Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 03:57:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777295.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_SRR1777295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777295_1.fastq.gz SRR1777295_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 03:57:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,794,730
Mapped reads	1,769,925 / 98.62%
Unmapped reads	24,805 / 1.38%
Mapped paired reads	1,769,925 / 98.62%
Mapped reads, first in pair	887,093 / 49.43%
Mapped reads, second in pair	882,832 / 49.19%
Mapped reads, both in pair	1,761,022 / 98.12%
Mapped reads, singletons	8,903 / 0.5%
Secondary alignments	0
Supplementary alignments	52,530 / 2.93%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	115,566 / 6.44%
Duplication rate	4.96%
Clipped reads	366,443 / 20.42%

2.2. ACGT Content

Number/percentage of A's	50,600,473 / 29.14%
Number/percentage of C's	36,322,343 / 20.92%
Number/percentage of T's	49,648,307 / 28.59%
Number/percentage of G's	37,064,850 / 21.35%
Number/percentage of N's	2,951 / 0%

GC Percentage	42.26%

2.3. Coverage

Mean	0.0561
Standard Deviation	0.7536

2.4. Mapping Quality

Mean Mapping Quality	53.31

2.5. Insert size

Mean	159,072.46
Standard Deviation	3,813,913.93
P25/Median/P75	131 / 174 / 228

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	1,096,751
Insertions	35,524
Mapped reads with at least one insertion	1.95%
Deletions	24,049
Mapped reads with at least one deletion	1.31%
Homopolymer indels	44.2%

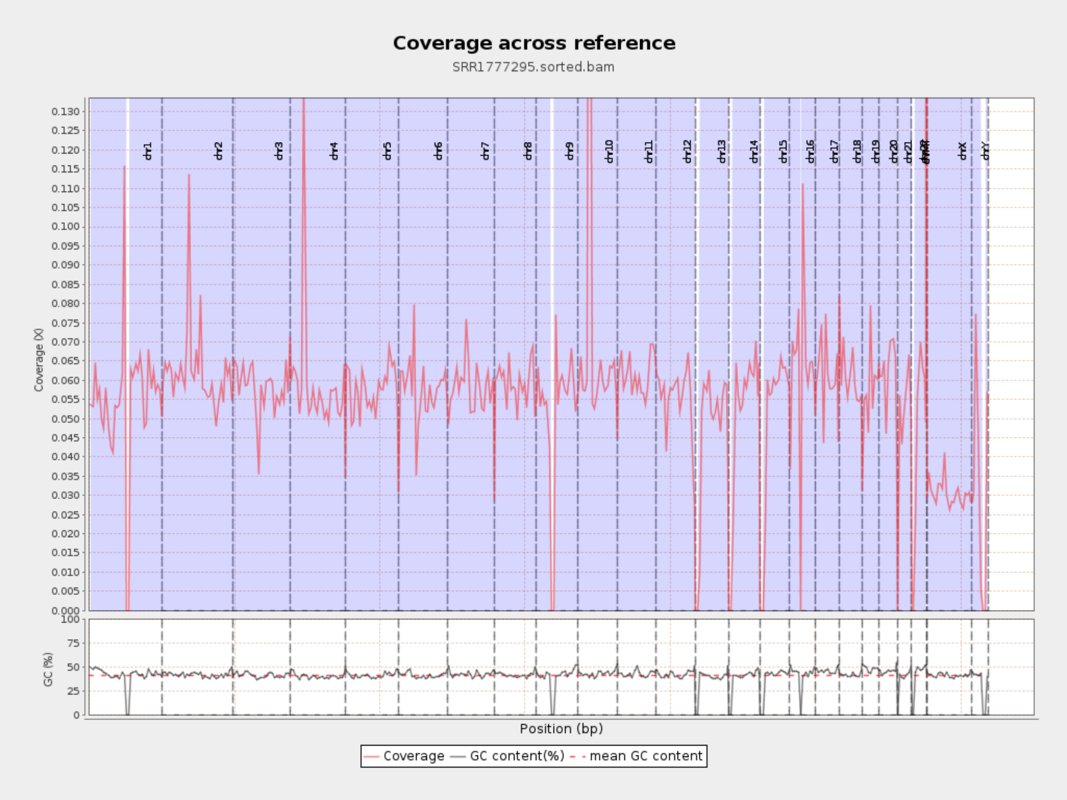
2.7. Chromosome stats

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

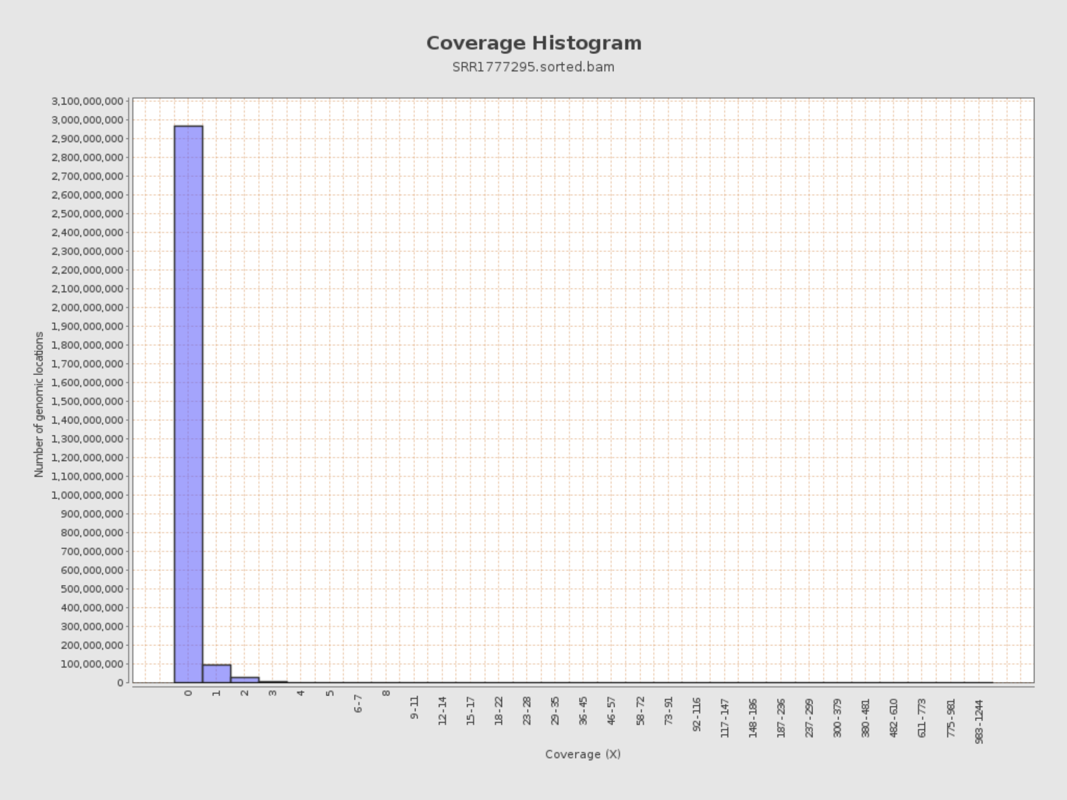
		bases	coverage	deviation
chr1	249250621	13583164	0.0545	1.2359
chr2	243199373	15193490	0.0625	0.5031
chr3	198022430	11439478	0.0578	0.3525
chr4	191154276	11277579	0.059	0.6743
chr5	180915260	10421177	0.0576	0.2954
chr6	171115067	9768719	0.0571	0.4013
chr7	159138663	9292147	0.0584	0.4813
chr8	146364022	8690346	0.0594	0.3578
chr9	141213431	7318548	0.0518	0.622
chr10	135534747	9939967	0.0733	2.228
chr11	135006516	8240816	0.061	0.3733
chr12	133851895	7438134	0.0556	0.2885
chr13	115169878	5260001	0.0457	0.2614
chr14	107349540	5317769	0.0495	0.2744
chr15	102531392	5023635	0.049	0.2688
chr16	90354753	5667188	0.0627	0.4945
chr17	81195210	4970701	0.0612	0.4321
chr18	78077248	4786911	0.0613	0.7525
chr19	59128983	3404581	0.0576	0.6821
chr20	63025520	3916932	0.0621	0.3352
chr21	48129895	2392939	0.0497	0.3578
chr22	51304566	2199251	0.0429	0.2554
chrMT	16571	1626514	98.1542	23.402
chrX	155270560	4775958	0.0308	0.2326

chrY	59373566	1755191	0.0296	0.6046

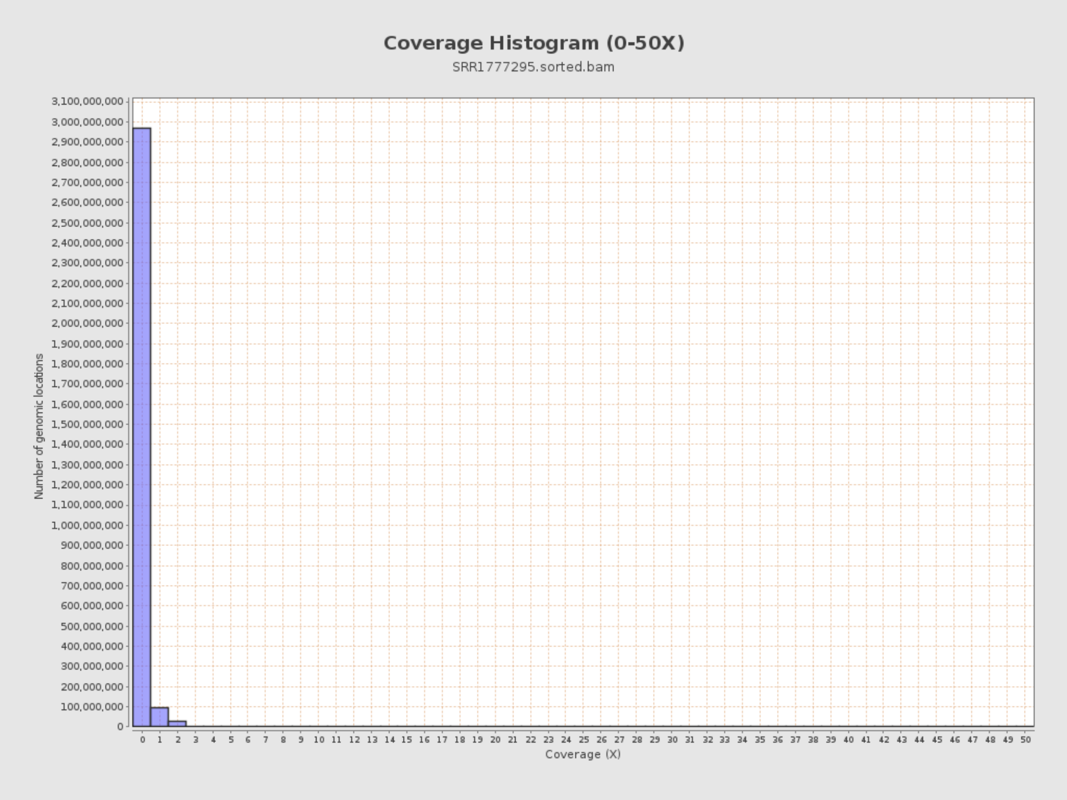
3. Results : Coverage across reference



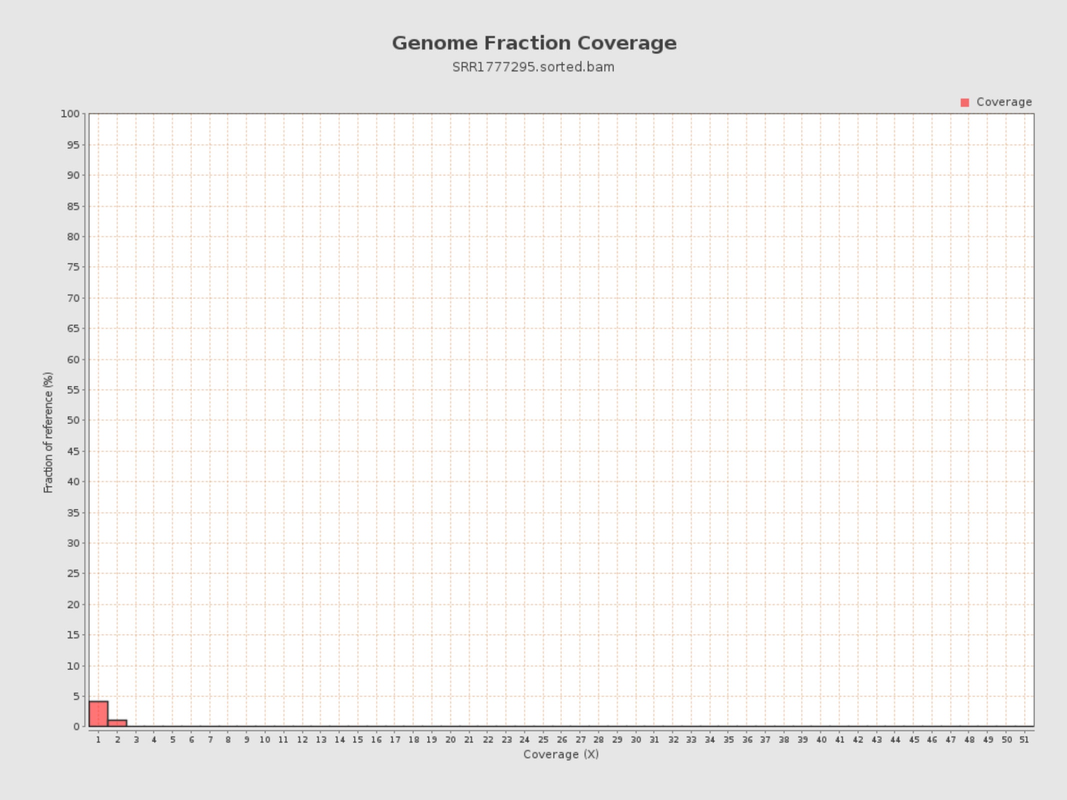
4. Results : Coverage Histogram



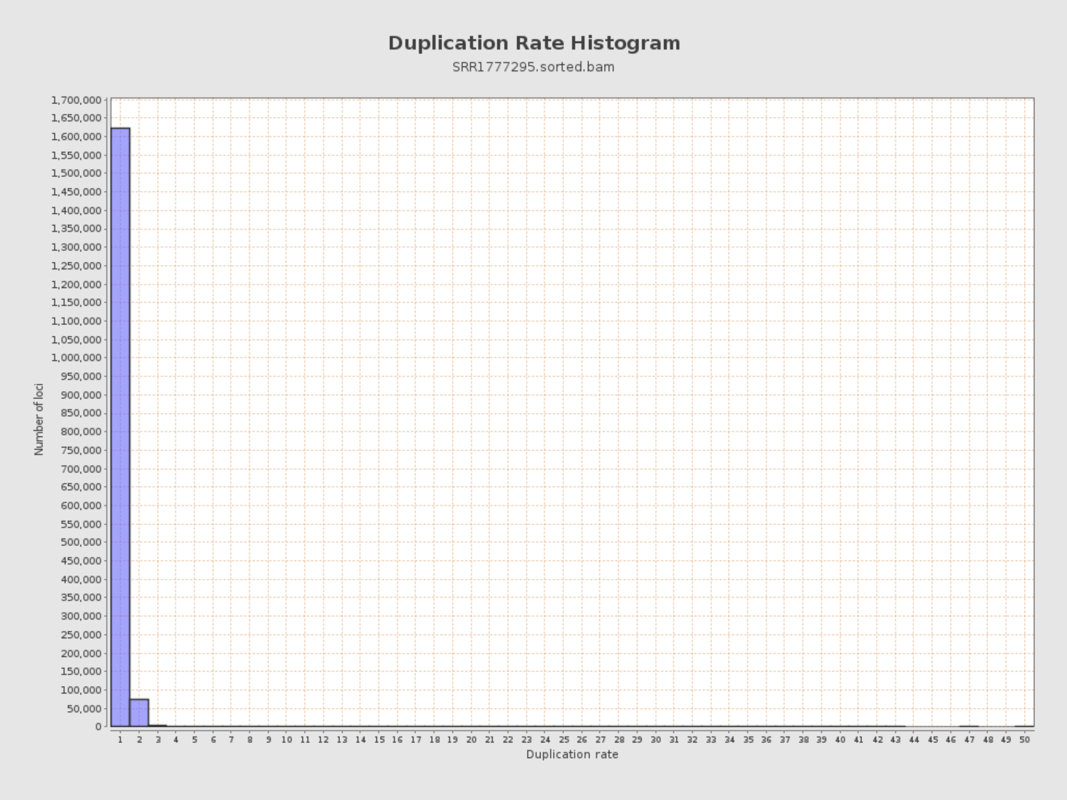
5. Results : Coverage Histogram (0-50X)



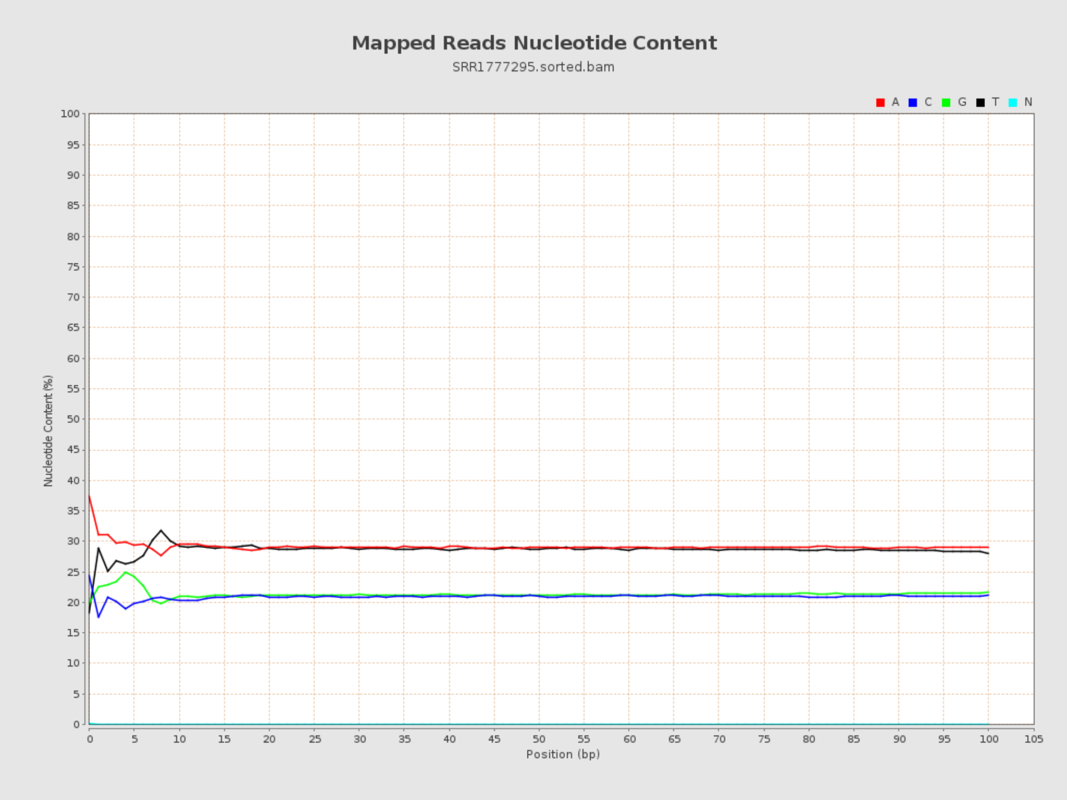
6. Results : Genome Fraction Coverage



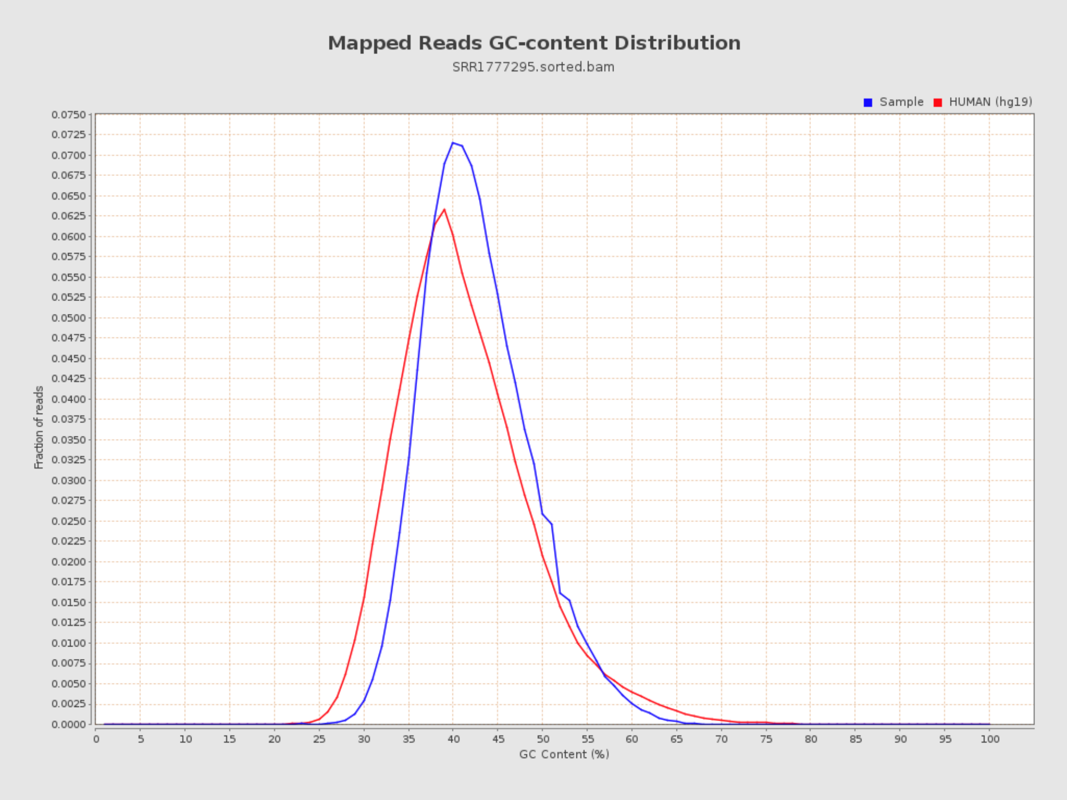
7. Results : Duplication Rate Histogram



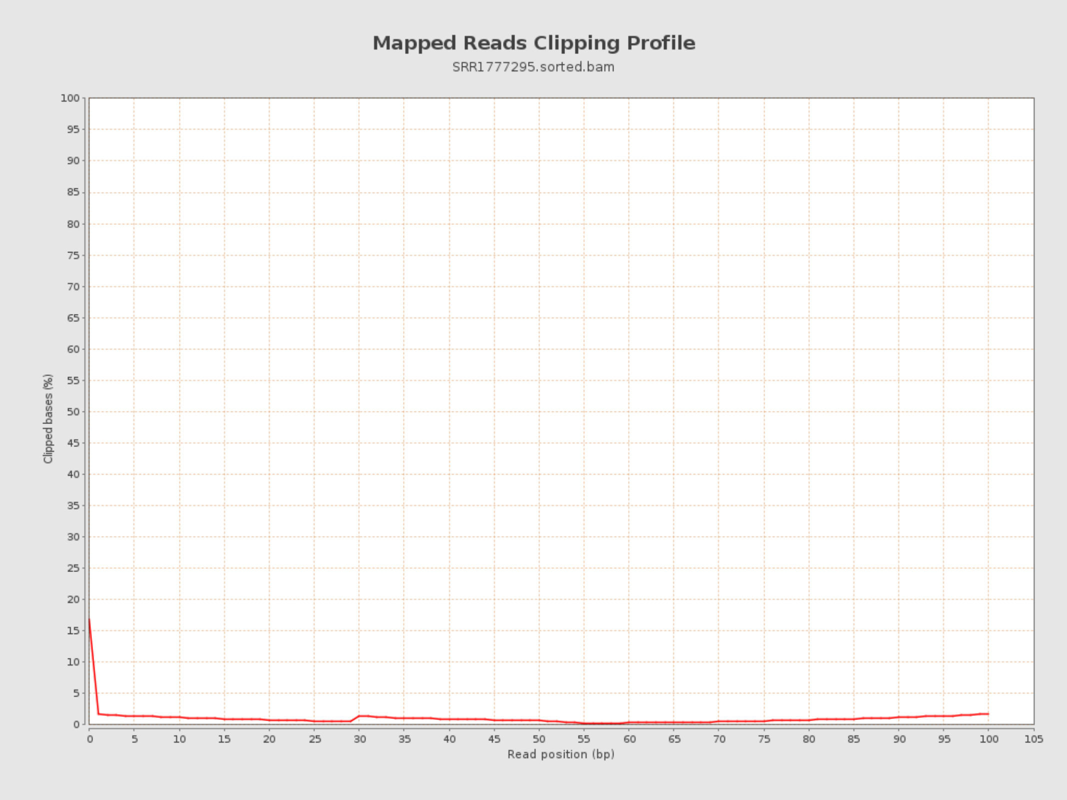
8. Results : Mapped Reads Nucleotide Content



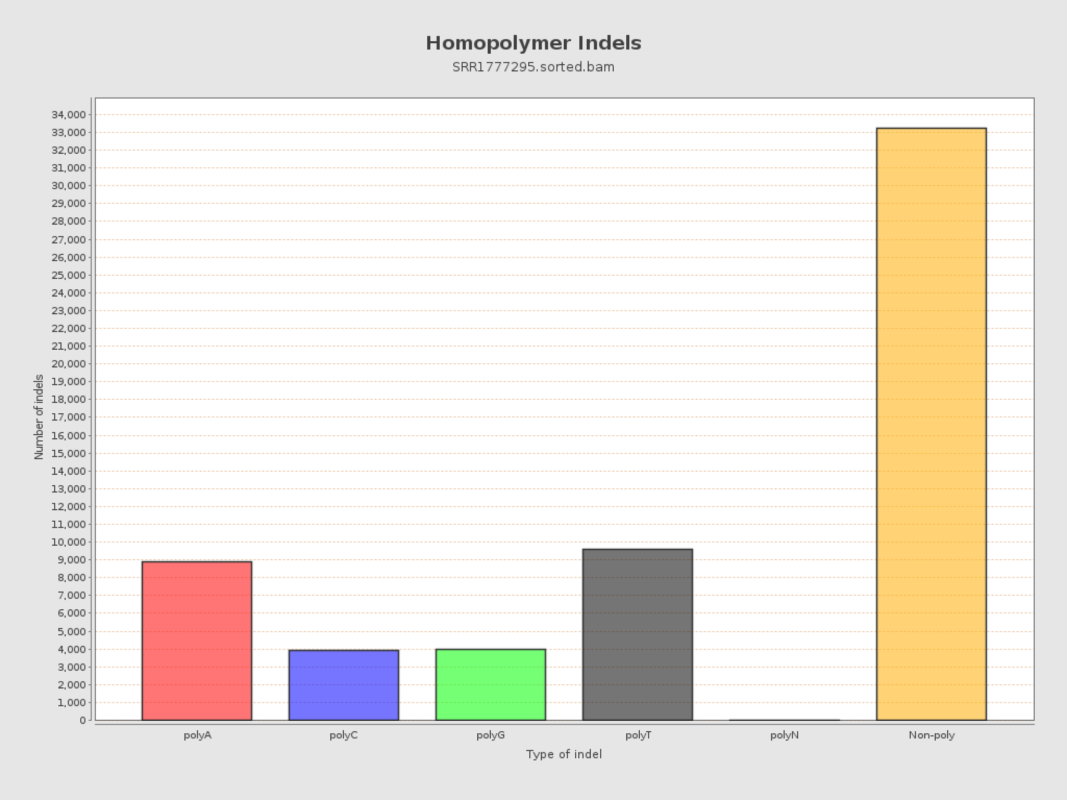
9. Results : Mapped Reads GC-content Distribution



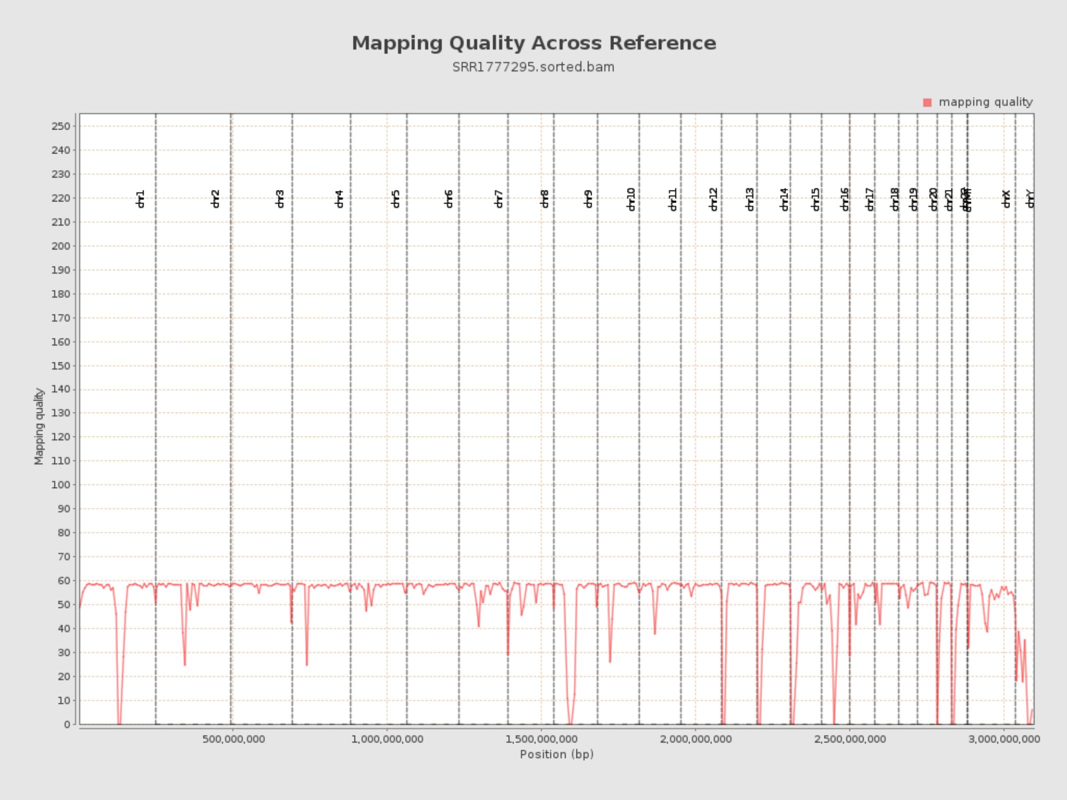
10. Results : Mapped Reads Clipping Profile



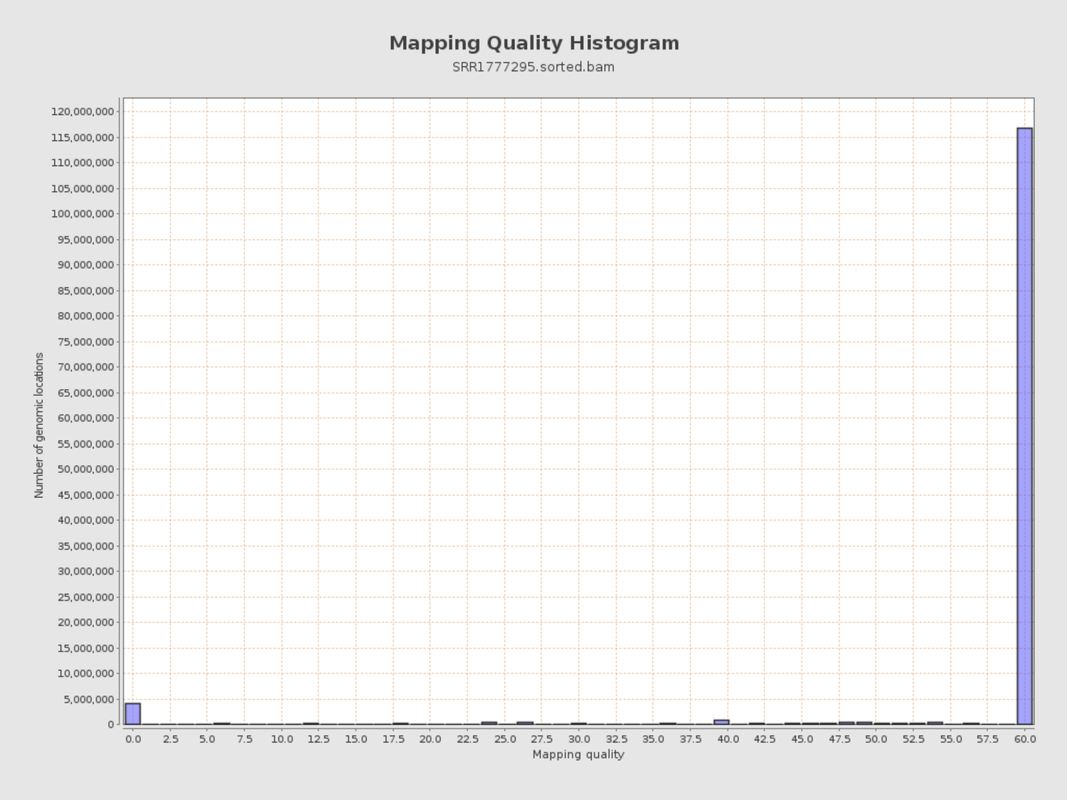
11. Results : Homopolymer Indels



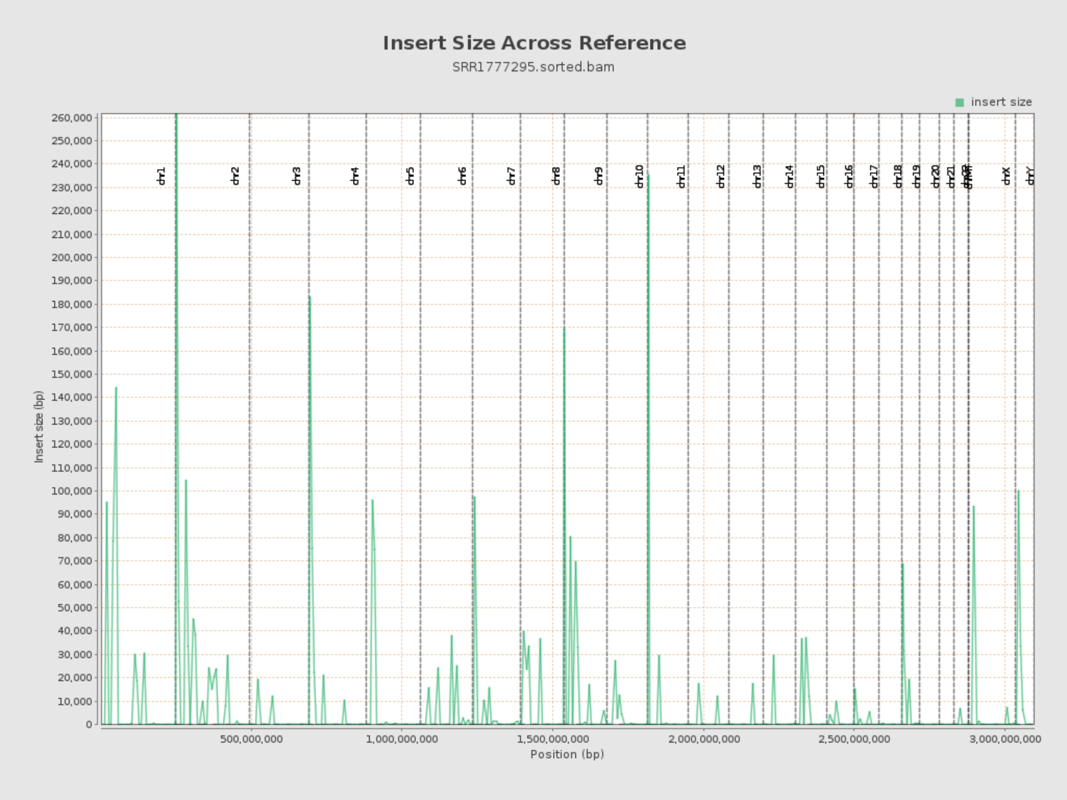
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram