Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779285.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_SRR1779285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779285_1.fastq.gz SRR1779285_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:26:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,465,932
Mapped reads	10,116,366 / 96.66%
Unmapped reads	349,566 / 3.34%
Mapped paired reads	10,116,366 / 96.66%
Mapped reads, first in pair	5,093,351 / 48.67%
Mapped reads, second in pair	5,023,015 / 47.99%
Mapped reads, both in pair	10,030,976 / 95.84%
Mapped reads, singletons	85,390 / 0.82%
Secondary alignments	0
Supplementary alignments	25,127 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	219,982 / 2.1%
Duplication rate	2%
Clipped reads	328,350 / 3.14%

2.2. ACGT Content

Number/percentage of A's	248,064,948 / 30.82%
Number/percentage of C's	153,921,752 / 19.12%
Number/percentage of T's	245,932,385 / 30.55%
Number/percentage of G's	156,927,997 / 19.49%
Number/percentage of N's	153,427 / 0.02%

GC Percentage	38.61%

2.3. Coverage

Mean	0.2601
Standard Deviation	1.0441

2.4. Mapping Quality

Mean Mapping Quality	53.01

2.5. Insert size

Mean	47,913.01
Standard Deviation	2,095,287.57
P25/Median/P75	147 / 194 / 261

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	2,984,661
Insertions	58,648
Mapped reads with at least one insertion	0.57%
Deletions	74,885
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.46%

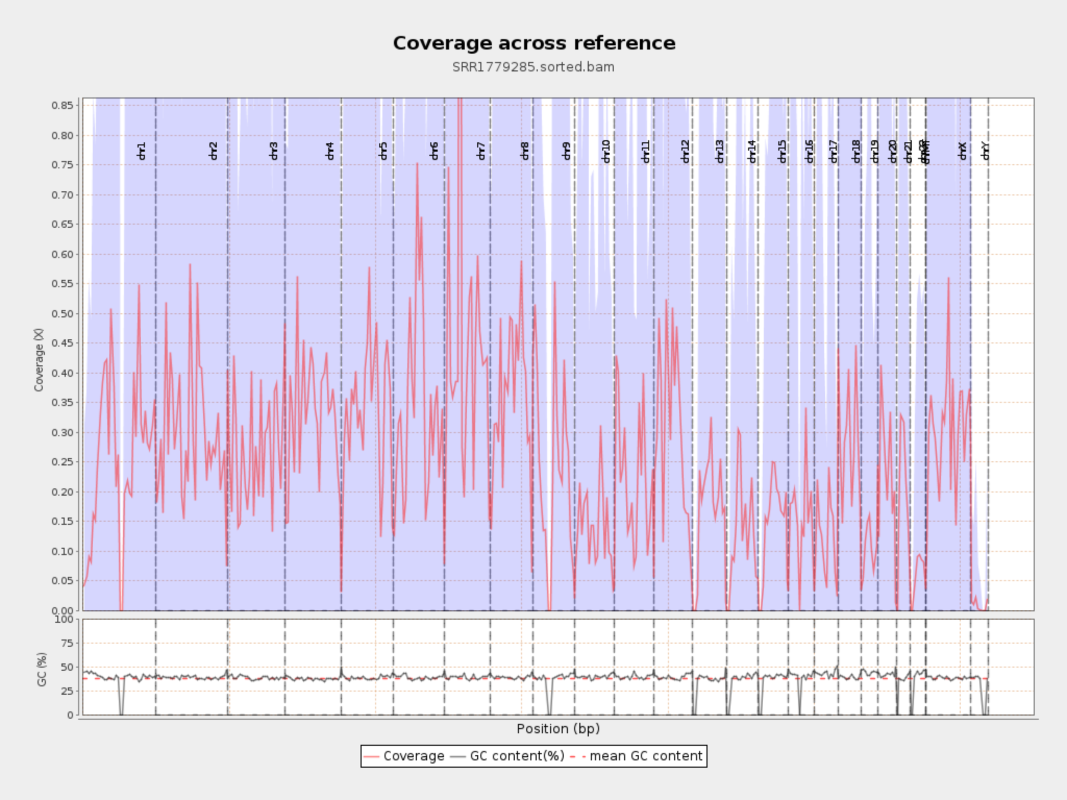
2.7. Chromosome stats

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

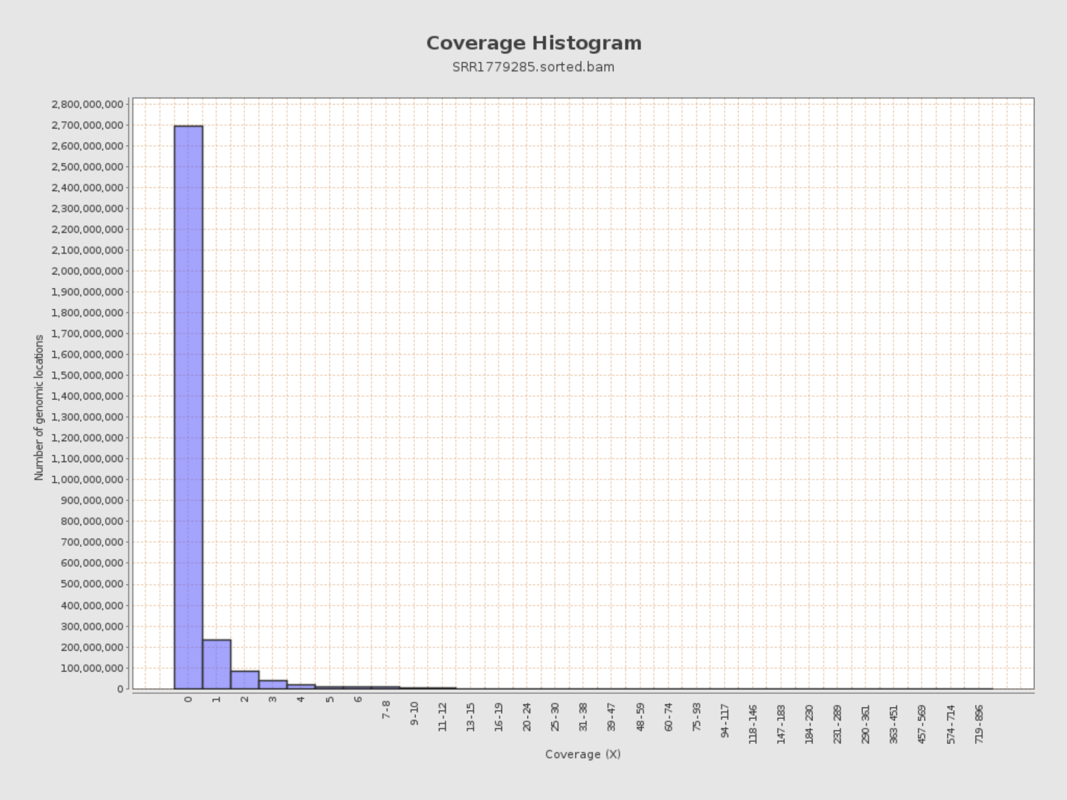
		bases	**coverage**	**deviation**
chr1	249250621	63937473	0.2565	1.2924
chr2	243199373	72345153	0.2975	1.0396
chr3	198022430	54289452	0.2742	0.9698
chr4	191154276	63339473	0.3314	1.0435
chr5	180915260	60476237	0.3343	1.0588
chr6	171115067	60082815	0.3511	1.1358
chr7	159138663	75026235	0.4715	1.8435
chr8	146364022	52493625	0.3587	1.0722
chr9	141213431	34219745	0.2423	0.8717
chr10	135534747	19160699	0.1414	1.1579
chr11	135006516	30298115	0.2244	0.8946
chr12	133851895	40966263	0.3061	1.0696
chr13	115169878	20171657	0.1751	0.6926
chr14	107349540	14458098	0.1347	0.6162
chr15	102531392	15147327	0.1477	0.7291
chr16	90354753	13681618	0.1514	0.6793
chr17	81195210	10192177	0.1255	0.6465
chr18	78077248	22459272	0.2877	0.9316
chr19	59128983	6473526	0.1095	0.7854
chr20	63025520	15328211	0.2432	0.8505
chr21	48129895	9154482	0.1902	0.7192
chr22	51304566	3064548	0.0597	0.3651
chrMT	16571	959	0.0579	0.2693
chrX	155270560	47872741	0.3083	1.078

chrY	59373566	515713	0.0087	0.1397

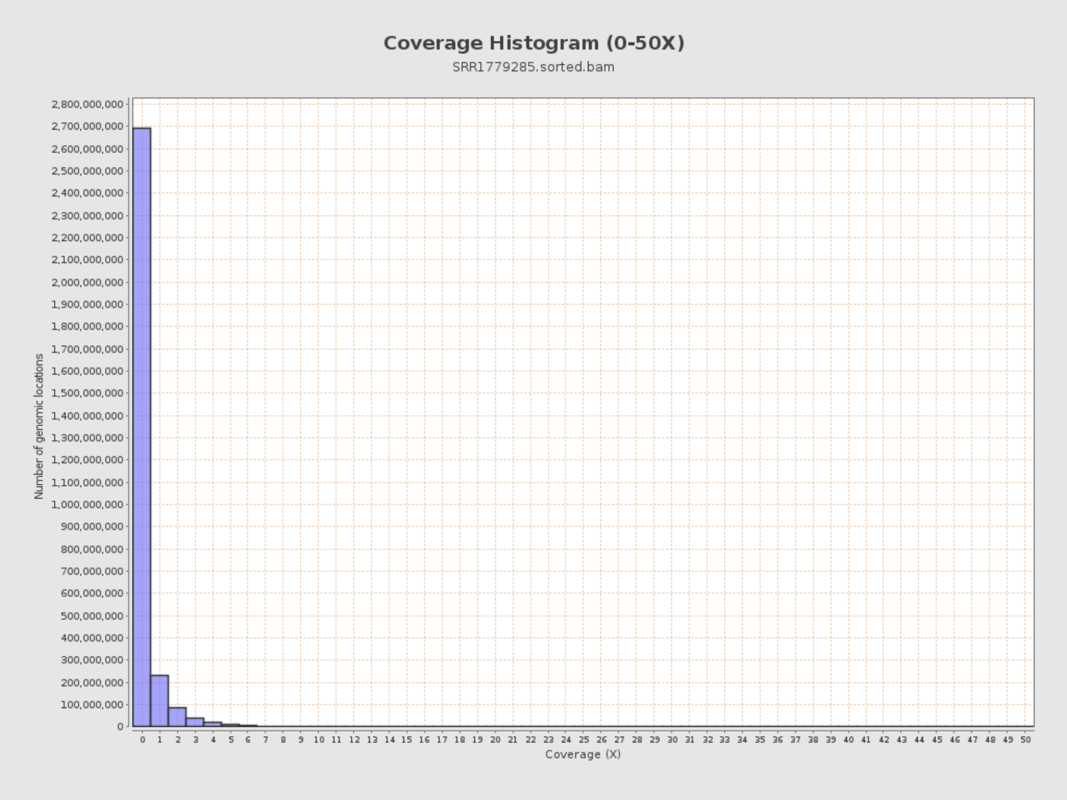
3. Results : Coverage across reference



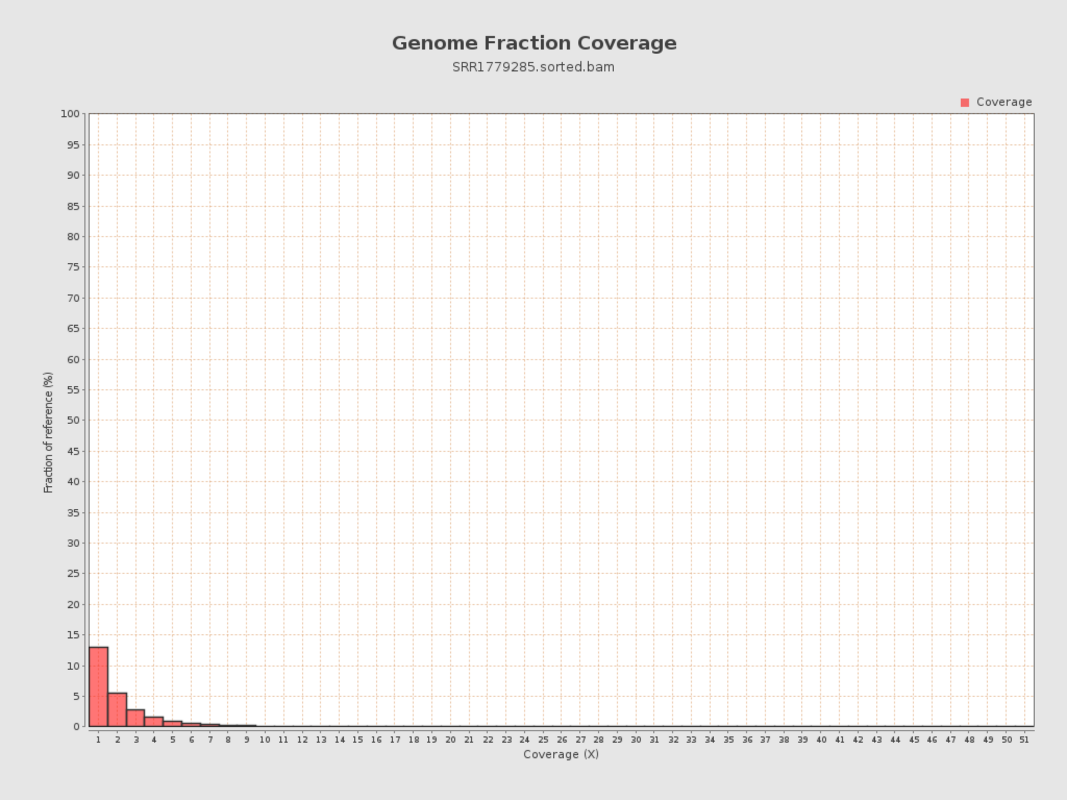
4. Results : Coverage Histogram



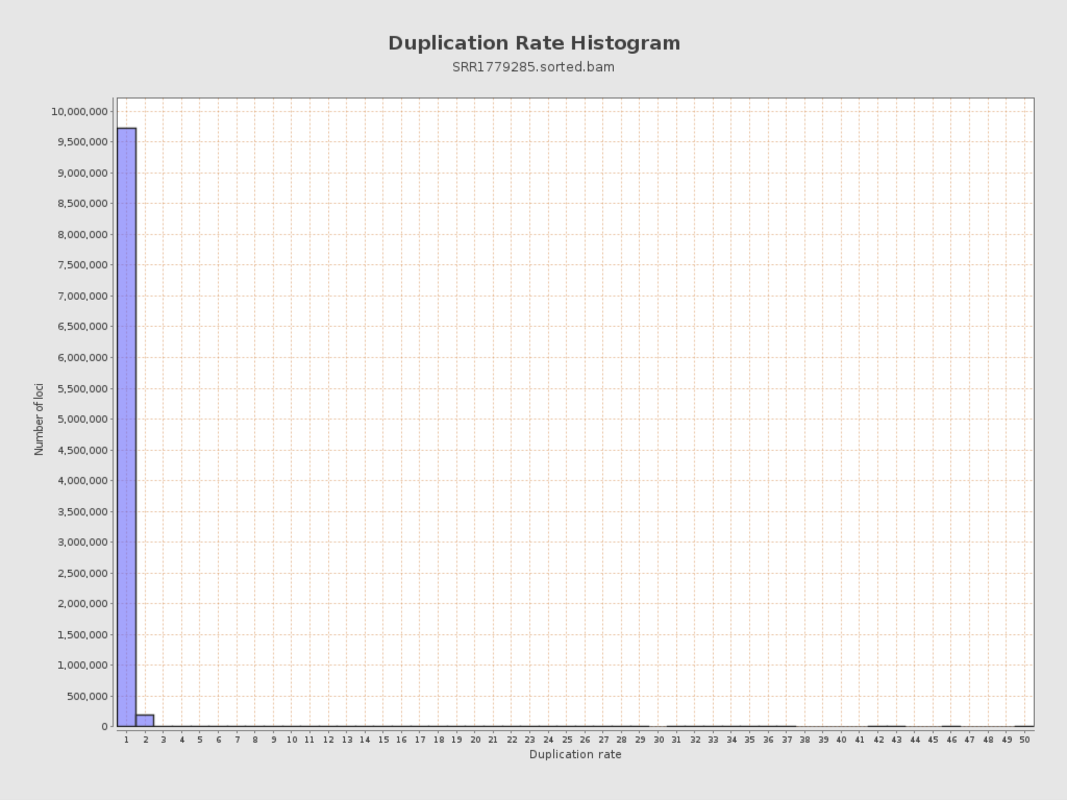
5. Results : Coverage Histogram (0-50X)



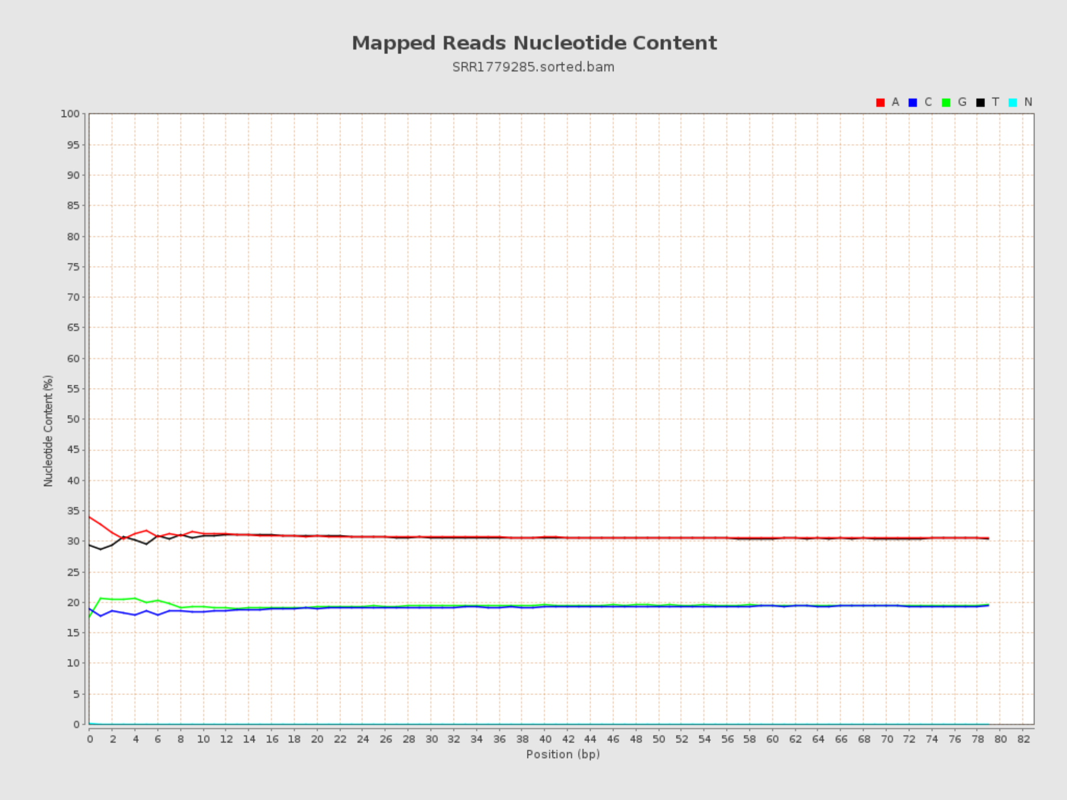
6. Results : Genome Fraction Coverage



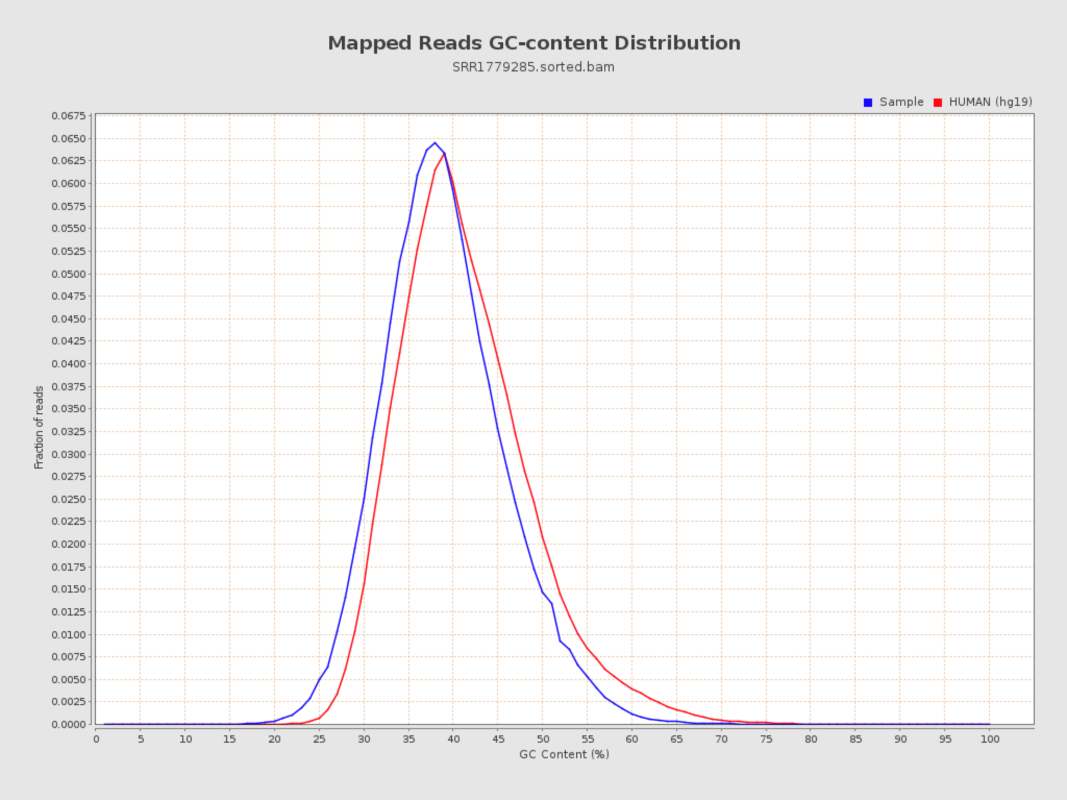
7. Results : Duplication Rate Histogram



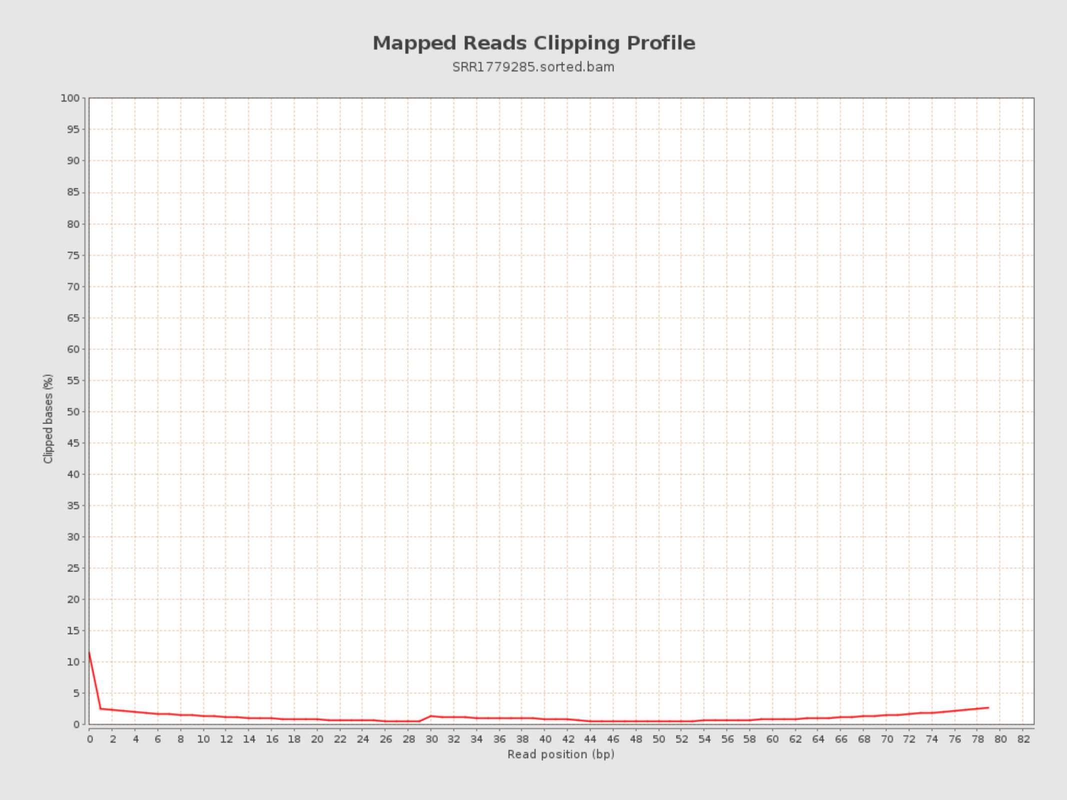
8. Results : Mapped Reads Nucleotide Content



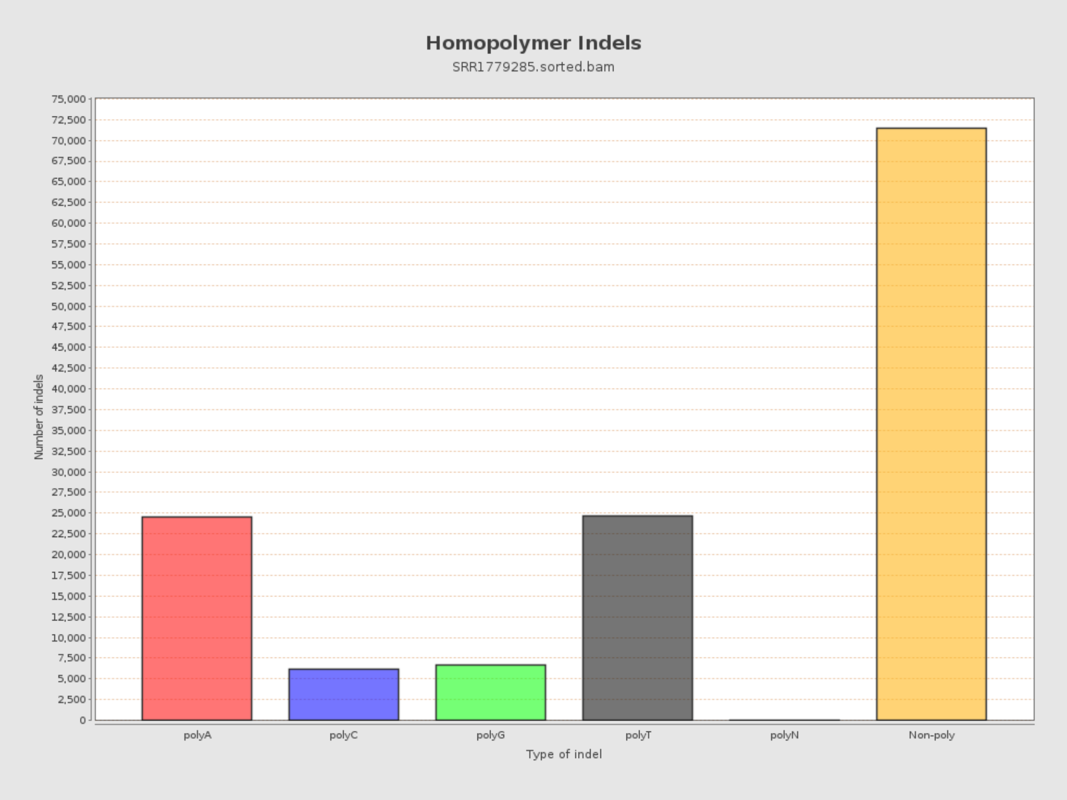
9. Results : Mapped Reads GC-content Distribution



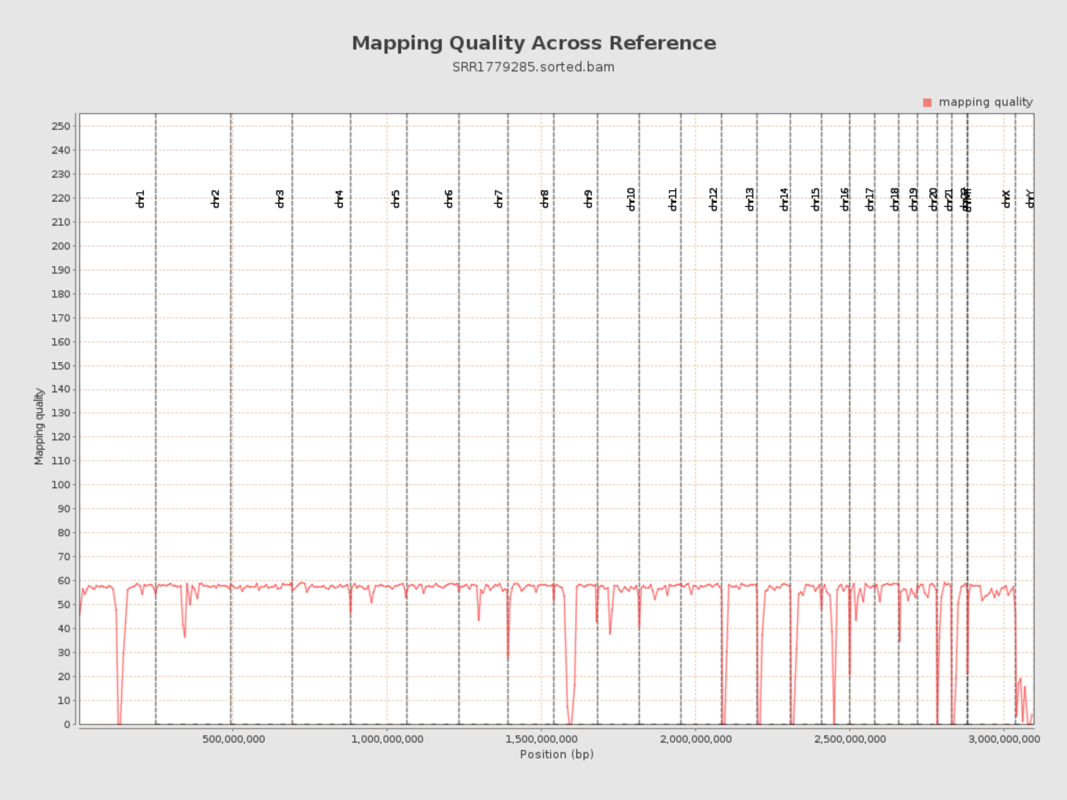
10. Results : Mapped Reads Clipping Profile



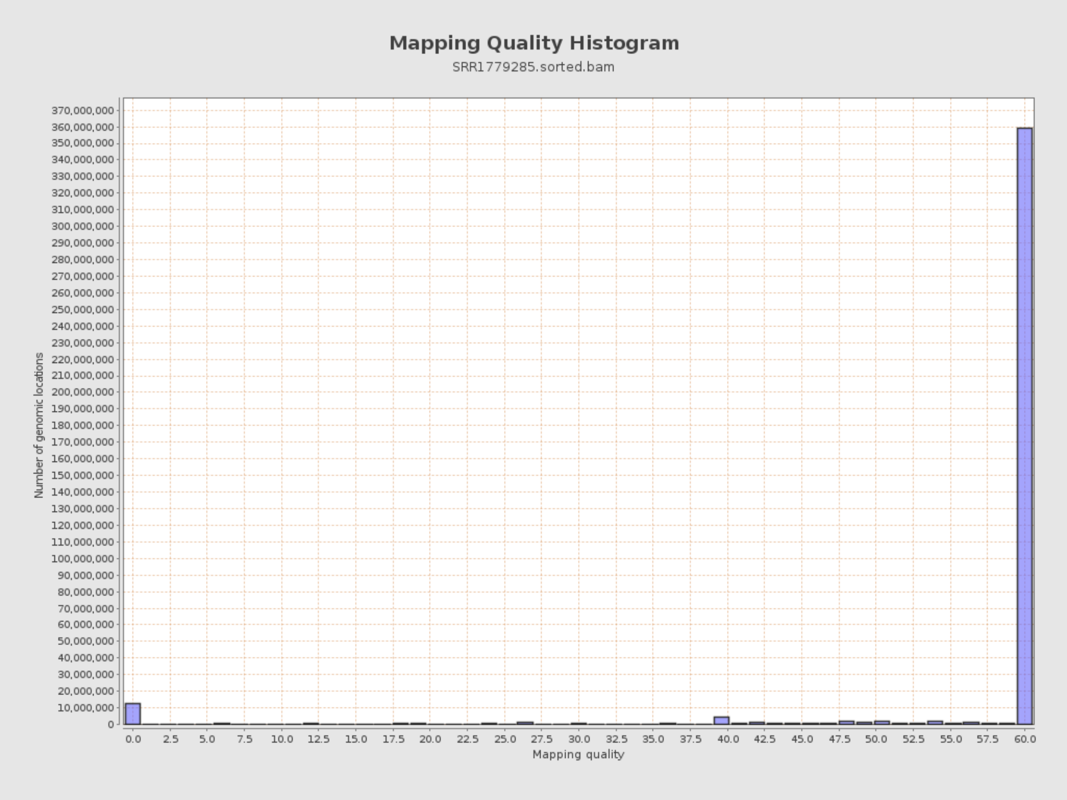
11. Results : Homopolymer Indels



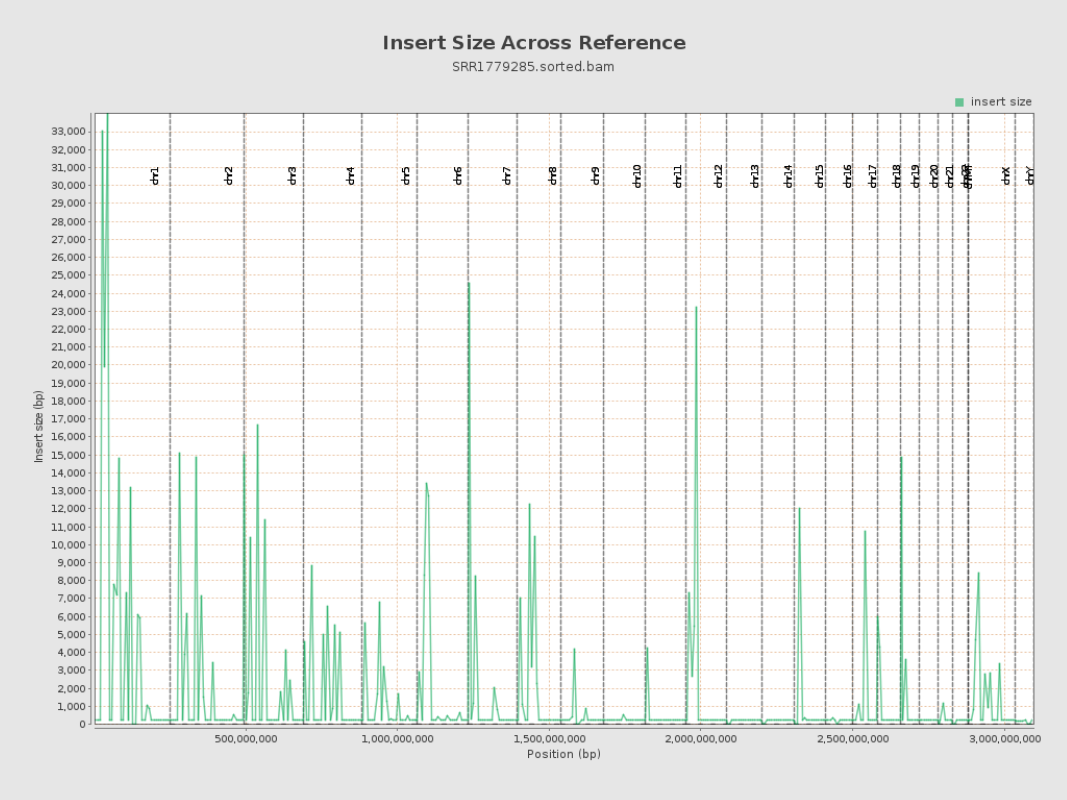
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram