Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 16:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777257.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_SRR1777257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777257_1.fastq.gz SRR1777257_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 16:30:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,248,054
Mapped reads	6,123,074 / 98%
Unmapped reads	124,980 / 2%
Mapped paired reads	6,123,074 / 98%
Mapped reads, first in pair	3,075,135 / 49.22%
Mapped reads, second in pair	3,047,939 / 48.78%
Mapped reads, both in pair	6,084,622 / 97.38%
Mapped reads, singletons	38,452 / 0.62%
Secondary alignments	0
Supplementary alignments	182,510 / 2.92%
Read min/max/mean length	30 / 101 / 102.21
Duplicated reads (estimated)	384,545 / 6.15%
Duplication rate	4.71%
Clipped reads	1,211,483 / 19.39%

2.2. ACGT Content

Number/percentage of A's	178,662,676 / 29.62%
Number/percentage of C's	123,570,162 / 20.49%
Number/percentage of T's	175,488,899 / 29.1%
Number/percentage of G's	125,323,422 / 20.78%
Number/percentage of N's	54,855 / 0.01%

GC Percentage	41.27%

2.3. Coverage

Mean	0.1949
Standard Deviation	1.861

2.4. Mapping Quality

Mean Mapping Quality	53.17

2.5. Insert size

Mean	104,394.55
Standard Deviation	3,122,721.75
P25/Median/P75	128 / 171 / 230

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	2,787,013
Insertions	147,732
Mapped reads with at least one insertion	2.37%
Deletions	68,797
Mapped reads with at least one deletion	1.1%
Homopolymer indels	49.02%

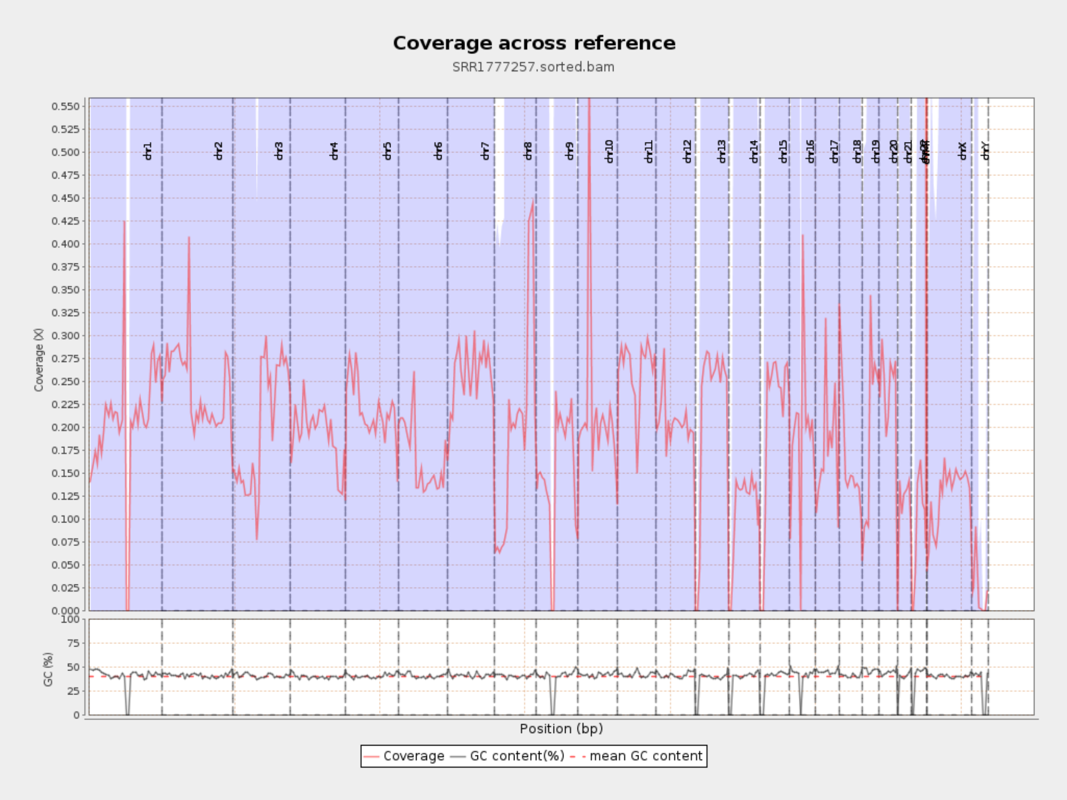
2.7. Chromosome stats

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

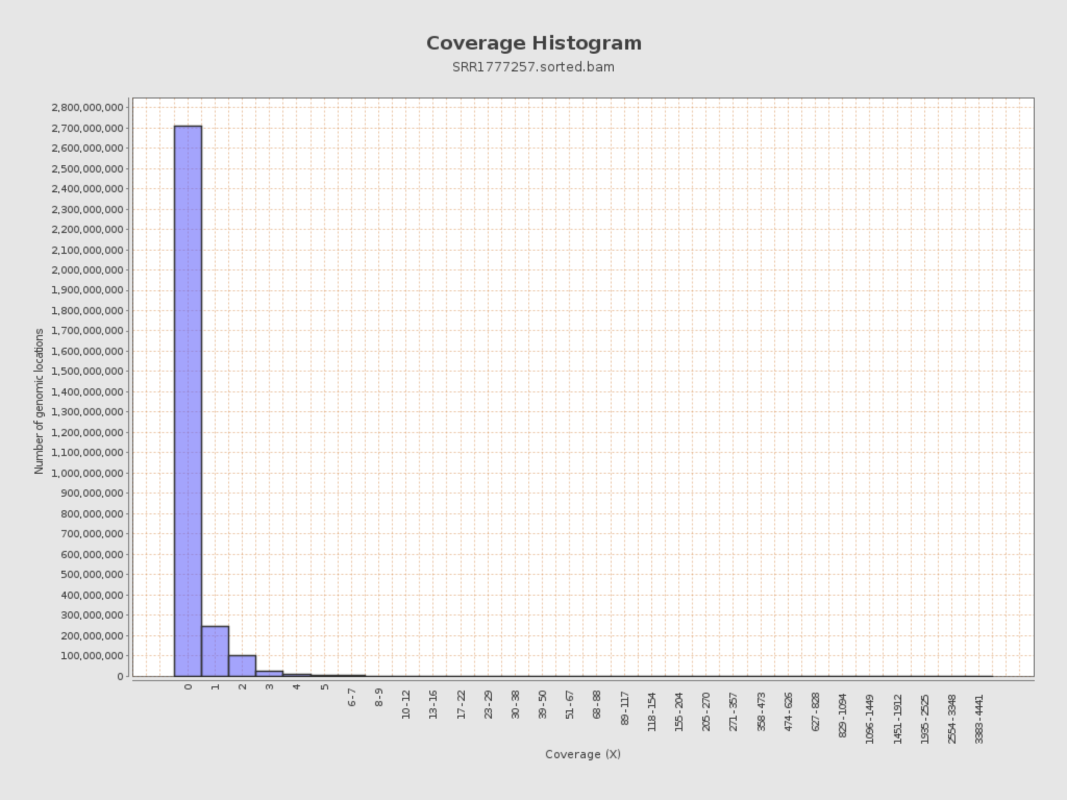
		bases	coverage	deviation
chr1	249250621	51339842	0.206	4.6111
chr2	243199373	59616399	0.2451	1.3481
chr3	198022430	39564336	0.1998	0.665
chr4	191154276	36837437	0.1927	0.8365
chr5	180915260	39656830	0.2192	0.6269
chr6	171115067	28469492	0.1664	0.8076
chr7	159138663	41420797	0.2603	1.6656
chr8	146364022	29440044	0.2011	0.9618
chr9	141213431	21832363	0.1546	1.8001
chr10	135534747	29567634	0.2182	3.4073
chr11	135006516	35099563	0.26	1.07
chr12	133851895	27384204	0.2046	0.6054
chr13	115169878	25148193	0.2184	0.6229
chr14	107349540	11736629	0.1093	0.4529
chr15	102531392	21188499	0.2067	0.6144
chr16	90354753	17342268	0.1919	1.7165
chr17	81195210	14254863	0.1756	0.8902
chr18	78077248	13178616	0.1688	1.9766
chr19	59128983	11466235	0.1939	2.4152
chr20	63025520	15195408	0.2411	0.6839
chr21	48129895	5420747	0.1126	0.5493
chr22	51304566	4564482	0.089	0.4008
chrMT	16571	2833878	171.0143	43.7416
chrX	155270560	19491508	0.1255	0.59

chrY	59373566	1207750	0.0203	0.9207

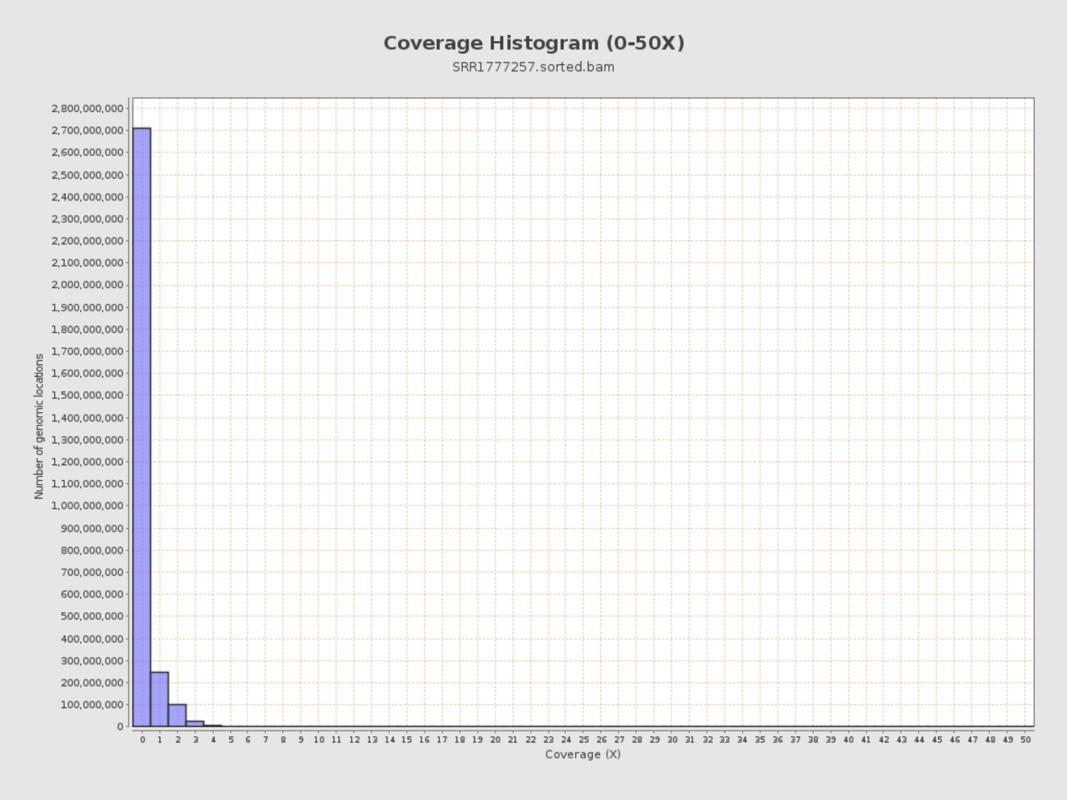
3. Results : Coverage across reference



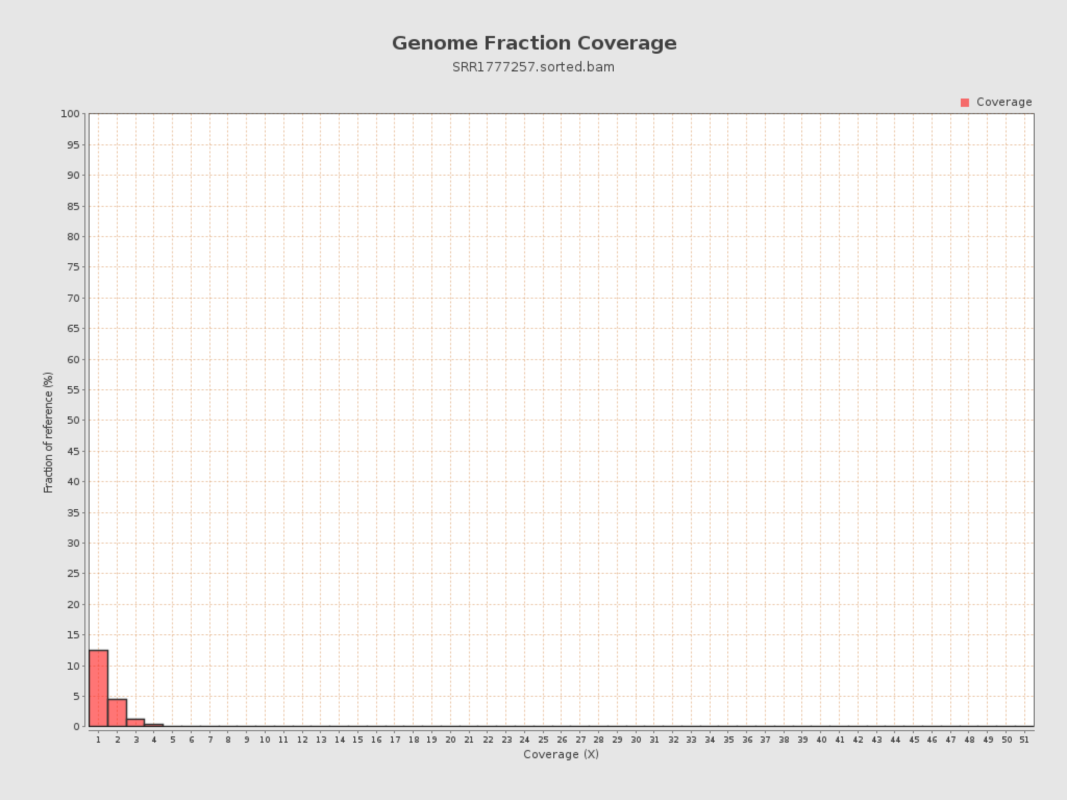
4. Results : Coverage Histogram



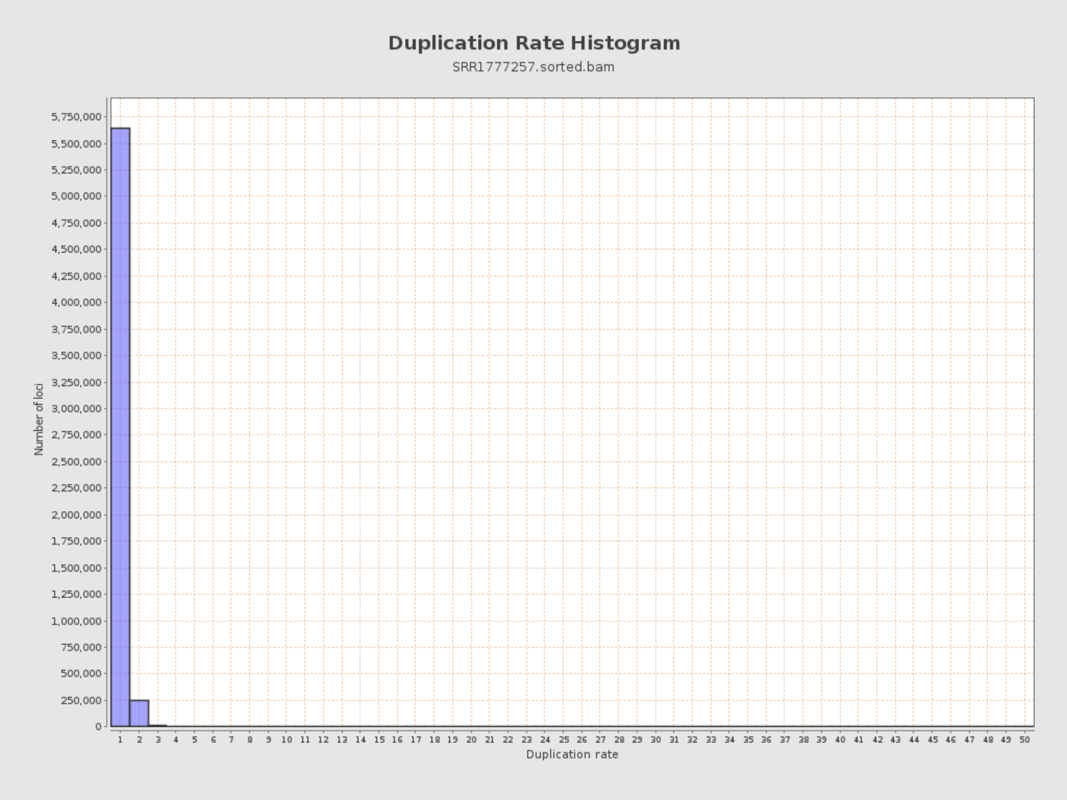
5. Results : Coverage Histogram (0-50X)



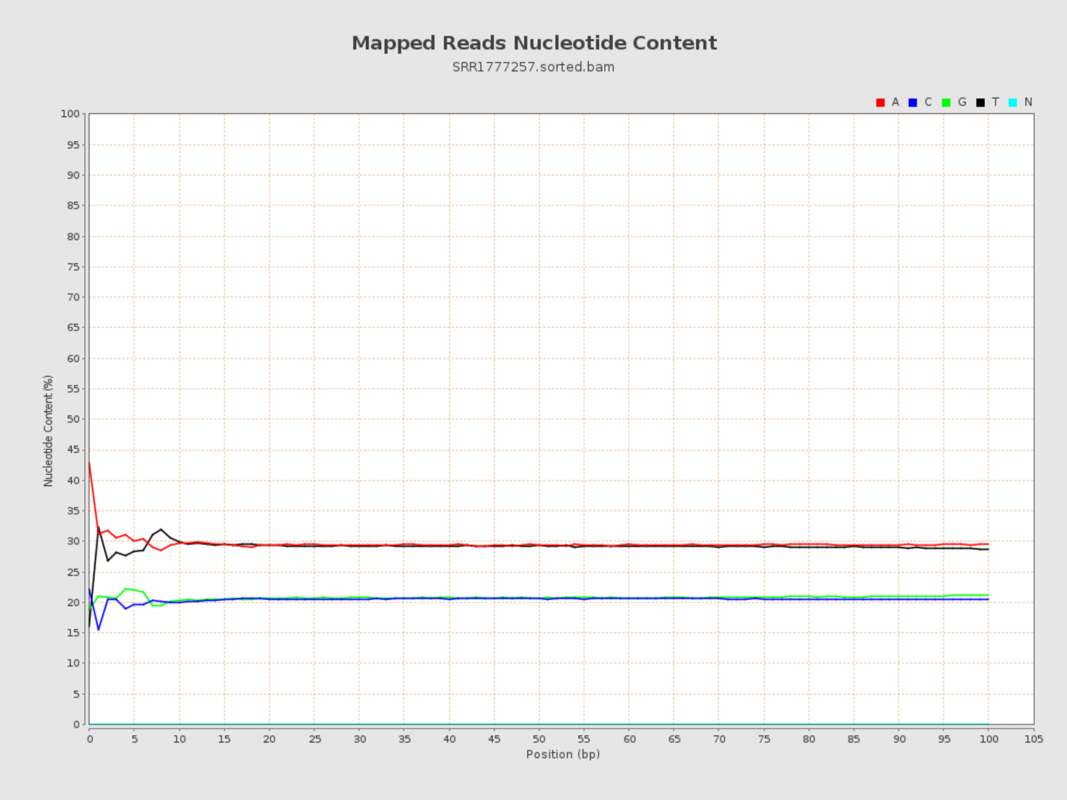
6. Results : Genome Fraction Coverage



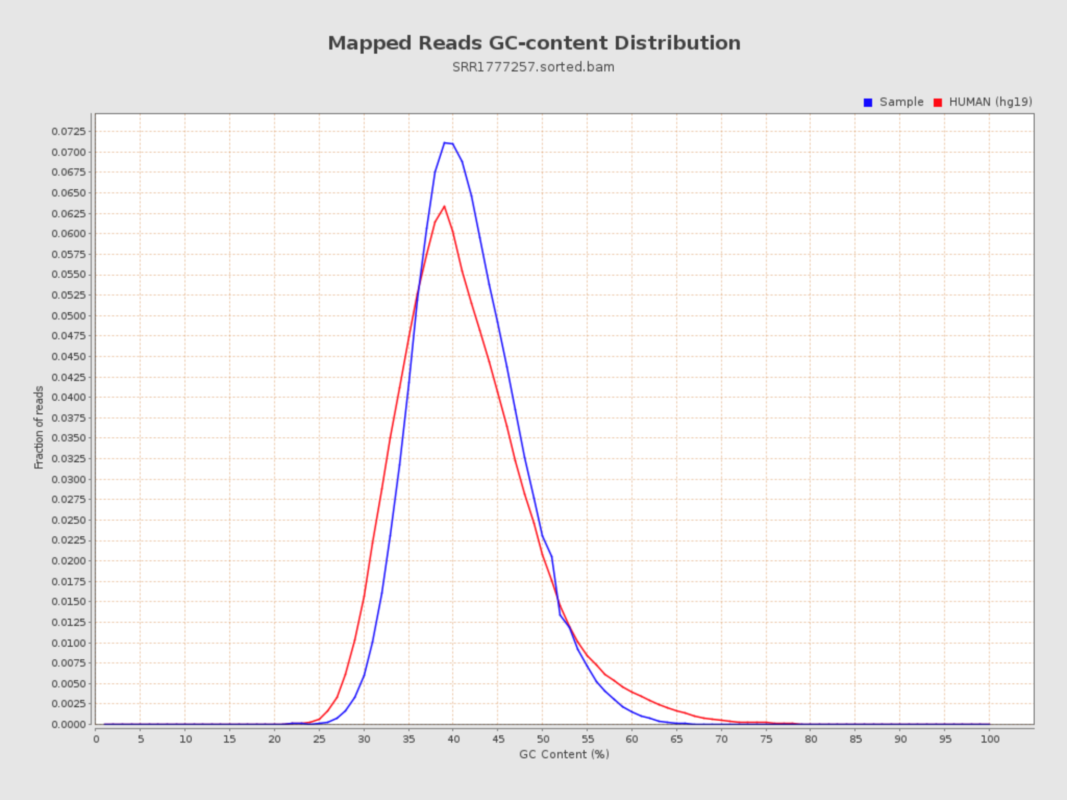
7. Results : Duplication Rate Histogram



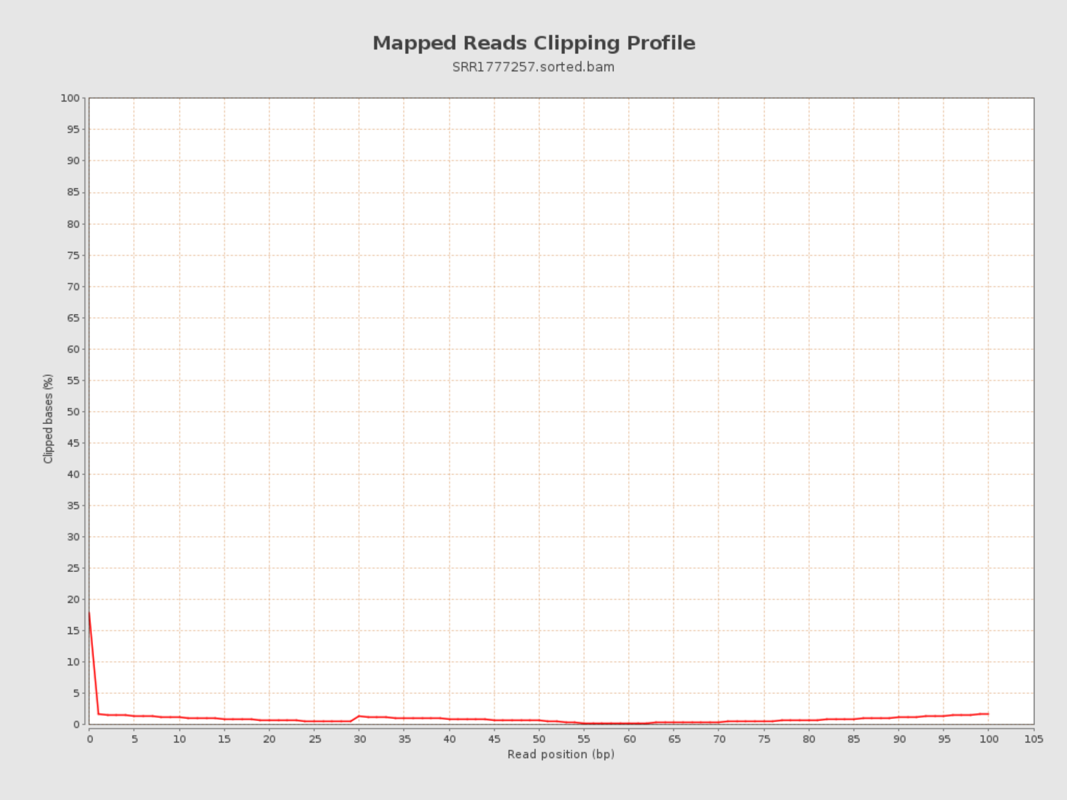
8. Results : Mapped Reads Nucleotide Content



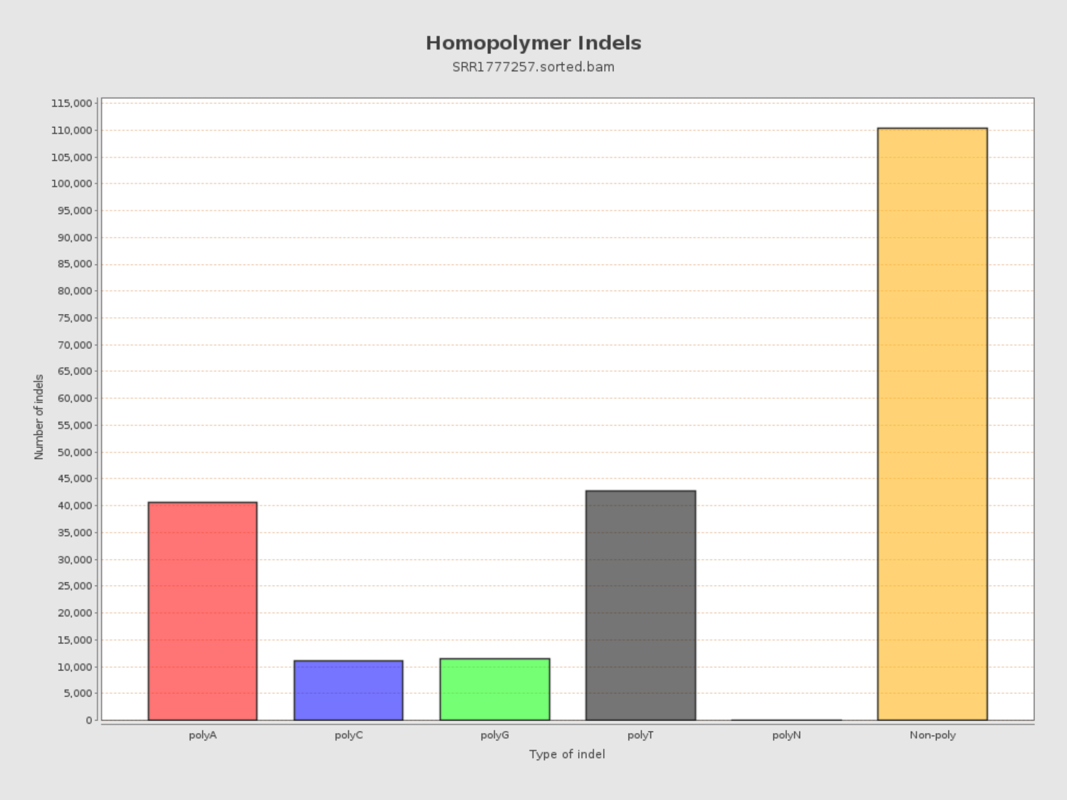
9. Results : Mapped Reads GC-content Distribution



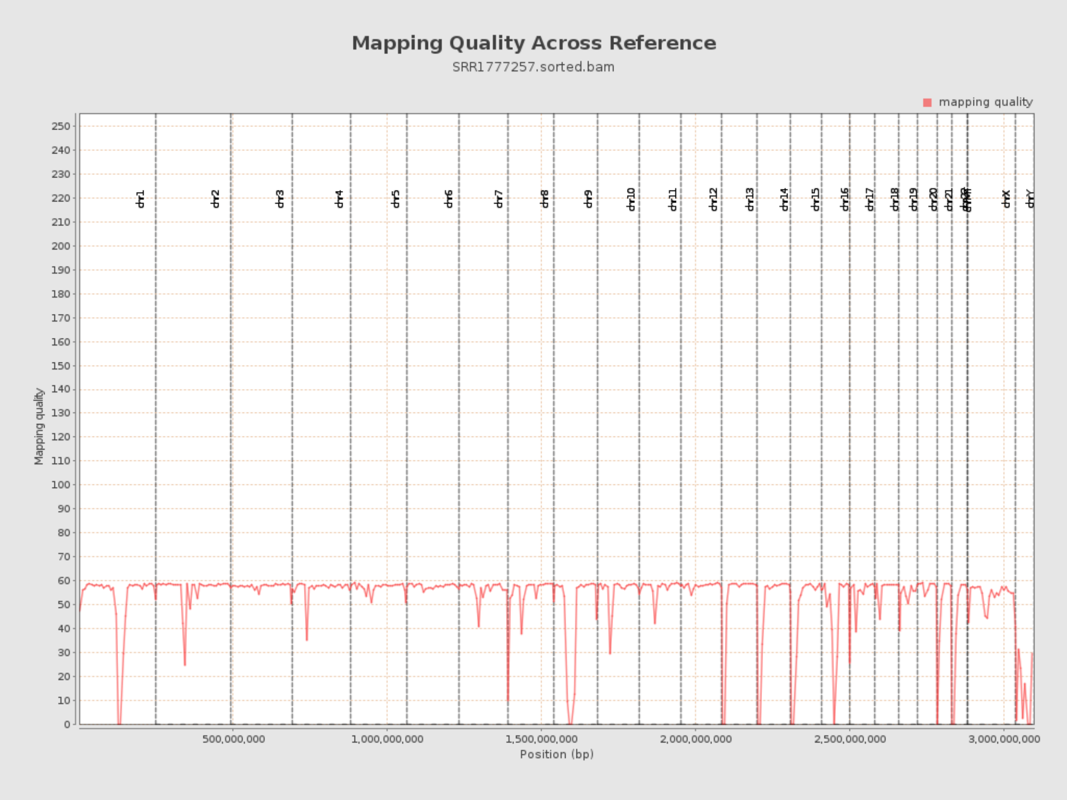
10. Results : Mapped Reads Clipping Profile



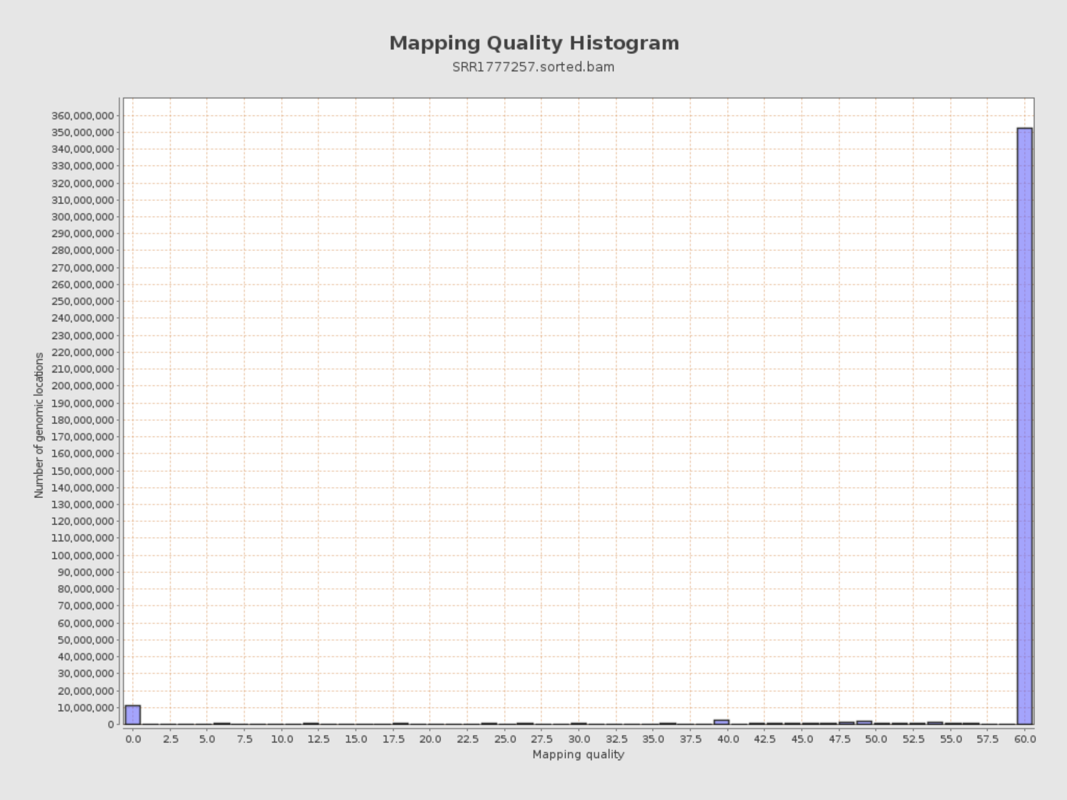
11. Results : Homopolymer Indels



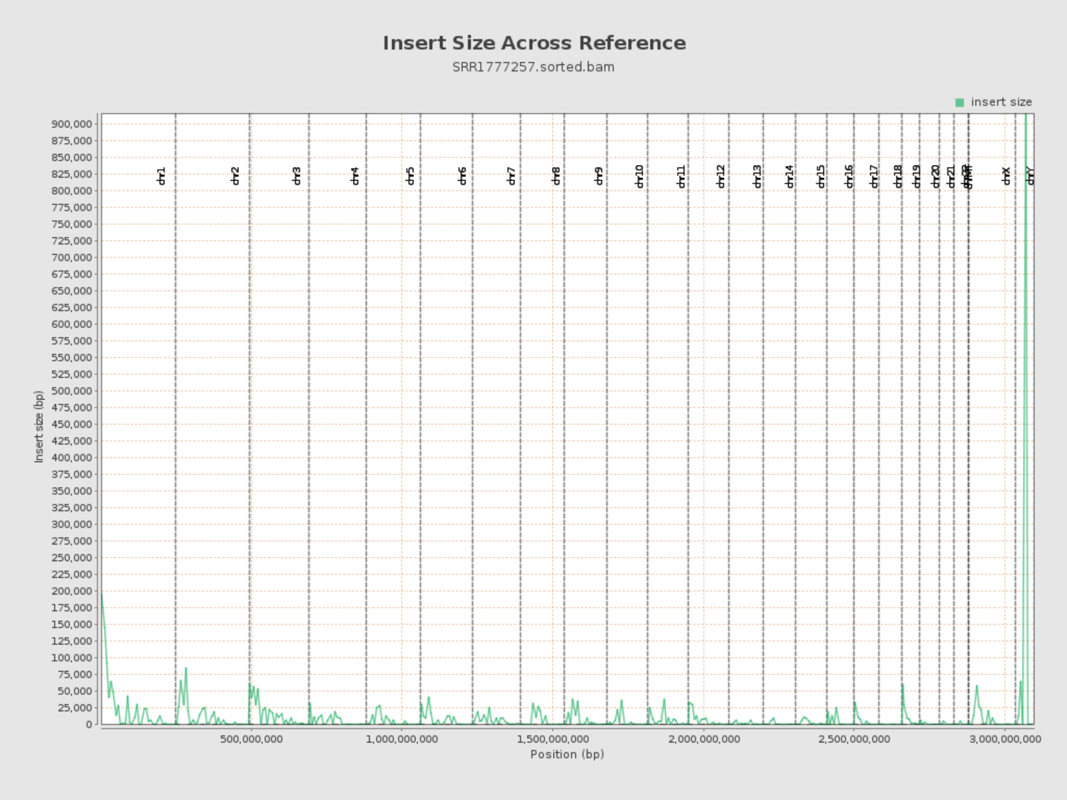
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram