Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 23:43:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779097.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_SRR1779097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779097_1.fastq.gz SRR1779097_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 23:43:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,219,998
Mapped reads	15,776,913 / 97.27%
Unmapped reads	443,085 / 2.73%
Mapped paired reads	15,776,913 / 97.27%
Mapped reads, first in pair	7,939,989 / 48.95%
Mapped reads, second in pair	7,836,924 / 48.32%
Mapped reads, both in pair	15,616,606 / 96.28%
Mapped reads, singletons	160,307 / 0.99%
Secondary alignments	0
Supplementary alignments	87,078 / 0.54%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	380,590 / 2.35%
Duplication rate	2.14%
Clipped reads	961,991 / 5.93%

2.2. ACGT Content

Number/percentage of A's	485,197,851 / 30.79%
Number/percentage of C's	301,144,336 / 19.11%
Number/percentage of T's	483,126,159 / 30.66%
Number/percentage of G's	305,849,203 / 19.41%
Number/percentage of N's	634,540 / 0.04%

GC Percentage	38.52%

2.3. Coverage

Mean	0.5092
Standard Deviation	1.4608

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	64,258.95
Standard Deviation	2,442,827.03
P25/Median/P75	163 / 217 / 294

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	6,639,828
Insertions	135,225
Mapped reads with at least one insertion	0.84%
Deletions	165,969
Mapped reads with at least one deletion	1.03%
Homopolymer indels	46.77%

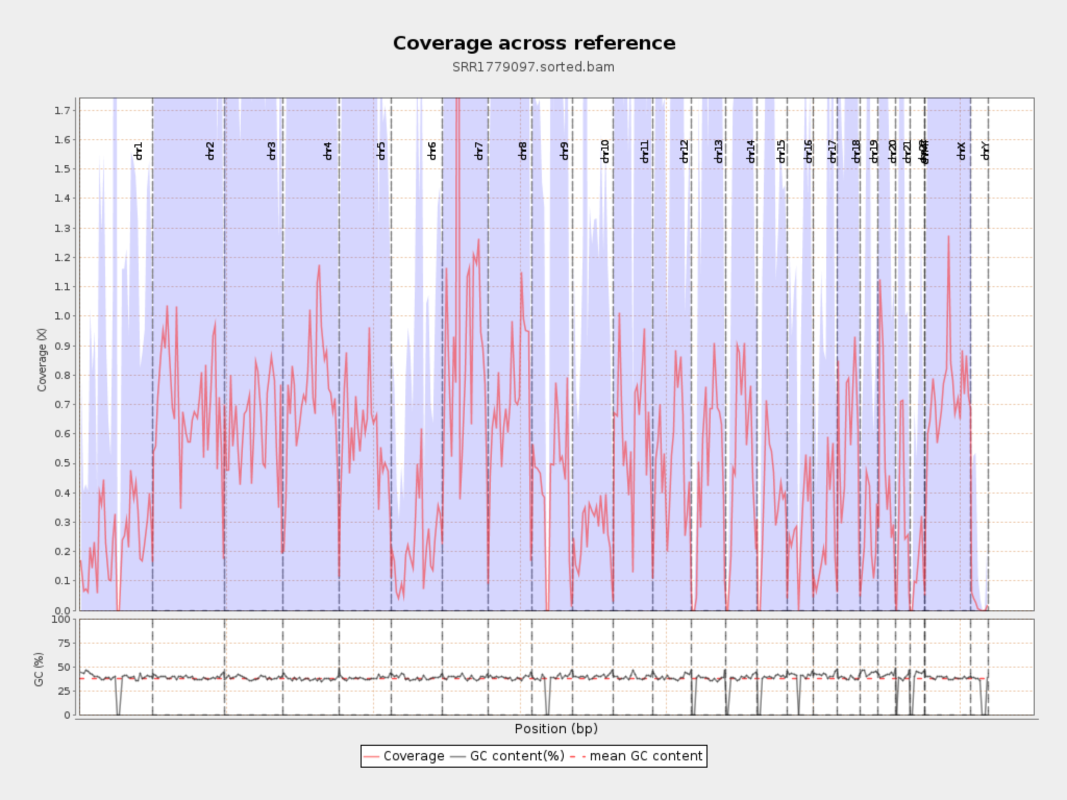
2.7. Chromosome stats

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

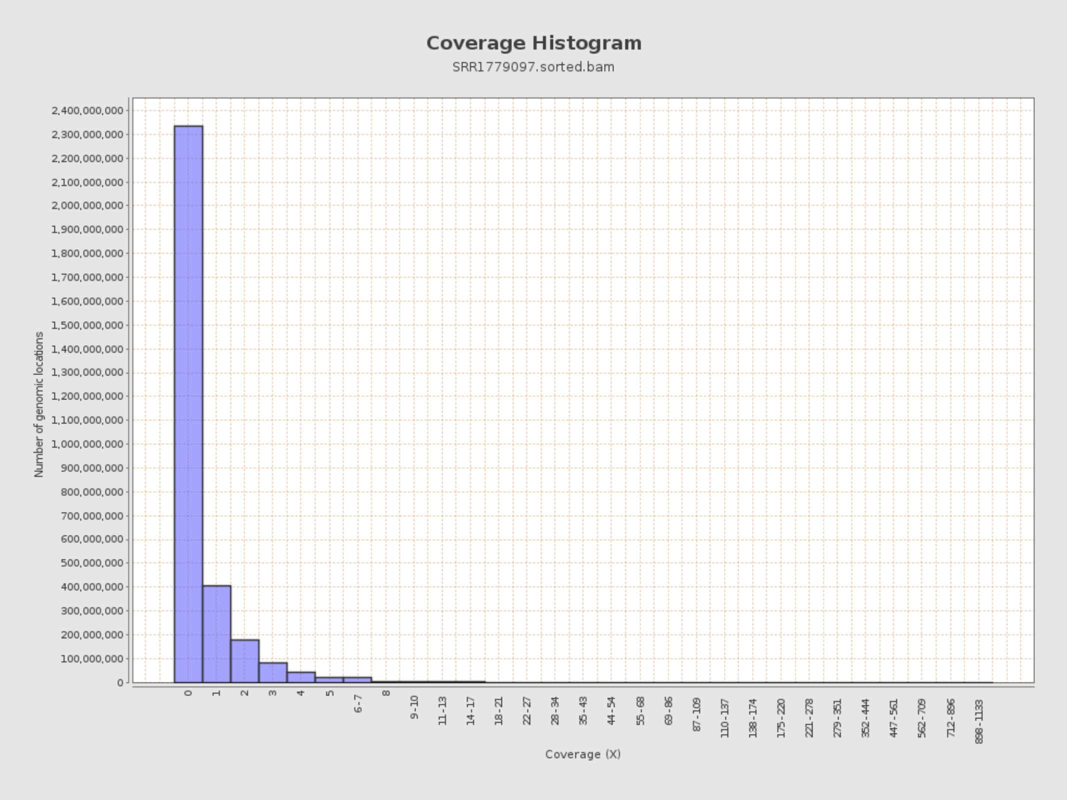
		bases	coverage	deviation
chr1	249250621	57772585	0.2318	1.373
chr2	243199373	171184930	0.7039	1.5998
chr3	198022430	124537803	0.6289	1.3698
chr4	191154276	142309025	0.7445	1.453
chr5	180915260	105004432	0.5804	1.2915
chr6	171115067	38630034	0.2258	0.757
chr7	159138663	154742603	0.9724	2.9039
chr8	146364022	105263595	0.7192	1.4337
chr9	141213431	59711168	0.4228	1.1957
chr10	135534747	37202216	0.2745	1.9423
chr11	135006516	83395750	0.6177	1.4305
chr12	133851895	68456879	0.5114	1.2646
chr13	115169878	56318788	0.489	1.2266
chr14	107349540	56052157	0.5221	1.2445
chr15	102531392	37768603	0.3684	1.0454
chr16	90354753	24914580	0.2757	0.8499
chr17	81195210	20107746	0.2476	0.9676
chr18	78077248	47857688	0.613	1.3593
chr19	59128983	14311691	0.242	1.0005
chr20	63025520	31353048	0.4975	1.2858
chr21	48129895	17302088	0.3595	1.0887
chr22	51304566	6417473	0.1251	0.5575
chrMT	16571	844	0.0509	0.238
chrX	155270560	114646415	0.7384	1.5189

chrY	59373566	1061658	0.0179	0.2899

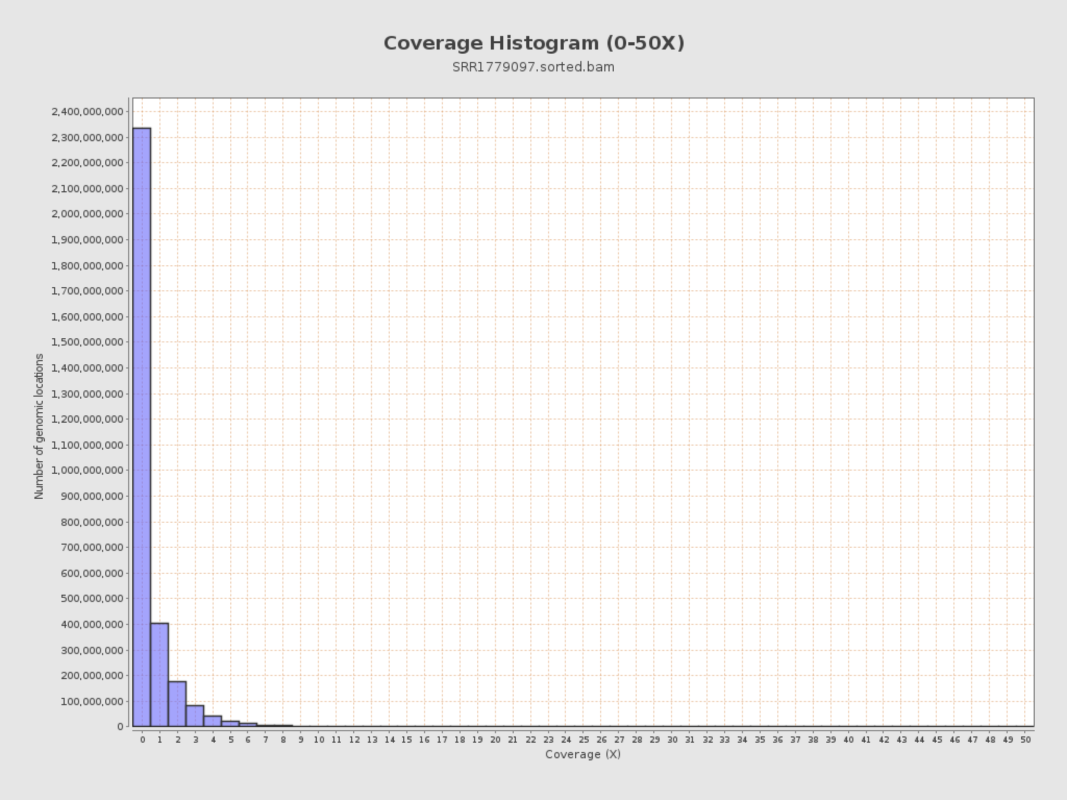
3. Results : Coverage across reference



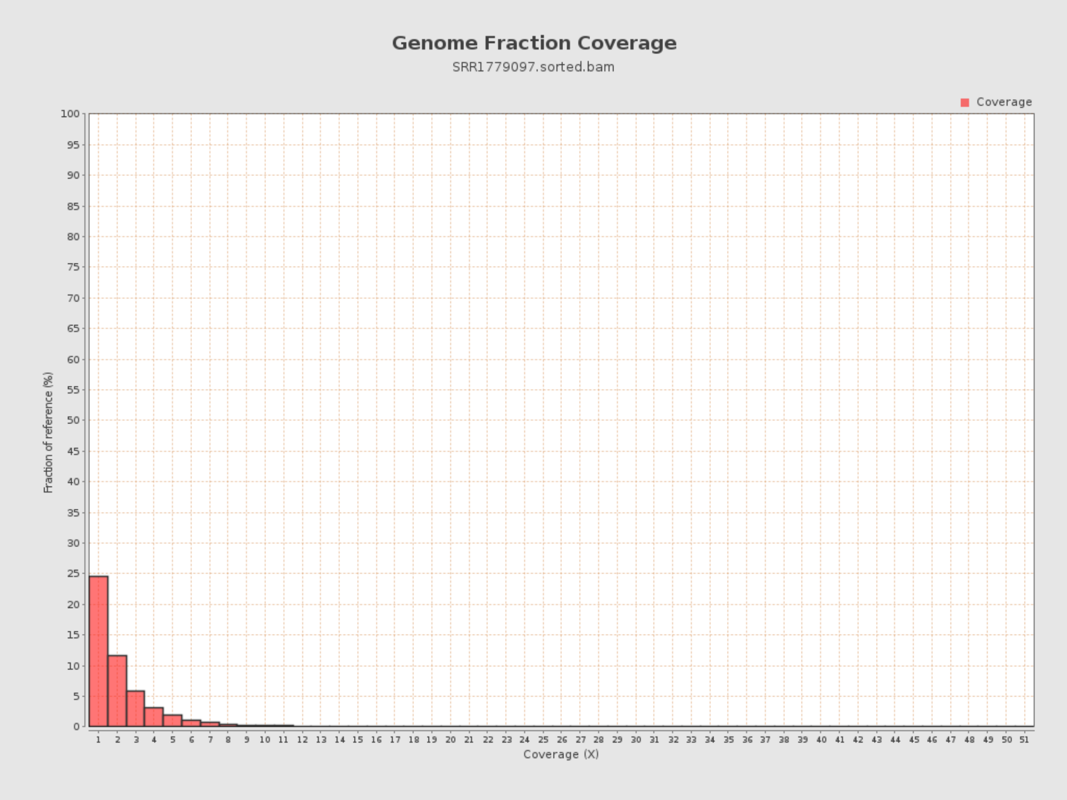
4. Results : Coverage Histogram



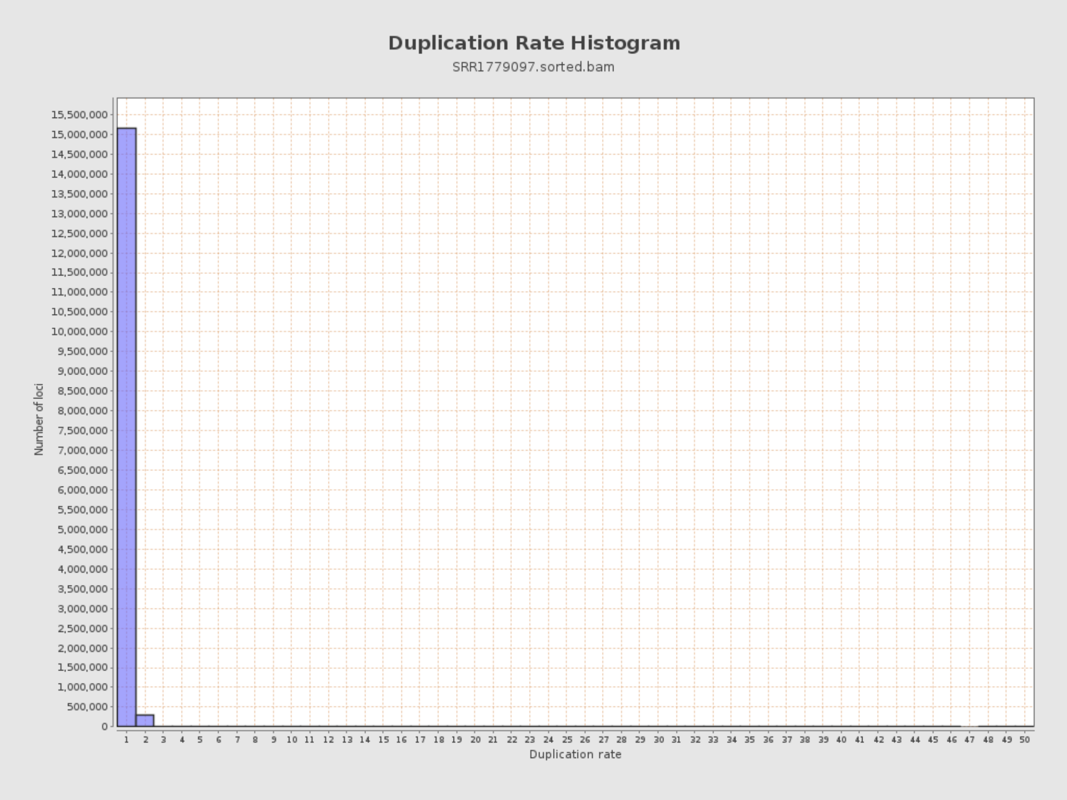
5. Results : Coverage Histogram (0-50X)



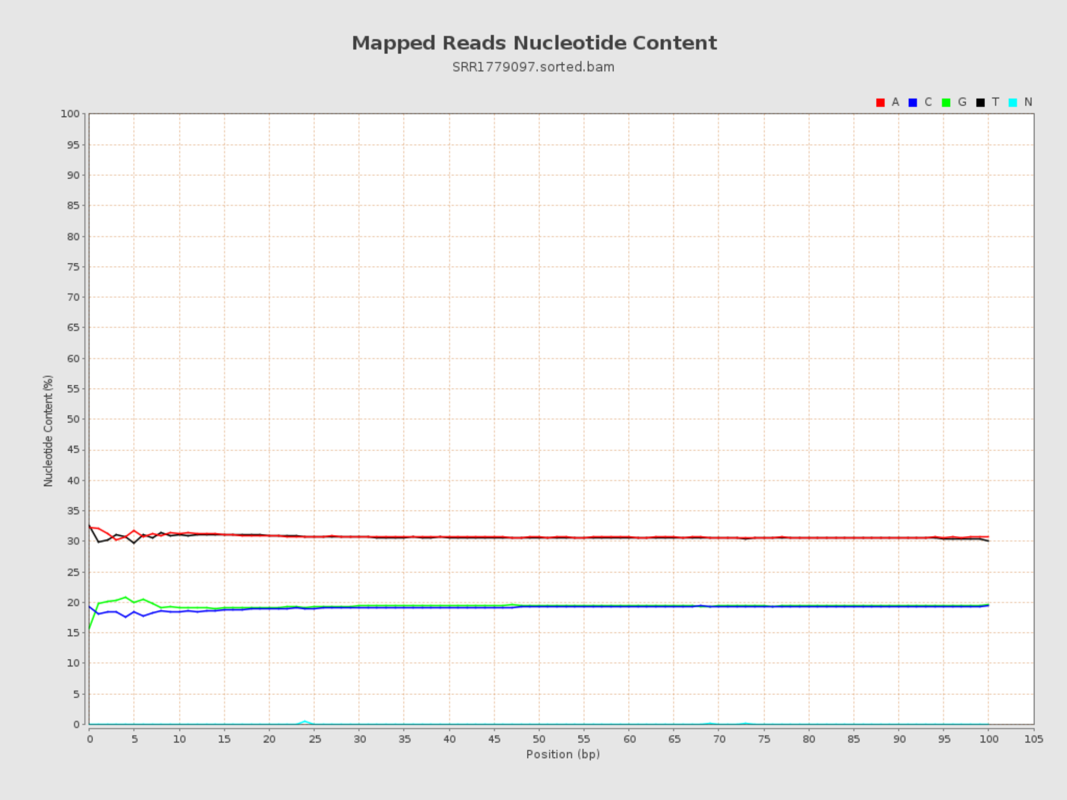
6. Results : Genome Fraction Coverage



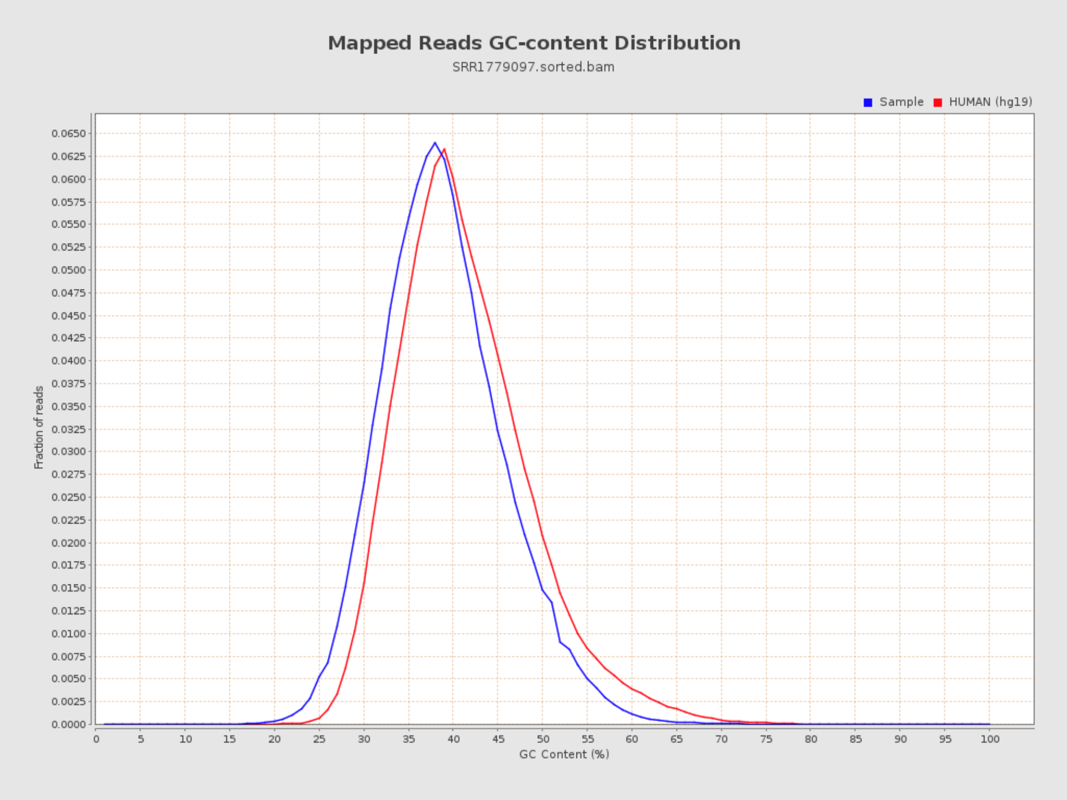
7. Results : Duplication Rate Histogram



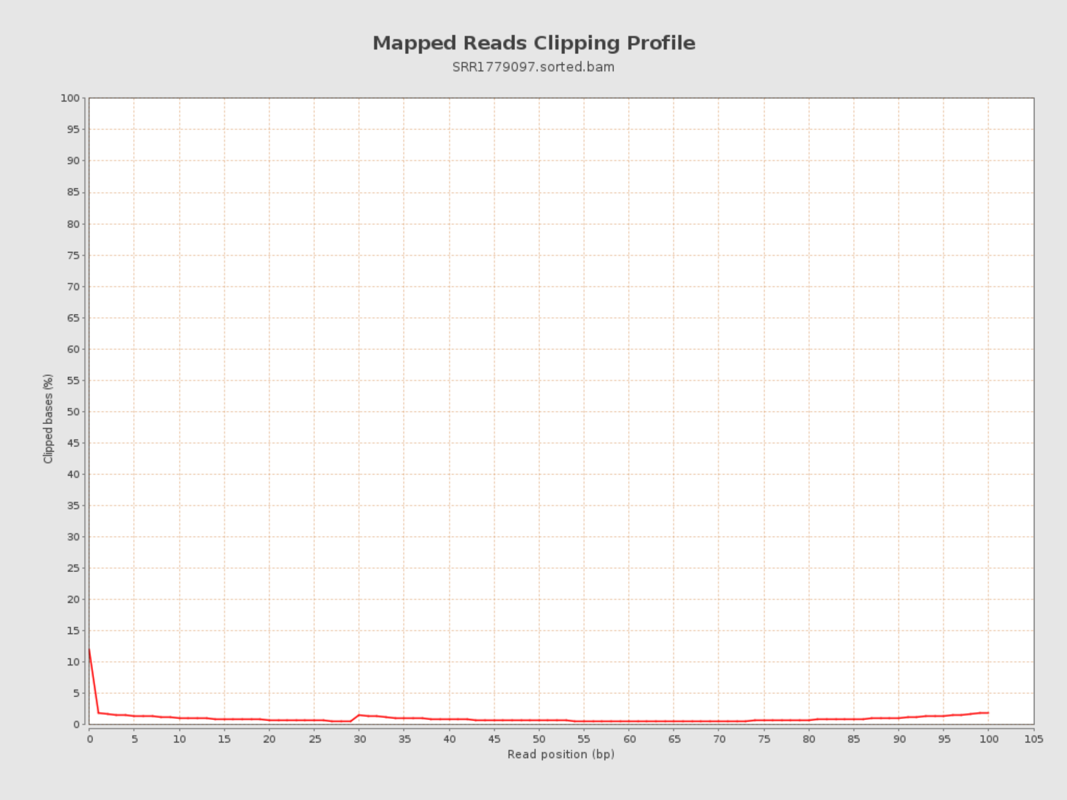
8. Results : Mapped Reads Nucleotide Content



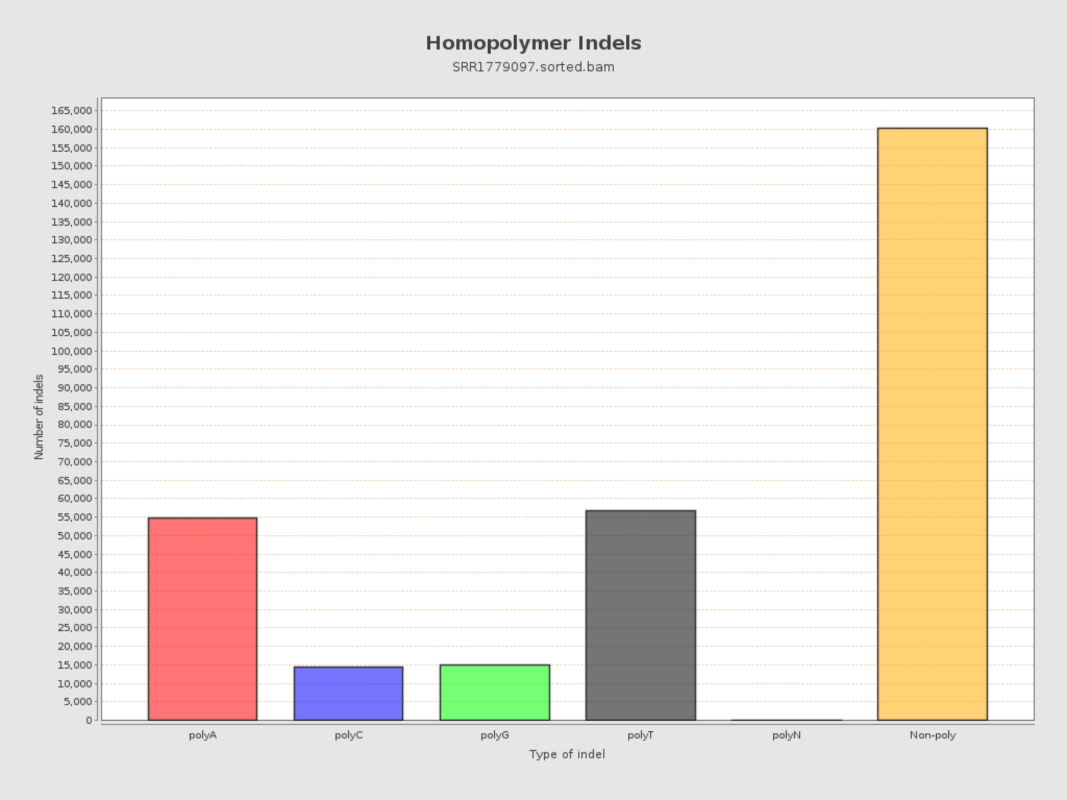
9. Results : Mapped Reads GC-content Distribution



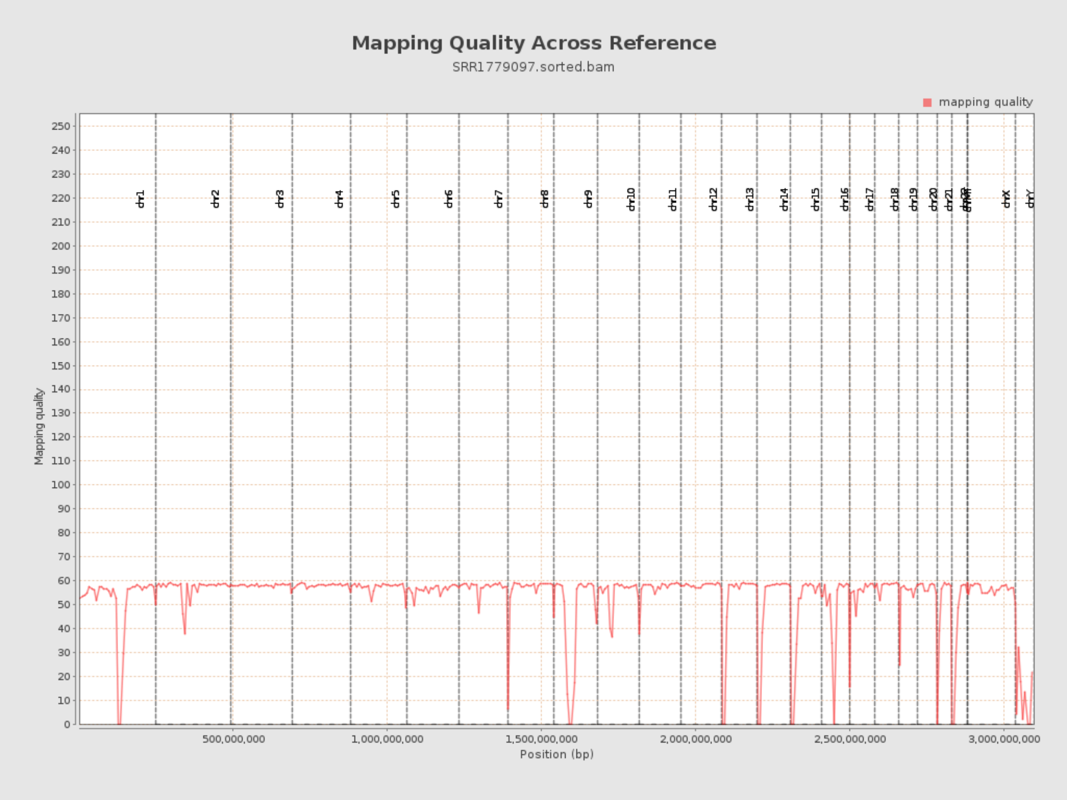
10. Results : Mapped Reads Clipping Profile



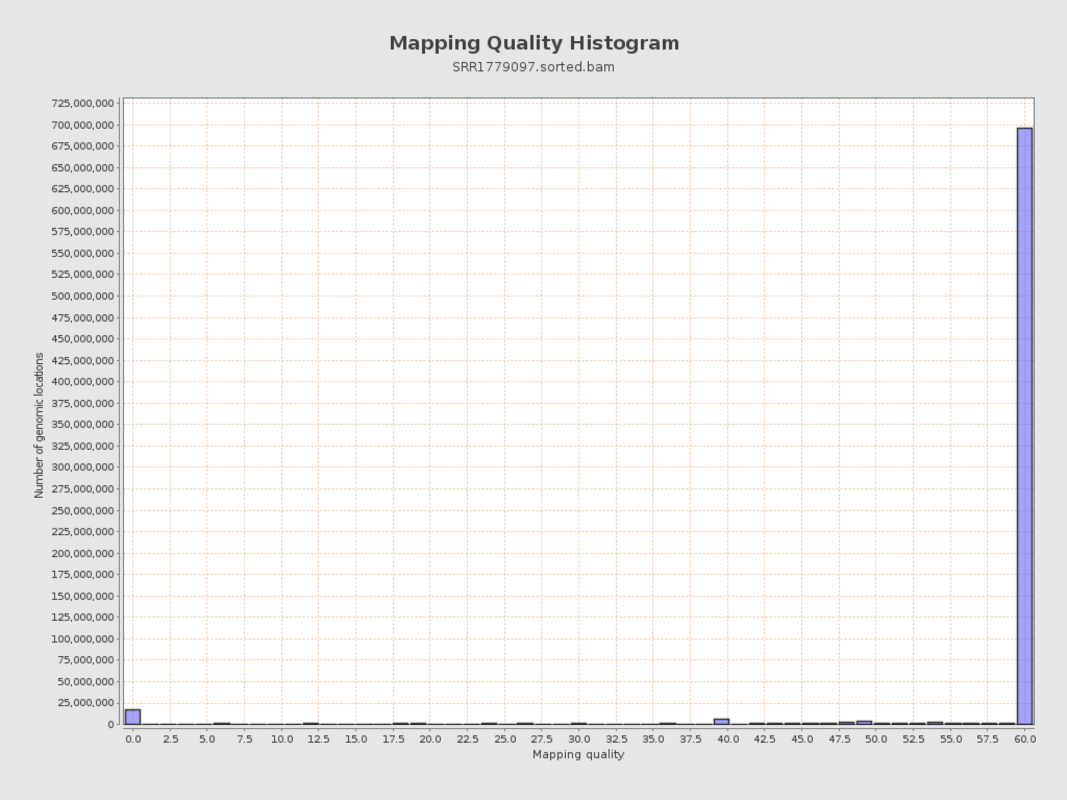
11. Results : Homopolymer Indels



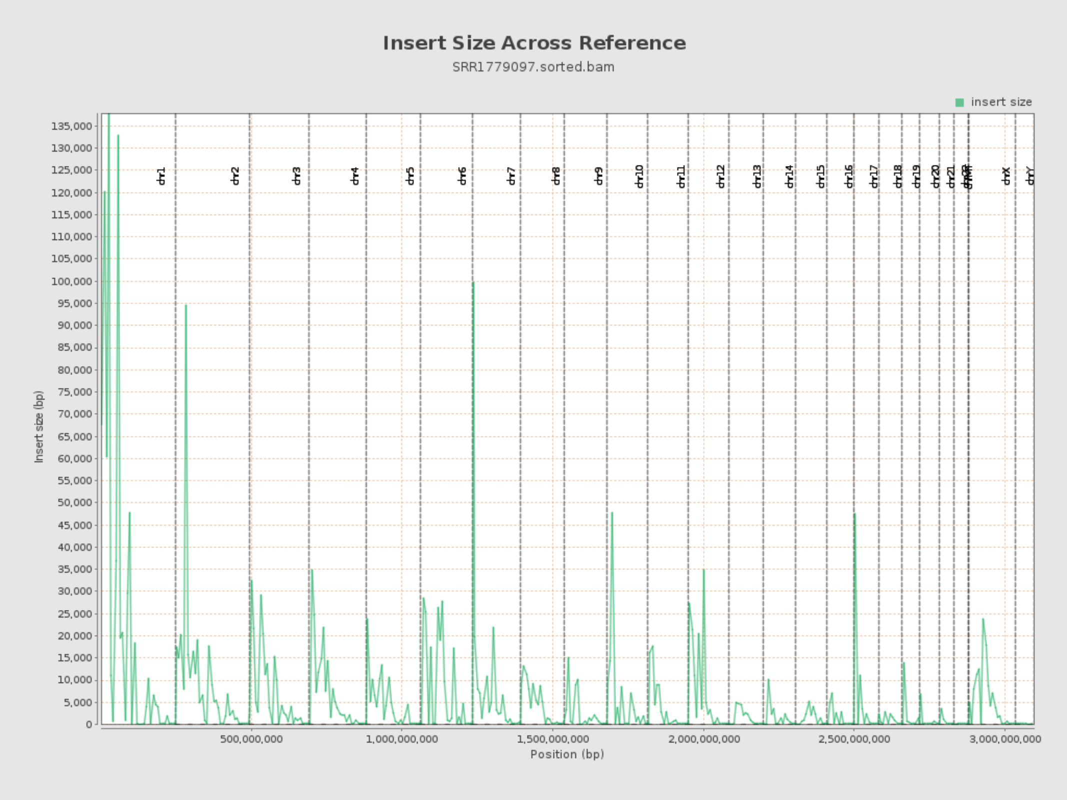
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram