Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 21:59:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779410.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_SRR1779410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779410_1.fastq.gz SRR1779410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 21:59:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,407,908
Mapped reads	15,098,377 / 97.99%
Unmapped reads	309,531 / 2.01%
Mapped paired reads	15,098,377 / 97.99%
Mapped reads, first in pair	7,604,938 / 49.36%
Mapped reads, second in pair	7,493,439 / 48.63%
Mapped reads, both in pair	14,960,882 / 97.1%
Mapped reads, singletons	137,495 / 0.89%
Secondary alignments	0
Supplementary alignments	54,303 / 0.35%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	475,752 / 3.09%
Duplication rate	2.84%
Clipped reads	582,229 / 3.78%

2.2. ACGT Content

Number/percentage of A's	365,270,550 / 30.42%
Number/percentage of C's	235,349,366 / 19.6%
Number/percentage of T's	358,469,801 / 29.85%
Number/percentage of G's	241,368,719 / 20.1%
Number/percentage of N's	268,648 / 0.02%

GC Percentage	39.7%

2.3. Coverage

Mean	0.388
Standard Deviation	1.5047

2.4. Mapping Quality

Mean Mapping Quality	52.98

2.5. Insert size

Mean	132,419.89
Standard Deviation	3,583,439.52
P25/Median/P75	146 / 186 / 239

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,969,762
Insertions	106,150
Mapped reads with at least one insertion	0.7%
Deletions	122,307
Mapped reads with at least one deletion	0.8%
Homopolymer indels	47.17%

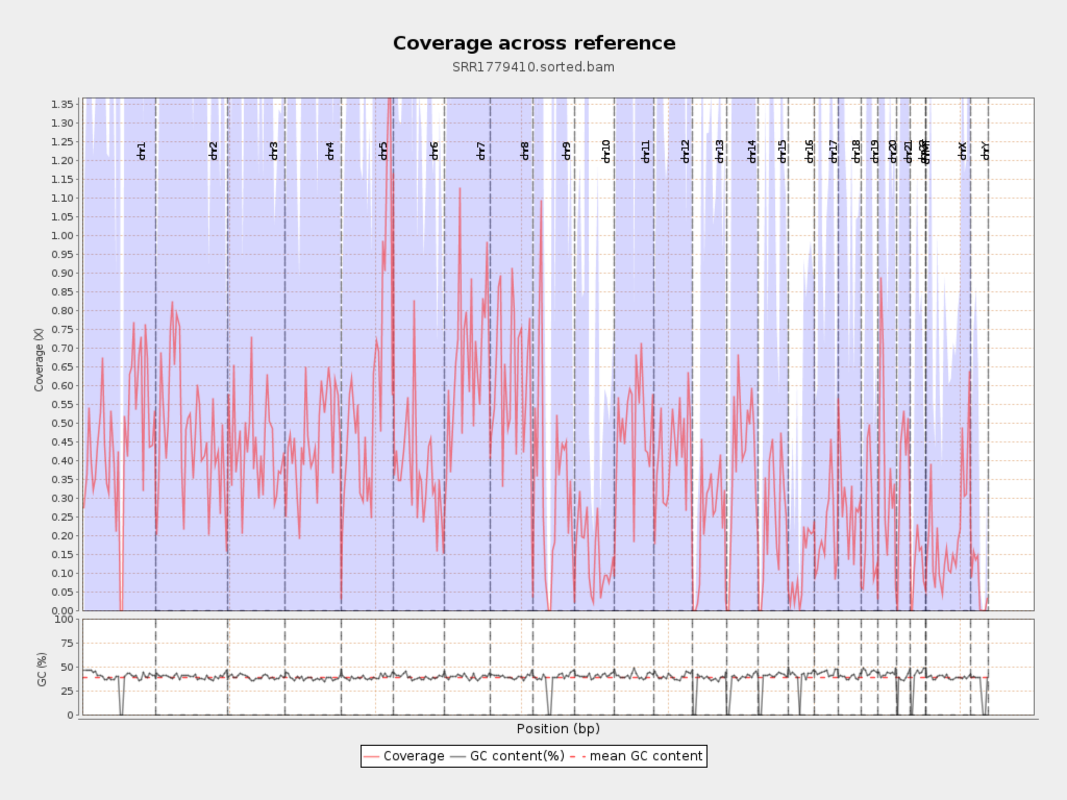
2.7. Chromosome stats

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

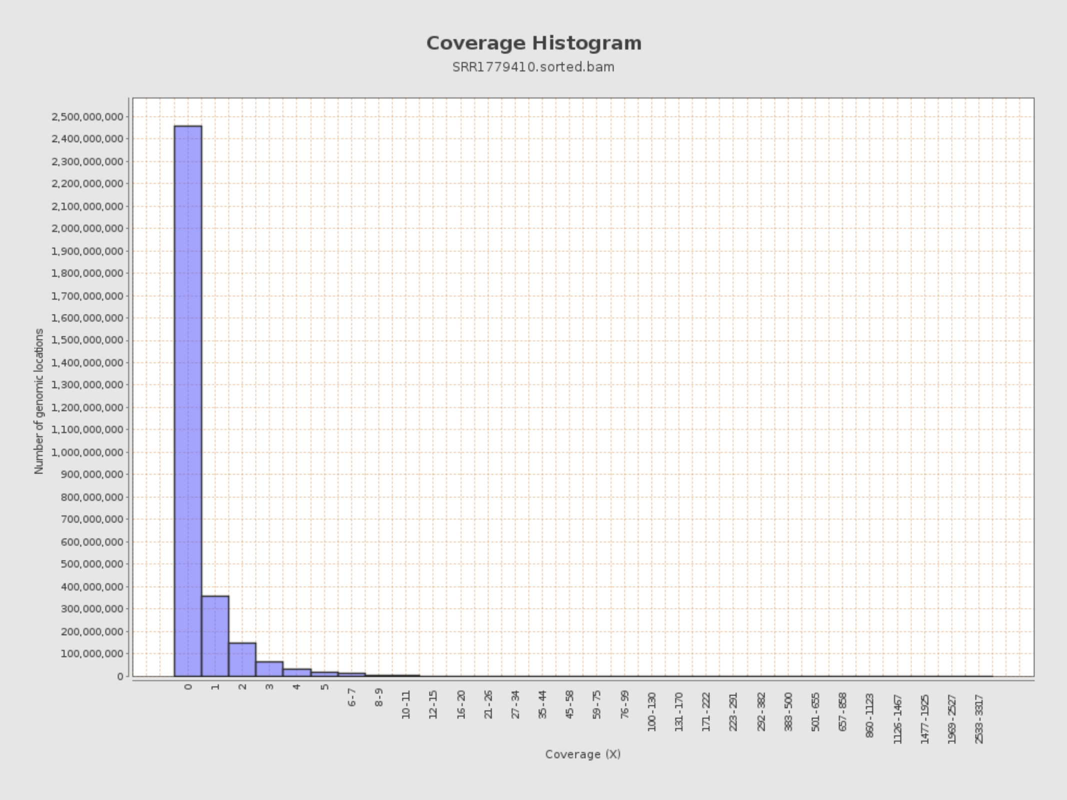
		bases	coverage	deviation
chr1	249250621	113674137	0.4561	3.5776
chr2	243199373	115424556	0.4746	1.1336
chr3	198022430	85977886	0.4342	1.0086
chr4	191154276	87664785	0.4586	1.0342
chr5	180915260	105922776	0.5855	1.2401
chr6	171115067	63408969	0.3706	1.03
chr7	159138663	104892559	0.6591	1.7122
chr8	146364022	90035538	0.6151	1.296
chr9	141213431	48808647	0.3456	1.1098
chr10	135534747	19500423	0.1439	1.9566
chr11	135006516	66744636	0.4944	1.1776
chr12	133851895	55212758	0.4125	1.0086
chr13	115169878	27769220	0.2411	0.7766
chr14	107349540	44330775	0.413	1.0211
chr15	102531392	24289048	0.2369	0.7679
chr16	90354753	10060879	0.1113	0.5146
chr17	81195210	16892656	0.208	0.8893
chr18	78077248	22100120	0.2831	1.0185
chr19	59128983	13438619	0.2273	1.9139
chr20	63025520	24920089	0.3954	1.0032
chr21	48129895	17289186	0.3592	0.925
chr22	51304566	5917306	0.1153	0.5724
chrMT	16571	937	0.0565	0.3045
chrX	155270560	32576644	0.2098	0.7225

chrY	59373566	4126580	0.0695	0.4141

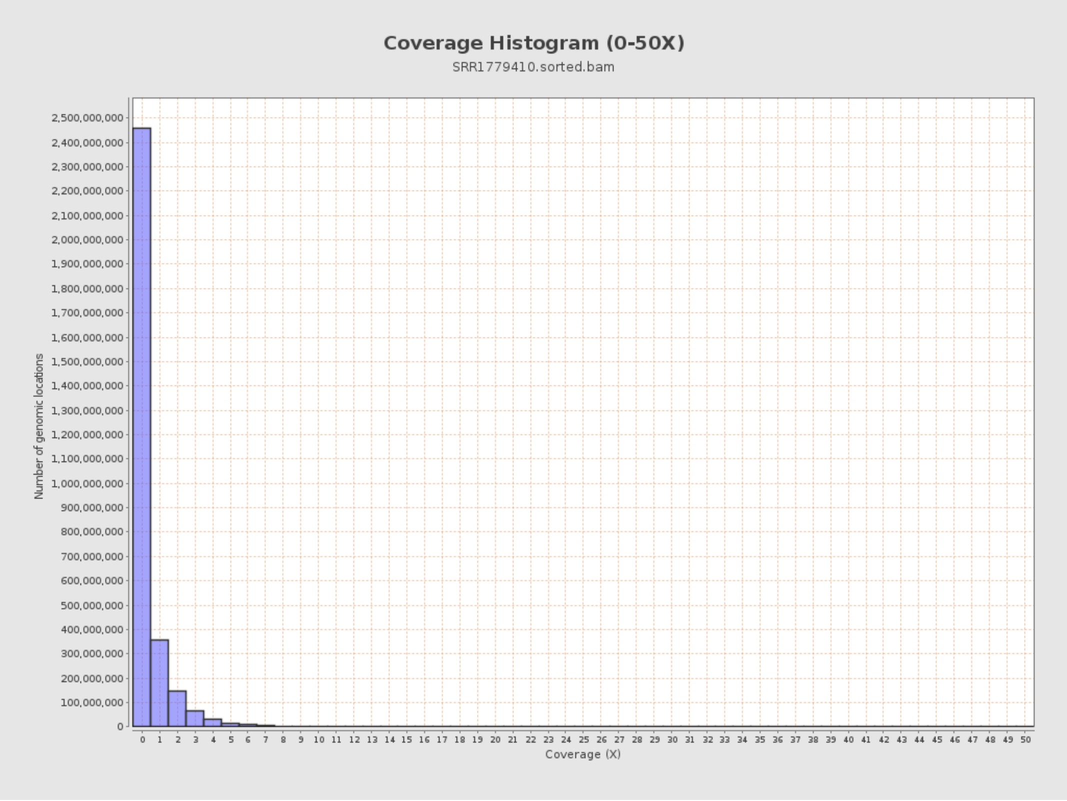
3. Results : Coverage across reference



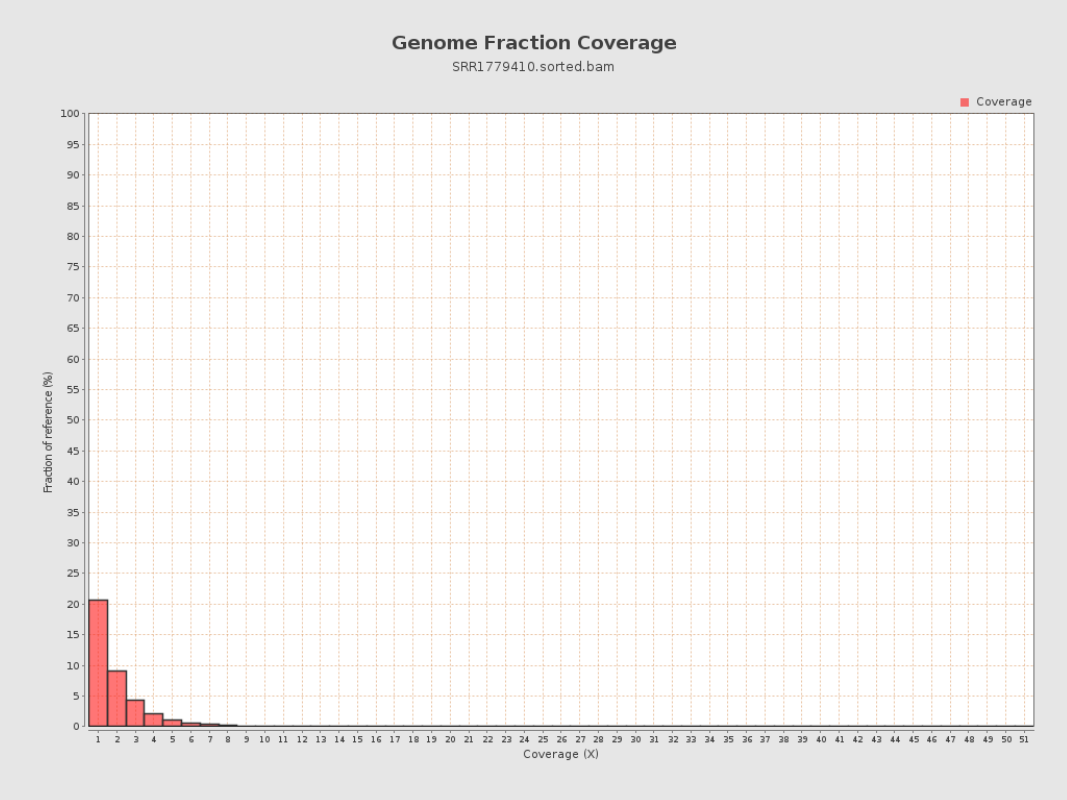
4. Results : Coverage Histogram



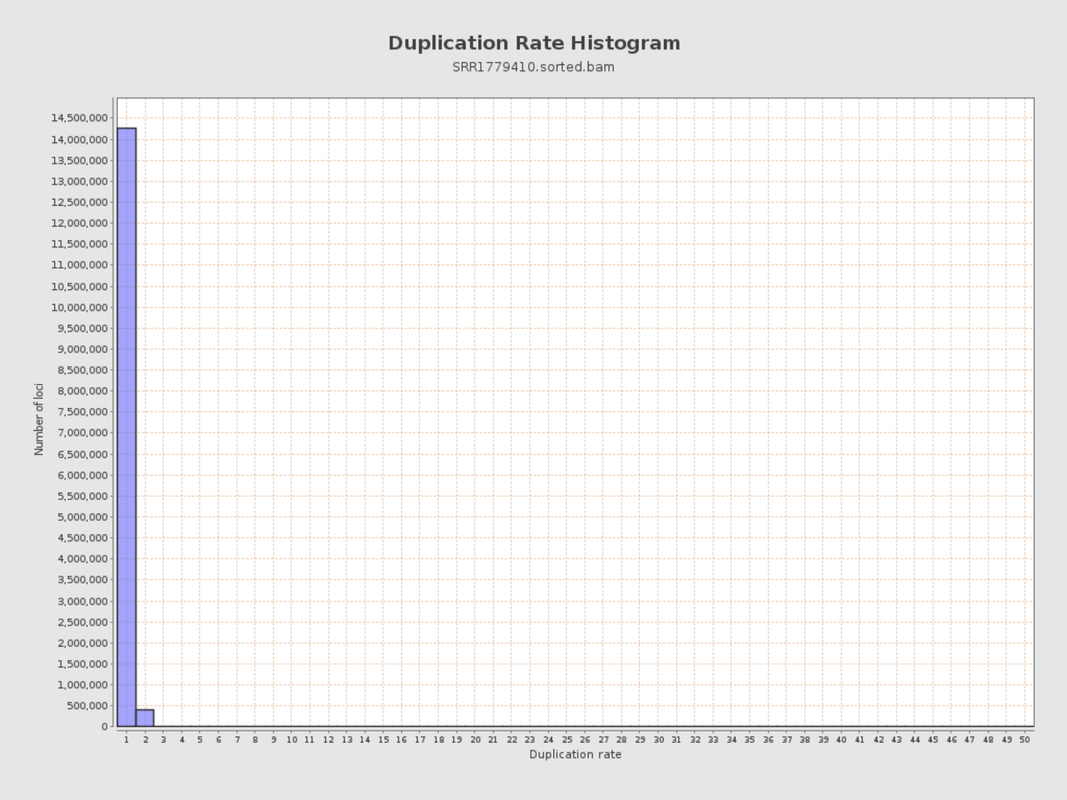
5. Results : Coverage Histogram (0-50X)



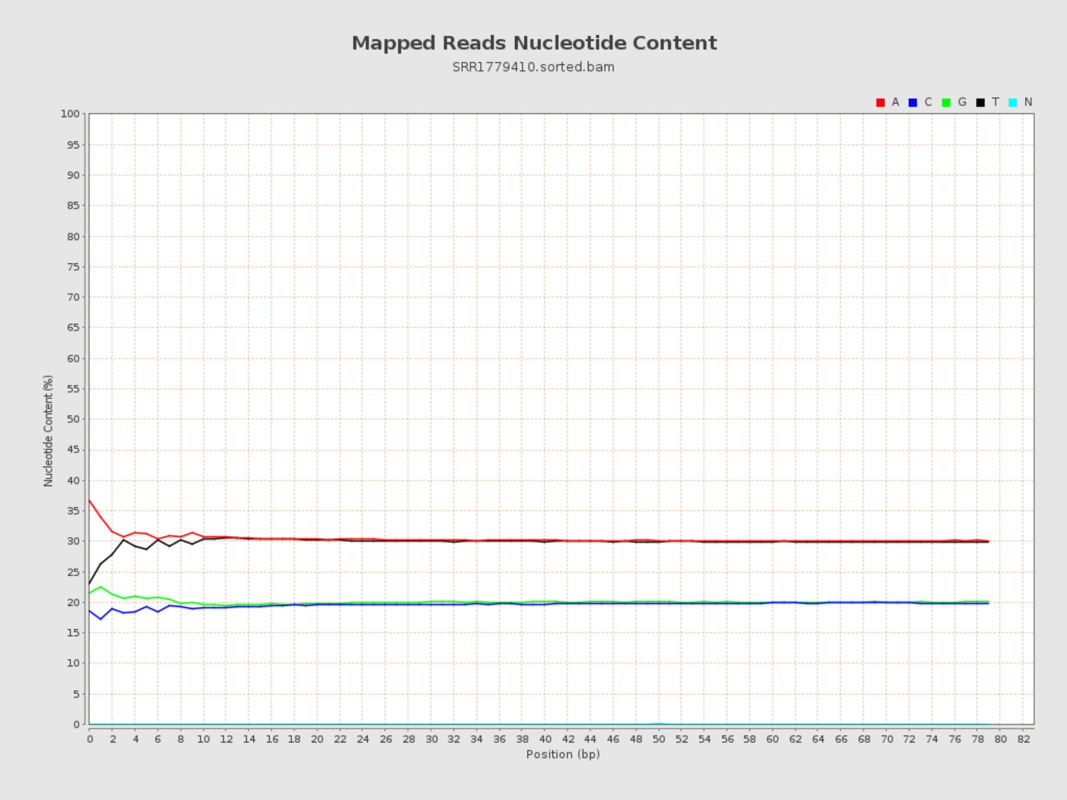
6. Results : Genome Fraction Coverage



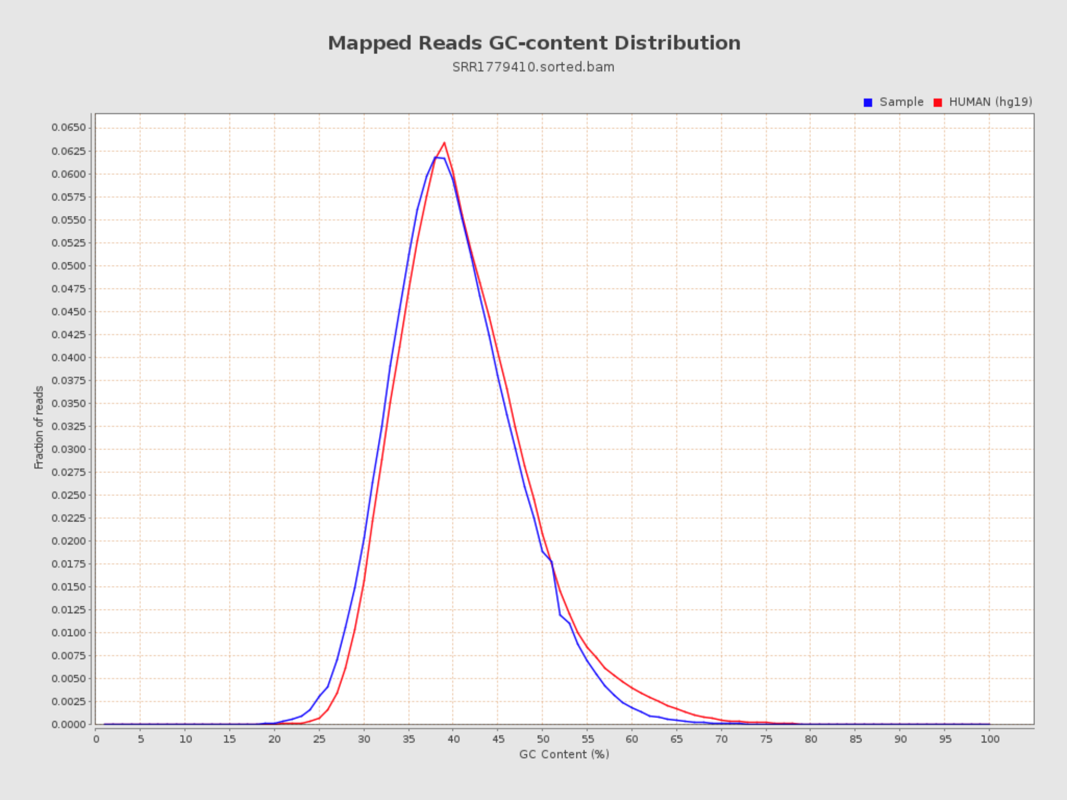
7. Results : Duplication Rate Histogram



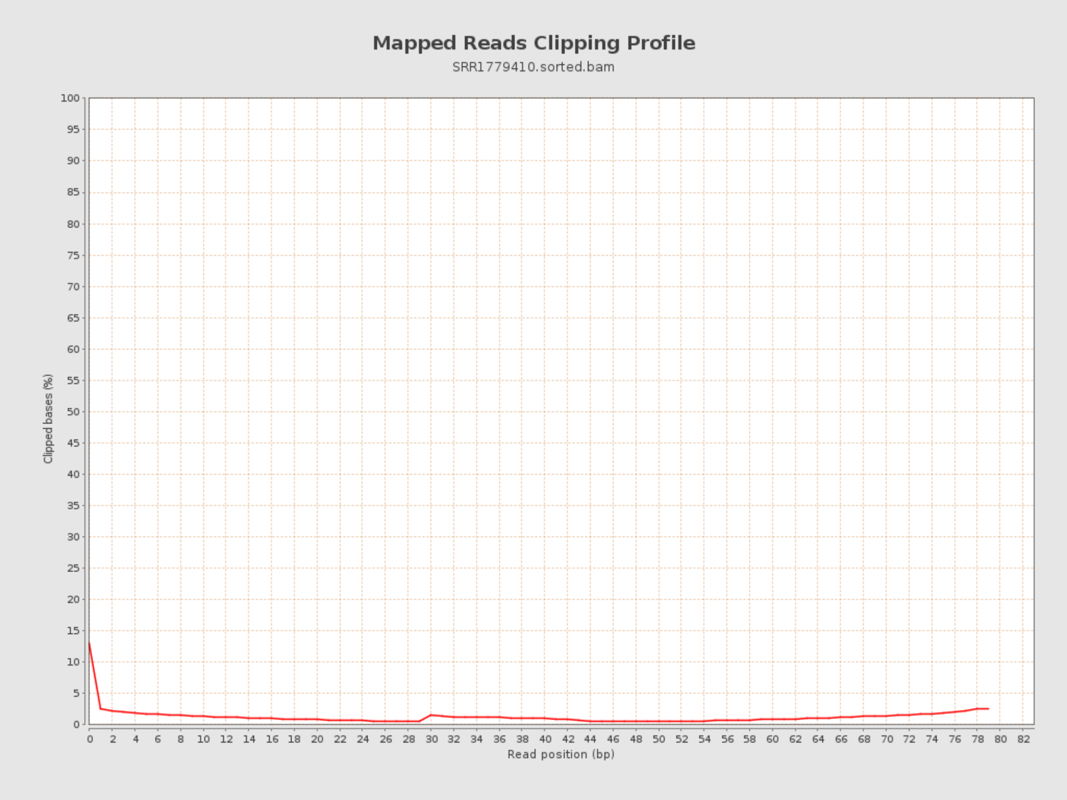
8. Results : Mapped Reads Nucleotide Content



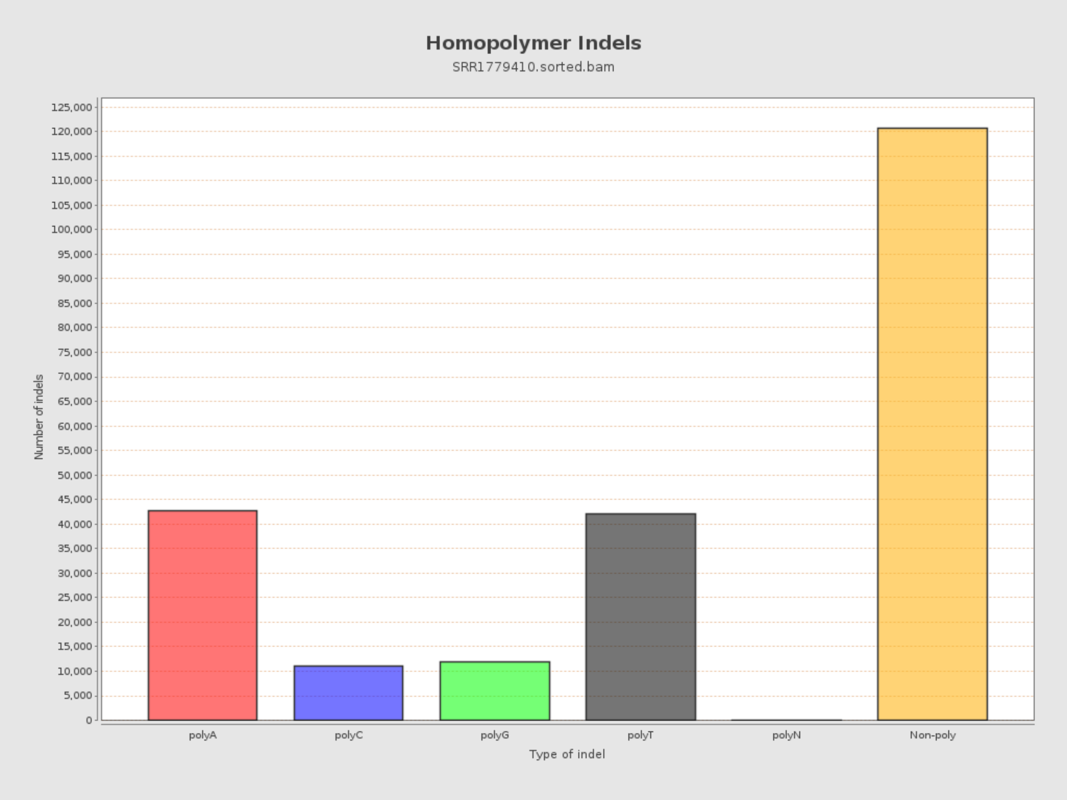
9. Results : Mapped Reads GC-content Distribution



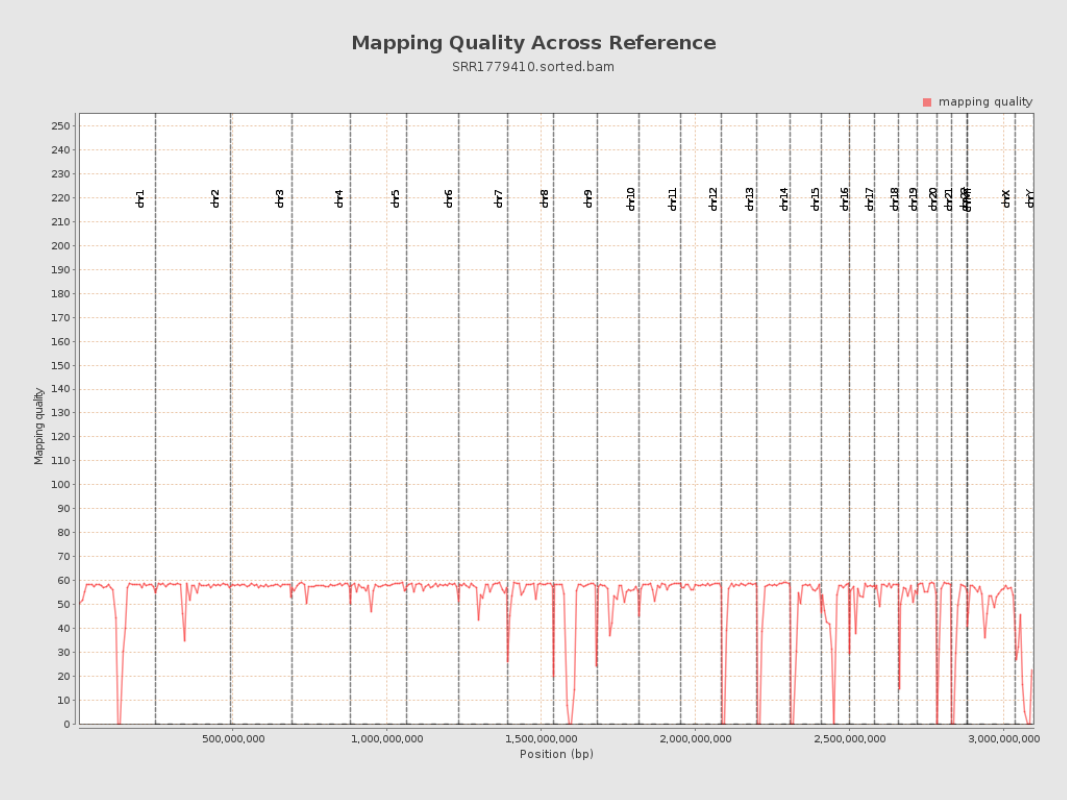
10. Results : Mapped Reads Clipping Profile



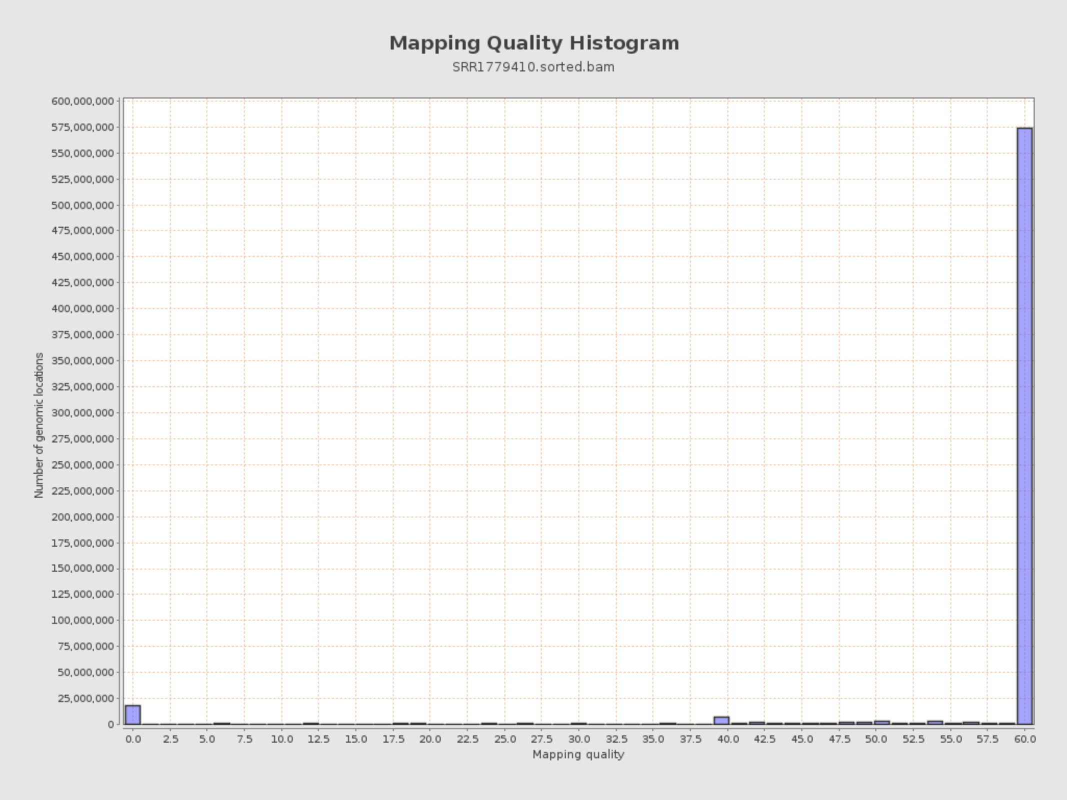
11. Results : Homopolymer Indels



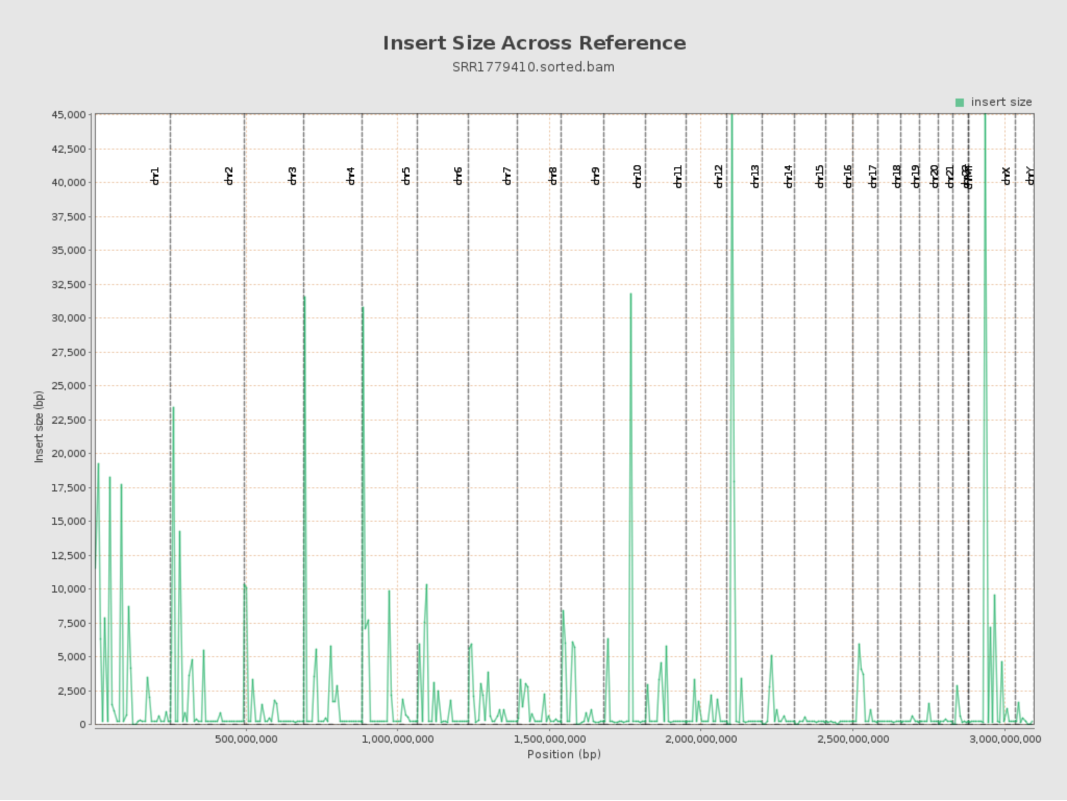
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram