Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/11 02:15:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438261.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_SRR8438261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438261_1.fastq.gz SRR8438261_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 11 02:15:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	758,121,248
Mapped reads	755,837,574 / 99.7%
Unmapped reads	2,283,674 / 0.3%
Mapped paired reads	755,837,574 / 99.7%
Mapped reads, first in pair	378,151,399 / 49.88%
Mapped reads, second in pair	377,686,175 / 49.82%
Mapped reads, both in pair	754,511,470 / 99.52%
Mapped reads, singletons	1,326,104 / 0.17%
Secondary alignments	0
Supplementary alignments	14,591,773 / 1.92%
Read min/max/mean length	30 / 149 / 126.67
Duplicated reads (estimated)	270,851,417 / 35.73%
Duplication rate	34.83%
Clipped reads	168,709,329 / 22.25%

2.2. ACGT Content

Number/percentage of A's	28,112,766,094 / 30.69%
Number/percentage of C's	17,889,493,766 / 19.53%
Number/percentage of T's	27,496,074,245 / 30.02%
Number/percentage of G's	18,091,062,540 / 19.75%
Number/percentage of N's	213,479 / 0%

GC Percentage	39.28%

2.3. Coverage

Mean	29.5925
Standard Deviation	188.538

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	158,913.43
Standard Deviation	3,928,626.78
P25/Median/P75	97 / 168 / 238

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	243,379,986
Insertions	13,197,834
Mapped reads with at least one insertion	1.73%
Deletions	8,697,778
Mapped reads with at least one deletion	1.14%
Homopolymer indels	49.59%

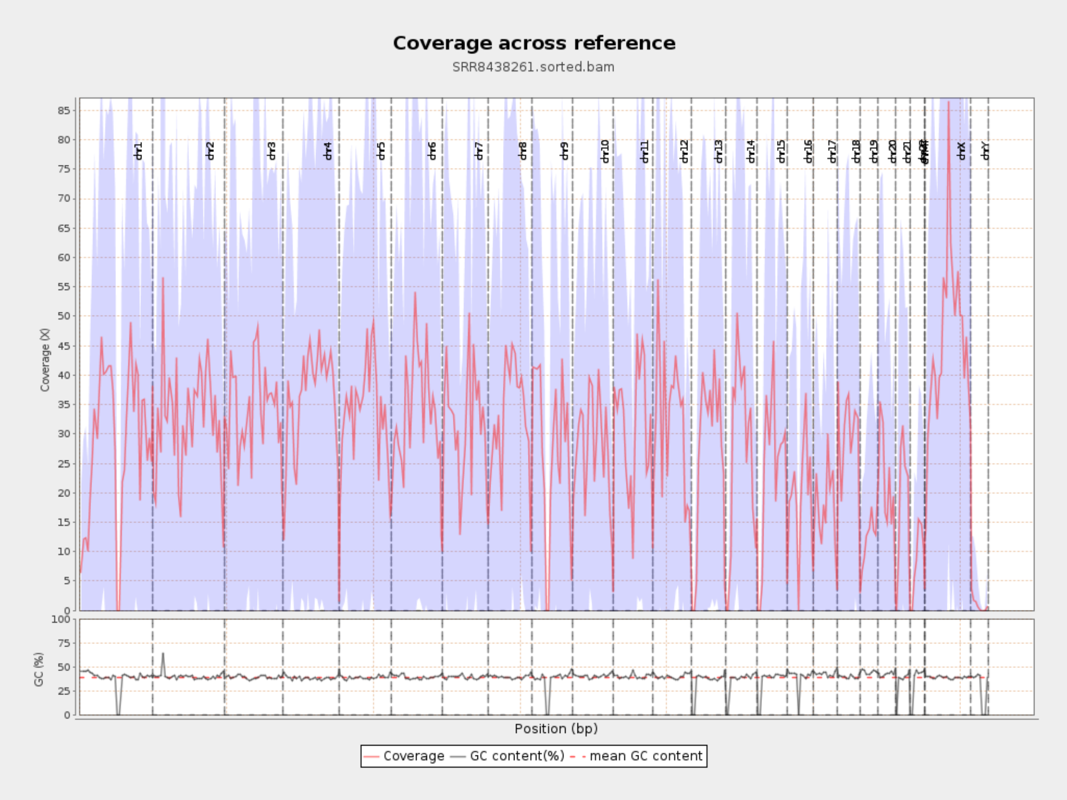
2.7. Chromosome stats

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

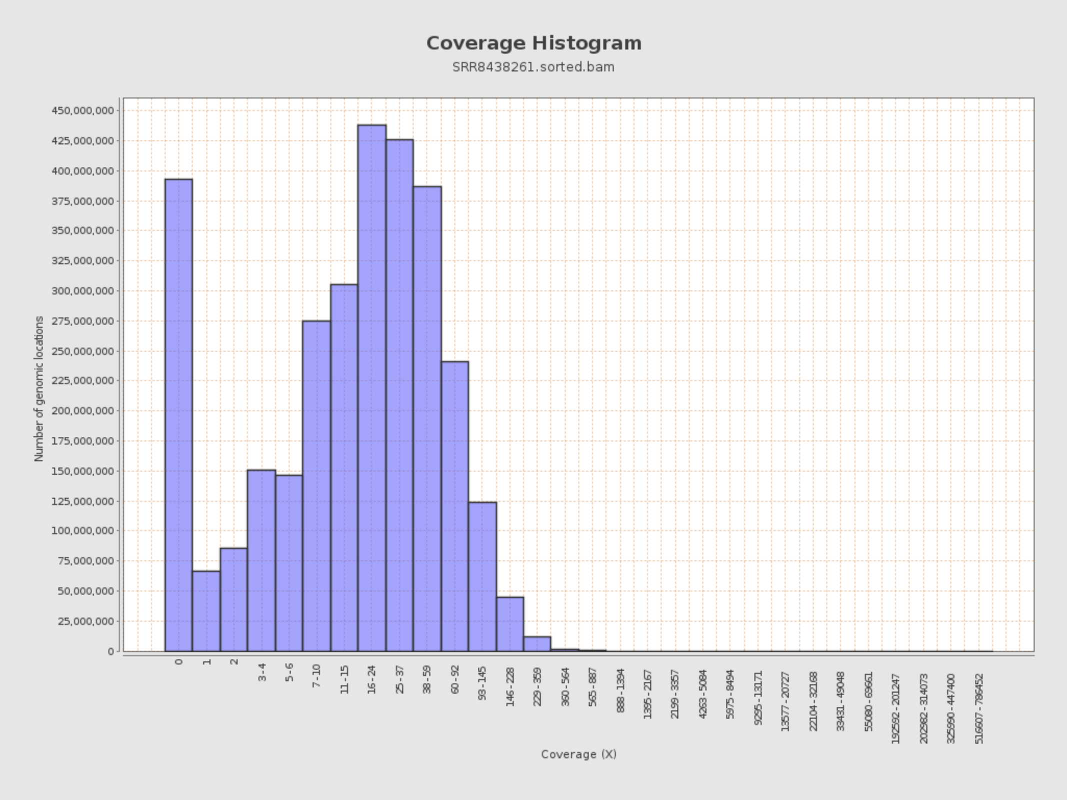
		bases	coverage	deviation
chr1	249250621	7154911991	28.7057	38.9715
chr2	243199373	7897742720	32.4744	659.76
chr3	198022430	6811235531	34.3963	39.0434
chr4	191154276	7013360644	36.6895	39.4189
chr5	180915260	6106880526	33.7555	38.0609
chr6	171115067	5901877973	34.4907	39.6871
chr7	159138663	5027427804	31.5915	37.9599
chr8	146364022	4885758292	33.3809	38.4605
chr9	141213431	3760589471	26.6305	36.9585
chr10	135534747	3817799780	28.1684	34.5086
chr11	135006516	4219738146	31.2558	38.5888
chr12	133851895	4298626938	32.1148	39.5784
chr13	115169878	3173857602	27.5581	35.0928
chr14	107349540	2929994209	27.294	37.4398
chr15	102531392	2465027856	24.0417	37.5792
chr16	90354753	1705825933	18.8792	28.8683
chr17	81195210	1415811498	17.4371	26.5562
chr18	78077248	2351000290	30.1112	34.6887
chr19	59128983	713924429	12.074	20.0822
chr20	63025520	1361544162	21.6031	32.4976
chr21	48129895	939342253	19.5168	31.1919
chr22	51304566	430891212	8.3987	17.5221
chrMT	16571	198971	12.0072	6.2034
chrX	155270560	7171353014	46.1862	53.5042

chrY	59373566	54486278	0.9177	6.327

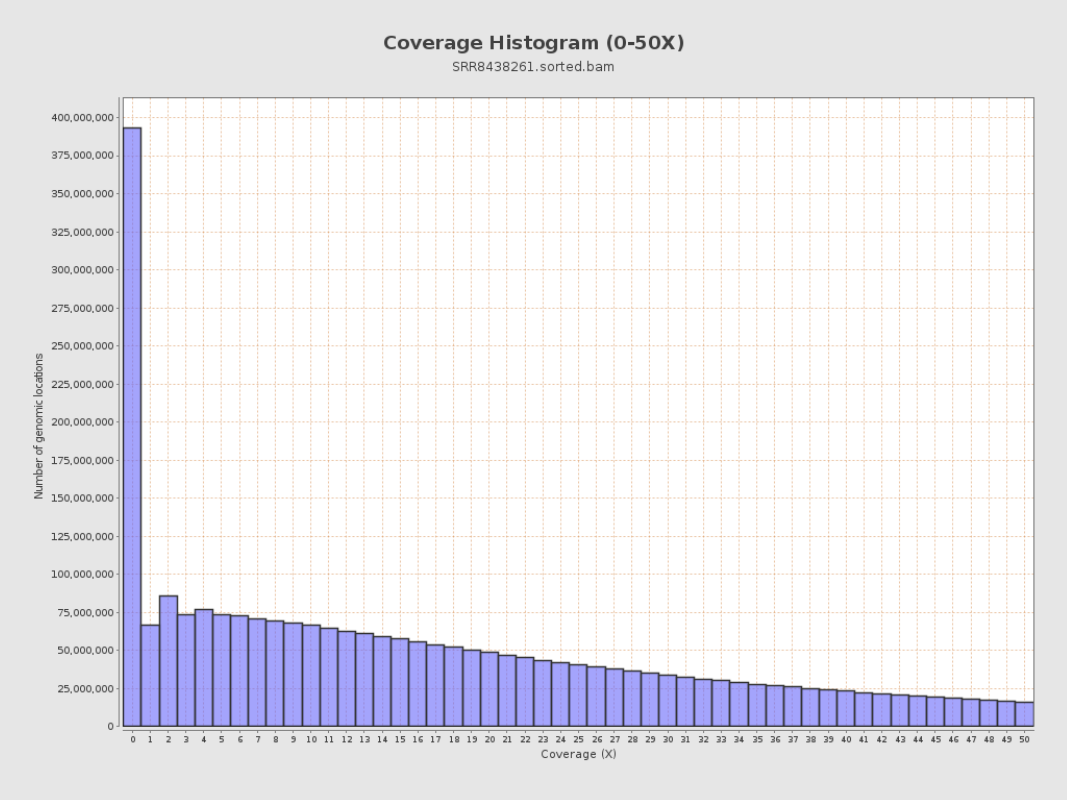
3. Results : Coverage across reference



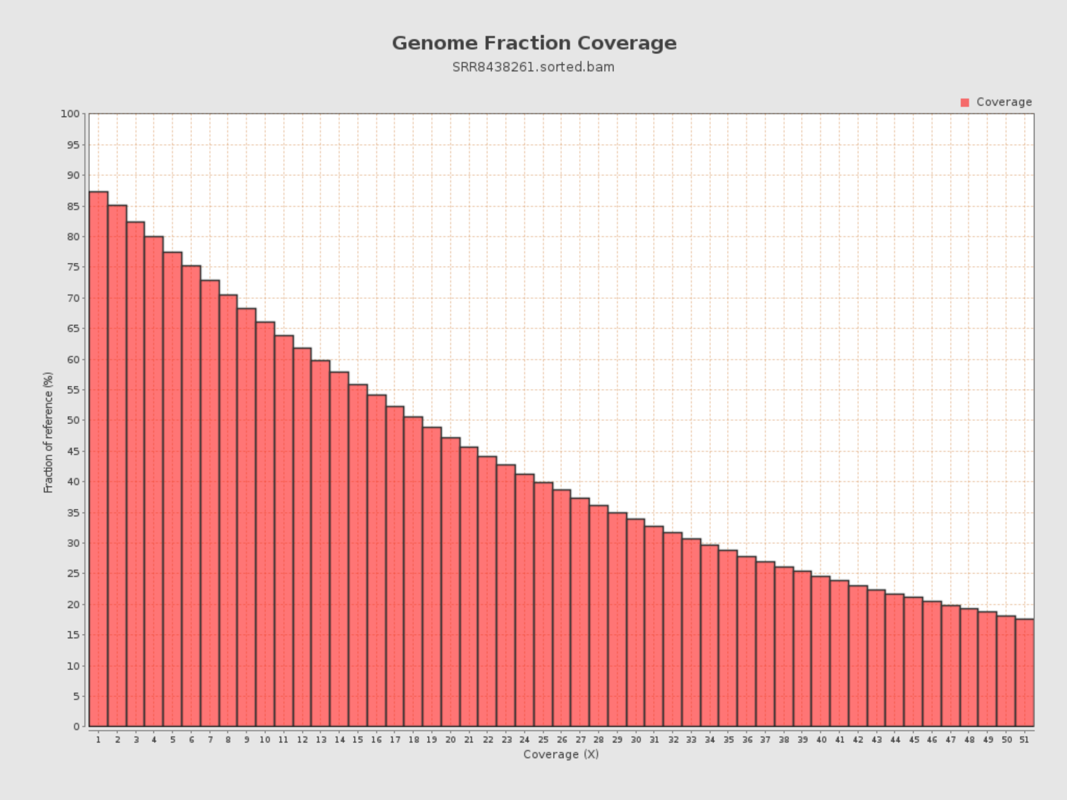
4. Results : Coverage Histogram



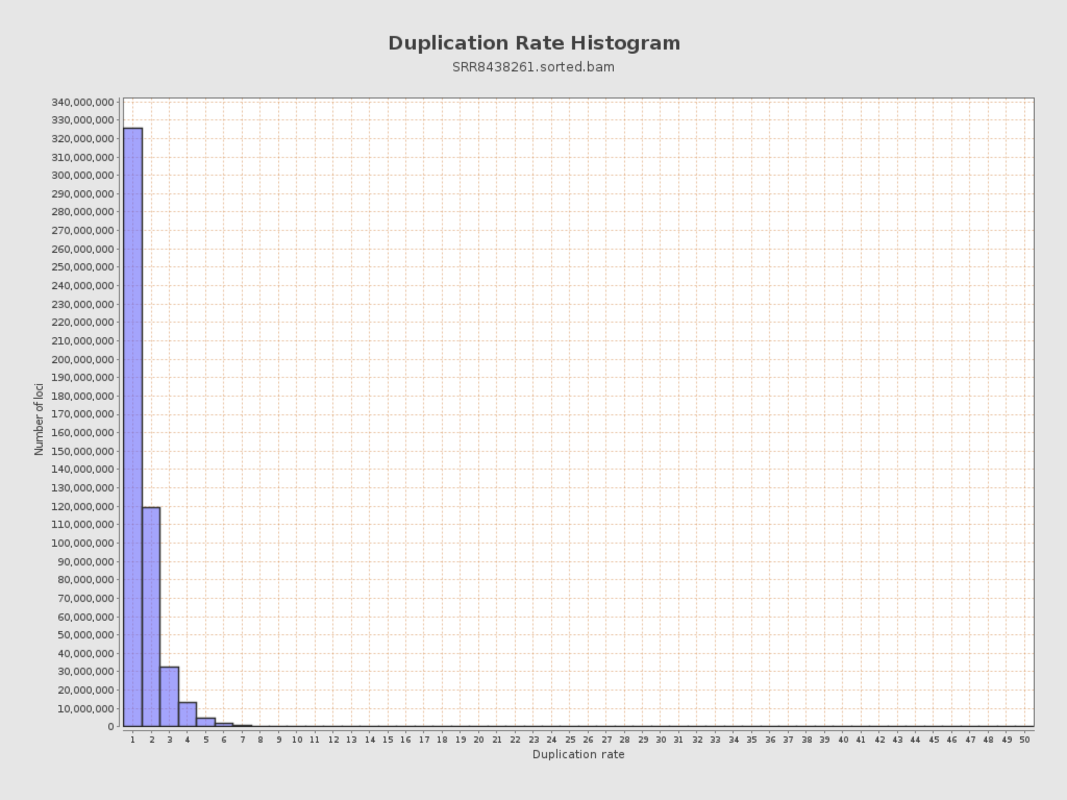
5. Results : Coverage Histogram (0-50X)



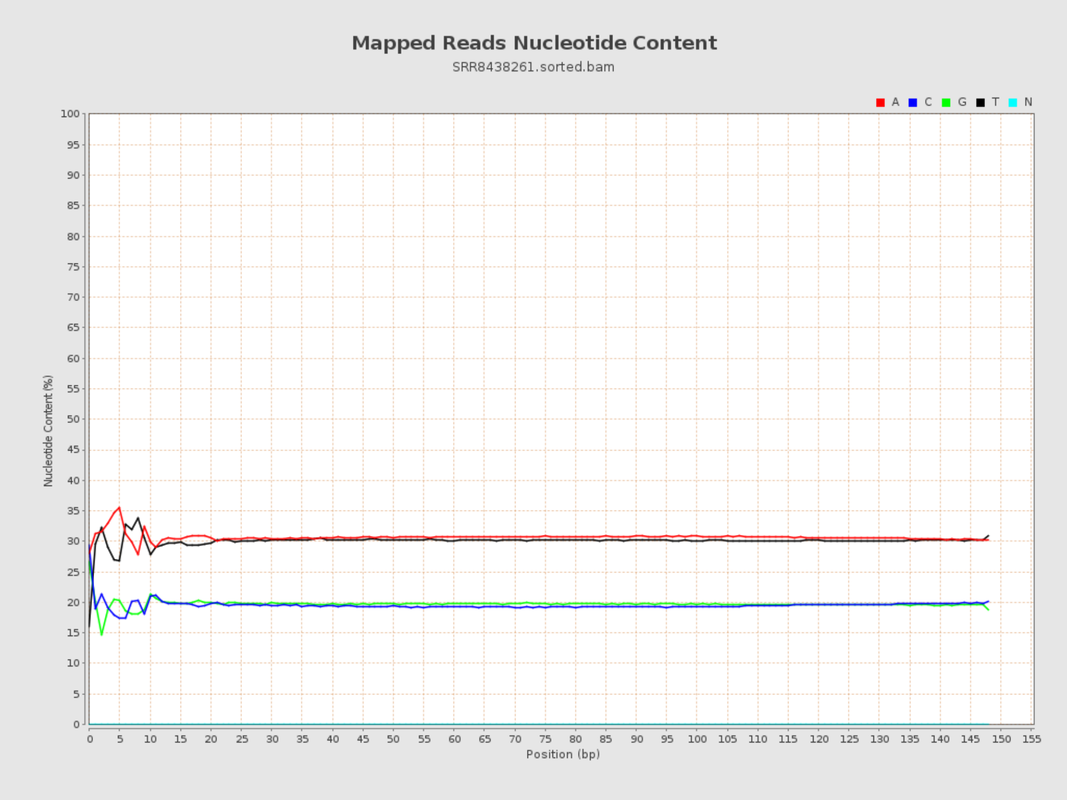
6. Results : Genome Fraction Coverage



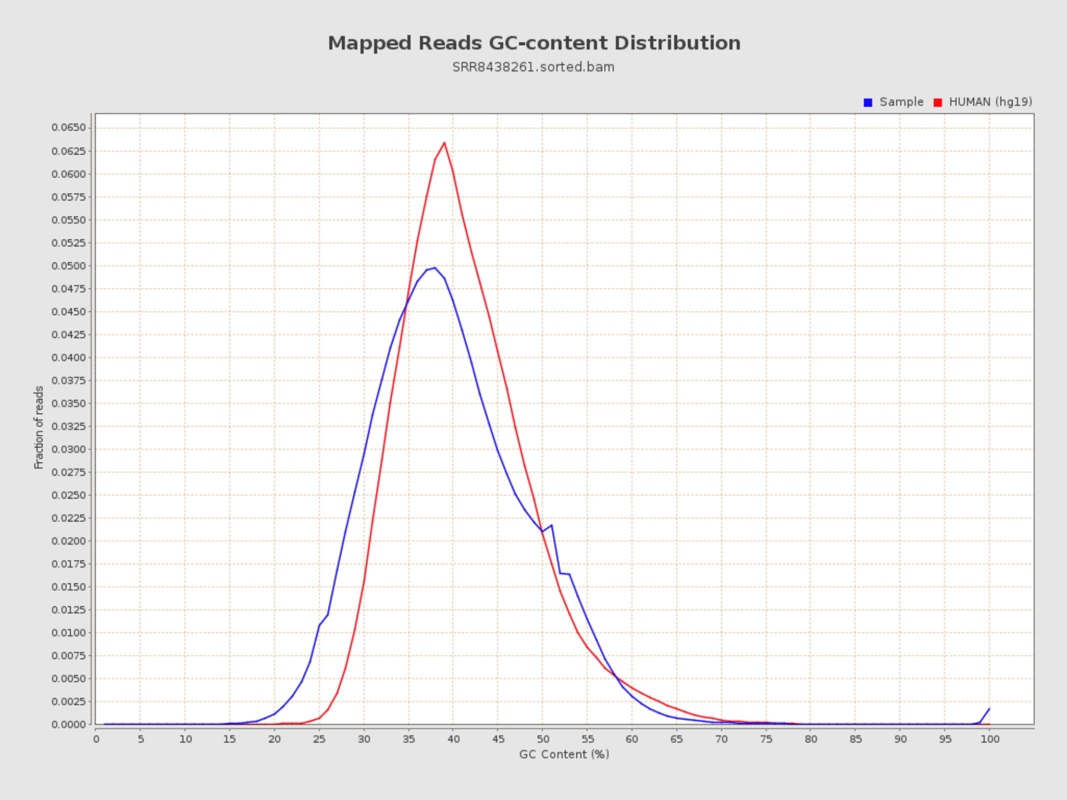
7. Results : Duplication Rate Histogram



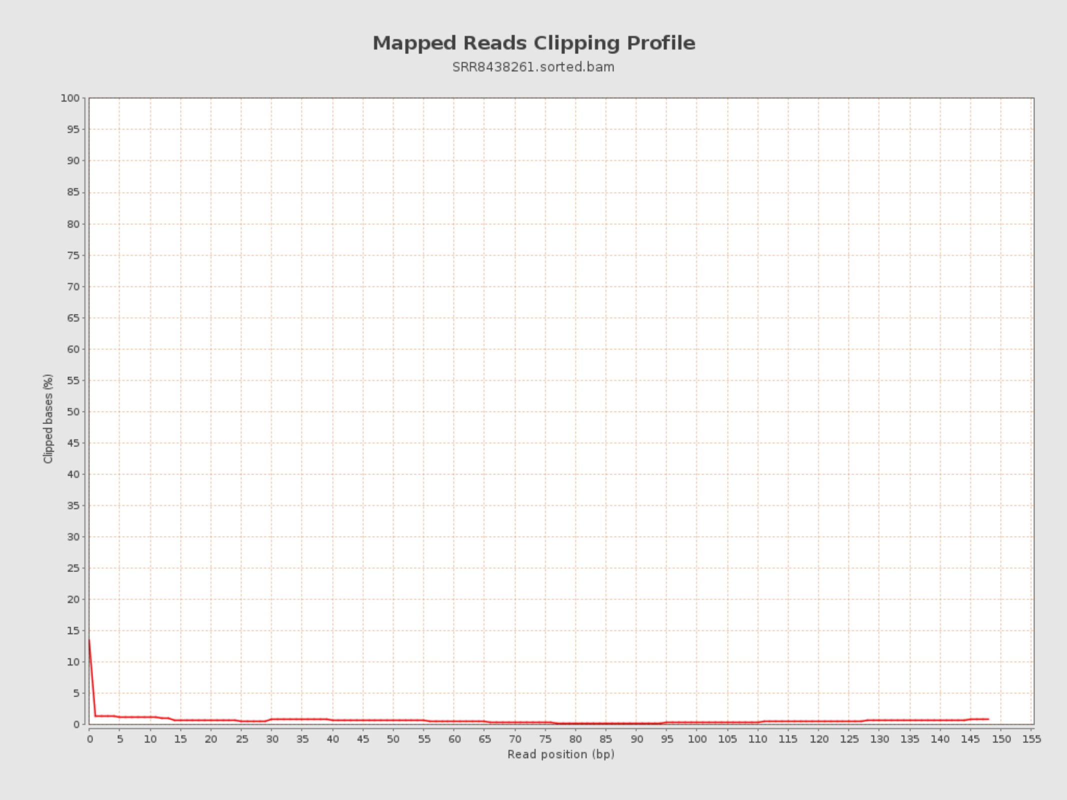
8. Results : Mapped Reads Nucleotide Content



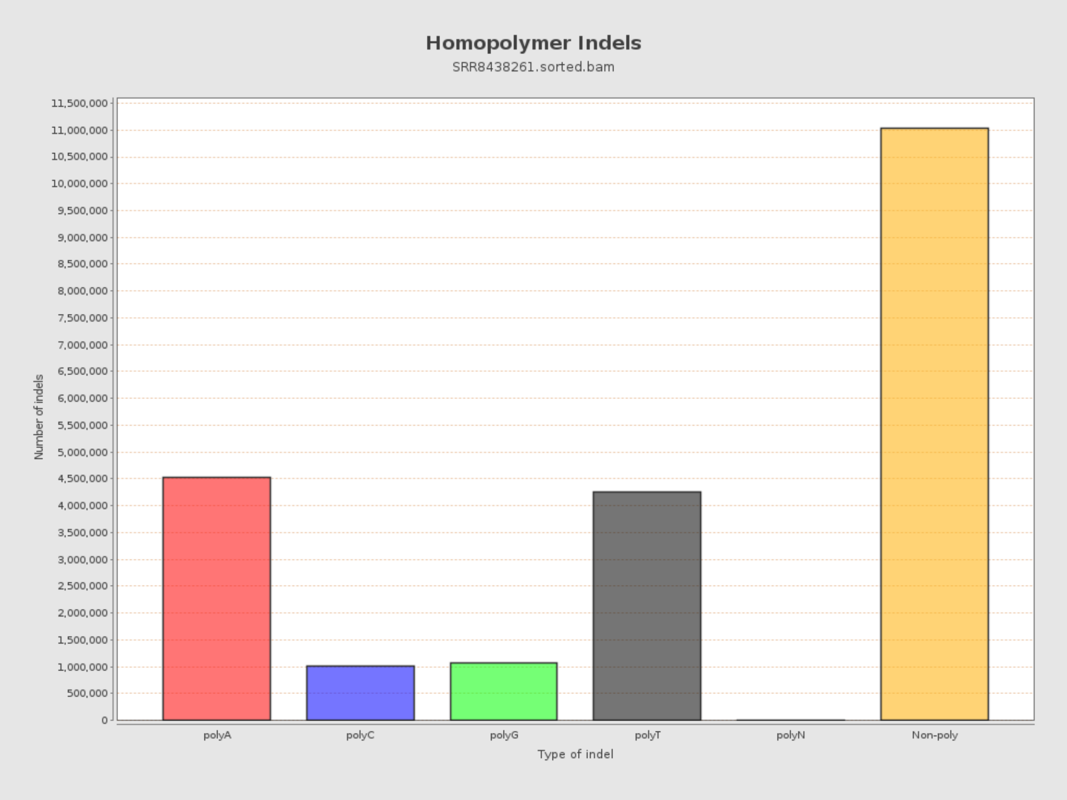
9. Results : Mapped Reads GC-content Distribution



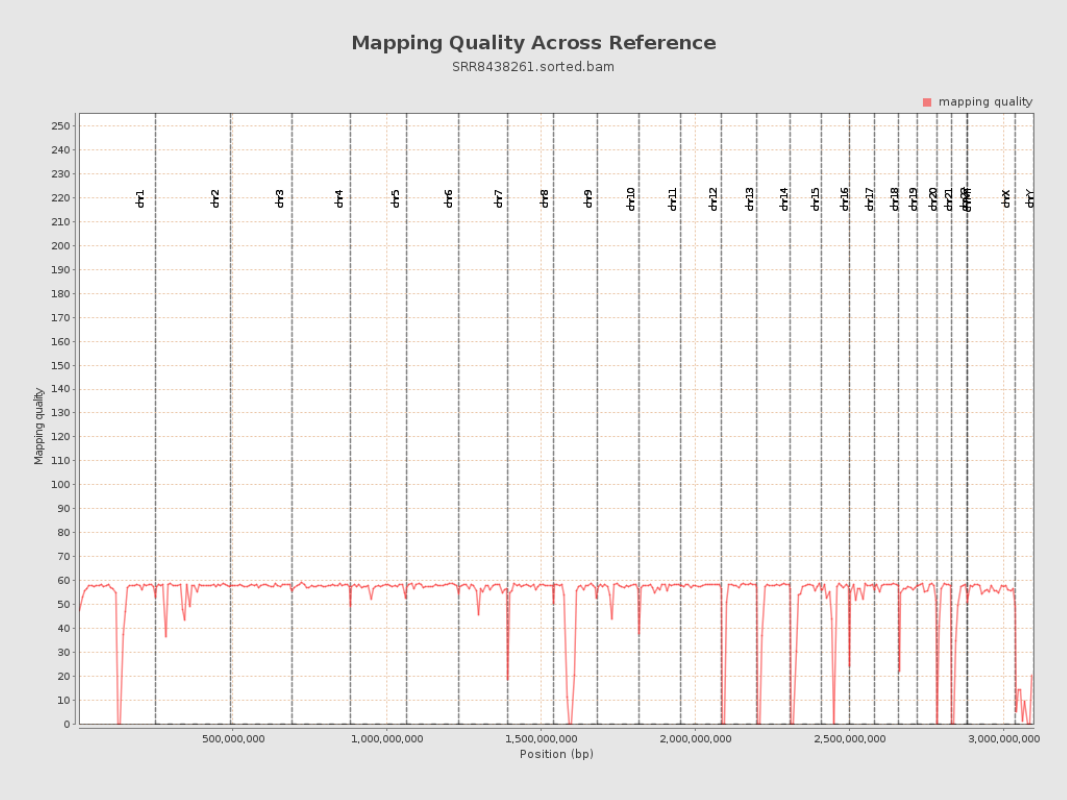
10. Results : Mapped Reads Clipping Profile



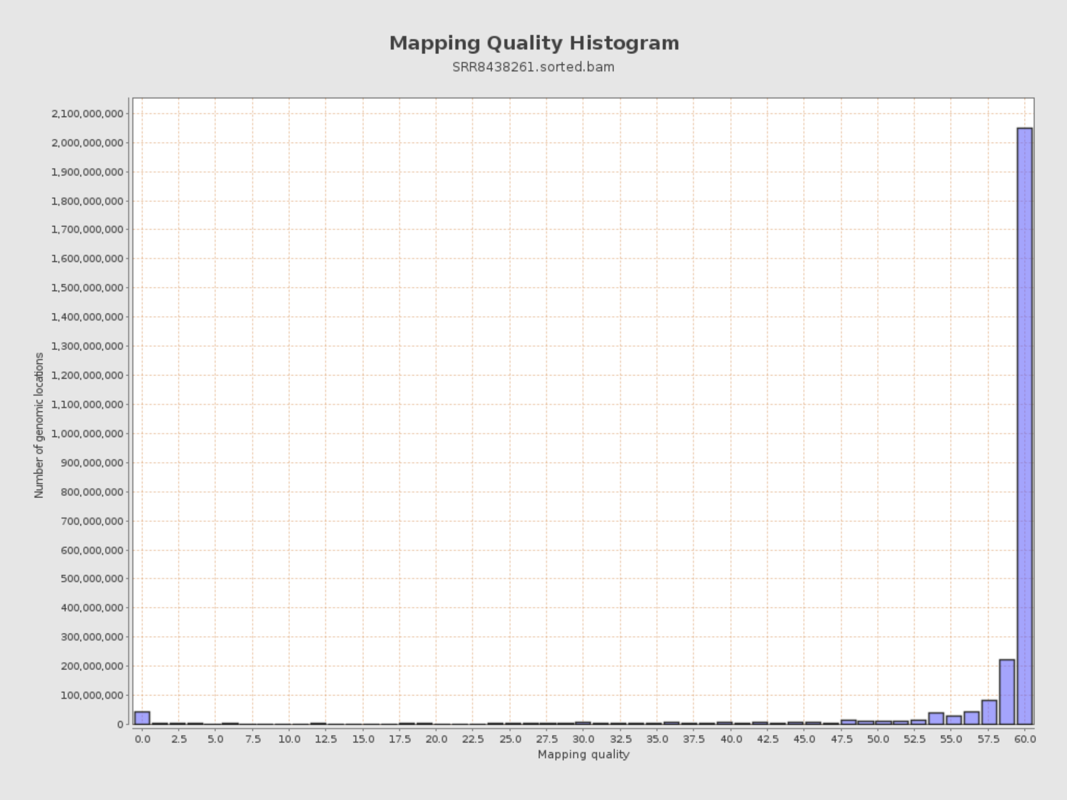
11. Results : Homopolymer Indels



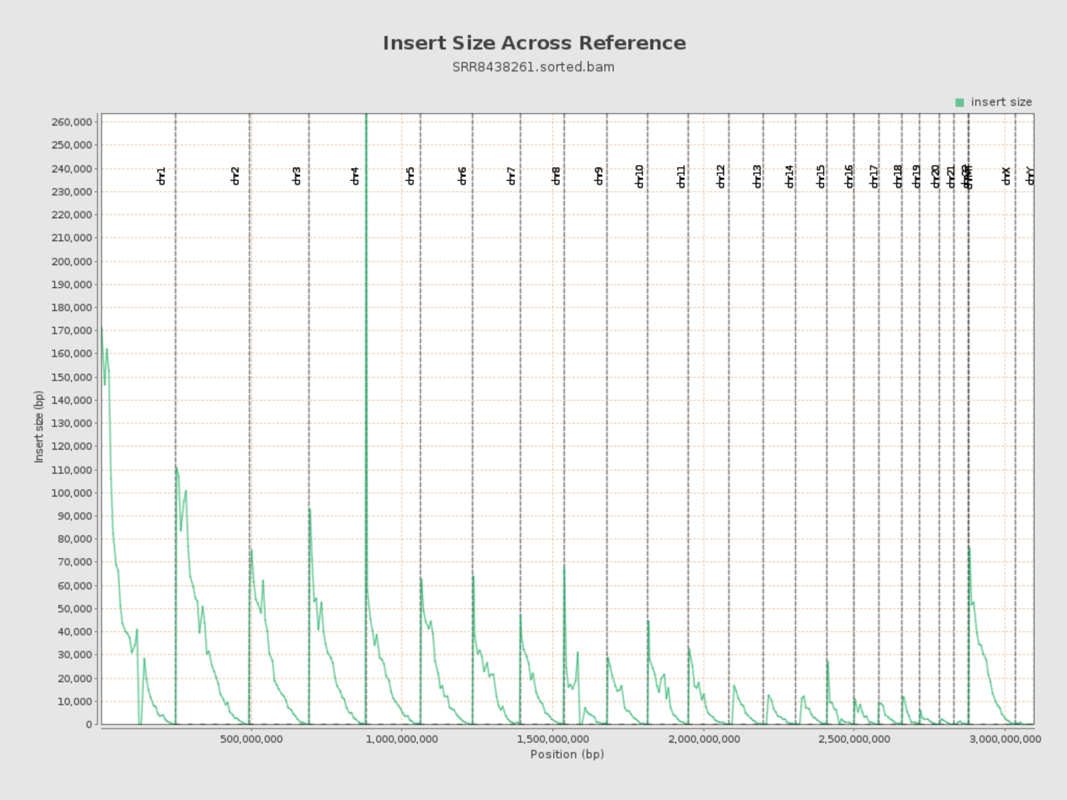
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram