Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 17:58:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438283.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_SRR8438283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438283_1.fastq.gz SRR8438283_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 17:58:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	817,262,372
Mapped reads	814,634,826 / 99.68%
Unmapped reads	2,627,546 / 0.32%
Mapped paired reads	814,634,826 / 99.68%
Mapped reads, first in pair	407,532,973 / 49.87%
Mapped reads, second in pair	407,101,853 / 49.81%
Mapped reads, both in pair	812,791,418 / 99.45%
Mapped reads, singletons	1,843,408 / 0.23%
Secondary alignments	0
Supplementary alignments	13,114,161 / 1.6%
Read min/max/mean length	28 / 151 / 145.06
Duplicated reads (estimated)	371,245,518 / 45.43%
Duplication rate	42.86%
Clipped reads	150,046,503 / 18.36%

2.2. ACGT Content

Number/percentage of A's	35,416,120,324 / 30.24%
Number/percentage of C's	23,401,884,939 / 19.98%
Number/percentage of T's	33,803,569,130 / 28.87%
Number/percentage of G's	24,479,893,821 / 20.9%
Number/percentage of N's	719,321 / 0%

GC Percentage	40.89%

2.3. Coverage

Mean	37.8379
Standard Deviation	82.6456

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	42,308.72
Standard Deviation	2,018,918.21
P25/Median/P75	182 / 240 / 339

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	605,841,587
Insertions	14,787,813
Mapped reads with at least one insertion	1.78%
Deletions	13,159,225
Mapped reads with at least one deletion	1.59%
Homopolymer indels	48.38%

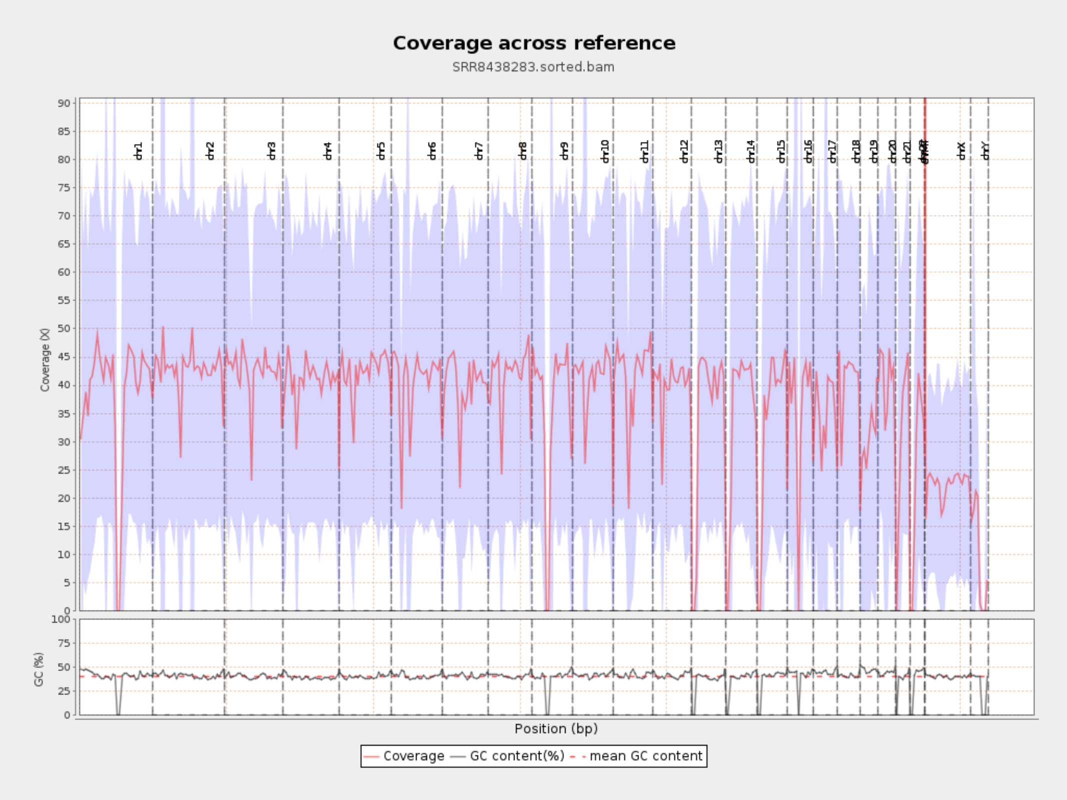
2.7. Chromosome stats

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

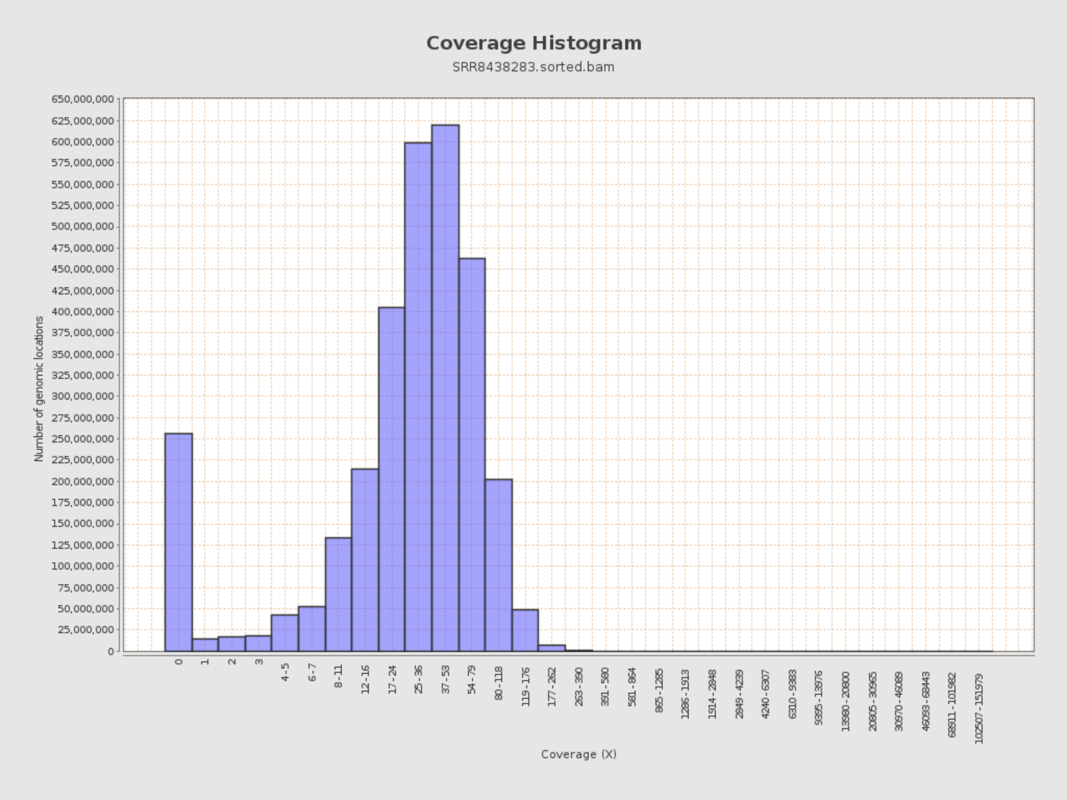
		bases	coverage	deviation
chr1	249250621	9583727762	38.4502	35.7081
chr2	243199373	10402048642	42.7717	147.2769
chr3	198022430	8424973298	42.5456	28.6312
chr4	191154276	7892020885	41.2861	28.5688
chr5	180915260	7644442683	42.2543	28.9238
chr6	171115067	7034509148	41.1098	30.6715
chr7	159138663	6349019241	39.8961	29.3487
chr8	146364022	6100051600	41.6773	29.9813
chr9	141213431	5065203119	35.8691	37.3967
chr10	135534747	5633523270	41.5652	41.1838
chr11	135006516	5624802104	41.6632	31.1005
chr12	133851895	5390721310	40.2738	28.917
chr13	115169878	4007580964	34.7971	29.8291
chr14	107349540	3714985731	34.6064	32.0548
chr15	102531392	3434780162	33.4998	32.8178
chr16	90354753	3161493094	34.9898	58.2066
chr17	81195210	2829463218	34.8477	41.2693
chr18	78077248	3248915331	41.6116	31.9309
chr19	59128983	1781039646	30.1213	31.4131
chr20	63025520	2549605418	40.4535	33.6465
chr21	48129895	1491833263	30.996	35.9654
chr22	51304566	1270478278	24.7635	31.869
chrMT	16571	426106042	25,713.9607	10,216.8167
chrX	155270560	3481341394	22.4211	17.8901

chrY	59373566	591903724	9.9691	31.3495

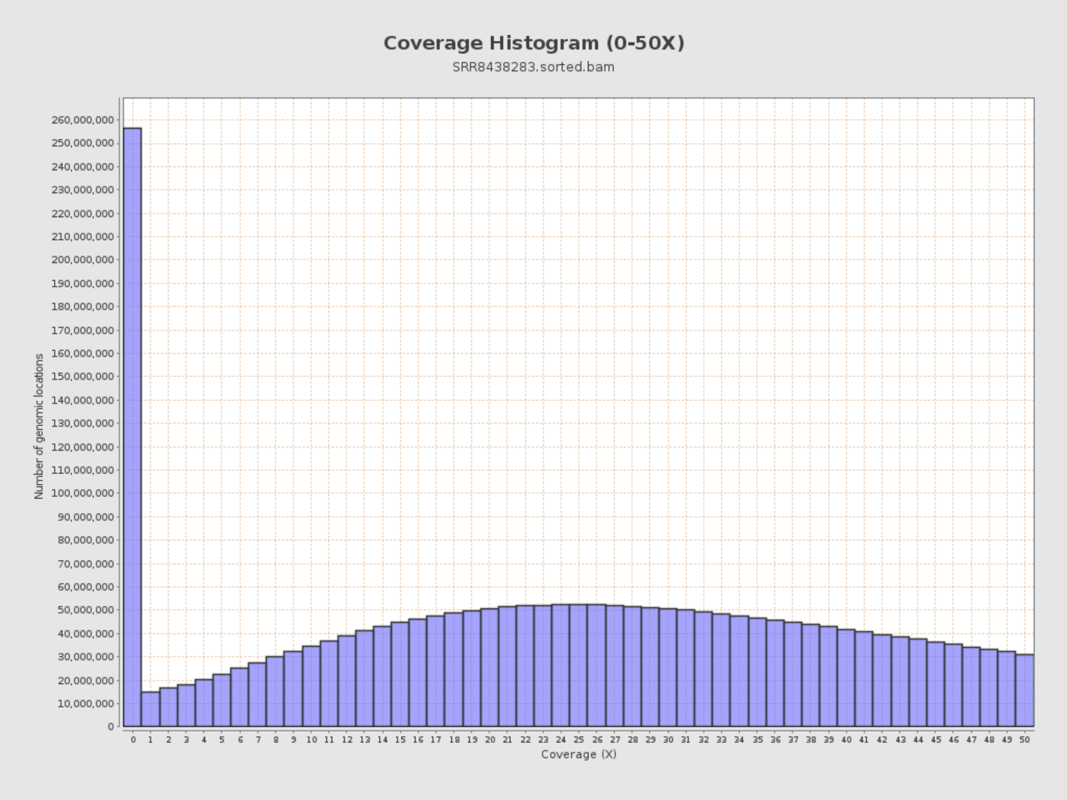
3. Results : Coverage across reference



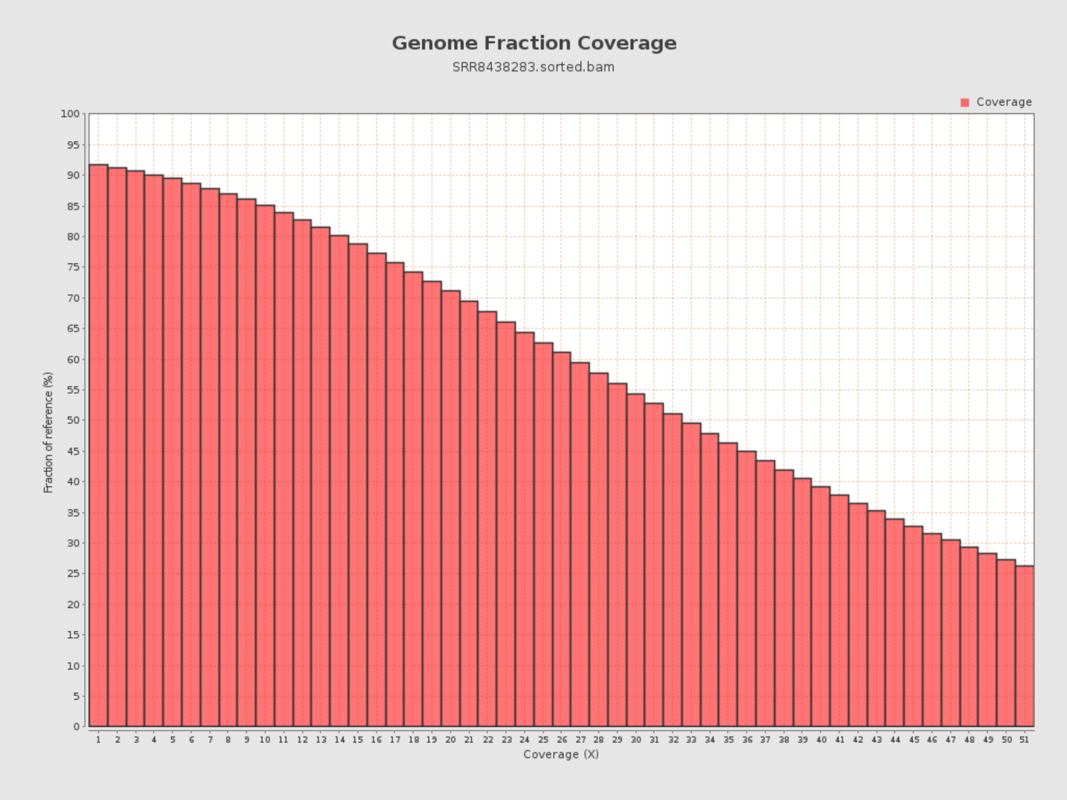
4. Results : Coverage Histogram



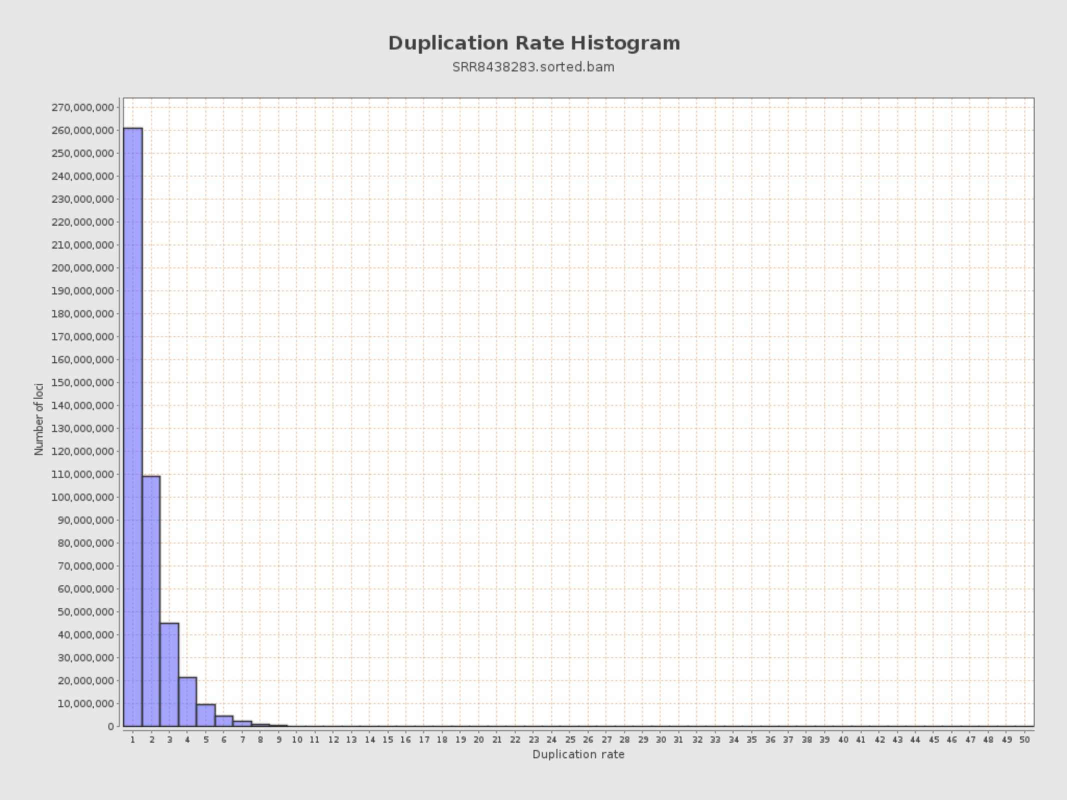
5. Results : Coverage Histogram (0-50X)



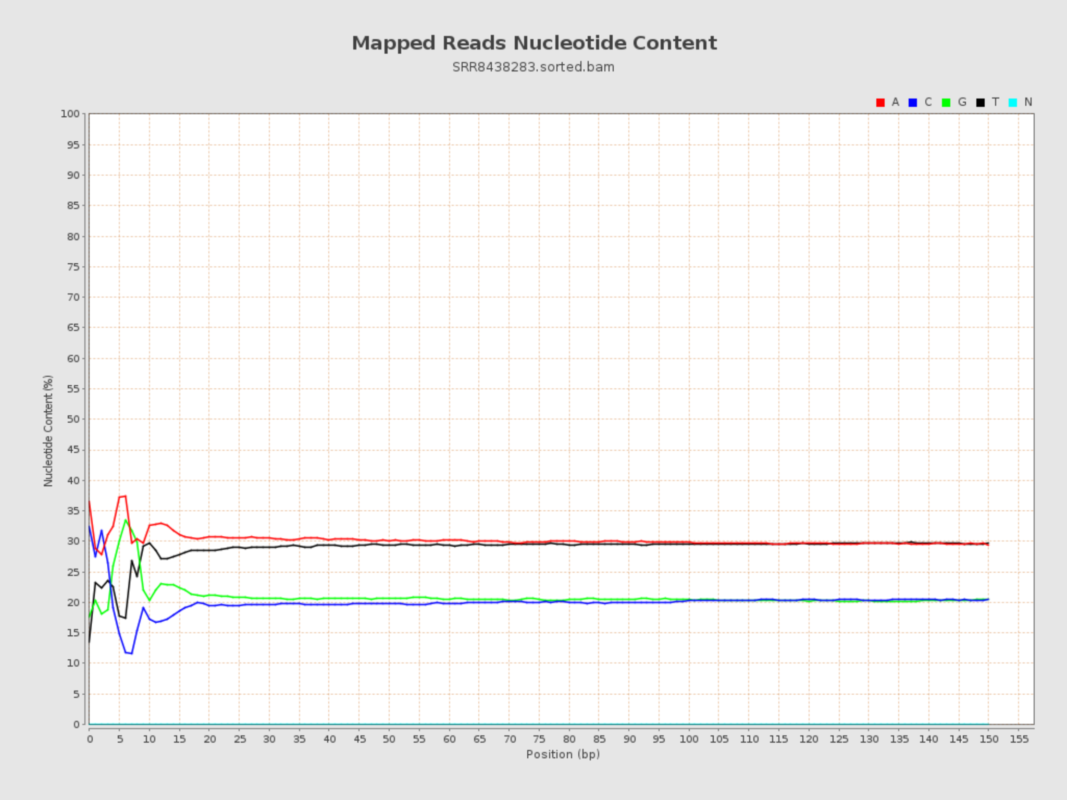
6. Results : Genome Fraction Coverage



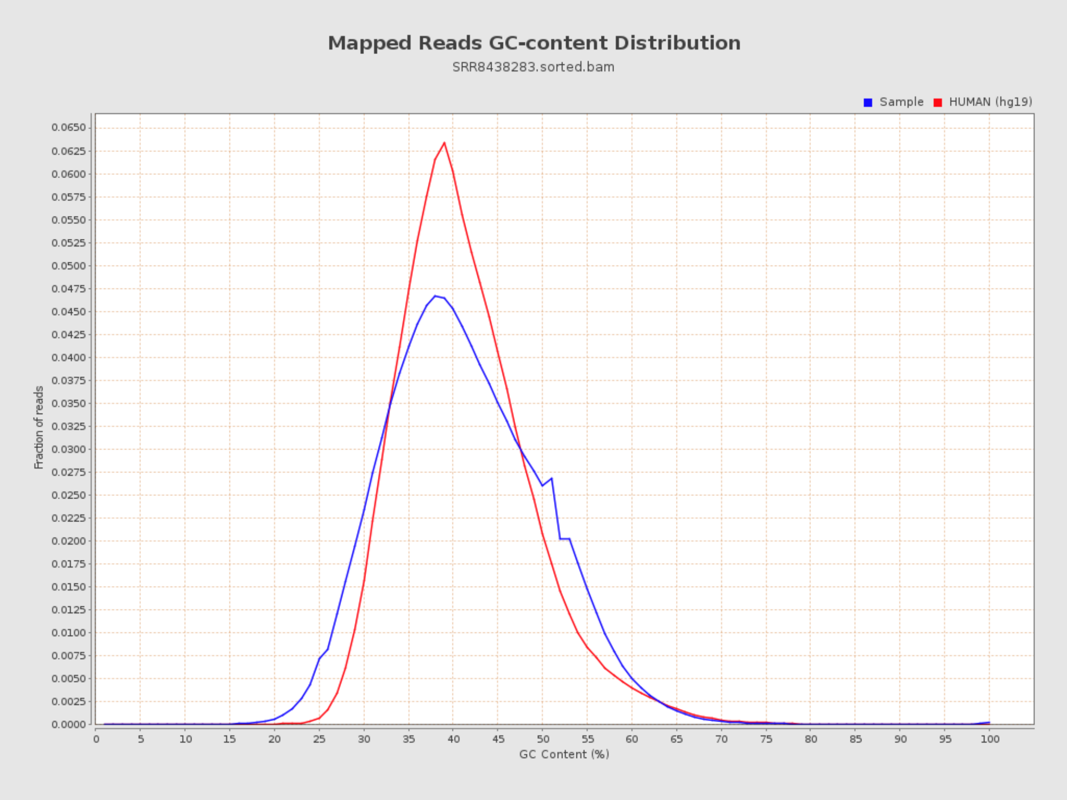
7. Results : Duplication Rate Histogram



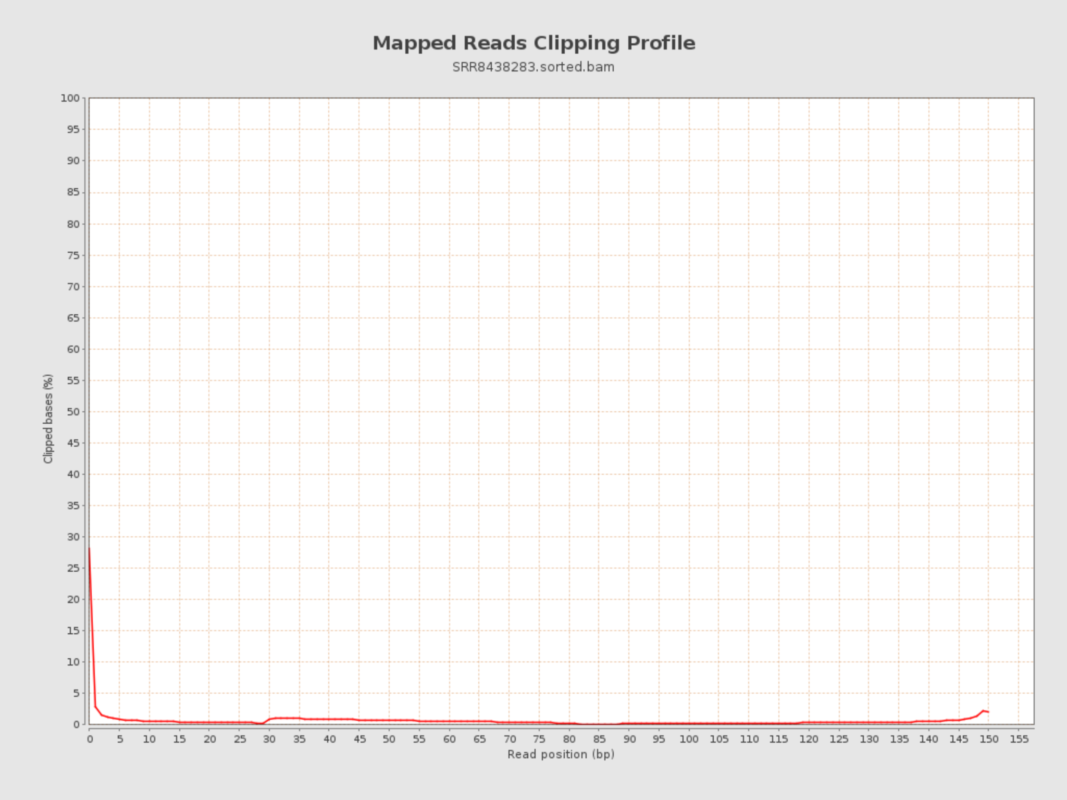
8. Results : Mapped Reads Nucleotide Content



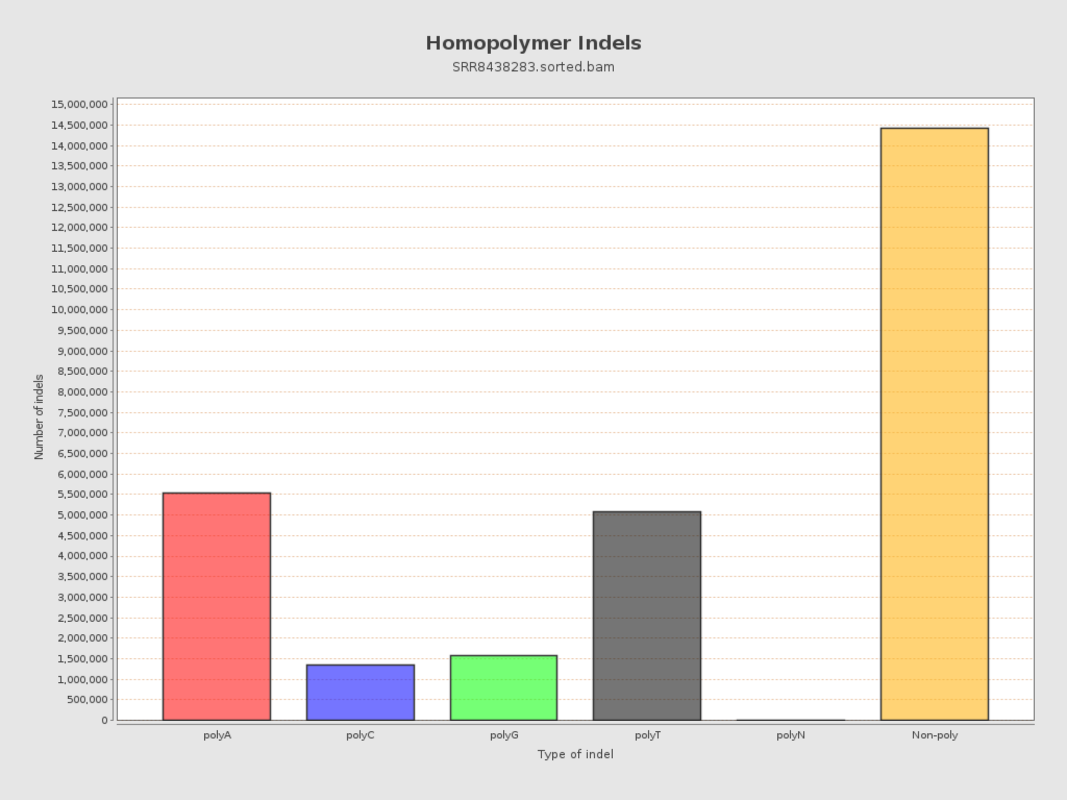
9. Results : Mapped Reads GC-content Distribution



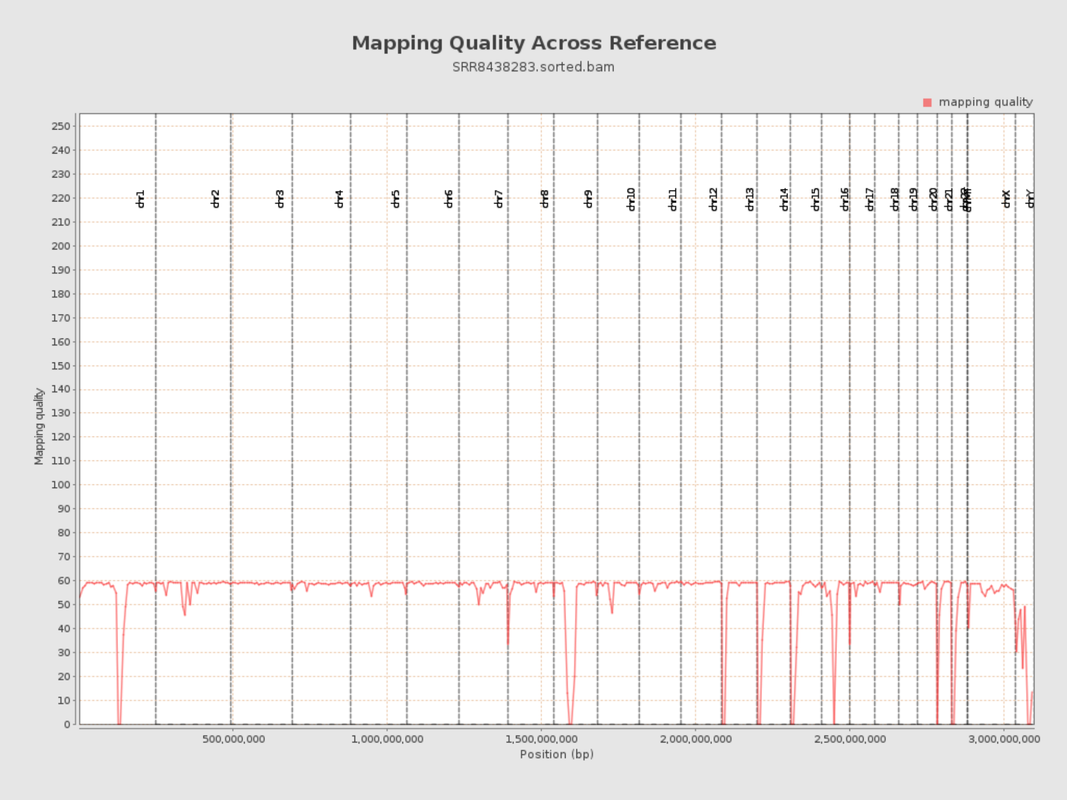
10. Results : Mapped Reads Clipping Profile



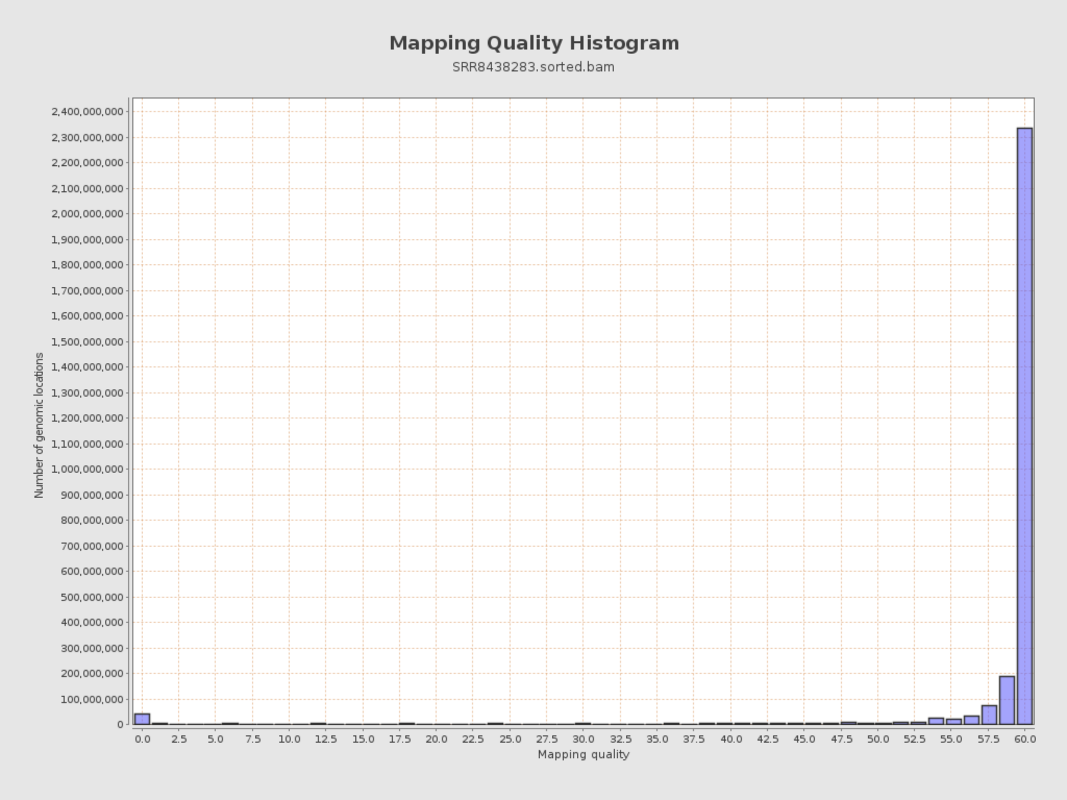
11. Results : Homopolymer Indels



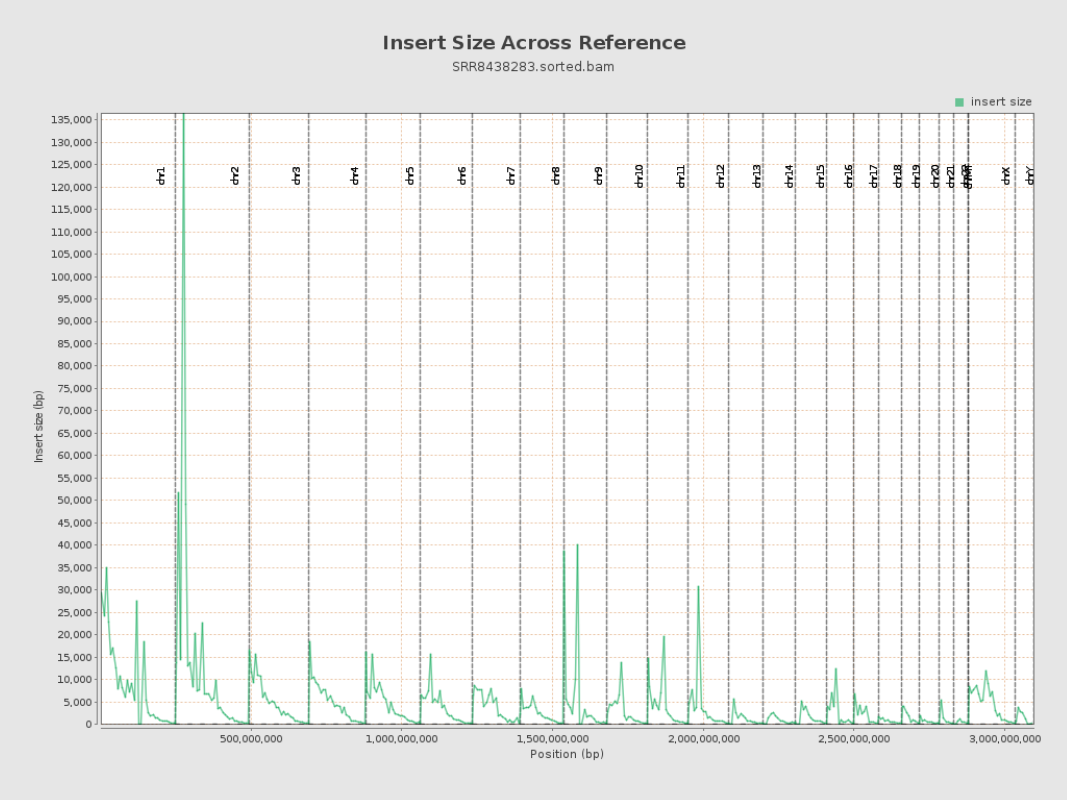
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram