Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 13:06:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779373.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_SRR1779373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779373_1.fastq.gz SRR1779373_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 13:06:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,469,292
Mapped reads	12,190,597 / 90.51%
Unmapped reads	1,278,695 / 9.49%
Mapped paired reads	12,190,597 / 90.51%
Mapped reads, first in pair	6,134,262 / 45.54%
Mapped reads, second in pair	6,056,335 / 44.96%
Mapped reads, both in pair	12,074,090 / 89.64%
Mapped reads, singletons	116,507 / 0.86%
Secondary alignments	0
Supplementary alignments	176,751 / 1.31%
Read min/max/mean length	30 / 80 / 80.47
Duplicated reads (estimated)	7,353,888 / 54.6%
Duplication rate	21.12%
Clipped reads	1,333,348 / 9.9%

2.2. ACGT Content

Number/percentage of A's	299,081,582 / 31.09%
Number/percentage of C's	180,934,000 / 18.81%
Number/percentage of T's	298,060,763 / 30.98%
Number/percentage of G's	183,748,547 / 19.1%
Number/percentage of N's	209,289 / 0.02%

GC Percentage	37.91%

2.3. Coverage

Mean	0.3108
Standard Deviation	33.644

2.4. Mapping Quality

Mean Mapping Quality	51.81

2.5. Insert size

Mean	43,199.3
Standard Deviation	1,884,834.09
P25/Median/P75	119 / 160 / 211

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	3,406,088
Insertions	107,060
Mapped reads with at least one insertion	0.87%
Deletions	100,693
Mapped reads with at least one deletion	0.82%
Homopolymer indels	47.12%

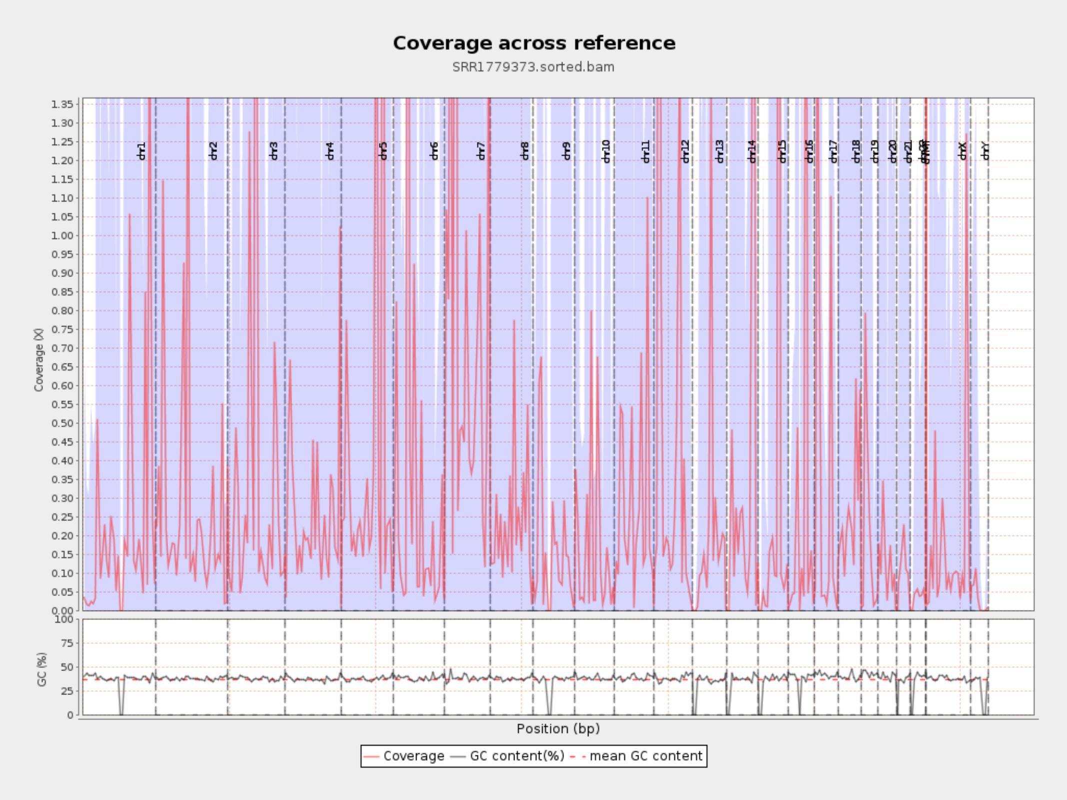
2.7. Chromosome stats

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

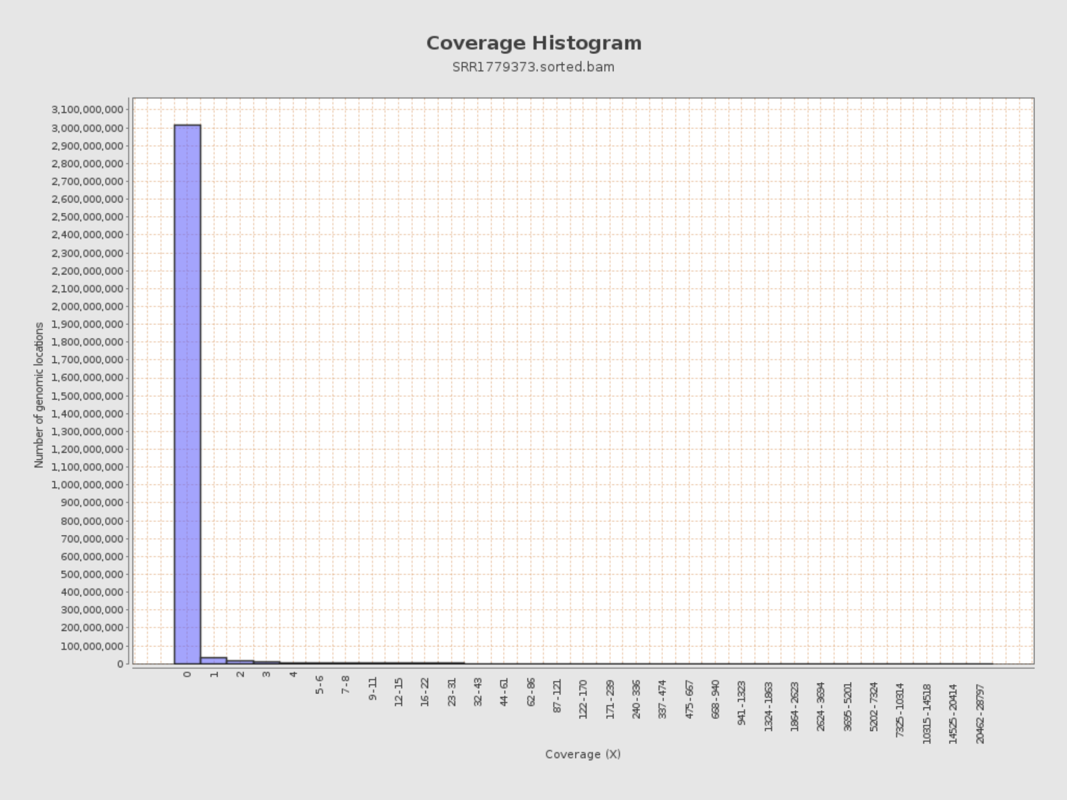
		bases	coverage	deviation
chr1	249250621	57604672	0.2311	24.8467
chr2	243199373	72657067	0.2988	13.8452
chr3	198022430	70910232	0.3581	29.0055
chr4	191154276	51448210	0.2691	13.8867
chr5	180915260	81897065	0.4527	66.885
chr6	171115067	60159931	0.3516	28.515
chr7	159138663	133952030	0.8417	60.5253
chr8	146364022	34980290	0.239	8.9683
chr9	141213431	23501837	0.1664	4.8775
chr10	135534747	23374291	0.1725	16.2727
chr11	135006516	40337838	0.2988	20.9757
chr12	133851895	73301629	0.5476	59.3289
chr13	115169878	24905722	0.2163	28.9922
chr14	107349540	46417389	0.4324	62.829
chr15	102531392	30771429	0.3001	41.9859
chr16	90354753	28020317	0.3101	28.2091
chr17	81195210	30742612	0.3786	40.3813
chr18	78077248	20618471	0.2641	12.1438
chr19	59128983	12963567	0.2192	19.9891
chr20	63025520	8338536	0.1323	3.549
chr21	48129895	4985818	0.1036	1.5918
chr22	51304566	1862599	0.0363	0.8322
chrMT	16571	330303	19.9326	11.9873
chrX	155270560	26046623	0.1677	17.0759

chrY	59373566	2114011	0.0356	0.6579

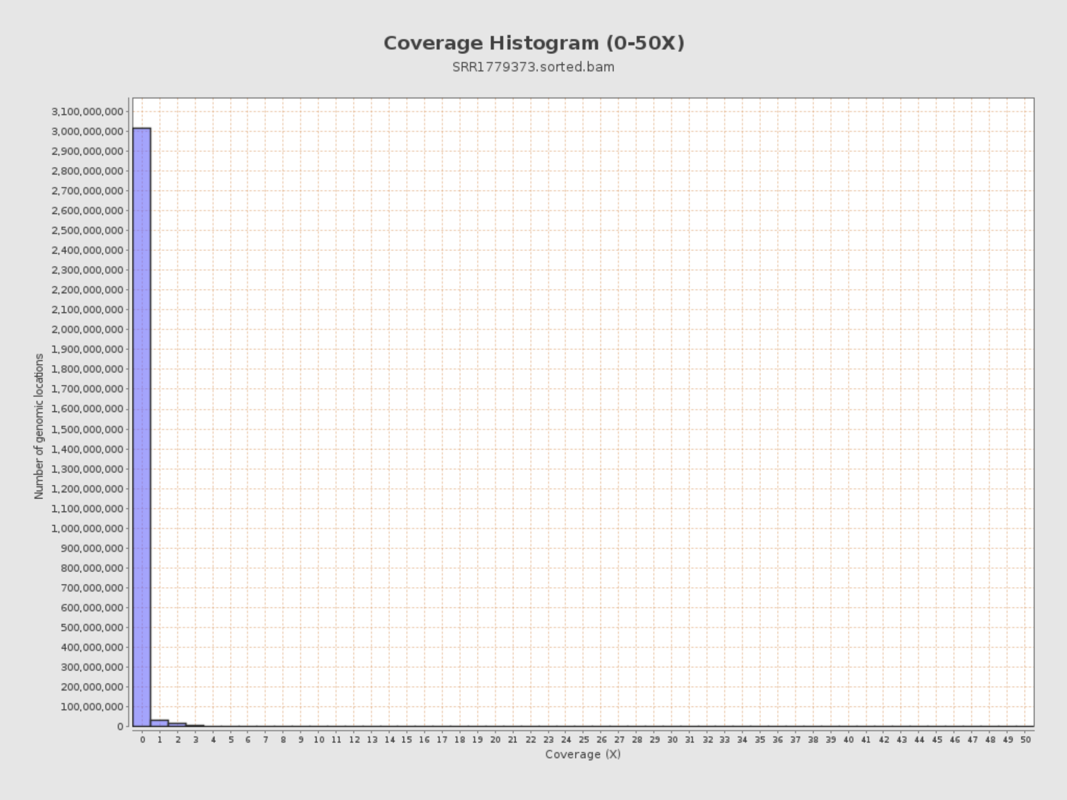
3. Results : Coverage across reference



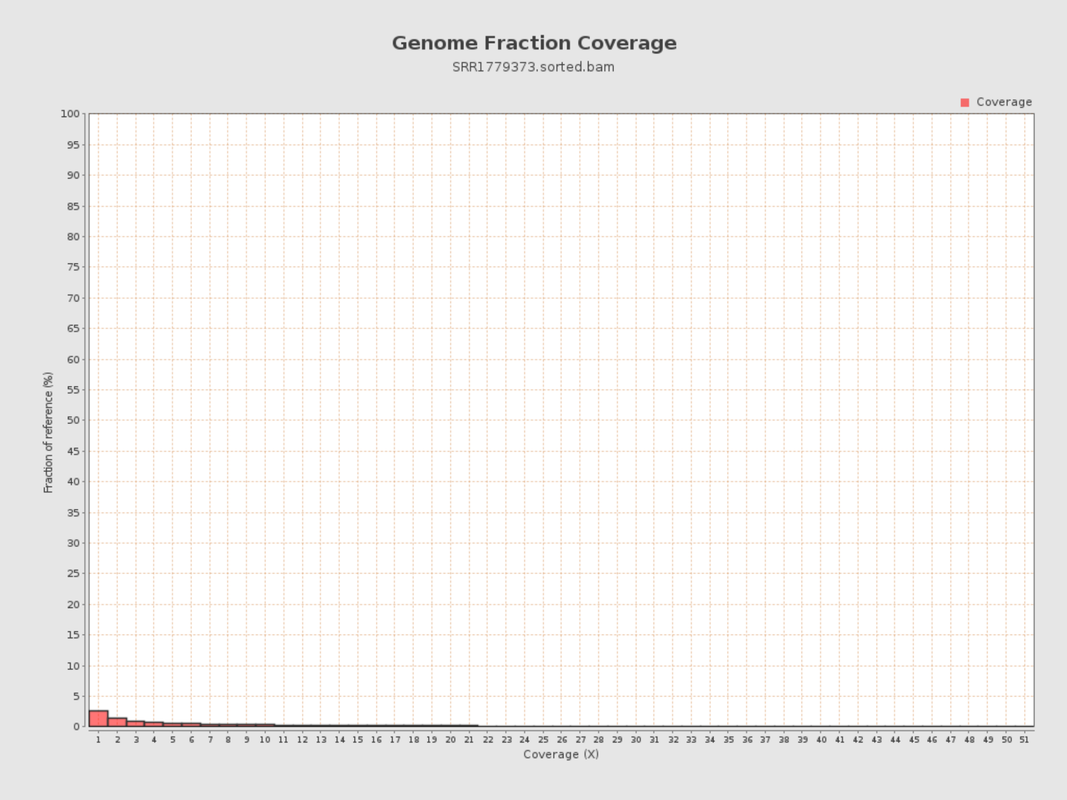
4. Results : Coverage Histogram



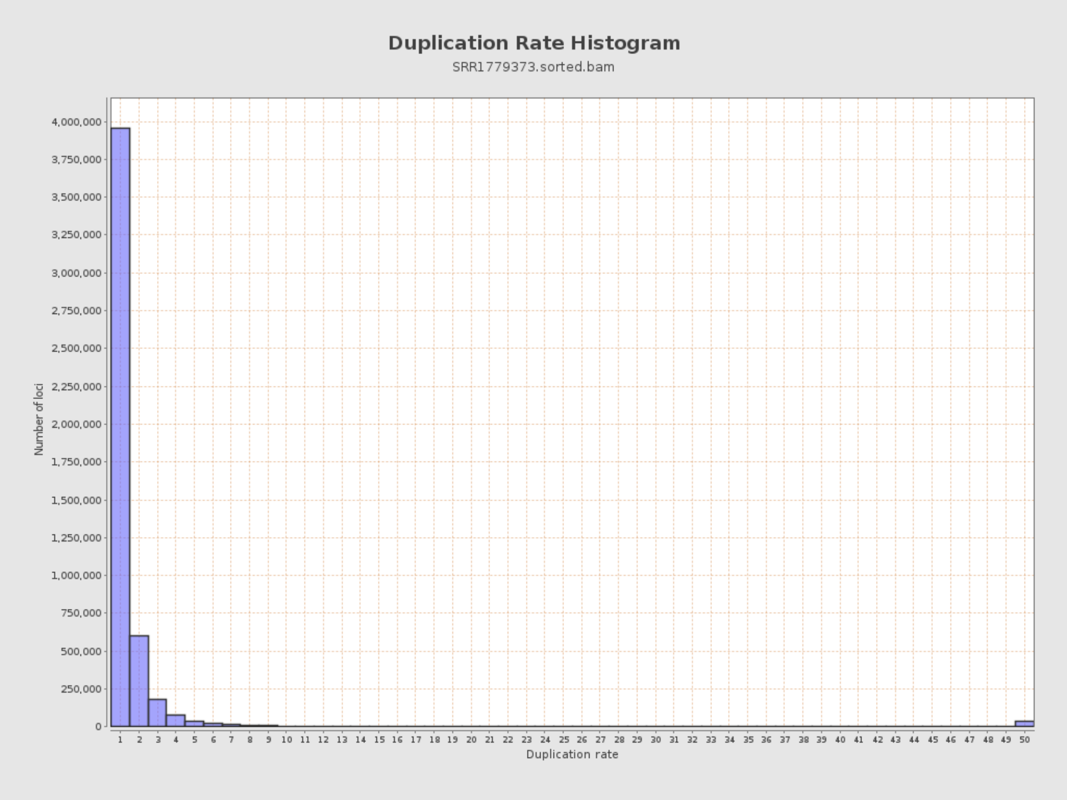
5. Results : Coverage Histogram (0-50X)



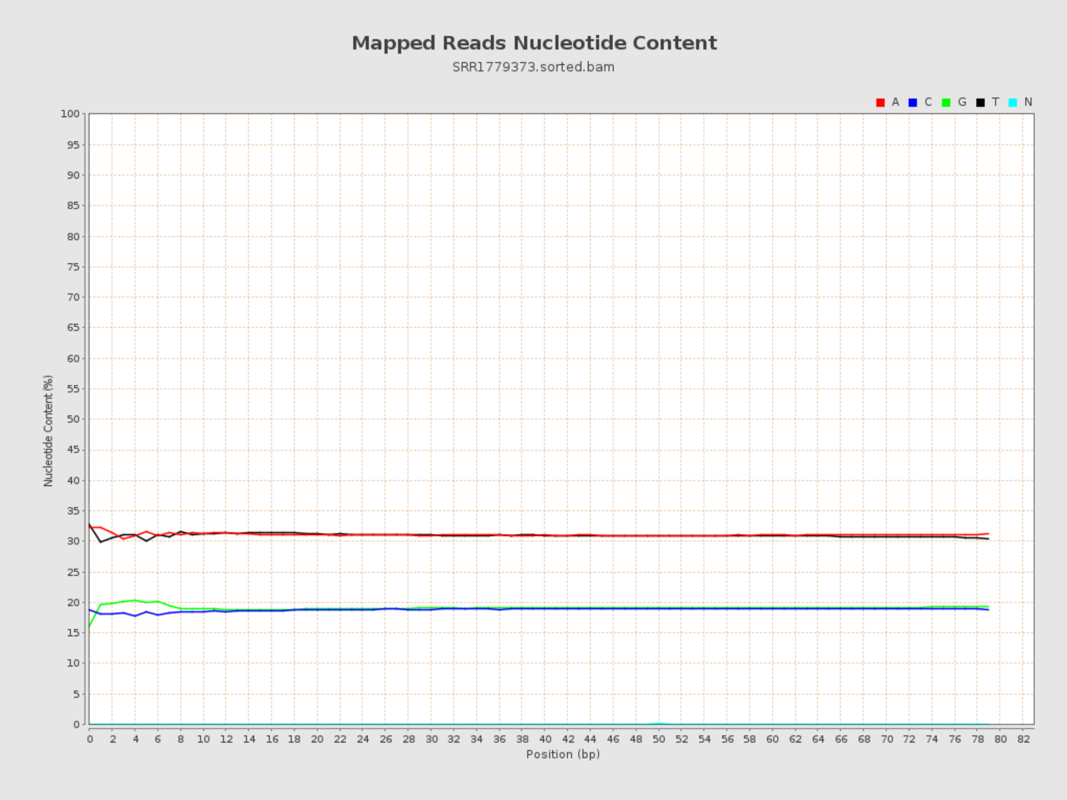
6. Results : Genome Fraction Coverage



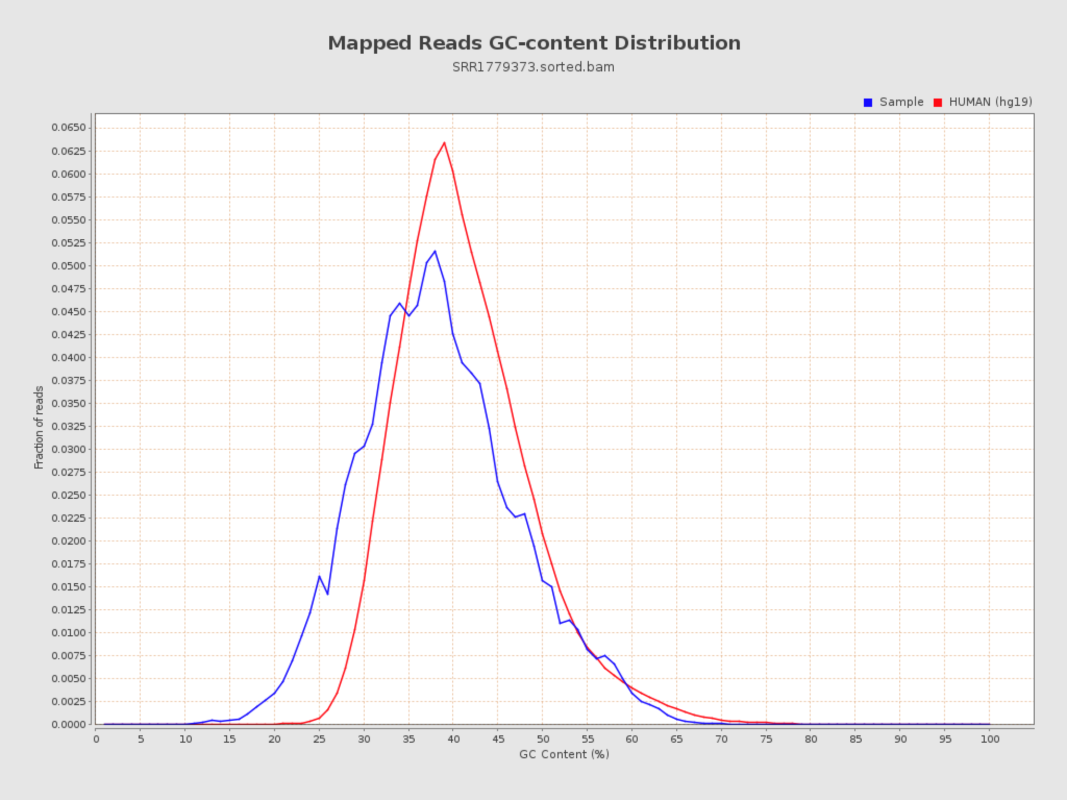
7. Results : Duplication Rate Histogram



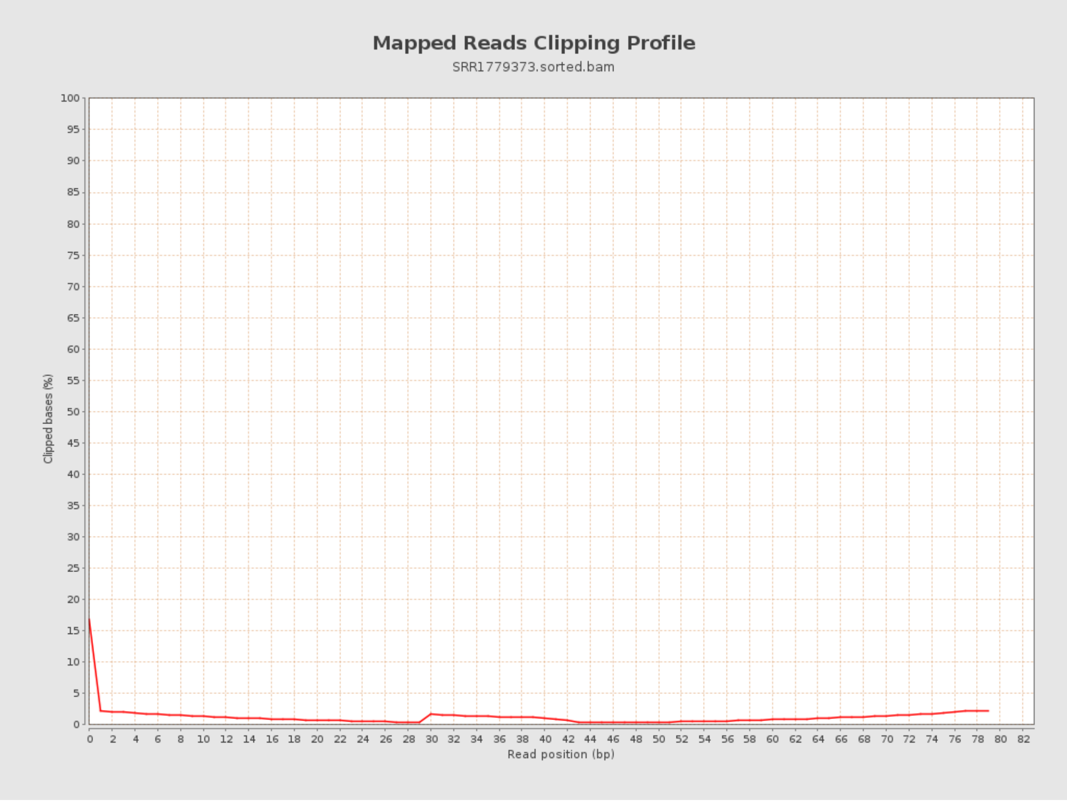
8. Results : Mapped Reads Nucleotide Content



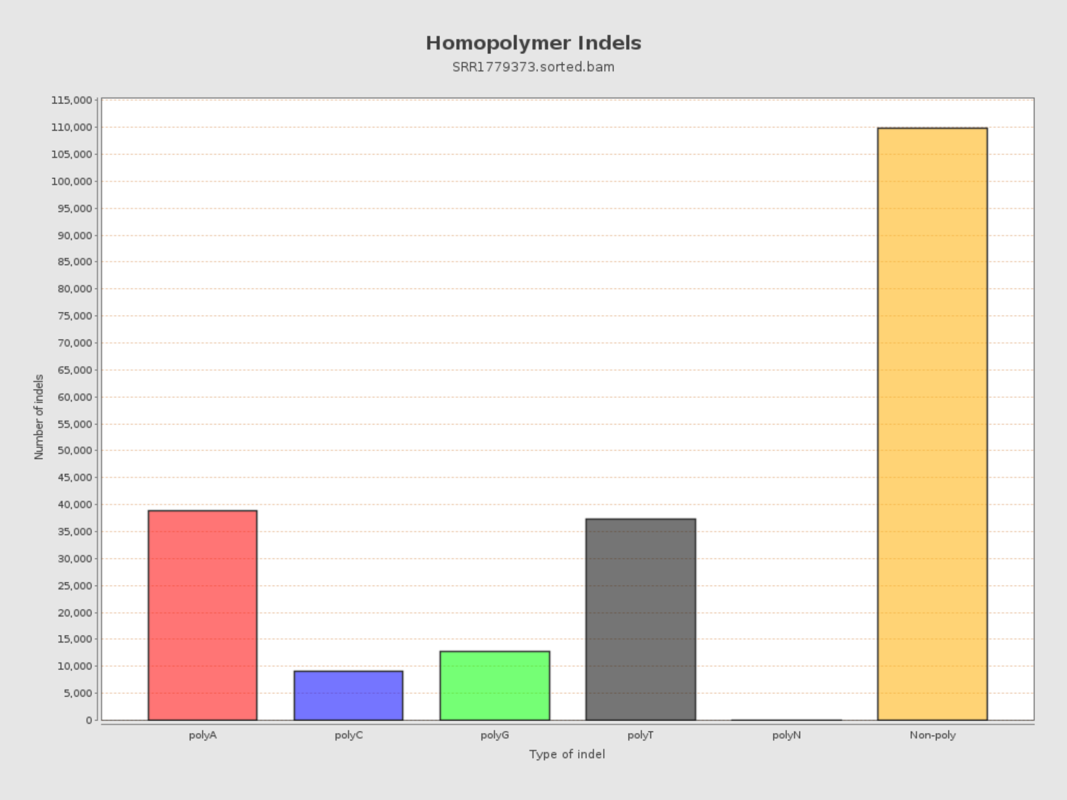
9. Results : Mapped Reads GC-content Distribution



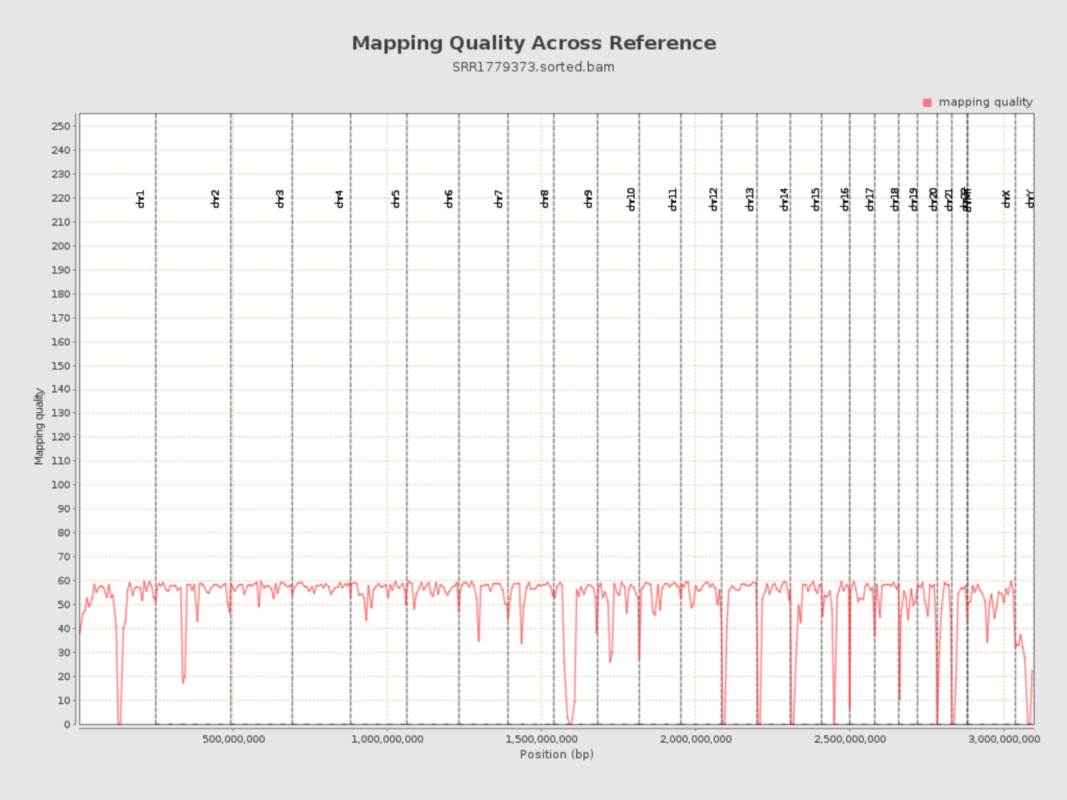
10. Results : Mapped Reads Clipping Profile



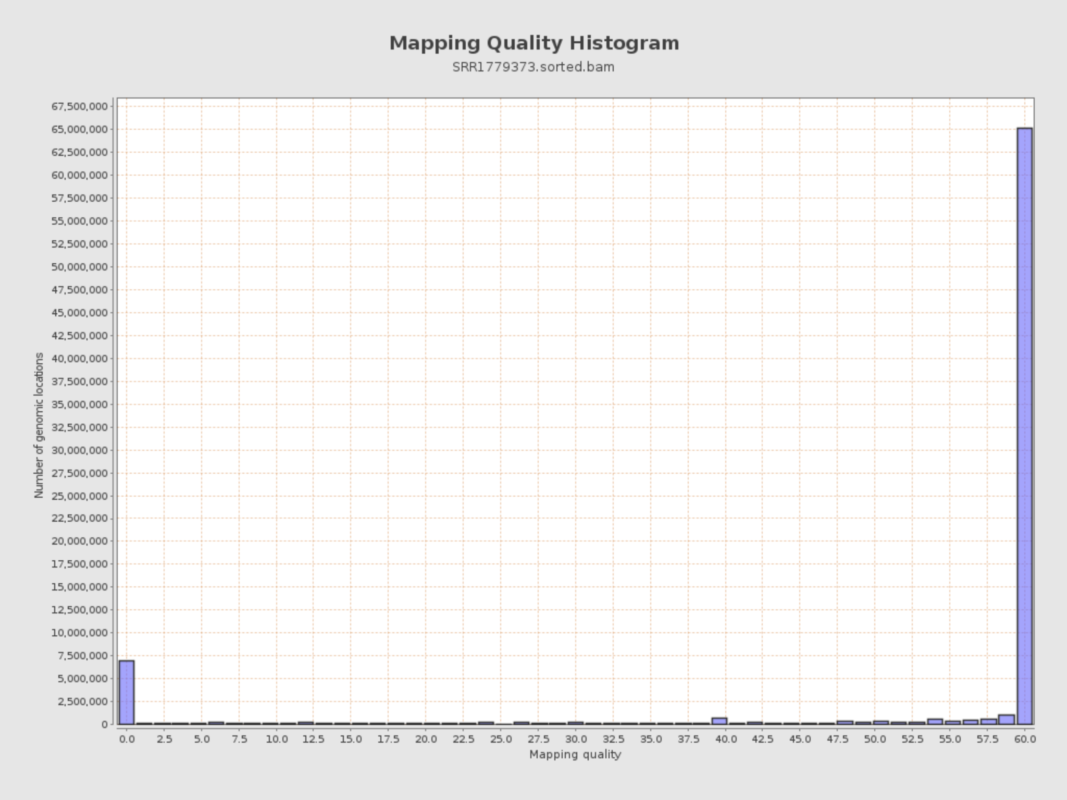
11. Results : Homopolymer Indels



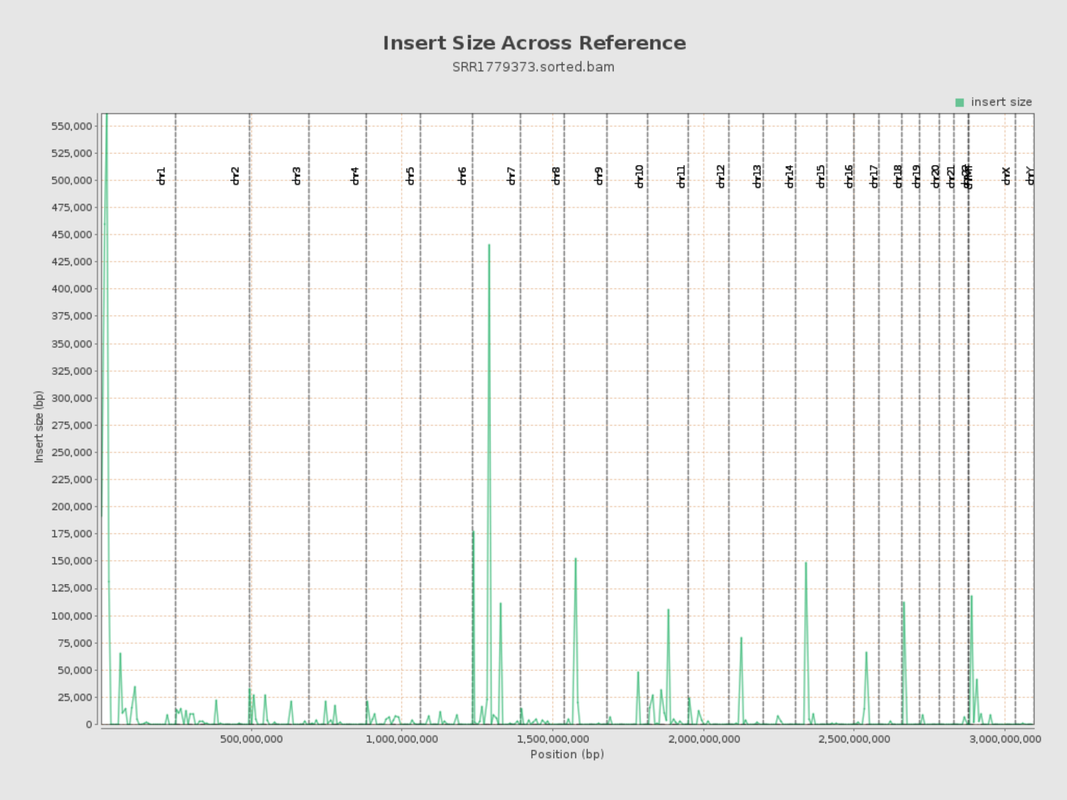
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram