Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 12:53:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779177.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_SRR1779177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779177_1.fastq.gz SRR1779177_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 12:53:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,587,636
Mapped reads	29,569,604 / 96.67%
Unmapped reads	1,018,032 / 3.33%
Mapped paired reads	29,569,604 / 96.67%
Mapped reads, first in pair	14,936,328 / 48.83%
Mapped reads, second in pair	14,633,276 / 47.84%
Mapped reads, both in pair	29,161,790 / 95.34%
Mapped reads, singletons	407,814 / 1.33%
Secondary alignments	0
Supplementary alignments	172,187 / 0.56%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	1,027,948 / 3.36%
Duplication rate	3.06%
Clipped reads	1,930,270 / 6.31%

2.2. ACGT Content

Number/percentage of A's	898,701,520 / 30.44%
Number/percentage of C's	574,778,823 / 19.47%
Number/percentage of T's	895,593,074 / 30.34%
Number/percentage of G's	581,830,460 / 19.71%
Number/percentage of N's	1,197,678 / 0.04%

GC Percentage	39.18%

2.3. Coverage

Mean	0.9538
Standard Deviation	2.4156

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	63,976.63
Standard Deviation	2,387,515.83
P25/Median/P75	154 / 206 / 280

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	12,521,989
Insertions	246,432
Mapped reads with at least one insertion	0.82%
Deletions	303,598
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.63%

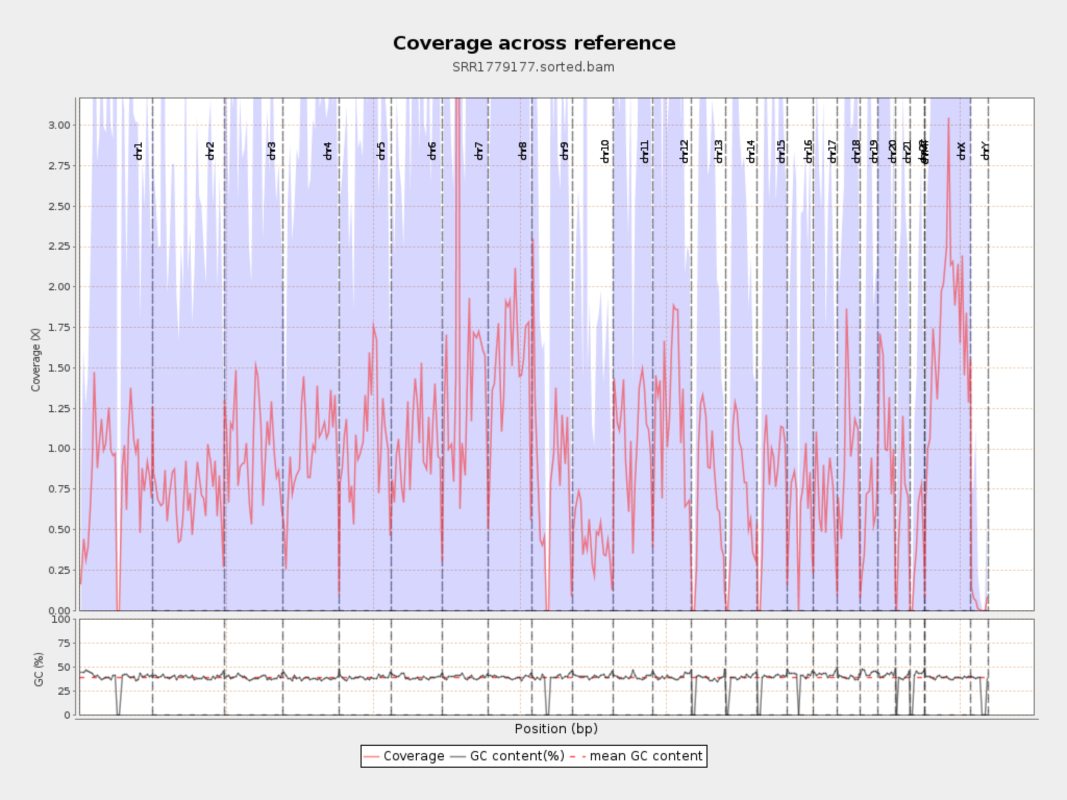
2.7. Chromosome stats

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

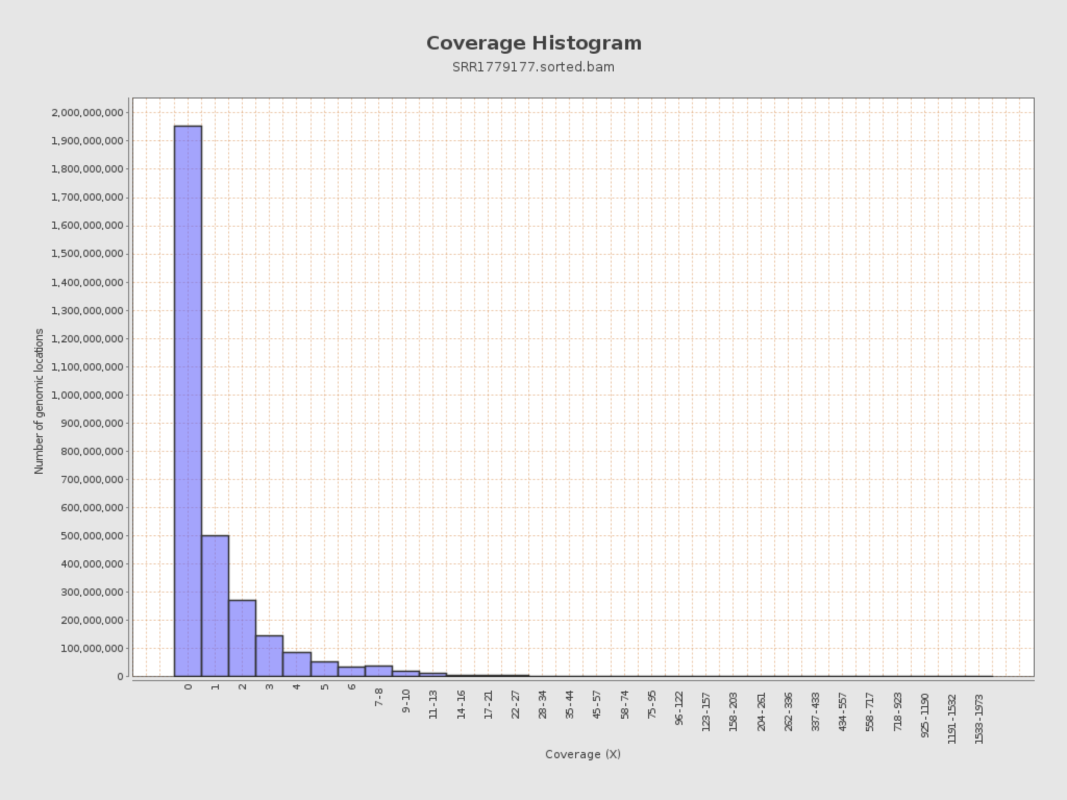
		bases	coverage	deviation
chr1	249250621	205279449	0.8236	2.6187
chr2	243199373	171939211	0.707	1.9644
chr3	198022430	197386867	0.9968	1.9169
chr4	191154276	189744140	0.9926	1.9165
chr5	180915260	189480924	1.0473	1.9154
chr6	171115067	175930124	1.0281	2.0168
chr7	159138663	251337148	1.5794	5.5331
chr8	146364022	224951056	1.5369	2.4473
chr9	141213431	116295003	0.8235	1.9392
chr10	135534747	59984248	0.4426	2.6445
chr11	135006516	145143254	1.0751	2.0485
chr12	133851895	163552639	1.2219	2.2152
chr13	115169878	84143519	0.7306	1.6923
chr14	107349540	73193144	0.6818	1.6211
chr15	102531392	81634480	0.7962	1.8763
chr16	90354753	56791555	0.6285	1.4847
chr17	81195210	54893228	0.6761	1.7164
chr18	78077248	79322386	1.0159	1.9769
chr19	59128983	33434793	0.5655	1.7581
chr20	63025520	71948113	1.1416	2.2525
chr21	48129895	31267073	0.6496	1.5045
chr22	51304566	19267568	0.3756	1.1724
chrMT	16571	1314	0.0793	0.4243
chrX	155270560	273326058	1.7603	2.9605

chrY	59373566	2534561	0.0427	0.5378

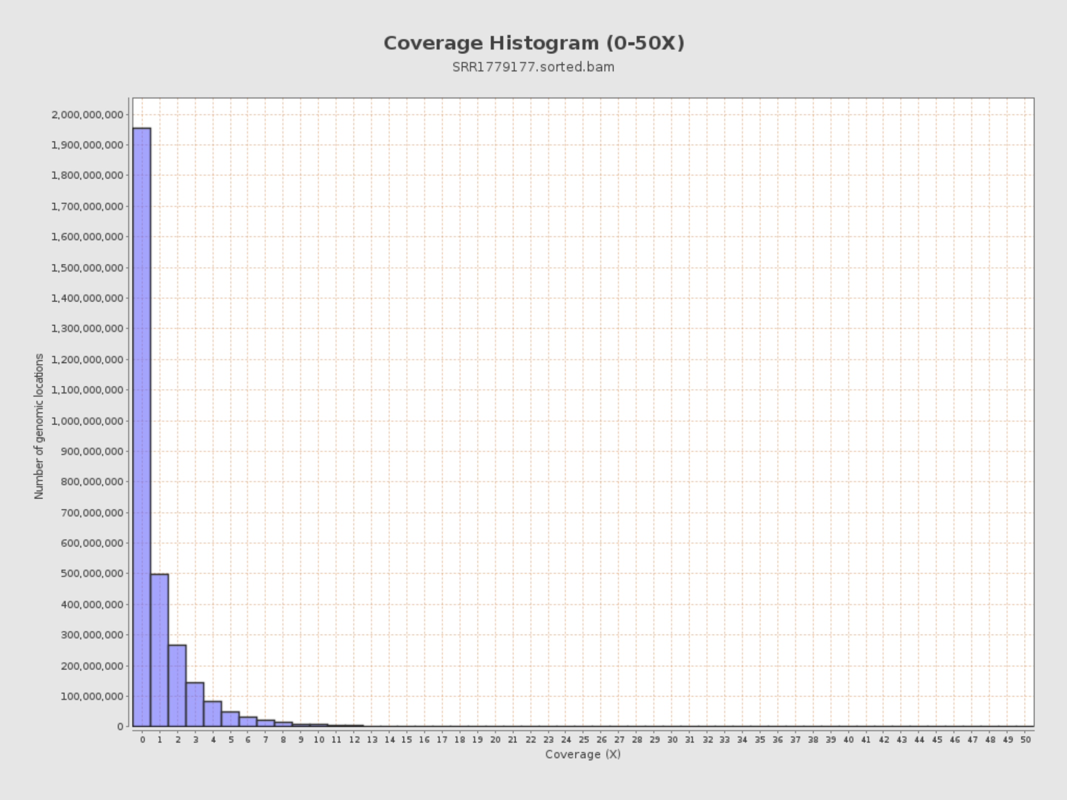
3. Results : Coverage across reference



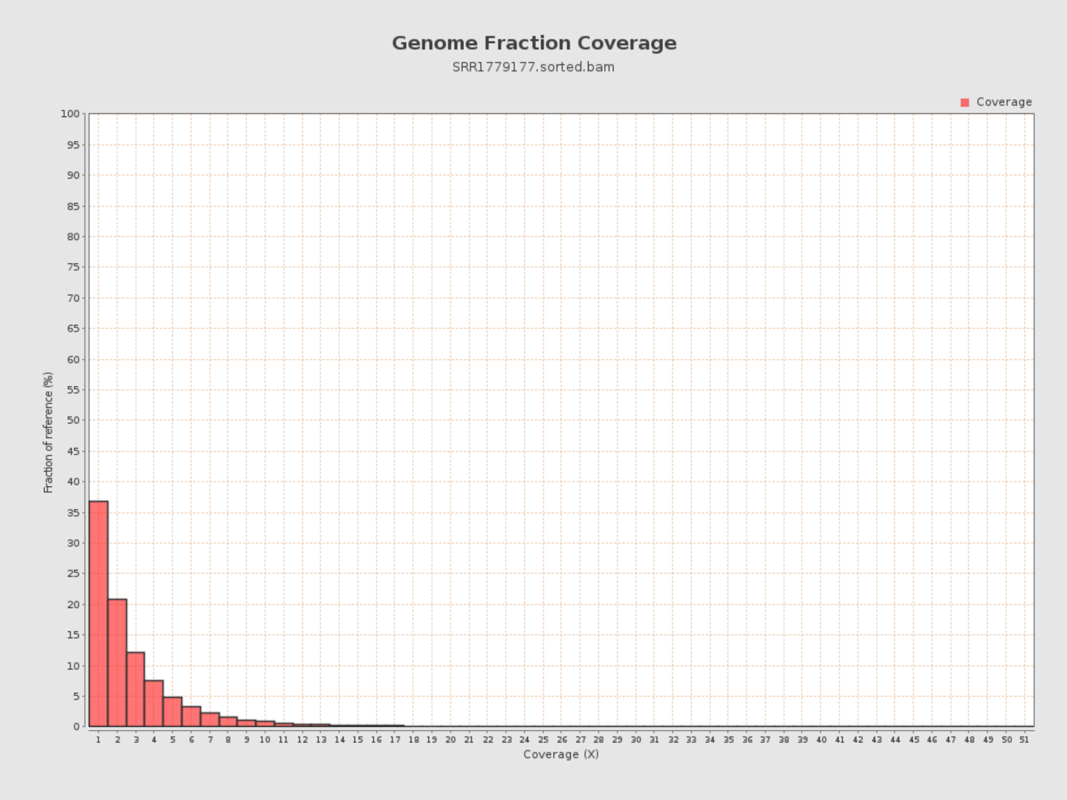
4. Results : Coverage Histogram



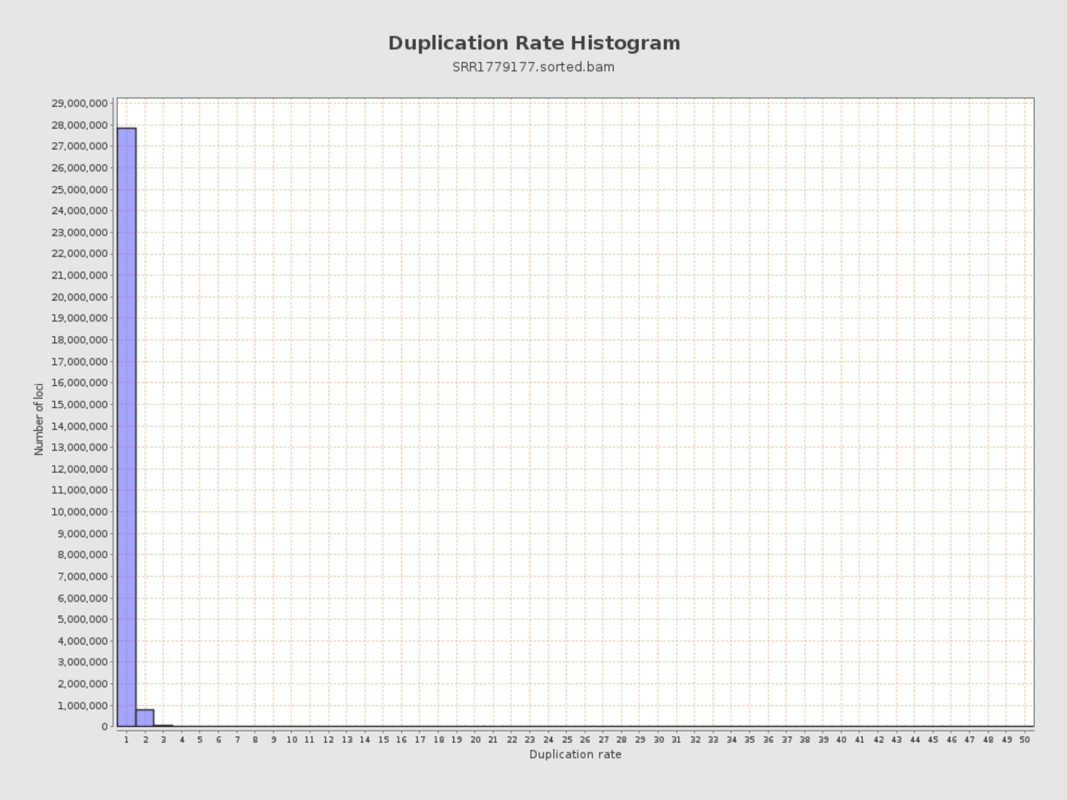
5. Results : Coverage Histogram (0-50X)



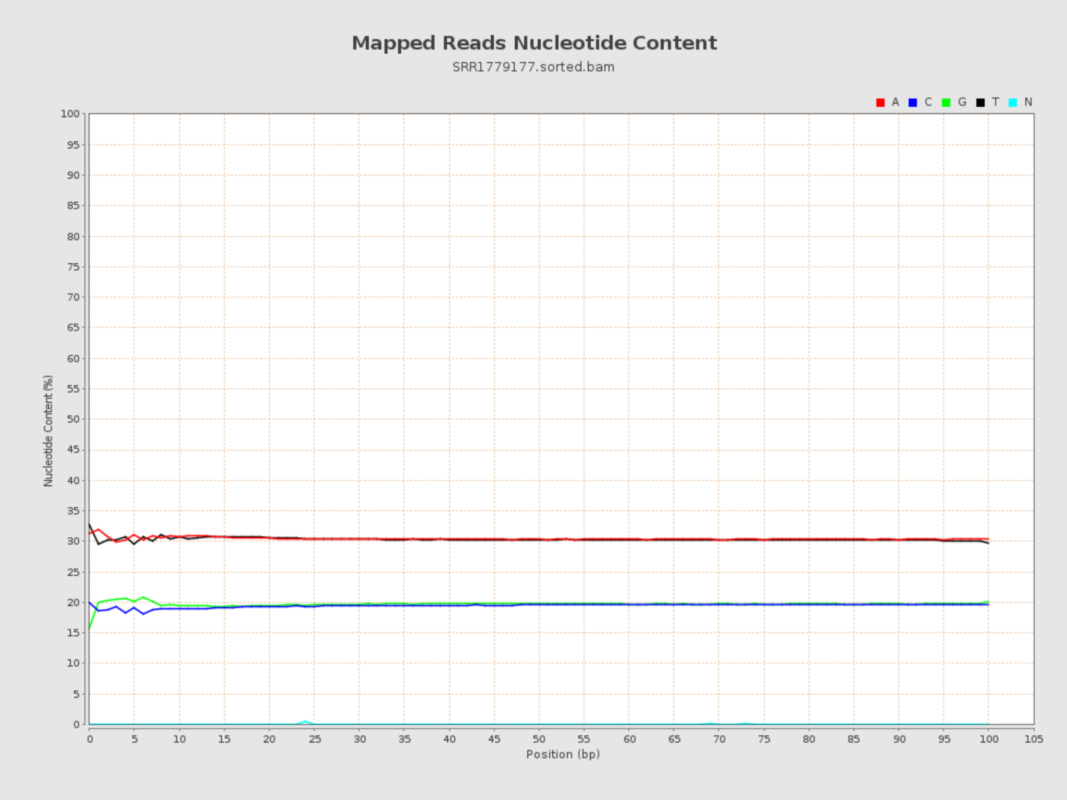
6. Results : Genome Fraction Coverage



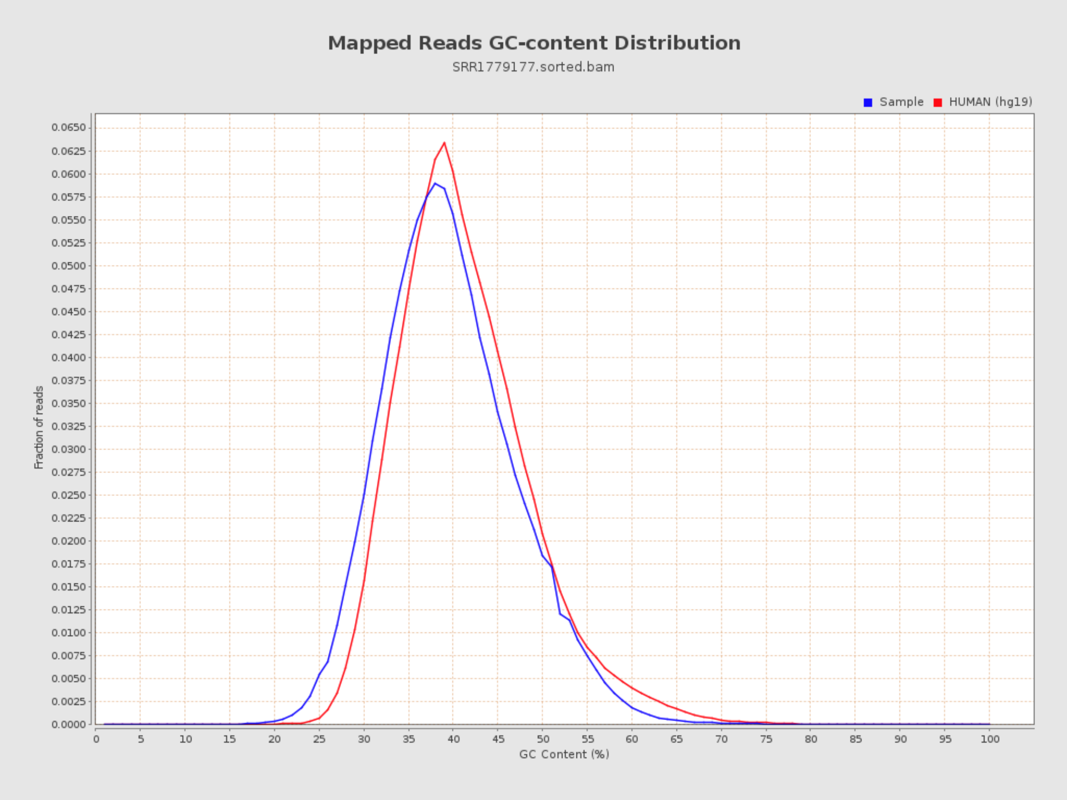
7. Results : Duplication Rate Histogram



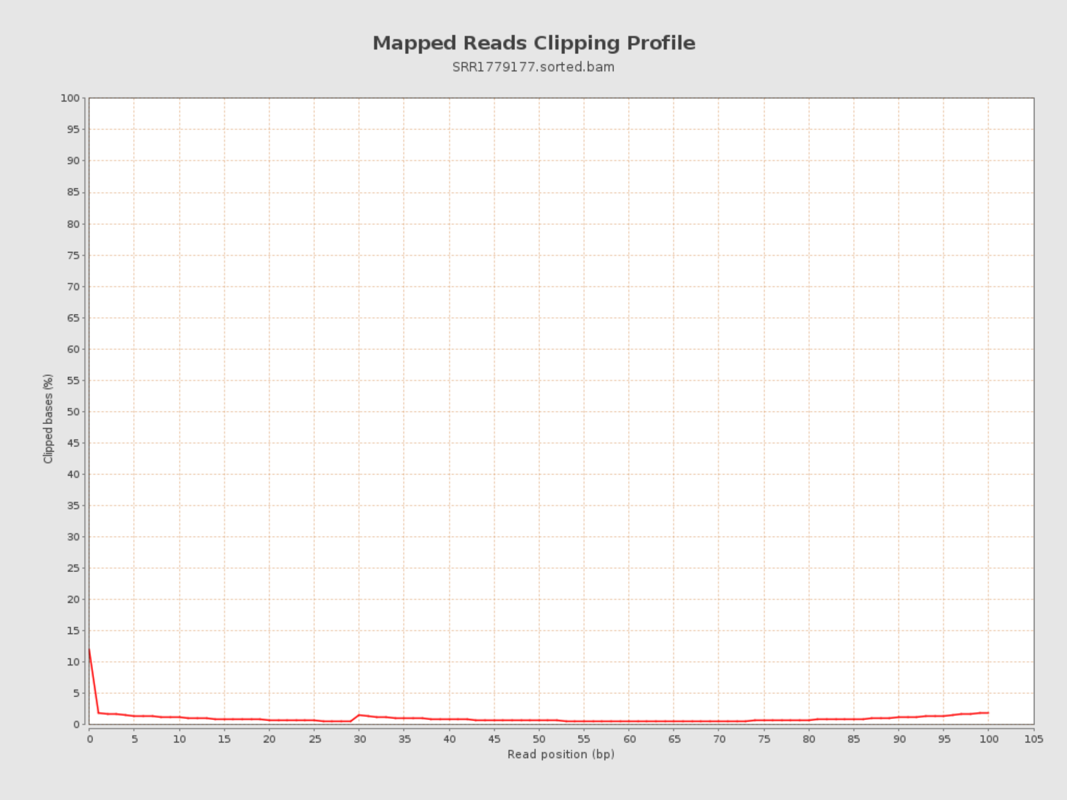
8. Results : Mapped Reads Nucleotide Content



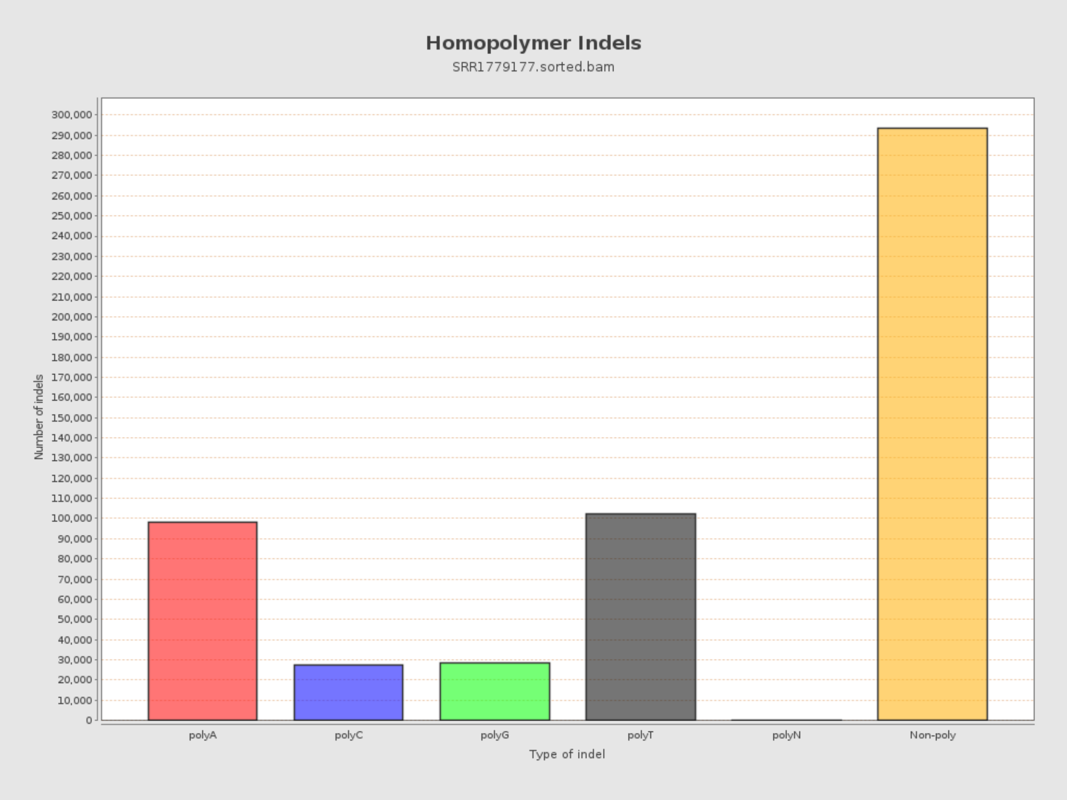
9. Results : Mapped Reads GC-content Distribution



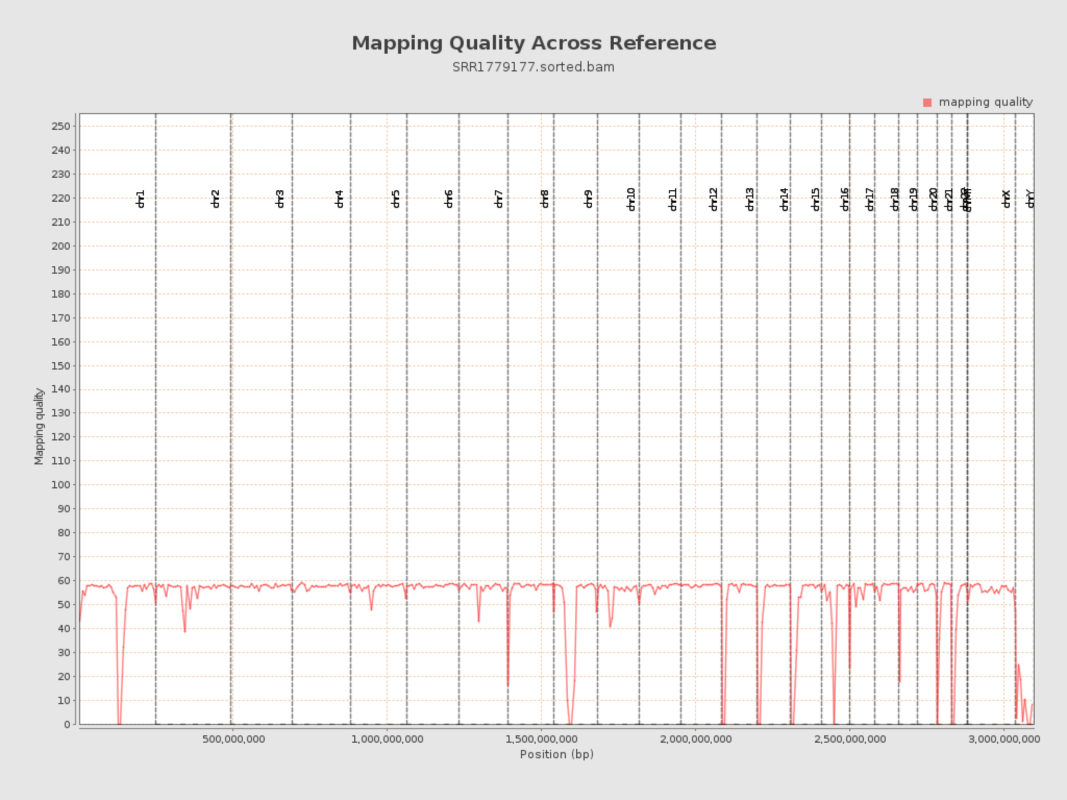
10. Results : Mapped Reads Clipping Profile



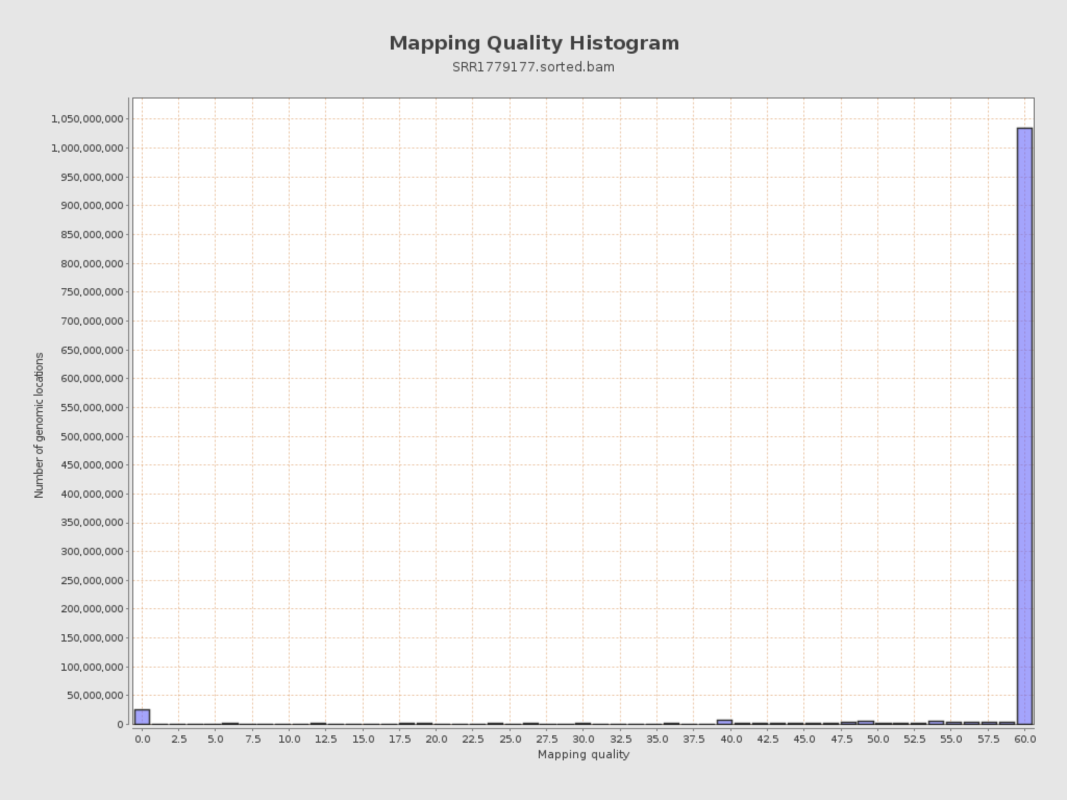
11. Results : Homopolymer Indels



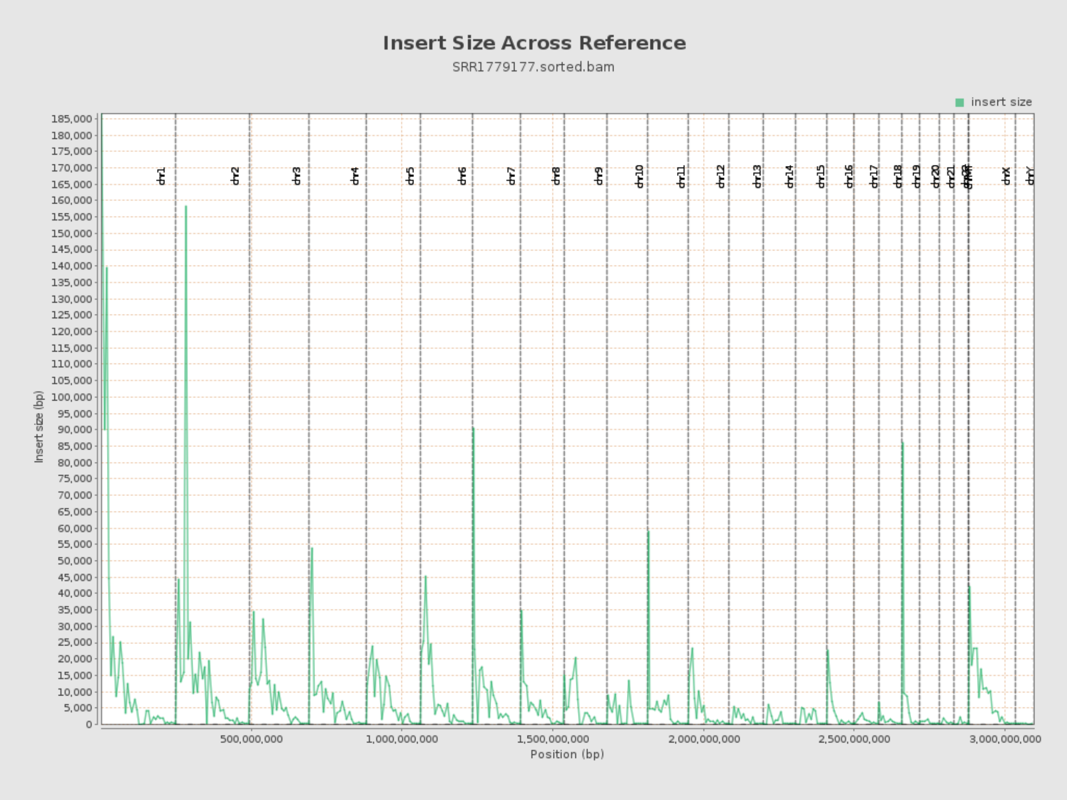
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram