Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 19:32:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779401.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_SRR1779401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779401_1.fastq.gz SRR1779401_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 19:32:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,238,542
Mapped reads	15,495,830 / 95.43%
Unmapped reads	742,712 / 4.57%
Mapped paired reads	15,495,830 / 95.43%
Mapped reads, first in pair	7,798,329 / 48.02%
Mapped reads, second in pair	7,697,501 / 47.4%
Mapped reads, both in pair	15,349,396 / 94.52%
Mapped reads, singletons	146,434 / 0.9%
Secondary alignments	0
Supplementary alignments	51,248 / 0.32%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	509,975 / 3.14%
Duplication rate	2.83%
Clipped reads	639,744 / 3.94%

2.2. ACGT Content

Number/percentage of A's	367,118,189 / 29.81%
Number/percentage of C's	246,661,863 / 20.03%
Number/percentage of T's	365,767,967 / 29.7%
Number/percentage of G's	251,594,322 / 20.43%
Number/percentage of N's	271,024 / 0.02%

GC Percentage	40.46%

2.3. Coverage

Mean	0.3979
Standard Deviation	1.612

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	38,214.93
Standard Deviation	1,825,060.08
P25/Median/P75	152 / 196 / 246

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,262,723
Insertions	115,895
Mapped reads with at least one insertion	0.74%
Deletions	137,116
Mapped reads with at least one deletion	0.87%
Homopolymer indels	47.12%

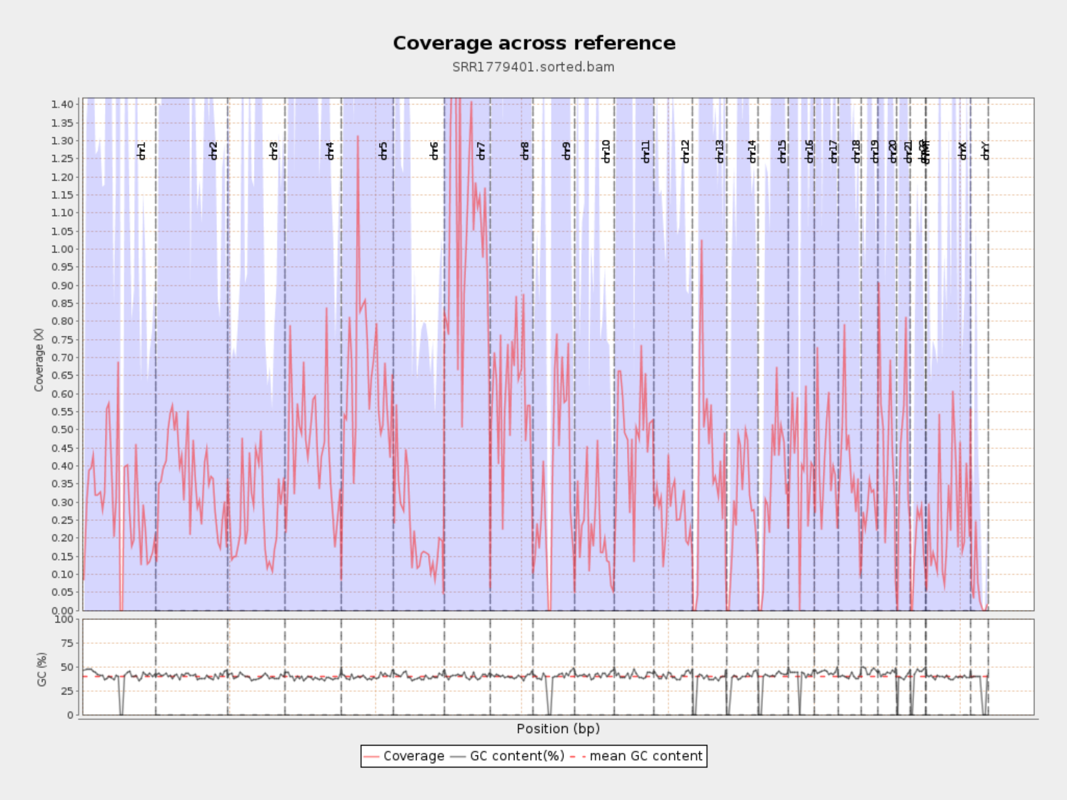
2.7. Chromosome stats

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

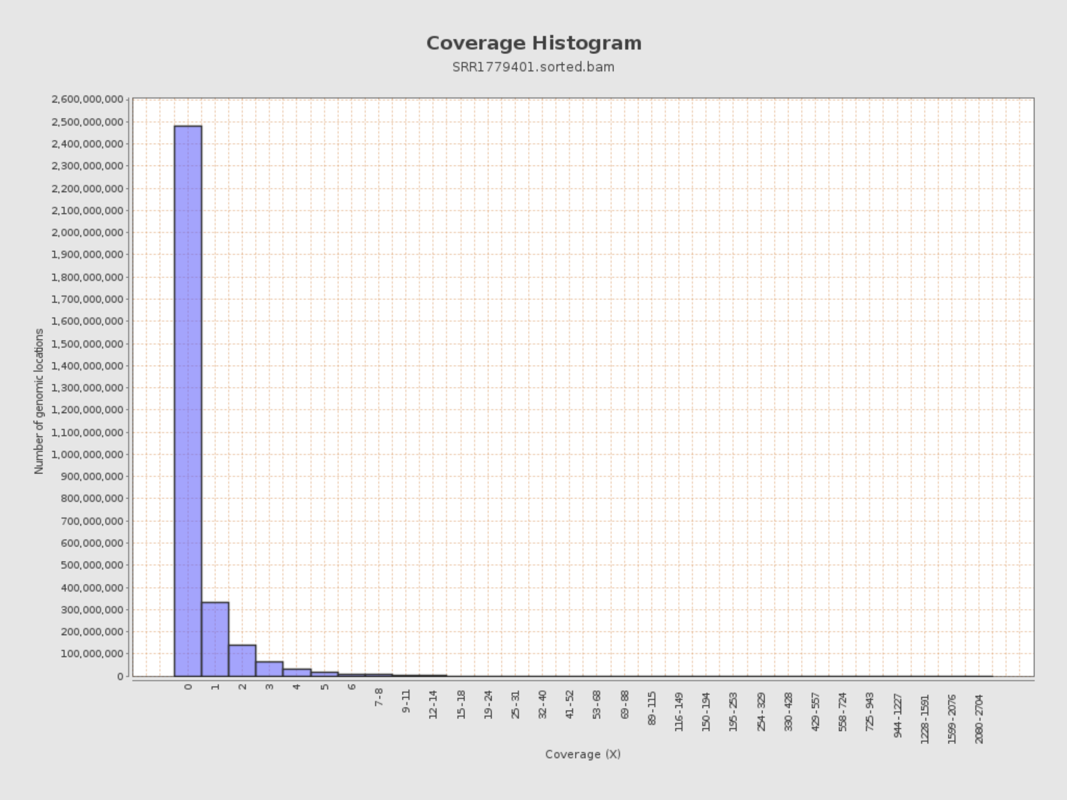
		bases	coverage	deviation
chr1	249250621	72784070	0.292	2.9459
chr2	243199373	89170500	0.3667	1.1295
chr3	198022430	53104065	0.2682	0.8073
chr4	191154276	88212506	0.4615	1.0902
chr5	180915260	115979643	0.6411	1.281
chr6	171115067	37419552	0.2187	0.8041
chr7	159138663	169371859	1.0643	2.319
chr8	146364022	88140202	0.6022	1.3145
chr9	141213431	52748172	0.3735	1.3214
chr10	135534747	29350189	0.2166	3.2897
chr11	135006516	65873641	0.4879	1.256
chr12	133851895	36893509	0.2756	0.8566
chr13	115169878	47496024	0.4124	1.1178
chr14	107349540	31278667	0.2914	0.8911
chr15	102531392	33660369	0.3283	0.9725
chr16	90354753	36128212	0.3998	1.1363
chr17	81195210	33813568	0.4164	1.2117
chr18	78077248	32166686	0.412	1.4577
chr19	59128983	17055085	0.2884	3.0073
chr20	63025520	29124074	0.4621	1.1384
chr21	48129895	19816975	0.4117	1.1517
chr22	51304566	8827517	0.1721	0.6472
chrMT	16571	1190	0.0718	0.4463
chrX	155270560	39841519	0.2566	0.8532

chrY	59373566	3442346	0.058	0.3744

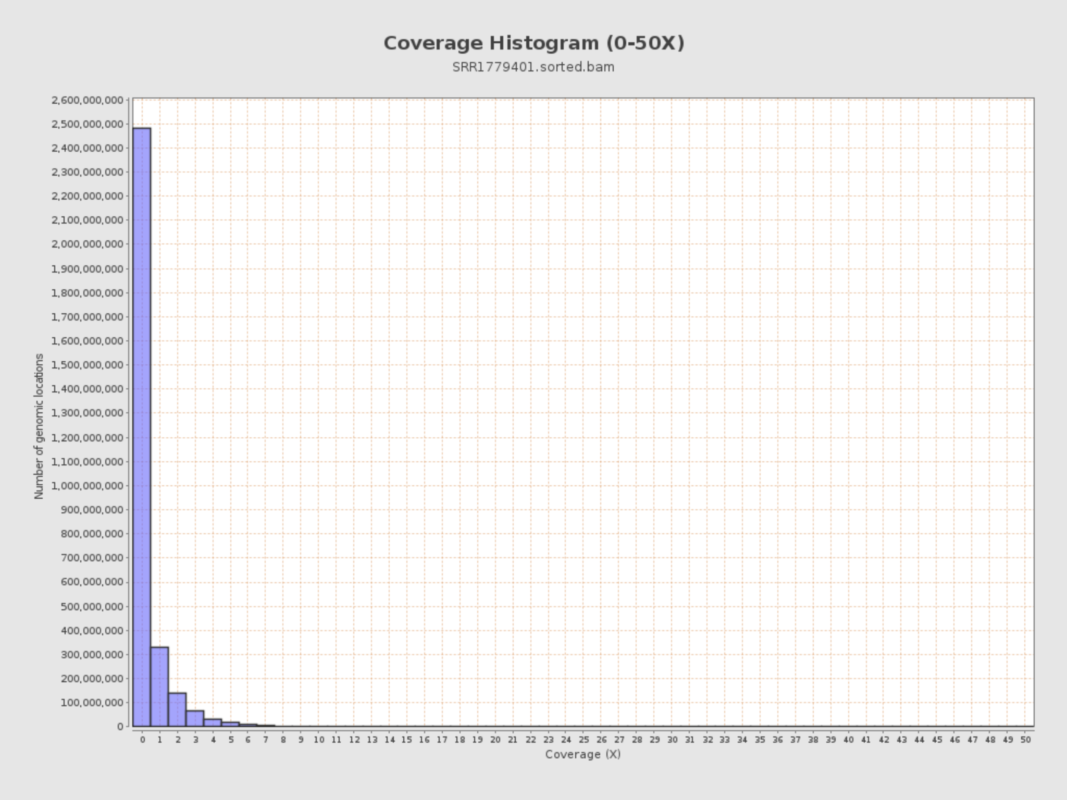
3. Results : Coverage across reference



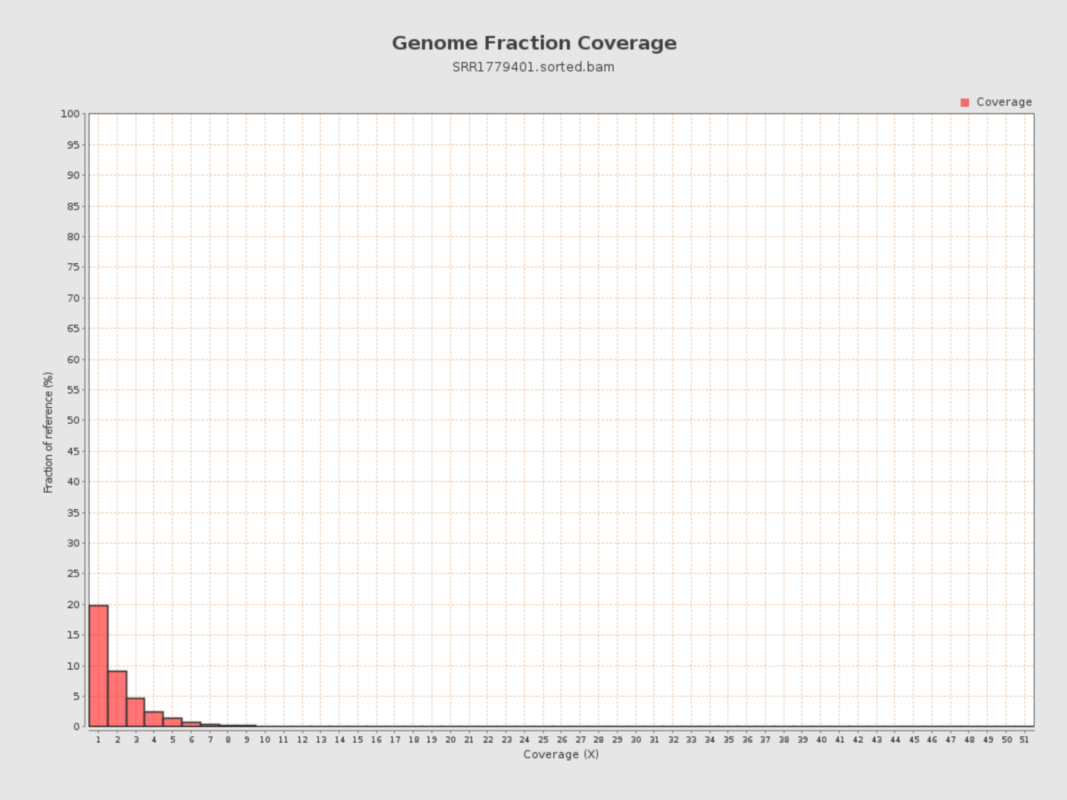
4. Results : Coverage Histogram



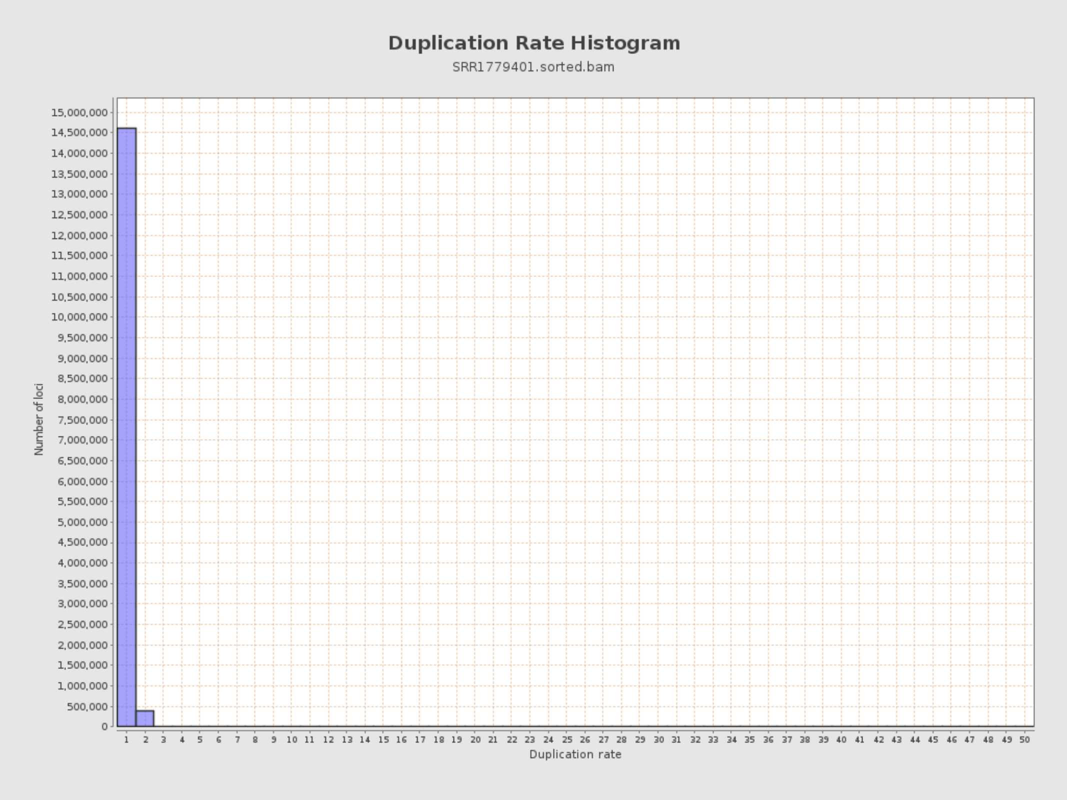
5. Results : Coverage Histogram (0-50X)



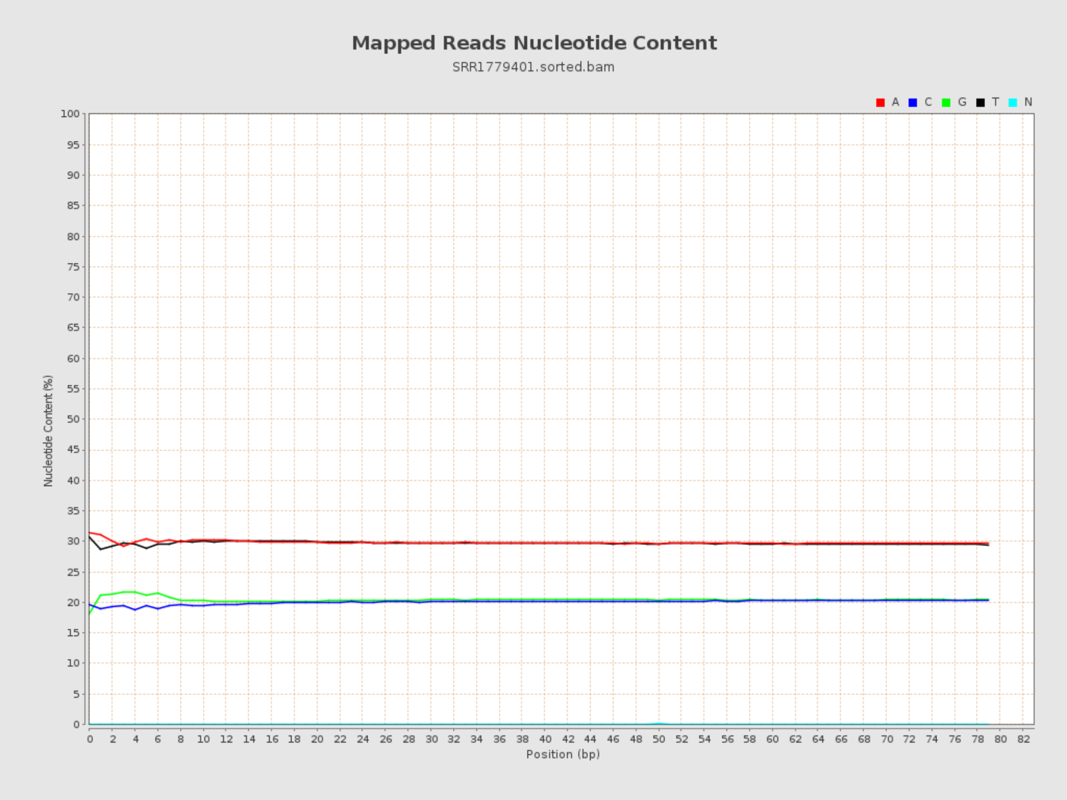
6. Results : Genome Fraction Coverage



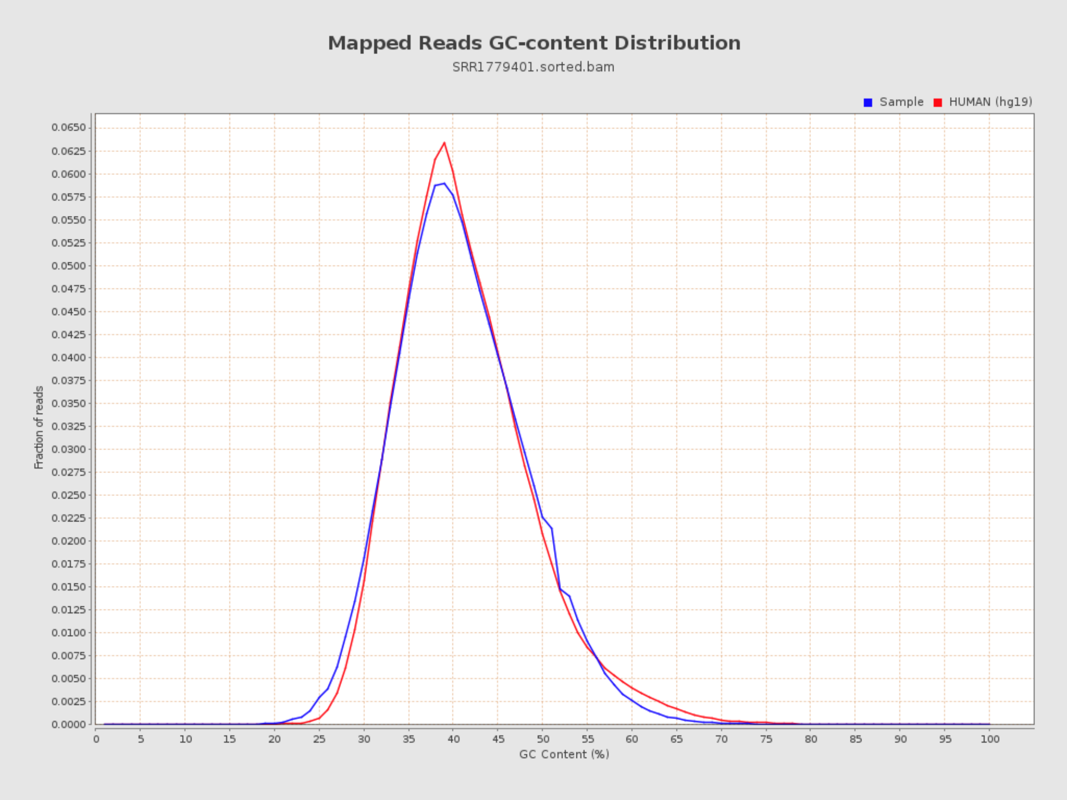
7. Results : Duplication Rate Histogram



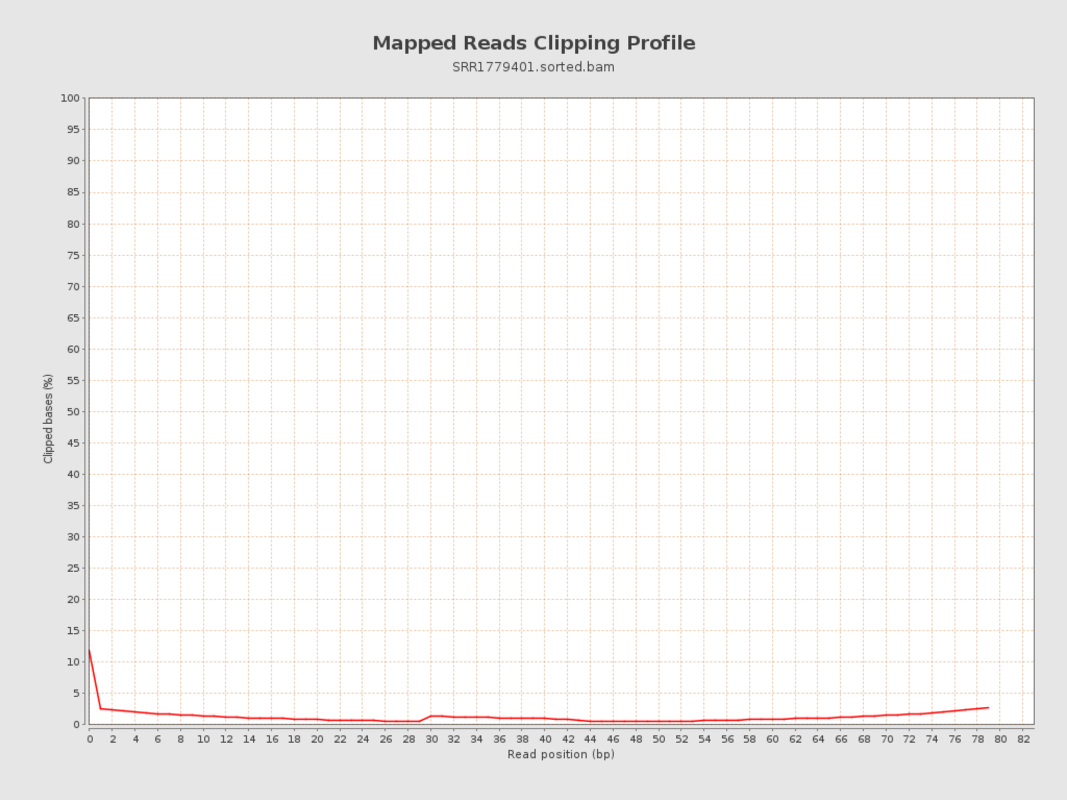
8. Results : Mapped Reads Nucleotide Content



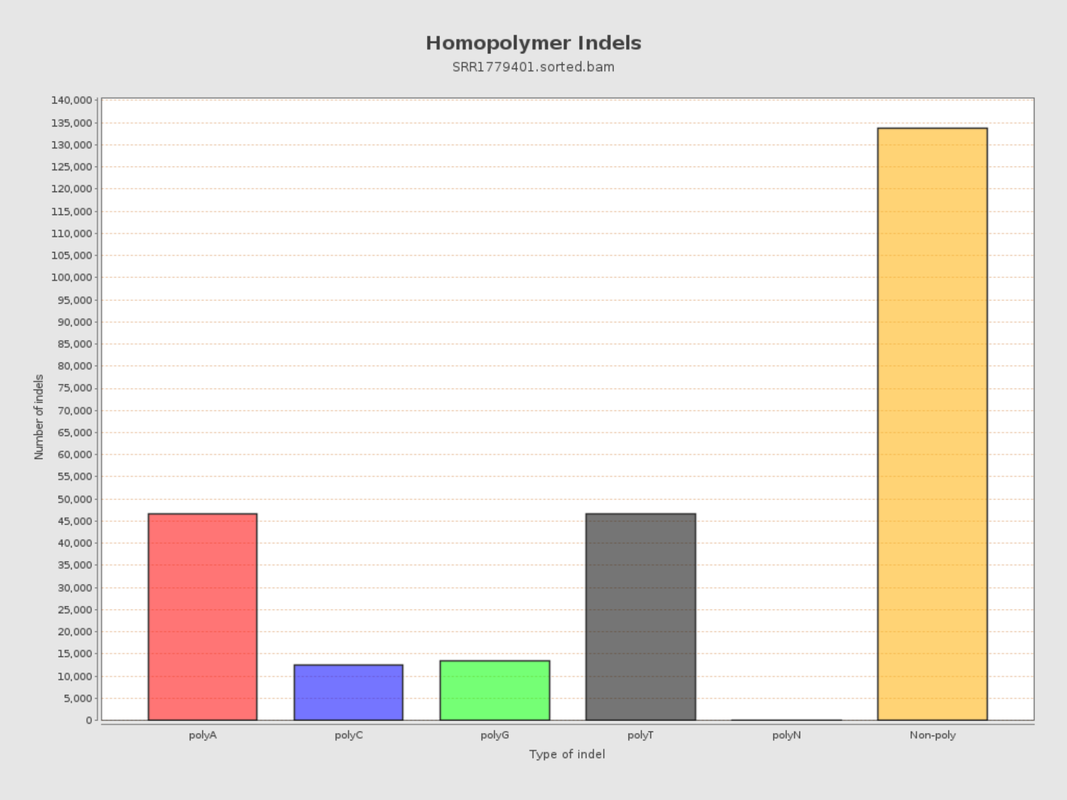
9. Results : Mapped Reads GC-content Distribution



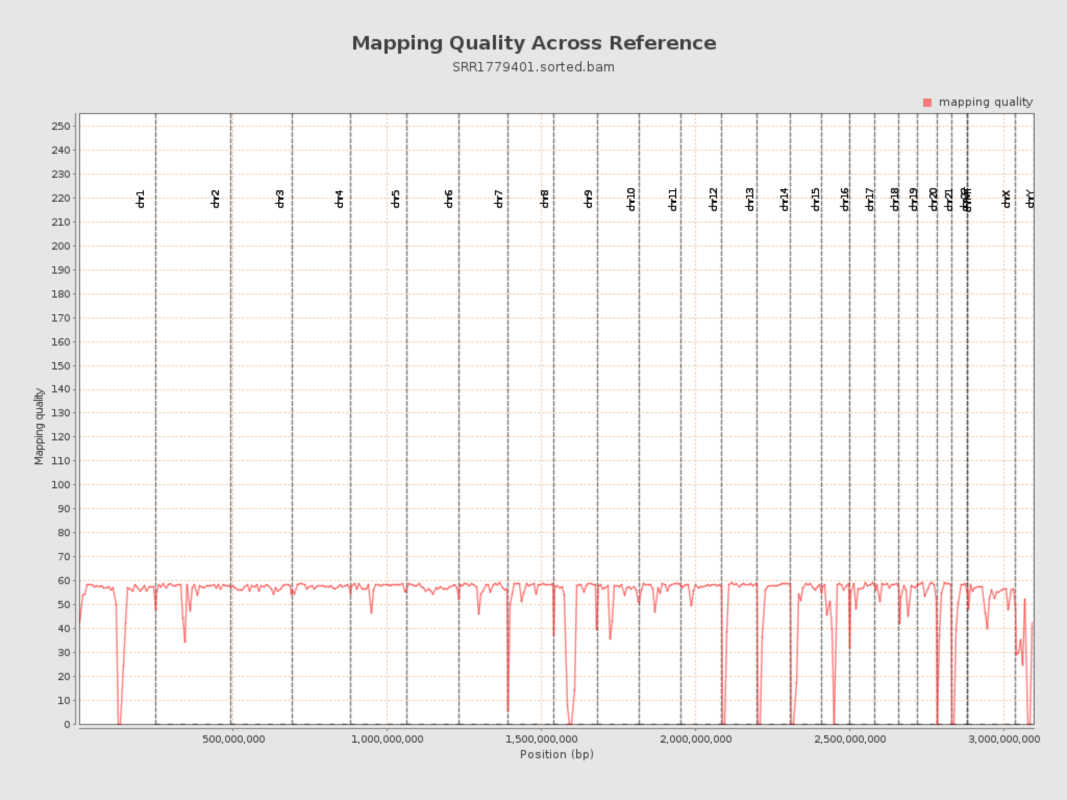
10. Results : Mapped Reads Clipping Profile



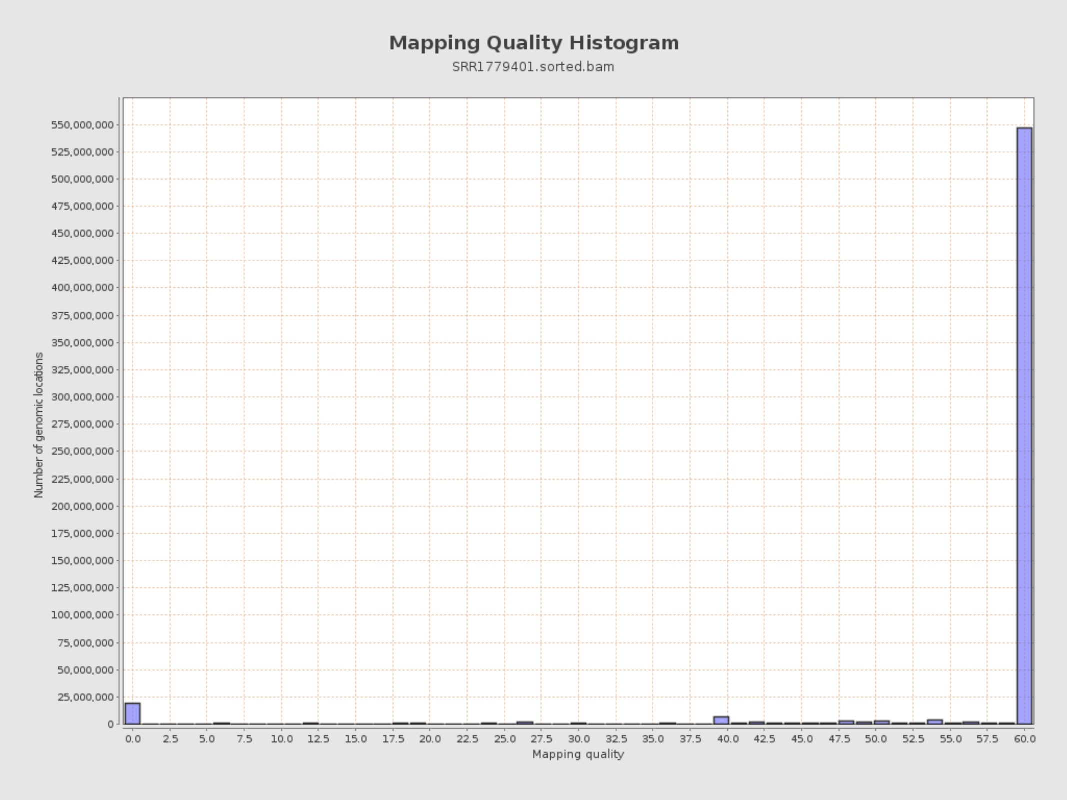
11. Results : Homopolymer Indels



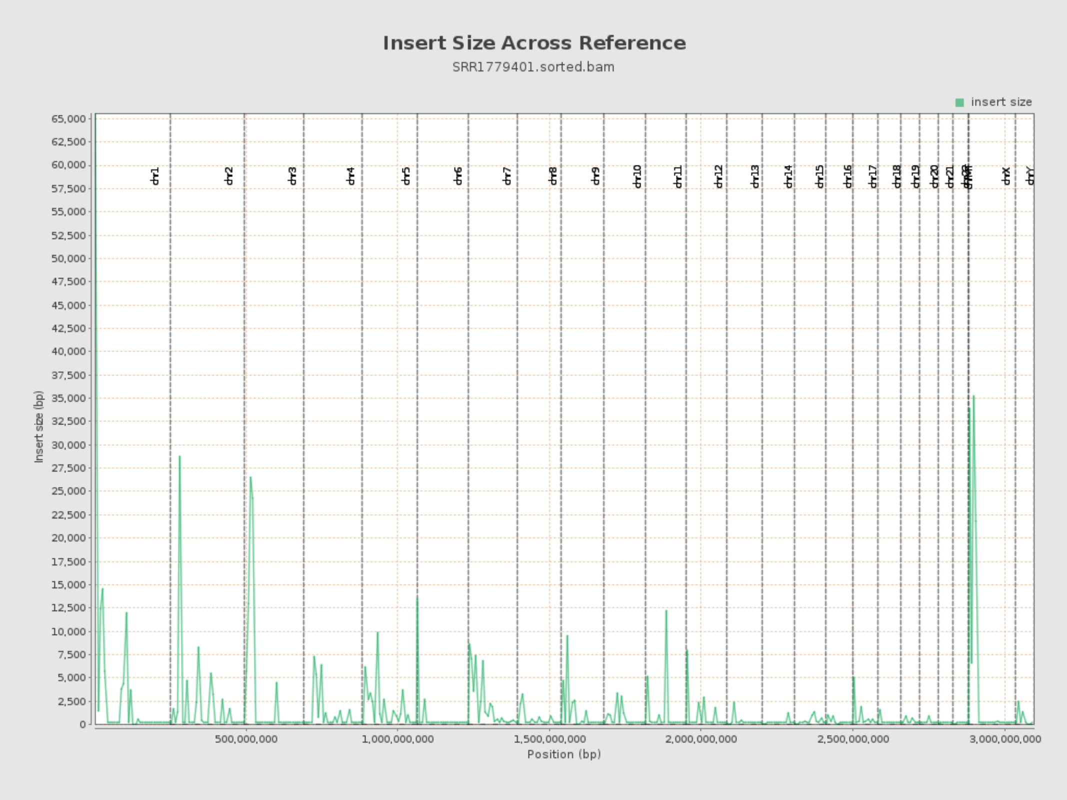
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram