Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/06 03:16:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778040.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_SRR1778040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778040_1.fastq.gz SRR1778040_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 06 03:16:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	193,952,890
Mapped reads	181,564,854 / 93.61%
Unmapped reads	12,388,036 / 6.39%
Mapped paired reads	181,564,854 / 93.61%
Mapped reads, first in pair	91,632,028 / 47.24%
Mapped reads, second in pair	89,932,826 / 46.37%
Mapped reads, both in pair	178,991,988 / 92.29%
Mapped reads, singletons	2,572,866 / 1.33%
Secondary alignments	0
Supplementary alignments	229,853 / 0.12%
Read min/max/mean length	30 / 76 / 70.02
Duplicated reads (estimated)	102,734,637 / 52.97%
Duplication rate	40.97%
Clipped reads	15,425,241 / 7.95%

2.2. ACGT Content

Number/percentage of A's	3,187,563,292 / 25.34%
Number/percentage of C's	3,112,775,897 / 24.75%
Number/percentage of T's	3,184,501,022 / 25.32%
Number/percentage of G's	3,092,411,610 / 24.58%
Number/percentage of N's	1,502,505 / 0.01%

GC Percentage	49.33%

2.3. Coverage

Mean	4.0637
Standard Deviation	40.2608

2.4. Mapping Quality

Mean Mapping Quality	51.9

2.5. Insert size

Mean	23,008.86
Standard Deviation	1,485,655.66
P25/Median/P75	87 / 103 / 127

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	65,018,852
Insertions	432,961
Mapped reads with at least one insertion	0.24%
Deletions	579,866
Mapped reads with at least one deletion	0.31%
Homopolymer indels	36.72%

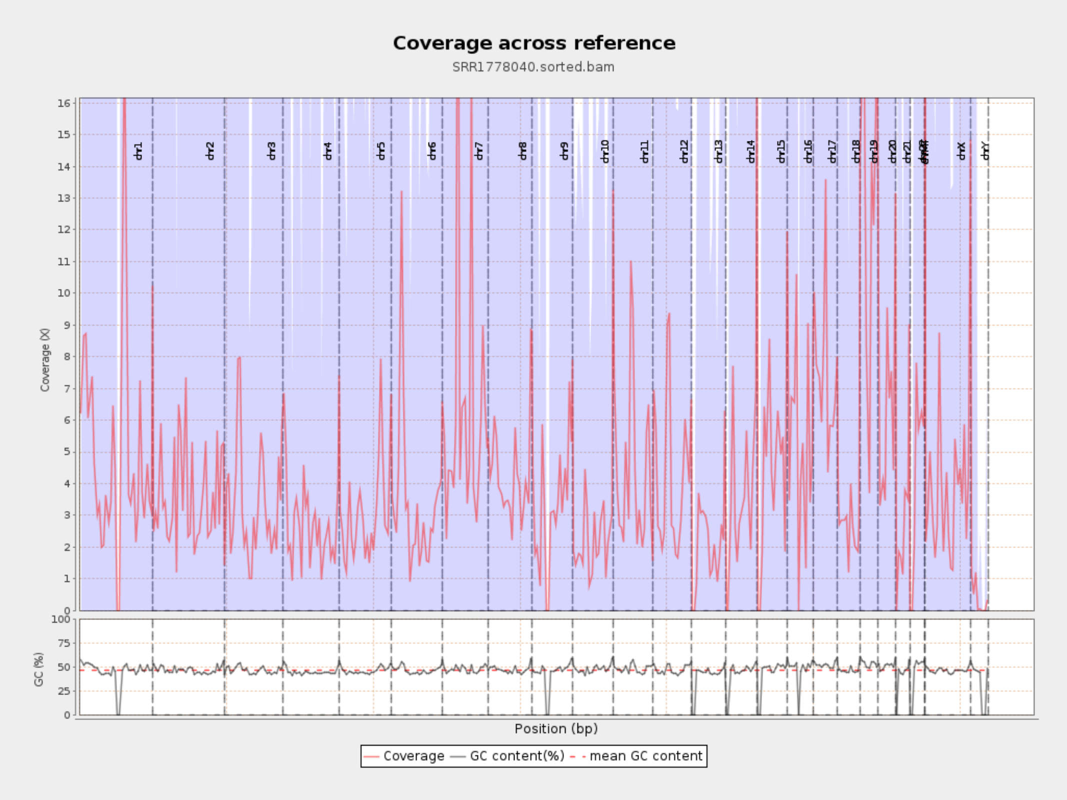
2.7. Chromosome stats

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

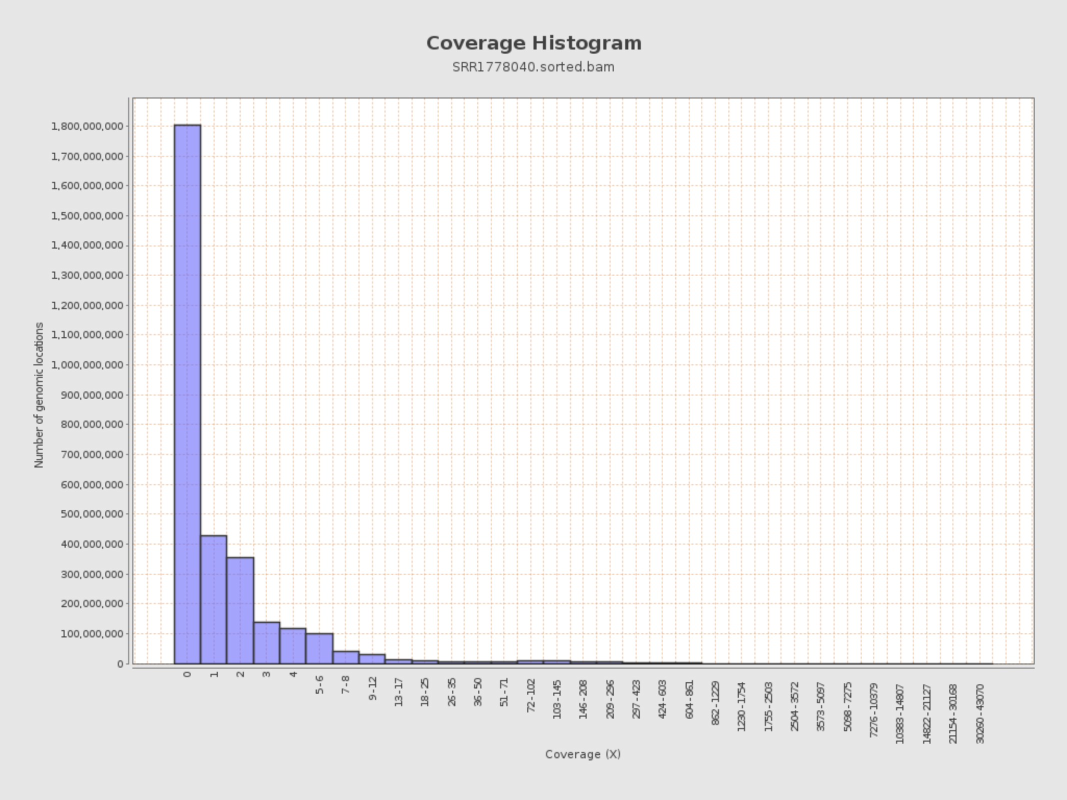
		bases	coverage	deviation
chr1	249250621	1267357111	5.0847	48.4681
chr2	243199373	884097047	3.6353	31.6767
chr3	198022430	663587987	3.3511	31.972
chr4	191154276	514835276	2.6933	23.6943
chr5	180915260	560916022	3.1004	24.3599
chr6	171115067	574786404	3.3591	28.1565
chr7	159138663	1051254425	6.6059	100.1854
chr8	146364022	610415615	4.1705	33.6375
chr9	141213431	473267757	3.3514	28.0457
chr10	135534747	295888145	2.1831	28.4309
chr11	135006516	634443690	4.6994	34.4773
chr12	133851895	569388109	4.2539	29.9836
chr13	115169878	231006234	2.0058	19.9376
chr14	107349540	382454637	3.5627	29.9486
chr15	102531392	424567172	4.1409	32.7679
chr16	90354753	489510530	5.4177	36.9307
chr17	81195210	615914219	7.5856	50.3891
chr18	78077248	205664746	2.6341	23.912
chr19	59128983	764973579	12.9374	67.1629
chr20	63025520	392823561	6.2328	40.8771
chr21	48129895	137324229	2.8532	26.8203
chr22	51304566	230191314	4.4868	31.017
chrMT	16571	670379	40.455	18.8265
chrX	155270560	582448345	3.7512	40.3296

chrY	59373566	22237799	0.3745	20.973

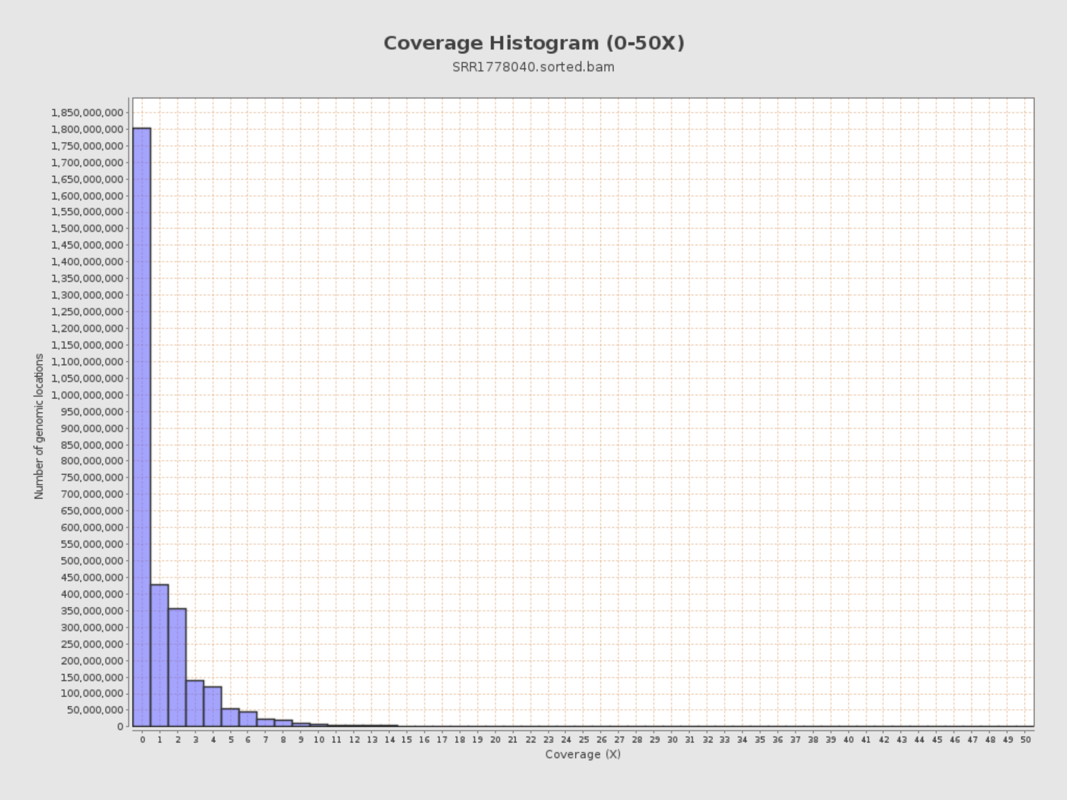
3. Results : Coverage across reference



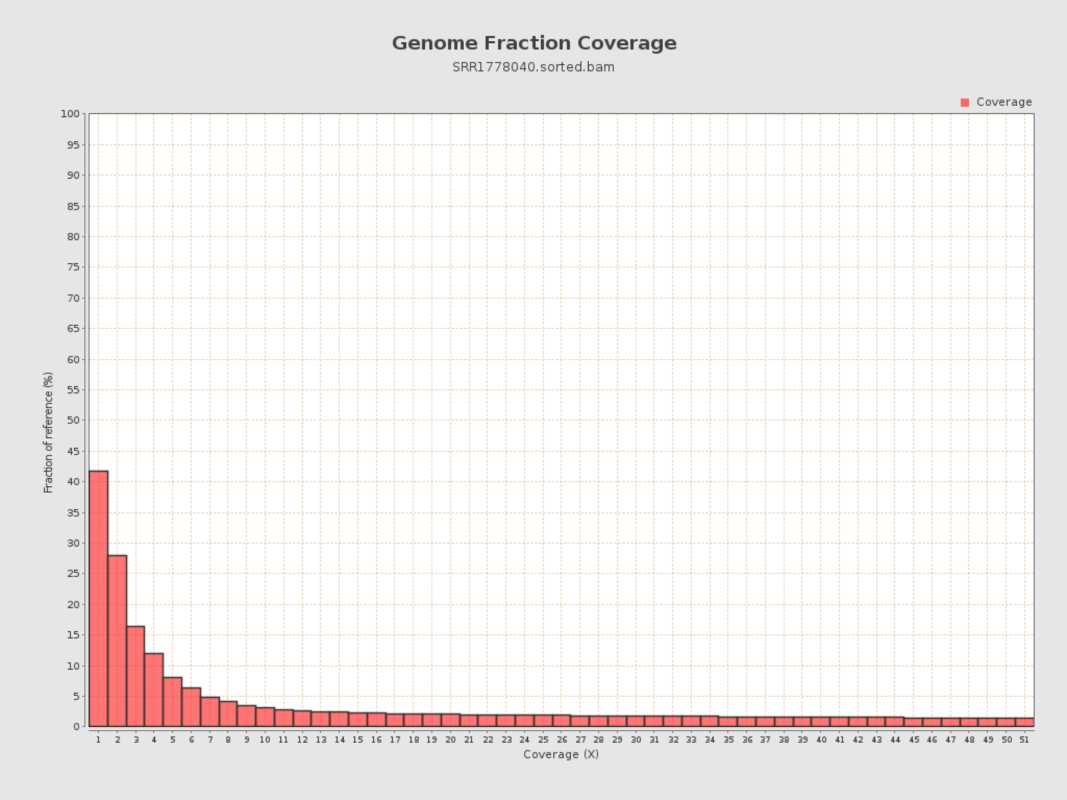
4. Results : Coverage Histogram



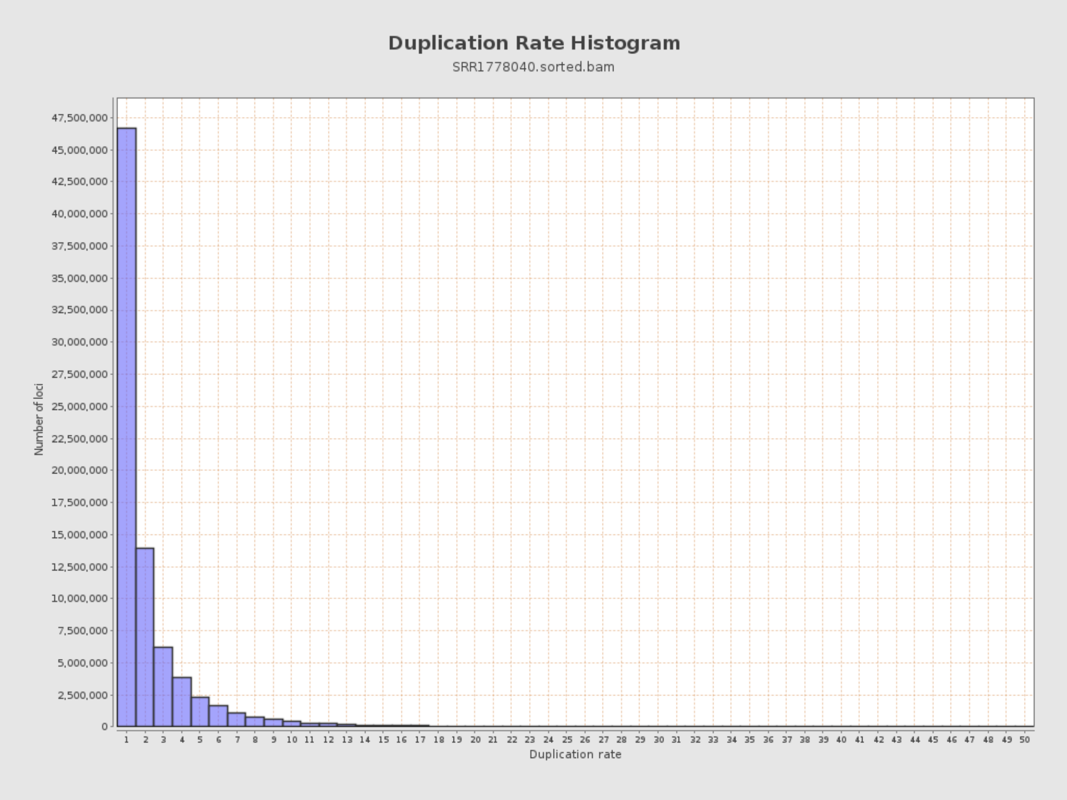
5. Results : Coverage Histogram (0-50X)



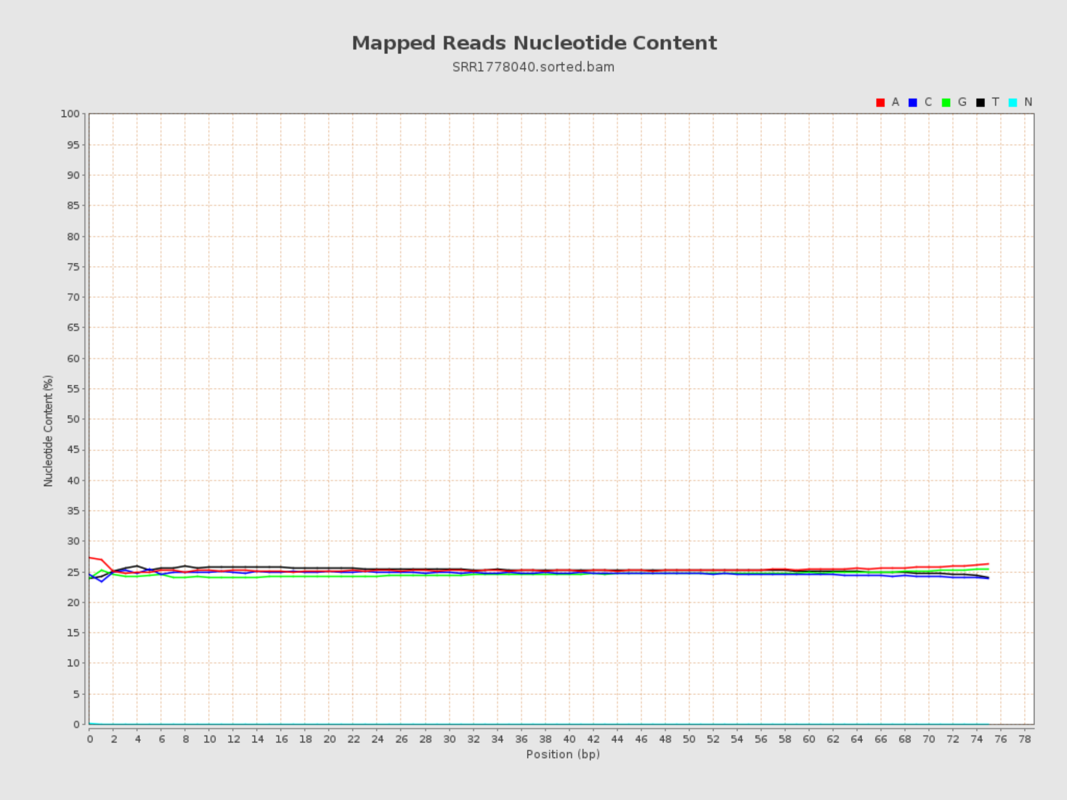
6. Results : Genome Fraction Coverage



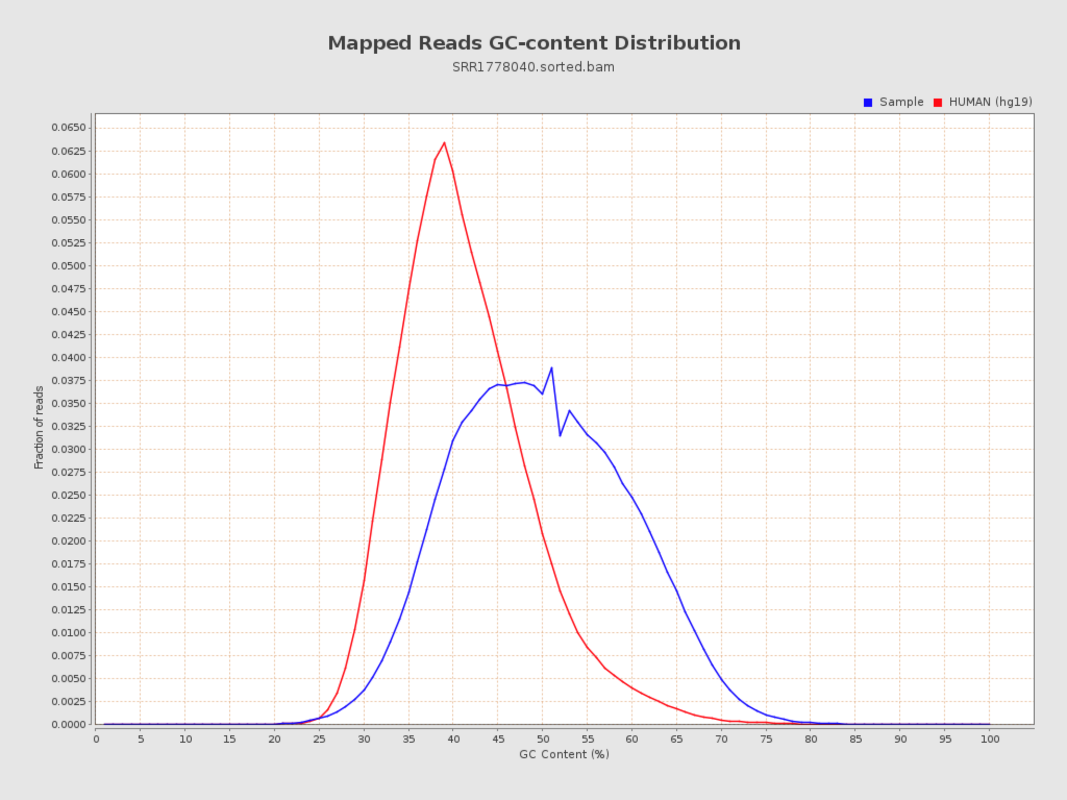
7. Results : Duplication Rate Histogram



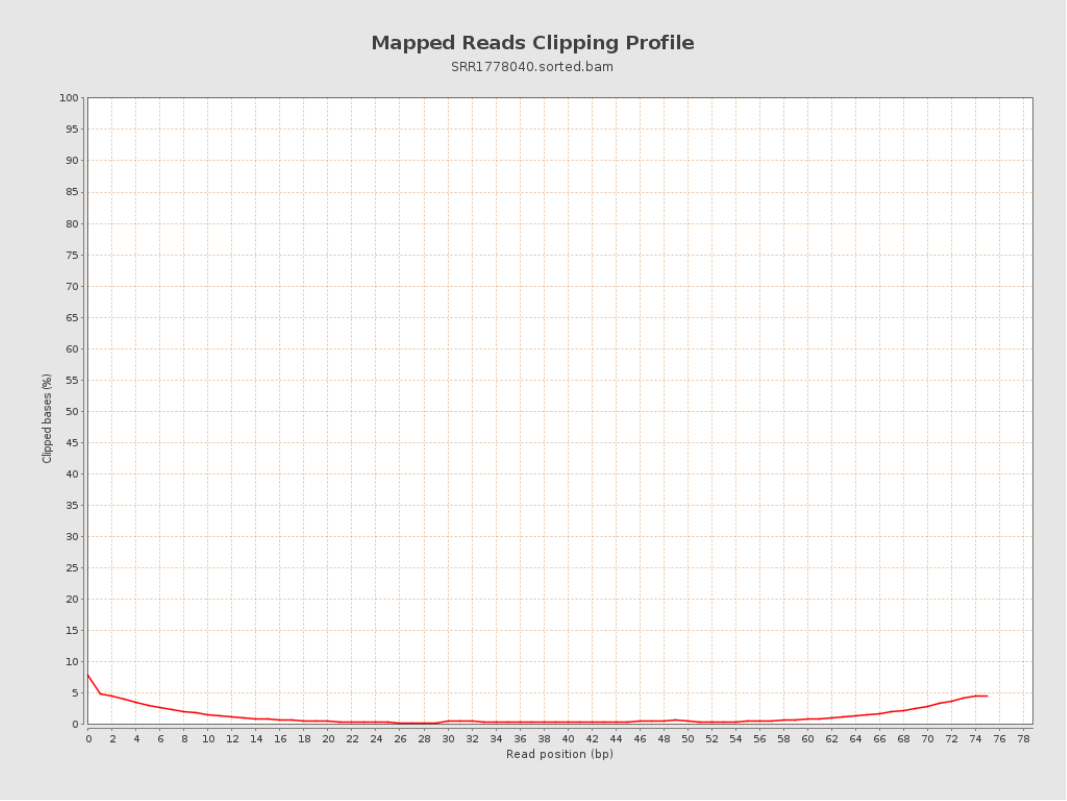
8. Results : Mapped Reads Nucleotide Content



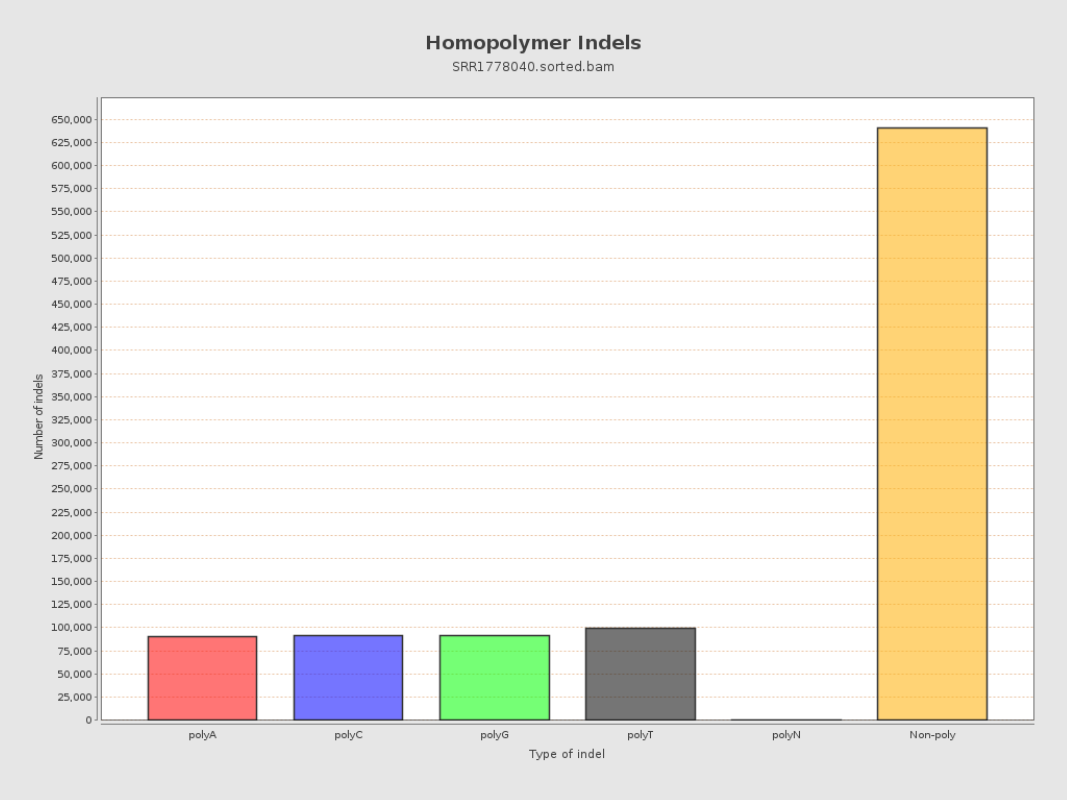
9. Results : Mapped Reads GC-content Distribution



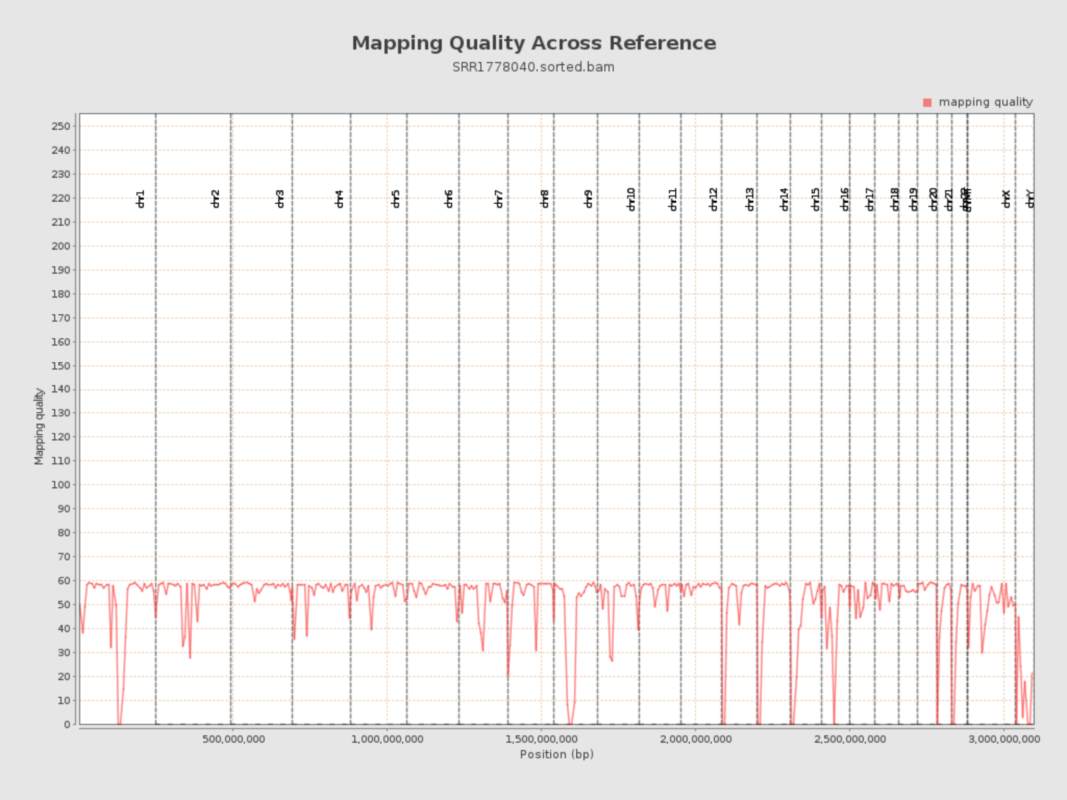
10. Results : Mapped Reads Clipping Profile



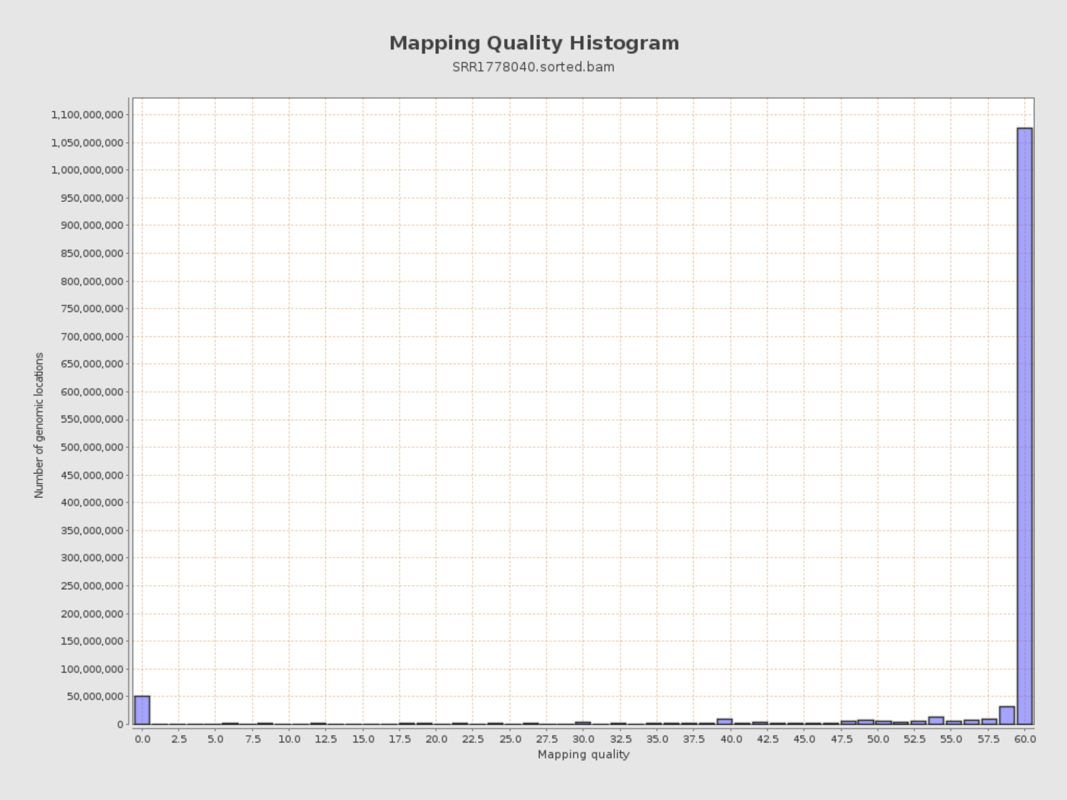
11. Results : Homopolymer Indels



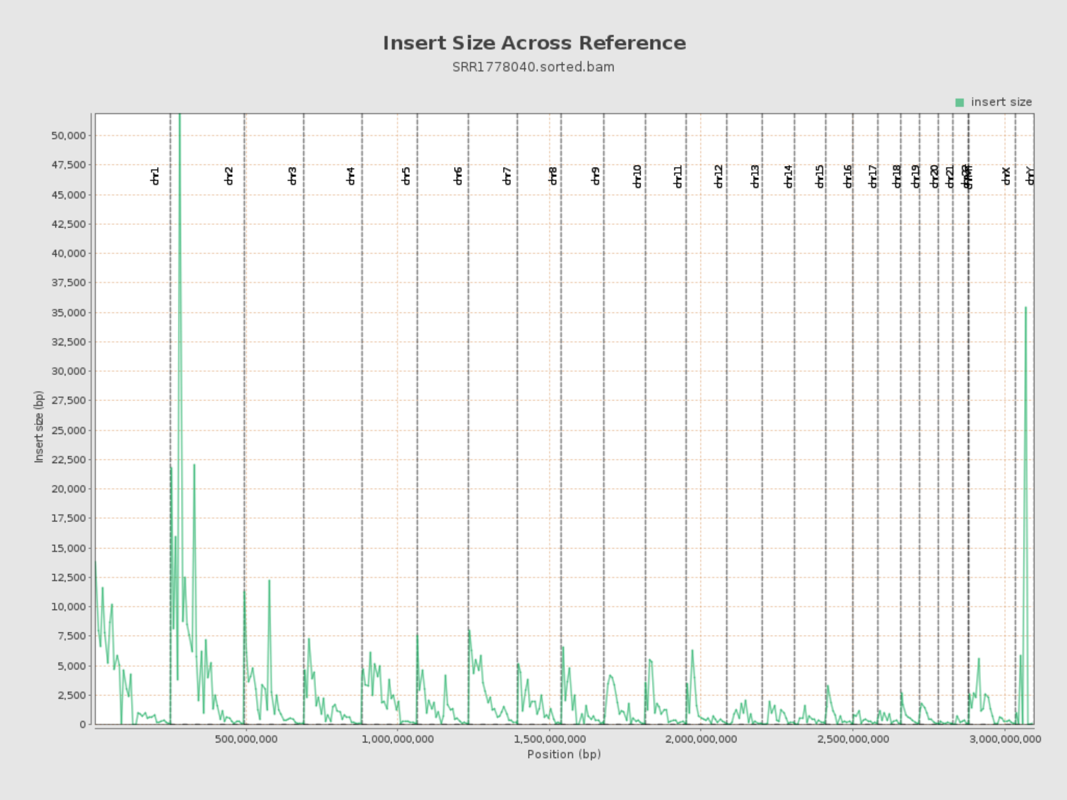
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram