Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 05:00:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779304.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_SRR1779304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779304_1.fastq.gz SRR1779304_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 05:00:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,442,556
Mapped reads	19,558,529 / 95.68%
Unmapped reads	884,027 / 4.32%
Mapped paired reads	19,558,529 / 95.68%
Mapped reads, first in pair	9,869,208 / 48.28%
Mapped reads, second in pair	9,689,321 / 47.4%
Mapped reads, both in pair	19,347,308 / 94.64%
Mapped reads, singletons	211,221 / 1.03%
Secondary alignments	0
Supplementary alignments	46,911 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	852,110 / 4.17%
Duplication rate	3.98%
Clipped reads	585,669 / 2.86%

2.2. ACGT Content

Number/percentage of A's	481,402,558 / 30.92%
Number/percentage of C's	294,862,376 / 18.94%
Number/percentage of T's	480,829,858 / 30.88%
Number/percentage of G's	299,552,476 / 19.24%
Number/percentage of N's	407,942 / 0.03%

GC Percentage	38.18%

2.3. Coverage

Mean	0.5031
Standard Deviation	1.9854

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	34,743.09
Standard Deviation	1,774,224
P25/Median/P75	164 / 218 / 294

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	5,580,365
Insertions	111,773
Mapped reads with at least one insertion	0.57%
Deletions	142,914
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.86%

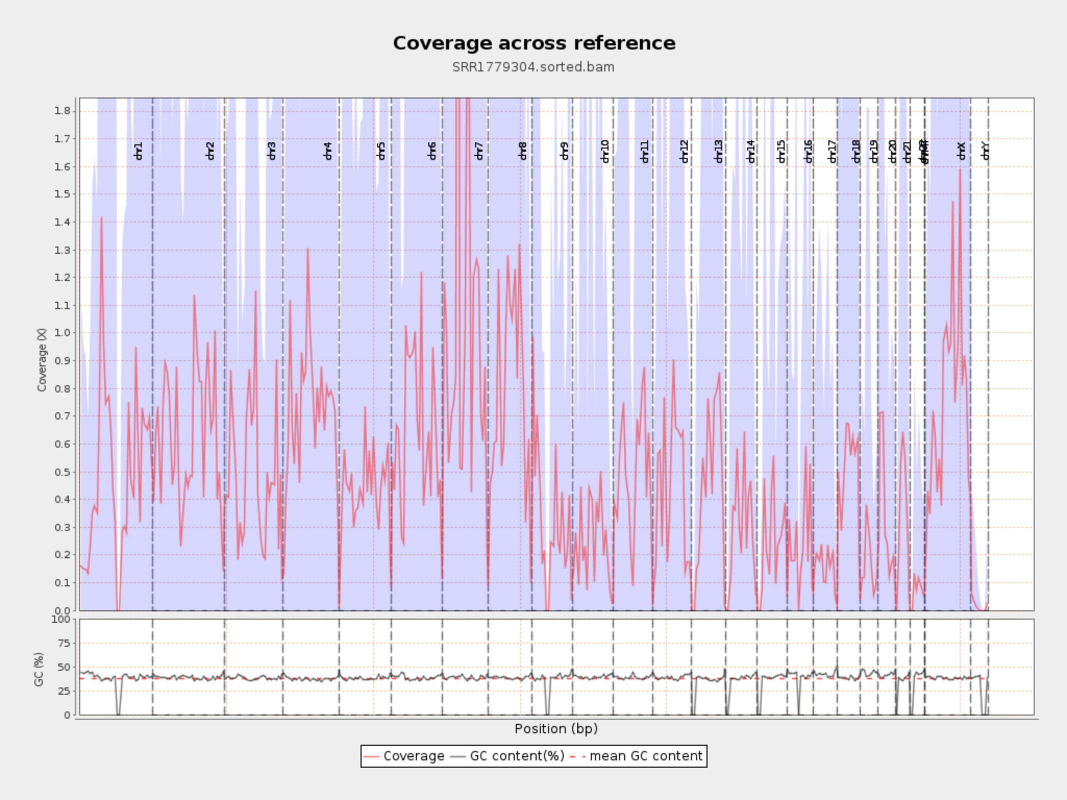
2.7. Chromosome stats

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

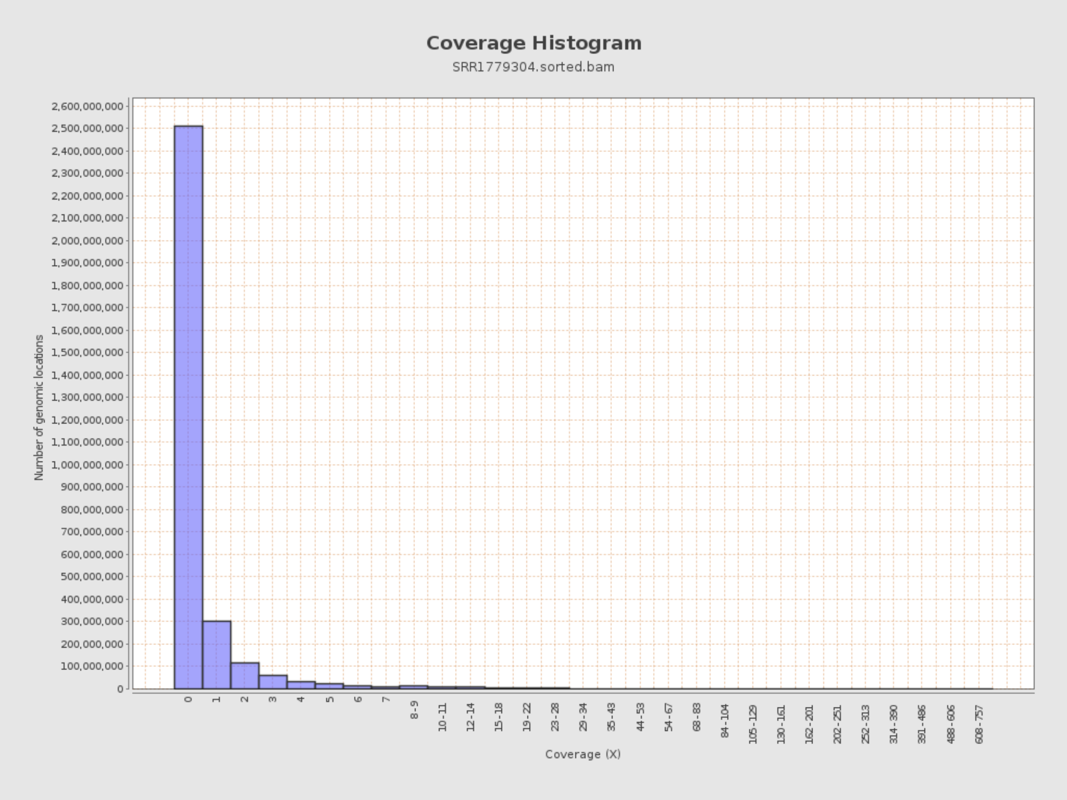
		bases	**coverage**	**deviation**
chr1	249250621	122035767	0.4896	1.8247
chr2	243199373	152198205	0.6258	1.8835
chr3	198022430	98257382	0.4962	1.8802
chr4	191154276	140393310	0.7345	2.0041
chr5	180915260	77938079	0.4308	1.4513
chr6	171115067	112969550	0.6602	2.0199
chr7	159138663	175159070	1.1007	4.603
chr8	146364022	118166076	0.8073	2.3106
chr9	141213431	45165717	0.3198	1.3733
chr10	135534747	33581379	0.2478	1.6185
chr11	135006516	67478417	0.4998	1.6964
chr12	133851895	58355987	0.436	1.5924
chr13	115169878	52278804	0.4539	1.5418
chr14	107349540	31172877	0.2904	1.1975
chr15	102531392	25592131	0.2496	1.089
chr16	90354753	21486065	0.2378	1.0746
chr17	81195210	12610133	0.1553	0.8353
chr18	78077248	41091310	0.5263	1.6996
chr19	59128983	9548825	0.1615	0.8664
chr20	63025520	20423269	0.324	1.4885
chr21	48129895	16985979	0.3529	1.3344
chr22	51304566	3744178	0.073	0.4513
chrMT	16571	1906	0.115	0.4307
chrX	155270560	119731422	0.7711	2.6194

chrY	59373566	984927	0.0166	0.2109

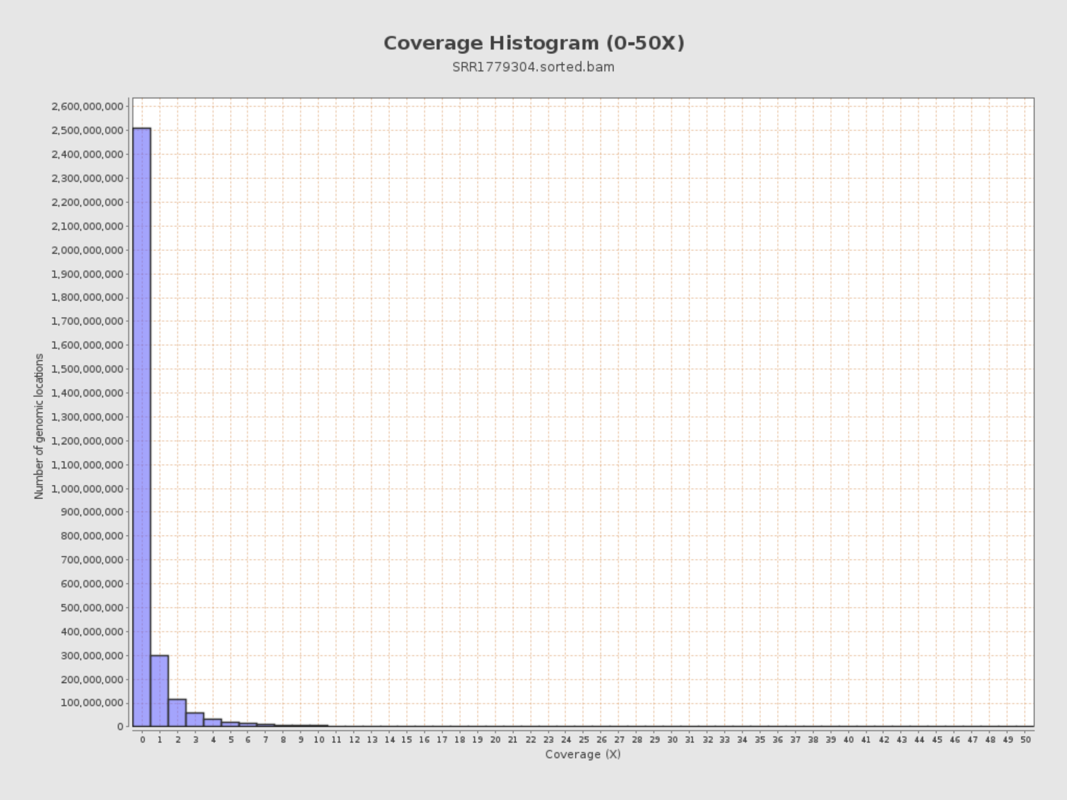
3. Results : Coverage across reference



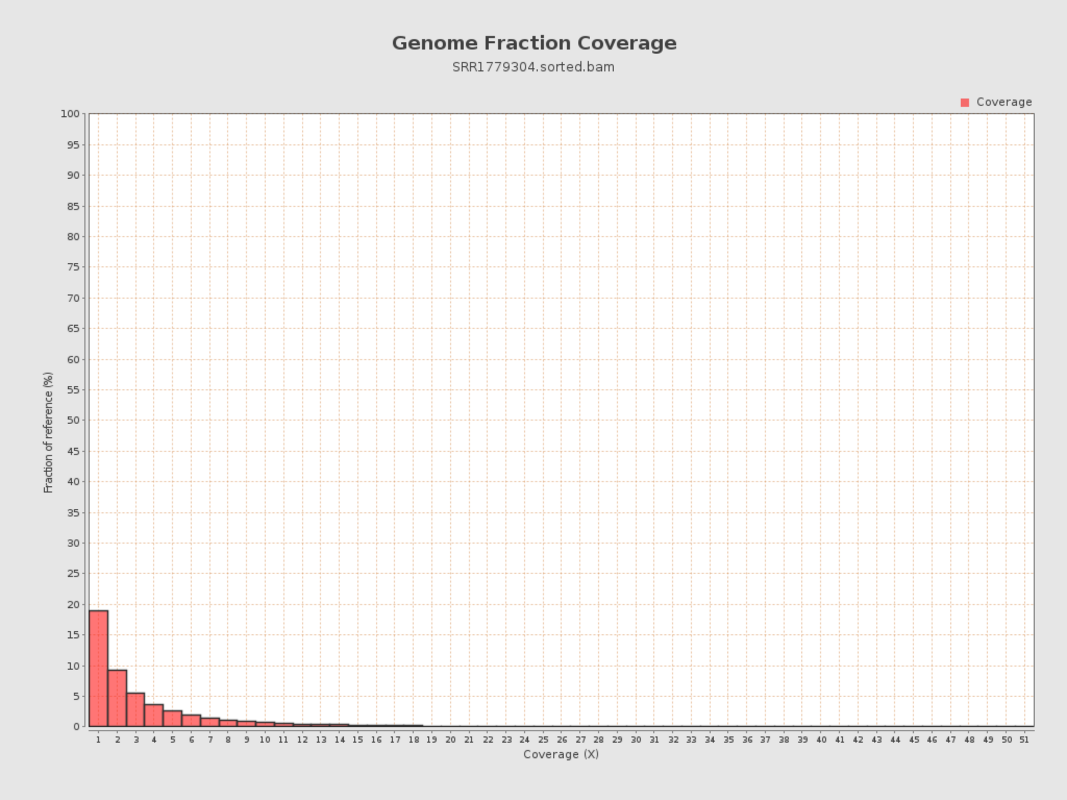
4. Results : Coverage Histogram



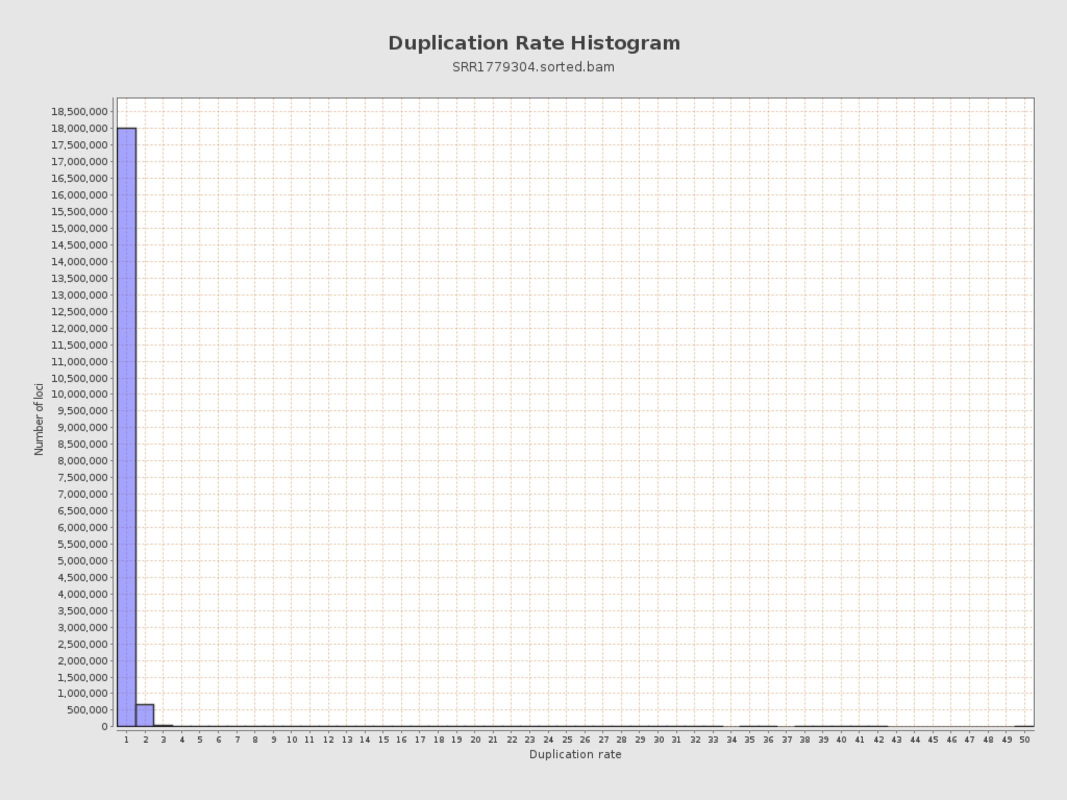
5. Results : Coverage Histogram (0-50X)



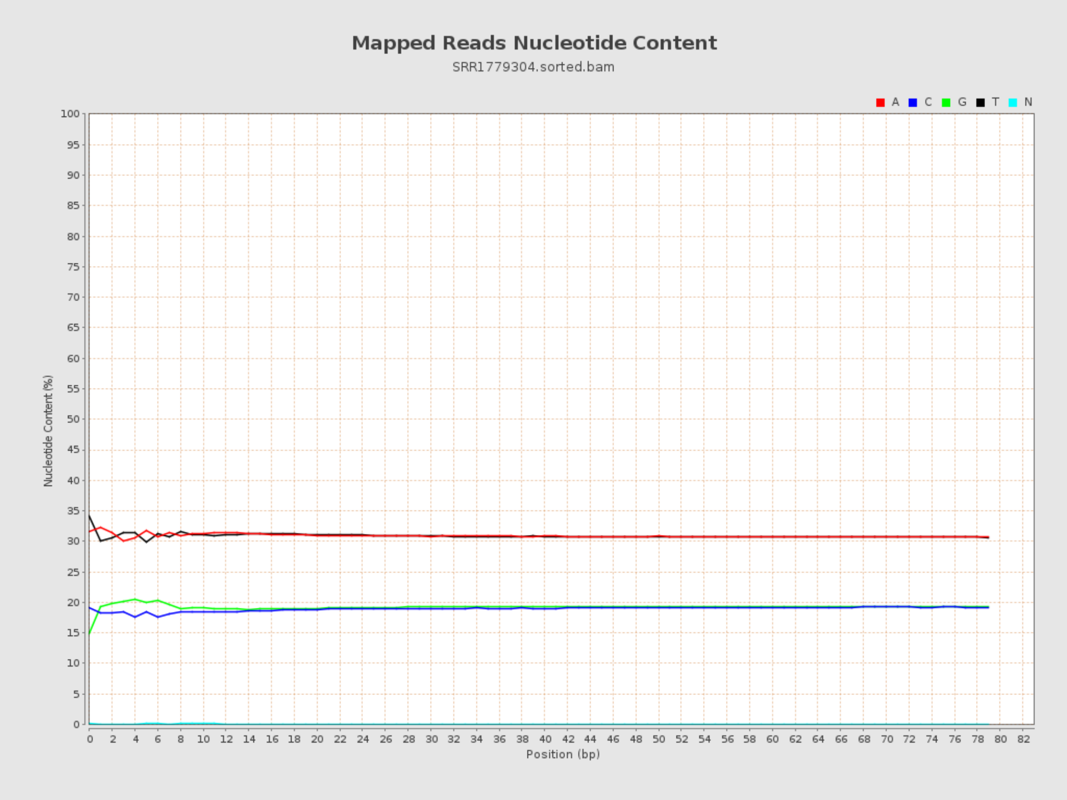
6. Results : Genome Fraction Coverage



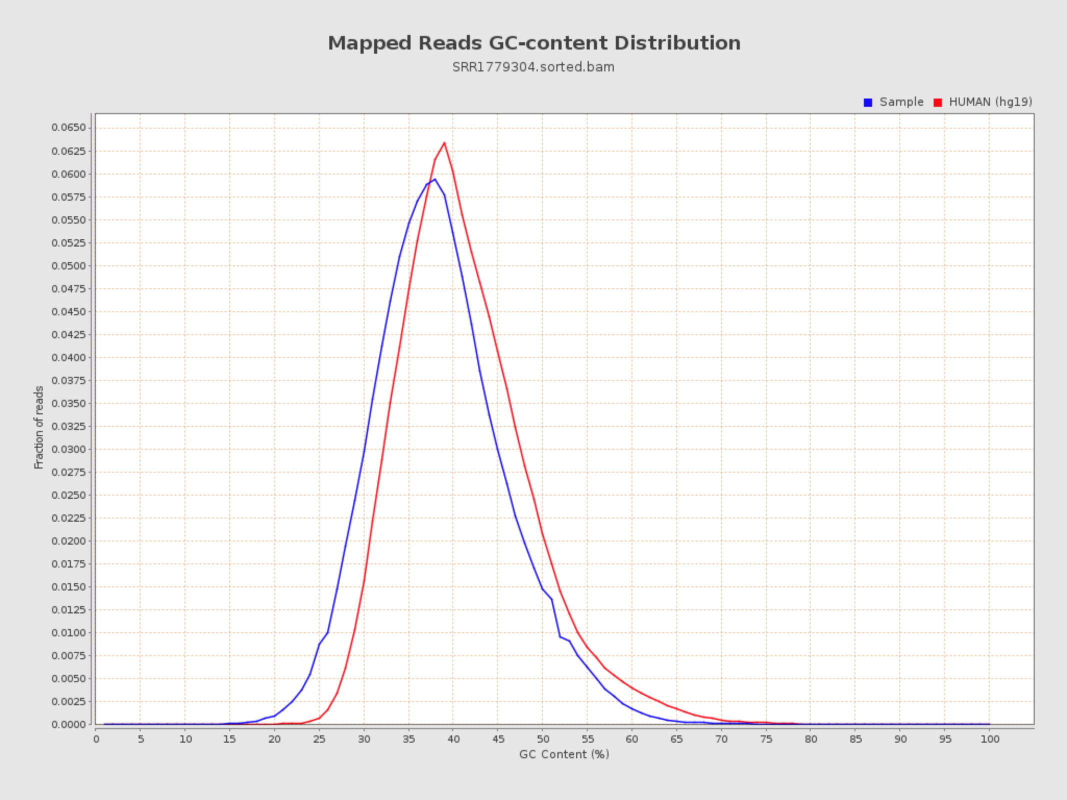
7. Results : Duplication Rate Histogram



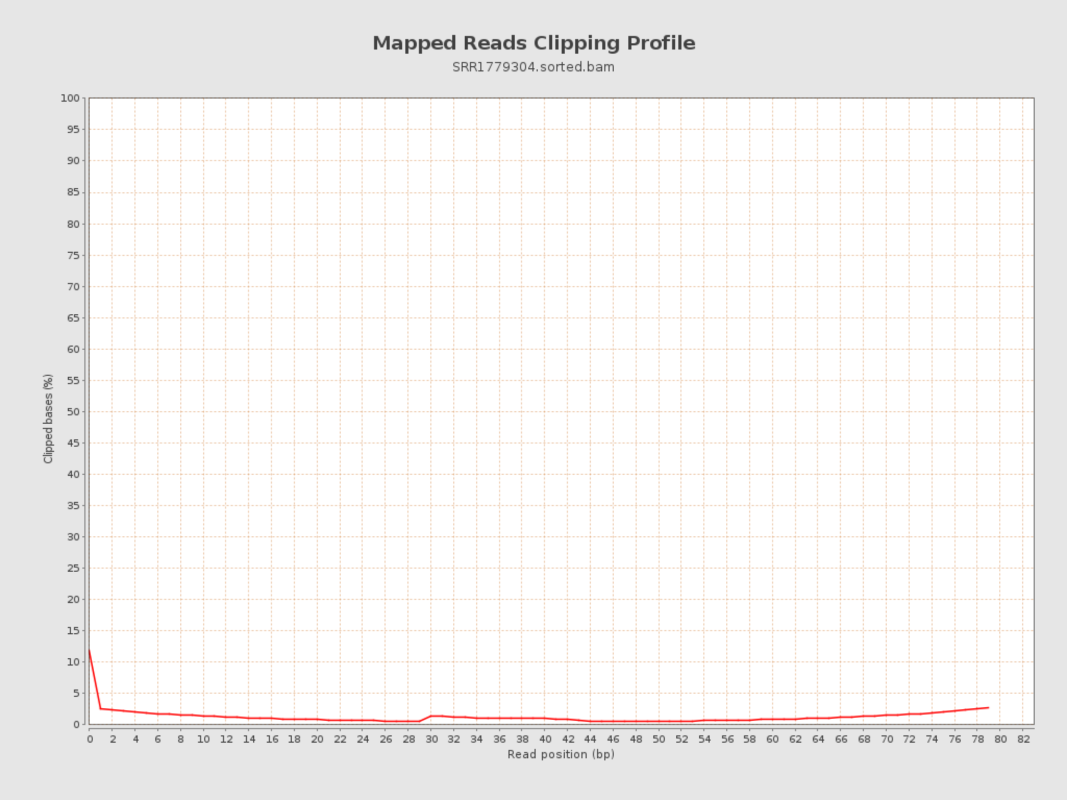
8. Results : Mapped Reads Nucleotide Content



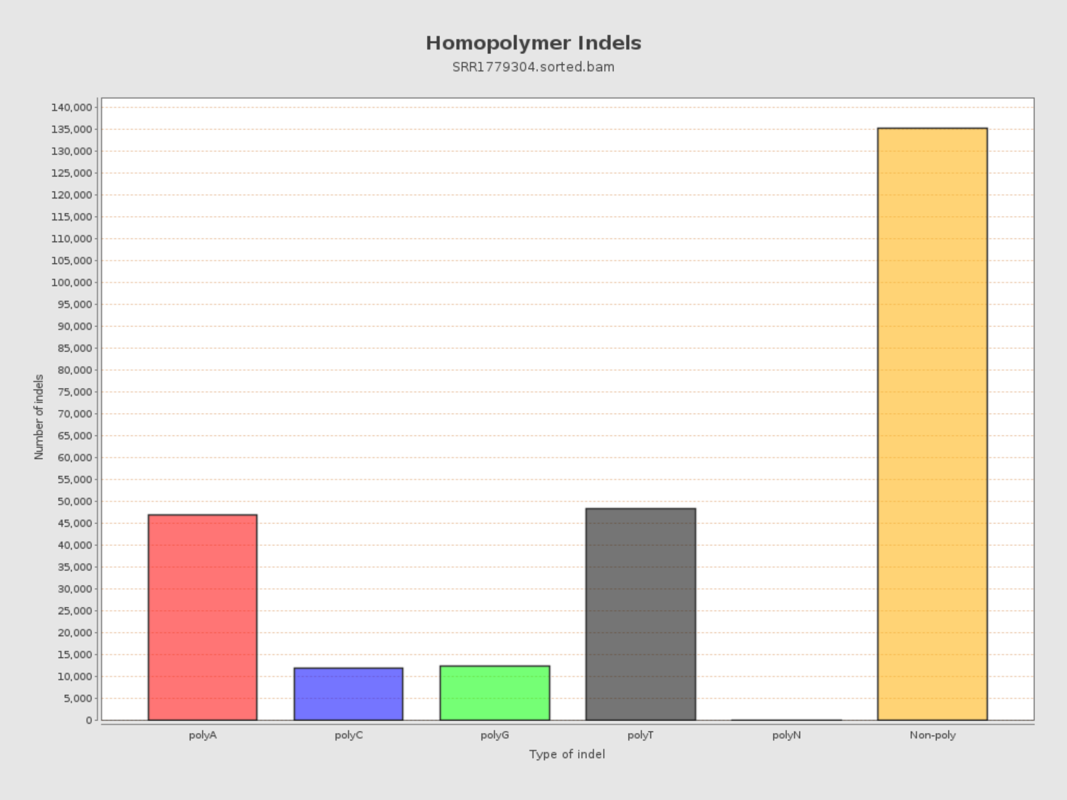
9. Results : Mapped Reads GC-content Distribution



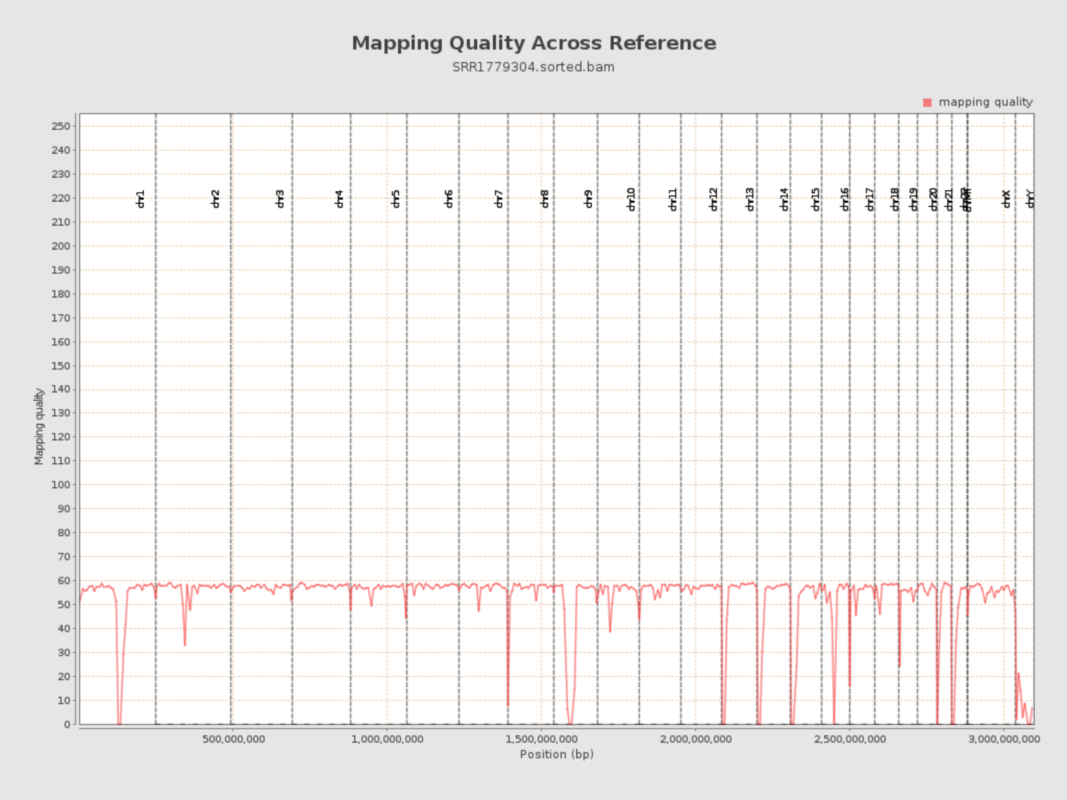
10. Results : Mapped Reads Clipping Profile



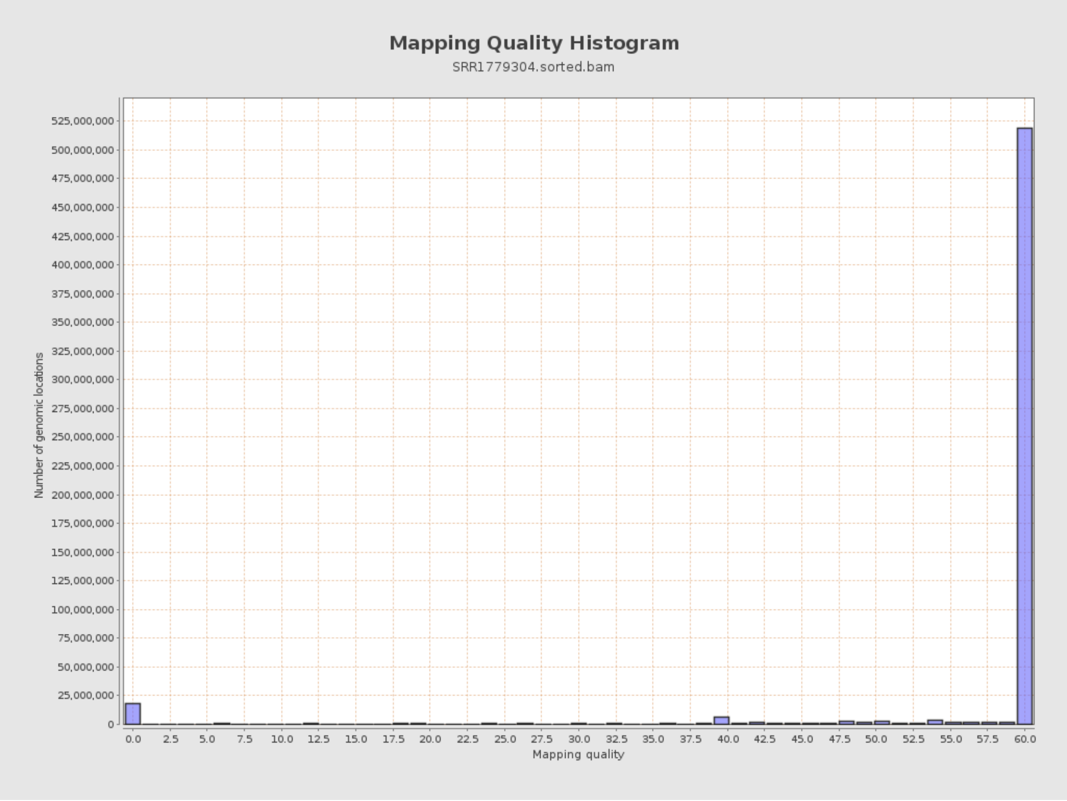
11. Results : Homopolymer Indels



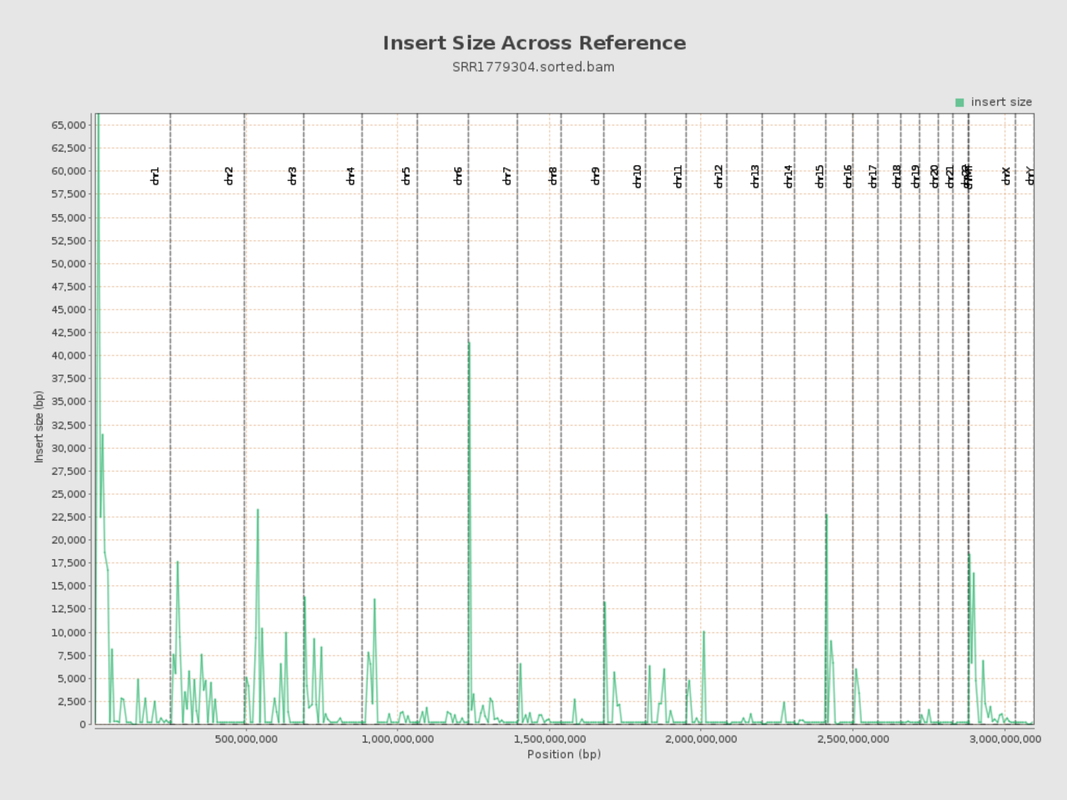
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram