Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 08:22:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779000.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_SRR1779000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779000_1.fastq.gz SRR1779000_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 08:22:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,601,106
Mapped reads	19,924,070 / 96.71%
Unmapped reads	677,036 / 3.29%
Mapped paired reads	19,924,070 / 96.71%
Mapped reads, first in pair	10,058,110 / 48.82%
Mapped reads, second in pair	9,865,960 / 47.89%
Mapped reads, both in pair	19,659,152 / 95.43%
Mapped reads, singletons	264,918 / 1.29%
Secondary alignments	0
Supplementary alignments	108,284 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	429,225 / 2.08%
Duplication rate	1.88%
Clipped reads	1,135,394 / 5.51%

2.2. ACGT Content

Number/percentage of A's	612,246,795 / 30.76%
Number/percentage of C's	380,772,853 / 19.13%
Number/percentage of T's	609,892,986 / 30.64%
Number/percentage of G's	386,842,030 / 19.44%
Number/percentage of N's	673,795 / 0.03%

GC Percentage	38.57%

2.3. Coverage

Mean	0.6431
Standard Deviation	1.5791

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	77,170.59
Standard Deviation	2,659,316.9
P25/Median/P75	214 / 278 / 351

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	9,603,225
Insertions	175,704
Mapped reads with at least one insertion	0.87%
Deletions	216,869
Mapped reads with at least one deletion	1.07%
Homopolymer indels	47.31%

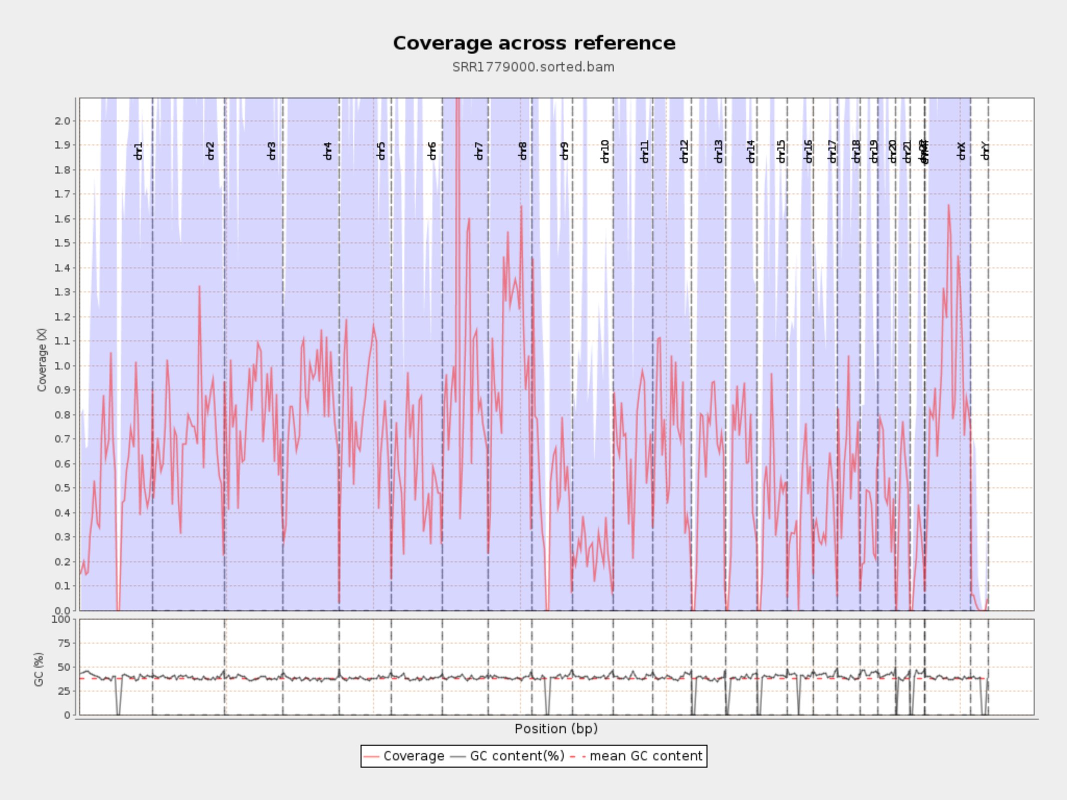
2.7. Chromosome stats

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

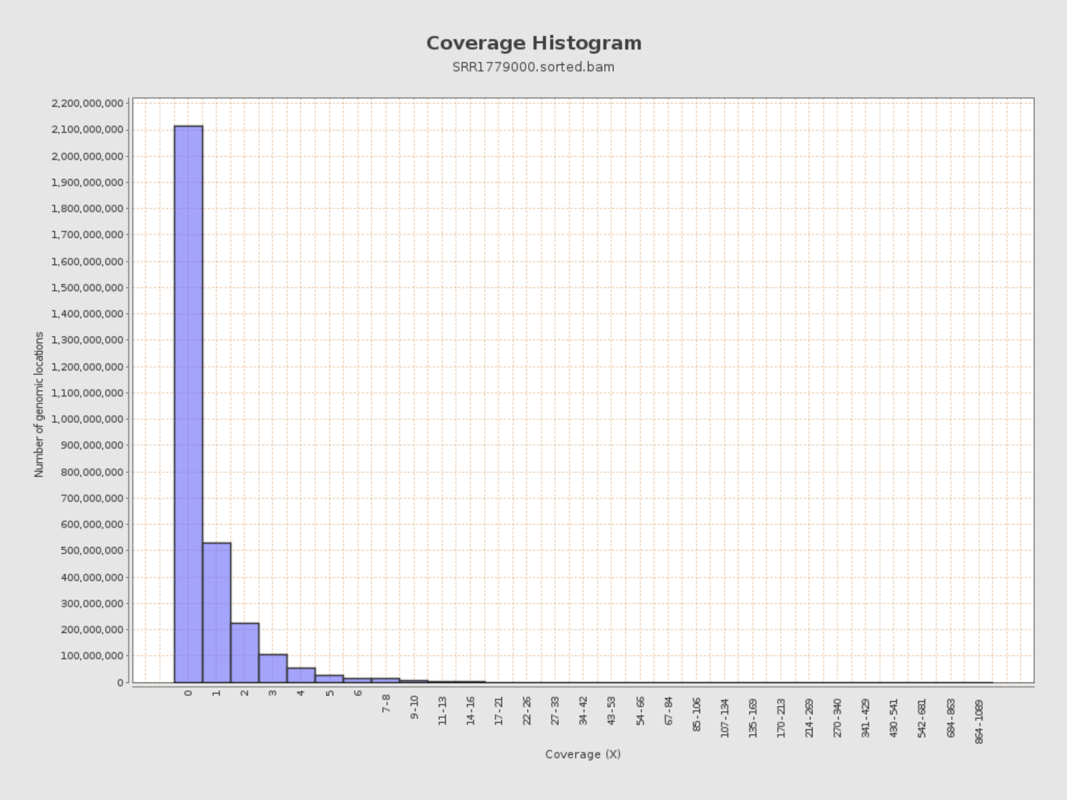
		bases	coverage	deviation
chr1	249250621	126196850	0.5063	1.4929
chr2	243199373	172573878	0.7096	1.5088
chr3	198022430	156460155	0.7901	1.4403
chr4	191154276	162500894	0.8501	1.4914
chr5	180915260	140828082	0.7784	1.394
chr6	171115067	97448657	0.5695	1.2364
chr7	159138663	164752126	1.0353	3.395
chr8	146364022	159495744	1.0897	1.7948
chr9	141213431	71360261	0.5053	1.2678
chr10	135534747	32770091	0.2418	1.7157
chr11	135006516	90691823	0.6718	1.3338
chr12	133851895	93225320	0.6965	1.4486
chr13	115169878	69587683	0.6042	1.2623
chr14	107349540	61219178	0.5703	1.229
chr15	102531392	44179010	0.4309	1.1071
chr16	90354753	34275198	0.3793	1.0094
chr17	81195210	29322508	0.3611	1
chr18	78077248	49051492	0.6282	1.2288
chr19	59128983	18698399	0.3162	1.0806
chr20	63025520	32311369	0.5127	1.2708
chr21	48129895	22972506	0.4773	1.1252
chr22	51304566	9907982	0.1931	0.6883
chrMT	16571	1215	0.0733	0.3154
chrX	155270560	149659500	0.9639	1.8026

chrY	59373566	1422644	0.024	0.3685

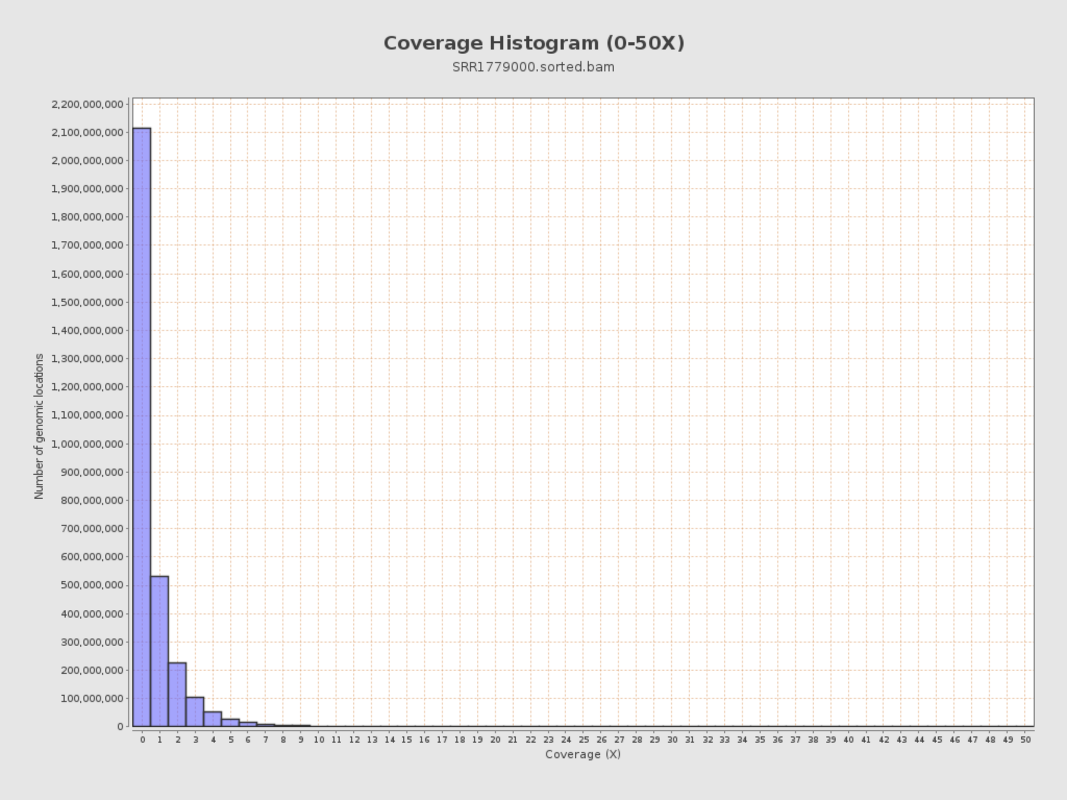
3. Results : Coverage across reference



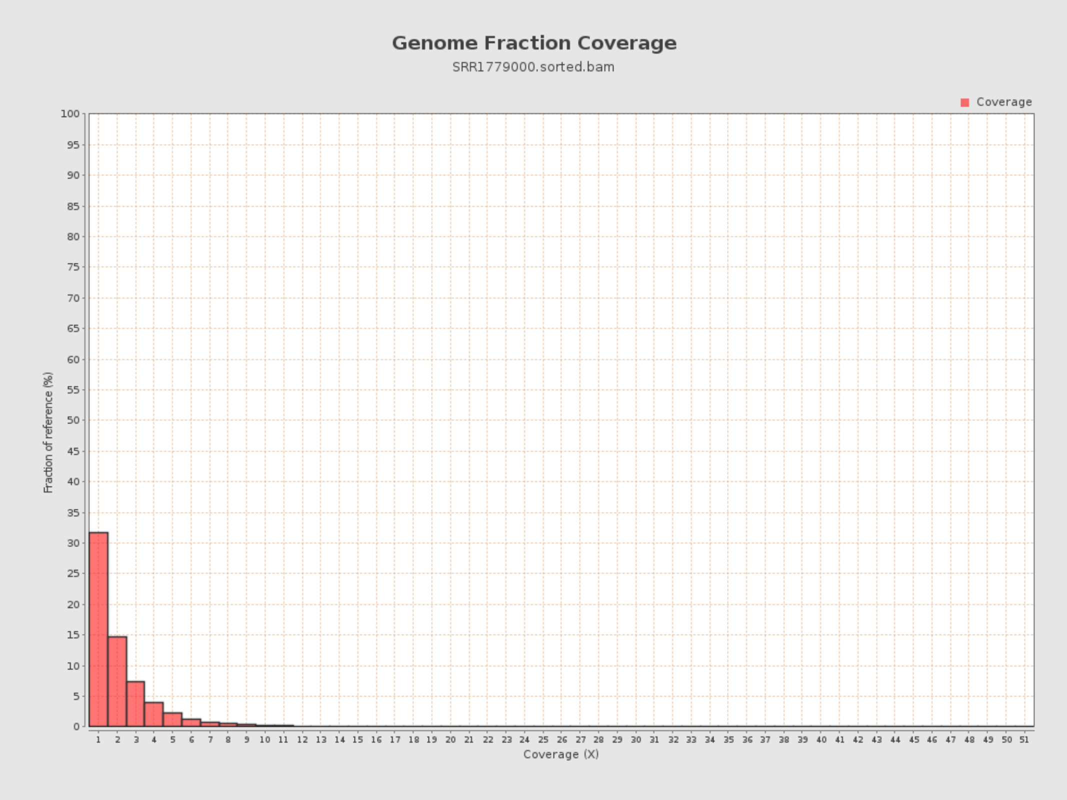
4. Results : Coverage Histogram



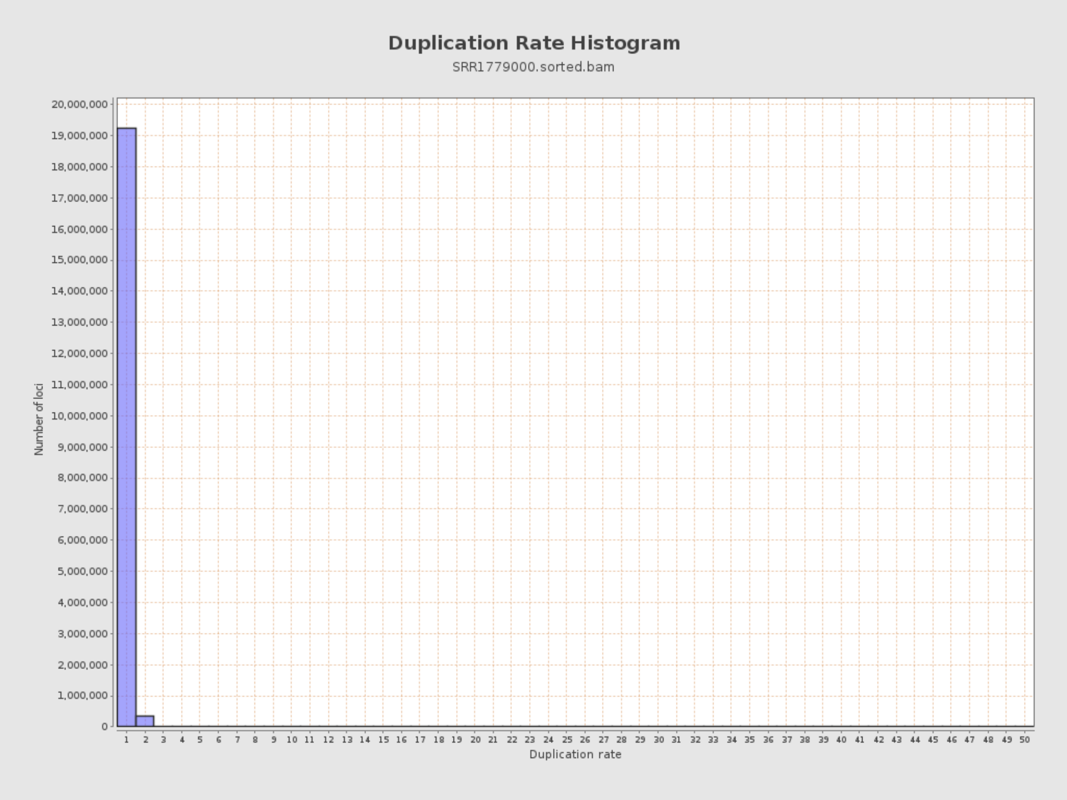
5. Results : Coverage Histogram (0-50X)



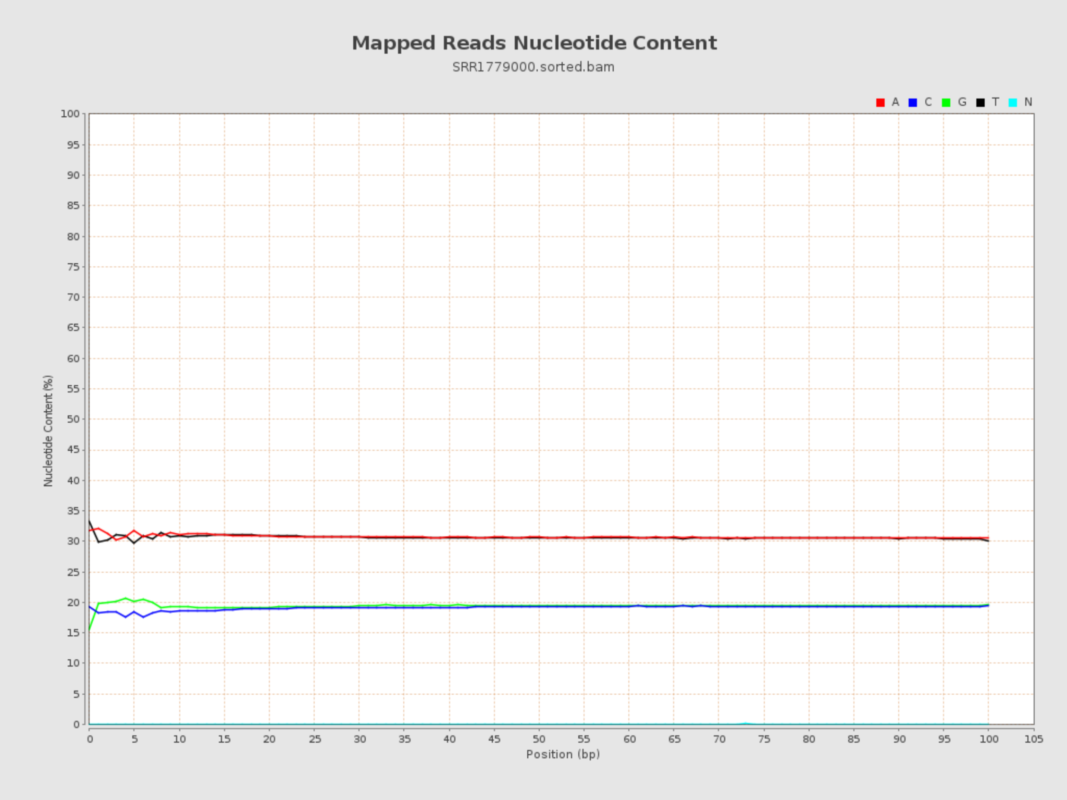
6. Results : Genome Fraction Coverage



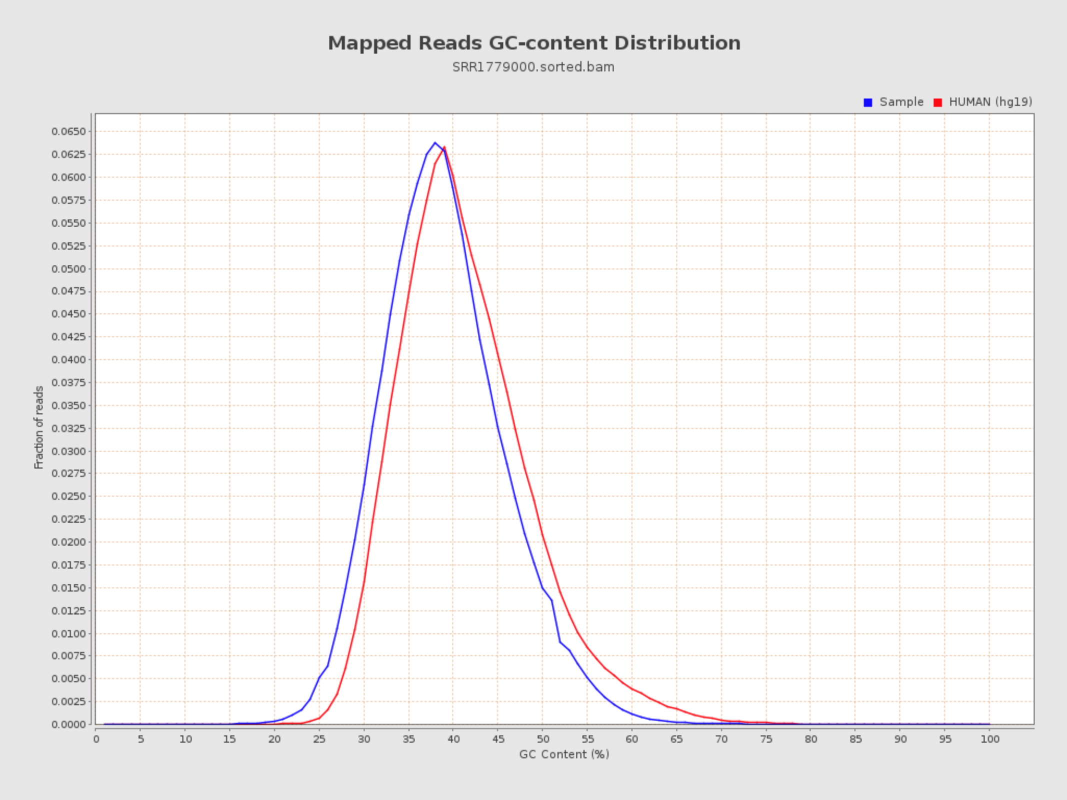
7. Results : Duplication Rate Histogram



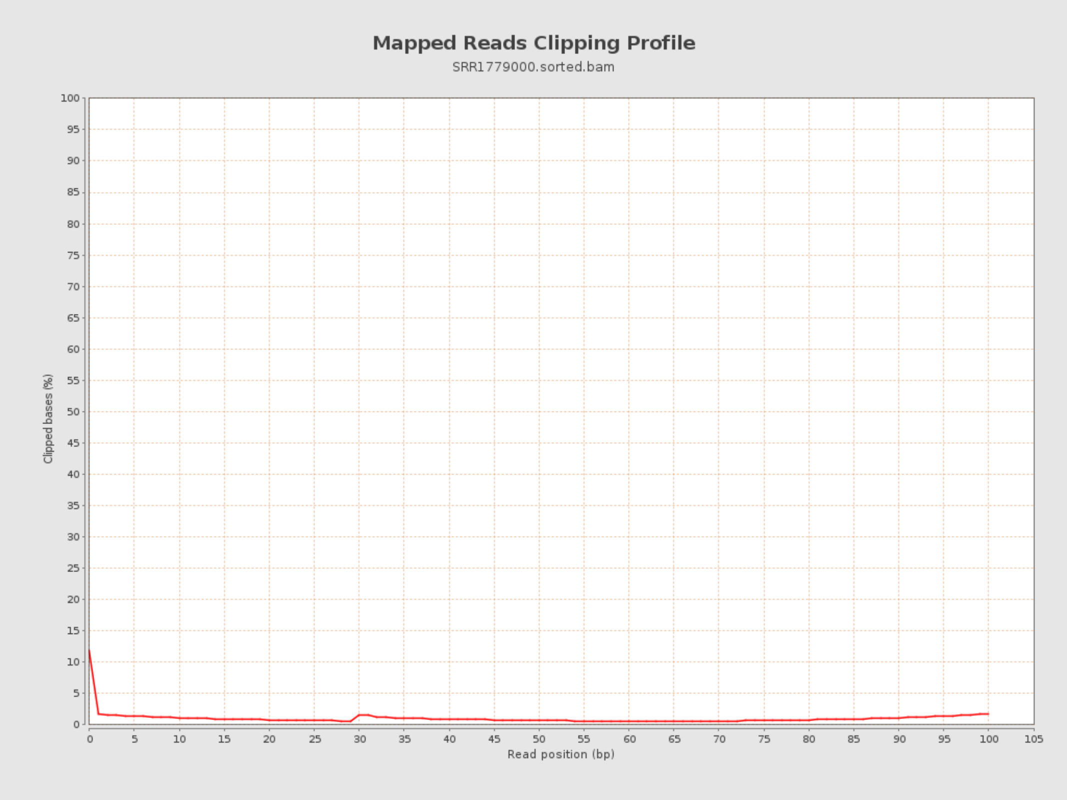
8. Results : Mapped Reads Nucleotide Content



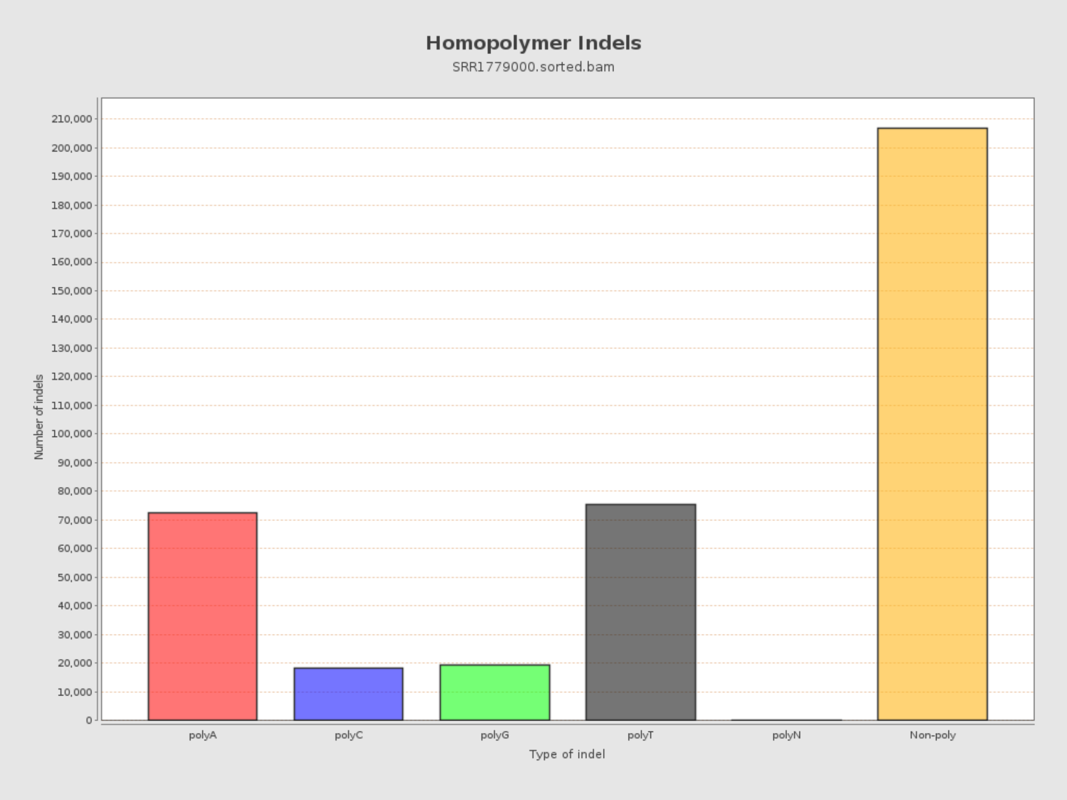
9. Results : Mapped Reads GC-content Distribution



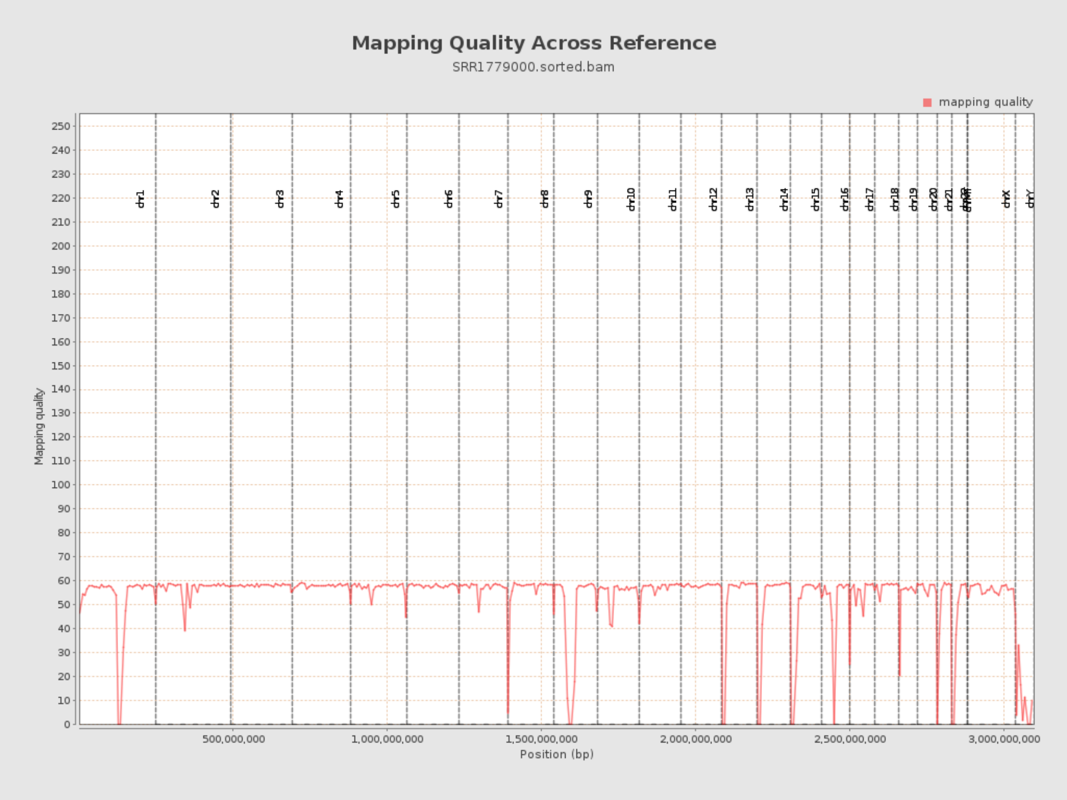
10. Results : Mapped Reads Clipping Profile



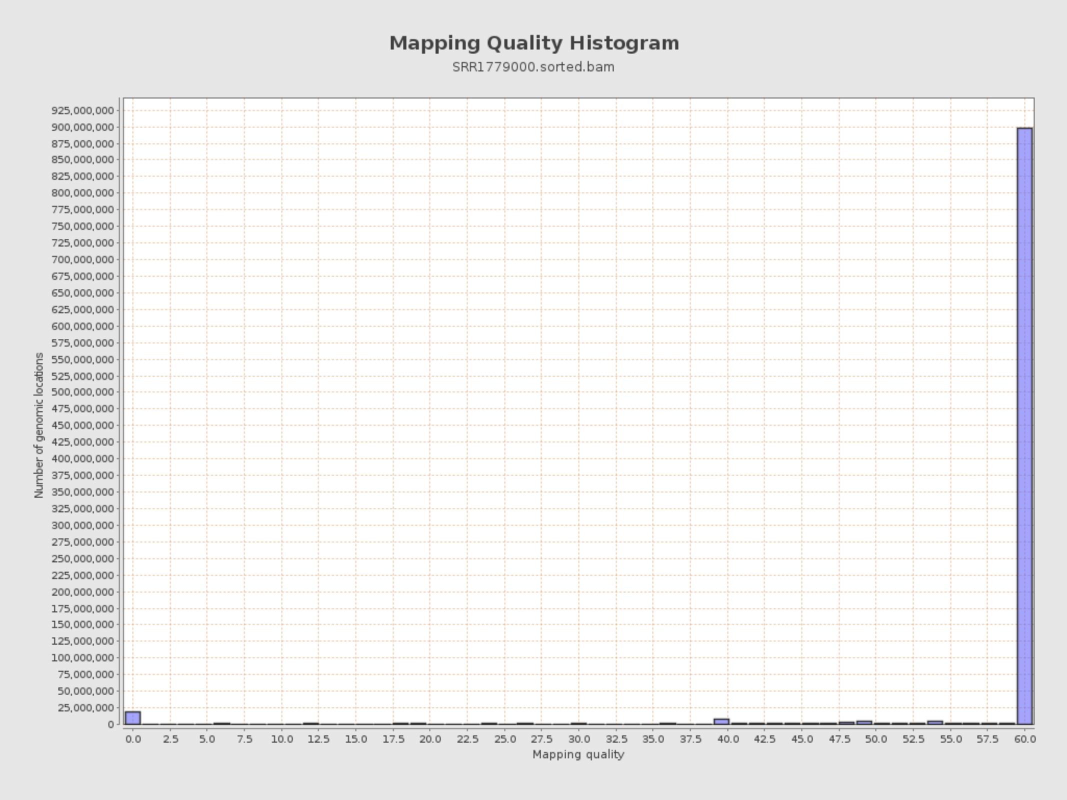
11. Results : Homopolymer Indels



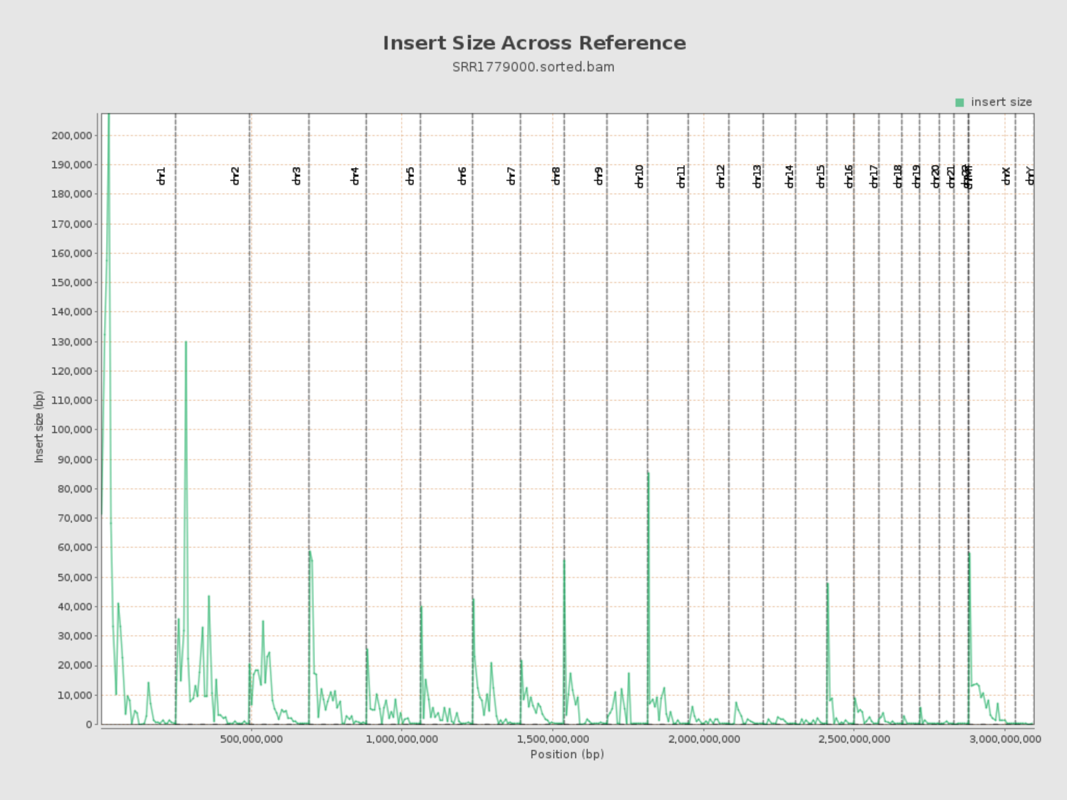
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram