Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 08:06:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438272.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_SRR8438272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438272_1.fastq.gz SRR8438272_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 08:06:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	739,091,198
Mapped reads	736,831,887 / 99.69%
Unmapped reads	2,259,311 / 0.31%
Mapped paired reads	736,831,887 / 99.69%
Mapped reads, first in pair	368,577,977 / 49.87%
Mapped reads, second in pair	368,253,910 / 49.83%
Mapped reads, both in pair	735,284,662 / 99.48%
Mapped reads, singletons	1,547,225 / 0.21%
Secondary alignments	0
Supplementary alignments	12,453,145 / 1.68%
Read min/max/mean length	28 / 151 / 145.46
Duplicated reads (estimated)	302,903,615 / 40.98%
Duplication rate	38.28%
Clipped reads	133,590,451 / 18.07%

2.2. ACGT Content

Number/percentage of A's	32,114,259,968 / 30.24%
Number/percentage of C's	21,232,512,428 / 19.99%
Number/percentage of T's	30,645,600,541 / 28.86%
Number/percentage of G's	22,199,679,463 / 20.91%
Number/percentage of N's	651,199 / 0%

GC Percentage	40.9%

2.3. Coverage

Mean	34.3126
Standard Deviation	75.5434

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	40,447.7
Standard Deviation	1,959,376.7
P25/Median/P75	185 / 243 / 343

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	539,852,840
Insertions	13,146,844
Mapped reads with at least one insertion	1.75%
Deletions	11,658,552
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.37%

2.7. Chromosome stats

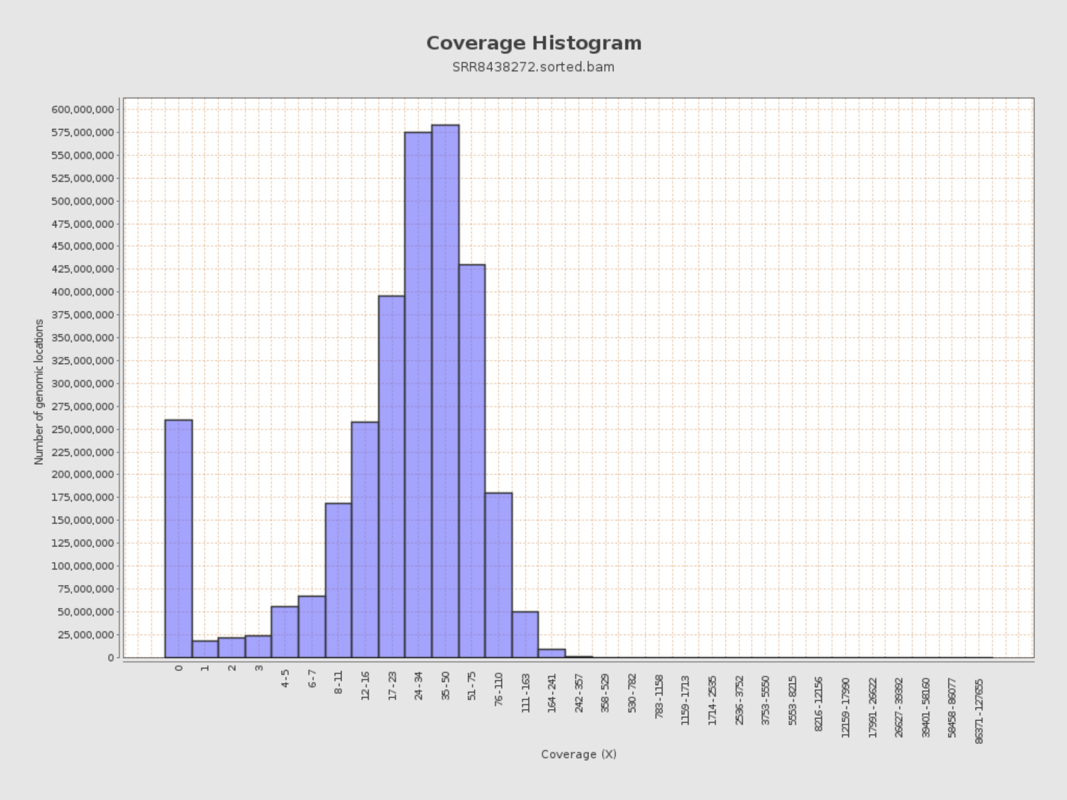
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	8645050949	34.6842	32.1852
chr2	243199373	9417895698	38.725	117.8814
chr3	198022430	7642443917	38.5938	78.9852
chr4	191154276	7155427730	37.4327	27.4324
chr5	180915260	6866311511	37.9532	29.6963
chr6	171115067	6521133880	38.1096	29.2268
chr7	159138663	5672249187	35.6434	28.353
chr8	146364022	5545557845	37.8888	28.5308
chr9	141213431	4688137190	33.1989	34.4191
chr10	135534747	5143925069	37.9528	37.5897
chr11	135006516	5016560318	37.1579	29.2935
chr12	133851895	4976530359	37.1794	27.8745
chr13	115169878	3744144833	32.5098	28.7501
chr14	107349540	3356603864	31.268	30.0411
chr15	102531392	3053383085	29.78	29.7678
chr16	90354753	2863610097	31.693	52.5102
chr17	81195210	2542289492	31.3108	37.361
chr18	78077248	3001686651	38.4451	29.9442
chr19	59128983	1528860236	25.8564	108.1654
chr20	63025520	2328843109	36.9508	31.8933
chr21	48129895	1399449560	29.0765	52.2599
chr22	51304566	1116470998	21.7616	28.7752
chrMT	16571	374398644	22,593.6059	8,596.4524
chrX	155270560	3089505532	19.8976	19.7748

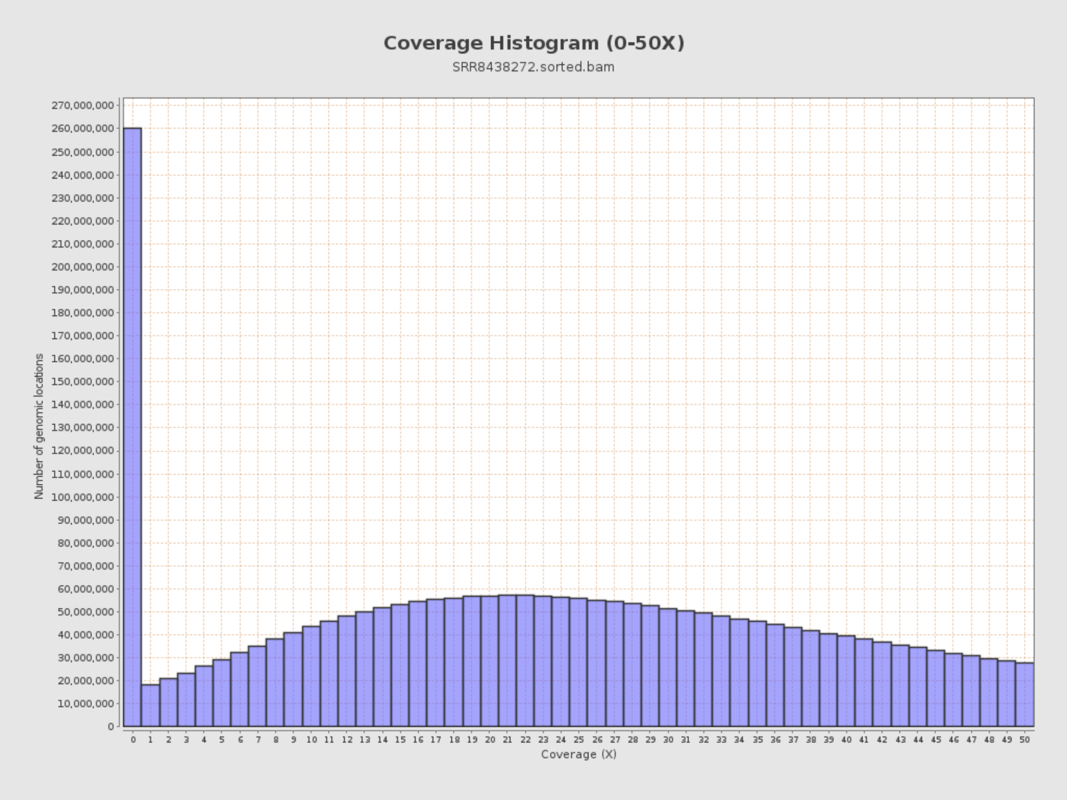
chrY	59373566	530963557	8.9428	27.0621

3. Results : Coverage across reference

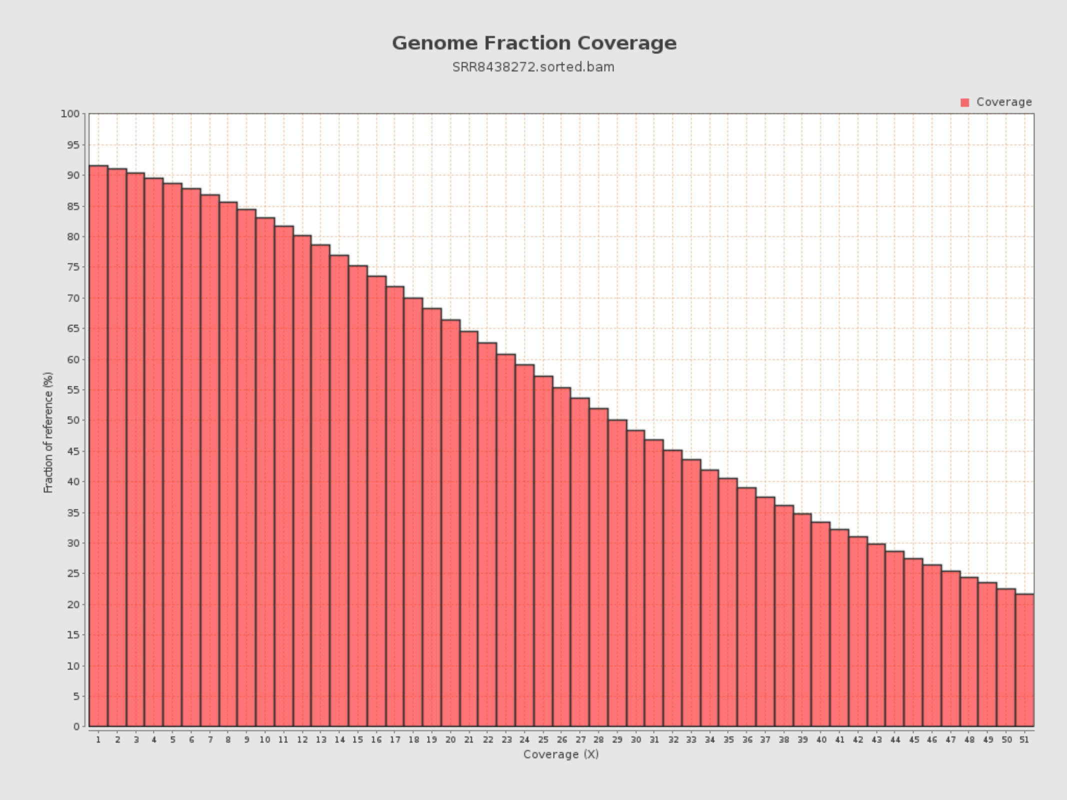
4. Results : Coverage Histogram



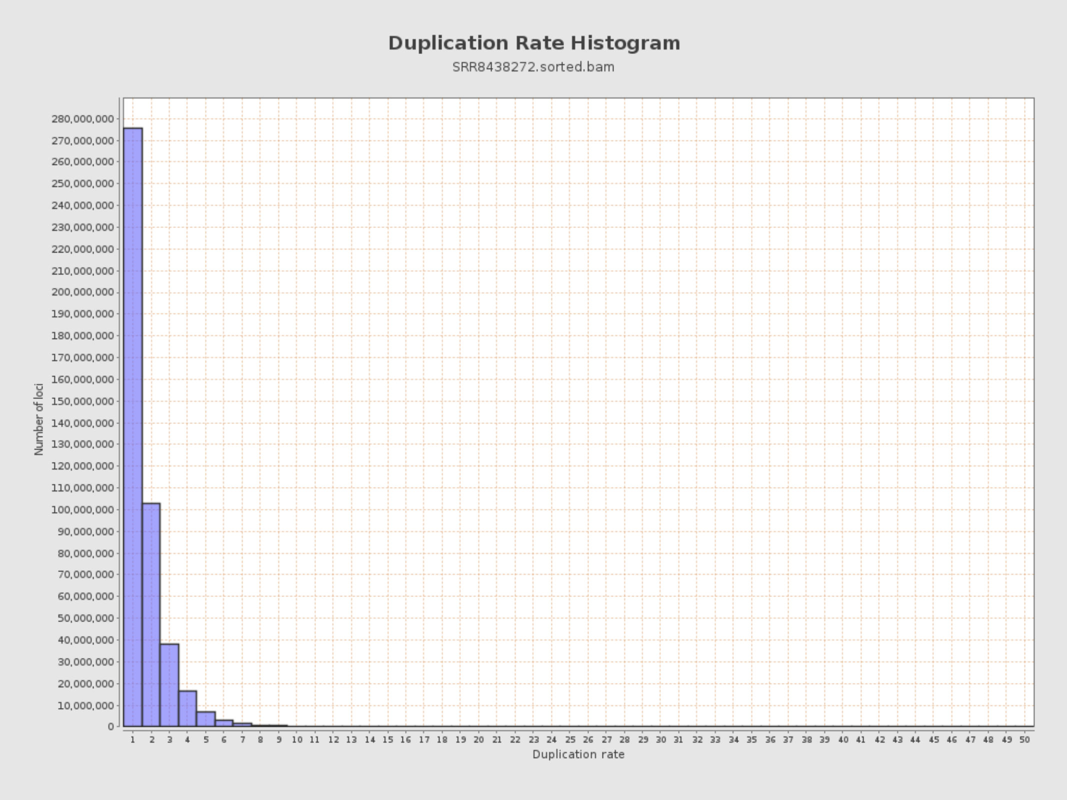
5. Results : Coverage Histogram (0-50X)



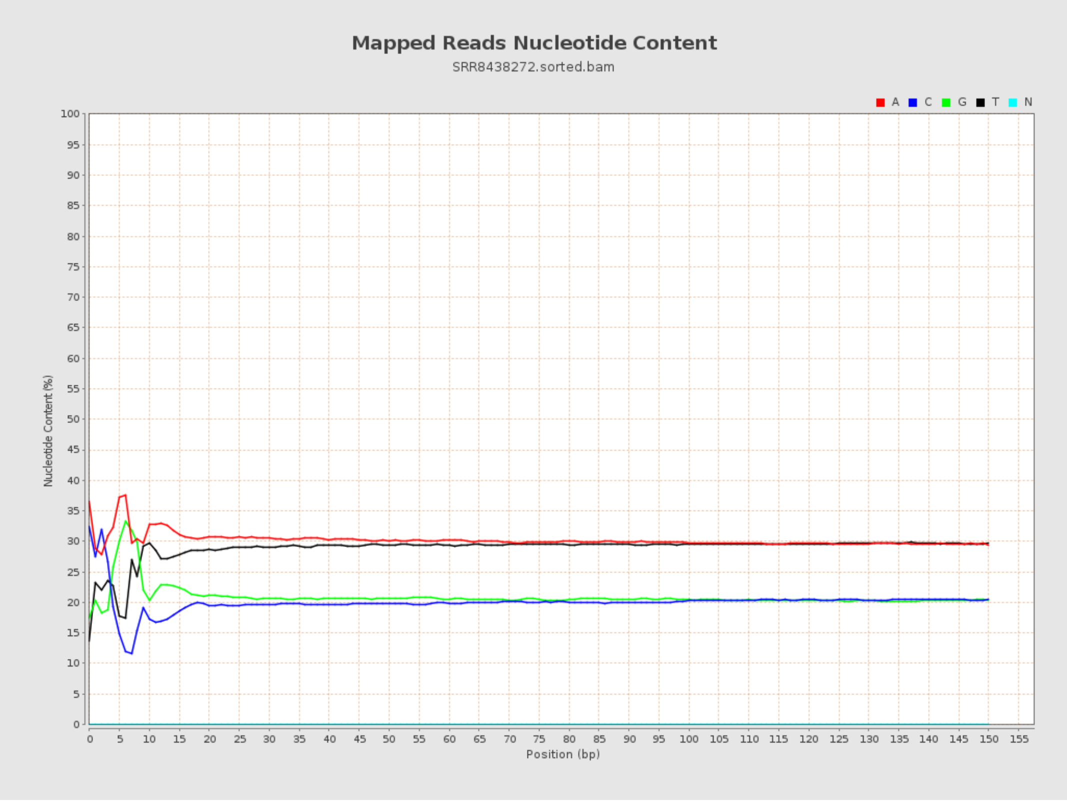
6. Results : Genome Fraction Coverage



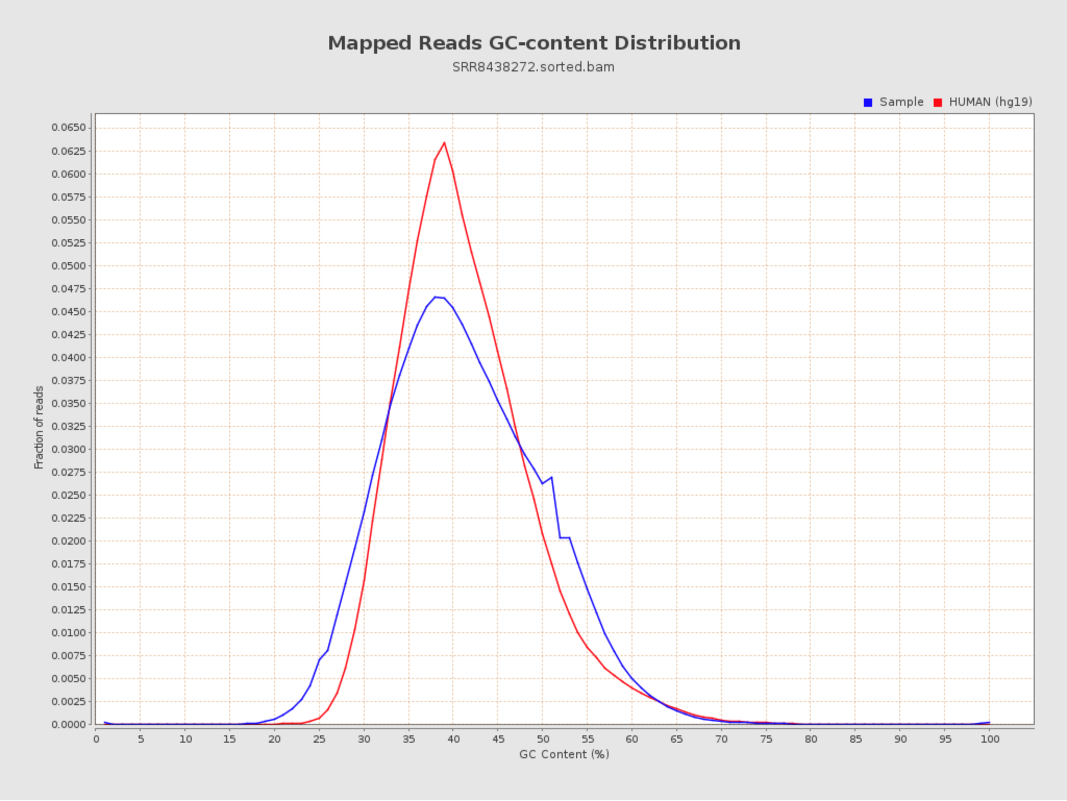
7. Results : Duplication Rate Histogram



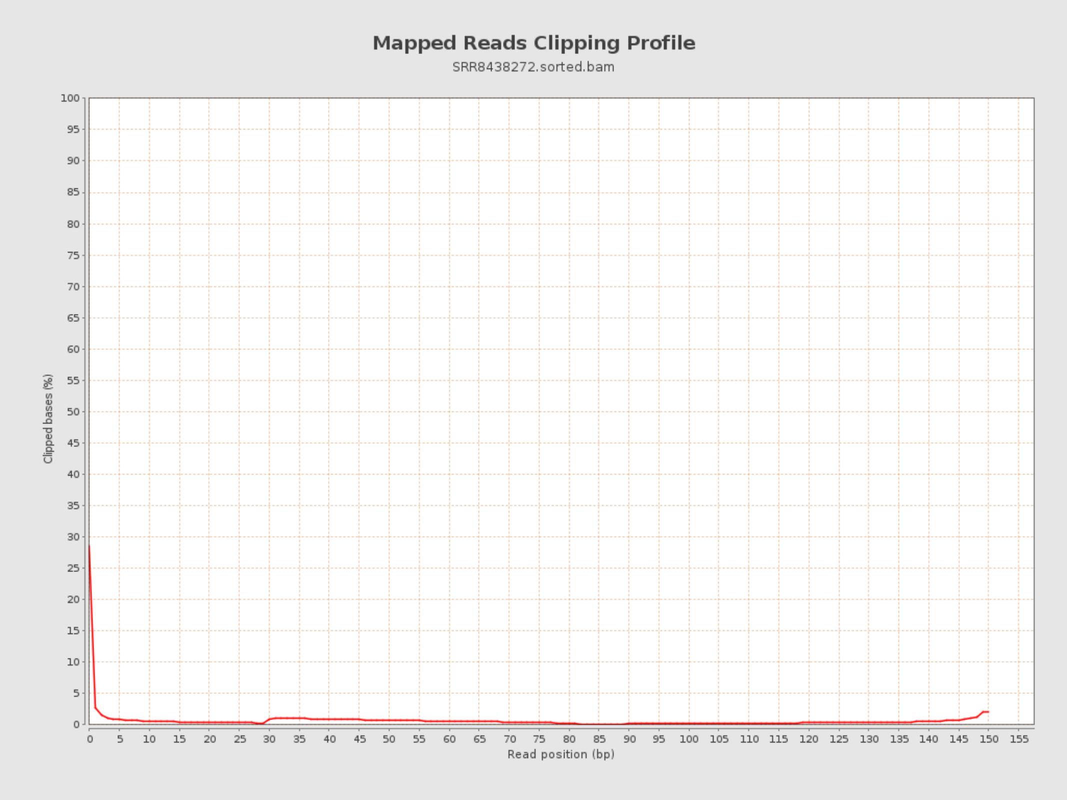
8. Results : Mapped Reads Nucleotide Content



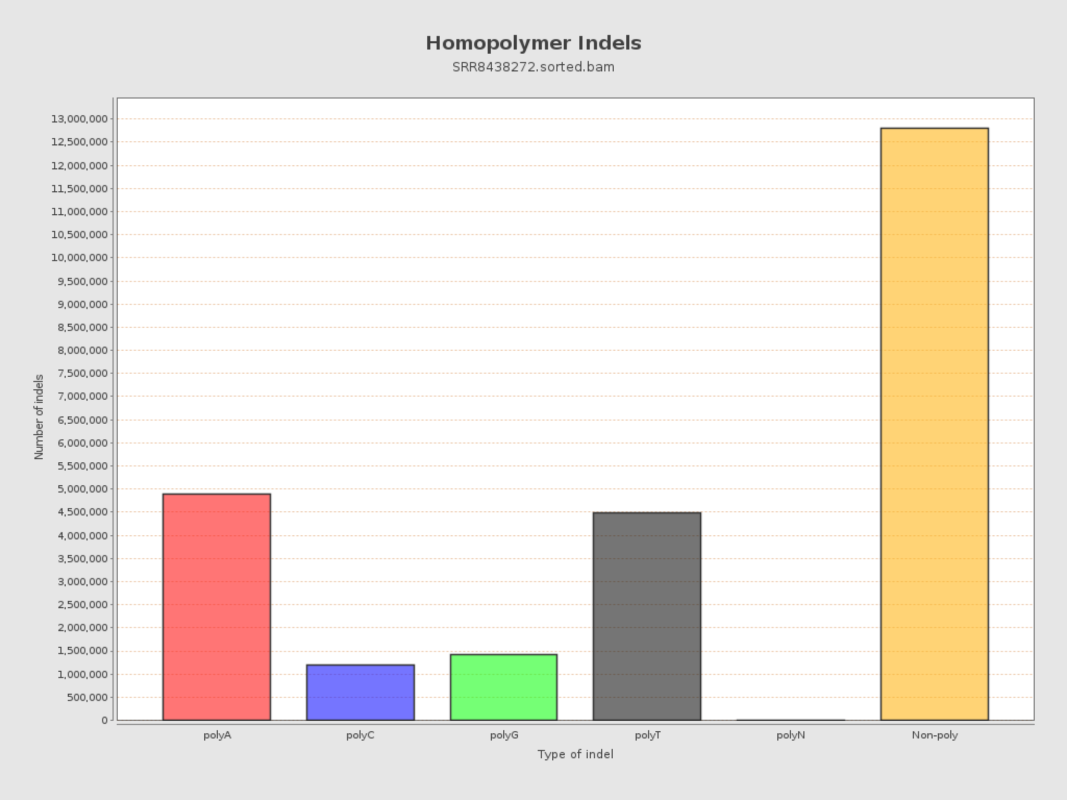
9. Results : Mapped Reads GC-content Distribution



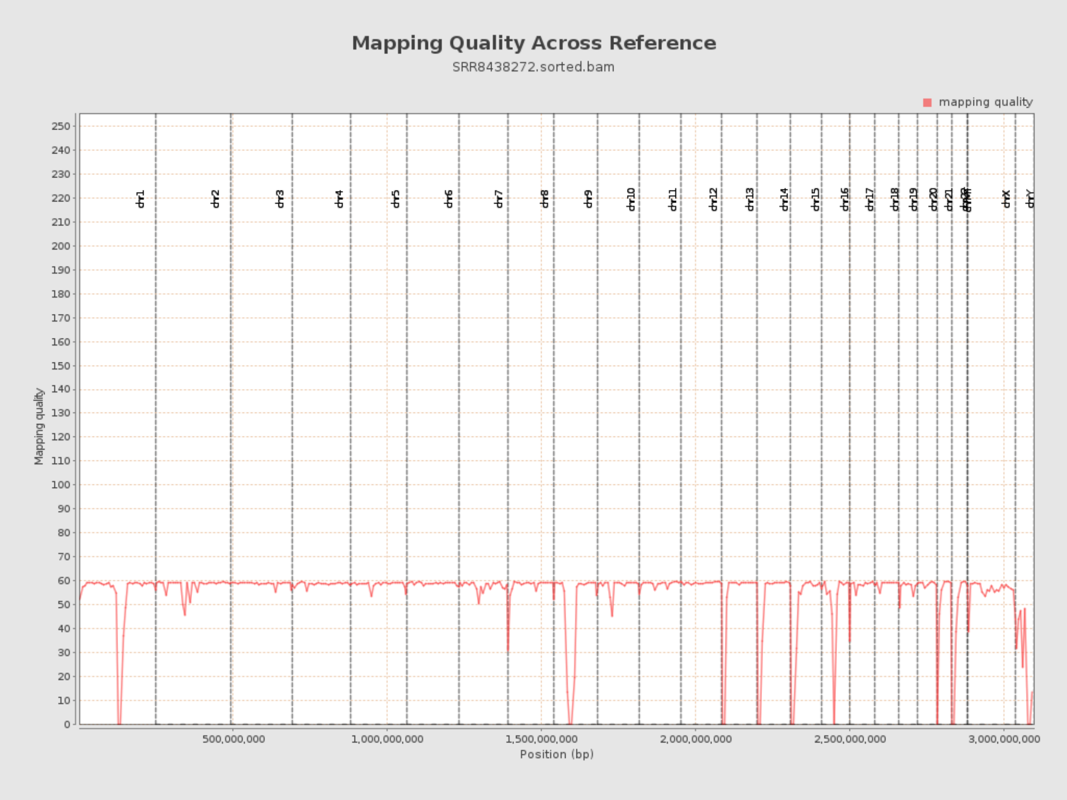
10. Results : Mapped Reads Clipping Profile



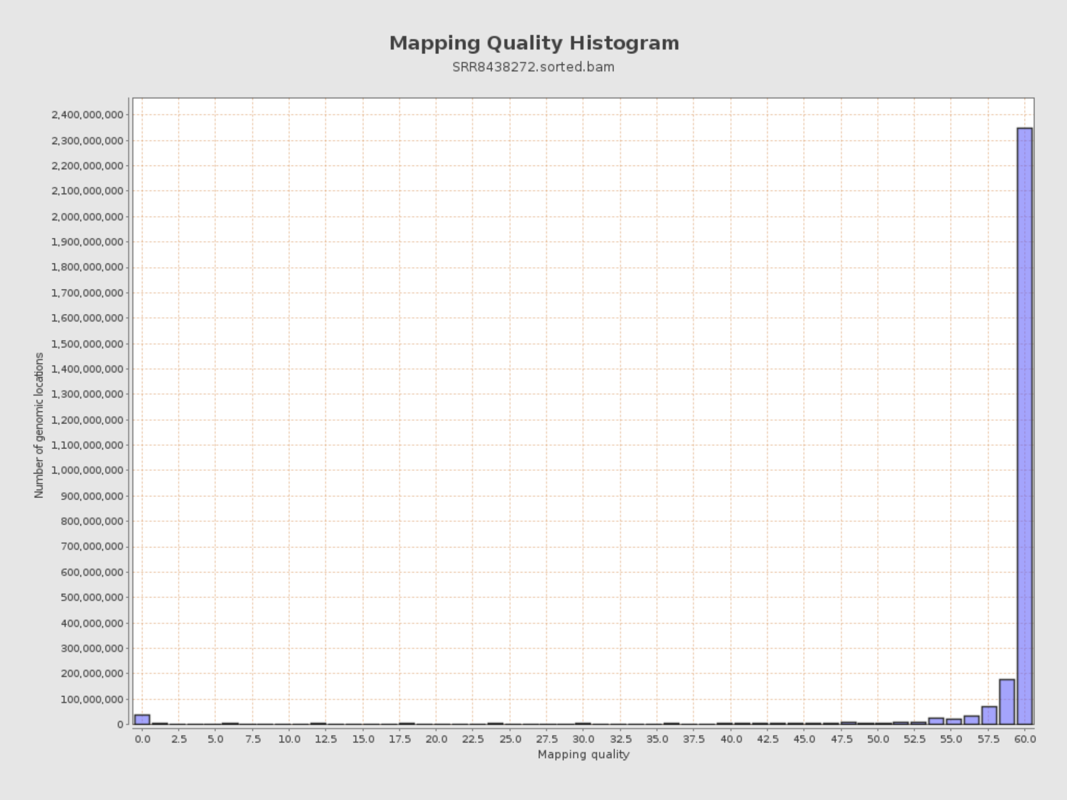
11. Results : Homopolymer Indels



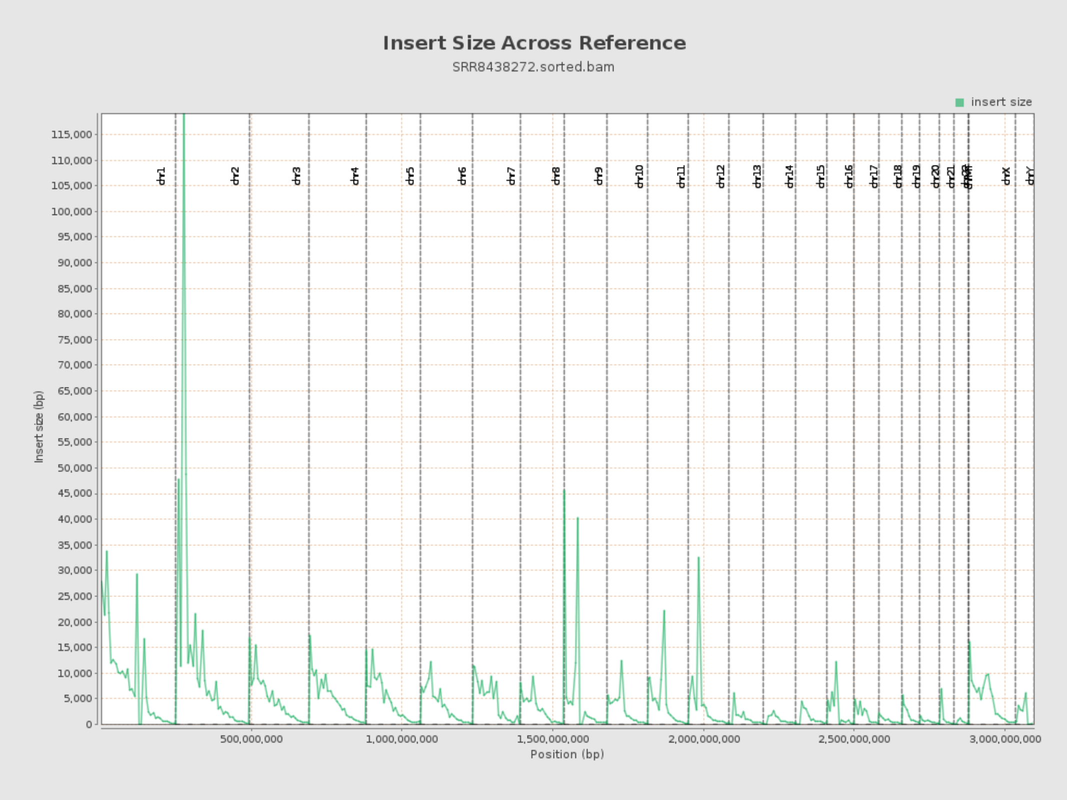
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram