Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 20:44:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779275.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_SRR1779275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779275_1.fastq.gz SRR1779275_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 20:44:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,382,504
Mapped reads	13,059,878 / 97.59%
Unmapped reads	322,626 / 2.41%
Mapped paired reads	13,059,878 / 97.59%
Mapped reads, first in pair	6,573,748 / 49.12%
Mapped reads, second in pair	6,486,130 / 48.47%
Mapped reads, both in pair	12,955,244 / 96.81%
Mapped reads, singletons	104,634 / 0.78%
Secondary alignments	0
Supplementary alignments	29,871 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	197,023 / 1.47%
Duplication rate	1.39%
Clipped reads	426,695 / 3.19%

2.2. ACGT Content

Number/percentage of A's	319,868,782 / 30.78%
Number/percentage of C's	198,380,470 / 19.09%
Number/percentage of T's	318,805,763 / 30.68%
Number/percentage of G's	201,950,923 / 19.43%
Number/percentage of N's	196,671 / 0.02%

GC Percentage	38.52%

2.3. Coverage

Mean	0.3358
Standard Deviation	0.9895

2.4. Mapping Quality

Mean Mapping Quality	52.91

2.5. Insert size

Mean	42,876.58
Standard Deviation	1,960,584.05
P25/Median/P75	158 / 208 / 277

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	4,117,632
Insertions	76,789
Mapped reads with at least one insertion	0.58%
Deletions	96,824
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.78%

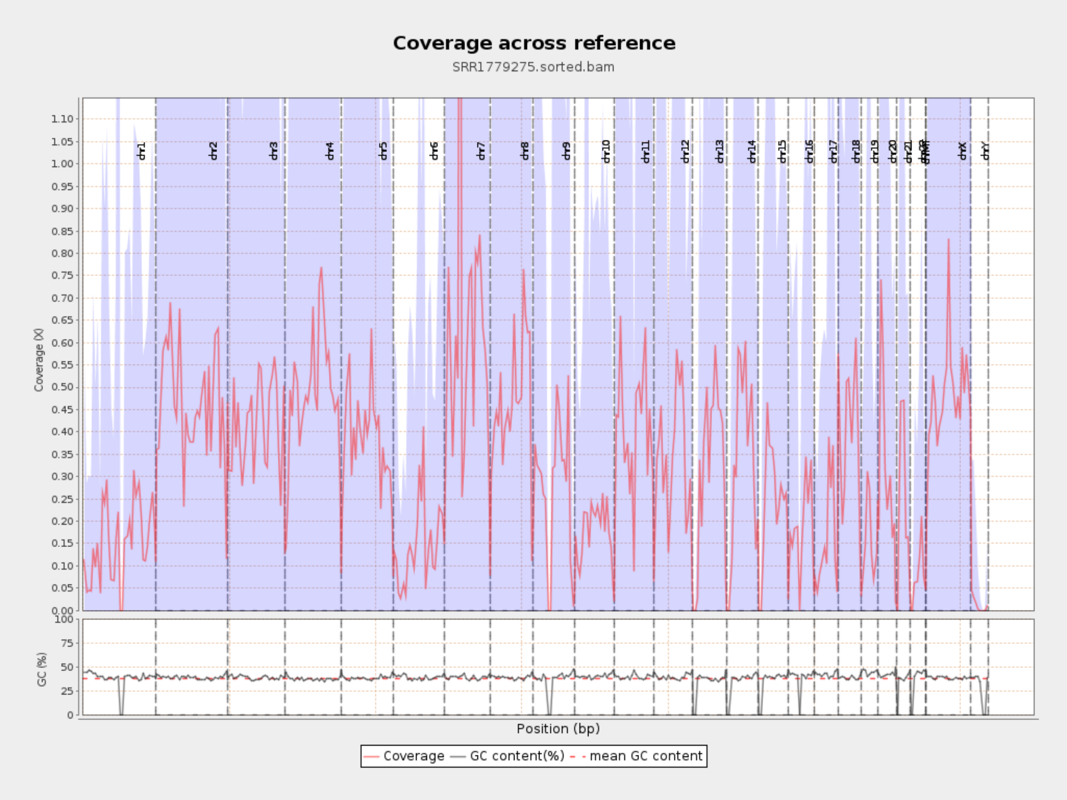
2.7. Chromosome stats

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

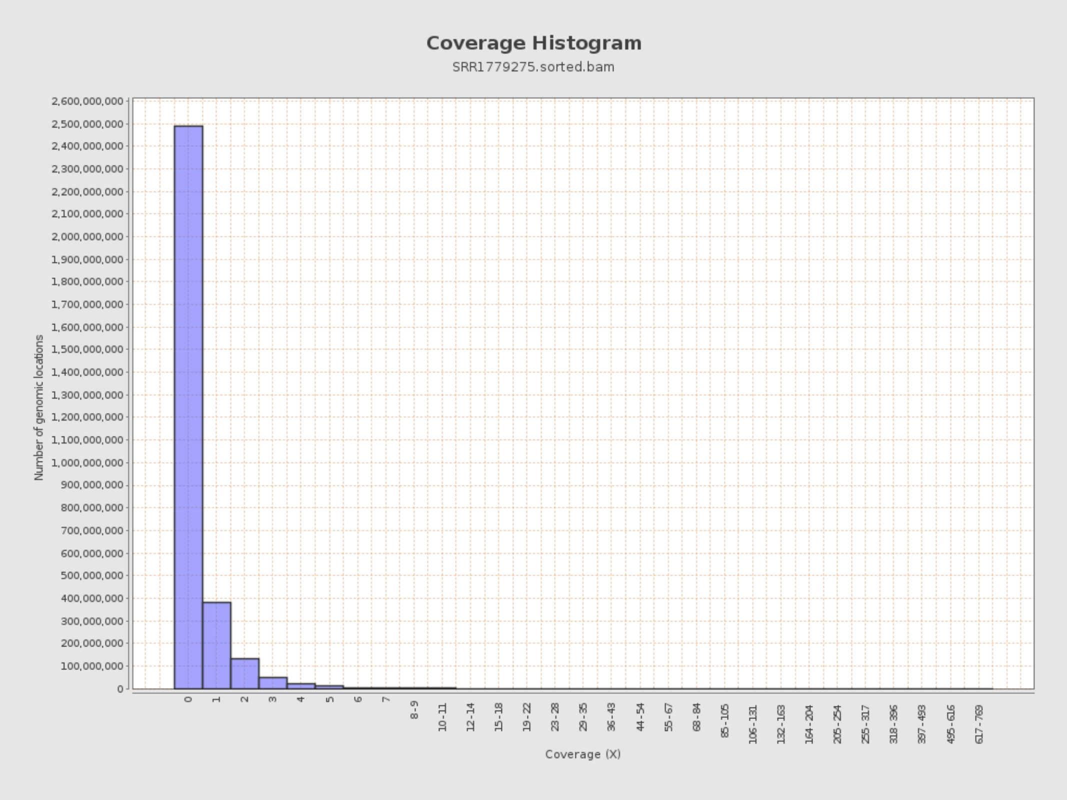
		bases	**coverage**	**deviation**
chr1	249250621	38123206	0.153	0.9035
chr2	243199373	112899274	0.4642	1.0432
chr3	198022430	82211500	0.4152	0.9657
chr4	191154276	93853510	0.491	1.0255
chr5	180915260	68960915	0.3812	0.9108
chr6	171115067	25356958	0.1482	0.5284
chr7	159138663	102271668	0.6427	1.9494
chr8	146364022	69634494	0.4758	1.0182
chr9	141213431	39262245	0.278	0.819
chr10	135534747	24643648	0.1818	1.1466
chr11	135006516	54881965	0.4065	1.0039
chr12	133851895	45165123	0.3374	0.8693
chr13	115169878	37281052	0.3237	0.8474
chr14	107349540	36875187	0.3435	0.8749
chr15	102531392	24938554	0.2432	0.7117
chr16	90354753	16344155	0.1809	0.5936
chr17	81195210	13233145	0.163	0.6405
chr18	78077248	31669773	0.4056	0.9629
chr19	59128983	9434013	0.1595	0.6939
chr20	63025520	20667427	0.3279	0.8936
chr21	48129895	11378483	0.2364	0.7641
chr22	51304566	4214072	0.0821	0.3915
chrMT	16571	1245	0.0751	0.3097
chrX	155270560	75359407	0.4853	1.0588

chrY	59373566	743499	0.0125	0.1686

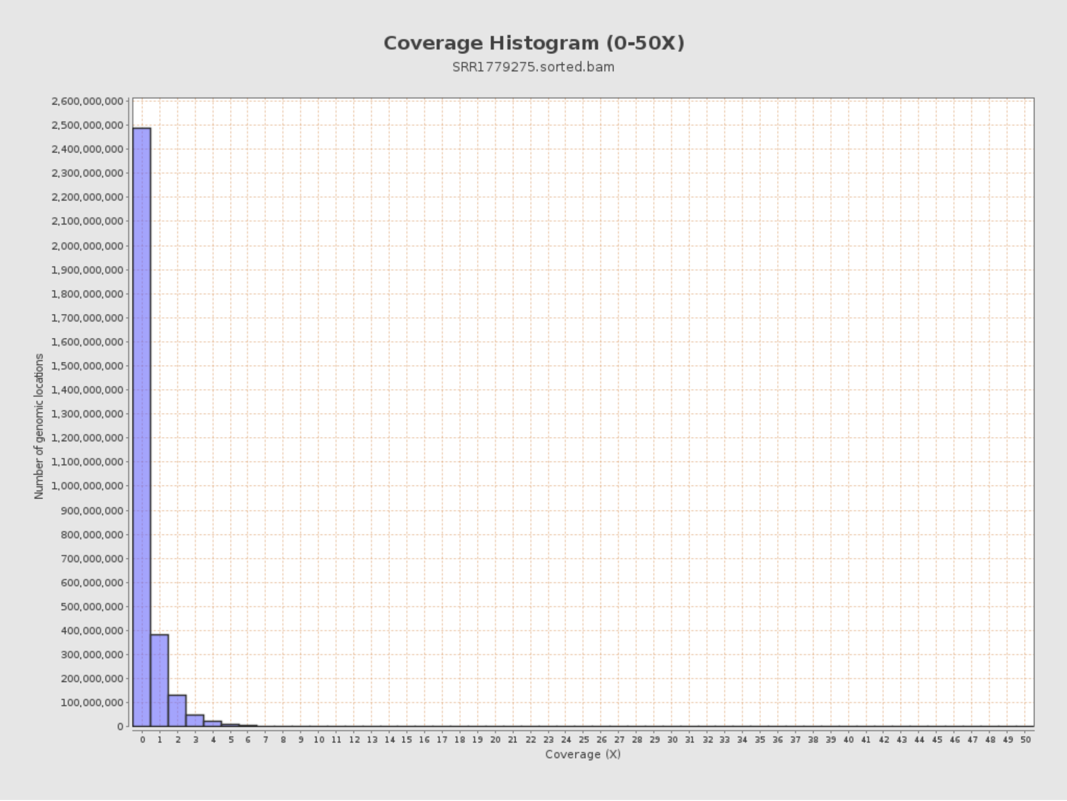
3. Results : Coverage across reference



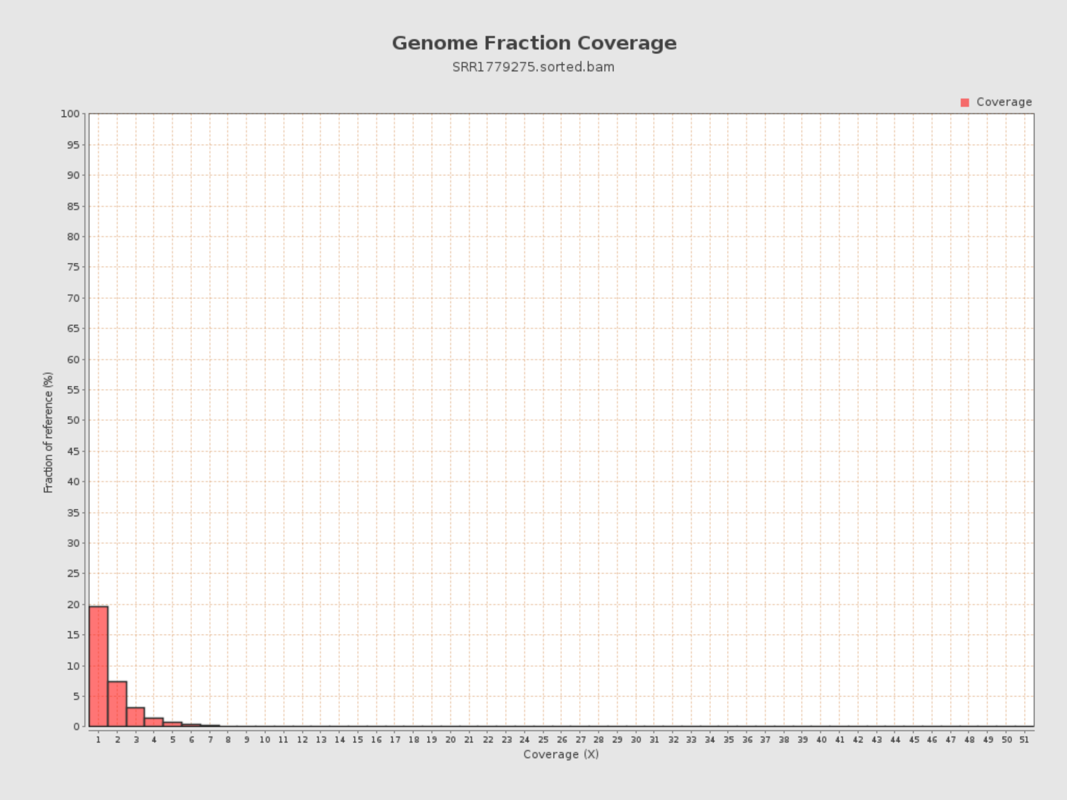
4. Results : Coverage Histogram



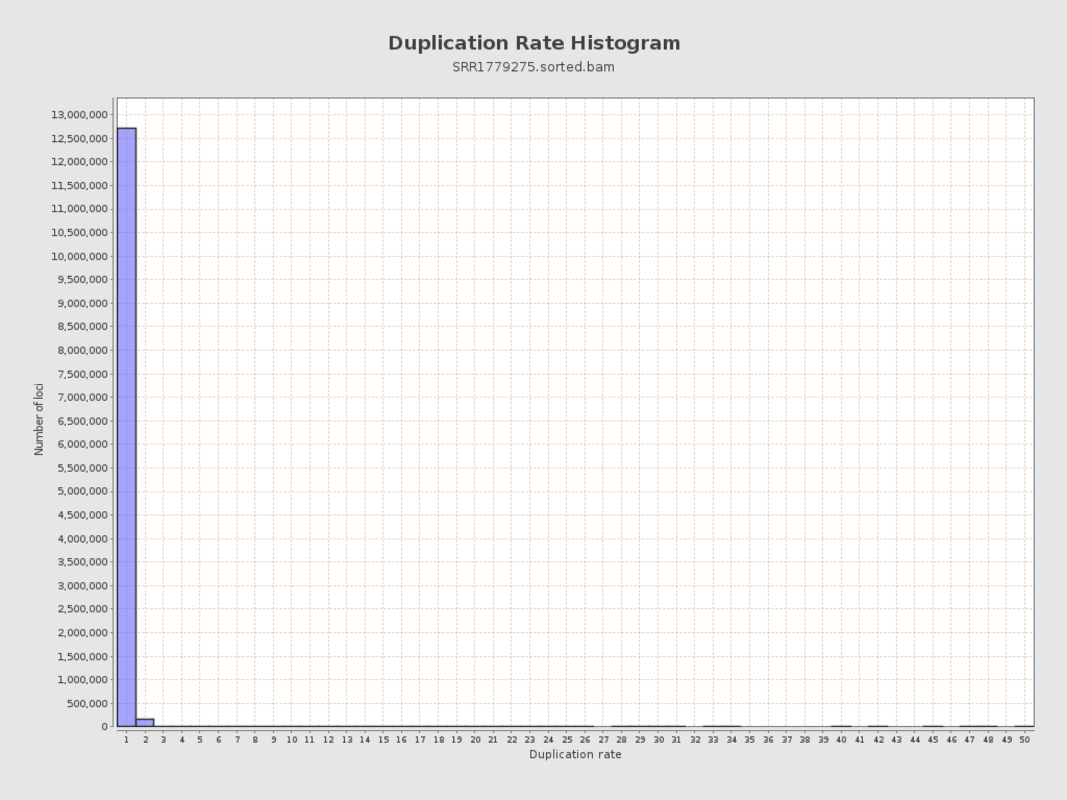
5. Results : Coverage Histogram (0-50X)



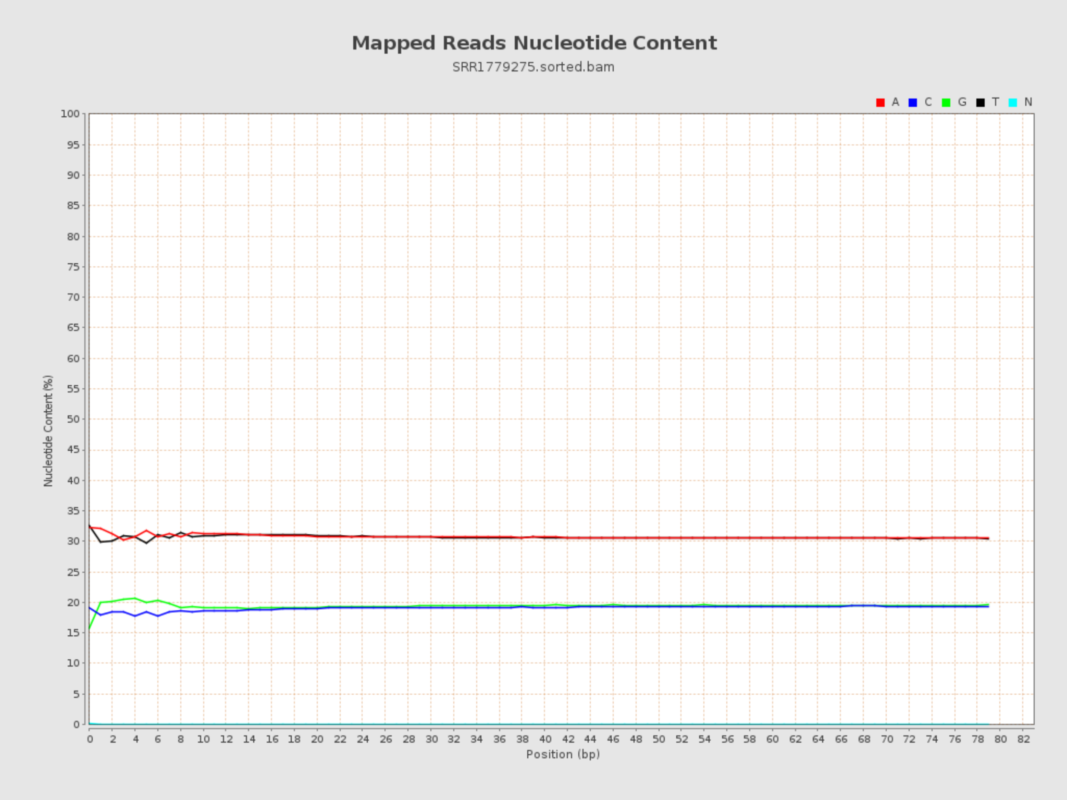
6. Results : Genome Fraction Coverage



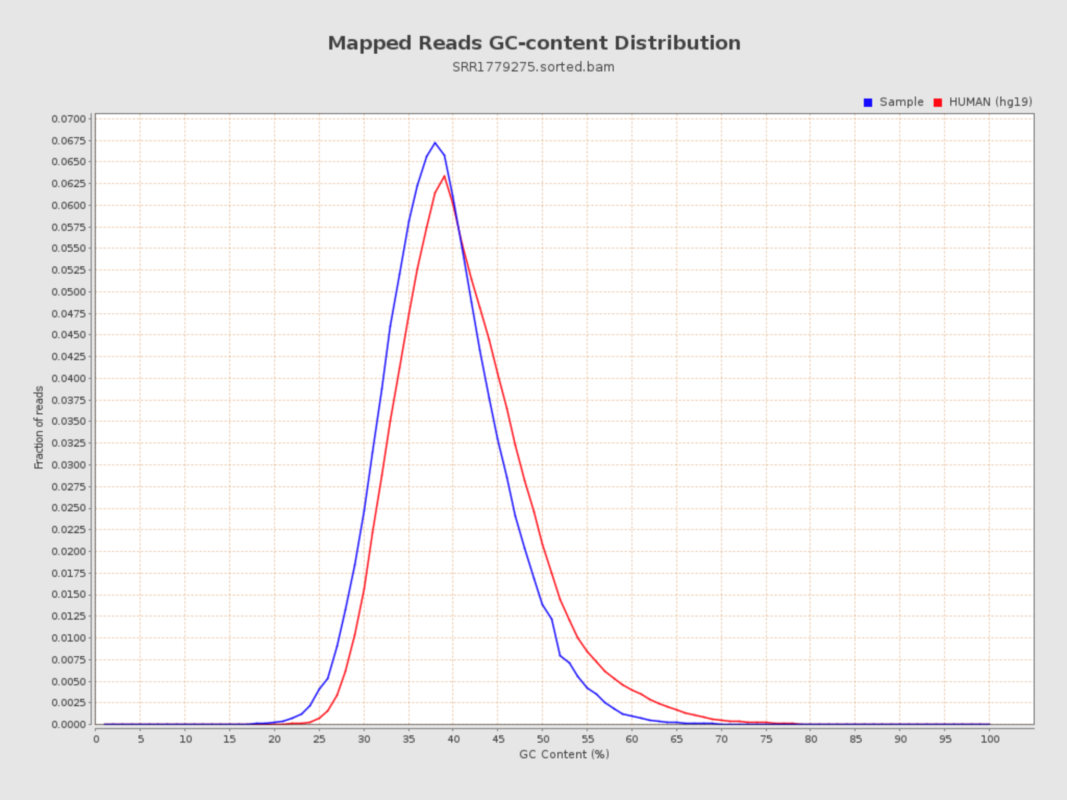
7. Results : Duplication Rate Histogram



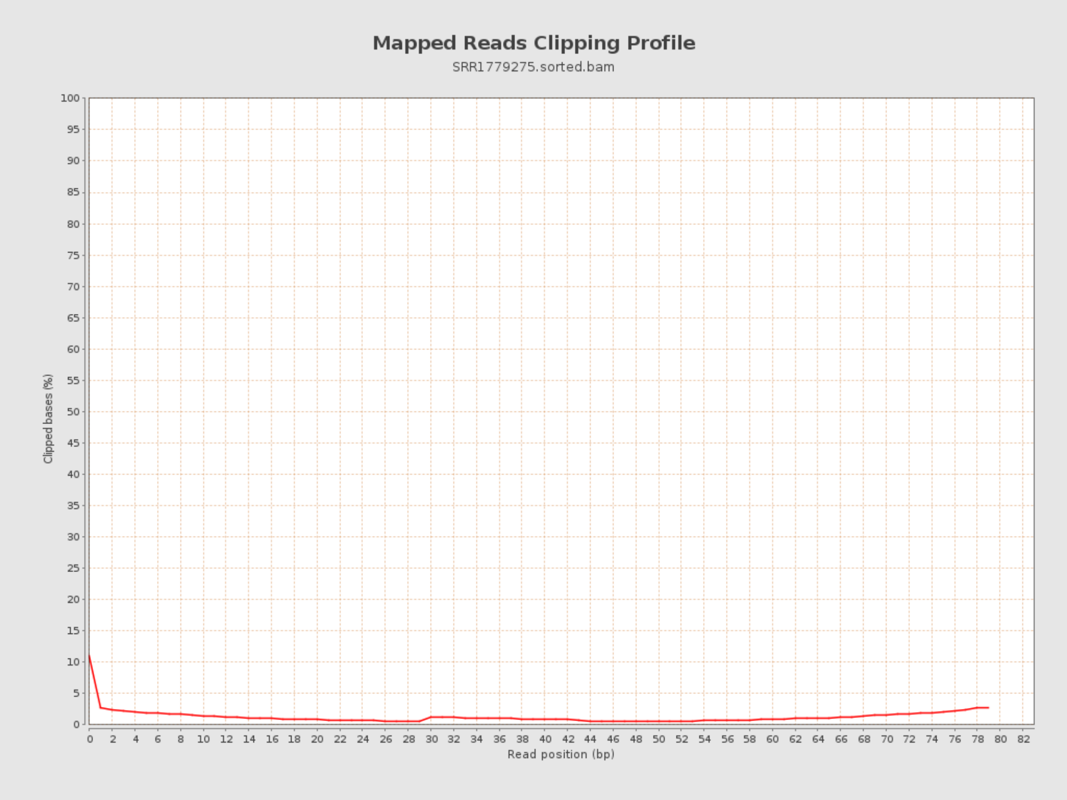
8. Results : Mapped Reads Nucleotide Content



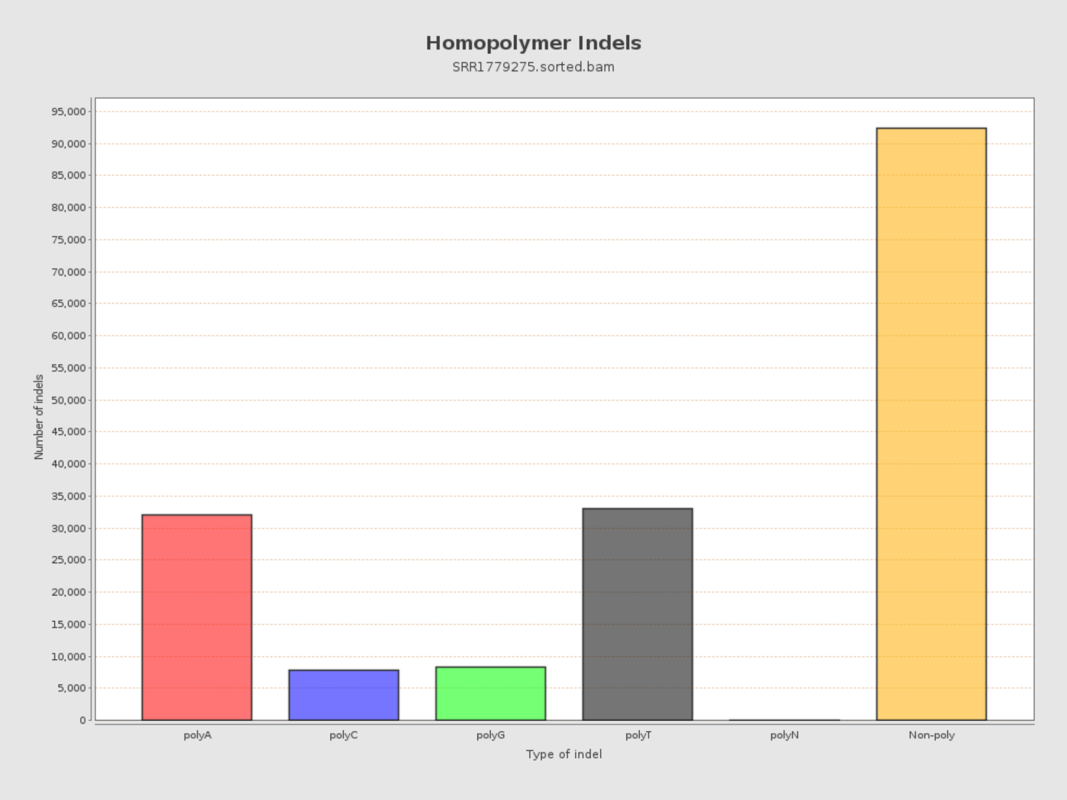
9. Results : Mapped Reads GC-content Distribution



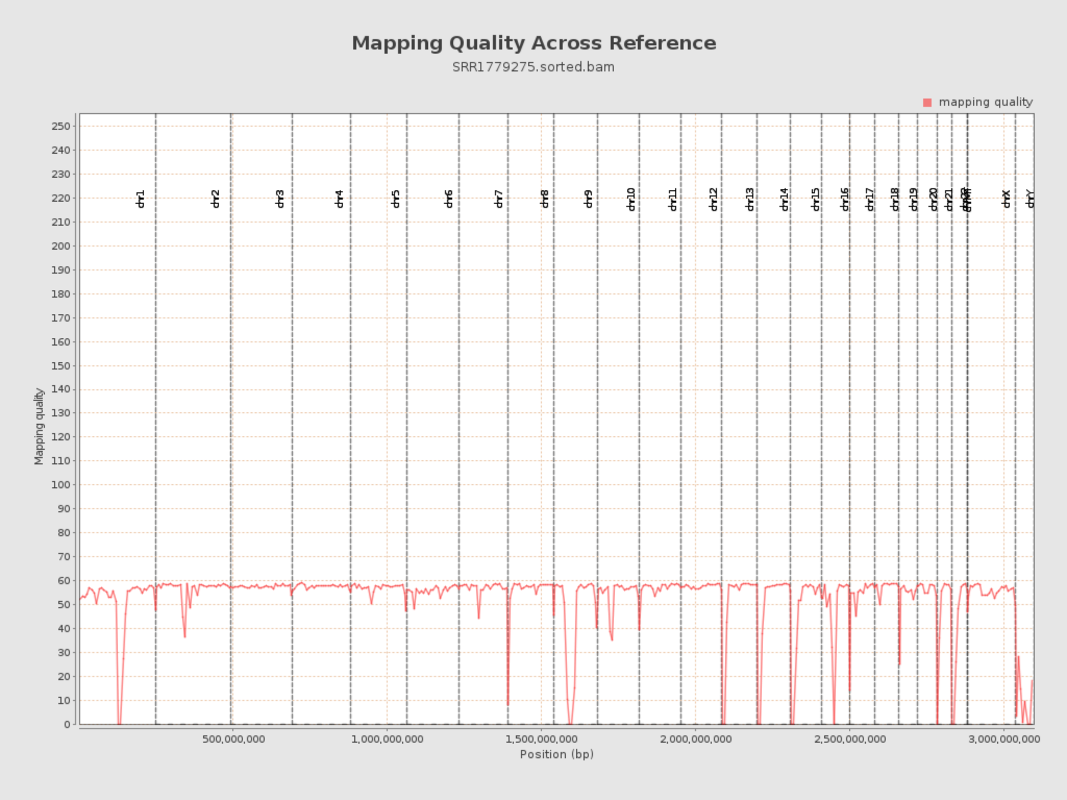
10. Results : Mapped Reads Clipping Profile



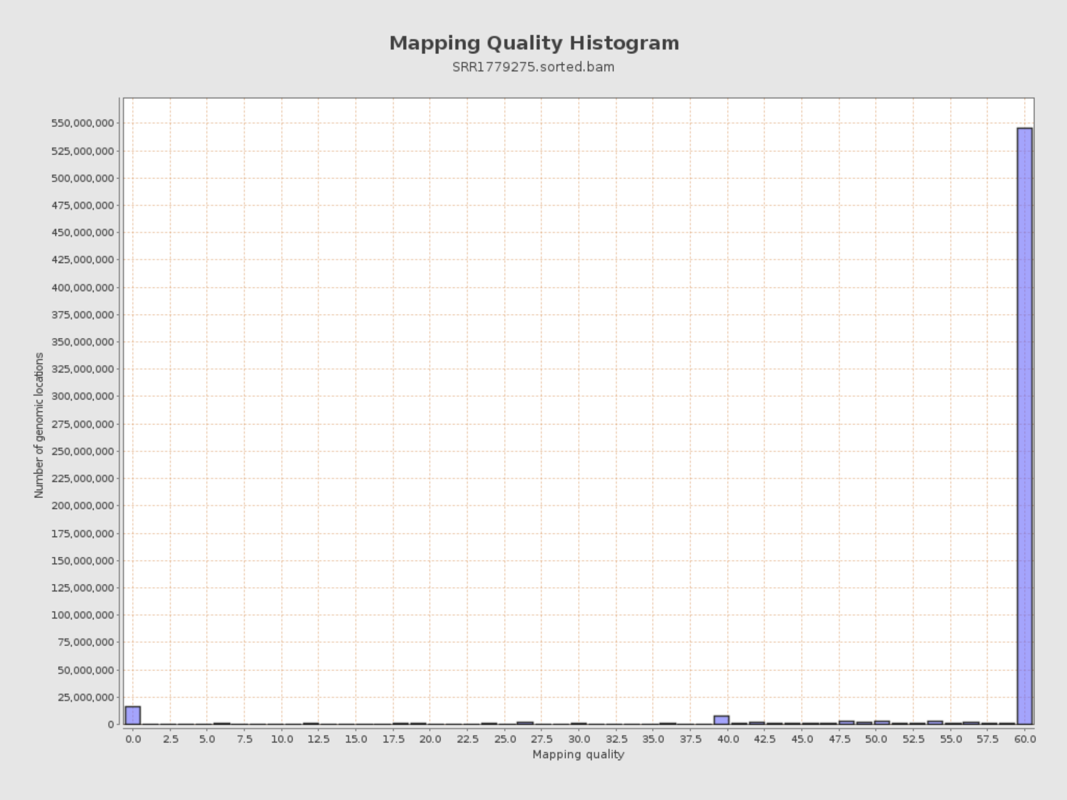
11. Results : Homopolymer Indels



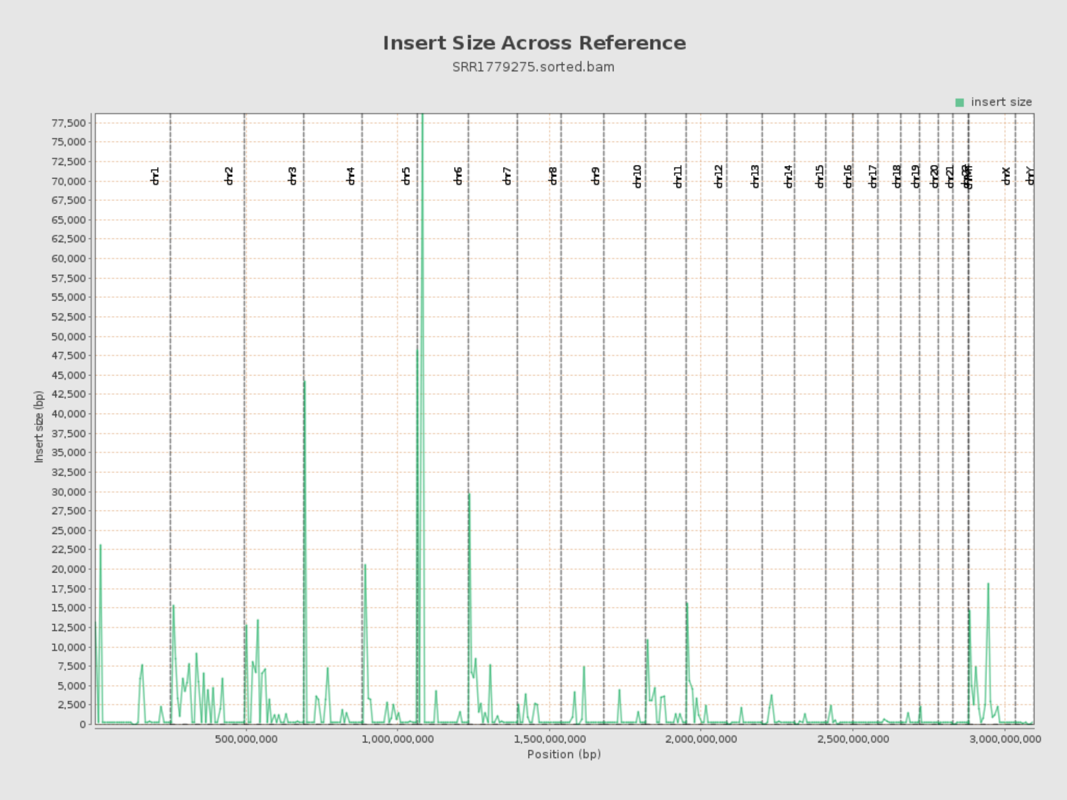
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram