Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 14:35:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779381.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_SRR1779381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779381_1.fastq.gz SRR1779381_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 14:35:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,171,528
Mapped reads	14,334,968 / 94.49%
Unmapped reads	836,560 / 5.51%
Mapped paired reads	14,334,968 / 94.49%
Mapped reads, first in pair	7,244,122 / 47.75%
Mapped reads, second in pair	7,090,846 / 46.74%
Mapped reads, both in pair	14,151,204 / 93.27%
Mapped reads, singletons	183,764 / 1.21%
Secondary alignments	0
Supplementary alignments	57,862 / 0.38%
Read min/max/mean length	30 / 80 / 80.14
Duplicated reads (estimated)	727,908 / 4.8%
Duplication rate	4.73%
Clipped reads	672,863 / 4.44%

2.2. ACGT Content

Number/percentage of A's	343,066,059 / 30.12%
Number/percentage of C's	224,905,832 / 19.75%
Number/percentage of T's	342,459,820 / 30.07%
Number/percentage of G's	228,209,958 / 20.04%
Number/percentage of N's	252,566 / 0.02%

GC Percentage	39.79%

2.3. Coverage

Mean	0.368
Standard Deviation	1.7621

2.4. Mapping Quality

Mean Mapping Quality	52.66

2.5. Insert size

Mean	38,038.81
Standard Deviation	1,836,516.69
P25/Median/P75	136 / 178 / 232

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,788,014
Insertions	100,732
Mapped reads with at least one insertion	0.7%
Deletions	119,807
Mapped reads with at least one deletion	0.83%
Homopolymer indels	47.14%

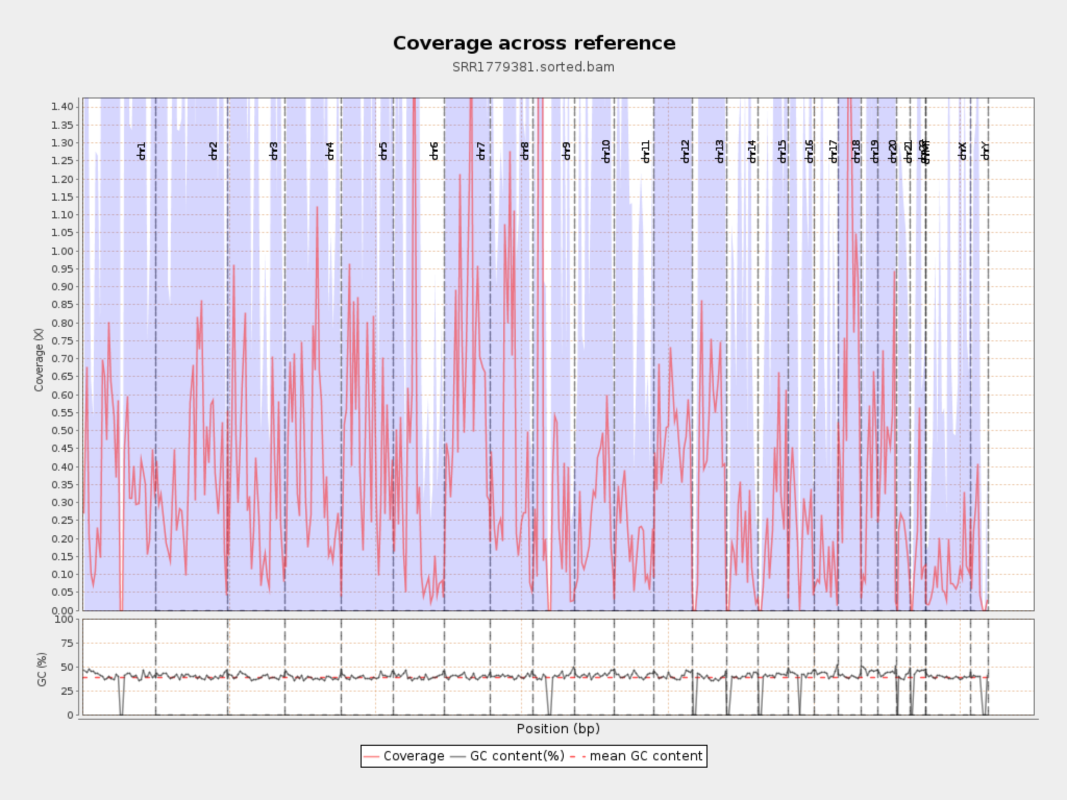
2.7. Chromosome stats

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

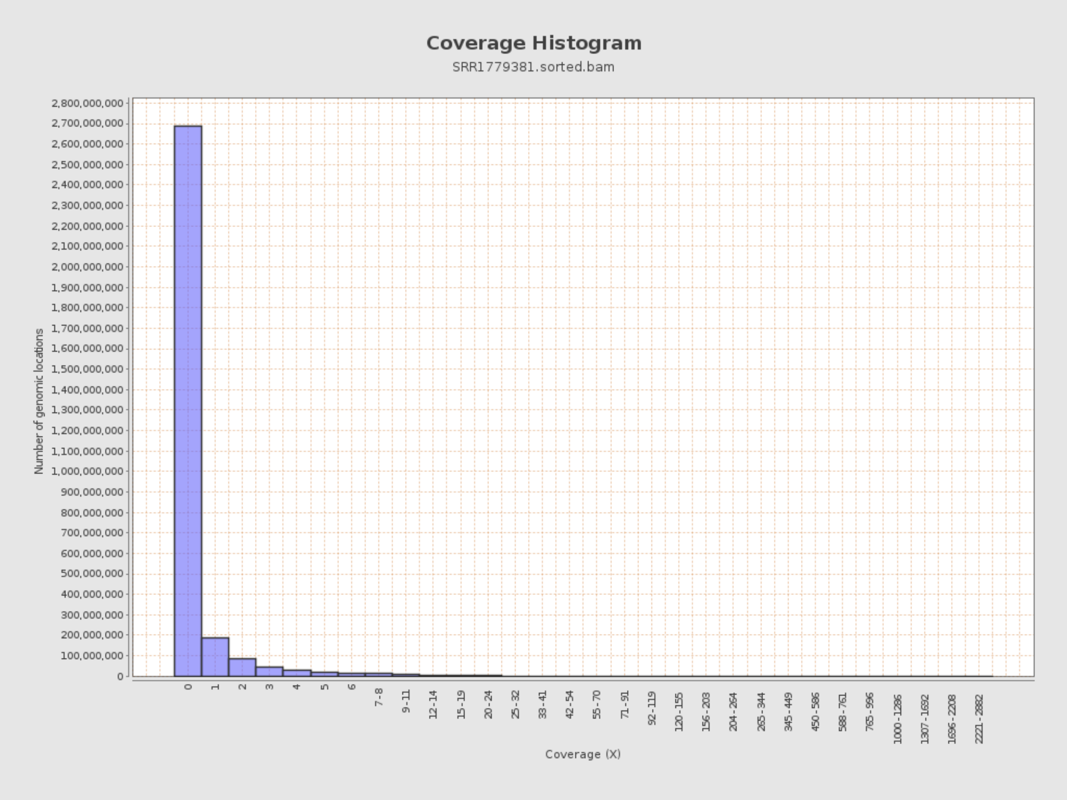
		bases	coverage	deviation
chr1	249250621	89679707	0.3598	3.0939
chr2	243199373	92603665	0.3808	1.4808
chr3	198022430	69359582	0.3503	1.47
chr4	191154276	82751982	0.4329	1.516
chr5	180915260	87316688	0.4826	1.6798
chr6	171115067	50131119	0.293	1.6293
chr7	159138663	108044258	0.6789	2.15
chr8	146364022	64058292	0.4377	1.6815
chr9	141213431	81380325	0.5763	2.8854
chr10	135534747	38074088	0.2809	1.2348
chr11	135006516	26947422	0.1996	0.9268
chr12	133851895	65548869	0.4897	1.6464
chr13	115169878	54276538	0.4713	1.4757
chr14	107349540	16440820	0.1532	0.854
chr15	102531392	27234671	0.2656	1.1293
chr16	90354753	20809775	0.2303	1.0842
chr17	81195210	8982473	0.1106	0.8091
chr18	78077248	62730117	0.8034	2.3822
chr19	59128983	20100001	0.3399	2.1522
chr20	63025520	32005893	0.5078	1.7927
chr21	48129895	8658007	0.1799	0.8047
chr22	51304566	8705176	0.1697	1.0409
chrMT	16571	411	0.0248	0.1555
chrX	155270560	15347177	0.0988	0.8425

chrY	59373566	7957033	0.134	0.7426

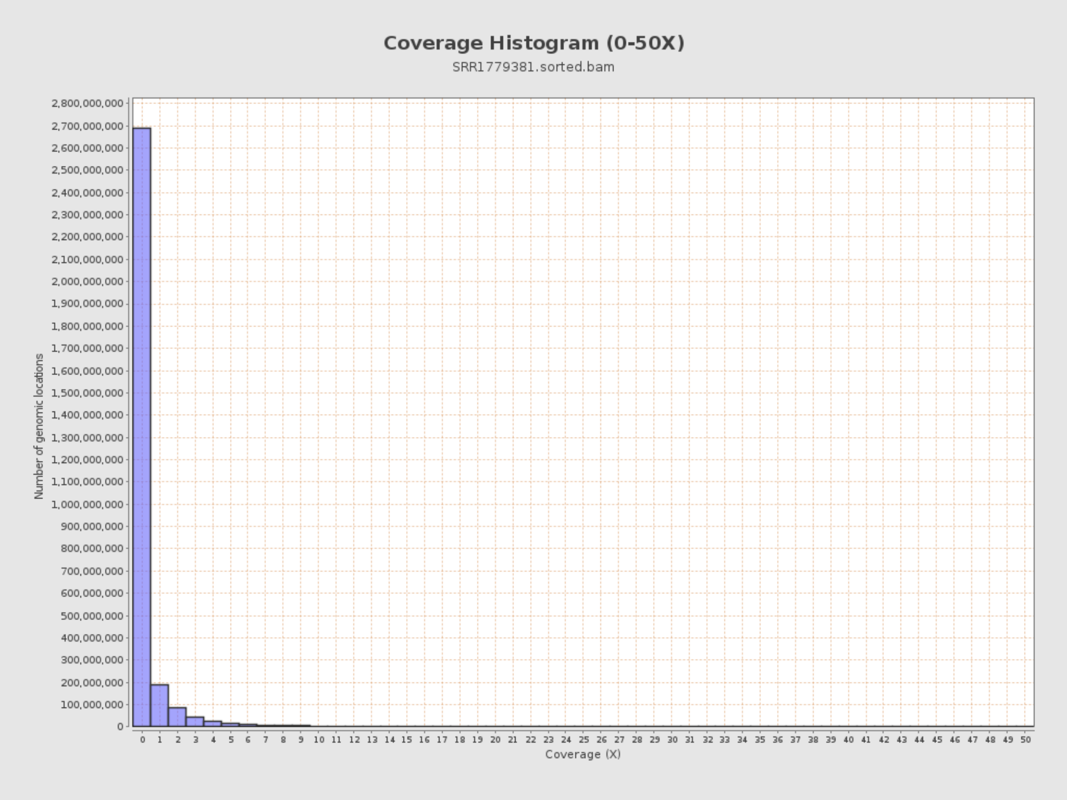
3. Results : Coverage across reference



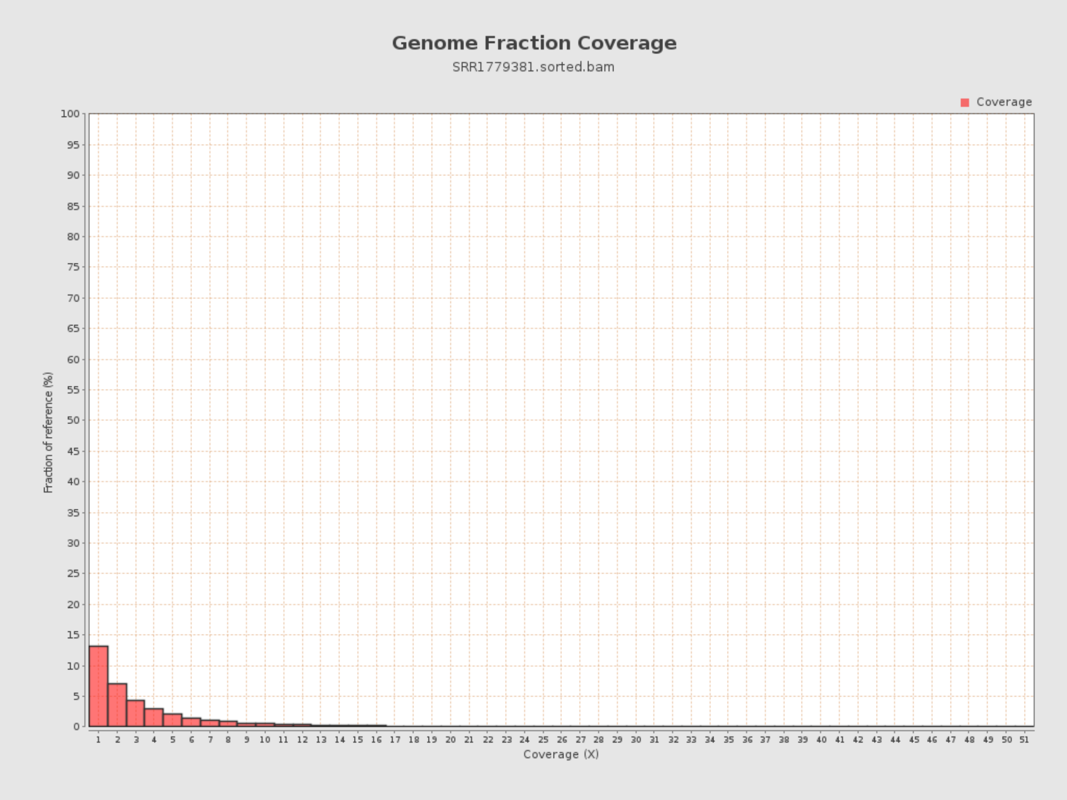
4. Results : Coverage Histogram



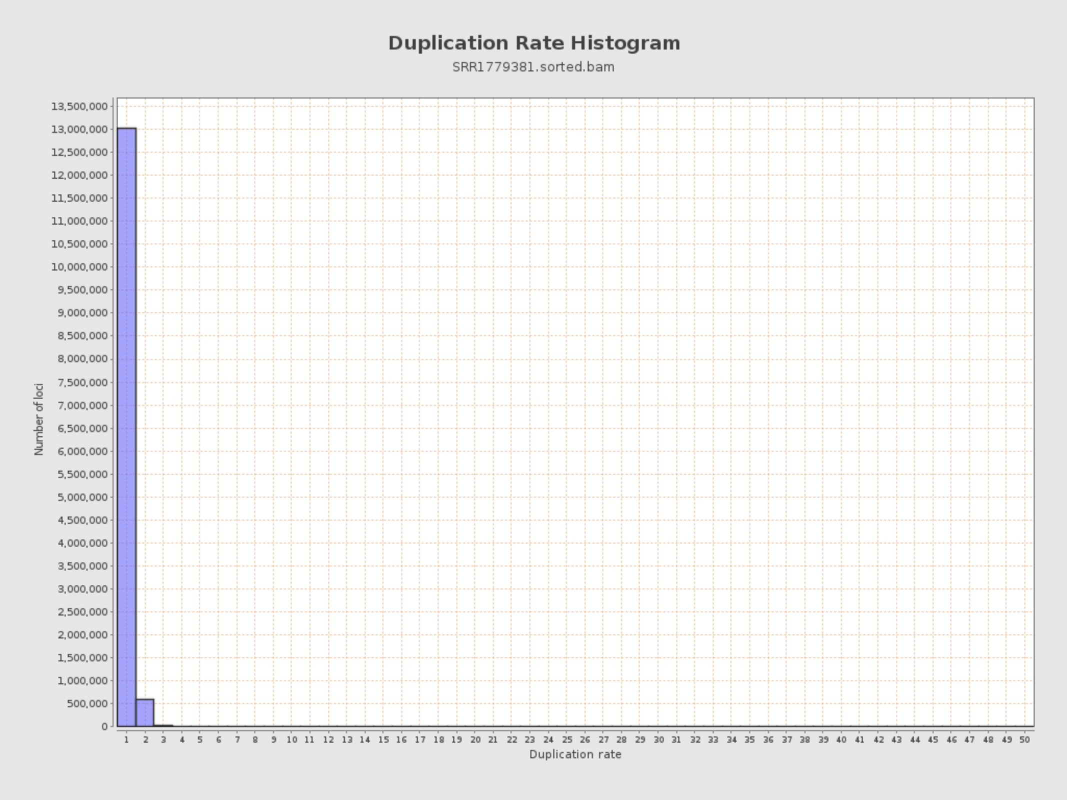
5. Results : Coverage Histogram (0-50X)



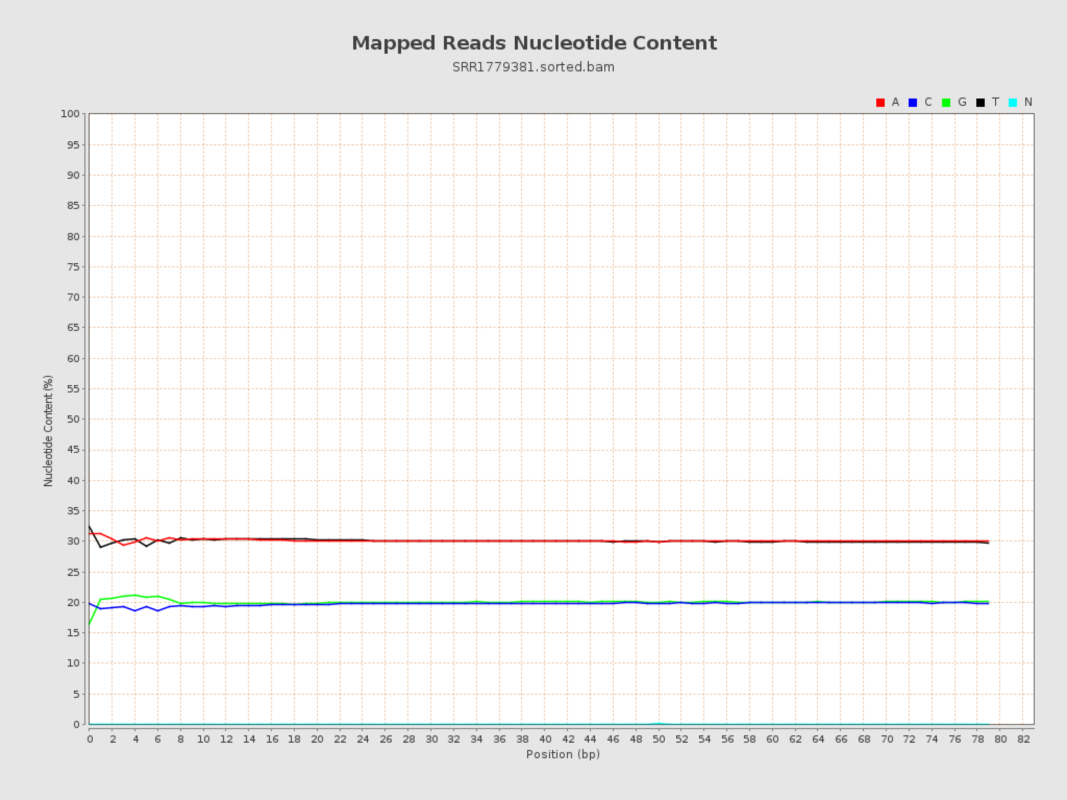
6. Results : Genome Fraction Coverage



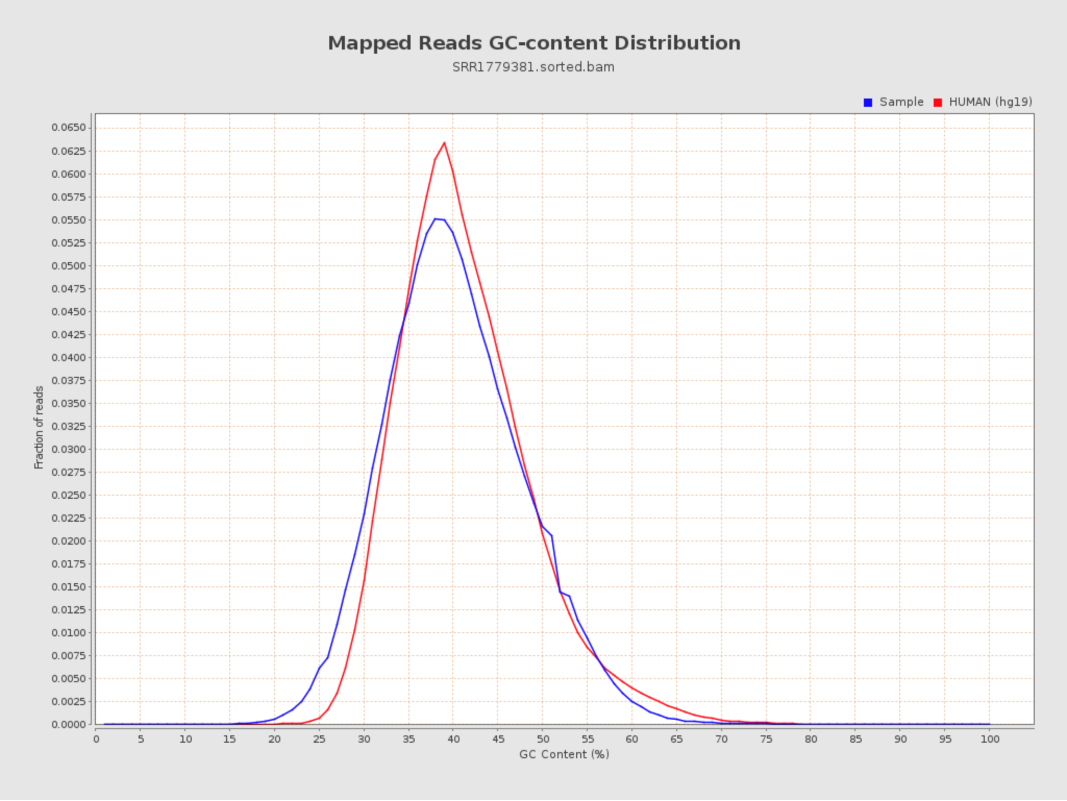
7. Results : Duplication Rate Histogram



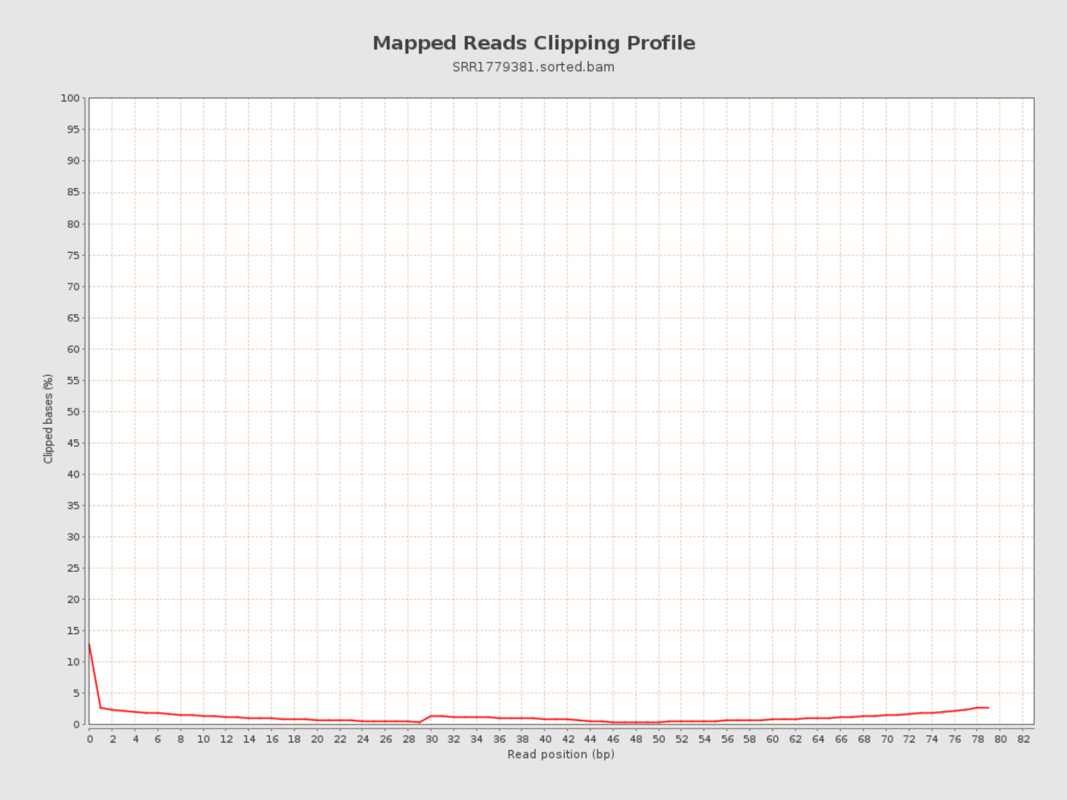
8. Results : Mapped Reads Nucleotide Content



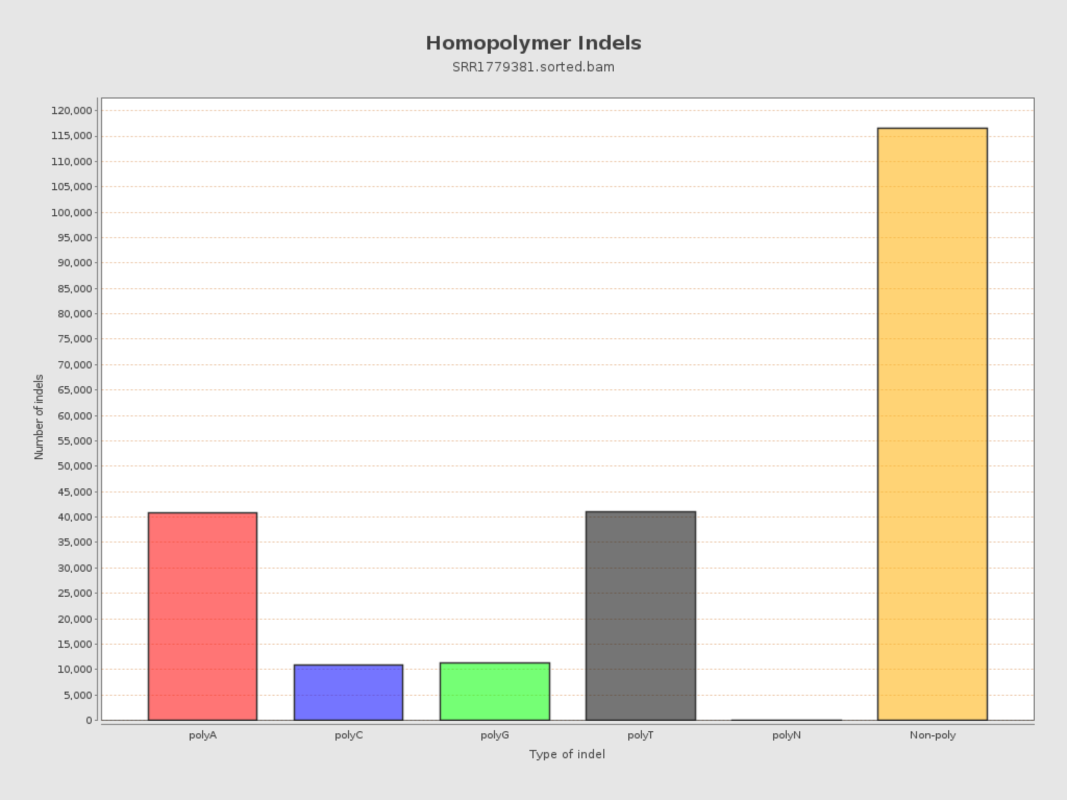
9. Results : Mapped Reads GC-content Distribution



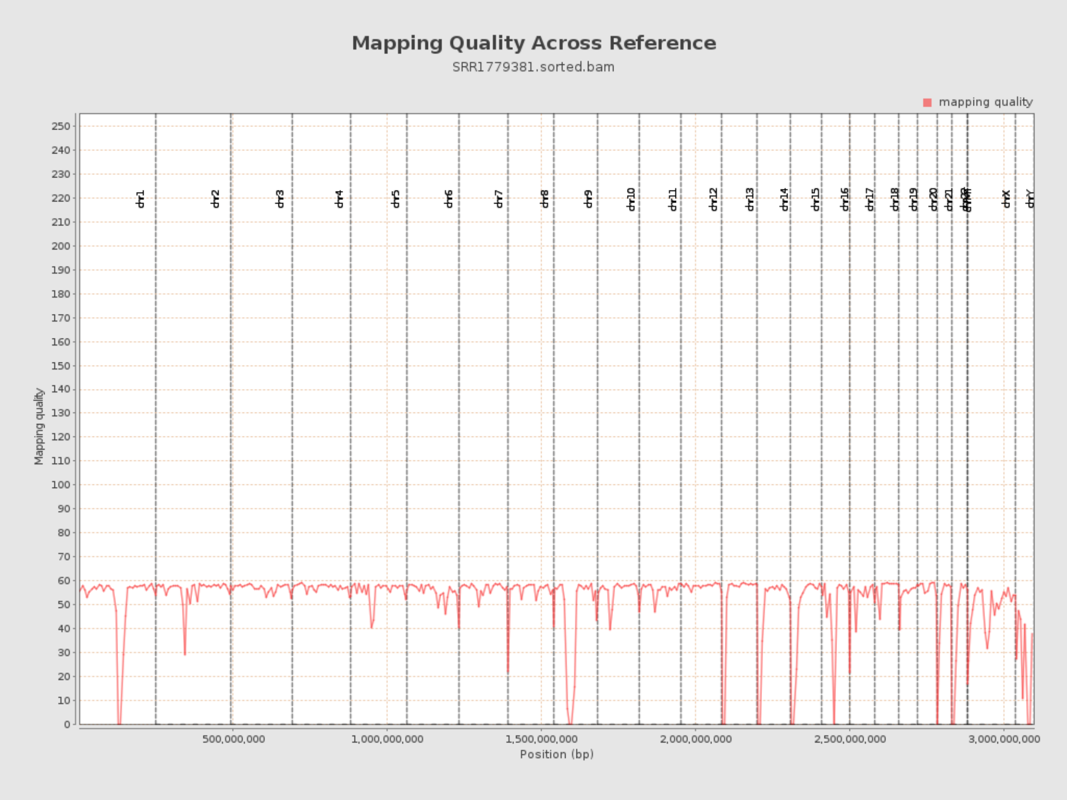
10. Results : Mapped Reads Clipping Profile



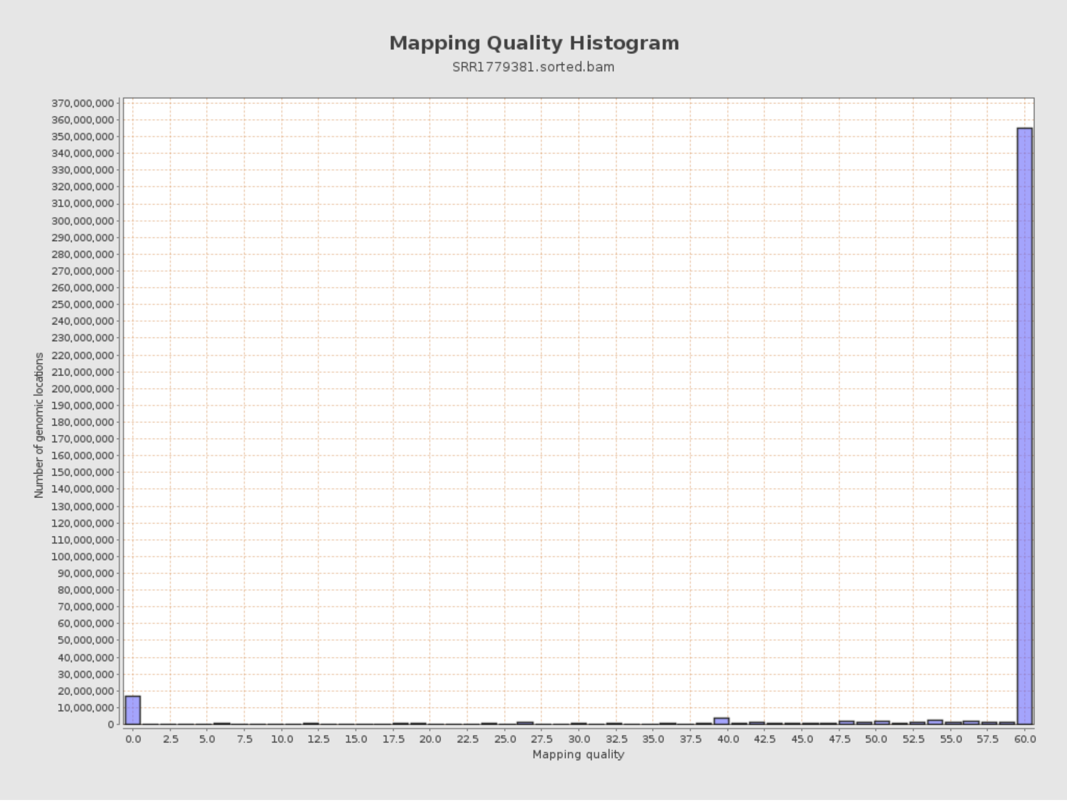
11. Results : Homopolymer Indels



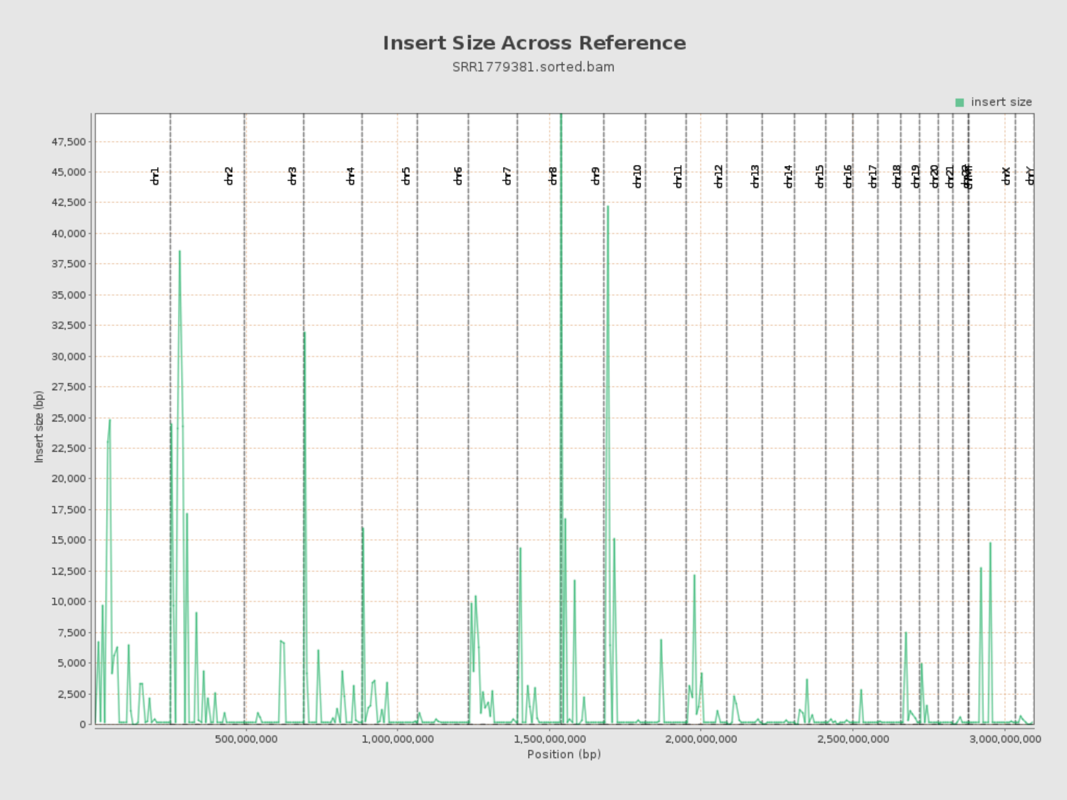
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram