Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 14:19:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779380.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_SRR1779380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779380_1.fastq.gz SRR1779380_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 14:19:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,665,860
Mapped reads	12,989,894 / 95.05%
Unmapped reads	675,966 / 4.95%
Mapped paired reads	12,989,894 / 95.05%
Mapped reads, first in pair	6,545,060 / 47.89%
Mapped reads, second in pair	6,444,834 / 47.16%
Mapped reads, both in pair	12,856,326 / 94.08%
Mapped reads, singletons	133,568 / 0.98%
Secondary alignments	0
Supplementary alignments	58,916 / 0.43%
Read min/max/mean length	30 / 80 / 80.16
Duplicated reads (estimated)	870,388 / 6.37%
Duplication rate	6.17%
Clipped reads	575,960 / 4.21%

2.2. ACGT Content

Number/percentage of A's	311,475,849 / 30.18%
Number/percentage of C's	203,117,020 / 19.68%
Number/percentage of T's	310,327,053 / 30.07%
Number/percentage of G's	206,995,443 / 20.05%
Number/percentage of N's	229,806 / 0.02%

GC Percentage	39.73%

2.3. Coverage

Mean	0.3335
Standard Deviation	1.8924

2.4. Mapping Quality

Mean Mapping Quality	52.31

2.5. Insert size

Mean	48,349.64
Standard Deviation	2,093,346.25
P25/Median/P75	176 / 226 / 281

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	3,605,835
Insertions	100,265
Mapped reads with at least one insertion	0.76%
Deletions	115,823
Mapped reads with at least one deletion	0.88%
Homopolymer indels	47.62%

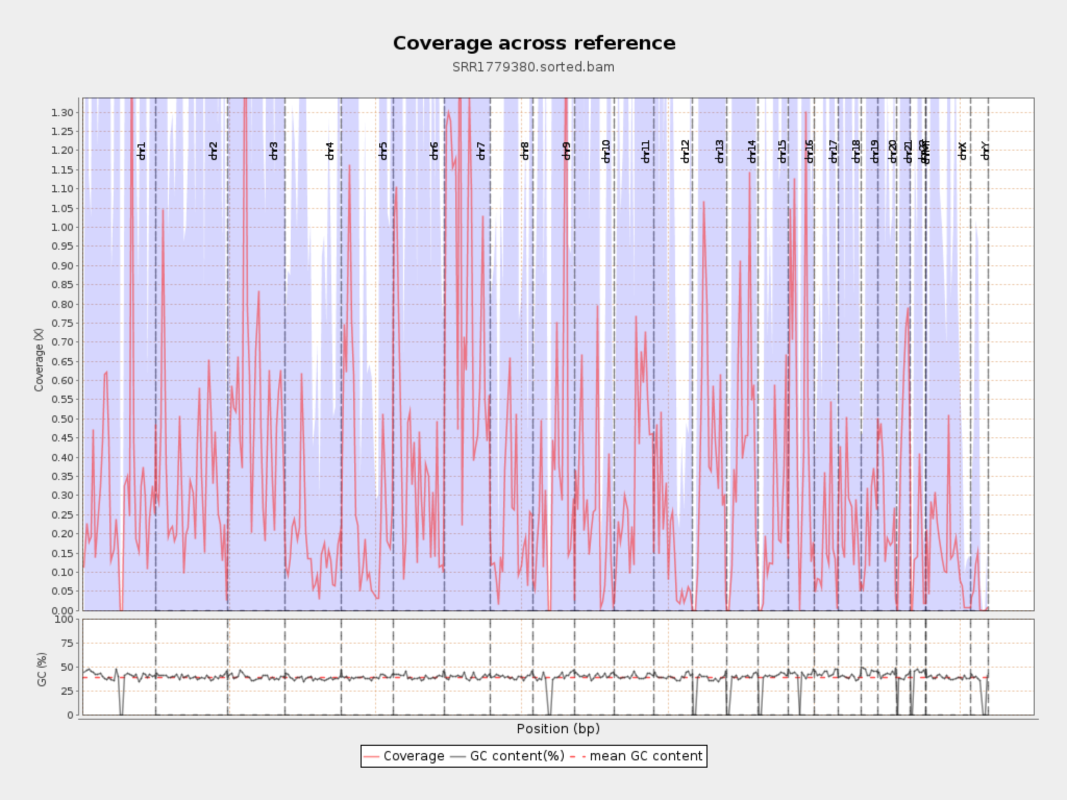
2.7. Chromosome stats

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

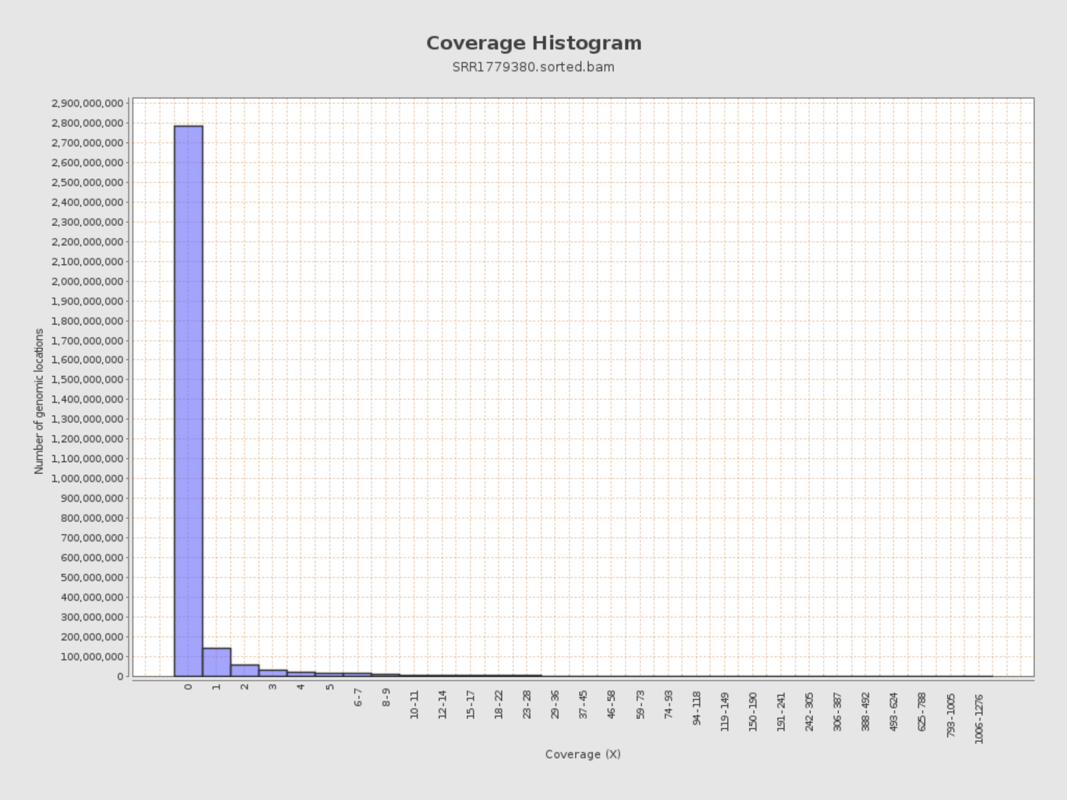
		bases	coverage	deviation
chr1	249250621	77488448	0.3109	2.2049
chr2	243199373	80238031	0.3299	1.6099
chr3	198022430	104220874	0.5263	2.438
chr4	191154276	32308488	0.169	0.9852
chr5	180915260	57142169	0.3159	1.9437
chr6	171115067	64540811	0.3772	1.9111
chr7	159138663	134266418	0.8437	2.8733
chr8	146364022	33360511	0.2279	1.5645
chr9	141213431	53133317	0.3763	1.9585
chr10	135534747	36728672	0.271	2.3547
chr11	135006516	49932484	0.3699	1.7084
chr12	133851895	23640201	0.1766	1.2
chr13	115169878	47864312	0.4156	2.0302
chr14	107349540	47506321	0.4425	2.2572
chr15	102531392	23306119	0.2273	1.2975
chr16	90354753	46801668	0.518	2.5846
chr17	81195210	13497568	0.1662	1.2153
chr18	78077248	19757363	0.253	1.7495
chr19	59128983	13377034	0.2262	1.9348
chr20	63025520	16692499	0.2649	1.4473
chr21	48129895	22746546	0.4726	1.966
chr22	51304566	7347631	0.1432	1.1831
chrMT	16571	2178	0.1314	0.5261
chrX	155270560	23708742	0.1527	1.0061

chrY	59373566	2778509	0.0468	0.4705

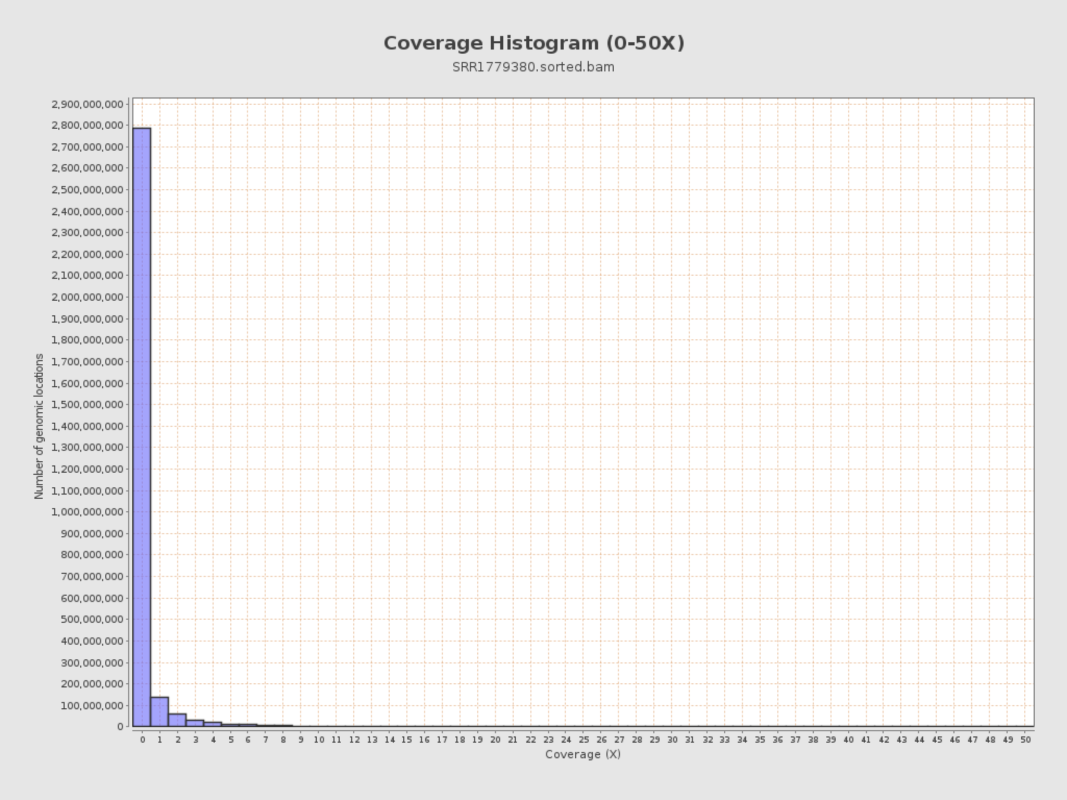
3. Results : Coverage across reference



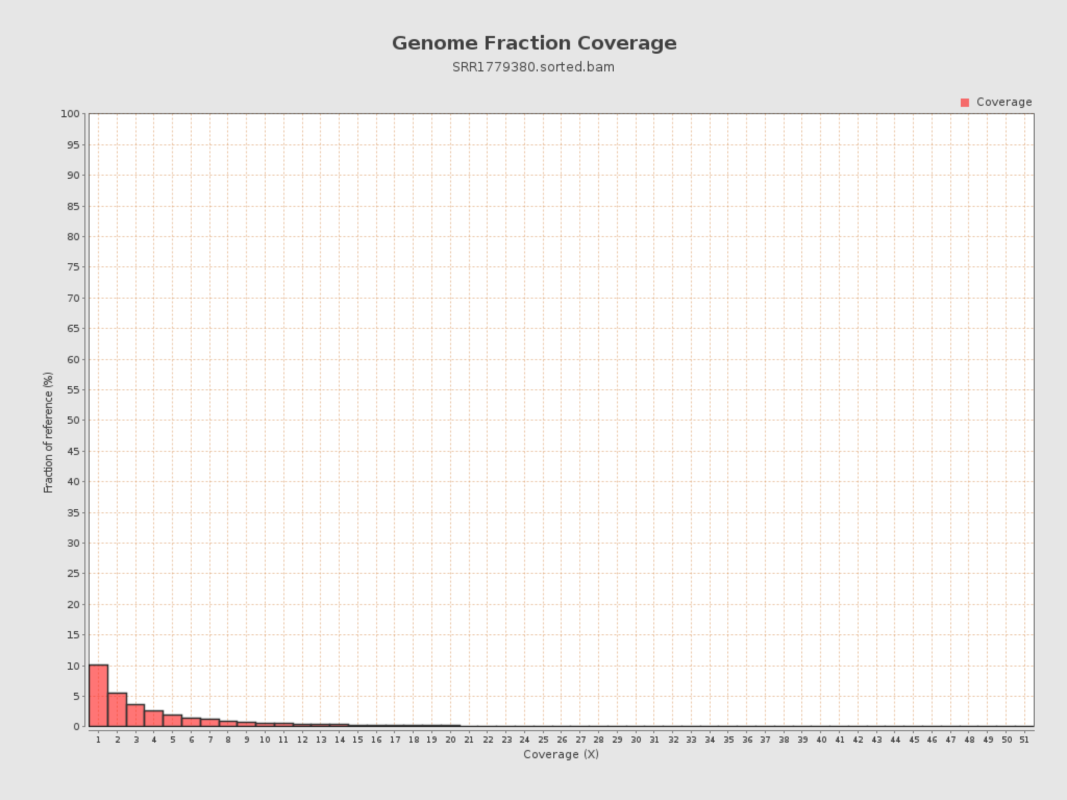
4. Results : Coverage Histogram



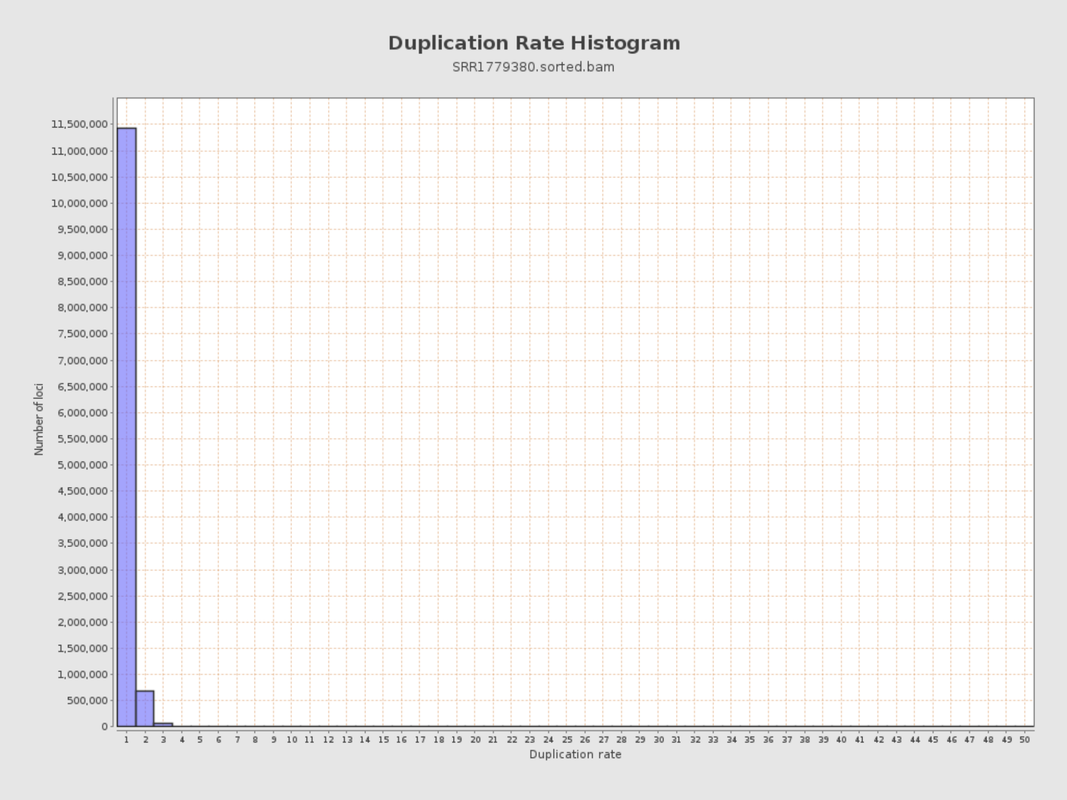
5. Results : Coverage Histogram (0-50X)



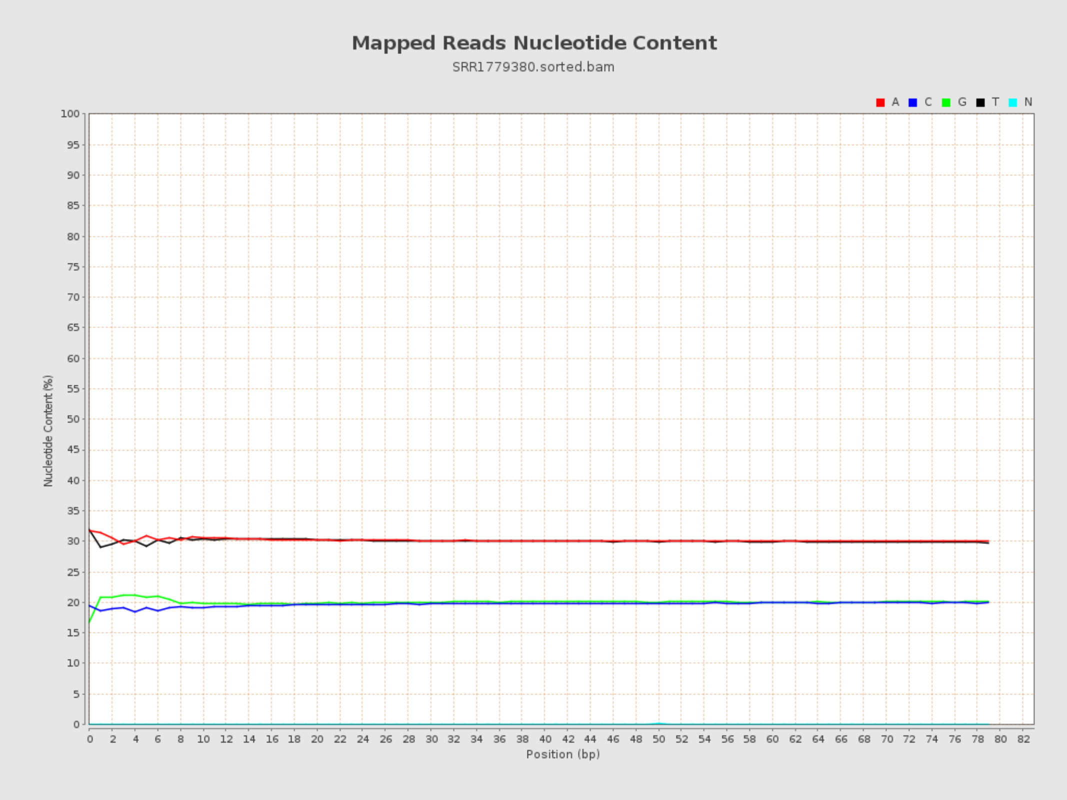
6. Results : Genome Fraction Coverage



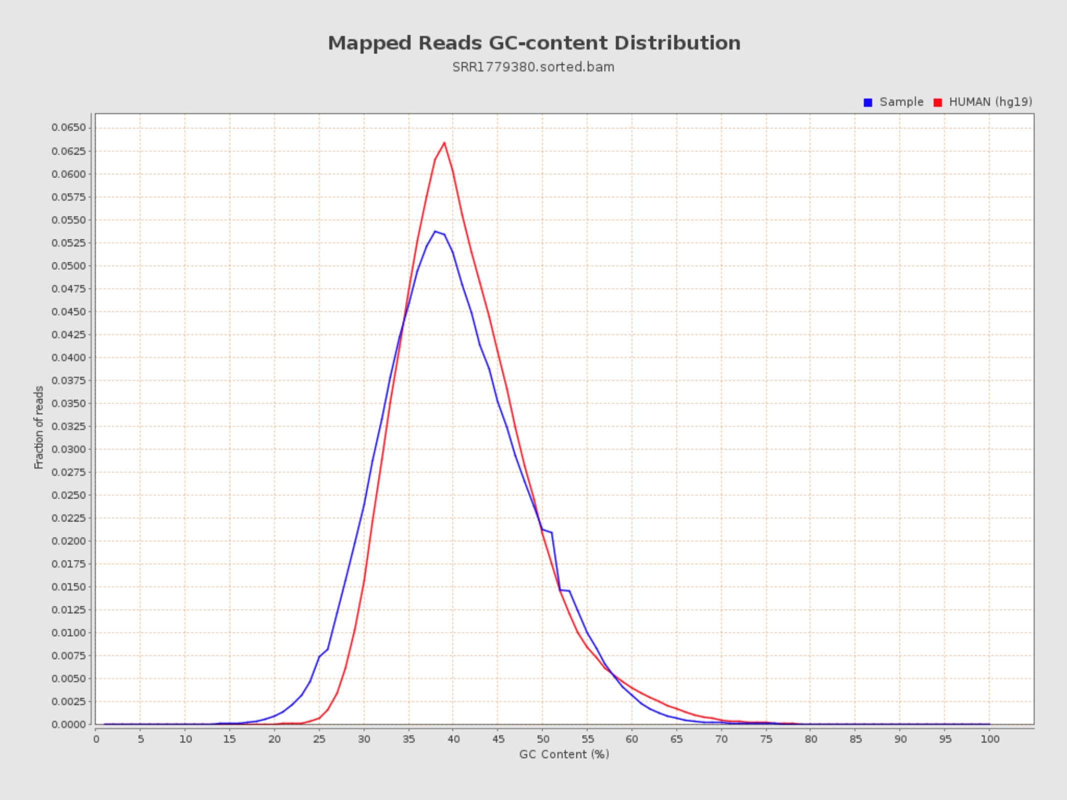
7. Results : Duplication Rate Histogram



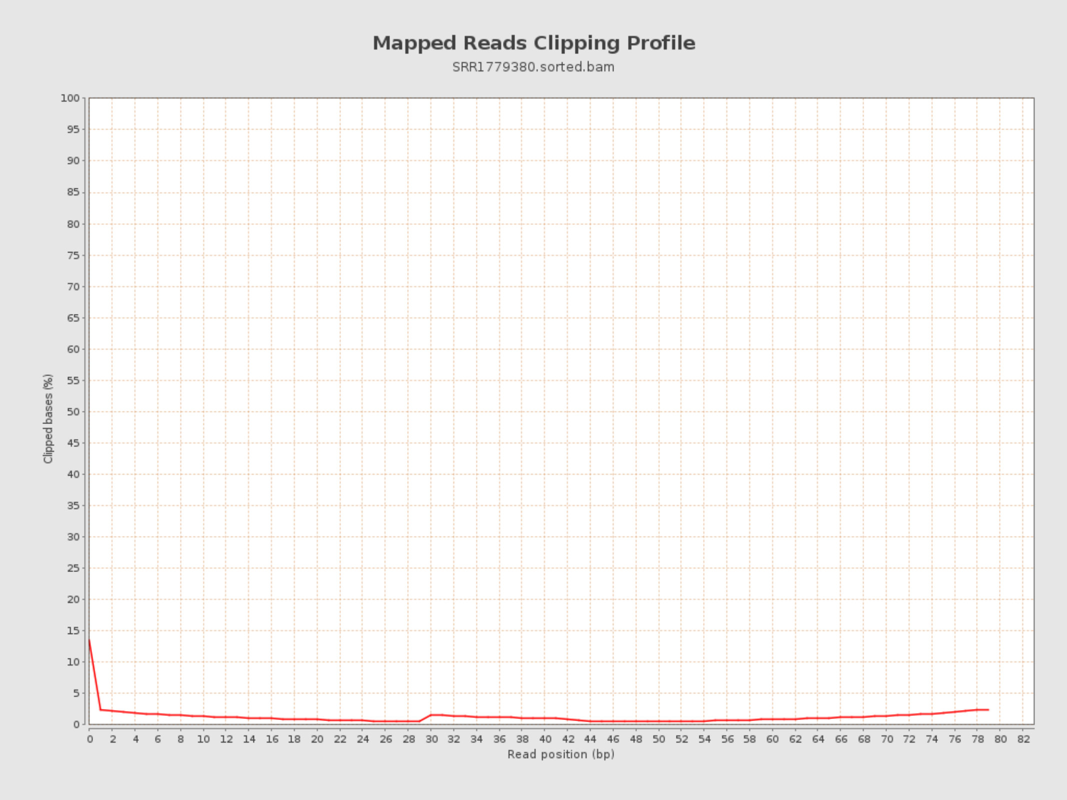
8. Results : Mapped Reads Nucleotide Content



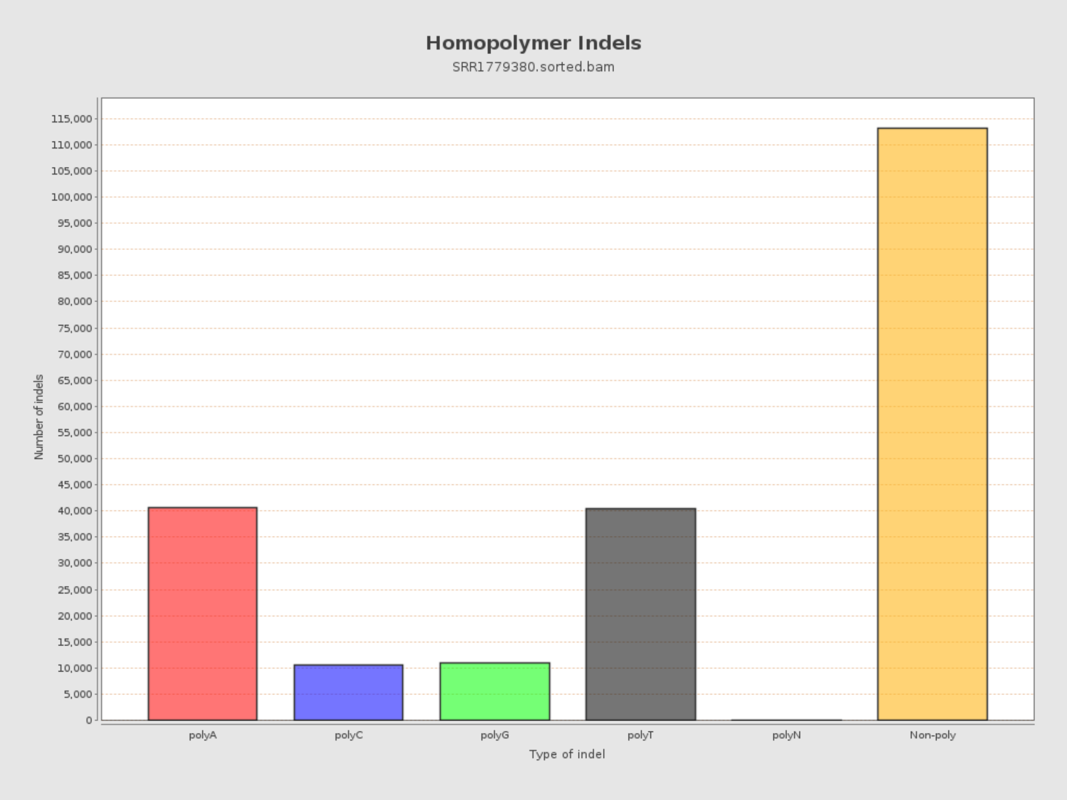
9. Results : Mapped Reads GC-content Distribution



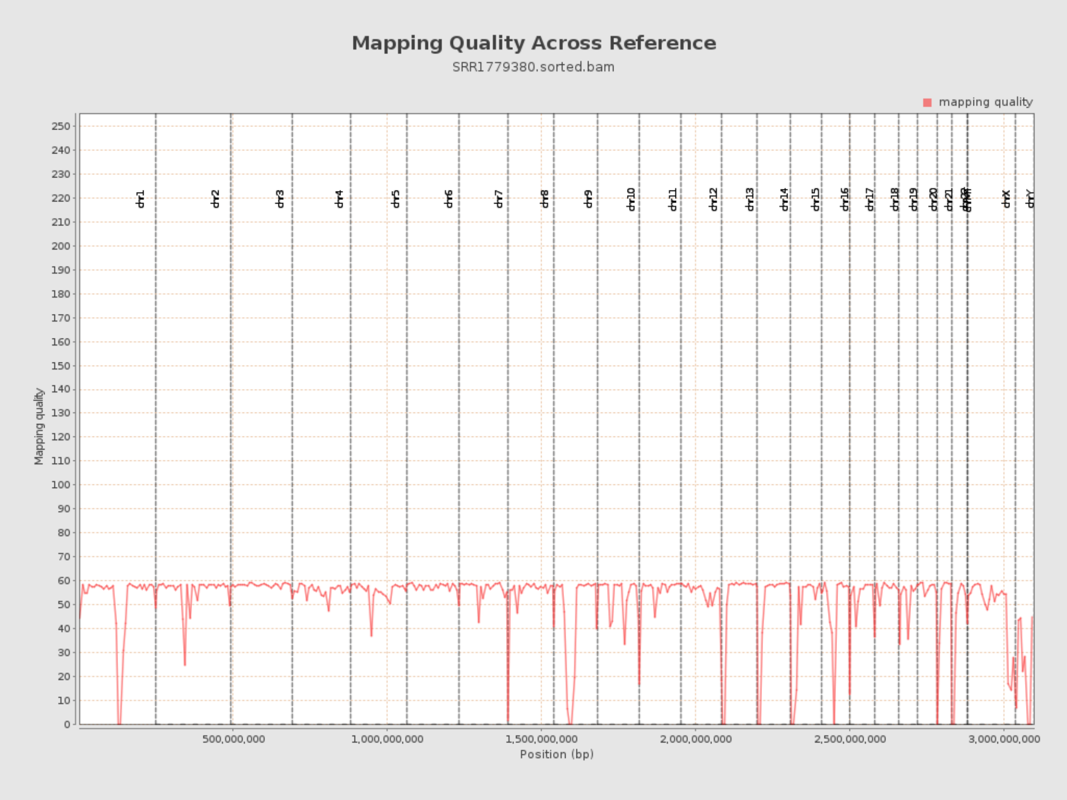
10. Results : Mapped Reads Clipping Profile



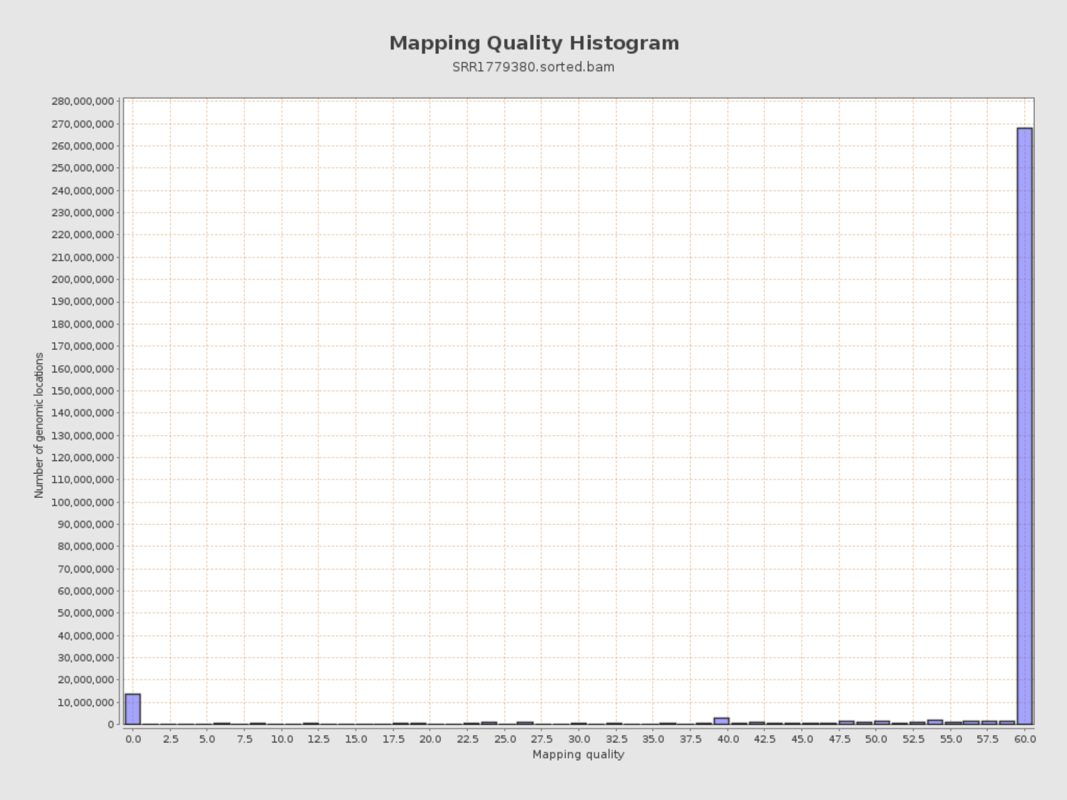
11. Results : Homopolymer Indels



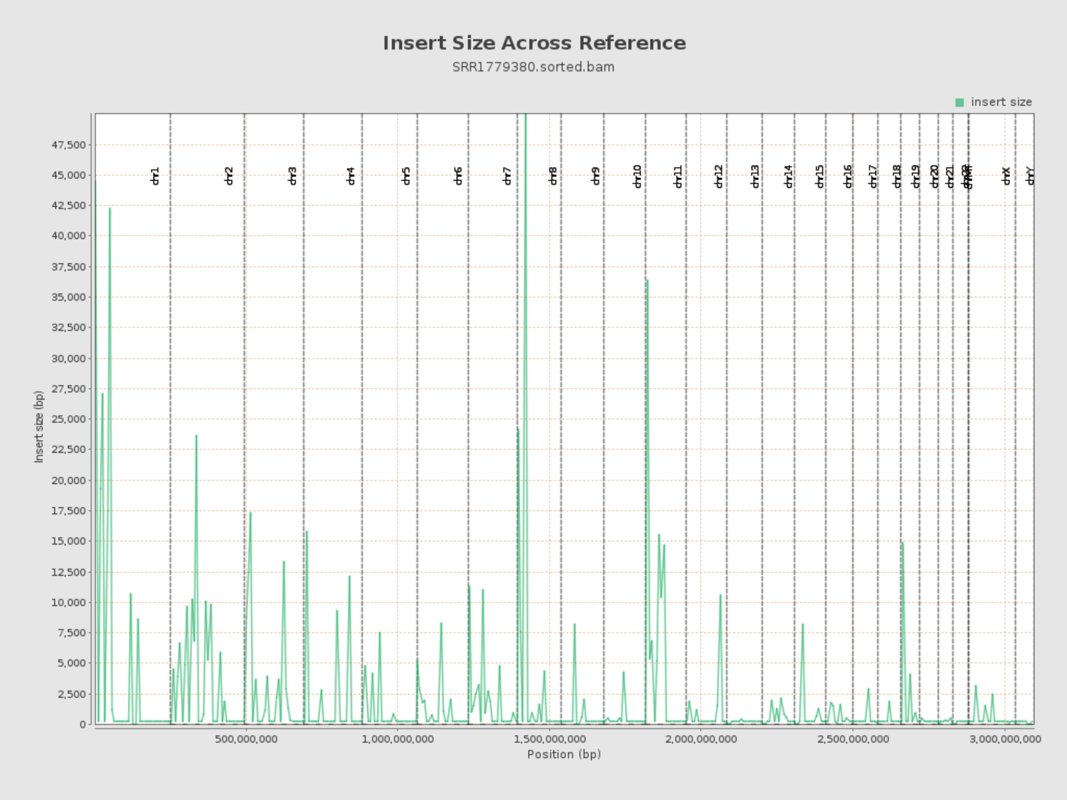
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram