Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 03:08:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779157.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_SRR1779157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779157_1.fastq.gz SRR1779157_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 03:08:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,312,532
Mapped reads	37,303,688 / 97.37%
Unmapped reads	1,008,844 / 2.63%
Mapped paired reads	37,303,688 / 97.37%
Mapped reads, first in pair	18,777,887 / 49.01%
Mapped reads, second in pair	18,525,801 / 48.35%
Mapped reads, both in pair	36,915,384 / 96.35%
Mapped reads, singletons	388,304 / 1.01%
Secondary alignments	0
Supplementary alignments	225,172 / 0.59%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	2,865,500 / 7.48%
Duplication rate	6.55%
Clipped reads	2,443,057 / 6.38%

2.2. ACGT Content

Number/percentage of A's	1,147,927,499 / 30.81%
Number/percentage of C's	712,838,192 / 19.13%
Number/percentage of T's	1,137,564,501 / 30.54%
Number/percentage of G's	725,502,809 / 19.47%
Number/percentage of N's	1,511,669 / 0.04%

GC Percentage	38.61%

2.3. Coverage

Mean	1.2037
Standard Deviation	4.837

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	68,165.06
Standard Deviation	2,502,078.91
P25/Median/P75	155 / 206 / 278

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	15,334,237
Insertions	305,554
Mapped reads with at least one insertion	0.81%
Deletions	380,140
Mapped reads with at least one deletion	1%
Homopolymer indels	46.34%

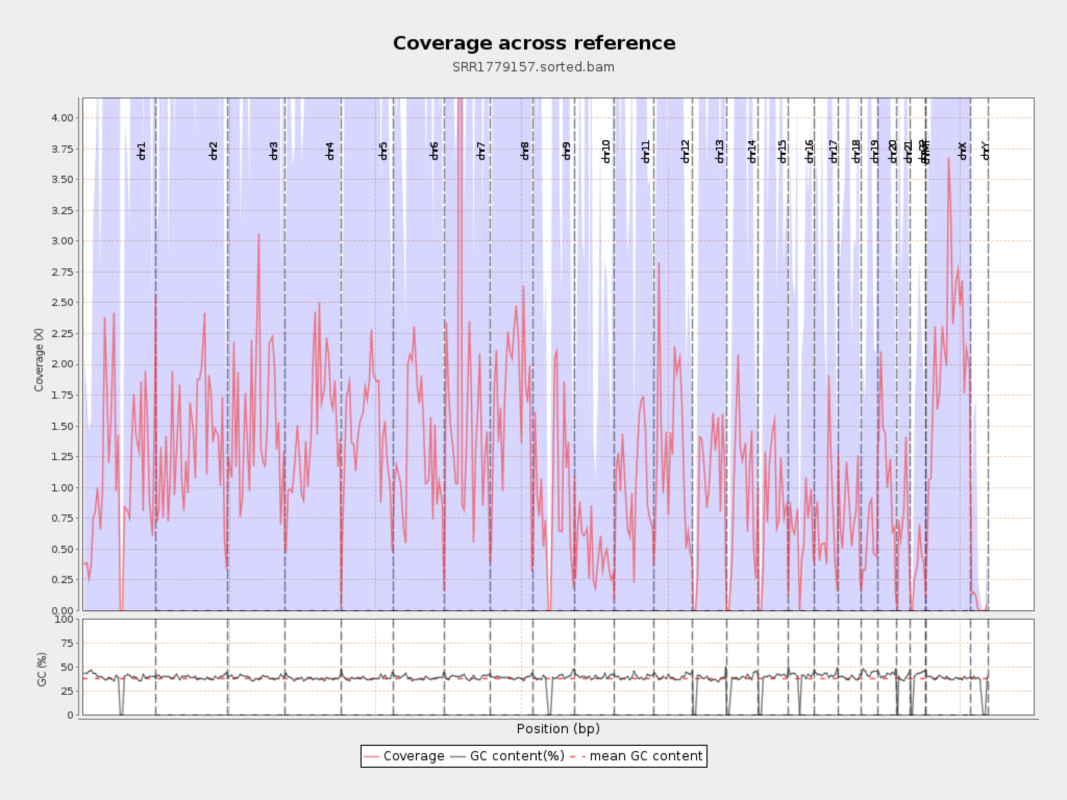
2.7. Chromosome stats

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

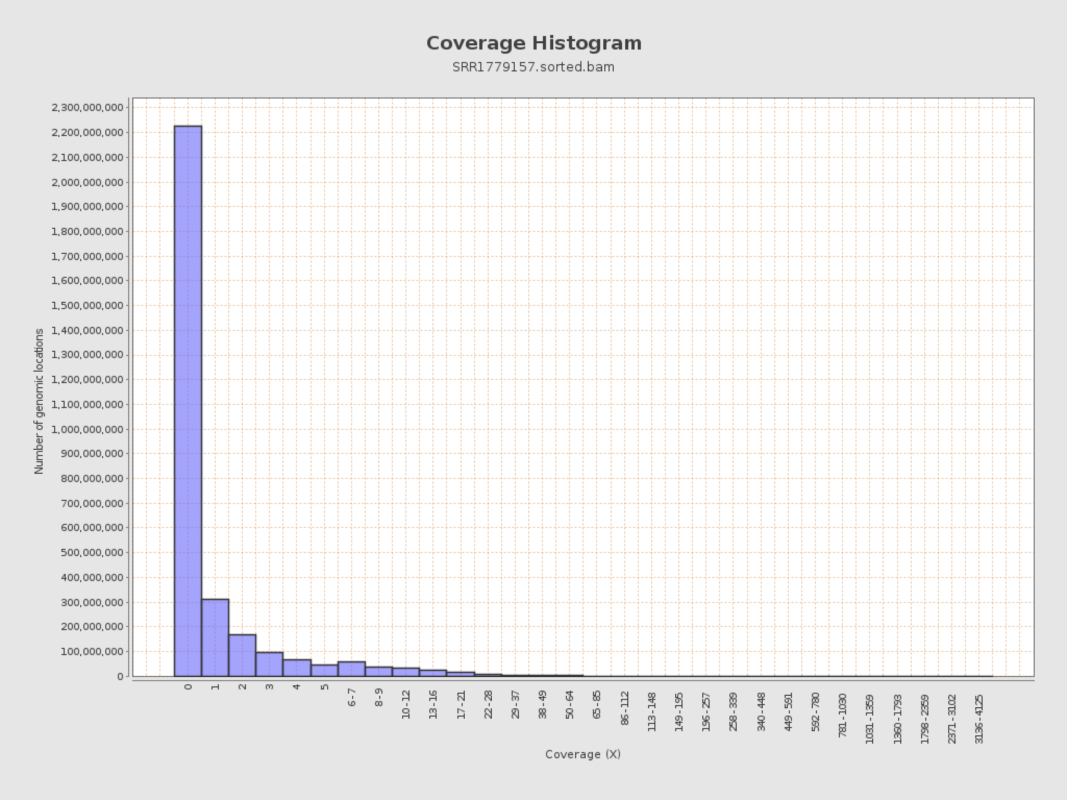
		bases	coverage	deviation
chr1	249250621	275134885	1.1038	5.6485
chr2	243199373	323028363	1.3282	4.2486
chr3	198022430	298552234	1.5077	4.0555
chr4	191154276	283881042	1.4851	4.0729
chr5	180915260	261295903	1.4443	3.8184
chr6	171115067	228223992	1.3337	3.9965
chr7	159138663	303435140	1.9067	12.2338
chr8	146364022	258381844	1.7653	4.5216
chr9	141213431	133896956	0.9482	3.4633
chr10	135534747	63840413	0.471	5.6431
chr11	135006516	141409152	1.0474	3.249
chr12	133851895	174249309	1.3018	3.9543
chr13	115169878	120437119	1.0457	3.1624
chr14	107349540	101974424	0.9499	2.9852
chr15	102531392	86158669	0.8403	2.7605
chr16	90354753	56516624	0.6255	2.2174
chr17	81195210	61531329	0.7578	2.9634
chr18	78077248	63630913	0.815	2.4999
chr19	59128983	34017675	0.5753	2.948
chr20	63025520	74642483	1.1843	3.7688
chr21	48129895	33884643	0.704	2.8584
chr22	51304566	17034913	0.332	1.4933
chrMT	16571	5128	0.3095	0.7329
chrX	155270560	327804096	2.1112	5.5781

chrY	59373566	3229590	0.0544	0.8269

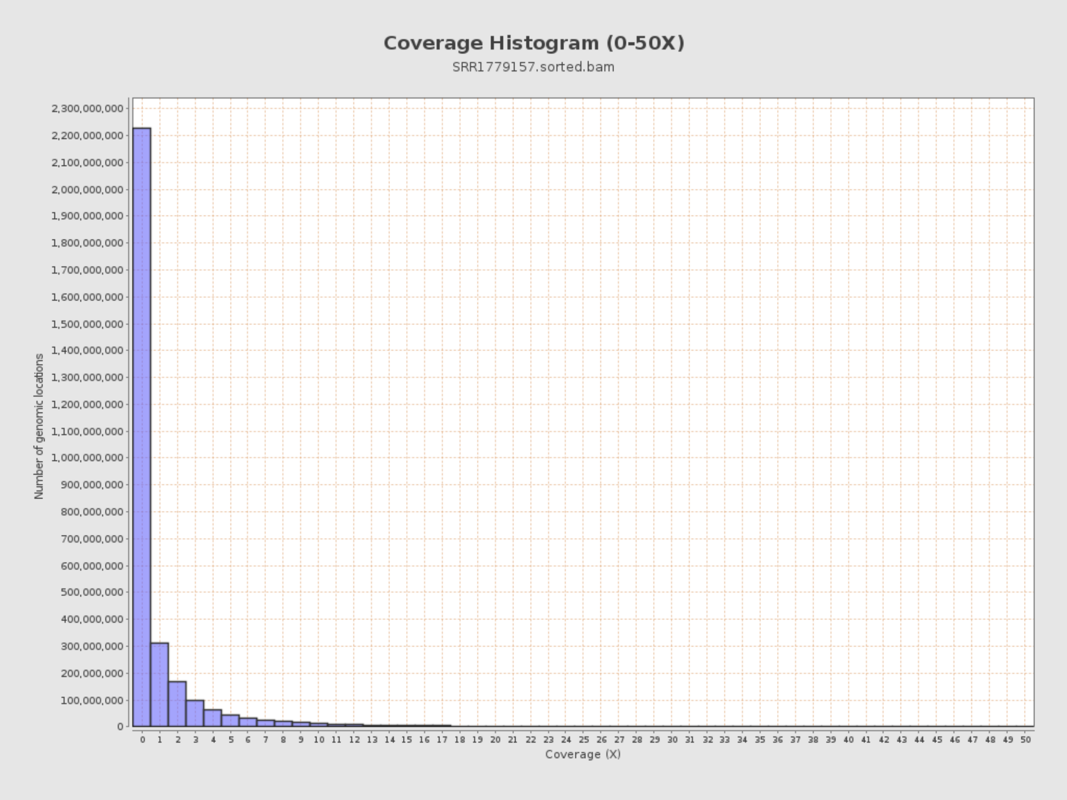
3. Results : Coverage across reference



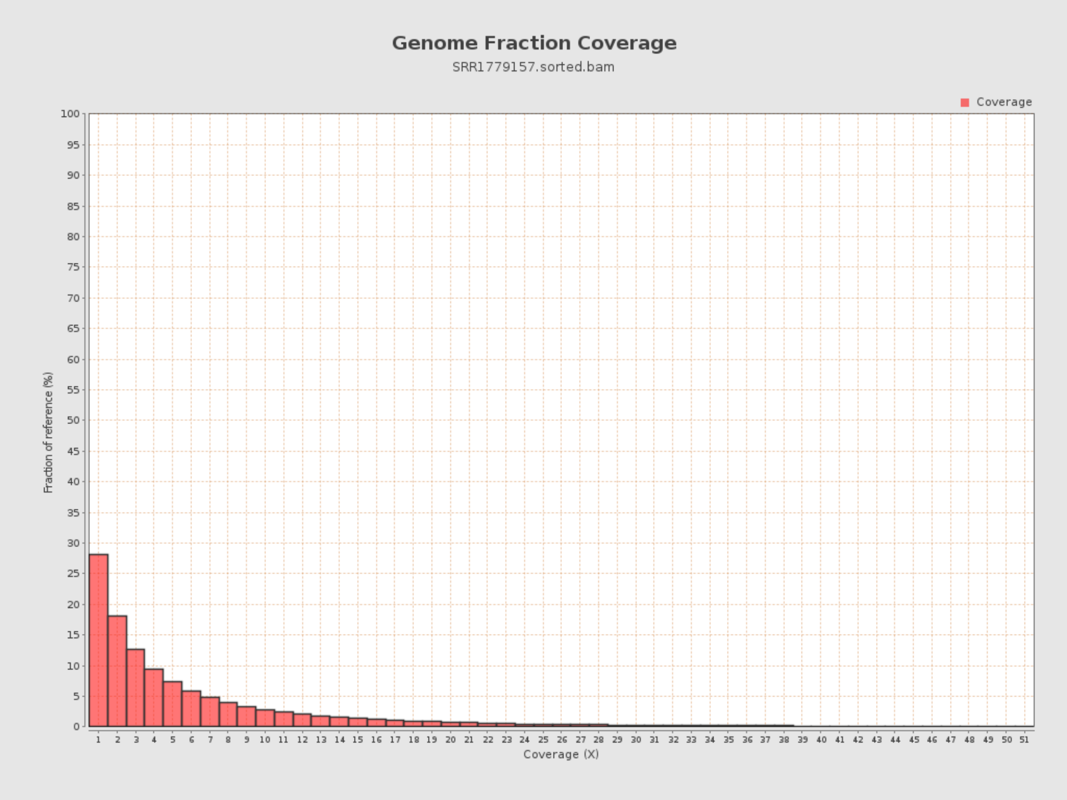
4. Results : Coverage Histogram



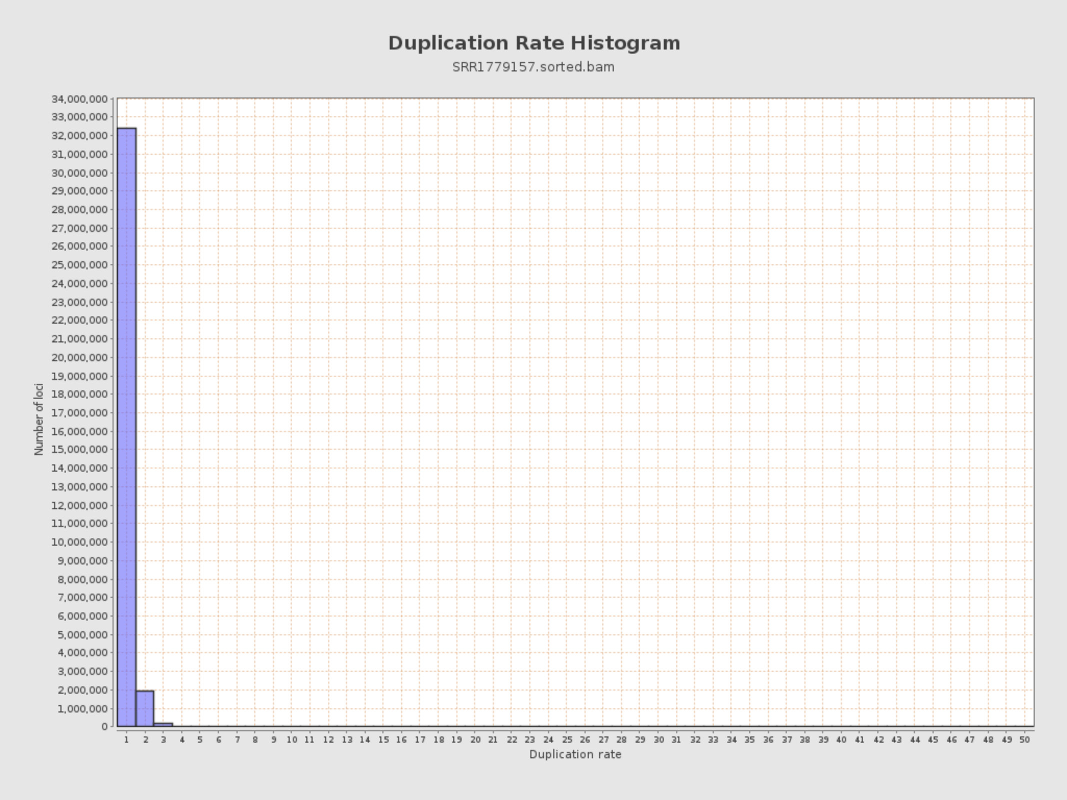
5. Results : Coverage Histogram (0-50X)



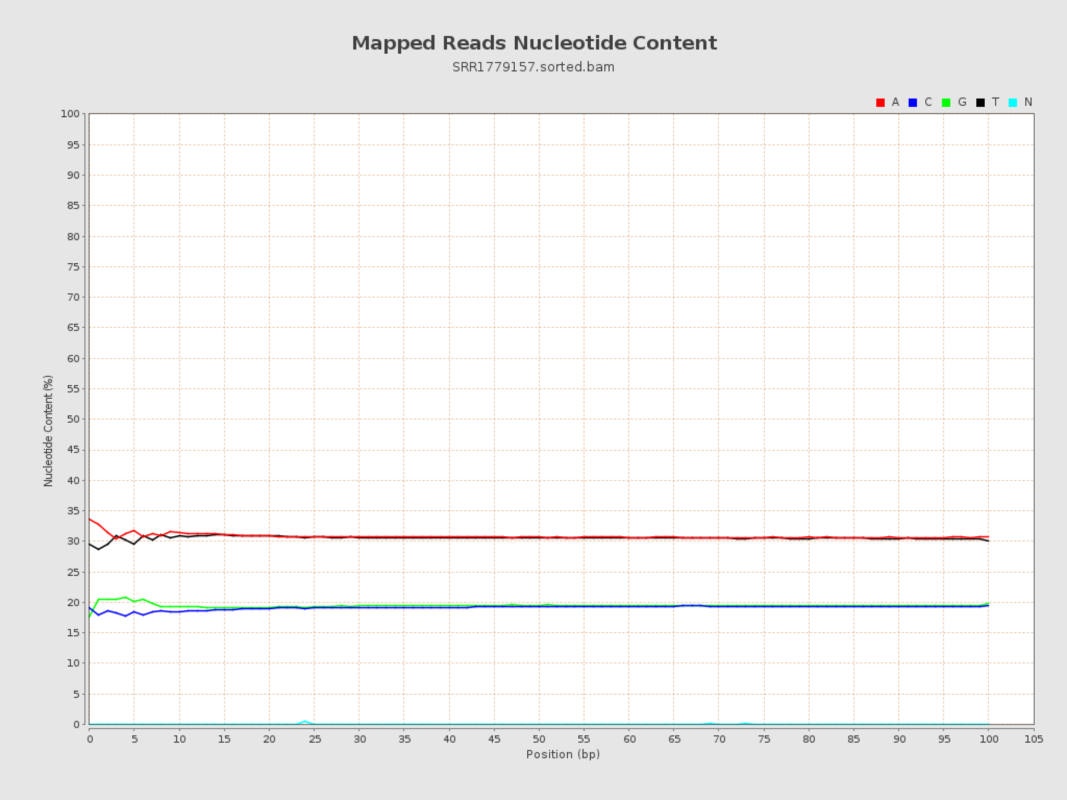
6. Results : Genome Fraction Coverage



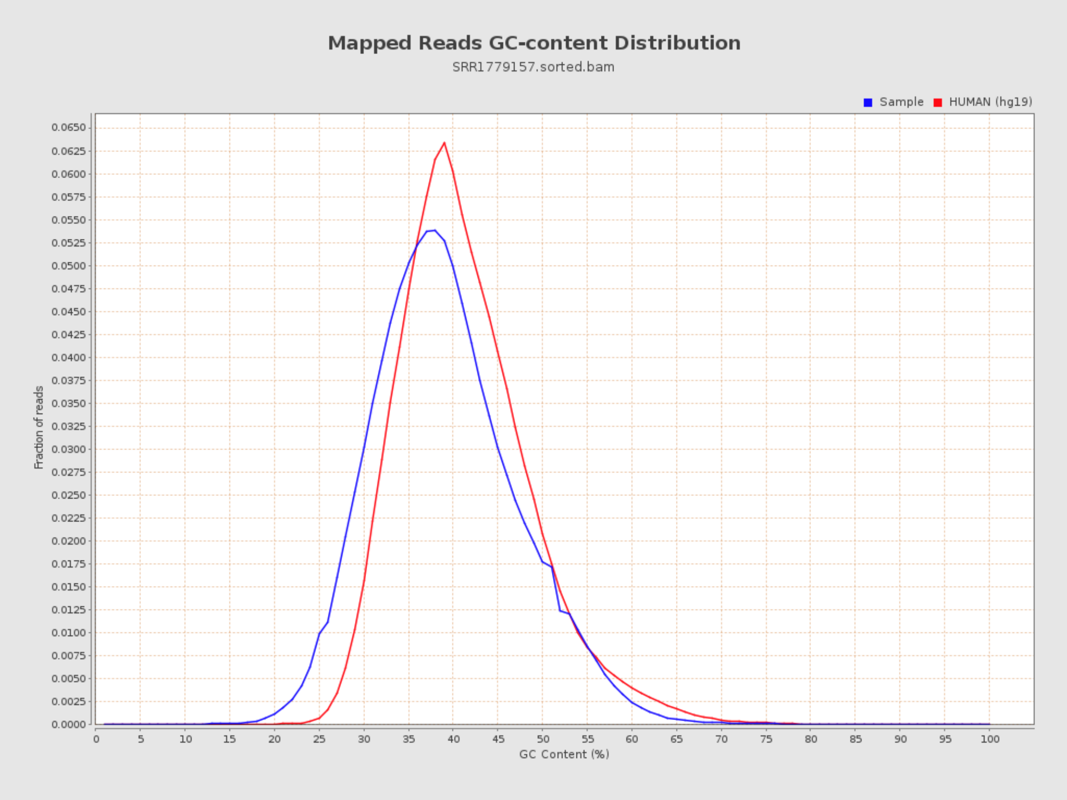
7. Results : Duplication Rate Histogram



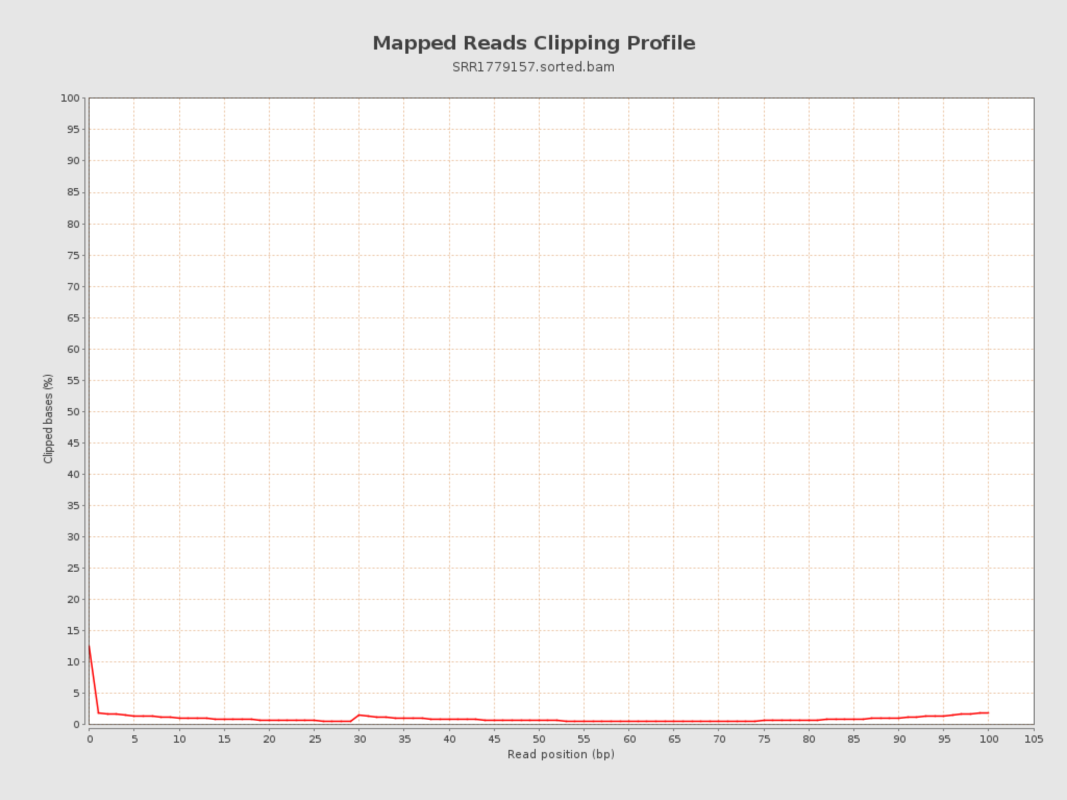
8. Results : Mapped Reads Nucleotide Content



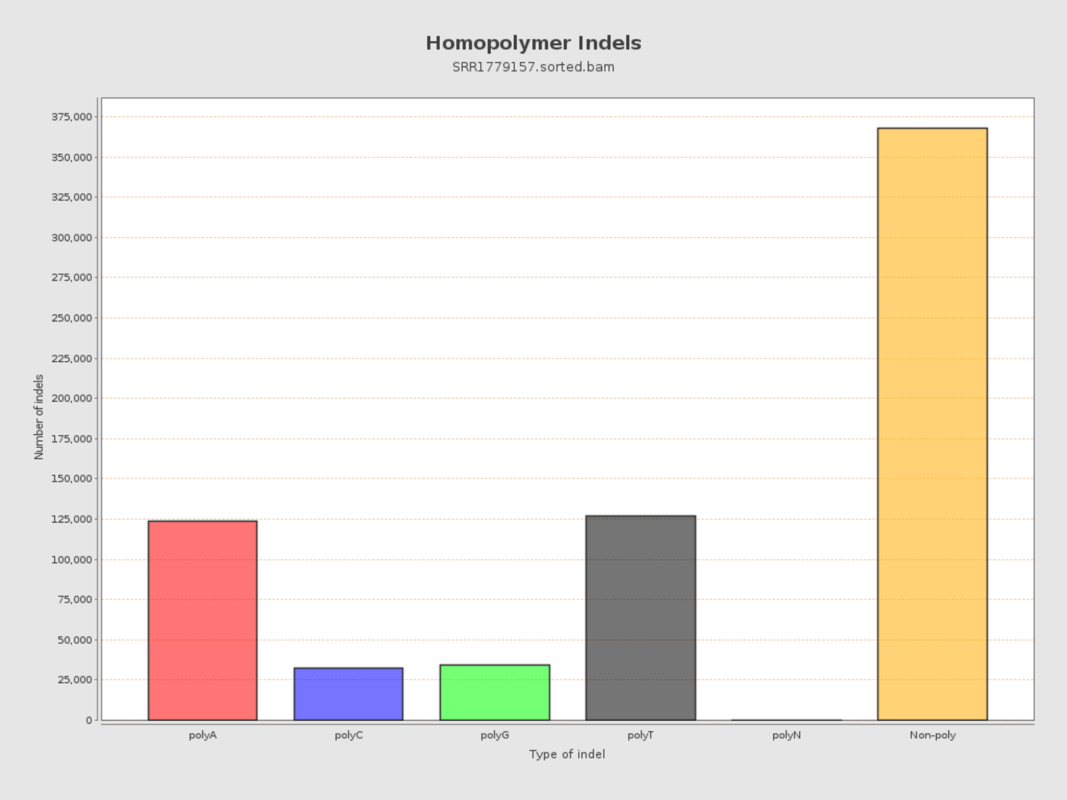
9. Results : Mapped Reads GC-content Distribution



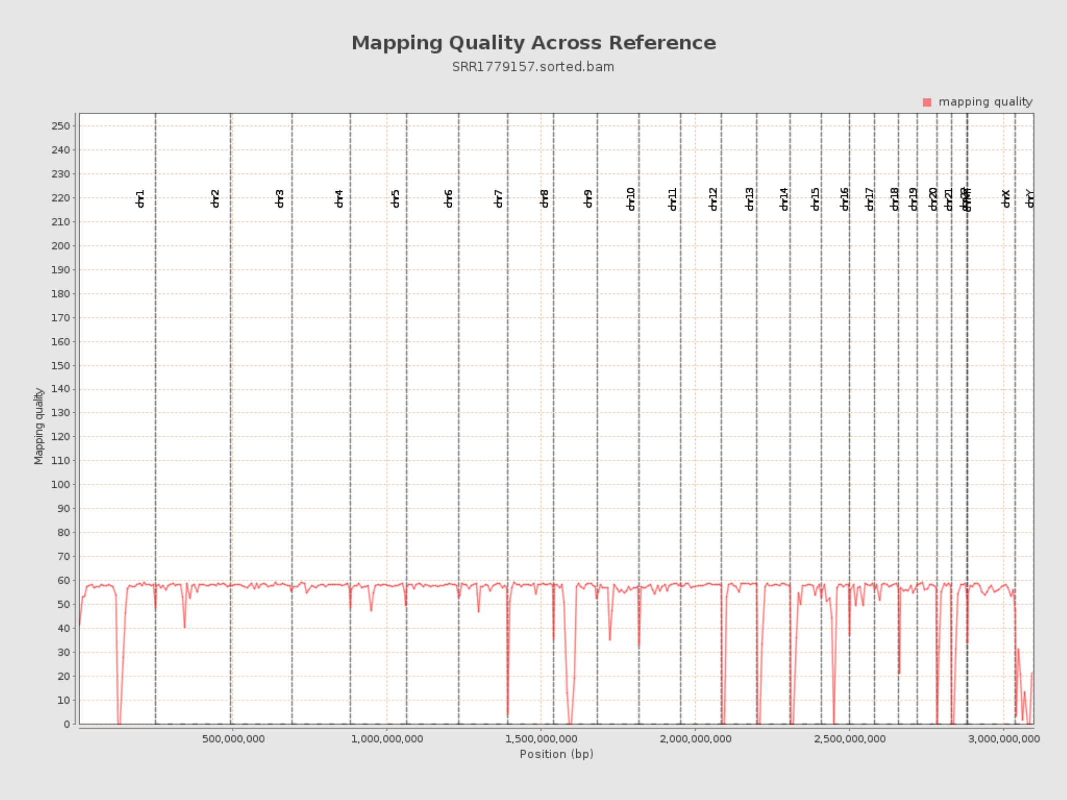
10. Results : Mapped Reads Clipping Profile



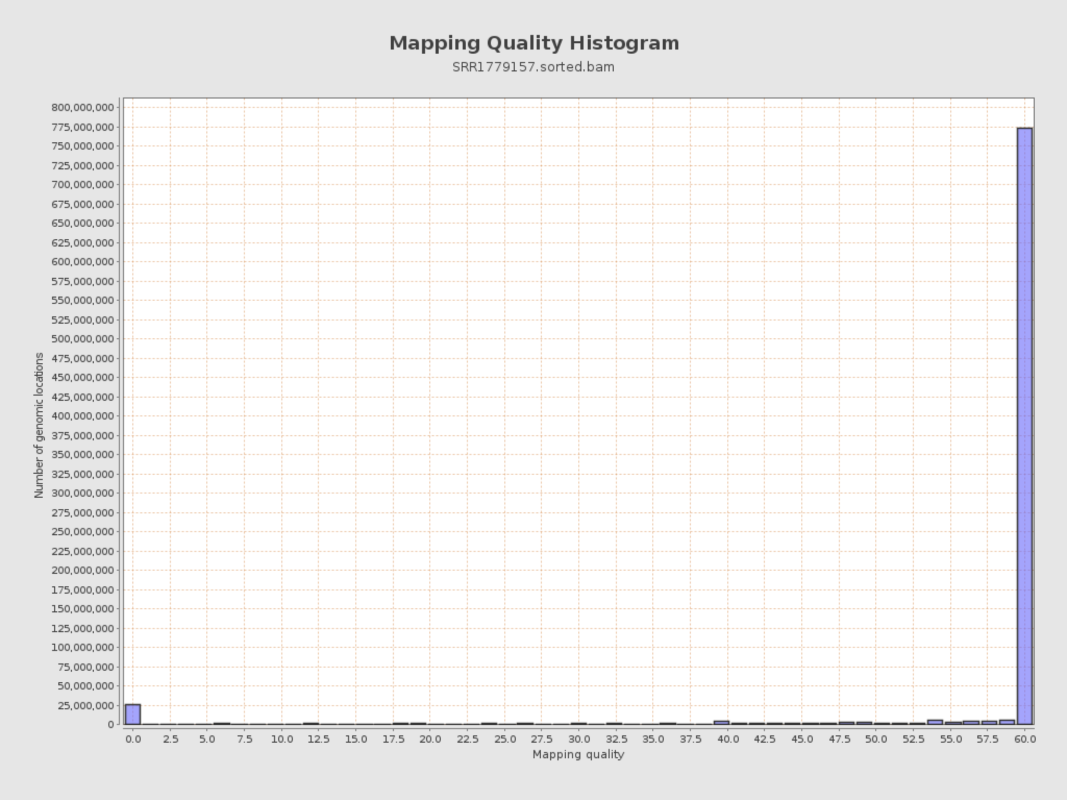
11. Results : Homopolymer Indels



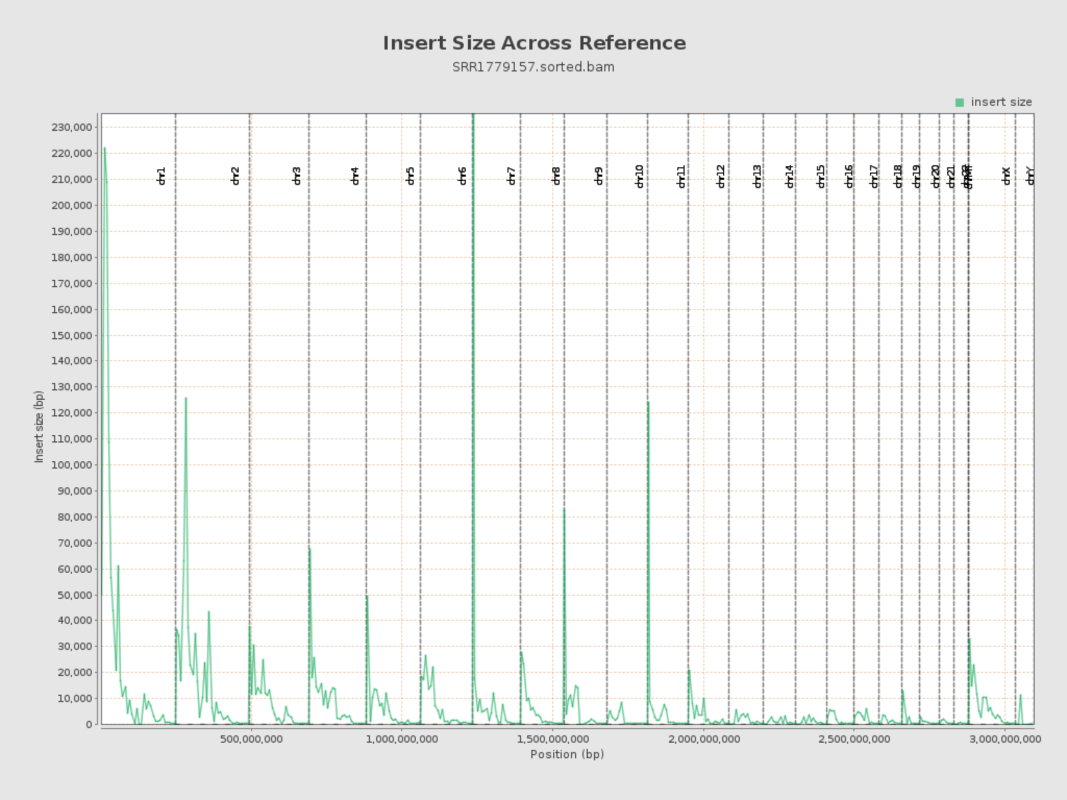
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram