Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 11:01:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779078.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_SRR1779078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779078_1.fastq.gz SRR1779078_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 11:01:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,501,420
Mapped reads	28,522,693 / 96.68%
Unmapped reads	978,727 / 3.32%
Mapped paired reads	28,522,693 / 96.68%
Mapped reads, first in pair	14,406,147 / 48.83%
Mapped reads, second in pair	14,116,546 / 47.85%
Mapped reads, both in pair	28,125,140 / 95.33%
Mapped reads, singletons	397,553 / 1.35%
Secondary alignments	0
Supplementary alignments	168,335 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	1,215,574 / 4.12%
Duplication rate	3.66%
Clipped reads	2,120,709 / 7.19%

2.2. ACGT Content

Number/percentage of A's	864,236,528 / 30.38%
Number/percentage of C's	555,963,721 / 19.54%
Number/percentage of T's	858,346,498 / 30.17%
Number/percentage of G's	565,511,114 / 19.88%
Number/percentage of N's	943,858 / 0.03%

GC Percentage	39.42%

2.3. Coverage

Mean	0.9192
Standard Deviation	2.739

2.4. Mapping Quality

Mean Mapping Quality	53.54

2.5. Insert size

Mean	70,745.97
Standard Deviation	2,582,604.91
P25/Median/P75	150 / 202 / 276

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	13,076,637
Insertions	239,941
Mapped reads with at least one insertion	0.83%
Deletions	292,411
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.3%

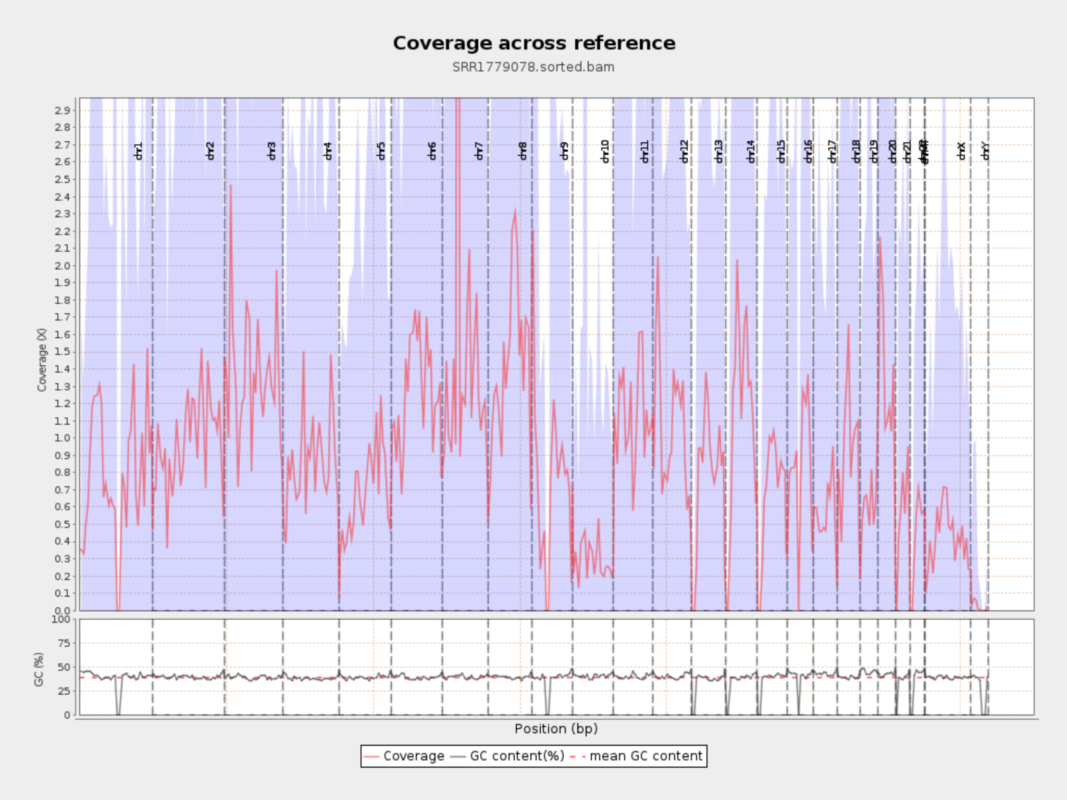
2.7. Chromosome stats

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

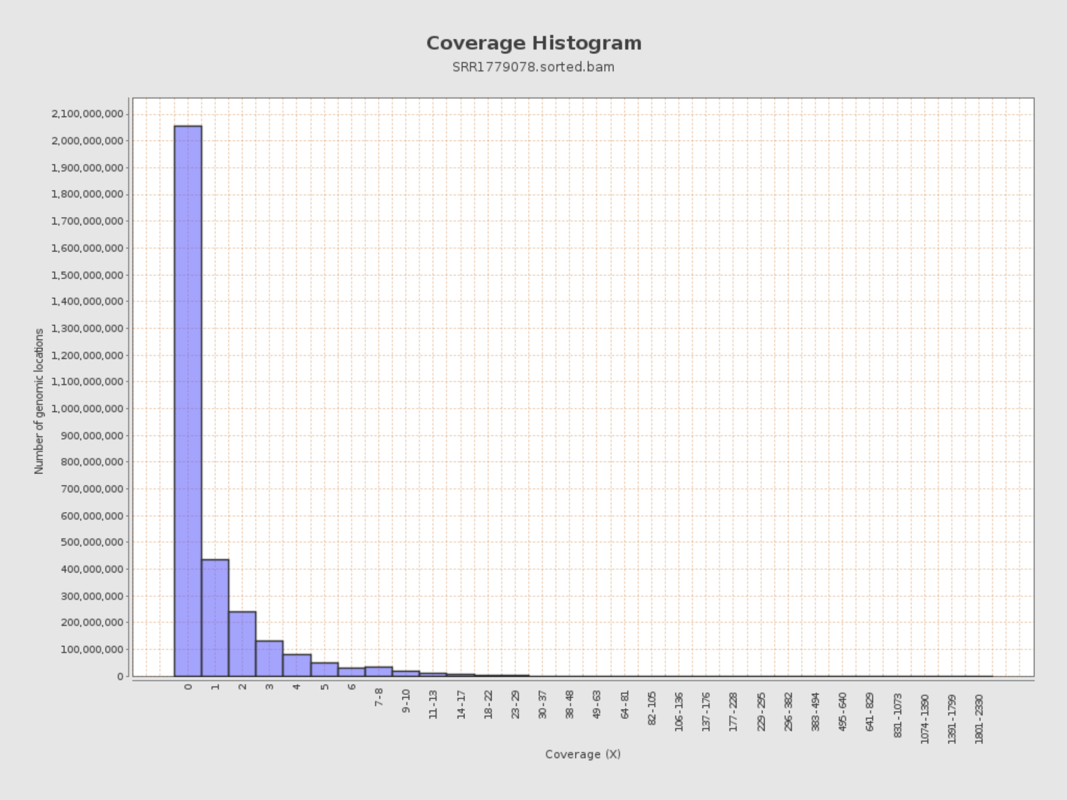
		bases	coverage	deviation
chr1	249250621	196270707	0.7874	2.2701
chr2	243199373	239791614	0.986	2.3222
chr3	198022430	268445858	1.3556	2.4546
chr4	191154276	166723782	0.8722	1.8792
chr5	180915260	123889919	0.6848	1.5978
chr6	171115067	220065104	1.2861	2.4117
chr7	159138663	262012397	1.6464	7.5559
chr8	146364022	211090825	1.4422	2.5032
chr9	141213431	106115793	0.7515	2.1206
chr10	135534747	40590021	0.2995	3.5157
chr11	135006516	150437840	1.1143	2.2627
chr12	133851895	144252661	1.0777	2.1496
chr13	115169878	91618303	0.7955	1.7293
chr14	107349540	123228414	1.1479	2.2731
chr15	102531392	69115316	0.6741	1.71
chr16	90354753	73454581	0.813	1.8589
chr17	81195210	46075876	0.5675	1.5821
chr18	78077248	75312965	0.9646	2.1317
chr19	59128983	35473883	0.5999	2.0391
chr20	63025520	84115149	1.3346	2.6464
chr21	48129895	28251384	0.587	1.554
chr22	51304566	22221612	0.4331	1.2021
chrMT	16571	4674	0.2821	0.7175
chrX	155270560	65570078	0.4223	1.4112

chrY	59373566	1530206	0.0258	0.4894

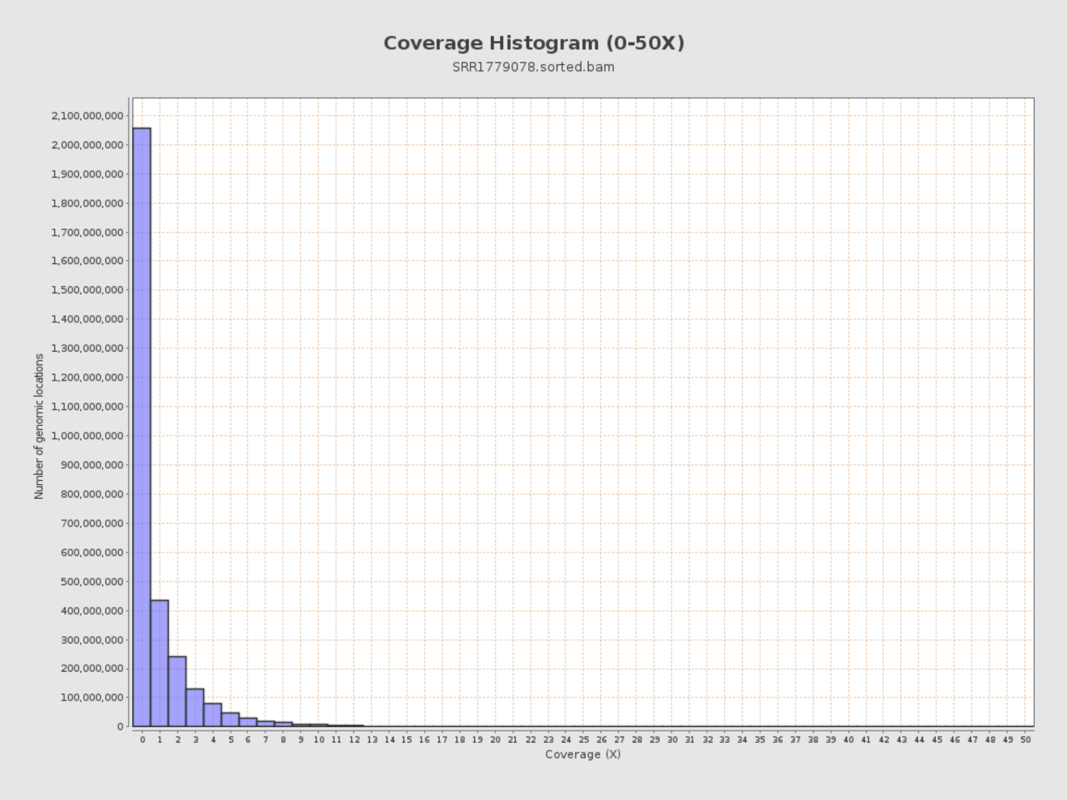
3. Results : Coverage across reference



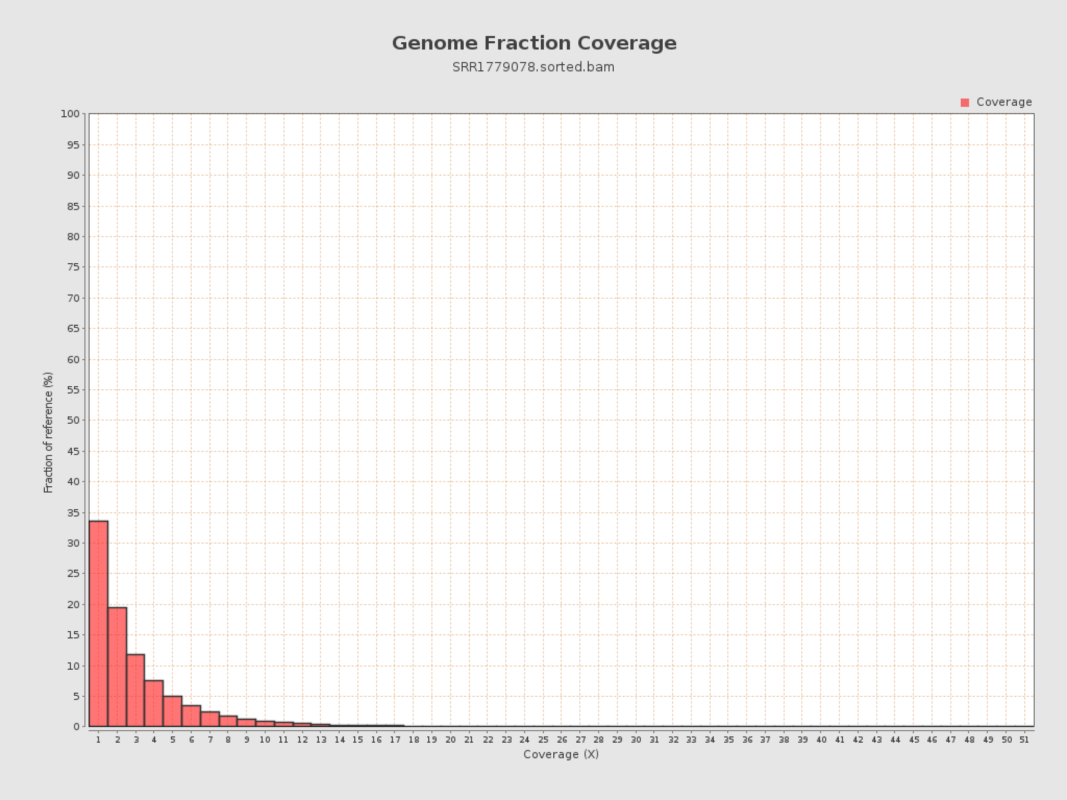
4. Results : Coverage Histogram



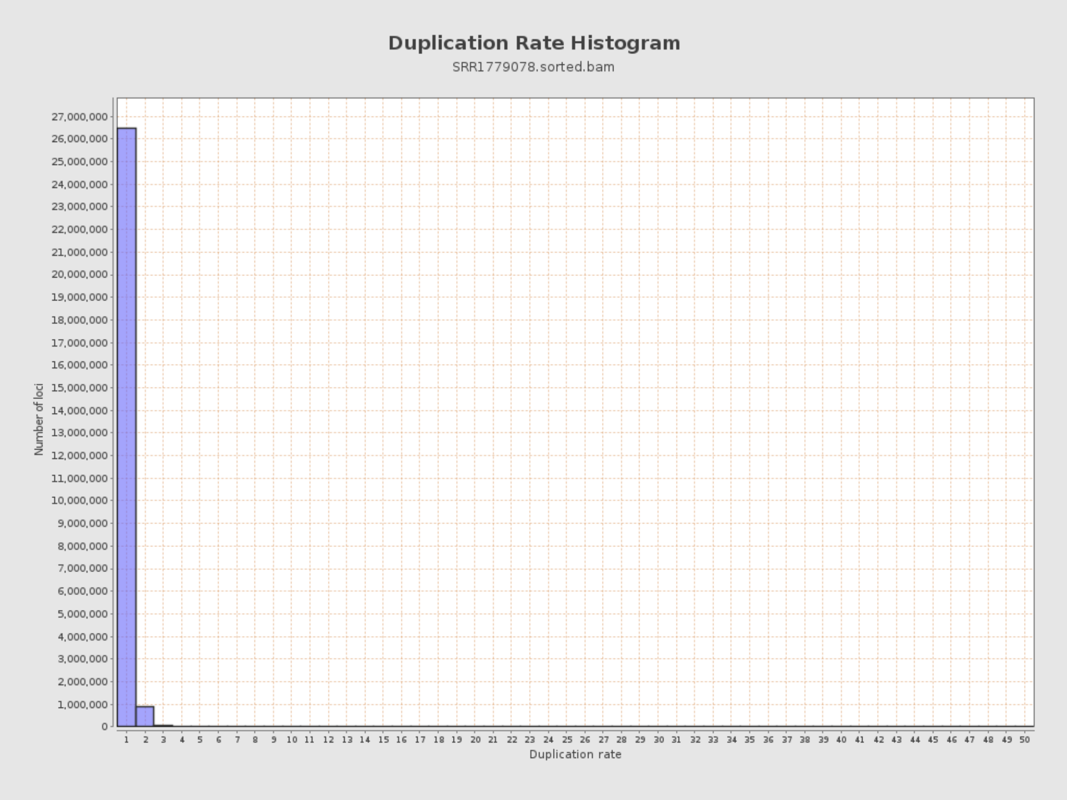
5. Results : Coverage Histogram (0-50X)



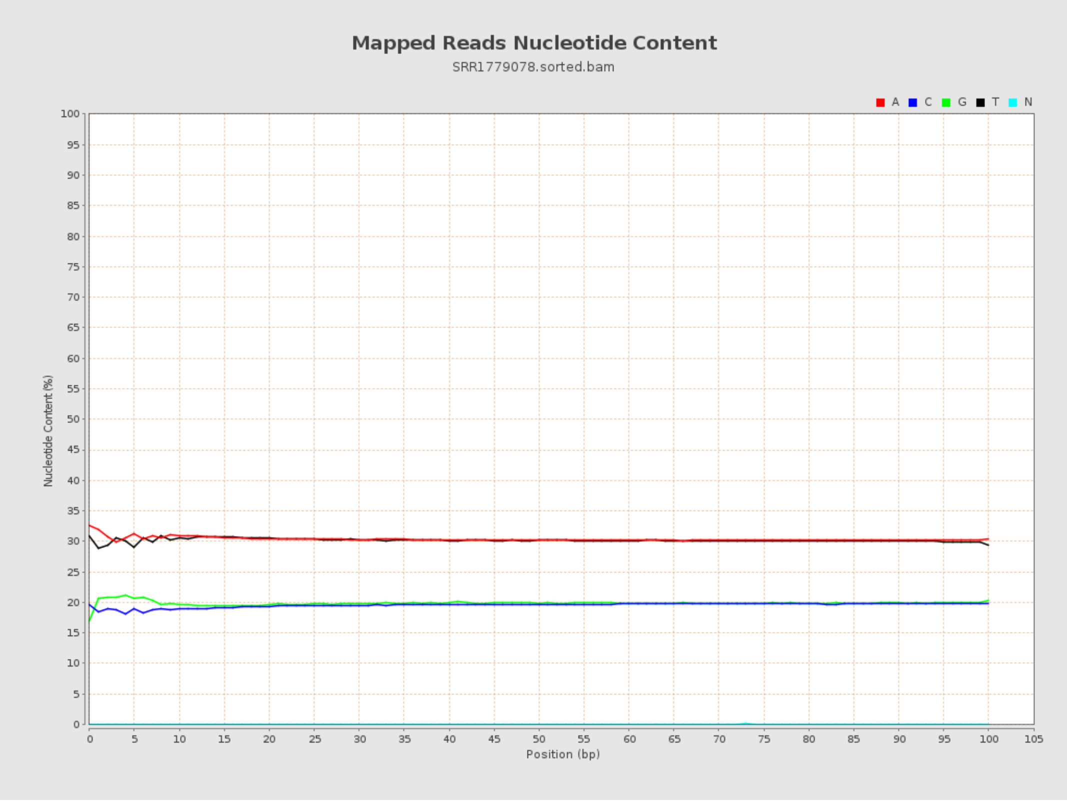
6. Results : Genome Fraction Coverage



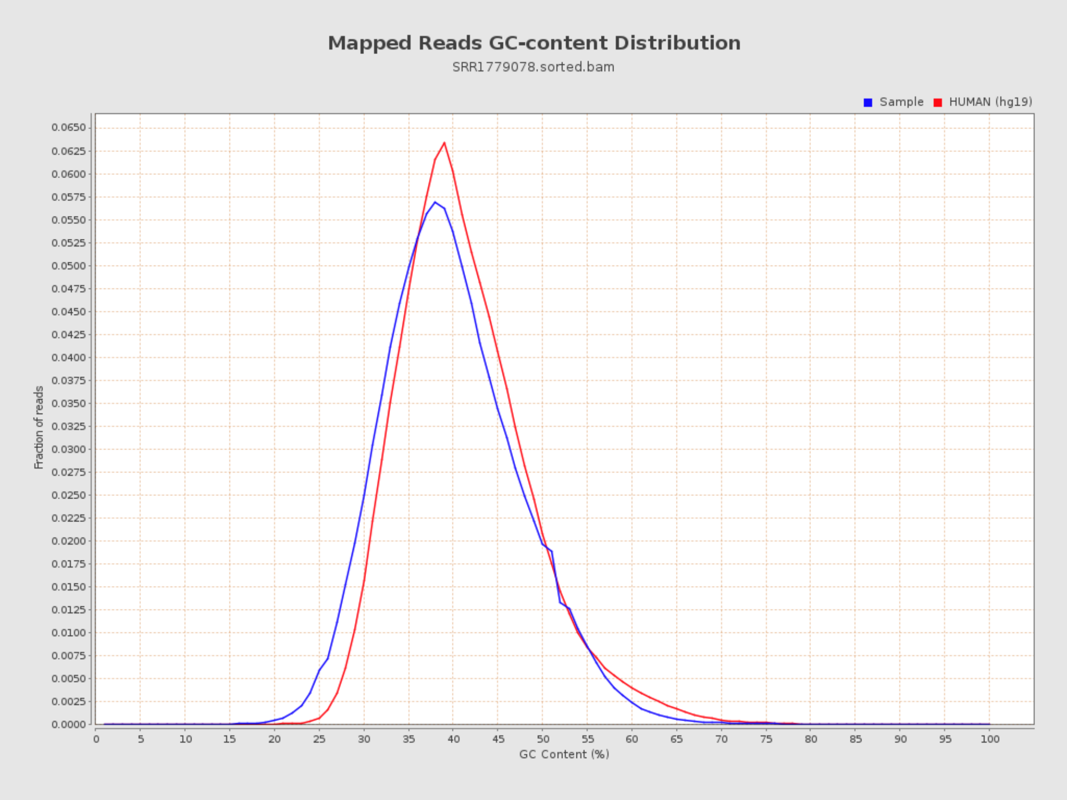
7. Results : Duplication Rate Histogram



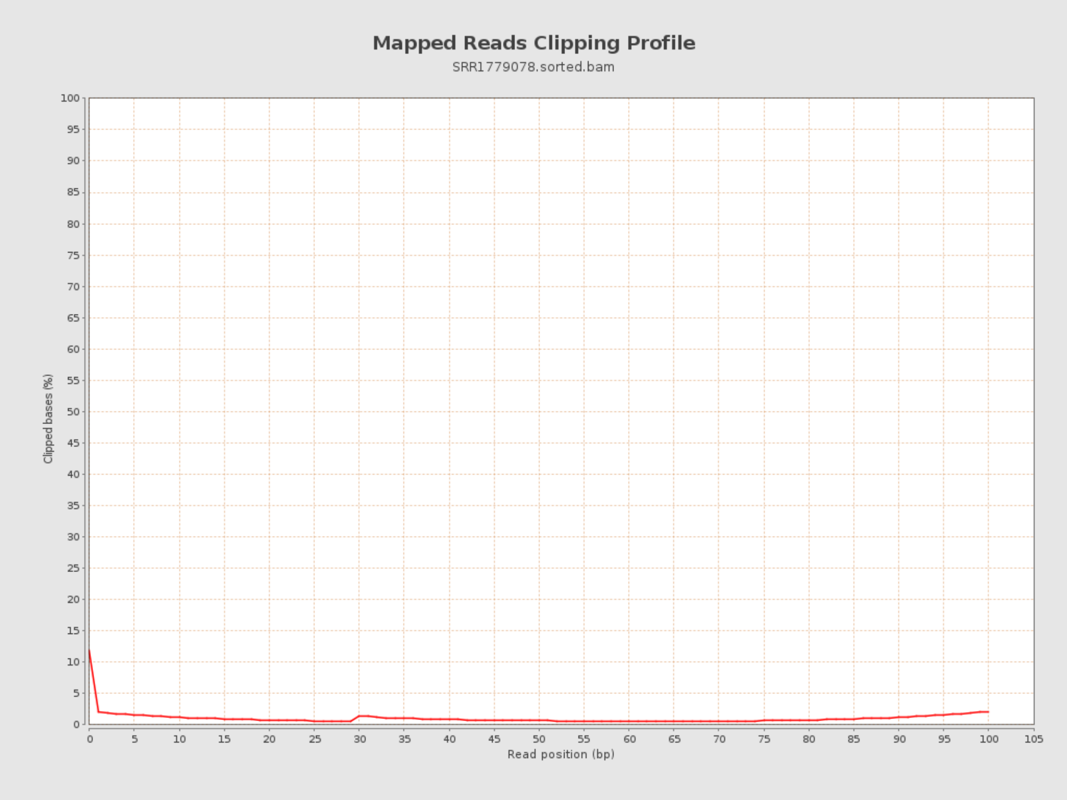
8. Results : Mapped Reads Nucleotide Content



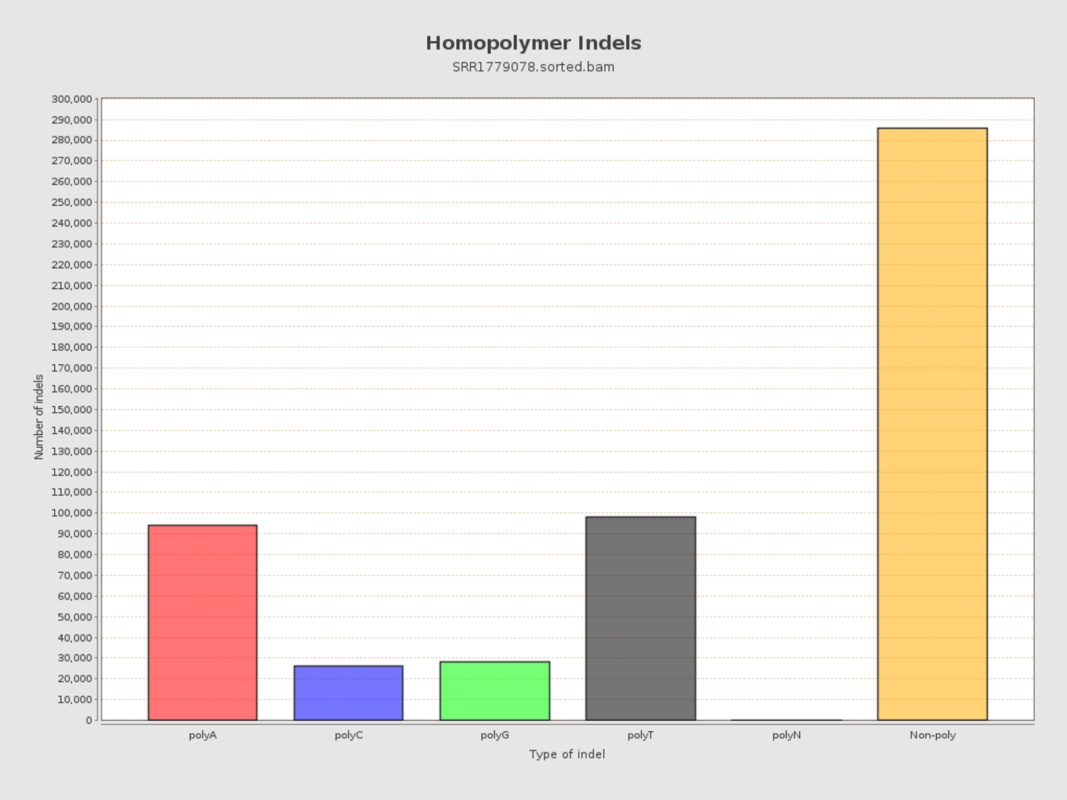
9. Results : Mapped Reads GC-content Distribution



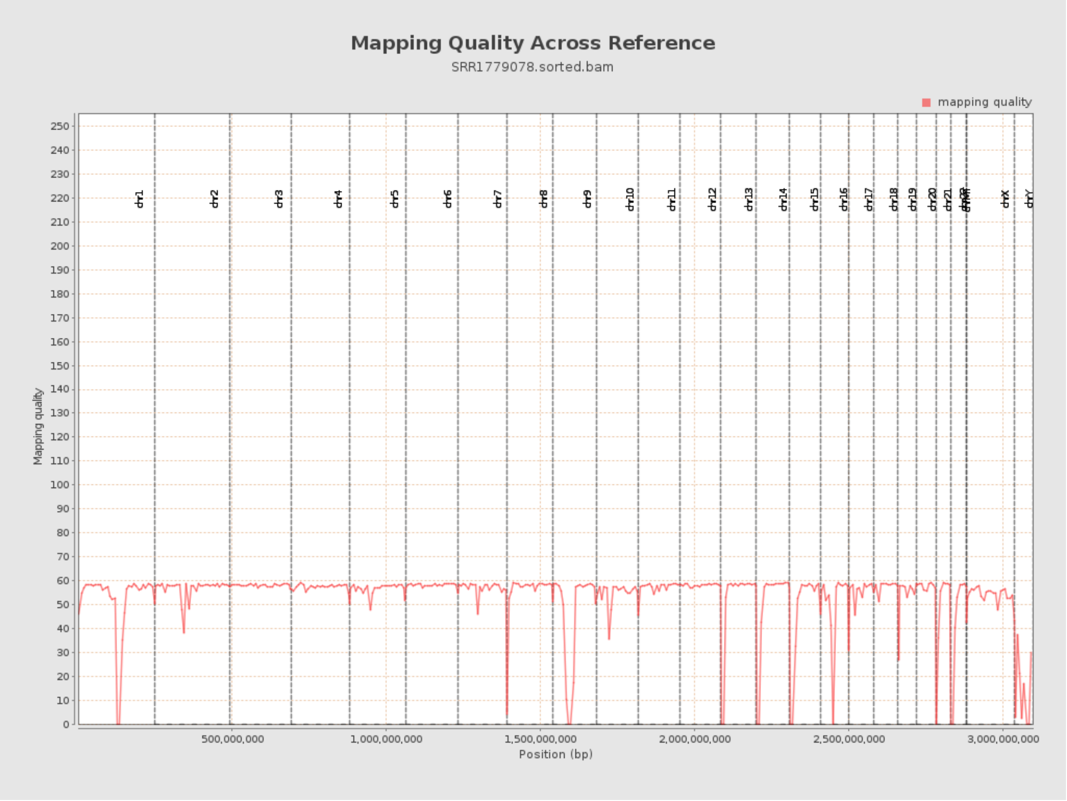
10. Results : Mapped Reads Clipping Profile



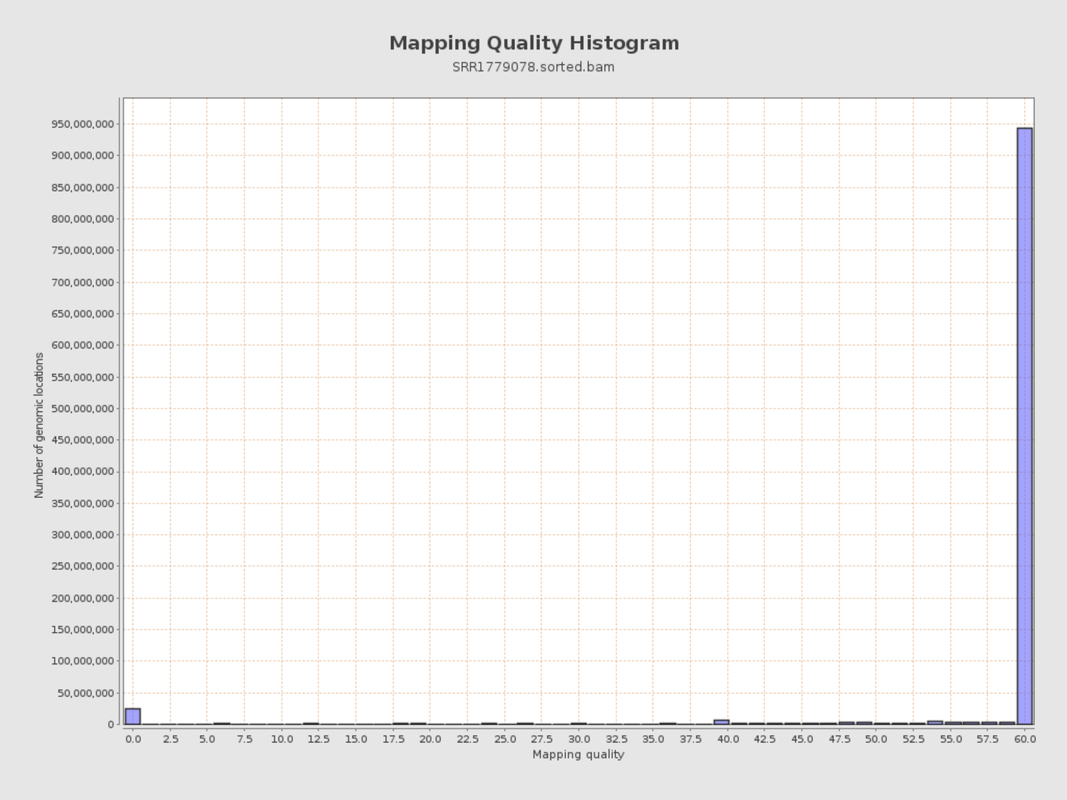
11. Results : Homopolymer Indels



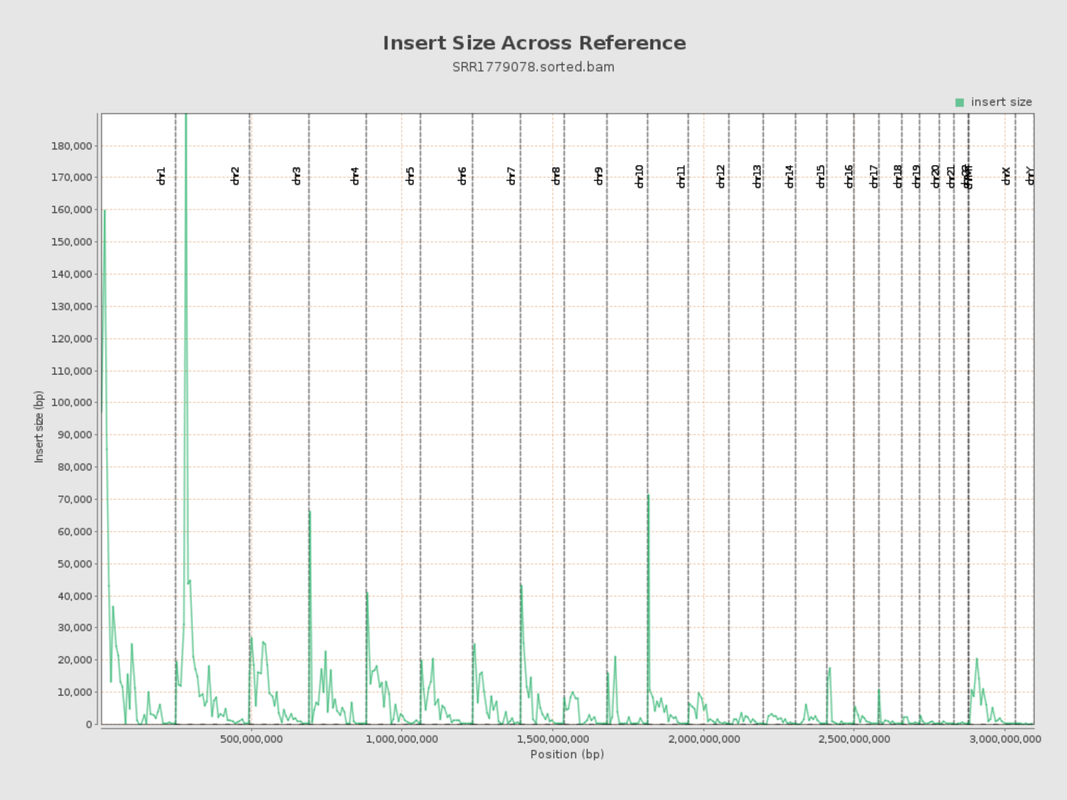
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram