Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 19:12:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779228.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_SRR1779228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779228_1.fastq.gz SRR1779228_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 19:12:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,512,070
Mapped reads	10,210,900 / 97.14%
Unmapped reads	301,170 / 2.86%
Mapped paired reads	10,210,900 / 97.14%
Mapped reads, first in pair	5,146,469 / 48.96%
Mapped reads, second in pair	5,064,431 / 48.18%
Mapped reads, both in pair	10,113,604 / 96.21%
Mapped reads, singletons	97,296 / 0.93%
Secondary alignments	0
Supplementary alignments	24,518 / 0.23%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	117,529 / 1.12%
Duplication rate	1.04%
Clipped reads	356,996 / 3.4%

2.2. ACGT Content

Number/percentage of A's	248,422,619 / 30.58%
Number/percentage of C's	157,035,974 / 19.33%
Number/percentage of T's	246,167,196 / 30.31%
Number/percentage of G's	160,483,553 / 19.76%
Number/percentage of N's	153,545 / 0.02%

GC Percentage	39.09%

2.3. Coverage

Mean	0.2624
Standard Deviation	0.789

2.4. Mapping Quality

Mean Mapping Quality	53.01

2.5. Insert size

Mean	53,977.85
Standard Deviation	2,192,968.38
P25/Median/P75	148 / 199 / 271

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,156,256
Insertions	58,268
Mapped reads with at least one insertion	0.57%
Deletions	73,757
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.34%

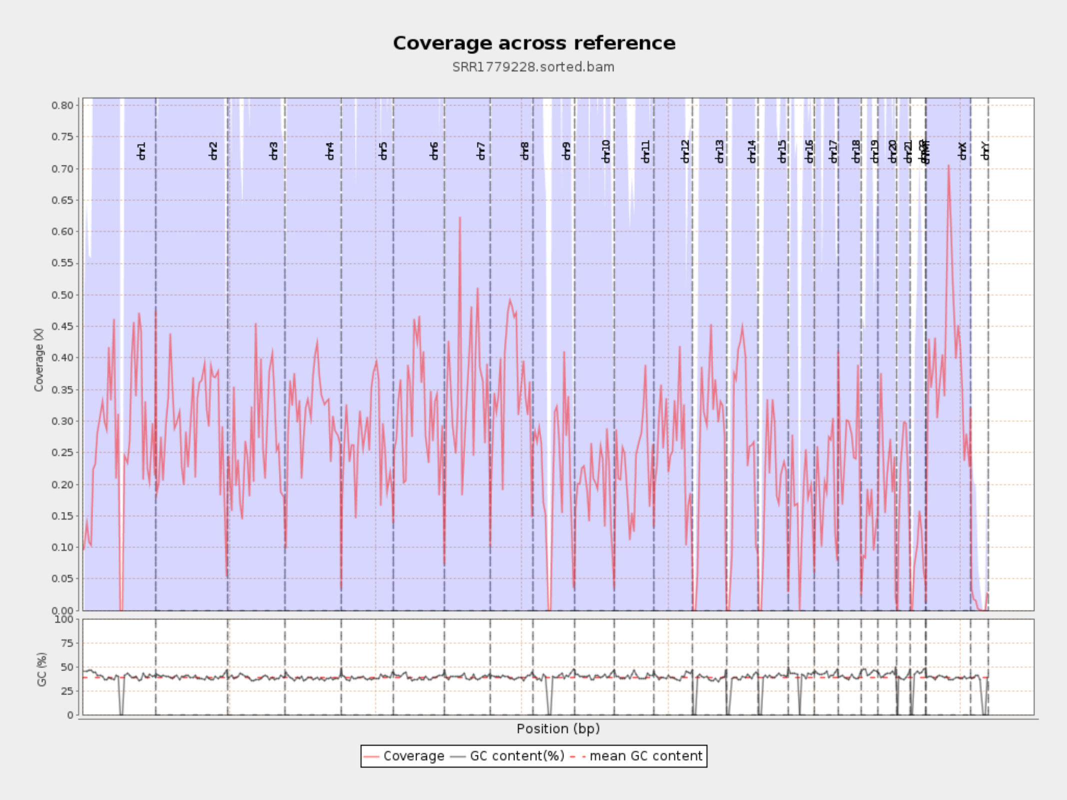
2.7. Chromosome stats

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

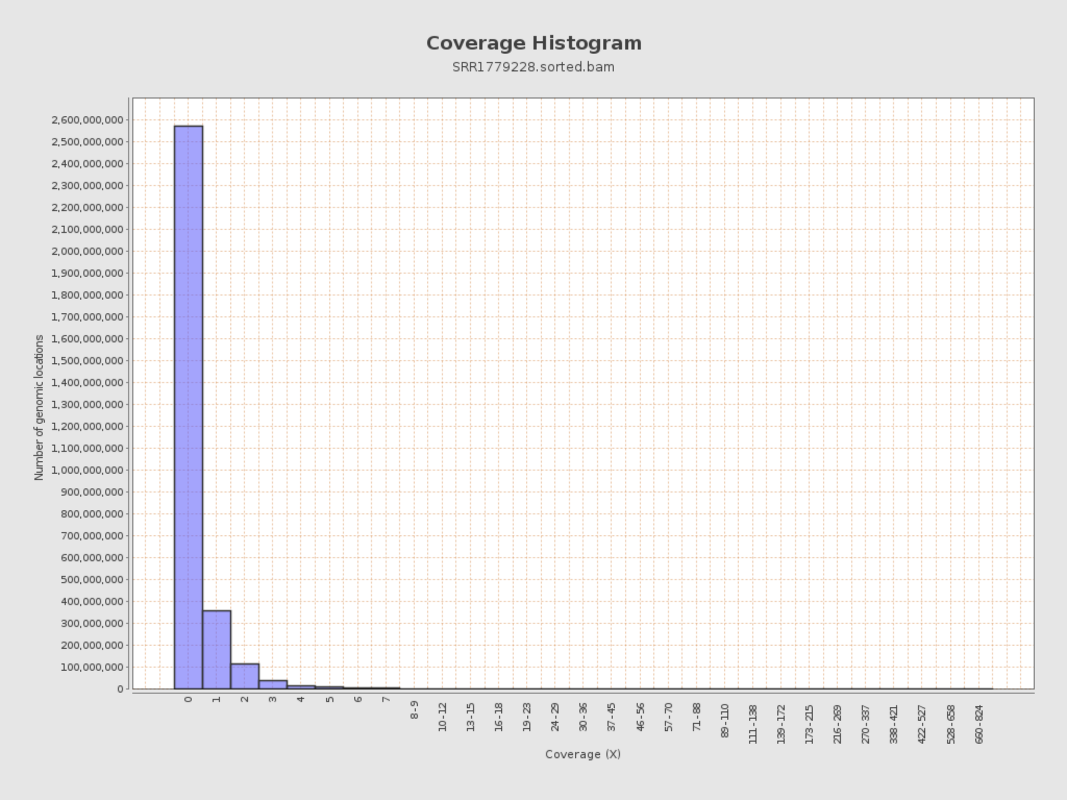
		bases	coverage	deviation
chr1	249250621	66414446	0.2665	1.088
chr2	243199373	71299724	0.2932	0.7536
chr3	198022430	52049721	0.2628	0.7041
chr4	191154276	59998180	0.3139	0.7698
chr5	180915260	47912258	0.2648	0.6954
chr6	171115067	54642519	0.3193	0.7877
chr7	159138663	54982165	0.3455	0.9739
chr8	146364022	52548164	0.359	0.8198
chr9	141213431	30688853	0.2173	0.6755
chr10	135534747	27302136	0.2014	1.1181
chr11	135006516	30969264	0.2294	0.6475
chr12	133851895	34647346	0.2588	0.705
chr13	115169878	31421958	0.2728	0.7097
chr14	107349540	28273074	0.2634	0.7269
chr15	102531392	19842527	0.1935	0.6106
chr16	90354753	14135547	0.1564	0.5277
chr17	81195210	16177358	0.1992	0.6354
chr18	78077248	20836885	0.2669	0.7362
chr19	59128983	7707923	0.1304	0.7224
chr20	63025520	14656477	0.2325	0.6372
chr21	48129895	9382275	0.1949	0.6048
chr22	51304566	4121755	0.0803	0.3621
chrMT	16571	240	0.0145	0.1195
chrX	155270560	61724114	0.3975	0.9191

chrY	59373566	680644	0.0115	0.1484

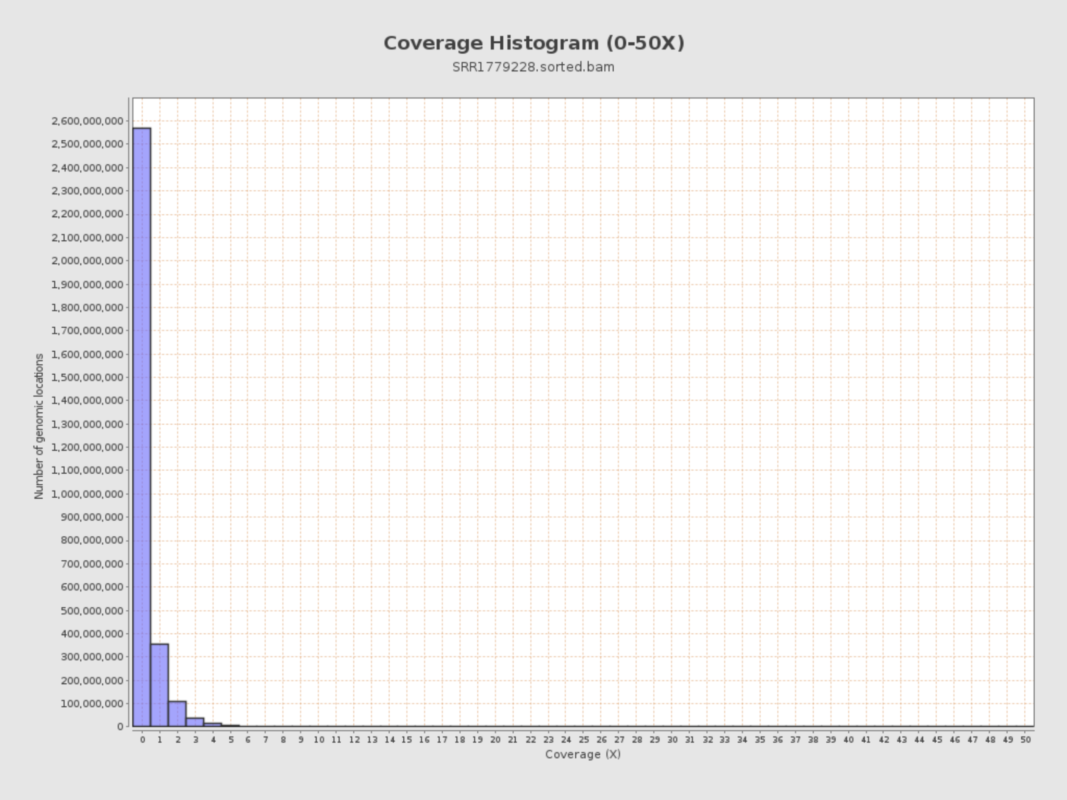
3. Results : Coverage across reference



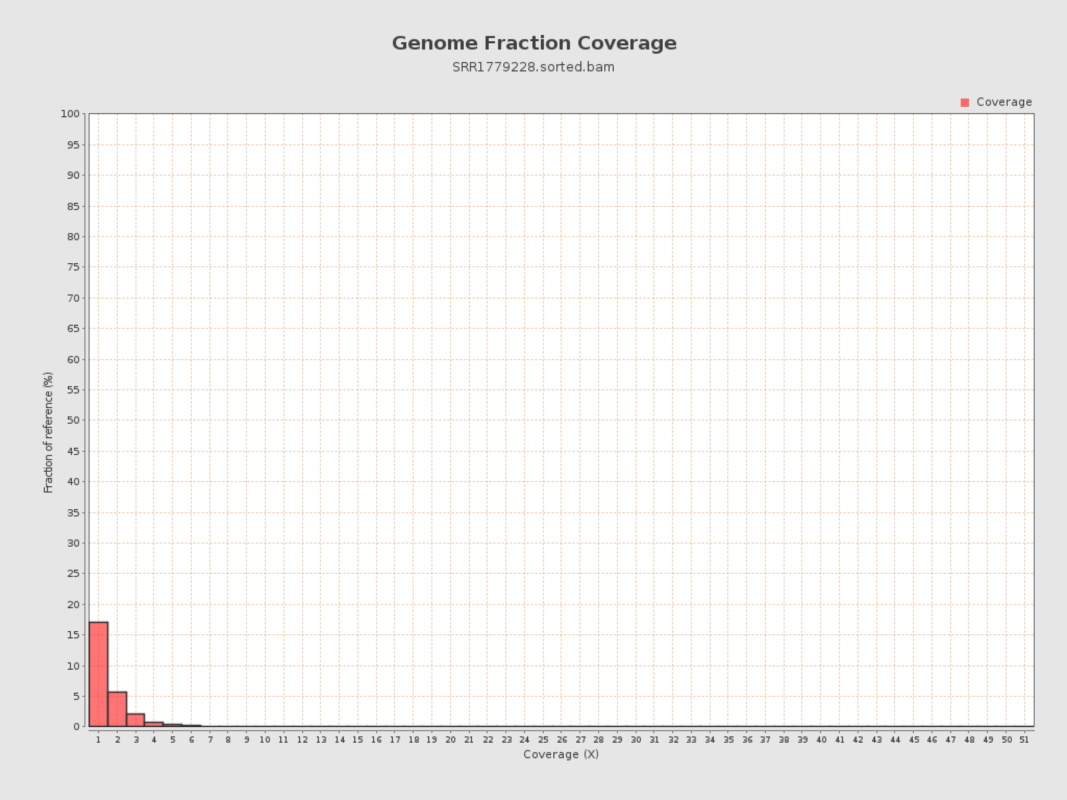
4. Results : Coverage Histogram



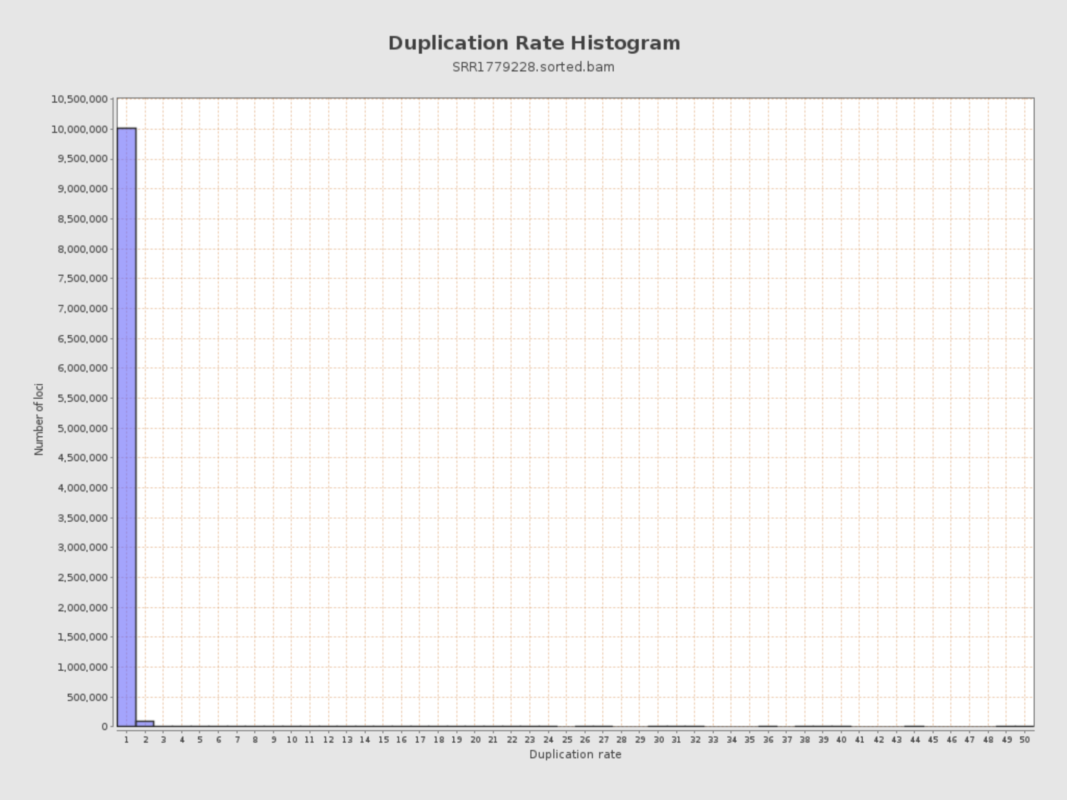
5. Results : Coverage Histogram (0-50X)



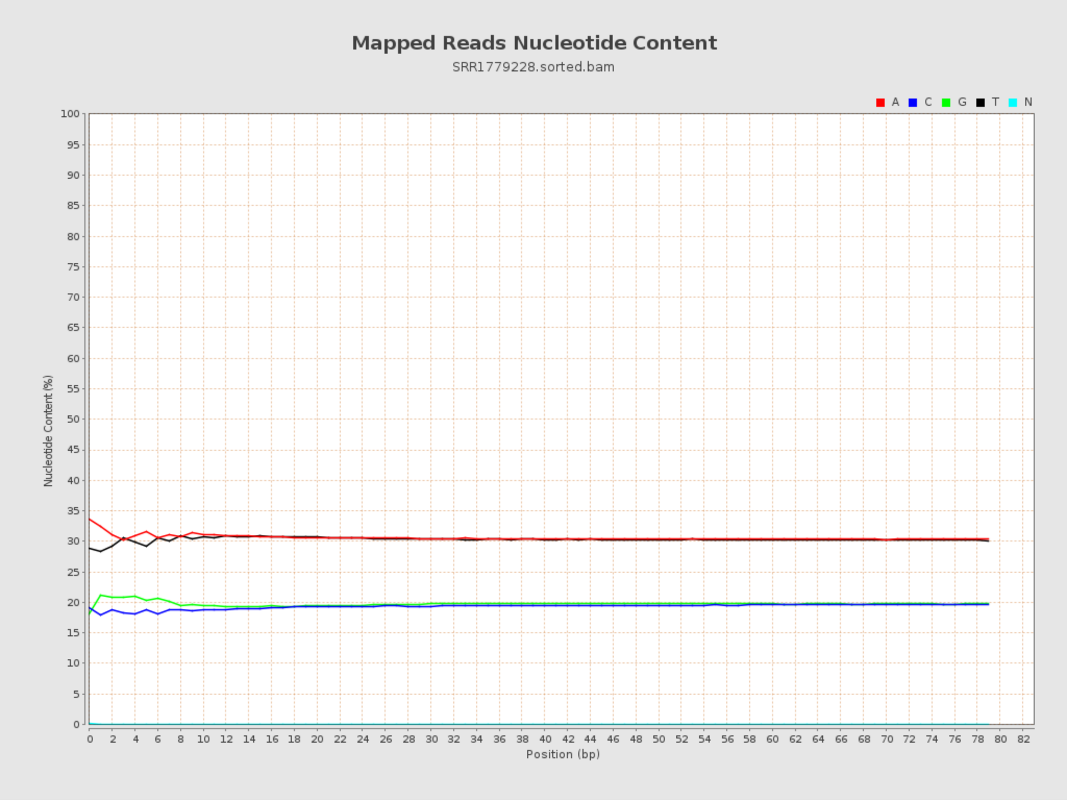
6. Results : Genome Fraction Coverage



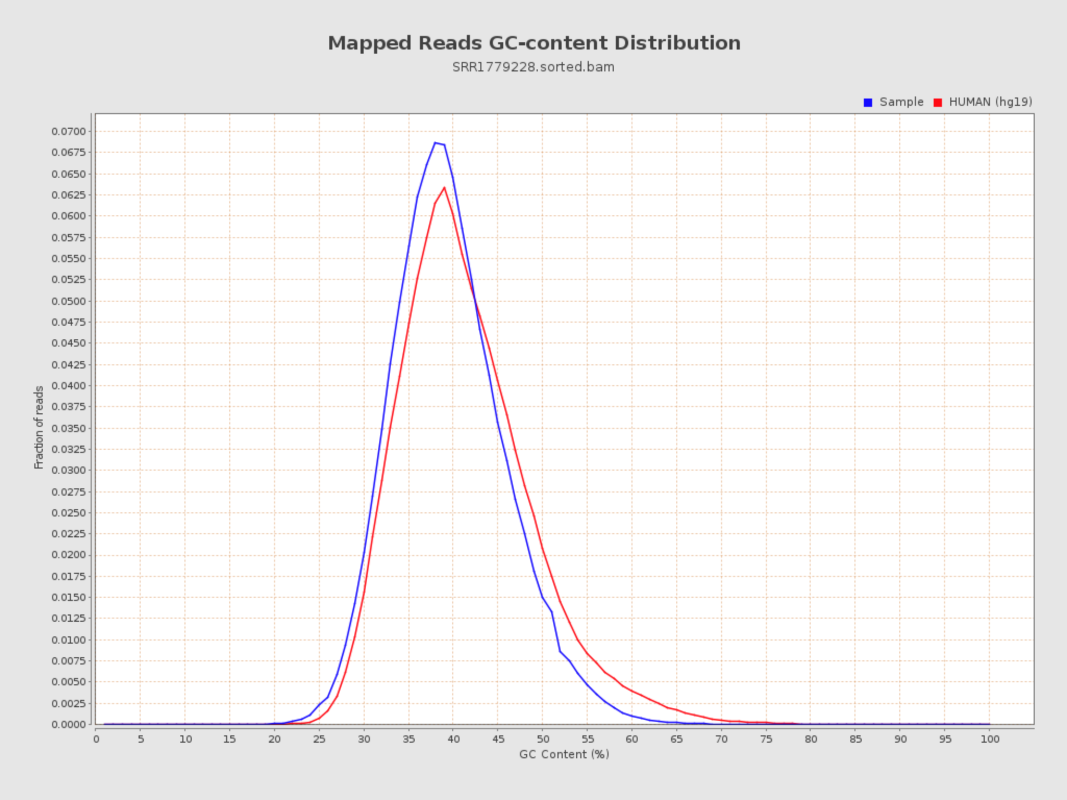
7. Results : Duplication Rate Histogram



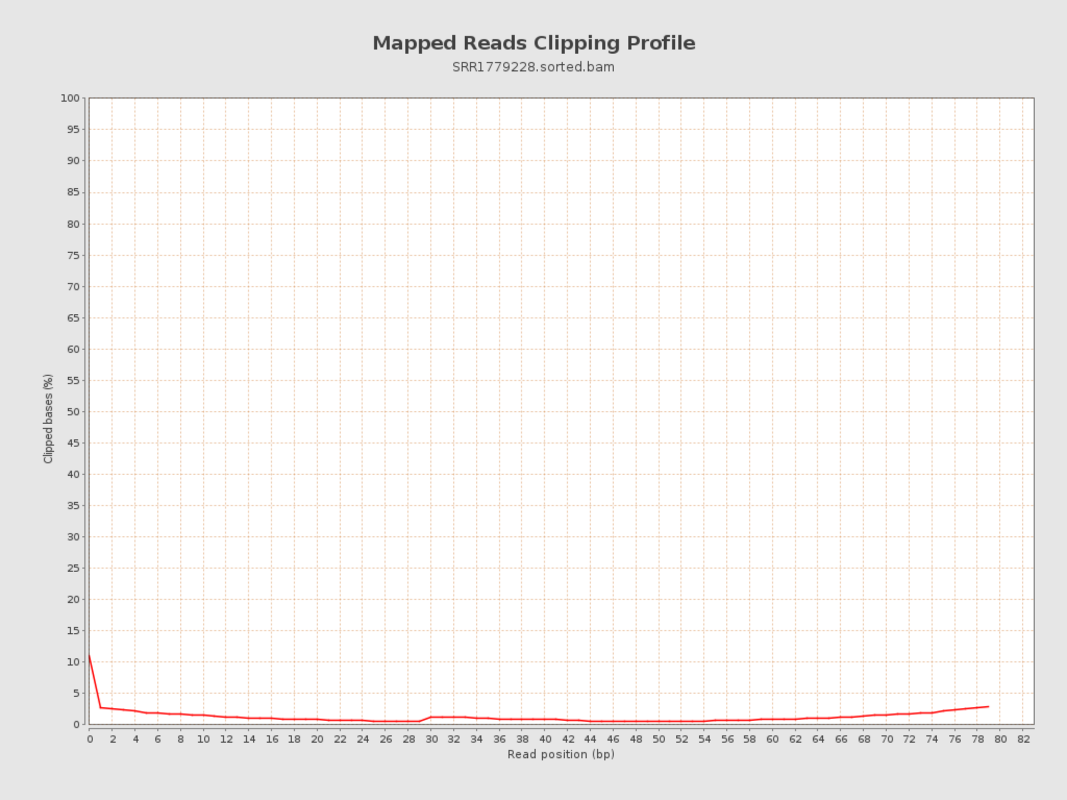
8. Results : Mapped Reads Nucleotide Content



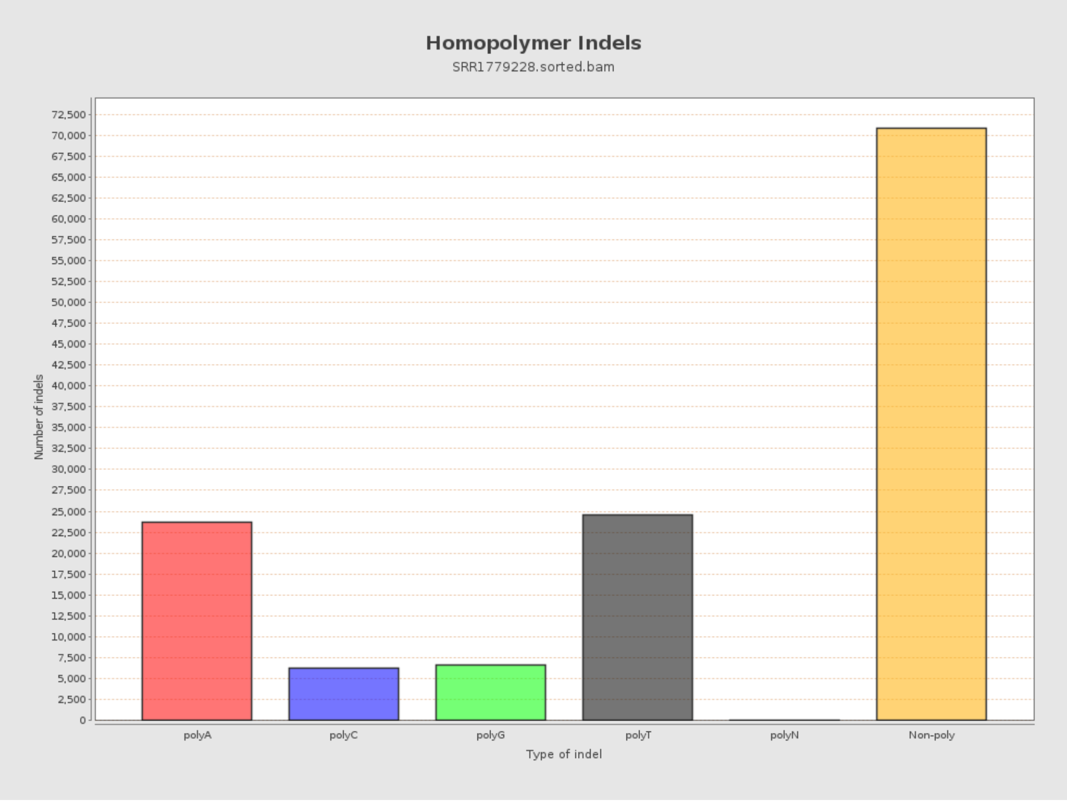
9. Results : Mapped Reads GC-content Distribution



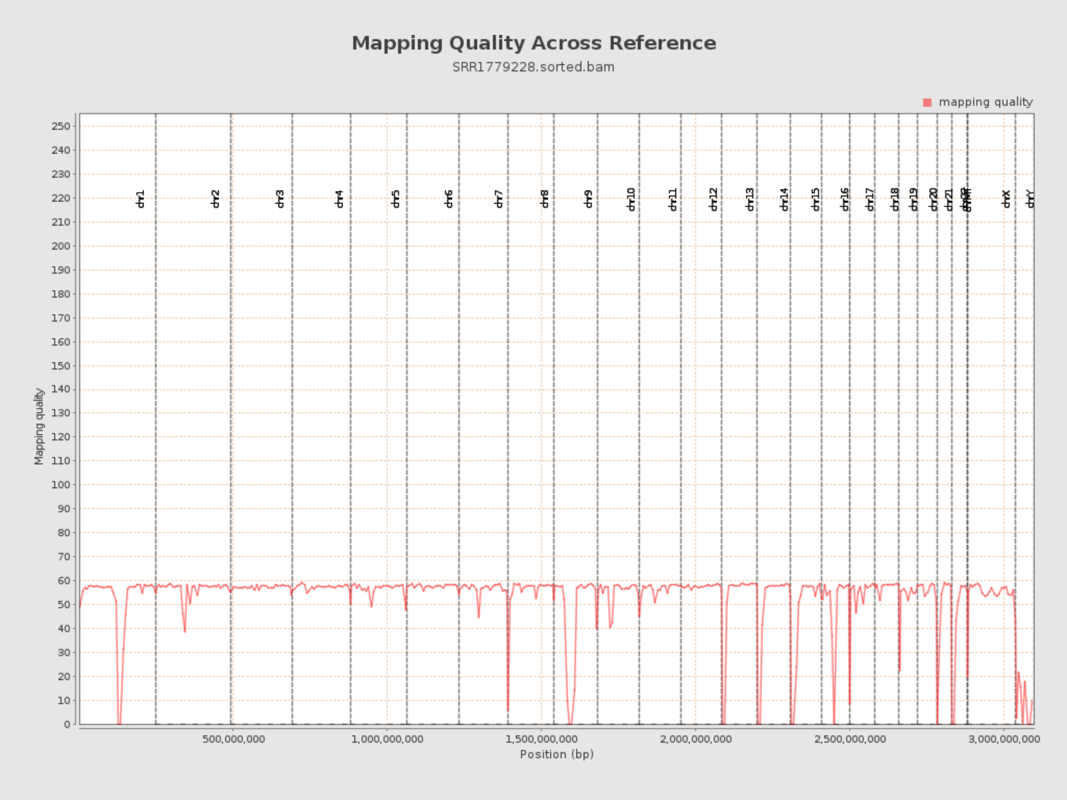
10. Results : Mapped Reads Clipping Profile



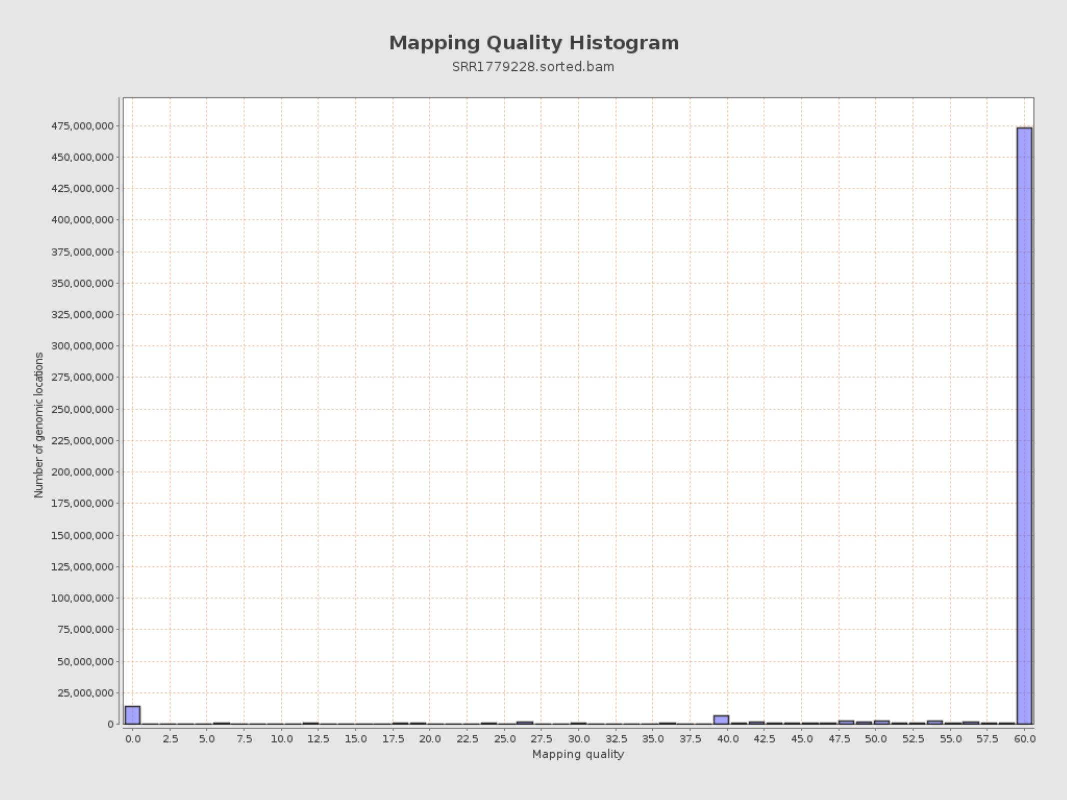
11. Results : Homopolymer Indels



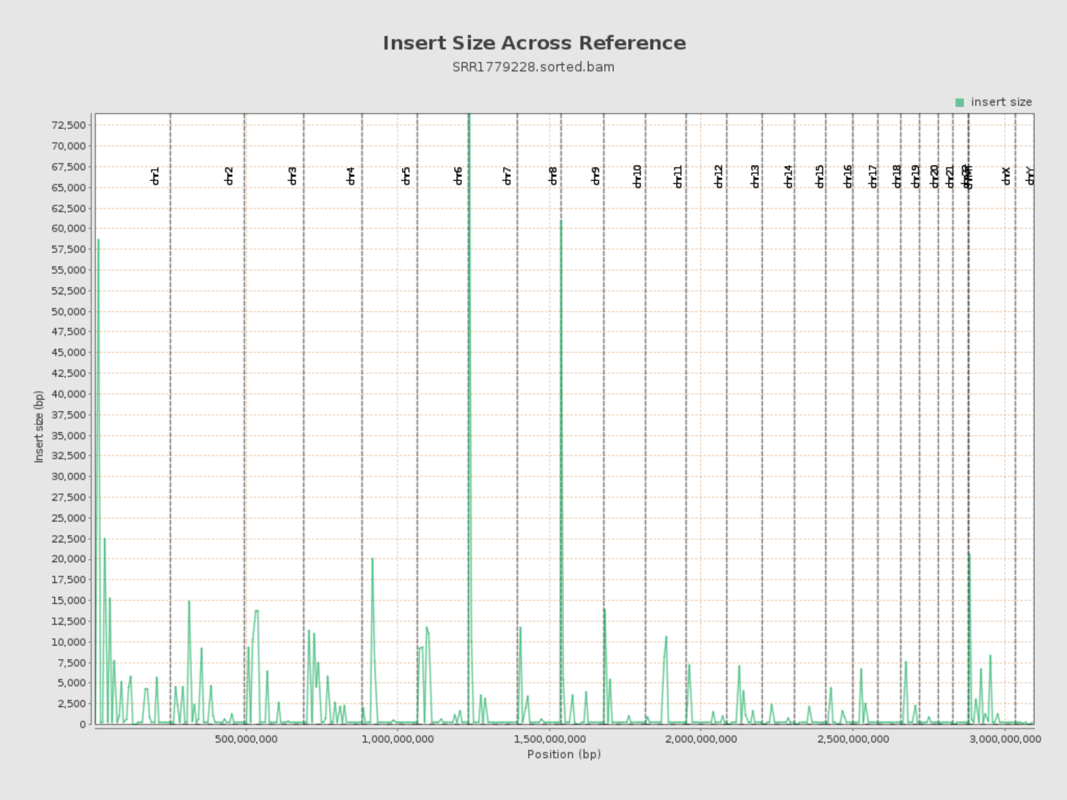
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram