Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 03:36:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777260.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_SRR1777260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777260_1.fastq.gz SRR1777260_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 03:36:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,087,630
Mapped reads	15,822,941 / 98.35%
Unmapped reads	264,689 / 1.65%
Mapped paired reads	15,822,941 / 98.35%
Mapped reads, first in pair	7,926,988 / 49.27%
Mapped reads, second in pair	7,895,953 / 49.08%
Mapped reads, both in pair	15,746,360 / 97.88%
Mapped reads, singletons	76,581 / 0.48%
Secondary alignments	0
Supplementary alignments	584,804 / 3.64%
Read min/max/mean length	30 / 101 / 102.5
Duplicated reads (estimated)	852,482 / 5.3%
Duplication rate	4.35%
Clipped reads	3,238,076 / 20.13%

2.2. ACGT Content

Number/percentage of A's	463,928,447 / 29.74%
Number/percentage of C's	317,052,503 / 20.33%
Number/percentage of T's	454,355,645 / 29.13%
Number/percentage of G's	324,536,565 / 20.81%
Number/percentage of N's	11,465 / 0%

GC Percentage	41.13%

2.3. Coverage

Mean	0.504
Standard Deviation	2.3483

2.4. Mapping Quality

Mean Mapping Quality	53.27

2.5. Insert size

Mean	172,815.24
Standard Deviation	4,043,668.77
P25/Median/P75	133 / 178 / 241

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	6,415,362
Insertions	394,542
Mapped reads with at least one insertion	2.45%
Deletions	163,872
Mapped reads with at least one deletion	1.02%
Homopolymer indels	50.42%

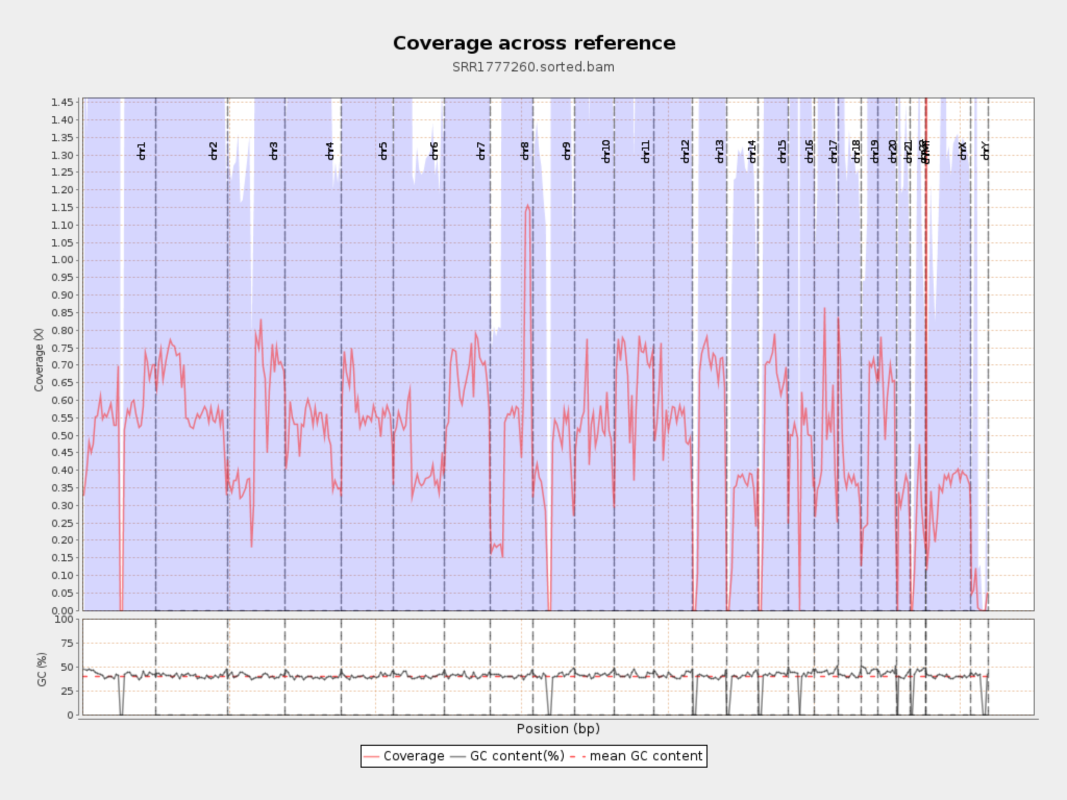
2.7. Chromosome stats

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

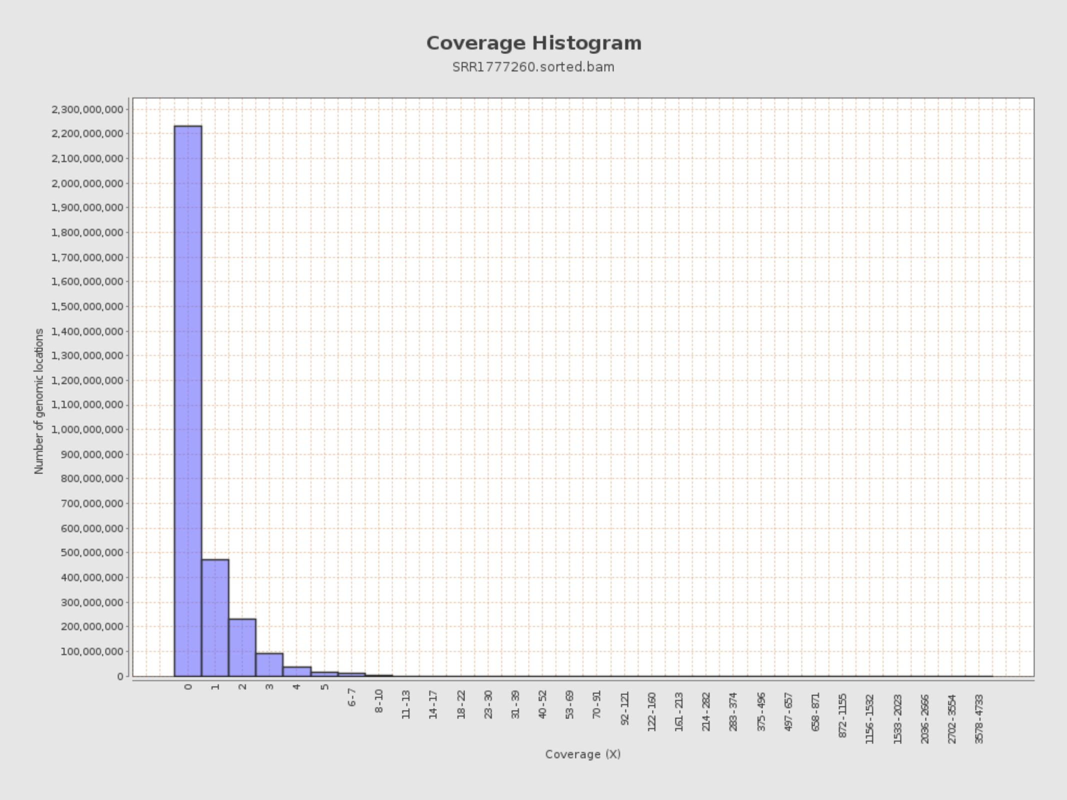
		bases	coverage	deviation
chr1	249250621	132491576	0.5316	4.8421
chr2	243199373	148708915	0.6115	1.7599
chr3	198022430	104195058	0.5262	1.0506
chr4	191154276	96064447	0.5025	1.0619
chr5	180915260	105172736	0.5813	1.0768
chr6	171115067	74625093	0.4361	1.4174
chr7	159138663	105391851	0.6623	2.0237
chr8	146364022	77034926	0.5263	1.262
chr9	141213431	55466709	0.3928	2.408
chr10	135534747	71589697	0.5282	3.4411
chr11	135006516	90876330	0.6731	1.5681
chr12	133851895	72824225	0.5441	1.0477
chr13	115169878	67748644	0.5882	1.0984
chr14	107349540	31876402	0.2969	0.7744
chr15	102531392	57439582	0.5602	1.1397
chr16	90354753	40933778	0.453	1.9334
chr17	81195210	38199414	0.4705	1.3779
chr18	78077248	33804454	0.433	2.7889
chr19	59128983	28874684	0.4883	2.8716
chr20	63025520	39593905	0.6282	1.1477
chr21	48129895	14470823	0.3007	0.948
chr22	51304566	11543317	0.225	0.6832
chrMT	16571	7347898	443.4191	90.6389
chrX	155270560	51895525	0.3342	0.9548

chrY	59373566	2079377	0.035	0.9295

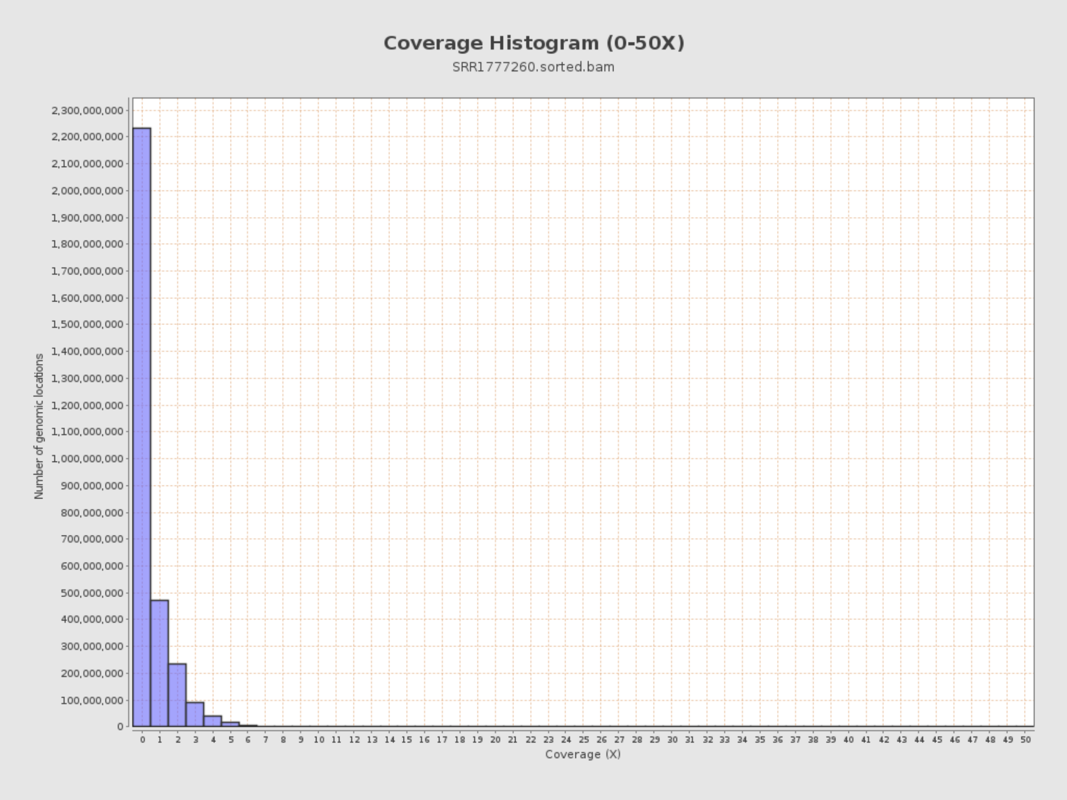
3. Results : Coverage across reference



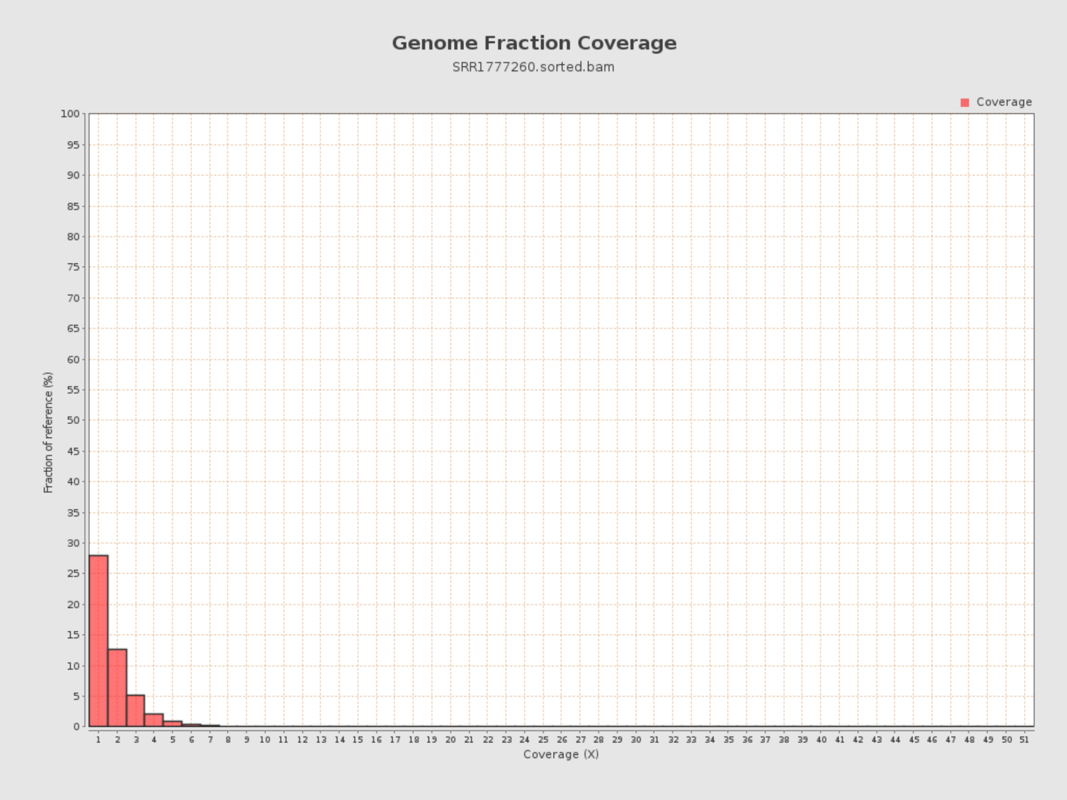
4. Results : Coverage Histogram



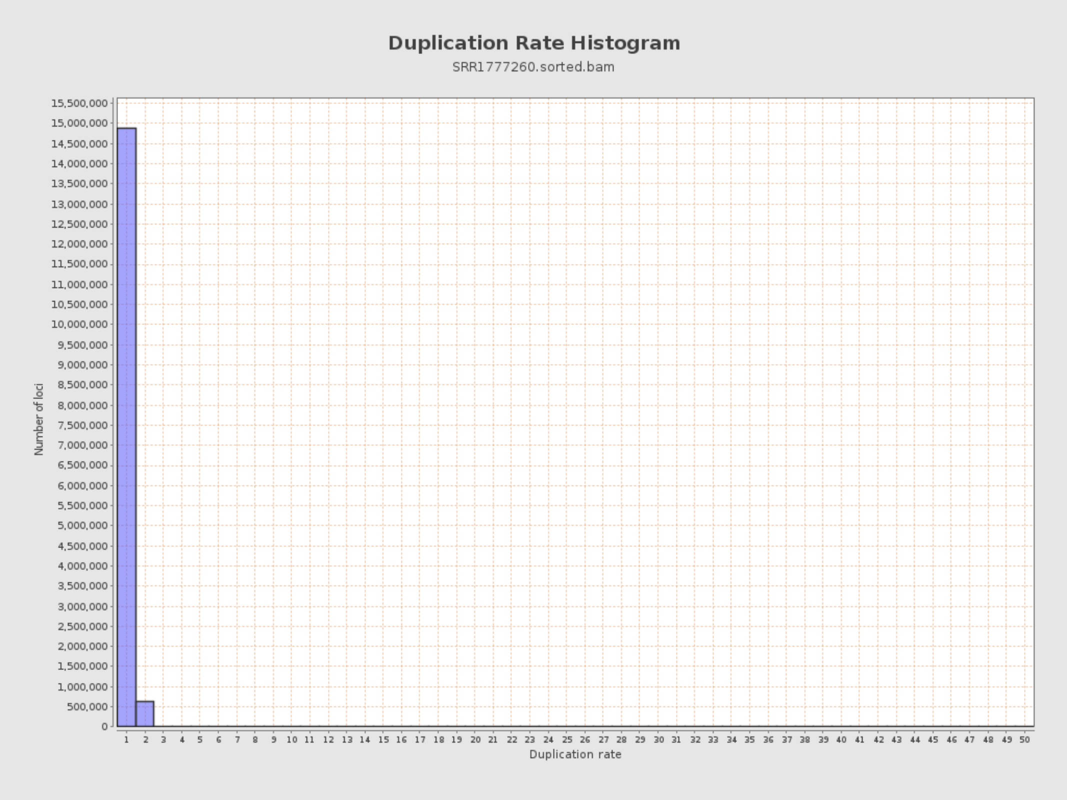
5. Results : Coverage Histogram (0-50X)



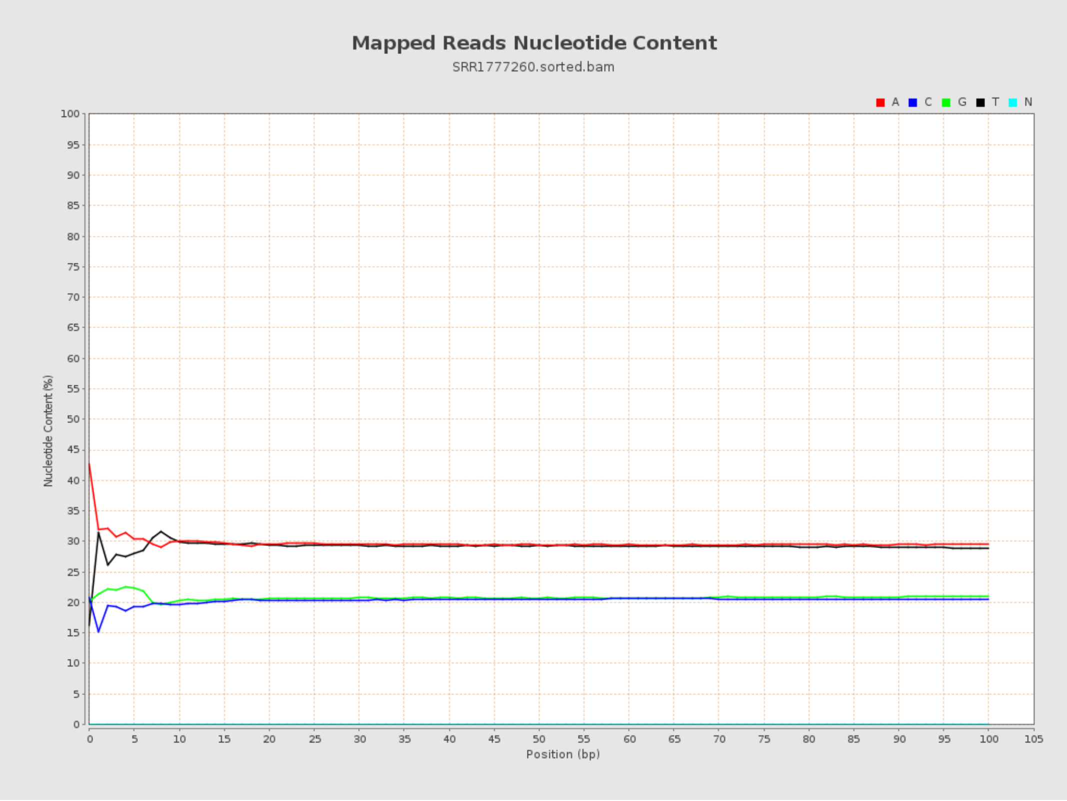
6. Results : Genome Fraction Coverage



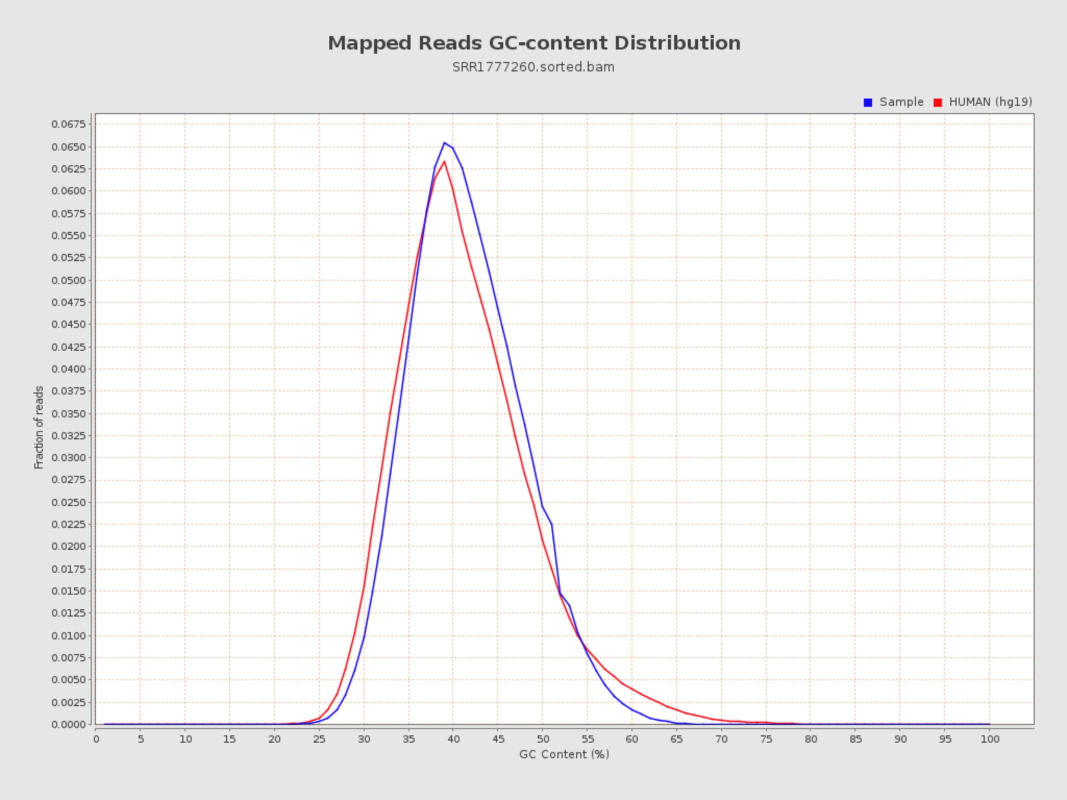
7. Results : Duplication Rate Histogram



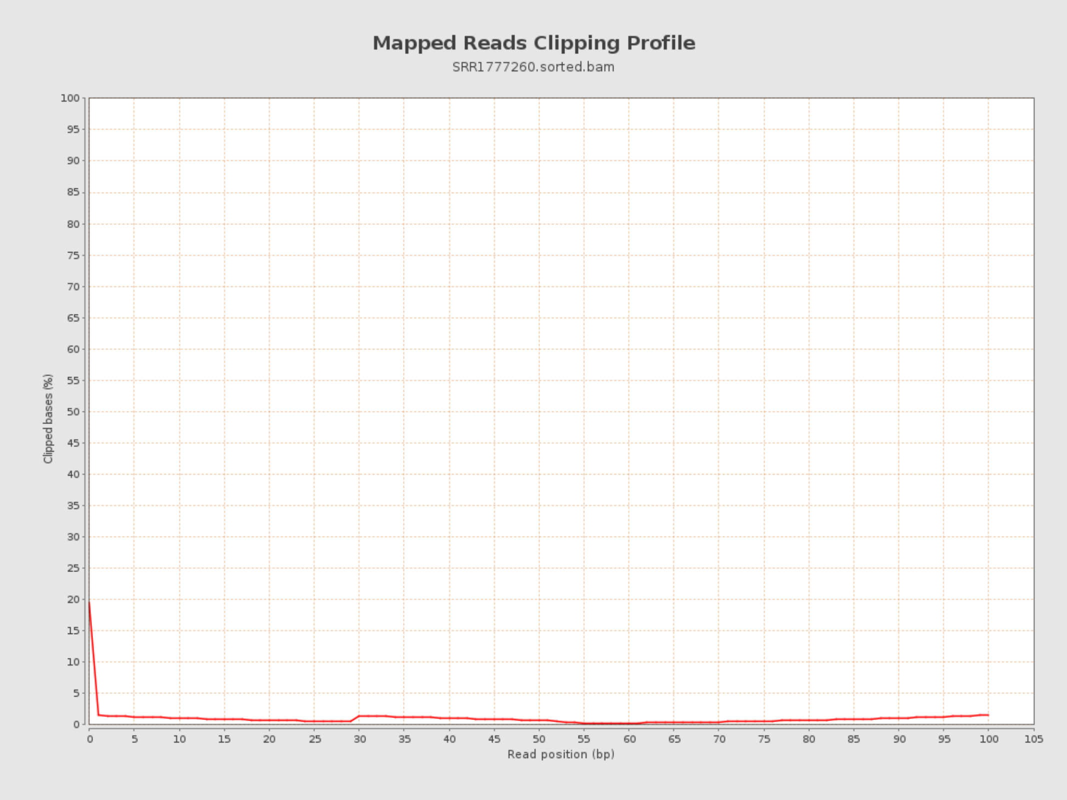
8. Results : Mapped Reads Nucleotide Content



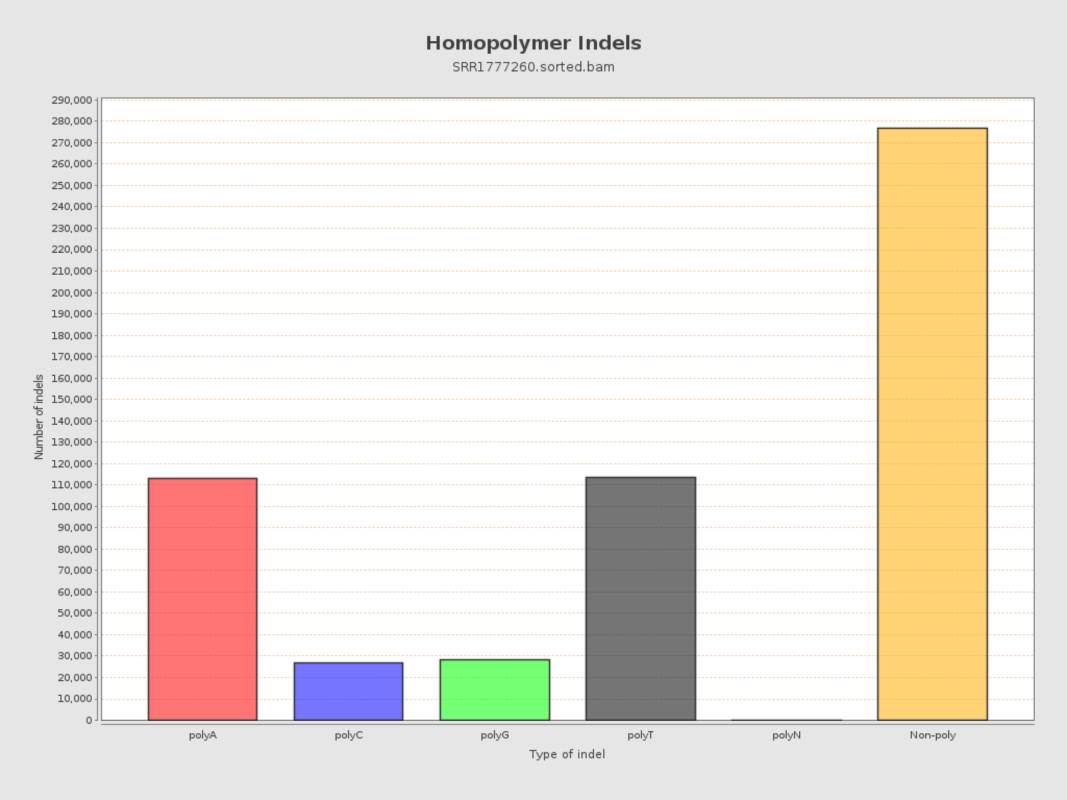
9. Results : Mapped Reads GC-content Distribution



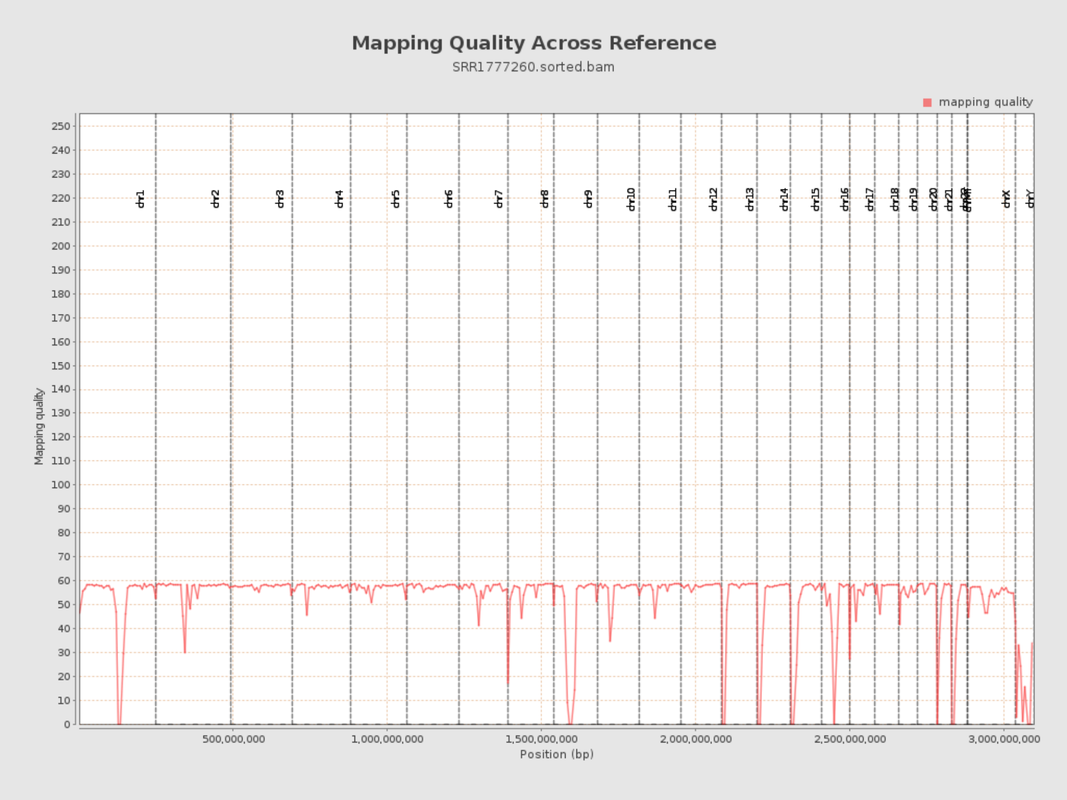
10. Results : Mapped Reads Clipping Profile



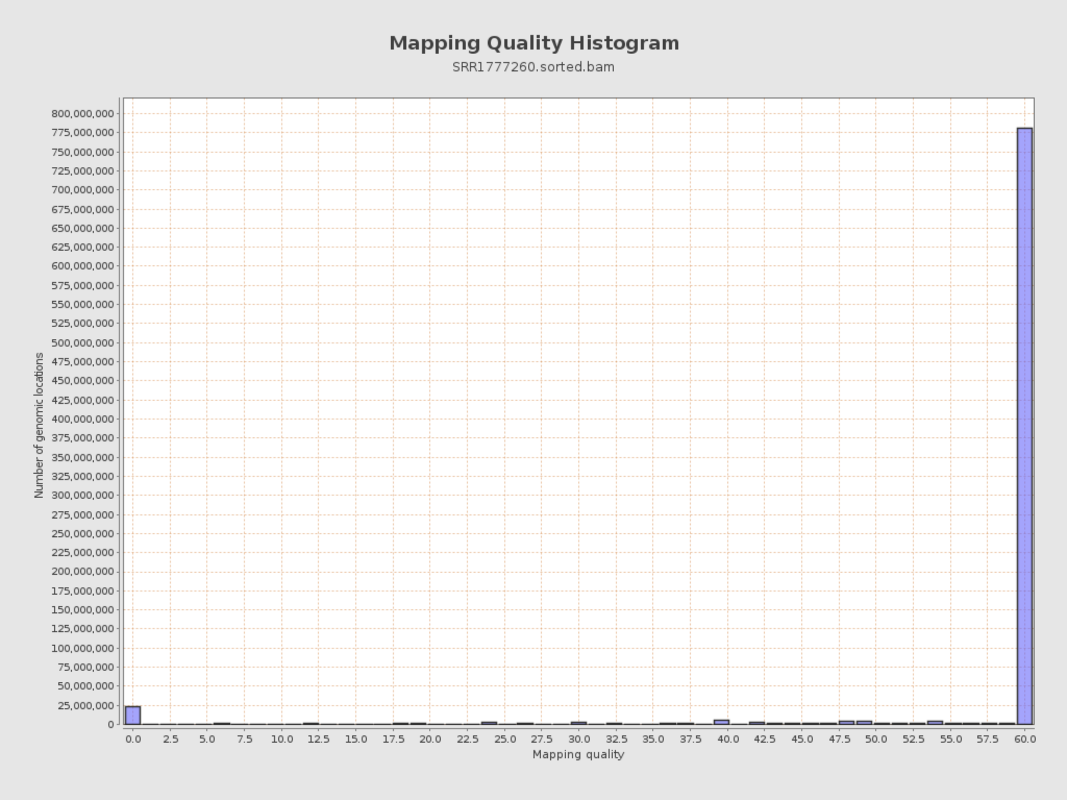
11. Results : Homopolymer Indels



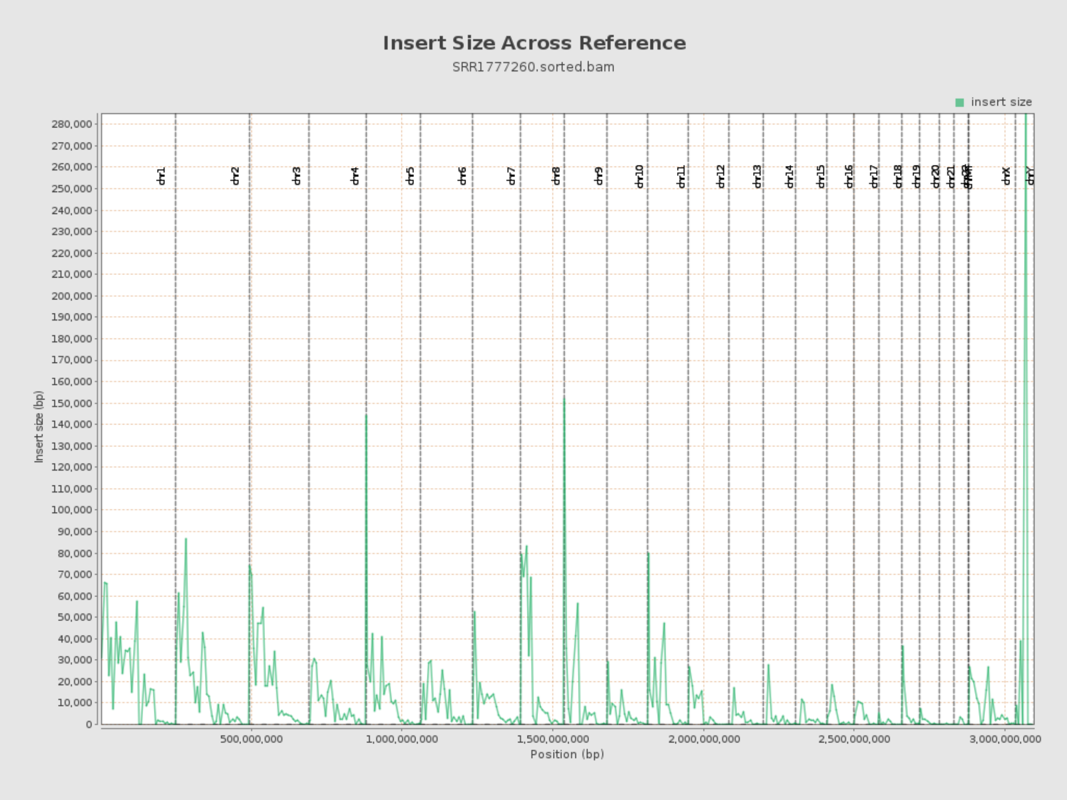
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram