Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 06:45:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779310.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_SRR1779310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779310_1.fastq.gz SRR1779310_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 06:45:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,574,426
Mapped reads	17,657,864 / 95.07%
Unmapped reads	916,562 / 4.93%
Mapped paired reads	17,657,864 / 95.07%
Mapped reads, first in pair	8,912,148 / 47.98%
Mapped reads, second in pair	8,745,716 / 47.08%
Mapped reads, both in pair	17,462,926 / 94.02%
Mapped reads, singletons	194,938 / 1.05%
Secondary alignments	0
Supplementary alignments	43,035 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	559,810 / 3.01%
Duplication rate	3.01%
Clipped reads	530,424 / 2.86%

2.2. ACGT Content

Number/percentage of A's	434,154,239 / 30.89%
Number/percentage of C's	266,509,167 / 18.96%
Number/percentage of T's	433,742,148 / 30.86%
Number/percentage of G's	270,757,293 / 19.26%
Number/percentage of N's	368,148 / 0.03%

GC Percentage	38.23%

2.3. Coverage

Mean	0.4541
Standard Deviation	1.5438

2.4. Mapping Quality

Mean Mapping Quality	53.48

2.5. Insert size

Mean	30,266.38
Standard Deviation	1,614,014.28
P25/Median/P75	163 / 219 / 301

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,924,663
Insertions	102,647
Mapped reads with at least one insertion	0.58%
Deletions	131,153
Mapped reads with at least one deletion	0.73%
Homopolymer indels	47.06%

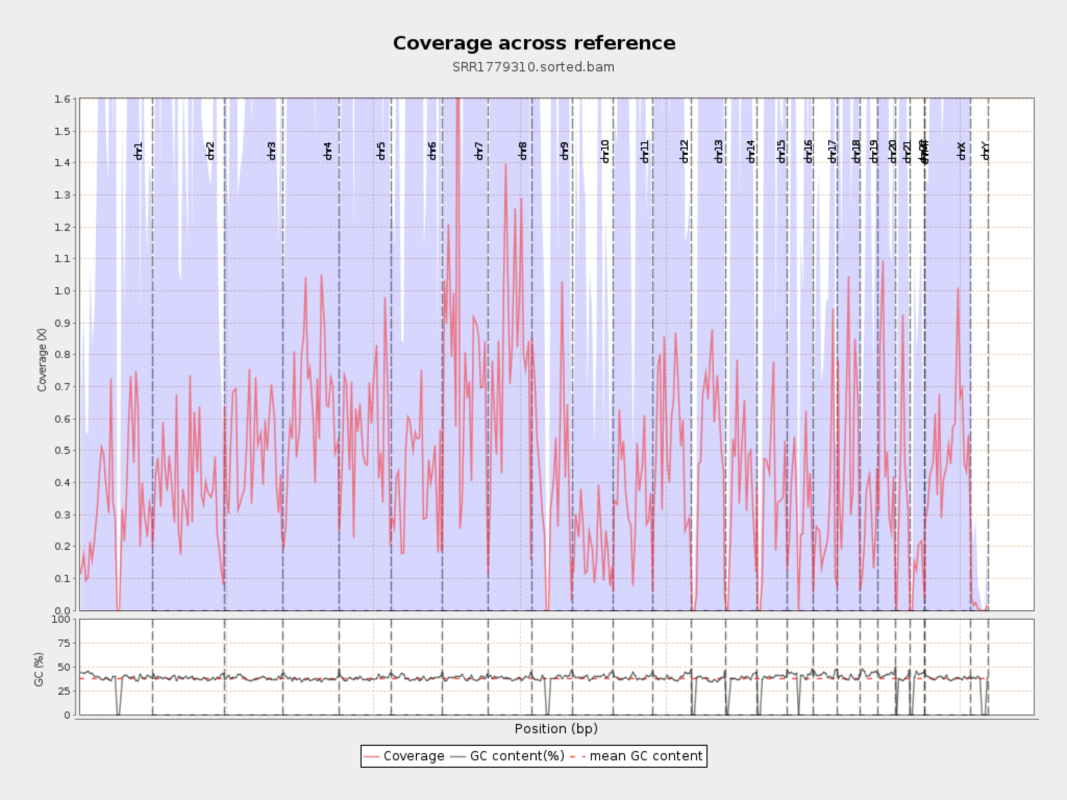
2.7. Chromosome stats

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

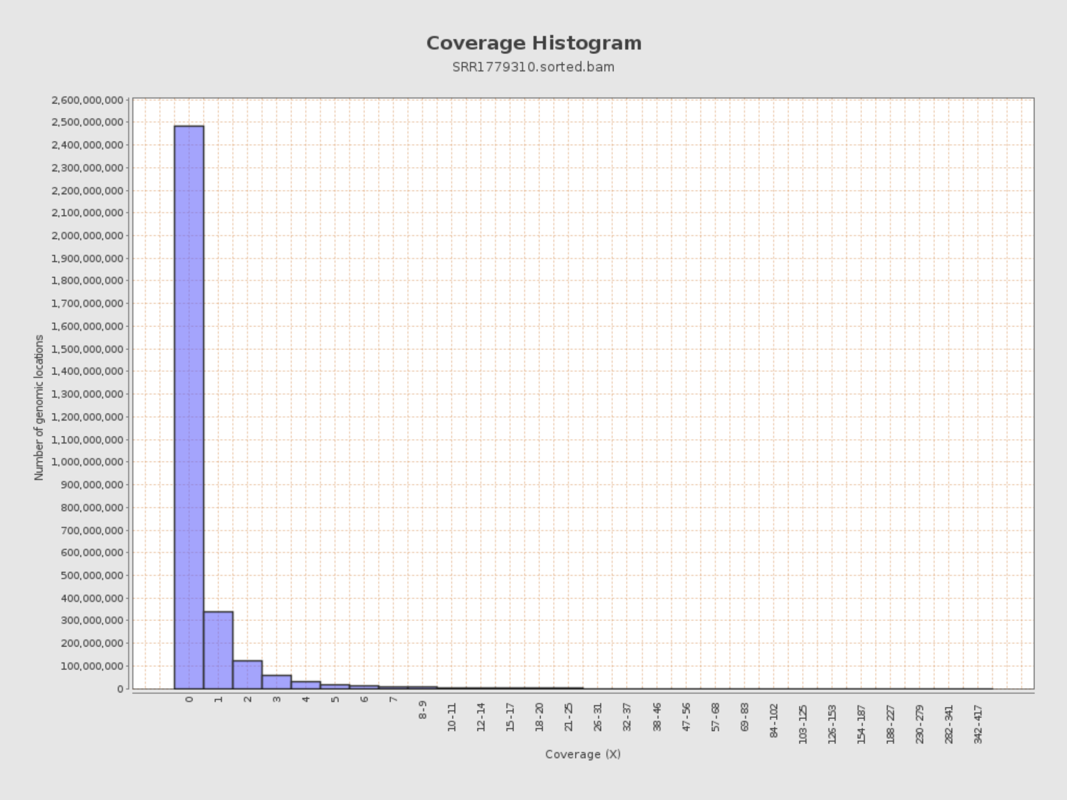
		bases	coverage	deviation
chr1	249250621	83355271	0.3344	1.22
chr2	243199373	93041615	0.3826	1.3362
chr3	198022430	97787504	0.4938	1.4576
chr4	191154276	123488067	0.646	1.808
chr5	180915260	99632976	0.5507	1.7933
chr6	171115067	73608722	0.4302	1.4226
chr7	159138663	127134270	0.7989	2.4871
chr8	146364022	119045846	0.8134	2.1222
chr9	141213431	59355650	0.4203	1.3663
chr10	135534747	27581867	0.2035	0.9554
chr11	135006516	49857341	0.3693	1.2174
chr12	133851895	70998058	0.5304	1.4961
chr13	115169878	58653886	0.5093	1.5005
chr14	107349540	41308941	0.3848	1.2294
chr15	102531392	36655385	0.3575	1.4586
chr16	90354753	28290938	0.3131	1.0881
chr17	81195210	21877986	0.2694	1.4164
chr18	78077248	42248726	0.5411	1.6435
chr19	59128983	14961225	0.253	0.9565
chr20	63025520	31158504	0.4944	1.6906
chr21	48129895	19535826	0.4059	1.4417
chr22	51304566	6122195	0.1193	0.6623
chrMT	16571	4063	0.2452	0.6436
chrX	155270560	79428276	0.5115	1.795

chrY	59373566	674206	0.0114	0.1605

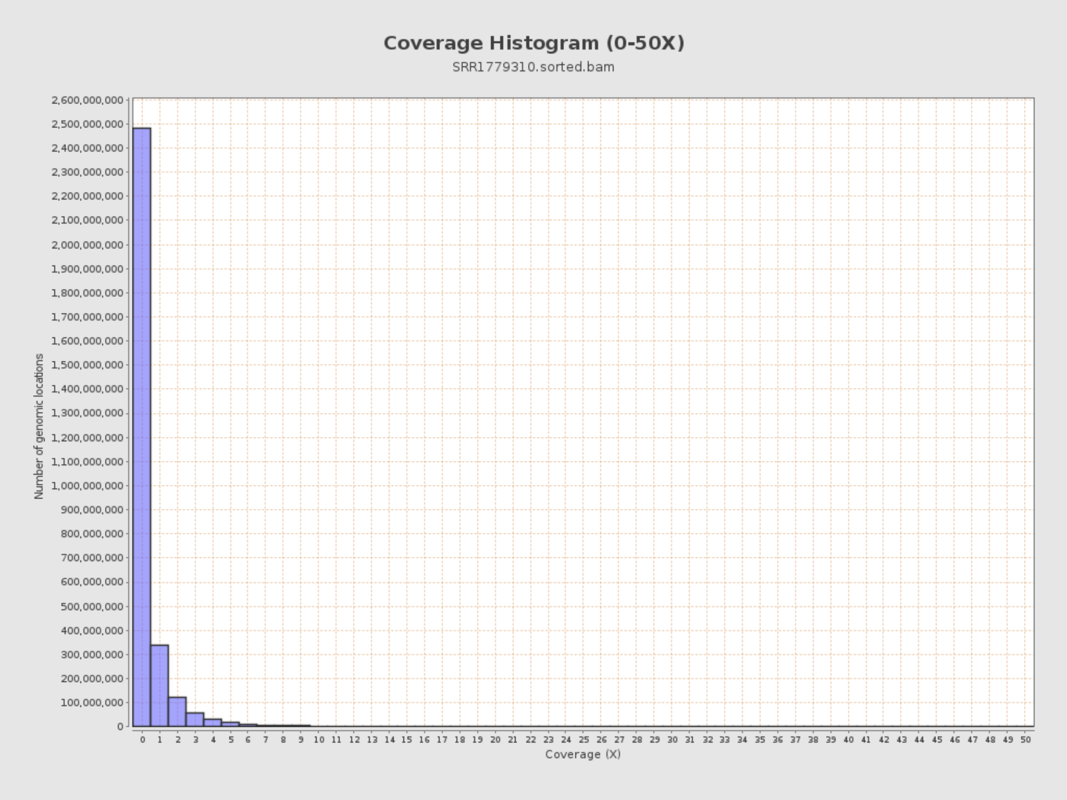
3. Results : Coverage across reference



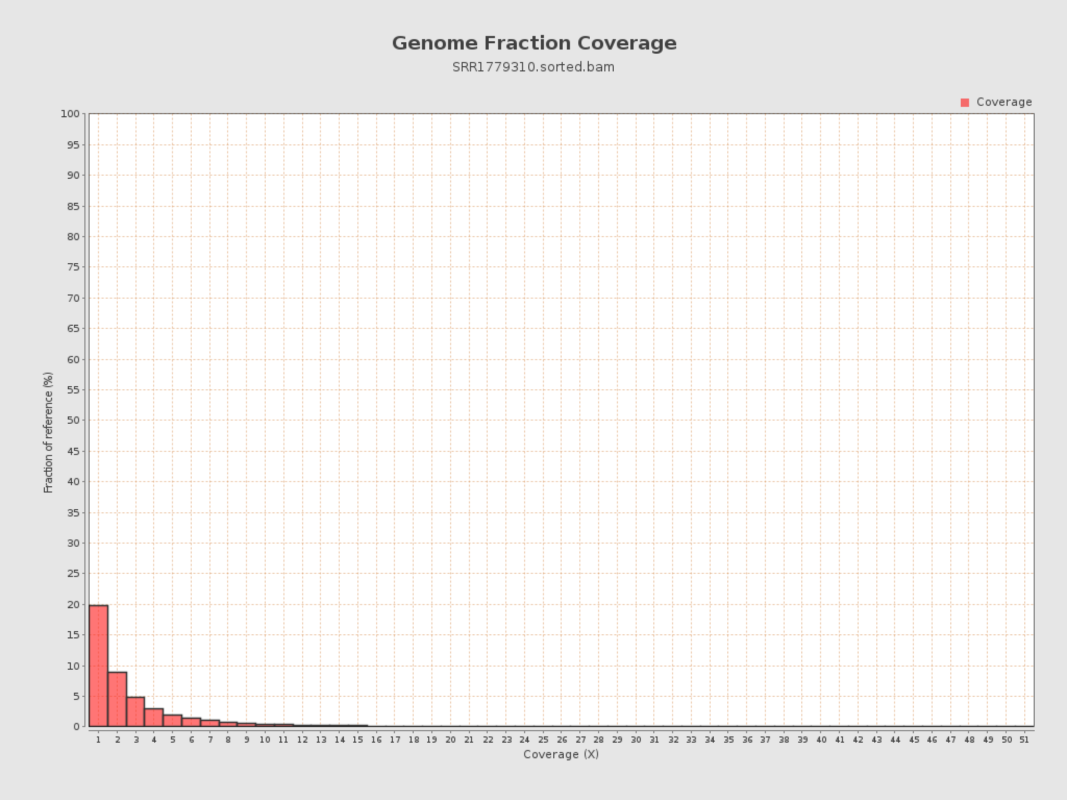
4. Results : Coverage Histogram



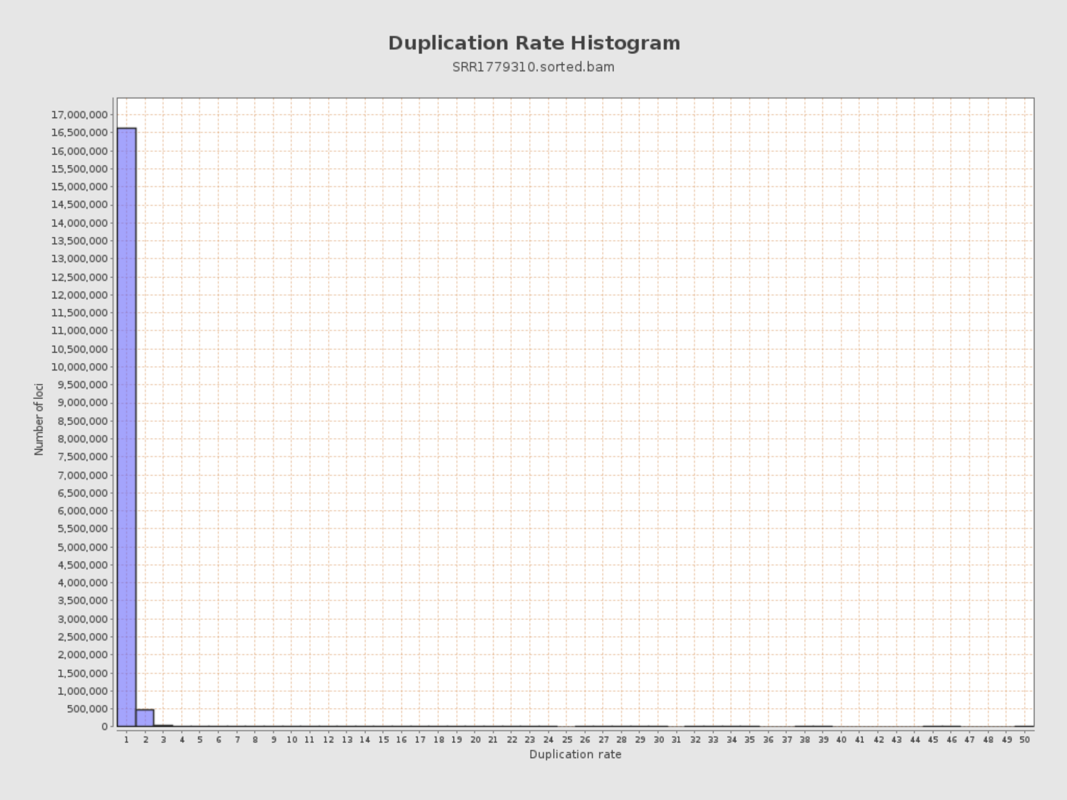
5. Results : Coverage Histogram (0-50X)



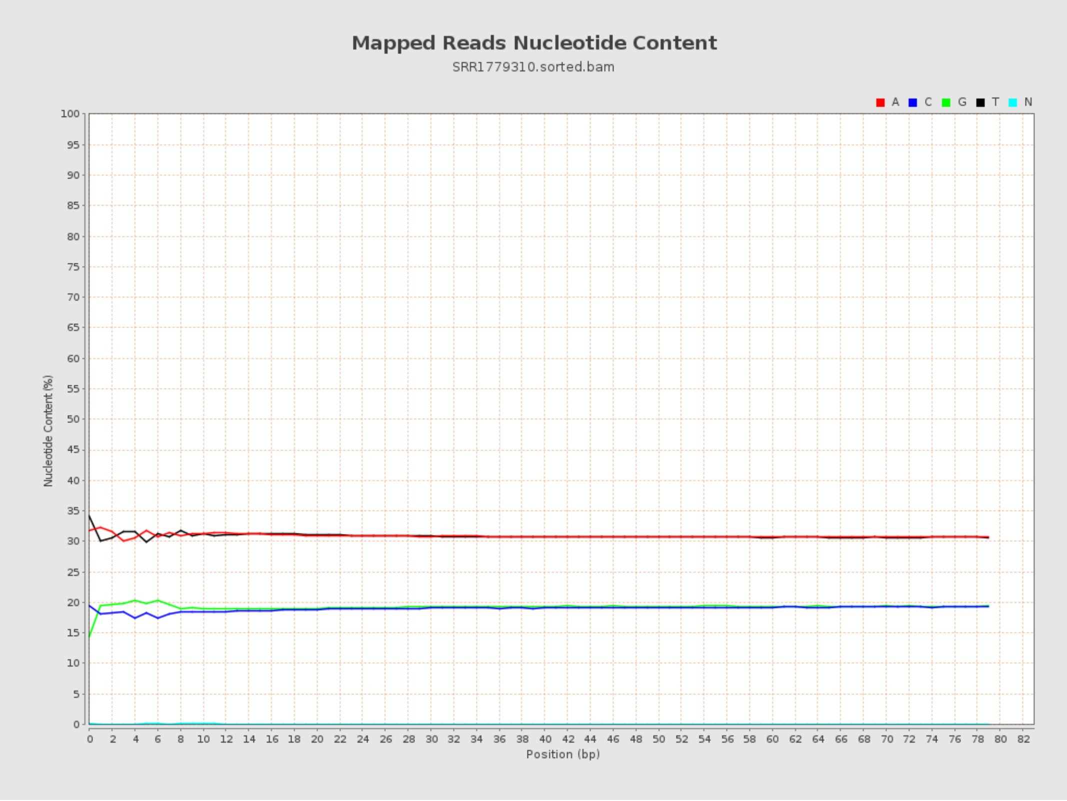
6. Results : Genome Fraction Coverage



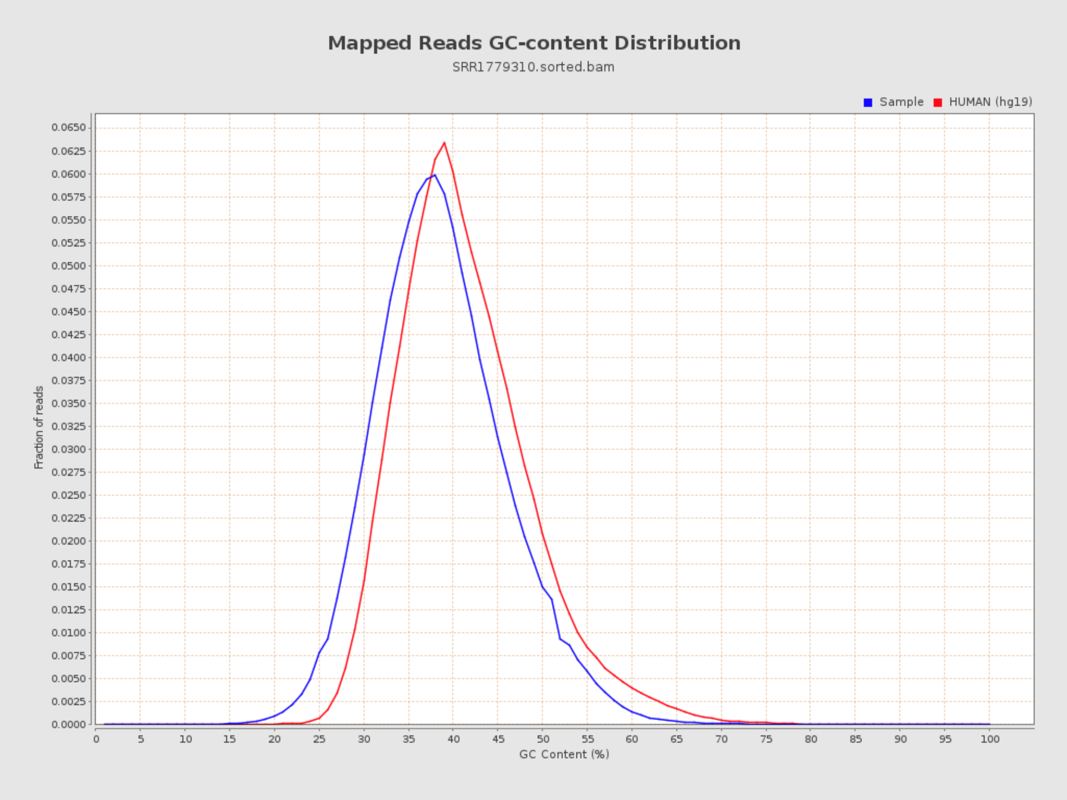
7. Results : Duplication Rate Histogram



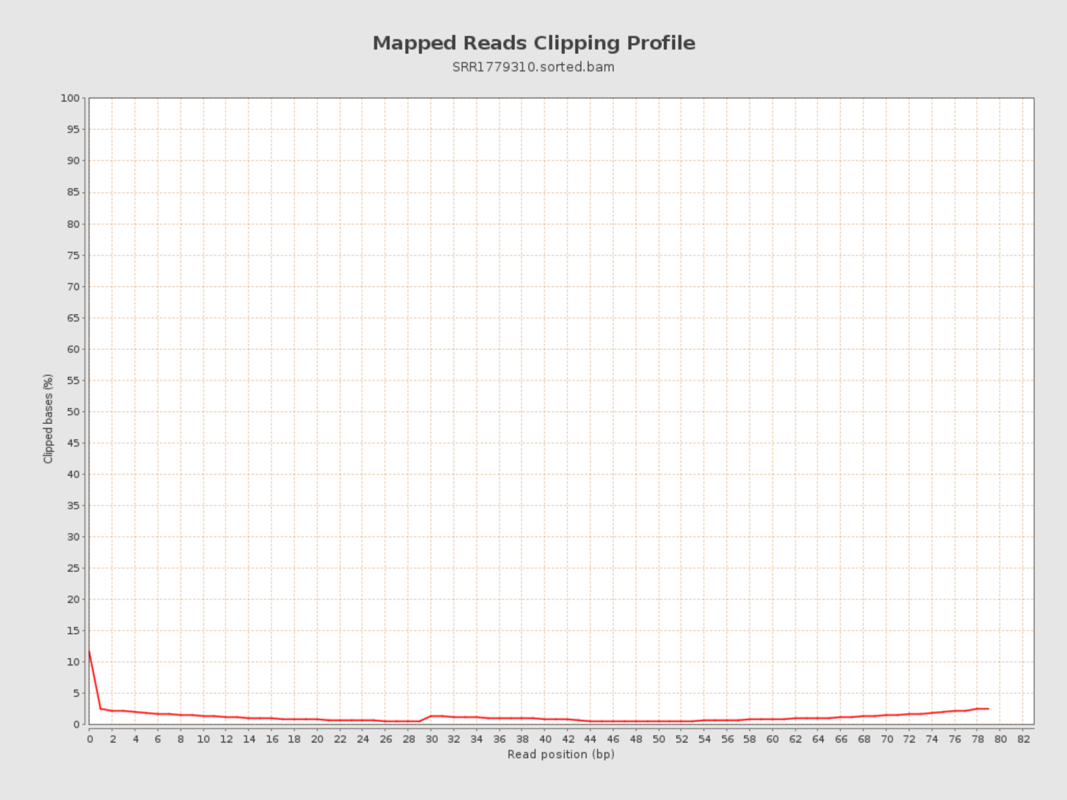
8. Results : Mapped Reads Nucleotide Content



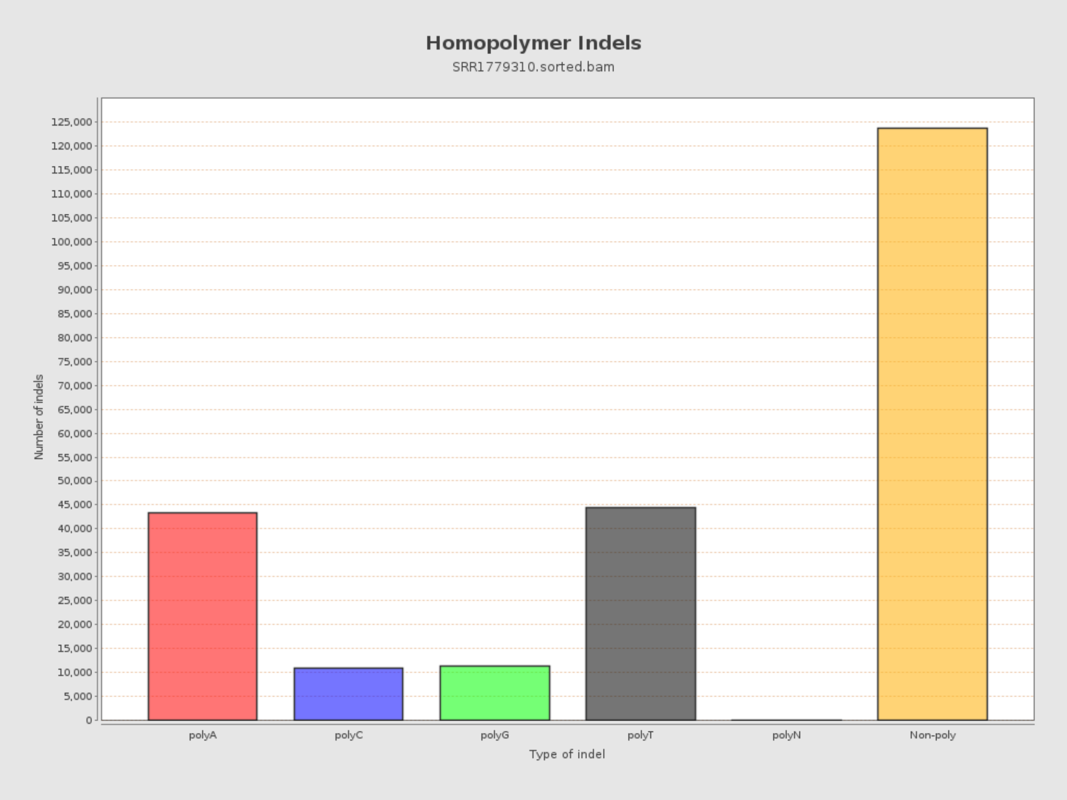
9. Results : Mapped Reads GC-content Distribution



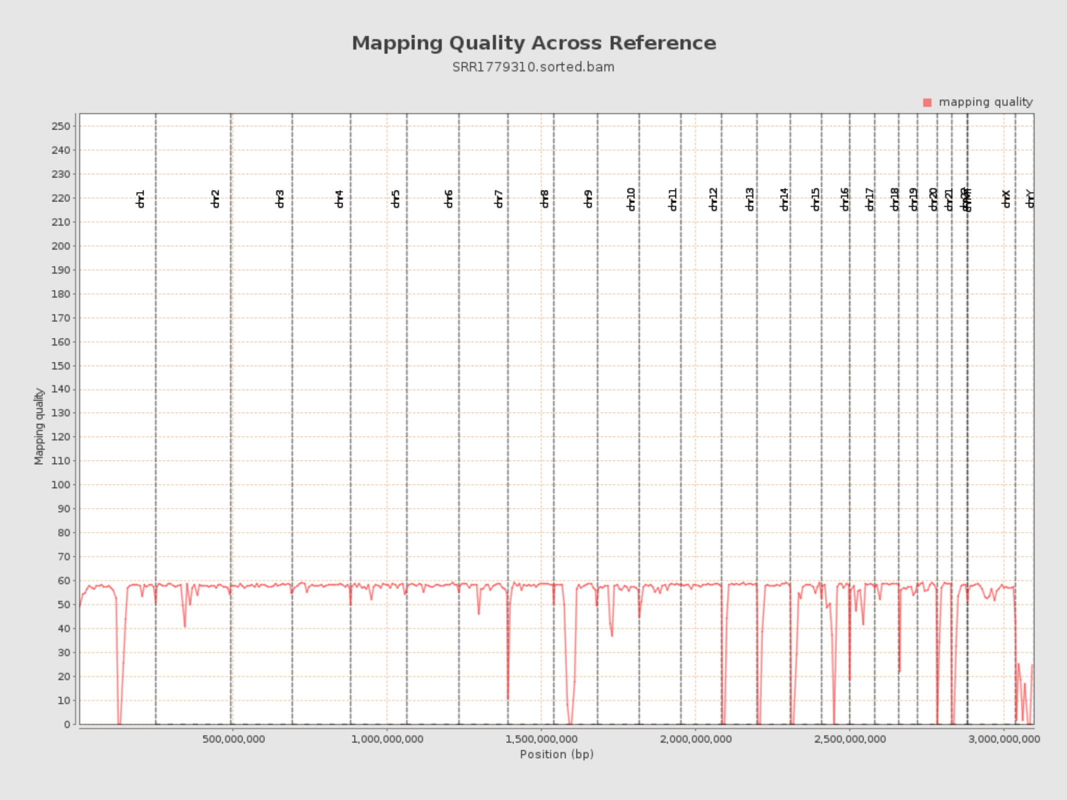
10. Results : Mapped Reads Clipping Profile



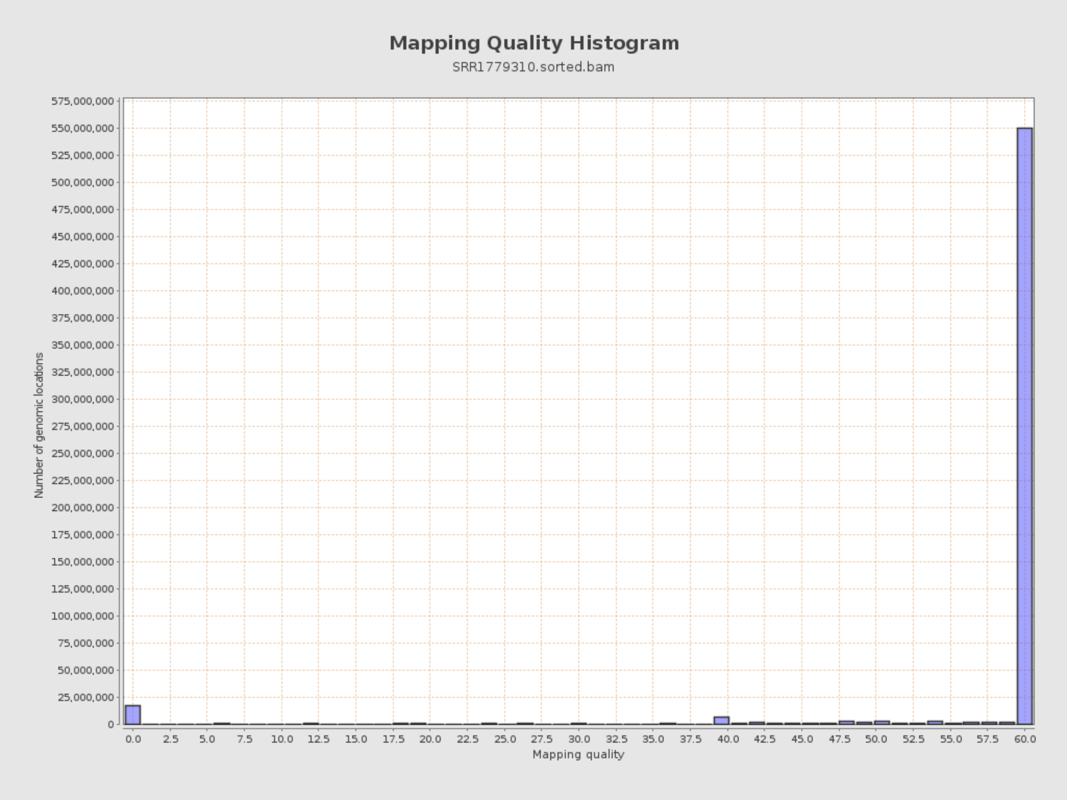
11. Results : Homopolymer Indels



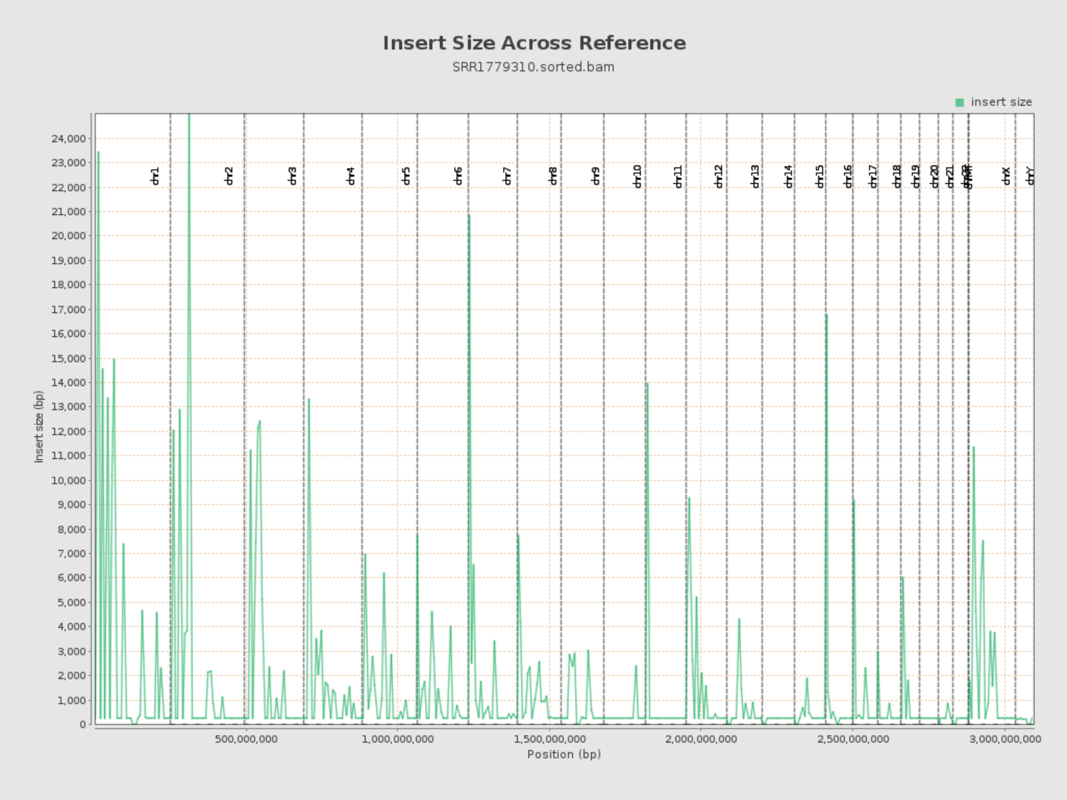
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram