Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 17:35:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779395.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_SRR1779395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779395_1.fastq.gz SRR1779395_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 17:35:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,785,756
Mapped reads	17,608,041 / 93.73%
Unmapped reads	1,177,715 / 6.27%
Mapped paired reads	17,608,041 / 93.73%
Mapped reads, first in pair	8,875,190 / 47.24%
Mapped reads, second in pair	8,732,851 / 46.49%
Mapped reads, both in pair	17,416,998 / 92.71%
Mapped reads, singletons	191,043 / 1.02%
Secondary alignments	0
Supplementary alignments	63,948 / 0.34%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	794,239 / 4.23%
Duplication rate	4.15%
Clipped reads	934,316 / 4.97%

2.2. ACGT Content

Number/percentage of A's	420,945,872 / 30.14%
Number/percentage of C's	277,936,937 / 19.9%
Number/percentage of T's	413,423,629 / 29.6%
Number/percentage of G's	284,095,340 / 20.34%
Number/percentage of N's	305,022 / 0.02%

GC Percentage	40.24%

2.3. Coverage

Mean	0.4513
Standard Deviation	1.6791

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	244,144.66
Standard Deviation	4,731,780.1
P25/Median/P75	132 / 173 / 217

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,649,973
Insertions	137,191
Mapped reads with at least one insertion	0.77%
Deletions	161,648
Mapped reads with at least one deletion	0.91%
Homopolymer indels	46.65%

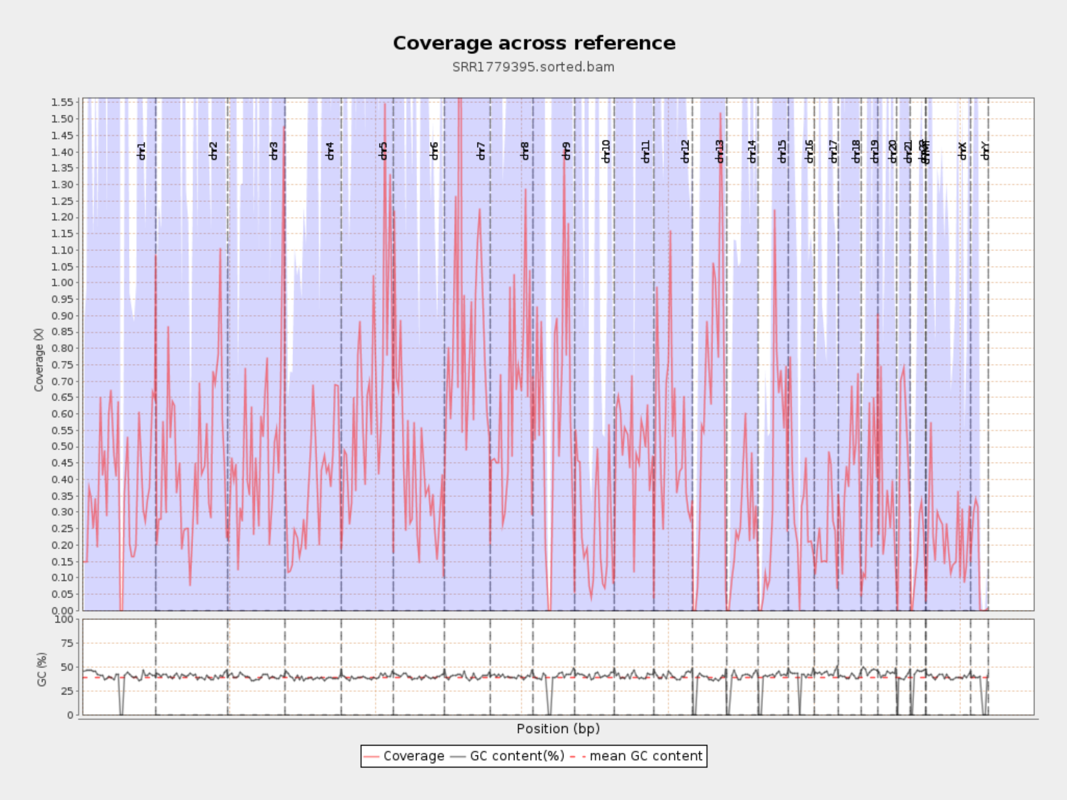
2.7. Chromosome stats

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

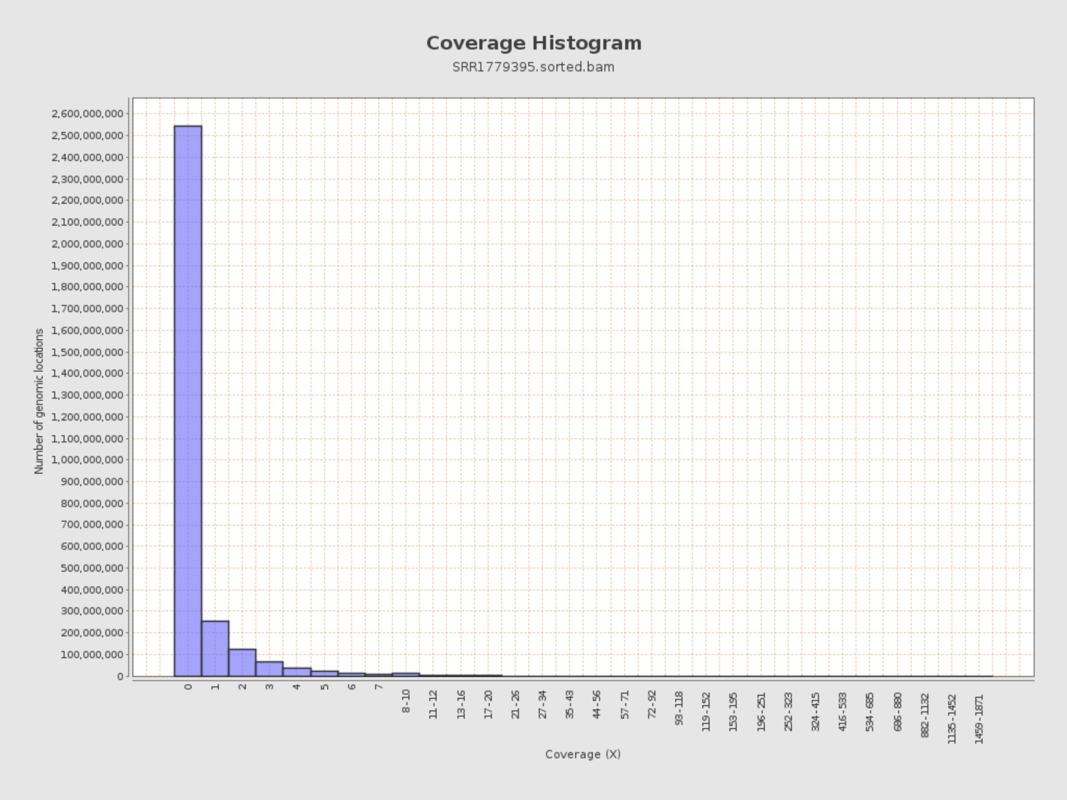
		bases	coverage	deviation
chr1	249250621	92576477	0.3714	2.2612
chr2	243199373	110488198	0.4543	1.4536
chr3	198022430	94936181	0.4794	1.4901
chr4	191154276	69230978	0.3622	1.1868
chr5	180915260	117595067	0.65	1.6434
chr6	171115067	72689286	0.4248	1.3395
chr7	159138663	140615828	0.8836	3.1523
chr8	146364022	94451781	0.6453	1.7216
chr9	141213431	87190346	0.6174	1.8183
chr10	135534747	33926953	0.2503	2.0148
chr11	135006516	68021228	0.5038	1.4621
chr12	133851895	72731347	0.5434	1.4969
chr13	115169878	76208458	0.6617	1.8028
chr14	107349540	27600084	0.2571	1.0525
chr15	102531392	41920417	0.4089	1.4991
chr16	90354753	29262492	0.3239	1.2155
chr17	81195210	19260608	0.2372	0.9835
chr18	78077248	32386114	0.4148	1.4135
chr19	59128983	21093434	0.3567	1.9317
chr20	63025520	20137935	0.3195	1.1897
chr21	48129895	22262114	0.4625	1.3829
chr22	51304566	8674631	0.1691	0.7912
chrMT	16571	480	0.029	0.1934
chrX	155270560	35206673	0.2267	1.0062

chrY	59373566	8586481	0.1446	0.8302

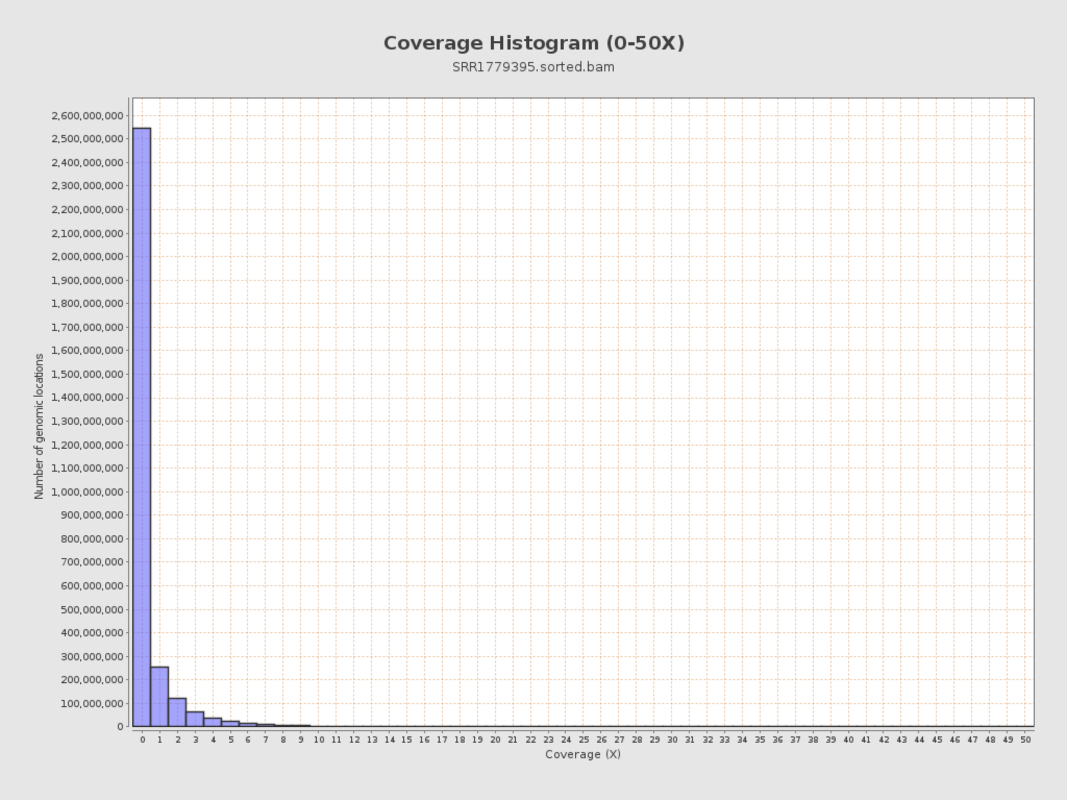
3. Results : Coverage across reference



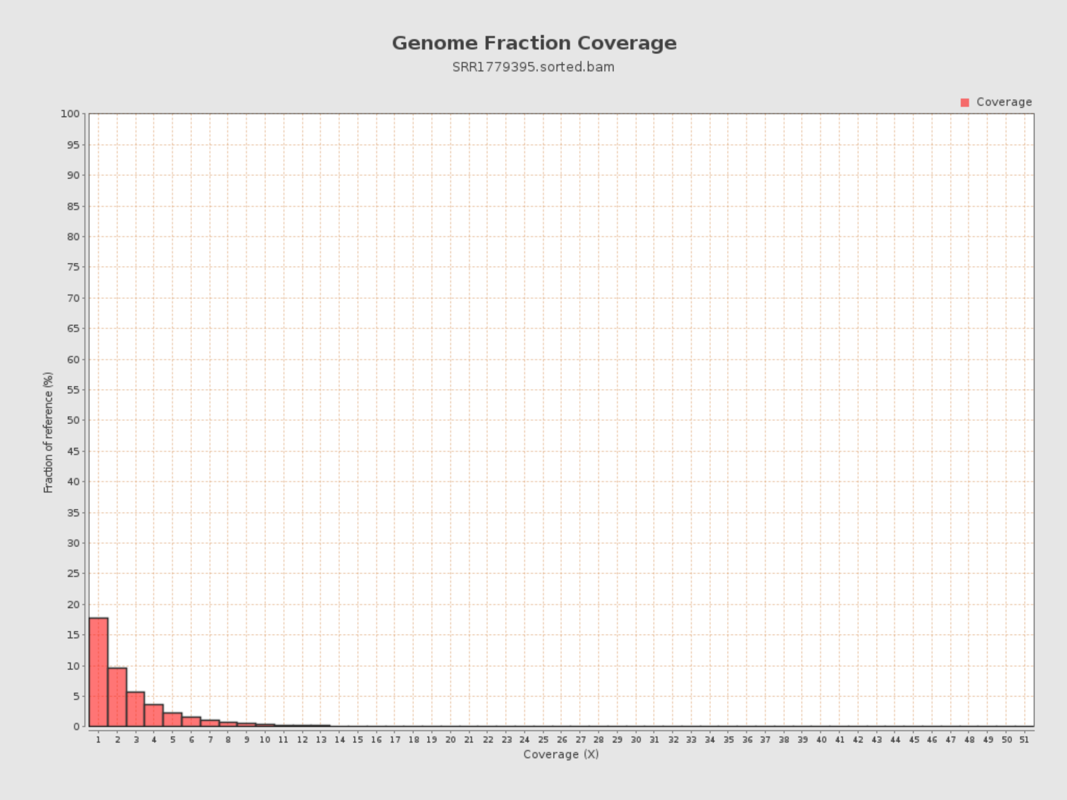
4. Results : Coverage Histogram



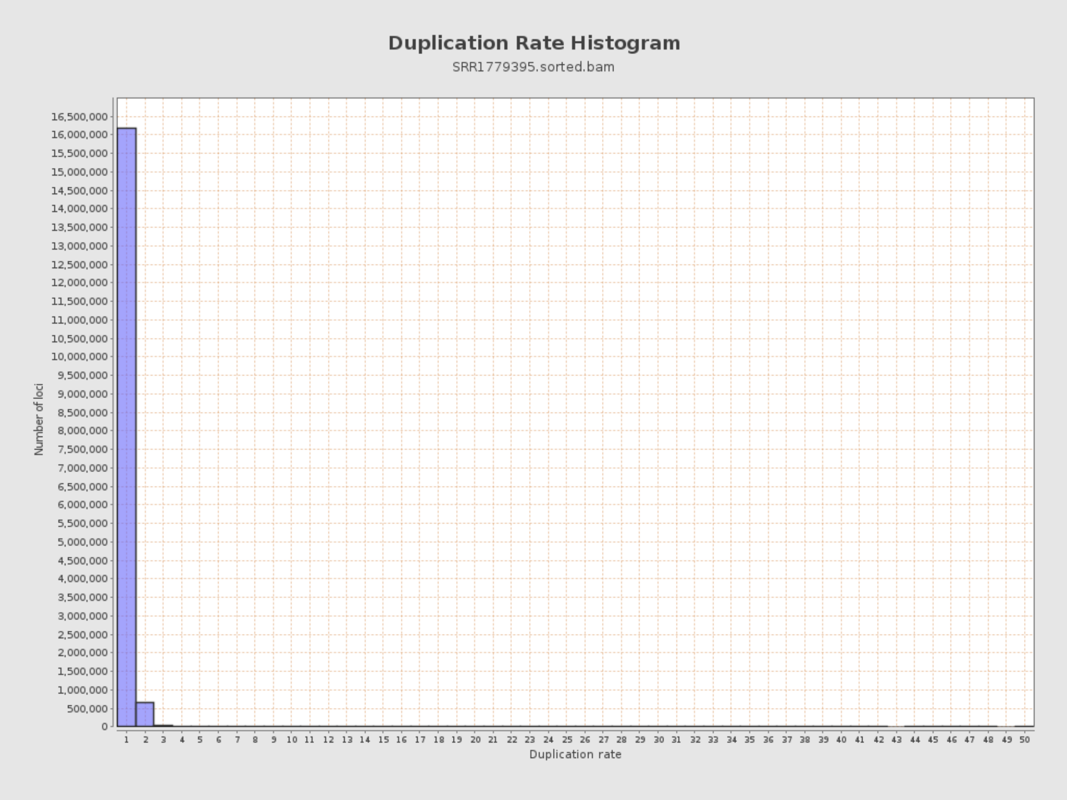
5. Results : Coverage Histogram (0-50X)



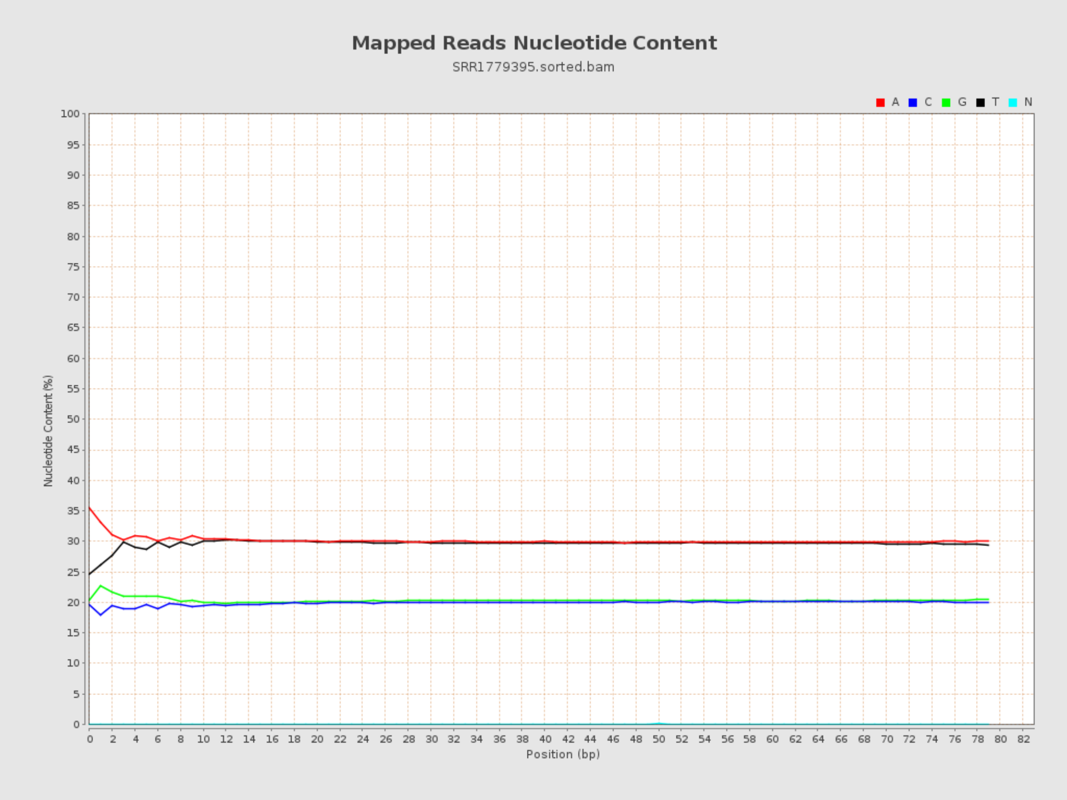
6. Results : Genome Fraction Coverage



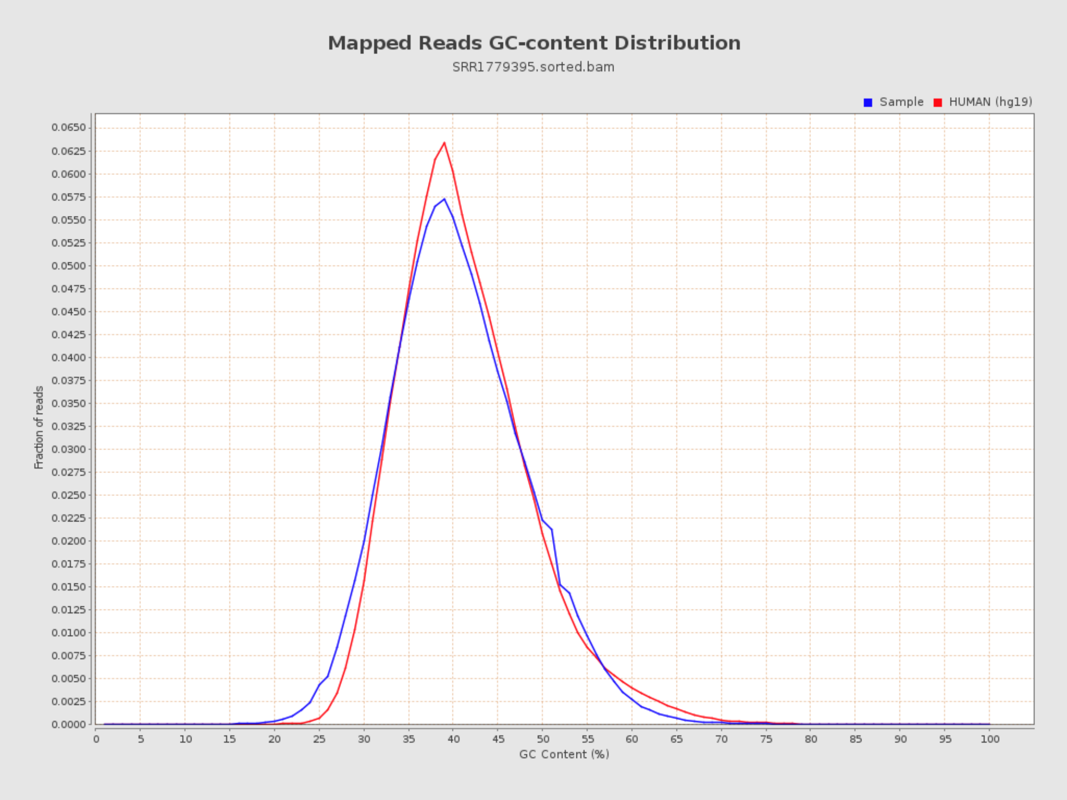
7. Results : Duplication Rate Histogram



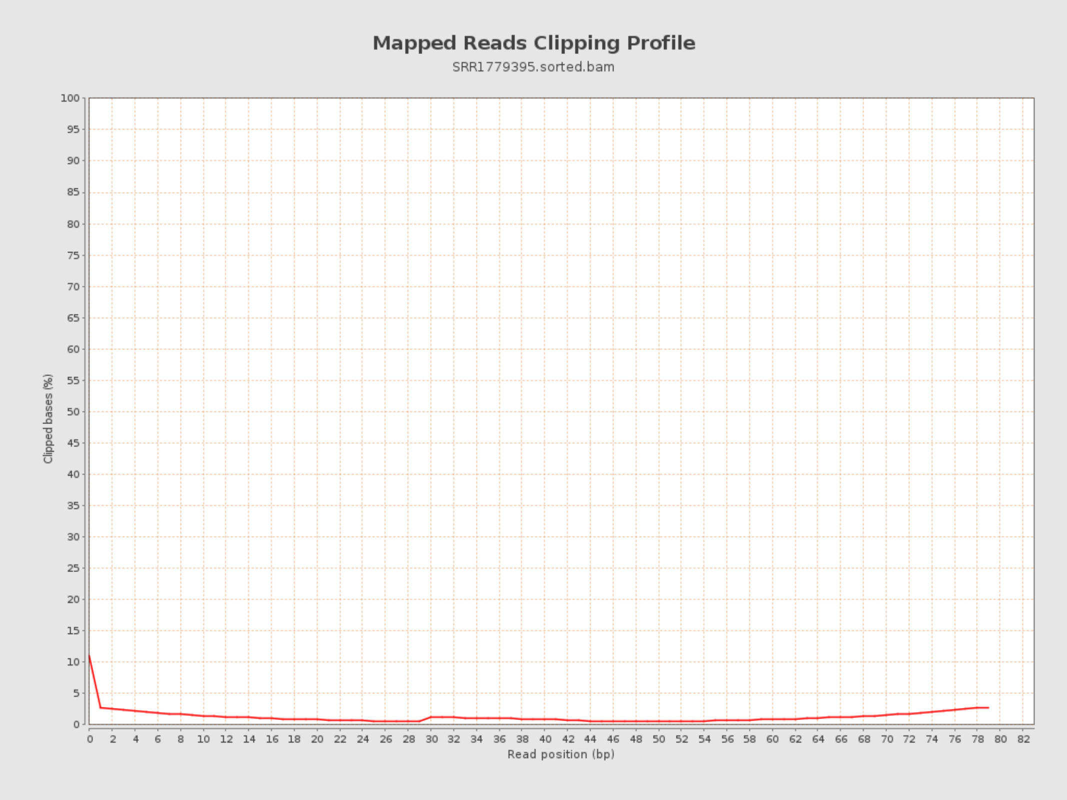
8. Results : Mapped Reads Nucleotide Content



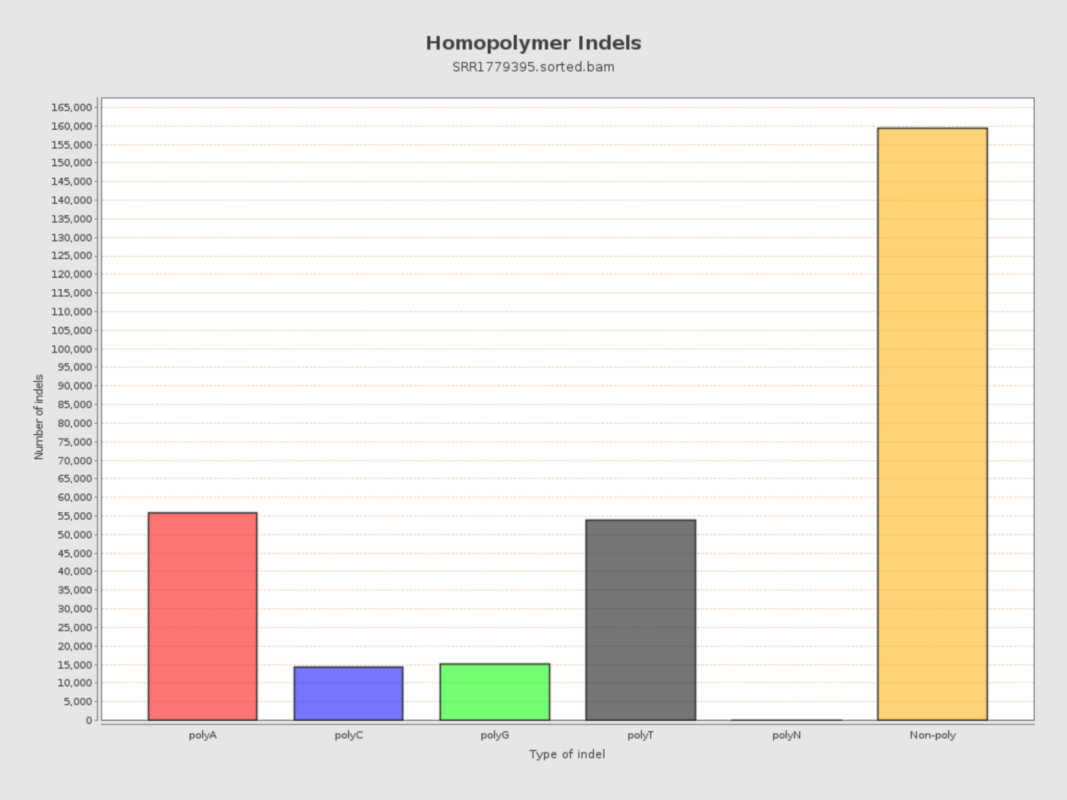
9. Results : Mapped Reads GC-content Distribution



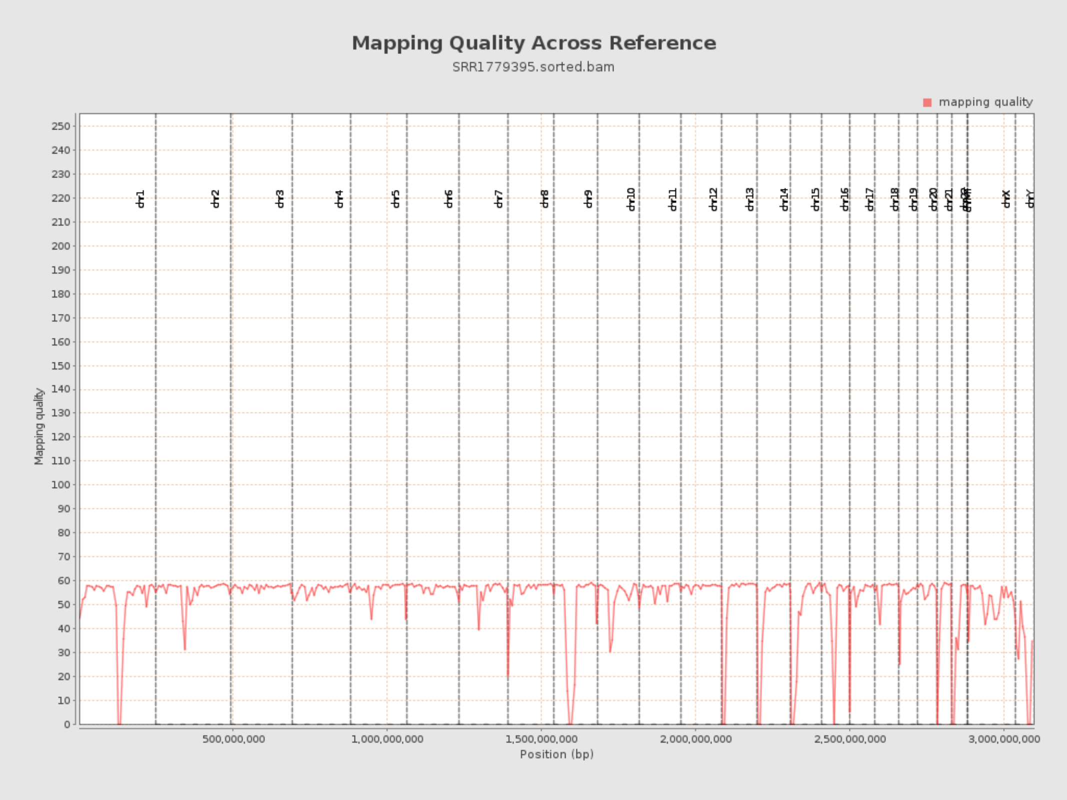
10. Results : Mapped Reads Clipping Profile



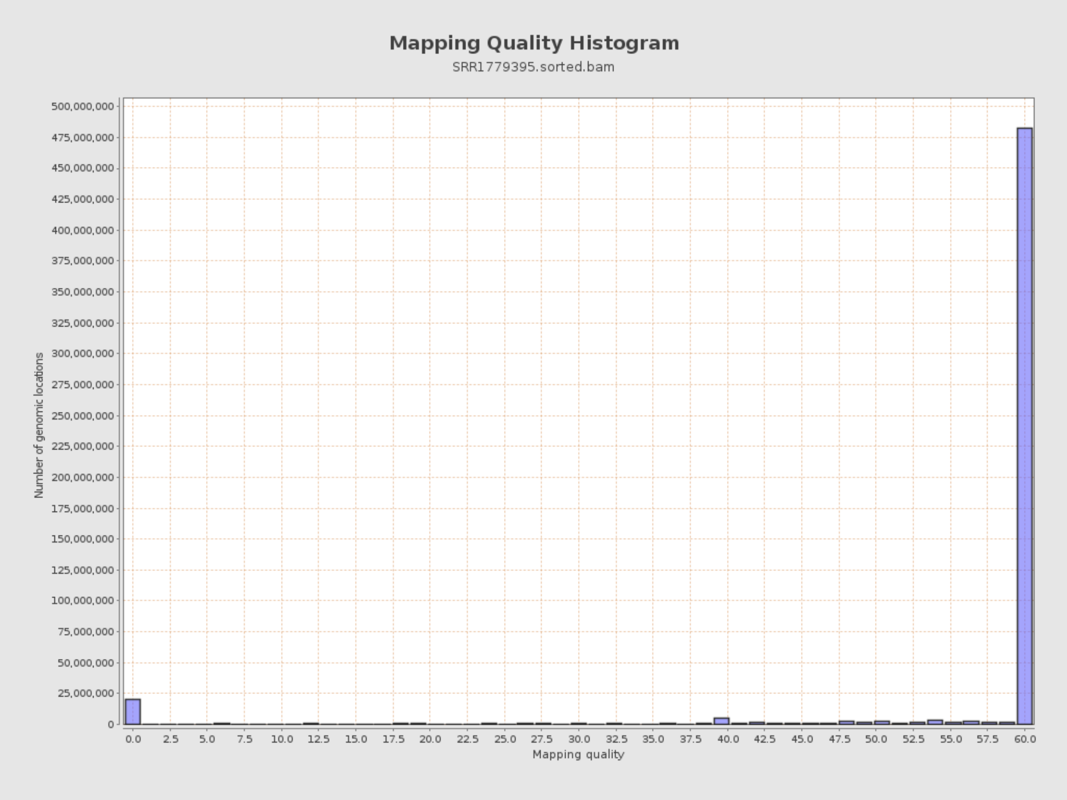
11. Results : Homopolymer Indels



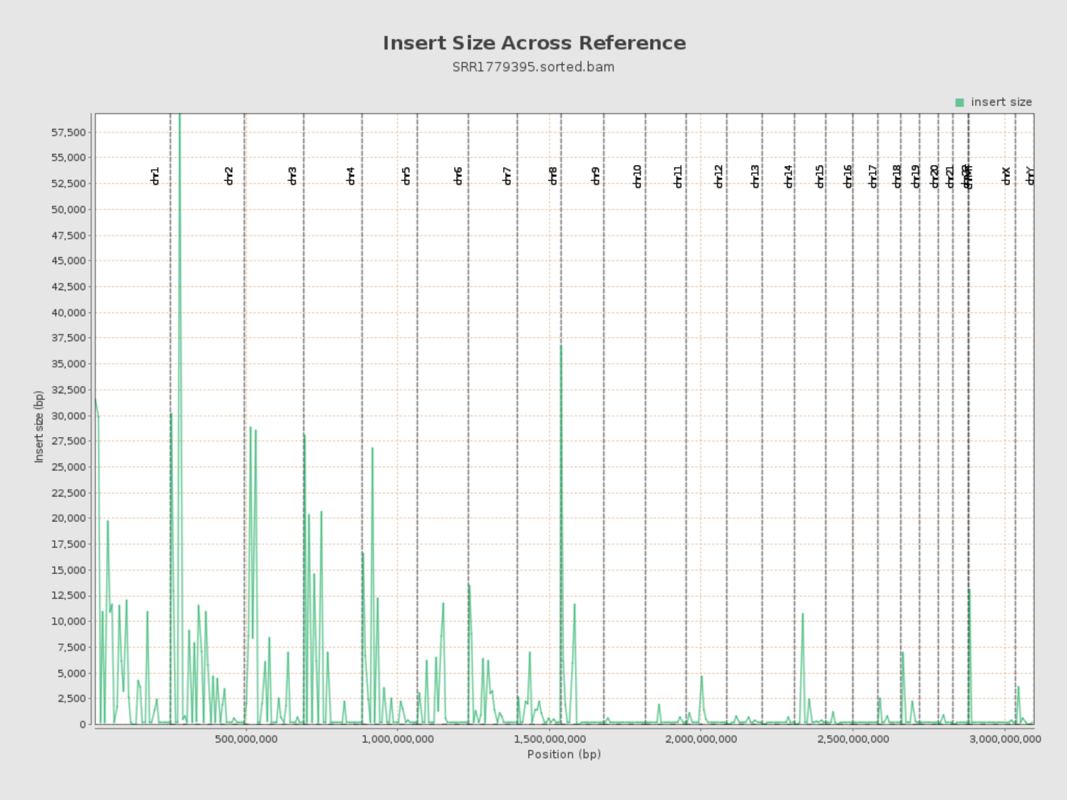
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram