Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 05:09:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778461.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_SRR1778461 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778461_1.fastq.gz SRR1778461_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 05:09:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778461.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	203,204,212
Mapped reads	193,298,758 / 95.13%
Unmapped reads	9,905,454 / 4.87%
Mapped paired reads	193,298,758 / 95.13%
Mapped reads, first in pair	97,251,256 / 47.86%
Mapped reads, second in pair	96,047,502 / 47.27%
Mapped reads, both in pair	191,158,150 / 94.07%
Mapped reads, singletons	2,140,608 / 1.05%
Secondary alignments	0
Supplementary alignments	432,877 / 0.21%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	151,098,519 / 74.36%
Duplication rate	62.52%
Clipped reads	40,107,762 / 19.74%

2.2. ACGT Content

Number/percentage of A's	3,485,548,122 / 24.34%
Number/percentage of C's	3,694,722,306 / 25.8%
Number/percentage of T's	3,434,577,984 / 23.99%
Number/percentage of G's	3,702,541,361 / 25.86%
Number/percentage of N's	2,039,640 / 0.01%

GC Percentage	51.66%

2.3. Coverage

Mean	4.626
Standard Deviation	60.1845

2.4. Mapping Quality

Mean Mapping Quality	51.93

2.5. Insert size

Mean	30,493.6
Standard Deviation	1,733,455.2
P25/Median/P75	77 / 89 / 107

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	70,189,409
Insertions	430,787
Mapped reads with at least one insertion	0.22%
Deletions	593,148
Mapped reads with at least one deletion	0.3%
Homopolymer indels	33.03%

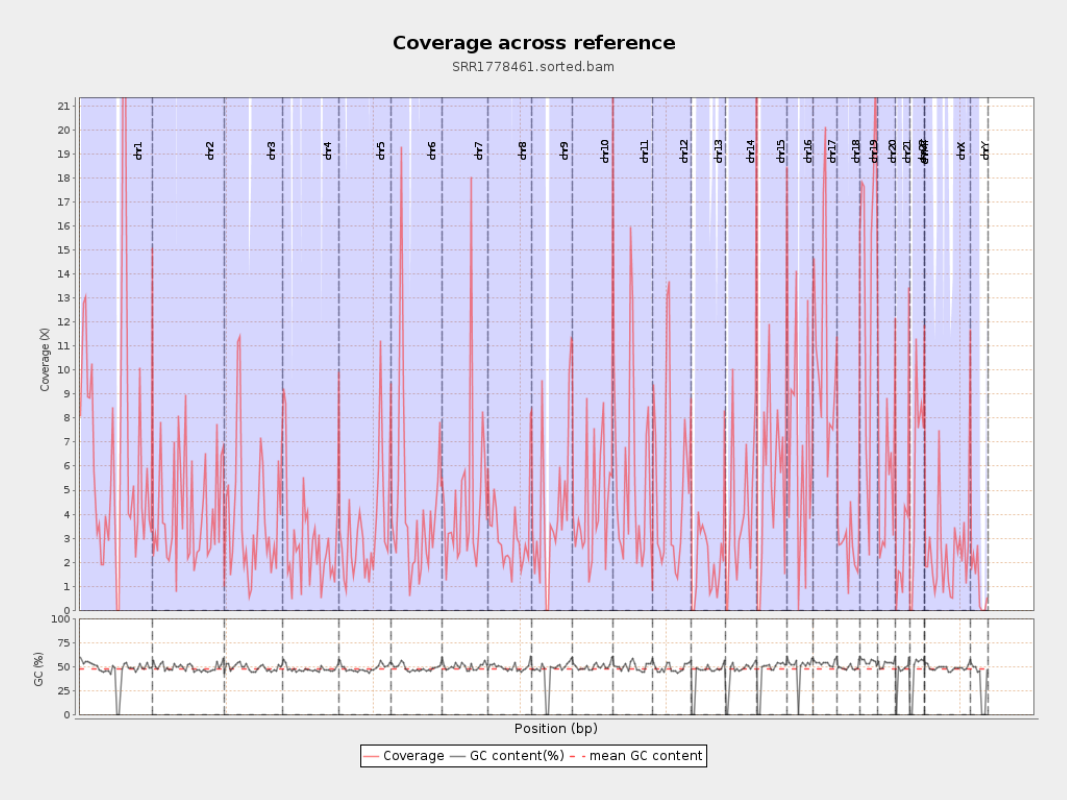
2.7. Chromosome stats

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

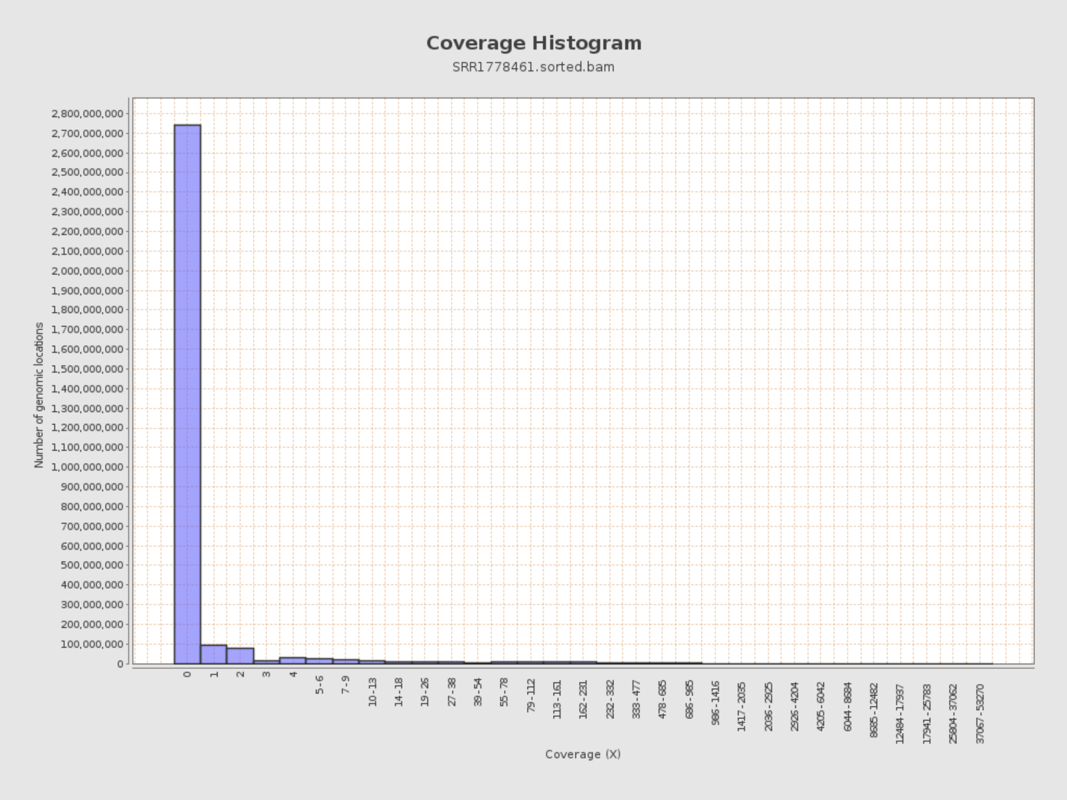
		bases	coverage	deviation
chr1	249250621	1700156636	6.8211	92.8187
chr2	243199373	999872988	4.1113	50.624
chr3	198022430	770475686	3.8909	51.172
chr4	191154276	552437914	2.89	42.2236
chr5	180915260	624936970	3.4543	41.8446
chr6	171115067	727864111	4.2537	68.3095
chr7	159138663	726106794	4.5627	67.7087
chr8	146364022	446682348	3.0519	38.1506
chr9	141213431	605594899	4.2885	48.5305
chr10	135534747	586944191	4.3306	47.0339
chr11	135006516	804887743	5.9618	61.3798
chr12	133851895	704307800	5.2618	52.6063
chr13	115169878	232574936	2.0194	33.0699
chr14	107349540	459716739	4.2824	51.7556
chr15	102531392	533613398	5.2044	55.6643
chr16	90354753	636741437	7.0471	63.8913
chr17	81195210	898454843	11.0654	133.1622
chr18	78077248	206128674	2.6401	36.6719
chr19	59128983	861072287	14.5626	95.2484
chr20	63025520	329883500	5.2341	49.8721
chr21	48129895	159981965	3.324	45.859
chr22	51304566	317379266	6.1862	58.5738
chrMT	16571	180672	10.9029	12.0041
chrX	155270560	370166287	2.384	41.3879

chrY	59373566	64556198	1.0873	44.4149

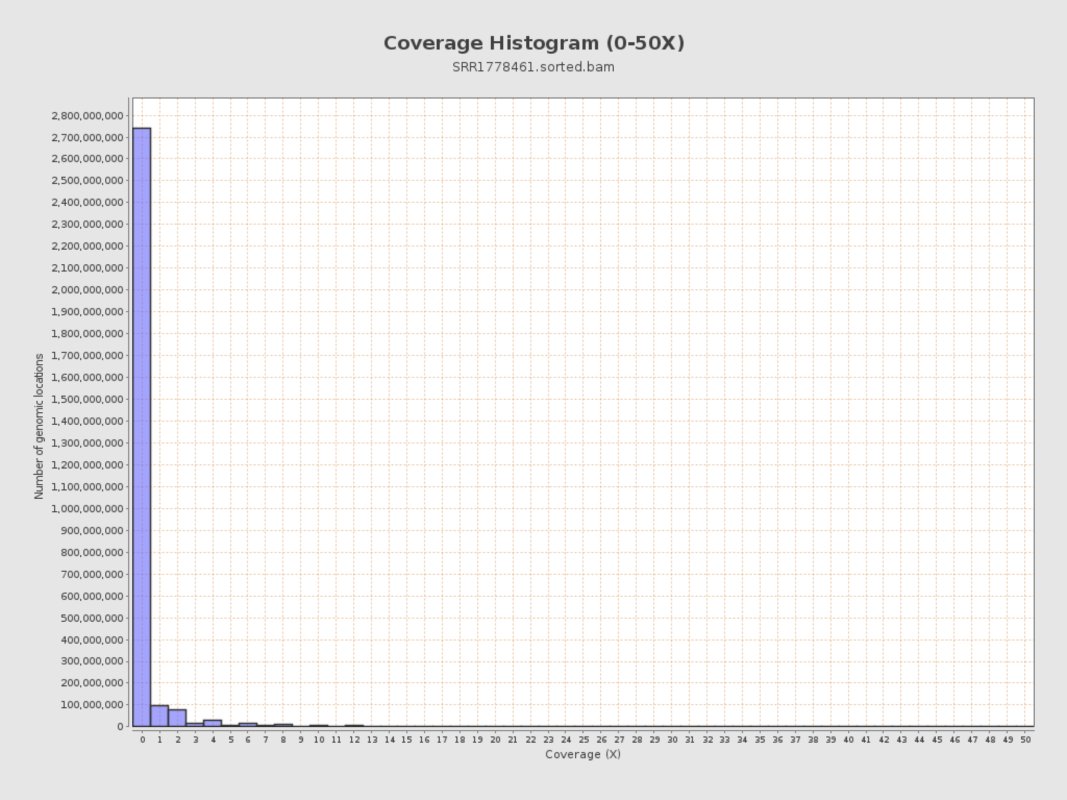
3. Results : Coverage across reference



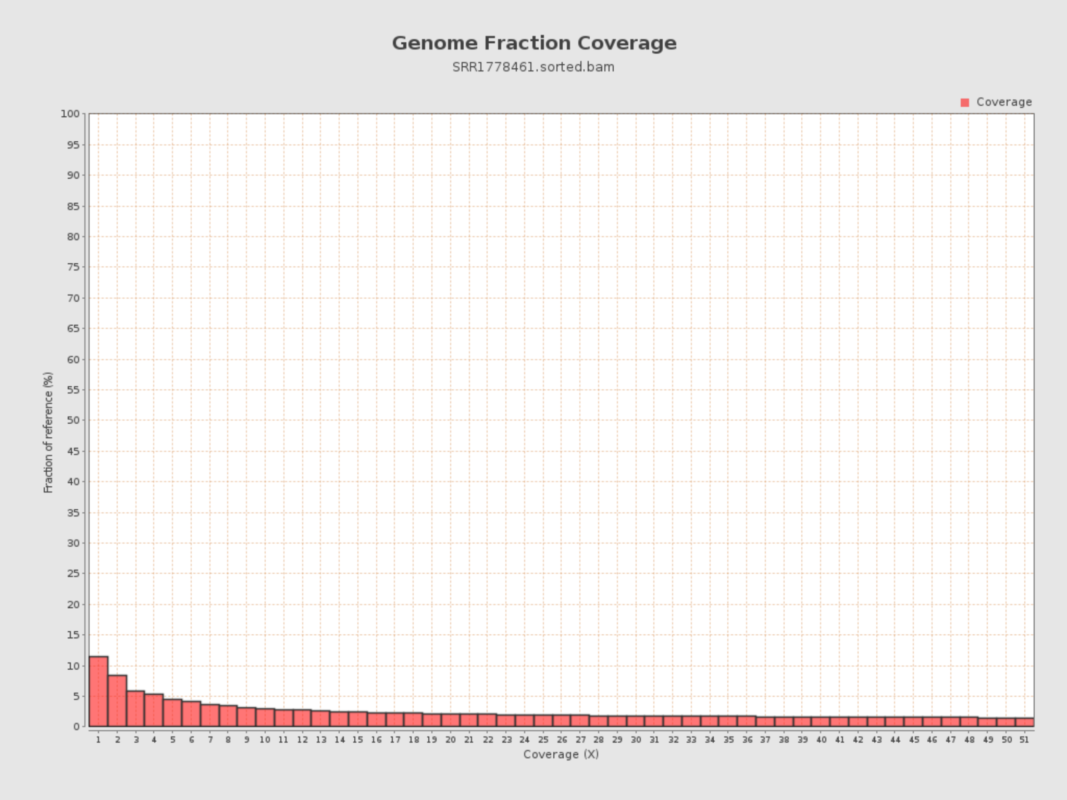
4. Results : Coverage Histogram



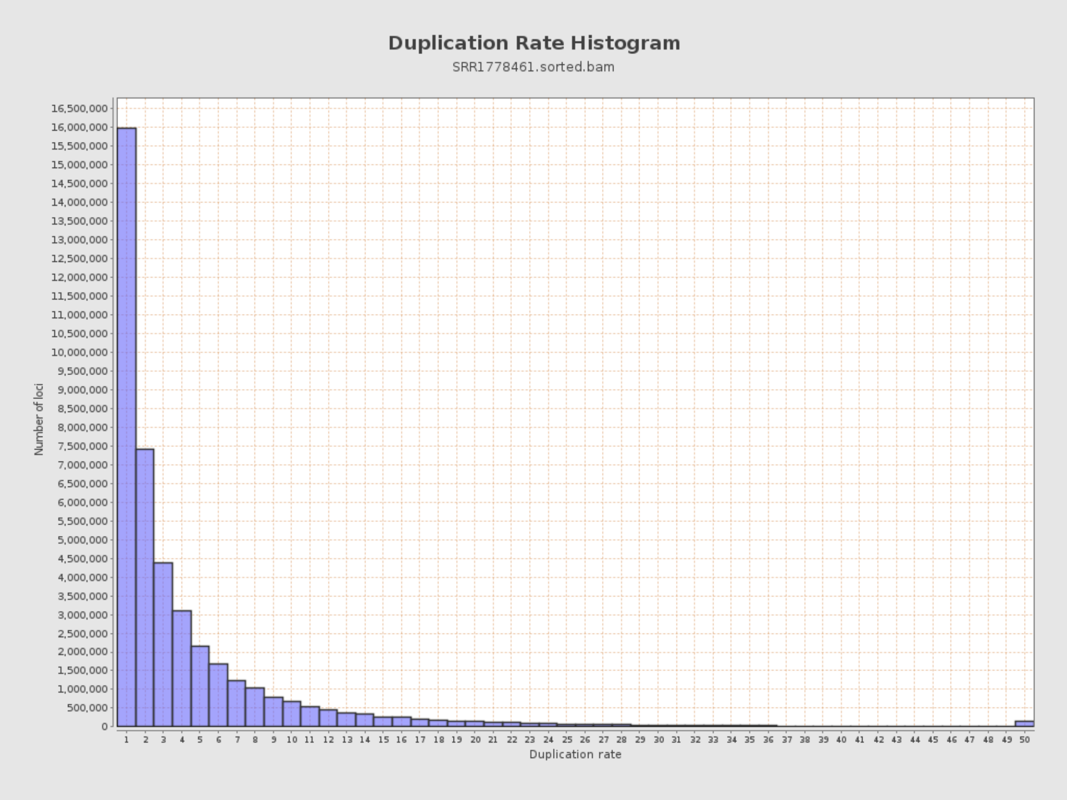
5. Results : Coverage Histogram (0-50X)



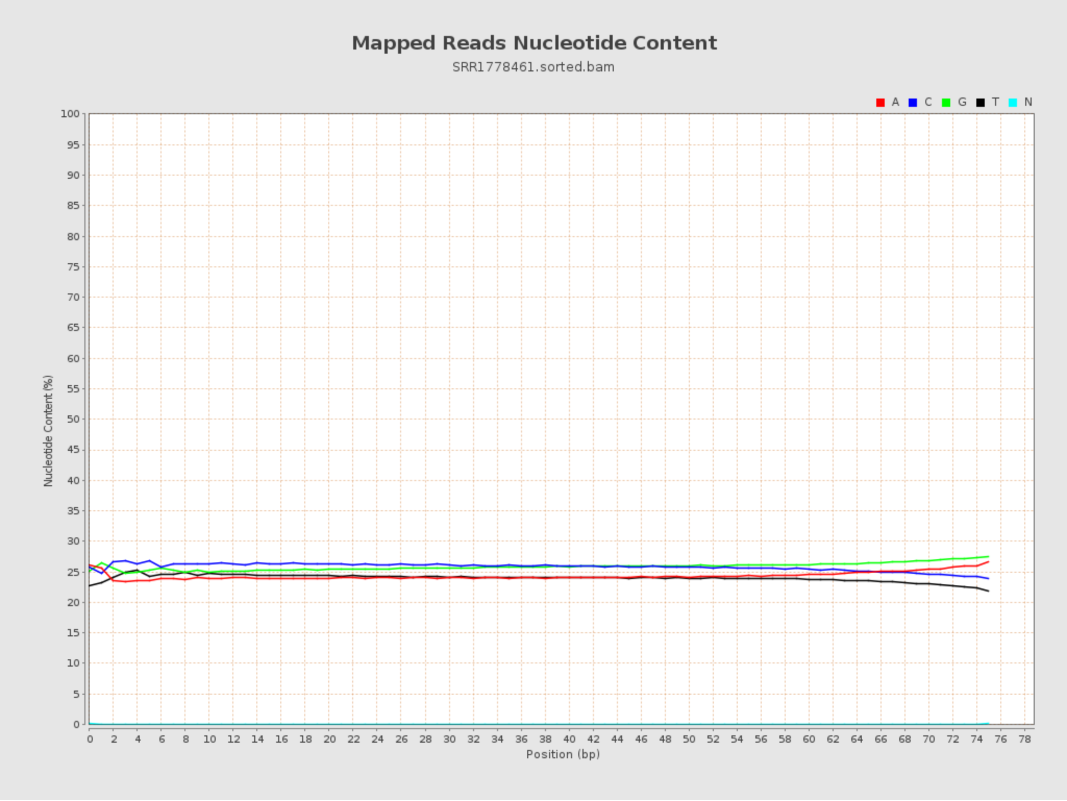
6. Results : Genome Fraction Coverage



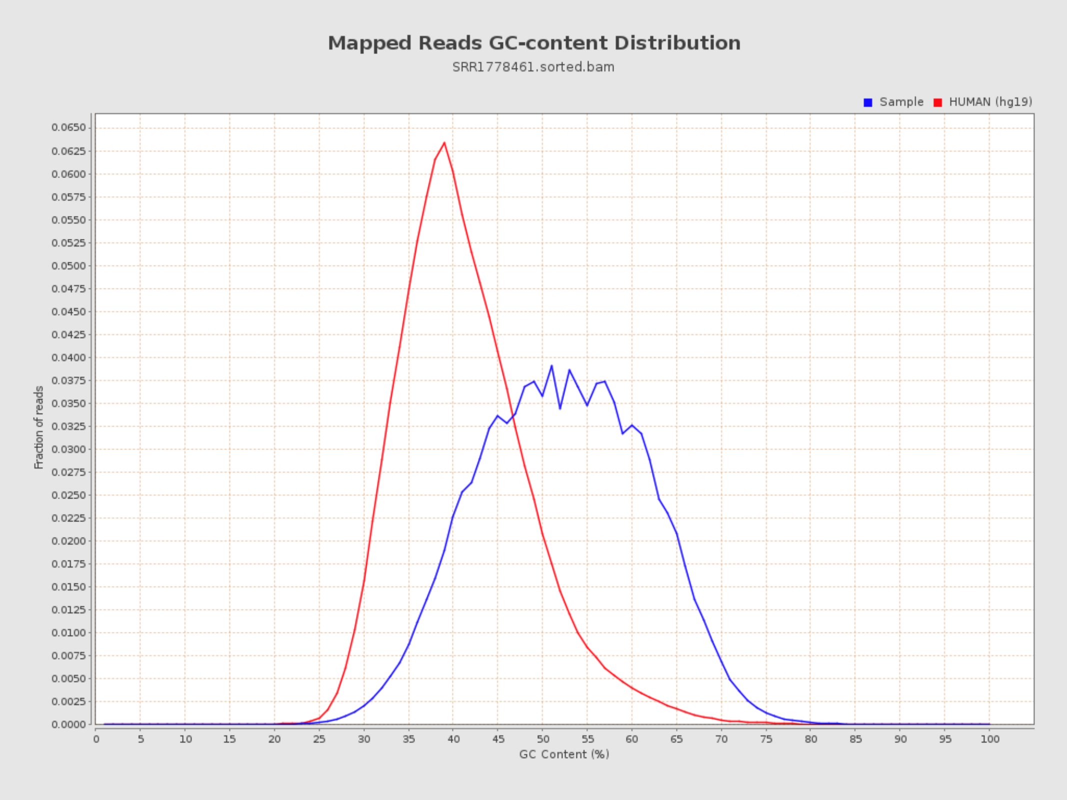
7. Results : Duplication Rate Histogram



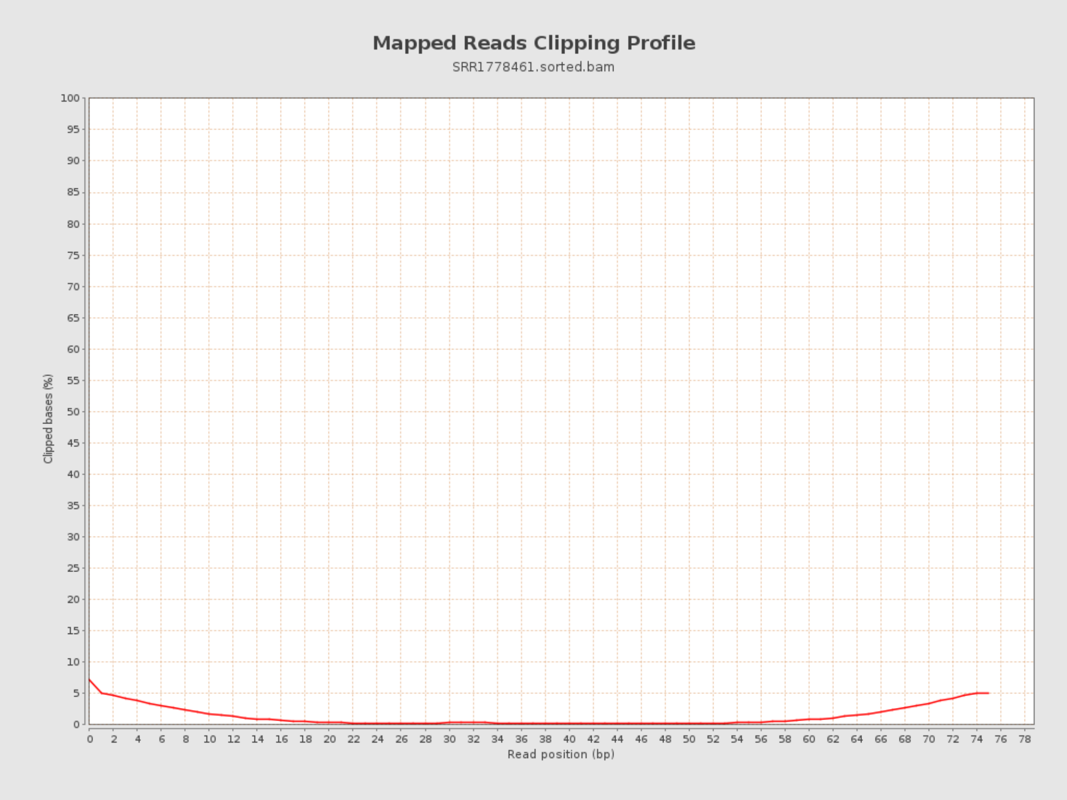
8. Results : Mapped Reads Nucleotide Content



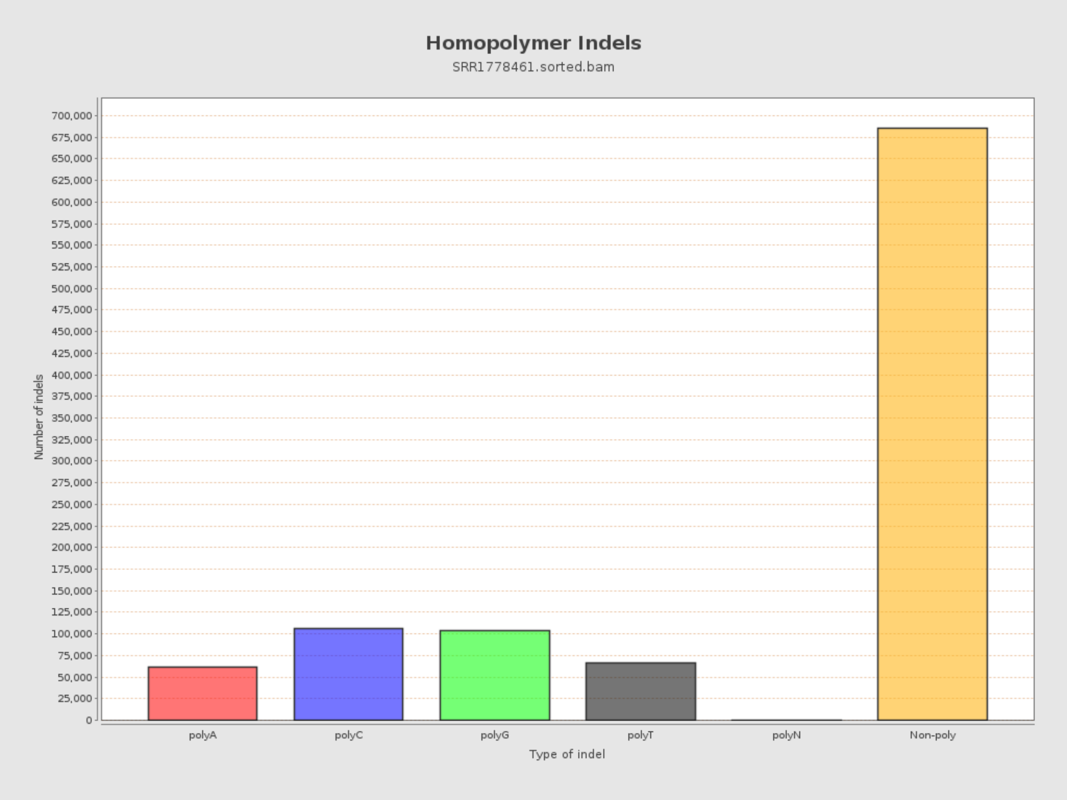
9. Results : Mapped Reads GC-content Distribution



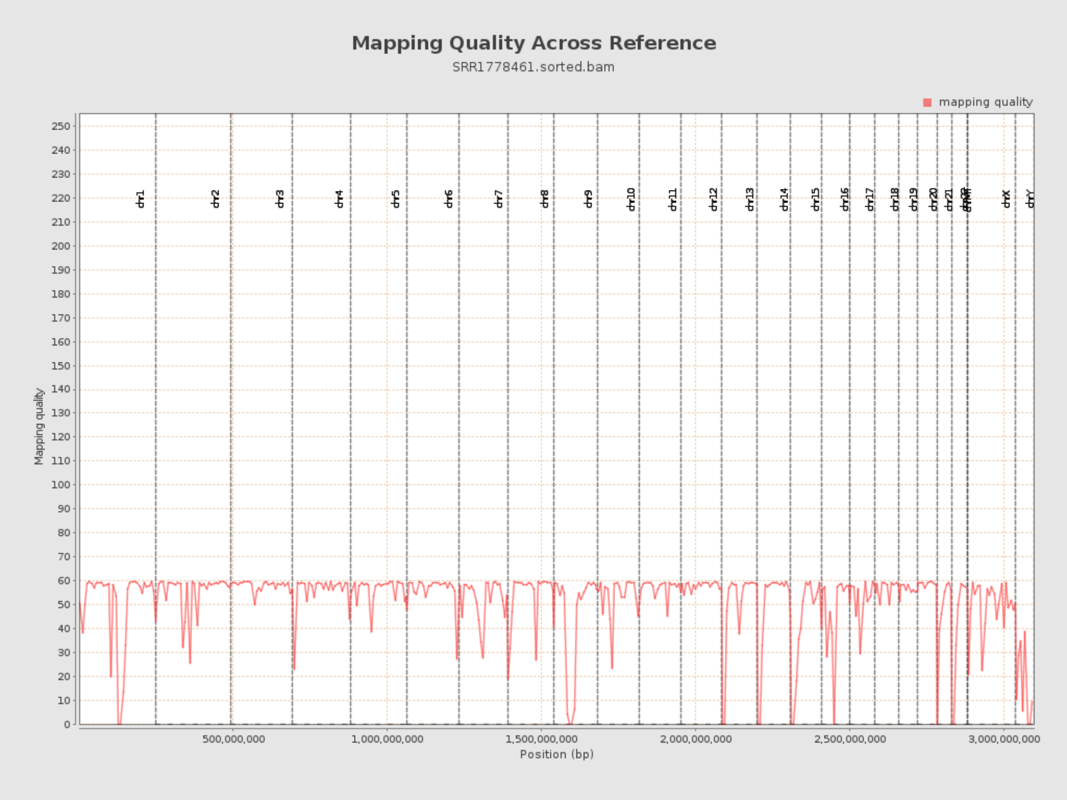
10. Results : Mapped Reads Clipping Profile



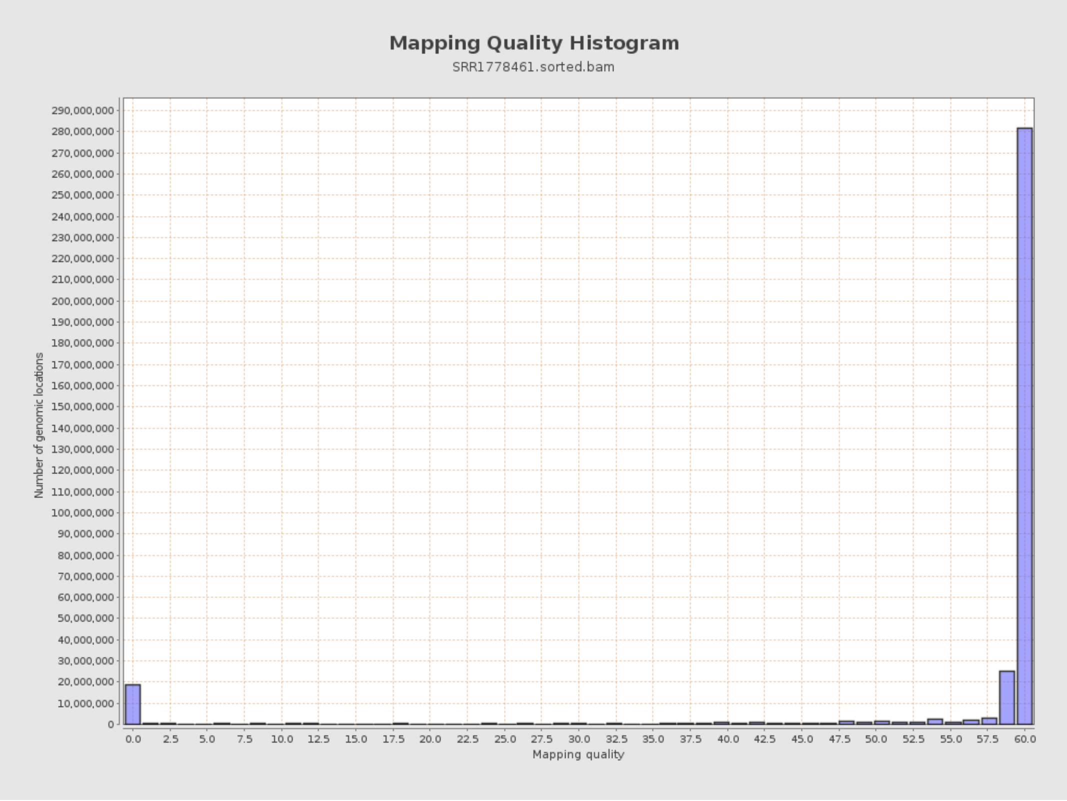
11. Results : Homopolymer Indels



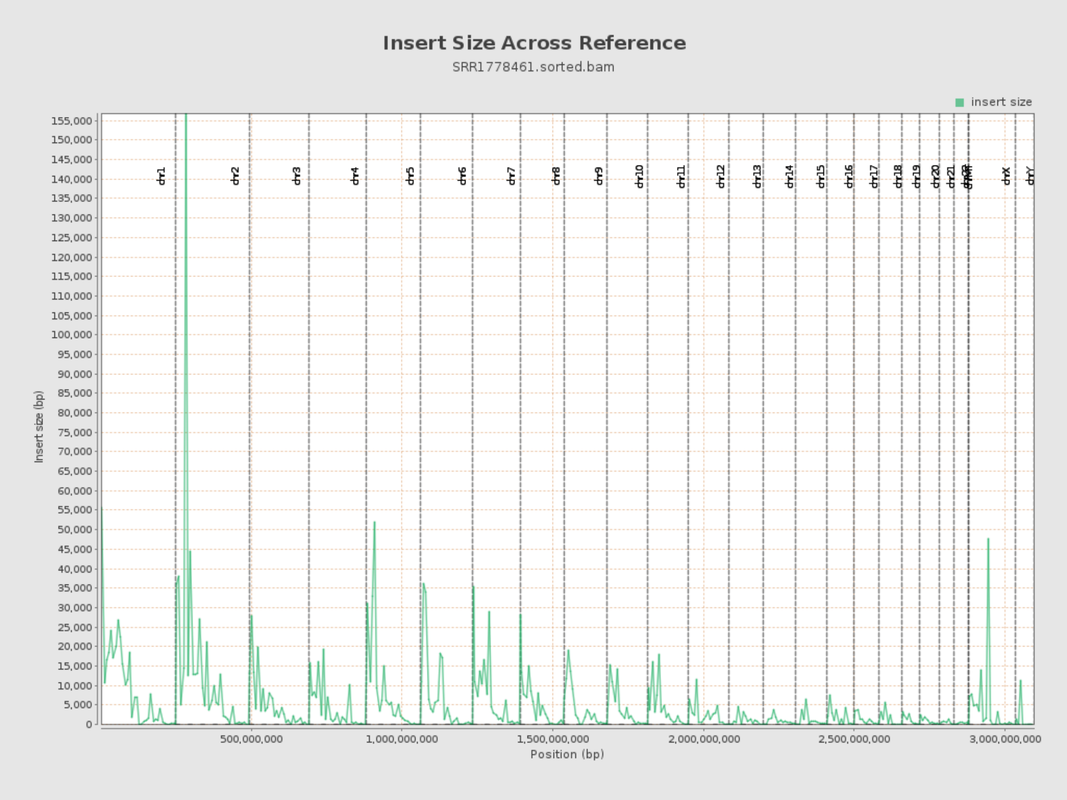
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram