Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 01:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779297.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_SRR1779297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779297_1.fastq.gz SRR1779297_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 01:35:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,928,918
Mapped reads	17,901,180 / 94.57%
Unmapped reads	1,027,738 / 5.43%
Mapped paired reads	17,901,180 / 94.57%
Mapped reads, first in pair	9,022,981 / 47.67%
Mapped reads, second in pair	8,878,199 / 46.9%
Mapped reads, both in pair	17,727,212 / 93.65%
Mapped reads, singletons	173,968 / 0.92%
Secondary alignments	0
Supplementary alignments	42,099 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	904,749 / 4.78%
Duplication rate	4.68%
Clipped reads	534,421 / 2.82%

2.2. ACGT Content

Number/percentage of A's	439,051,806 / 30.81%
Number/percentage of C's	271,428,700 / 19.05%
Number/percentage of T's	438,053,058 / 30.74%
Number/percentage of G's	276,157,204 / 19.38%
Number/percentage of N's	378,479 / 0.03%

GC Percentage	38.43%

2.3. Coverage

Mean	0.4604
Standard Deviation	2.0272

2.4. Mapping Quality

Mean Mapping Quality	52.86

2.5. Insert size

Mean	34,248.29
Standard Deviation	1,759,497.79
P25/Median/P75	158 / 212 / 288

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,897,642
Insertions	102,755
Mapped reads with at least one insertion	0.57%
Deletions	131,106
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.92%

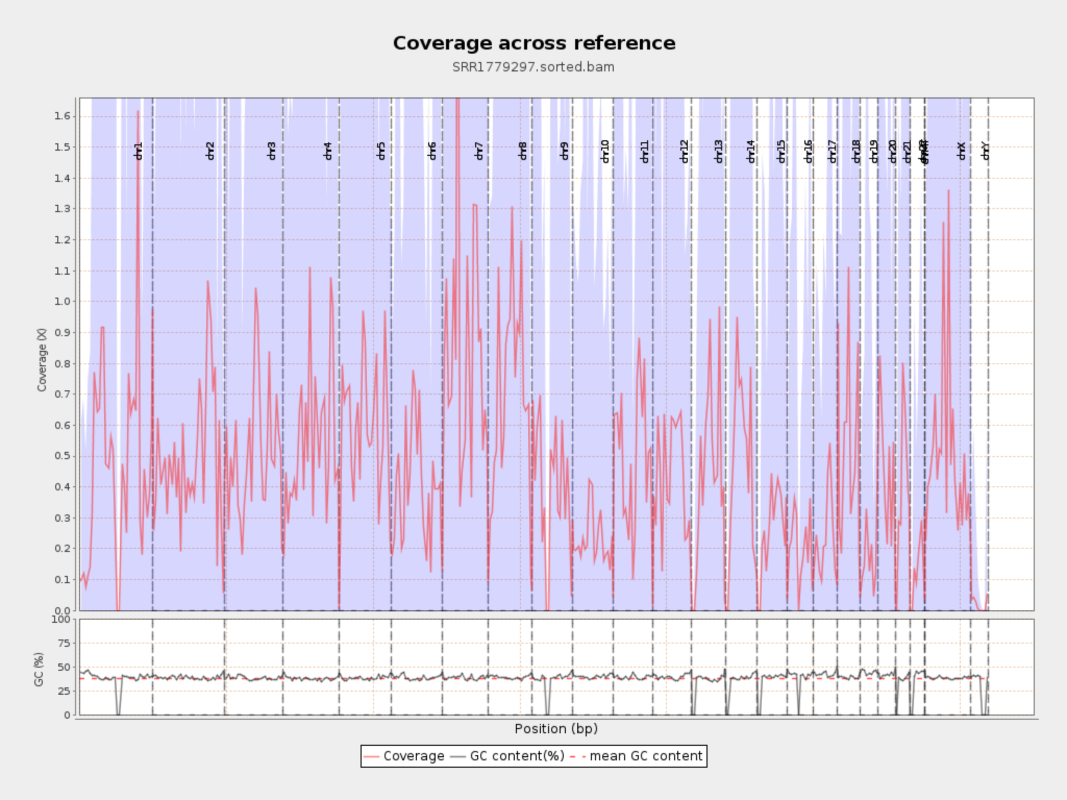
2.7. Chromosome stats

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

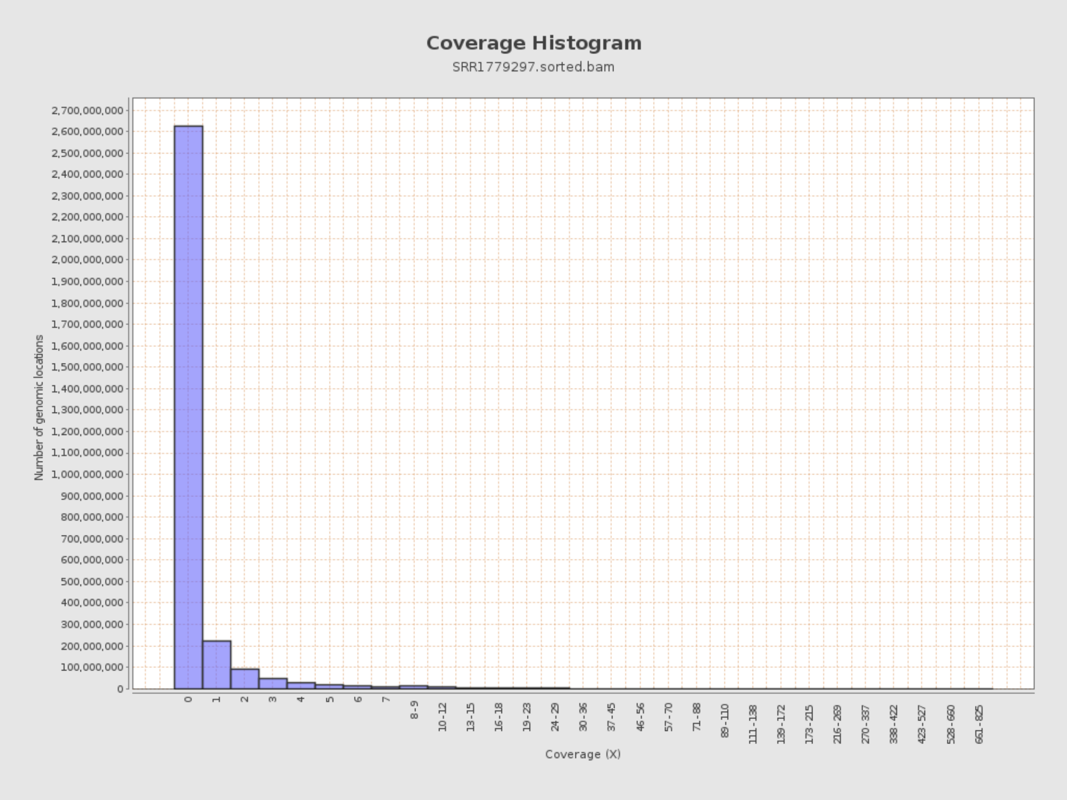
		bases	coverage	deviation
chr1	249250621	115623082	0.4639	2.3054
chr2	243199373	119145230	0.4899	1.9184
chr3	198022430	102412166	0.5172	1.9448
chr4	191154276	105051029	0.5496	2.339
chr5	180915260	105344153	0.5823	2.1647
chr6	171115067	70058971	0.4094	1.6122
chr7	159138663	137739953	0.8655	3.4242
chr8	146364022	105668795	0.722	2.1943
chr9	141213431	54107236	0.3832	1.5086
chr10	135534747	30852817	0.2276	1.681
chr11	135006516	67144296	0.4973	1.9521
chr12	133851895	58373147	0.4361	1.9754
chr13	115169878	51846746	0.4502	1.897
chr14	107349540	50876602	0.4739	1.8912
chr15	102531392	26567263	0.2591	1.4045
chr16	90354753	17706041	0.196	1
chr17	81195210	19074813	0.2349	1.0466
chr18	78077248	41403060	0.5303	2.1221
chr19	59128983	9259824	0.1566	0.9962
chr20	63025520	28714180	0.4556	1.6323
chr21	48129895	20492087	0.4258	2.0902
chr22	51304566	6387609	0.1245	0.6545
chrMT	16571	5429	0.3276	0.6468
chrX	155270560	80286000	0.5171	2.5598

chrY	59373566	1196575	0.0202	0.3253

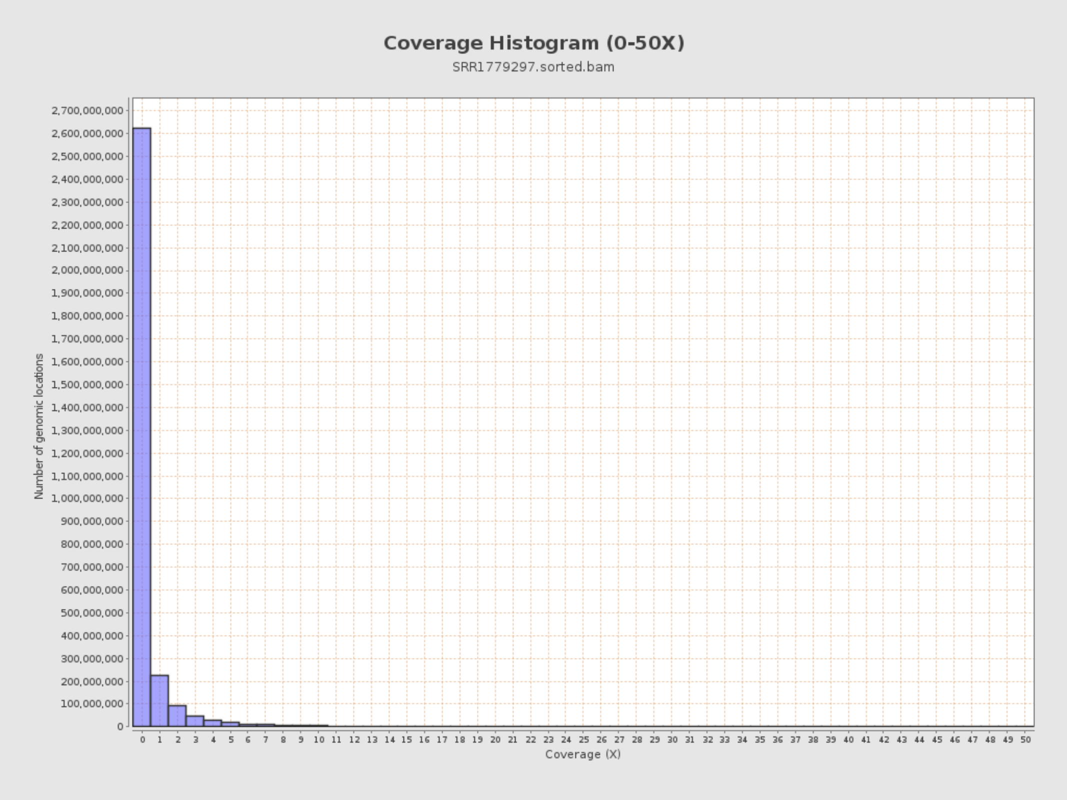
3. Results : Coverage across reference



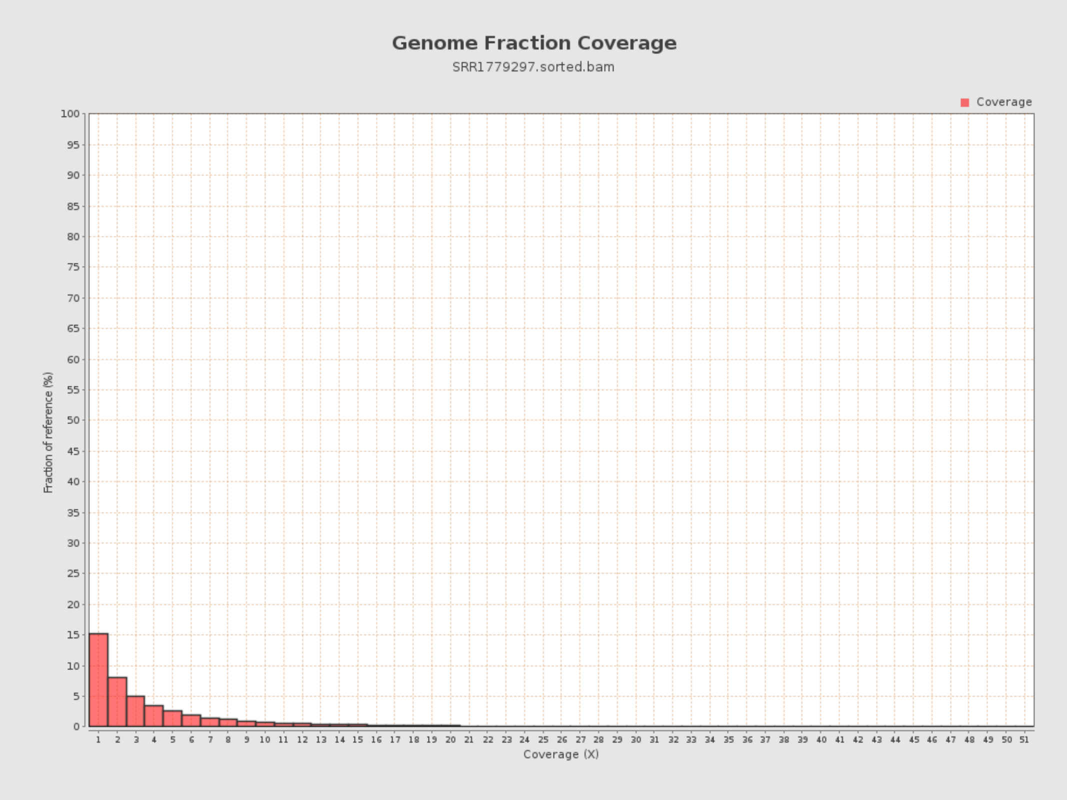
4. Results : Coverage Histogram



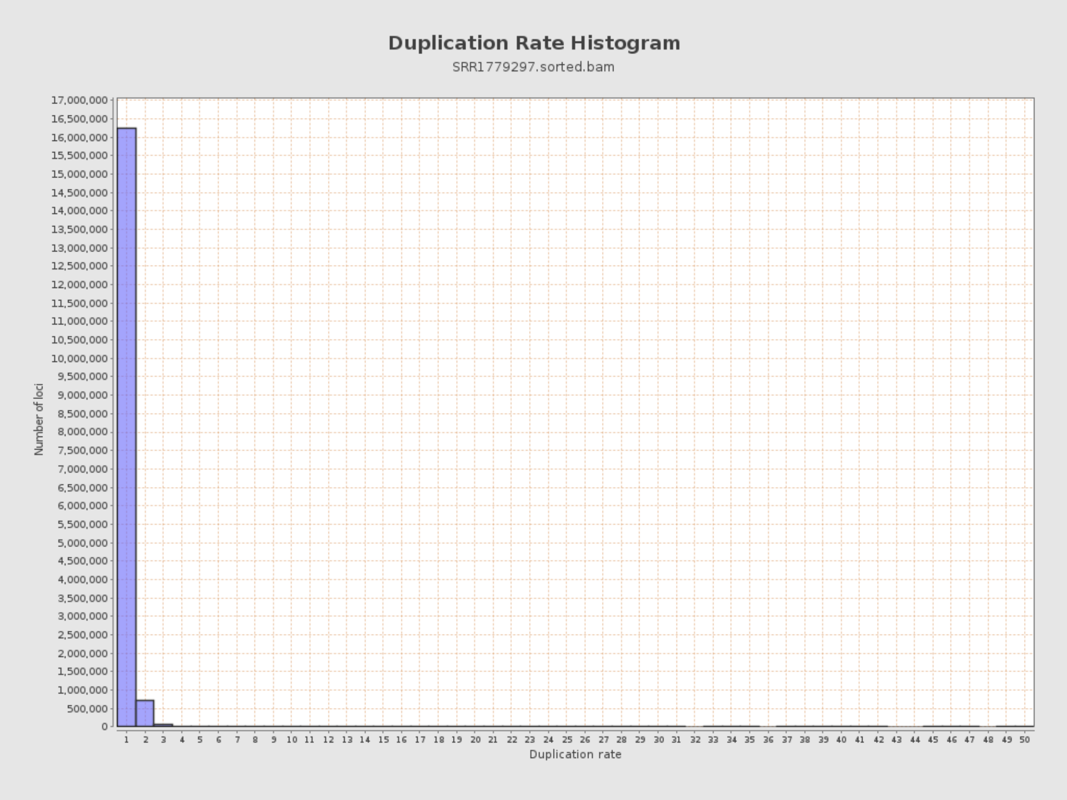
5. Results : Coverage Histogram (0-50X)



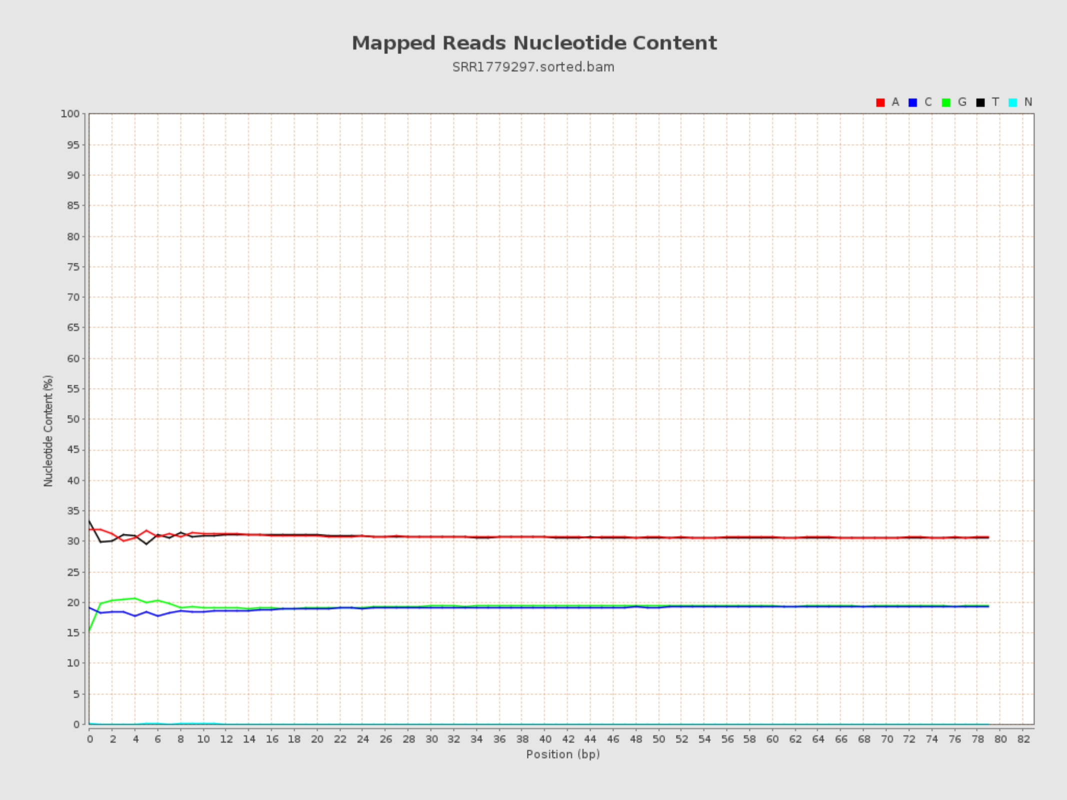
6. Results : Genome Fraction Coverage



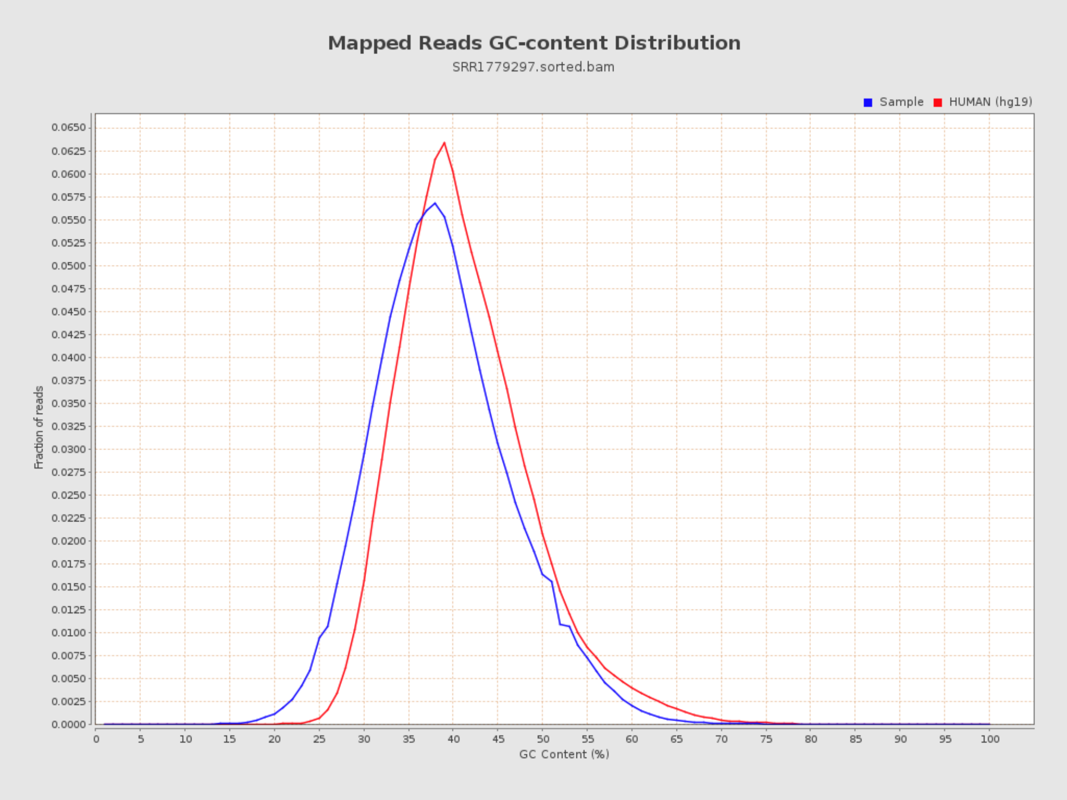
7. Results : Duplication Rate Histogram



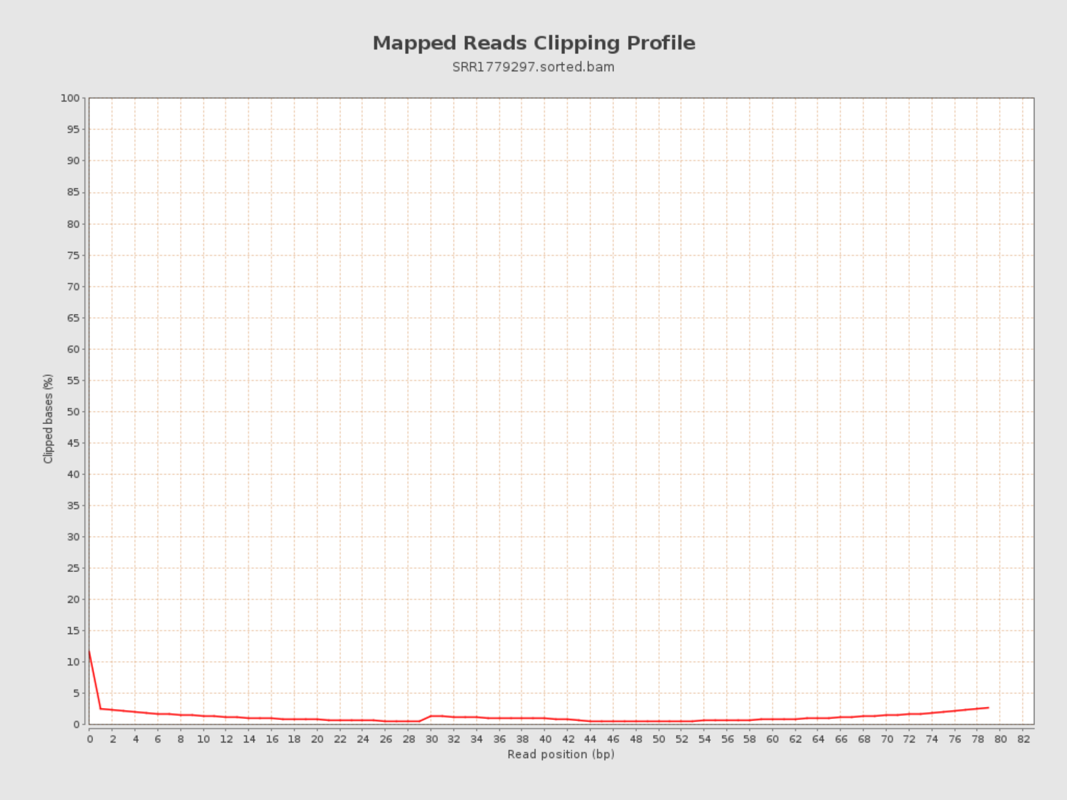
8. Results : Mapped Reads Nucleotide Content



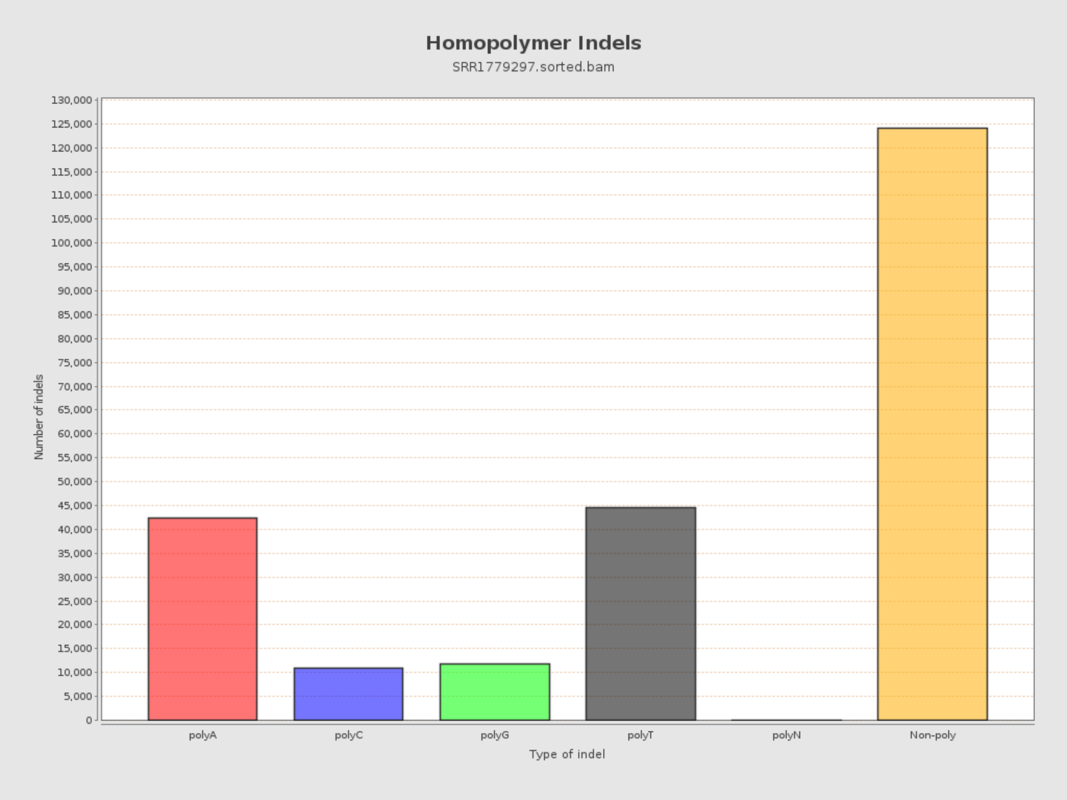
9. Results : Mapped Reads GC-content Distribution



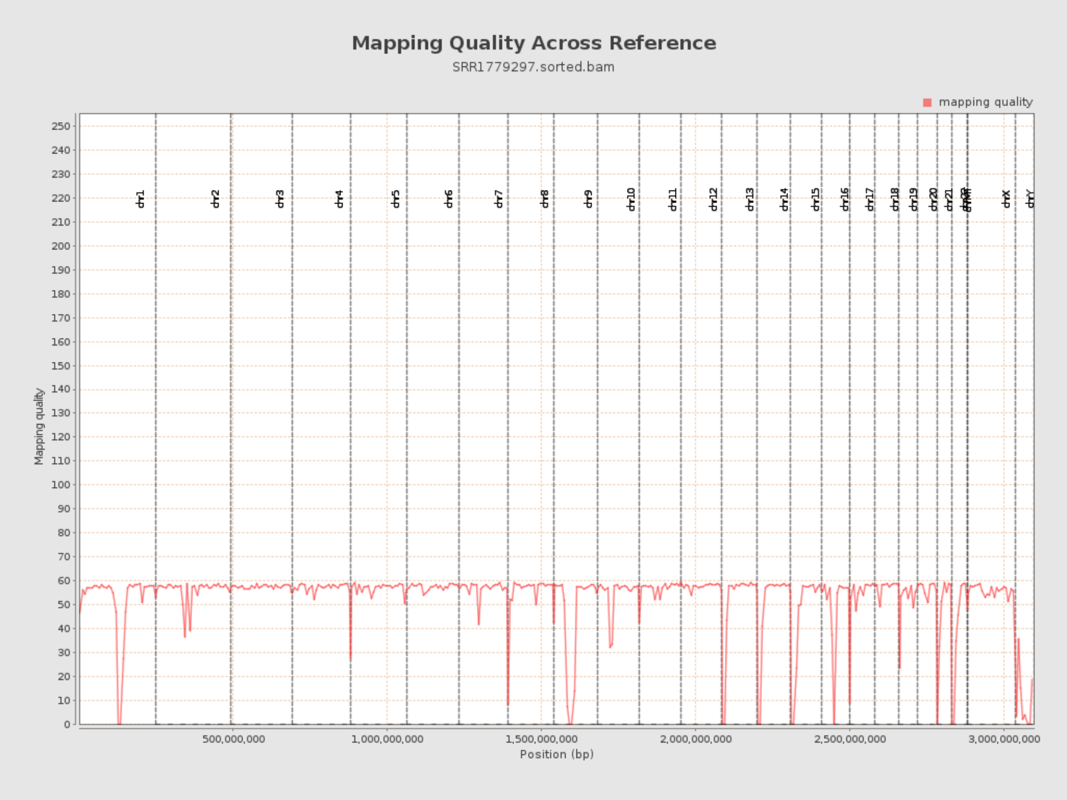
10. Results : Mapped Reads Clipping Profile



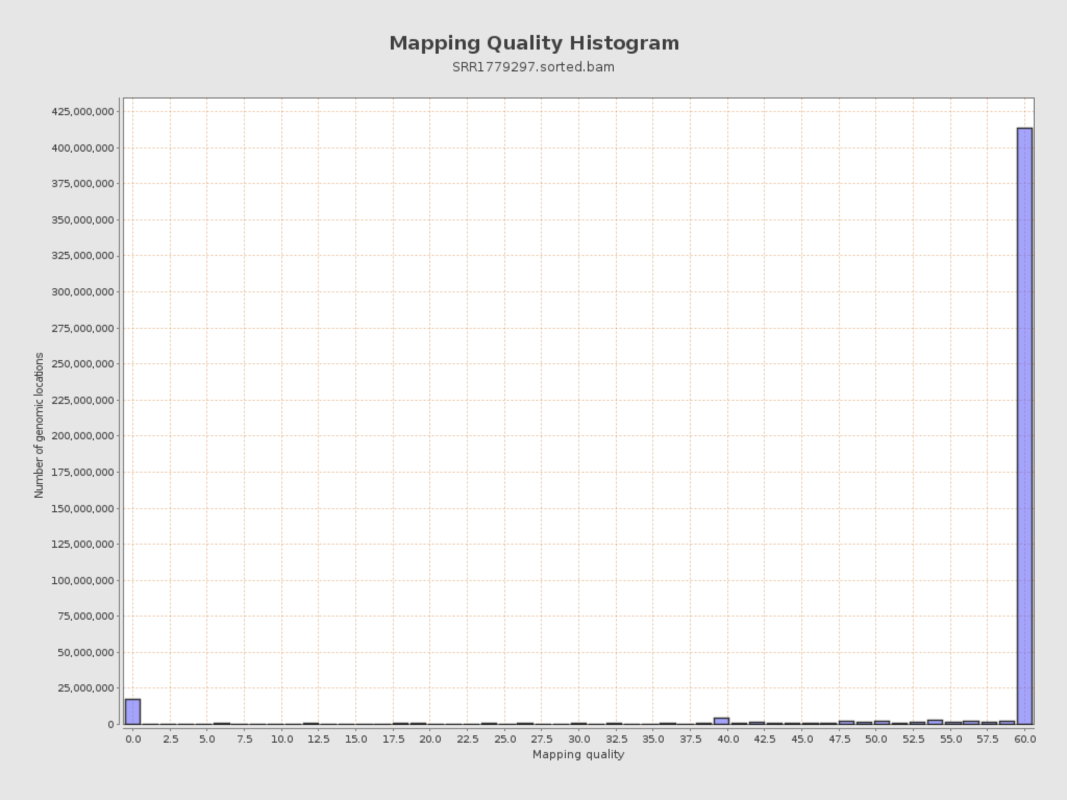
11. Results : Homopolymer Indels



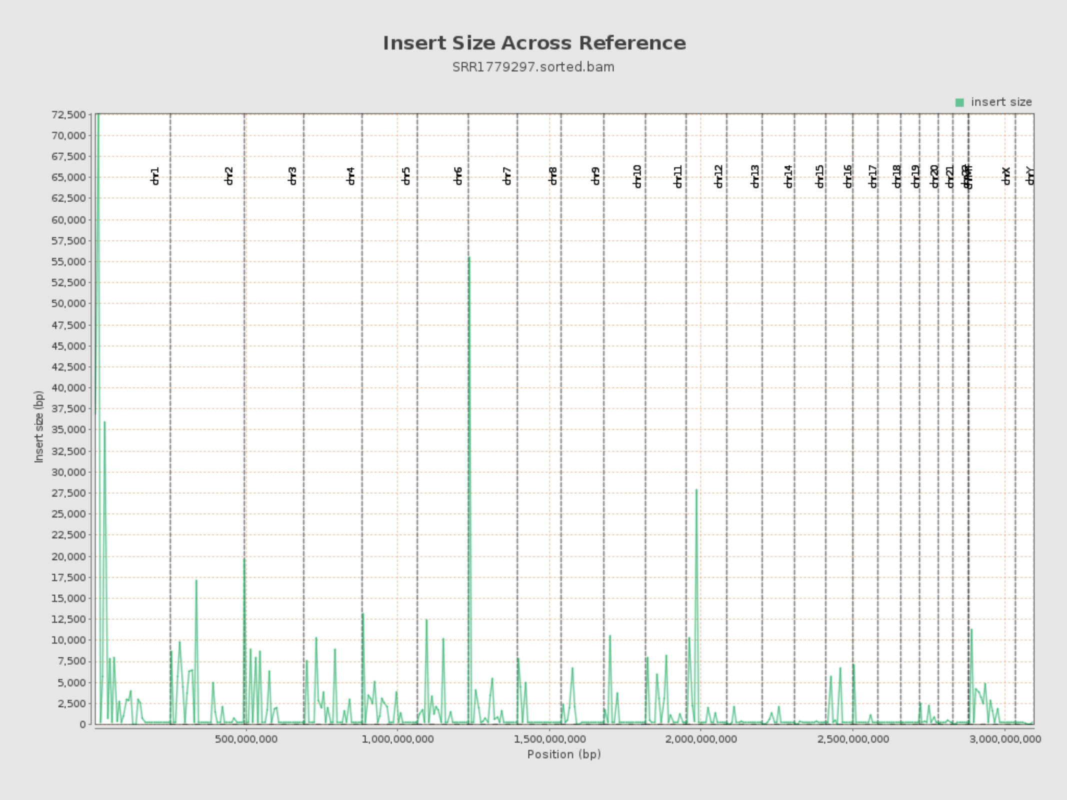
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram