Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 20:06:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779273.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_SRR1779273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779273_1.fastq.gz SRR1779273_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 20:06:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,734,440
Mapped reads	11,333,821 / 96.59%
Unmapped reads	400,619 / 3.41%
Mapped paired reads	11,333,821 / 96.59%
Mapped reads, first in pair	5,727,862 / 48.81%
Mapped reads, second in pair	5,605,959 / 47.77%
Mapped reads, both in pair	11,193,638 / 95.39%
Mapped reads, singletons	140,183 / 1.19%
Secondary alignments	0
Supplementary alignments	25,901 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	193,231 / 1.65%
Duplication rate	1.46%
Clipped reads	377,388 / 3.22%

2.2. ACGT Content

Number/percentage of A's	274,561,539 / 30.45%
Number/percentage of C's	175,179,910 / 19.43%
Number/percentage of T's	273,803,400 / 30.36%
Number/percentage of G's	178,042,855 / 19.74%
Number/percentage of N's	170,216 / 0.02%

GC Percentage	39.17%

2.3. Coverage

Mean	0.2913
Standard Deviation	1.0347

2.4. Mapping Quality

Mean Mapping Quality	52.92

2.5. Insert size

Mean	47,324.53
Standard Deviation	2,009,278.75
P25/Median/P75	145 / 193 / 261

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	3,389,723
Insertions	64,189
Mapped reads with at least one insertion	0.56%
Deletions	81,153
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.58%

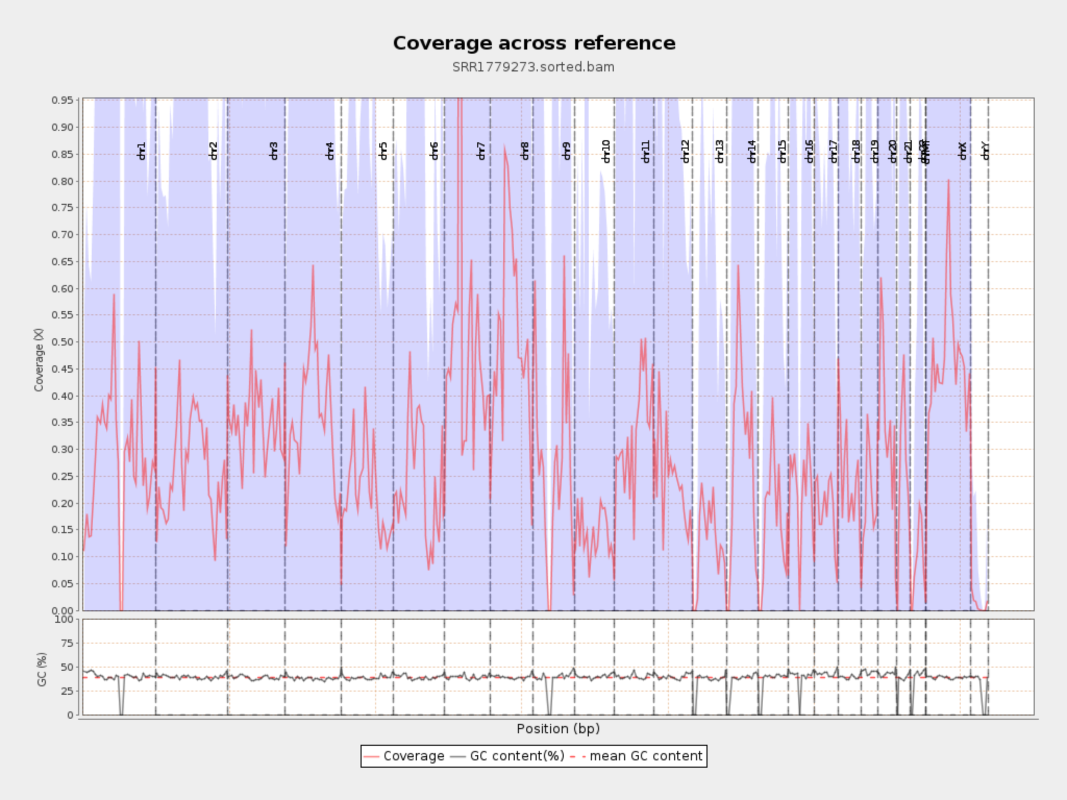
2.7. Chromosome stats

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

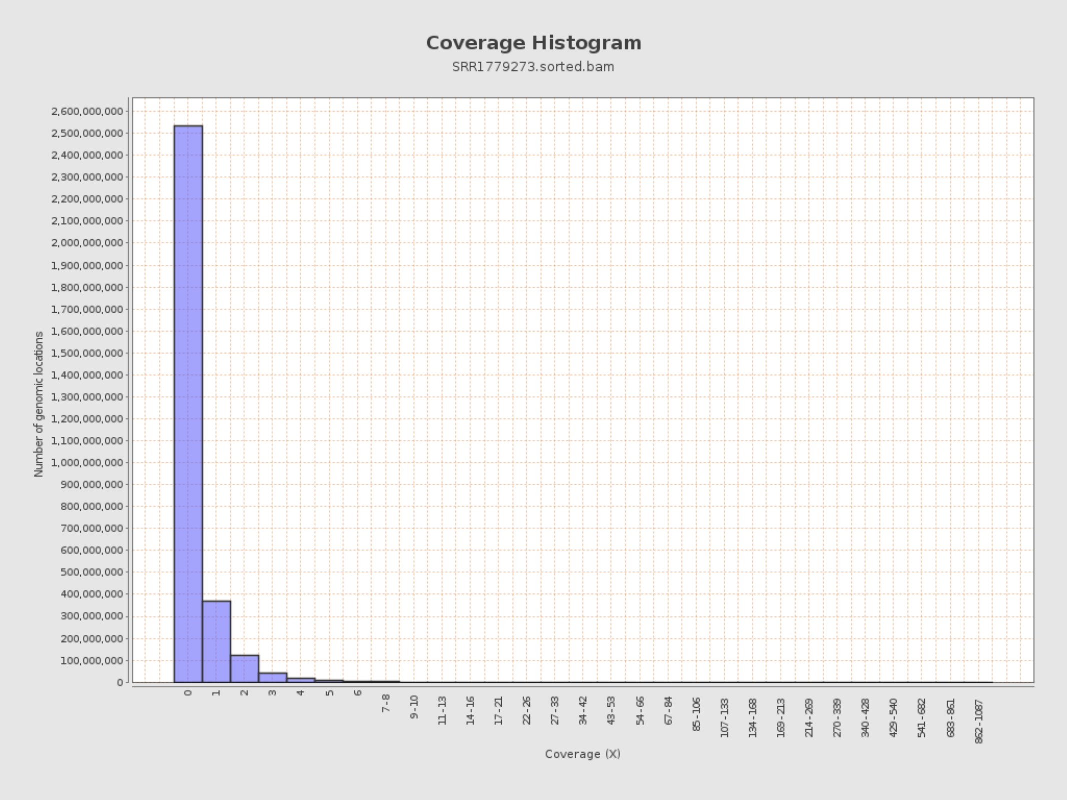
		bases	coverage	deviation
chr1	249250621	70032487	0.281	1.2742
chr2	243199373	63200616	0.2599	0.707
chr3	198022430	69469325	0.3508	0.7952
chr4	191154276	69119796	0.3616	0.8242
chr5	180915260	39761018	0.2198	0.6397
chr6	171115067	41881019	0.2448	0.6962
chr7	159138663	93156726	0.5854	2.792
chr8	146364022	75714053	0.5173	1.024
chr9	141213431	38515534	0.2727	0.7779
chr10	135534747	19331015	0.1426	1.1646
chr11	135006516	44584385	0.3302	0.8197
chr12	133851895	32700961	0.2443	0.6792
chr13	115169878	14774762	0.1283	0.4873
chr14	107349540	32530529	0.303	0.7889
chr15	102531392	16900314	0.1648	0.5555
chr16	90354753	19389697	0.2146	0.6224
chr17	81195210	15621057	0.1924	0.5955
chr18	78077248	19677758	0.252	0.7097
chr19	59128983	12714476	0.215	0.9463
chr20	63025520	22591197	0.3584	0.8223
chr21	48129895	11827730	0.2457	0.6793
chr22	51304566	4854761	0.0946	0.4802
chrMT	16571	1238	0.0747	0.3662
chrX	155270560	72919840	0.4696	0.9957

chrY	59373566	656033	0.011	0.142

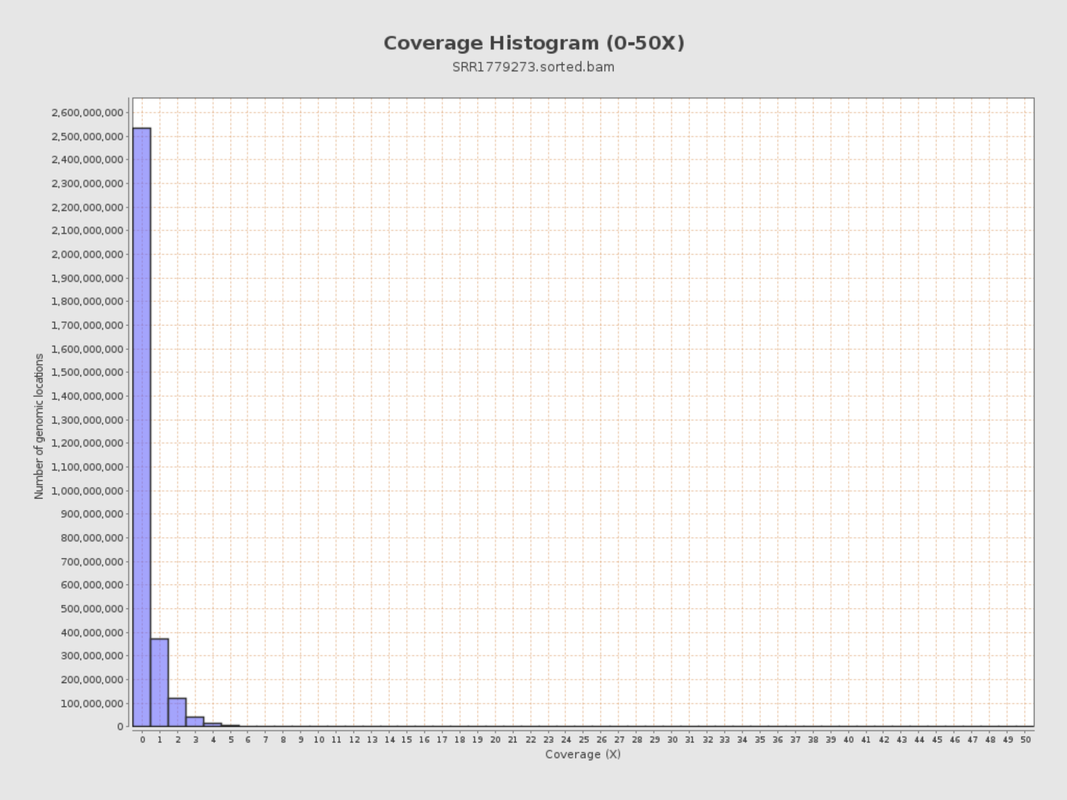
3. Results : Coverage across reference



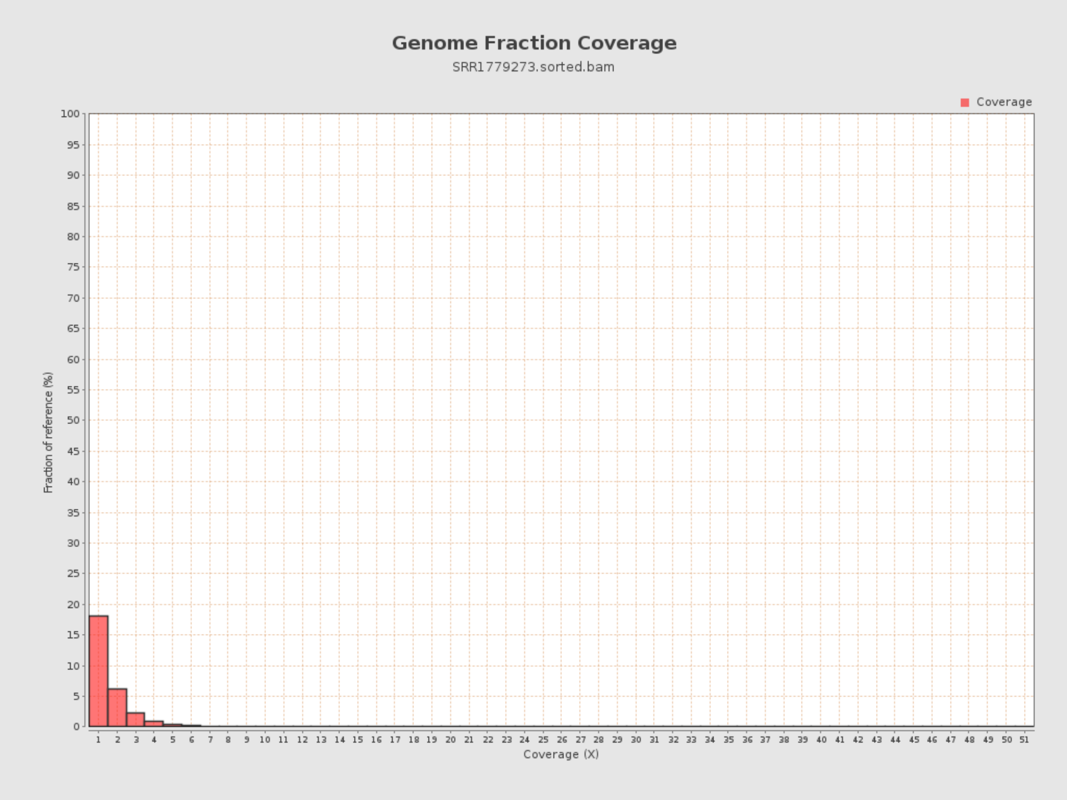
4. Results : Coverage Histogram



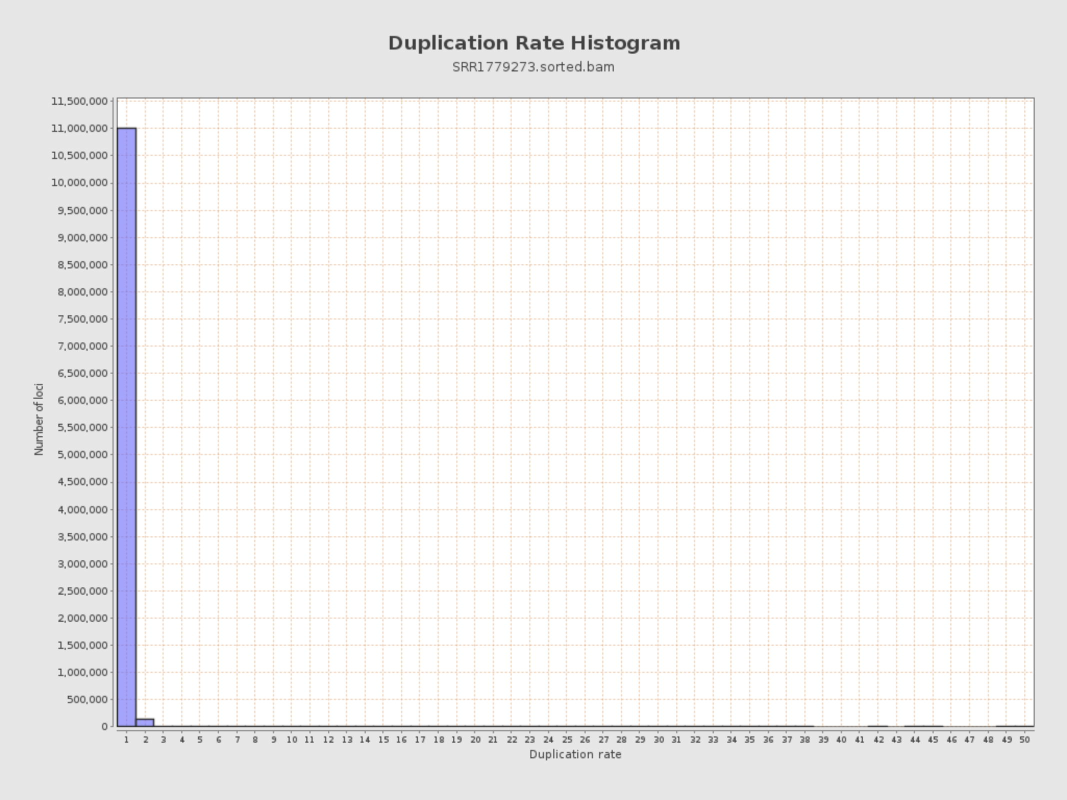
5. Results : Coverage Histogram (0-50X)



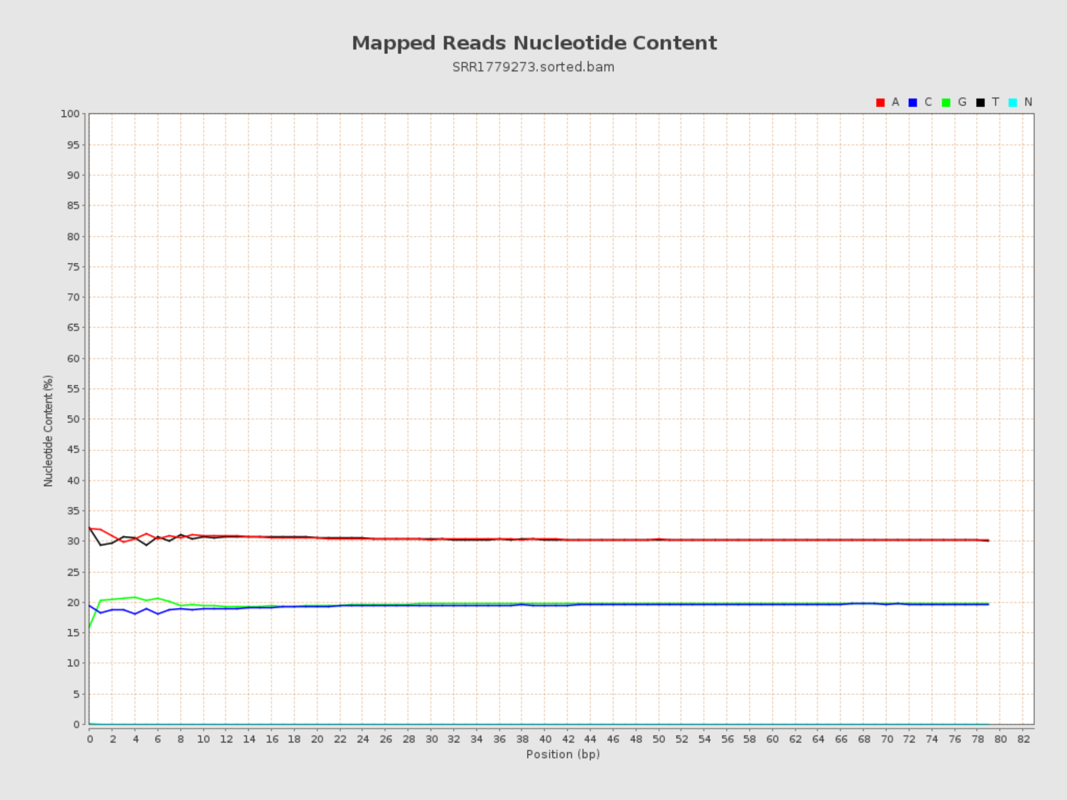
6. Results : Genome Fraction Coverage



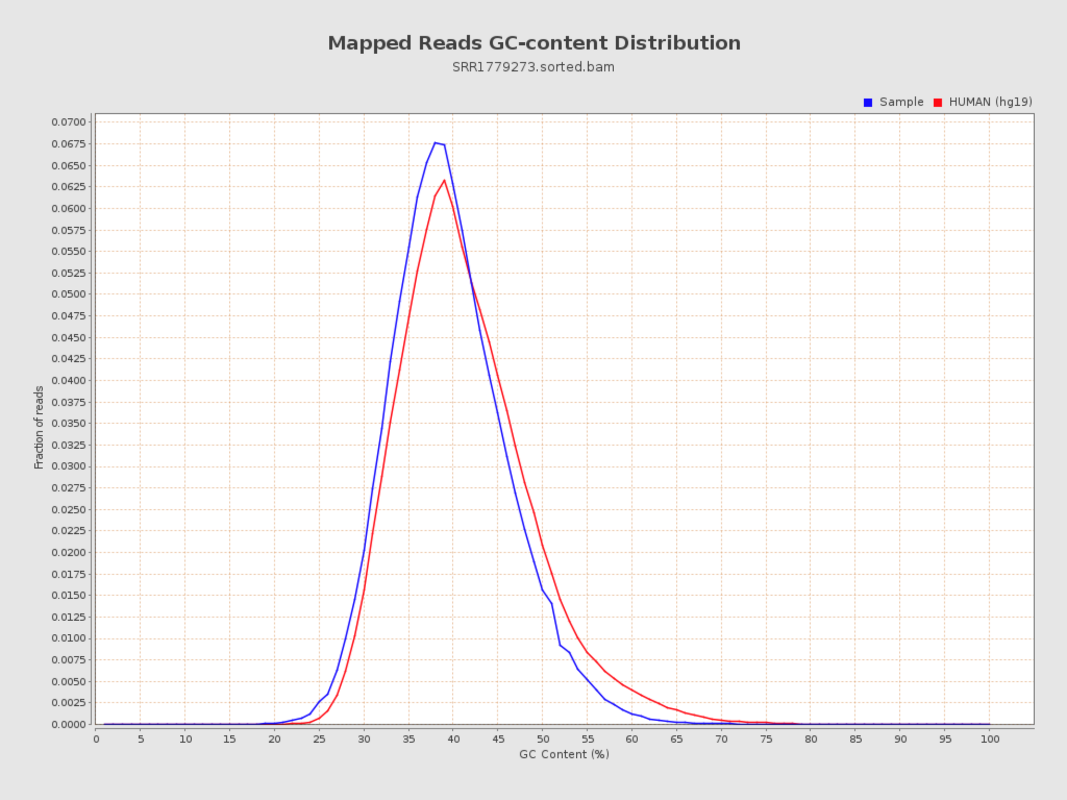
7. Results : Duplication Rate Histogram



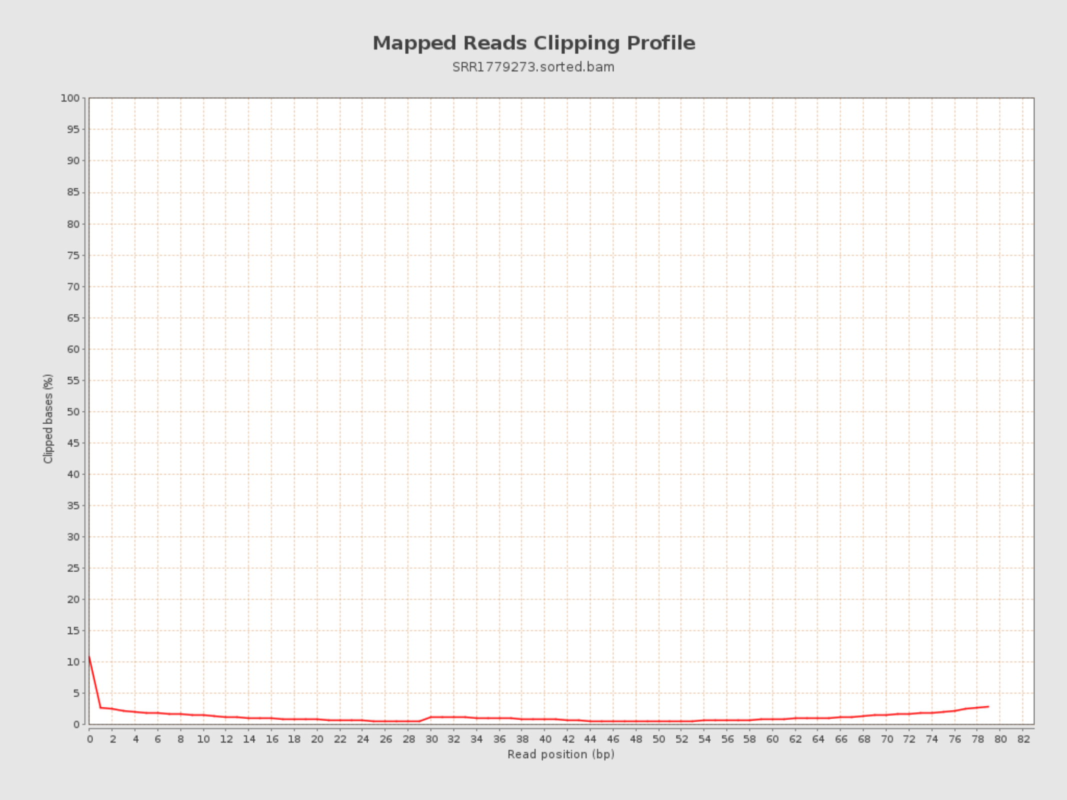
8. Results : Mapped Reads Nucleotide Content



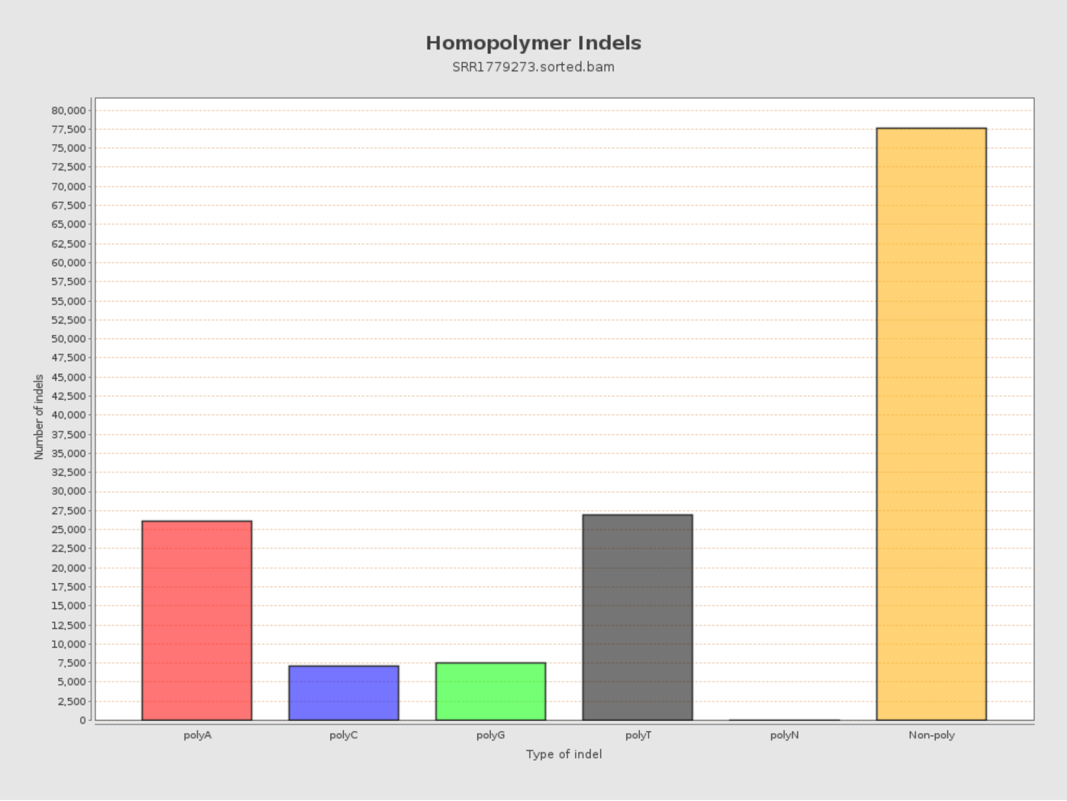
9. Results : Mapped Reads GC-content Distribution



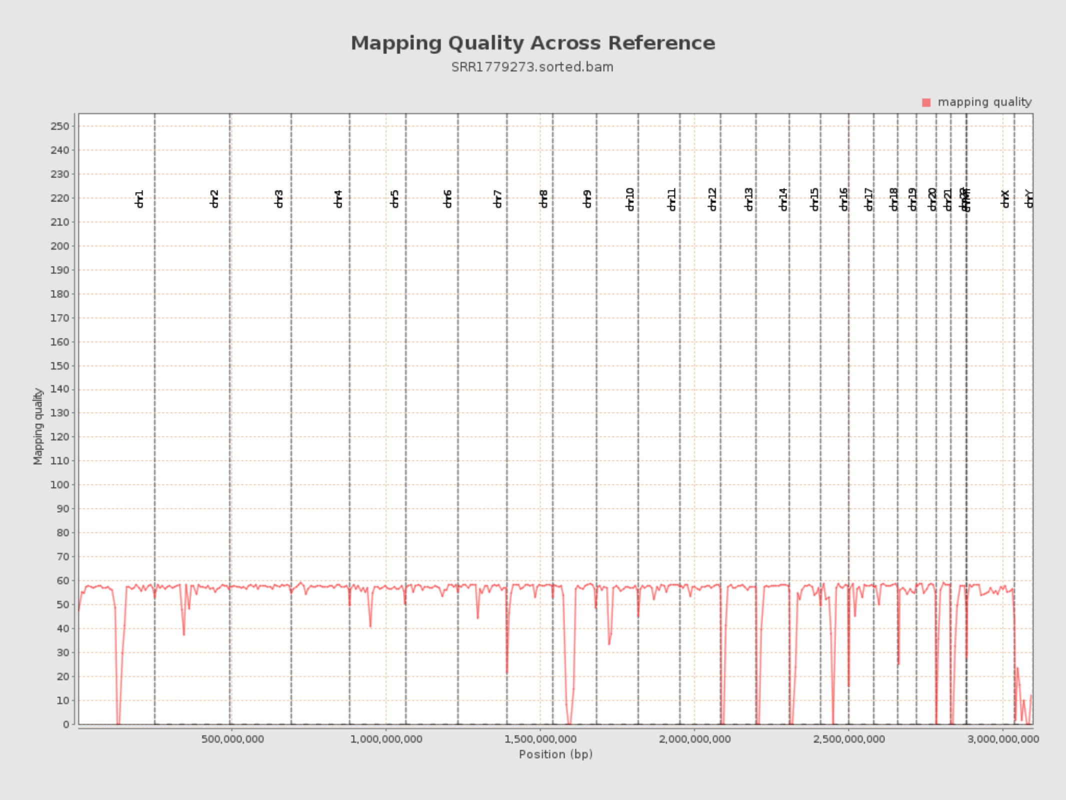
10. Results : Mapped Reads Clipping Profile



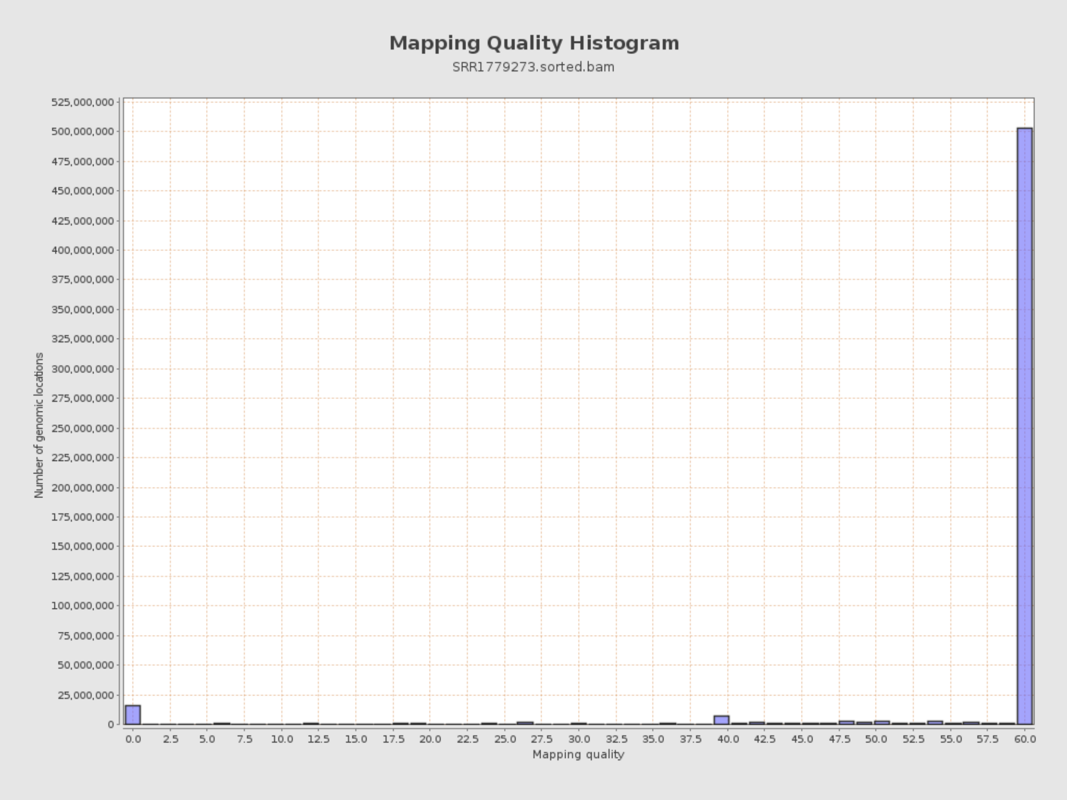
11. Results : Homopolymer Indels



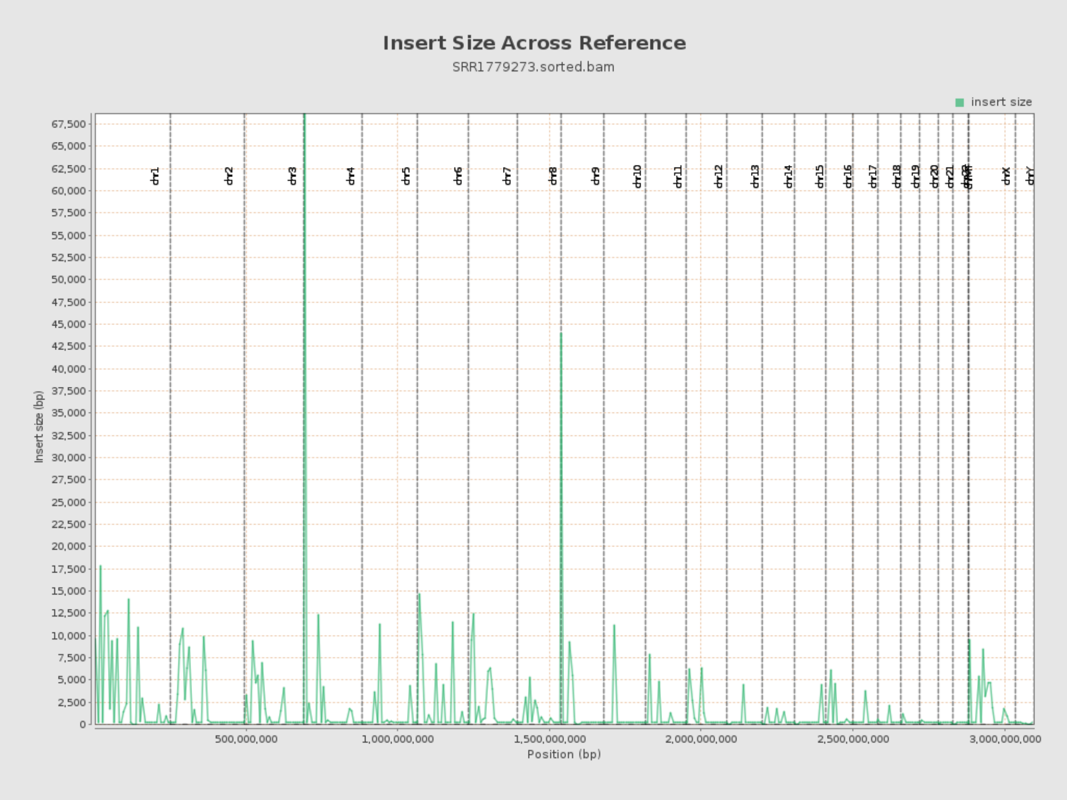
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram