Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 23:07:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779096.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_SRR1779096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779096_1.fastq.gz SRR1779096_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 23:07:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779096.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,043,322
Mapped reads	17,519,765 / 97.1%
Unmapped reads	523,557 / 2.9%
Mapped paired reads	17,519,765 / 97.1%
Mapped reads, first in pair	8,835,376 / 48.97%
Mapped reads, second in pair	8,684,389 / 48.13%
Mapped reads, both in pair	17,306,998 / 95.92%
Mapped reads, singletons	212,767 / 1.18%
Secondary alignments	0
Supplementary alignments	106,893 / 0.59%
Read min/max/mean length	30 / 101 / 101.24
Duplicated reads (estimated)	472,538 / 2.62%
Duplication rate	2.42%
Clipped reads	1,071,585 / 5.94%

2.2. ACGT Content

Number/percentage of A's	534,604,430 / 30.55%
Number/percentage of C's	338,868,793 / 19.36%
Number/percentage of T's	532,587,605 / 30.43%
Number/percentage of G's	343,400,295 / 19.62%
Number/percentage of N's	704,171 / 0.04%

GC Percentage	38.98%

2.3. Coverage

Mean	0.5655
Standard Deviation	1.6454

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	62,541.09
Standard Deviation	2,308,209.8
P25/Median/P75	167 / 219 / 289

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	7,321,141
Insertions	146,957
Mapped reads with at least one insertion	0.83%
Deletions	178,121
Mapped reads with at least one deletion	1%
Homopolymer indels	46.94%

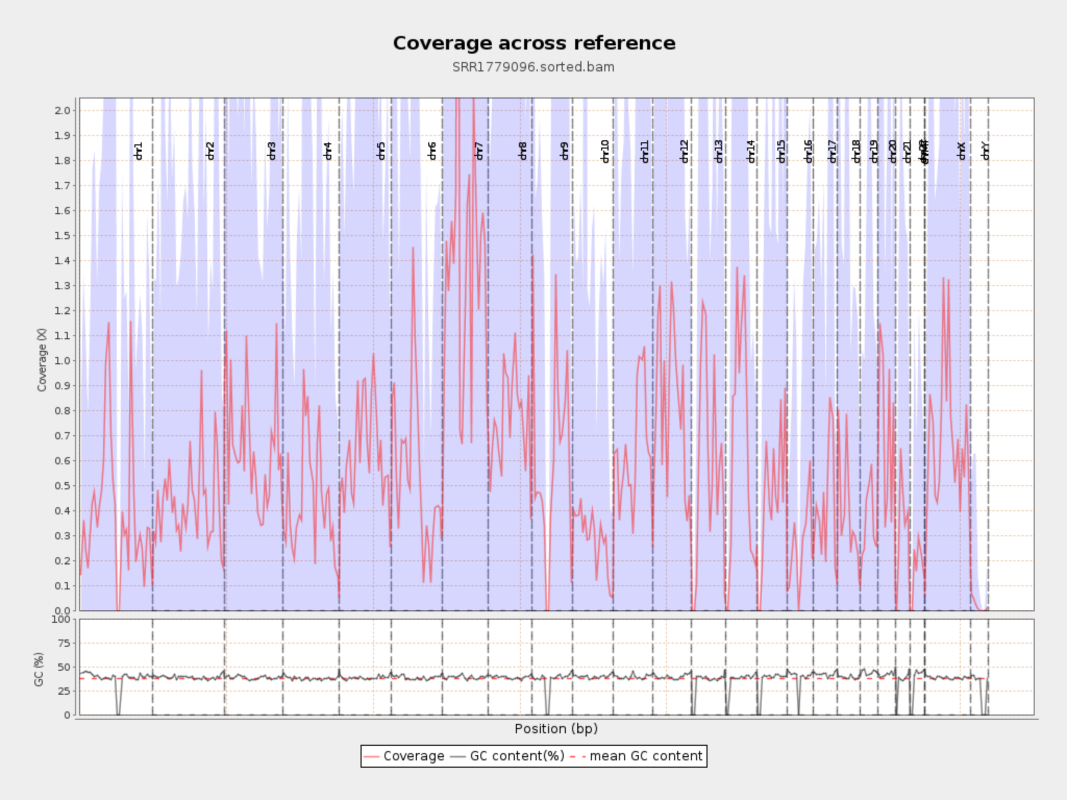
2.7. Chromosome stats

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

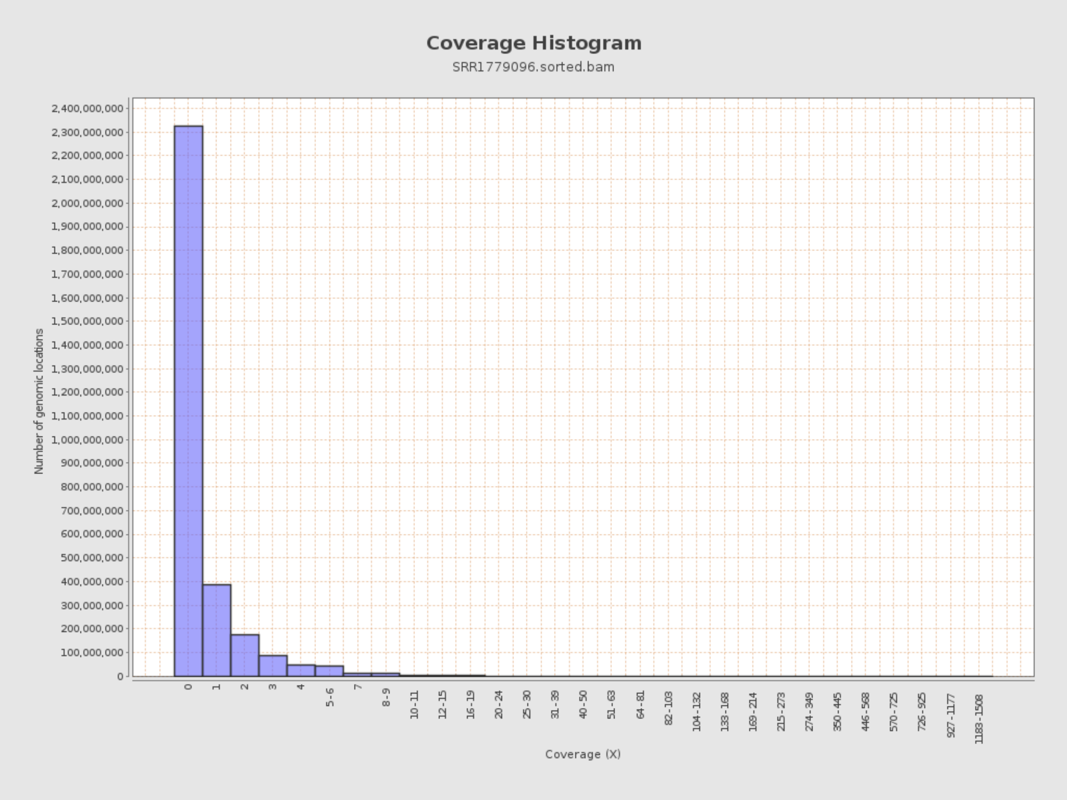
		bases	coverage	deviation
chr1	249250621	96688500	0.3879	1.2556
chr2	243199373	105892112	0.4354	1.3921
chr3	198022430	127600206	0.6444	1.4591
chr4	191154276	85756169	0.4486	1.2556
chr5	180915260	112815079	0.6236	1.4924
chr6	171115067	95009606	0.5552	1.4741
chr7	159138663	227666101	1.4306	3.3532
chr8	146364022	112037351	0.7655	1.5927
chr9	141213431	84044860	0.5952	1.5299
chr10	135534747	38954380	0.2874	2.4752
chr11	135006516	86247539	0.6388	1.5067
chr12	133851895	109838895	0.8206	1.7216
chr13	115169878	66898119	0.5809	1.4416
chr14	107349540	68327077	0.6365	1.6663
chr15	102531392	46287438	0.4514	1.2971
chr16	90354753	23187397	0.2566	0.8703
chr17	81195210	33652951	0.4145	1.1557
chr18	78077248	32391509	0.4149	1.2711
chr19	59128983	20732126	0.3506	1.0859
chr20	63025520	44443481	0.7052	1.5497
chr21	48129895	16815465	0.3494	1.131
chr22	51304566	8487262	0.1654	0.6334
chrMT	16571	1035	0.0625	0.2518
chrX	155270560	105732970	0.681	1.7231

chrY	59373566	1055006	0.0178	0.339

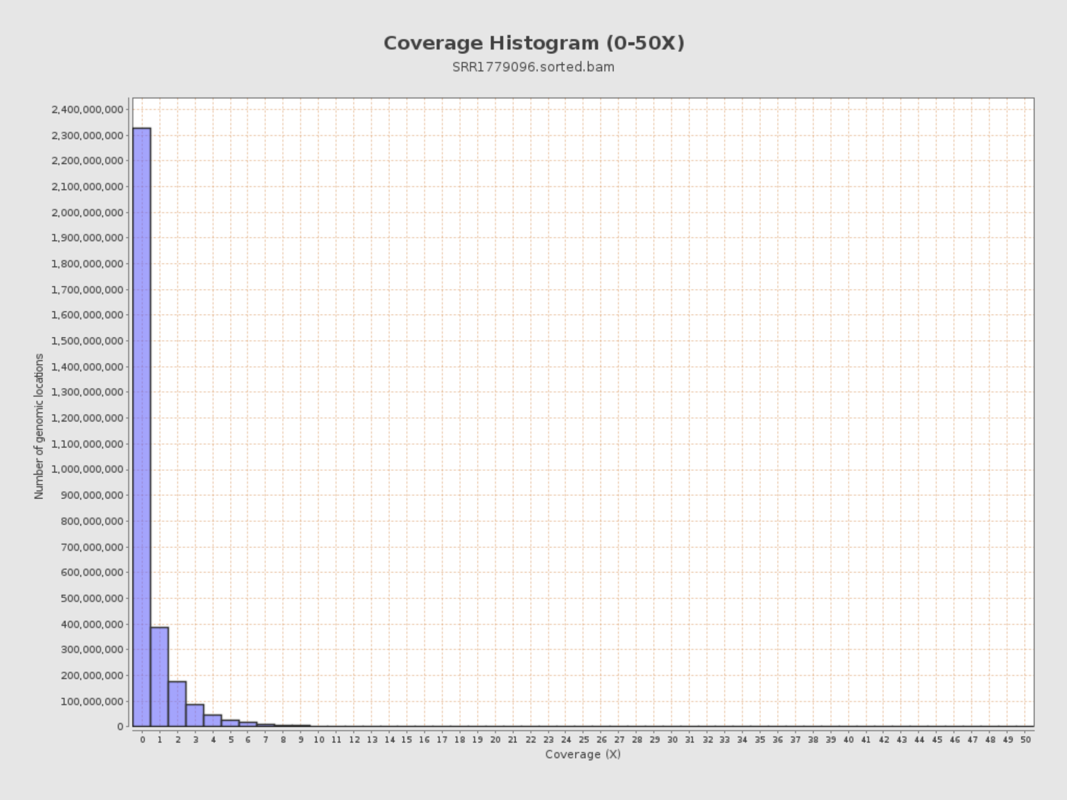
3. Results : Coverage across reference



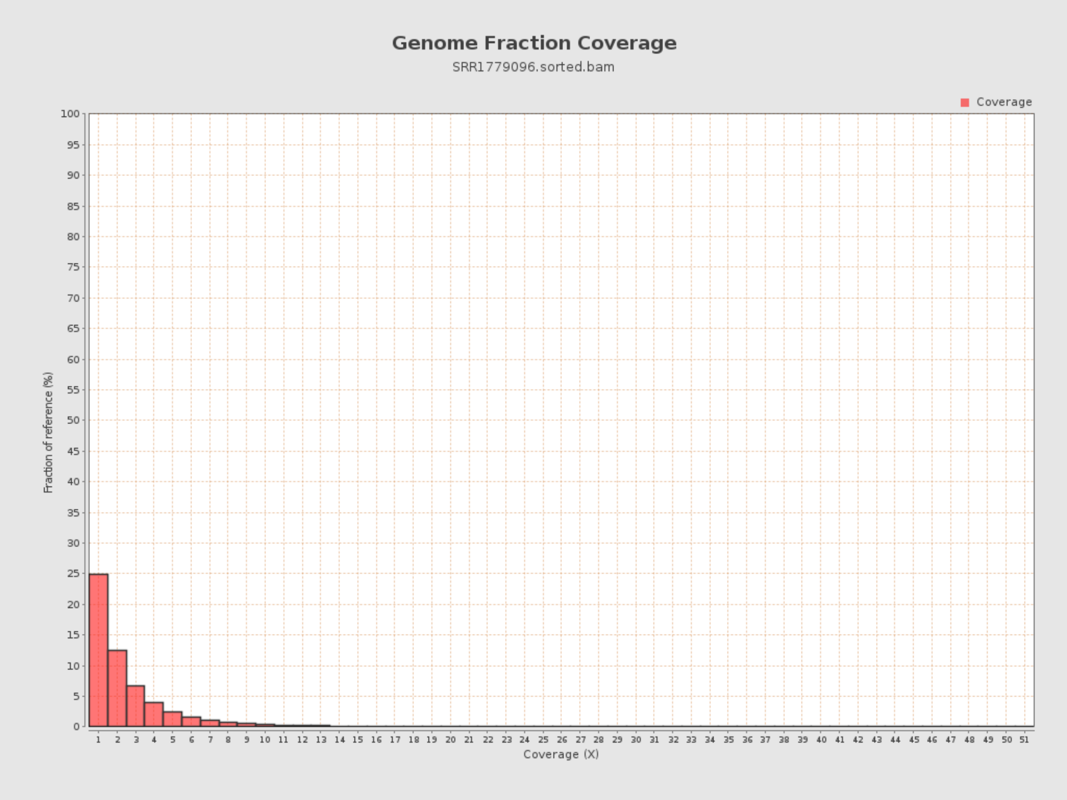
4. Results : Coverage Histogram



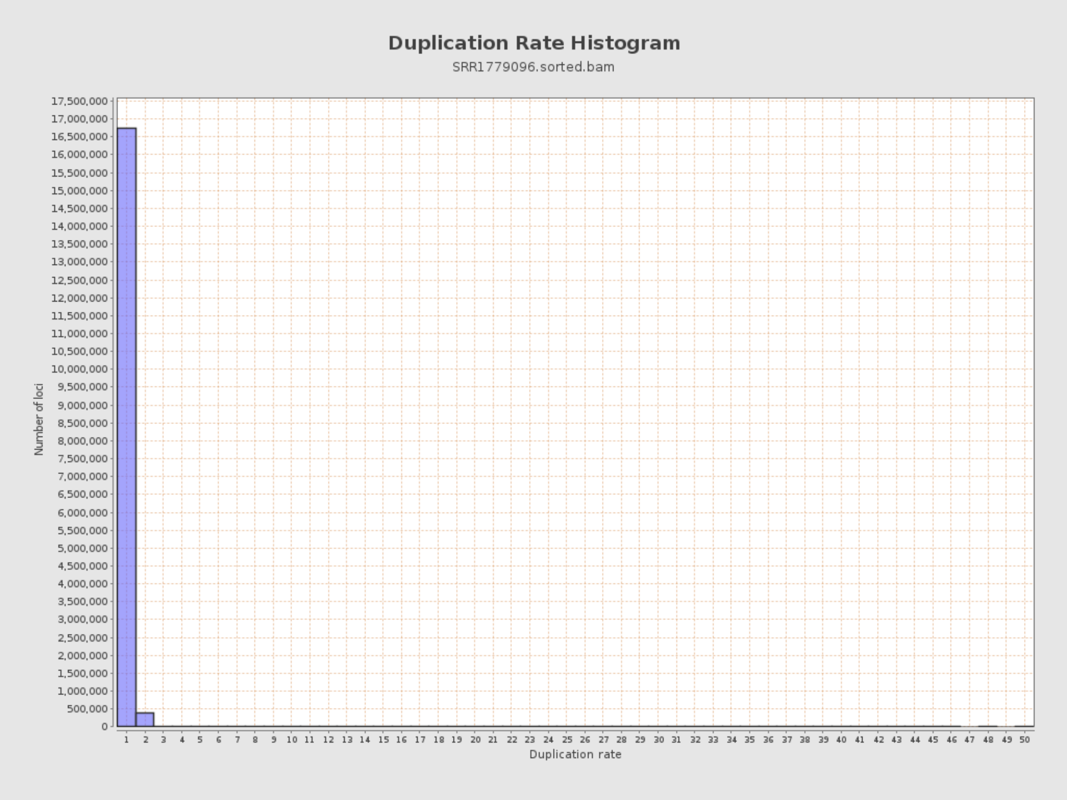
5. Results : Coverage Histogram (0-50X)



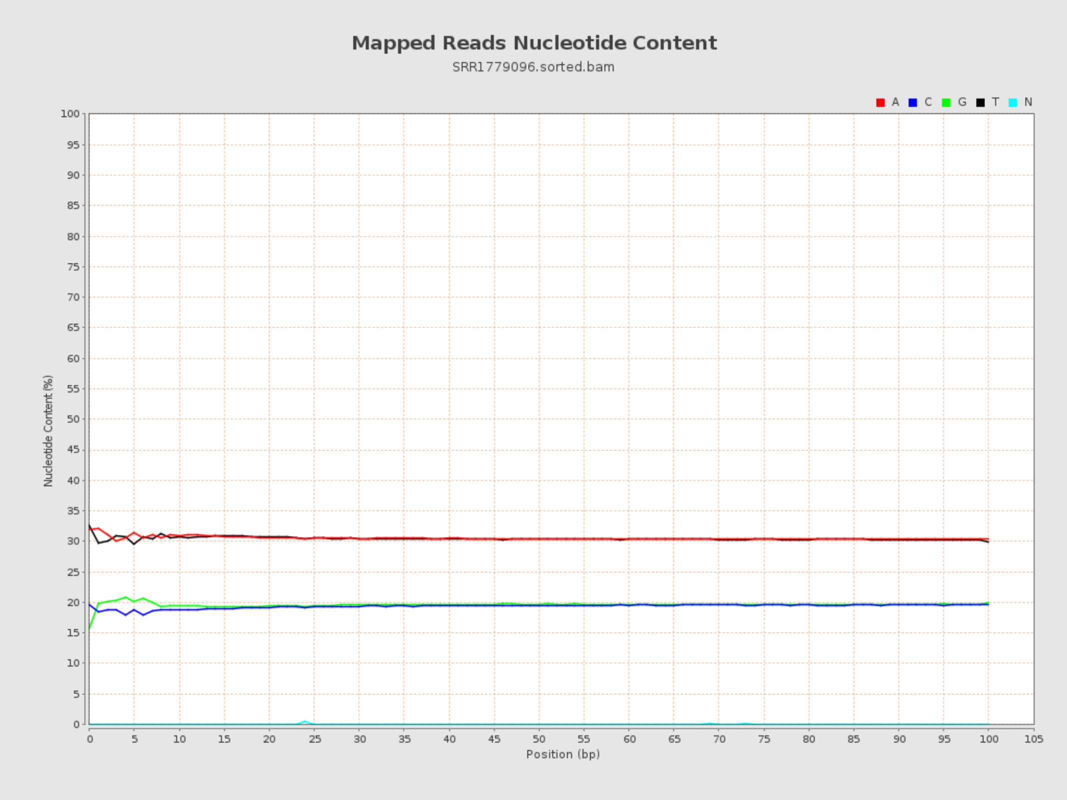
6. Results : Genome Fraction Coverage



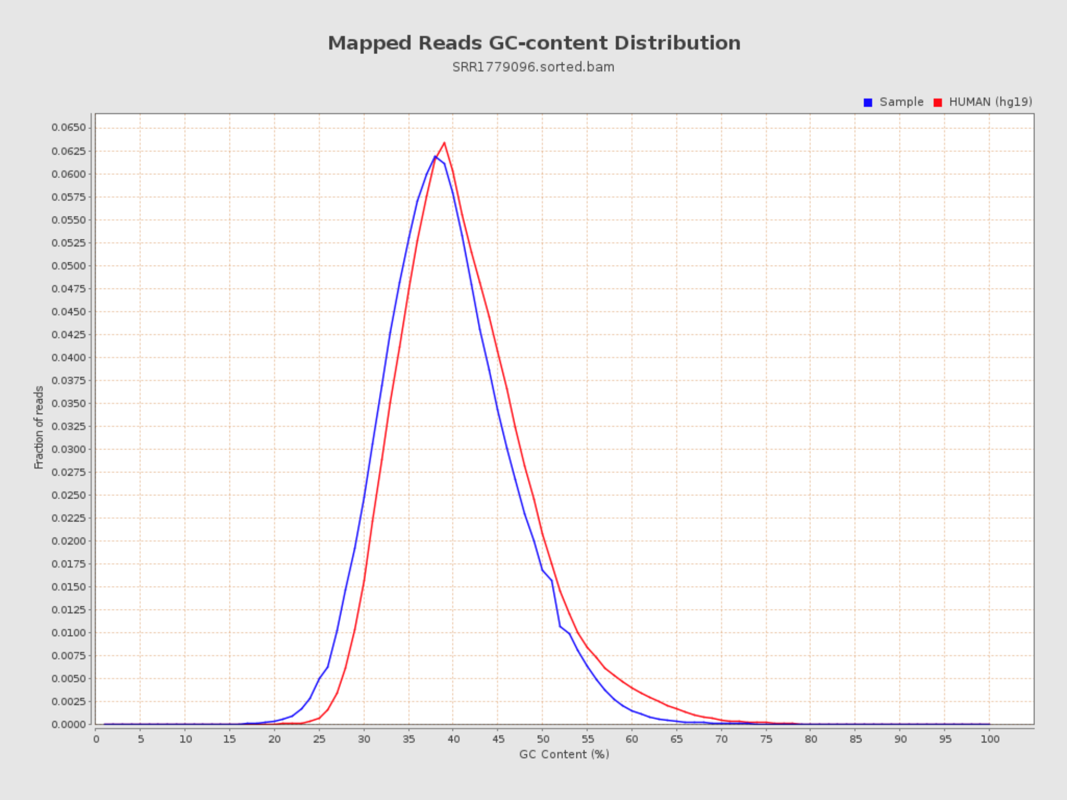
7. Results : Duplication Rate Histogram



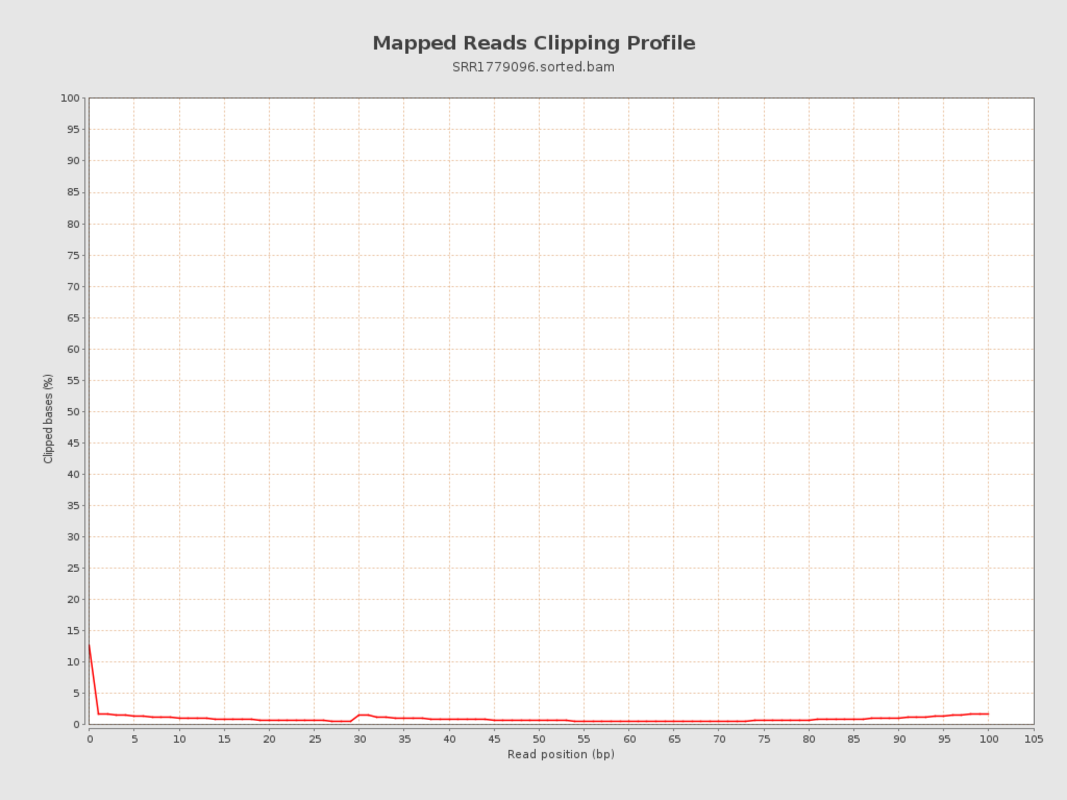
8. Results : Mapped Reads Nucleotide Content



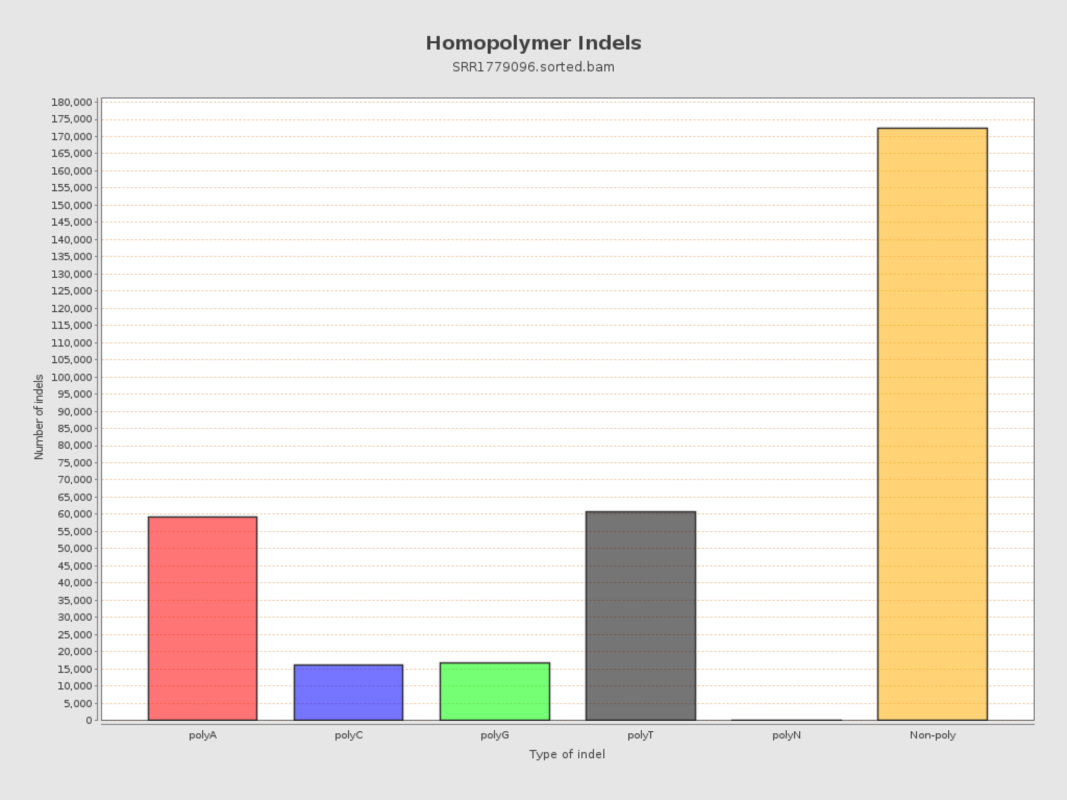
9. Results : Mapped Reads GC-content Distribution



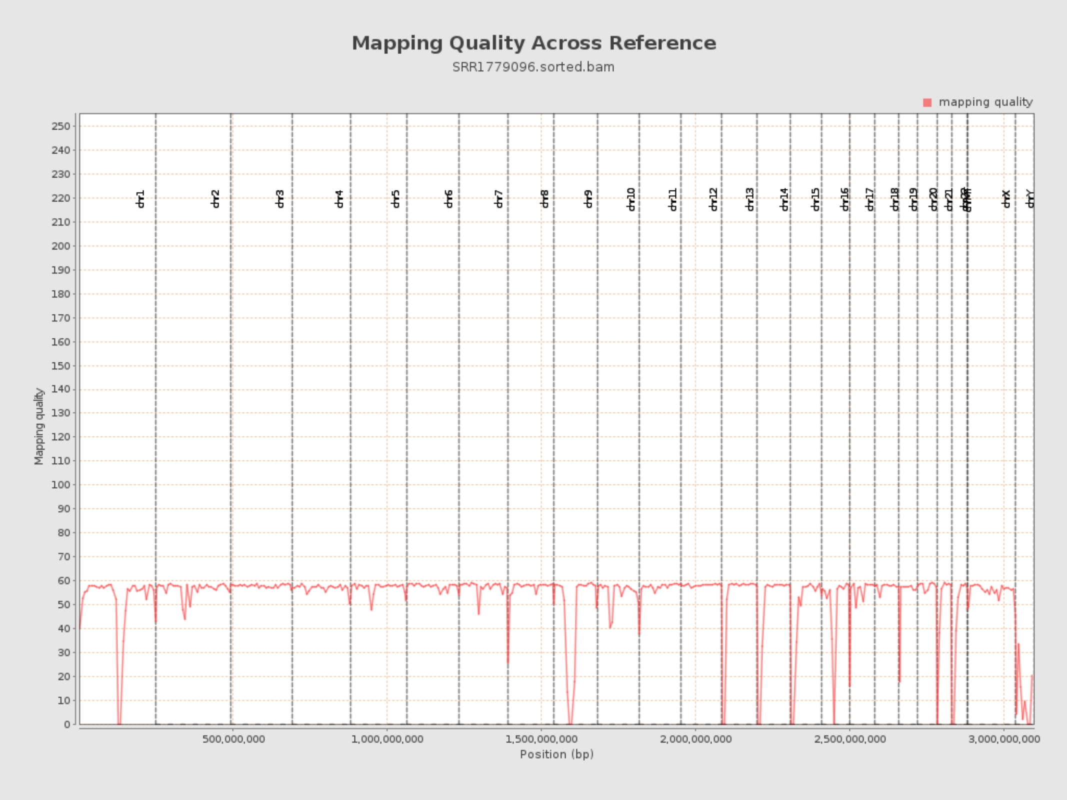
10. Results : Mapped Reads Clipping Profile



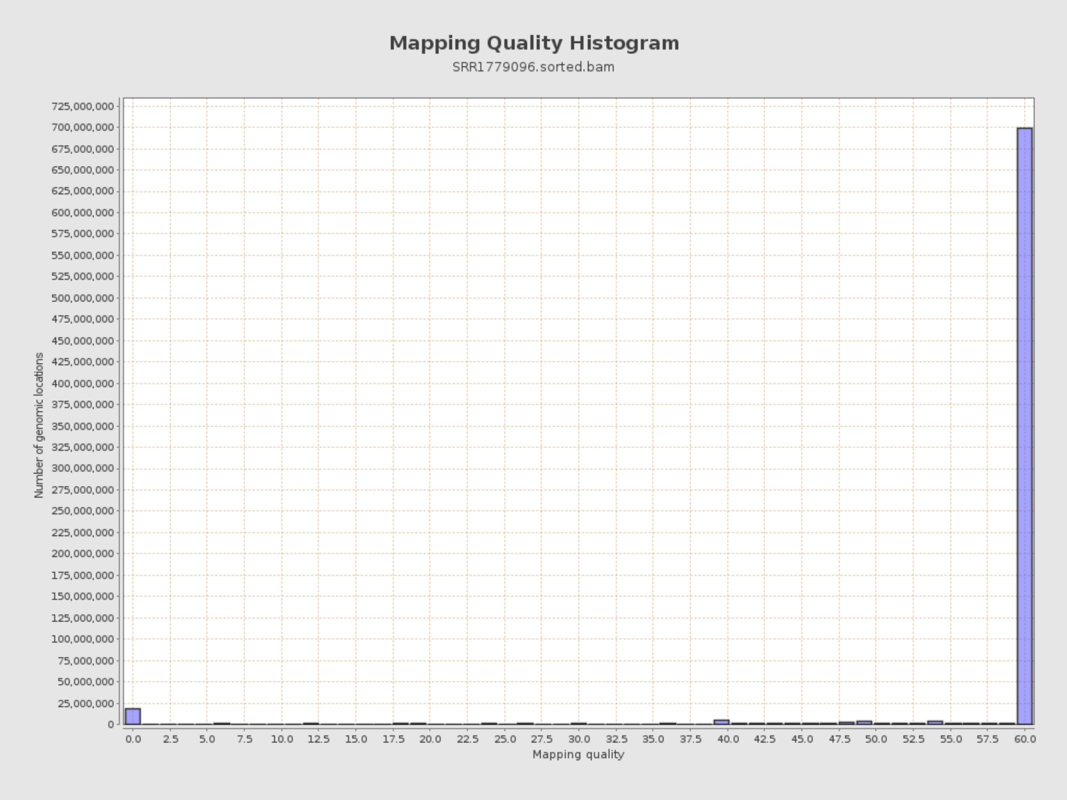
11. Results : Homopolymer Indels



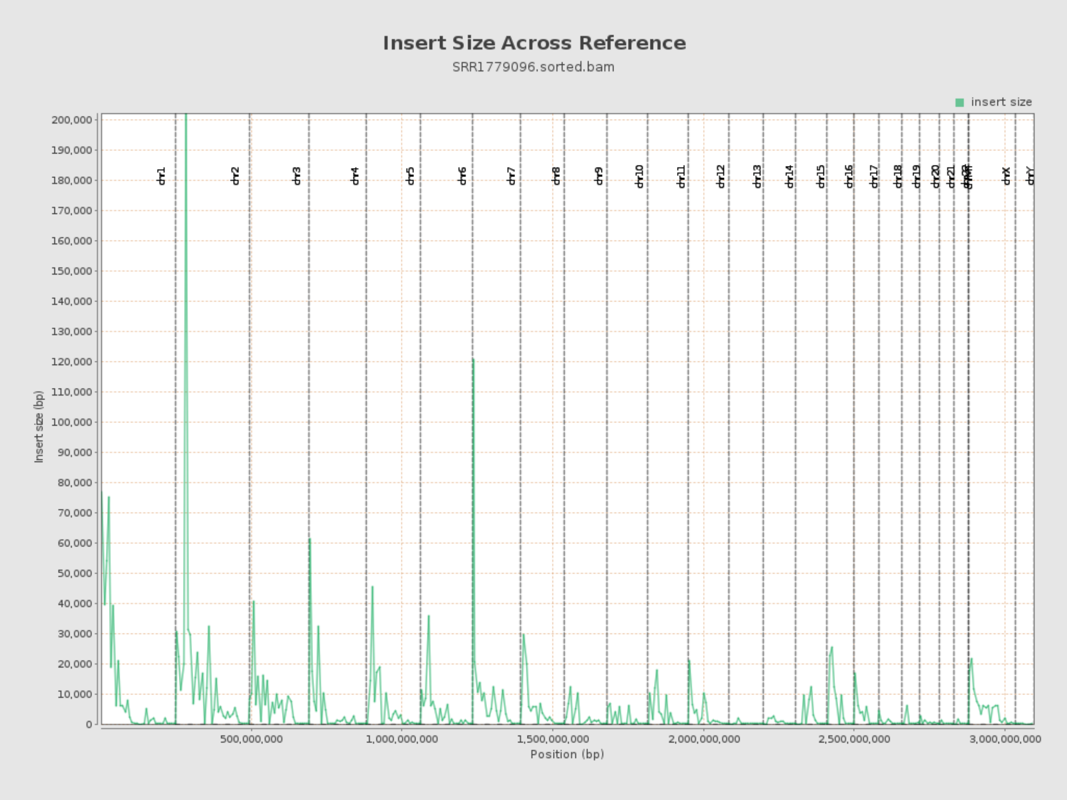
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram