Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 07:35:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779168.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_SRR1779168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779168_1.fastq.gz SRR1779168_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 07:35:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,909,572
Mapped reads	5,740,060 / 97.13%
Unmapped reads	169,512 / 2.87%
Mapped paired reads	5,740,060 / 97.13%
Mapped reads, first in pair	2,896,915 / 49.02%
Mapped reads, second in pair	2,843,145 / 48.11%
Mapped reads, both in pair	5,664,950 / 95.86%
Mapped reads, singletons	75,110 / 1.27%
Secondary alignments	0
Supplementary alignments	34,896 / 0.59%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	82,319 / 1.39%
Duplication rate	1.3%
Clipped reads	344,439 / 5.83%

2.2. ACGT Content

Number/percentage of A's	175,576,227 / 30.62%
Number/percentage of C's	110,665,008 / 19.3%
Number/percentage of T's	174,723,830 / 30.47%
Number/percentage of G's	112,296,720 / 19.58%
Number/percentage of N's	233,997 / 0.04%

GC Percentage	38.88%

2.3. Coverage

Mean	0.1853
Standard Deviation	0.6745

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	70,833.77
Standard Deviation	2,525,903.76
P25/Median/P75	169 / 221 / 292

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	2,430,093
Insertions	48,215
Mapped reads with at least one insertion	0.83%
Deletions	59,556
Mapped reads with at least one deletion	1.02%
Homopolymer indels	46.83%

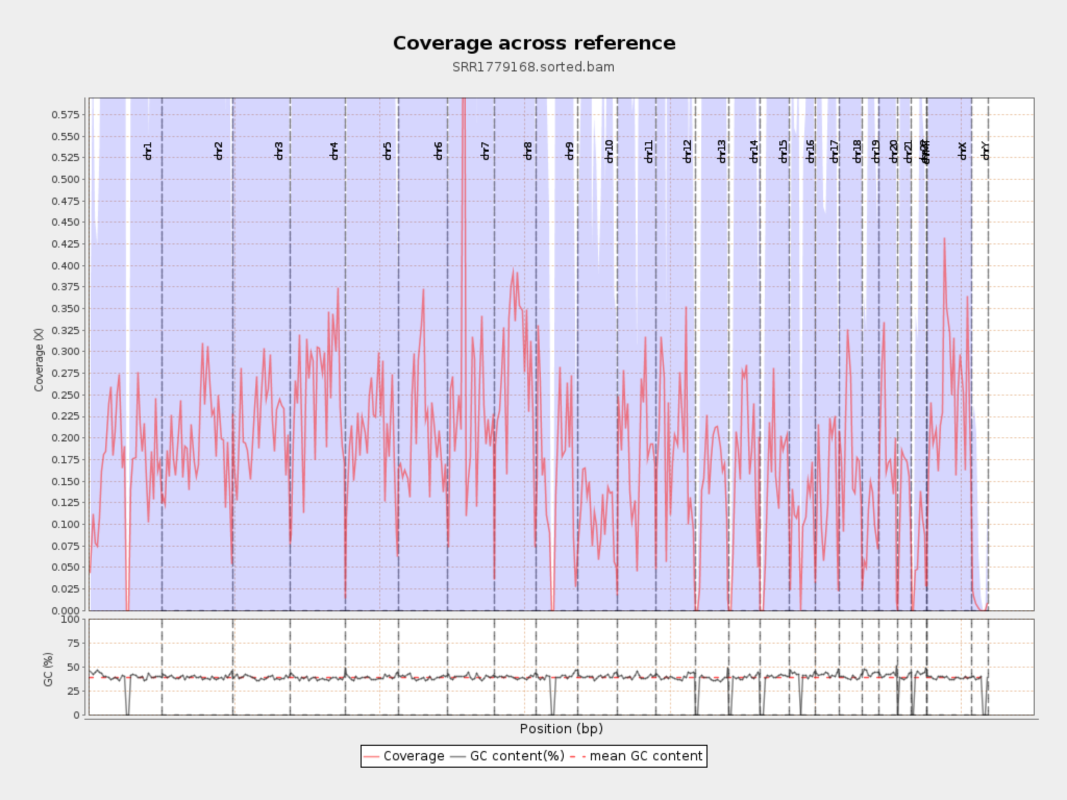
2.7. Chromosome stats

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

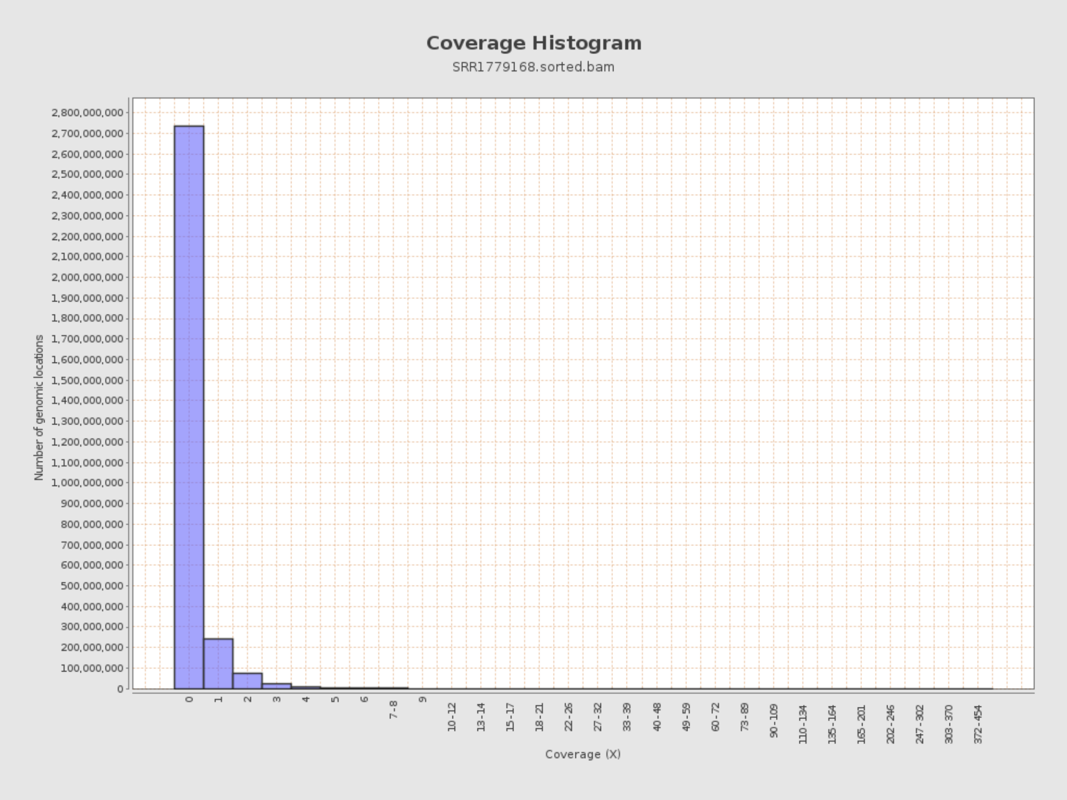
		bases	**coverage**	**deviation**
chr1	249250621	40863783	0.1639	0.6522
chr2	243199373	47278923	0.1944	0.68
chr3	198022430	43019501	0.2172	0.6712
chr4	191154276	49064686	0.2567	0.7367
chr5	180915260	36592811	0.2023	0.6604
chr6	171115067	35434060	0.2071	0.6735
chr7	159138663	40091467	0.2519	0.9532
chr8	146364022	41847942	0.2859	0.7971
chr9	141213431	23084892	0.1635	0.6362
chr10	135534747	15172799	0.1119	0.7918
chr11	135006516	25542390	0.1892	0.637
chr12	133851895	25566044	0.191	0.6398
chr13	115169878	16400533	0.1424	0.5532
chr14	107349540	17207636	0.1603	0.582
chr15	102531392	15049841	0.1468	0.5683
chr16	90354753	9589847	0.1061	0.4569
chr17	81195210	10760852	0.1325	0.5447
chr18	78077248	14597955	0.187	0.6273
chr19	59128983	5641904	0.0954	0.4808
chr20	63025520	12498384	0.1983	0.6575
chr21	48129895	6467316	0.1344	0.5219
chr22	51304566	3357562	0.0654	0.3618
chrMT	16571	467	0.0282	0.1726
chrX	155270560	38104829	0.2454	0.8081

chrY	59373566	392749	0.0066	0.1319

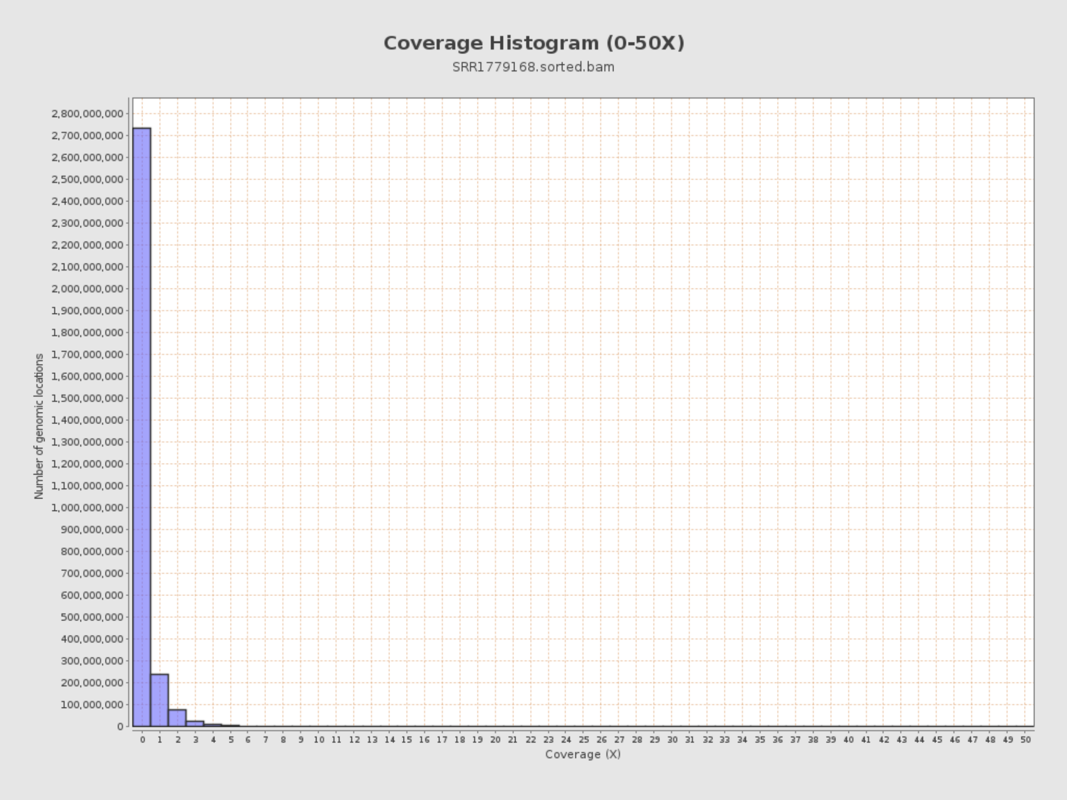
3. Results : Coverage across reference



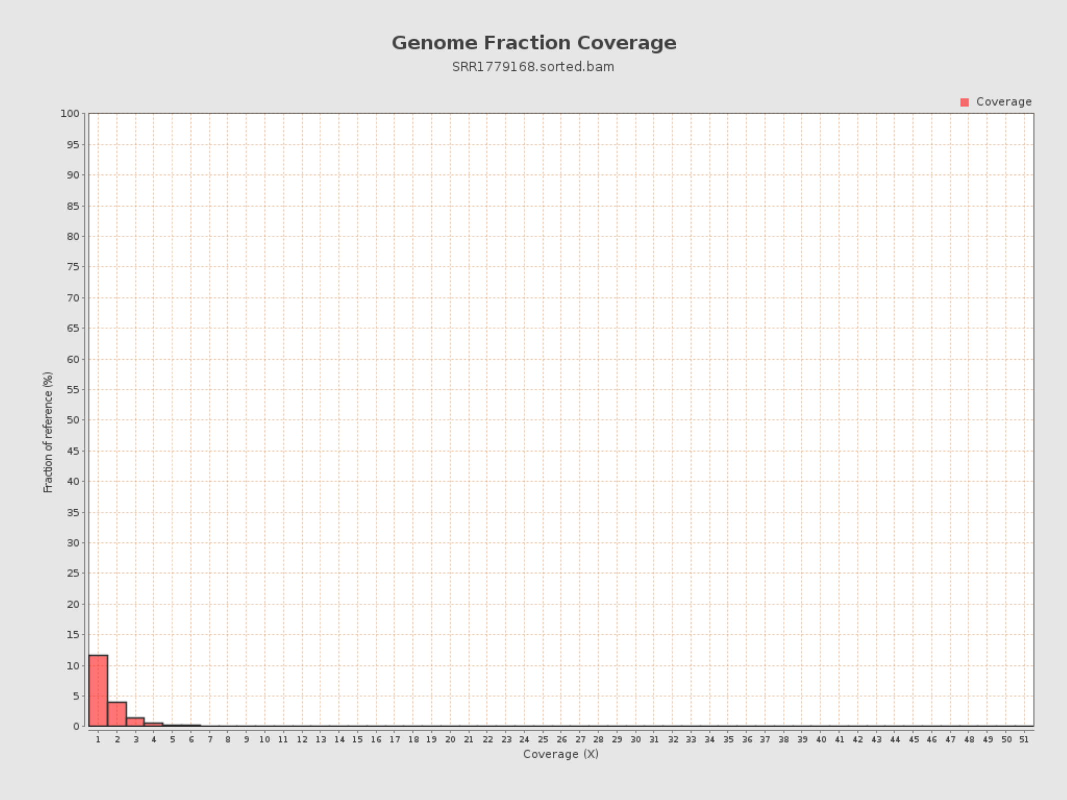
4. Results : Coverage Histogram



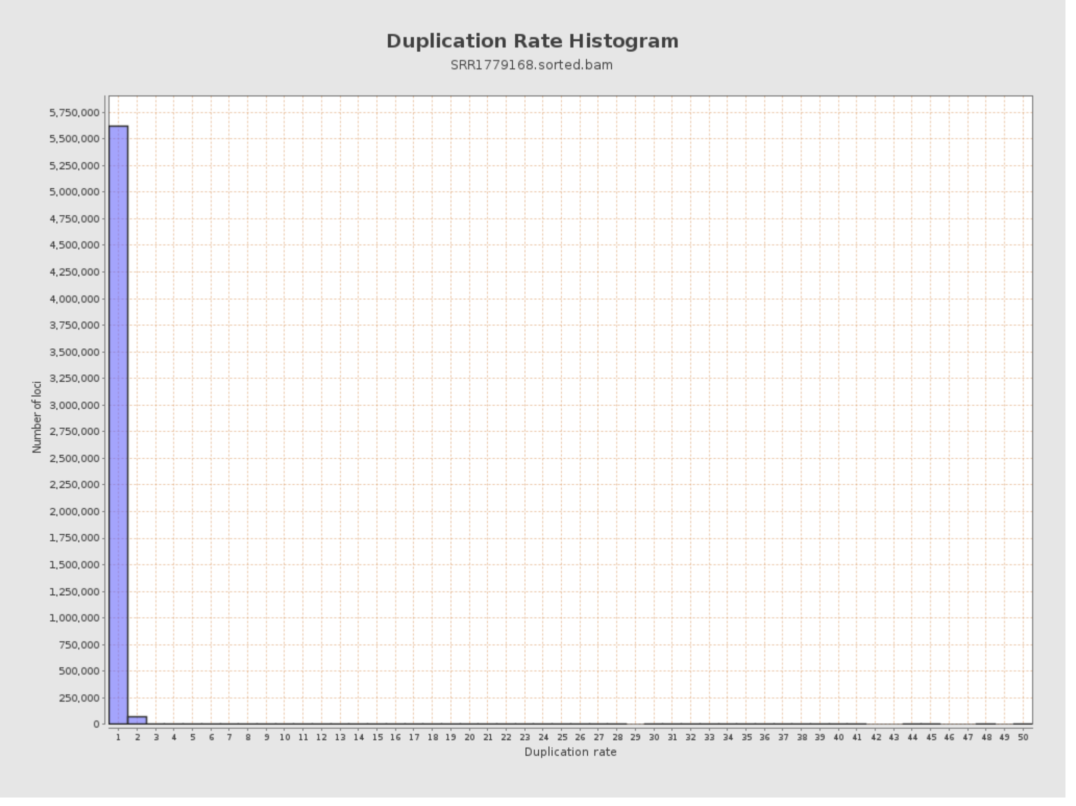
5. Results : Coverage Histogram (0-50X)



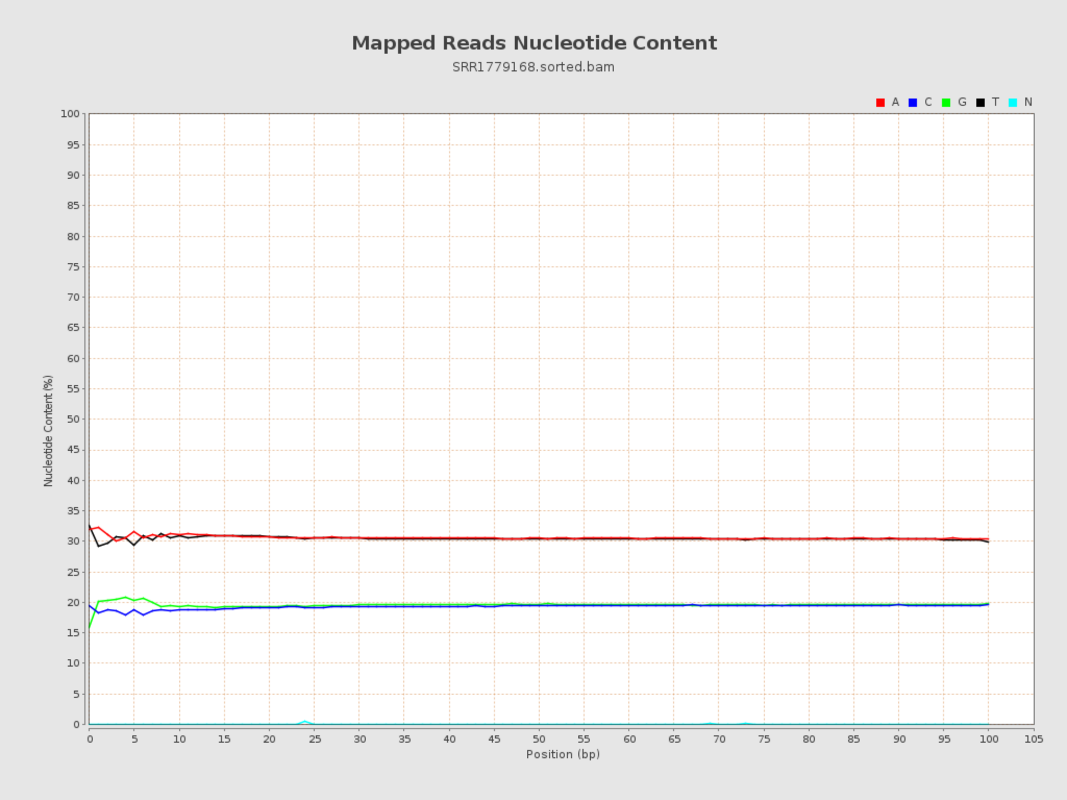
6. Results : Genome Fraction Coverage



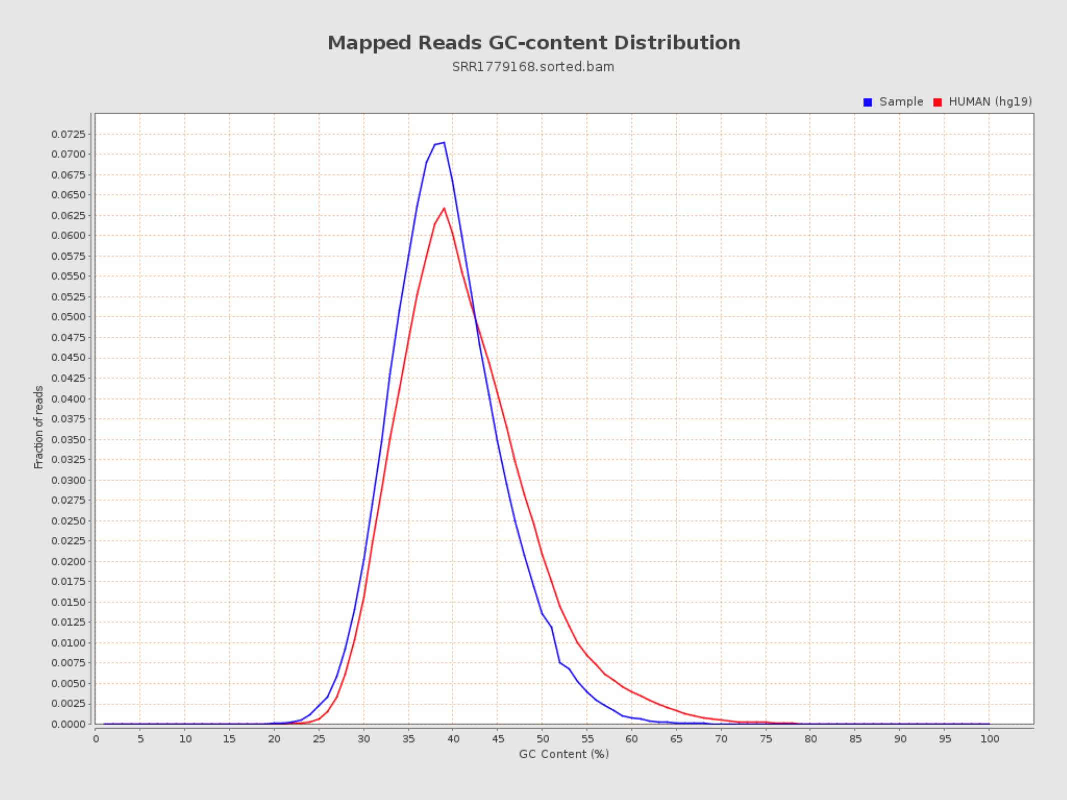
7. Results : Duplication Rate Histogram



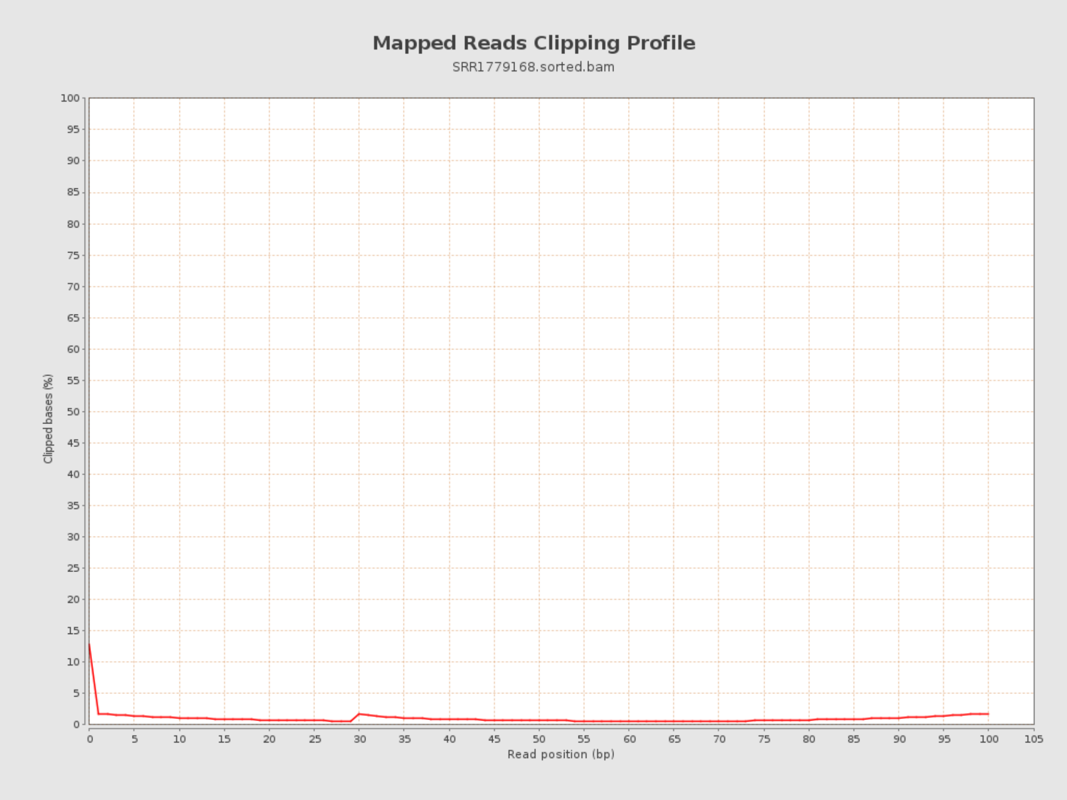
8. Results : Mapped Reads Nucleotide Content



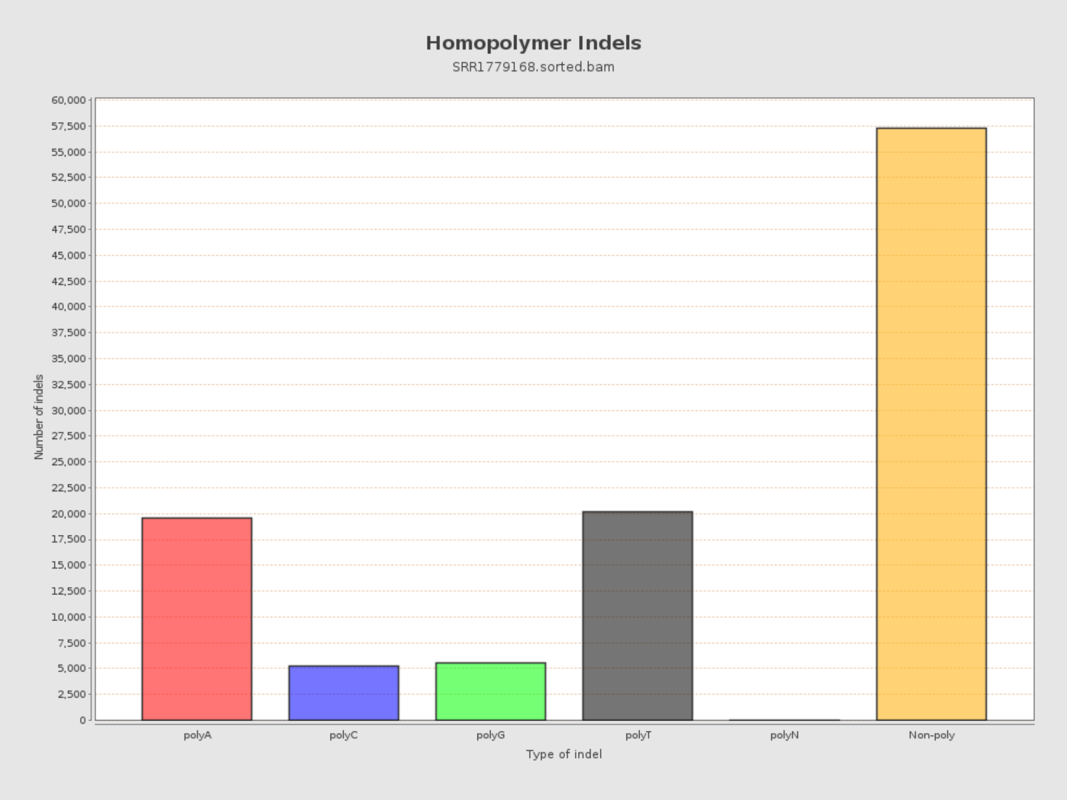
9. Results : Mapped Reads GC-content Distribution



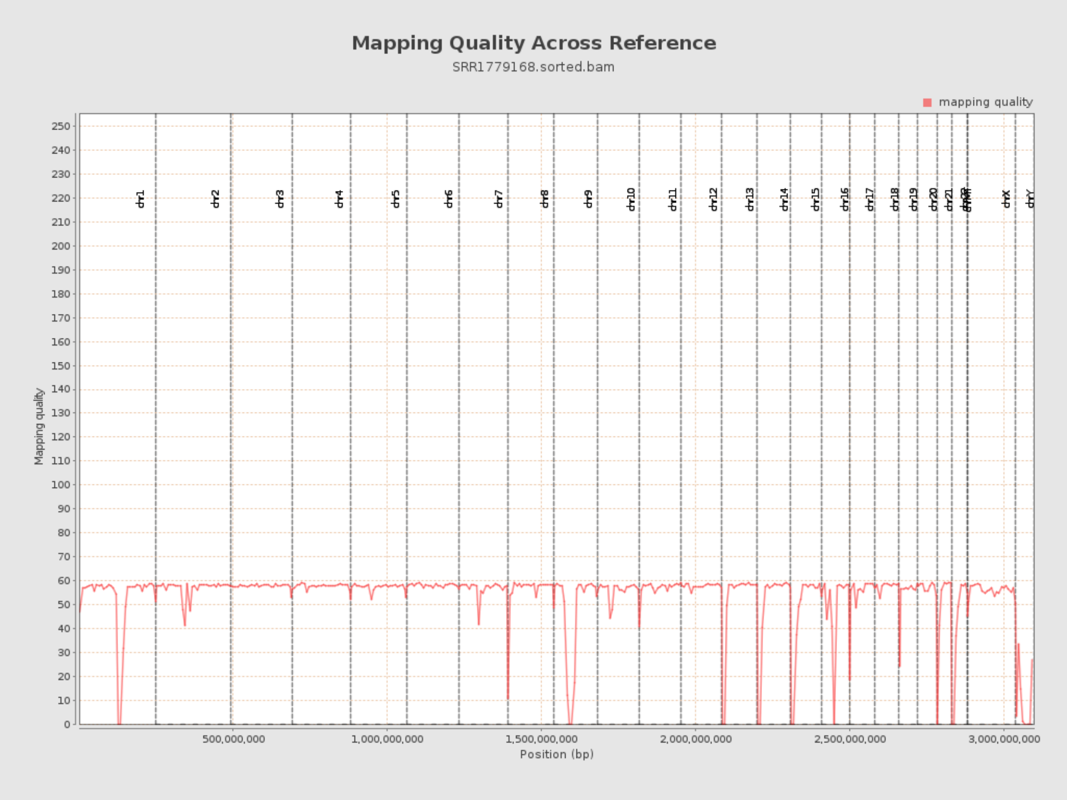
10. Results : Mapped Reads Clipping Profile



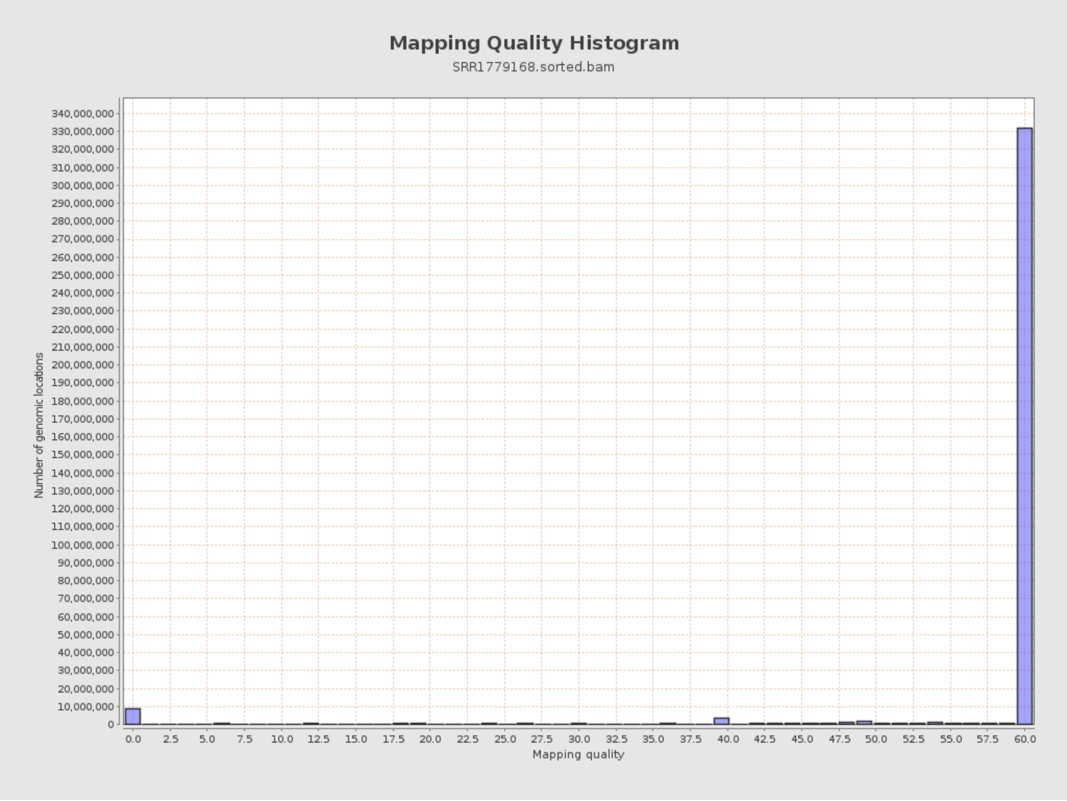
11. Results : Homopolymer Indels



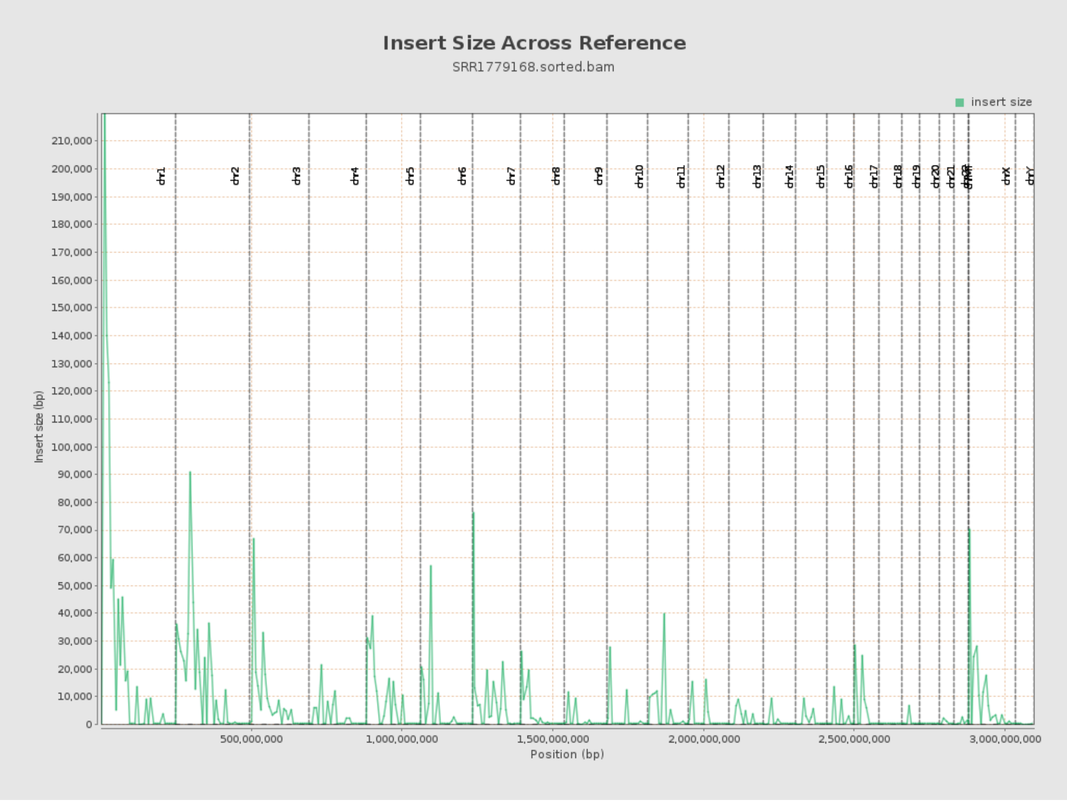
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram