Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 14:59:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779084.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_SRR1779084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779084_1.fastq.gz SRR1779084_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 14:59:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,288,790
Mapped reads	10,877,151 / 96.35%
Unmapped reads	411,639 / 3.65%
Mapped paired reads	10,877,151 / 96.35%
Mapped reads, first in pair	5,499,010 / 48.71%
Mapped reads, second in pair	5,378,141 / 47.64%
Mapped reads, both in pair	10,710,830 / 94.88%
Mapped reads, singletons	166,321 / 1.47%
Secondary alignments	0
Supplementary alignments	59,551 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	286,426 / 2.54%
Duplication rate	2.3%
Clipped reads	789,375 / 6.99%

2.2. ACGT Content

Number/percentage of A's	330,052,492 / 30.42%
Number/percentage of C's	211,446,191 / 19.49%
Number/percentage of T's	328,499,325 / 30.28%
Number/percentage of G's	214,617,788 / 19.78%
Number/percentage of N's	365,503 / 0.03%

GC Percentage	39.27%

2.3. Coverage

Mean	0.3506
Standard Deviation	1.2571

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Insert size

Mean	65,574.1
Standard Deviation	2,422,190.62
P25/Median/P75	149 / 200 / 273

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	4,967,481
Insertions	89,229
Mapped reads with at least one insertion	0.81%
Deletions	109,817
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.36%

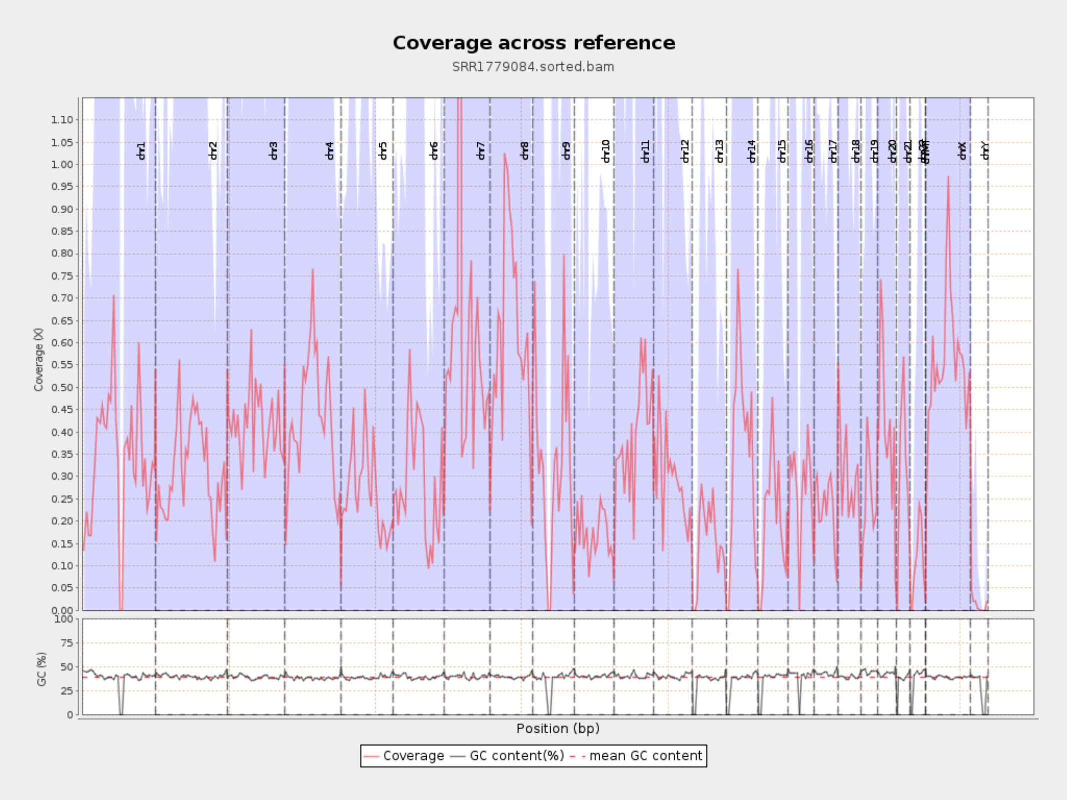
2.7. Chromosome stats

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

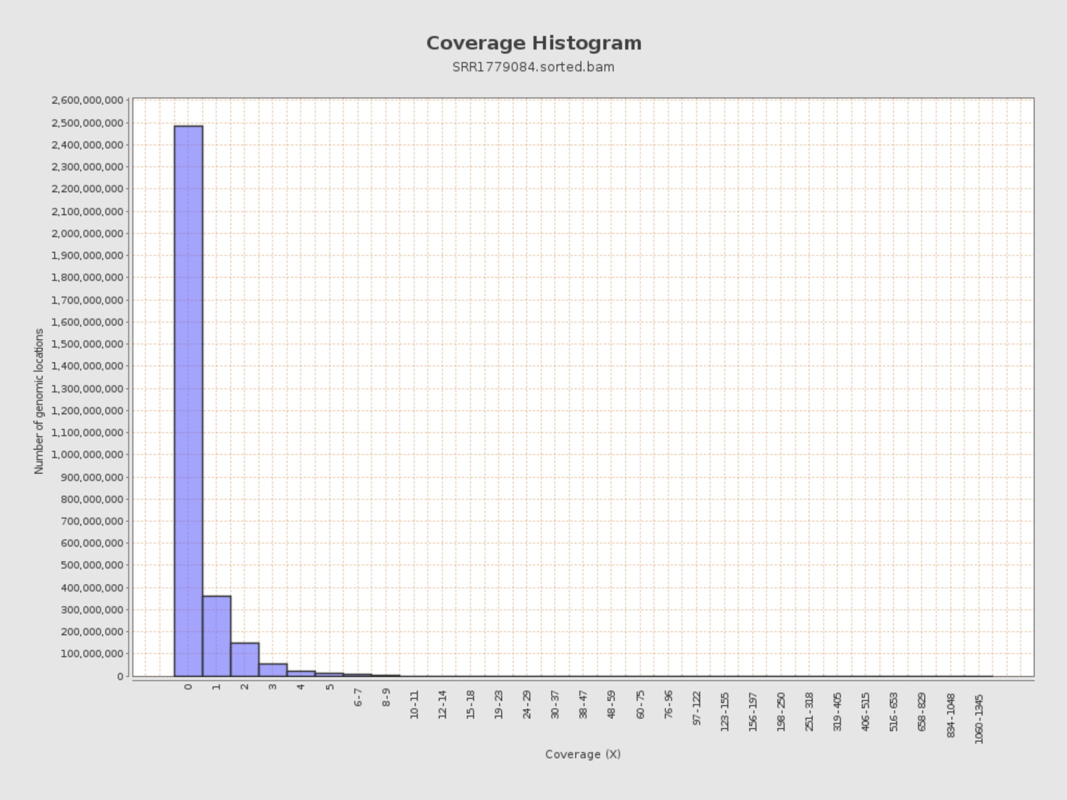
		bases	coverage	deviation
chr1	249250621	84376170	0.3385	1.6335
chr2	243199373	75875015	0.312	0.9166
chr3	198022430	83195818	0.4201	0.9323
chr4	191154276	83038980	0.4344	0.9809
chr5	180915260	48072192	0.2657	0.7549
chr6	171115067	50597901	0.2957	0.8281
chr7	159138663	111886146	0.7031	3.3334
chr8	146364022	91168423	0.6229	1.2077
chr9	141213431	46346657	0.3282	0.9354
chr10	135534747	23299986	0.1719	1.548
chr11	135006516	53429290	0.3958	0.9629
chr12	133851895	39372416	0.2941	0.8233
chr13	115169878	17884288	0.1553	0.5924
chr14	107349540	39026466	0.3635	0.9282
chr15	102531392	20574474	0.2007	0.6838
chr16	90354753	23334982	0.2583	0.7401
chr17	81195210	18888430	0.2326	0.7322
chr18	78077248	23635839	0.3027	0.8366
chr19	59128983	15140092	0.2561	1.1562
chr20	63025520	27044733	0.4291	0.9646
chr21	48129895	14303477	0.2972	0.8047
chr22	51304566	5866514	0.1143	0.5744
chrMT	16571	639	0.0386	0.256
chrX	155270560	88100972	0.5674	1.1803

chrY	59373566	765569	0.0129	0.2037

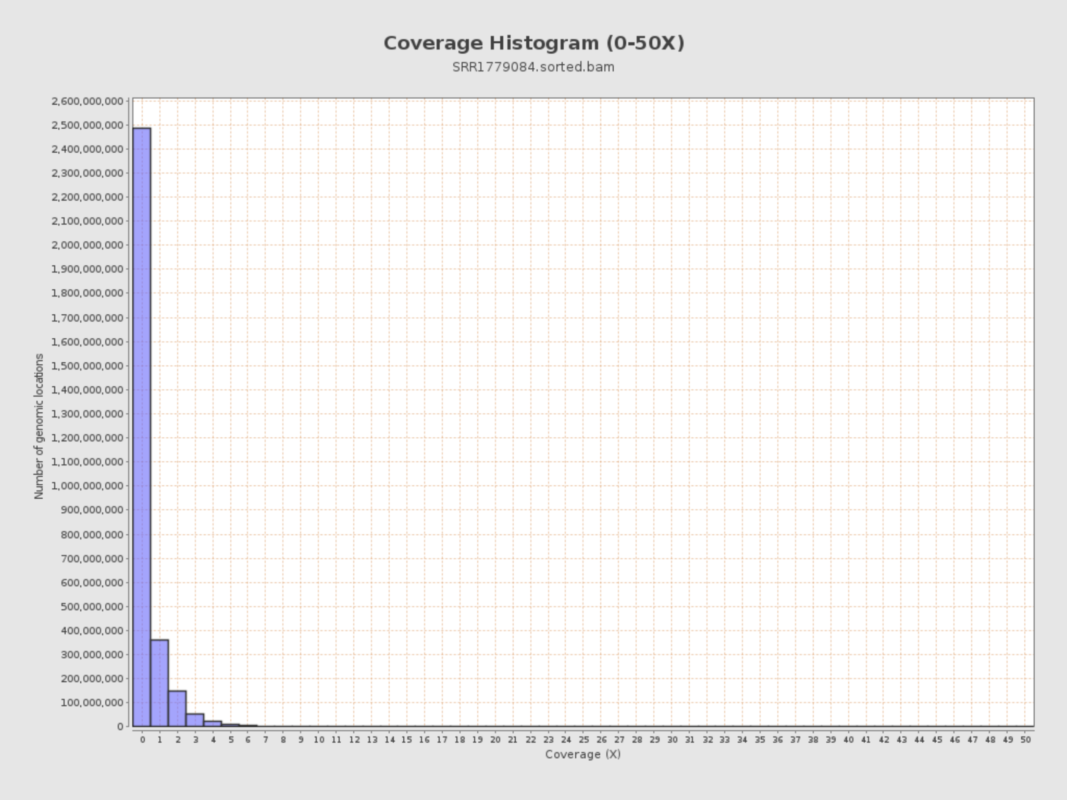
3. Results : Coverage across reference



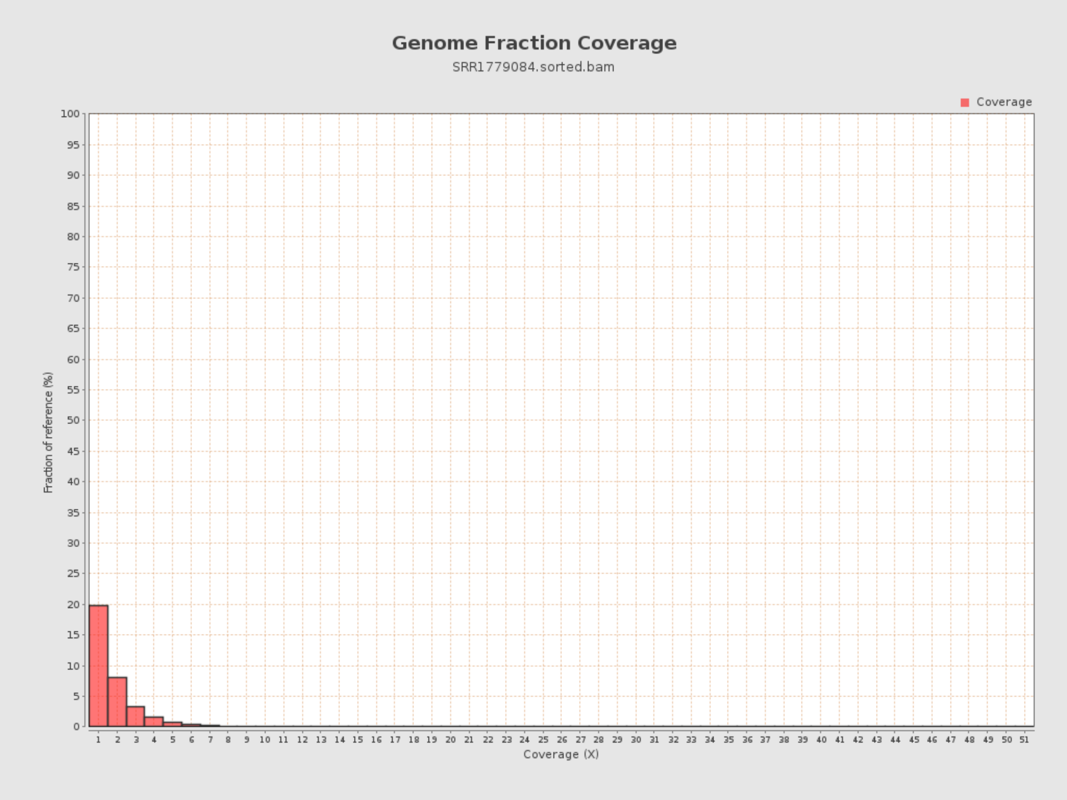
4. Results : Coverage Histogram



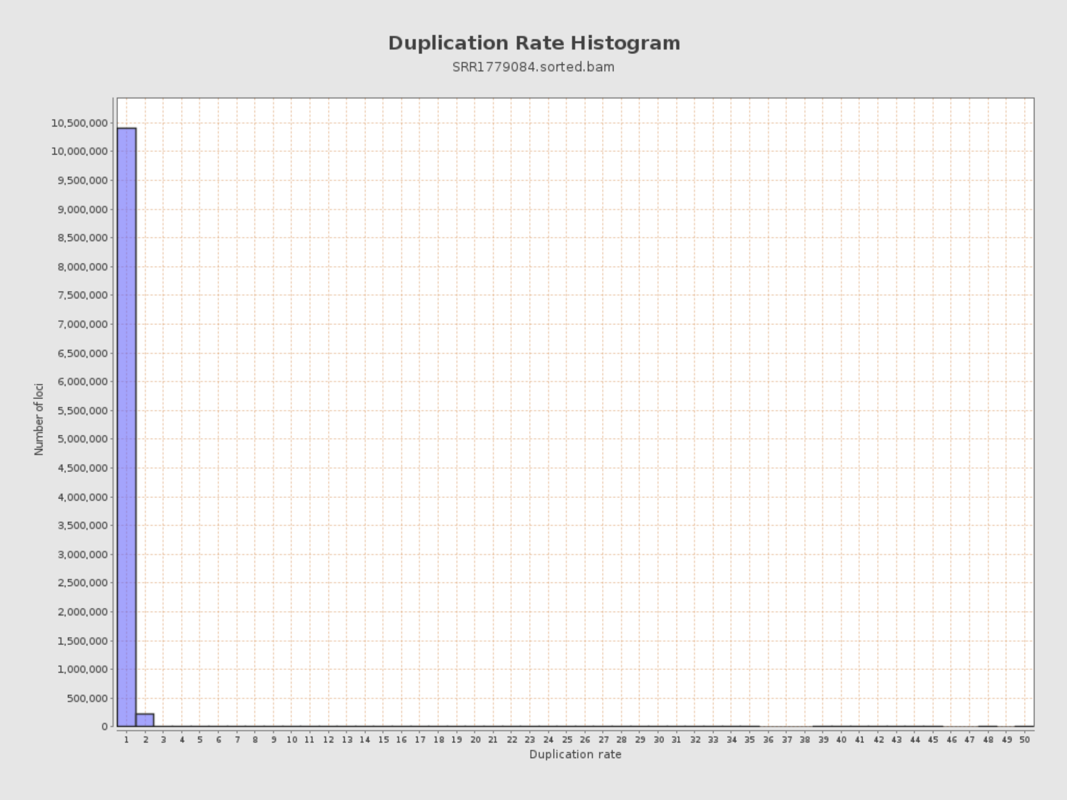
5. Results : Coverage Histogram (0-50X)



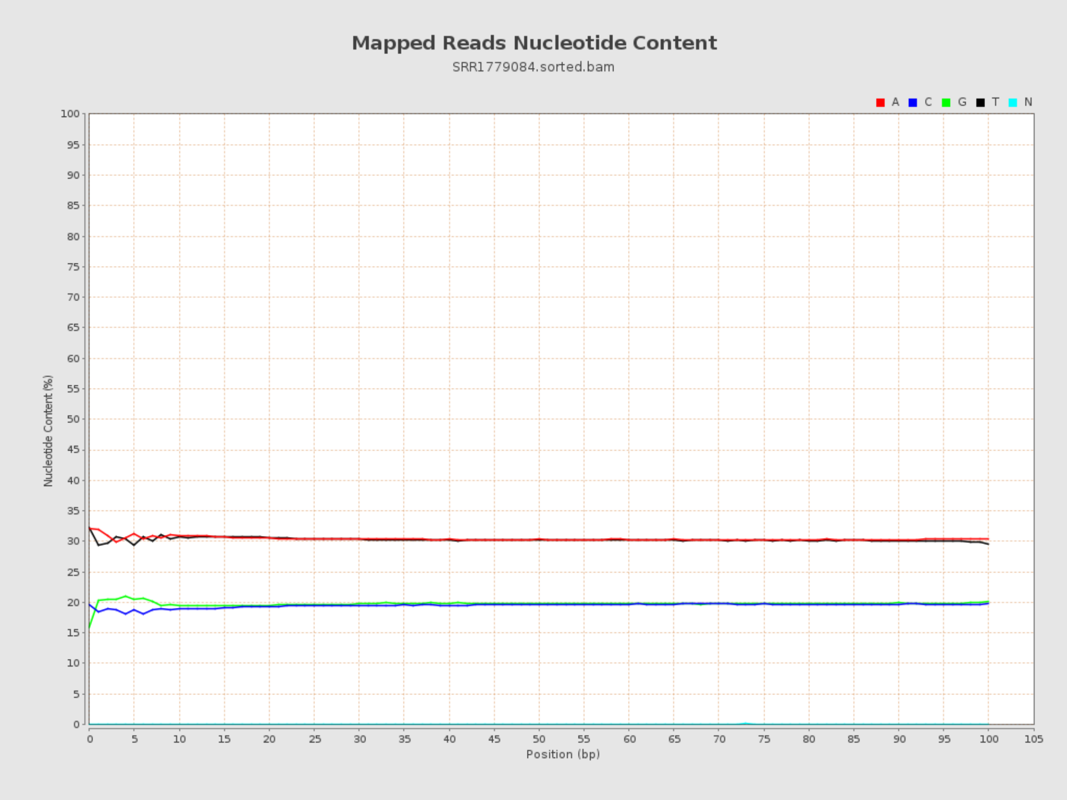
6. Results : Genome Fraction Coverage



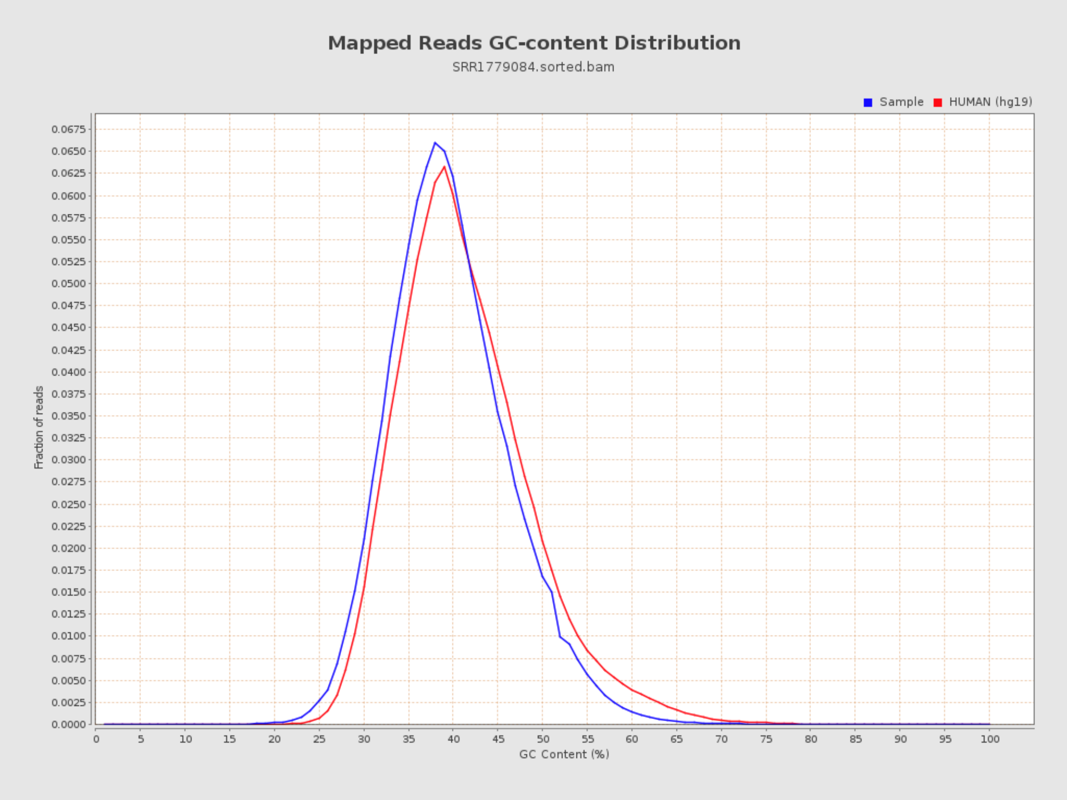
7. Results : Duplication Rate Histogram



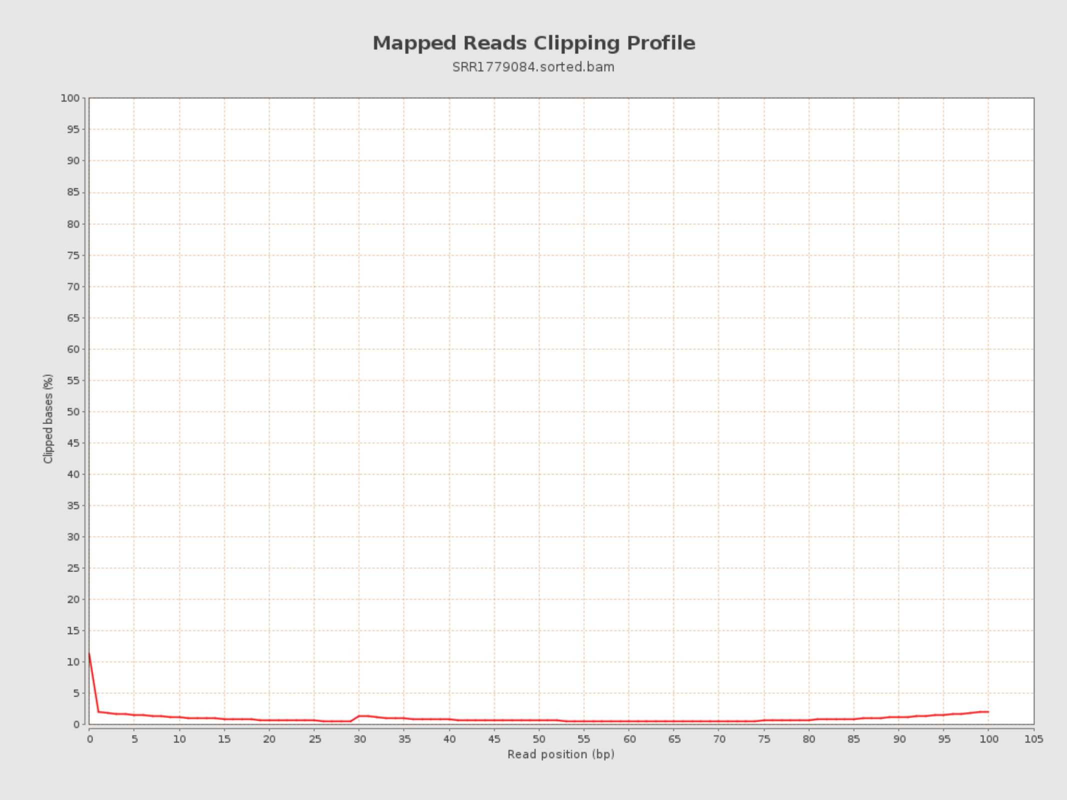
8. Results : Mapped Reads Nucleotide Content



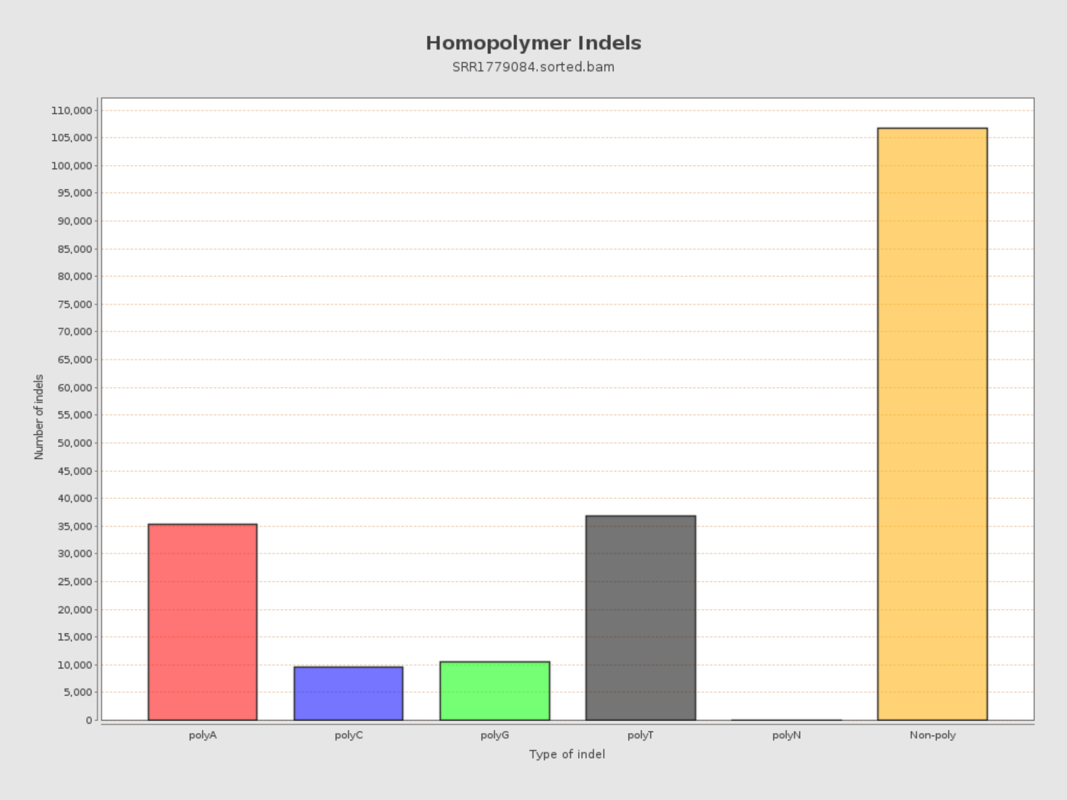
9. Results : Mapped Reads GC-content Distribution



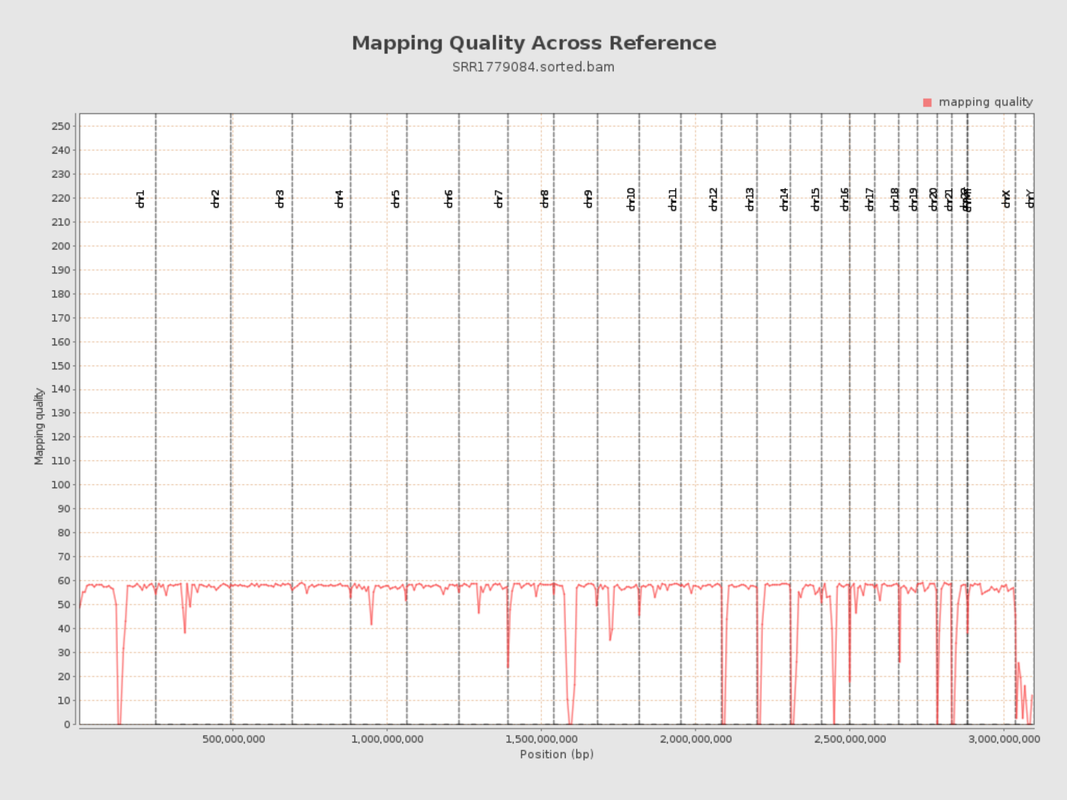
10. Results : Mapped Reads Clipping Profile



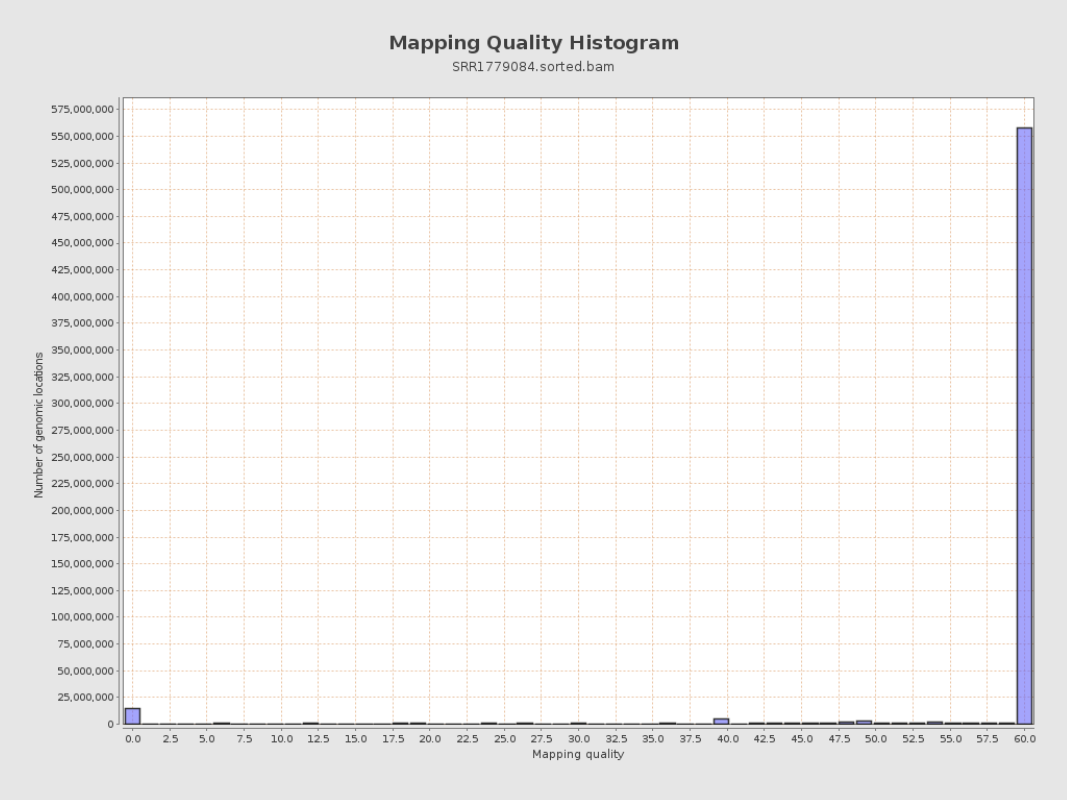
11. Results : Homopolymer Indels



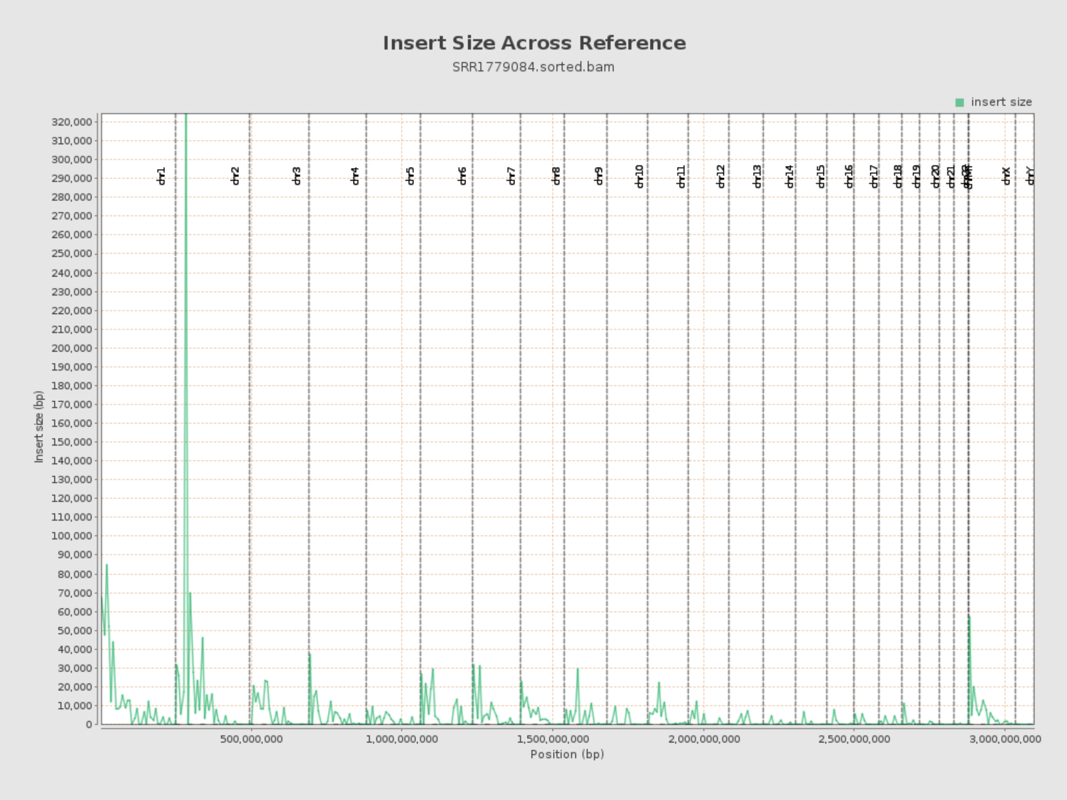
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram