Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 18:30:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779398.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_SRR1779398 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779398_1.fastq.gz SRR1779398_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 18:30:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779398.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,004,464
Mapped reads	13,450,221 / 96.04%
Unmapped reads	554,243 / 3.96%
Mapped paired reads	13,450,221 / 96.04%
Mapped reads, first in pair	6,763,385 / 48.29%
Mapped reads, second in pair	6,686,836 / 47.75%
Mapped reads, both in pair	13,346,644 / 95.3%
Mapped reads, singletons	103,577 / 0.74%
Secondary alignments	0
Supplementary alignments	44,177 / 0.32%
Read min/max/mean length	30 / 80 / 80.11
Duplicated reads (estimated)	430,254 / 3.07%
Duplication rate	2.75%
Clipped reads	592,171 / 4.23%

2.2. ACGT Content

Number/percentage of A's	319,734,823 / 29.92%
Number/percentage of C's	214,151,266 / 20.04%
Number/percentage of T's	316,436,767 / 29.61%
Number/percentage of G's	218,199,455 / 20.42%
Number/percentage of N's	239,355 / 0.02%

GC Percentage	40.45%

2.3. Coverage

Mean	0.3453
Standard Deviation	1.4071

2.4. Mapping Quality

Mean Mapping Quality	53.31

2.5. Insert size

Mean	73,613.16
Standard Deviation	2,602,703.97
P25/Median/P75	137 / 178 / 230

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,463,386
Insertions	94,236
Mapped reads with at least one insertion	0.69%
Deletions	112,280
Mapped reads with at least one deletion	0.82%
Homopolymer indels	47.14%

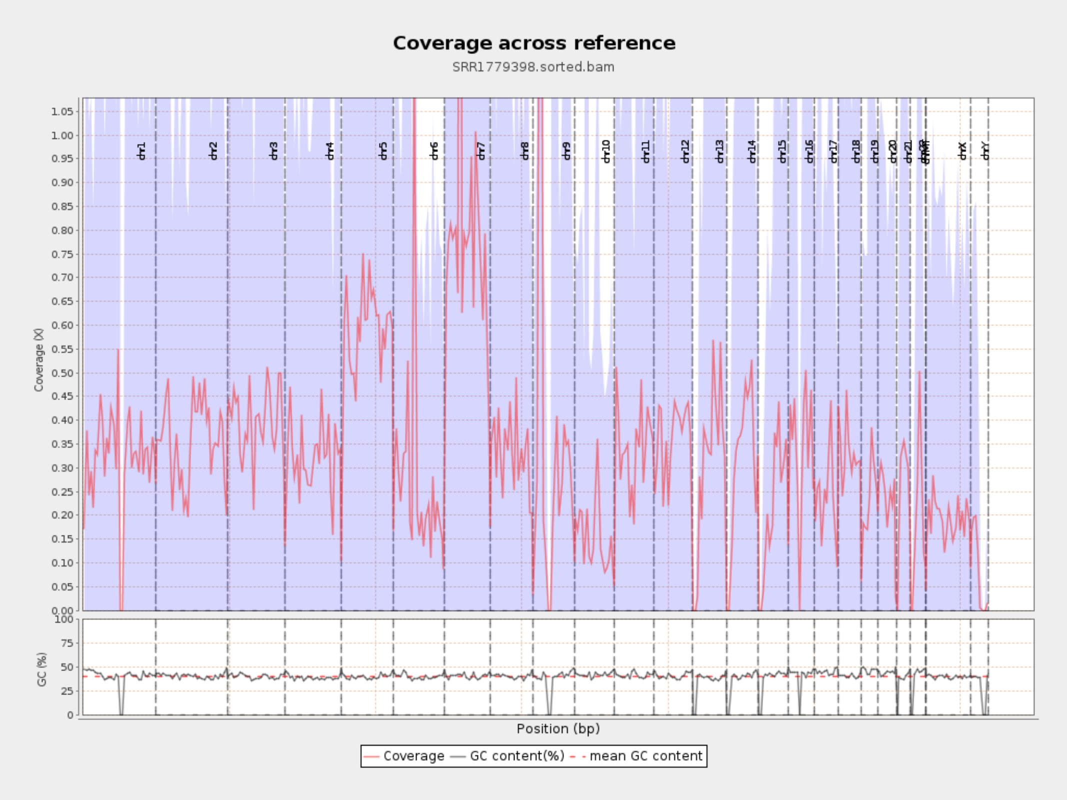
2.7. Chromosome stats

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

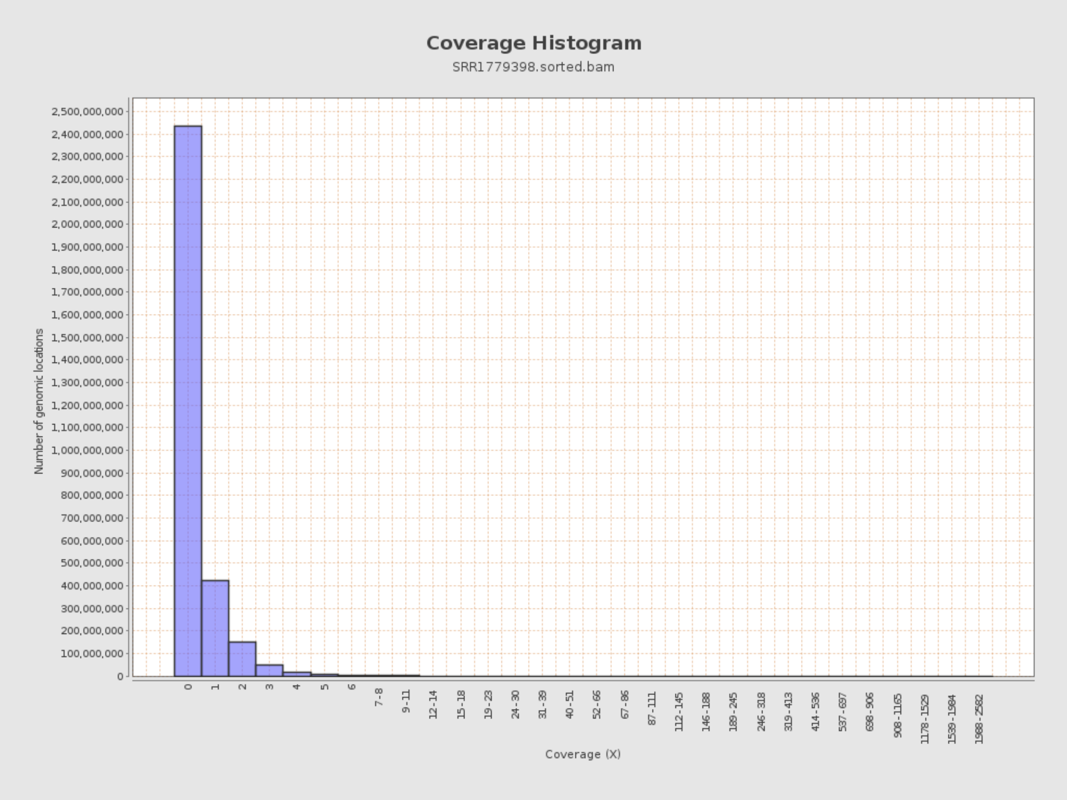
		bases	coverage	deviation
chr1	249250621	79226921	0.3179	2.7442
chr2	243199373	86410244	0.3553	0.8603
chr3	198022430	78546234	0.3967	0.8117
chr4	191154276	61885411	0.3237	0.7471
chr5	180915260	105005837	0.5804	1.0091
chr6	171115067	47472548	0.2774	0.9024
chr7	159138663	137769742	0.8657	3.4017
chr8	146364022	48716142	0.3328	0.7799
chr9	141213431	55210212	0.391	1.445
chr10	135534747	21175024	0.1562	1.5888
chr11	135006516	45752341	0.3389	0.8136
chr12	133851895	48130926	0.3596	0.7859
chr13	115169878	35487545	0.3081	0.7273
chr14	107349540	33806387	0.3149	0.7365
chr15	102531392	22422464	0.2187	0.6233
chr16	90354753	29581868	0.3274	0.7829
chr17	81195210	19857391	0.2446	0.8437
chr18	78077248	25962682	0.3325	1.0945
chr19	59128983	13902875	0.2351	1.8445
chr20	63025520	15355613	0.2436	0.6436
chr21	48129895	12085705	0.2511	0.6754
chr22	51304566	10263145	0.2	0.6297
chrMT	16571	720	0.0434	0.2239
chrX	155270560	29916820	0.1927	0.5908

chrY	59373566	5050515	0.0851	0.4001

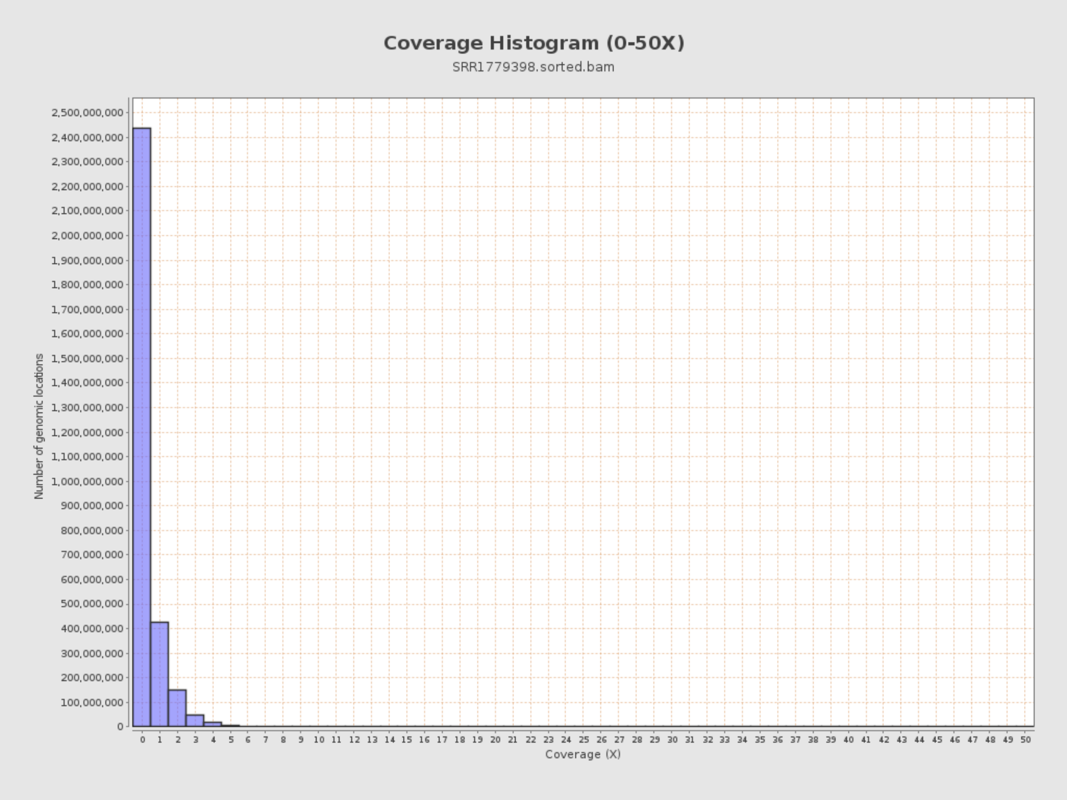
3. Results : Coverage across reference



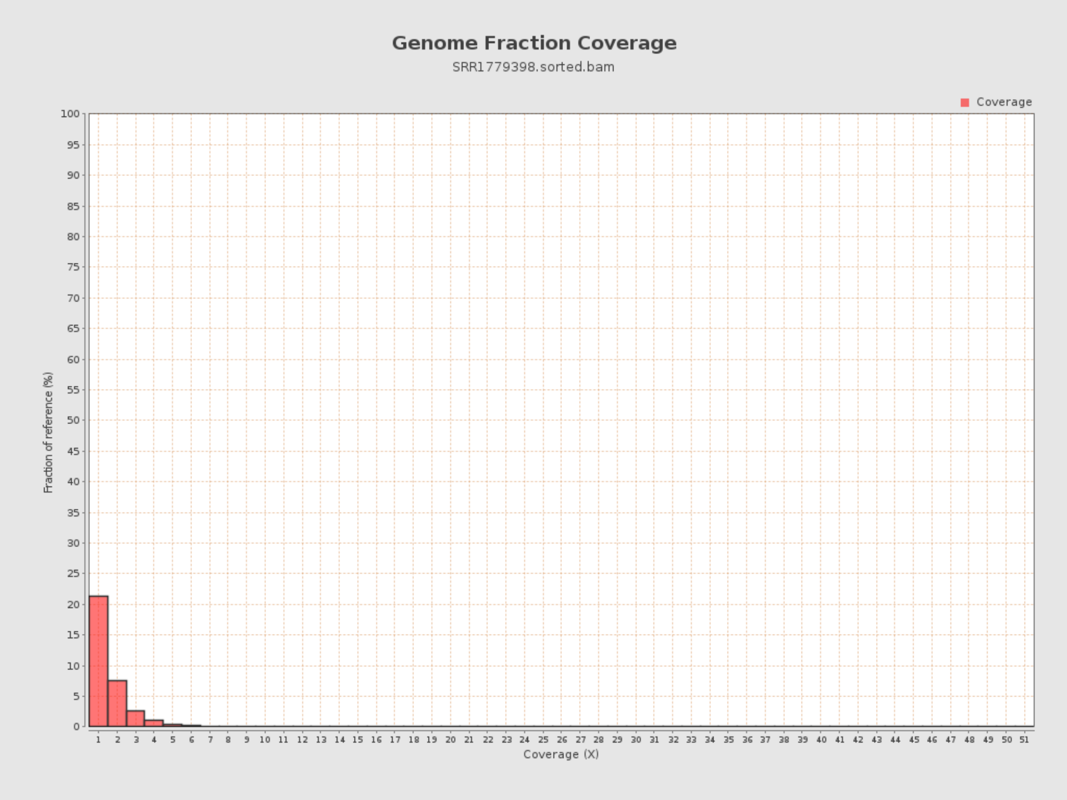
4. Results : Coverage Histogram



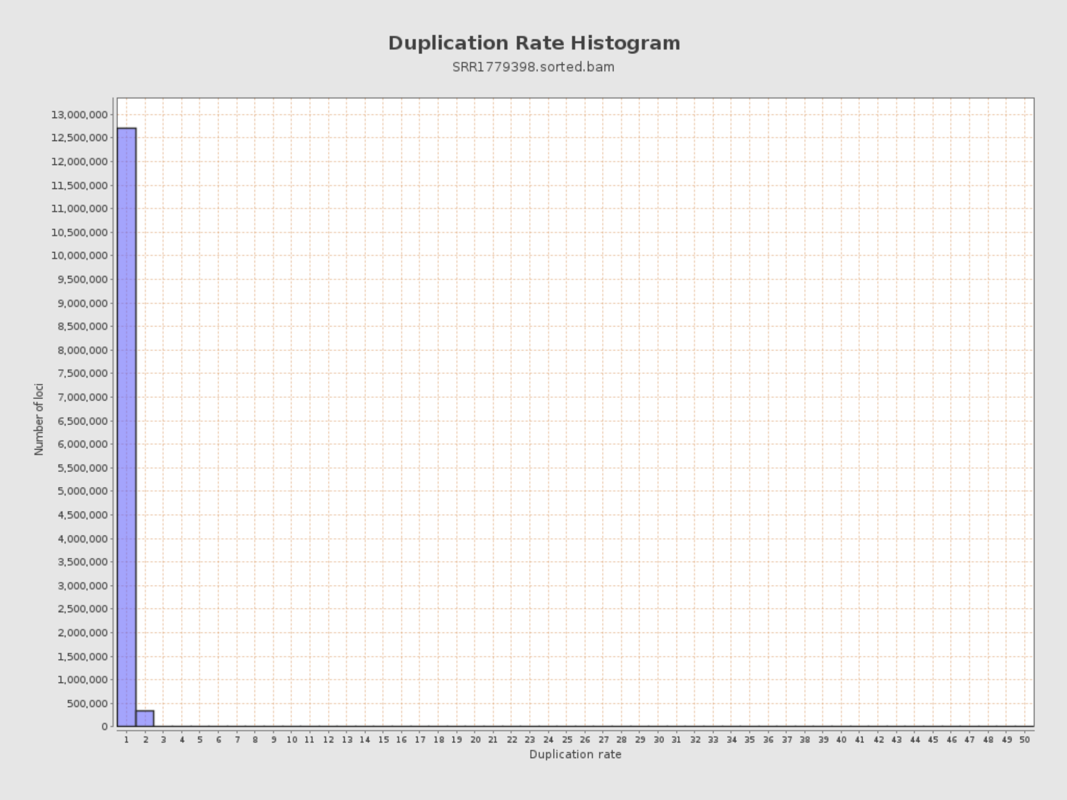
5. Results : Coverage Histogram (0-50X)



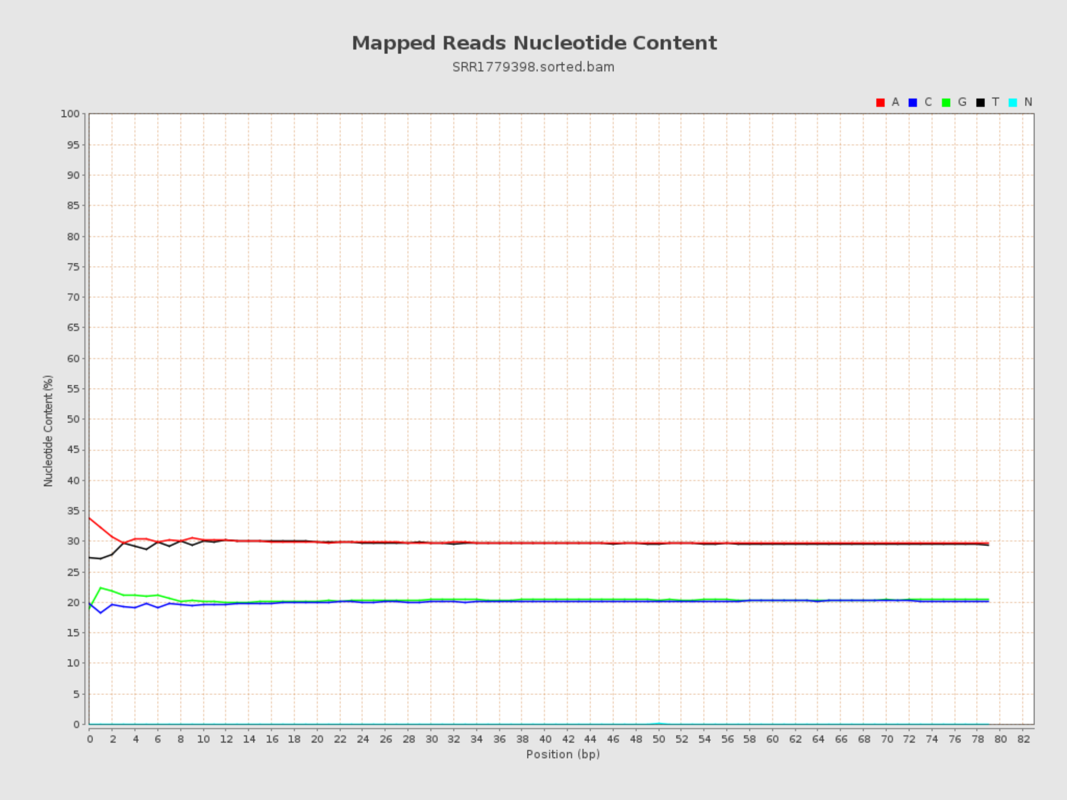
6. Results : Genome Fraction Coverage



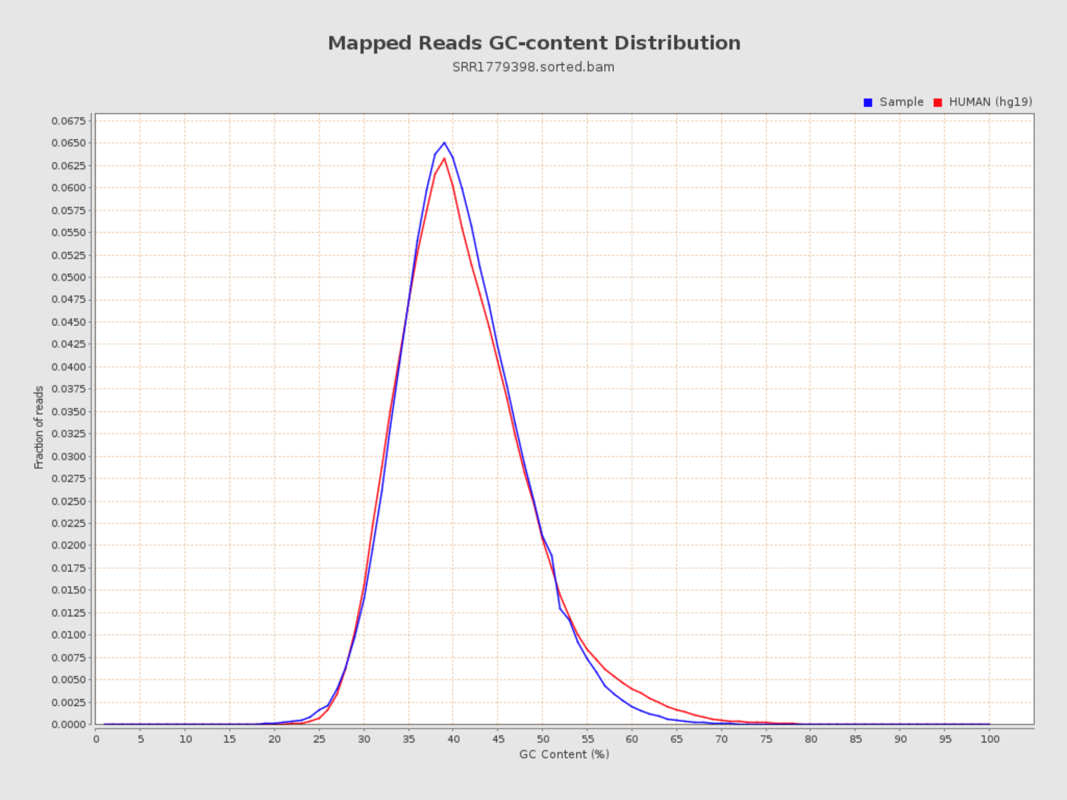
7. Results : Duplication Rate Histogram



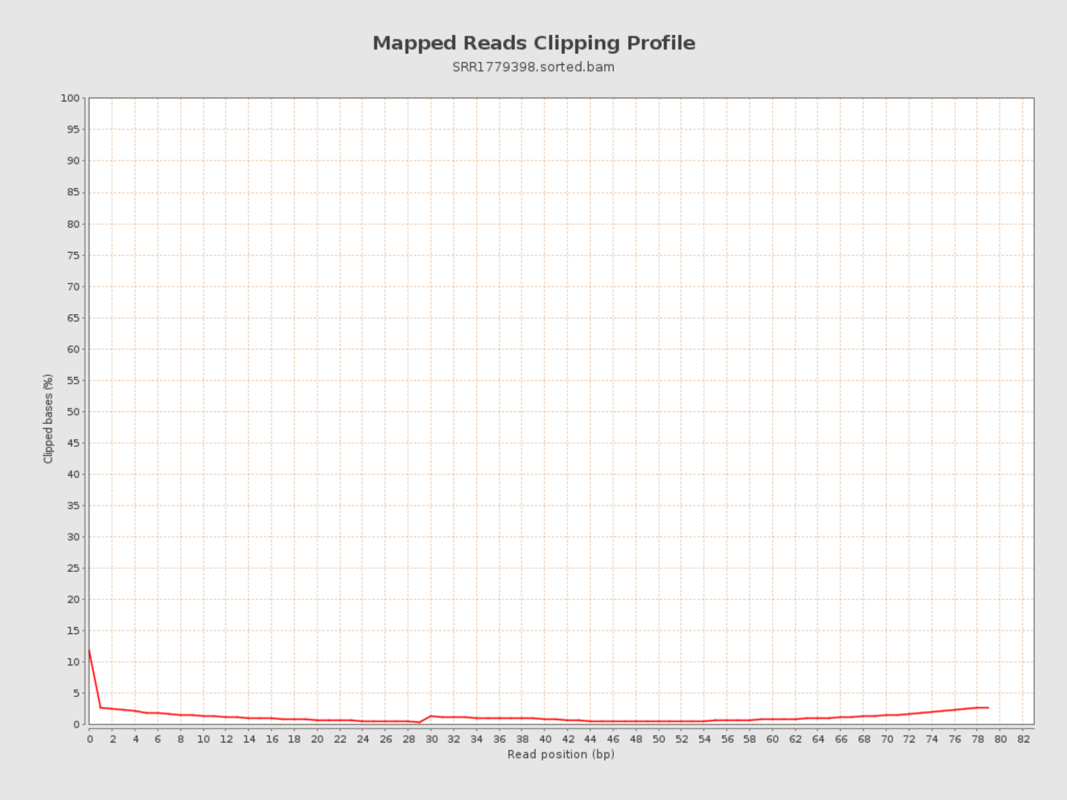
8. Results : Mapped Reads Nucleotide Content



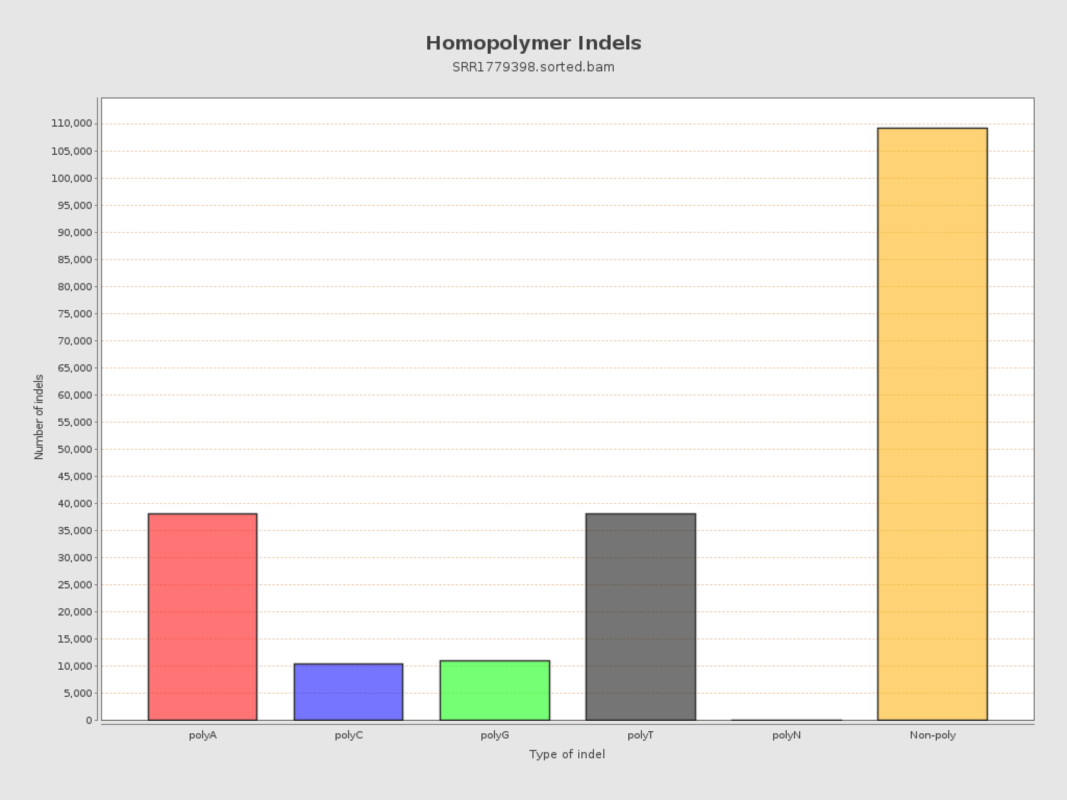
9. Results : Mapped Reads GC-content Distribution



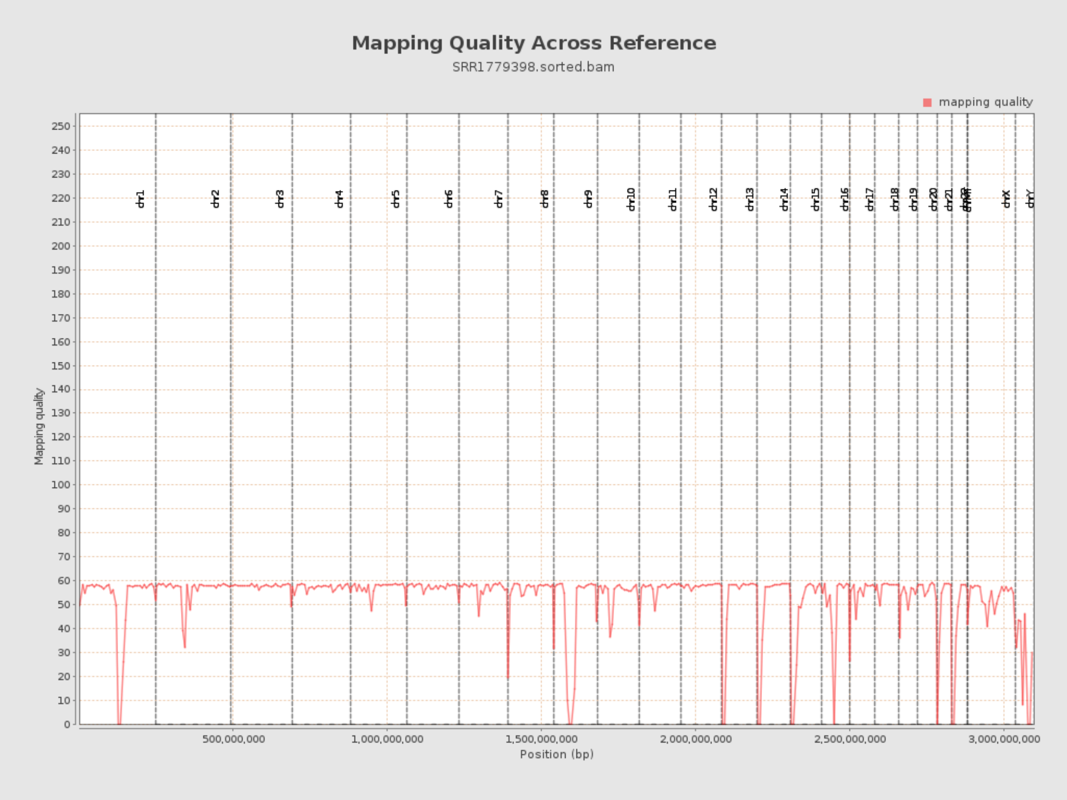
10. Results : Mapped Reads Clipping Profile



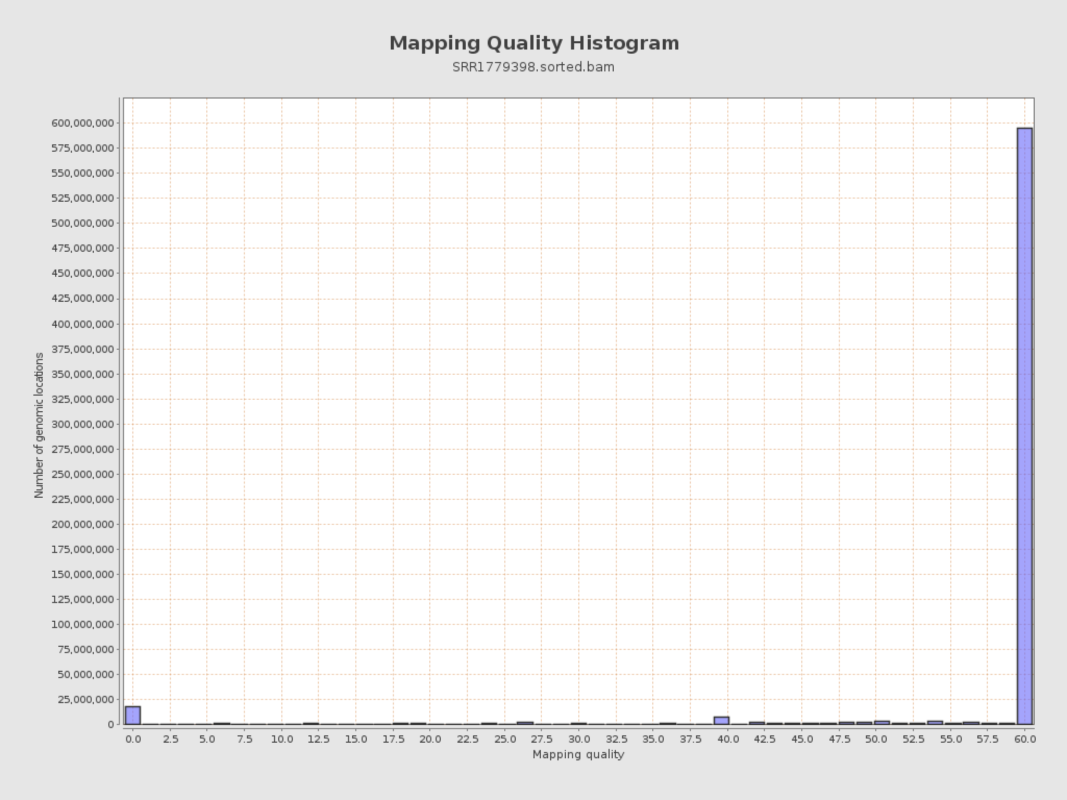
11. Results : Homopolymer Indels



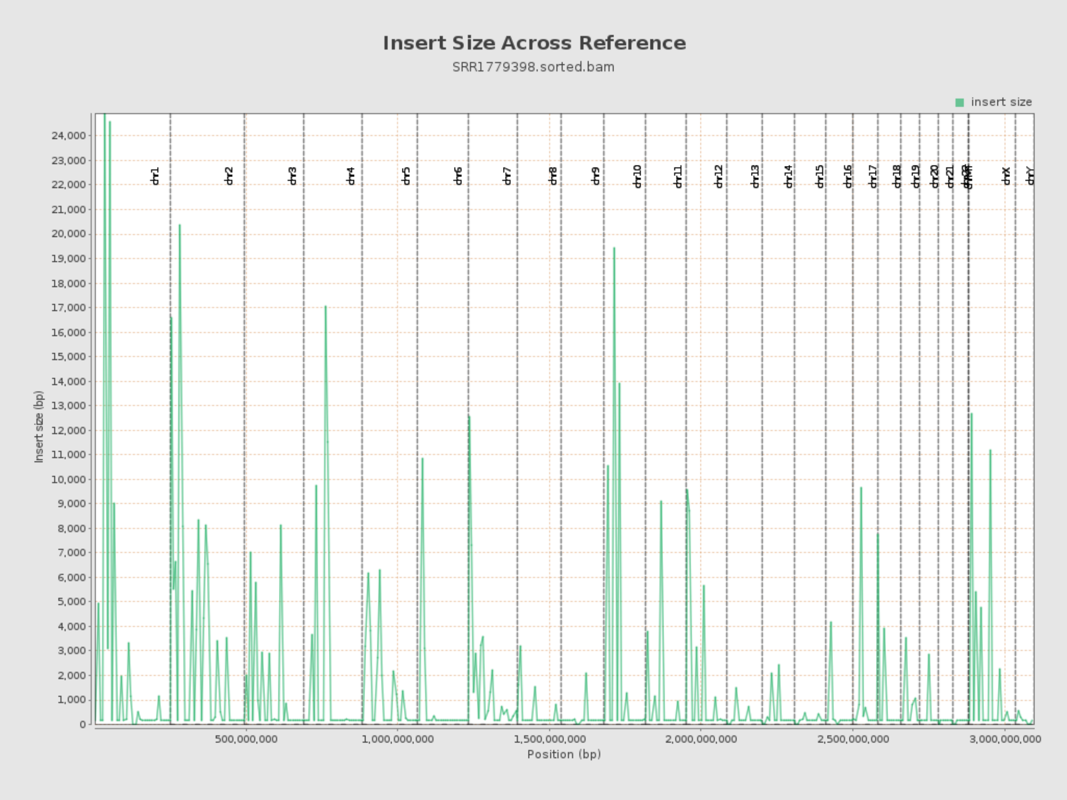
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram