Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:04:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777297.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_SRR1777297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777297_1.fastq.gz SRR1777297_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:04:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,363,470
Mapped reads	1,291,512 / 94.72%
Unmapped reads	71,958 / 5.28%
Mapped paired reads	1,291,512 / 94.72%
Mapped reads, first in pair	647,102 / 47.46%
Mapped reads, second in pair	644,410 / 47.26%
Mapped reads, both in pair	1,285,644 / 94.29%
Mapped reads, singletons	5,868 / 0.43%
Secondary alignments	0
Supplementary alignments	42,904 / 3.15%
Read min/max/mean length	30 / 101 / 102.31
Duplicated reads (estimated)	106,449 / 7.81%
Duplication rate	7.18%
Clipped reads	350,898 / 25.74%

2.2. ACGT Content

Number/percentage of A's	36,989,293 / 29.63%
Number/percentage of C's	25,477,487 / 20.41%
Number/percentage of T's	36,201,125 / 29%
Number/percentage of G's	26,161,296 / 20.96%
Number/percentage of N's	2,121 / 0%

GC Percentage	41.37%

2.3. Coverage

Mean	0.0403
Standard Deviation	0.5117

2.4. Mapping Quality

Mean Mapping Quality	53.18

2.5. Insert size

Mean	126,335.85
Standard Deviation	3,395,461.54
P25/Median/P75	114 / 158 / 217

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	763,340
Insertions	31,343
Mapped reads with at least one insertion	2.36%
Deletions	17,463
Mapped reads with at least one deletion	1.3%
Homopolymer indels	44.85%

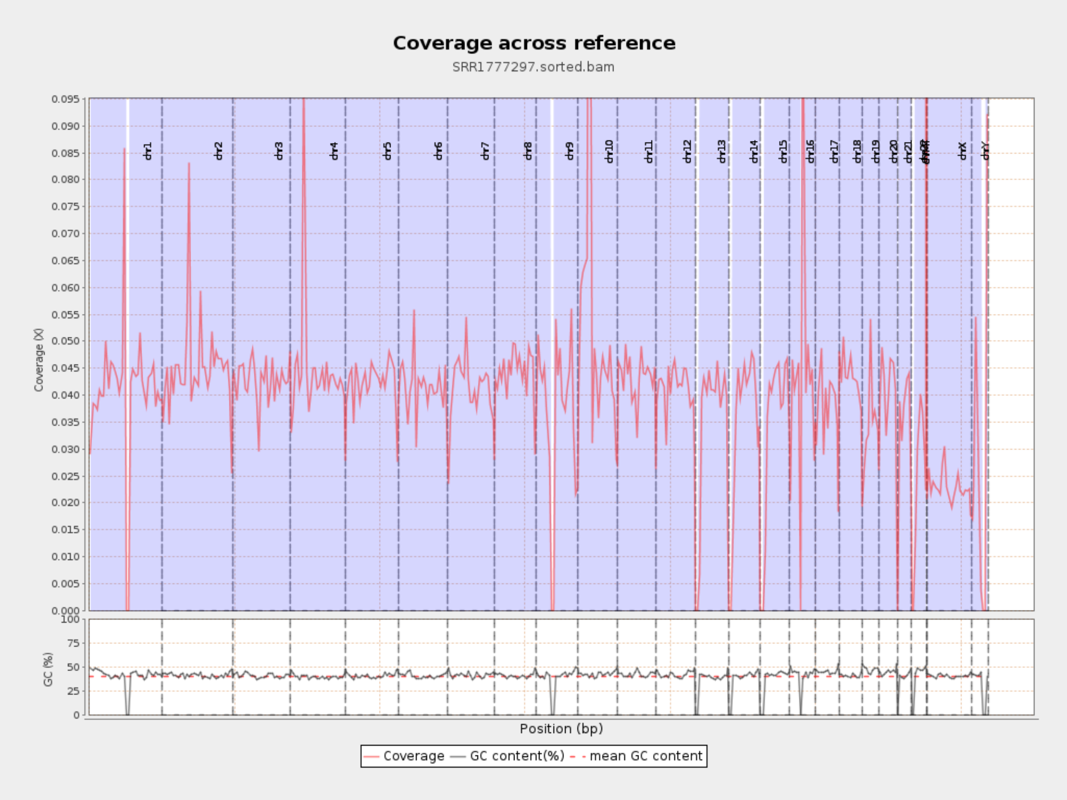
2.7. Chromosome stats

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

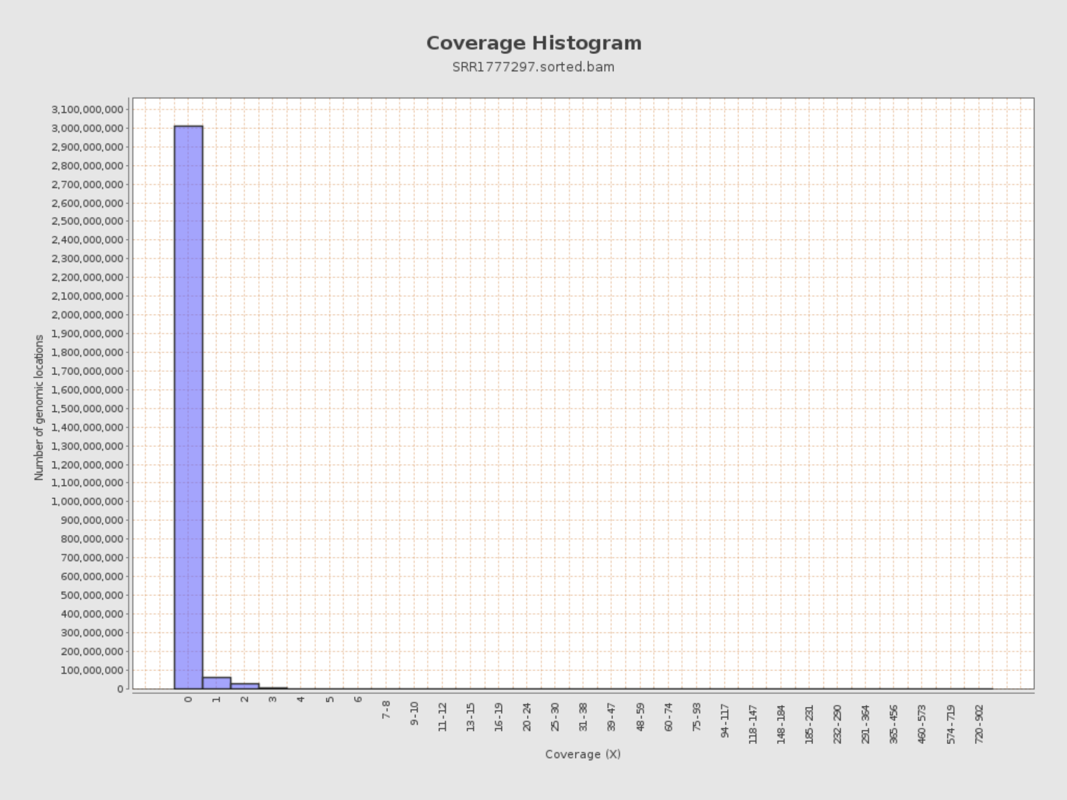
		bases	coverage	deviation
chr1	249250621	10149588	0.0407	0.9263
chr2	243199373	11012355	0.0453	0.4458
chr3	198022430	8453095	0.0427	0.2847
chr4	191154276	8528791	0.0446	0.4794
chr5	180915260	7677739	0.0424	0.2622
chr6	171115067	7114433	0.0416	0.2913
chr7	159138663	6653122	0.0418	0.3595
chr8	146364022	6487967	0.0443	0.3566
chr9	141213431	5246112	0.0372	0.4564
chr10	135534747	7521547	0.0555	1.2873
chr11	135006516	5818688	0.0431	0.2956
chr12	133851895	5547268	0.0414	0.2573
chr13	115169878	3939521	0.0342	0.2323
chr14	107349540	3714761	0.0346	0.2386
chr15	102531392	3445978	0.0336	0.2306
chr16	90354753	3984917	0.0441	0.571
chr17	81195210	3030069	0.0373	0.3106
chr18	78077248	3413226	0.0437	0.523
chr19	59128983	2052826	0.0347	0.5249
chr20	63025520	2581875	0.041	0.273
chr21	48129895	1622295	0.0337	0.2895
chr22	51304566	1195852	0.0233	0.1957
chrMT	16571	508909	30.7108	9.3512
chrX	155270560	3568810	0.023	0.2093

chrY	59373566	1608386	0.0271	0.5817

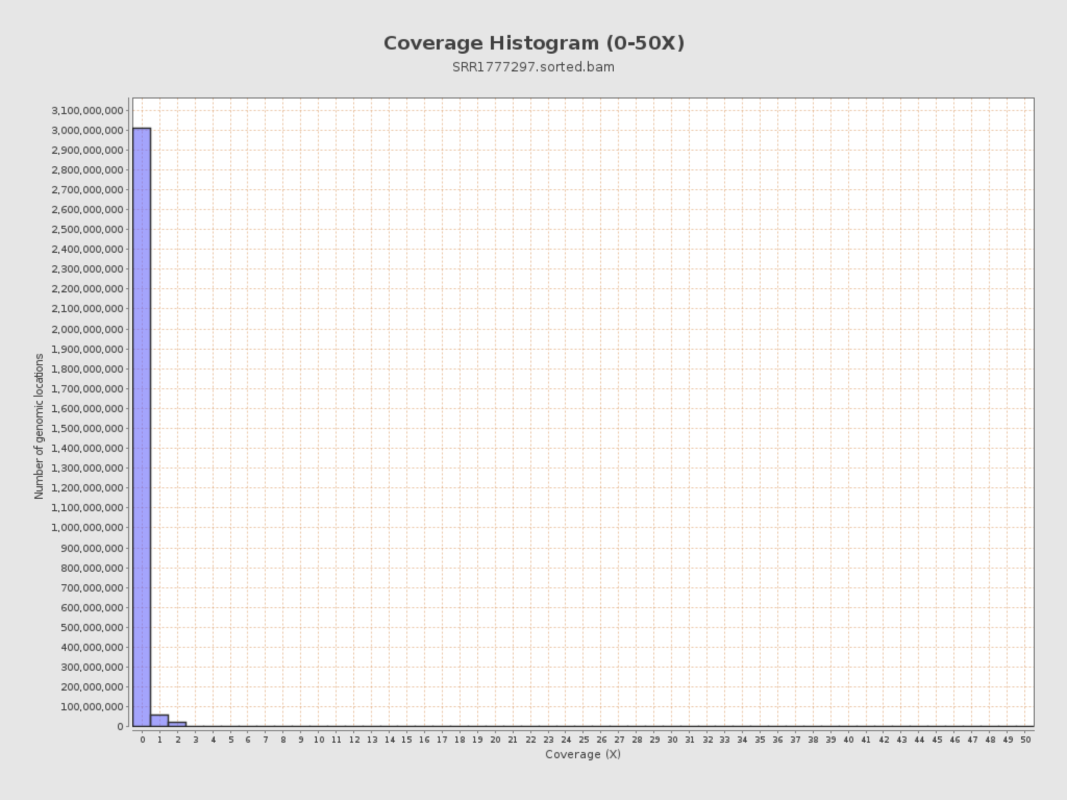
3. Results : Coverage across reference



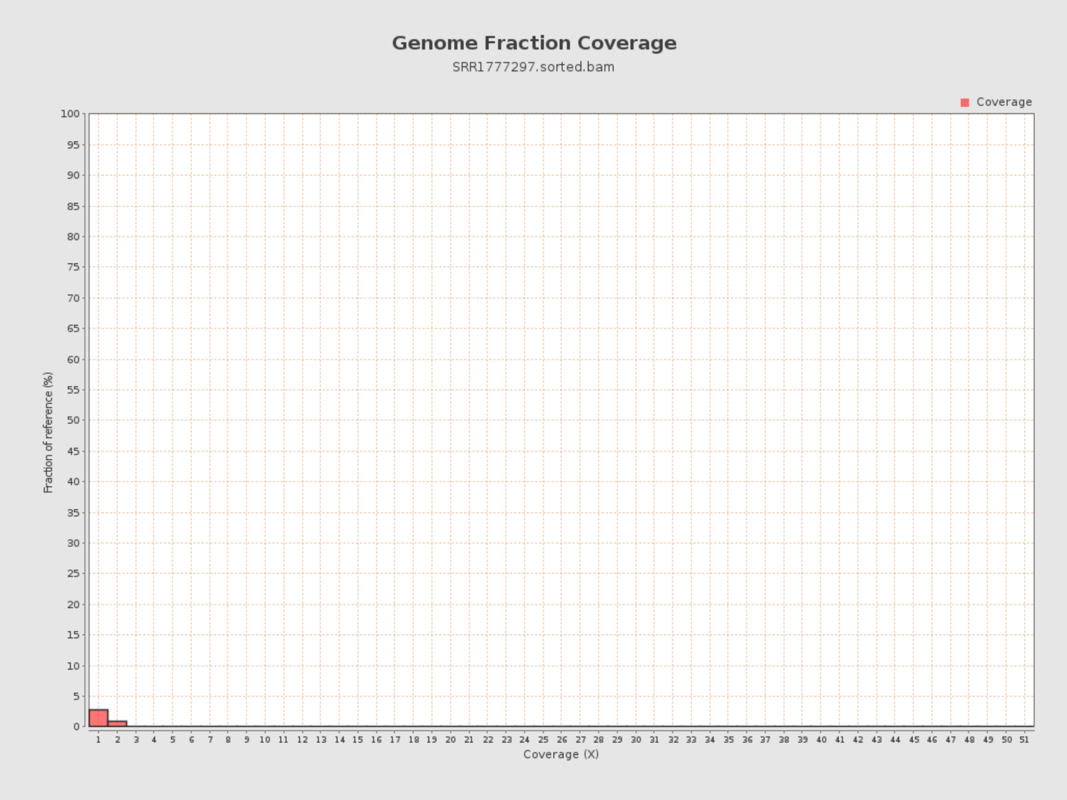
4. Results : Coverage Histogram



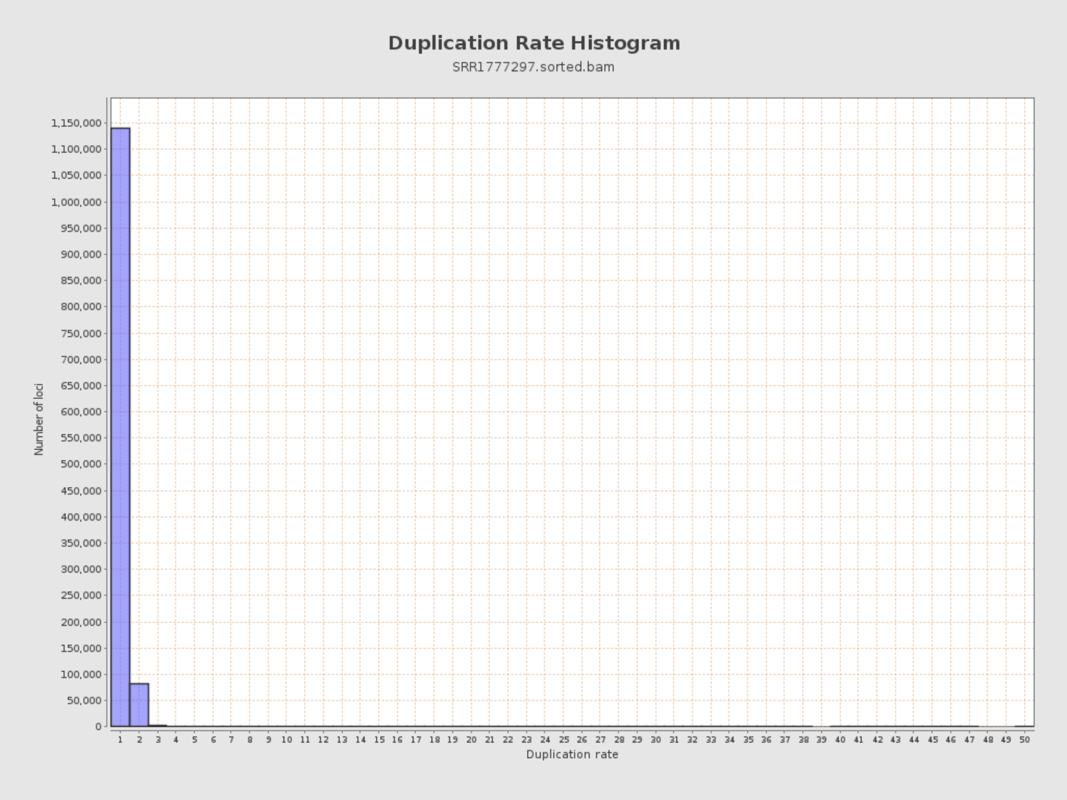
5. Results : Coverage Histogram (0-50X)



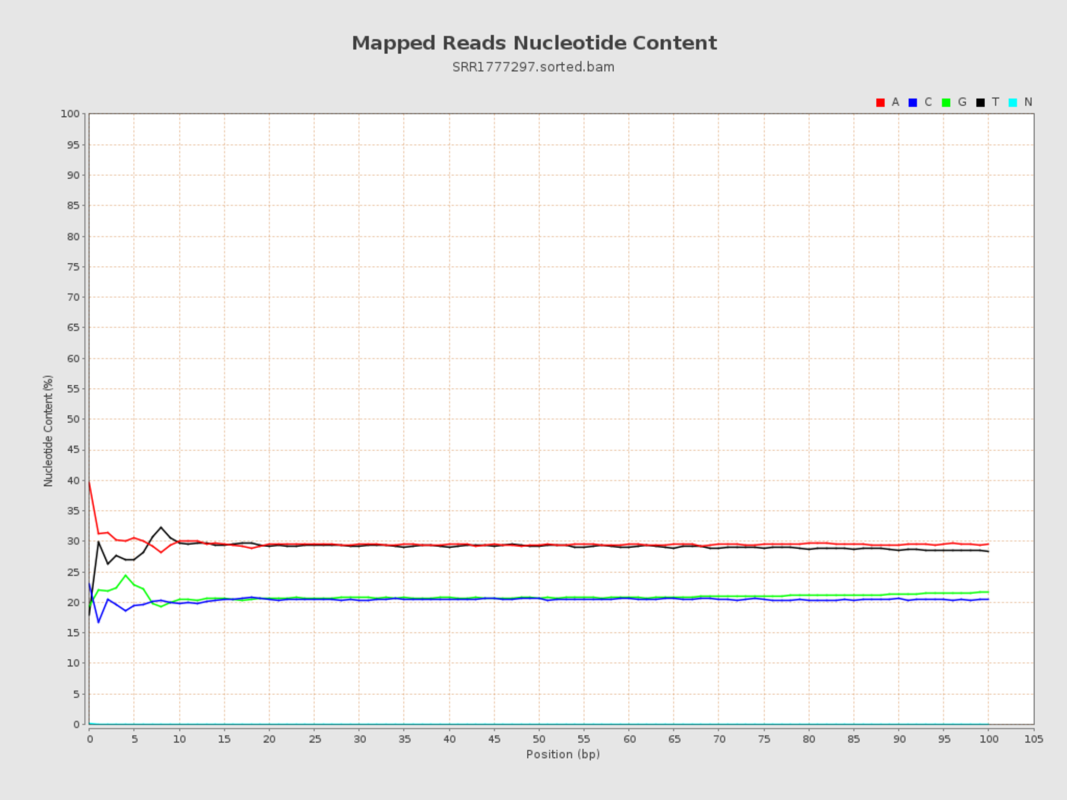
6. Results : Genome Fraction Coverage



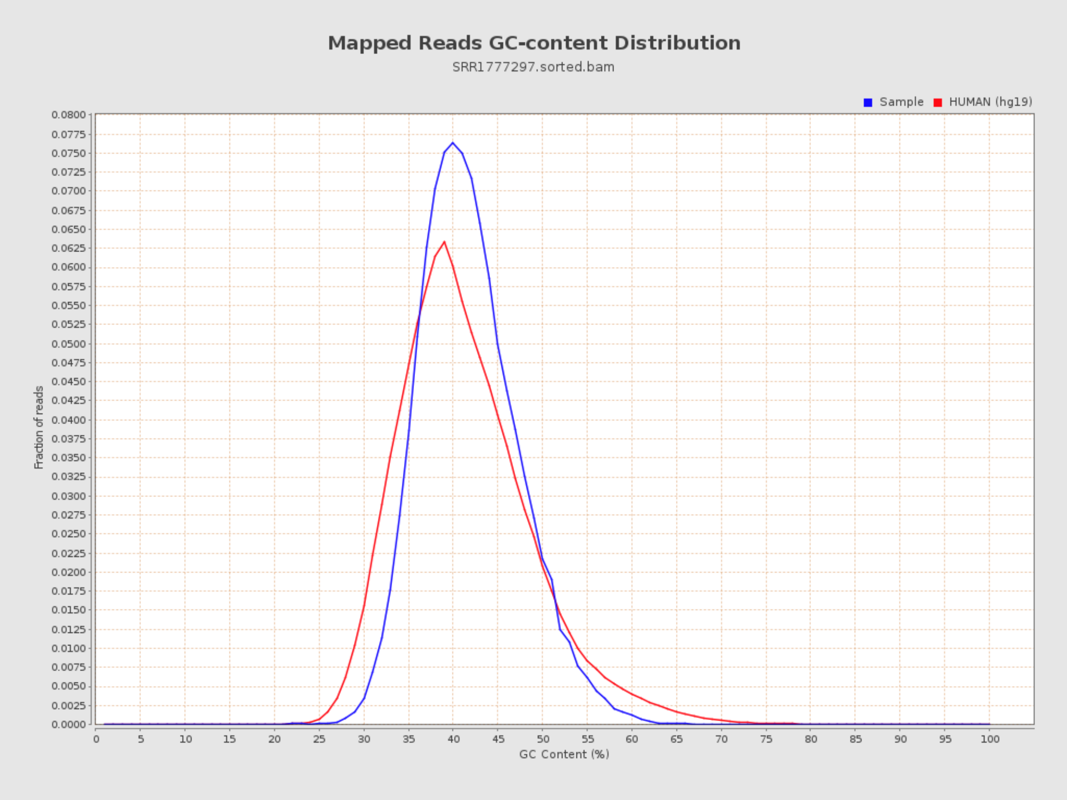
7. Results : Duplication Rate Histogram



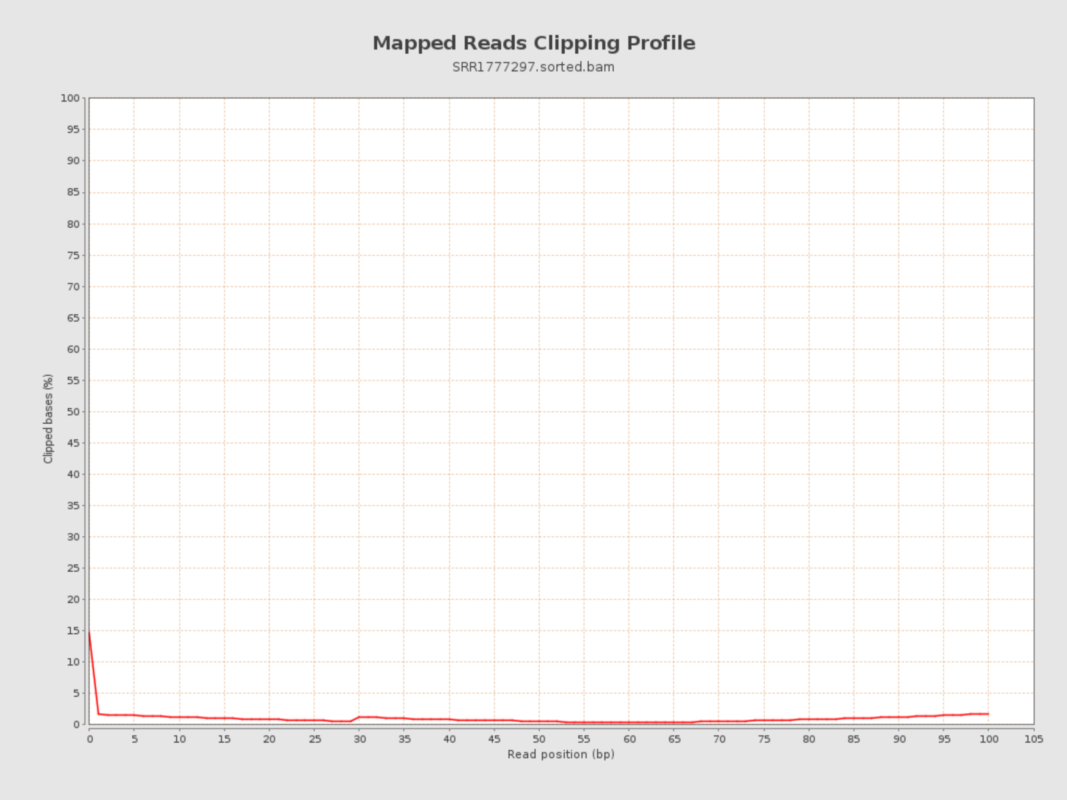
8. Results : Mapped Reads Nucleotide Content



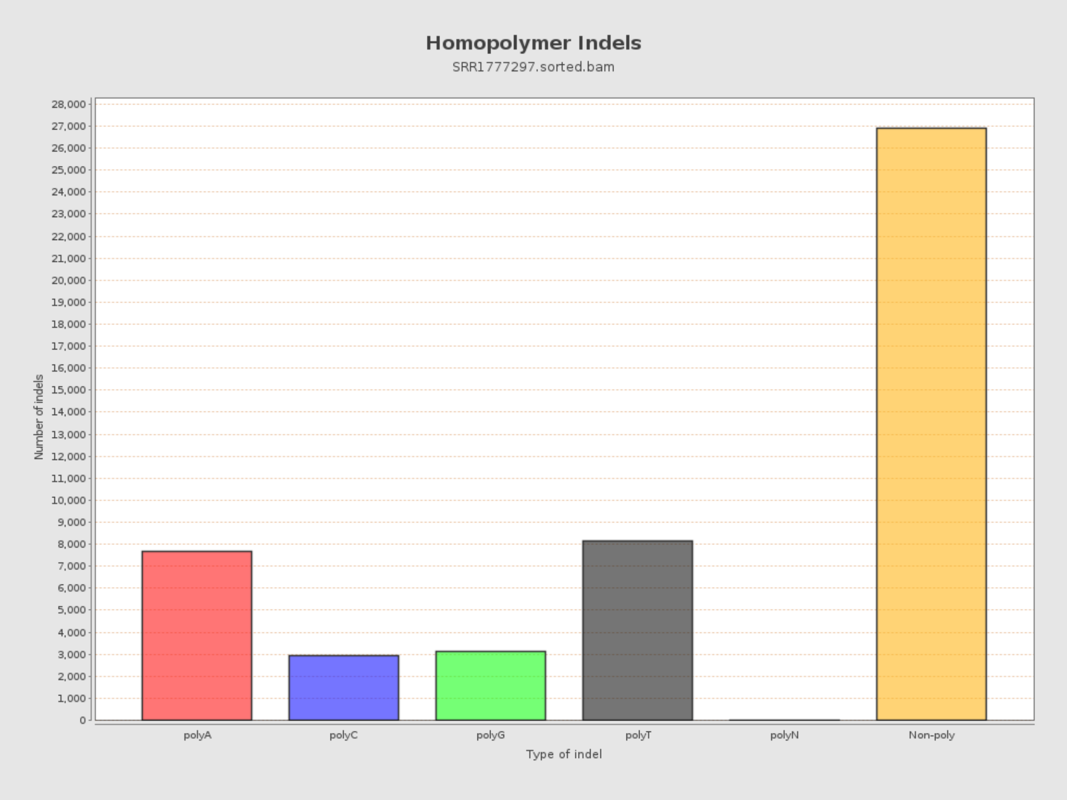
9. Results : Mapped Reads GC-content Distribution



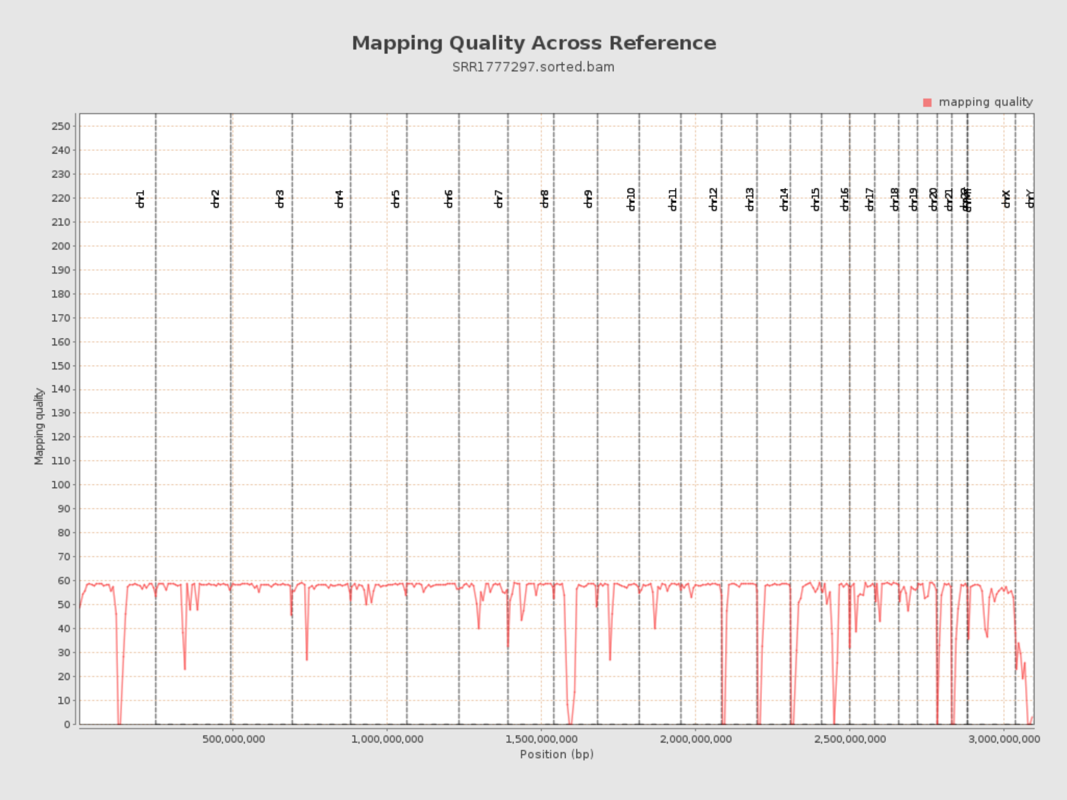
10. Results : Mapped Reads Clipping Profile



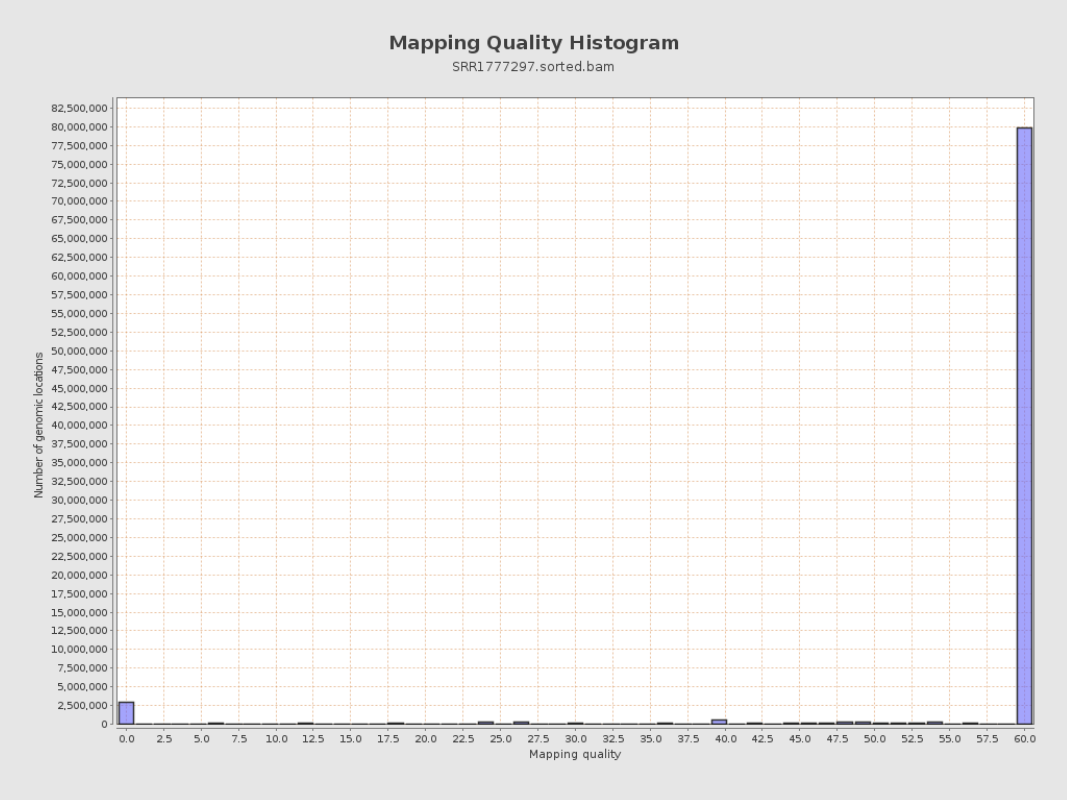
11. Results : Homopolymer Indels



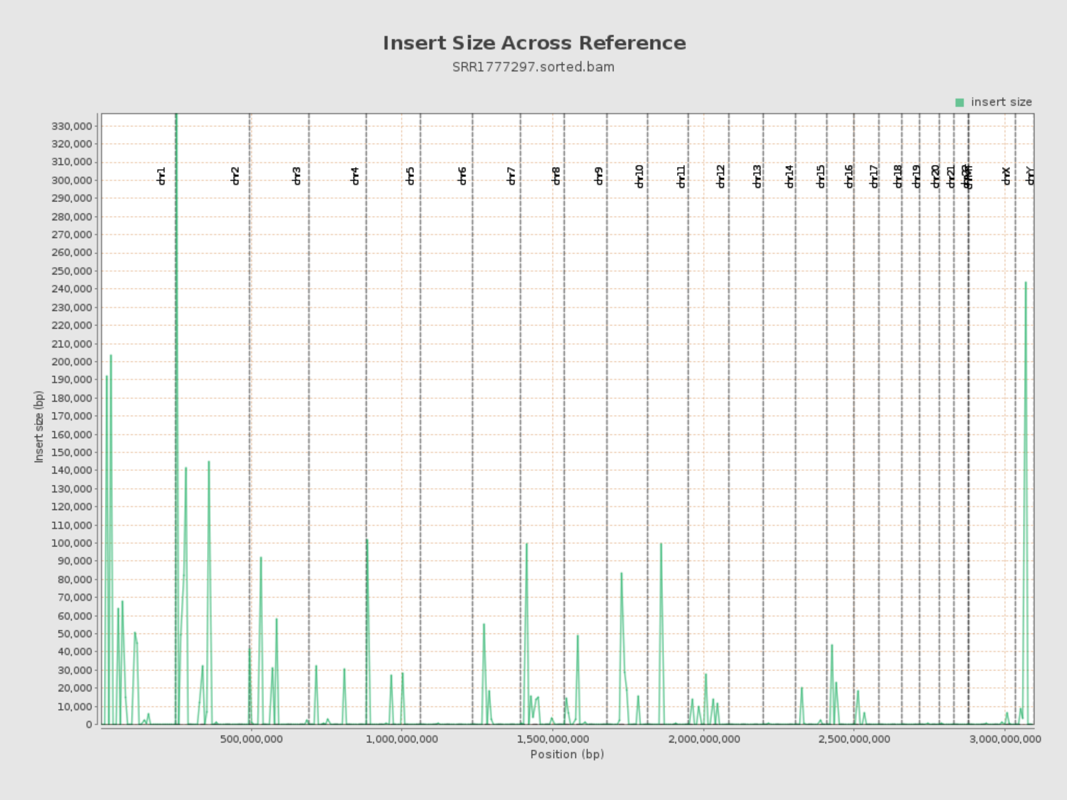
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram