Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/05 06:11:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438300.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_SRR8438300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438300_1.fastq.gz SRR8438300_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 05 06:11:27 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	778,937,652
Mapped reads	774,938,336 / 99.49%
Unmapped reads	3,999,316 / 0.51%
Mapped paired reads	774,938,336 / 99.49%
Mapped reads, first in pair	387,622,105 / 49.76%
Mapped reads, second in pair	387,316,231 / 49.72%
Mapped reads, both in pair	772,473,878 / 99.17%
Mapped reads, singletons	2,464,458 / 0.32%
Secondary alignments	0
Supplementary alignments	21,453,715 / 2.75%
Read min/max/mean length	30 / 149 / 143.43
Duplicated reads (estimated)	317,646,739 / 40.78%
Duplication rate	35.93%
Clipped reads	107,828,214 / 13.84%

2.2. ACGT Content

Number/percentage of A's	33,771,646,390 / 30.74%
Number/percentage of C's	20,806,433,729 / 18.94%
Number/percentage of T's	31,816,781,453 / 28.96%
Number/percentage of G's	23,454,804,092 / 21.35%
Number/percentage of N's	202,247 / 0%

GC Percentage	40.29%

2.3. Coverage

Mean	35.4962
Standard Deviation	128.4346

2.4. Mapping Quality

Mean Mapping Quality	54.27

2.5. Insert size

Mean	104,440.31
Standard Deviation	3,123,967.77
P25/Median/P75	379 / 454 / 572

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	599,185,493
Insertions	14,645,391
Mapped reads with at least one insertion	1.84%
Deletions	12,954,506
Mapped reads with at least one deletion	1.63%
Homopolymer indels	48.05%

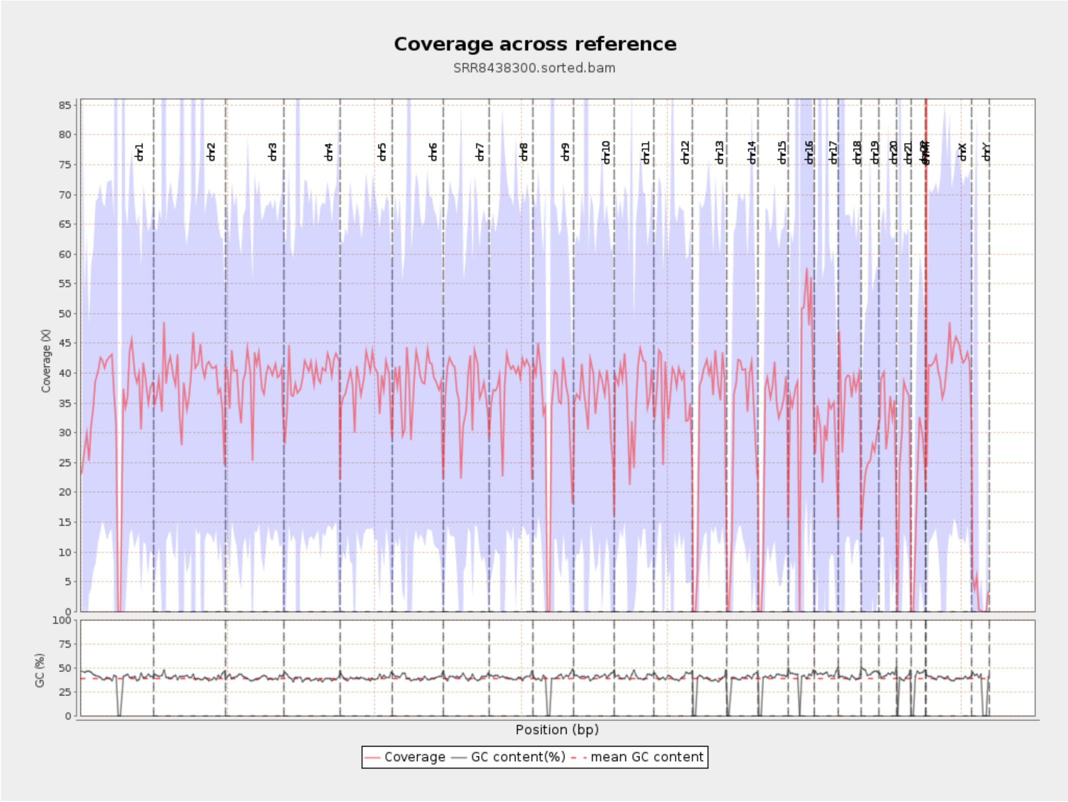
2.7. Chromosome stats

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

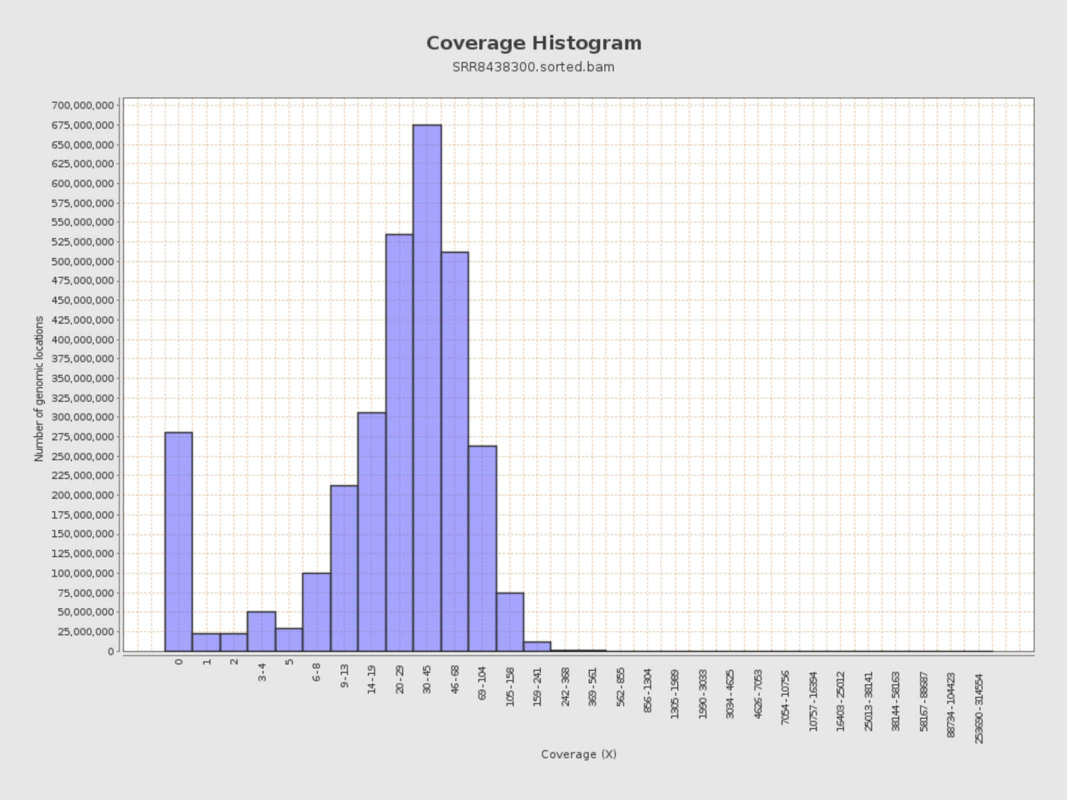
		bases	coverage	deviation
chr1	249250621	8646160993	34.6886	44.3153
chr2	243199373	9452295633	38.8664	235.0584
chr3	198022430	7747838956	39.1261	28.3863
chr4	191154276	7565224301	39.5765	38.4645
chr5	180915260	6915576473	38.2255	28.4021
chr6	171115067	6587593414	38.498	35.0785
chr7	159138663	5828127183	36.6229	31.0449
chr8	146364022	5586475143	38.1684	32.3585
chr9	141213431	4549113581	32.2145	58.3046
chr10	135534747	4925085173	36.3382	88.7392
chr11	135006516	4963023255	36.7614	32.2185
chr12	133851895	4927021161	36.8095	30.3598
chr13	115169878	3788300682	32.8932	29.4977
chr14	107349540	3322530948	30.9506	30.1608
chr15	102531392	3022397238	29.4778	29.2688
chr16	90354753	3552046938	39.3122	113.5182
chr17	81195210	2399986962	29.5582	49.8903
chr18	78077248	2945945748	37.7312	68.2919
chr19	59128983	1468662974	24.8383	31.144
chr20	63025520	2095338598	33.2459	32.641
chr21	48129895	1399674226	29.0812	46.4226
chr22	51304566	965748756	18.8238	25.8959
chrMT	16571	678460622	40,942.6481	15,244.2563
chrX	155270560	6417428191	41.3306	32.1437

chrY	59373566	135215144	2.2774	38.4464

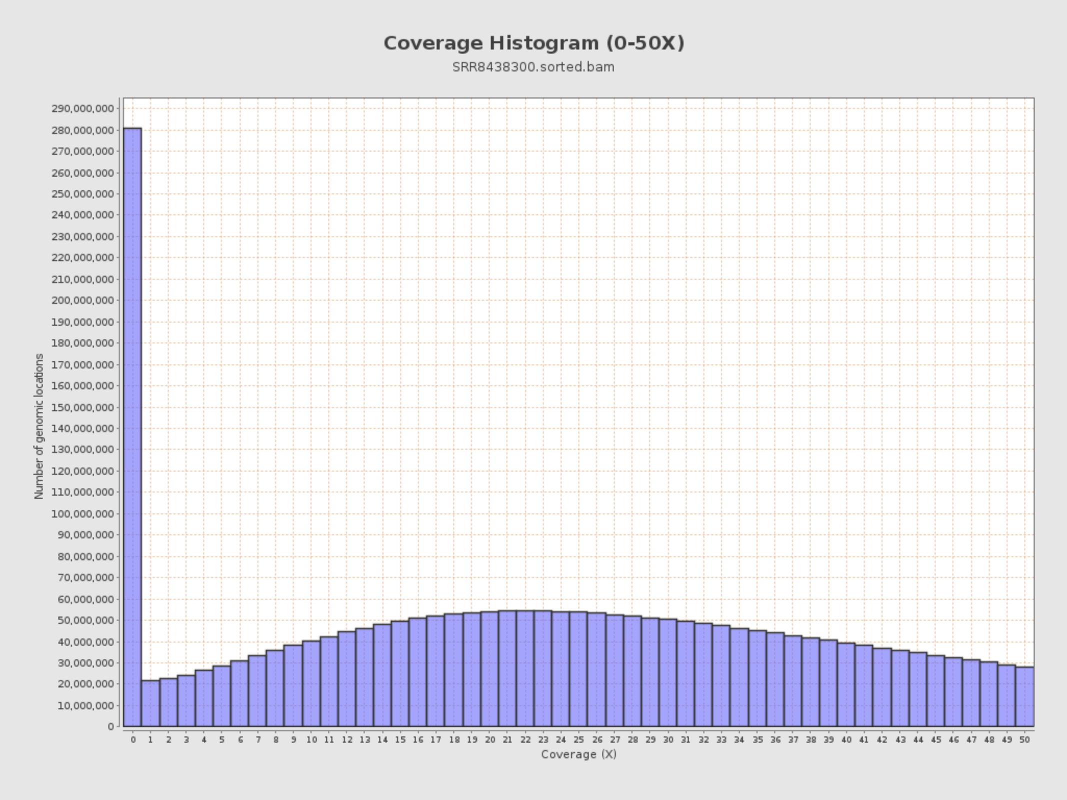
3. Results : Coverage across reference



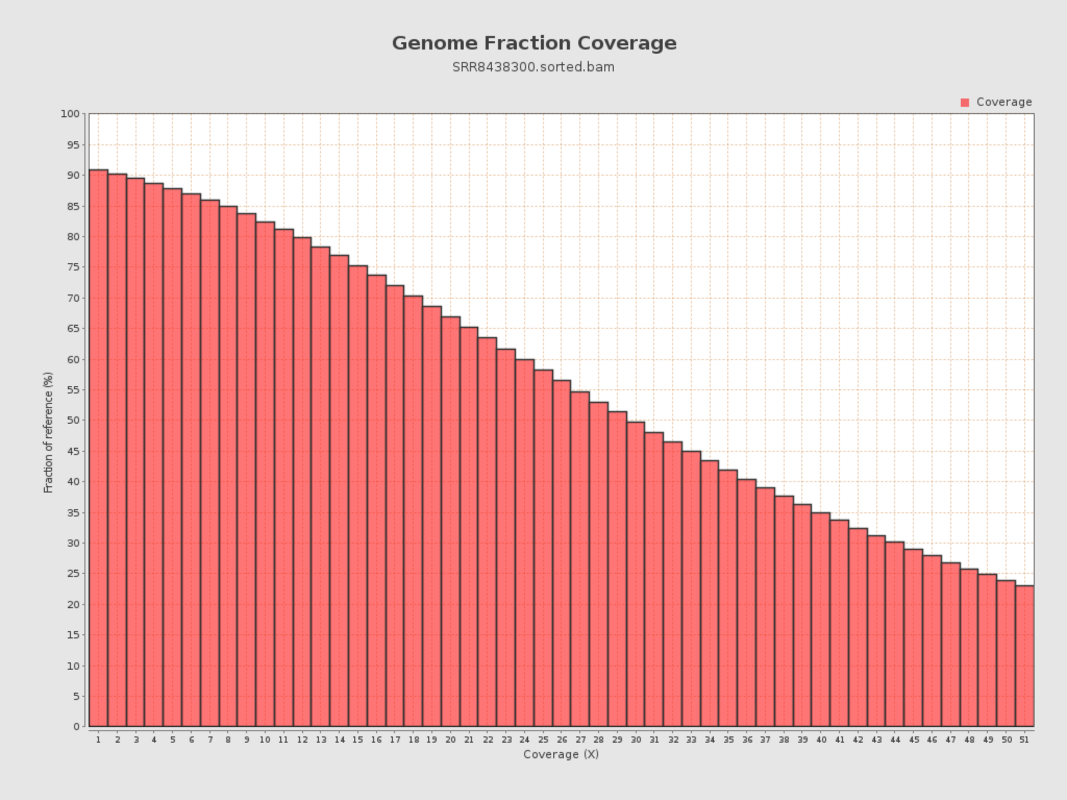
4. Results : Coverage Histogram



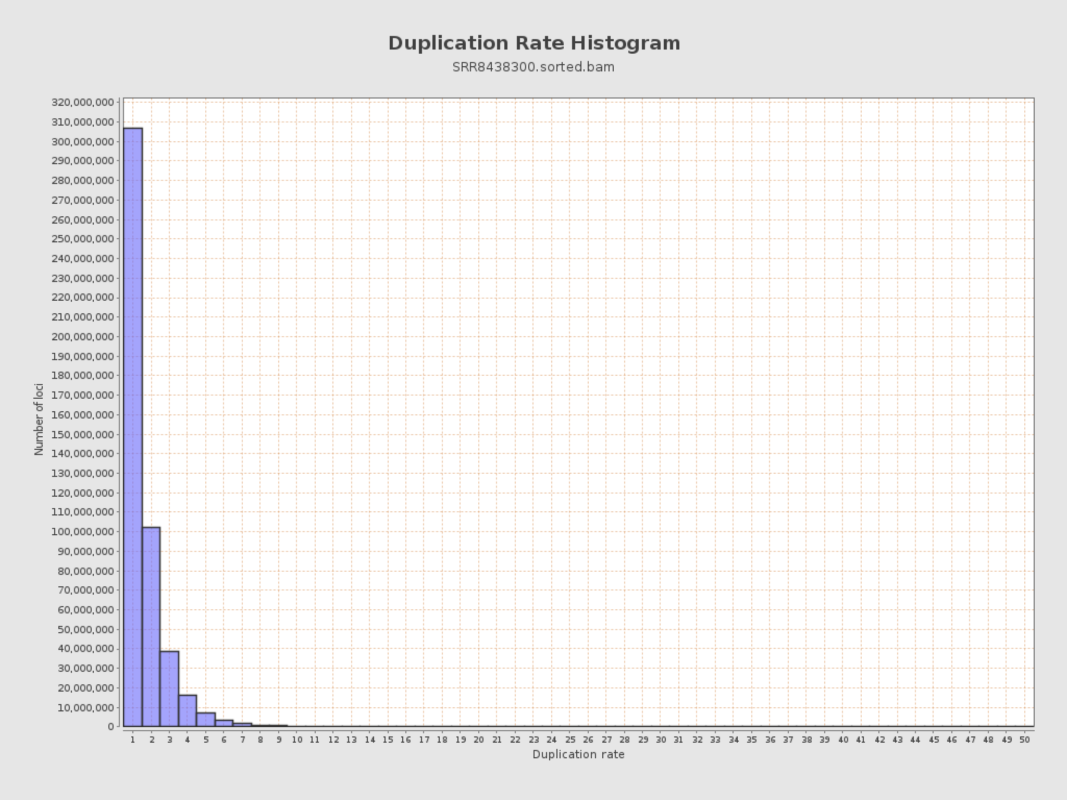
5. Results : Coverage Histogram (0-50X)



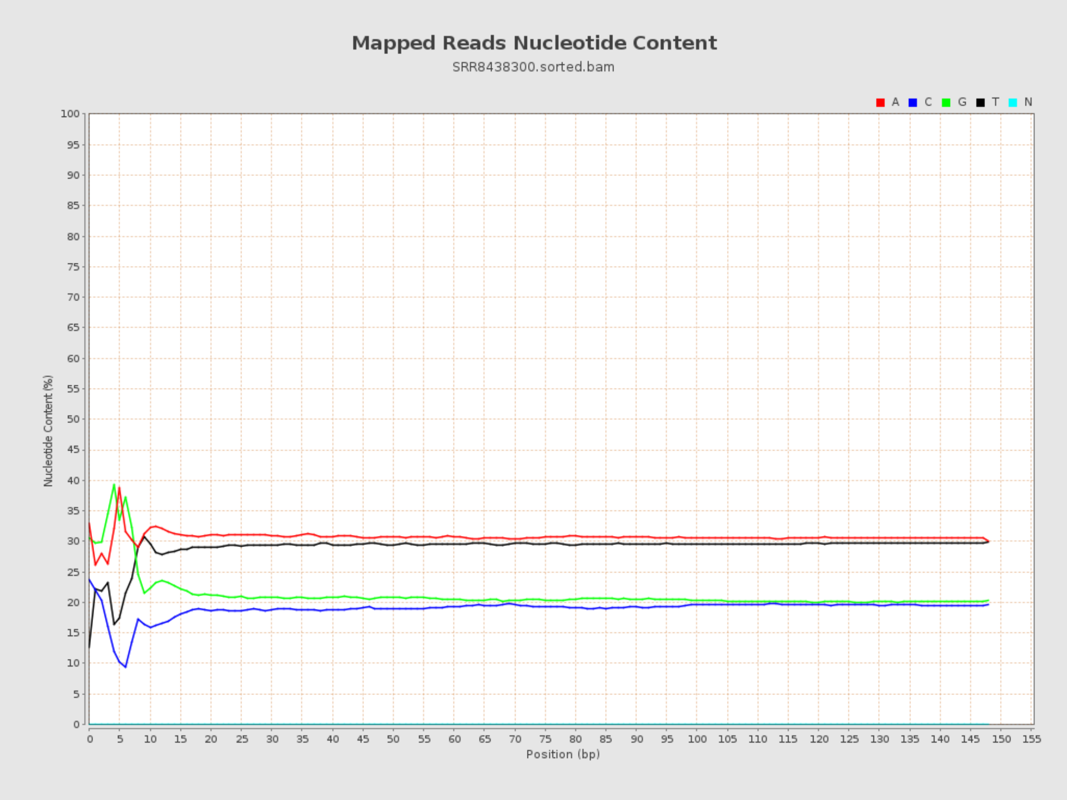
6. Results : Genome Fraction Coverage



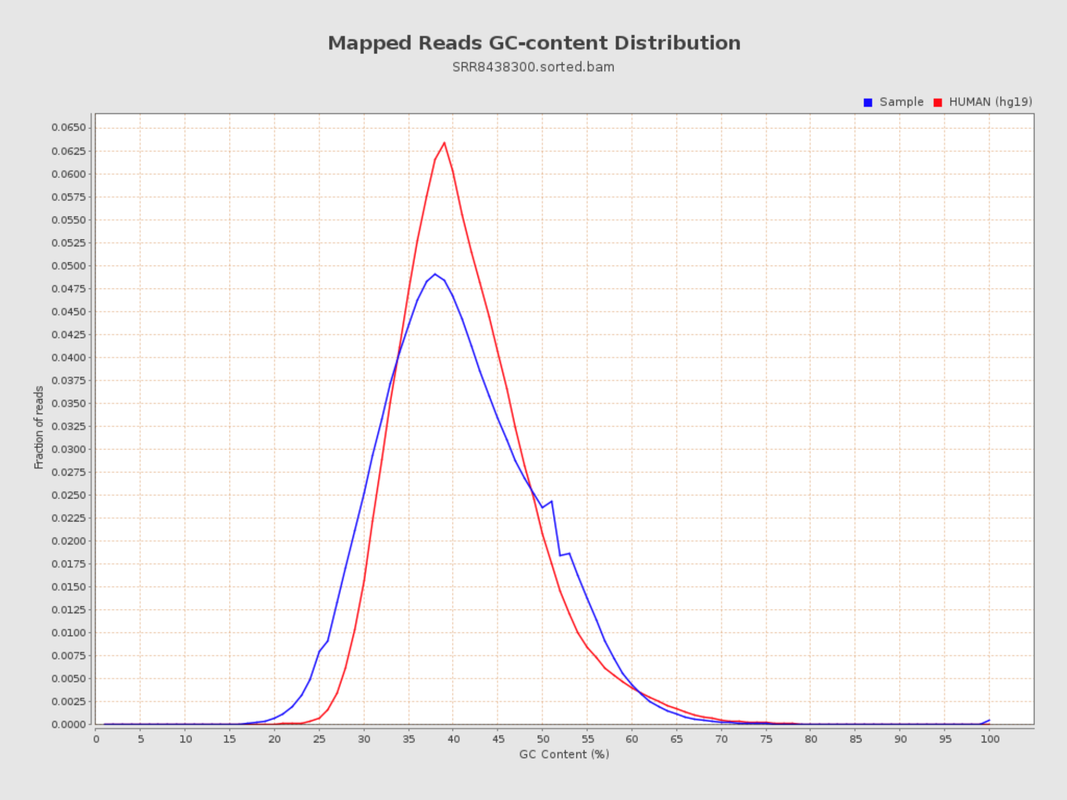
7. Results : Duplication Rate Histogram



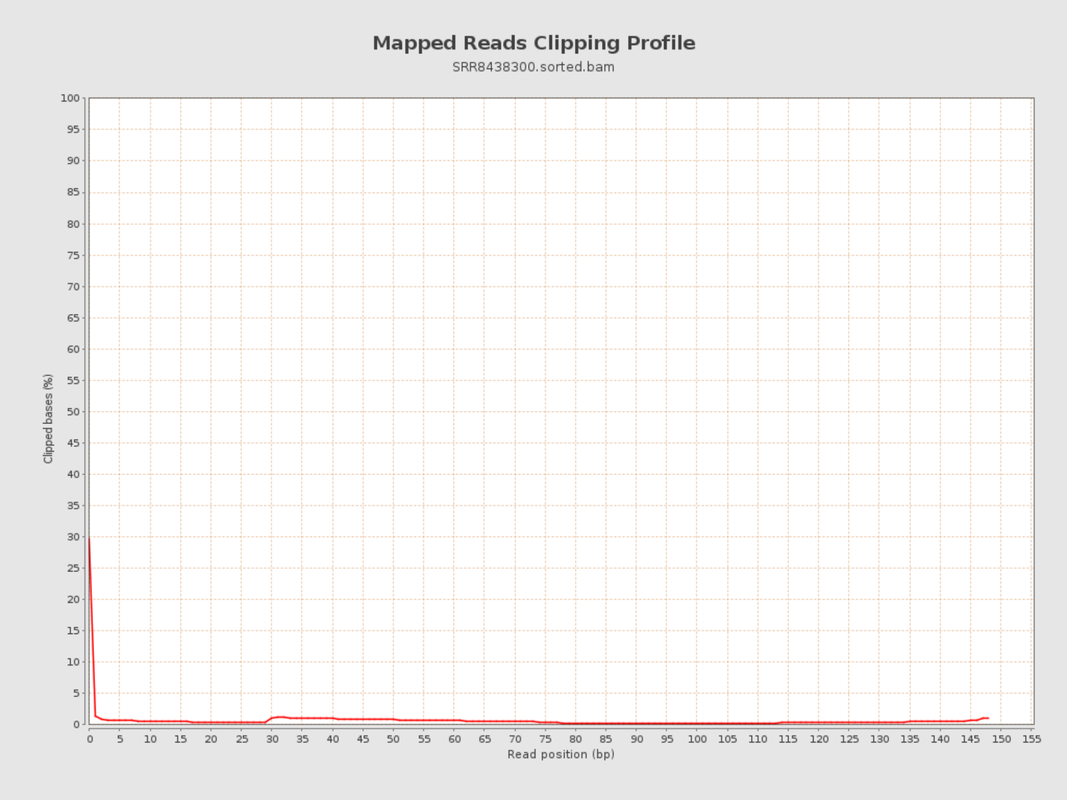
8. Results : Mapped Reads Nucleotide Content



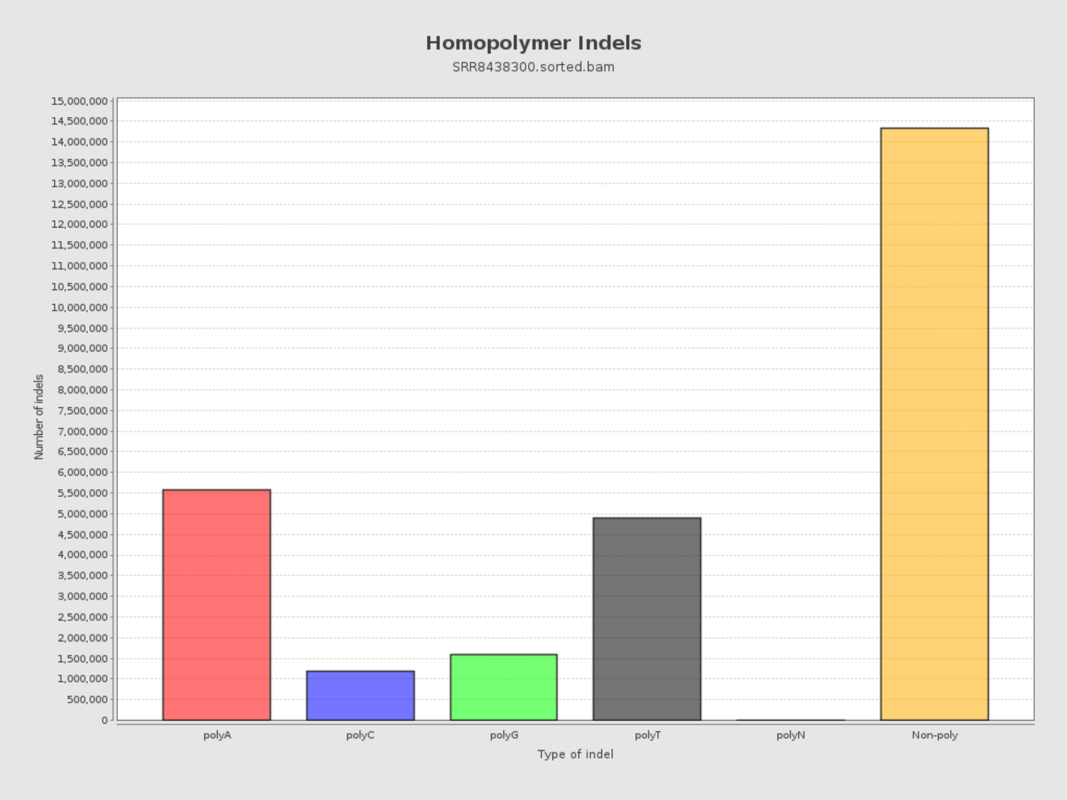
9. Results : Mapped Reads GC-content Distribution



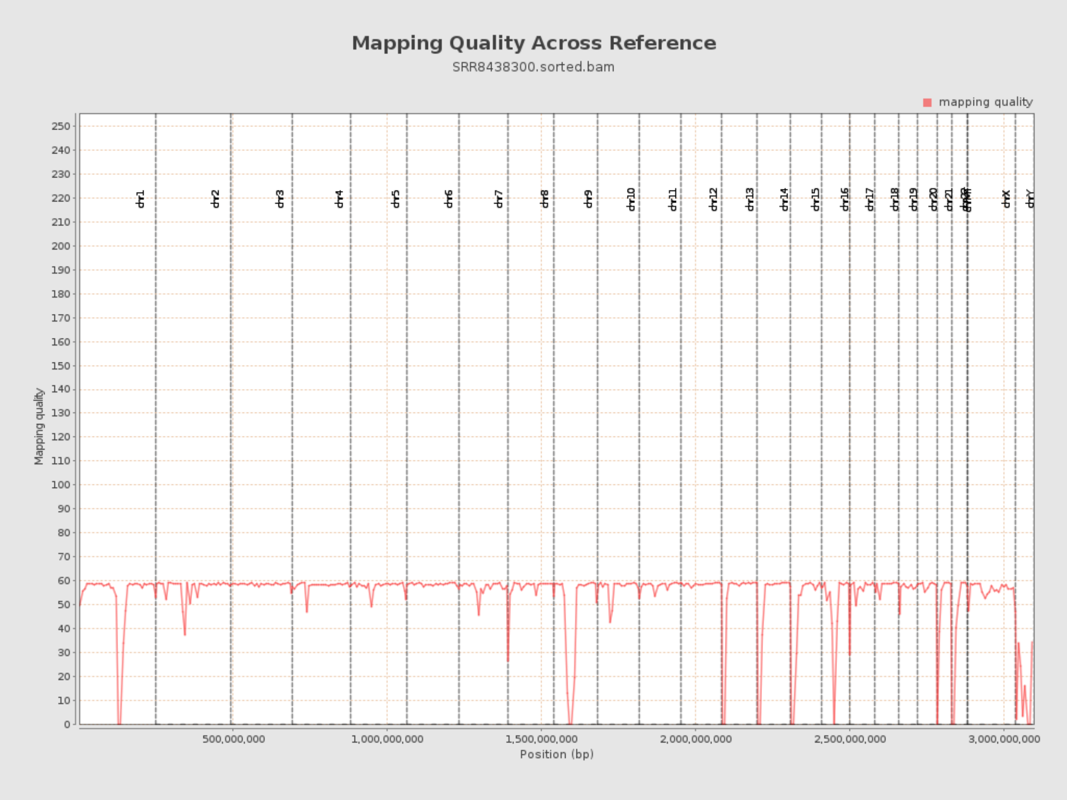
10. Results : Mapped Reads Clipping Profile



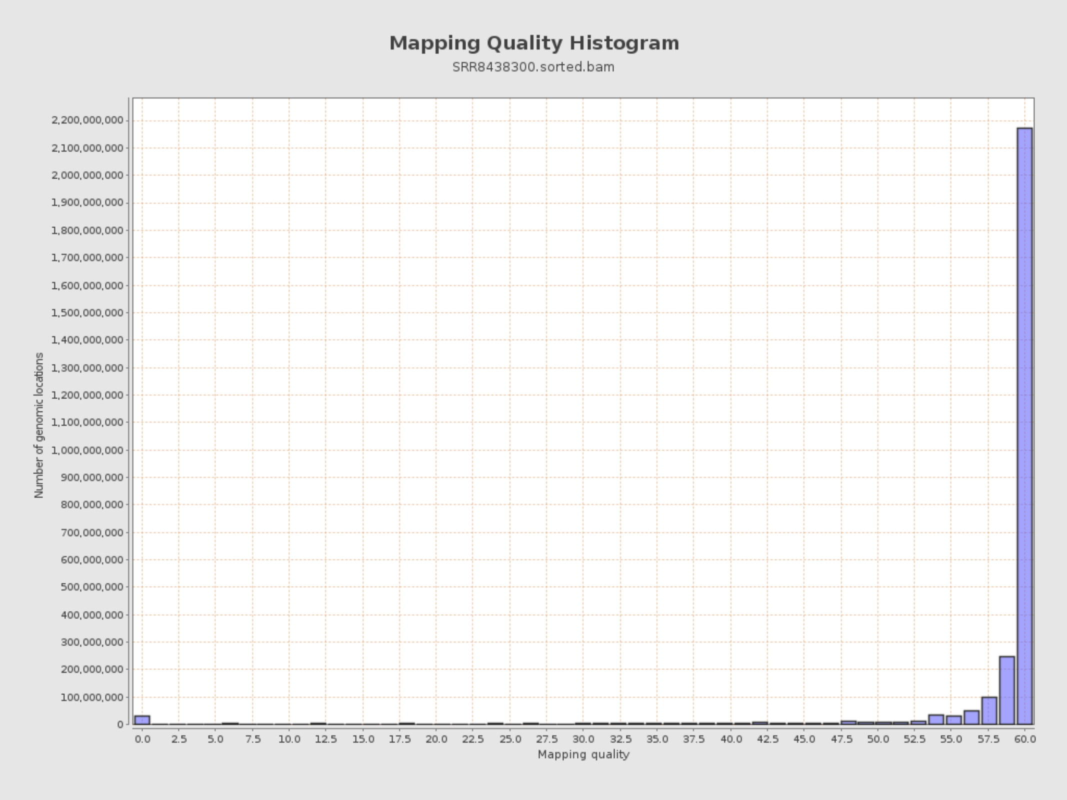
11. Results : Homopolymer Indels



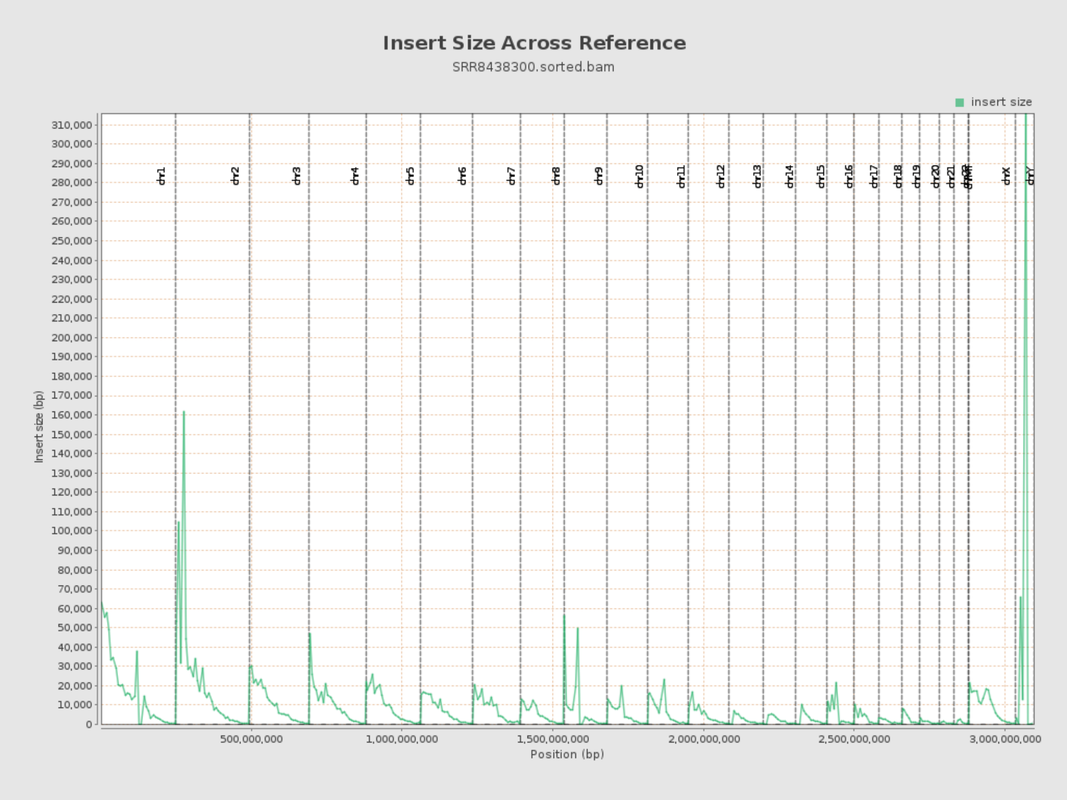
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram