Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 14:05:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438277.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_SRR8438277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438277_1.fastq.gz SRR8438277_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 14:05:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	724,014,094
Mapped reads	721,790,660 / 99.69%
Unmapped reads	2,223,434 / 0.31%
Mapped paired reads	721,790,660 / 99.69%
Mapped reads, first in pair	361,035,340 / 49.87%
Mapped reads, second in pair	360,755,320 / 49.83%
Mapped reads, both in pair	720,257,614 / 99.48%
Mapped reads, singletons	1,533,046 / 0.21%
Secondary alignments	0
Supplementary alignments	11,464,179 / 1.58%
Read min/max/mean length	28 / 151 / 144.77
Duplicated reads (estimated)	327,454,892 / 45.23%
Duplication rate	42.7%
Clipped reads	132,942,959 / 18.36%

2.2. ACGT Content

Number/percentage of A's	31,373,184,179 / 30.3%
Number/percentage of C's	20,638,421,159 / 19.93%
Number/percentage of T's	29,980,773,753 / 28.96%
Number/percentage of G's	21,548,210,362 / 20.81%
Number/percentage of N's	640,729 / 0%

GC Percentage	40.74%

2.3. Coverage

Mean	33.4558
Standard Deviation	99.8735

2.4. Mapping Quality

Mean Mapping Quality	55.03

2.5. Insert size

Mean	40,228.03
Standard Deviation	1,962,749.25
P25/Median/P75	179 / 234 / 325

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	529,032,462
Insertions	12,791,017
Mapped reads with at least one insertion	1.74%
Deletions	11,344,216
Mapped reads with at least one deletion	1.55%
Homopolymer indels	48.29%

2.7. Chromosome stats

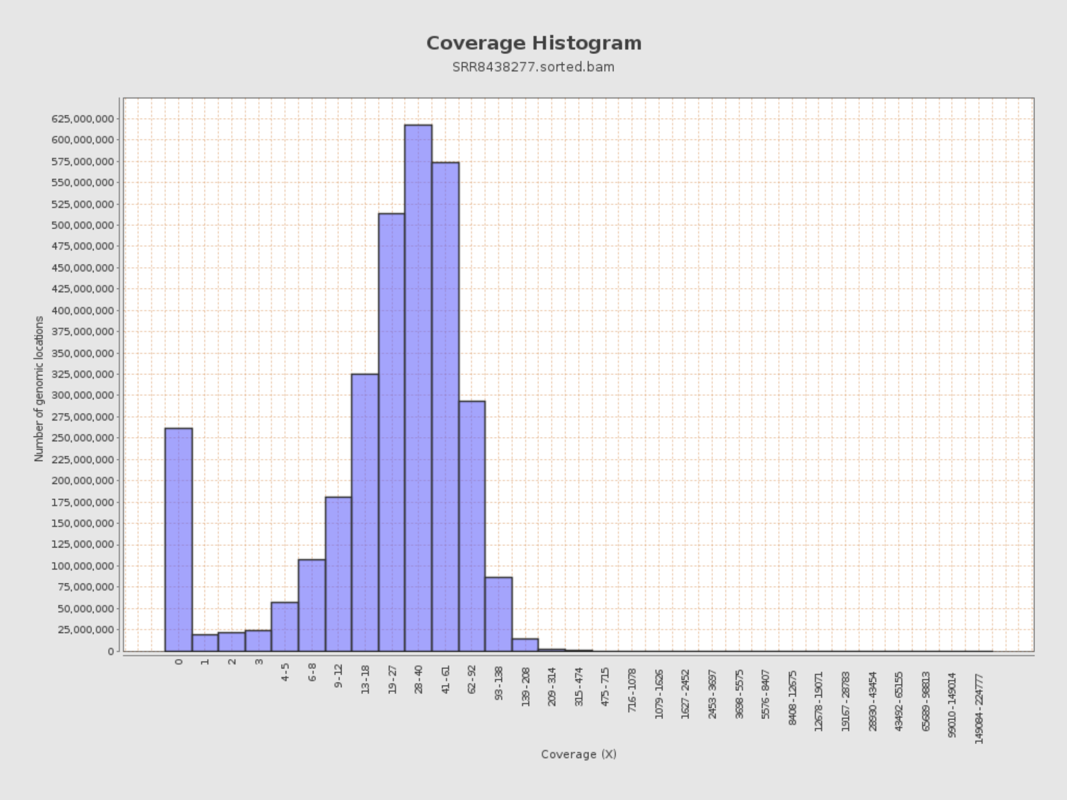
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	8454121509	33.9182	32.464
chr2	243199373	9169843150	37.705	130.5559
chr3	198022430	7513065222	37.9405	257.316
chr4	191154276	6981359301	36.5221	35.1651
chr5	180915260	6740440870	37.2574	52.503
chr6	171115067	6219419161	36.3464	29.4351
chr7	159138663	5658444055	35.5567	34.8714
chr8	146364022	5433653167	37.1242	29.5729
chr9	141213431	4494389222	31.8269	37.4853
chr10	135534747	4988632785	36.807	43.4475
chr11	135006516	4899817772	36.2932	28.8561
chr12	133851895	4850339075	36.2366	28.585
chr13	115169878	3604441735	31.2967	27.6667
chr14	107349540	3311545611	30.8483	32.8232
chr15	102531392	3019063982	29.4453	30.7476
chr16	90354753	2805710441	31.0522	53.1124
chr17	81195210	2489525568	30.661	37.4429
chr18	78077248	2908606508	37.2529	28.8283
chr19	59128983	1602743190	27.1059	370.2111
chr20	63025520	2266540970	35.9623	32.6926
chr21	48129895	1323374862	27.4959	135.1658
chr22	51304566	1115430734	21.7414	28.3648
chrMT	16571	134169340	8,096.6351	3,083.0674
chrX	155270560	3059184426	19.7023	41.7305

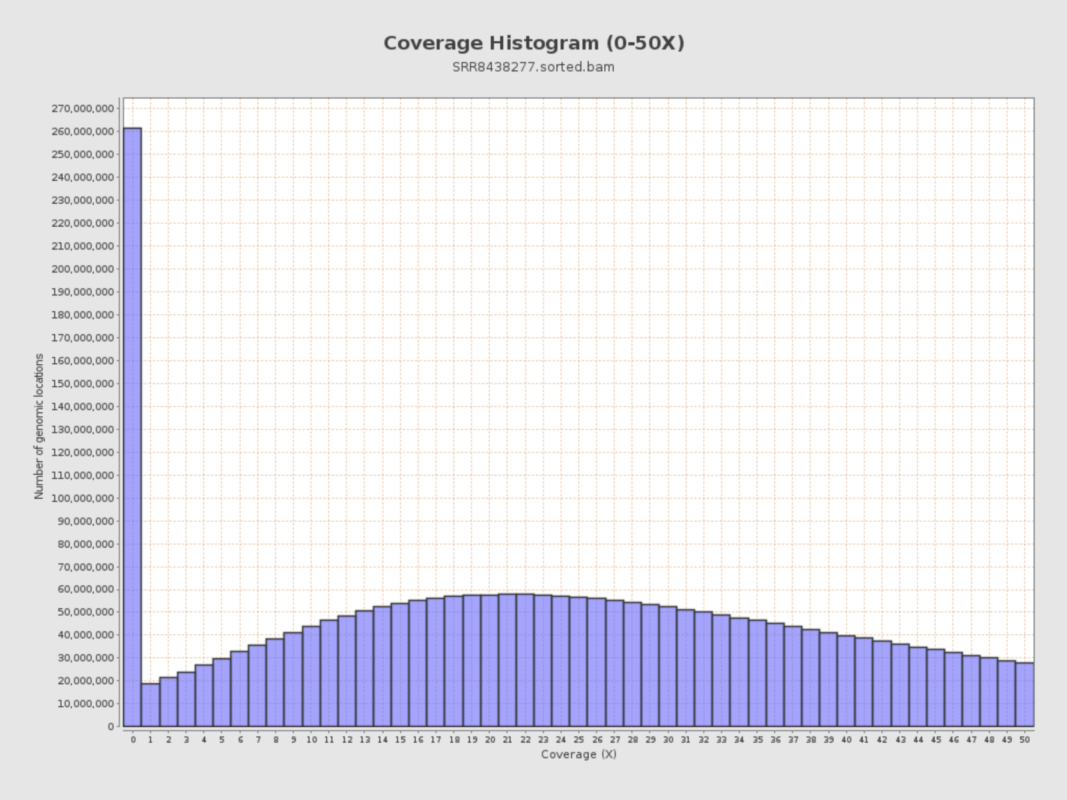
chrY	59373566	525064931	8.8434	27.2269

3. Results : Coverage across reference

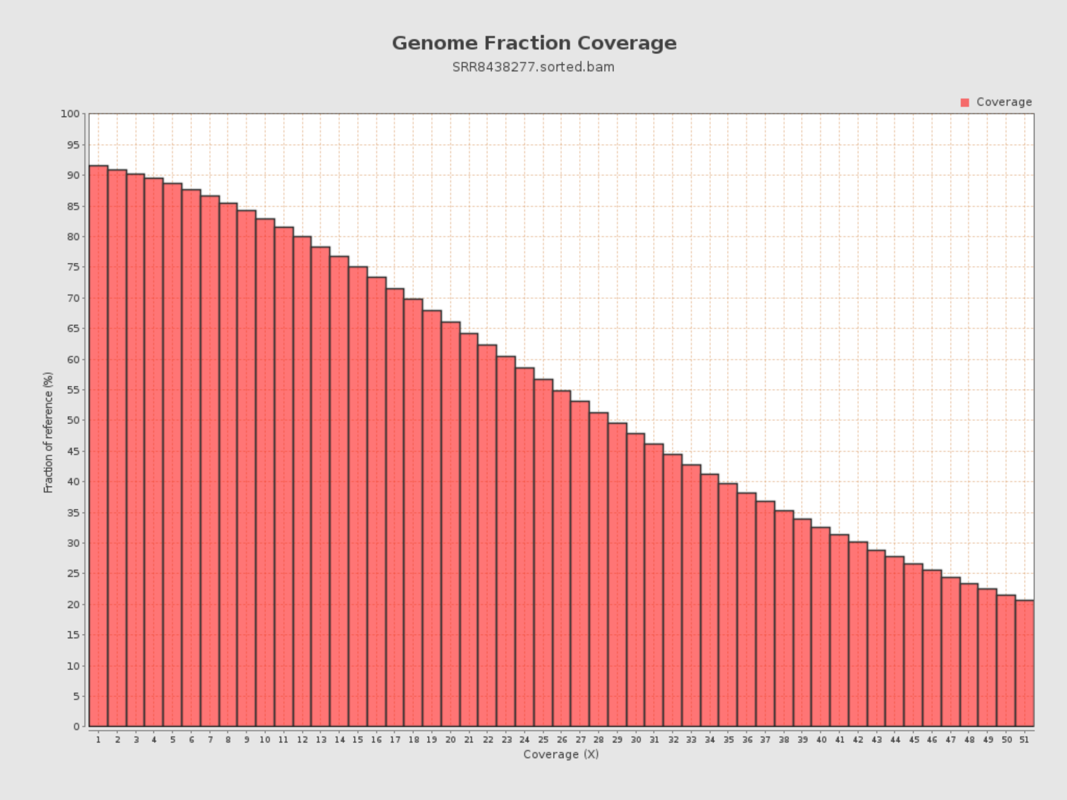
4. Results : Coverage Histogram



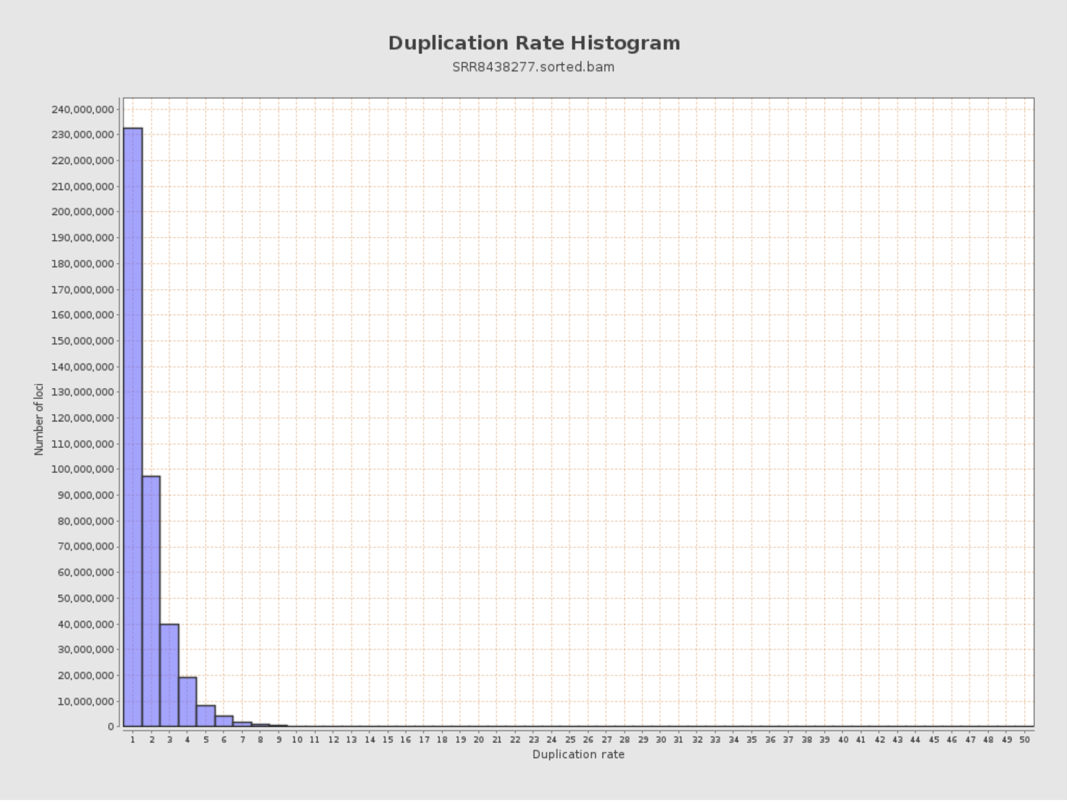
5. Results : Coverage Histogram (0-50X)



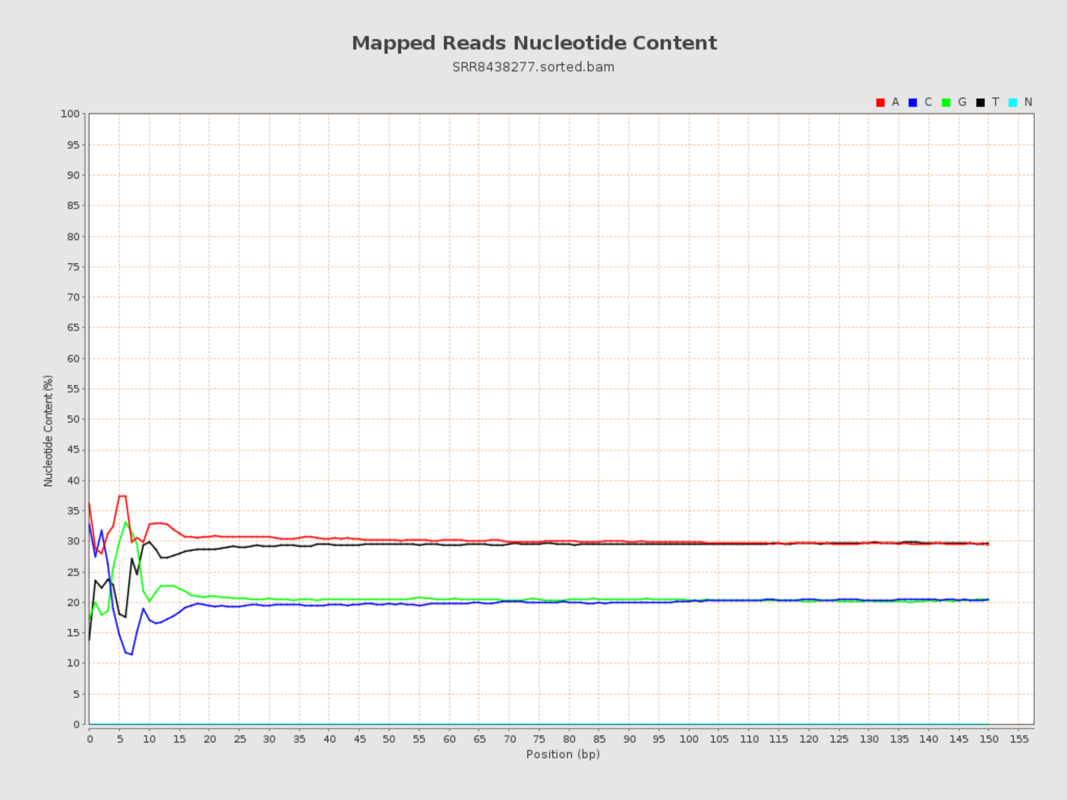
6. Results : Genome Fraction Coverage



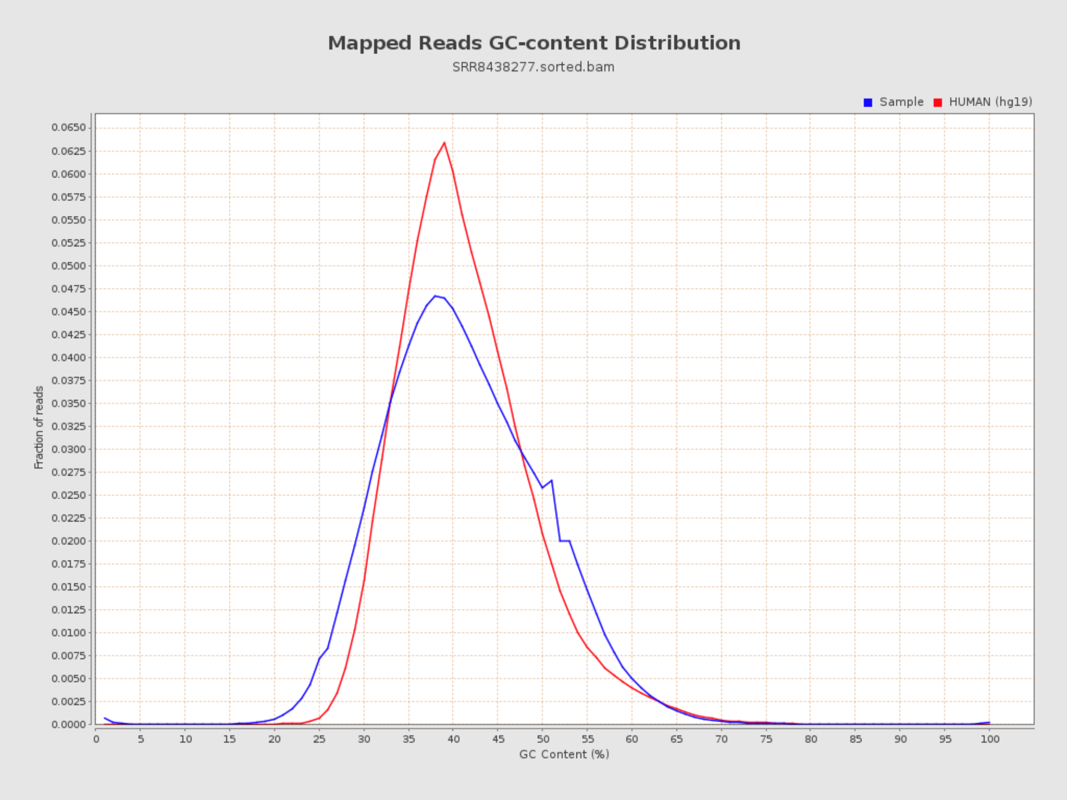
7. Results : Duplication Rate Histogram



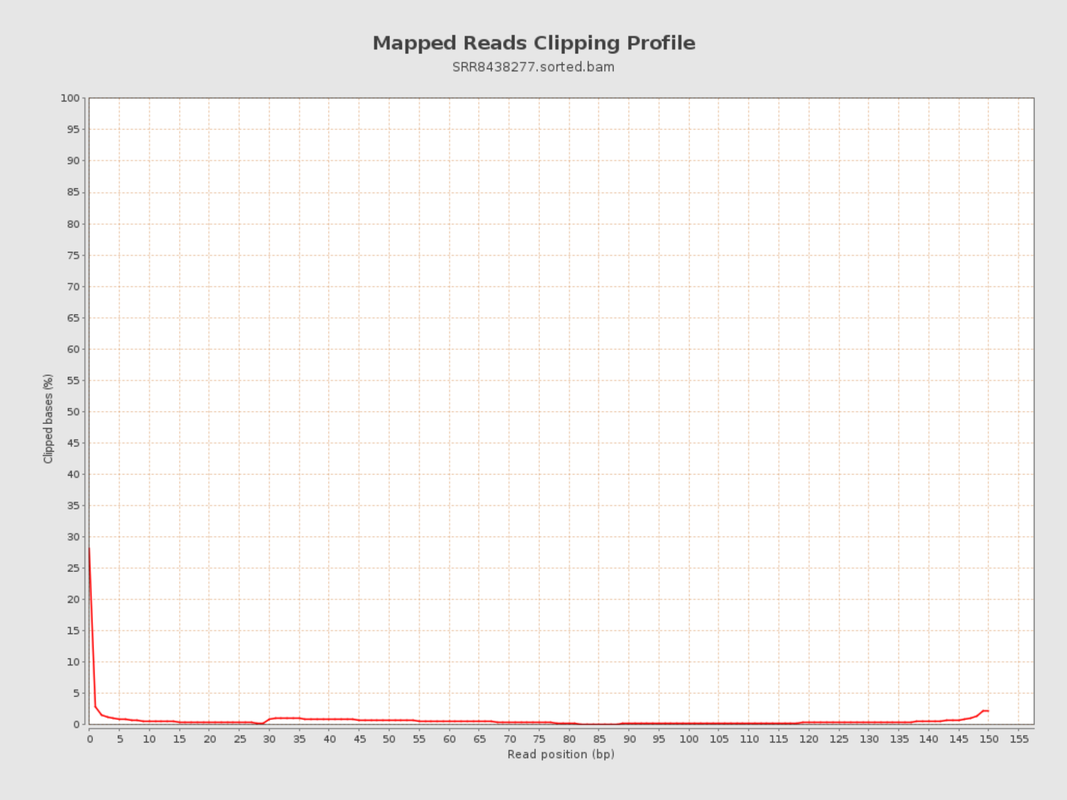
8. Results : Mapped Reads Nucleotide Content



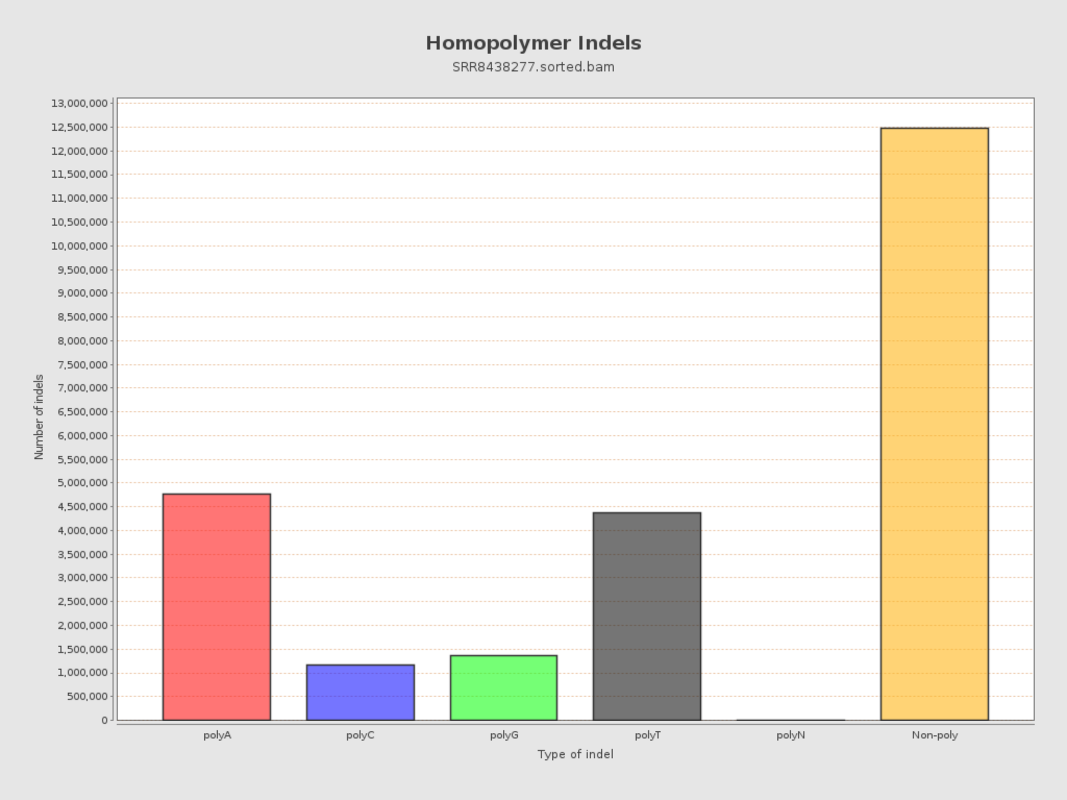
9. Results : Mapped Reads GC-content Distribution



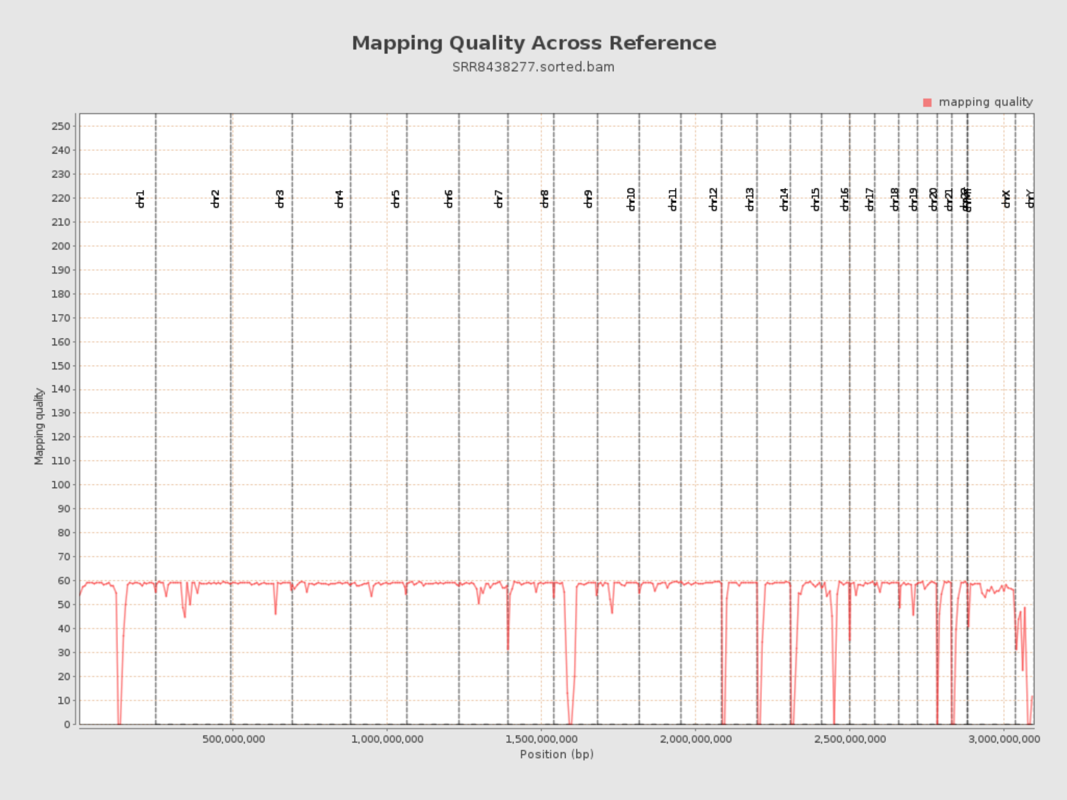
10. Results : Mapped Reads Clipping Profile



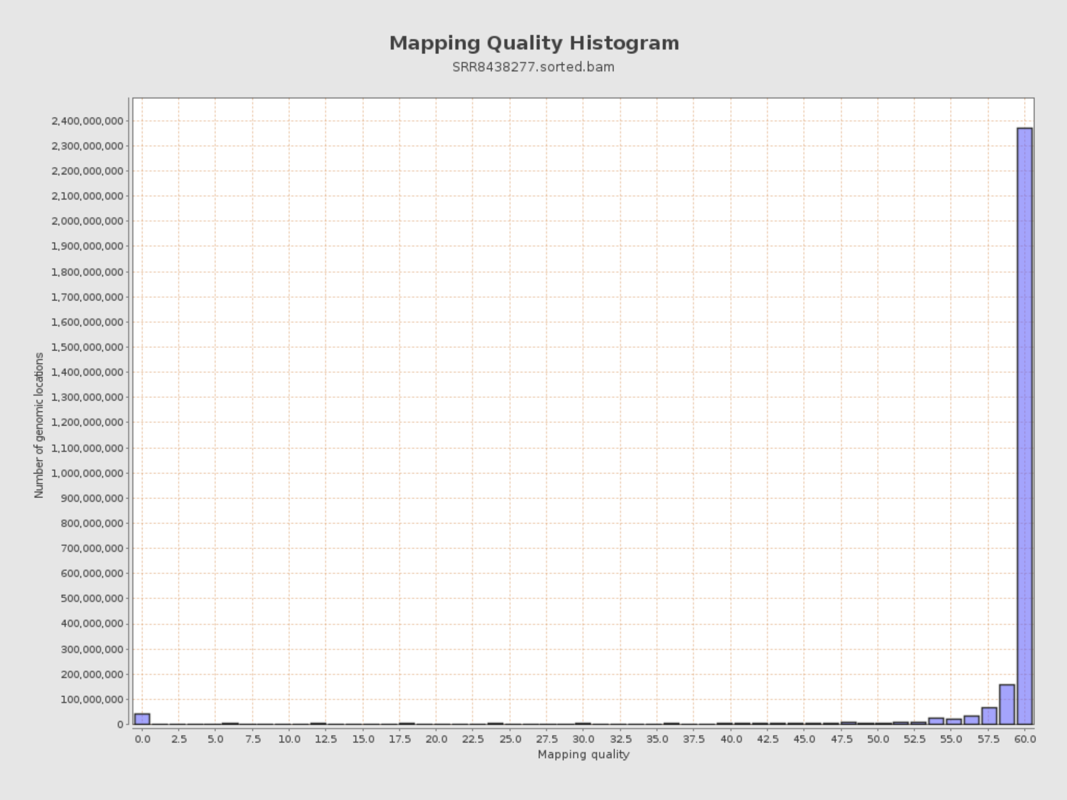
11. Results : Homopolymer Indels



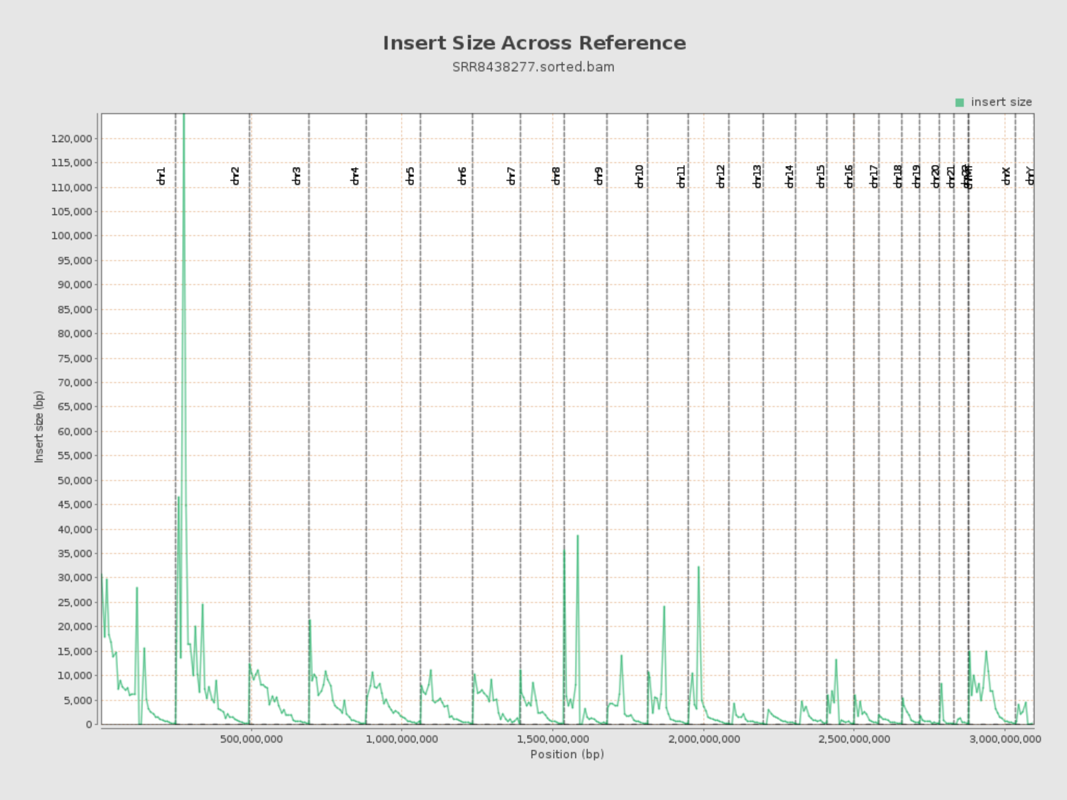
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram