Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/27 11:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438286.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_SRR8438286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438286_1.fastq.gz SRR8438286_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 27 11:47:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	587,328,756
Mapped reads	585,452,070 / 99.68%
Unmapped reads	1,876,686 / 0.32%
Mapped paired reads	585,452,070 / 99.68%
Mapped reads, first in pair	292,943,600 / 49.88%
Mapped reads, second in pair	292,508,470 / 49.8%
Mapped reads, both in pair	584,038,914 / 99.44%
Mapped reads, singletons	1,413,156 / 0.24%
Secondary alignments	0
Supplementary alignments	11,637,960 / 1.98%
Read min/max/mean length	28 / 151 / 146.25
Duplicated reads (estimated)	320,207,271 / 54.52%
Duplication rate	50.5%
Clipped reads	106,745,453 / 18.17%

2.2. ACGT Content

Number/percentage of A's	25,796,091,821 / 30.43%
Number/percentage of C's	16,782,161,596 / 19.79%
Number/percentage of T's	24,574,659,699 / 28.99%
Number/percentage of G's	17,627,433,960 / 20.79%
Number/percentage of N's	633,898 / 0%

GC Percentage	40.59%

2.3. Coverage

Mean	27.3947
Standard Deviation	156.1234

2.4. Mapping Quality

Mean Mapping Quality	54.29

2.5. Insert size

Mean	58,849.53
Standard Deviation	2,384,599.68
P25/Median/P75	199 / 257 / 342

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	429,938,247
Insertions	10,956,567
Mapped reads with at least one insertion	1.84%
Deletions	9,807,867
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.72%

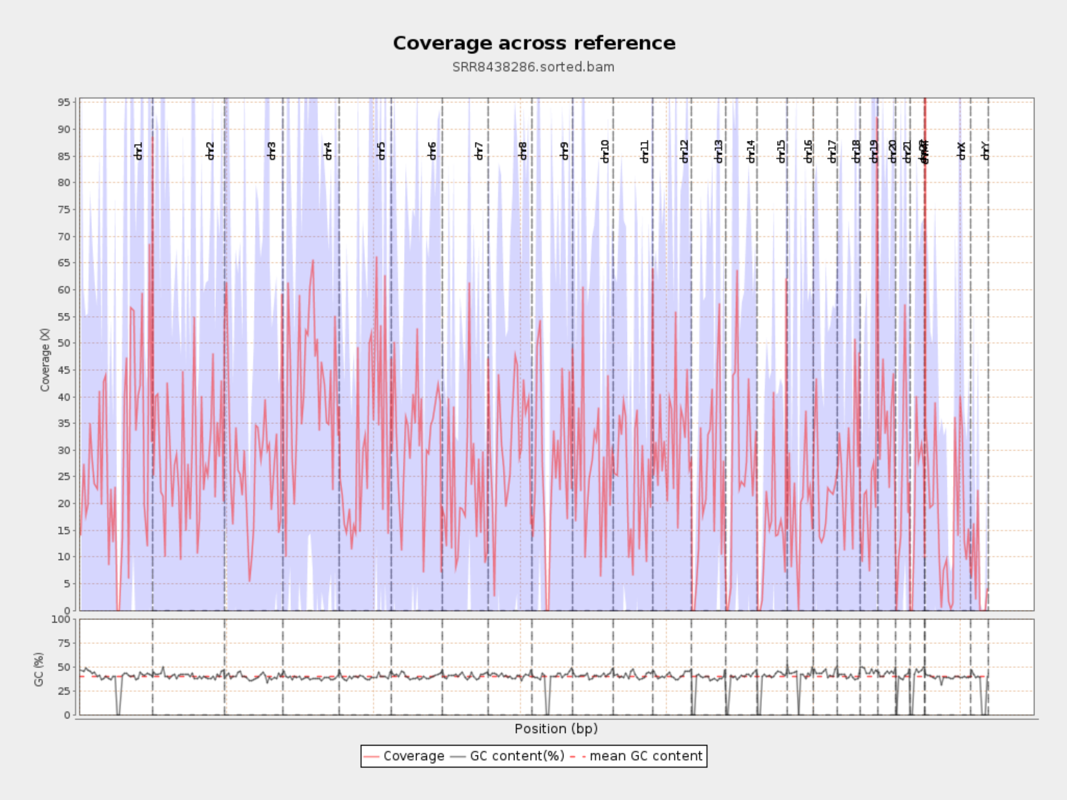
2.7. Chromosome stats

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

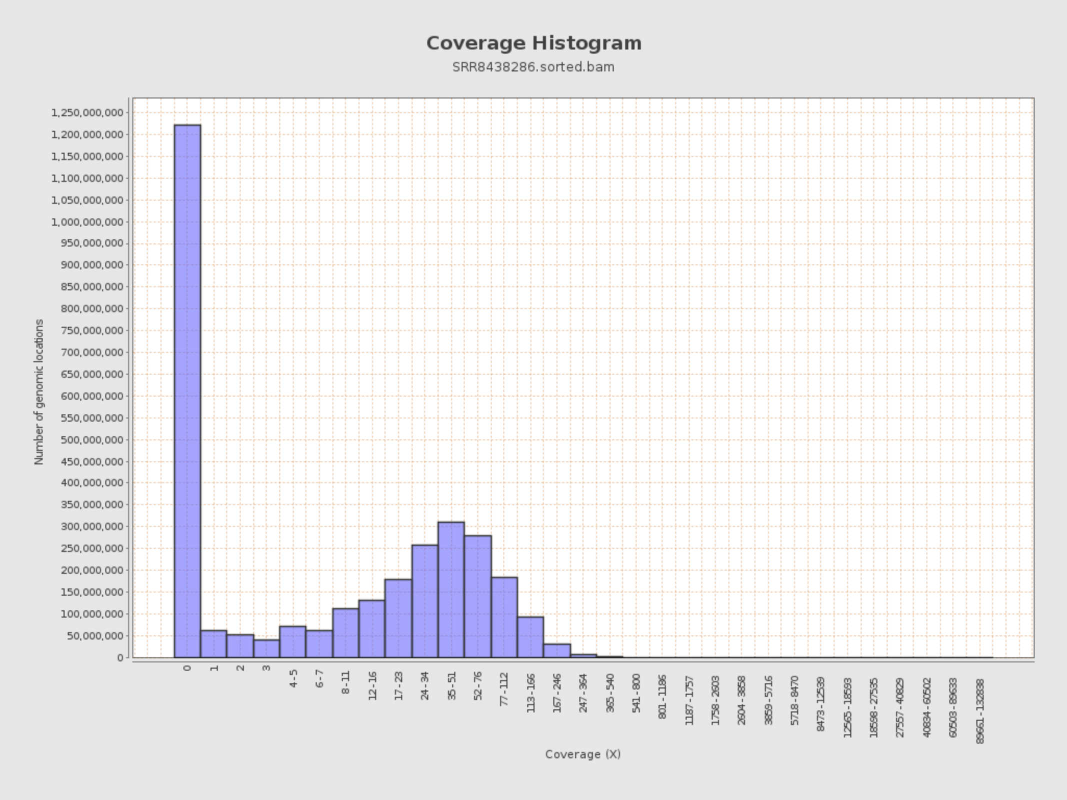
		bases	coverage	deviation
chr1	249250621	7338007882	29.4403	47.5653
chr2	243199373	6928542026	28.4891	114.9823
chr3	198022430	5463577627	27.5907	111.2138
chr4	191154276	7962304650	41.6538	46.623
chr5	180915260	5604116751	30.9765	44.7493
chr6	171115067	5577033311	32.5923	41.892
chr7	159138663	3554388829	22.3352	36.0249
chr8	146364022	4425073015	30.2333	41.6826
chr9	141213431	3726789393	26.3912	43.6209
chr10	135534747	3770709117	27.821	44.7081
chr11	135006516	3359867019	24.8867	37.6379
chr12	133851895	4308639887	32.1896	45.8537
chr13	115169878	2769351370	24.0458	38.8175
chr14	107349540	2990378302	27.8565	40.9316
chr15	102531392	1532128490	14.943	29.0706
chr16	90354753	1706332296	18.8848	46.4624
chr17	81195210	1828742131	22.5228	39.0159
chr18	78077248	2222610685	28.4668	42.9755
chr19	59128983	1271343412	21.5012	128.4606
chr20	63025520	2168718298	34.4102	45.1634
chr21	48129895	1132498657	23.53	49.6456
chr22	51304566	1105204366	21.542	38.8692
chrMT	16571	957917608	57,806.8679	23,044.9653
chrX	155270560	2719206466	17.5127	35.9289

chrY	59373566	382109106	6.4357	22.1494

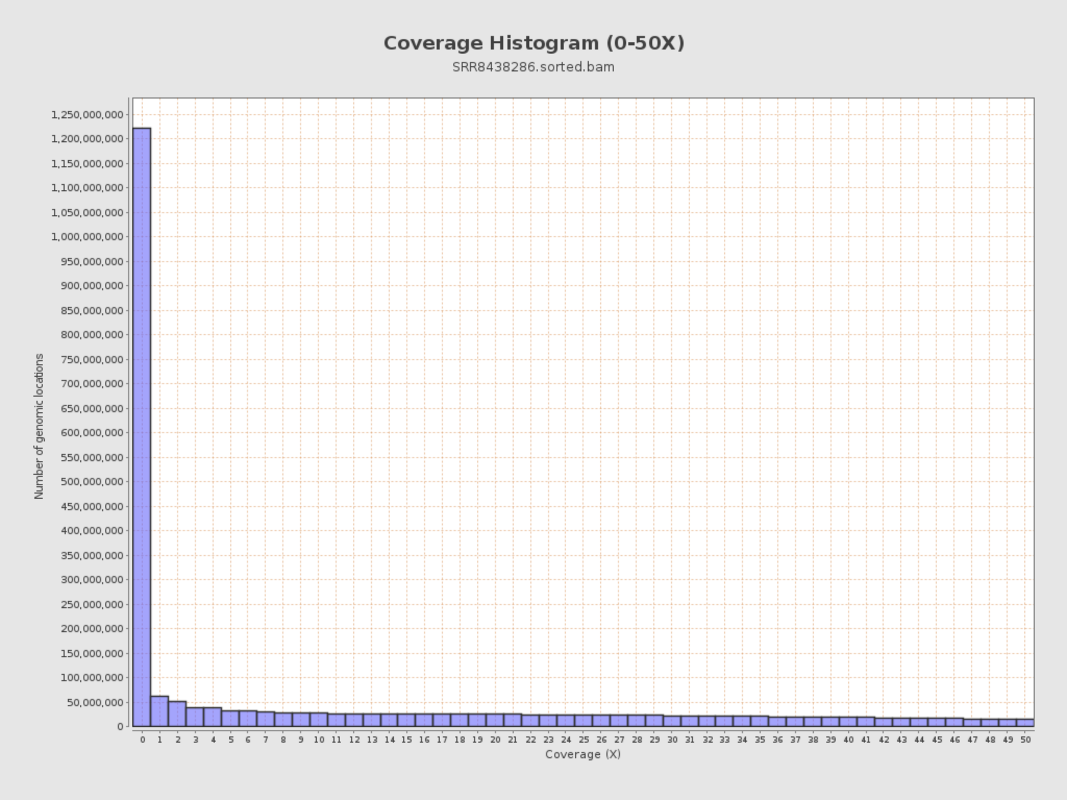
3. Results : Coverage across reference



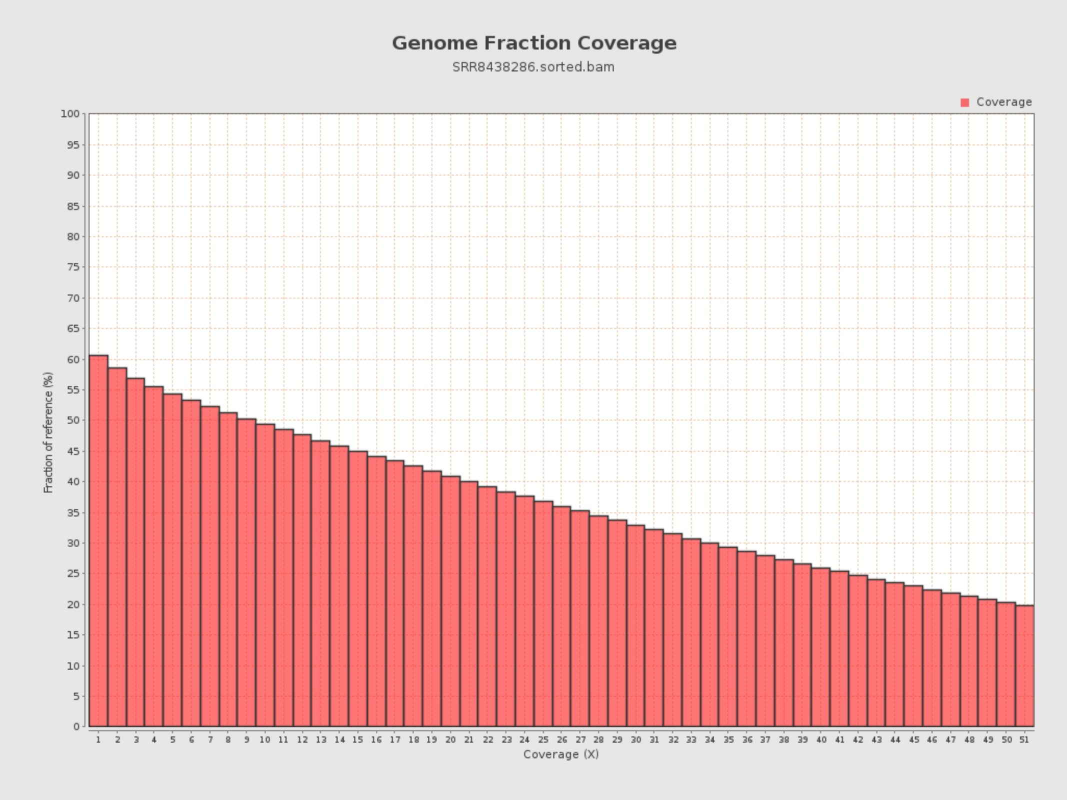
4. Results : Coverage Histogram



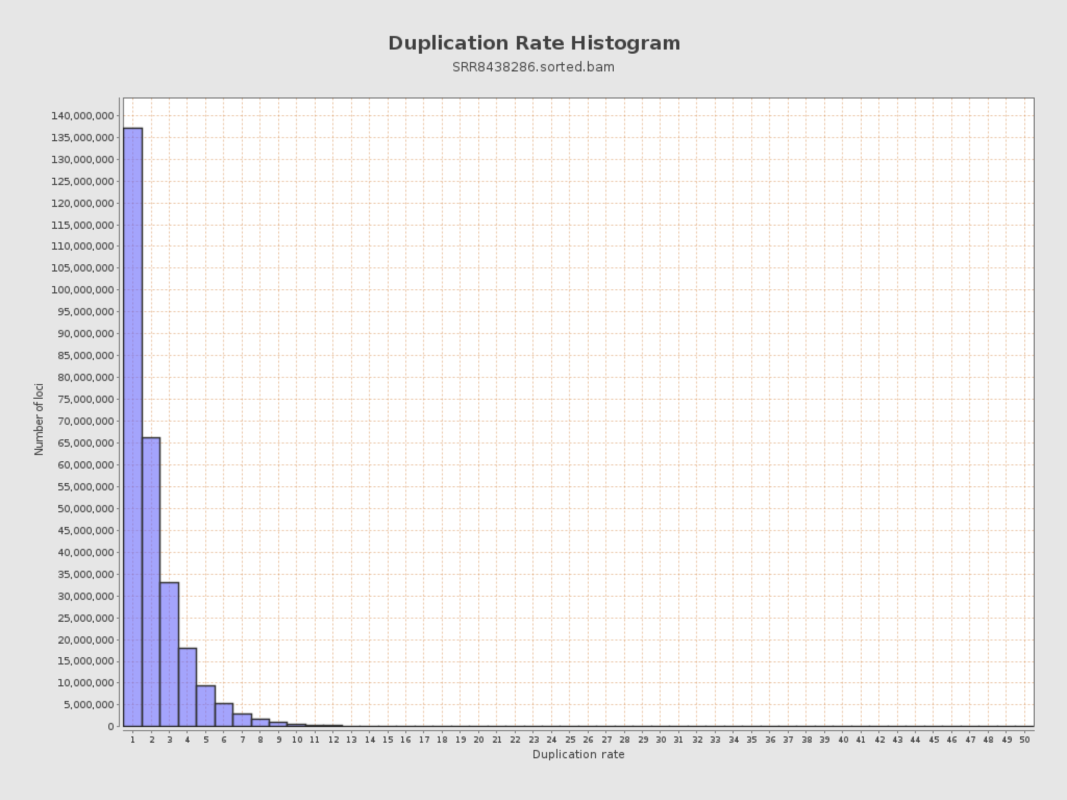
5. Results : Coverage Histogram (0-50X)



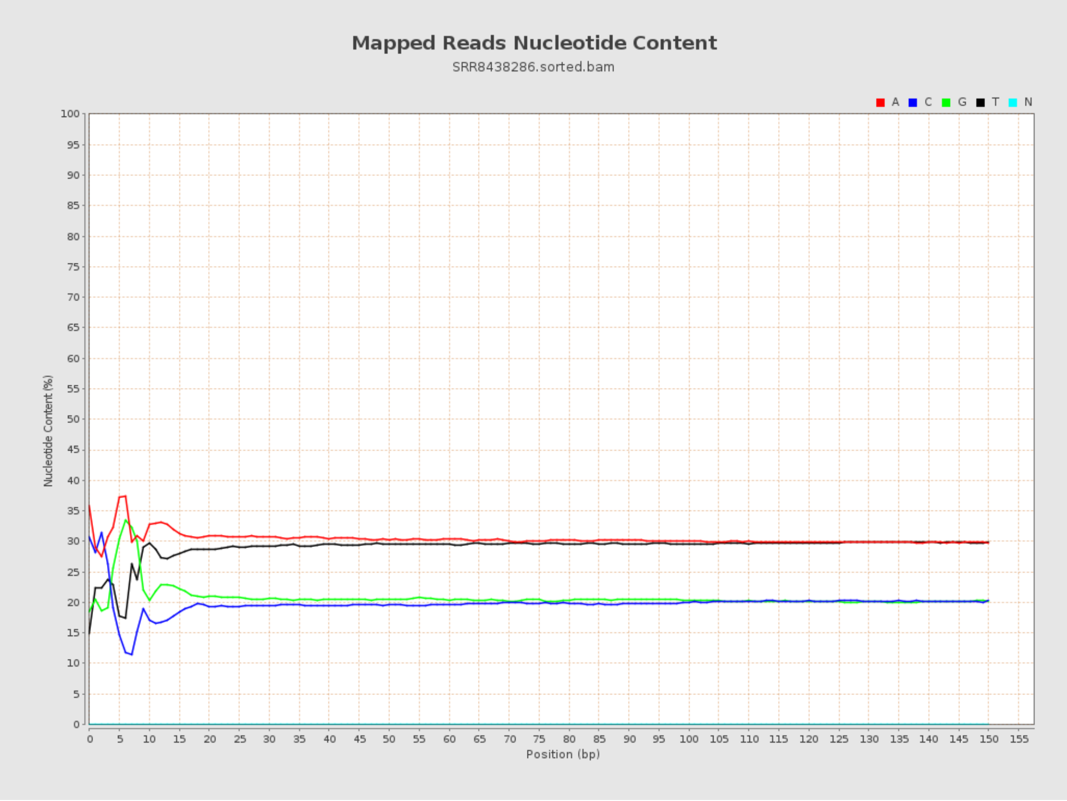
6. Results : Genome Fraction Coverage



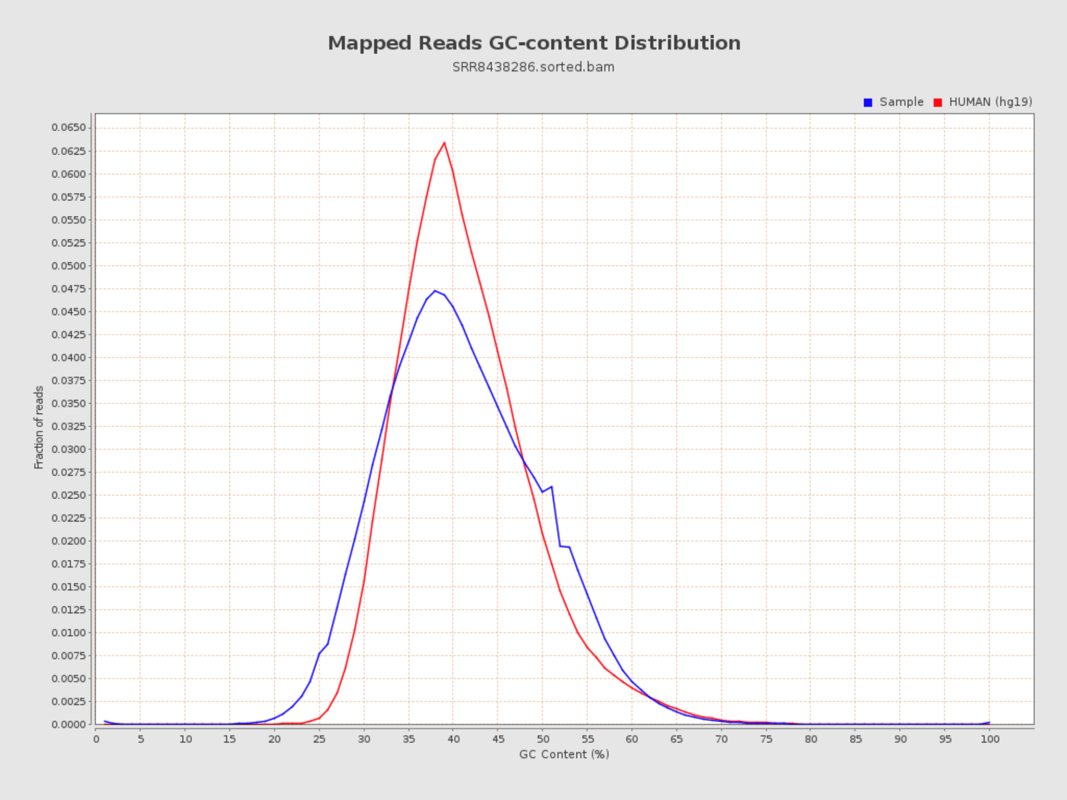
7. Results : Duplication Rate Histogram



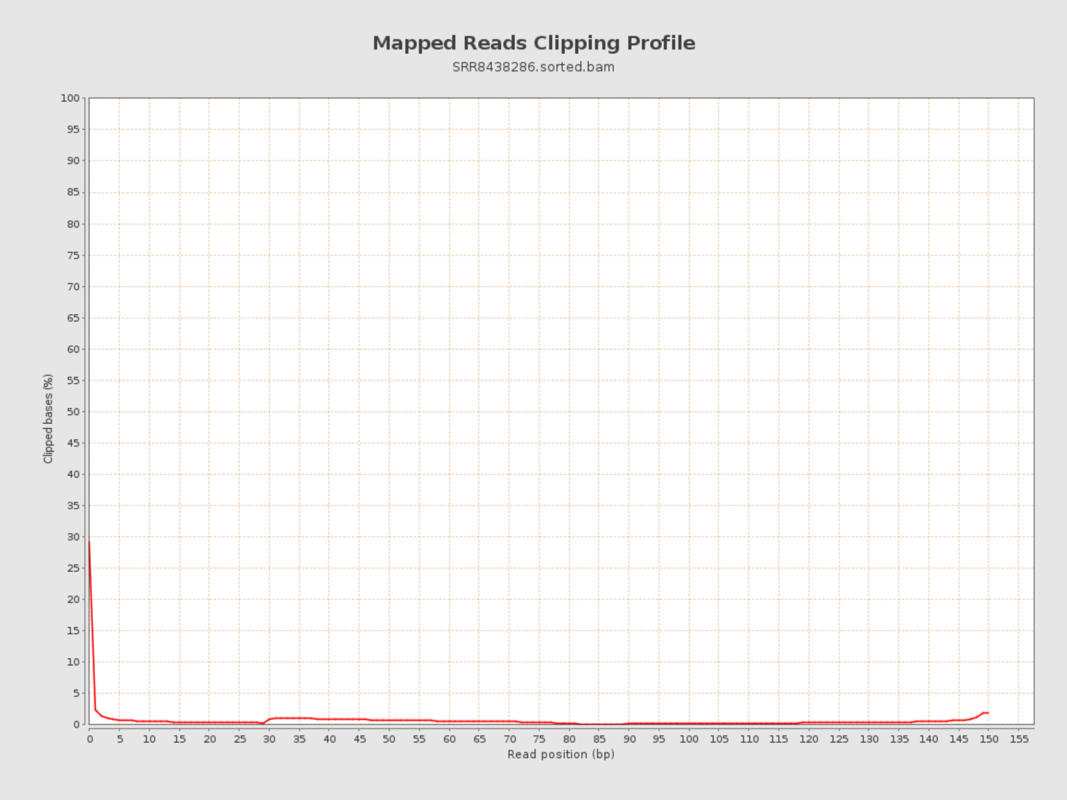
8. Results : Mapped Reads Nucleotide Content



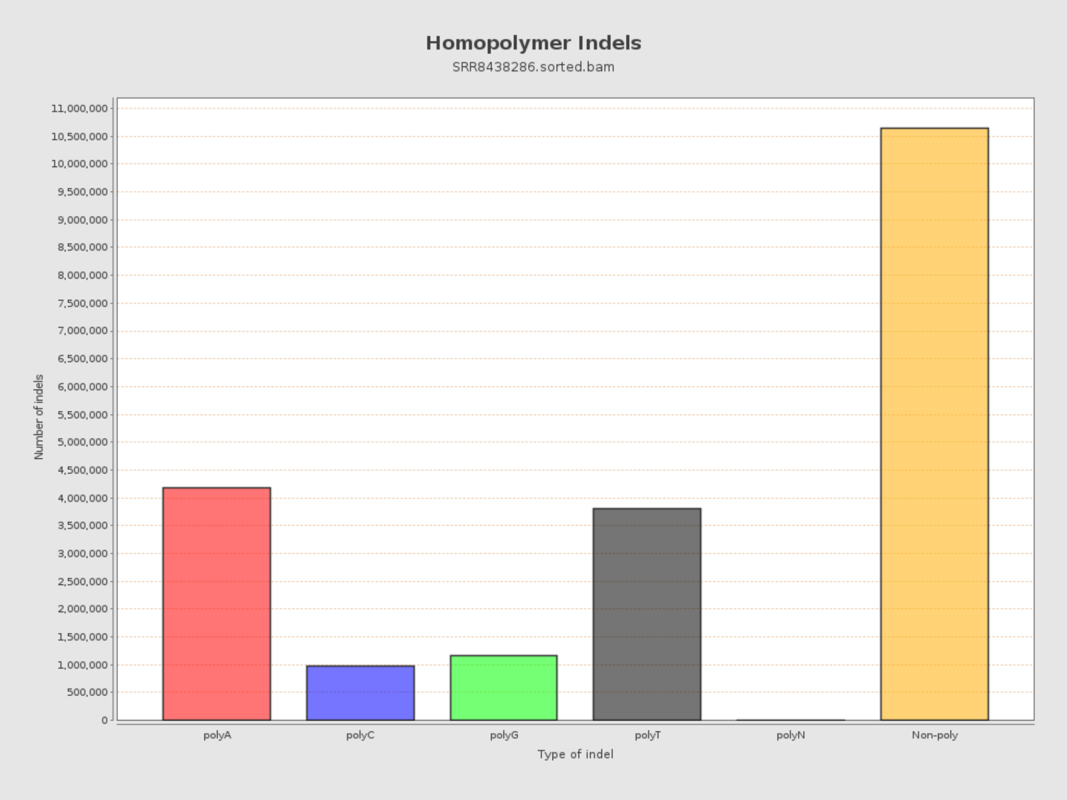
9. Results : Mapped Reads GC-content Distribution



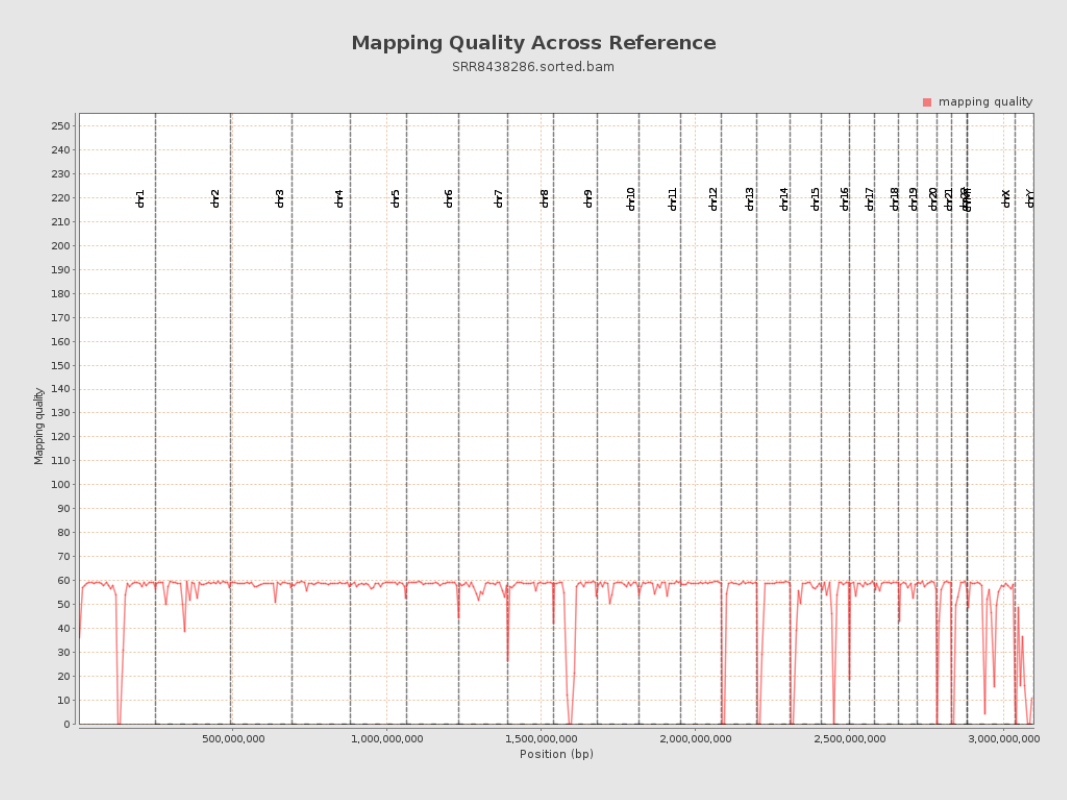
10. Results : Mapped Reads Clipping Profile



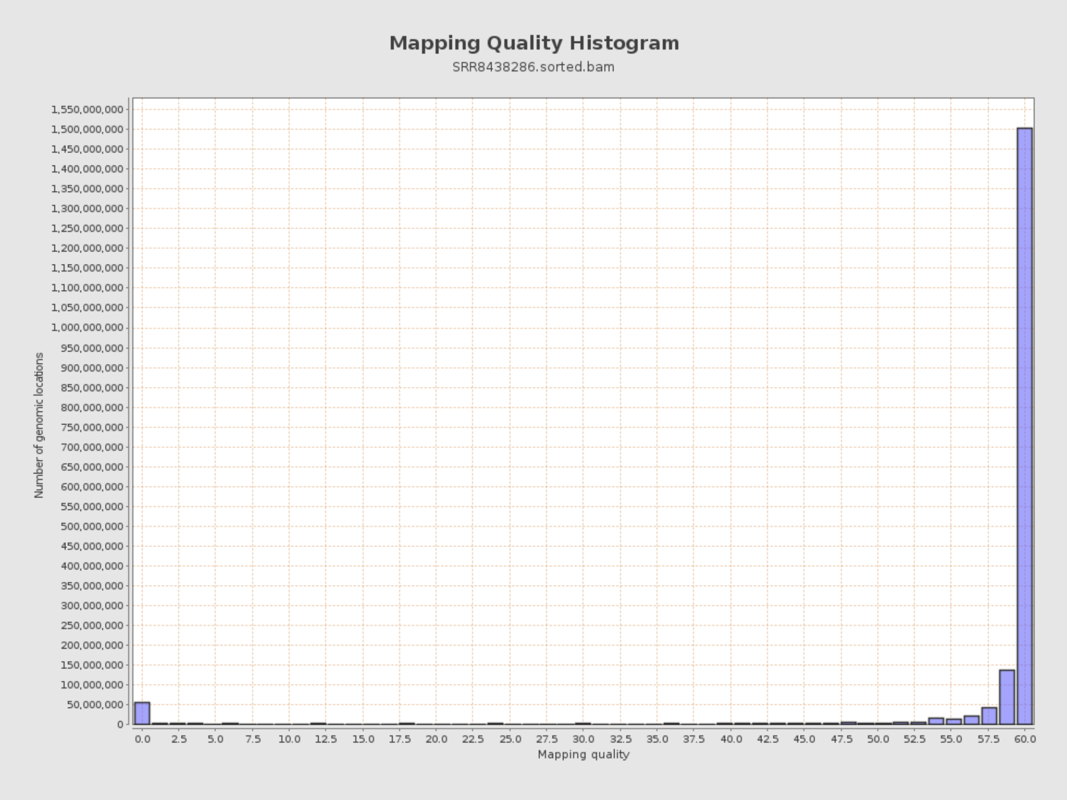
11. Results : Homopolymer Indels



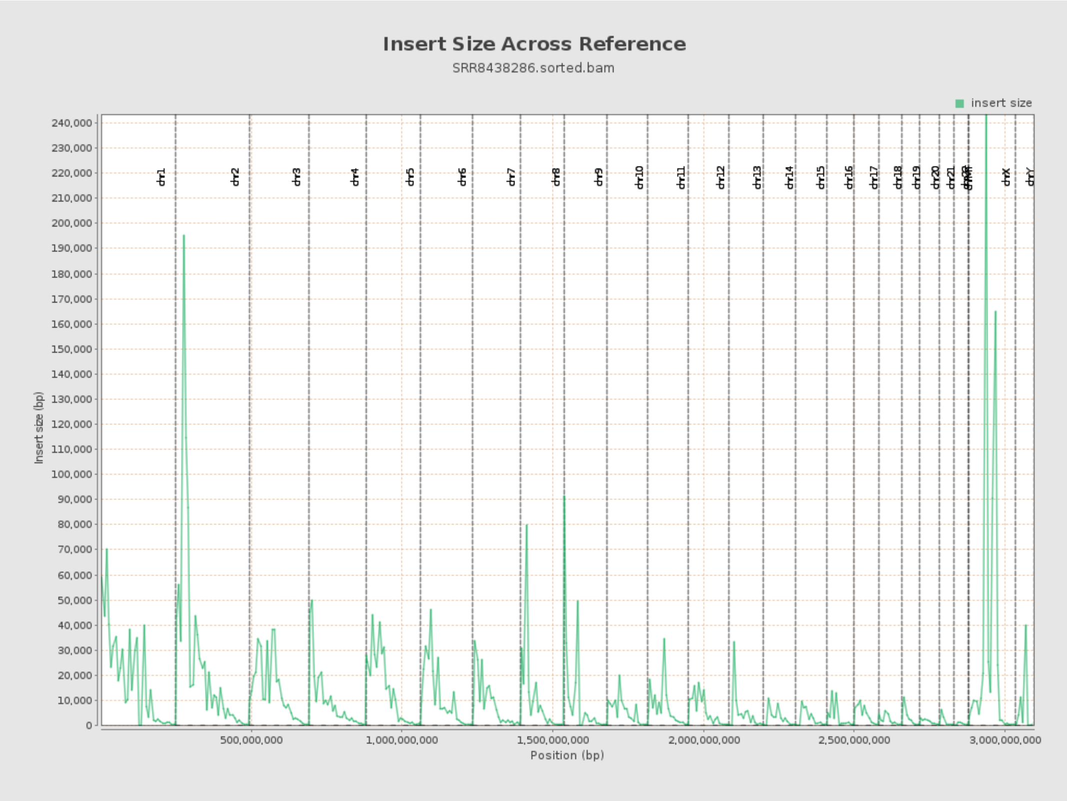
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram