Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:14:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779283.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_SRR1779283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779283_1.fastq.gz SRR1779283_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:14:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,602,682
Mapped reads	7,367,259 / 96.9%
Unmapped reads	235,423 / 3.1%
Mapped paired reads	7,367,259 / 96.9%
Mapped reads, first in pair	3,707,049 / 48.76%
Mapped reads, second in pair	3,660,210 / 48.14%
Mapped reads, both in pair	7,308,578 / 96.13%
Mapped reads, singletons	58,681 / 0.77%
Secondary alignments	0
Supplementary alignments	17,950 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	69,634 / 0.92%
Duplication rate	0.83%
Clipped reads	261,192 / 3.44%

2.2. ACGT Content

Number/percentage of A's	178,656,580 / 30.49%
Number/percentage of C's	113,562,986 / 19.38%
Number/percentage of T's	177,733,360 / 30.33%
Number/percentage of G's	115,902,559 / 19.78%
Number/percentage of N's	111,440 / 0.02%

GC Percentage	39.16%

2.3. Coverage

Mean	0.1893
Standard Deviation	0.65

2.4. Mapping Quality

Mean Mapping Quality	53.22

2.5. Insert size

Mean	53,681.38
Standard Deviation	2,202,186.71
P25/Median/P75	161 / 212 / 283

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	2,367,236
Insertions	42,731
Mapped reads with at least one insertion	0.58%
Deletions	53,863
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.7%

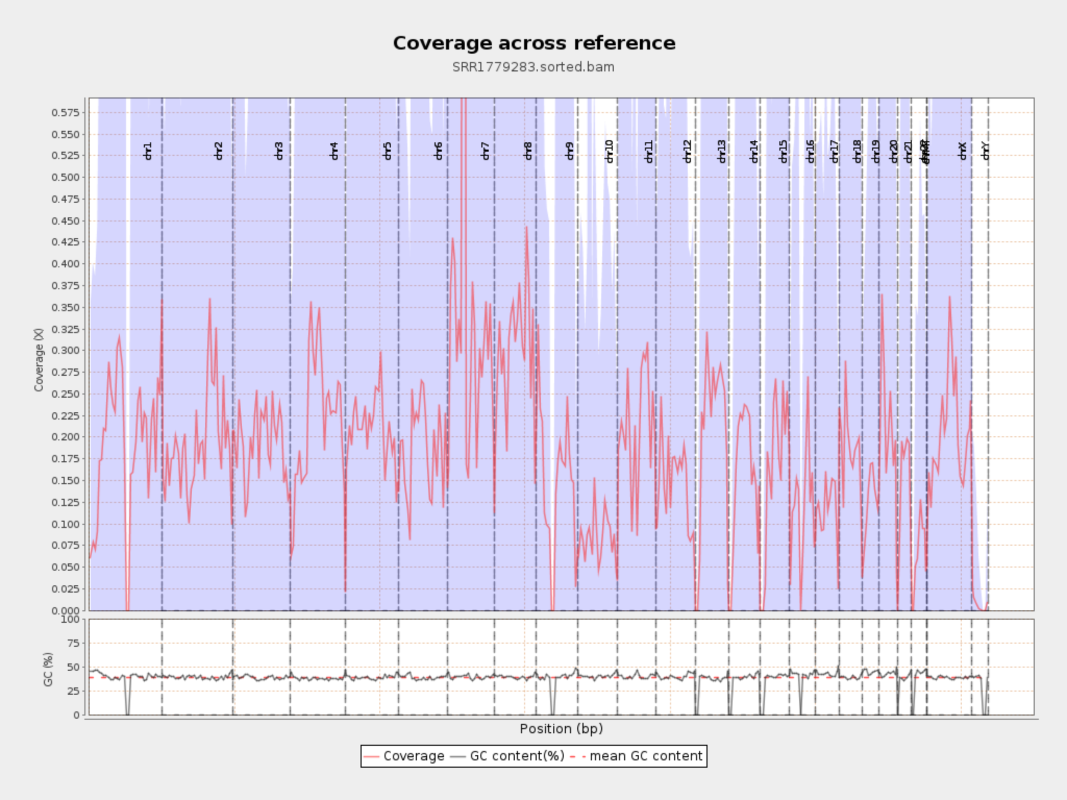
2.7. Chromosome stats

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

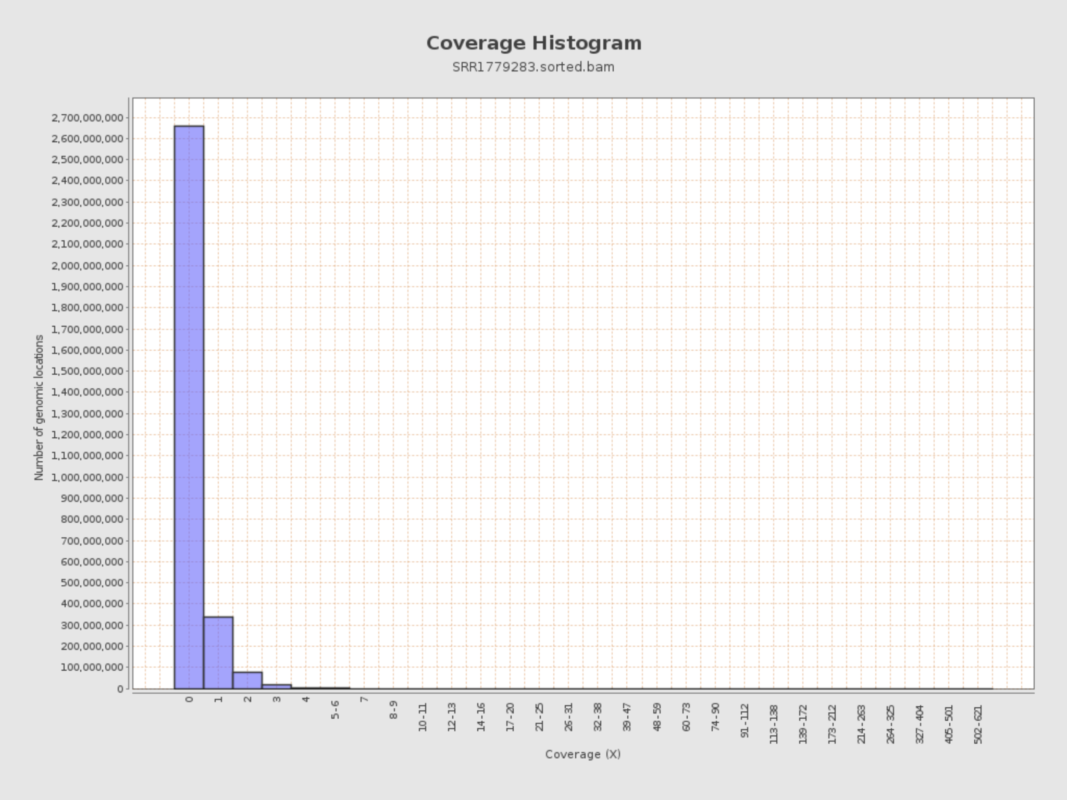
		bases	coverage	deviation
chr1	249250621	47709379	0.1914	0.7797
chr2	243199373	47331511	0.1946	0.5282
chr3	198022430	38455933	0.1942	0.5176
chr4	191154276	42376224	0.2217	0.5634
chr5	180915260	37908290	0.2095	0.54
chr6	171115067	31966880	0.1868	0.517
chr7	159138663	59291886	0.3726	1.5228
chr8	146364022	44446483	0.3037	0.6701
chr9	141213431	21121201	0.1496	0.4803
chr10	135534747	11566289	0.0853	0.8167
chr11	135006516	28392652	0.2103	0.5507
chr12	133851895	19693890	0.1471	0.4486
chr13	115169878	23990532	0.2083	0.5521
chr14	107349540	16468302	0.1534	0.4706
chr15	102531392	16470464	0.1606	0.4884
chr16	90354753	11049737	0.1223	0.4111
chr17	81195210	9416628	0.116	0.4063
chr18	78077248	14861569	0.1903	0.5313
chr19	59128983	7420083	0.1255	0.5621
chr20	63025520	13747967	0.2181	0.5732
chr21	48129895	6901099	0.1434	0.4577
chr22	51304566	3412033	0.0665	0.3041
chrMT	16571	877	0.0529	0.2286
chrX	155270560	31652615	0.2039	0.5569

chrY	59373566	426162	0.0072	0.1068

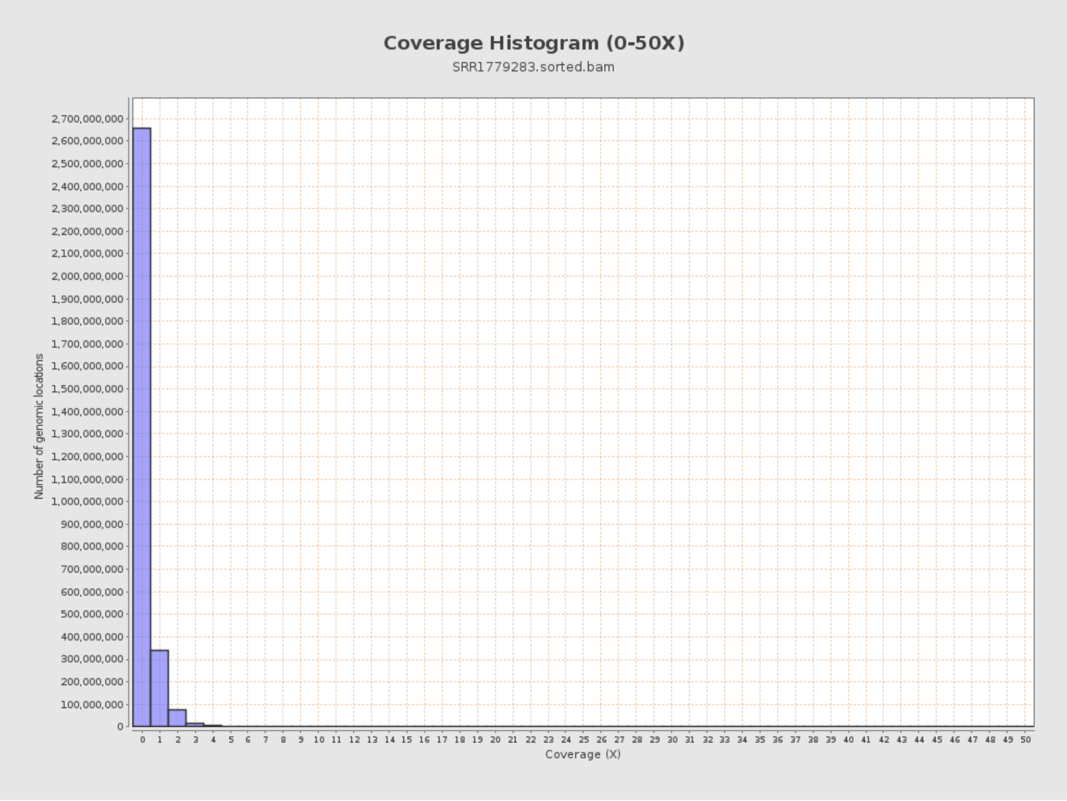
3. Results : Coverage across reference



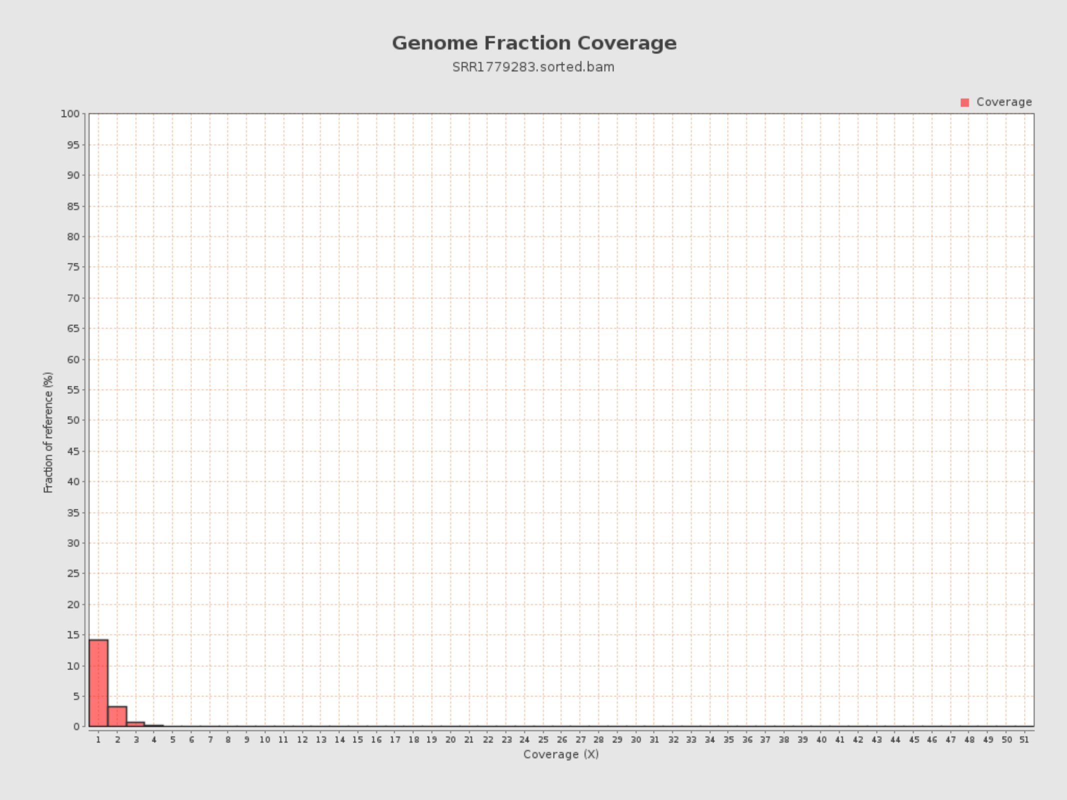
4. Results : Coverage Histogram



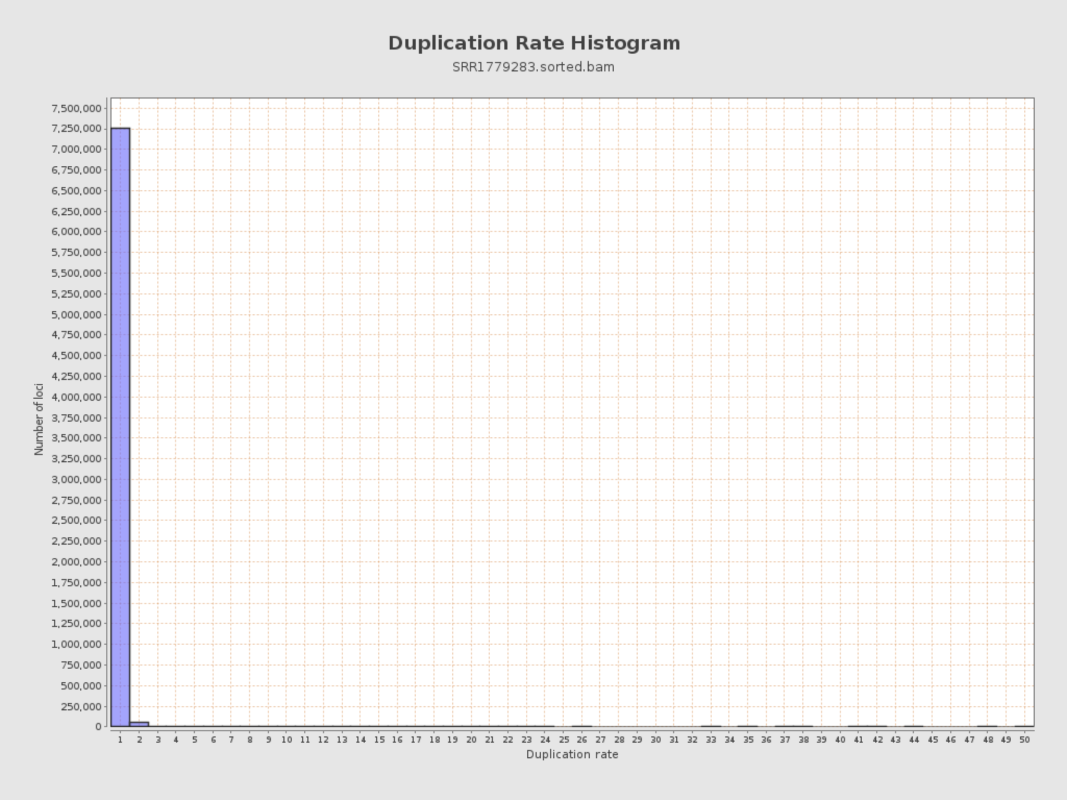
5. Results : Coverage Histogram (0-50X)



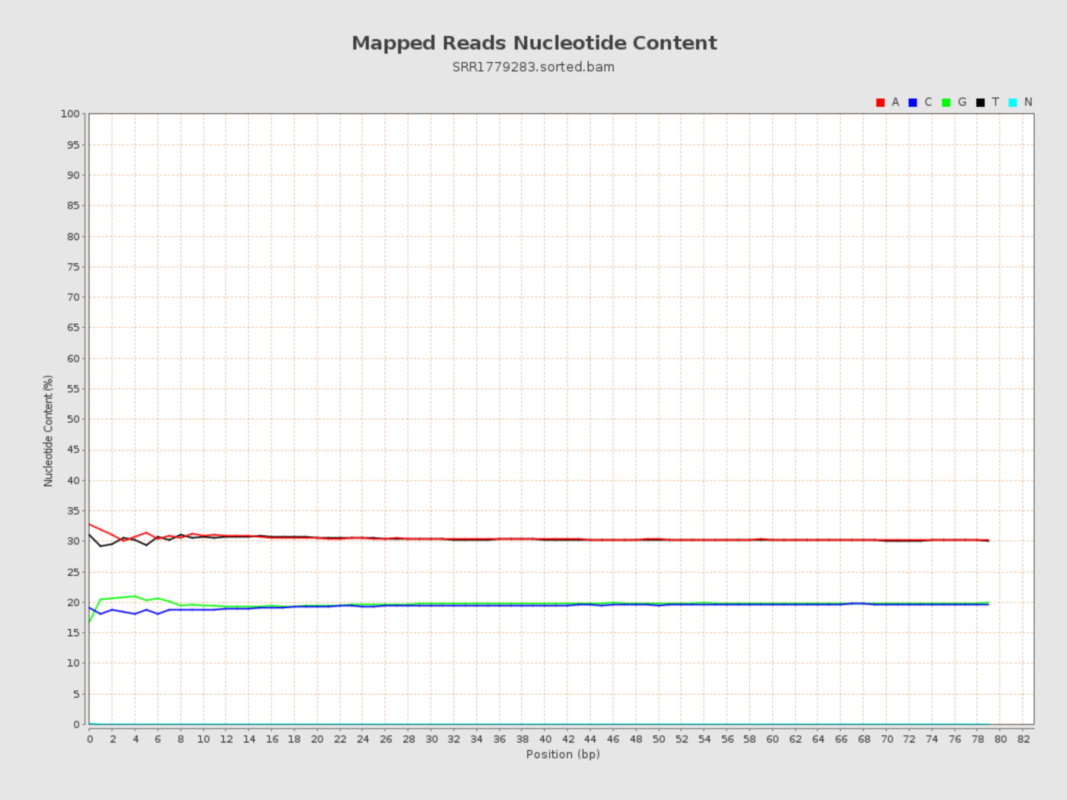
6. Results : Genome Fraction Coverage



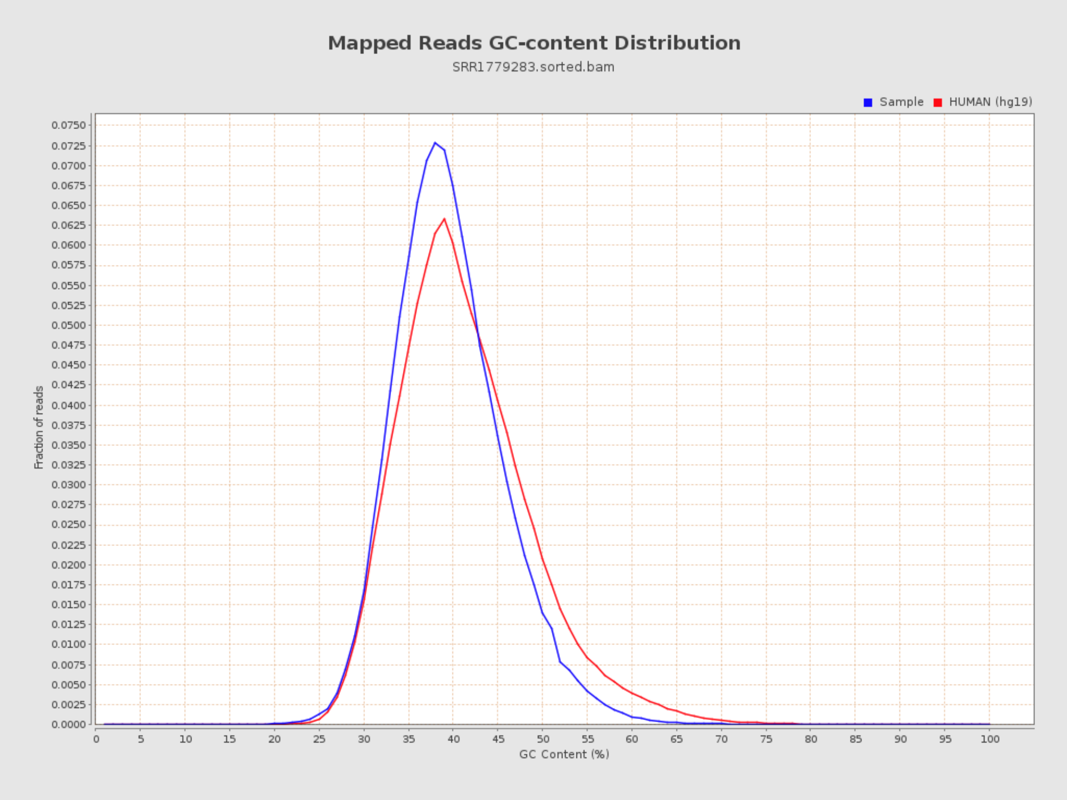
7. Results : Duplication Rate Histogram



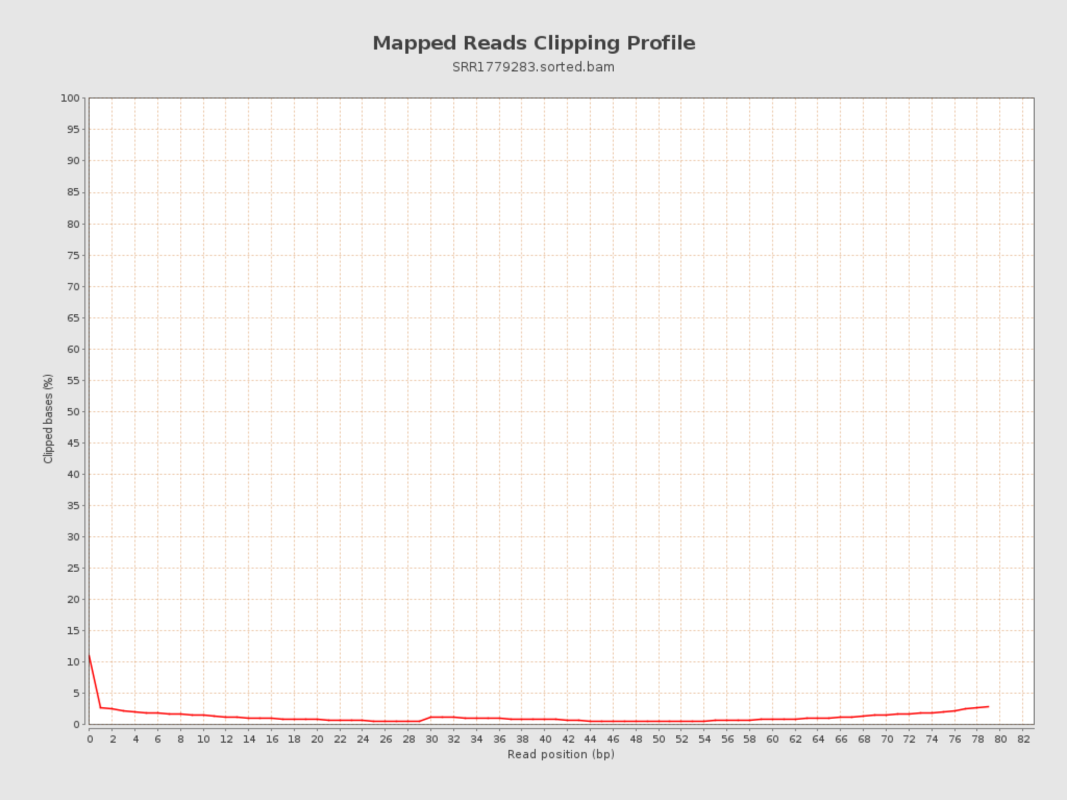
8. Results : Mapped Reads Nucleotide Content



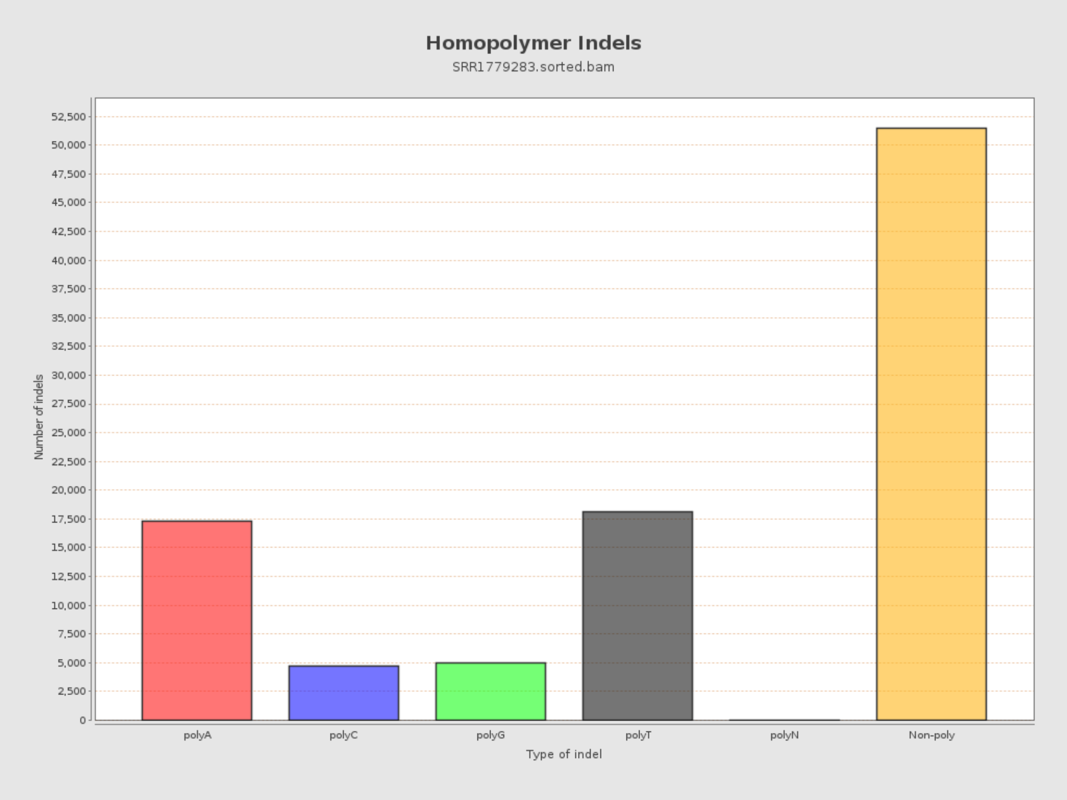
9. Results : Mapped Reads GC-content Distribution



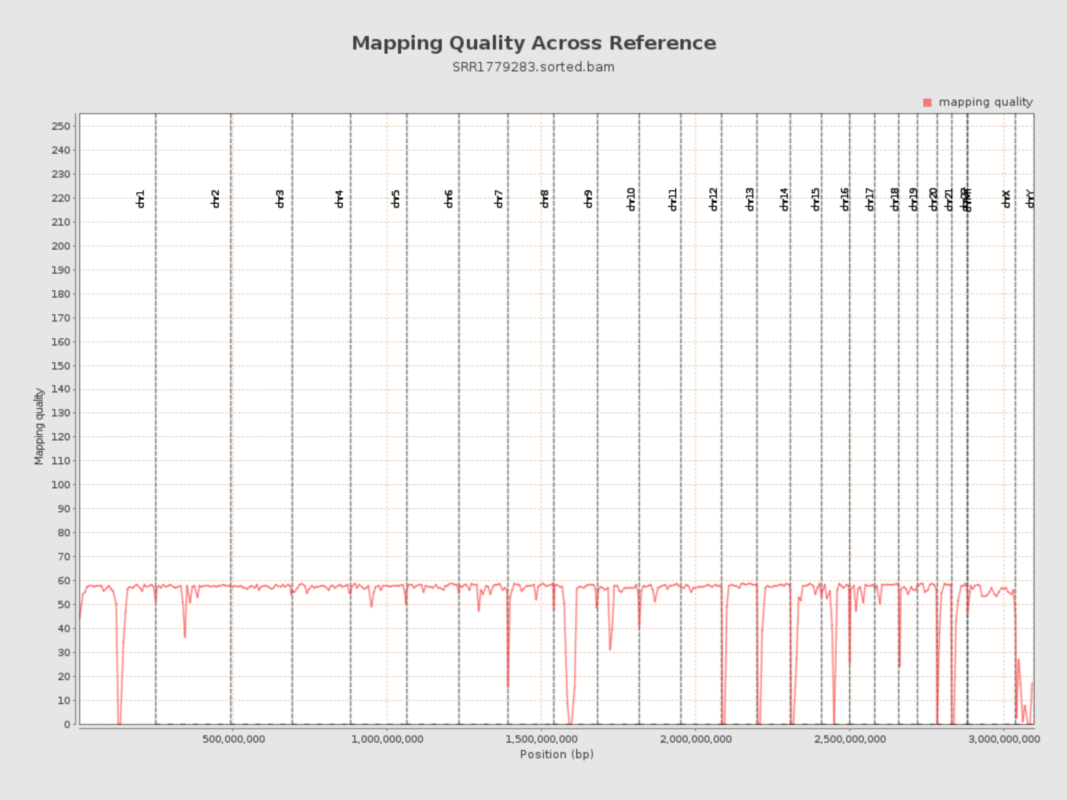
10. Results : Mapped Reads Clipping Profile



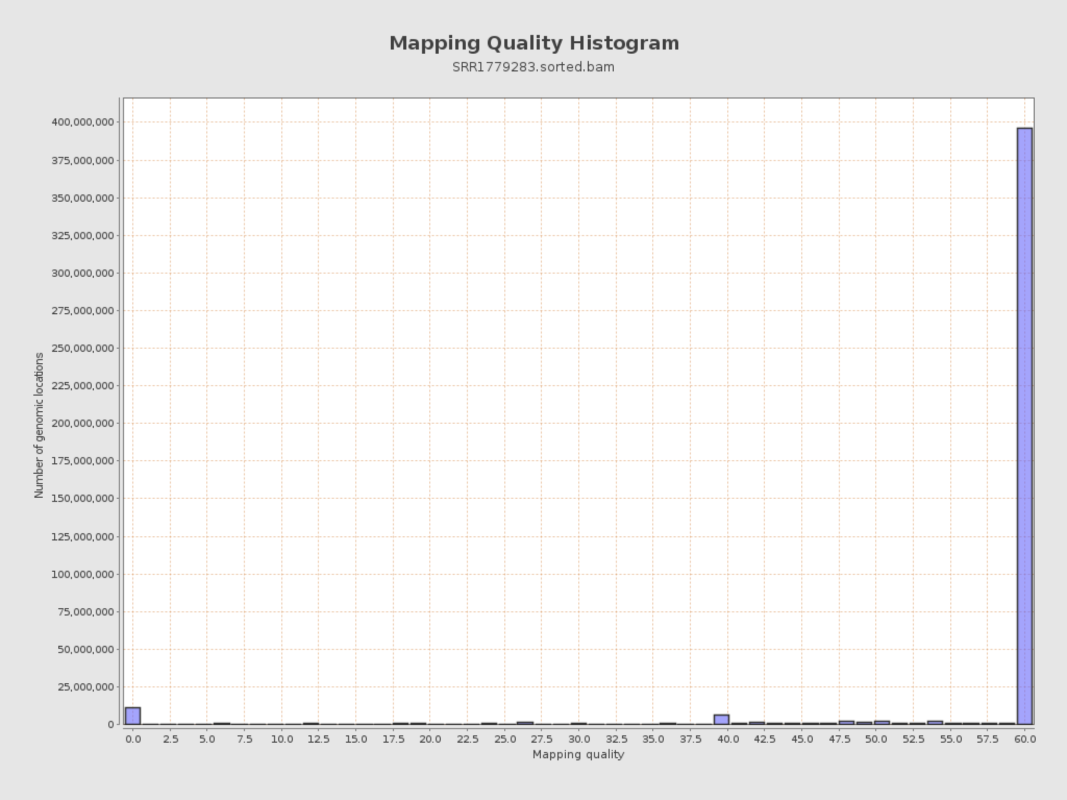
11. Results : Homopolymer Indels



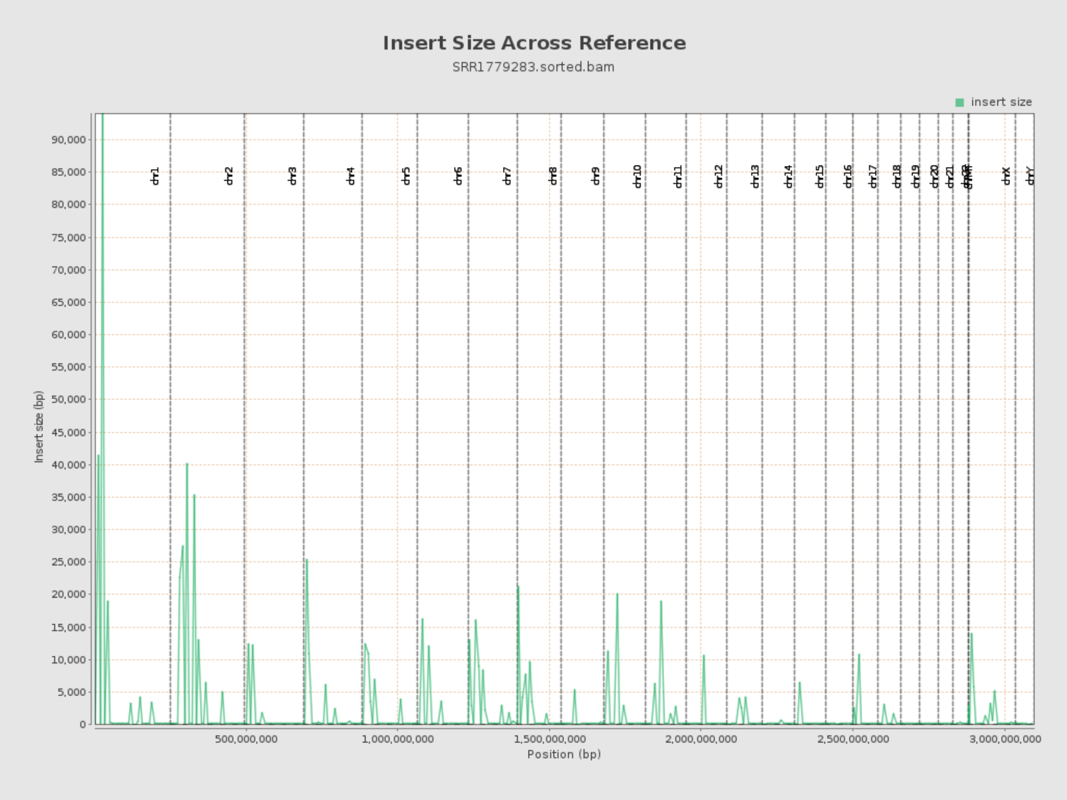
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram