Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 13:24:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779374.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_SRR1779374 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779374_1.fastq.gz SRR1779374_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 13:24:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779374.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,495,956
Mapped reads	15,223,210 / 87.01%
Unmapped reads	2,272,746 / 12.99%
Mapped paired reads	15,223,210 / 87.01%
Mapped reads, first in pair	7,659,589 / 43.78%
Mapped reads, second in pair	7,563,621 / 43.23%
Mapped reads, both in pair	15,069,196 / 86.13%
Mapped reads, singletons	154,014 / 0.88%
Secondary alignments	0
Supplementary alignments	206,214 / 1.18%
Read min/max/mean length	30 / 80 / 80.43
Duplicated reads (estimated)	6,661,011 / 38.07%
Duplication rate	18.63%
Clipped reads	1,717,527 / 9.82%

2.2. ACGT Content

Number/percentage of A's	370,318,783 / 30.84%
Number/percentage of C's	229,613,272 / 19.12%
Number/percentage of T's	367,567,098 / 30.61%
Number/percentage of G's	233,079,541 / 19.41%
Number/percentage of N's	260,287 / 0.02%

GC Percentage	38.53%

2.3. Coverage

Mean	0.388
Standard Deviation	39.1739

2.4. Mapping Quality

Mean Mapping Quality	51.41

2.5. Insert size

Mean	54,785.33
Standard Deviation	2,194,400.91
P25/Median/P75	112 / 151 / 201

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	4,305,440
Insertions	141,080
Mapped reads with at least one insertion	0.92%
Deletions	147,429
Mapped reads with at least one deletion	0.96%
Homopolymer indels	48.73%

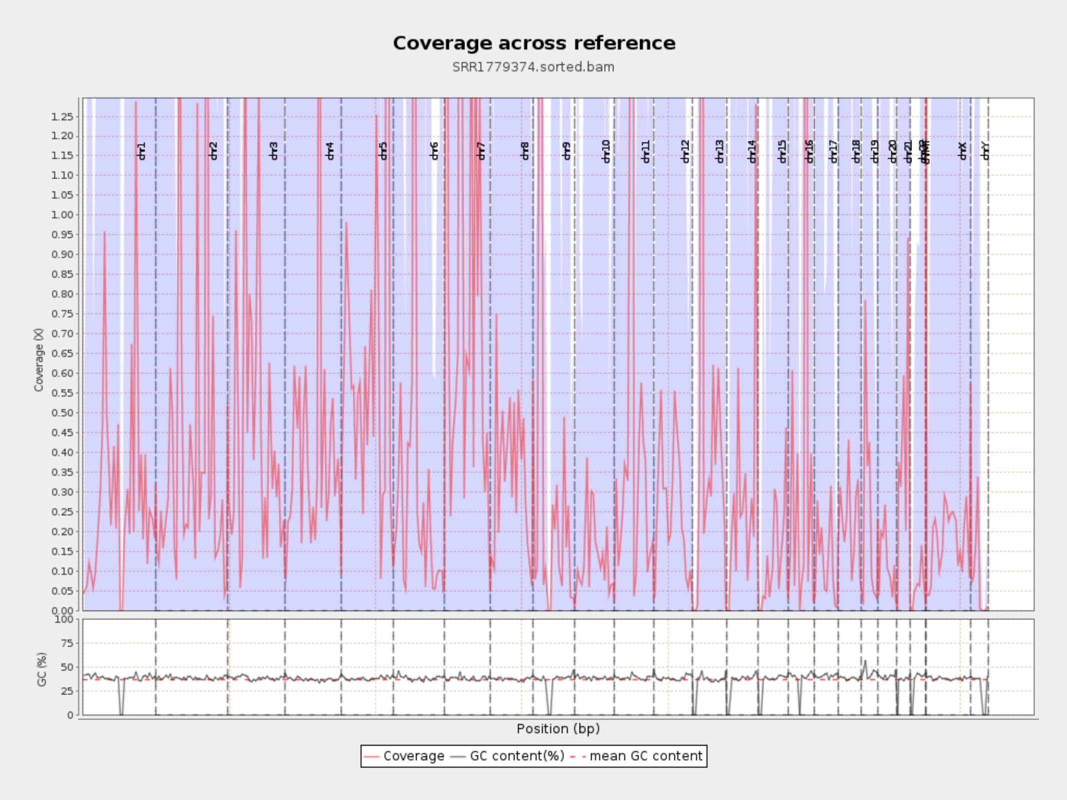
2.7. Chromosome stats

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

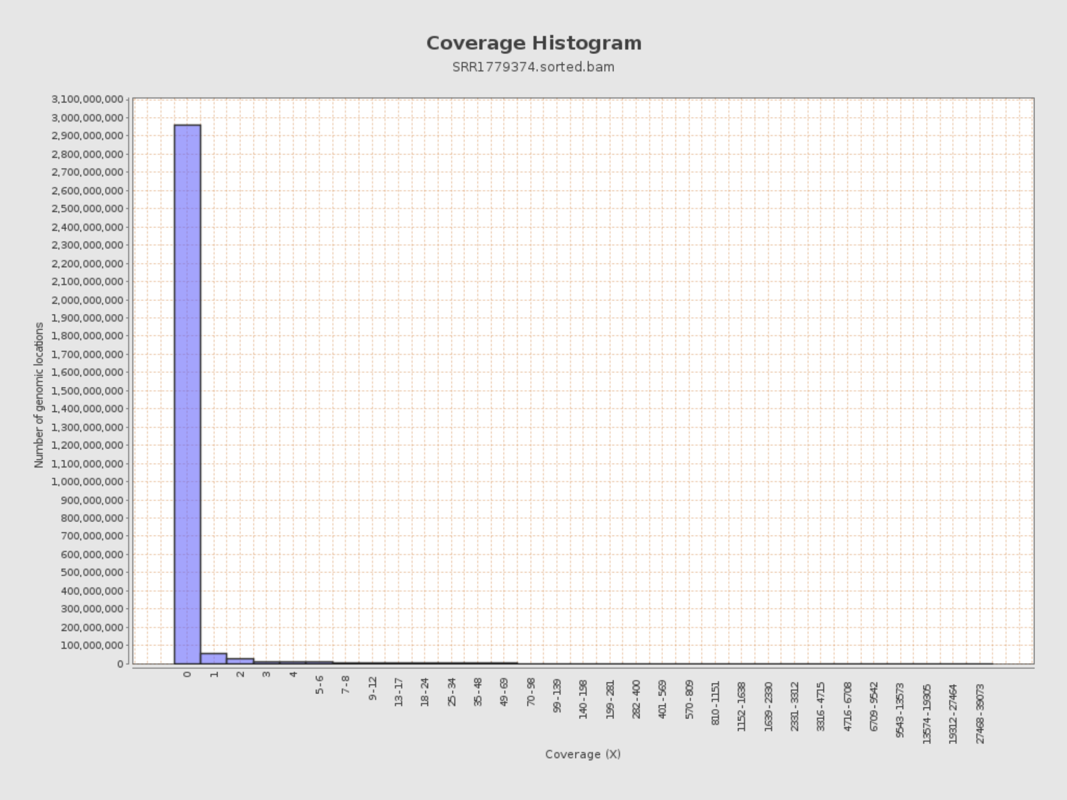
		bases	coverage	deviation
chr1	249250621	73478571	0.2948	15.1186
chr2	243199373	106381858	0.4374	47.0862
chr3	198022430	92098837	0.4651	29.3956
chr4	191154276	83200850	0.4353	41.6668
chr5	180915260	116254904	0.6426	43.8697
chr6	171115067	55155306	0.3223	6.9308
chr7	159138663	148346994	0.9322	43.2725
chr8	146364022	50334239	0.3439	10.6456
chr9	141213431	49281747	0.349	5.8975
chr10	135534747	18863568	0.1392	4.9399
chr11	135006516	121463483	0.8997	129.1255
chr12	133851895	35403689	0.2645	3.3633
chr13	115169878	60622713	0.5264	45.8829
chr14	107349540	31533594	0.2937	21.5428
chr15	102531392	14162918	0.1381	3.7265
chr16	90354753	37590551	0.416	47.3635
chr17	81195210	10539043	0.1298	5.0137
chr18	78077248	18168056	0.2327	3.8185
chr19	59128983	14224941	0.2406	57.4866
chr20	63025520	7989475	0.1268	2.0613
chr21	48129895	18893557	0.3926	21.9422
chr22	51304566	3260434	0.0636	1.1567
chrMT	16571	507075	30.6001	17.5239
chrX	155270560	28287321	0.1822	2.5074

chrY	59373566	5092325	0.0858	1.4314

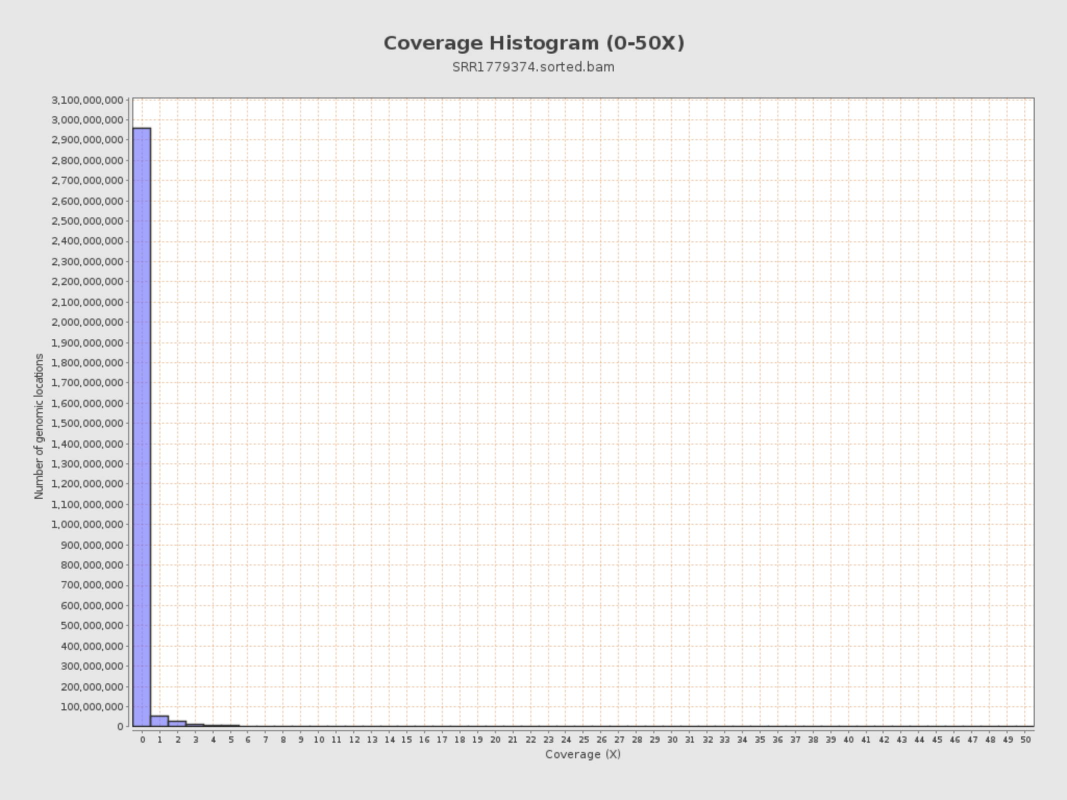
3. Results : Coverage across reference



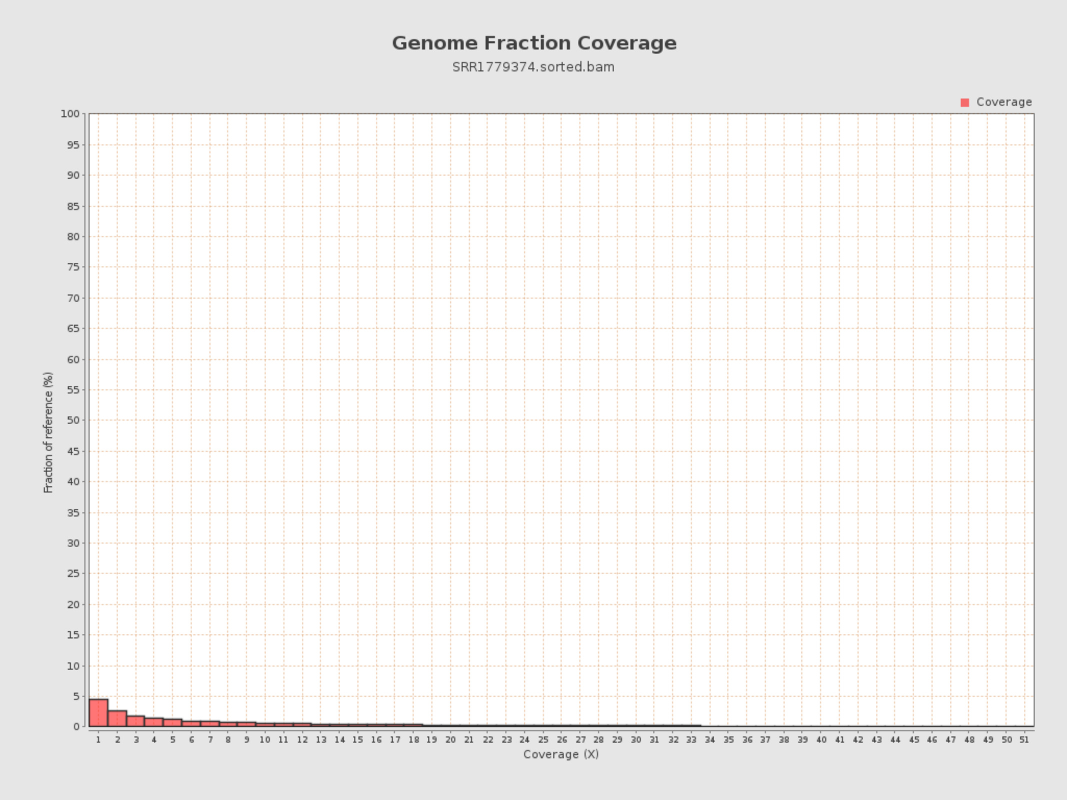
4. Results : Coverage Histogram



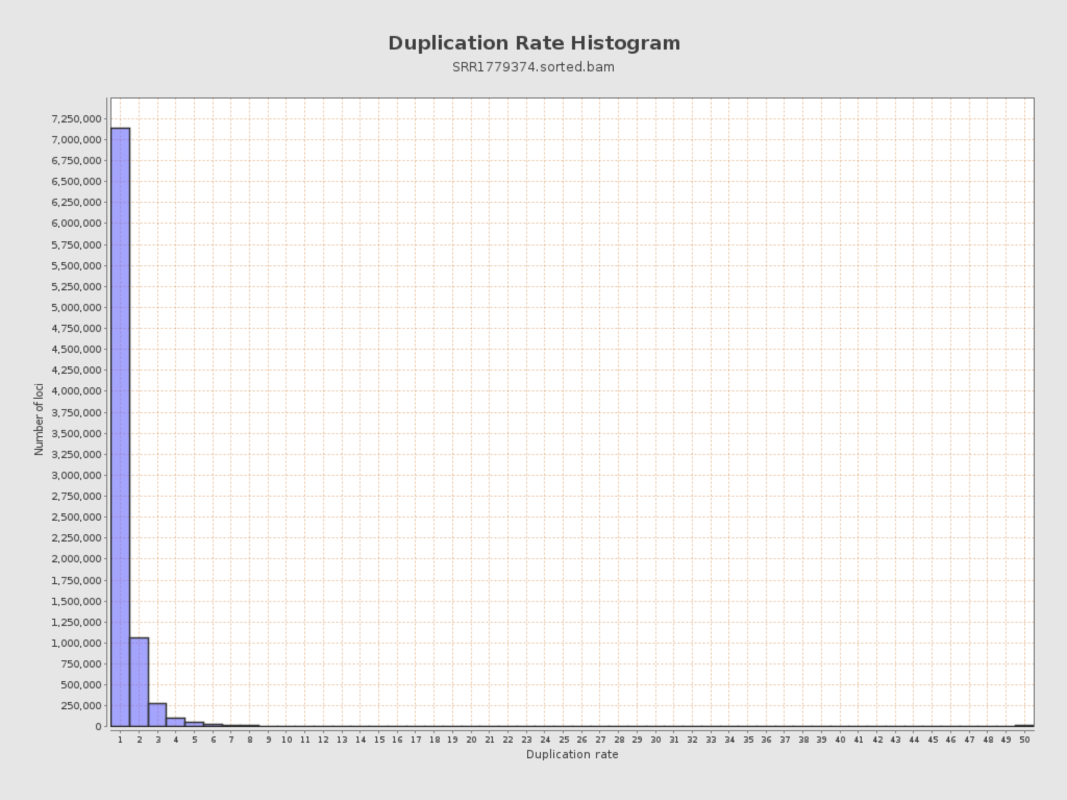
5. Results : Coverage Histogram (0-50X)



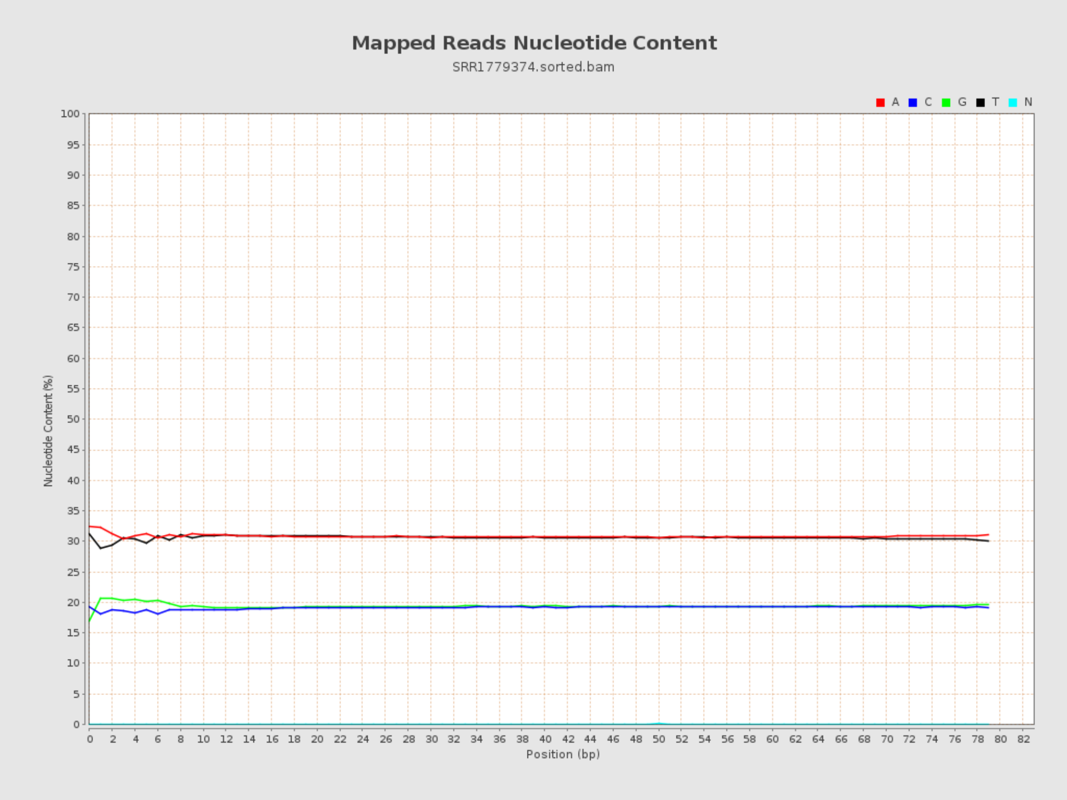
6. Results : Genome Fraction Coverage



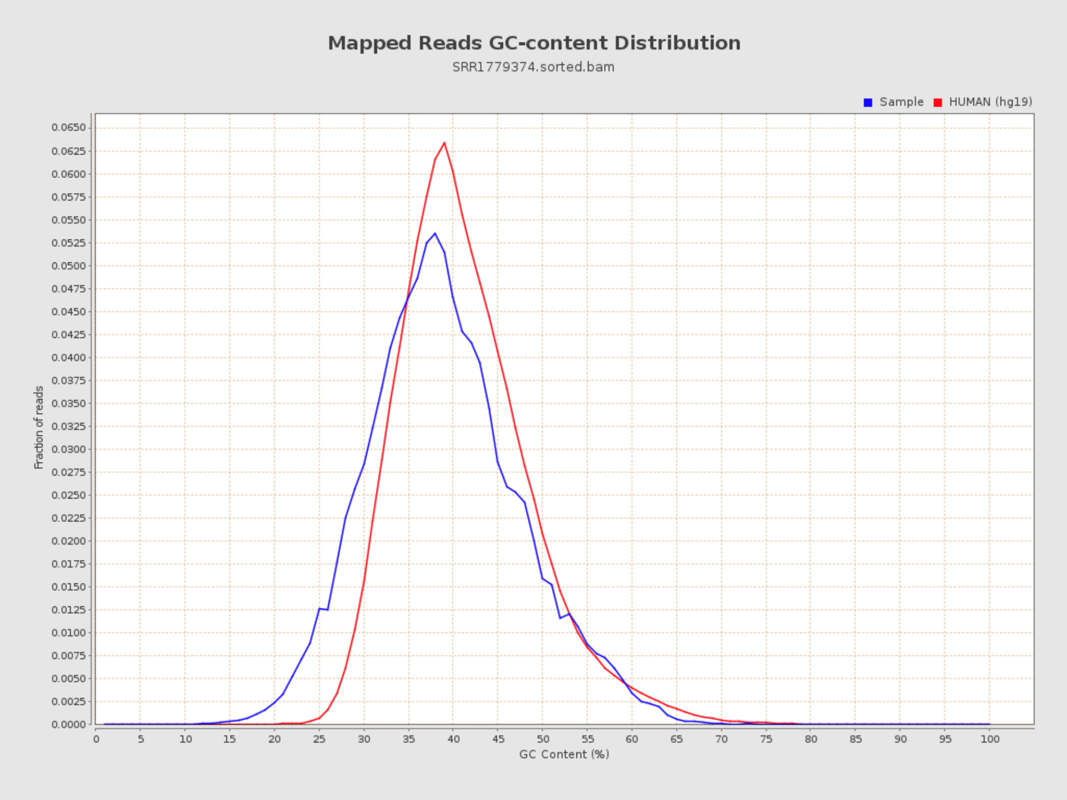
7. Results : Duplication Rate Histogram



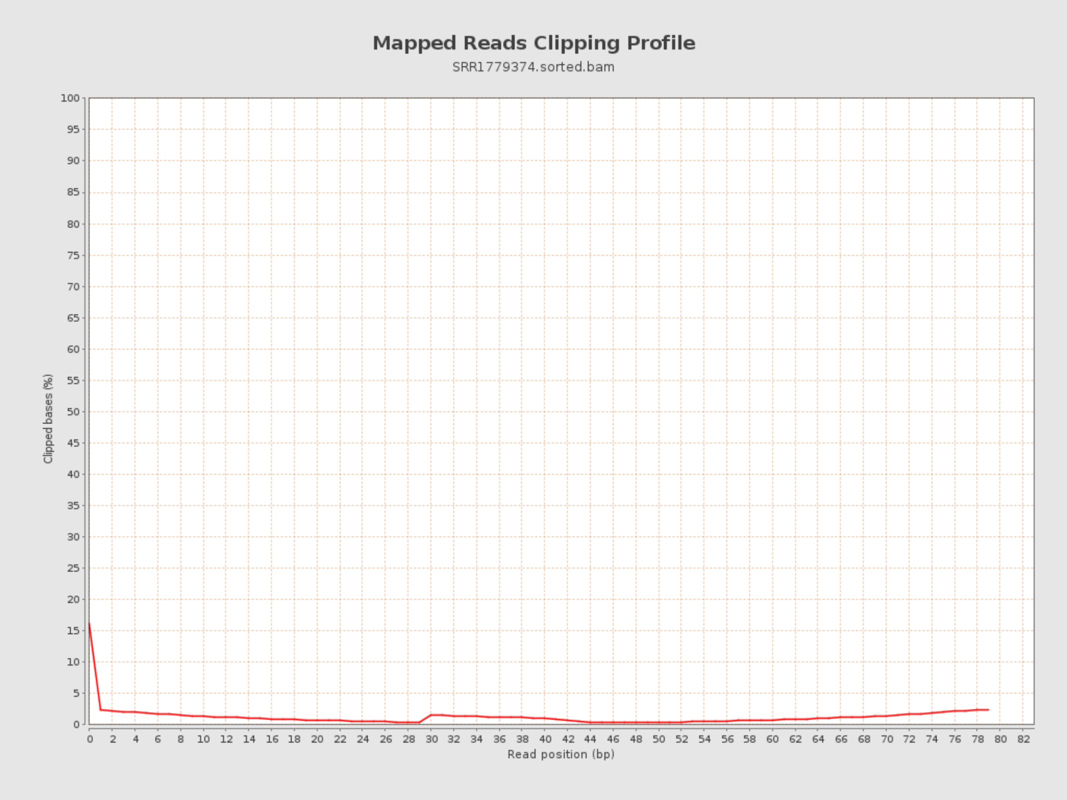
8. Results : Mapped Reads Nucleotide Content



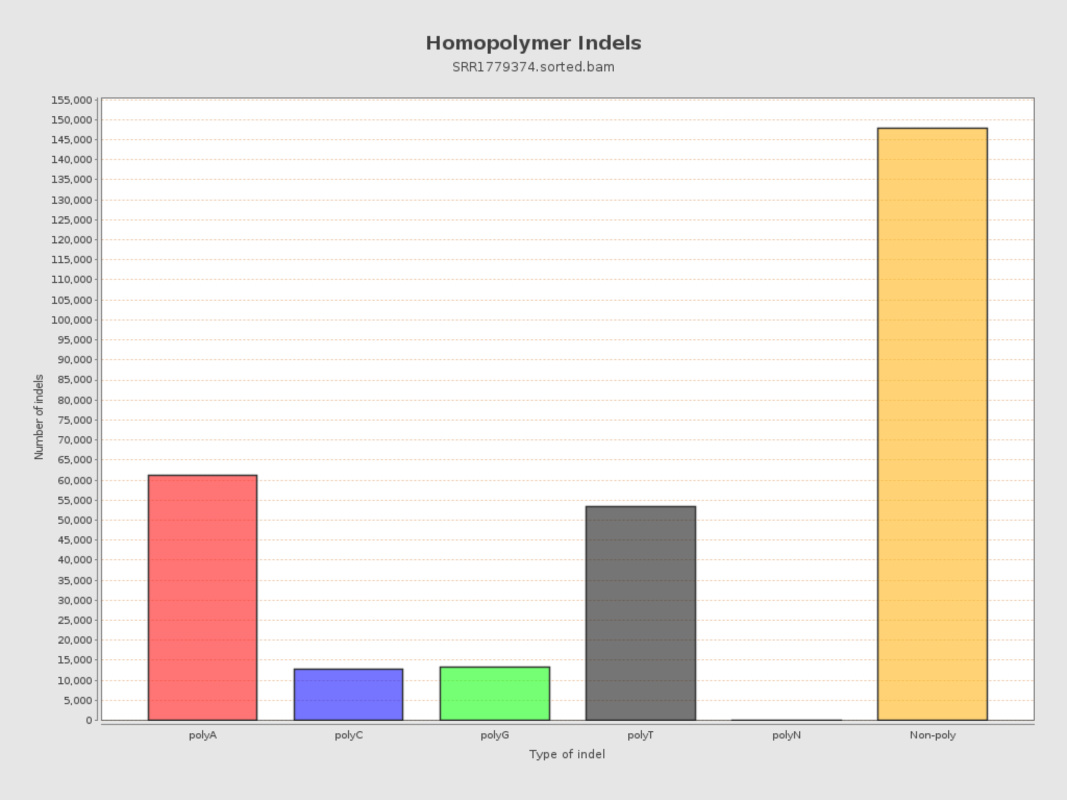
9. Results : Mapped Reads GC-content Distribution



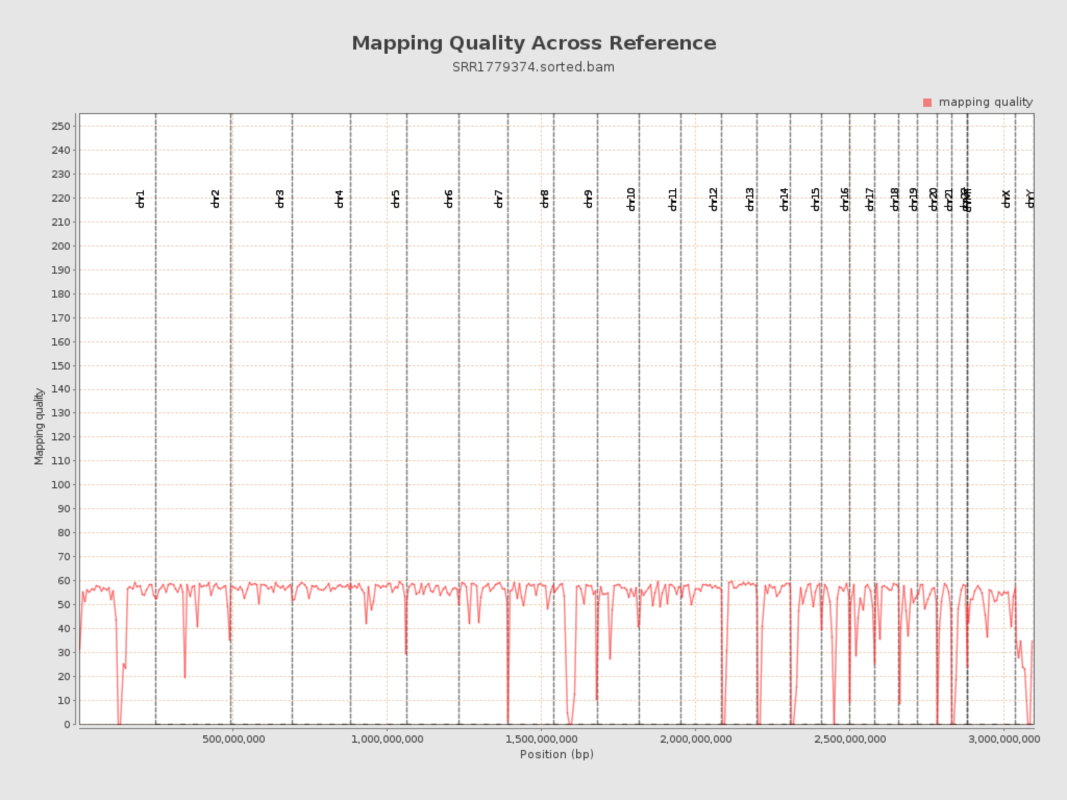
10. Results : Mapped Reads Clipping Profile



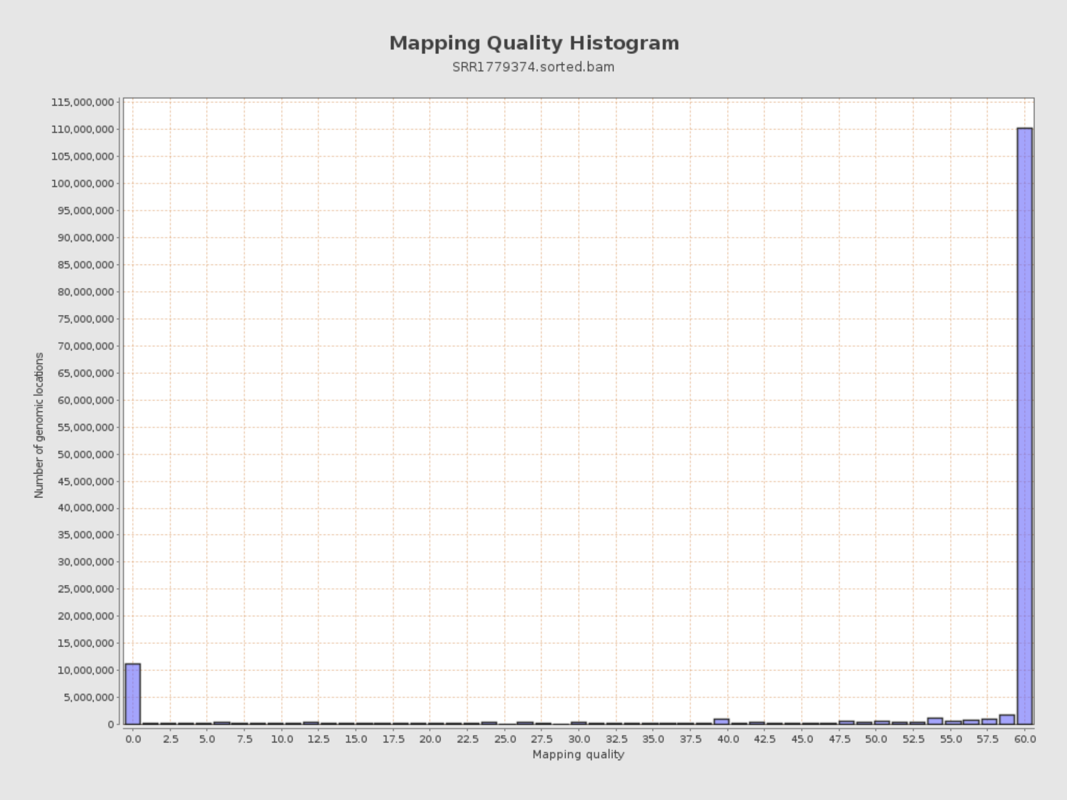
11. Results : Homopolymer Indels



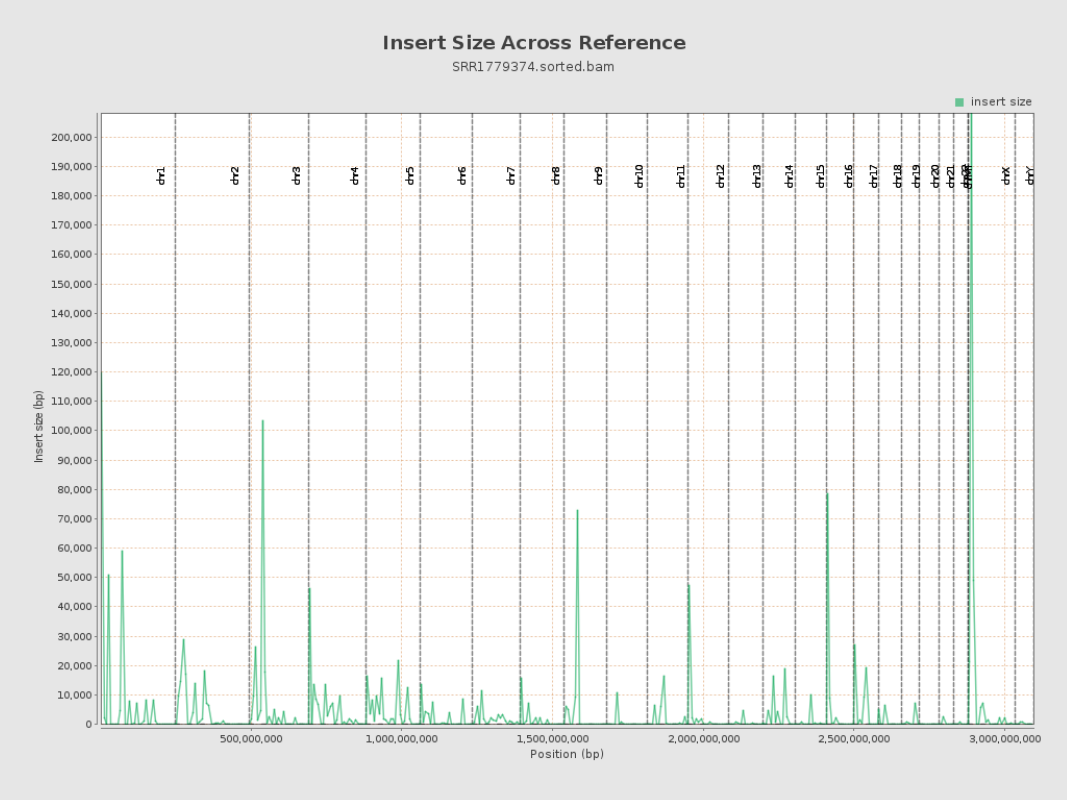
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram