Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 16:22:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777256.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_SRR1777256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777256_1.fastq.gz SRR1777256_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 16:22:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,299,740
Mapped reads	6,172,188 / 97.98%
Unmapped reads	127,552 / 2.02%
Mapped paired reads	6,172,188 / 97.98%
Mapped reads, first in pair	3,100,427 / 49.22%
Mapped reads, second in pair	3,071,761 / 48.76%
Mapped reads, both in pair	6,132,188 / 97.34%
Mapped reads, singletons	40,000 / 0.63%
Secondary alignments	0
Supplementary alignments	184,834 / 2.93%
Read min/max/mean length	30 / 101 / 102.21
Duplicated reads (estimated)	387,764 / 6.16%
Duplication rate	4.71%
Clipped reads	1,220,900 / 19.38%

2.2. ACGT Content

Number/percentage of A's	180,294,821 / 29.65%
Number/percentage of C's	124,409,636 / 20.46%
Number/percentage of T's	177,061,025 / 29.12%
Number/percentage of G's	126,174,992 / 20.75%
Number/percentage of N's	50,911 / 0.01%

GC Percentage	41.22%

2.3. Coverage

Mean	0.1965
Standard Deviation	1.8651

2.4. Mapping Quality

Mean Mapping Quality	53.17

2.5. Insert size

Mean	104,059.94
Standard Deviation	3,078,162.71
P25/Median/P75	128 / 171 / 231

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	2,822,424
Insertions	148,327
Mapped reads with at least one insertion	2.36%
Deletions	69,767
Mapped reads with at least one deletion	1.11%
Homopolymer indels	48.98%

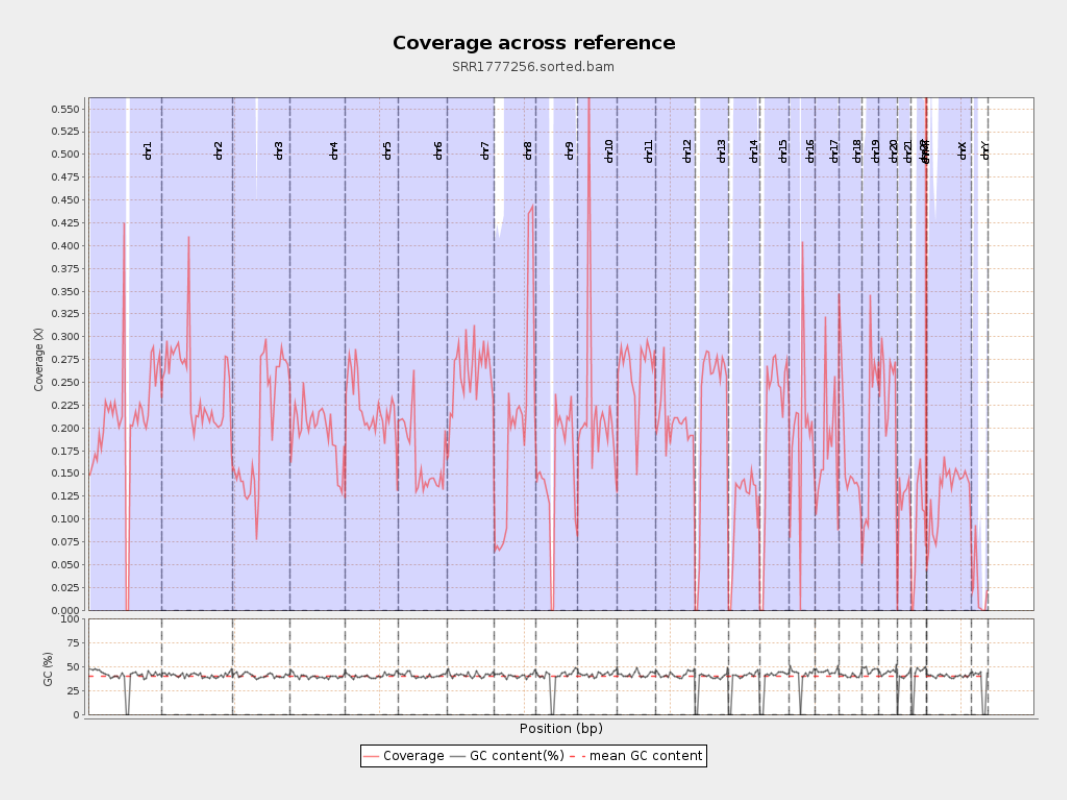
2.7. Chromosome stats

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

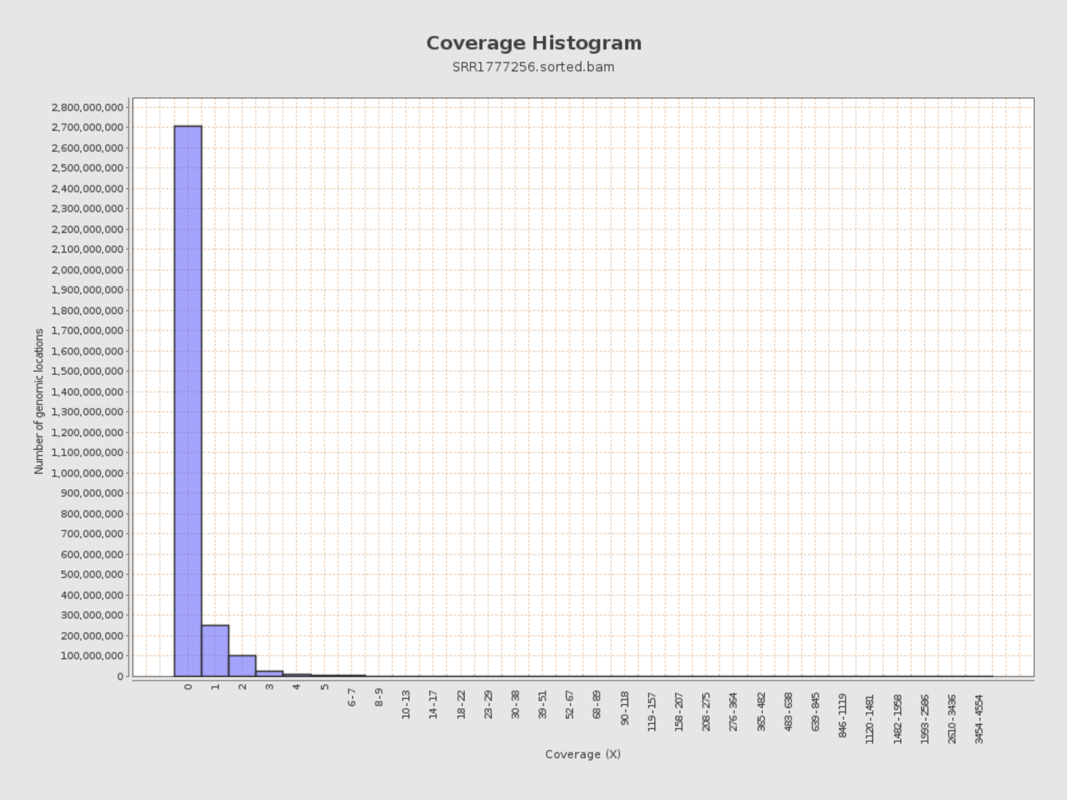
		bases	coverage	deviation
chr1	249250621	51801831	0.2078	4.5845
chr2	243199373	59895798	0.2463	1.3604
chr3	198022430	39794077	0.201	0.664
chr4	191154276	37364815	0.1955	0.8468
chr5	180915260	40040764	0.2213	0.6318
chr6	171115067	28774142	0.1682	0.8204
chr7	159138663	41678355	0.2619	1.7407
chr8	146364022	29909885	0.2044	0.9963
chr9	141213431	21950289	0.1554	1.7725
chr10	135534747	29787879	0.2198	3.4238
chr11	135006516	35255202	0.2611	1.082
chr12	133851895	27463678	0.2052	0.6087
chr13	115169878	25439577	0.2209	0.6277
chr14	107349540	11865696	0.1105	0.4524
chr15	102531392	21258708	0.2073	0.6156
chr16	90354753	17351911	0.192	1.6723
chr17	81195210	14302159	0.1761	0.8815
chr18	78077248	13375087	0.1713	1.9829
chr19	59128983	11518986	0.1948	2.5552
chr20	63025520	15364753	0.2438	0.6873
chr21	48129895	5534692	0.115	0.5565
chr22	51304566	4513847	0.088	0.3979
chrMT	16571	2854581	172.2637	43.4093
chrX	155270560	19826716	0.1277	0.5964

chrY	59373566	1228542	0.0207	0.9083

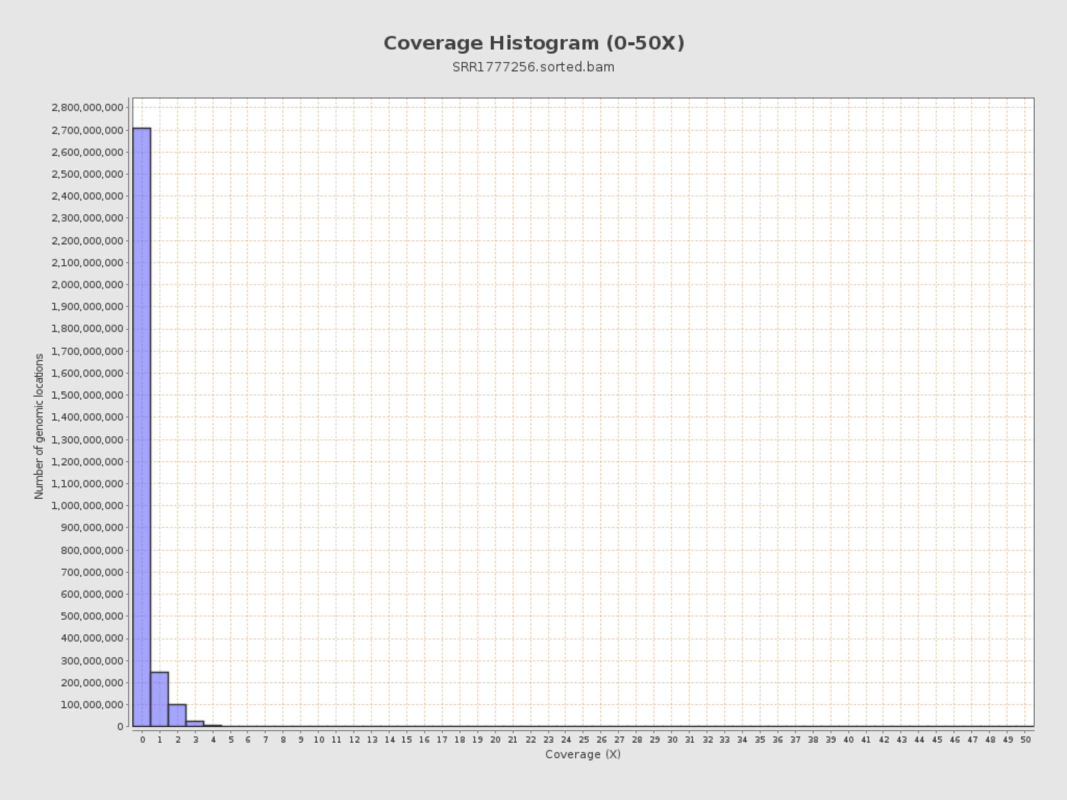
3. Results : Coverage across reference



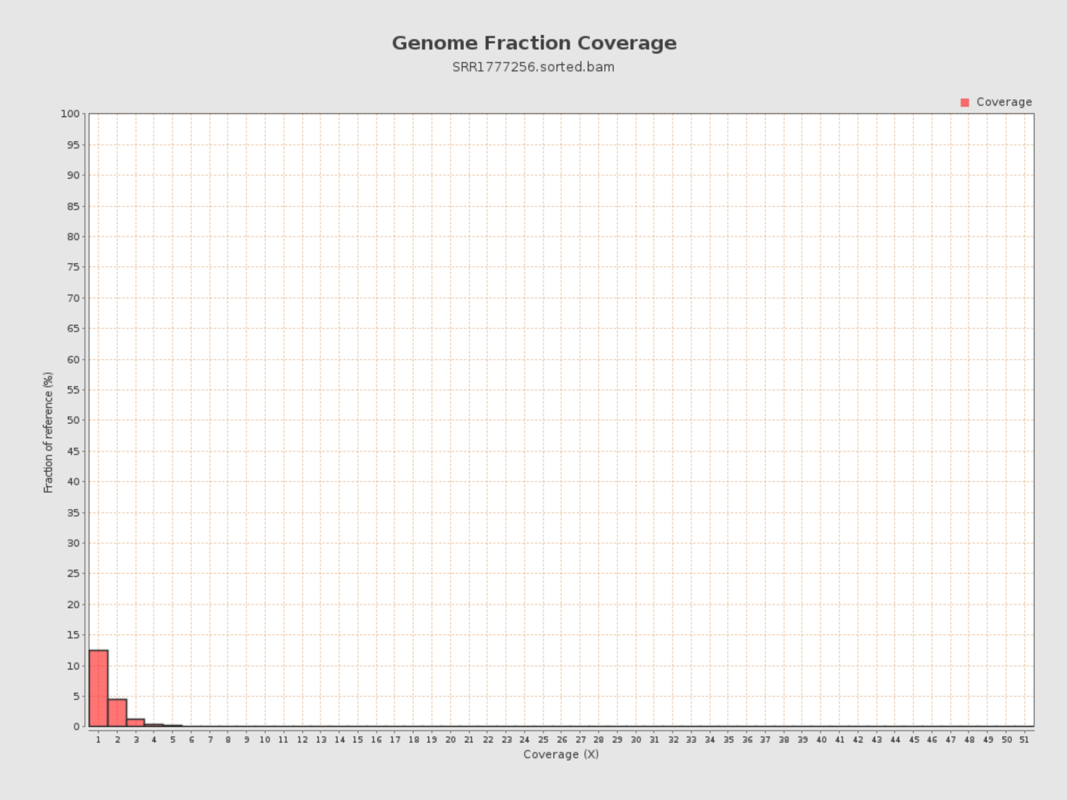
4. Results : Coverage Histogram



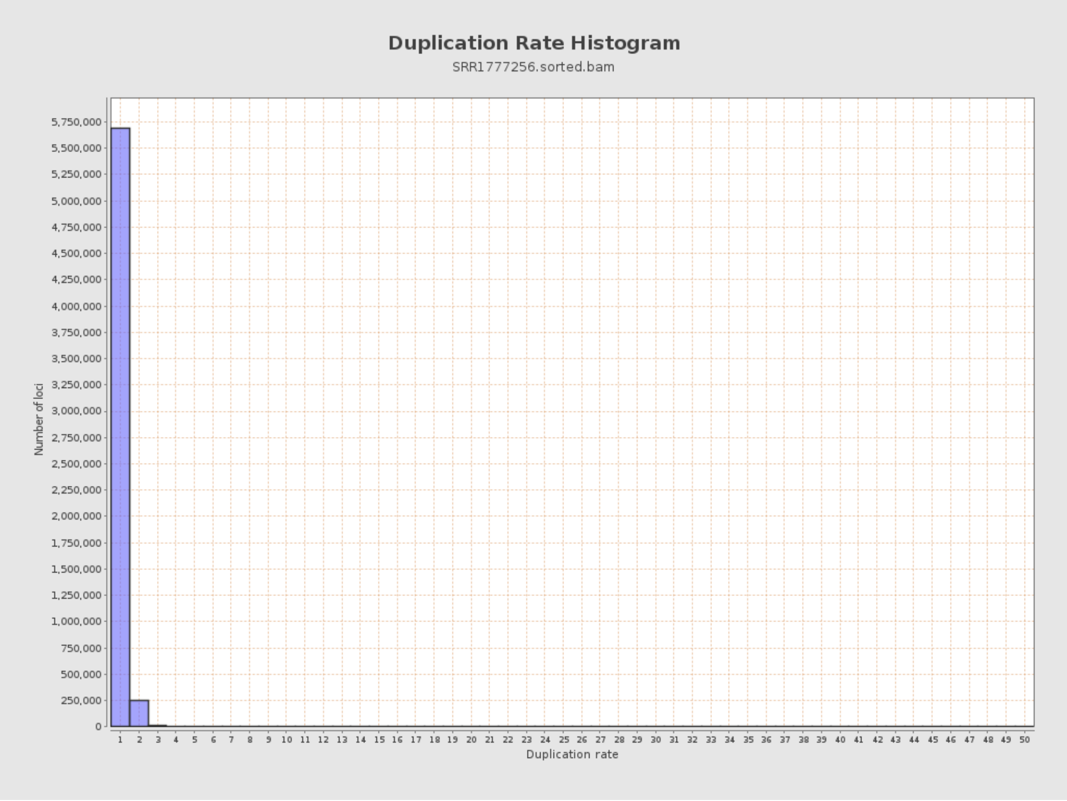
5. Results : Coverage Histogram (0-50X)



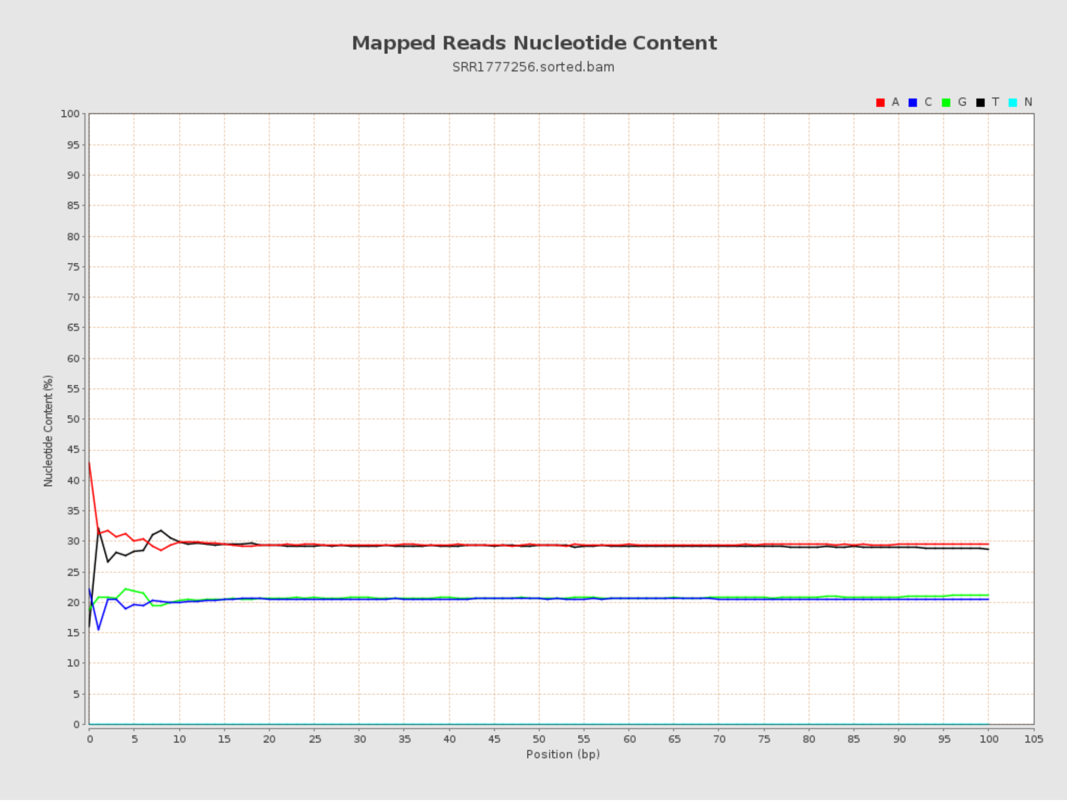
6. Results : Genome Fraction Coverage



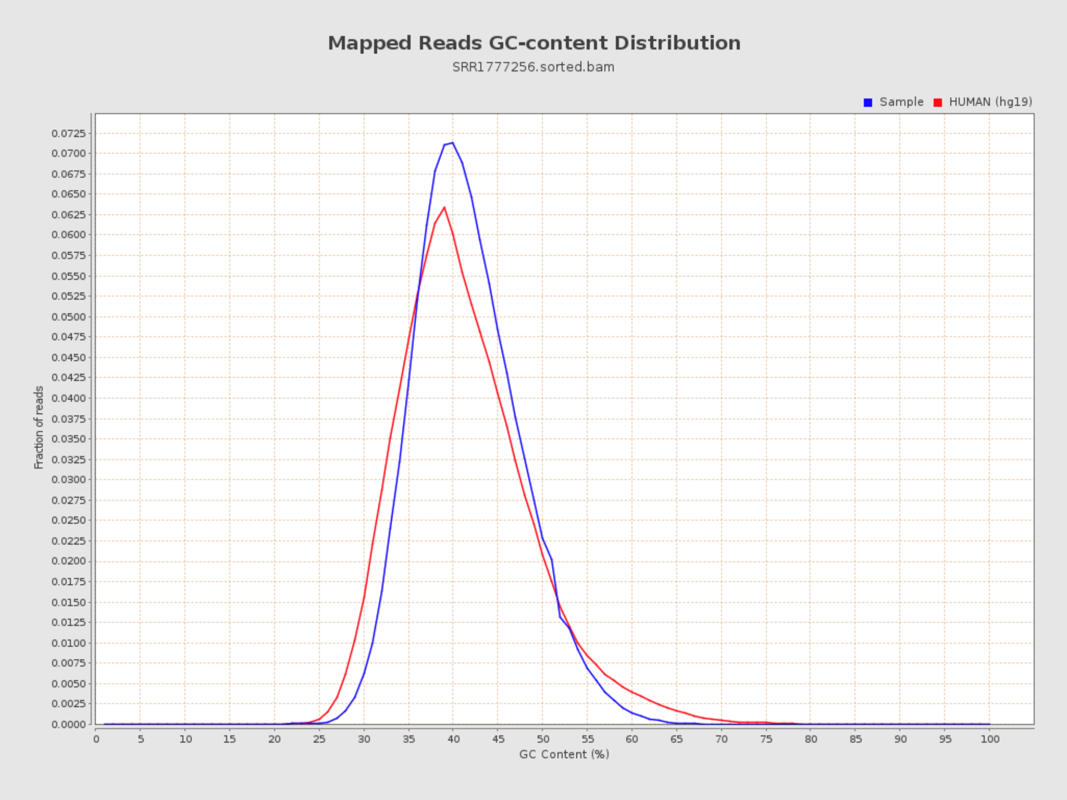
7. Results : Duplication Rate Histogram



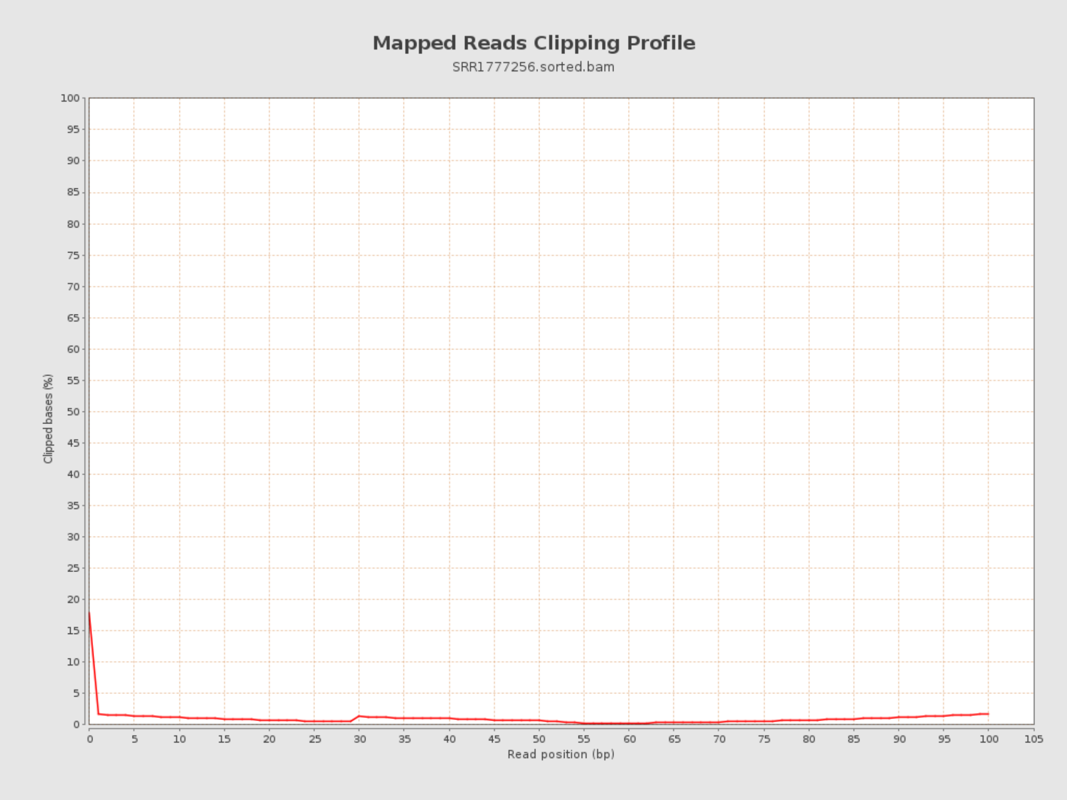
8. Results : Mapped Reads Nucleotide Content



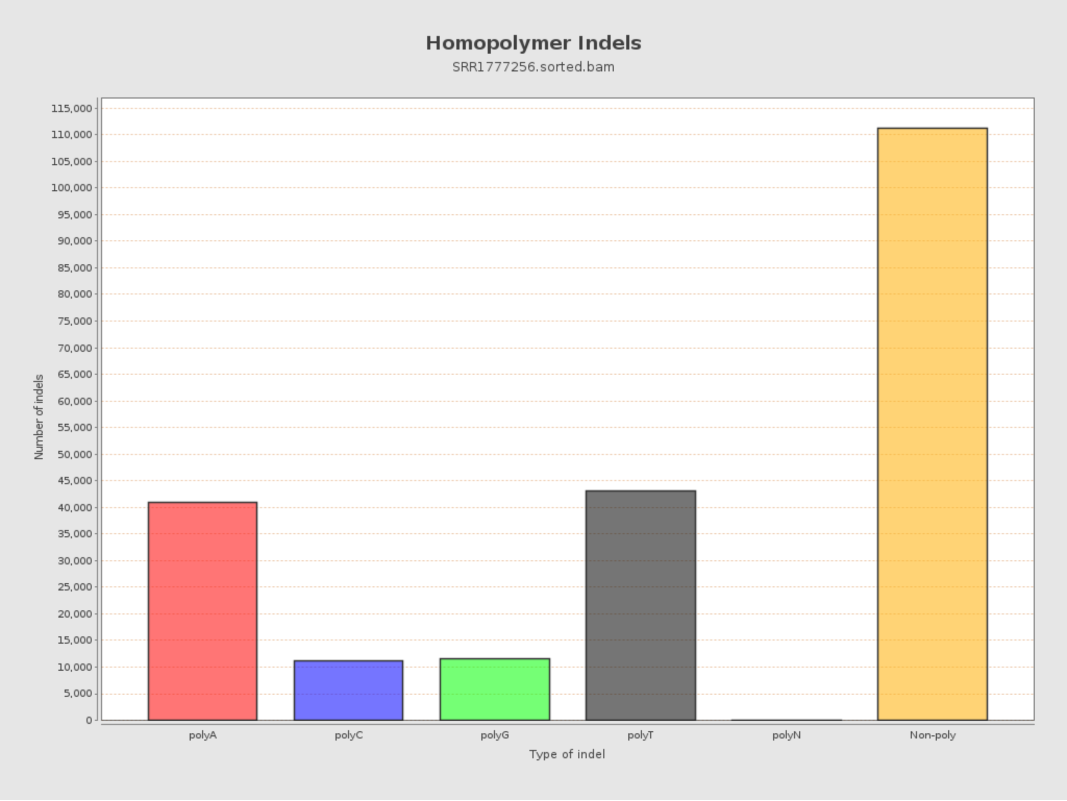
9. Results : Mapped Reads GC-content Distribution



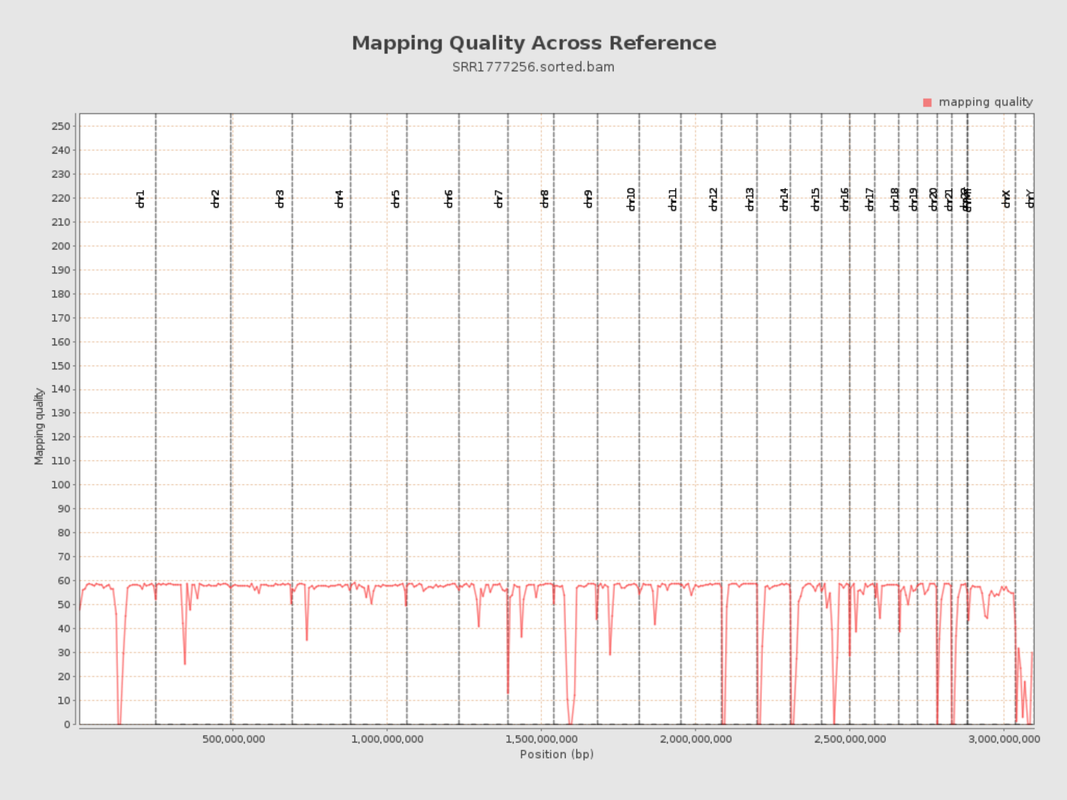
10. Results : Mapped Reads Clipping Profile



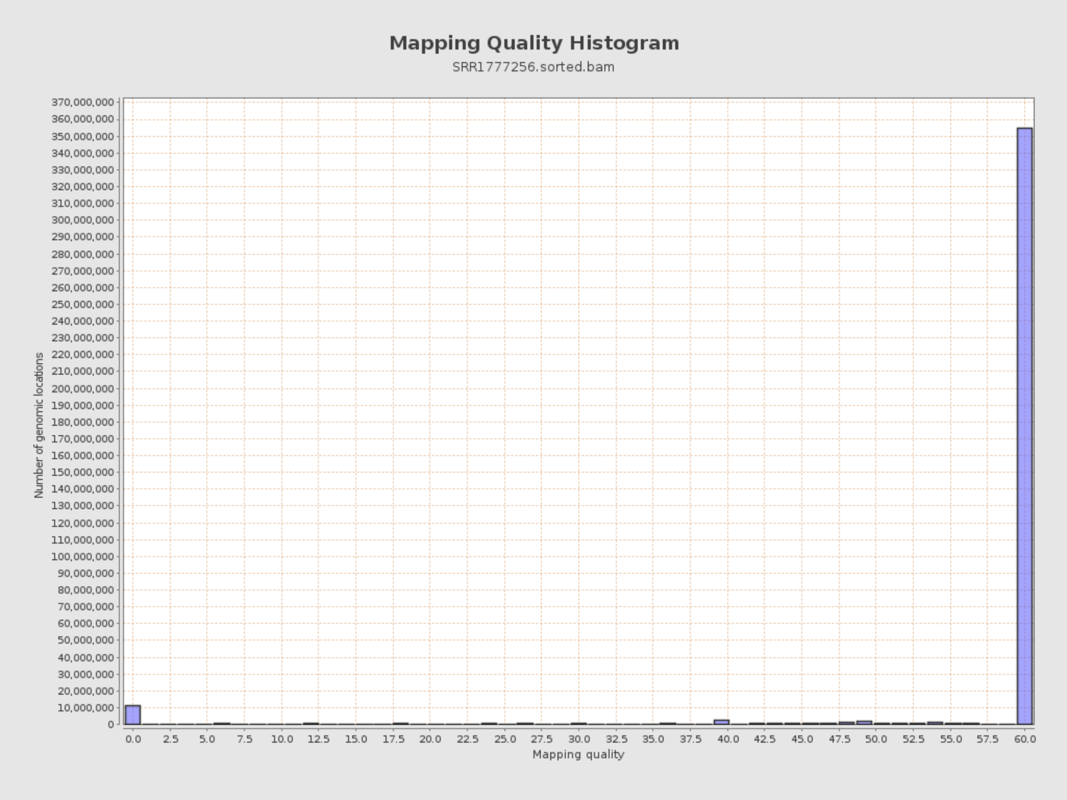
11. Results : Homopolymer Indels



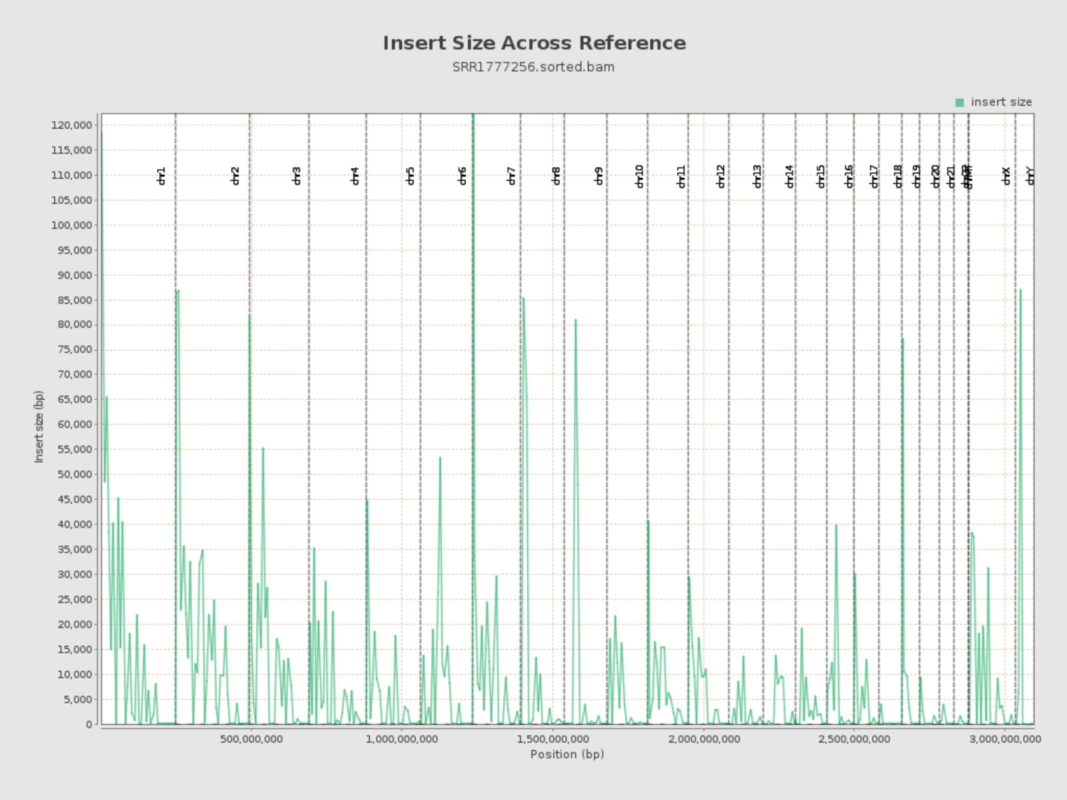
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram