Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 01:18:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778460.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_SRR1778460 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778460_1.fastq.gz SRR1778460_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 01:18:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778460.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	256,823,158
Mapped reads	234,444,435 / 91.29%
Unmapped reads	22,378,723 / 8.71%
Mapped paired reads	234,444,435 / 91.29%
Mapped reads, first in pair	118,550,238 / 46.16%
Mapped reads, second in pair	115,894,197 / 45.13%
Mapped reads, both in pair	230,629,984 / 89.8%
Mapped reads, singletons	3,814,451 / 1.49%
Secondary alignments	0
Supplementary alignments	232,865 / 0.09%
Read min/max/mean length	30 / 76 / 70.02
Duplicated reads (estimated)	157,233,537 / 61.22%
Duplication rate	50.5%
Clipped reads	22,133,966 / 8.62%

2.2. ACGT Content

Number/percentage of A's	4,106,998,423 / 25.31%
Number/percentage of C's	4,023,598,851 / 24.79%
Number/percentage of T's	4,098,142,039 / 25.25%
Number/percentage of G's	3,996,839,322 / 24.63%
Number/percentage of N's	1,929,186 / 0.01%

GC Percentage	49.42%

2.3. Coverage

Mean	5.2424
Standard Deviation	59.8045

2.4. Mapping Quality

Mean Mapping Quality	51.85

2.5. Insert size

Mean	22,643.94
Standard Deviation	1,474,471.28
P25/Median/P75	85 / 102 / 127

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	82,046,964
Insertions	500,441
Mapped reads with at least one insertion	0.21%
Deletions	685,817
Mapped reads with at least one deletion	0.29%
Homopolymer indels	37.05%

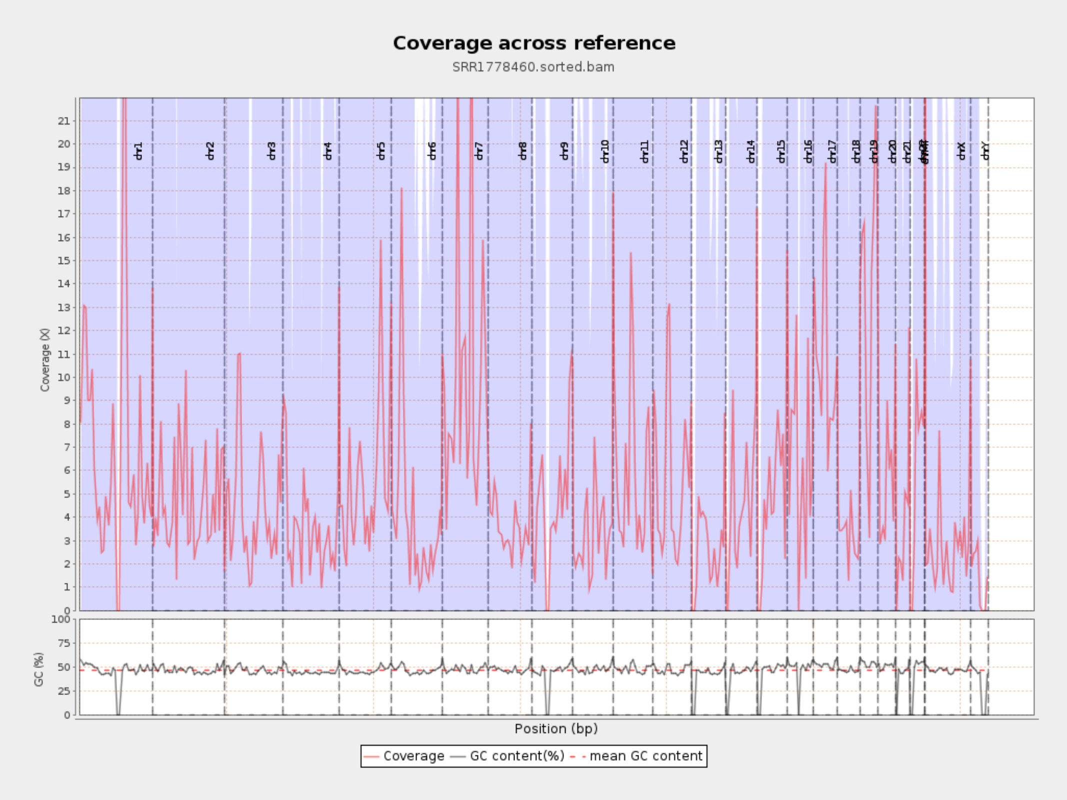
2.7. Chromosome stats

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

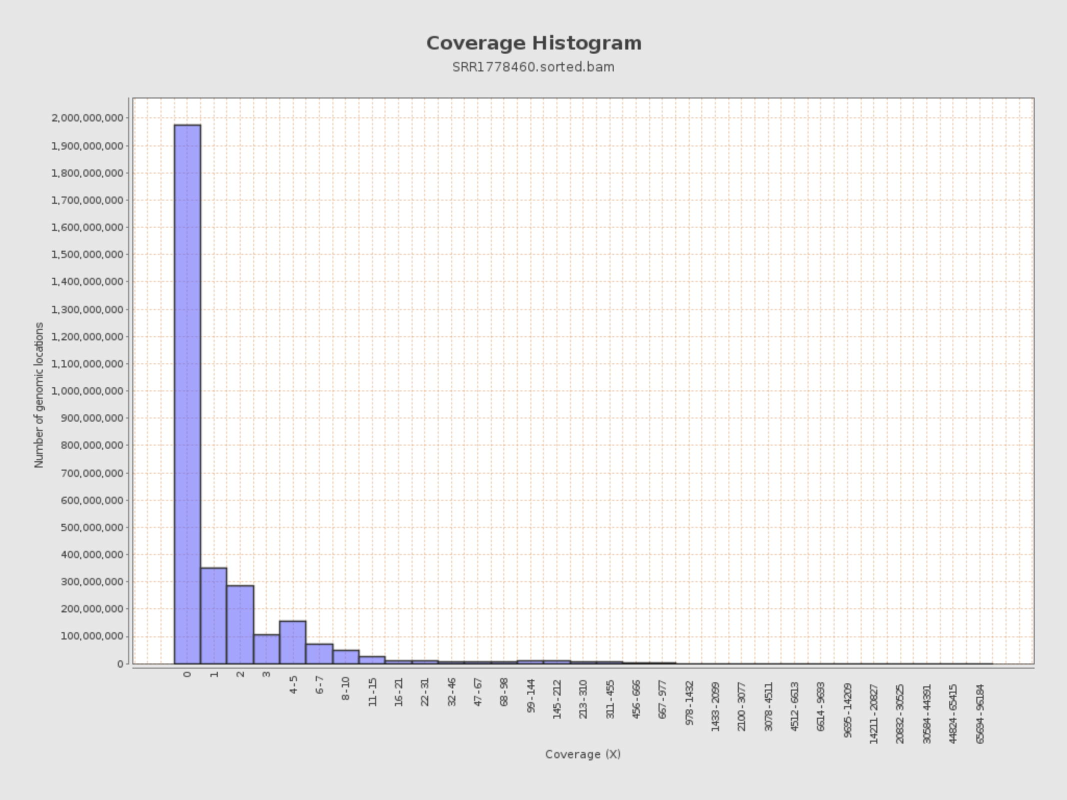
		bases	coverage	deviation
chr1	249250621	1785979294	7.1654	77.6531
chr2	243199373	1157956974	4.7613	46.4764
chr3	198022430	873722239	4.4122	48.203
chr4	191154276	659641950	3.4508	35.279
chr5	180915260	1036743026	5.7305	50.7811
chr6	171115067	662732502	3.873	45.4951
chr7	159138663	1666809125	10.4739	155.9659
chr8	146364022	535808983	3.6608	32.5942
chr9	141213431	642691111	4.5512	45.6981
chr10	135534747	439898052	3.2456	33.9257
chr11	135006516	841675929	6.2343	48.7154
chr12	133851895	765991607	5.7227	43.9065
chr13	115169878	294261771	2.555	26.3405
chr14	107349540	481313398	4.4836	40.9479
chr15	102531392	456148140	4.4489	37.8781
chr16	90354753	599319745	6.633	48.4916
chr17	81195210	893437177	11.0036	98.7591
chr18	78077248	254674412	3.2618	32.486
chr19	59128983	833015637	14.0881	77.9437
chr20	63025520	354231425	5.6204	41.4246
chr21	48129895	178225438	3.703	38.2074
chr22	51304566	315778821	6.155	46.6717
chrMT	16571	1646187	99.3414	39.777
chrX	155270560	413276893	2.6617	38.1685

chrY	59373566	83989340	1.4146	36.9505

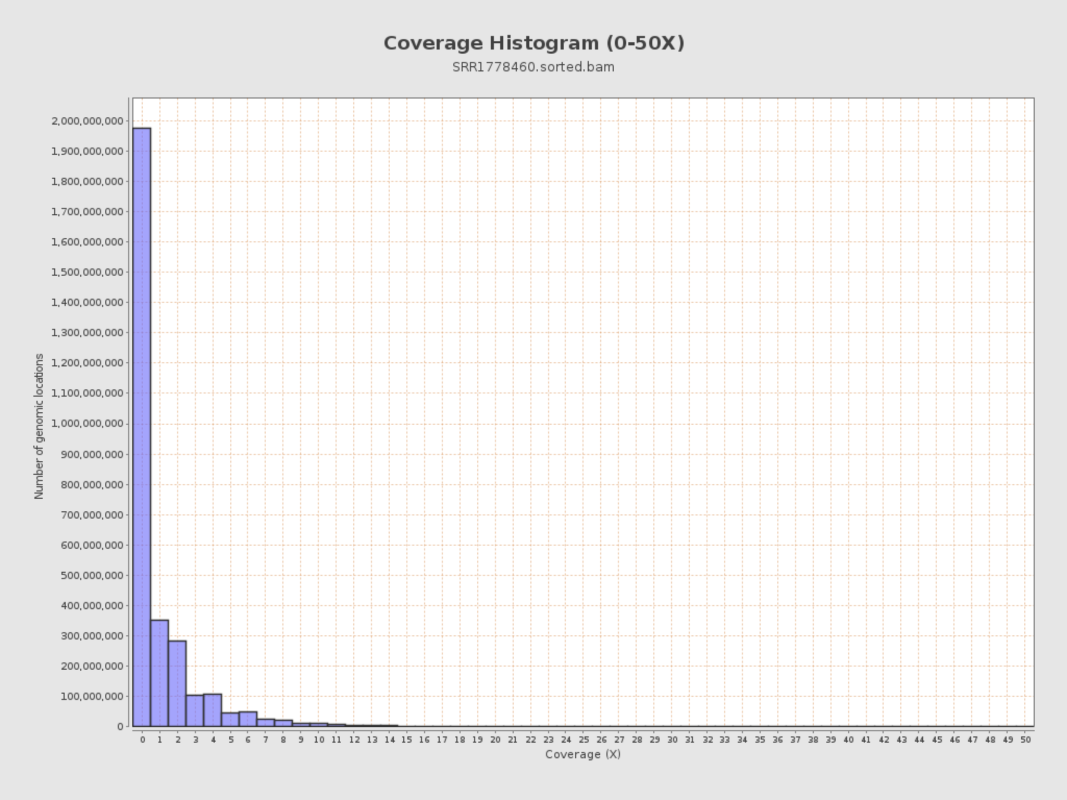
3. Results : Coverage across reference



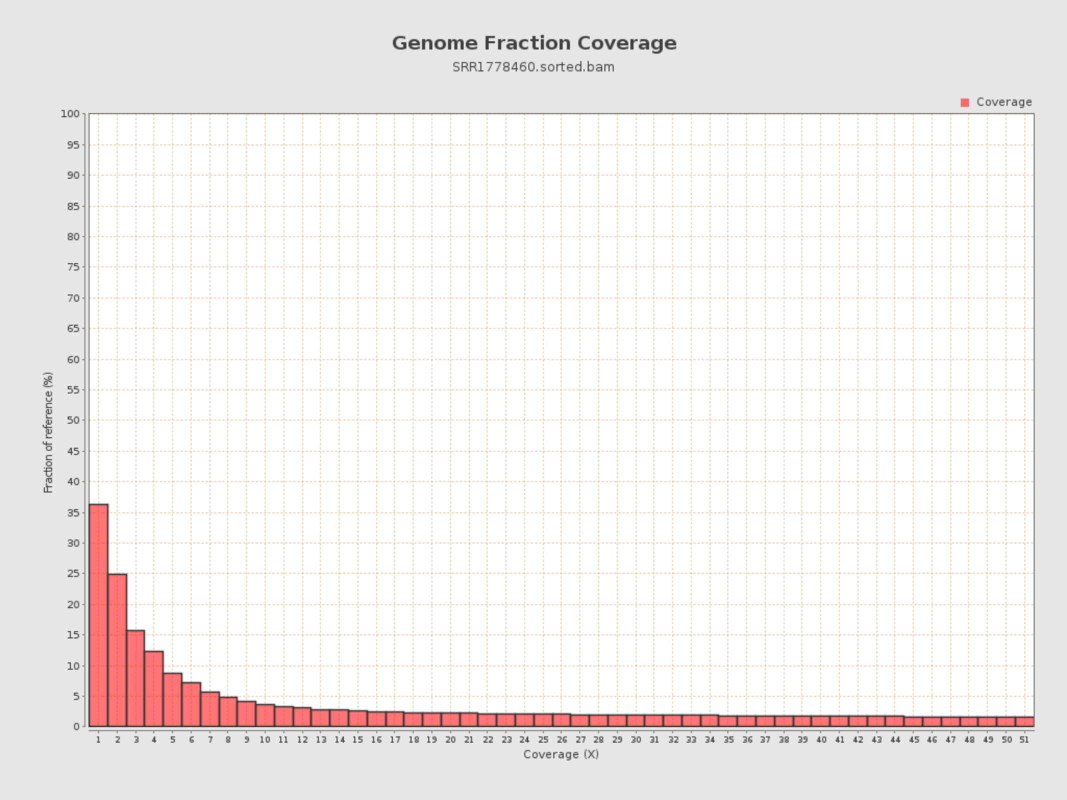
4. Results : Coverage Histogram



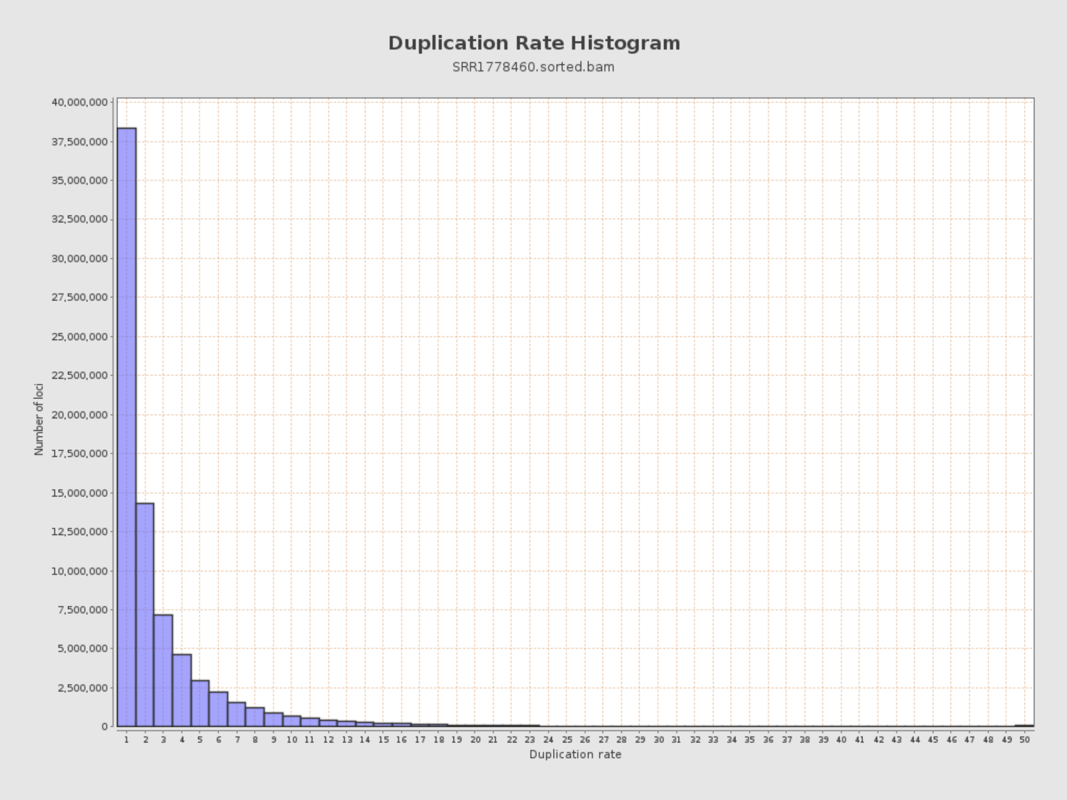
5. Results : Coverage Histogram (0-50X)



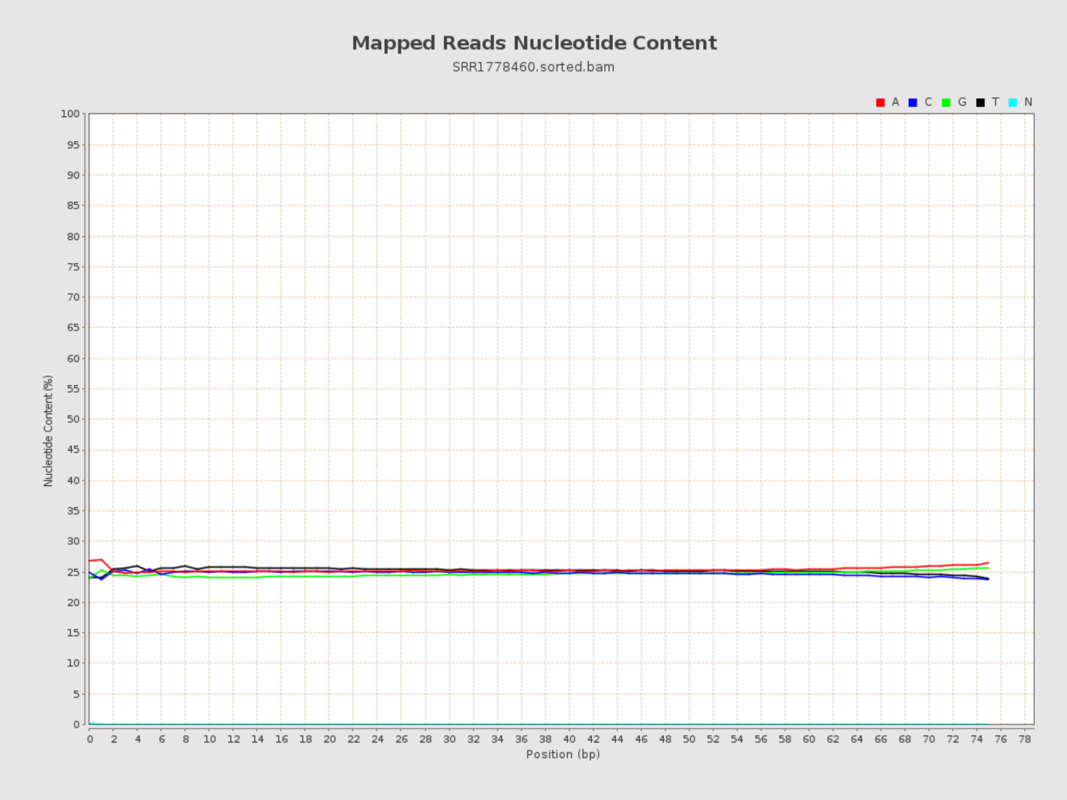
6. Results : Genome Fraction Coverage



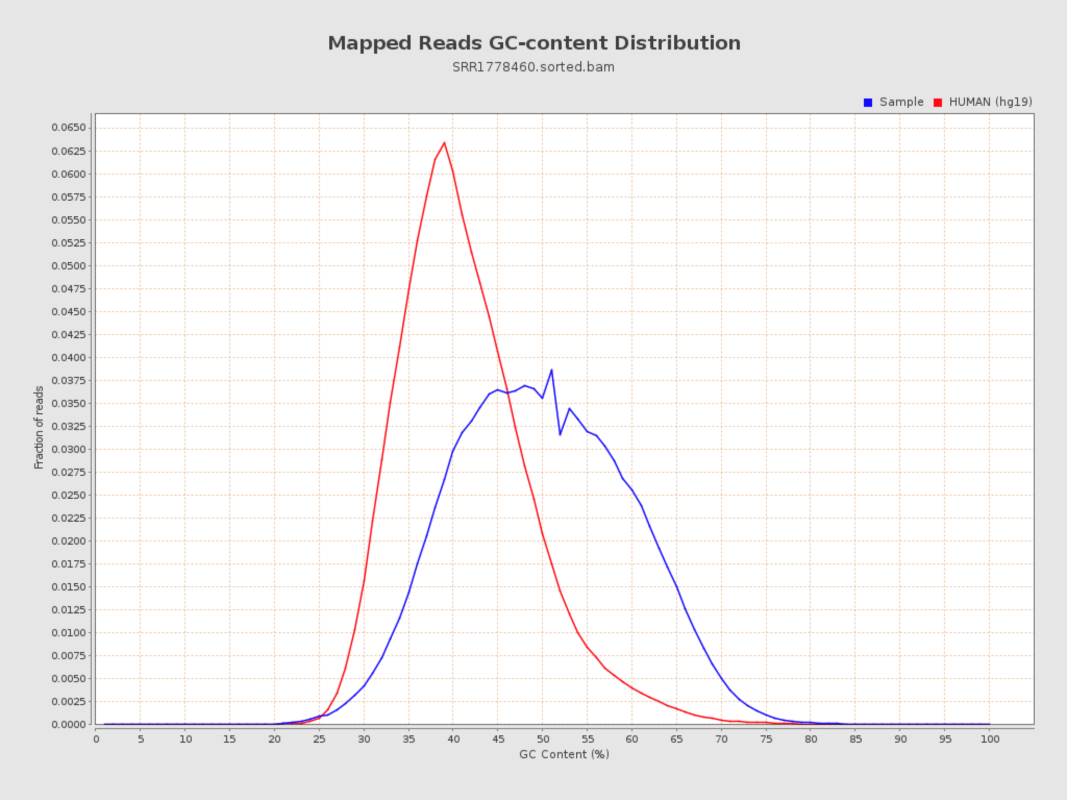
7. Results : Duplication Rate Histogram



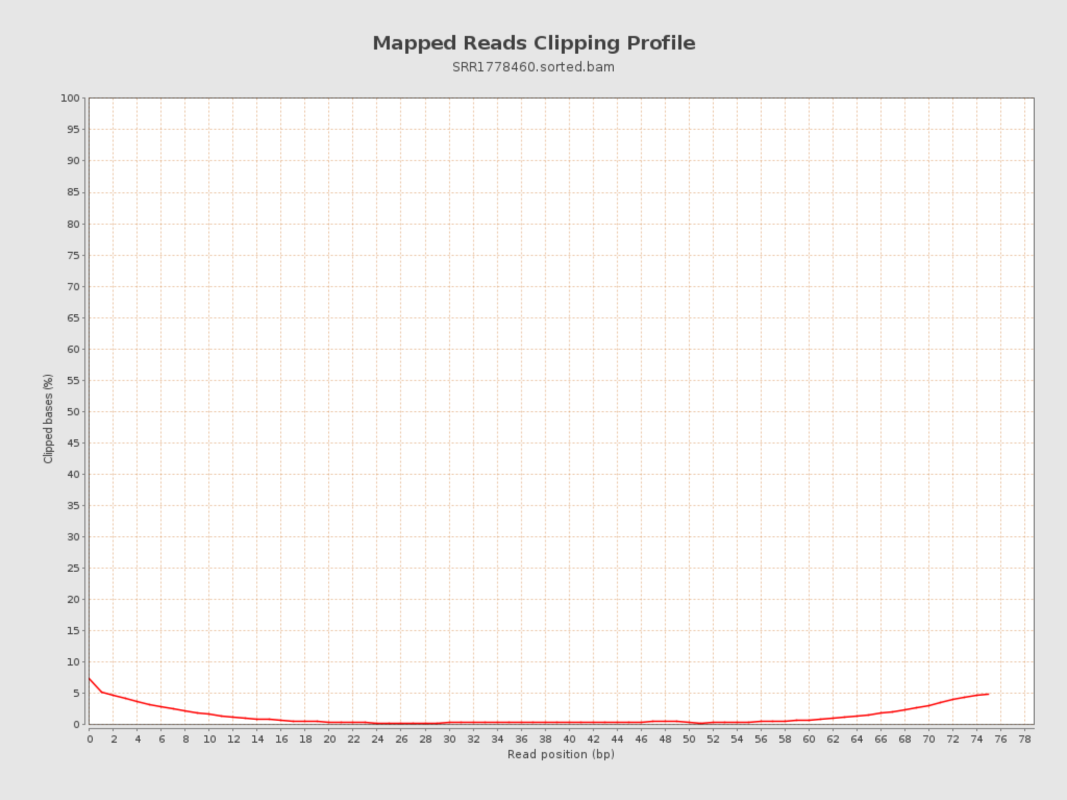
8. Results : Mapped Reads Nucleotide Content



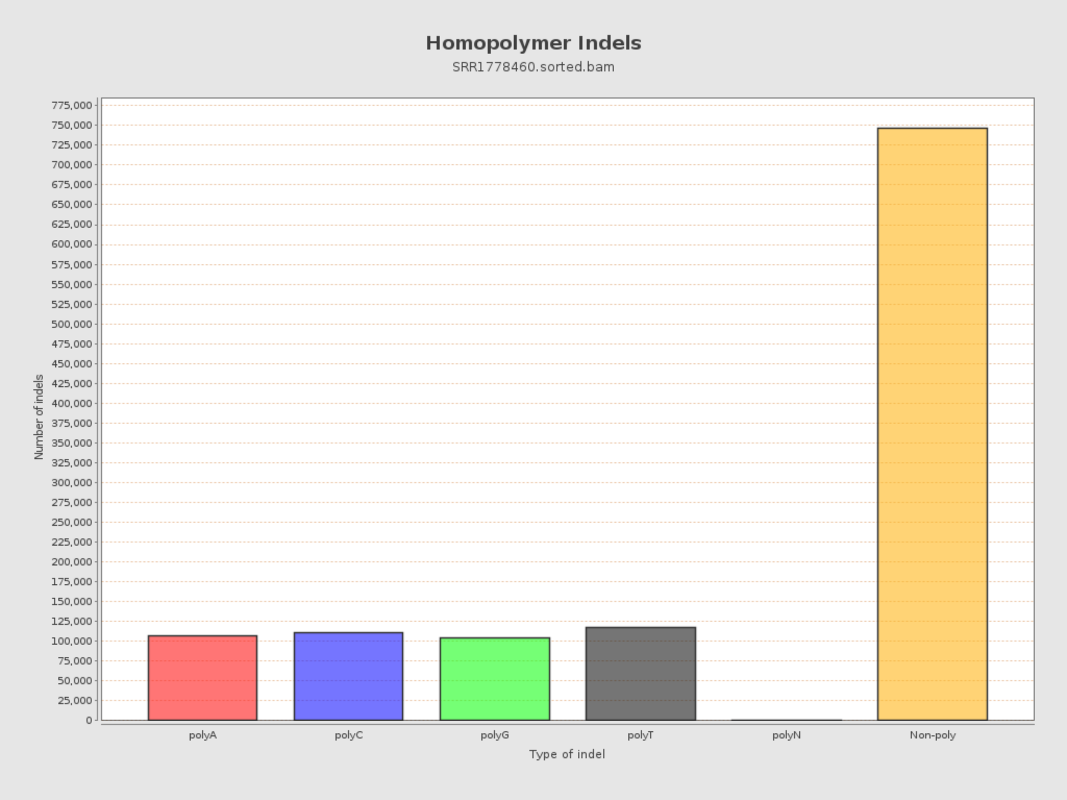
9. Results : Mapped Reads GC-content Distribution



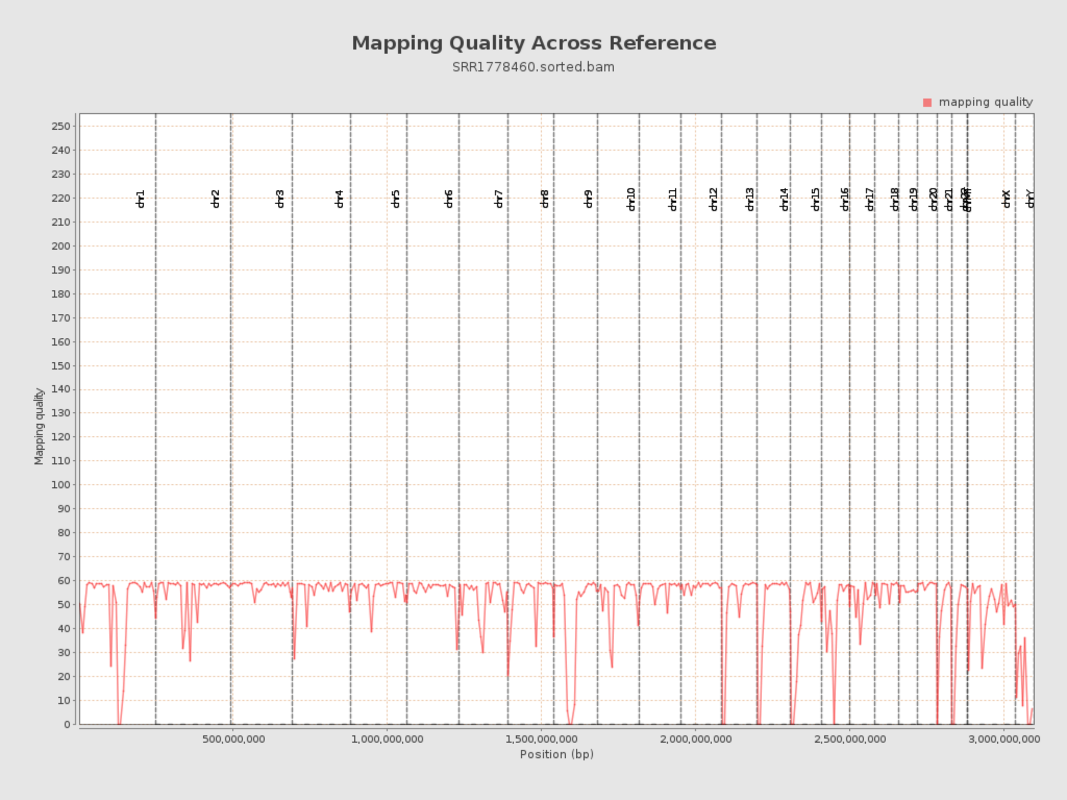
10. Results : Mapped Reads Clipping Profile



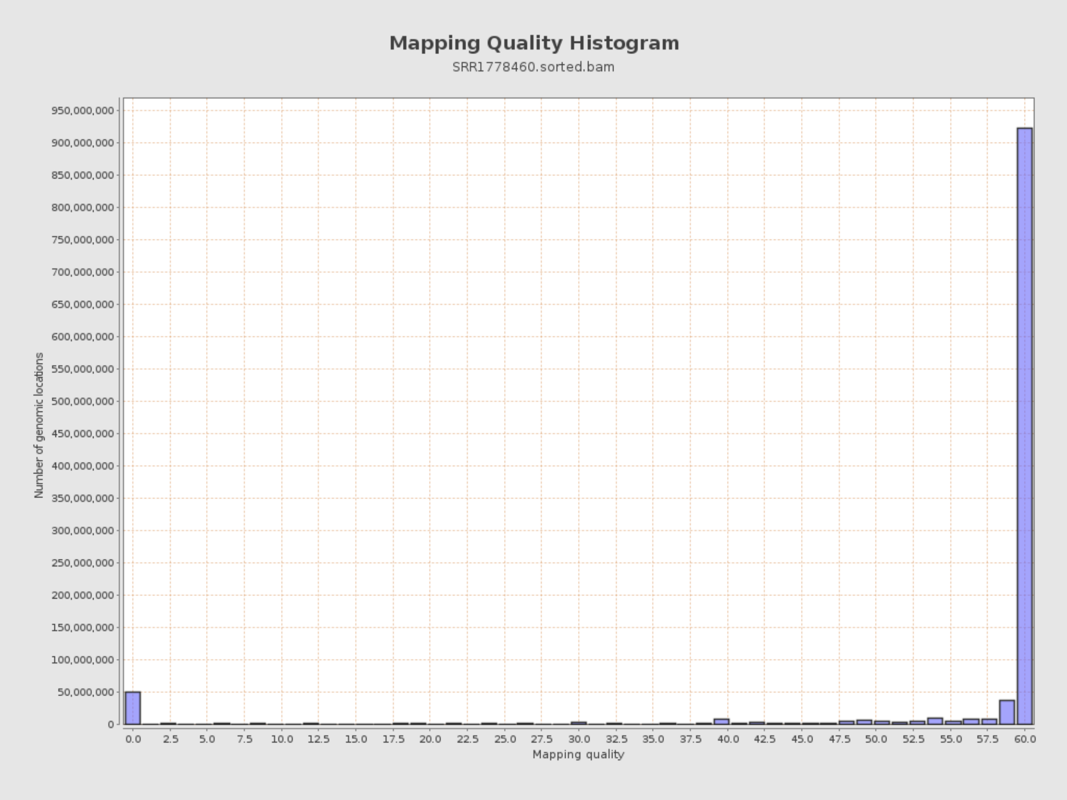
11. Results : Homopolymer Indels



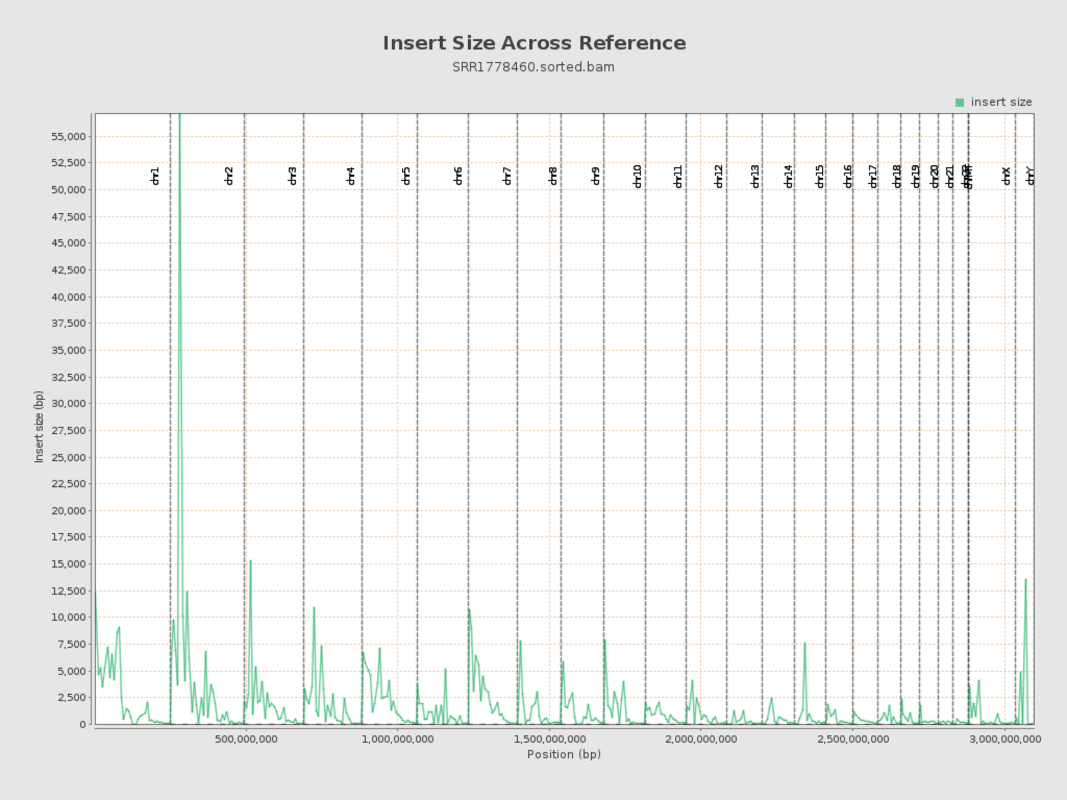
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram