Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 06:00:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779163.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_SRR1779163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779163_1.fastq.gz SRR1779163_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 06:00:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,352,896
Mapped reads	31,067,869 / 96.03%
Unmapped reads	1,285,027 / 3.97%
Mapped paired reads	31,067,869 / 96.03%
Mapped reads, first in pair	15,657,032 / 48.39%
Mapped reads, second in pair	15,410,837 / 47.63%
Mapped reads, both in pair	30,692,678 / 94.87%
Mapped reads, singletons	375,191 / 1.16%
Secondary alignments	0
Supplementary alignments	183,940 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	1,557,527 / 4.81%
Duplication rate	4.51%
Clipped reads	1,964,367 / 6.07%

2.2. ACGT Content

Number/percentage of A's	955,532,956 / 30.8%
Number/percentage of C's	592,146,776 / 19.09%
Number/percentage of T's	952,918,290 / 30.72%
Number/percentage of G's	600,287,907 / 19.35%
Number/percentage of N's	1,250,067 / 0.04%

GC Percentage	38.44%

2.3. Coverage

Mean	1.0023
Standard Deviation	3.1367

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	64,464.73
Standard Deviation	2,429,150.03
P25/Median/P75	163 / 219 / 298

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	13,084,834
Insertions	258,652
Mapped reads with at least one insertion	0.82%
Deletions	319,440
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.54%

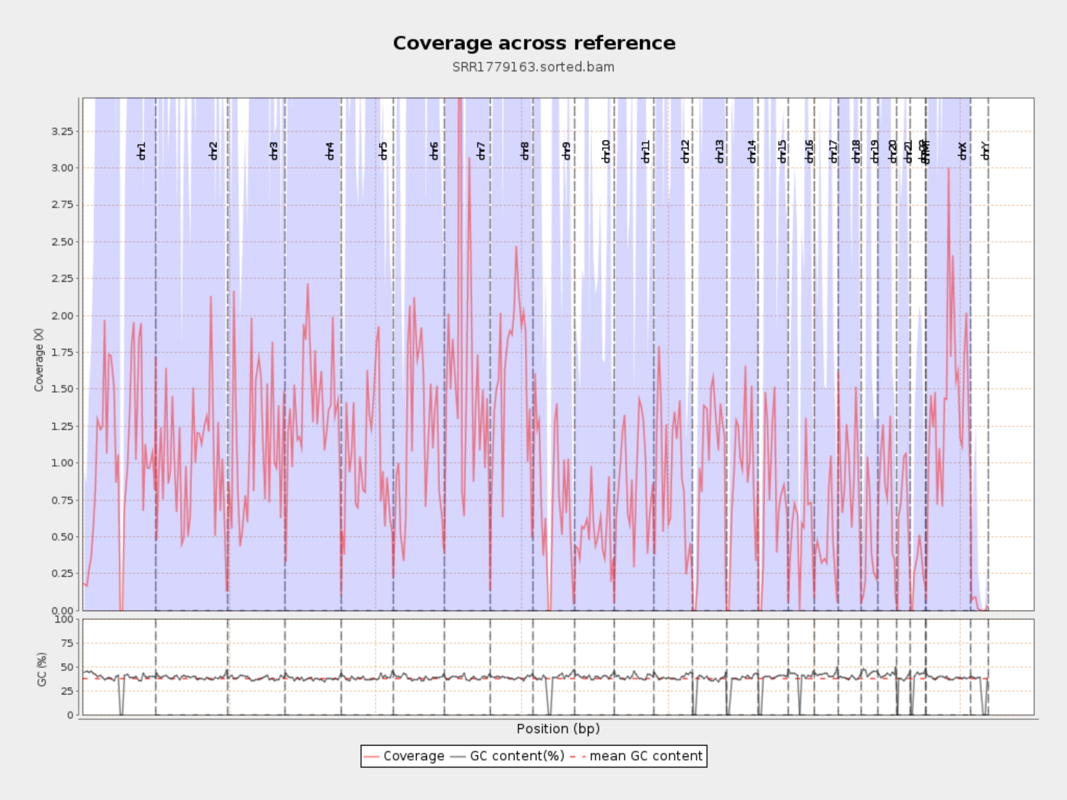
2.7. Chromosome stats

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

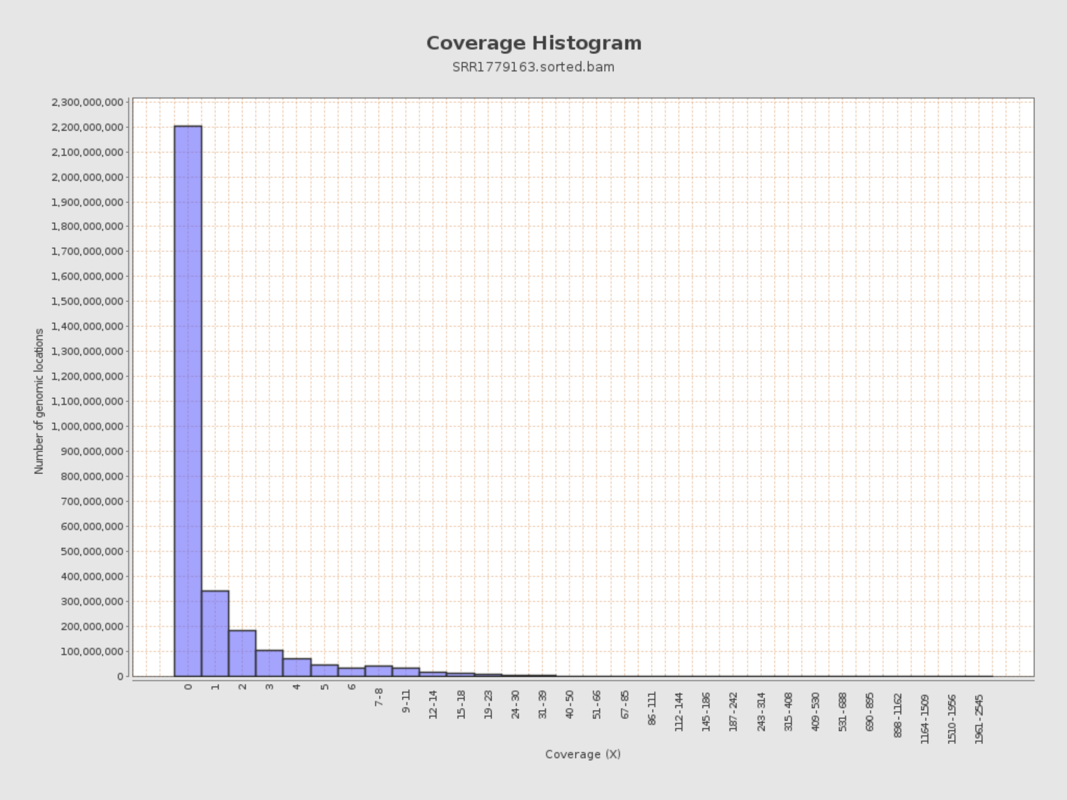
		bases	coverage	deviation
chr1	249250621	260450965	1.0449	3.8976
chr2	243199373	245408267	1.0091	2.95
chr3	198022430	220574630	1.1139	2.8164
chr4	191154276	266229462	1.3927	3.0369
chr5	180915260	182357417	1.008	2.5851
chr6	171115067	207797856	1.2144	3.0828
chr7	159138663	260183926	1.635	5.1794
chr8	146364022	235549407	1.6093	3.4764
chr9	141213431	107838642	0.7637	2.4217
chr10	135534747	71538335	0.5278	4.4144
chr11	135006516	118611848	0.8786	2.5054
chr12	133851895	122574339	0.9157	2.724
chr13	115169878	117459012	1.0199	2.674
chr14	107349540	96435046	0.8983	2.5699
chr15	102531392	79656523	0.7769	2.394
chr16	90354753	50552075	0.5595	1.9216
chr17	81195210	37687826	0.4642	1.9029
chr18	78077248	76140361	0.9752	2.8677
chr19	59128983	24838892	0.4201	2.1503
chr20	63025520	51330728	0.8144	2.4085
chr21	48129895	32435684	0.6739	2.0084
chr22	51304566	13715710	0.2673	1.1576
chrMT	16571	1144	0.069	0.3408
chrX	155270560	221362859	1.4257	3.8854

chrY	59373566	2119742	0.0357	0.5524

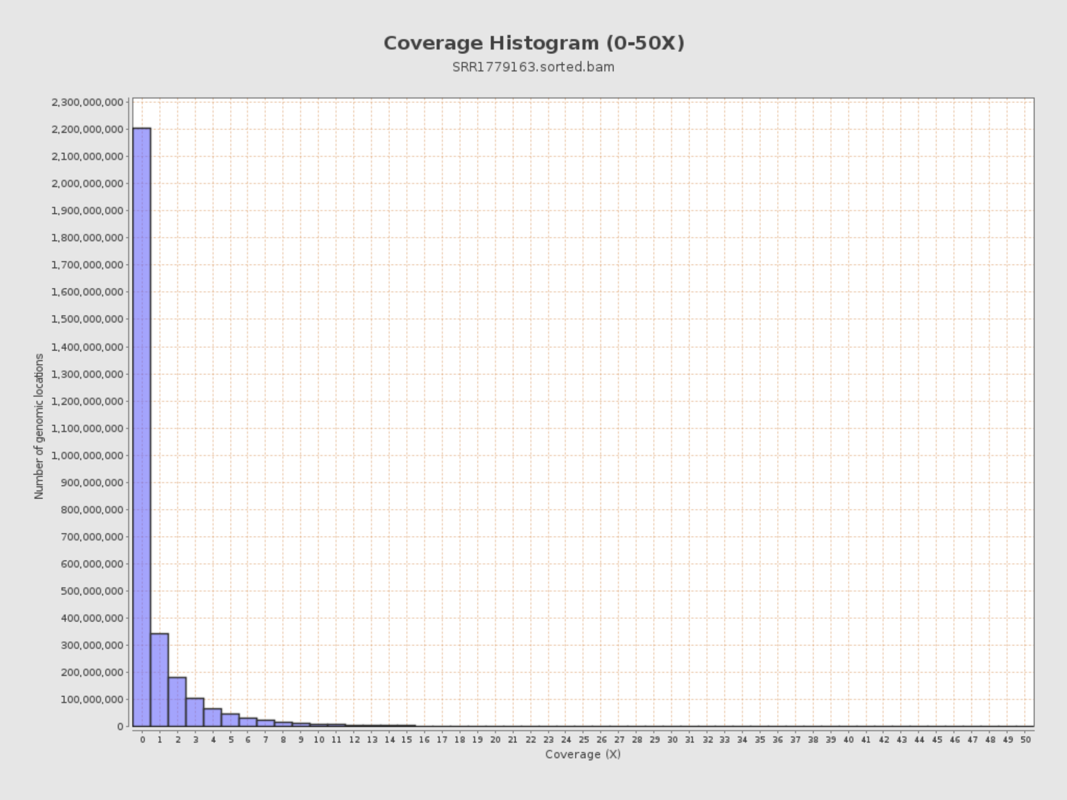
3. Results : Coverage across reference



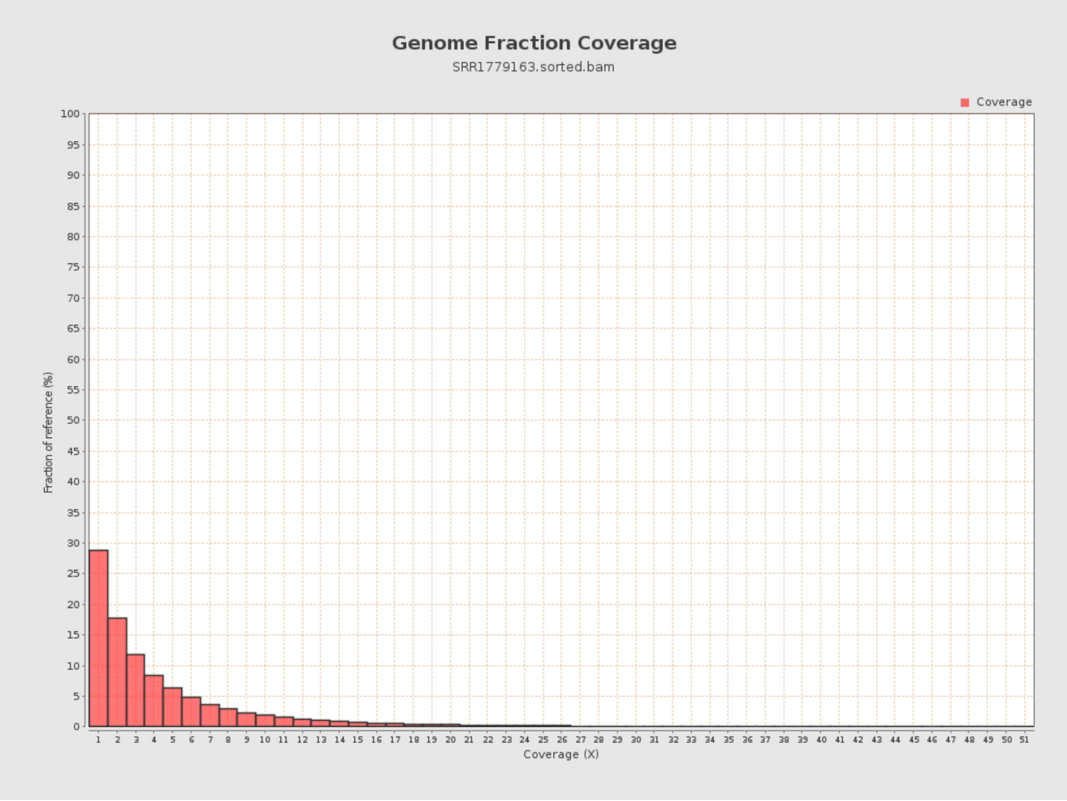
4. Results : Coverage Histogram



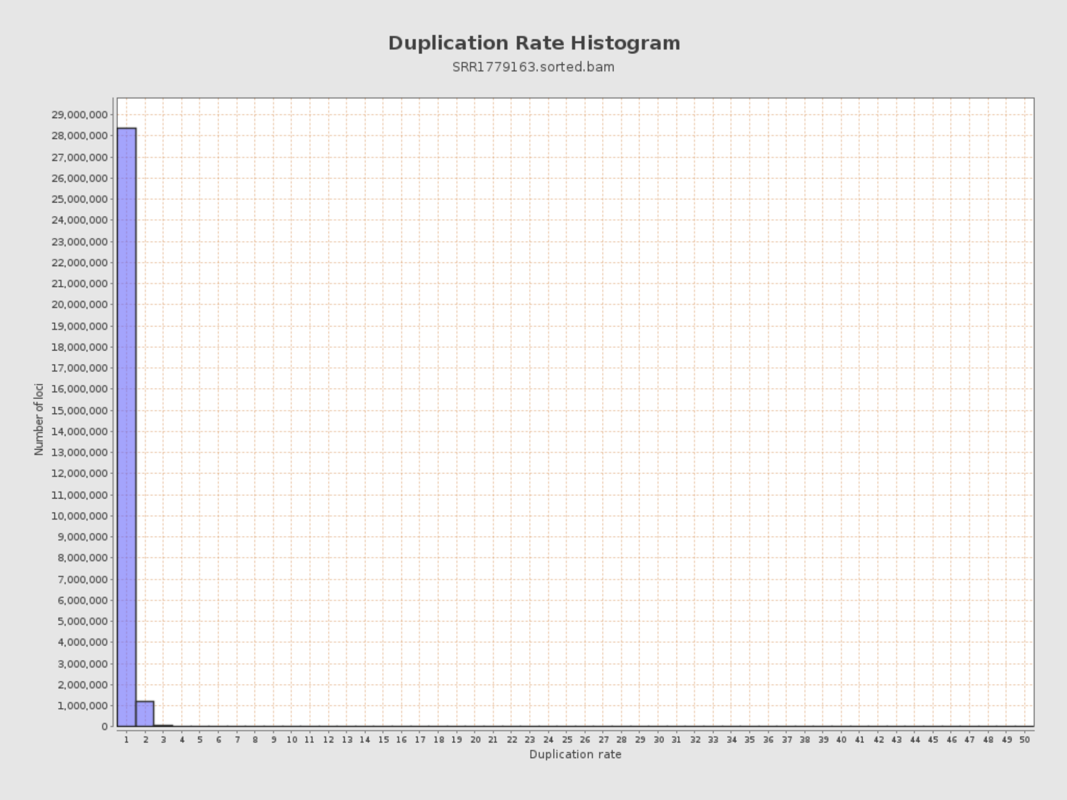
5. Results : Coverage Histogram (0-50X)



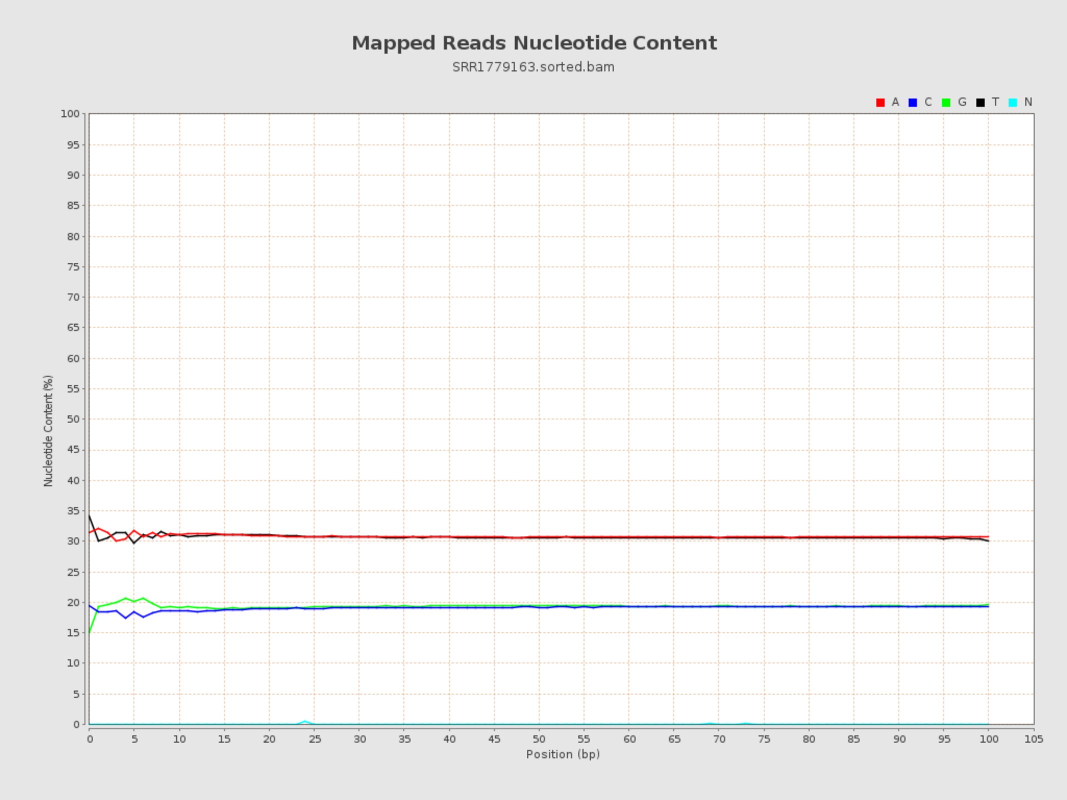
6. Results : Genome Fraction Coverage



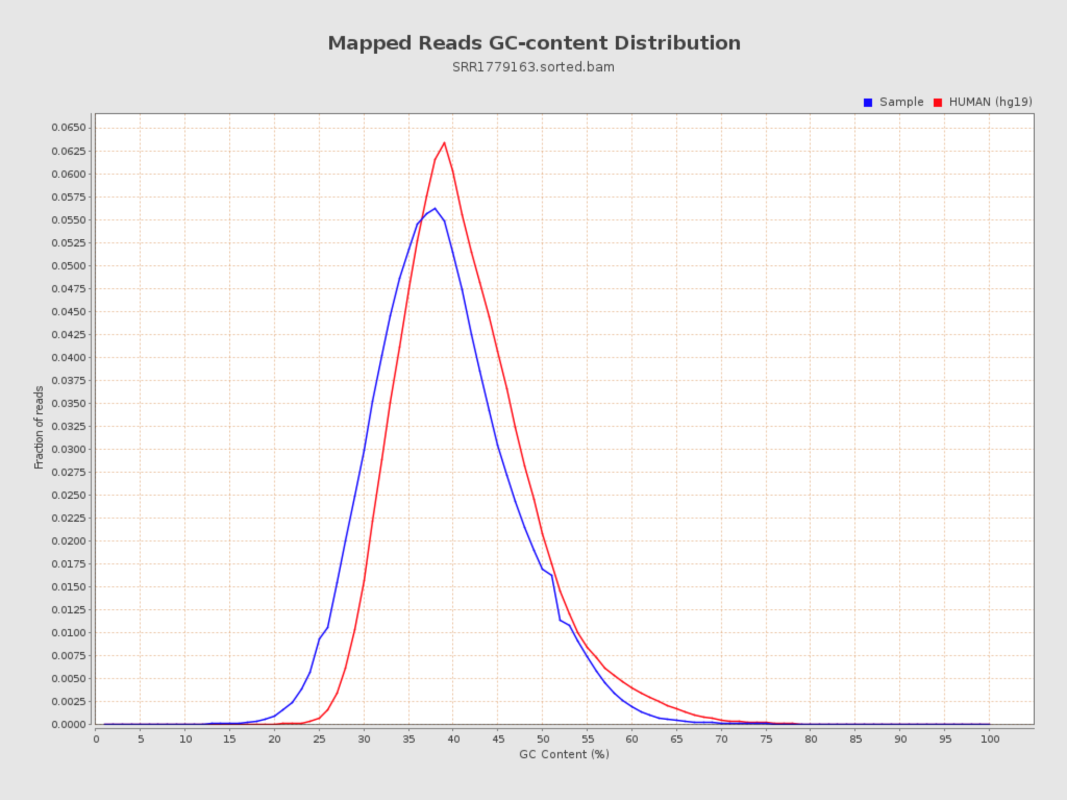
7. Results : Duplication Rate Histogram



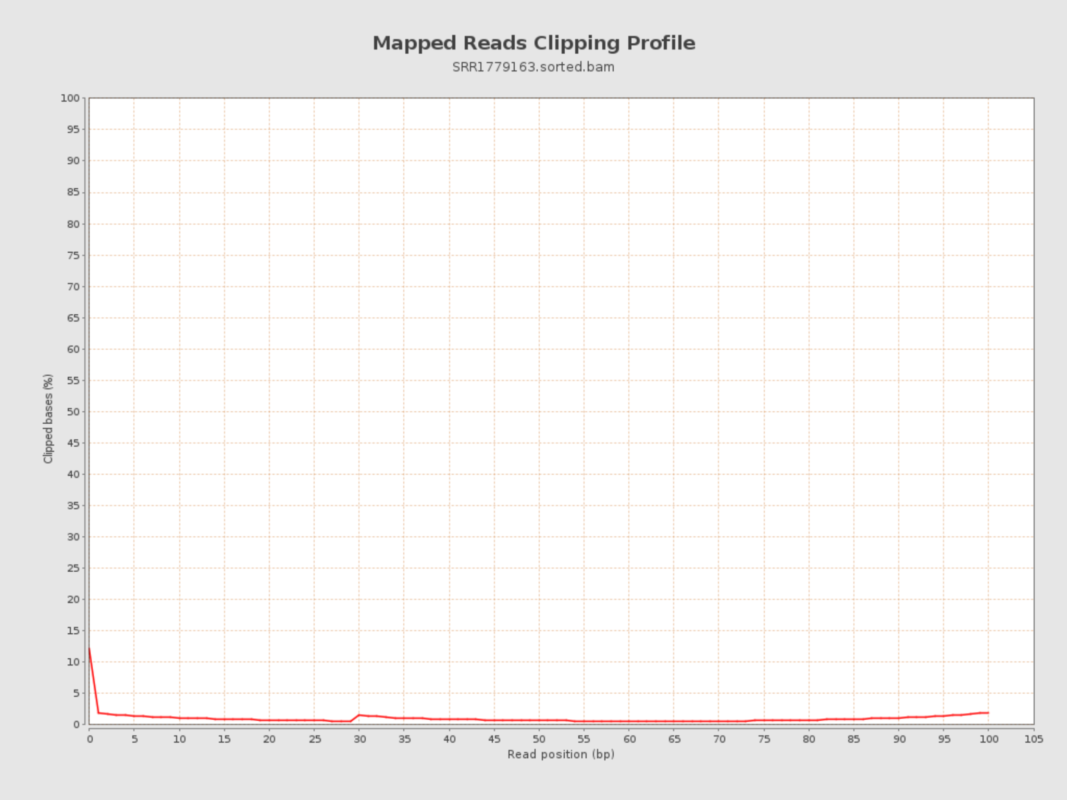
8. Results : Mapped Reads Nucleotide Content



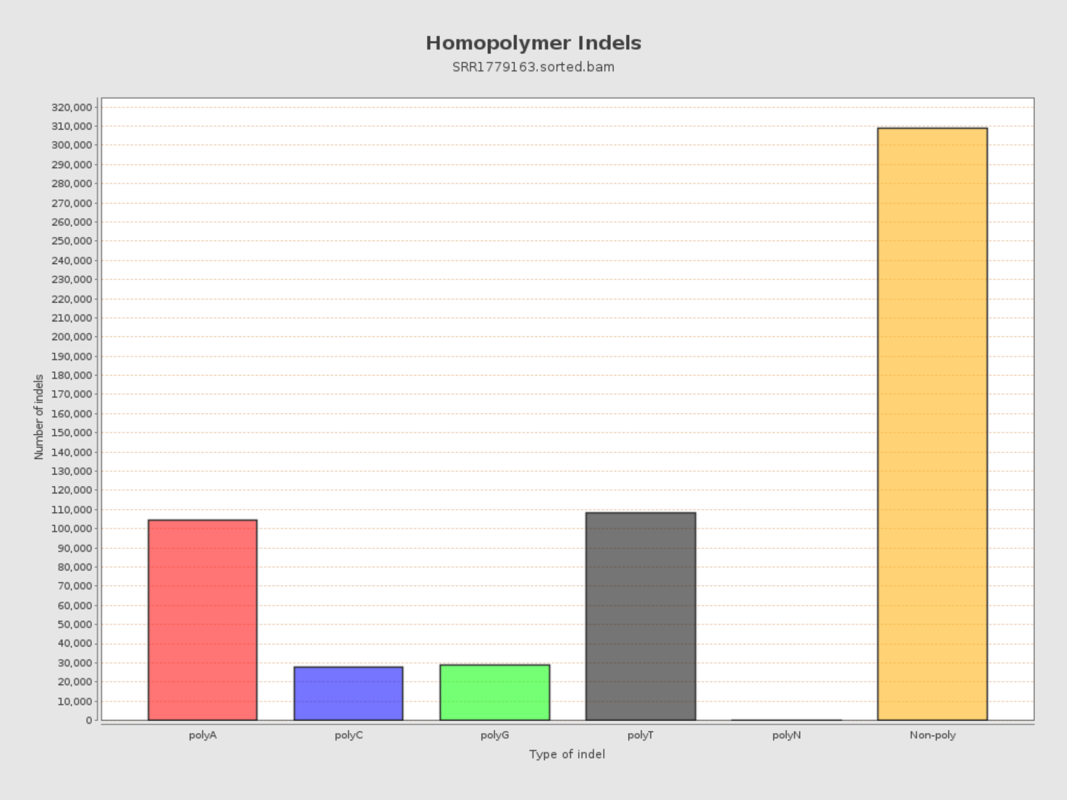
9. Results : Mapped Reads GC-content Distribution



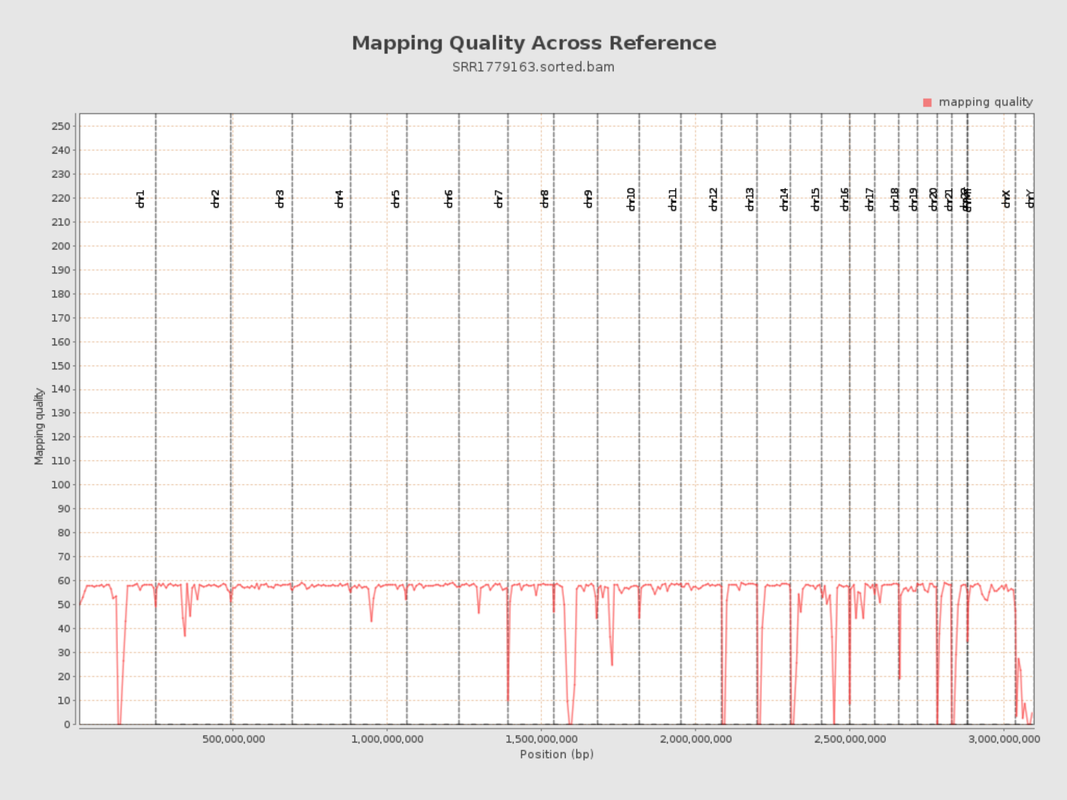
10. Results : Mapped Reads Clipping Profile



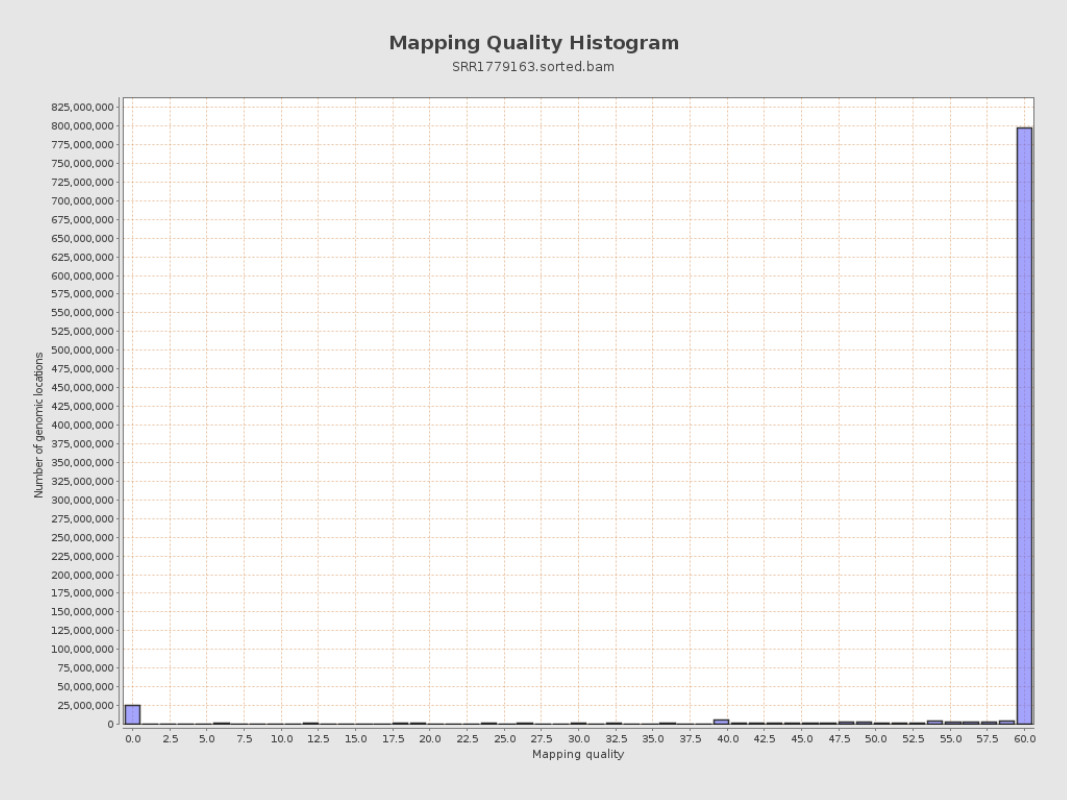
11. Results : Homopolymer Indels



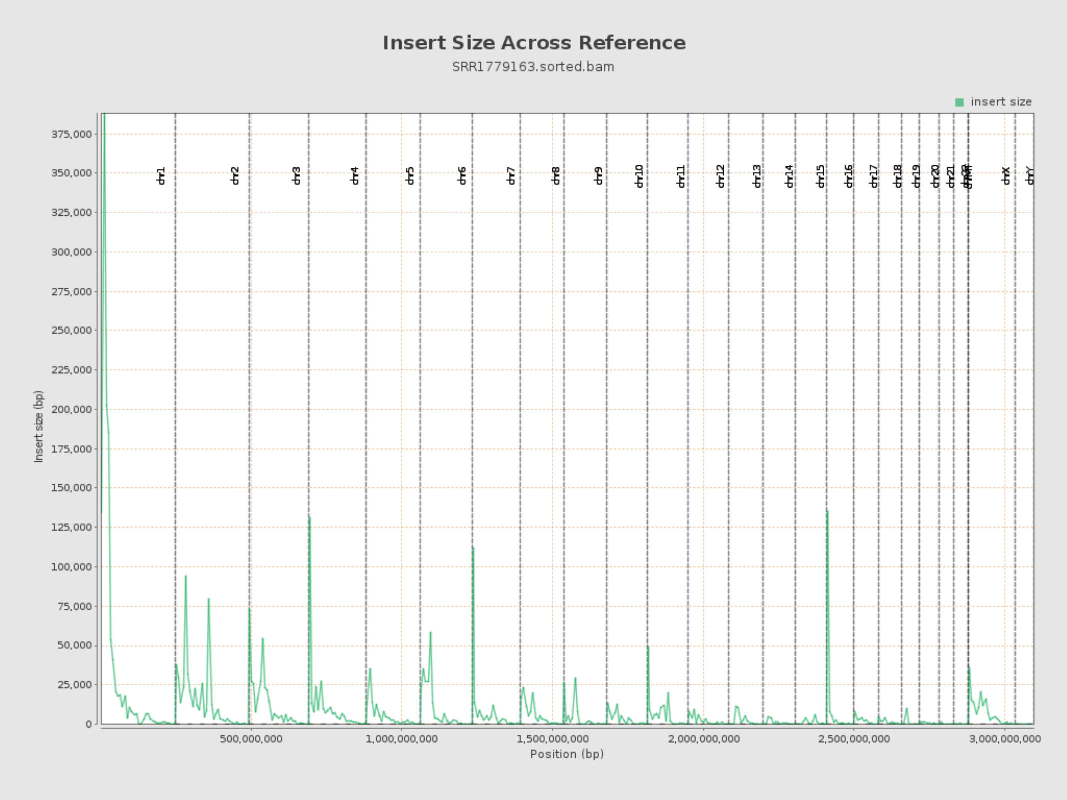
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram