Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 08:48:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777278.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_SRR1777278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777278_1.fastq.gz SRR1777278_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 08:48:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,666,134
Mapped reads	12,486,345 / 98.58%
Unmapped reads	179,789 / 1.42%
Mapped paired reads	12,486,345 / 98.58%
Mapped reads, first in pair	6,260,068 / 49.42%
Mapped reads, second in pair	6,226,277 / 49.16%
Mapped reads, both in pair	12,441,654 / 98.23%
Mapped reads, singletons	44,691 / 0.35%
Secondary alignments	0
Supplementary alignments	74,497 / 0.59%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	1,085,491 / 8.57%
Duplication rate	8.88%
Clipped reads	3,102,825 / 24.5%

2.2. ACGT Content

Number/percentage of A's	331,394,337 / 27.86%
Number/percentage of C's	262,209,293 / 22.04%
Number/percentage of T's	324,568,518 / 27.29%
Number/percentage of G's	271,332,065 / 22.81%
Number/percentage of N's	22,570 / 0%

GC Percentage	44.85%

2.3. Coverage

Mean	0.3845
Standard Deviation	1.4327

2.4. Mapping Quality

Mean Mapping Quality	53.93

2.5. Insert size

Mean	78,033.81
Standard Deviation	2,821,530.85
P25/Median/P75	108 / 150 / 204

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	8,733,141
Insertions	195,780
Mapped reads with at least one insertion	1.55%
Deletions	590,861
Mapped reads with at least one deletion	4.62%
Homopolymer indels	54.16%

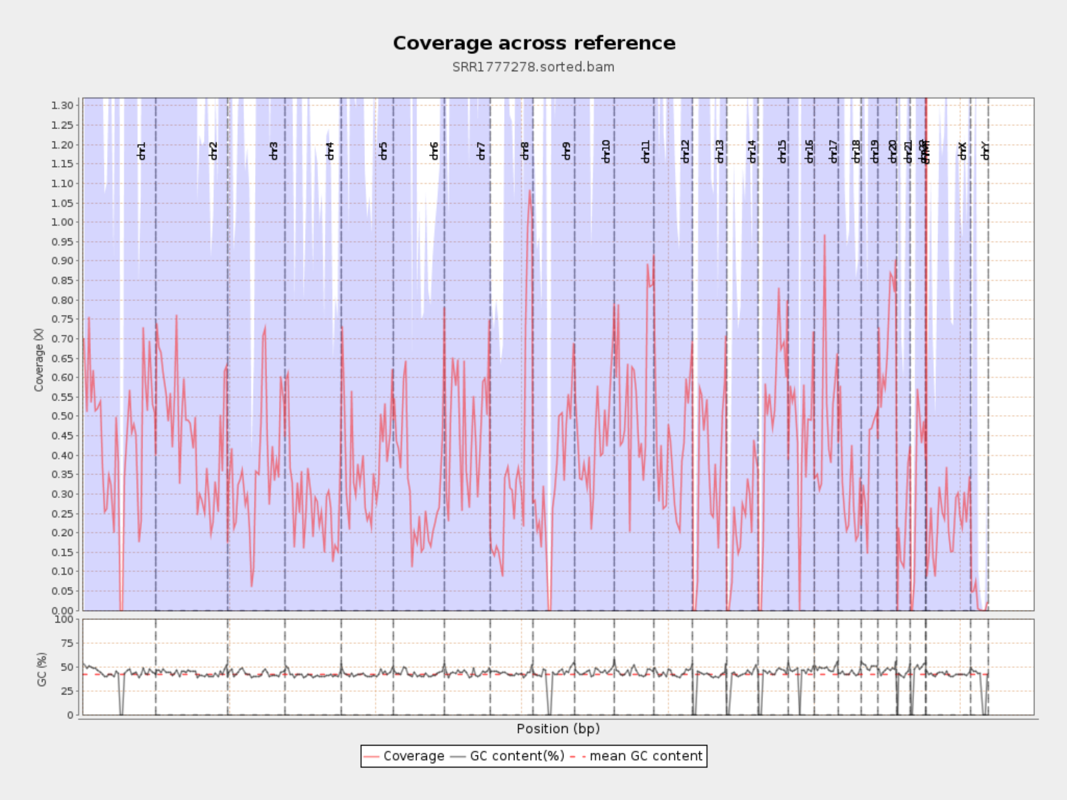
2.7. Chromosome stats

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

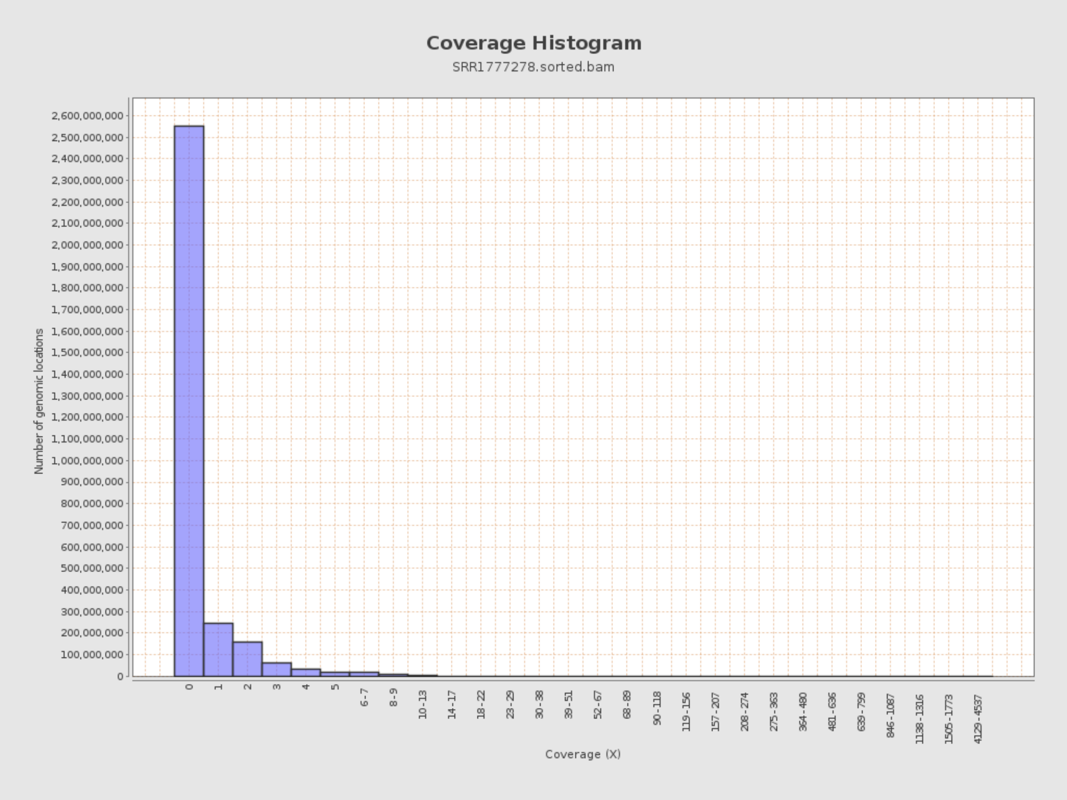
		bases	coverage	deviation
chr1	249250621	109744556	0.4403	1.3428
chr2	243199373	110796991	0.4556	1.5991
chr3	198022430	71845307	0.3628	1.0594
chr4	191154276	53958136	0.2823	0.9463
chr5	180915260	70686019	0.3907	1.0867
chr6	171115067	52305932	0.3057	3.3187
chr7	159138663	76079319	0.4781	1.2924
chr8	146364022	56842319	0.3884	1.2317
chr9	141213431	46802720	0.3314	1.2952
chr10	135534747	58469381	0.4314	1.2003
chr11	135006516	76366397	0.5656	1.4568
chr12	133851895	54705981	0.4087	1.1245
chr13	115169878	40575763	0.3523	1.0749
chr14	107349540	23894975	0.2226	0.7757
chr15	102531392	50810696	0.4956	1.3651
chr16	90354753	41676797	0.4613	1.5484
chr17	81195210	39441651	0.4858	1.3714
chr18	78077248	23693889	0.3035	1.2692
chr19	59128983	22304665	0.3772	1.1927
chr20	63025520	44942565	0.7131	1.6762
chr21	48129895	10401965	0.2161	1.0688
chr22	51304566	16831968	0.3281	1.0725
chrMT	16571	188632	11.3833	10.7733
chrX	155270560	35540830	0.2289	0.7668

chrY	59373566	1429536	0.0241	0.6313

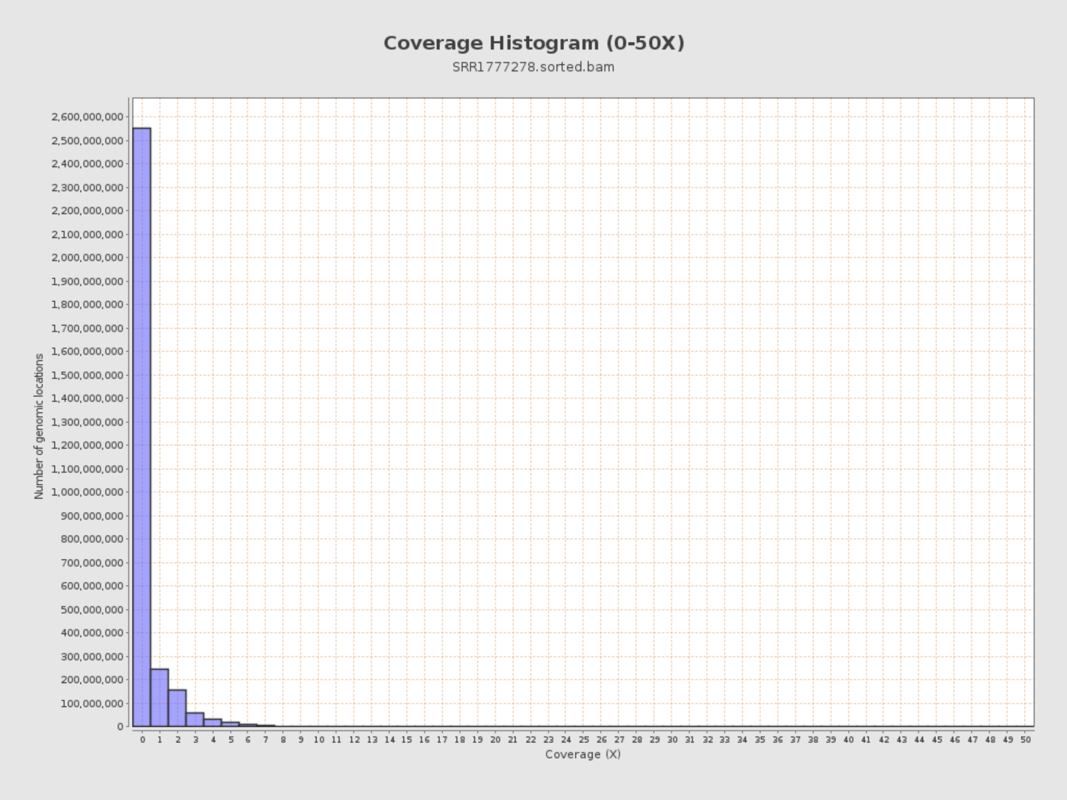
3. Results : Coverage across reference



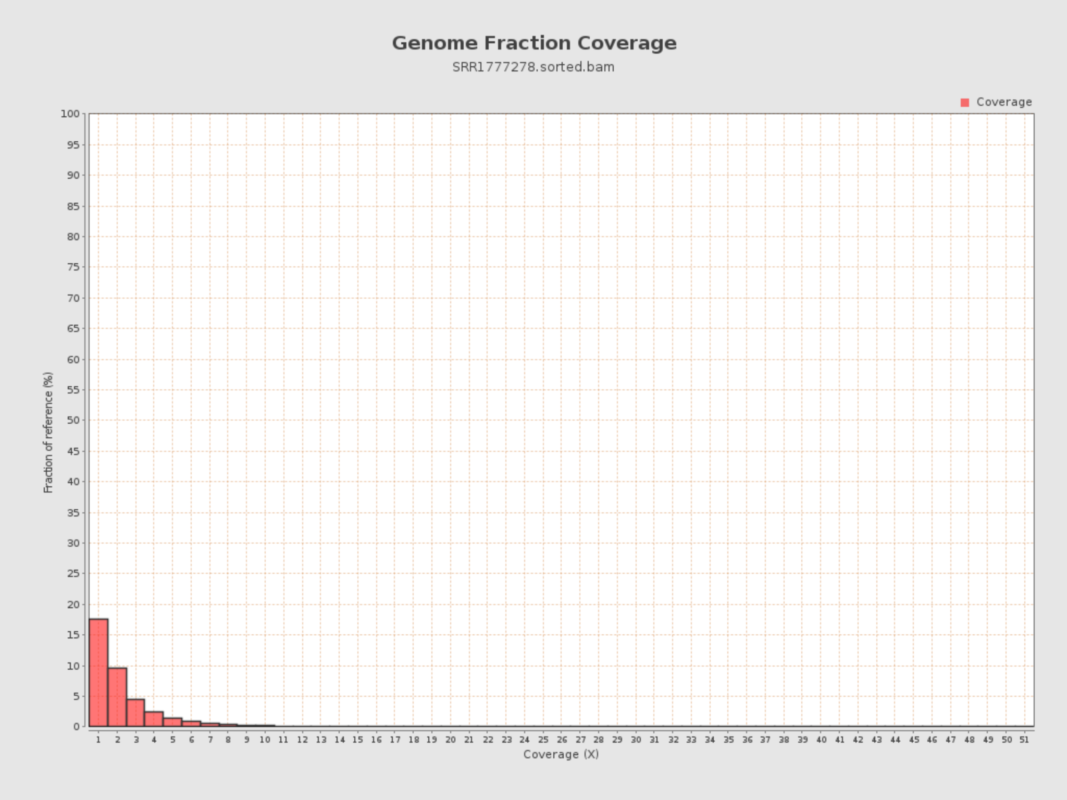
4. Results : Coverage Histogram



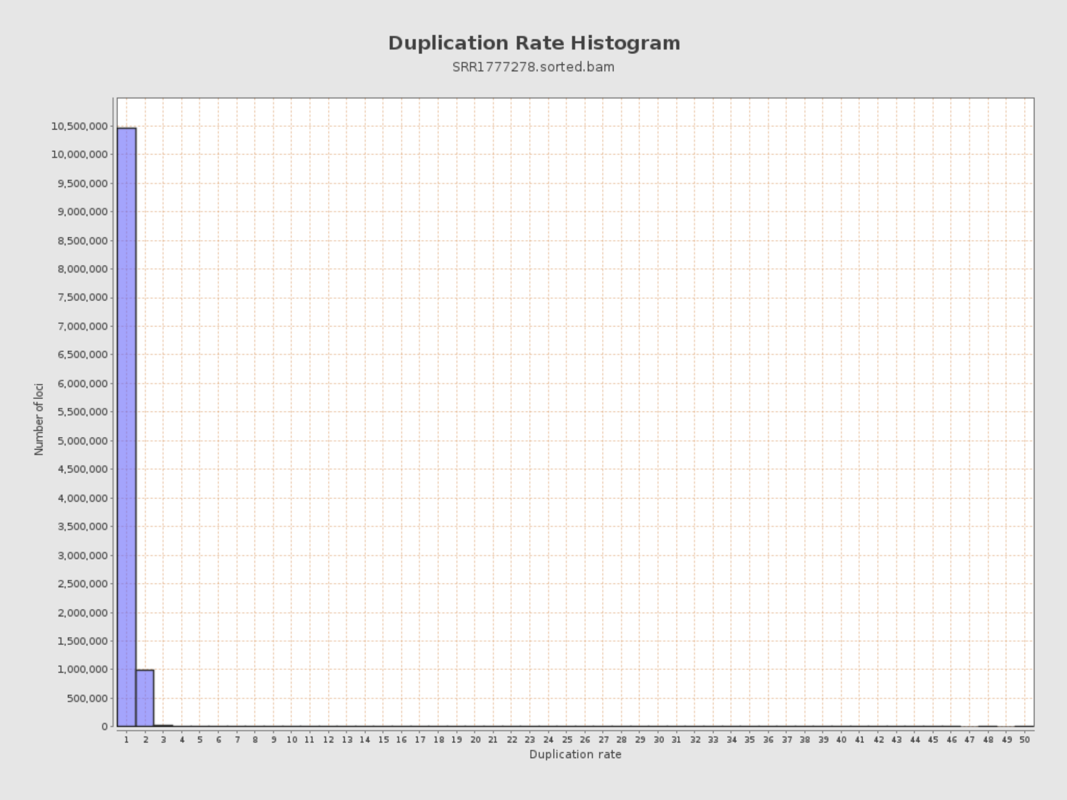
5. Results : Coverage Histogram (0-50X)



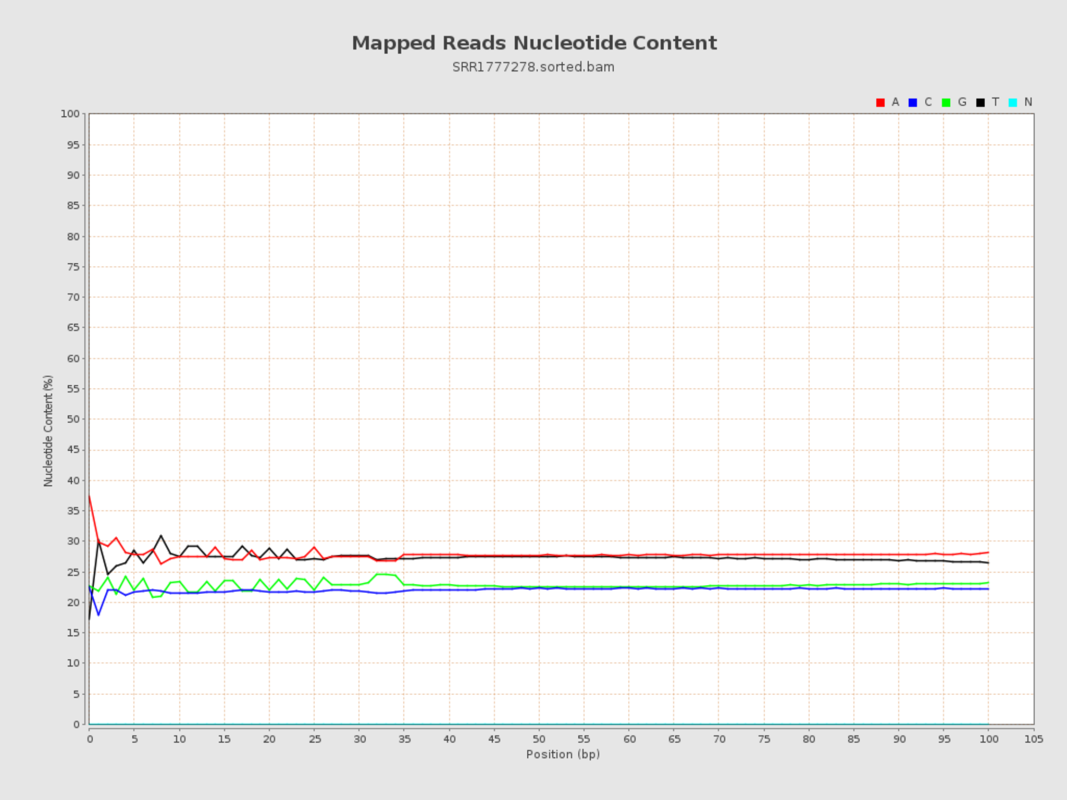
6. Results : Genome Fraction Coverage



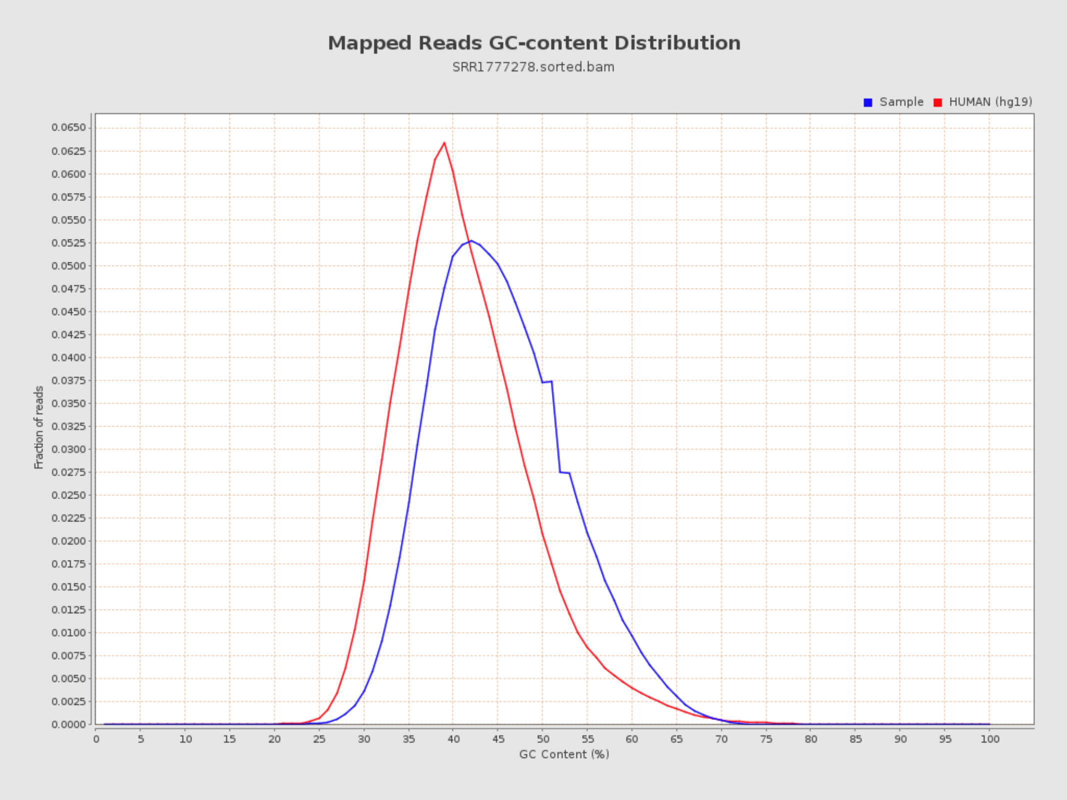
7. Results : Duplication Rate Histogram



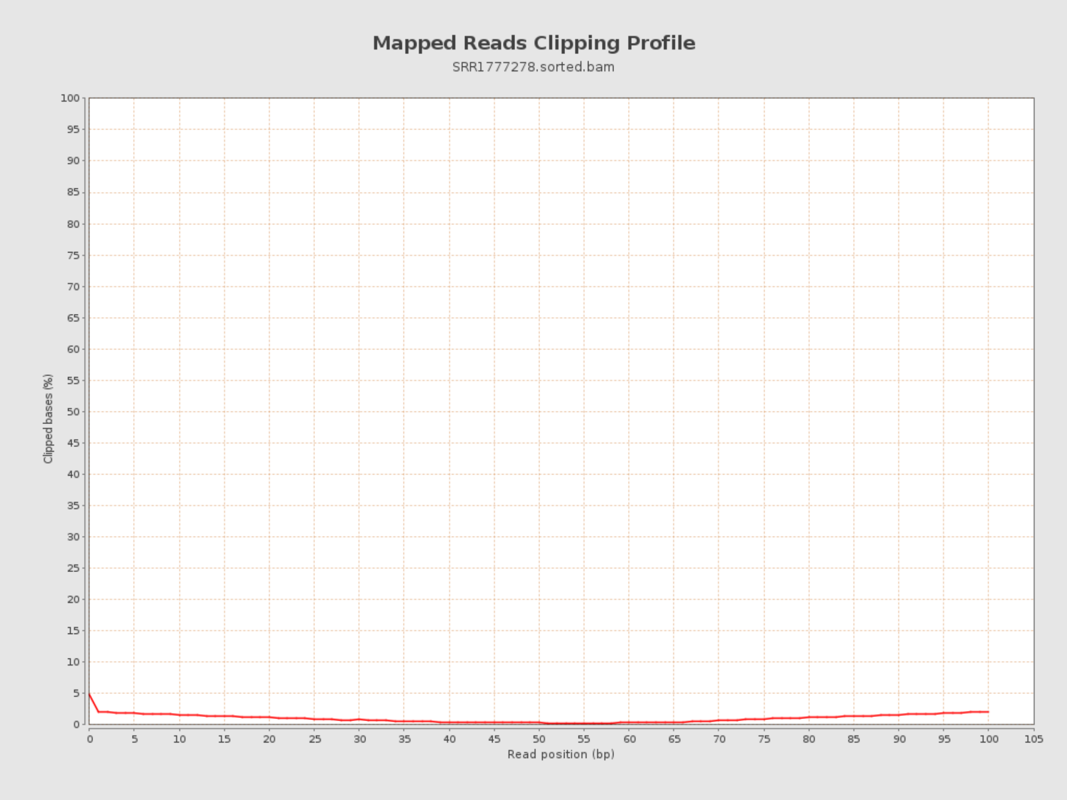
8. Results : Mapped Reads Nucleotide Content



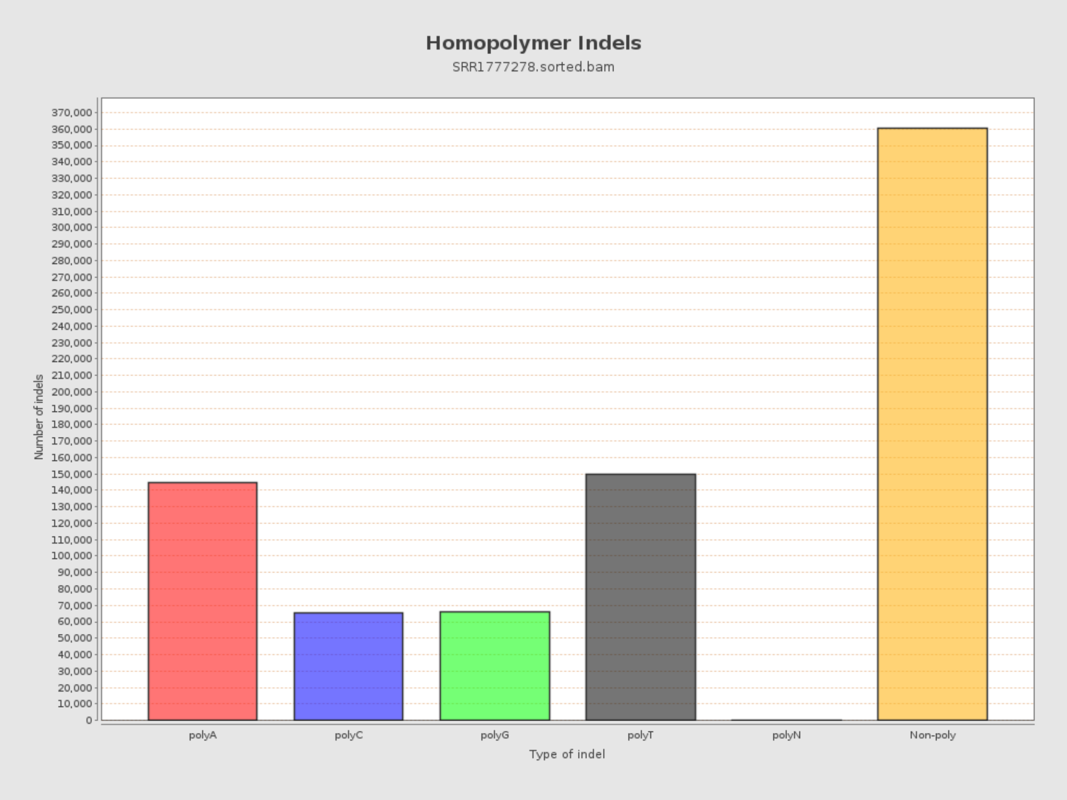
9. Results : Mapped Reads GC-content Distribution



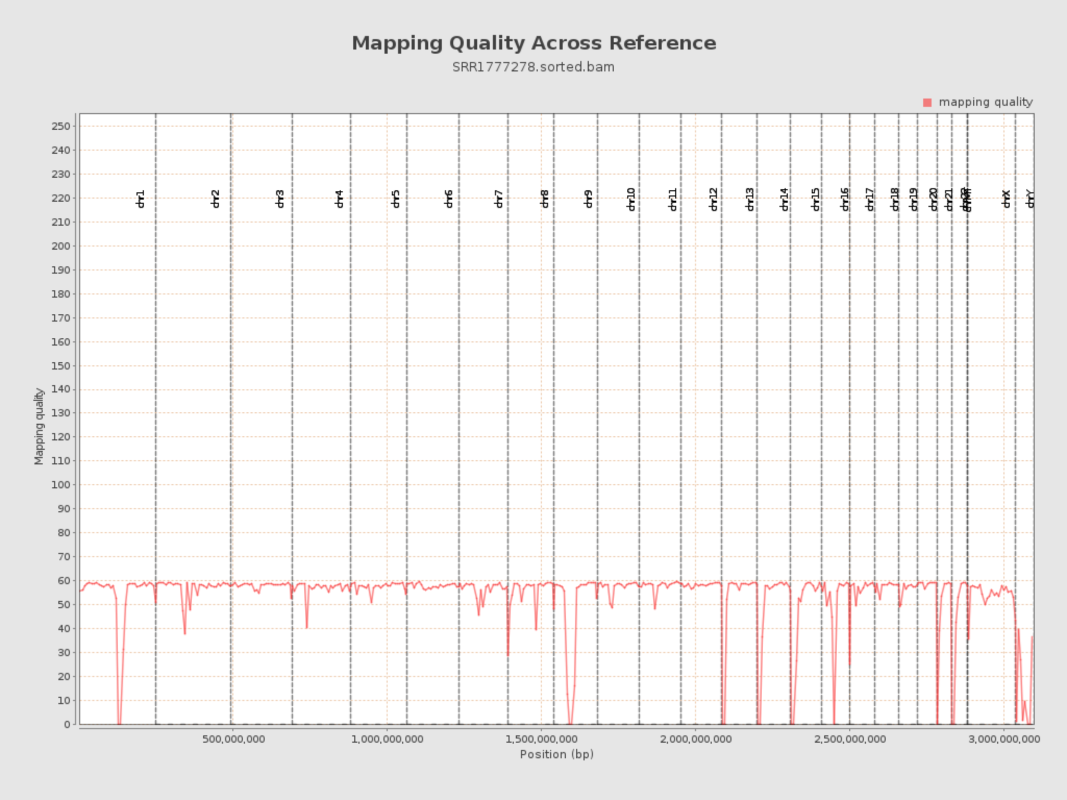
10. Results : Mapped Reads Clipping Profile



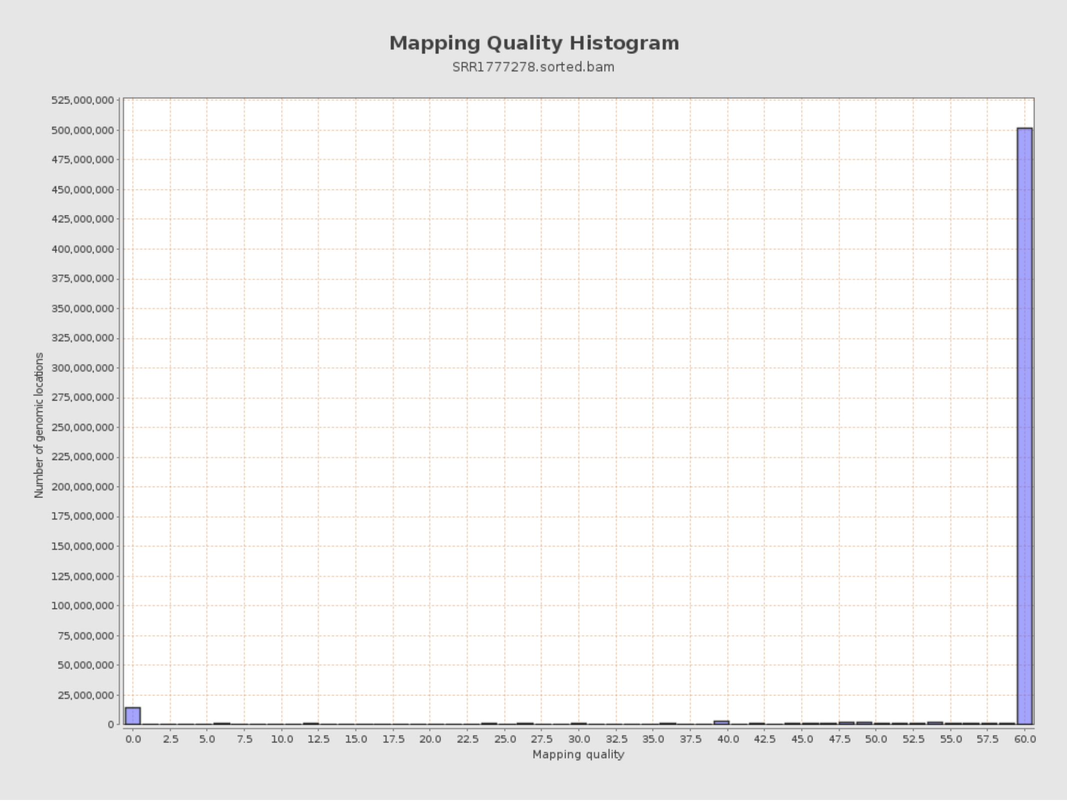
11. Results : Homopolymer Indels



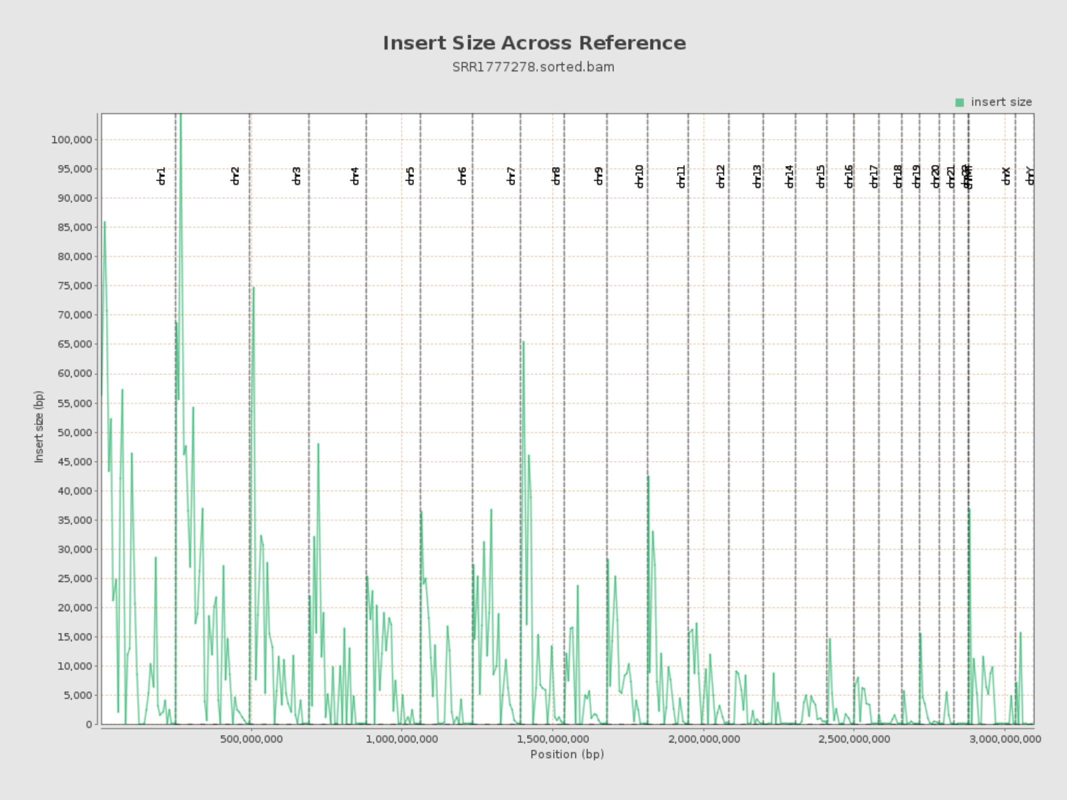
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram