Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 23:21:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779289.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_SRR1779289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779289_1.fastq.gz SRR1779289_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 23:21:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,855,742
Mapped reads	22,173,413 / 97.01%
Unmapped reads	682,329 / 2.99%
Mapped paired reads	22,173,413 / 97.01%
Mapped reads, first in pair	11,200,295 / 49%
Mapped reads, second in pair	10,973,118 / 48.01%
Mapped reads, both in pair	21,917,244 / 95.89%
Mapped reads, singletons	256,169 / 1.12%
Secondary alignments	0
Supplementary alignments	50,298 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	450,130 / 1.97%
Duplication rate	1.87%
Clipped reads	699,707 / 3.06%

2.2. ACGT Content

Number/percentage of A's	538,876,609 / 30.54%
Number/percentage of C's	341,129,957 / 19.33%
Number/percentage of T's	538,113,115 / 30.49%
Number/percentage of G's	346,277,183 / 19.62%
Number/percentage of N's	330,923 / 0.02%

GC Percentage	38.95%

2.3. Coverage

Mean	0.5702
Standard Deviation	1.4307

2.4. Mapping Quality

Mean Mapping Quality	52.97

2.5. Insert size

Mean	42,378.21
Standard Deviation	1,948,454.29
P25/Median/P75	158 / 205 / 270

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	6,705,894
Insertions	124,839
Mapped reads with at least one insertion	0.56%
Deletions	154,409
Mapped reads with at least one deletion	0.69%
Homopolymer indels	46.59%

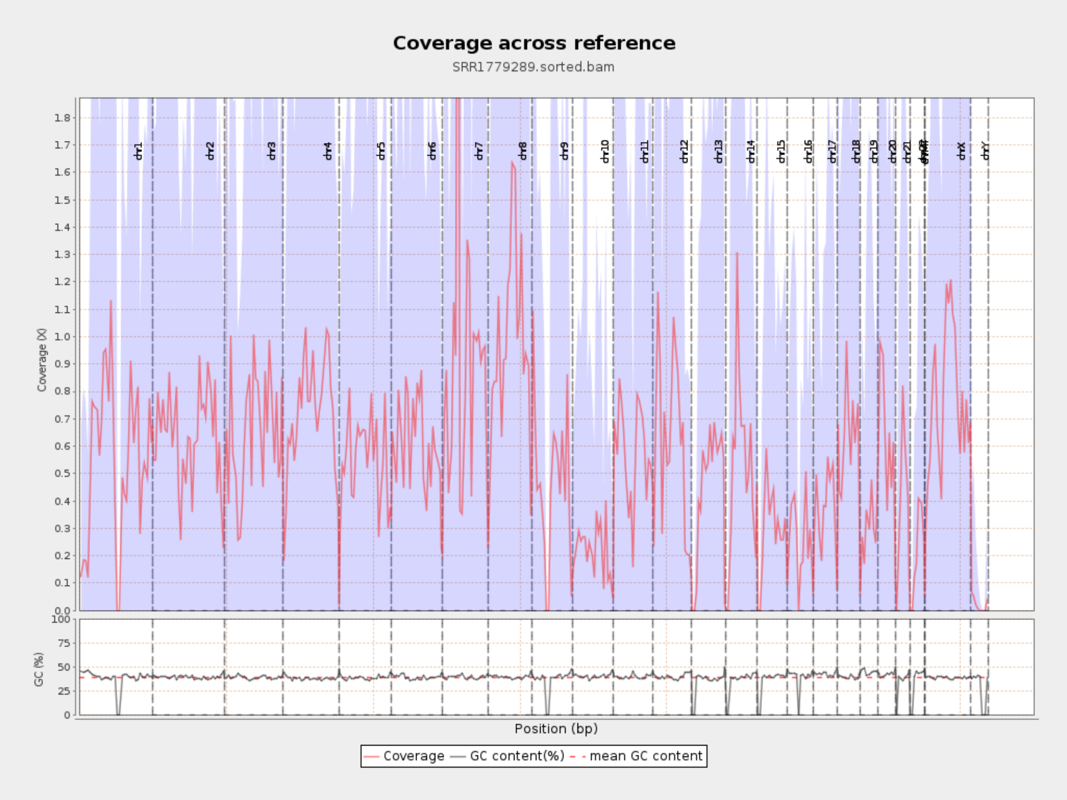
2.7. Chromosome stats

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

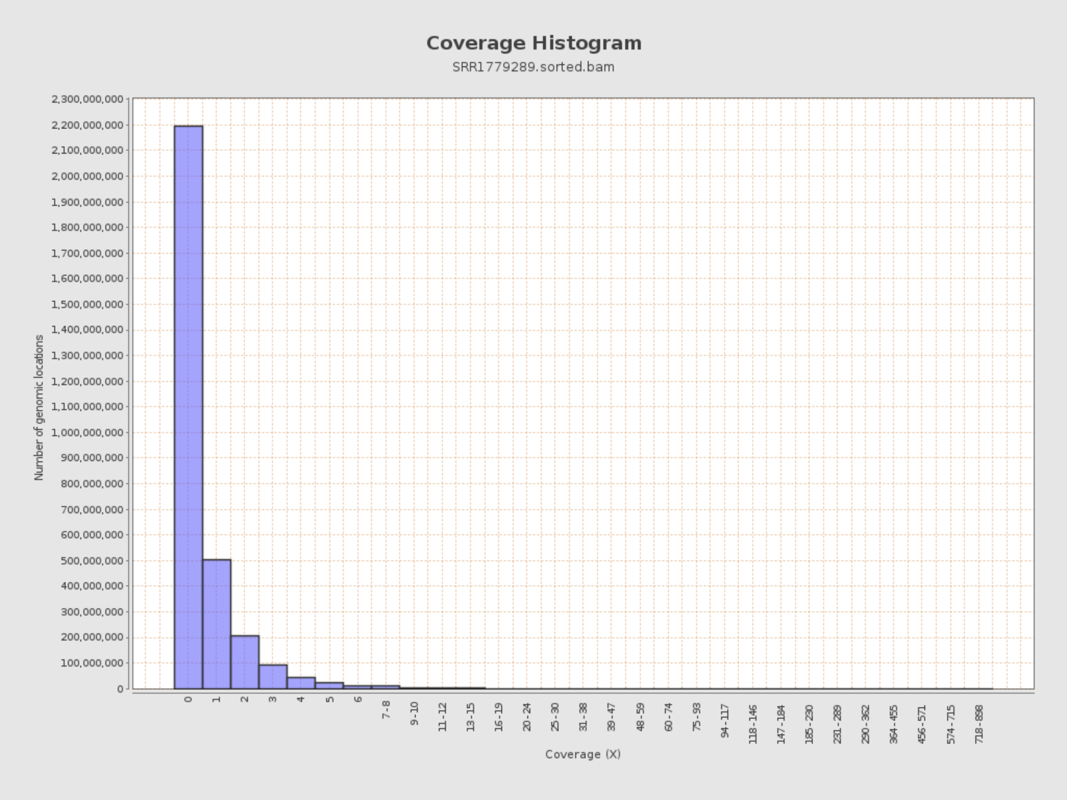
		bases	coverage	deviation
chr1	249250621	137930344	0.5534	1.398
chr2	243199373	154240719	0.6342	1.2421
chr3	198022430	128281074	0.6478	1.2986
chr4	191154276	138626426	0.7252	1.3885
chr5	180915260	98848421	0.5464	1.1595
chr6	171115067	105743968	0.618	1.2486
chr7	159138663	150606644	0.9464	3.2051
chr8	146364022	145164255	0.9918	1.657
chr9	141213431	64795634	0.4588	1.1237
chr10	135534747	30541575	0.2253	1.5137
chr11	135006516	76697037	0.5681	1.2042
chr12	133851895	83452785	0.6235	1.2683
chr13	115169878	52358144	0.4546	1.0441
chr14	107349540	56058085	0.5222	1.1802
chr15	102531392	29933134	0.2919	0.8456
chr16	90354753	22622601	0.2504	0.7211
chr17	81195210	30221392	0.3722	0.9455
chr18	78077248	49898692	0.6391	1.2464
chr19	59128983	17364789	0.2937	0.9166
chr20	63025520	39952074	0.6339	1.3217
chr21	48129895	19978553	0.4151	0.9911
chr22	51304566	10806572	0.2106	0.6929
chrMT	16571	889	0.0536	0.321
chrX	155270560	119617503	0.7704	1.5383

chrY	59373566	1305792	0.022	0.2524

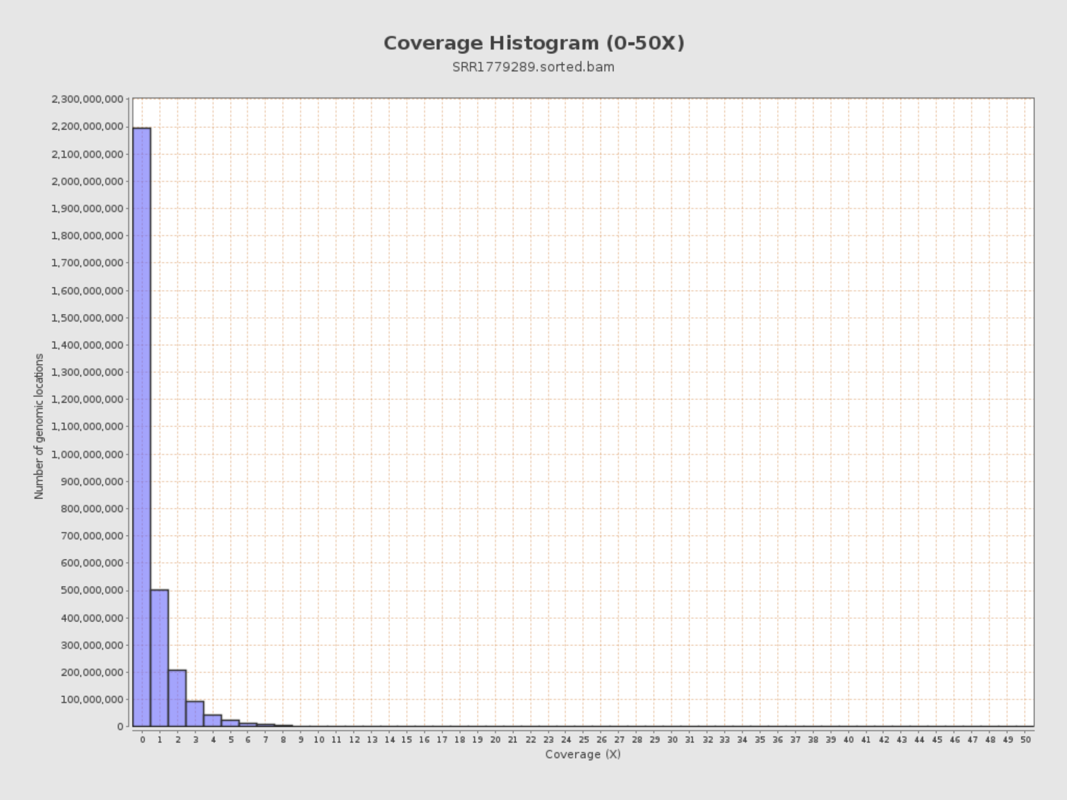
3. Results : Coverage across reference



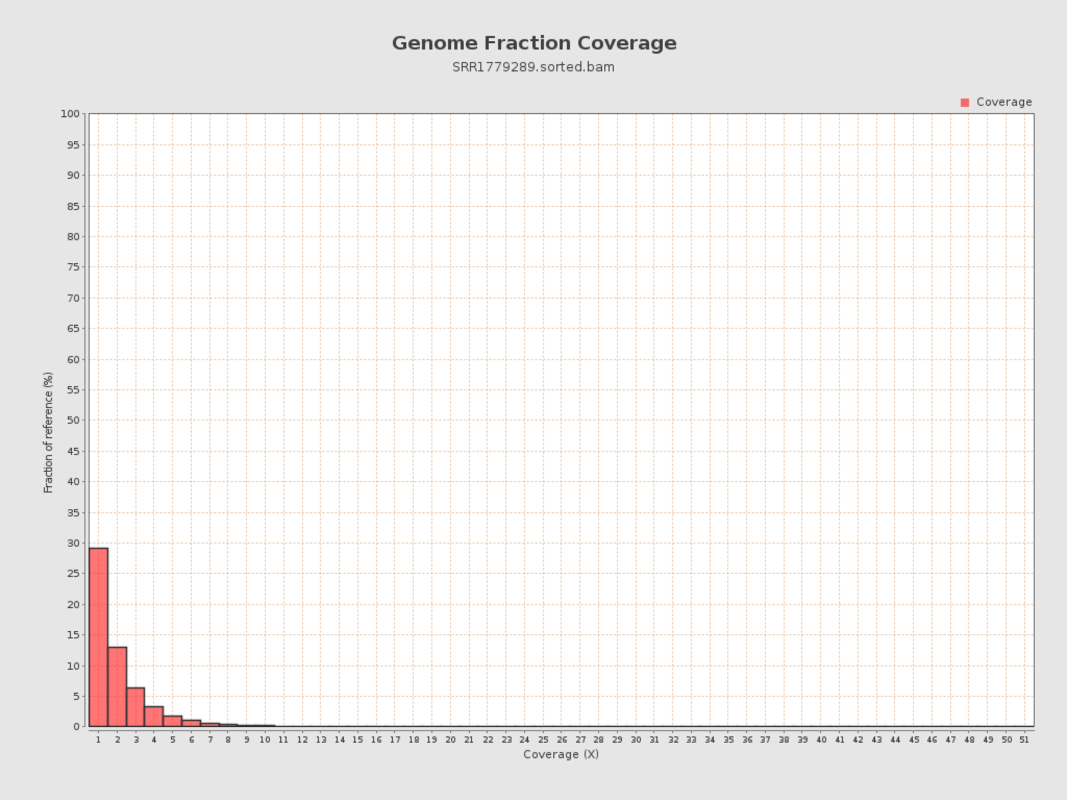
4. Results : Coverage Histogram



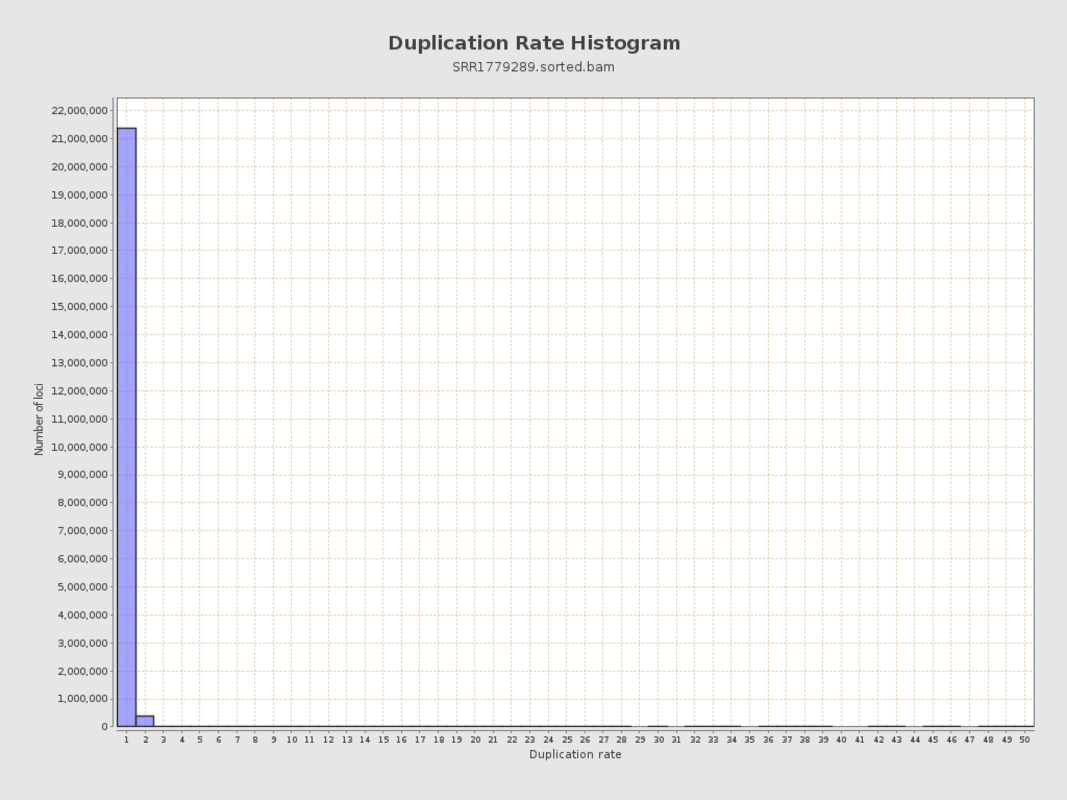
5. Results : Coverage Histogram (0-50X)



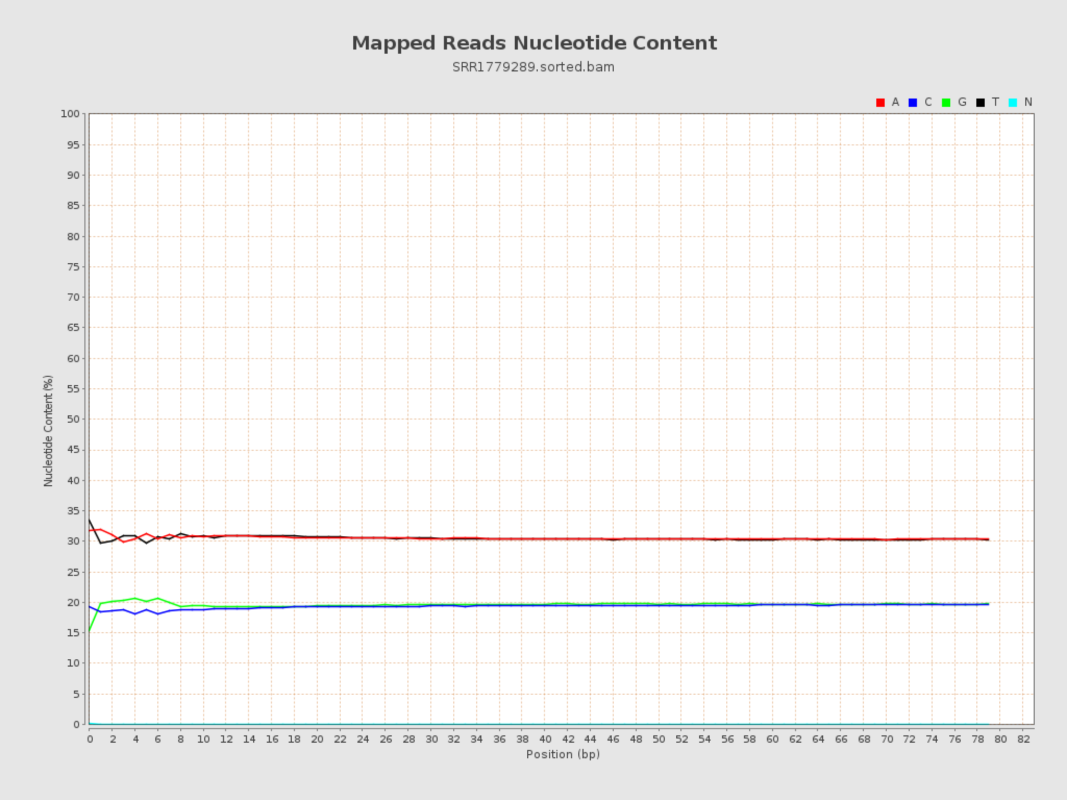
6. Results : Genome Fraction Coverage



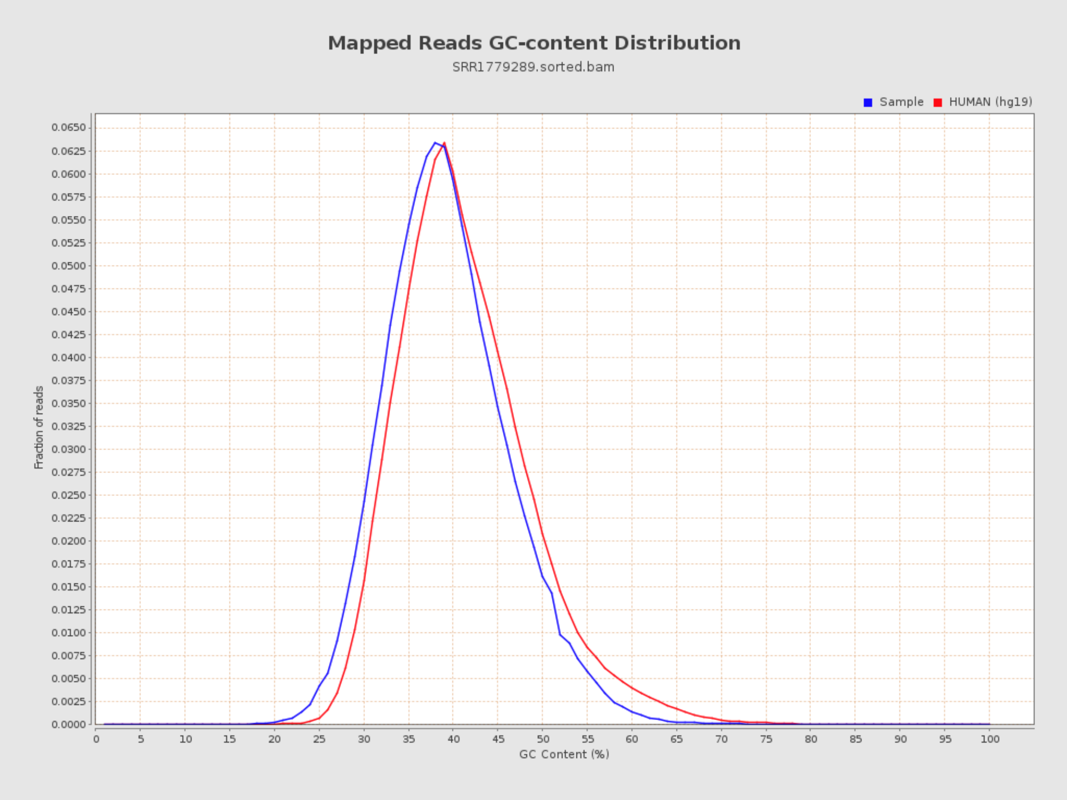
7. Results : Duplication Rate Histogram



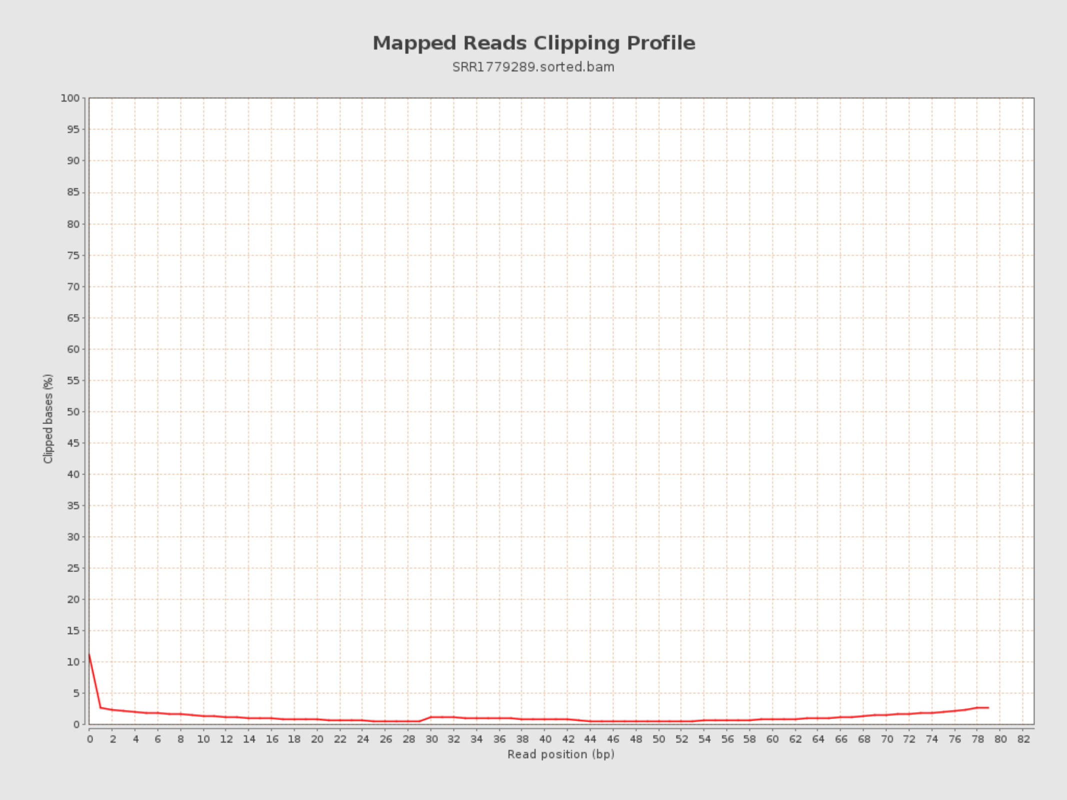
8. Results : Mapped Reads Nucleotide Content



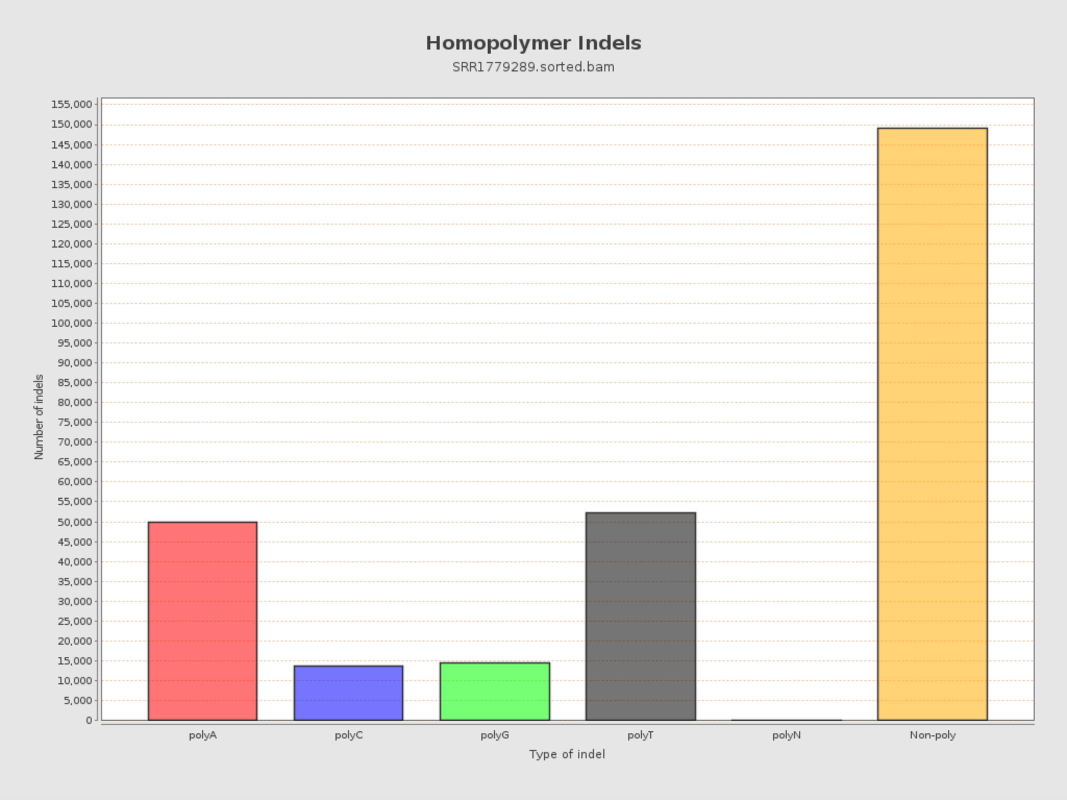
9. Results : Mapped Reads GC-content Distribution



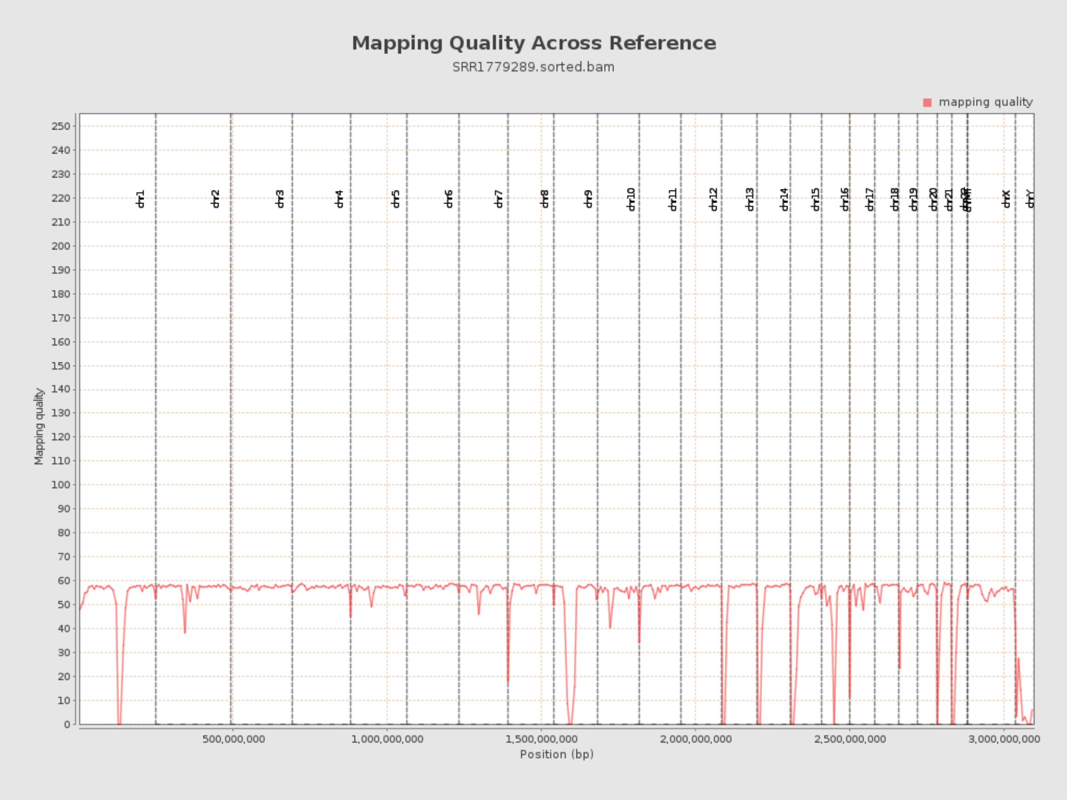
10. Results : Mapped Reads Clipping Profile



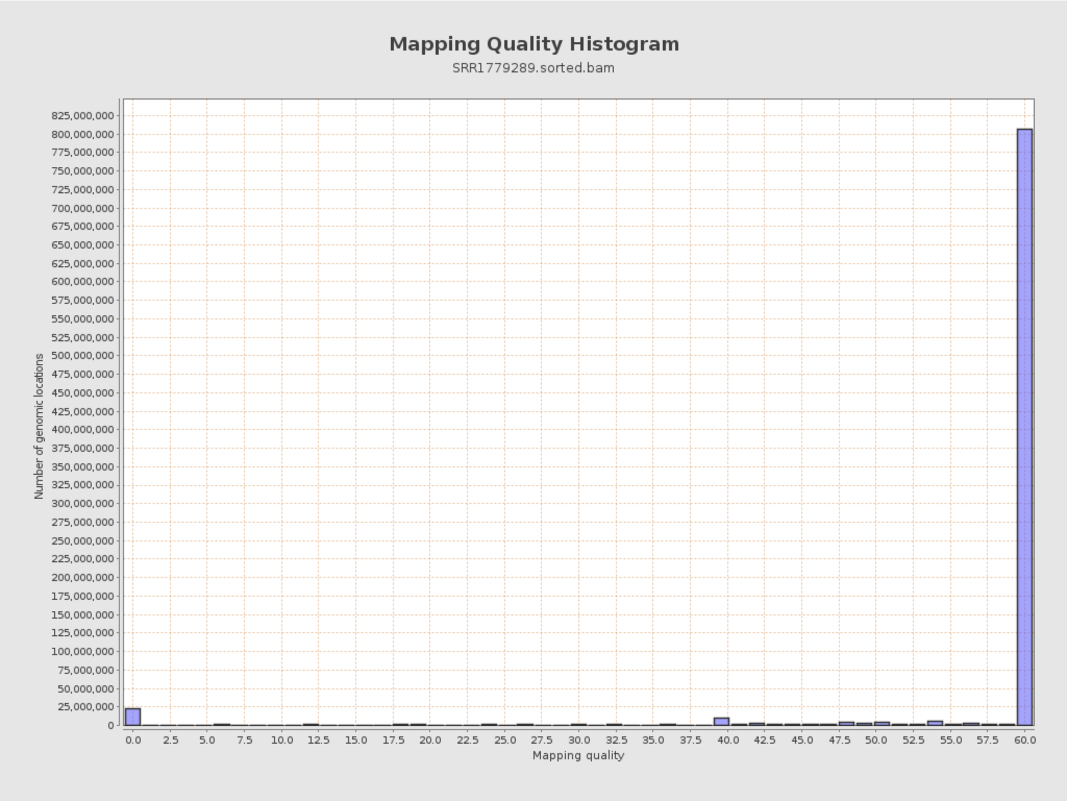
11. Results : Homopolymer Indels



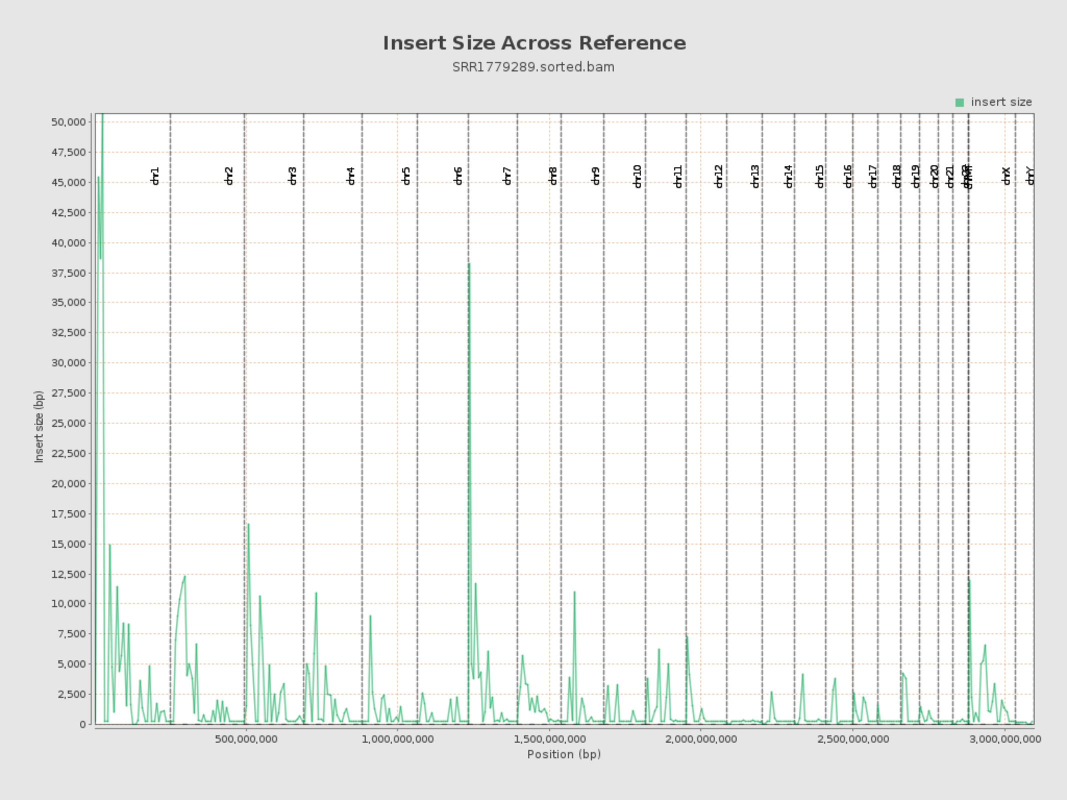
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram