Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 18:49:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779399.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_SRR1779399 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779399_1.fastq.gz SRR1779399_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 18:49:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779399.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,008,884
Mapped reads	15,985,391 / 93.98%
Unmapped reads	1,023,493 / 6.02%
Mapped paired reads	15,985,391 / 93.98%
Mapped reads, first in pair	8,054,378 / 47.35%
Mapped reads, second in pair	7,931,013 / 46.63%
Mapped reads, both in pair	15,813,578 / 92.97%
Mapped reads, singletons	171,813 / 1.01%
Secondary alignments	0
Supplementary alignments	74,795 / 0.44%
Read min/max/mean length	30 / 80 / 80.16
Duplicated reads (estimated)	985,000 / 5.79%
Duplication rate	4.94%
Clipped reads	833,101 / 4.9%

2.2. ACGT Content

Number/percentage of A's	388,804,300 / 30.63%
Number/percentage of C's	243,876,145 / 19.21%
Number/percentage of T's	387,139,553 / 30.5%
Number/percentage of G's	249,144,653 / 19.63%
Number/percentage of N's	282,441 / 0.02%

GC Percentage	38.84%

2.3. Coverage

Mean	0.4101
Standard Deviation	3.01

2.4. Mapping Quality

Mean Mapping Quality	52.84

2.5. Insert size

Mean	42,541.76
Standard Deviation	1,942,332.28
P25/Median/P75	139 / 178 / 226

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,749,697
Insertions	120,596
Mapped reads with at least one insertion	0.75%
Deletions	138,717
Mapped reads with at least one deletion	0.86%
Homopolymer indels	46.79%

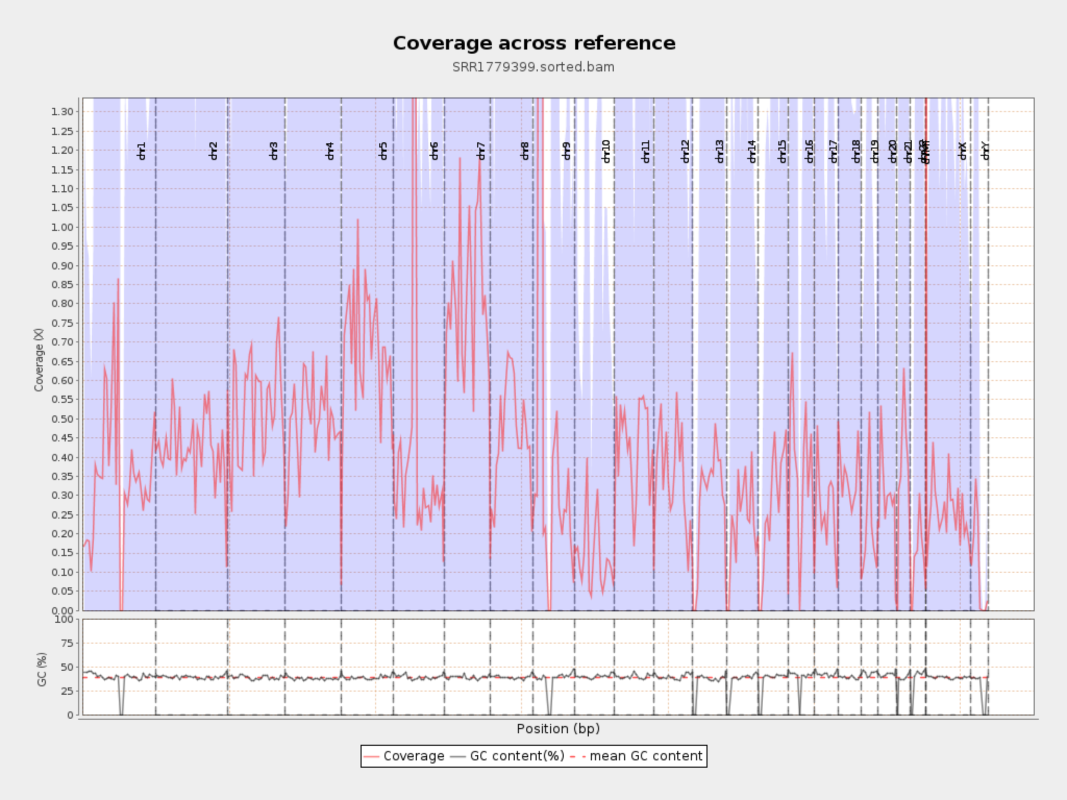
2.7. Chromosome stats

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

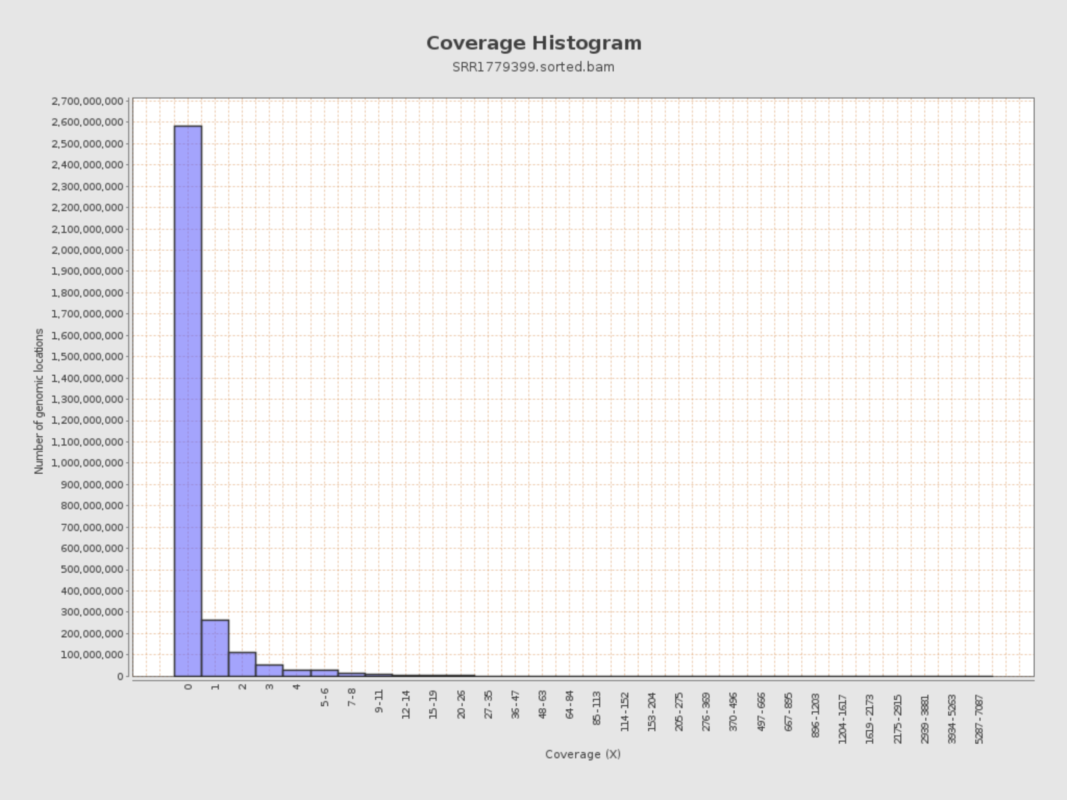
		bases	coverage	deviation
chr1	249250621	86968280	0.3489	7.3452
chr2	243199373	103160909	0.4242	1.6851
chr3	198022430	105149968	0.531	1.6922
chr4	191154276	94345986	0.4936	1.4899
chr5	180915260	124128728	0.6861	1.9748
chr6	171115067	72245925	0.4222	2.2022
chr7	159138663	128593182	0.8081	3.3396
chr8	146364022	68286464	0.4666	1.6598
chr9	141213431	92553231	0.6554	3.6263
chr10	135534747	18918851	0.1396	4.7529
chr11	135006516	58364744	0.4323	1.6991
chr12	133851895	46428752	0.3469	1.5423
chr13	115169878	33368656	0.2897	1.46
chr14	107349540	24525660	0.2285	1.5383
chr15	102531392	27686529	0.27	1.1449
chr16	90354753	32222581	0.3566	1.6003
chr17	81195210	21598178	0.266	1.8337
chr18	78077248	27156690	0.3478	2.318
chr19	59128983	12984806	0.2196	4.5553
chr20	63025520	19337243	0.3068	1.4482
chr21	48129895	17291996	0.3593	1.5035
chr22	51304566	7356649	0.1434	1.8428
chrMT	16571	108243	6.5321	3.5547
chrX	155270560	39796442	0.2563	1.1063

chrY	59373566	6953648	0.1171	1.2817

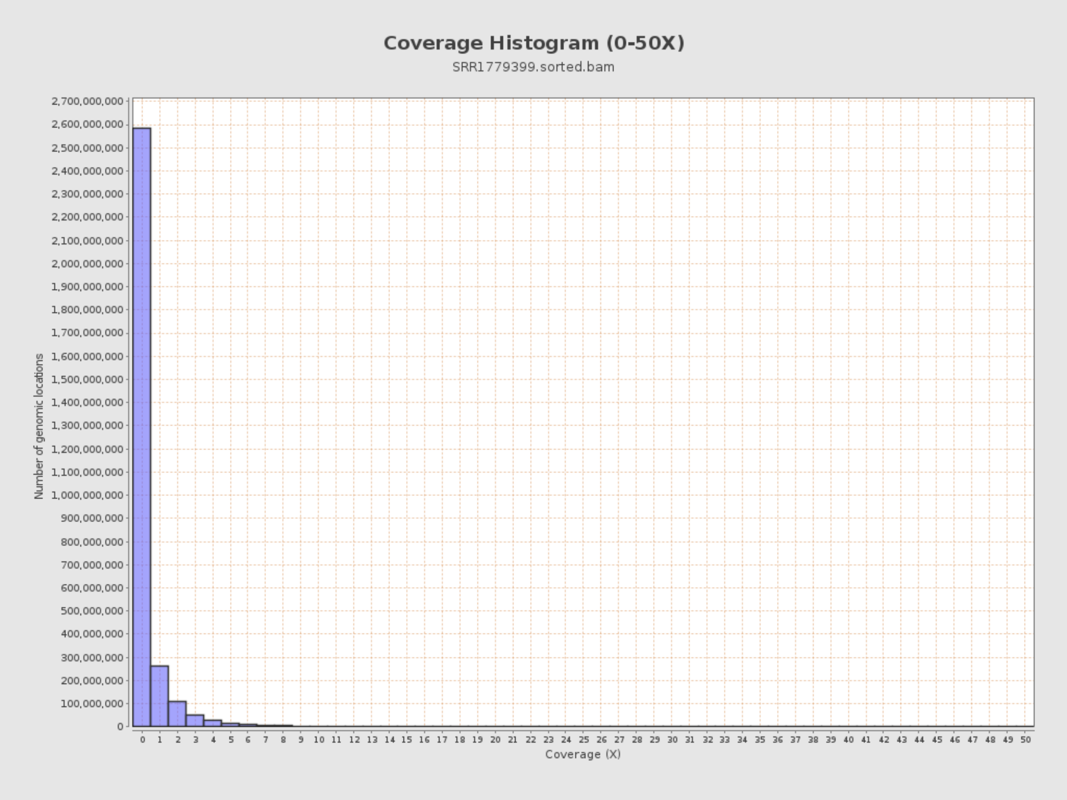
3. Results : Coverage across reference



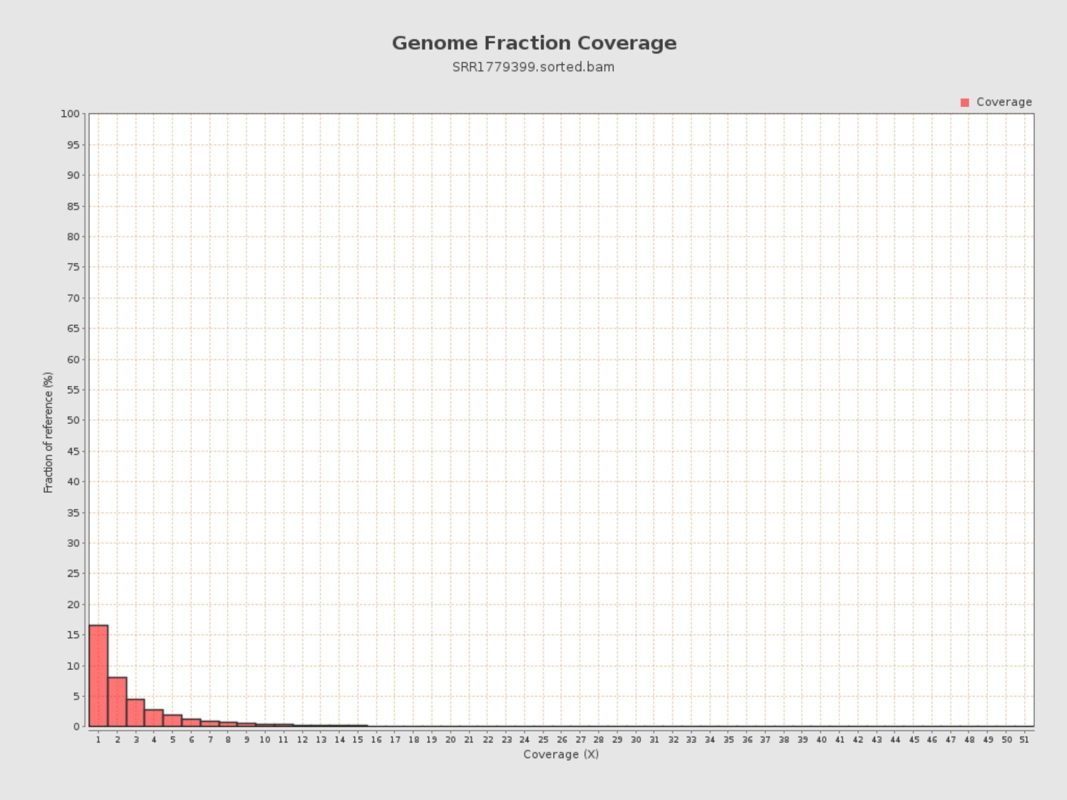
4. Results : Coverage Histogram



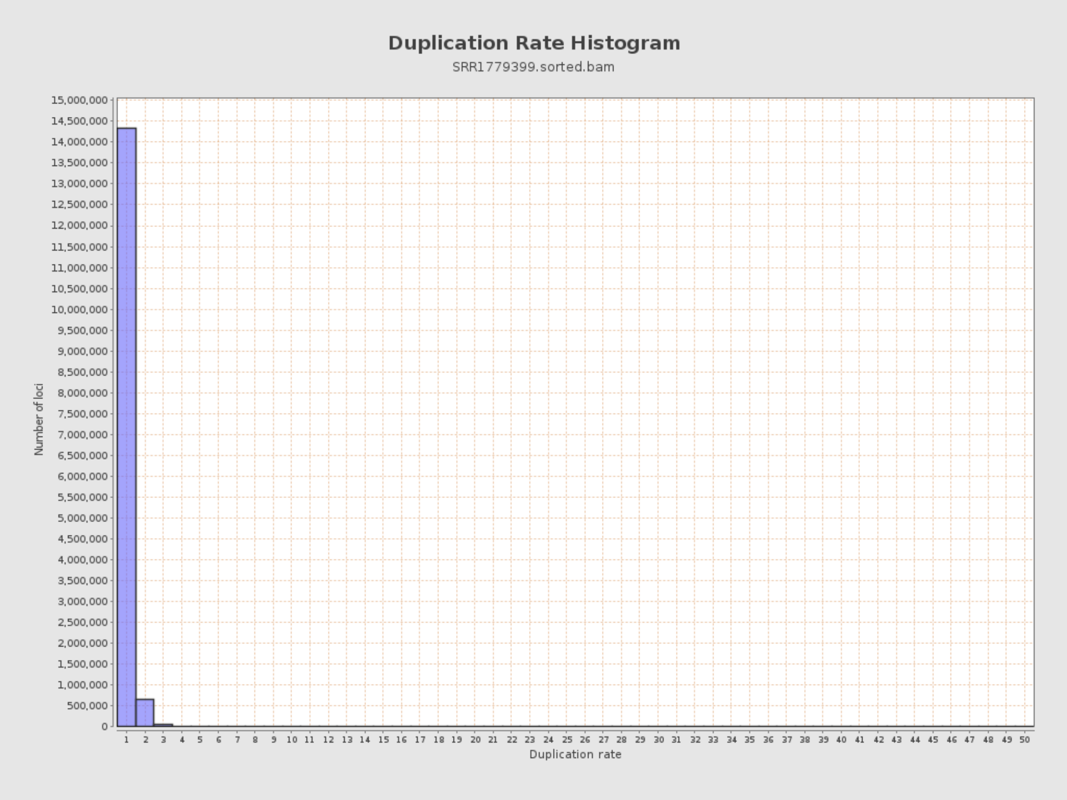
5. Results : Coverage Histogram (0-50X)



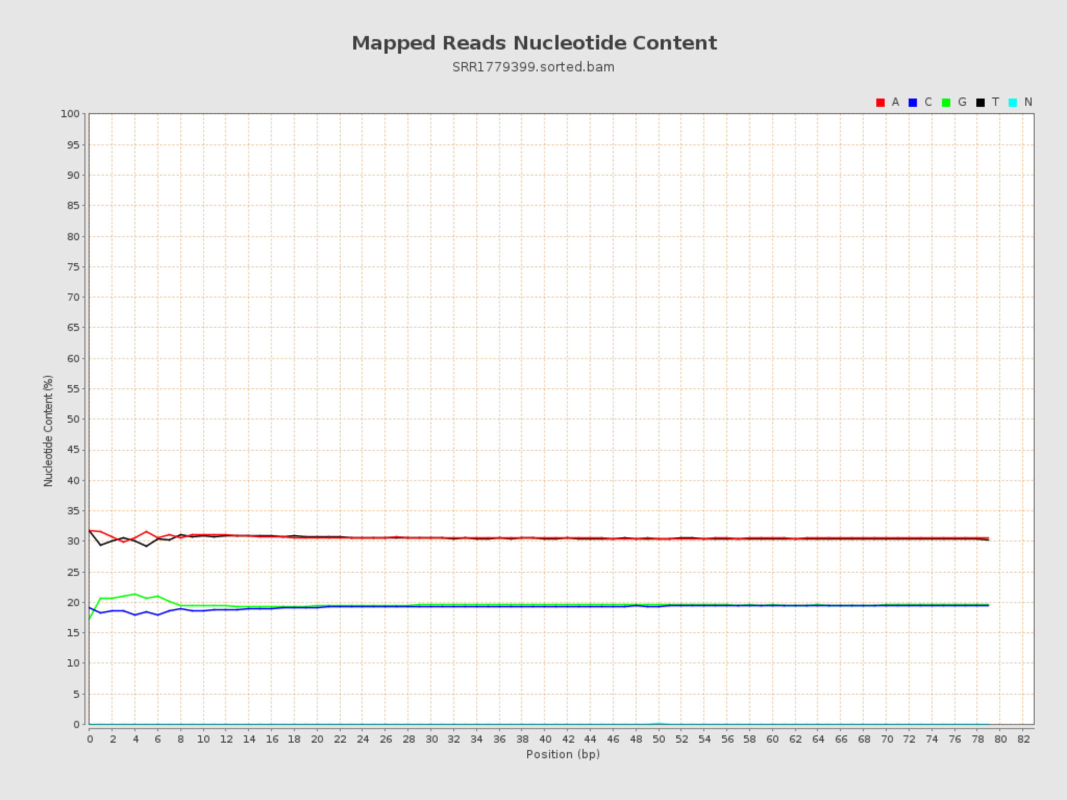
6. Results : Genome Fraction Coverage



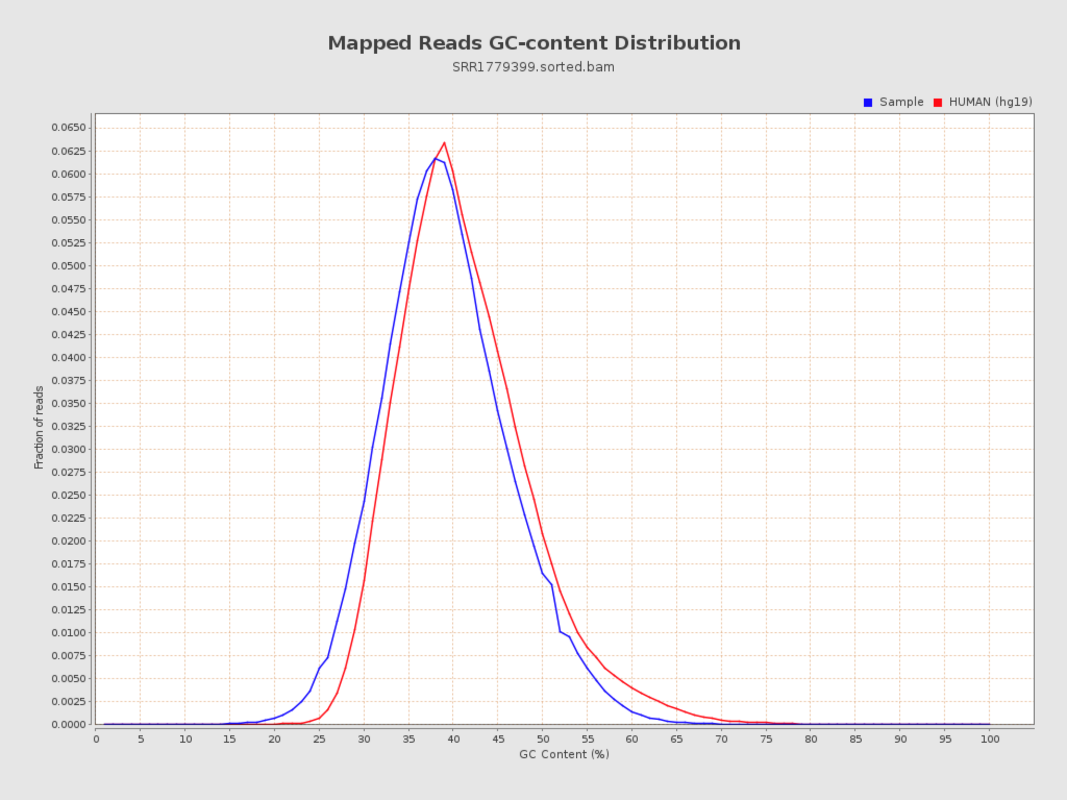
7. Results : Duplication Rate Histogram



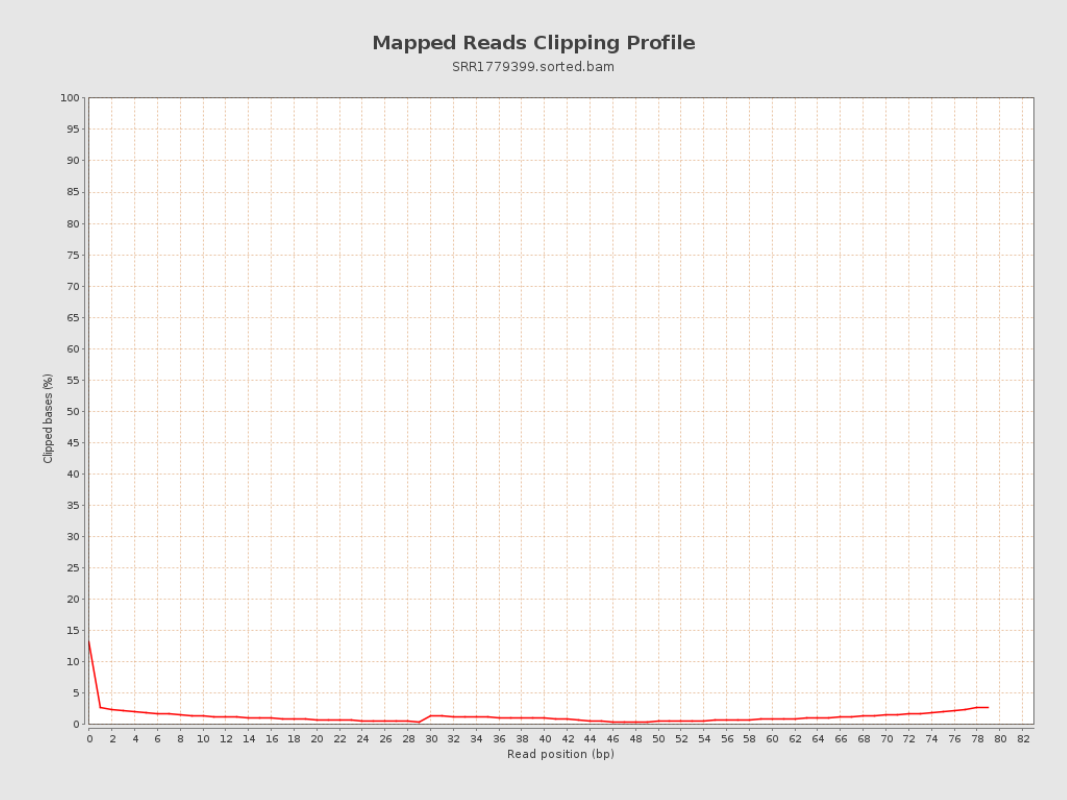
8. Results : Mapped Reads Nucleotide Content



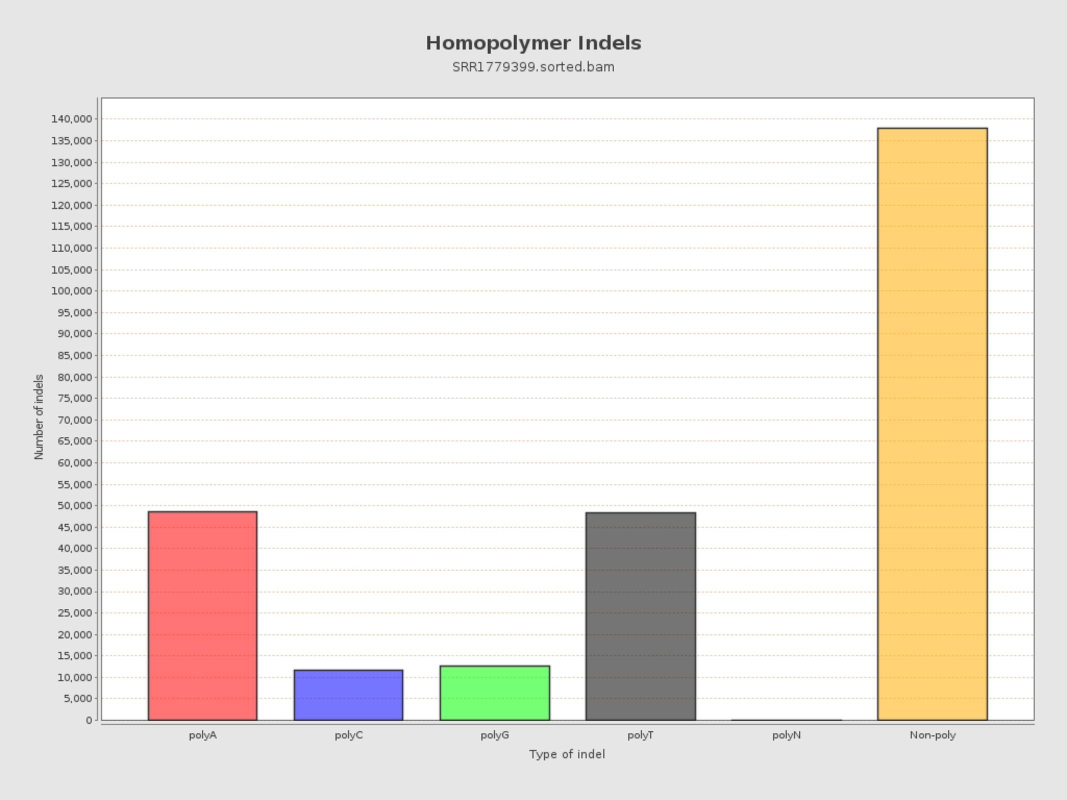
9. Results : Mapped Reads GC-content Distribution



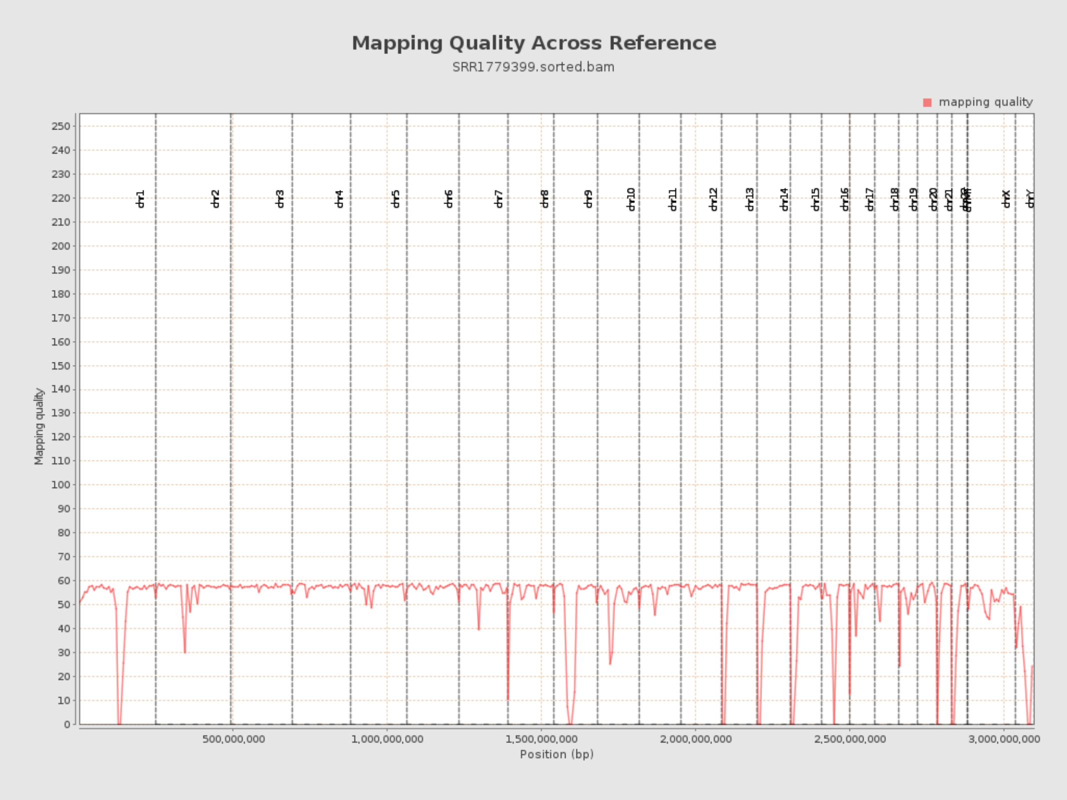
10. Results : Mapped Reads Clipping Profile



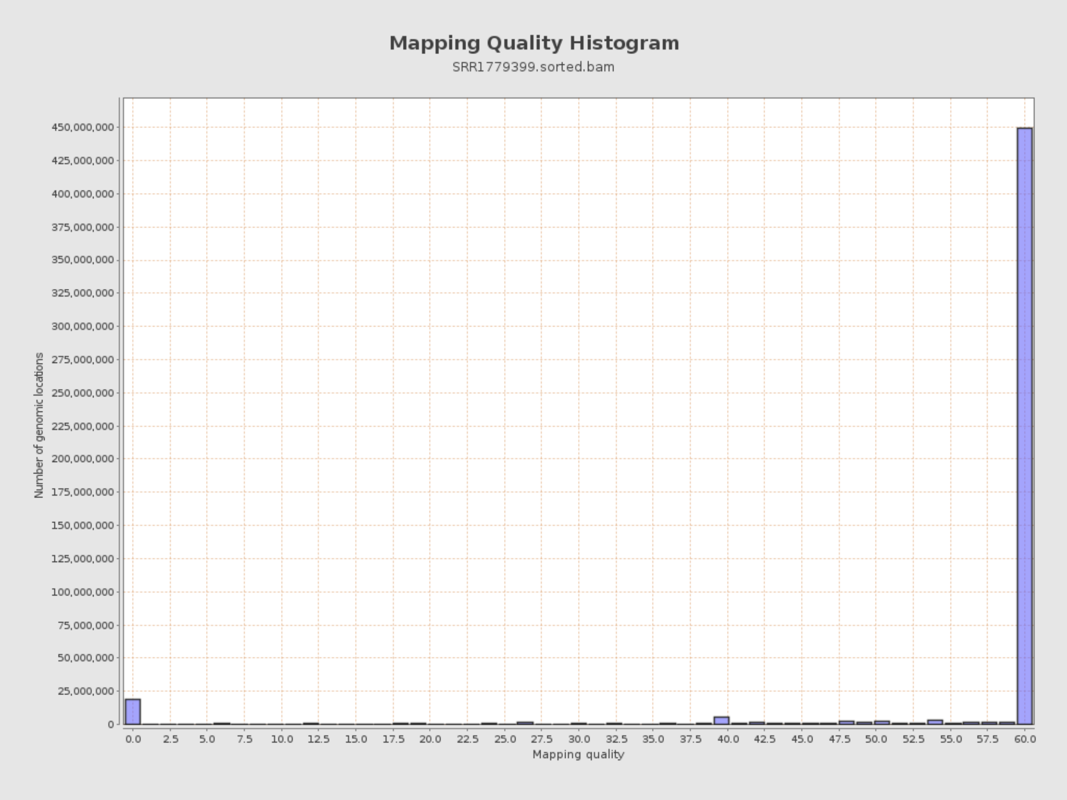
11. Results : Homopolymer Indels



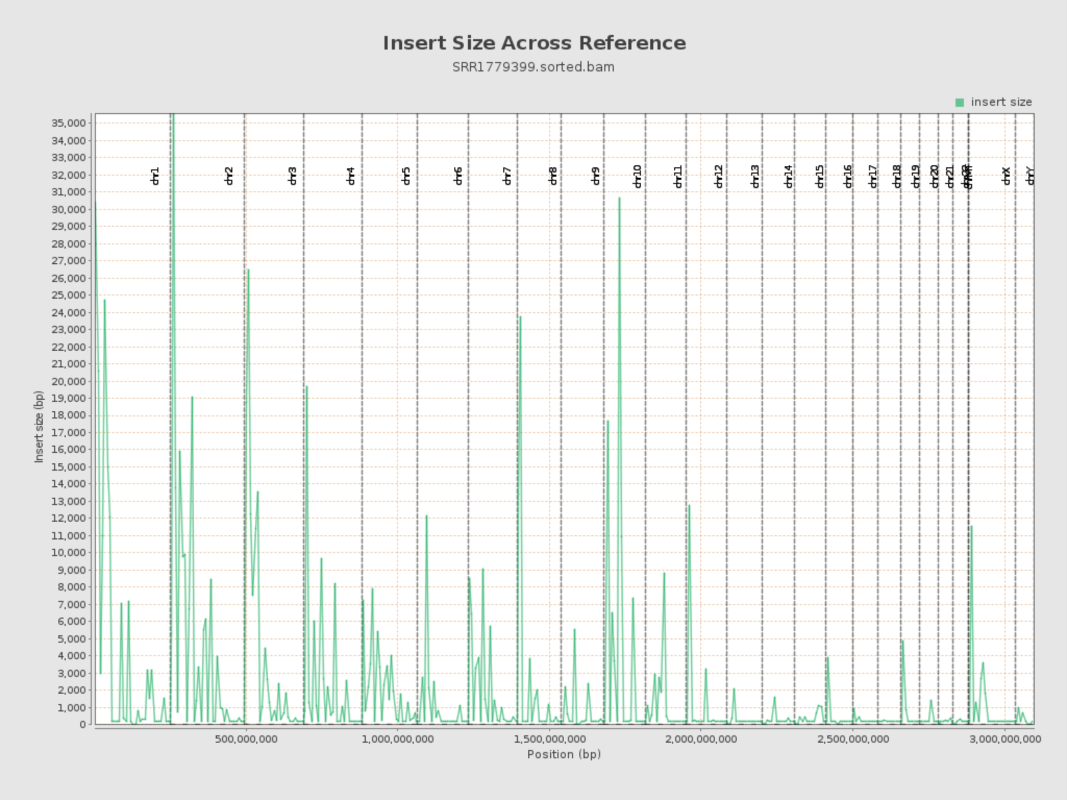
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram