Deviation	126.6405

2.4. Mapping Quality

Mean Mapping Quality	54.25

2.5. Insert size

Mean	112,445.8
Standard Deviation	3,250,794.31
P25/Median/P75	386 / 462 / 586

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	619,500,423
Insertions	14,627,632
Mapped reads with at least one insertion	1.82%
Deletions	12,997,456
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.03%

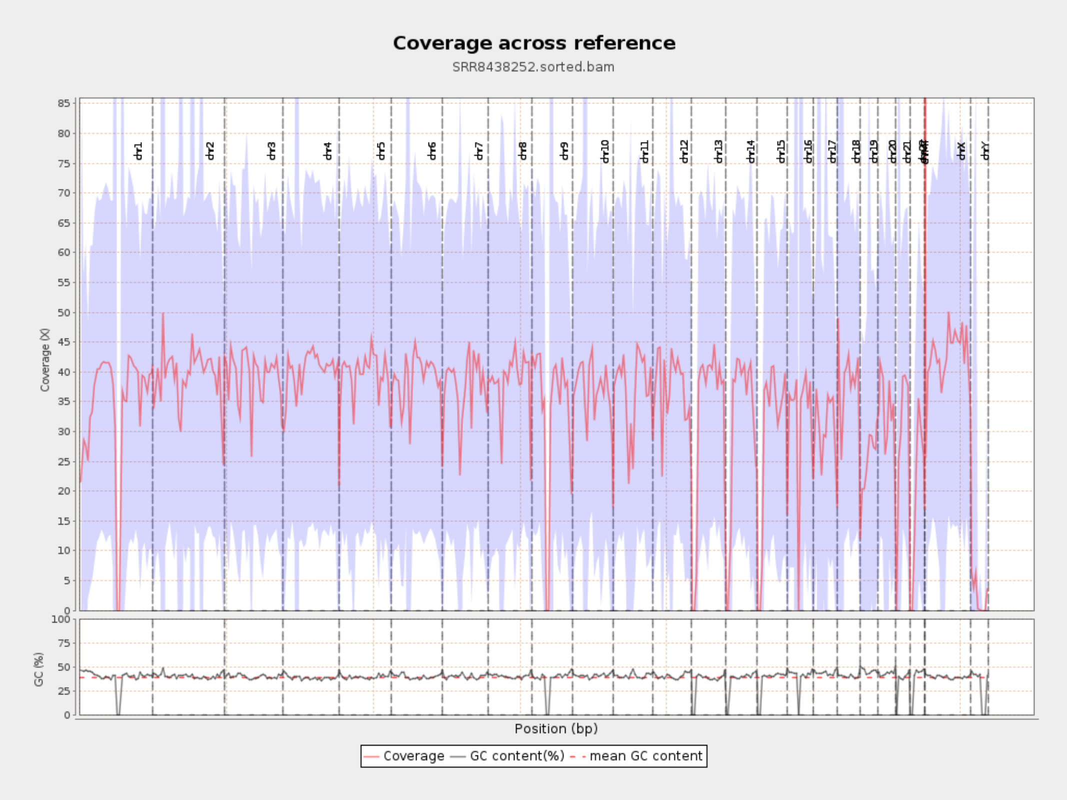
2.7. Chromosome stats

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

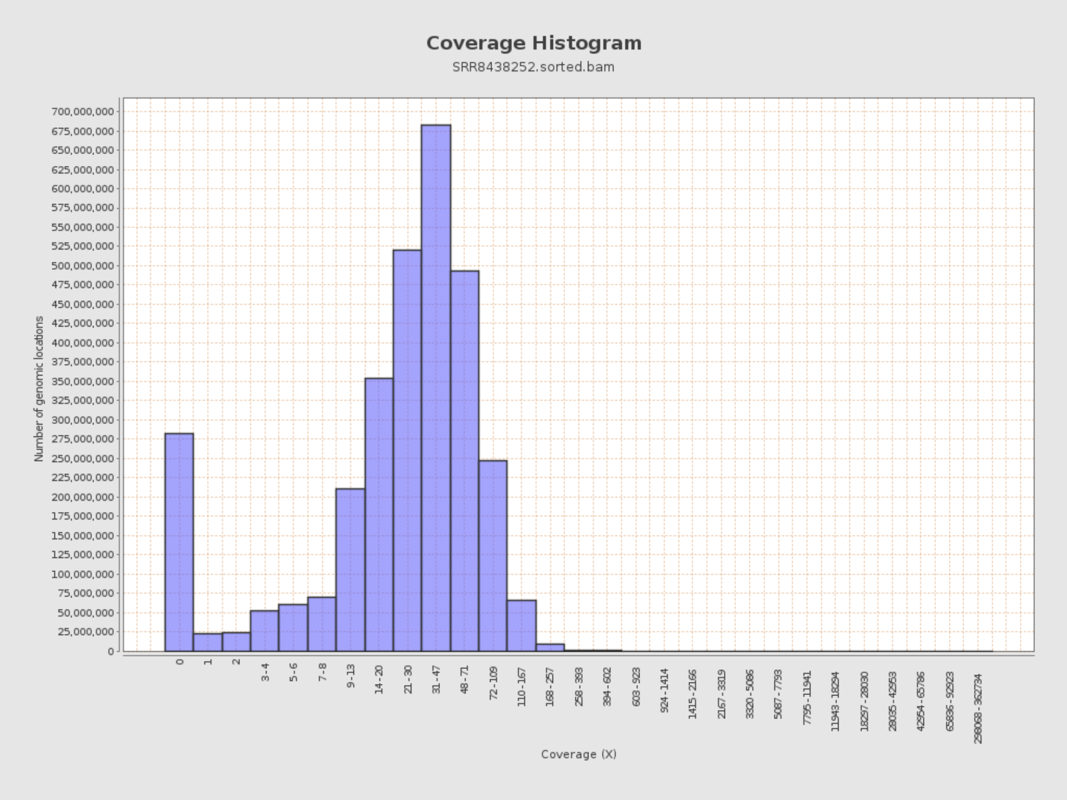
		bases	**coverage**	**deviation**
chr1	249250621	8606200123	34.5283	46.0053
chr2	243199373	9597691432	39.4643	271.1456
chr3	198022430	7799175257	39.3853	28.8413
chr4	191154276	7710419573	40.3361	39.2909
chr5	180915260	7130624538	39.4142	29.2937
chr6	171115067	6719772958	39.2705	35.1567
chr7	159138663	5935811489	37.2996	31.6224
chr8	146364022	5623103782	38.4186	32.2911
chr9	141213431	4660739910	33.0049	55.519
chr10	135534747	5049517877	37.2563	88.8791
chr11	135006516	4999682254	37.0329	31.9843
chr12	133851895	4994556489	37.3141	30.9164
chr13	115169878	3805505282	33.0425	29.6789
chr14	107349540	3364862423	31.3449	30.5582
chr15	102531392	3013277142	29.3888	29.2375
chr16	90354753	2841614503	31.4495	89.1703
chr17	81195210	2461396174	30.3145	48.8715
chr18	78077248	3003531693	38.4687	66.7839
chr19	59128983	1471944737	24.8938	33.6802
chr20	63025520	2100088915	33.3212	32.7704
chr21	48129895	1436807106	29.8527	46.753
chr22	51304566	1011305761	19.7118	27.5501
chrMT	16571	617994056	37,293.7093	13,721.8991
chrX	155270560	6627658095	42.6846	32.9524

chrY	59373566	142502537	2.4001	38.7692

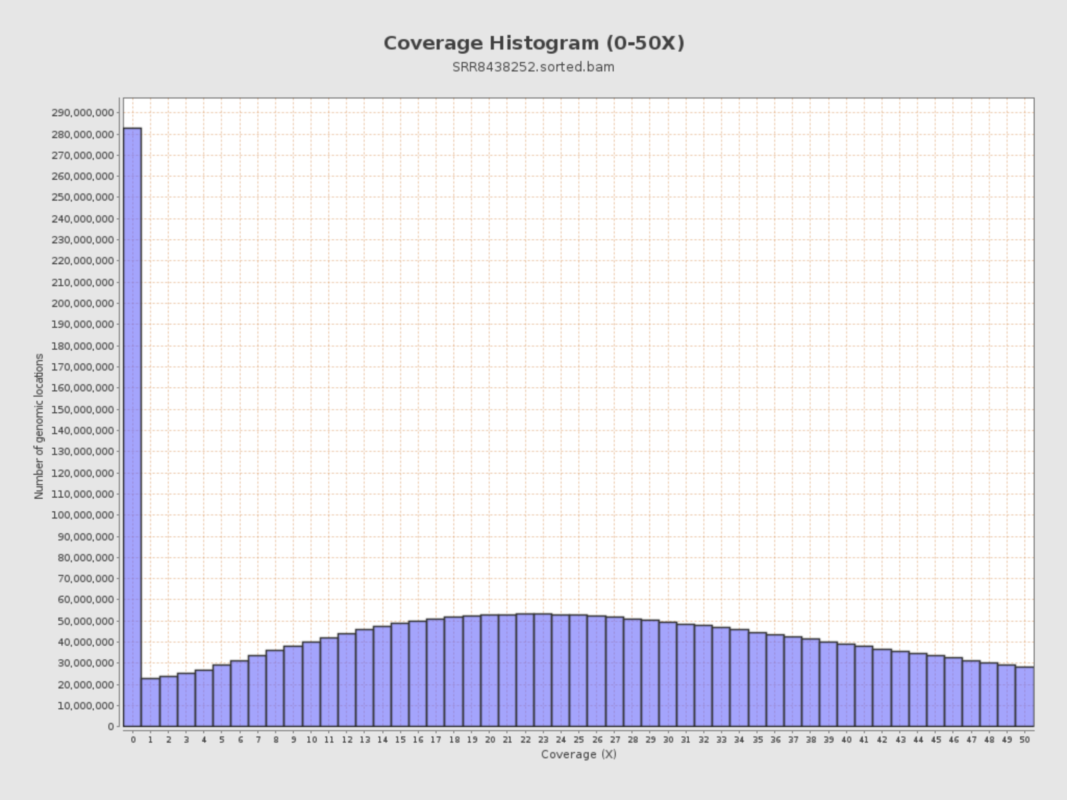
3. Results : Coverage across reference



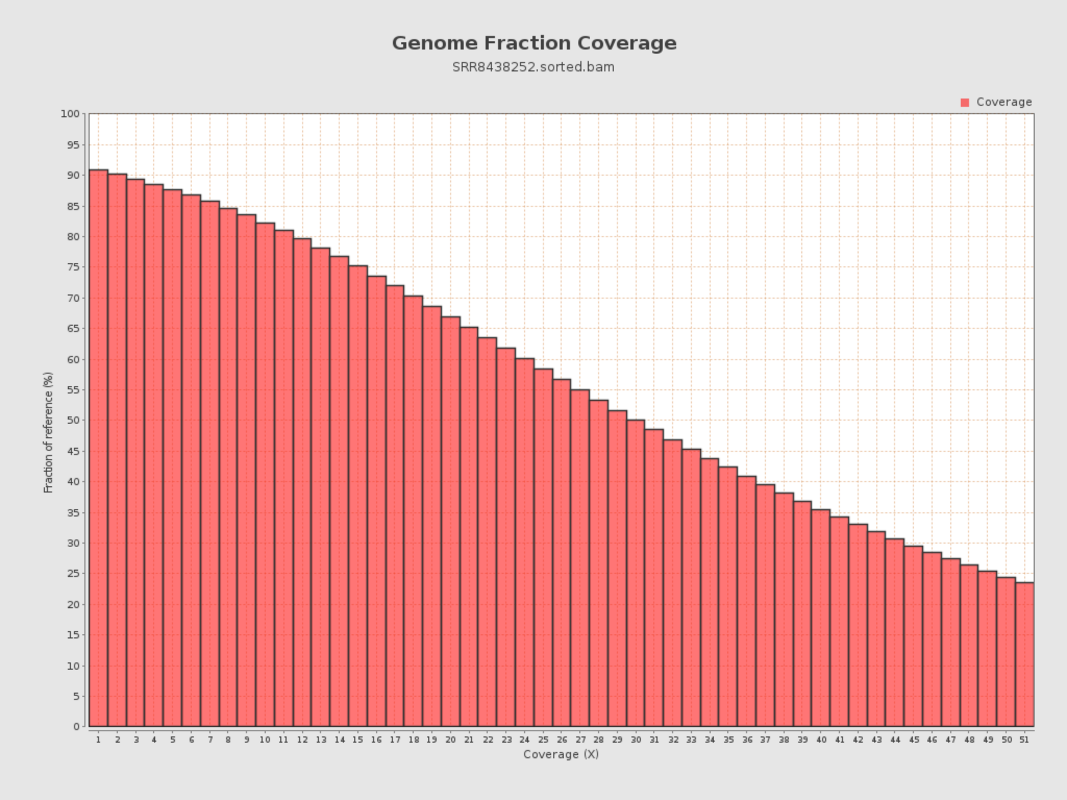
4. Results : Coverage Histogram



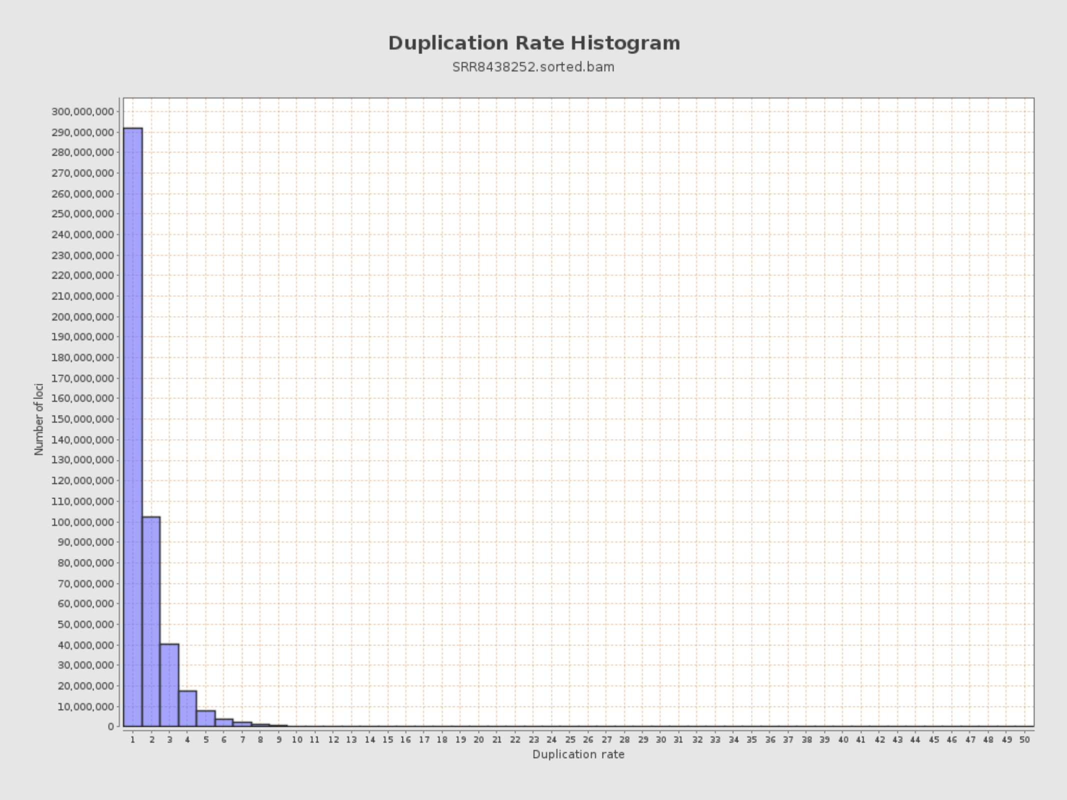
5. Results : Coverage Histogram (0-50X)



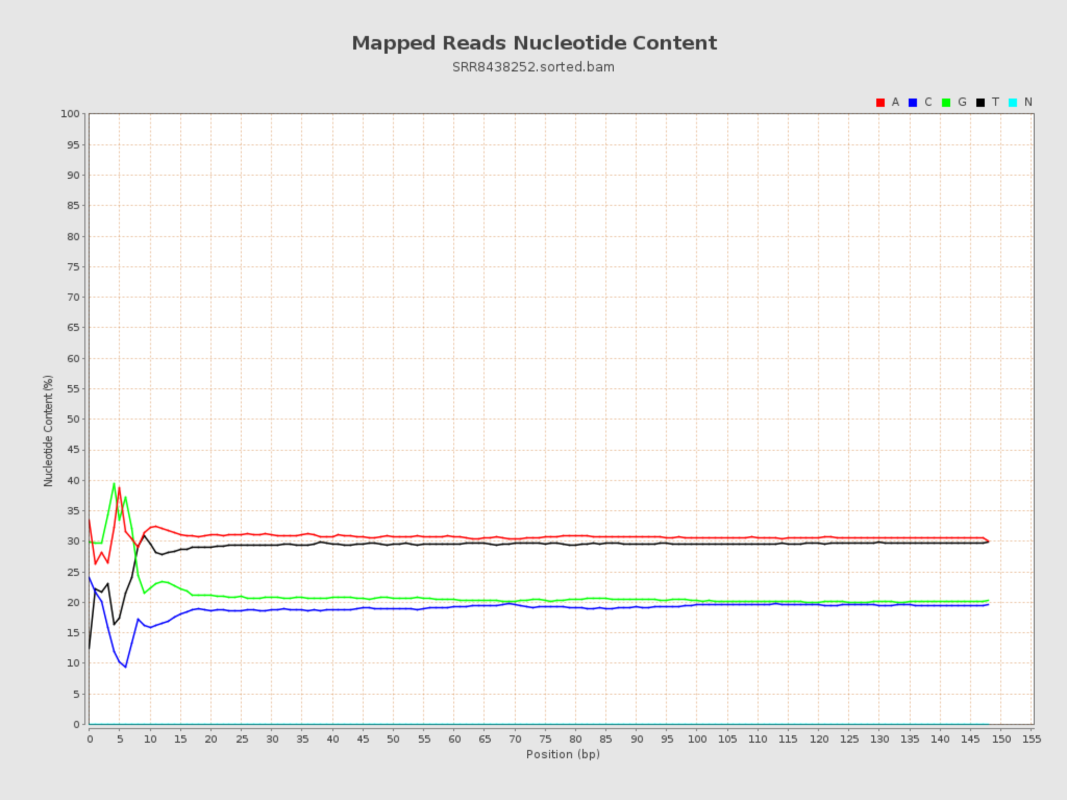
6. Results : Genome Fraction Coverage



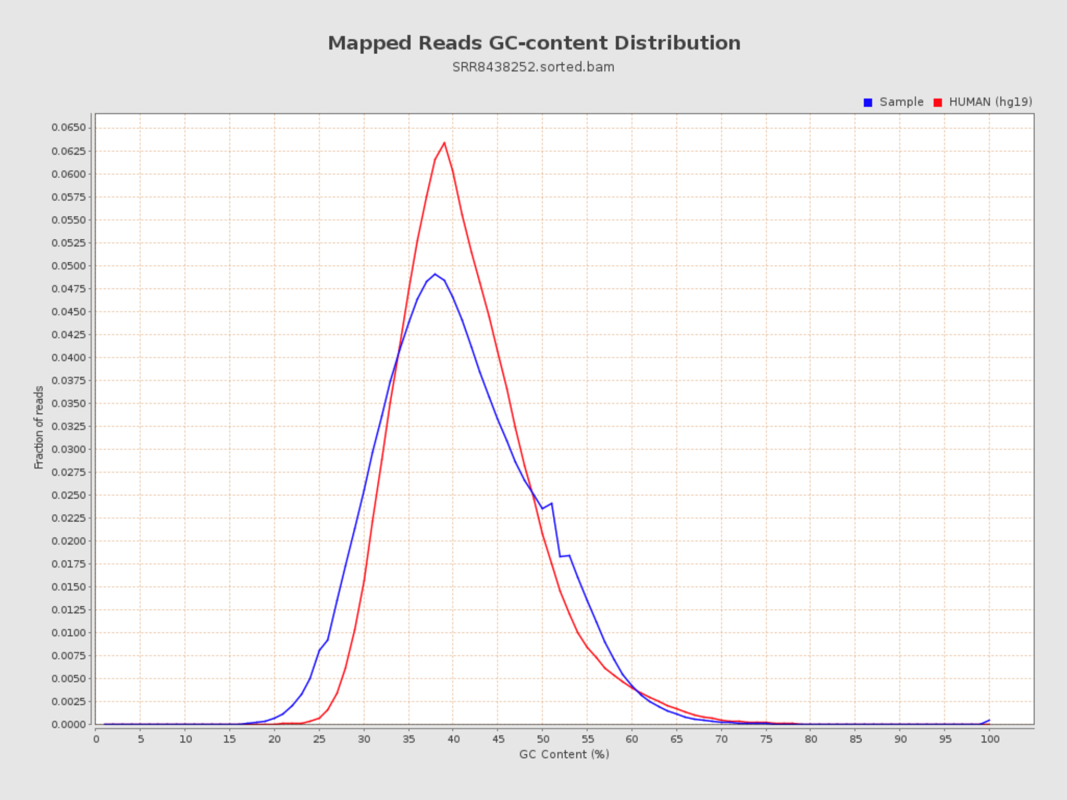
7. Results : Duplication Rate Histogram



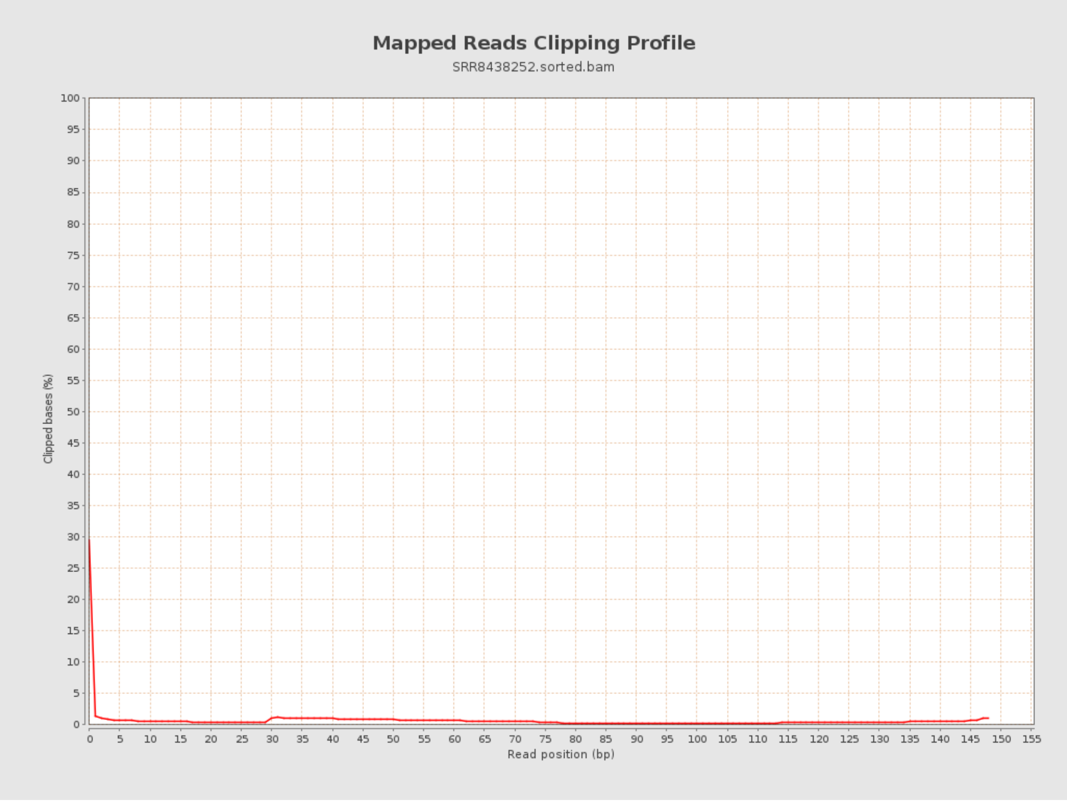
8. Results : Mapped Reads Nucleotide Content



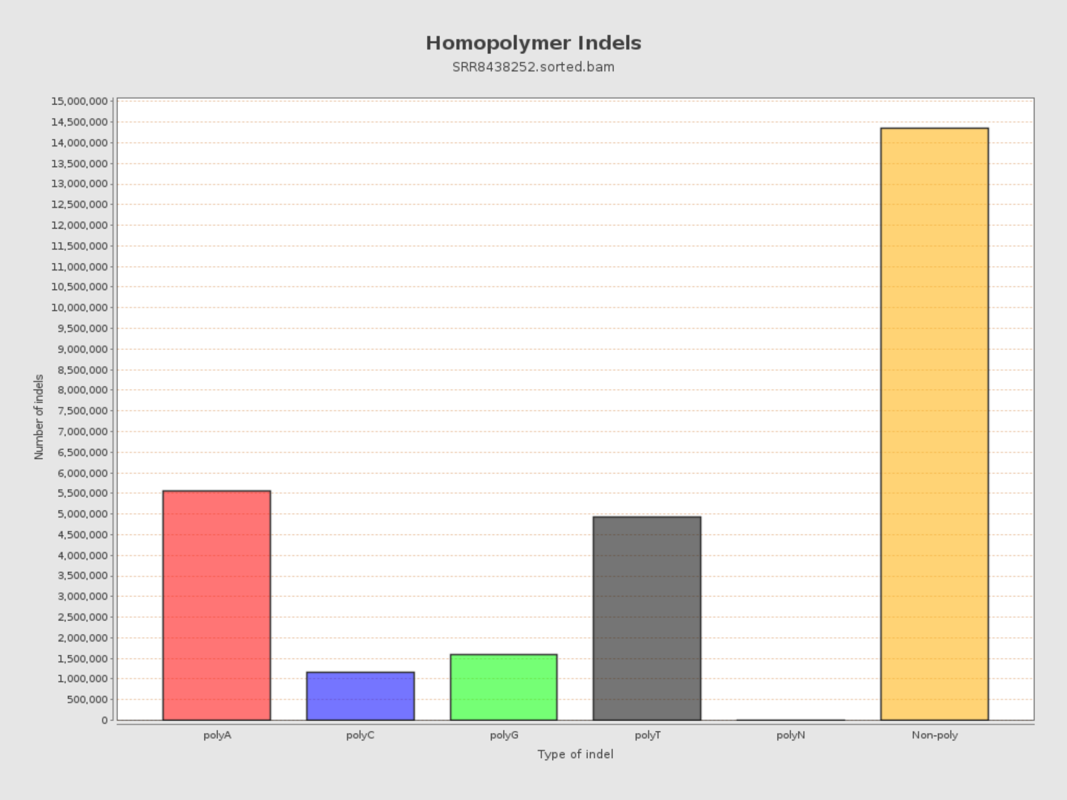
9. Results : Mapped Reads GC-content Distribution



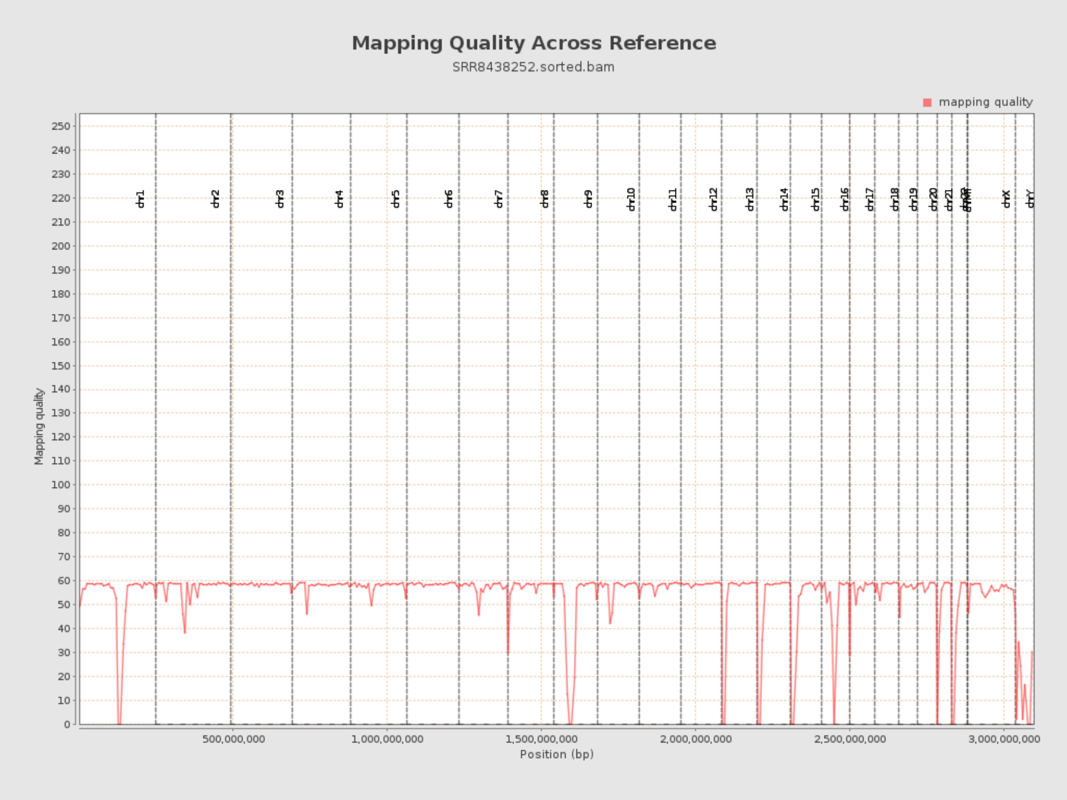
10. Results : Mapped Reads Clipping Profile



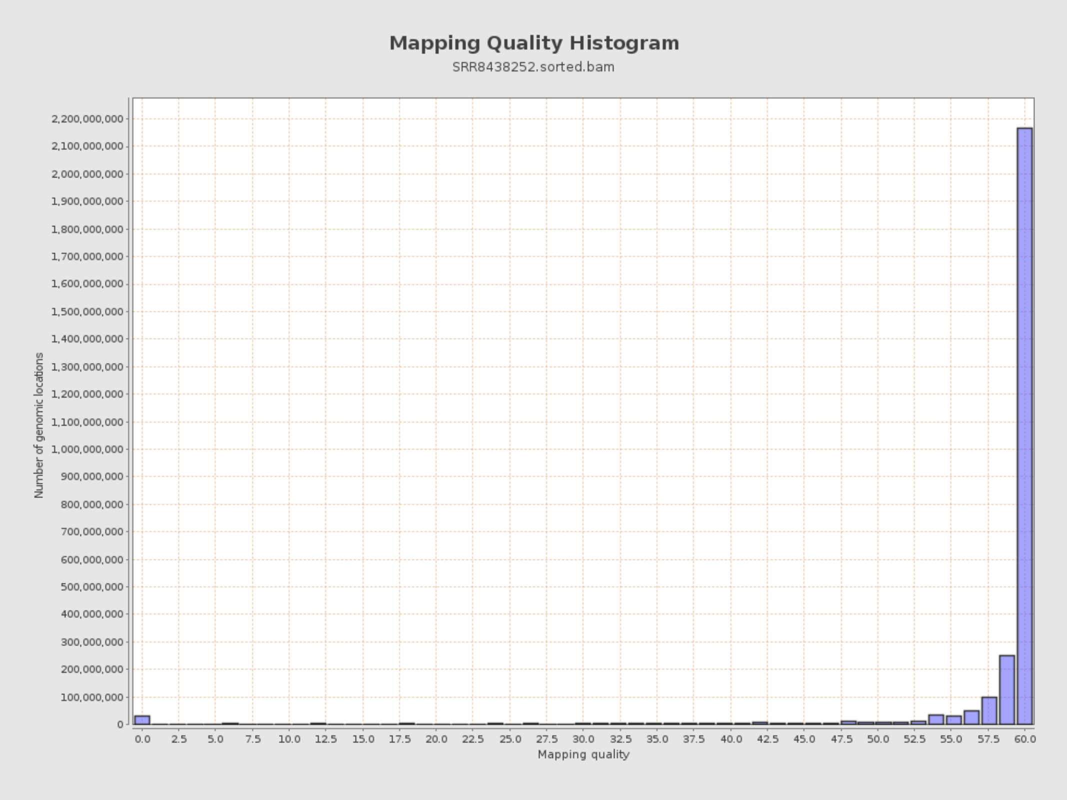
11. Results : Homopolymer Indels



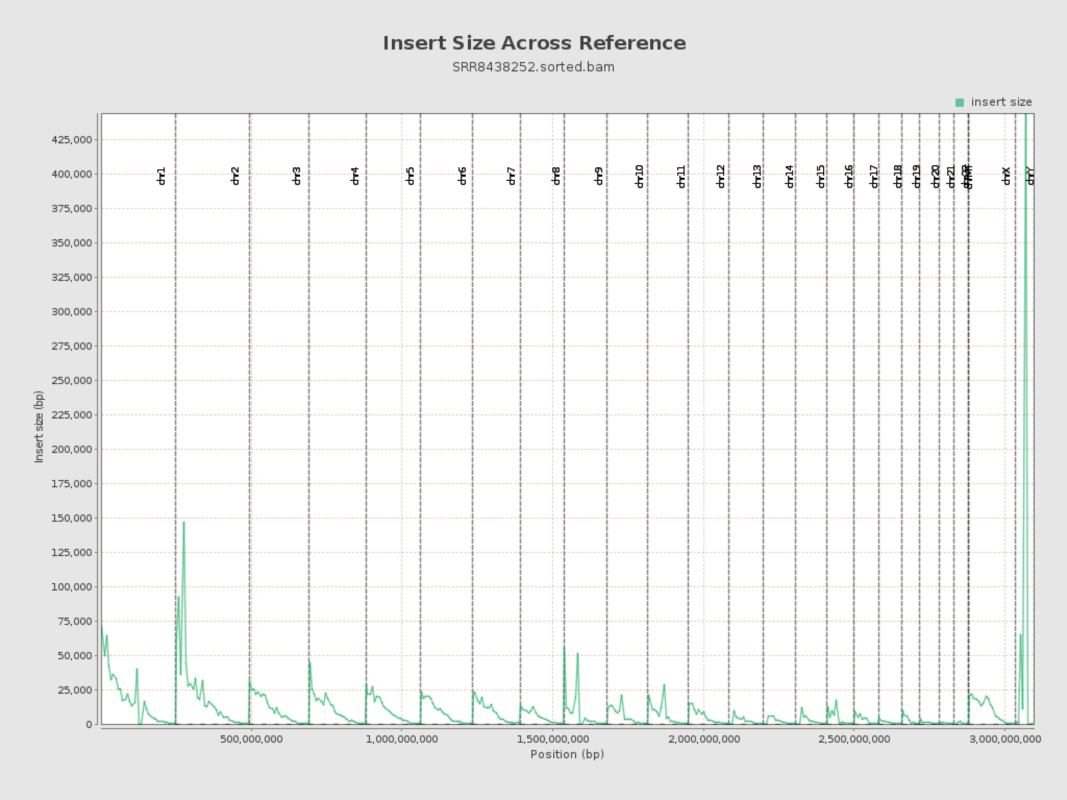
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram