Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 07:59:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438284.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_SRR8438284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438284_1.fastq.gz SRR8438284_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 07:59:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	684,039,712
Mapped reads	681,613,601 / 99.65%
Unmapped reads	2,426,111 / 0.35%
Mapped paired reads	681,613,601 / 99.65%
Mapped reads, first in pair	341,106,789 / 49.87%
Mapped reads, second in pair	340,506,812 / 49.78%
Mapped reads, both in pair	679,838,488 / 99.39%
Mapped reads, singletons	1,775,113 / 0.26%
Secondary alignments	0
Supplementary alignments	11,360,881 / 1.66%
Read min/max/mean length	28 / 151 / 145.77
Duplicated reads (estimated)	295,587,477 / 43.21%
Duplication rate	40.73%
Clipped reads	117,087,025 / 17.12%

2.2. ACGT Content

Number/percentage of A's	29,710,796,305 / 30.16%
Number/percentage of C's	19,747,824,220 / 20.05%
Number/percentage of T's	28,245,224,012 / 28.67%
Number/percentage of G's	20,807,572,250 / 21.12%
Number/percentage of N's	736,358 / 0%

GC Percentage	41.17%

2.3. Coverage

Mean	31.8317
Standard Deviation	62.8329

2.4. Mapping Quality

Mean Mapping Quality	55.17

2.5. Insert size

Mean	41,110.57
Standard Deviation	1,969,902.25
P25/Median/P75	204 / 269 / 372

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	504,769,674
Insertions	12,908,609
Mapped reads with at least one insertion	1.86%
Deletions	11,521,768
Mapped reads with at least one deletion	1.66%
Homopolymer indels	48.8%

2.7. Chromosome stats

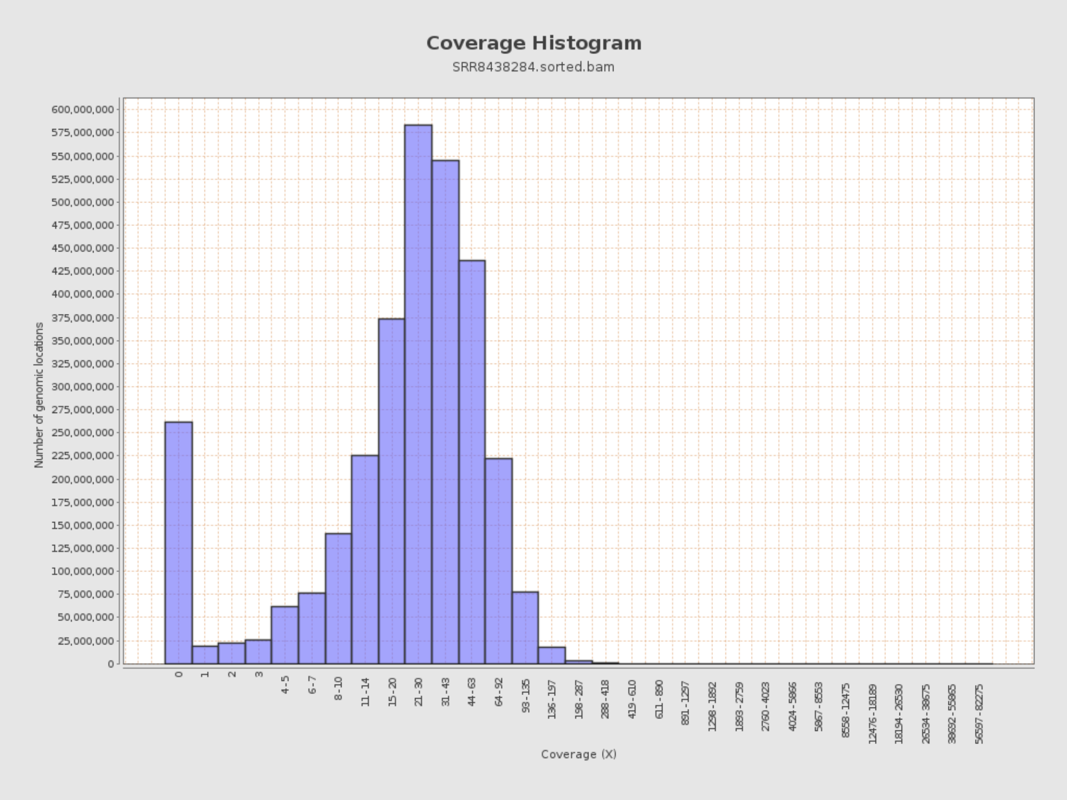
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	8254948405	33.1191	31.9144
chr2	243199373	8632627927	35.4961	80.2817
chr3	198022430	7000282622	35.351	34.9871
chr4	191154276	6352360266	33.2316	24.0988
chr5	180915260	6204804418	34.2967	26.0778
chr6	171115067	5829234857	34.0662	26.4271
chr7	159138663	5242094563	32.9404	26.2085
chr8	146364022	5015346053	34.2662	25.8451
chr9	141213431	4160213167	29.4605	31.9001
chr10	135534747	4628208262	34.1478	36.1417
chr11	135006516	4644712111	34.4036	28.2026
chr12	133851895	4815305259	35.9749	28.523
chr13	115169878	3196414228	27.7539	24.9977
chr14	107349540	3212268091	29.9234	28.9988
chr15	102531392	3035494780	29.6055	30.374
chr16	90354753	2837358427	31.4024	47.7639
chr17	81195210	2757253641	33.9583	38.1454
chr18	78077248	2507891043	32.1206	25.6231
chr19	59128983	1709095310	28.9045	41.3314
chr20	63025520	2284757203	36.2513	31.7639
chr21	48129895	1323639421	27.5014	34.6831
chr22	51304566	1215928103	23.7002	31.3016
chrMT	16571	338820906	20,446.6179	8,115.2436
chrX	155270560	2877798453	18.5341	16.362

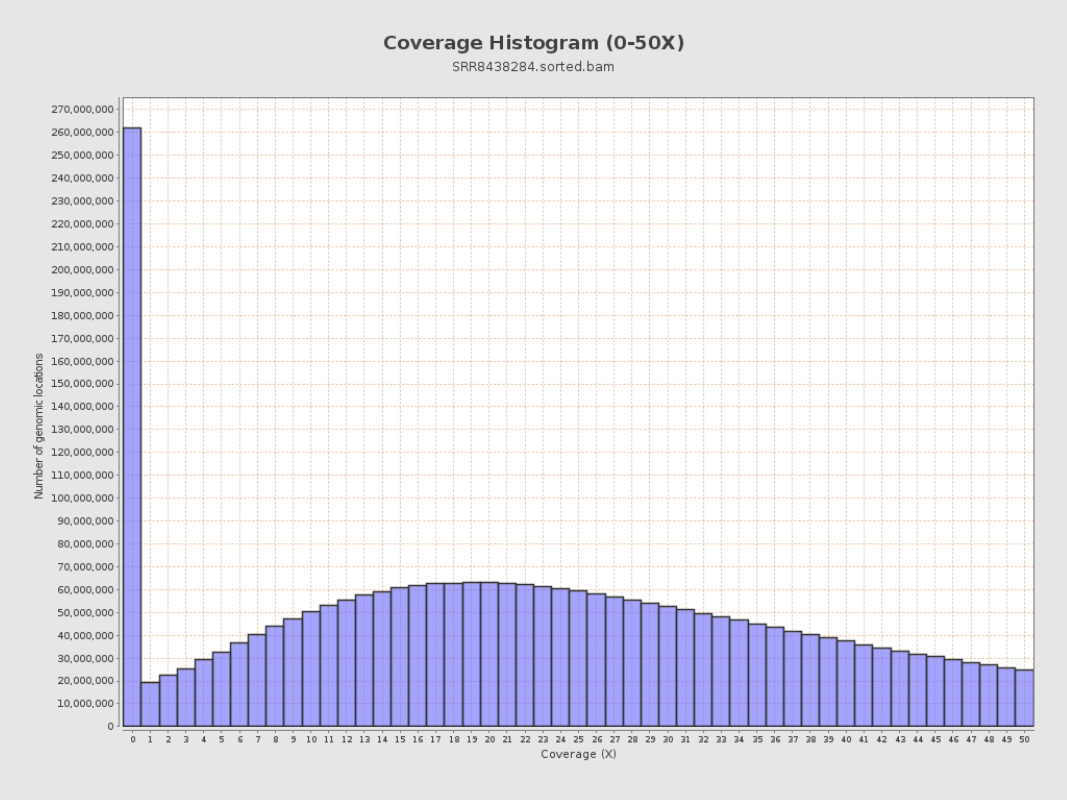
chrY	59373566	464481230	7.823	23.2879

3. Results : Coverage across reference

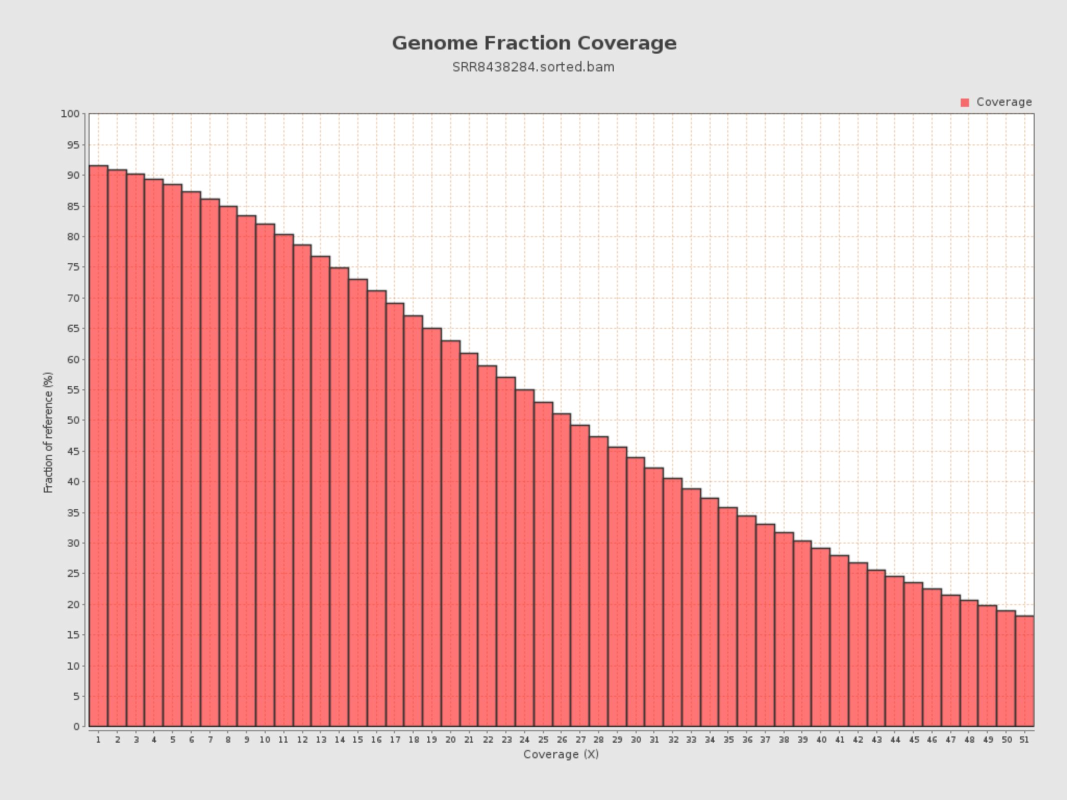
4. Results : Coverage Histogram



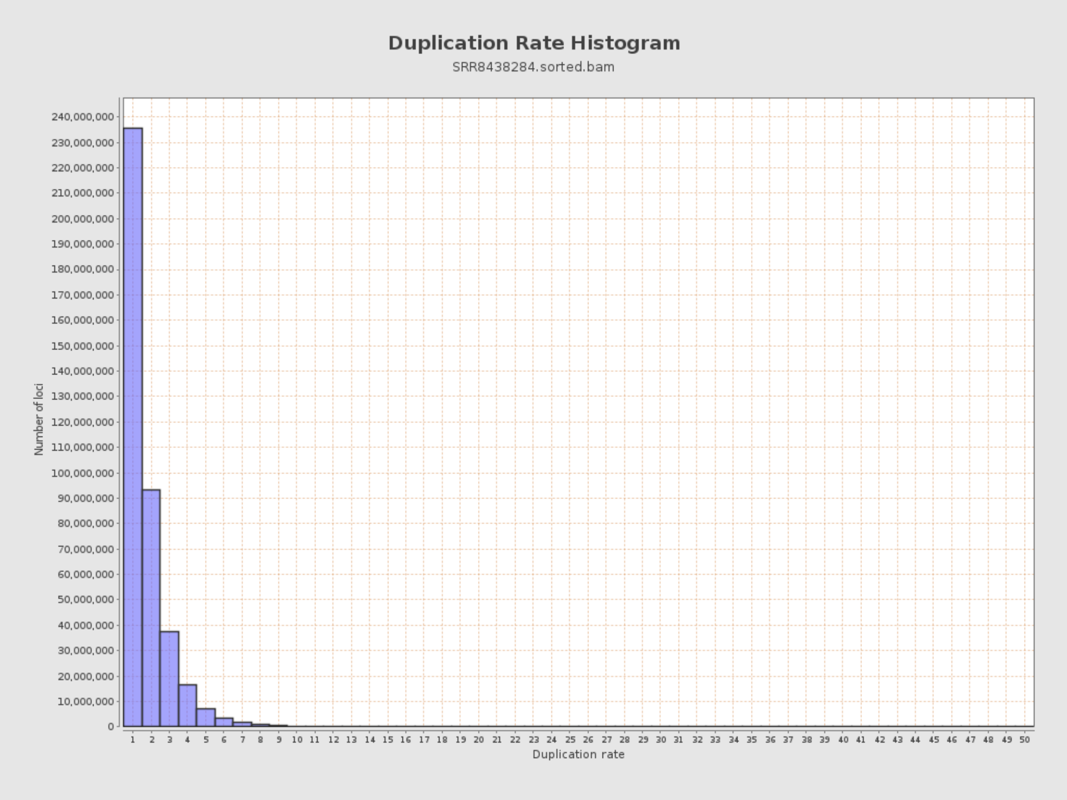
5. Results : Coverage Histogram (0-50X)



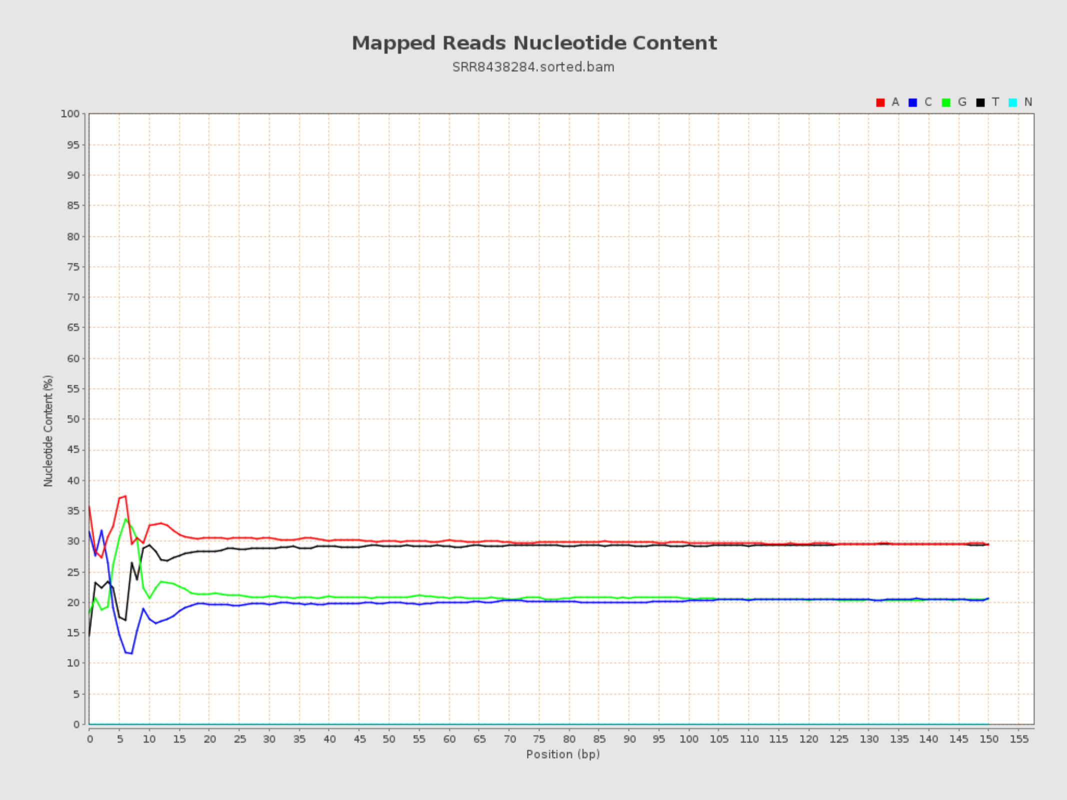
6. Results : Genome Fraction Coverage



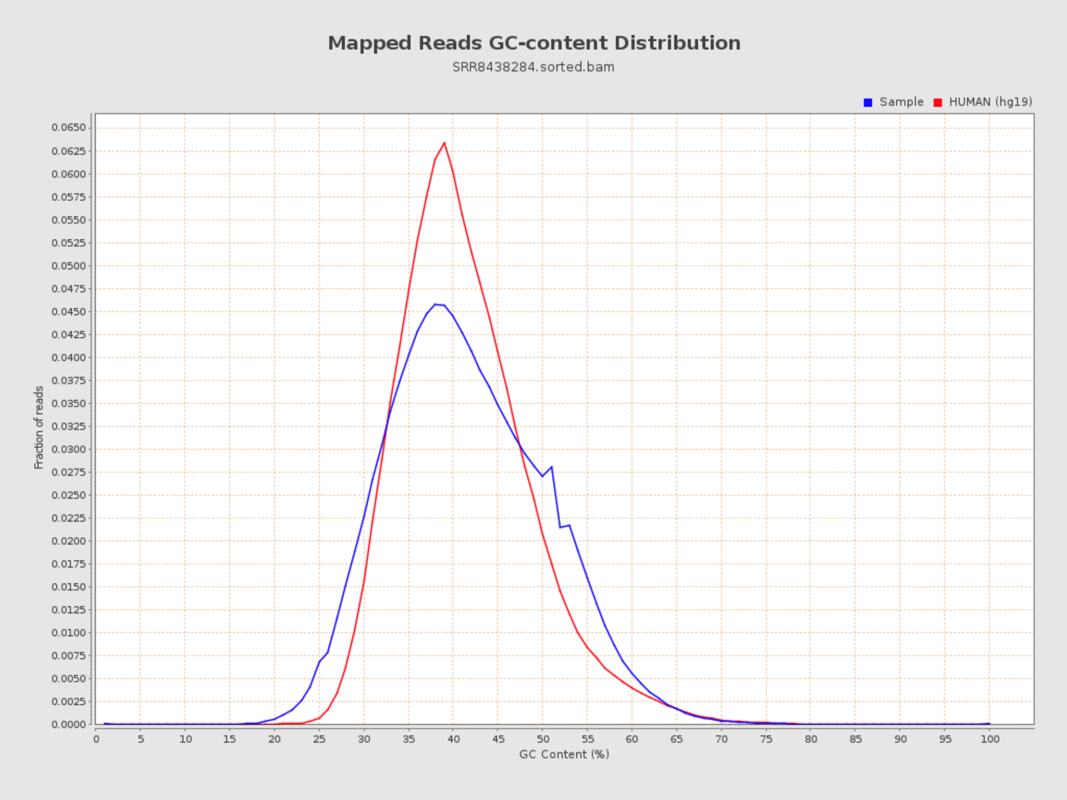
7. Results : Duplication Rate Histogram



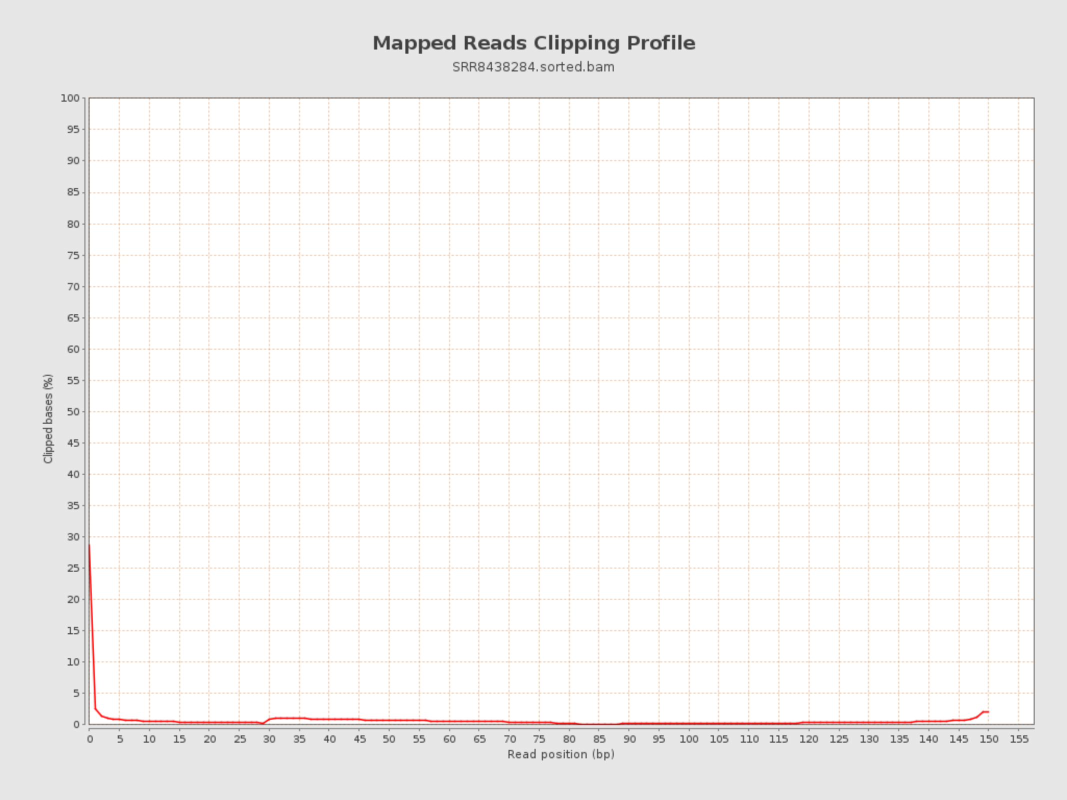
8. Results : Mapped Reads Nucleotide Content



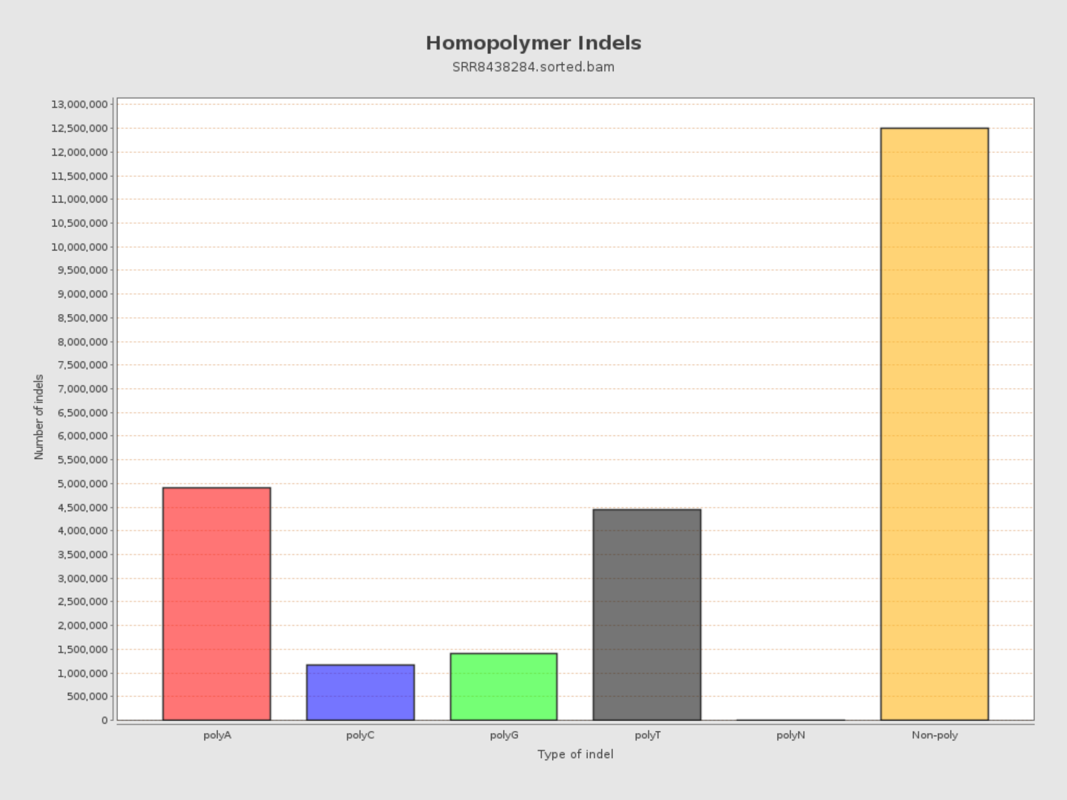
9. Results : Mapped Reads GC-content Distribution



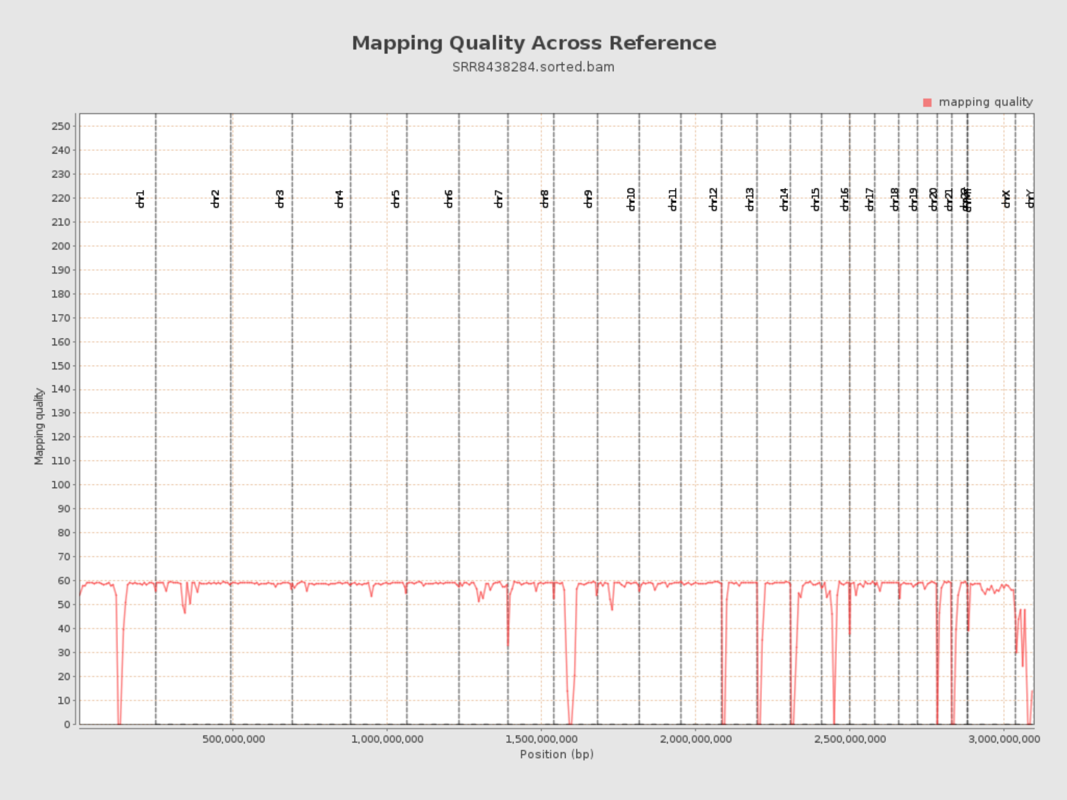
10. Results : Mapped Reads Clipping Profile



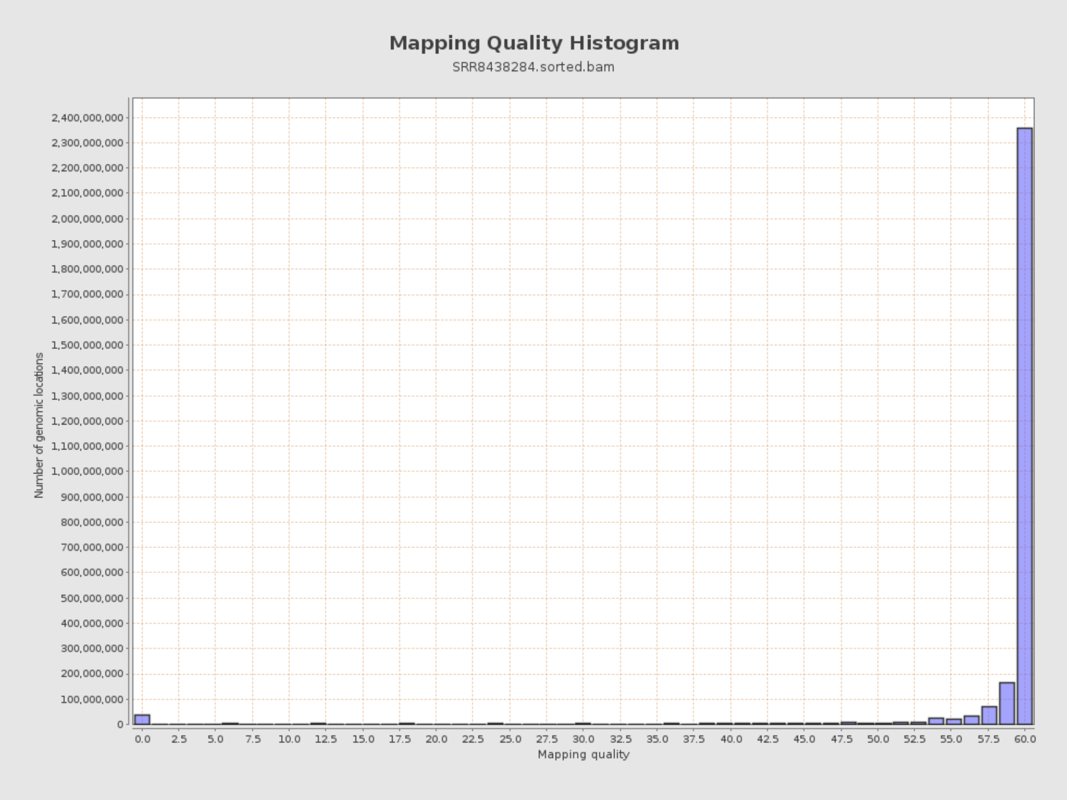
11. Results : Homopolymer Indels



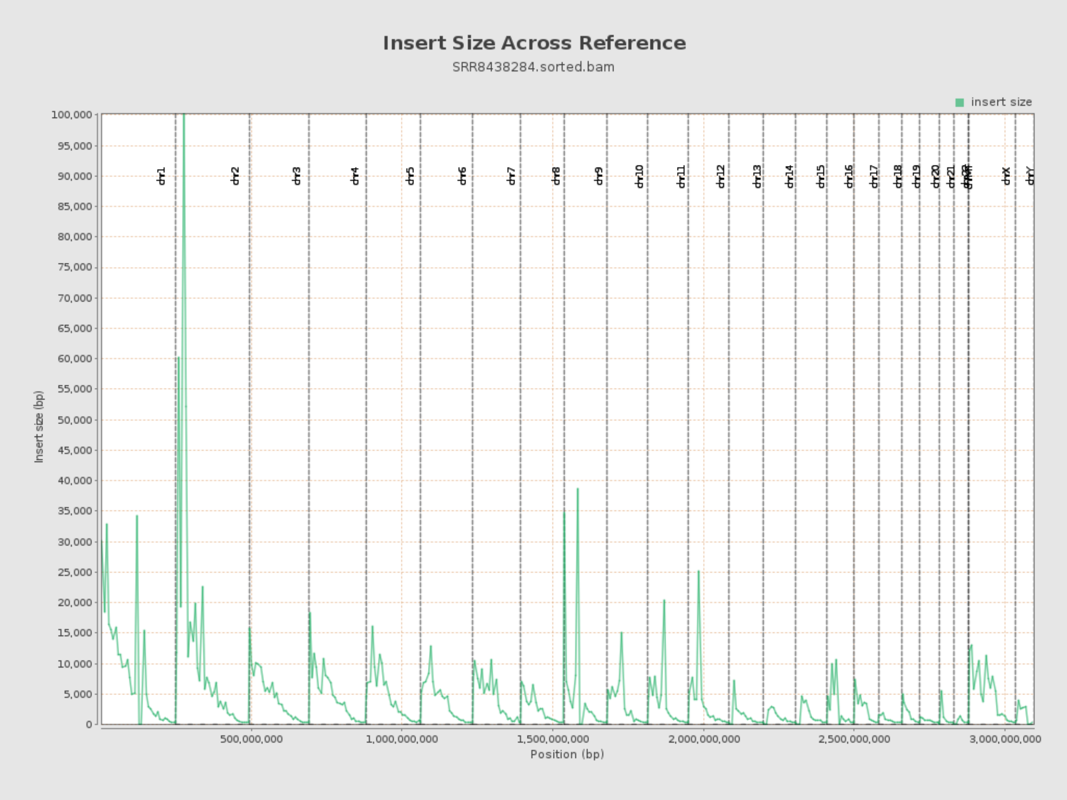
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram