Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 04:33:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779303.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_SRR1779303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779303_1.fastq.gz SRR1779303_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 04:33:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,741,818
Mapped reads	17,146,558 / 96.64%
Unmapped reads	595,260 / 3.36%
Mapped paired reads	17,146,558 / 96.64%
Mapped reads, first in pair	8,627,392 / 48.63%
Mapped reads, second in pair	8,519,166 / 48.02%
Mapped reads, both in pair	17,011,242 / 95.88%
Mapped reads, singletons	135,316 / 0.76%
Secondary alignments	0
Supplementary alignments	41,899 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	542,472 / 3.06%
Duplication rate	2.92%
Clipped reads	546,285 / 3.08%

2.2. ACGT Content

Number/percentage of A's	421,903,946 / 30.91%
Number/percentage of C's	258,719,787 / 18.96%
Number/percentage of T's	419,672,469 / 30.75%
Number/percentage of G's	264,077,147 / 19.35%
Number/percentage of N's	359,350 / 0.03%

GC Percentage	38.31%

2.3. Coverage

Mean	0.4409
Standard Deviation	1.6265

2.4. Mapping Quality

Mean Mapping Quality	52.94

2.5. Insert size

Mean	38,898.07
Standard Deviation	1,850,366.61
P25/Median/P75	165 / 223 / 306

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	5,053,116
Insertions	98,976
Mapped reads with at least one insertion	0.57%
Deletions	126,320
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.48%

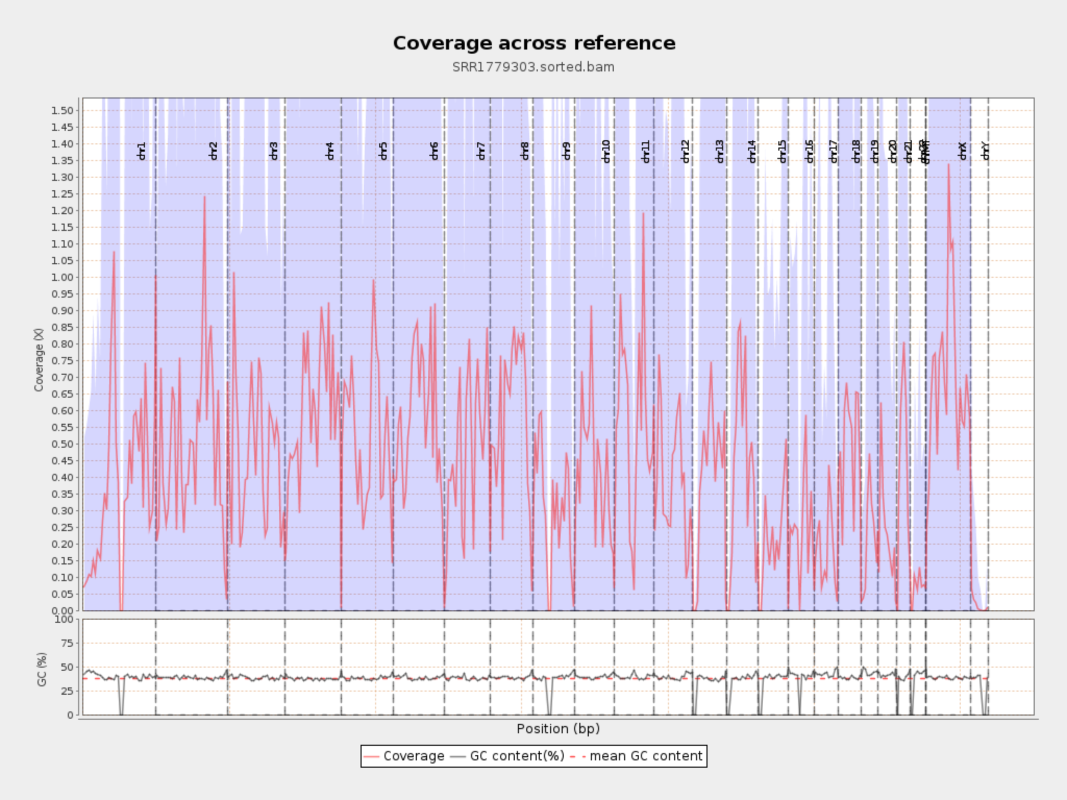
2.7. Chromosome stats

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

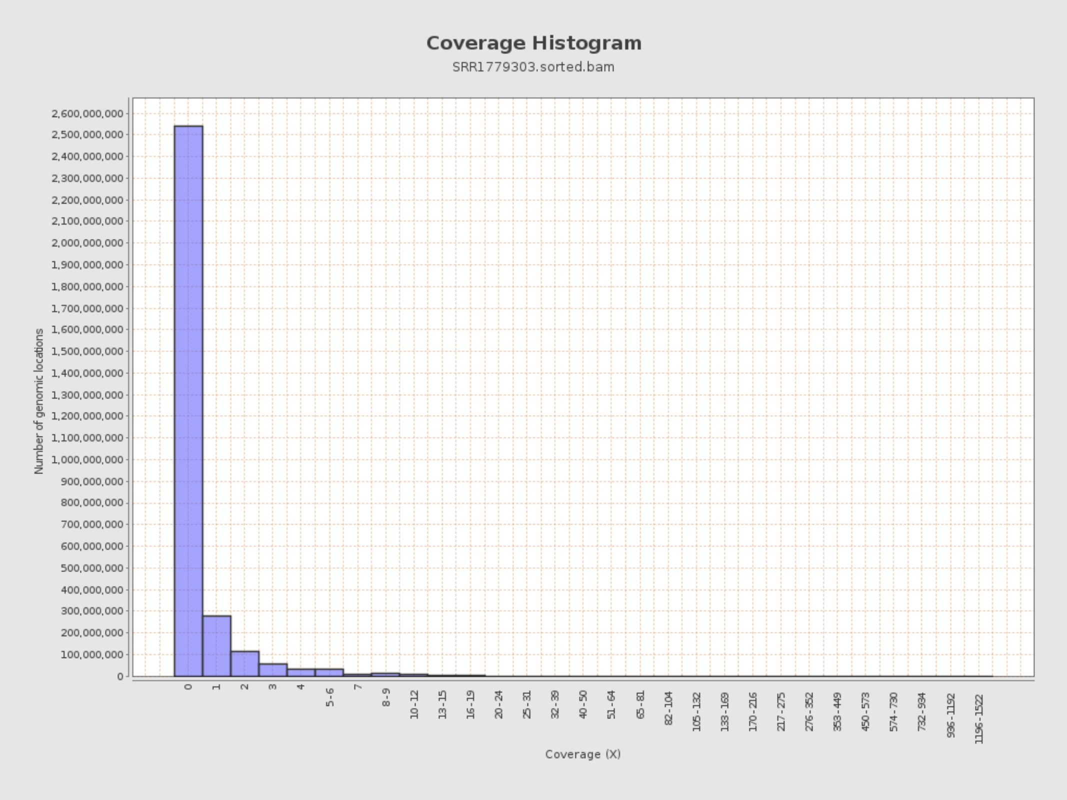
		bases	coverage	deviation
chr1	249250621	92161755	0.3698	1.9534
chr2	243199373	119040374	0.4895	1.5406
chr3	198022430	95270382	0.4811	1.5489
chr4	191154276	115608369	0.6048	1.7168
chr5	180915260	94091655	0.5201	1.652
chr6	171115067	99912821	0.5839	1.7562
chr7	159138663	76706634	0.482	1.7278
chr8	146364022	86376695	0.5901	1.6196
chr9	141213431	44006040	0.3116	1.1873
chr10	135534747	59191940	0.4367	2.8059
chr11	135006516	76196602	0.5644	1.6832
chr12	133851895	51680073	0.3861	1.3519
chr13	115169878	47812622	0.4151	1.394
chr14	107349540	46409919	0.4323	1.5592
chr15	102531392	22421555	0.2187	0.8942
chr16	90354753	21902571	0.2424	0.9025
chr17	81195210	15440399	0.1902	0.8768
chr18	78077248	39382977	0.5044	1.4469
chr19	59128983	13182321	0.2229	1.4541
chr20	63025520	15378293	0.244	1.0675
chr21	48129895	21022073	0.4368	1.457
chr22	51304566	3609711	0.0704	0.447
chrMT	16571	1066	0.0643	0.3444
chrX	155270560	107299736	0.6911	1.9732

chrY	59373566	885434	0.0149	0.1867

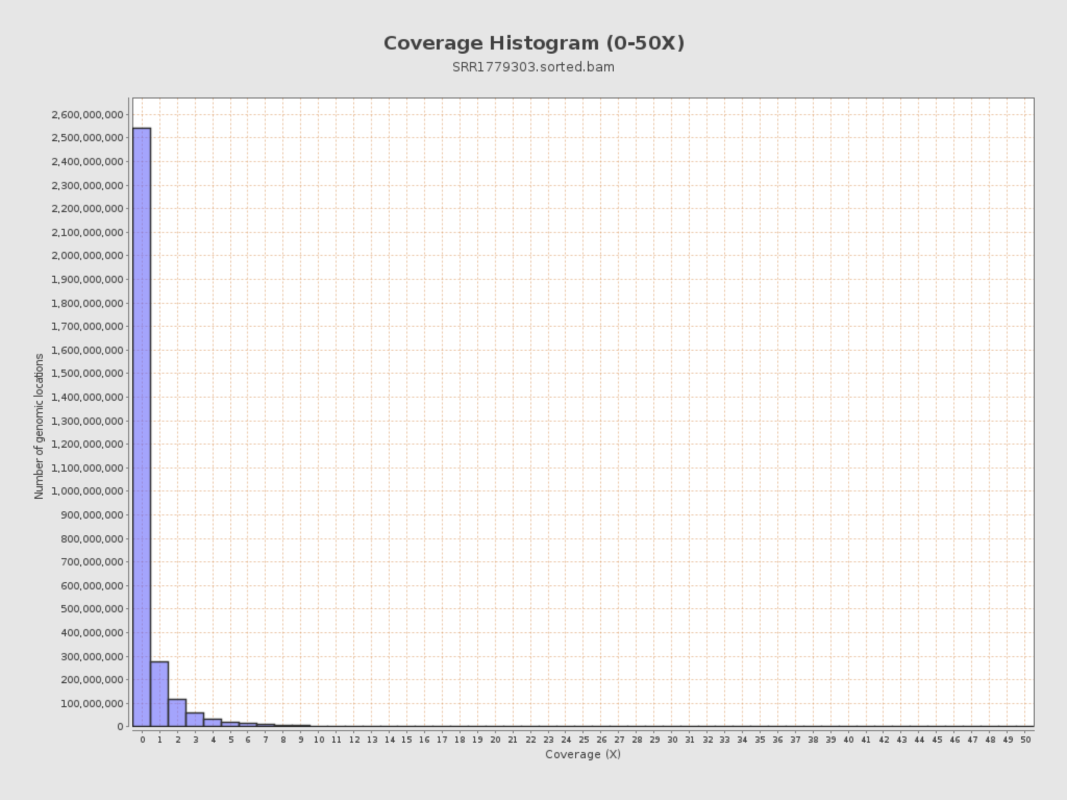
3. Results : Coverage across reference



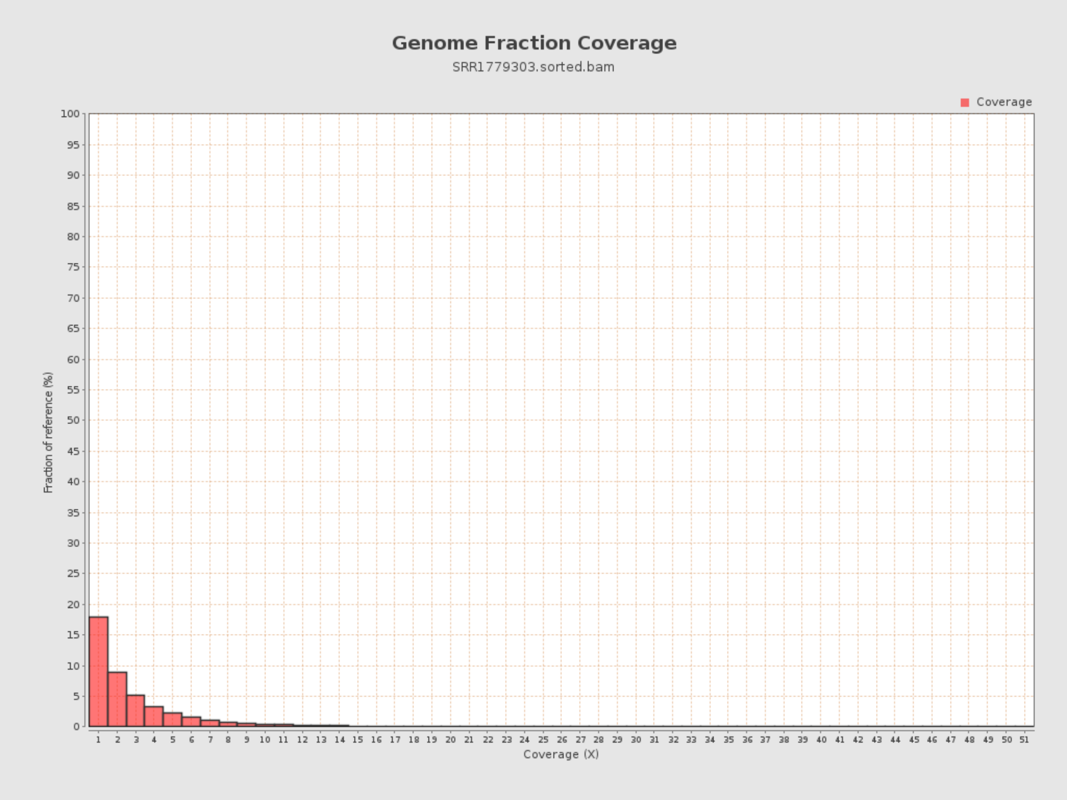
4. Results : Coverage Histogram



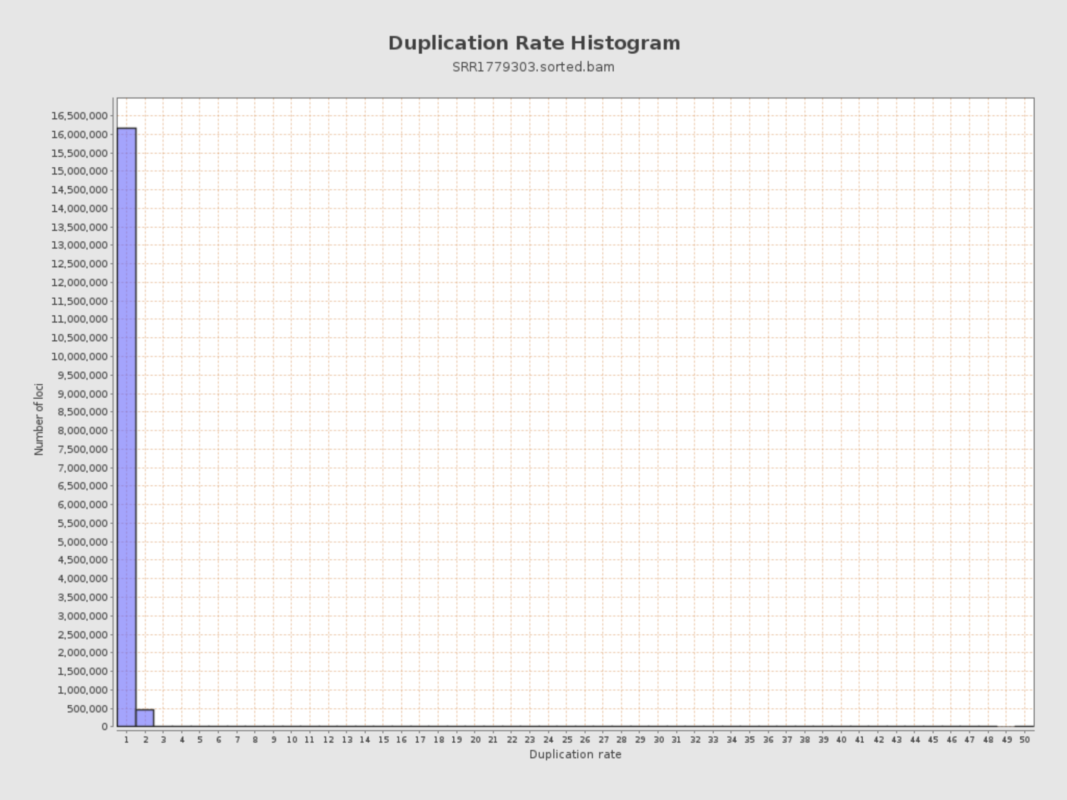
5. Results : Coverage Histogram (0-50X)



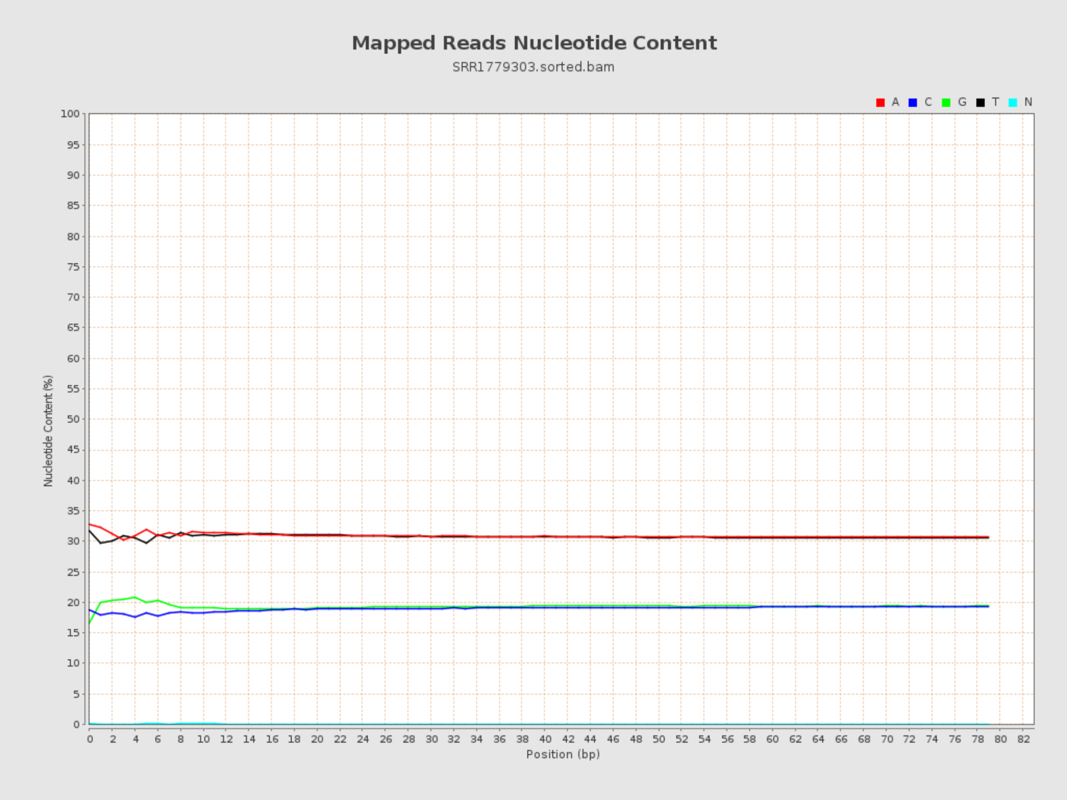
6. Results : Genome Fraction Coverage



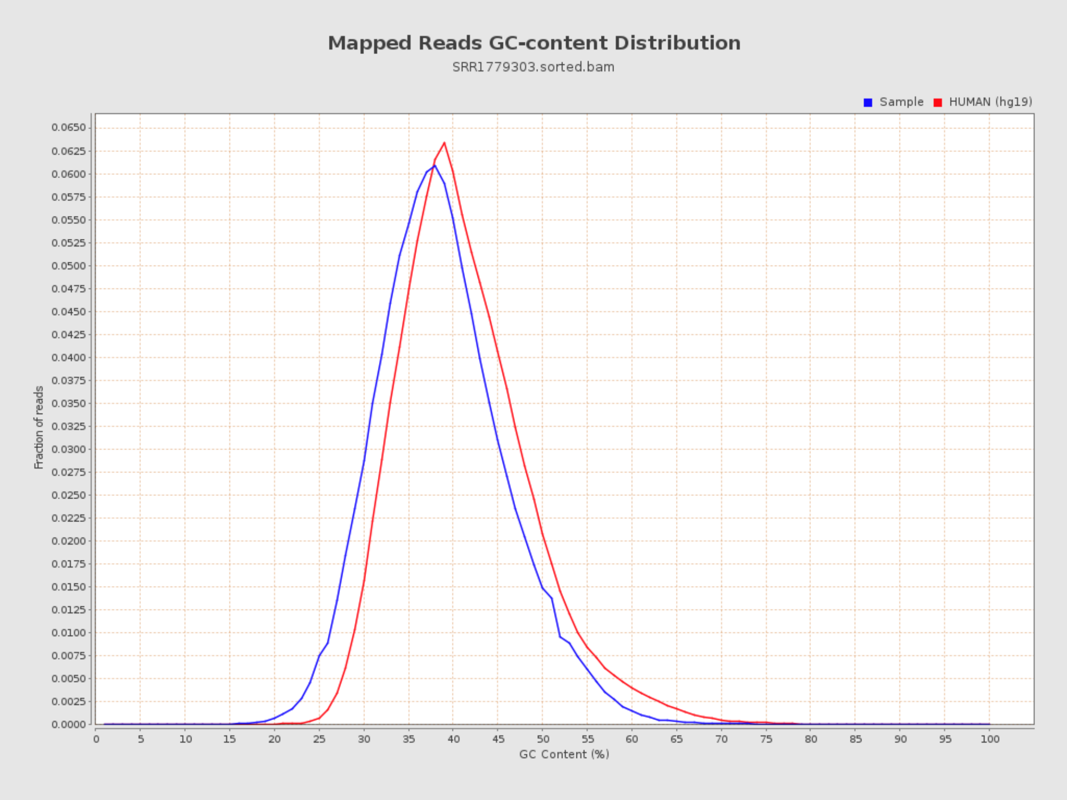
7. Results : Duplication Rate Histogram



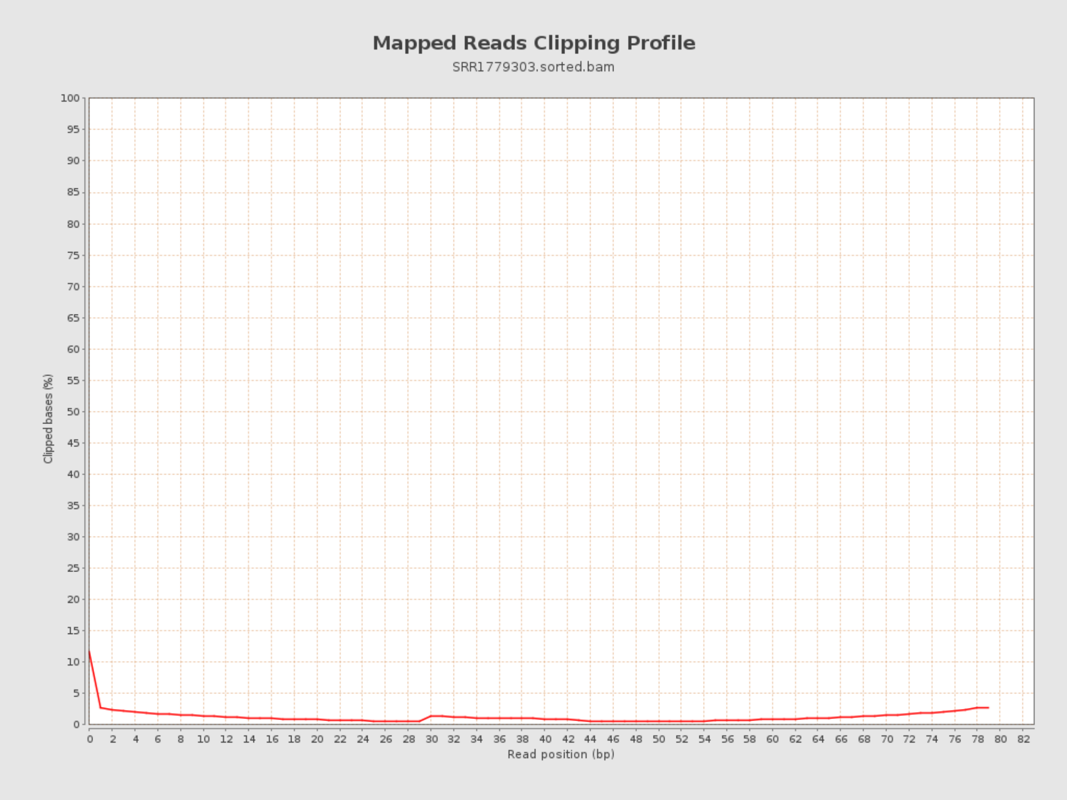
8. Results : Mapped Reads Nucleotide Content



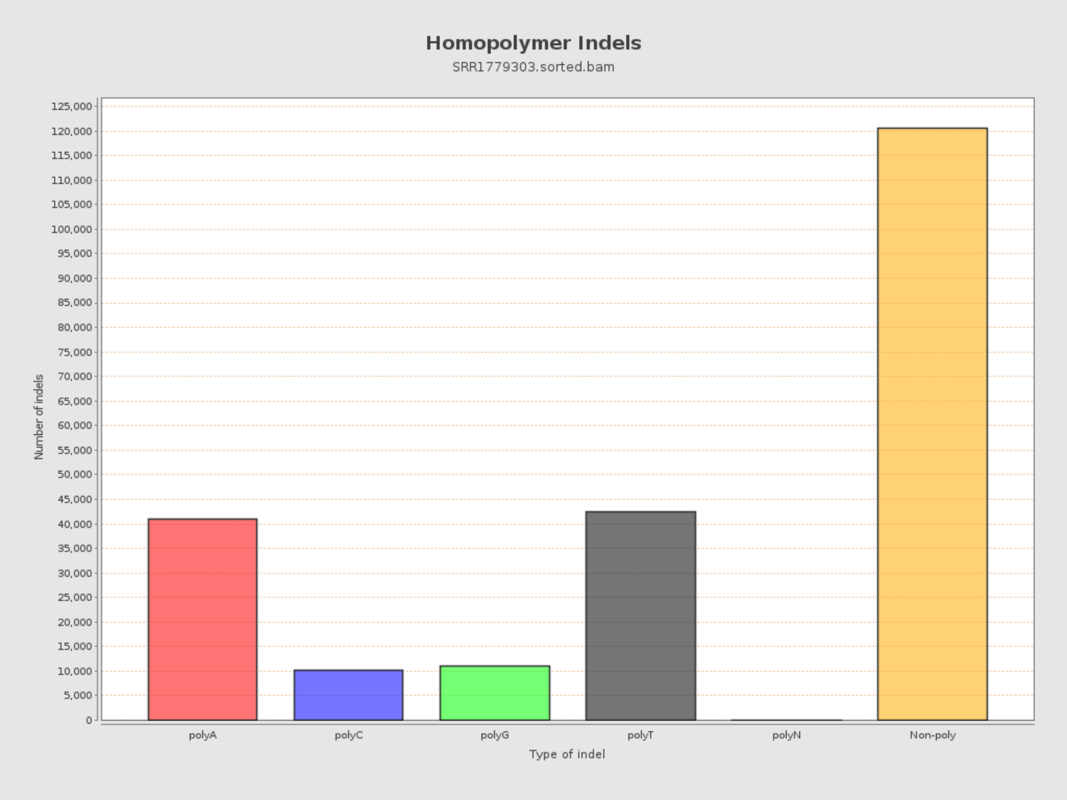
9. Results : Mapped Reads GC-content Distribution



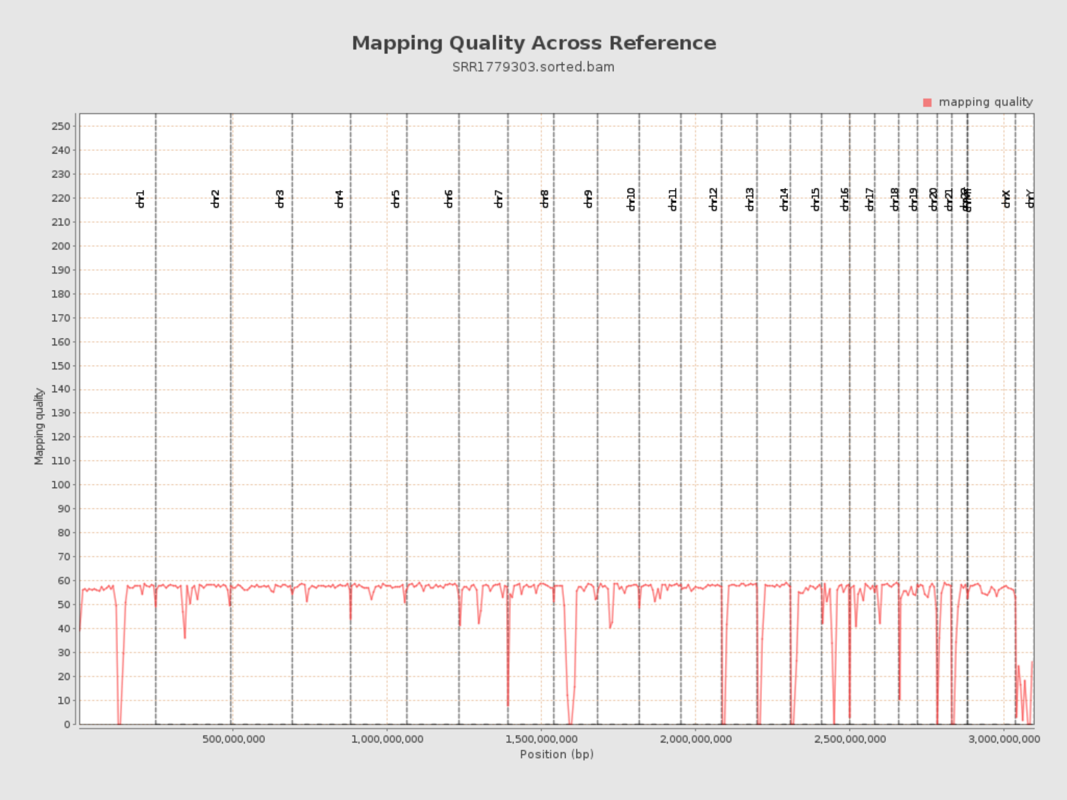
10. Results : Mapped Reads Clipping Profile



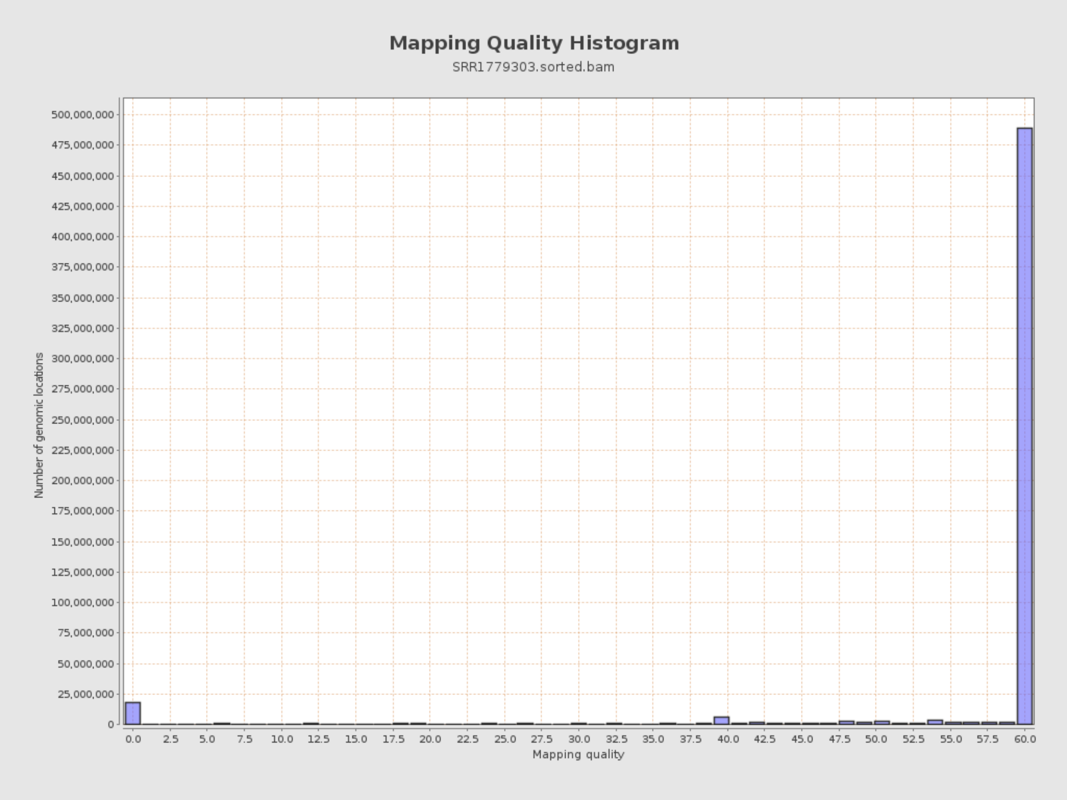
11. Results : Homopolymer Indels



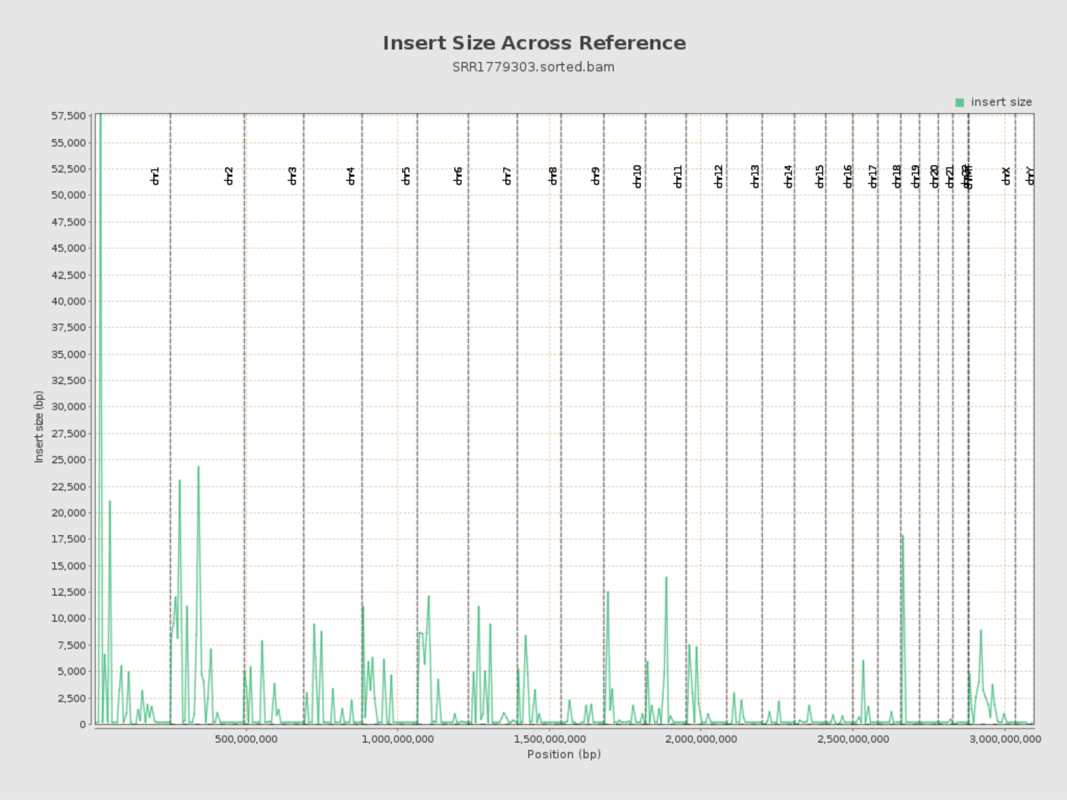
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram