Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 16:57:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779214.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_SRR1779214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779214_1.fastq.gz SRR1779214_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 16:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,850,168
Mapped reads	6,627,671 / 96.75%
Unmapped reads	222,497 / 3.25%
Mapped paired reads	6,627,671 / 96.75%
Mapped reads, first in pair	3,347,914 / 48.87%
Mapped reads, second in pair	3,279,757 / 47.88%
Mapped reads, both in pair	6,549,698 / 95.61%
Mapped reads, singletons	77,973 / 1.14%
Secondary alignments	0
Supplementary alignments	15,249 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	47,798 / 0.7%
Duplication rate	0.68%
Clipped reads	231,419 / 3.38%

2.2. ACGT Content

Number/percentage of A's	162,225,085 / 30.78%
Number/percentage of C's	100,547,267 / 19.08%
Number/percentage of T's	161,791,254 / 30.69%
Number/percentage of G's	102,447,970 / 19.44%
Number/percentage of N's	98,233 / 0.02%

GC Percentage	38.51%

2.3. Coverage

Mean	0.1703
Standard Deviation	0.5404

2.4. Mapping Quality

Mean Mapping Quality	52.96

2.5. Insert size

Mean	58,240.47
Standard Deviation	2,264,526.09
P25/Median/P75	207 / 269 / 338

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	2,266,092
Insertions	39,912
Mapped reads with at least one insertion	0.6%
Deletions	50,854
Mapped reads with at least one deletion	0.76%
Homopolymer indels	47.43%

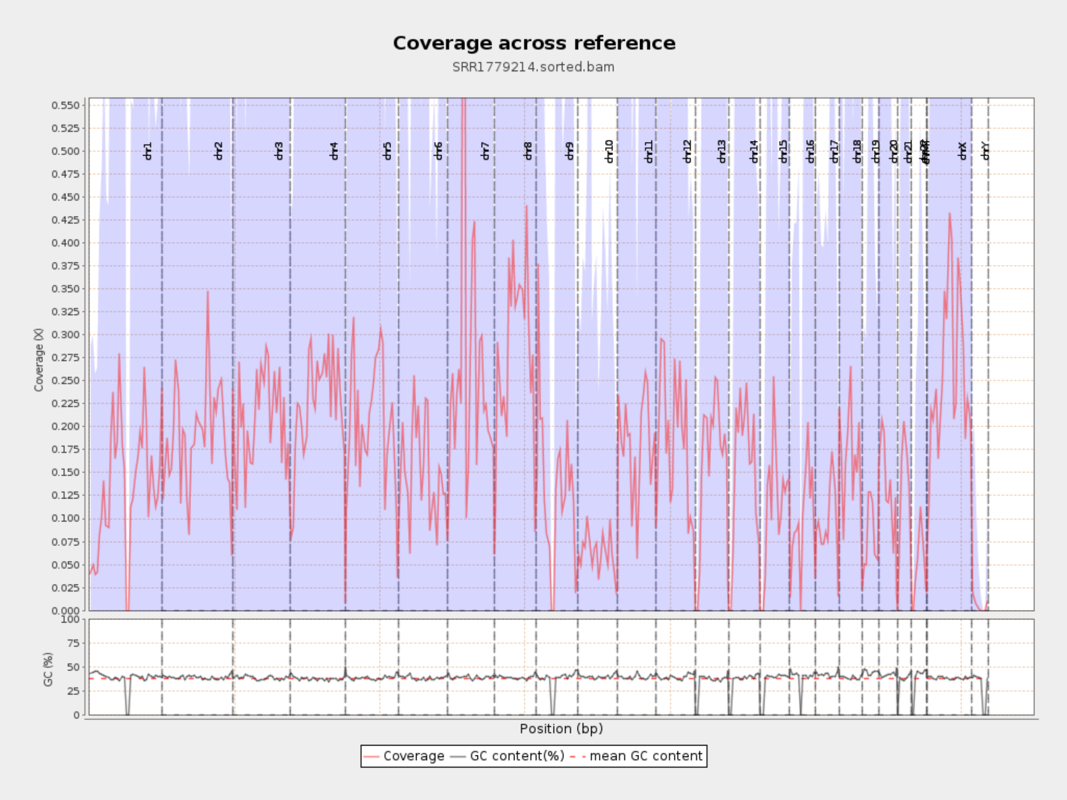
2.7. Chromosome stats

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

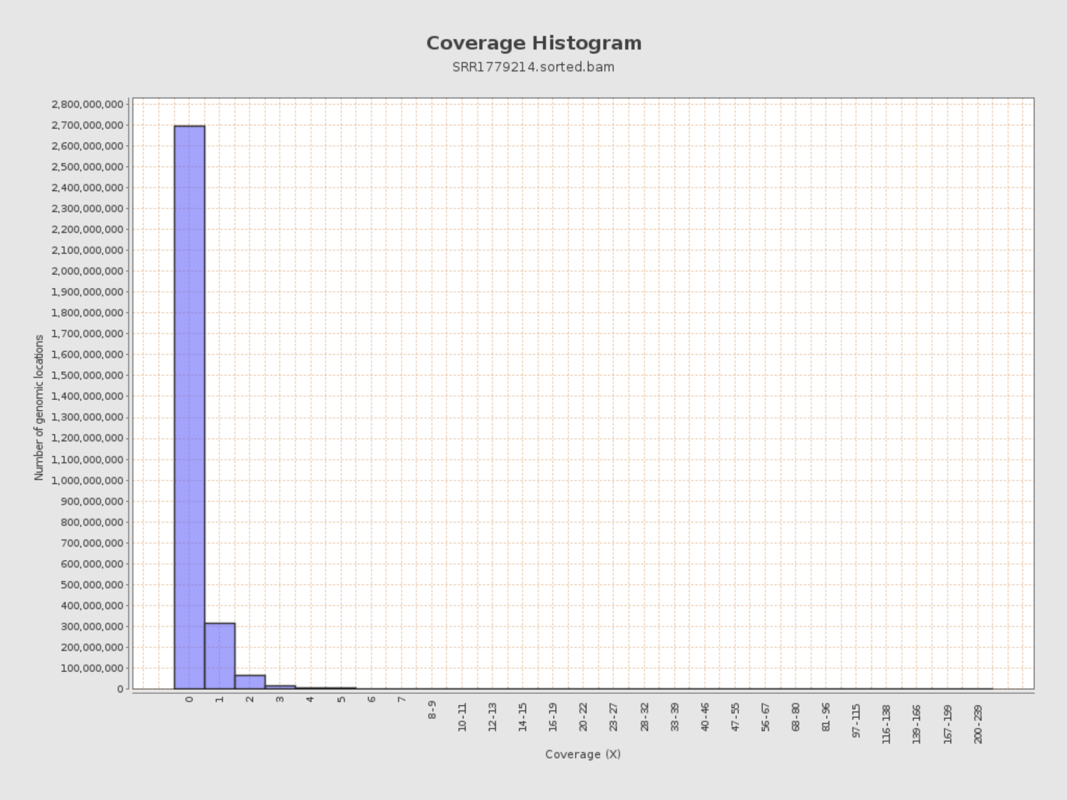
		bases	**coverage**	**deviation**
chr1	249250621	33392932	0.134	0.4949
chr2	243199373	45673686	0.1878	0.5163
chr3	198022430	41418676	0.2092	0.5488
chr4	191154276	43240400	0.2262	0.5681
chr5	180915260	37219797	0.2057	0.5375
chr6	171115067	25844061	0.151	0.4673
chr7	159138663	43467724	0.2731	0.9933
chr8	146364022	42108069	0.2877	0.6613
chr9	141213431	18806892	0.1332	0.4563
chr10	135534747	8712134	0.0643	0.4385
chr11	135006516	24137422	0.1788	0.5094
chr12	133851895	24717511	0.1847	0.5221
chr13	115169878	18536318	0.1609	0.4777
chr14	107349540	16249523	0.1514	0.4668
chr15	102531392	11773646	0.1148	0.4045
chr16	90354753	9033448	0.1	0.3788
chr17	81195210	7791166	0.096	0.3663
chr18	78077248	12934648	0.1657	0.4782
chr19	59128983	4977049	0.0842	0.3752
chr20	63025520	8544770	0.1356	0.4589
chr21	48129895	6100337	0.1267	0.4276
chr22	51304566	2598100	0.0506	0.2622
chrMT	16571	320	0.0193	0.1376
chrX	155270560	39563910	0.2548	0.6428

chrY	59373566	372093	0.0063	0.1018

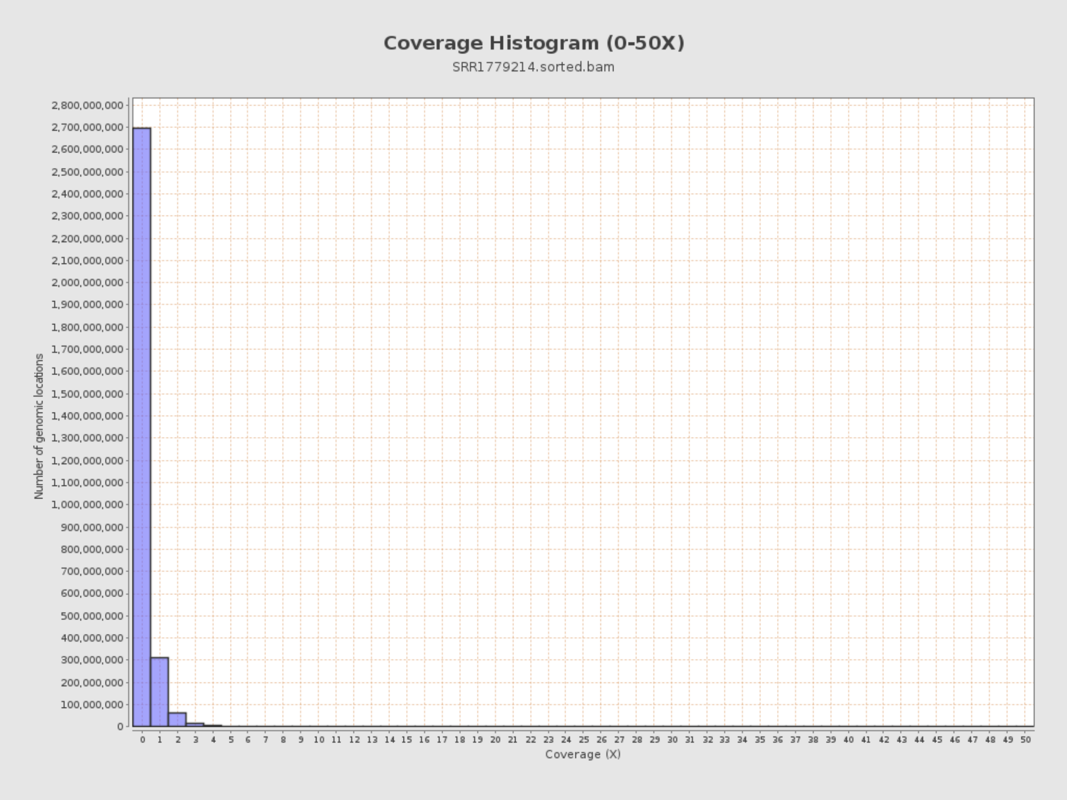
3. Results : Coverage across reference



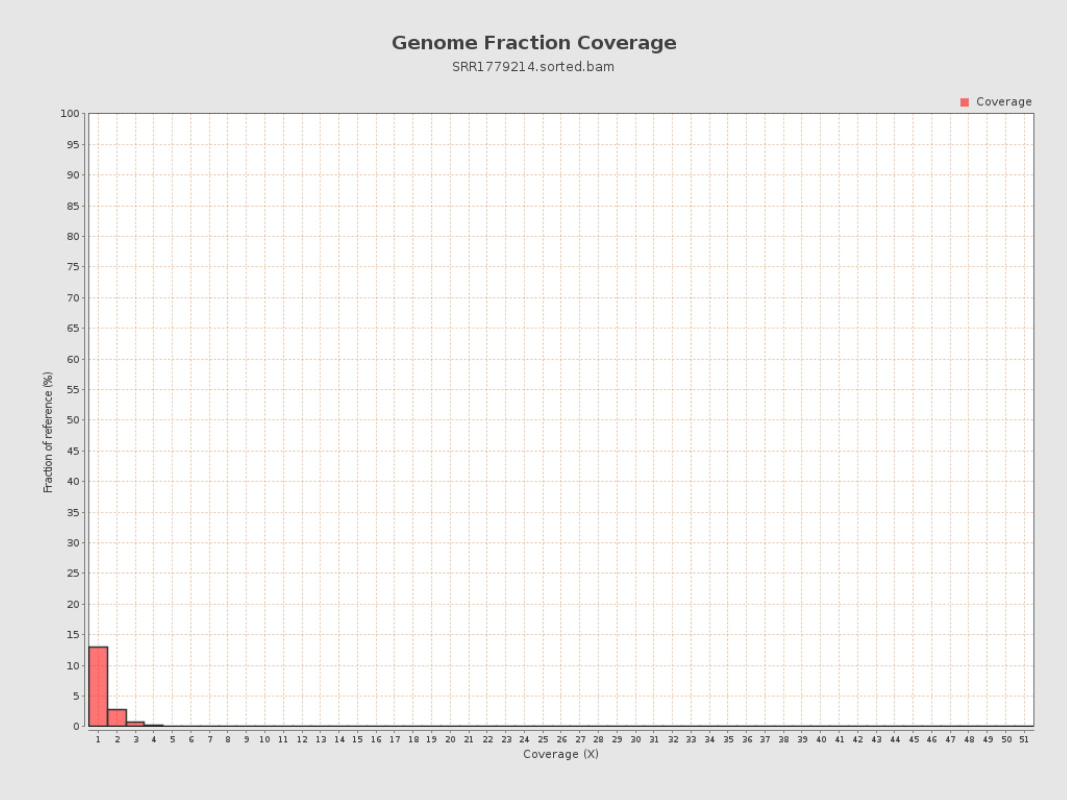
4. Results : Coverage Histogram



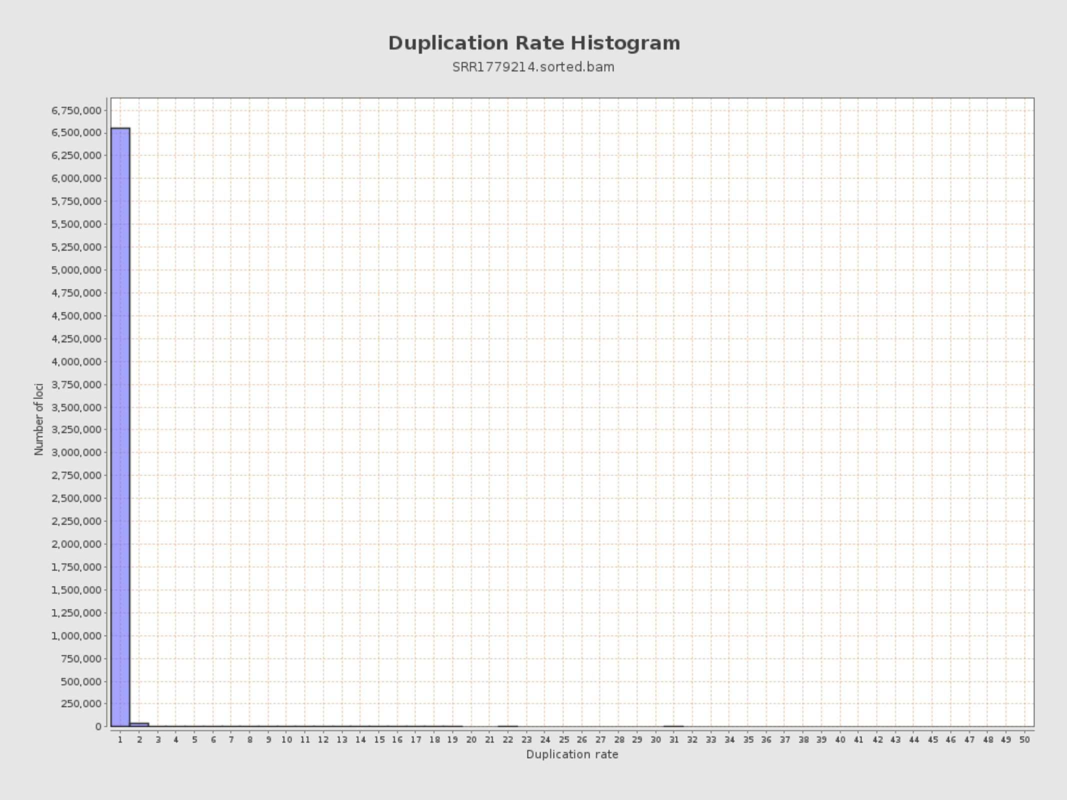
5. Results : Coverage Histogram (0-50X)



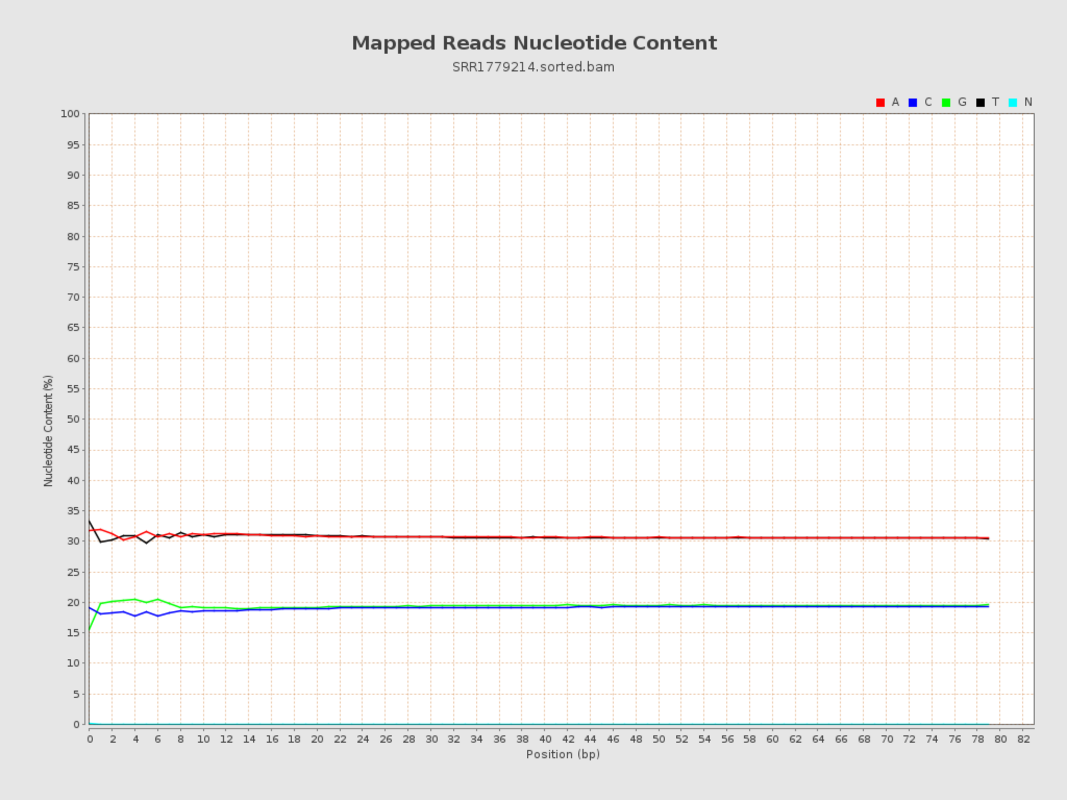
6. Results : Genome Fraction Coverage



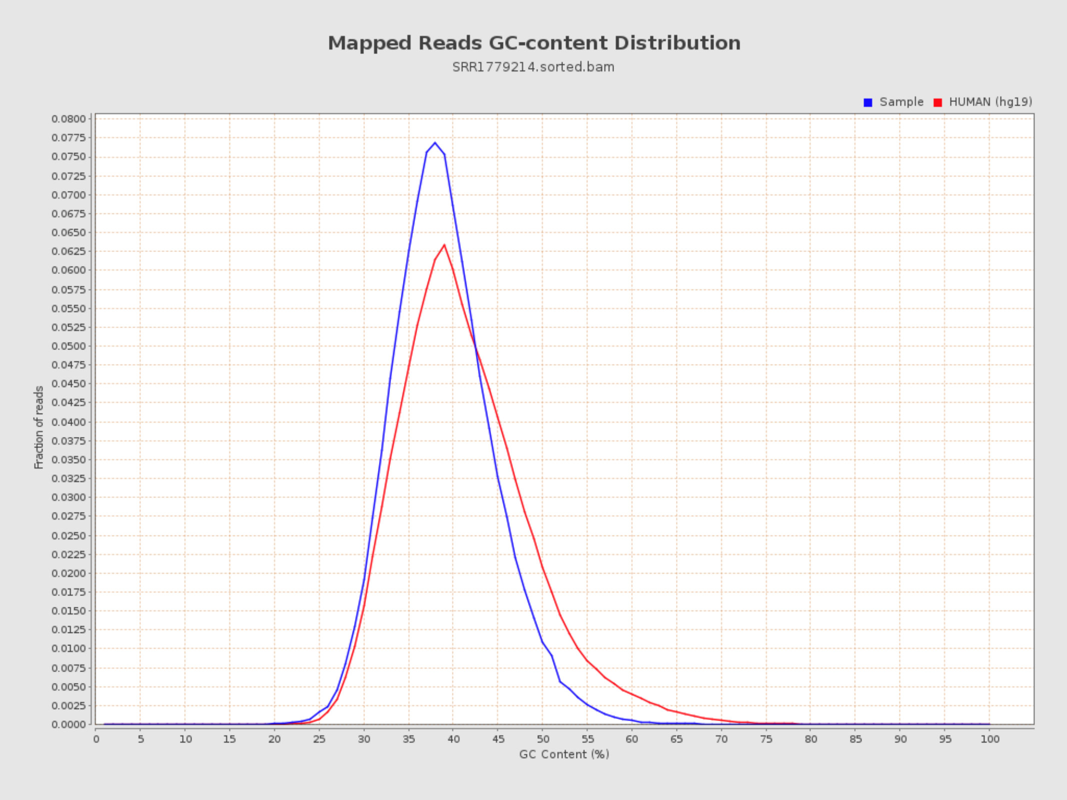
7. Results : Duplication Rate Histogram



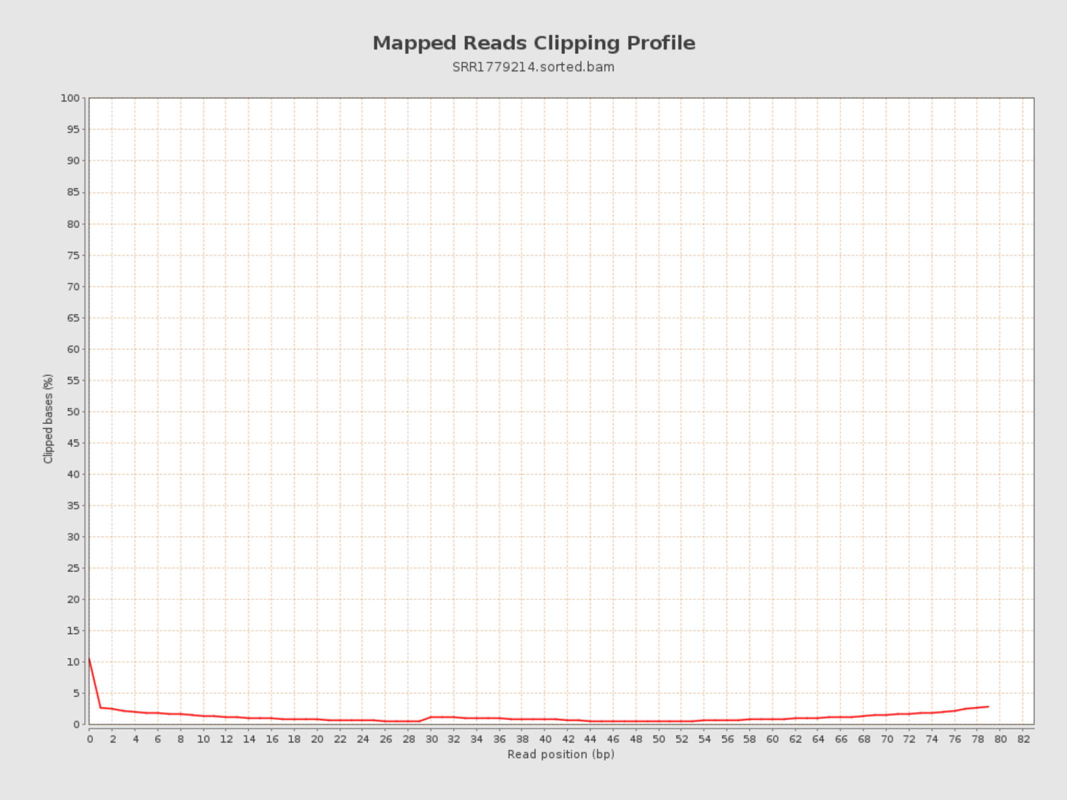
8. Results : Mapped Reads Nucleotide Content



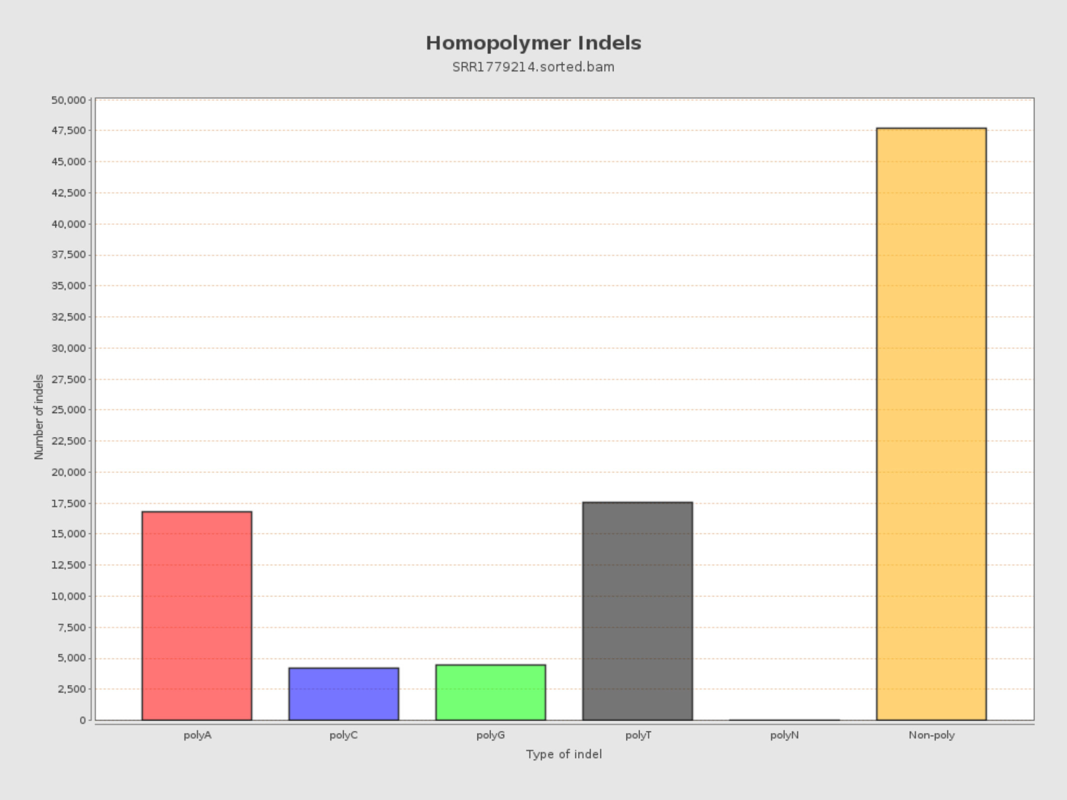
9. Results : Mapped Reads GC-content Distribution



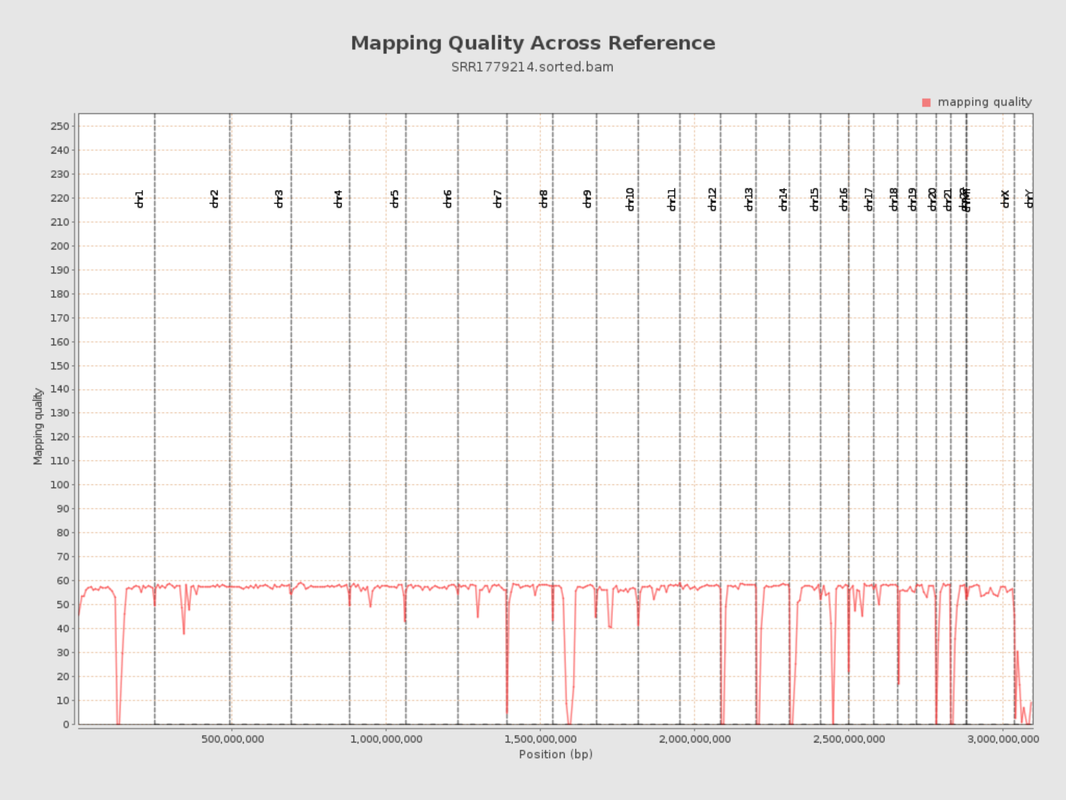
10. Results : Mapped Reads Clipping Profile



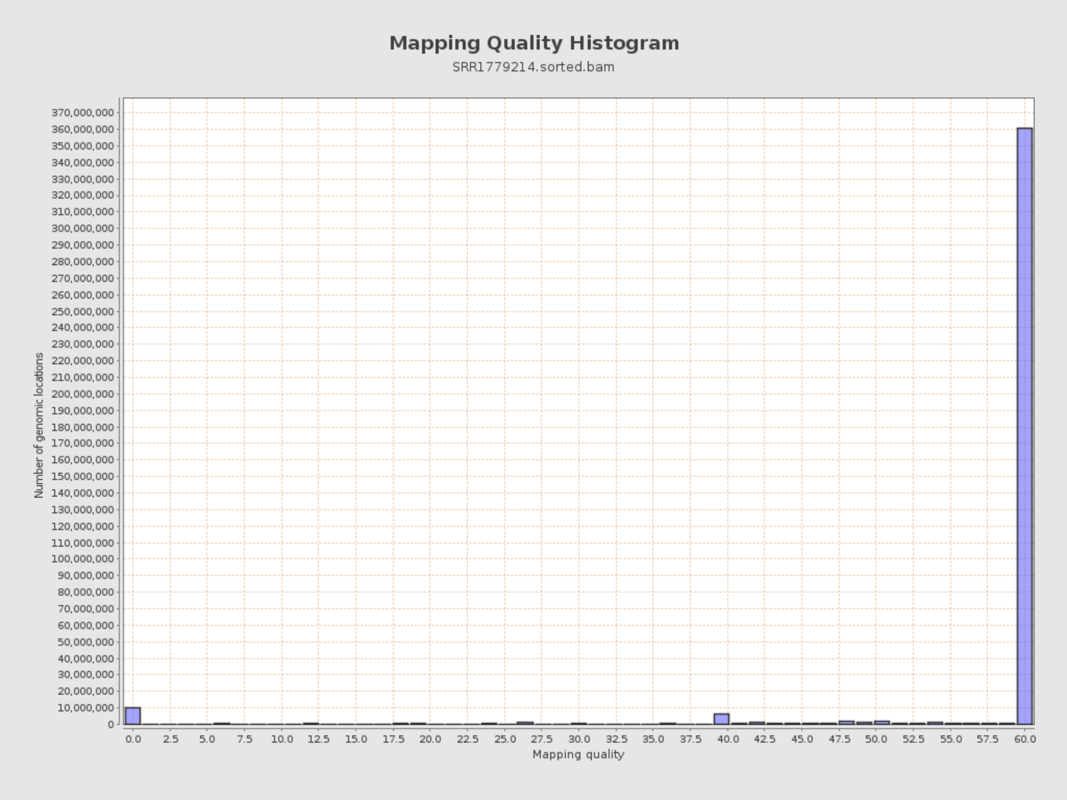
11. Results : Homopolymer Indels



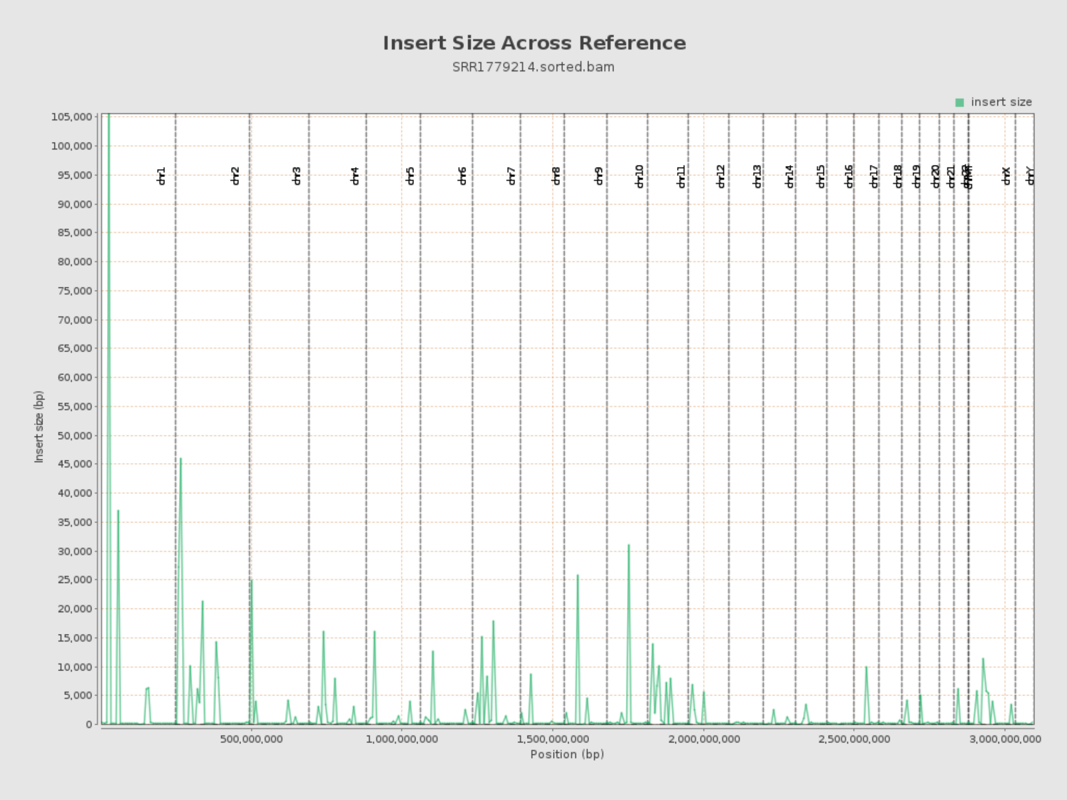
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram