Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 17:22:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779216.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_SRR1779216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779216_1.fastq.gz SRR1779216_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 17:22:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,078,610
Mapped reads	6,871,277 / 97.07%
Unmapped reads	207,333 / 2.93%
Mapped paired reads	6,871,277 / 97.07%
Mapped reads, first in pair	3,472,884 / 49.06%
Mapped reads, second in pair	3,398,393 / 48.01%
Mapped reads, both in pair	6,787,040 / 95.88%
Mapped reads, singletons	84,237 / 1.19%
Secondary alignments	0
Supplementary alignments	16,728 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	52,441 / 0.74%
Duplication rate	0.71%
Clipped reads	250,970 / 3.55%

2.2. ACGT Content

Number/percentage of A's	167,436,117 / 30.64%
Number/percentage of C's	104,952,257 / 19.21%
Number/percentage of T's	166,804,087 / 30.53%
Number/percentage of G's	107,088,236 / 19.6%
Number/percentage of N's	100,340 / 0.02%

GC Percentage	38.81%

2.3. Coverage

Mean	0.1765
Standard Deviation	0.5597

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	56,605
Standard Deviation	2,244,462.17
P25/Median/P75	200 / 264 / 335

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	2,438,601
Insertions	41,794
Mapped reads with at least one insertion	0.6%
Deletions	52,893
Mapped reads with at least one deletion	0.76%
Homopolymer indels	47.18%

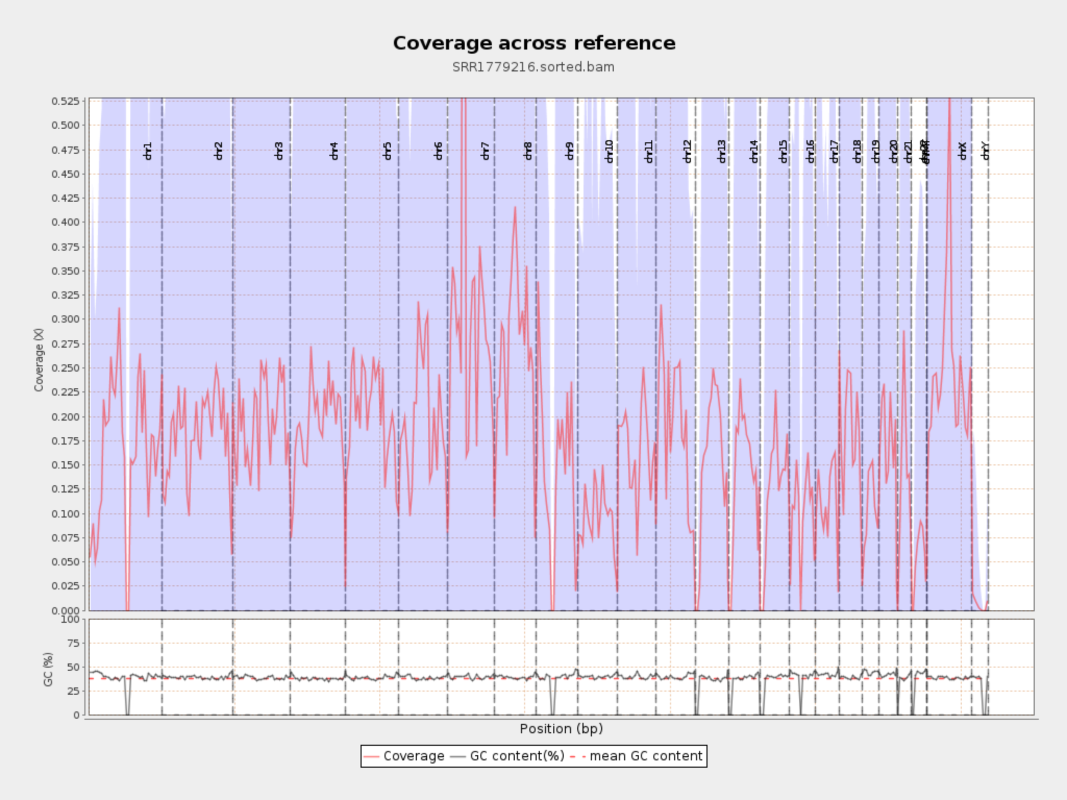
2.7. Chromosome stats

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

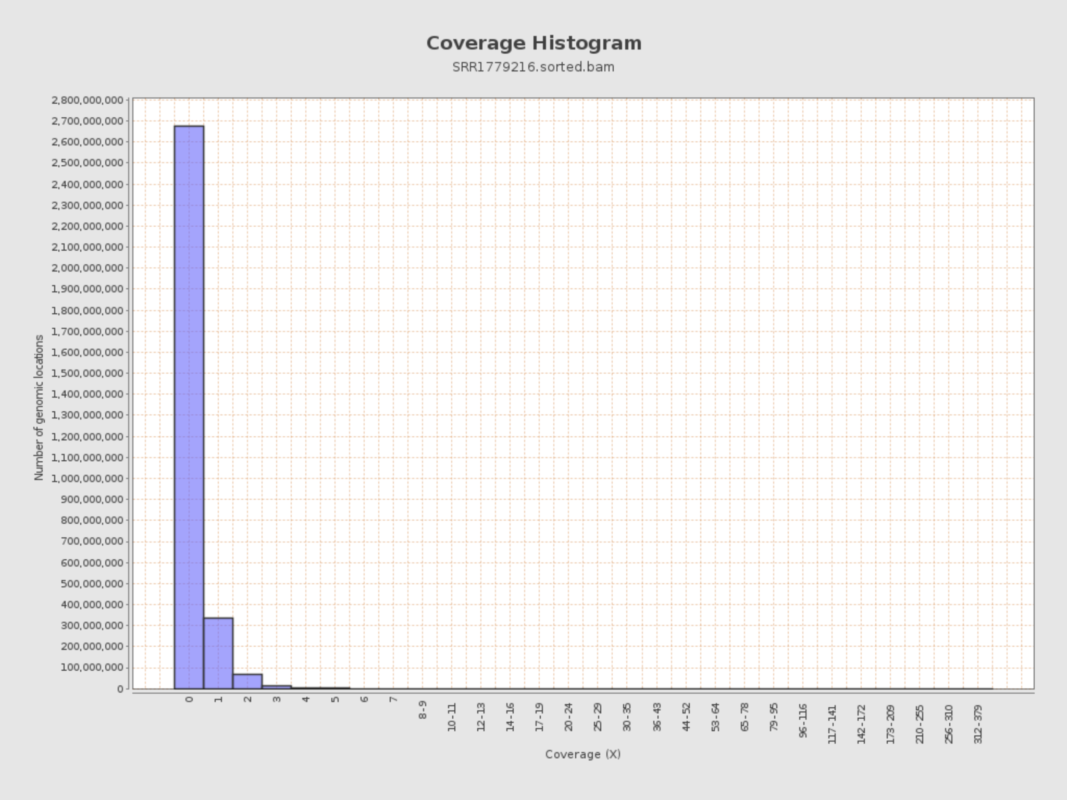
		bases	coverage	deviation
chr1	249250621	40862167	0.1639	0.5881
chr2	243199373	43949417	0.1807	0.5
chr3	198022430	38745575	0.1957	0.5155
chr4	191154276	36806004	0.1925	0.5106
chr5	180915260	36821485	0.2035	0.5261
chr6	171115067	33313784	0.1947	0.5205
chr7	159138663	51652165	0.3246	1.1707
chr8	146364022	40105876	0.274	0.6262
chr9	141213431	21068272	0.1492	0.469
chr10	135534747	13237873	0.0977	0.5126
chr11	135006516	22358896	0.1656	0.4785
chr12	133851895	25143913	0.1878	0.5075
chr13	115169878	17369625	0.1508	0.4542
chr14	107349540	14955042	0.1393	0.4416
chr15	102531392	12532608	0.1222	0.4143
chr16	90354753	9212597	0.102	0.3707
chr17	81195210	8816290	0.1086	0.3913
chr18	78077248	14333906	0.1836	0.5066
chr19	59128983	6367555	0.1077	0.4237
chr20	63025520	11062827	0.1755	0.5076
chr21	48129895	6631863	0.1378	0.4485
chr22	51304566	2800765	0.0546	0.2705
chrMT	16571	698	0.0421	0.2242
chrX	155270560	37967192	0.2445	0.6068

chrY	59373566	373219	0.0063	0.0997

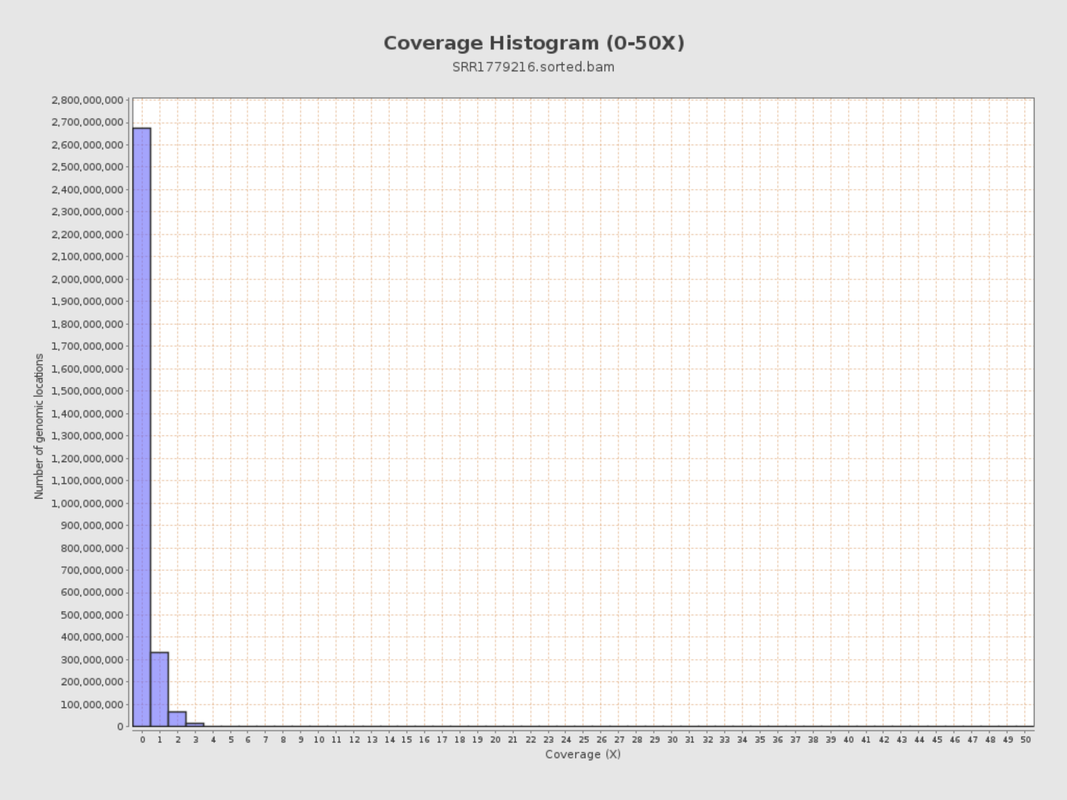
3. Results : Coverage across reference



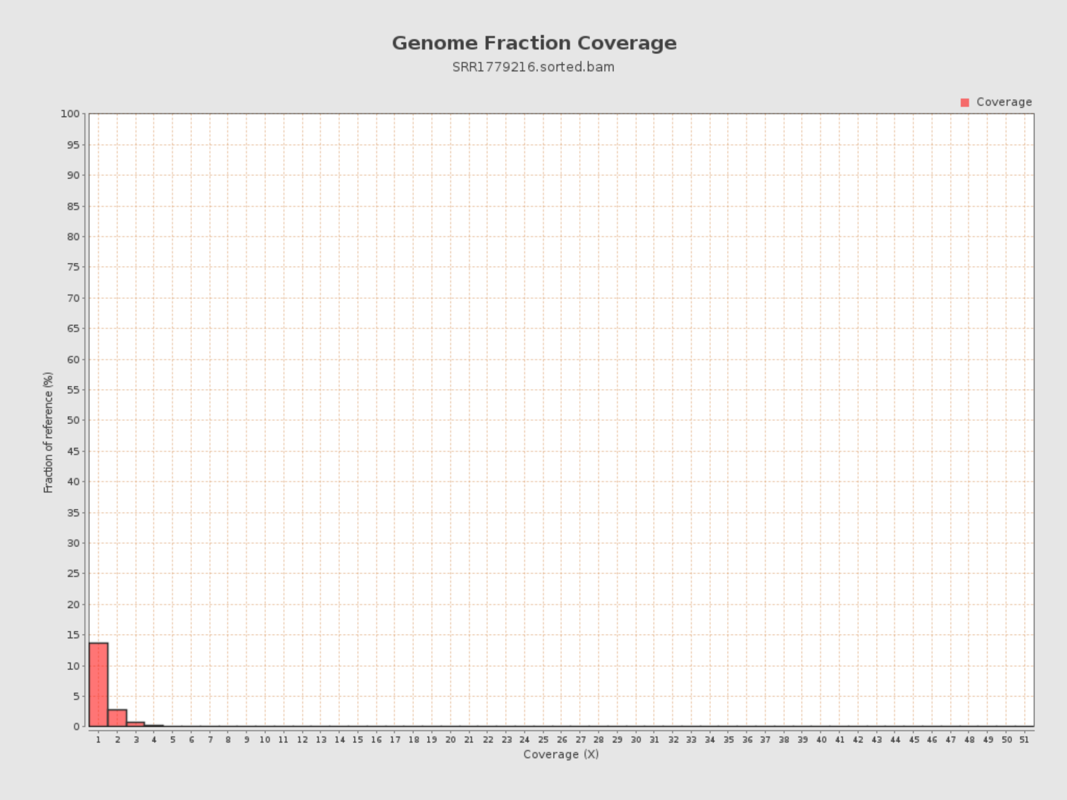
4. Results : Coverage Histogram



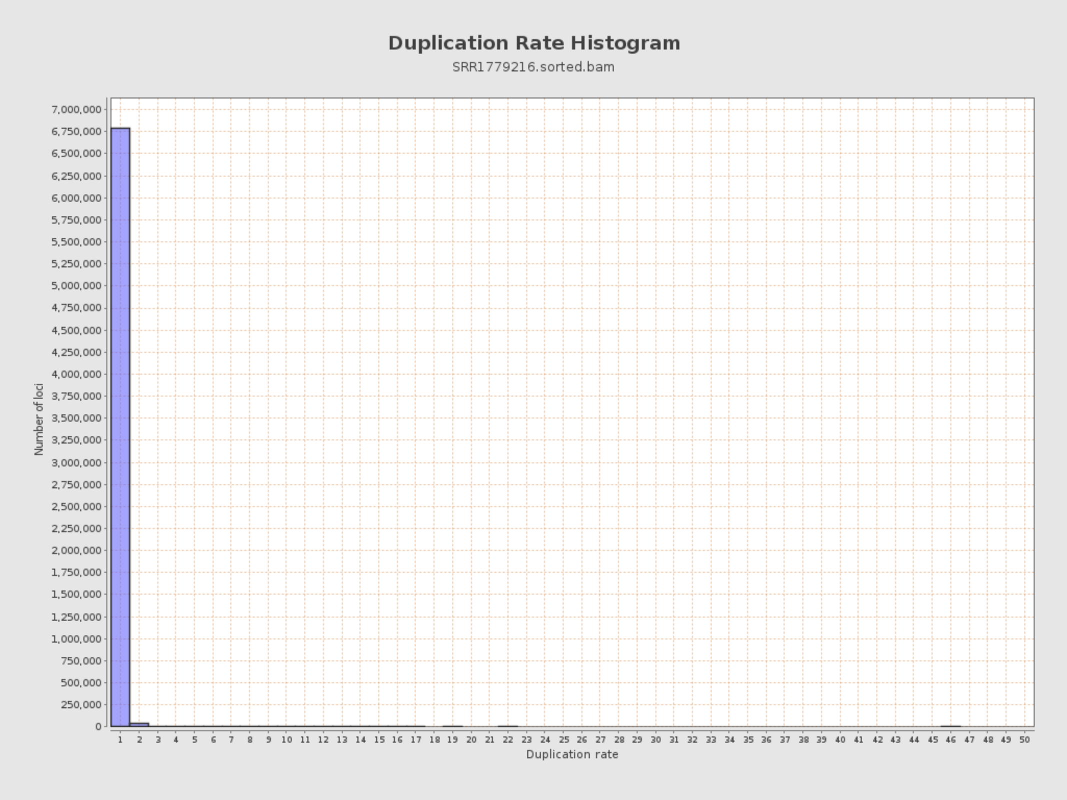
5. Results : Coverage Histogram (0-50X)



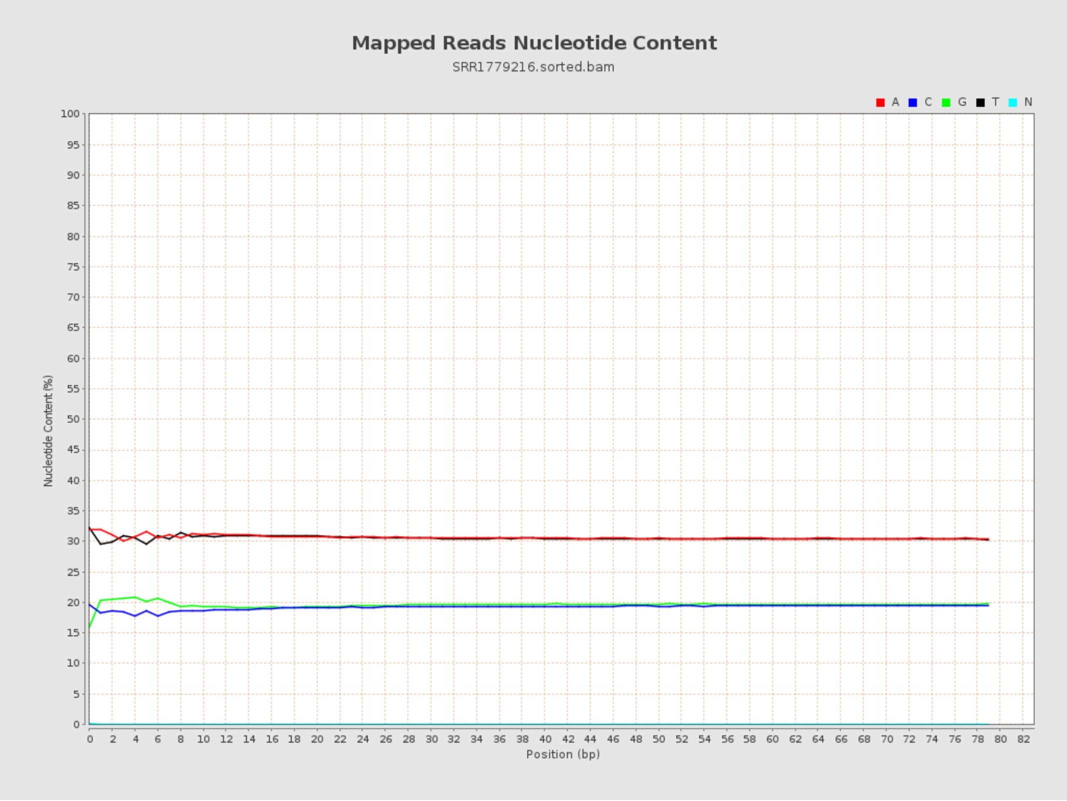
6. Results : Genome Fraction Coverage



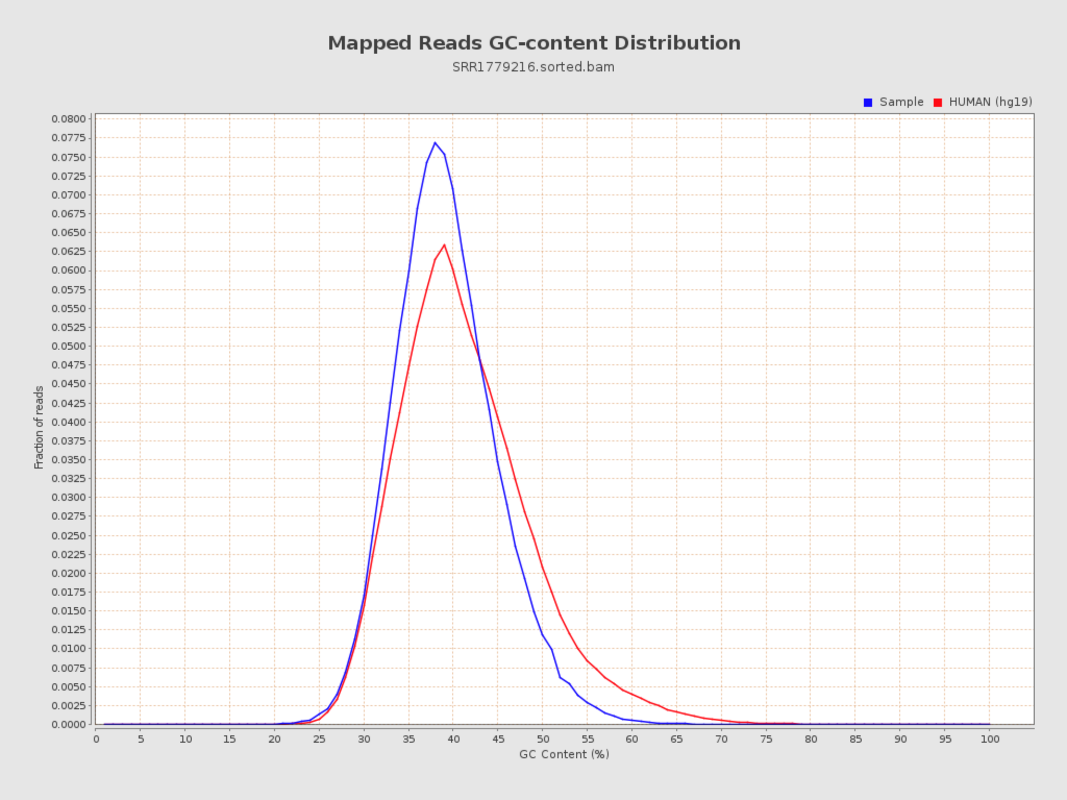
7. Results : Duplication Rate Histogram



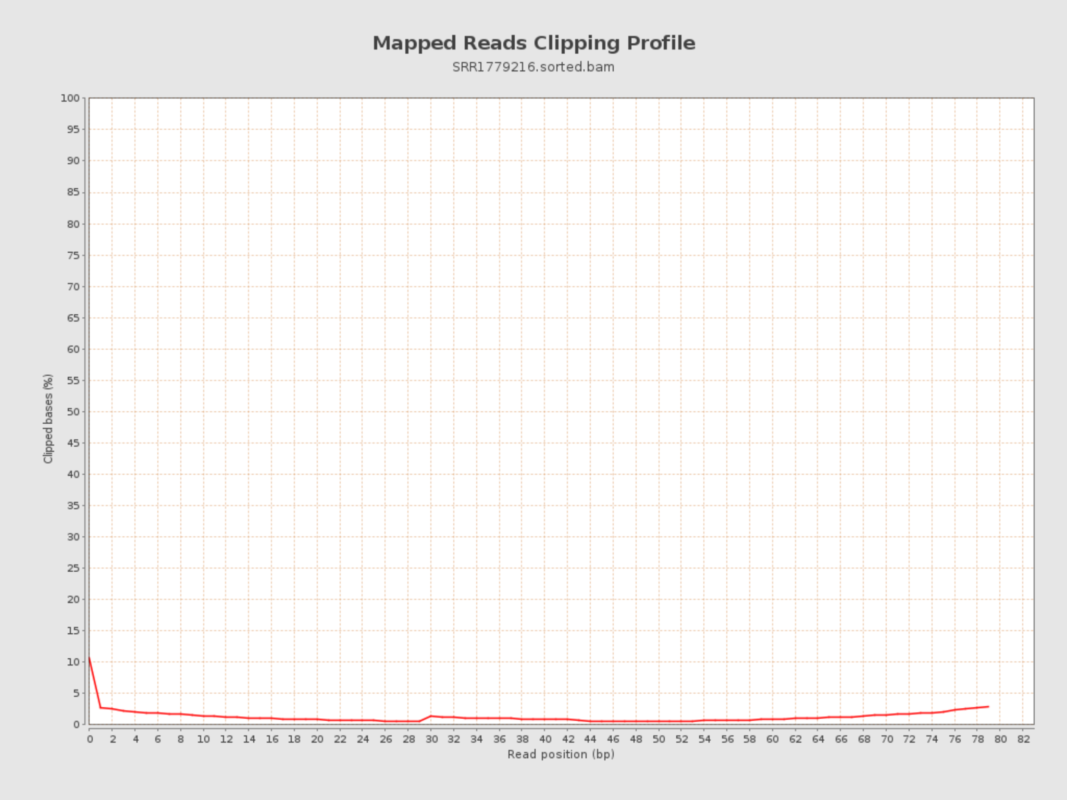
8. Results : Mapped Reads Nucleotide Content



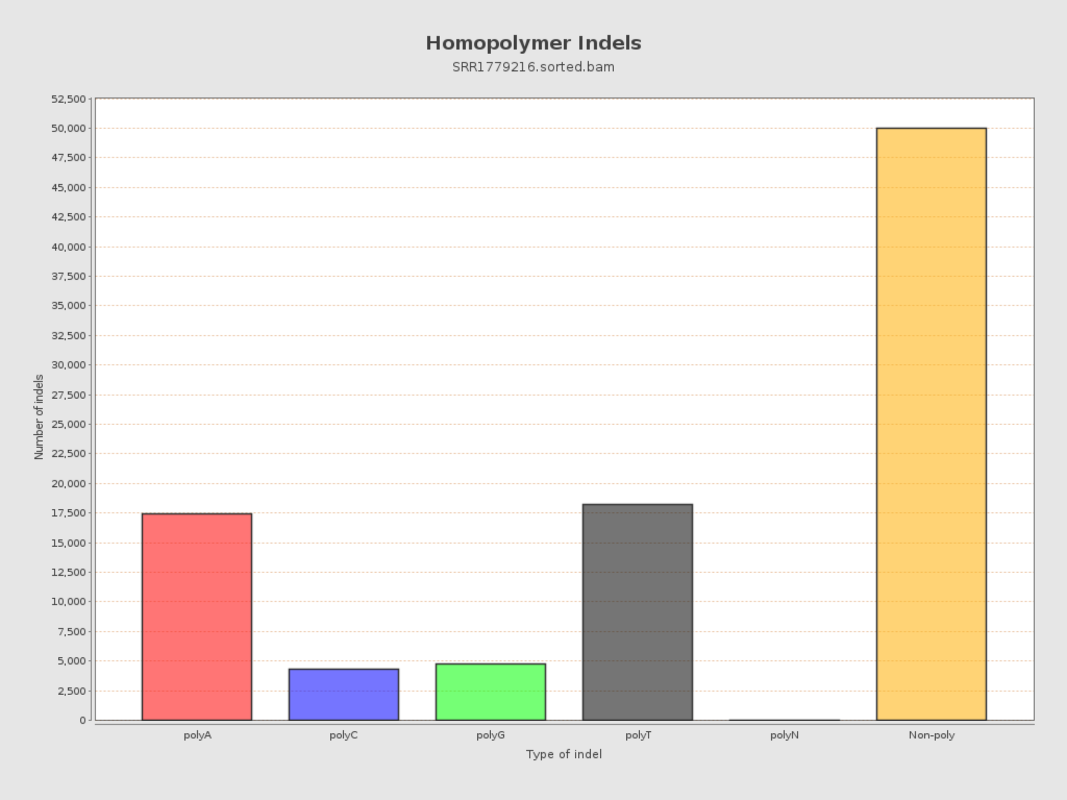
9. Results : Mapped Reads GC-content Distribution



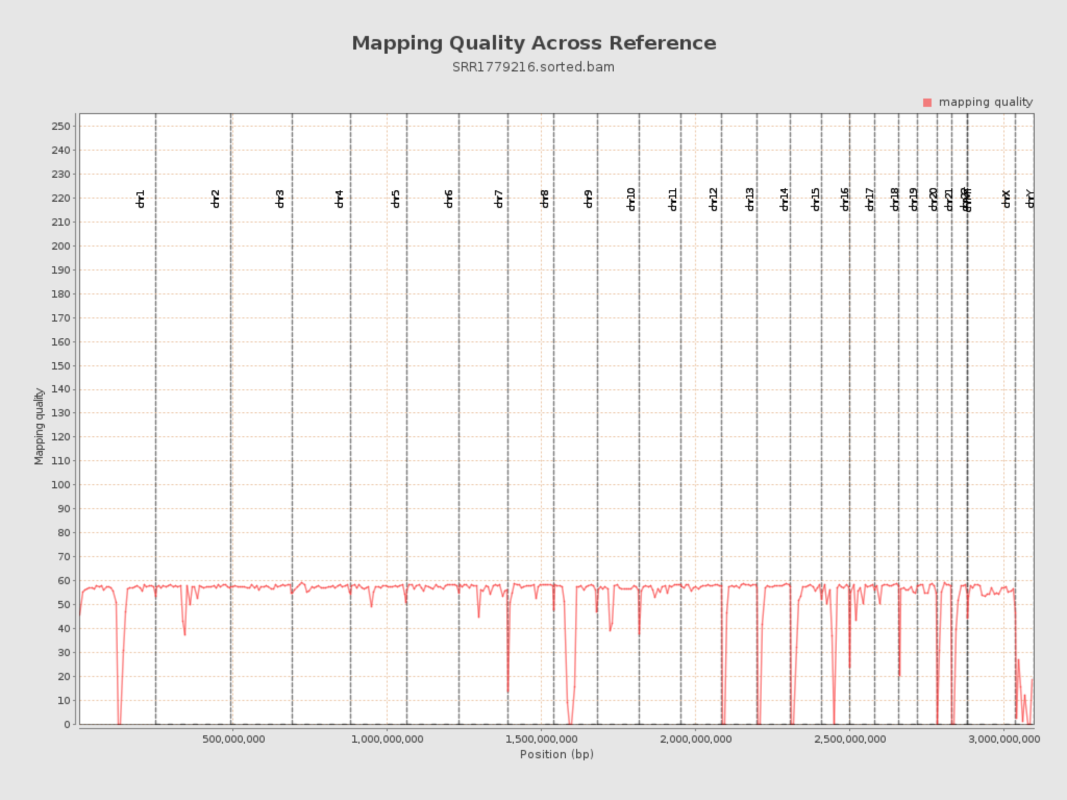
10. Results : Mapped Reads Clipping Profile



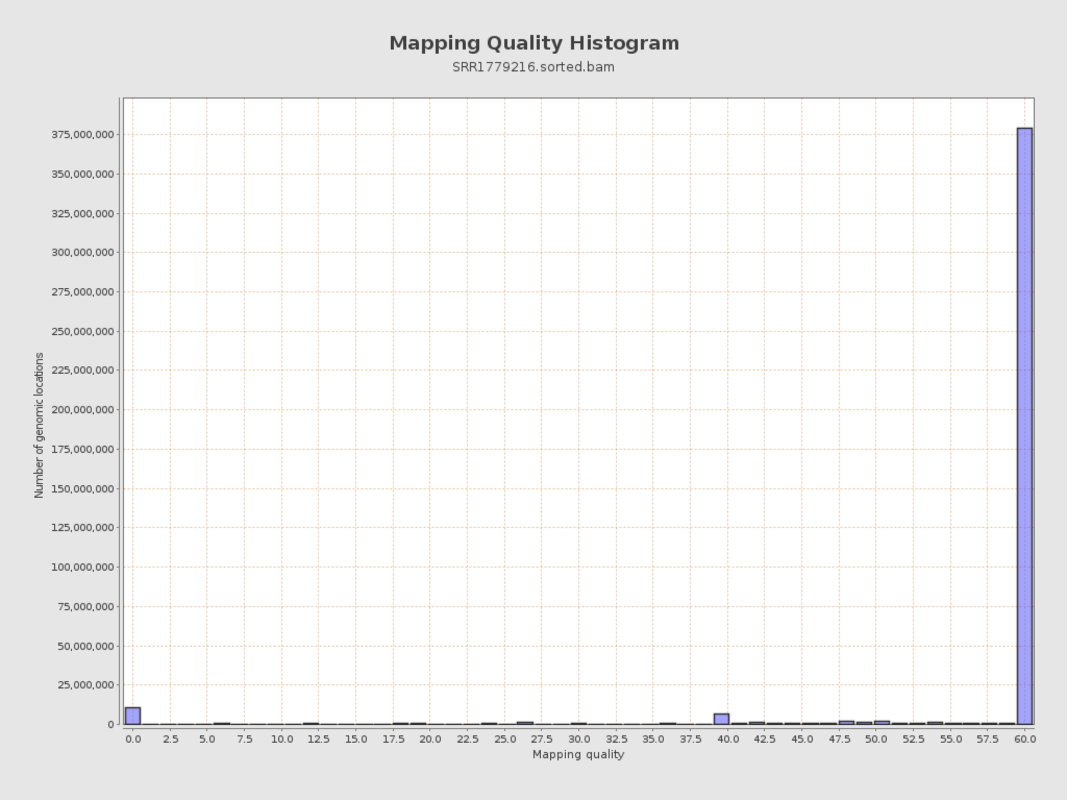
11. Results : Homopolymer Indels



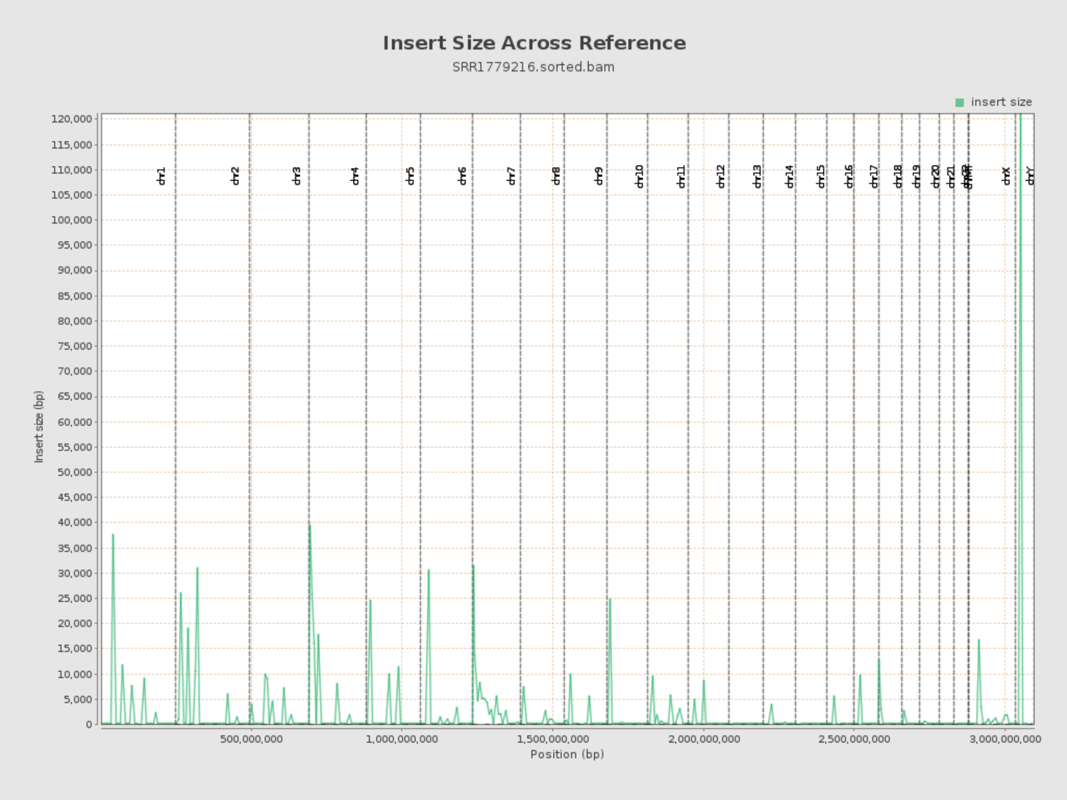
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram