Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 00:47:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779294.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_SRR1779294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779294_1.fastq.gz SRR1779294_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 00:47:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,007,720
Mapped reads	12,617,554 / 97%
Unmapped reads	390,166 / 3%
Mapped paired reads	12,617,554 / 97%
Mapped reads, first in pair	6,373,206 / 49%
Mapped reads, second in pair	6,244,348 / 48%
Mapped reads, both in pair	12,473,088 / 95.89%
Mapped reads, singletons	144,466 / 1.11%
Secondary alignments	0
Supplementary alignments	30,326 / 0.23%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	168,867 / 1.3%
Duplication rate	1.24%
Clipped reads	415,137 / 3.19%

2.2. ACGT Content

Number/percentage of A's	305,733,039 / 30.45%
Number/percentage of C's	195,093,209 / 19.43%
Number/percentage of T's	305,170,916 / 30.4%
Number/percentage of G's	197,825,290 / 19.7%
Number/percentage of N's	190,135 / 0.02%

GC Percentage	39.13%

2.3. Coverage

Mean	0.3244
Standard Deviation	0.9231

2.4. Mapping Quality

Mean Mapping Quality	52.9

2.5. Insert size

Mean	44,865.37
Standard Deviation	1,964,831.63
P25/Median/P75	150 / 198 / 266

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,924,991
Insertions	73,067
Mapped reads with at least one insertion	0.57%
Deletions	92,665
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.62%

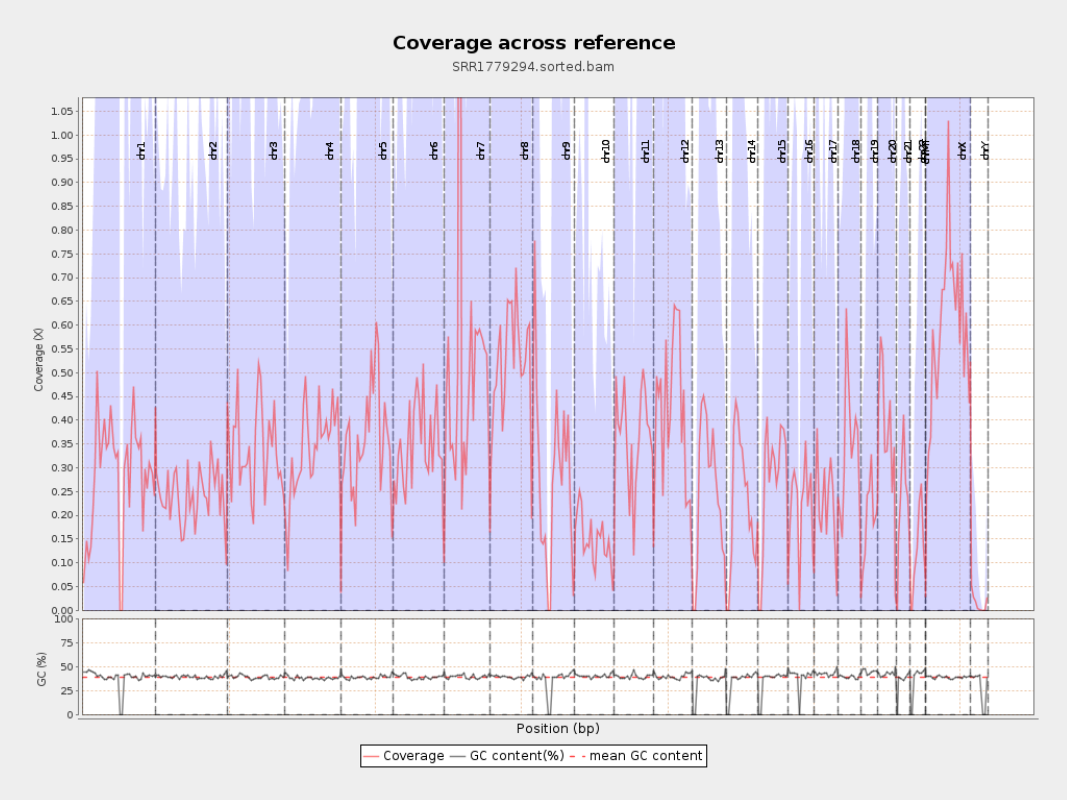
2.7. Chromosome stats

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

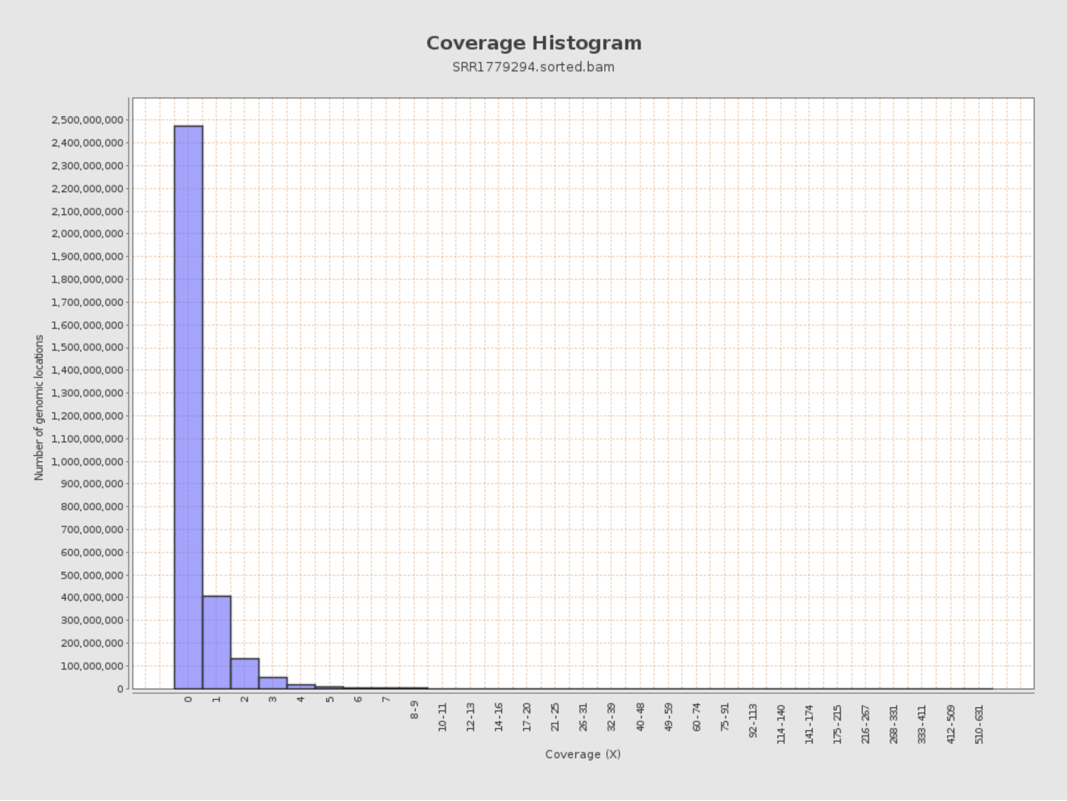
		bases	coverage	deviation
chr1	249250621	70243096	0.2818	0.9524
chr2	243199373	58509076	0.2406	0.6572
chr3	198022430	67019217	0.3384	0.8069
chr4	191154276	64639218	0.3382	0.8007
chr5	180915260	64320594	0.3555	0.8111
chr6	171115067	59858585	0.3498	0.8366
chr7	159138663	85681002	0.5384	1.9574
chr8	146364022	76422947	0.5221	1.0251
chr9	141213431	39625720	0.2806	0.7853
chr10	135534747	20343664	0.1501	0.8454
chr11	135006516	49202505	0.3644	0.8542
chr12	133851895	55701246	0.4161	0.9021
chr13	115169878	28757300	0.2497	0.6892
chr14	107349540	24756565	0.2306	0.671
chr15	102531392	27696631	0.2701	0.7452
chr16	90354753	19303654	0.2136	0.6189
chr17	81195210	18697600	0.2303	0.6702
chr18	78077248	26937154	0.345	0.8264
chr19	59128983	11406910	0.1929	0.6884
chr20	63025520	24411512	0.3873	0.9162
chr21	48129895	10657293	0.2214	0.6408
chr22	51304566	6602659	0.1287	0.494
chrMT	16571	455	0.0275	0.2029
chrX	155270560	92520081	0.5959	1.181

chrY	59373566	889590	0.015	0.1718

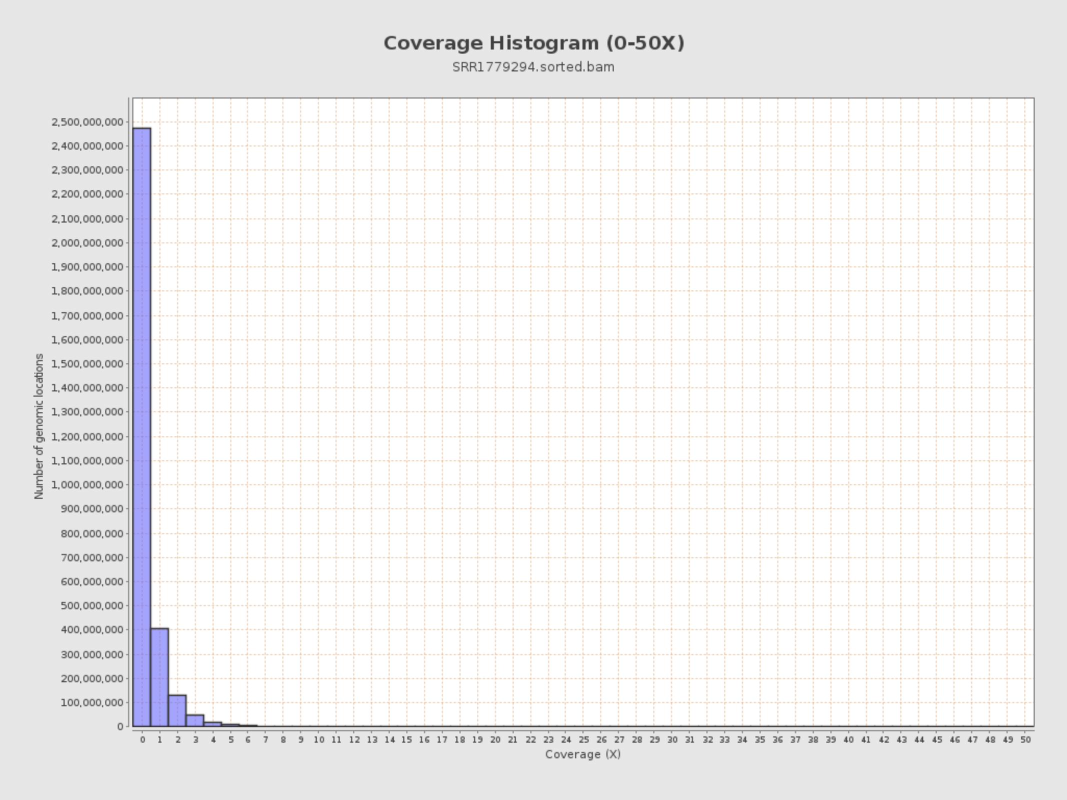
3. Results : Coverage across reference



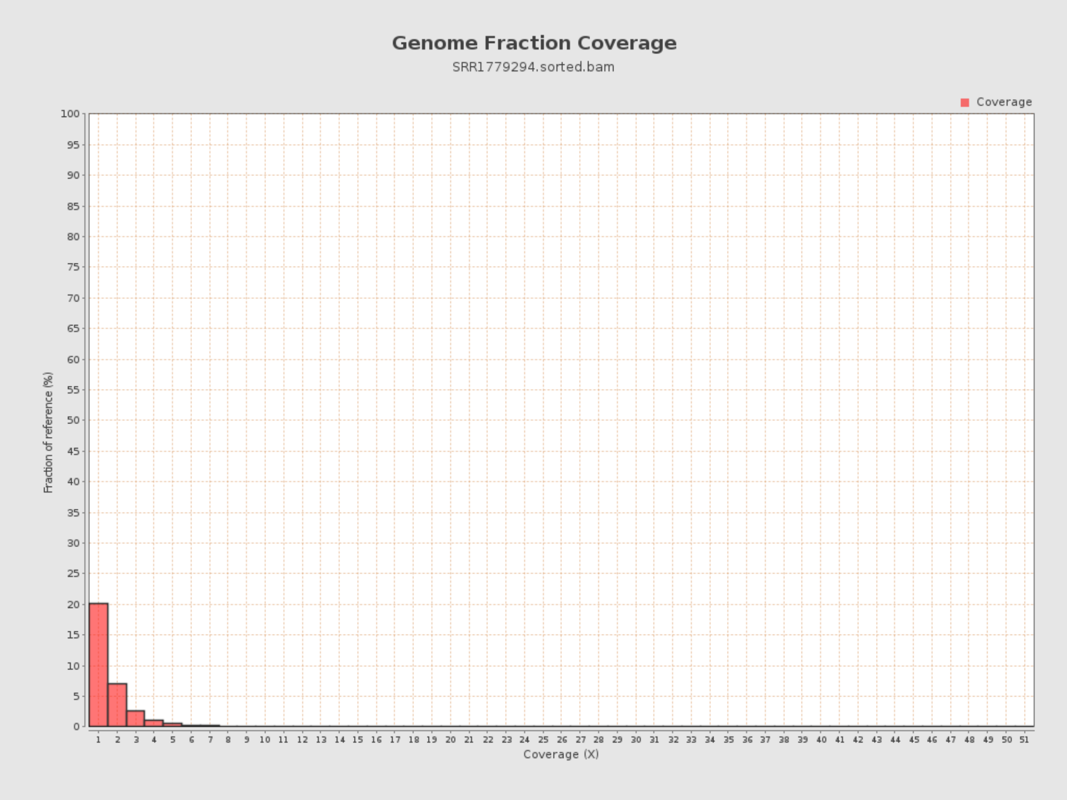
4. Results : Coverage Histogram



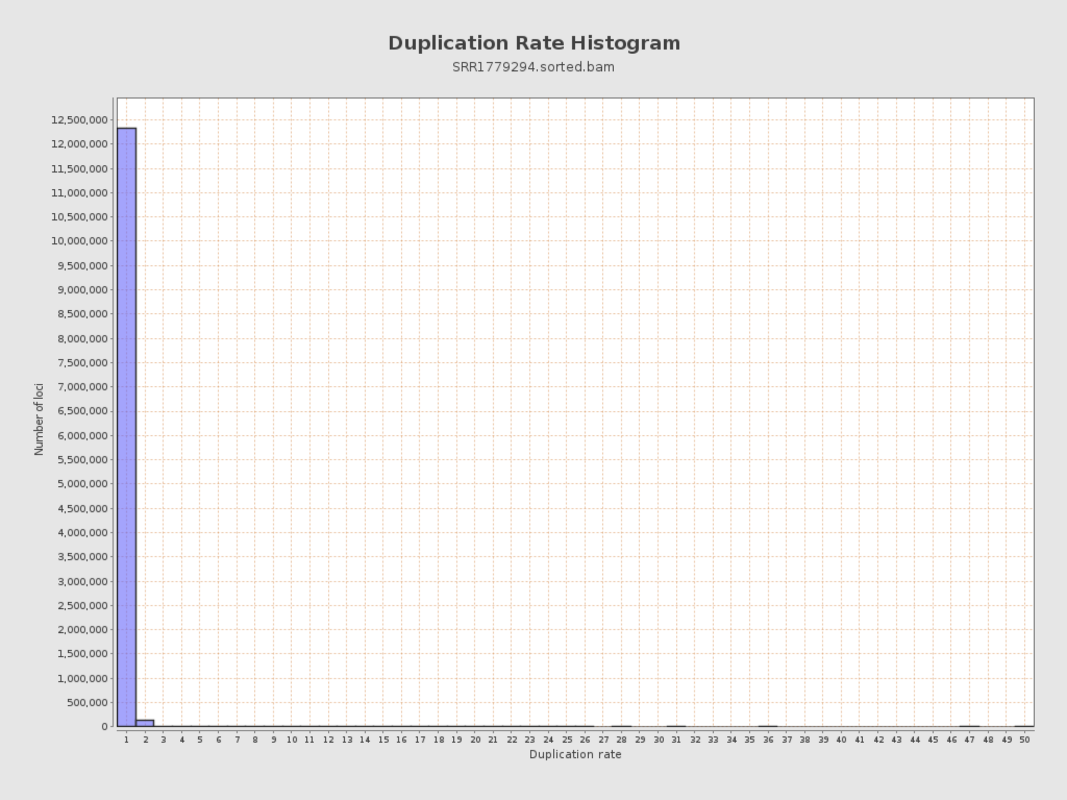
5. Results : Coverage Histogram (0-50X)



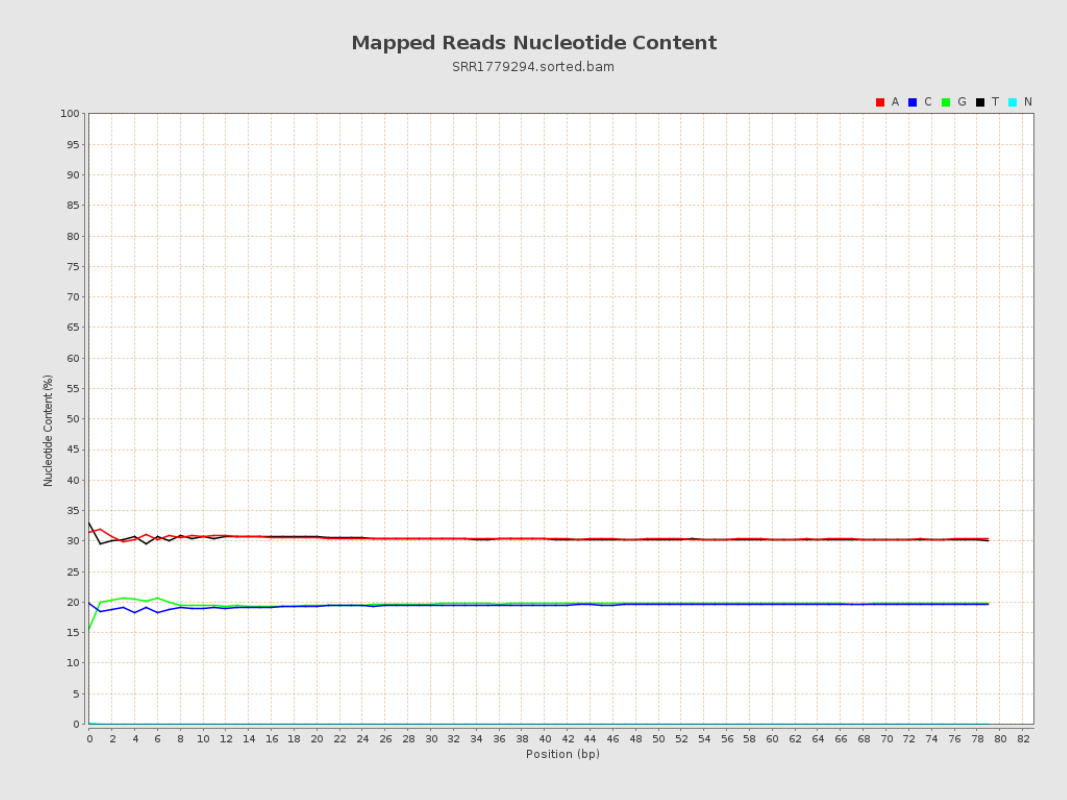
6. Results : Genome Fraction Coverage



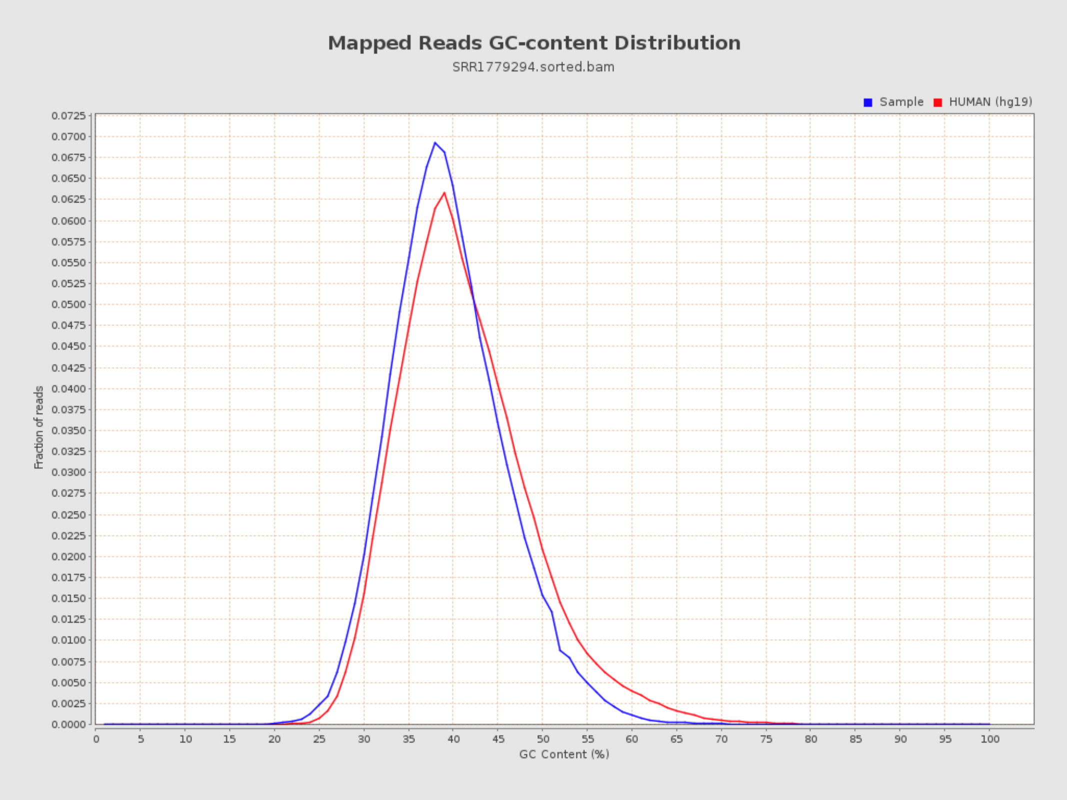
7. Results : Duplication Rate Histogram



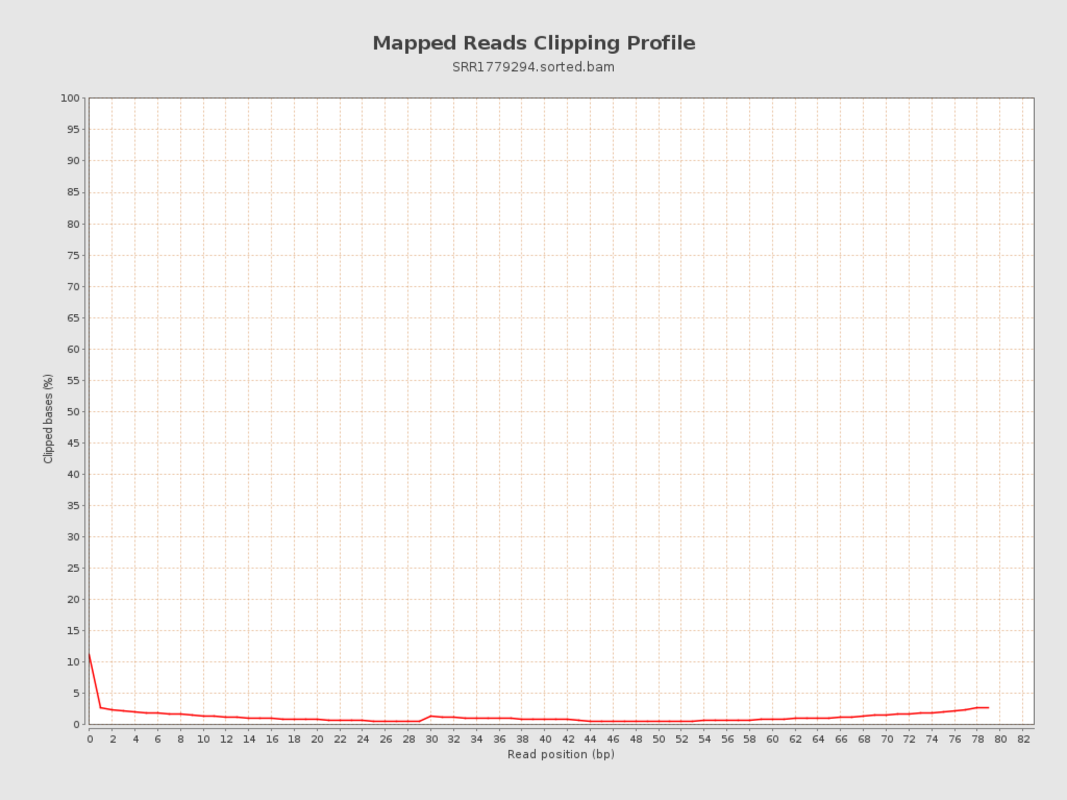
8. Results : Mapped Reads Nucleotide Content



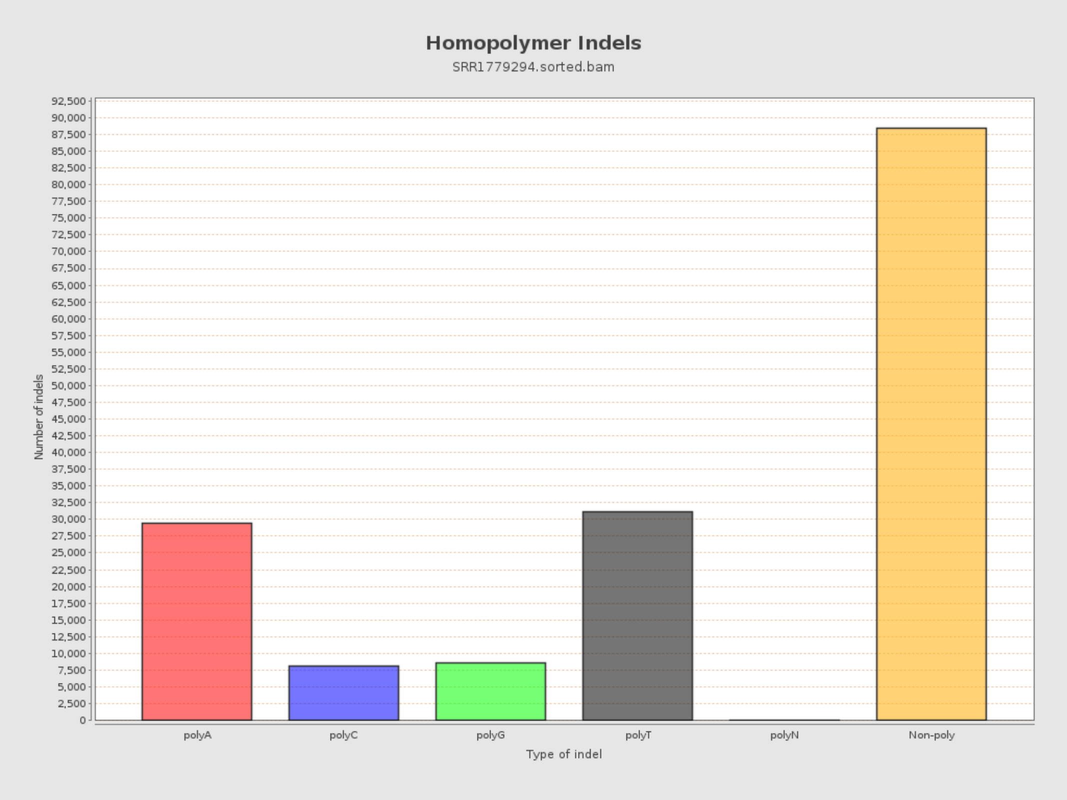
9. Results : Mapped Reads GC-content Distribution



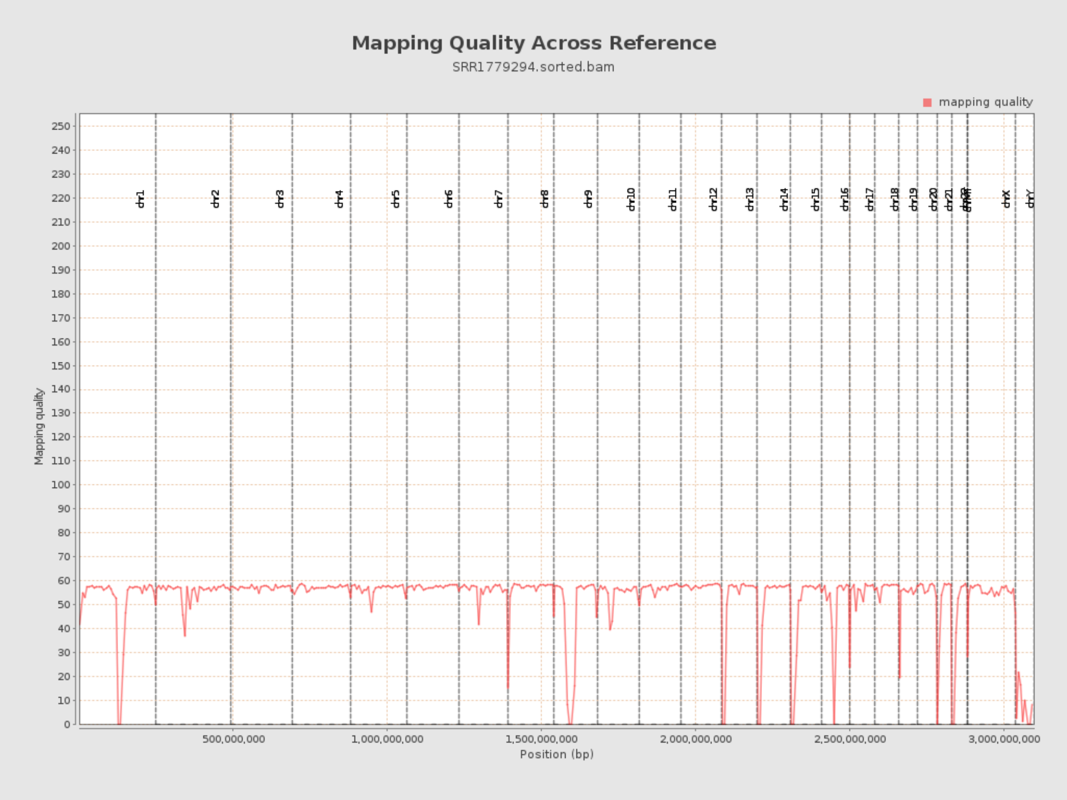
10. Results : Mapped Reads Clipping Profile



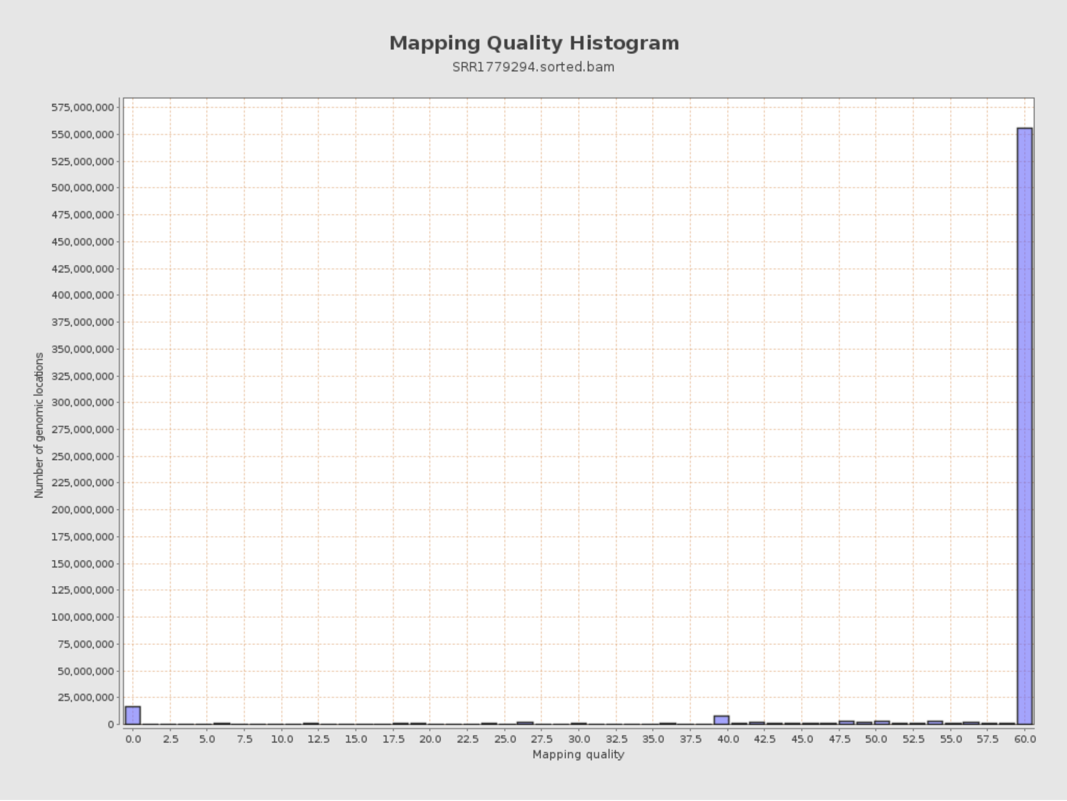
11. Results : Homopolymer Indels



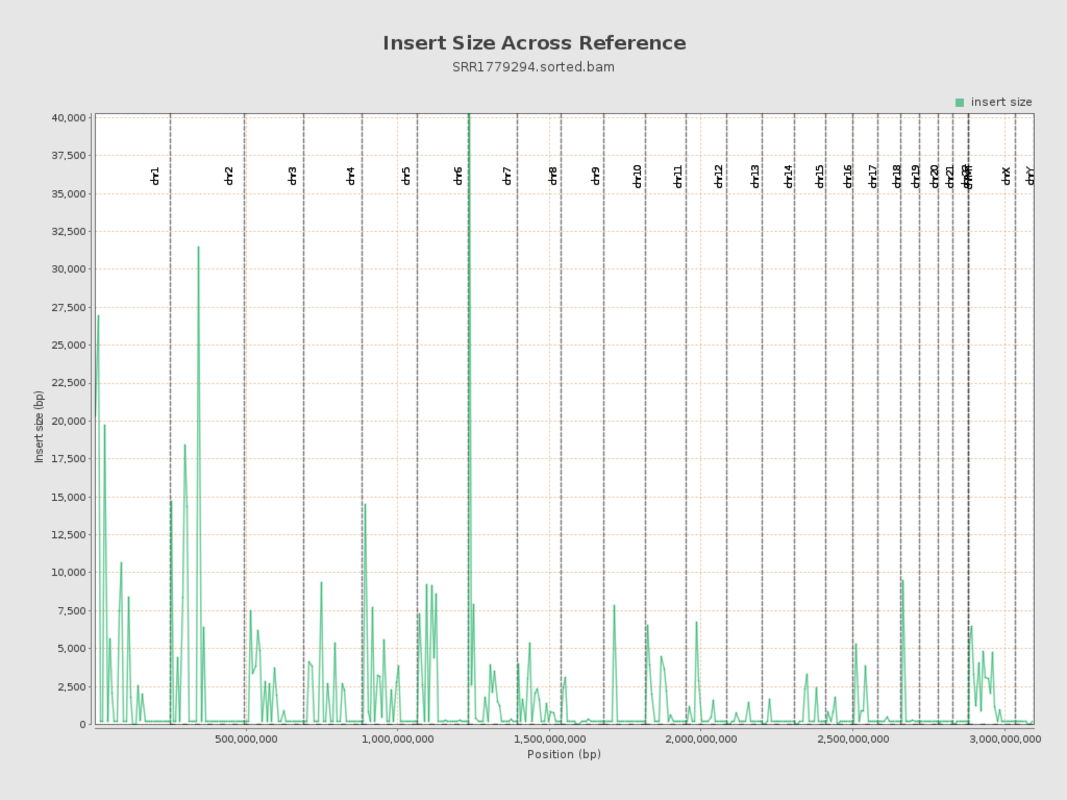
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram