Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 03:53:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777293.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_SRR1777293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777293_1.fastq.gz SRR1777293_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 03:53:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,124,874
Mapped reads	1,092,167 / 97.09%
Unmapped reads	32,707 / 2.91%
Mapped paired reads	1,092,167 / 97.09%
Mapped reads, first in pair	548,820 / 48.79%
Mapped reads, second in pair	543,347 / 48.3%
Mapped reads, both in pair	1,083,692 / 96.34%
Mapped reads, singletons	8,475 / 0.75%
Secondary alignments	0
Supplementary alignments	47,226 / 4.2%
Read min/max/mean length	30 / 101 / 102.74
Duplicated reads (estimated)	60,903 / 5.41%
Duplication rate	4.56%
Clipped reads	266,663 / 23.71%

2.2. ACGT Content

Number/percentage of A's	31,086,535 / 29.03%
Number/percentage of C's	22,547,336 / 21.05%
Number/percentage of T's	30,528,068 / 28.51%
Number/percentage of G's	22,929,315 / 21.41%
Number/percentage of N's	1,656 / 0%

GC Percentage	42.46%

2.3. Coverage

Mean	0.0346
Standard Deviation	0.4236

2.4. Mapping Quality

Mean Mapping Quality	53.03

2.5. Insert size

Mean	207,683.71
Standard Deviation	4,334,817.54
P25/Median/P75	130 / 175 / 232

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	630,171
Insertions	24,270
Mapped reads with at least one insertion	2.17%
Deletions	13,796
Mapped reads with at least one deletion	1.22%
Homopolymer indels	45.81%

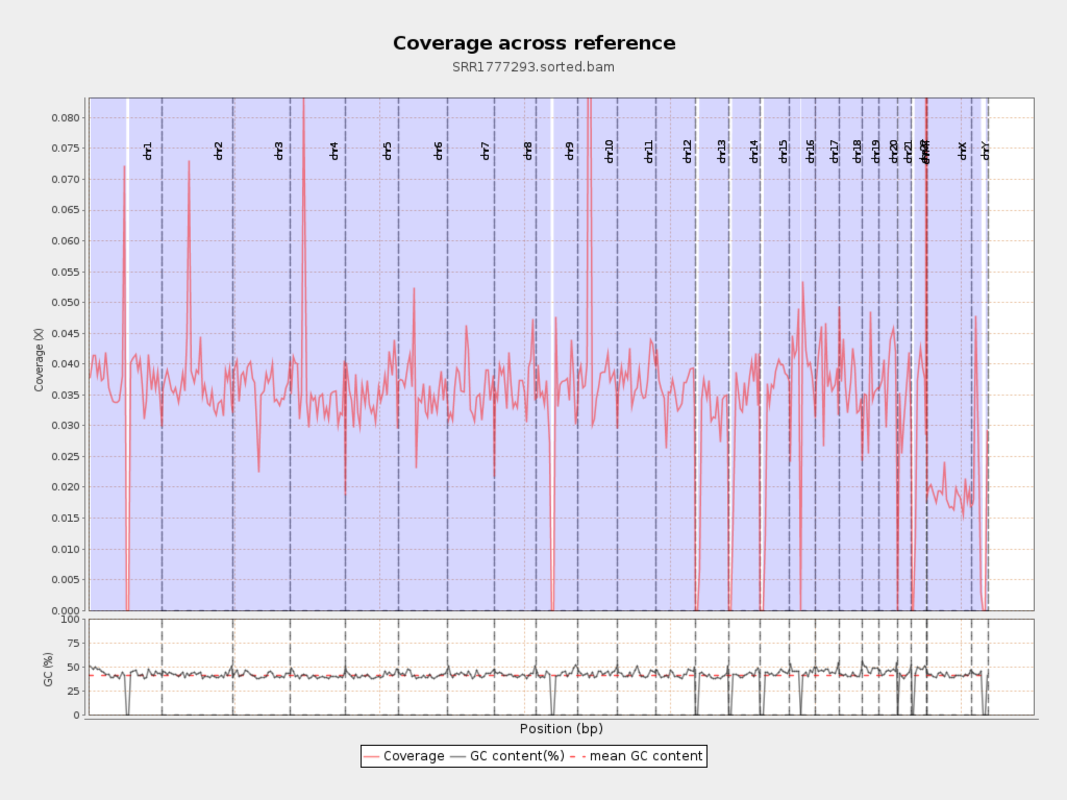
2.7. Chromosome stats

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

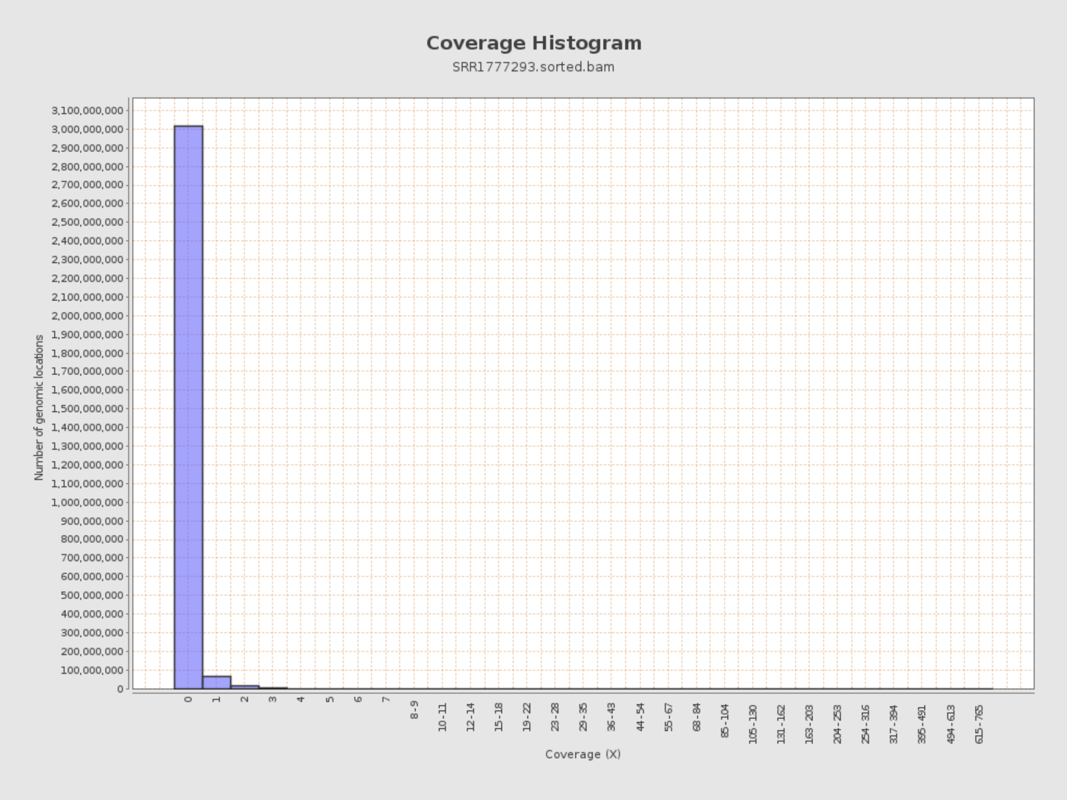
		bases	coverage	deviation
chr1	249250621	9046558	0.0363	0.785
chr2	243199373	9164208	0.0377	0.3434
chr3	198022430	7140382	0.0361	0.2443
chr4	191154276	6973544	0.0365	0.4129
chr5	180915260	6413322	0.0354	0.2273
chr6	171115067	6155737	0.036	0.2939
chr7	159138663	5692530	0.0358	0.3377
chr8	146364022	5396355	0.0369	0.2581
chr9	141213431	4587216	0.0325	0.4103
chr10	135534747	5864307	0.0433	1.0055
chr11	135006516	5092204	0.0377	0.2853
chr12	133851895	4794495	0.0358	0.226
chr13	115169878	3222274	0.028	0.1998
chr14	107349540	3245912	0.0302	0.21
chr15	102531392	3135527	0.0306	0.2089
chr16	90354753	3414632	0.0378	0.2883
chr17	81195210	3094270	0.0381	0.2848
chr18	78077248	2923775	0.0374	0.4915
chr19	59128983	2078627	0.0352	0.4744
chr20	63025520	2448008	0.0388	0.2488
chr21	48129895	1465869	0.0305	0.269
chr22	51304566	1363159	0.0266	0.1963
chrMT	16571	469349	28.3235	8.1615
chrX	155270560	2918741	0.0188	0.1782

chrY	59373566	1027730	0.0173	0.3953

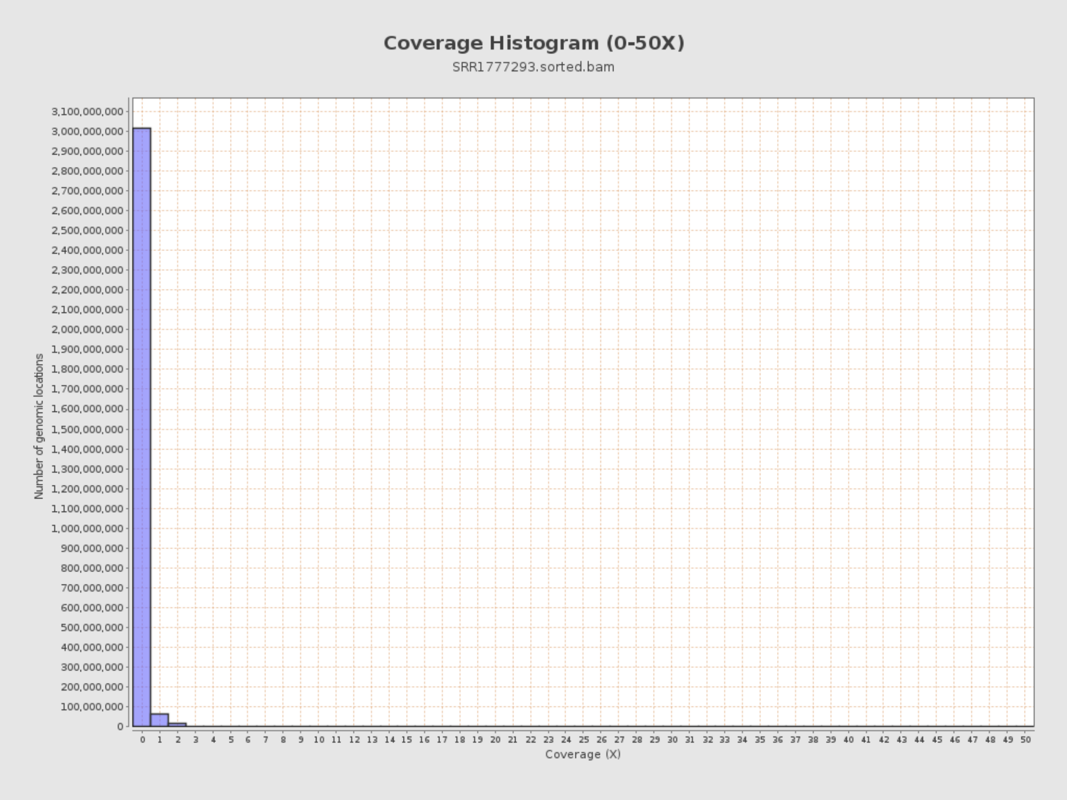
3. Results : Coverage across reference



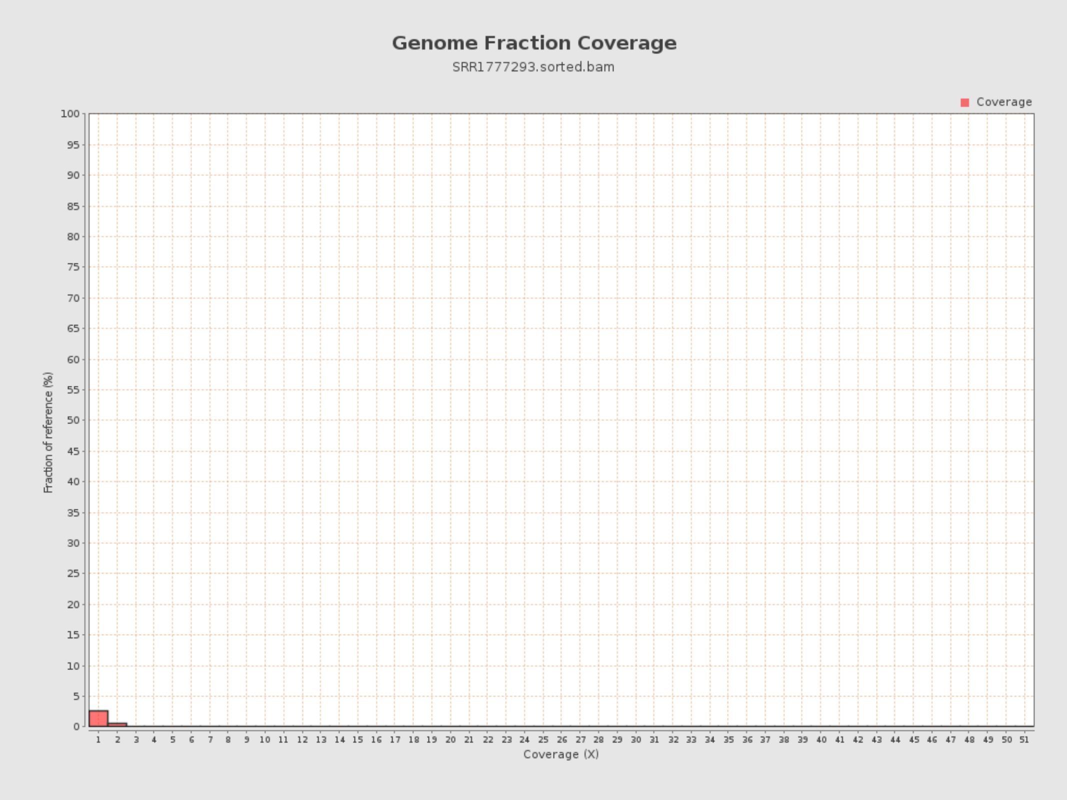
4. Results : Coverage Histogram



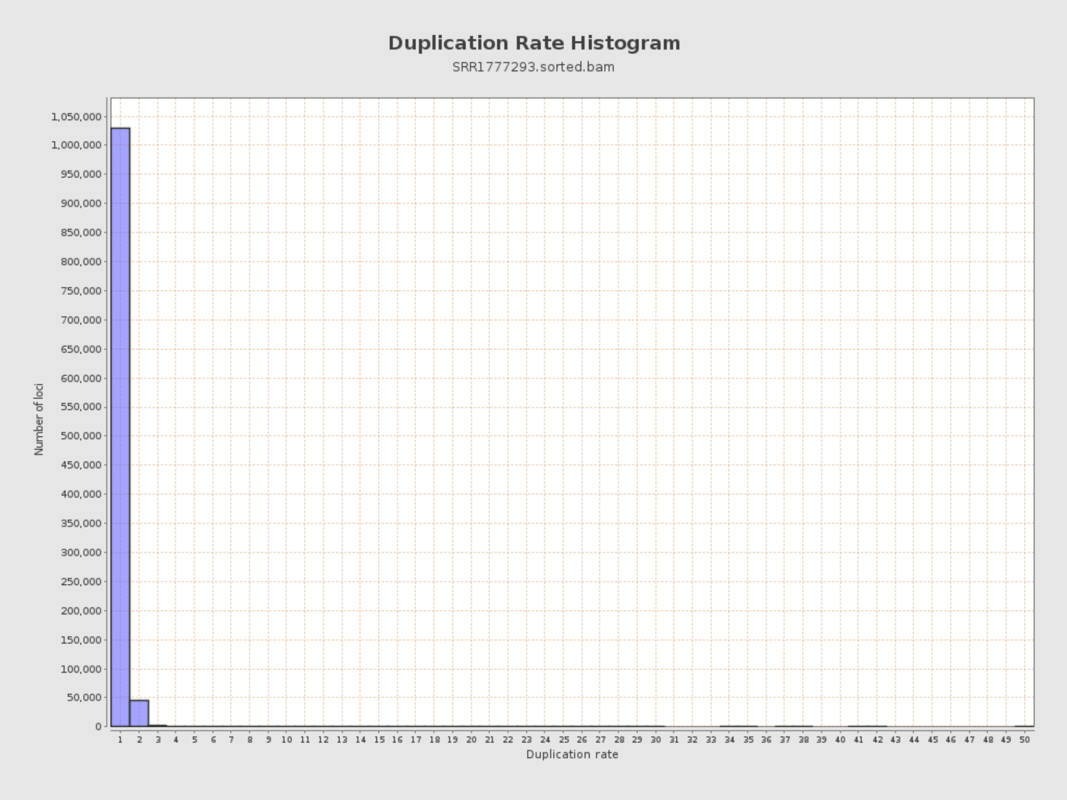
5. Results : Coverage Histogram (0-50X)



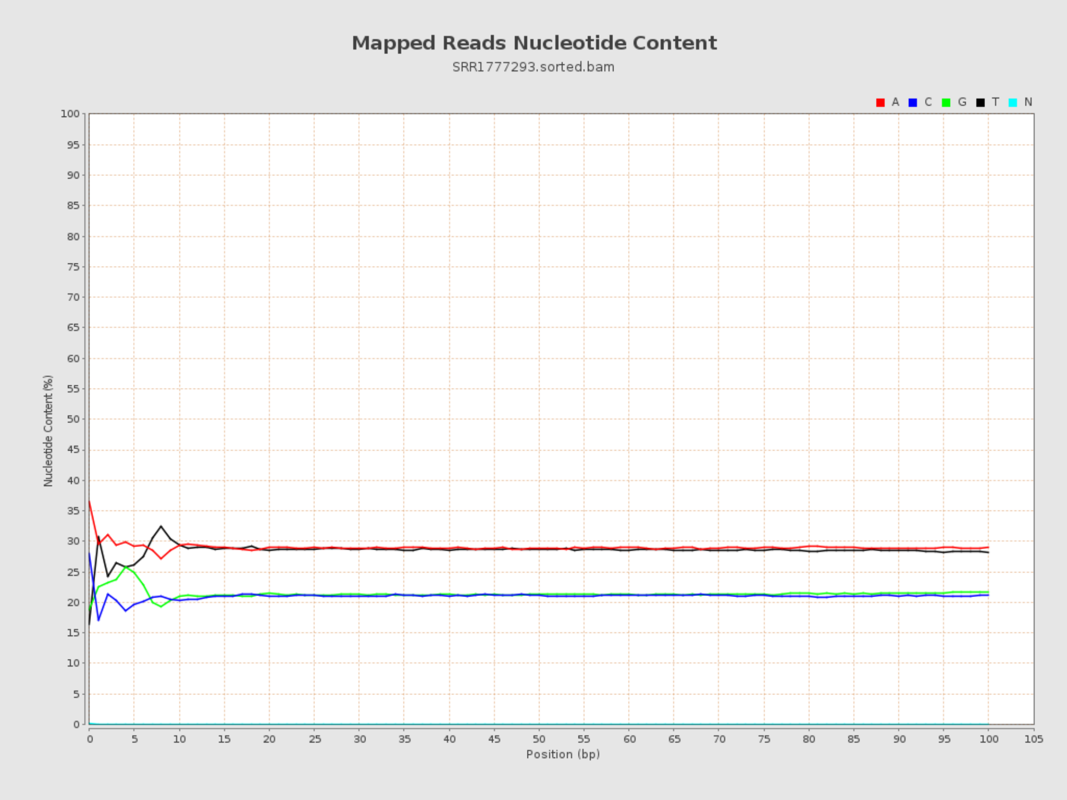
6. Results : Genome Fraction Coverage



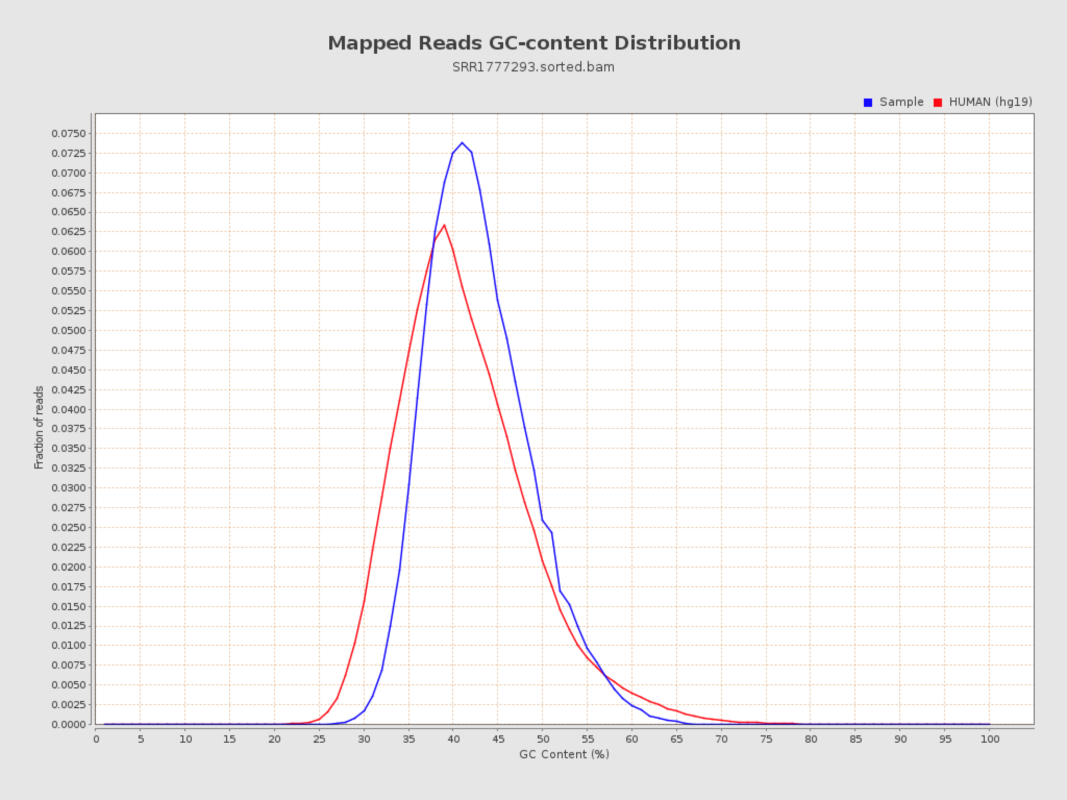
7. Results : Duplication Rate Histogram



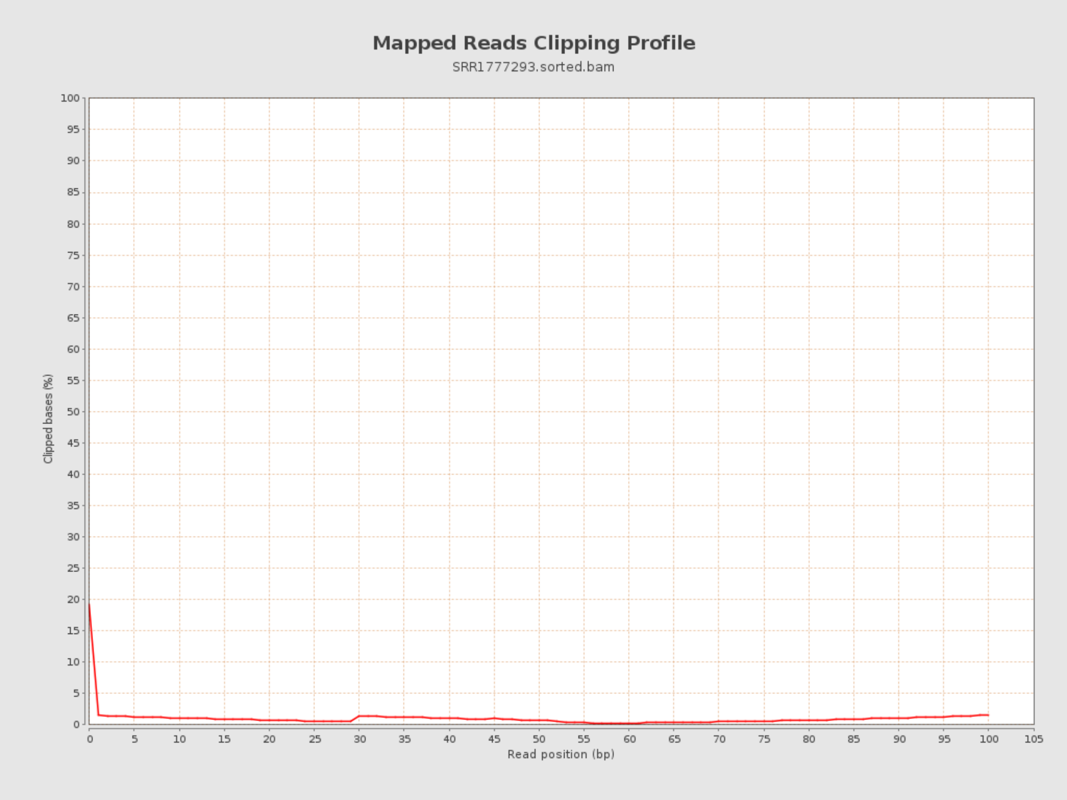
8. Results : Mapped Reads Nucleotide Content



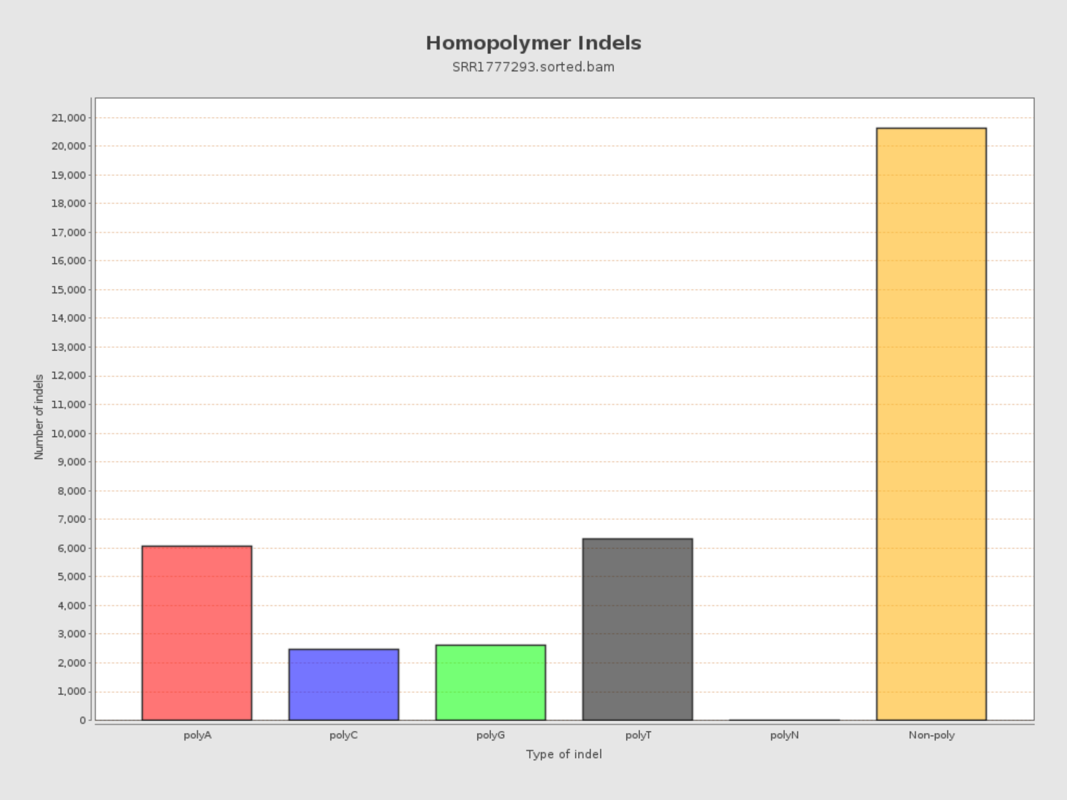
9. Results : Mapped Reads GC-content Distribution



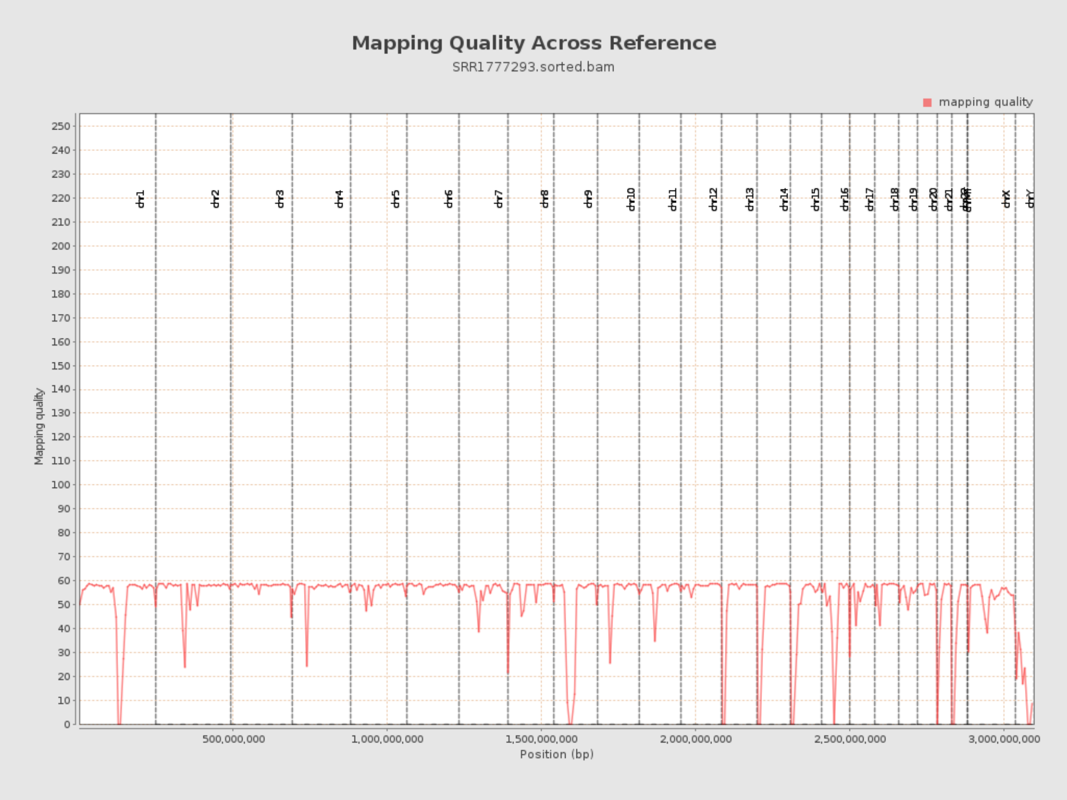
10. Results : Mapped Reads Clipping Profile



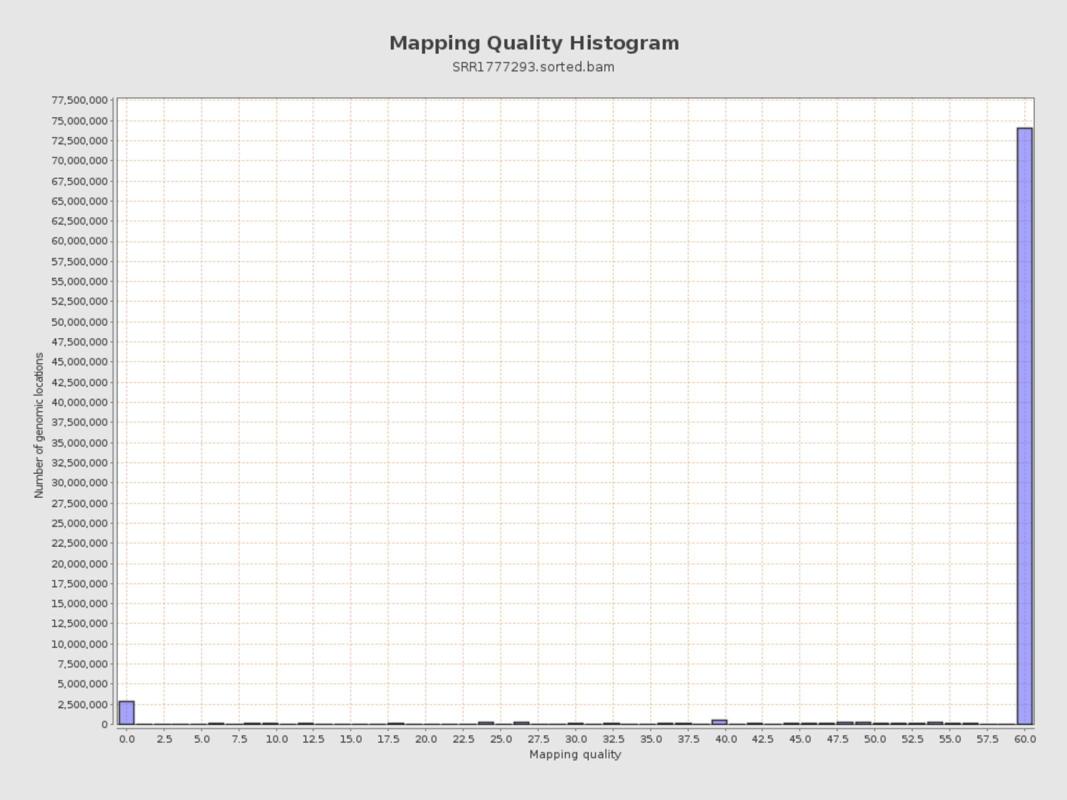
11. Results : Homopolymer Indels



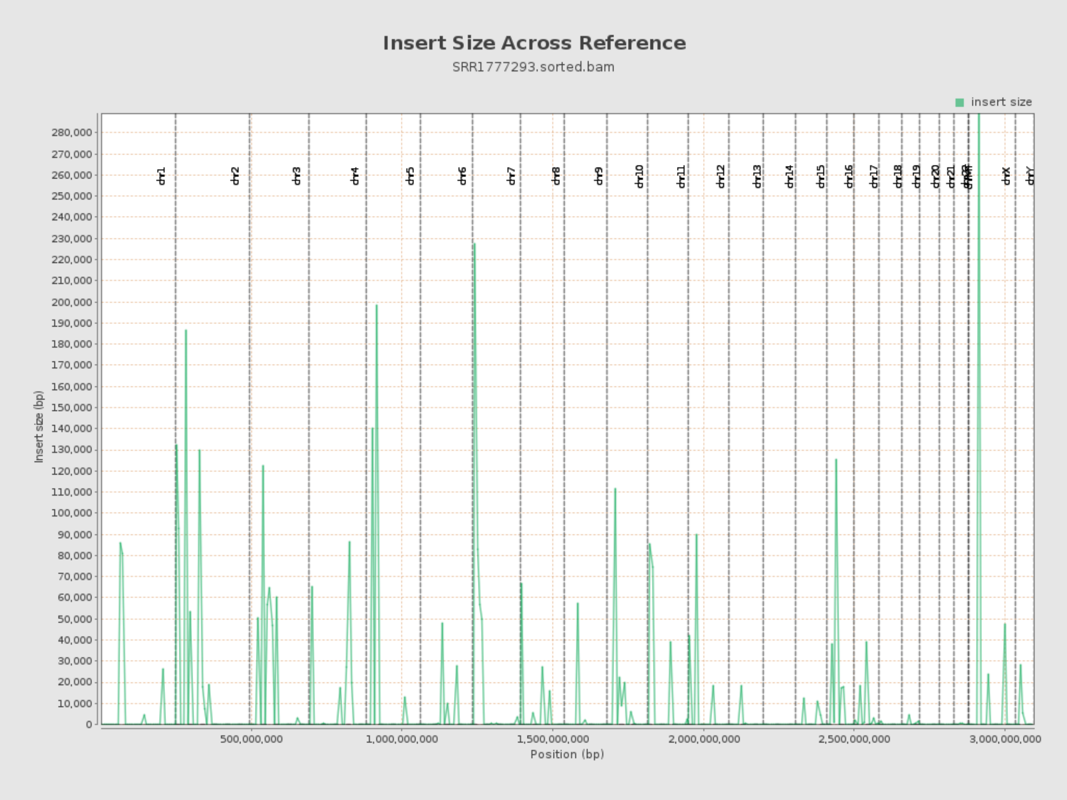
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram