Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 14:03:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779379.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_SRR1779379 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779379_1.fastq.gz SRR1779379_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 14:03:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779379.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,437,378
Mapped reads	15,136,962 / 98.05%
Unmapped reads	300,416 / 1.95%
Mapped paired reads	15,136,962 / 98.05%
Mapped reads, first in pair	7,616,566 / 49.34%
Mapped reads, second in pair	7,520,396 / 48.72%
Mapped reads, both in pair	15,018,646 / 97.29%
Mapped reads, singletons	118,316 / 0.77%
Secondary alignments	0
Supplementary alignments	63,329 / 0.41%
Read min/max/mean length	30 / 80 / 80.15
Duplicated reads (estimated)	638,972 / 4.14%
Duplication rate	3.97%
Clipped reads	709,048 / 4.59%

2.2. ACGT Content

Number/percentage of A's	360,718,186 / 29.99%
Number/percentage of C's	239,646,227 / 19.92%
Number/percentage of T's	358,826,217 / 29.83%
Number/percentage of G's	243,331,177 / 20.23%
Number/percentage of N's	264,955 / 0.02%

GC Percentage	40.15%

2.3. Coverage

Mean	0.3886
Standard Deviation	1.6347

2.4. Mapping Quality

Mean Mapping Quality	51.69

2.5. Insert size

Mean	63,217.97
Standard Deviation	2,376,535.14
P25/Median/P75	131 / 168 / 215

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	3,704,918
Insertions	105,154
Mapped reads with at least one insertion	0.69%
Deletions	120,576
Mapped reads with at least one deletion	0.79%
Homopolymer indels	47.37%

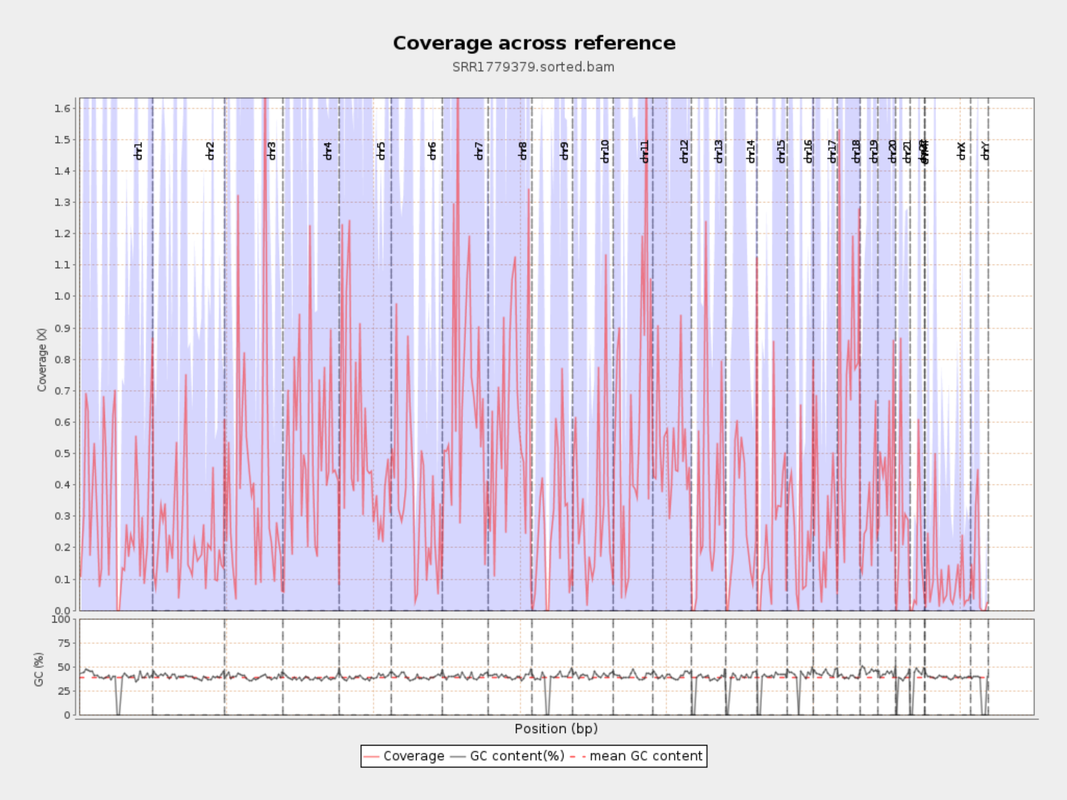
2.7. Chromosome stats

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

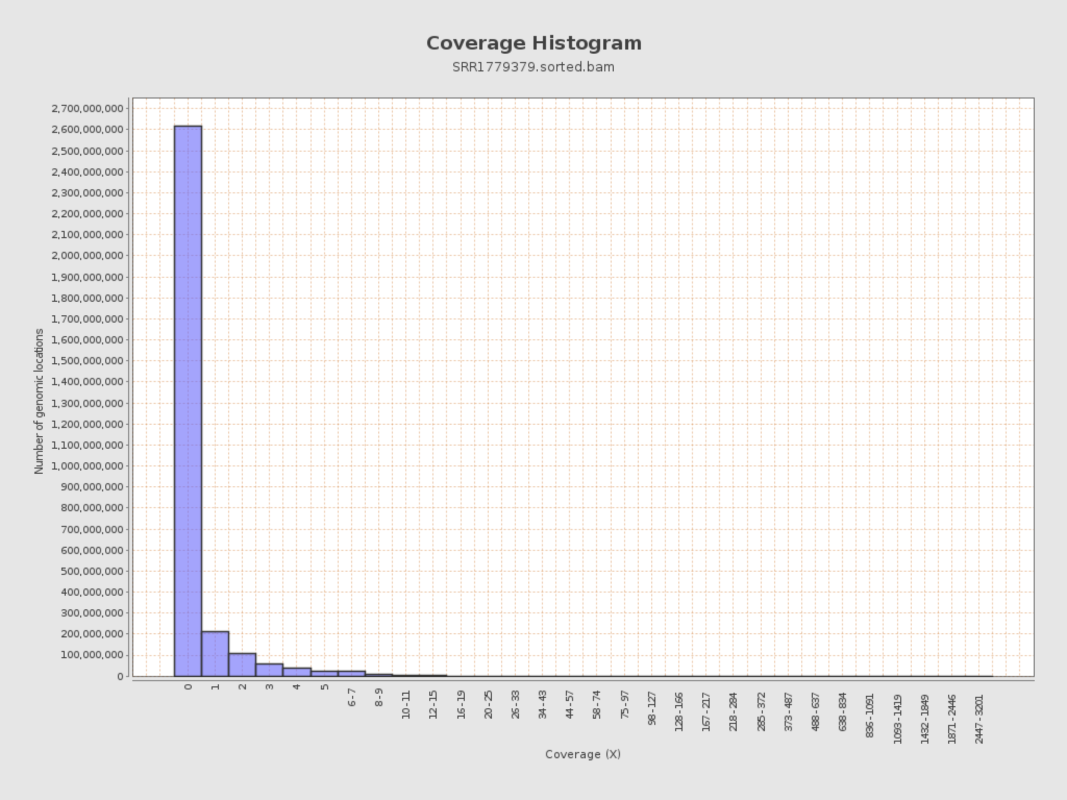
		bases	coverage	deviation
chr1	249250621	82072606	0.3293	3.4267
chr2	243199373	53648441	0.2206	0.9635
chr3	198022430	88024783	0.4445	1.4377
chr4	191154276	96733314	0.506	1.356
chr5	180915260	94510232	0.5224	1.4074
chr6	171115067	60855375	0.3556	1.1635
chr7	159138663	111677775	0.7018	2.161
chr8	146364022	87752932	0.5996	1.5881
chr9	141213431	36944157	0.2616	1.0542
chr10	135534747	45145332	0.3331	1.5559
chr11	135006516	81125375	0.6009	1.6415
chr12	133851895	68023522	0.5082	1.4365
chr13	115169878	42239386	0.3668	1.1903
chr14	107349540	30027896	0.2797	1.0819
chr15	102531392	26405663	0.2575	1.0258
chr16	90354753	22975222	0.2543	1.0449
chr17	81195210	21421318	0.2638	1.3185
chr18	78077248	62262027	0.7974	1.8631
chr19	59128983	18511285	0.3131	2.0506
chr20	63025520	28276099	0.4486	1.4059
chr21	48129895	14510530	0.3015	1.0838
chr22	51304566	6924027	0.135	0.7116
chrMT	16571	704	0.0425	0.2463
chrX	155270560	15560105	0.1002	0.6119

chrY	59373566	7411382	0.1248	0.6258

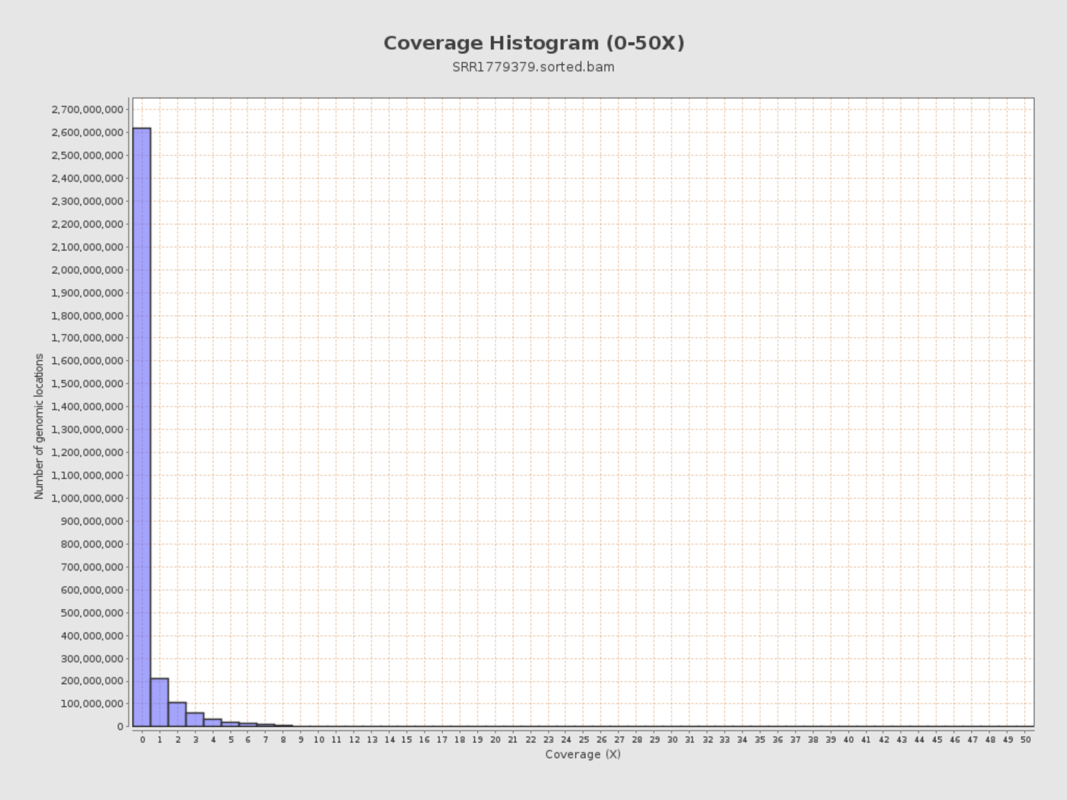
3. Results : Coverage across reference



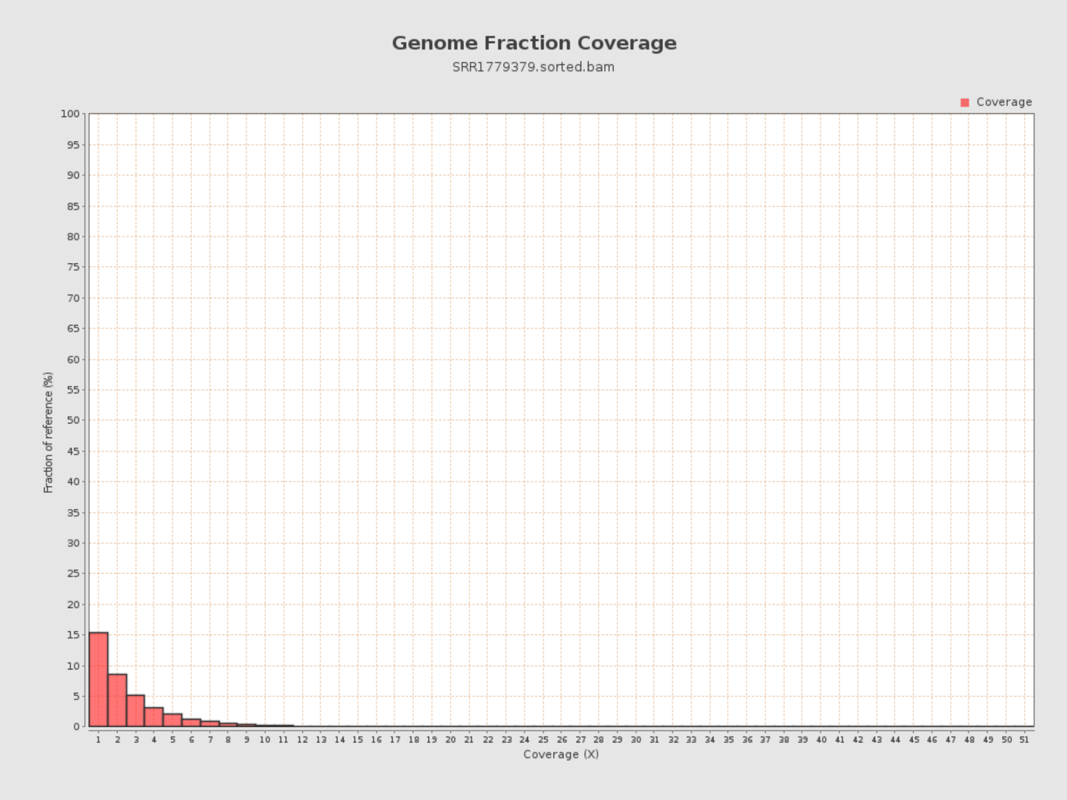
4. Results : Coverage Histogram



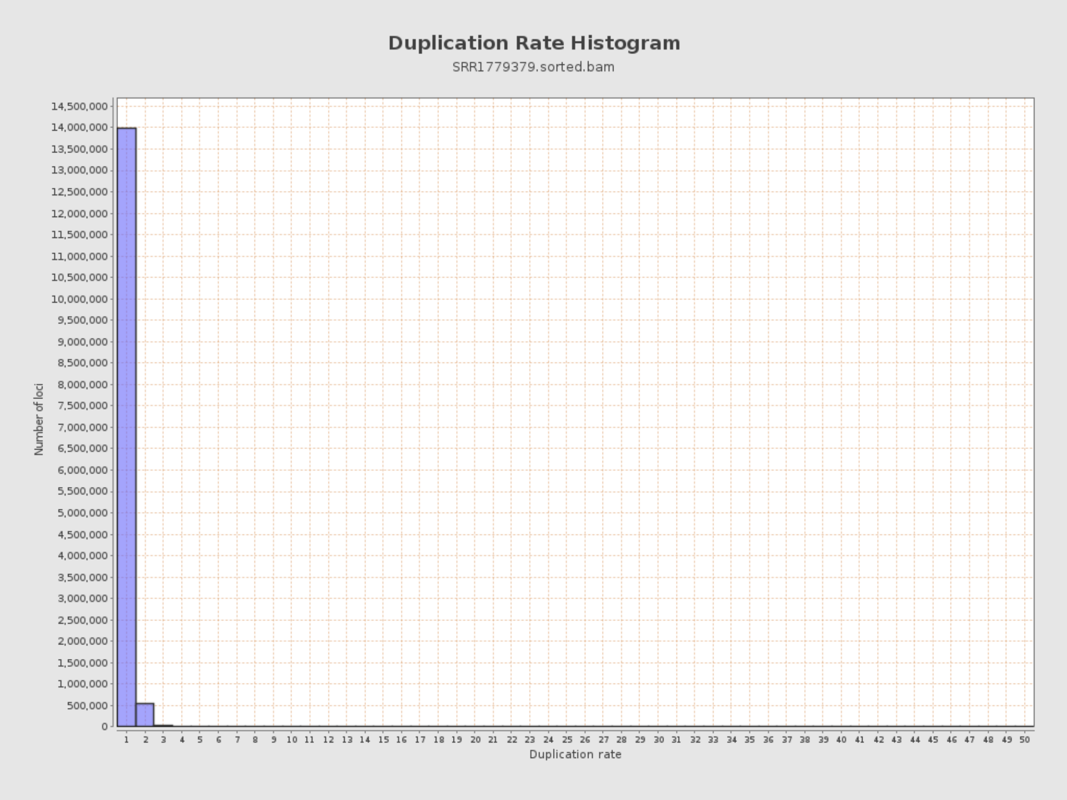
5. Results : Coverage Histogram (0-50X)



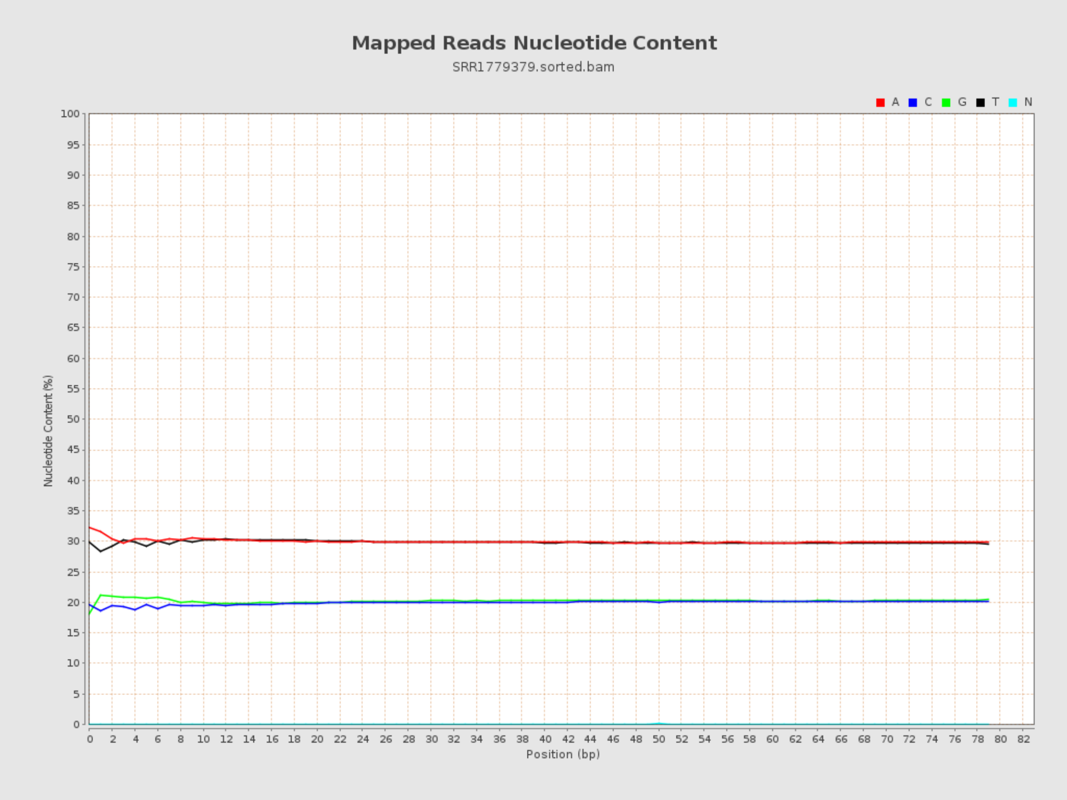
6. Results : Genome Fraction Coverage



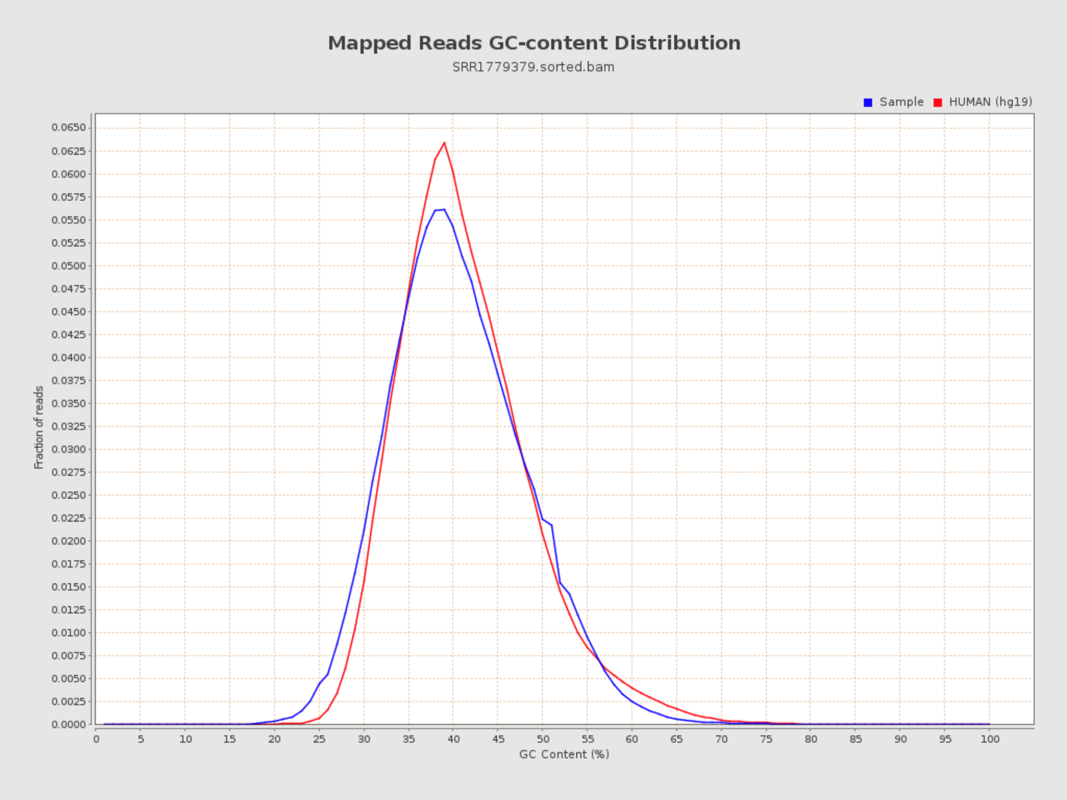
7. Results : Duplication Rate Histogram



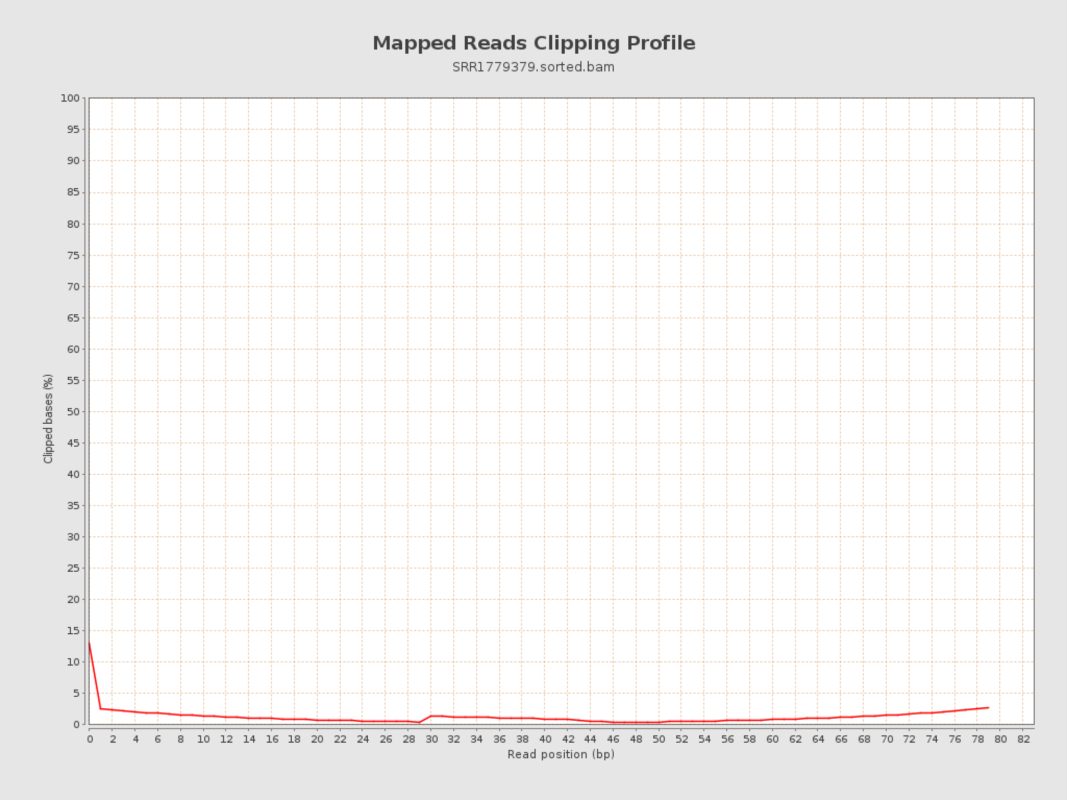
8. Results : Mapped Reads Nucleotide Content



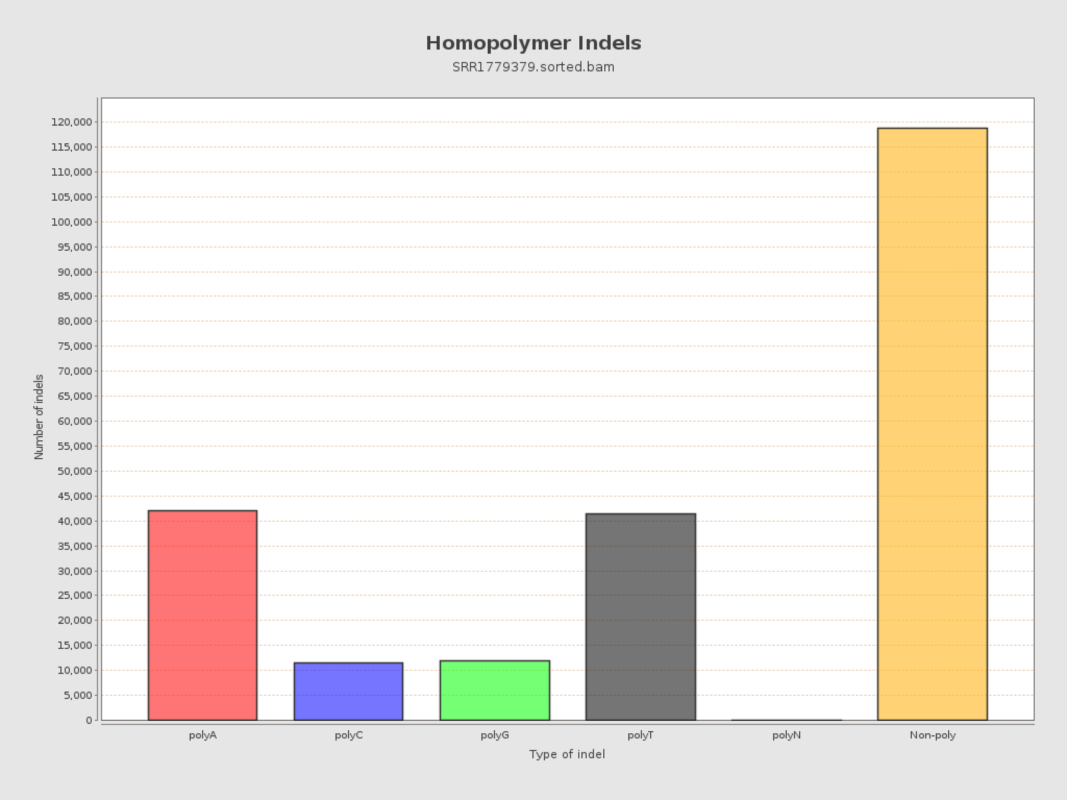
9. Results : Mapped Reads GC-content Distribution



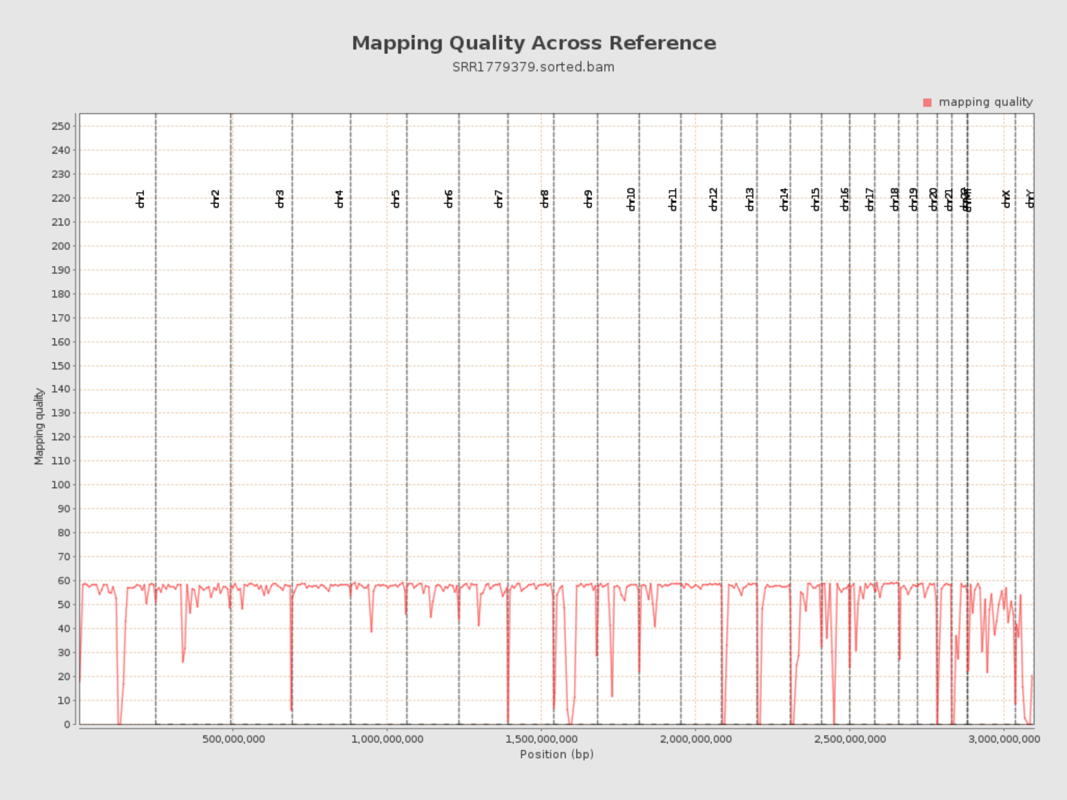
10. Results : Mapped Reads Clipping Profile



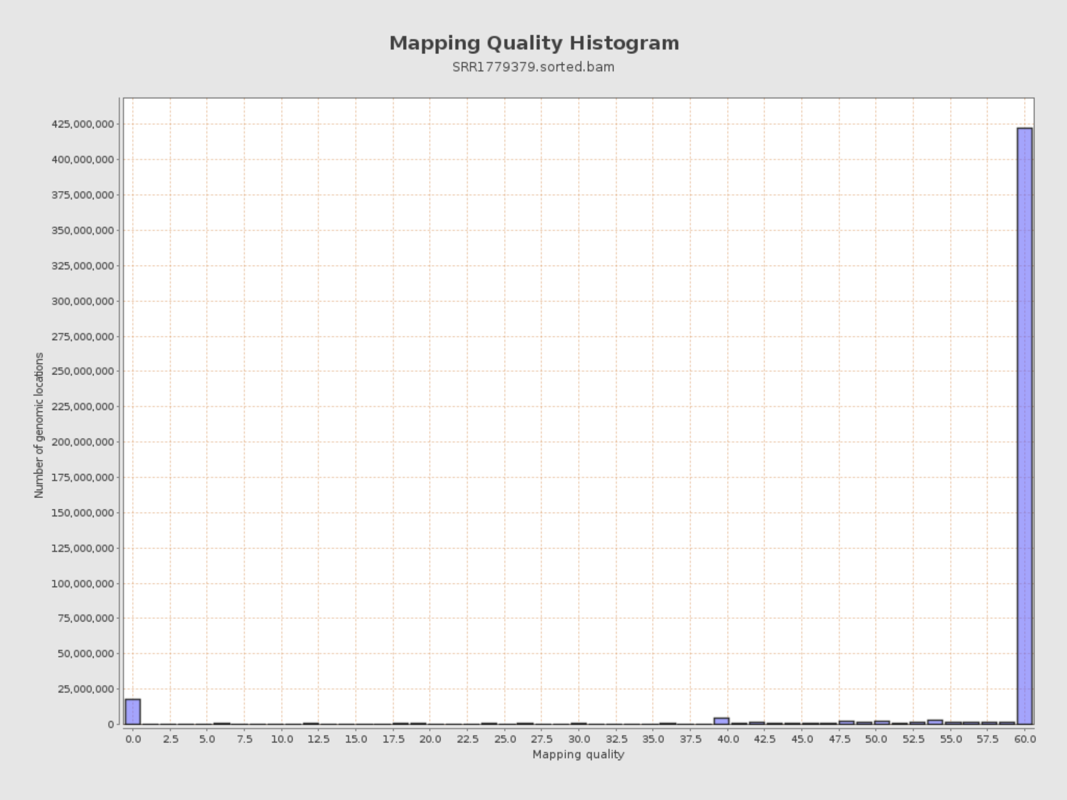
11. Results : Homopolymer Indels



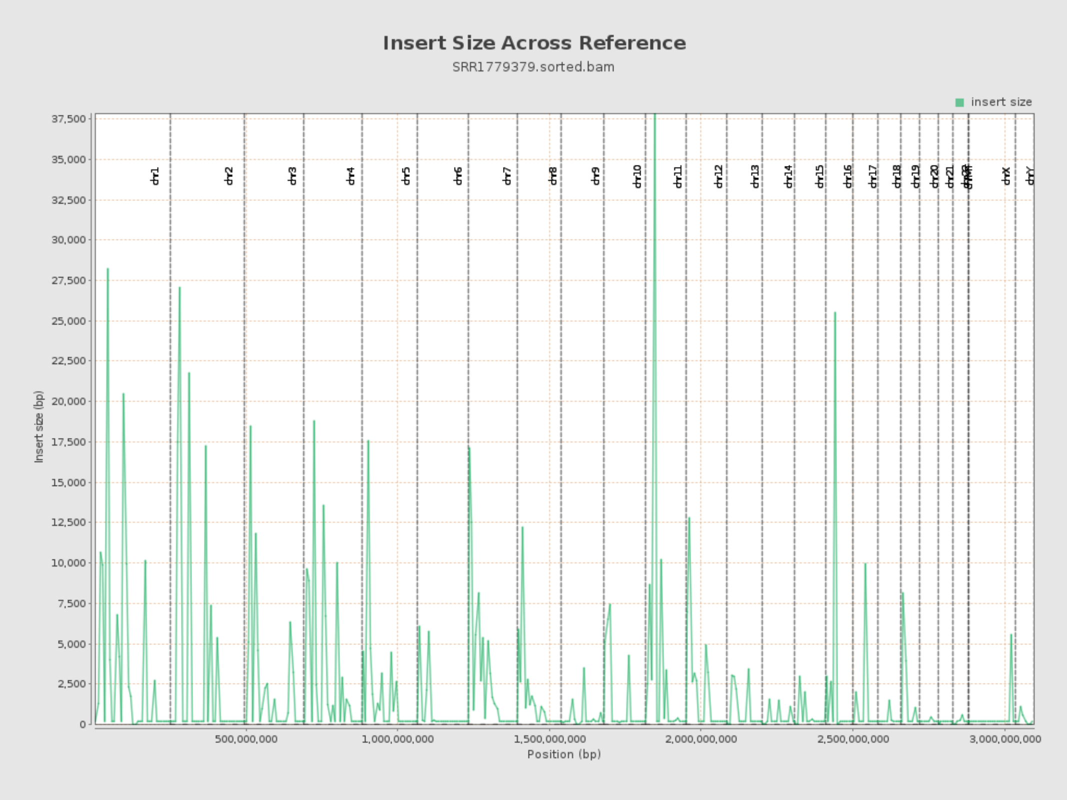
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram