Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 03:38:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779301.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_SRR1779301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779301_1.fastq.gz SRR1779301_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 03:38:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,822,656
Mapped reads	30,224,886 / 94.98%
Unmapped reads	1,597,770 / 5.02%
Mapped paired reads	30,224,886 / 94.98%
Mapped reads, first in pair	15,234,844 / 47.87%
Mapped reads, second in pair	14,990,042 / 47.1%
Mapped reads, both in pair	29,928,852 / 94.05%
Mapped reads, singletons	296,034 / 0.93%
Secondary alignments	0
Supplementary alignments	75,541 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	2,648,182 / 8.32%
Duplication rate	7.54%
Clipped reads	959,139 / 3.01%

2.2. ACGT Content

Number/percentage of A's	739,422,457 / 30.74%
Number/percentage of C's	459,907,306 / 19.12%
Number/percentage of T's	736,201,904 / 30.61%
Number/percentage of G's	469,161,151 / 19.51%
Number/percentage of N's	633,338 / 0.03%

GC Percentage	38.63%

2.3. Coverage

Mean	0.7771
Standard Deviation	3.7632

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	36,162.57
Standard Deviation	1,787,421.42
P25/Median/P75	172 / 227 / 302

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	8,799,326
Insertions	181,530
Mapped reads with at least one insertion	0.59%
Deletions	227,099
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.73%

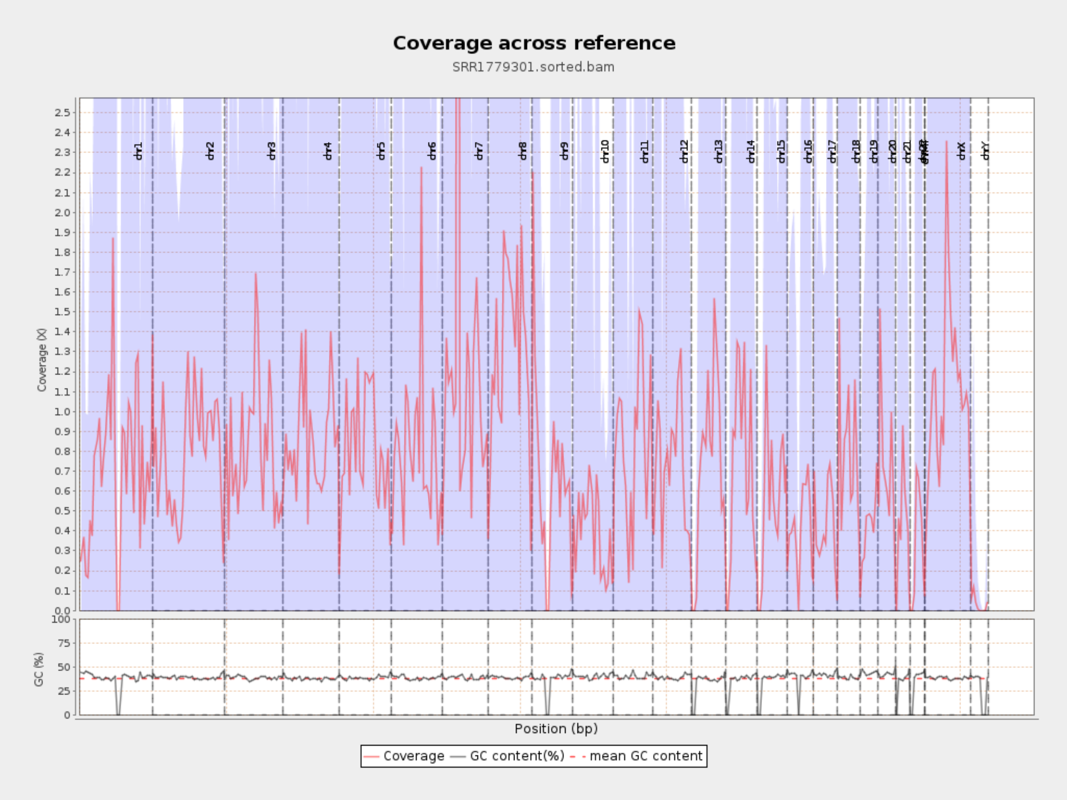
2.7. Chromosome stats

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

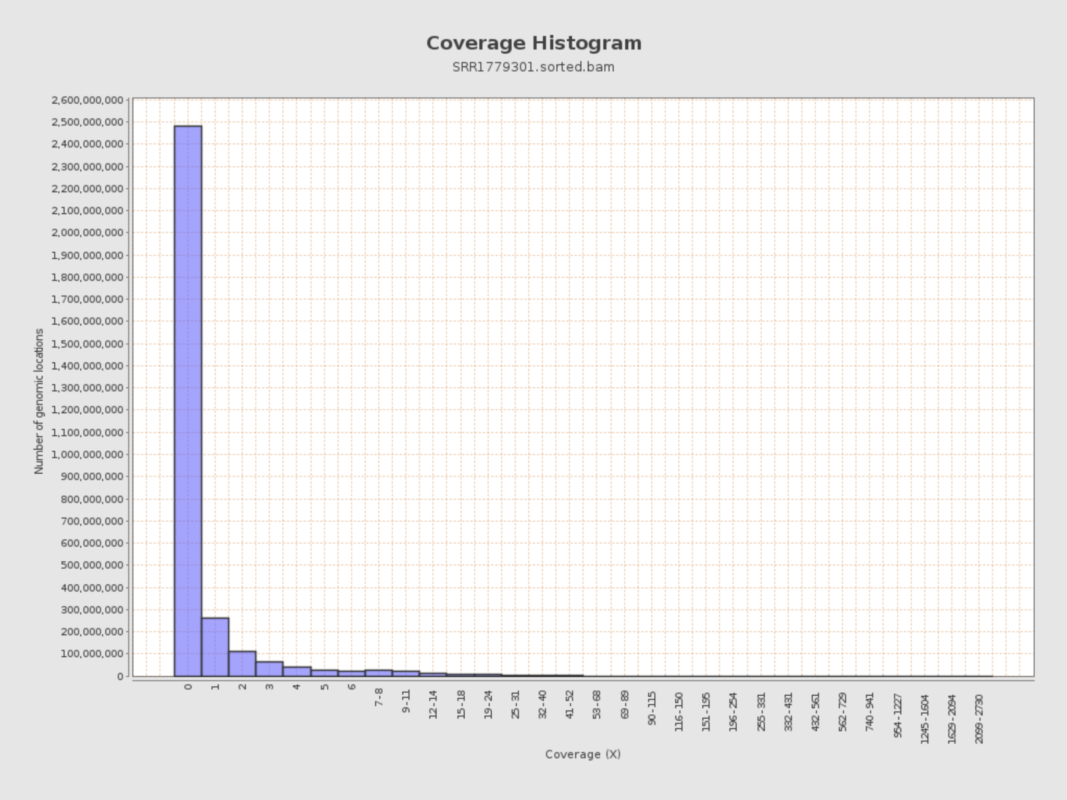
		bases	coverage	deviation
chr1	249250621	177560717	0.7124	4.554
chr2	243199373	192972856	0.7935	3.1385
chr3	198022430	162637367	0.8213	3.1322
chr4	191154276	166264984	0.8698	3.2282
chr5	180915260	147888689	0.8174	3.0308
chr6	171115067	138421542	0.8089	3.2798
chr7	159138663	232144917	1.4588	8.8929
chr8	146364022	197373571	1.3485	4.2839
chr9	141213431	93707455	0.6636	2.6001
chr10	135534747	53691587	0.3961	2.4537
chr11	135006516	112534996	0.8336	3.0118
chr12	133851895	96008659	0.7173	2.969
chr13	115169878	85451626	0.742	2.9411
chr14	107349540	76395615	0.7117	3.0361
chr15	102531392	56261923	0.5487	2.6762
chr16	90354753	36828016	0.4076	2.2202
chr17	81195210	34969643	0.4307	2.0625
chr18	78077248	62432930	0.7996	3.1971
chr19	59128983	24232250	0.4098	2.2714
chr20	63025520	45884392	0.728	2.9409
chr21	48129895	21695647	0.4508	1.943
chr22	51304566	16278851	0.3173	4.8777
chrMT	16571	2372	0.1431	0.4839
chrX	155270560	172209840	1.1091	4.0632

chrY	59373566	1948464	0.0328	0.5164

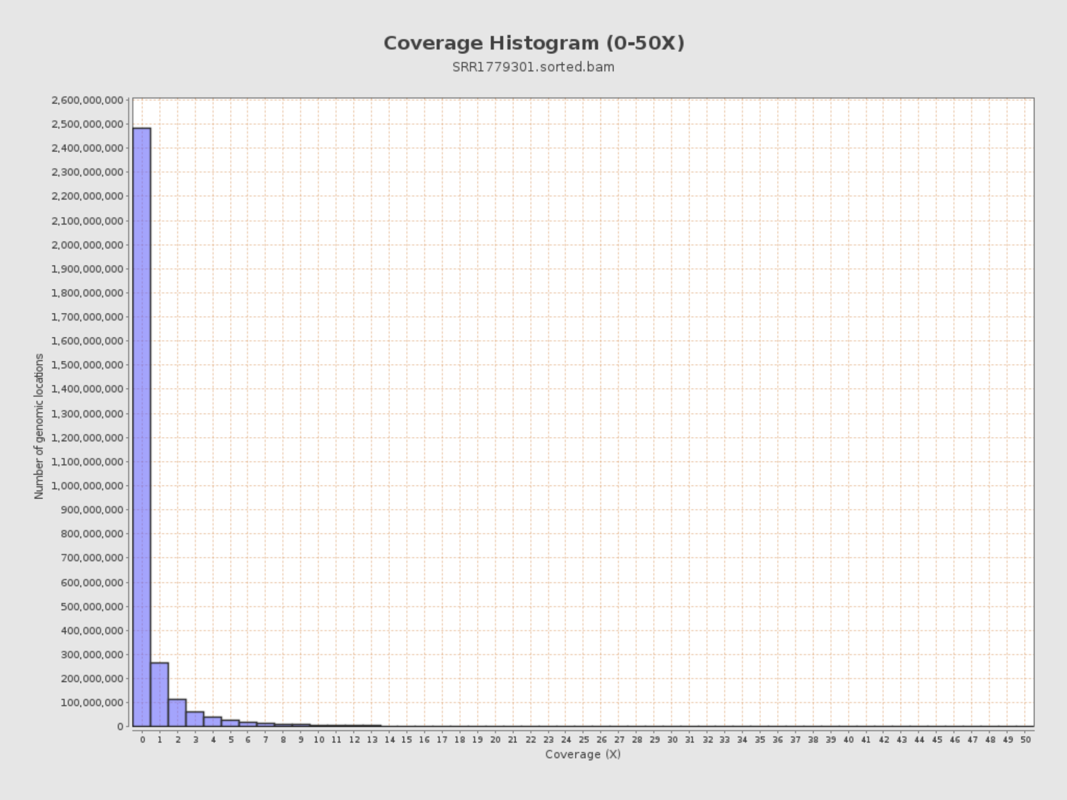
3. Results : Coverage across reference



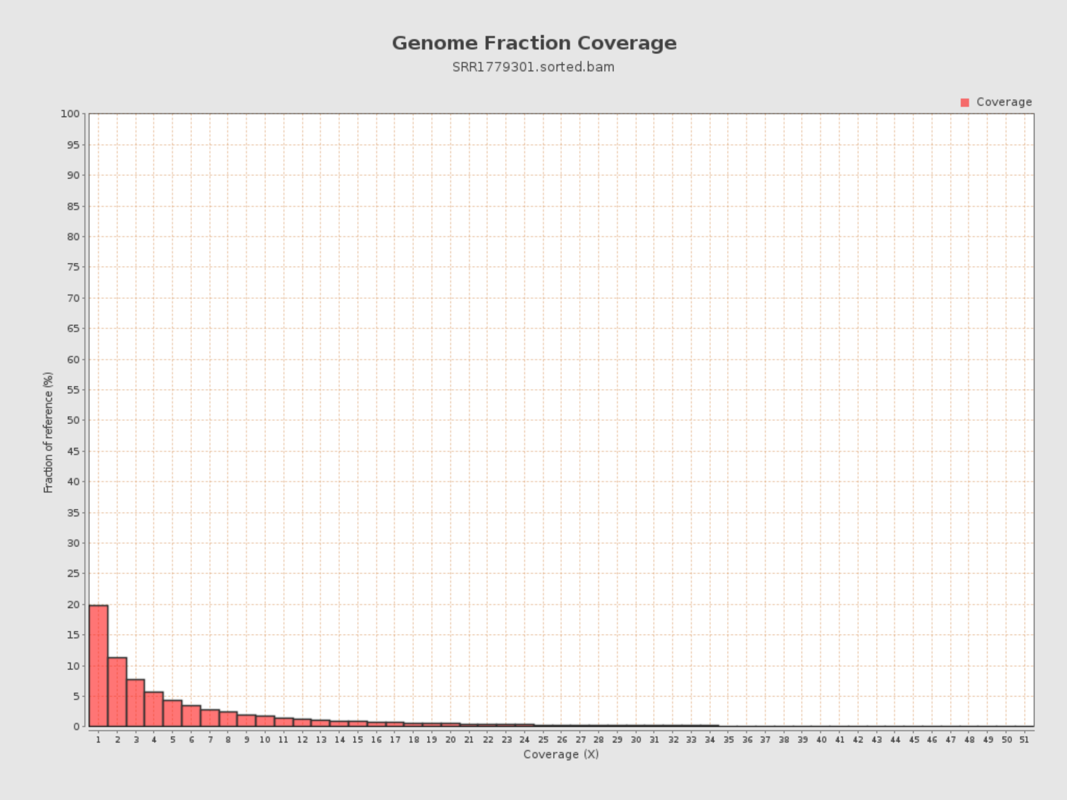
4. Results : Coverage Histogram



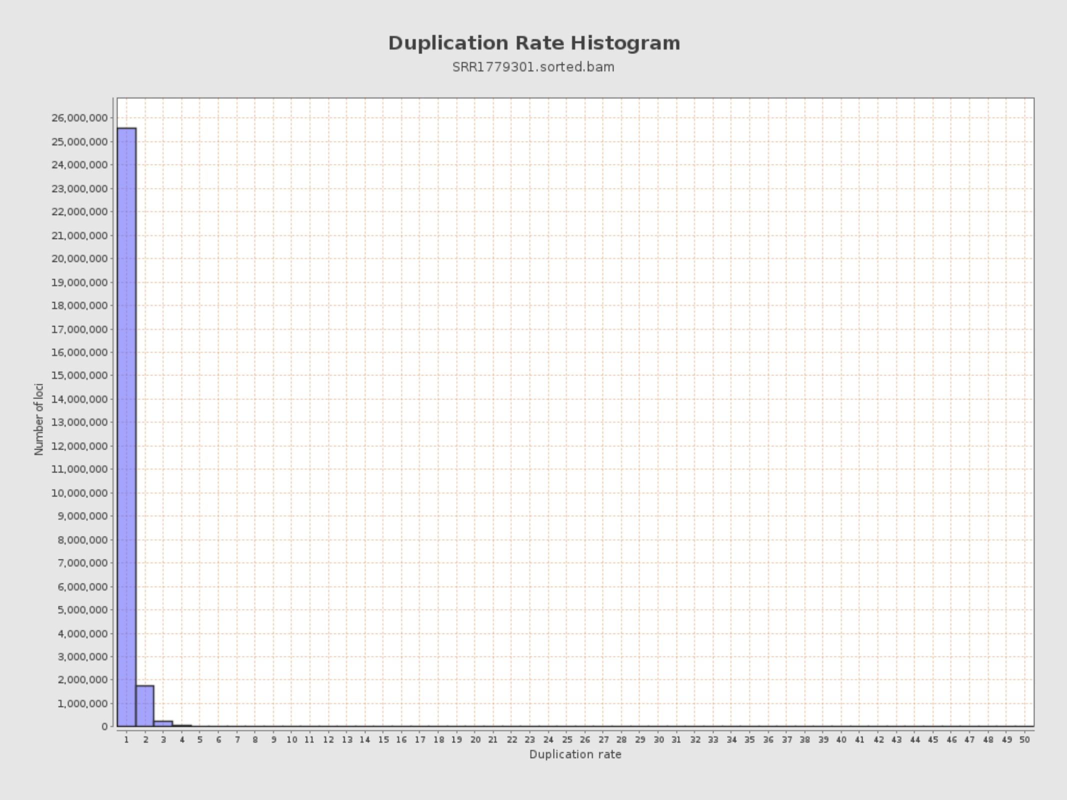
5. Results : Coverage Histogram (0-50X)



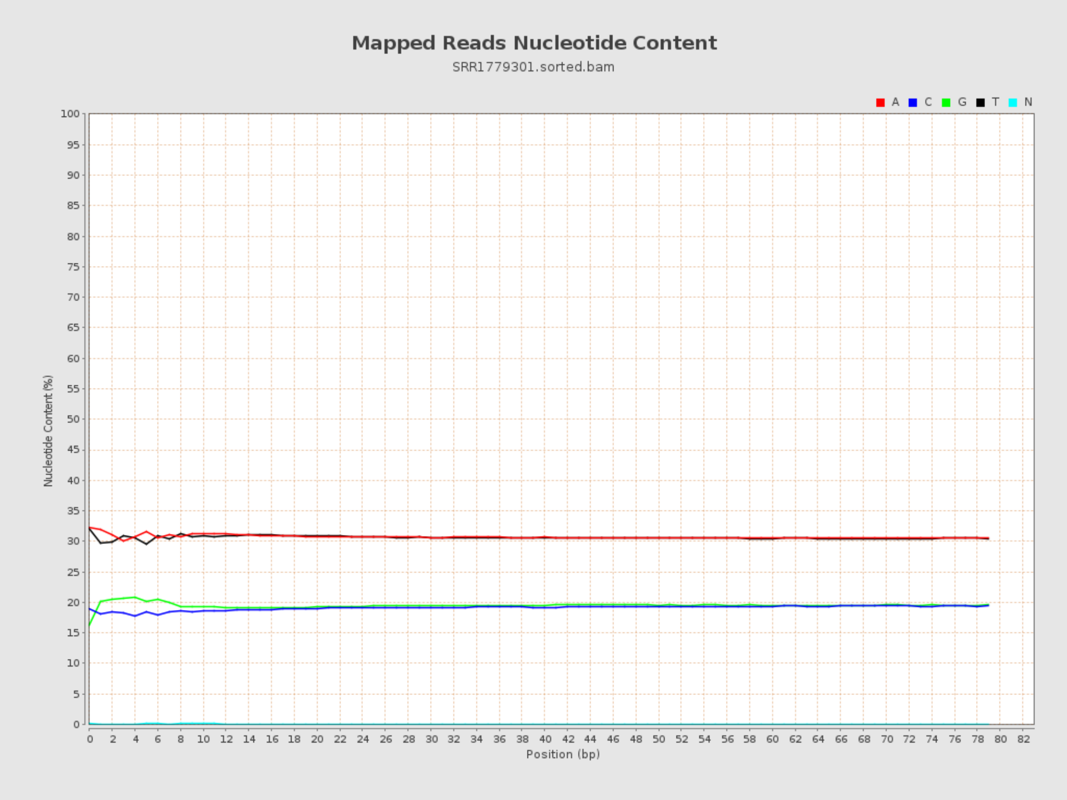
6. Results : Genome Fraction Coverage



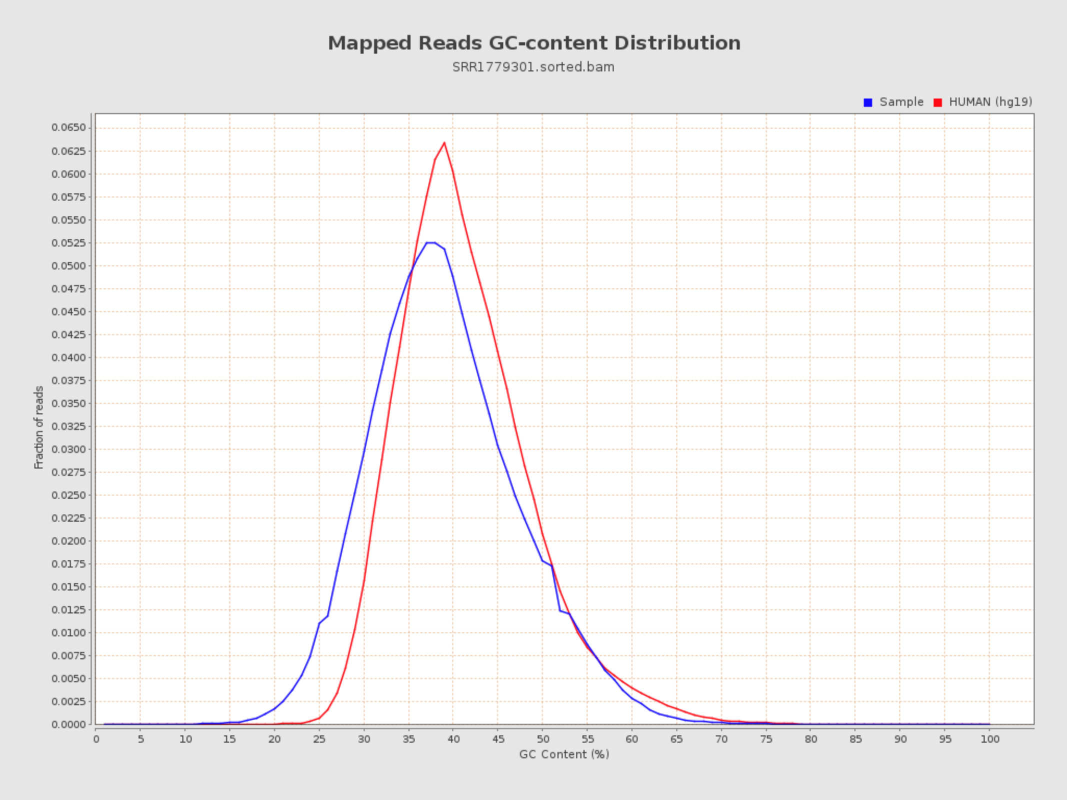
7. Results : Duplication Rate Histogram



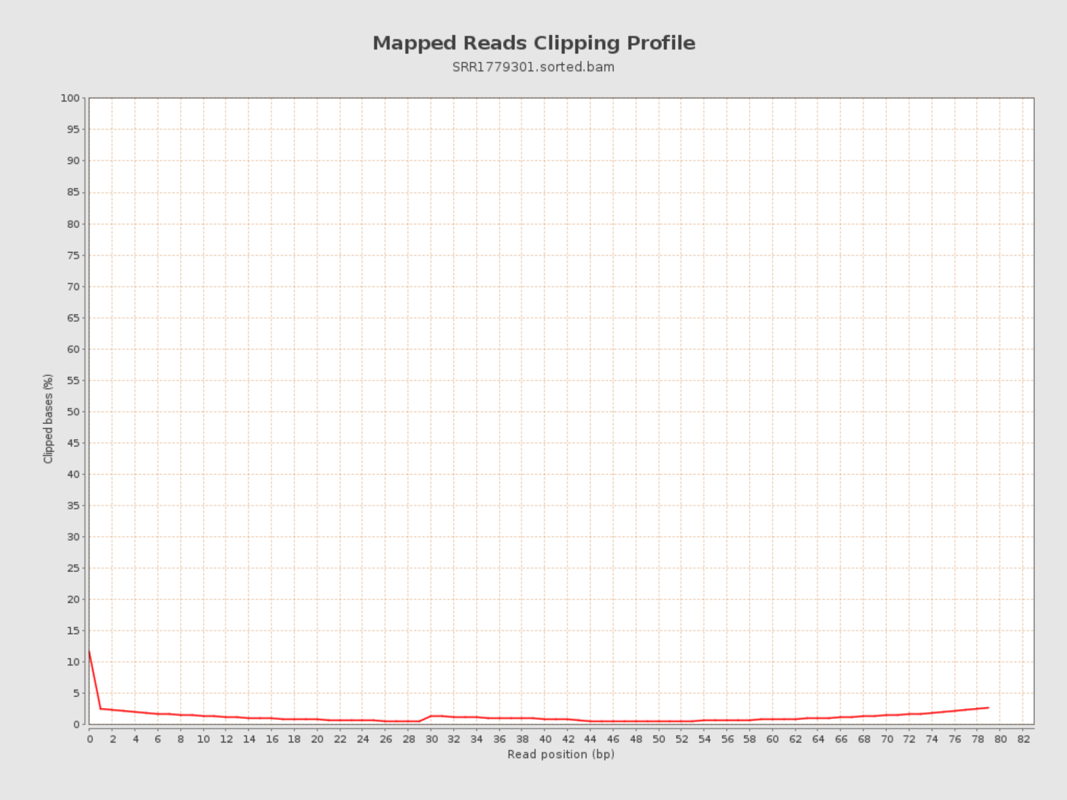
8. Results : Mapped Reads Nucleotide Content



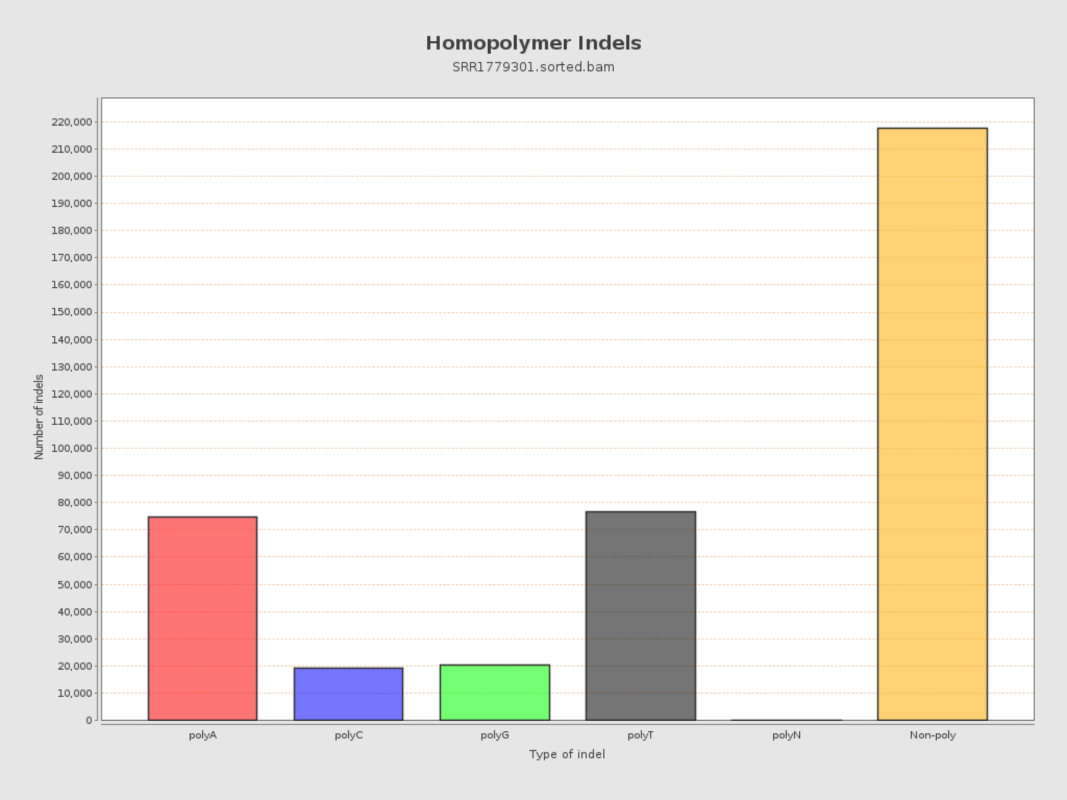
9. Results : Mapped Reads GC-content Distribution



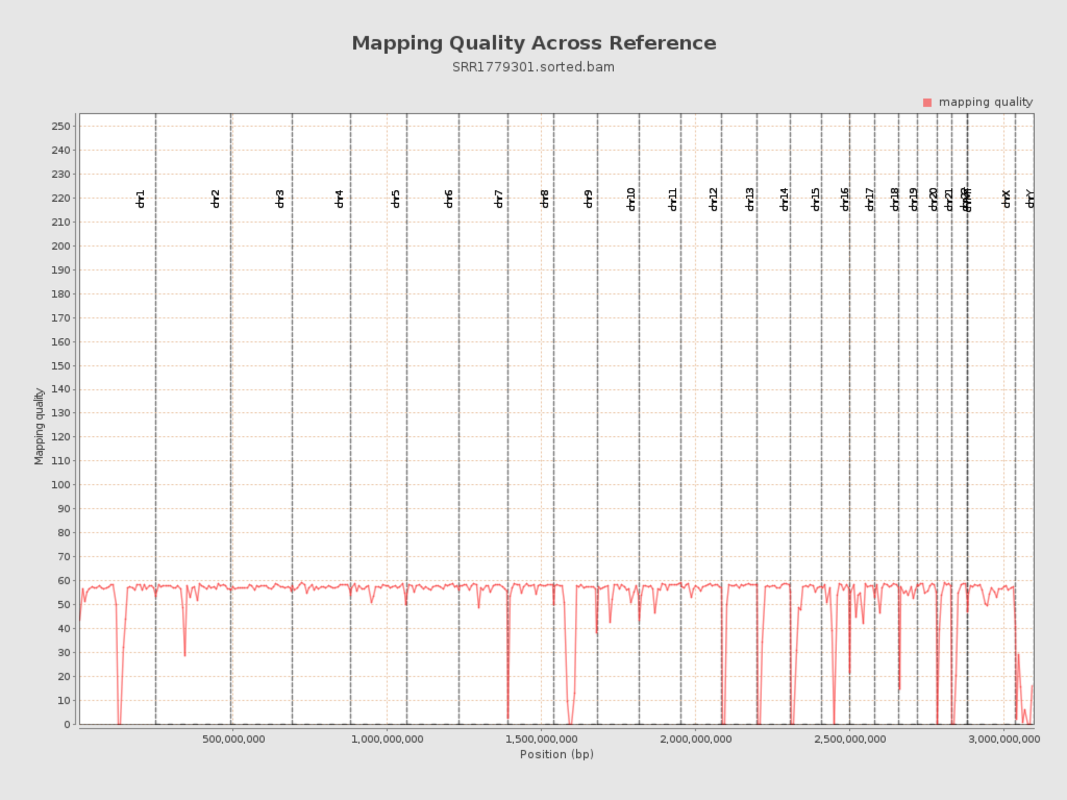
10. Results : Mapped Reads Clipping Profile



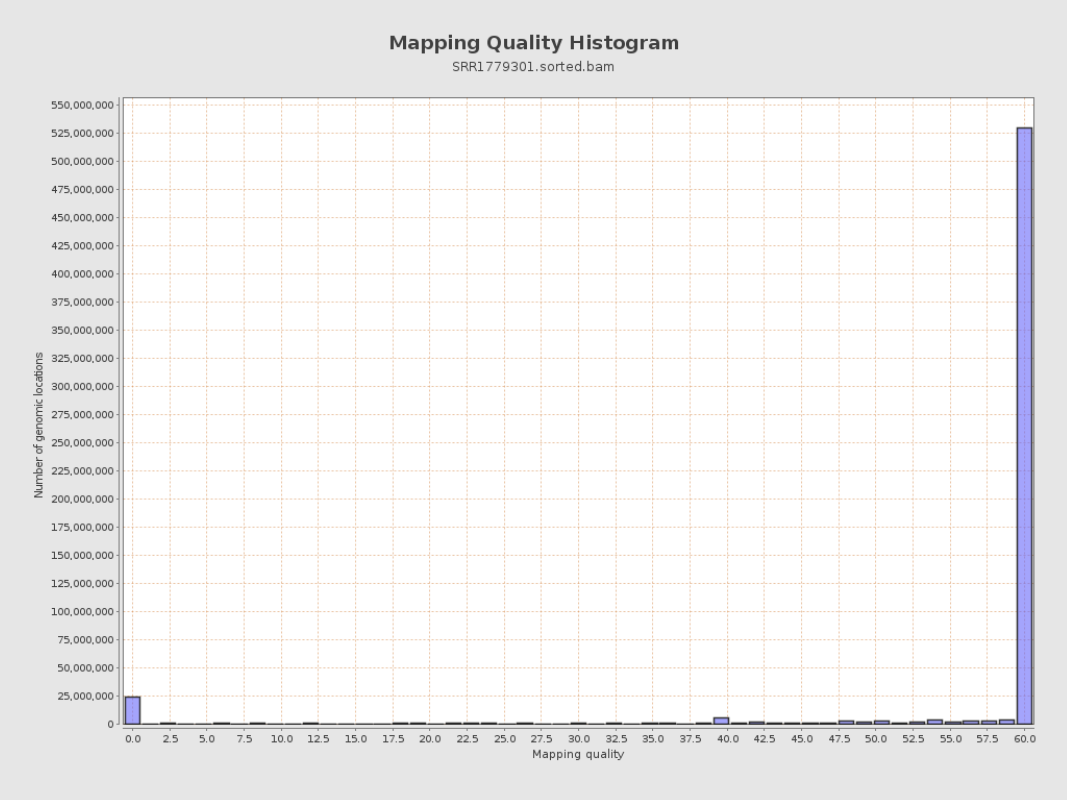
11. Results : Homopolymer Indels



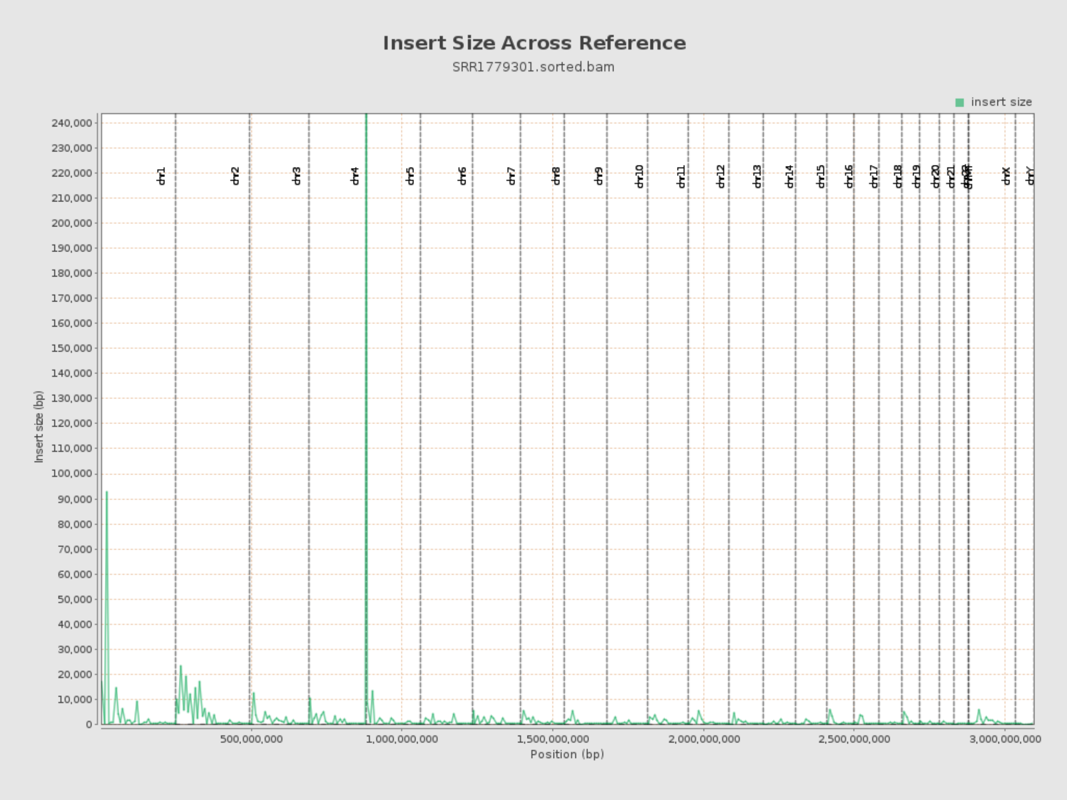
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram