Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 09:32:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779007.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_SRR1779007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779007_1.fastq.gz SRR1779007_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 09:32:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,702,358
Mapped reads	20,080,507 / 97%
Unmapped reads	621,851 / 3%
Mapped paired reads	20,080,507 / 97%
Mapped reads, first in pair	10,144,844 / 49%
Mapped reads, second in pair	9,935,663 / 47.99%
Mapped reads, both in pair	19,803,992 / 95.66%
Mapped reads, singletons	276,515 / 1.34%
Secondary alignments	0
Supplementary alignments	113,855 / 0.55%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	438,555 / 2.12%
Duplication rate	1.89%
Clipped reads	1,209,902 / 5.84%

2.2. ACGT Content

Number/percentage of A's	614,147,267 / 30.62%
Number/percentage of C's	386,498,604 / 19.27%
Number/percentage of T's	611,167,027 / 30.47%
Number/percentage of G's	393,152,737 / 19.6%
Number/percentage of N's	674,251 / 0.03%

GC Percentage	38.87%

2.3. Coverage

Mean	0.648
Standard Deviation	1.606

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	75,814.1
Standard Deviation	2,635,019.85
P25/Median/P75	207 / 274 / 348

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	9,977,788
Insertions	176,804
Mapped reads with at least one insertion	0.87%
Deletions	217,162
Mapped reads with at least one deletion	1.06%
Homopolymer indels	47.1%

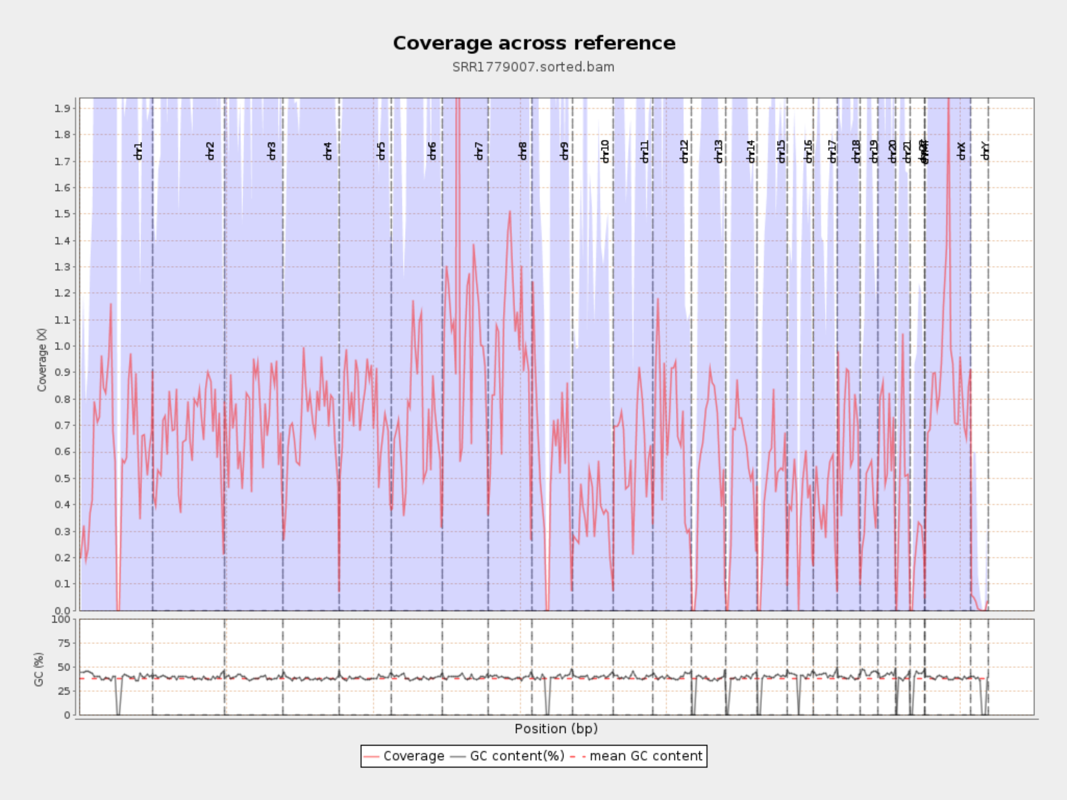
2.7. Chromosome stats

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

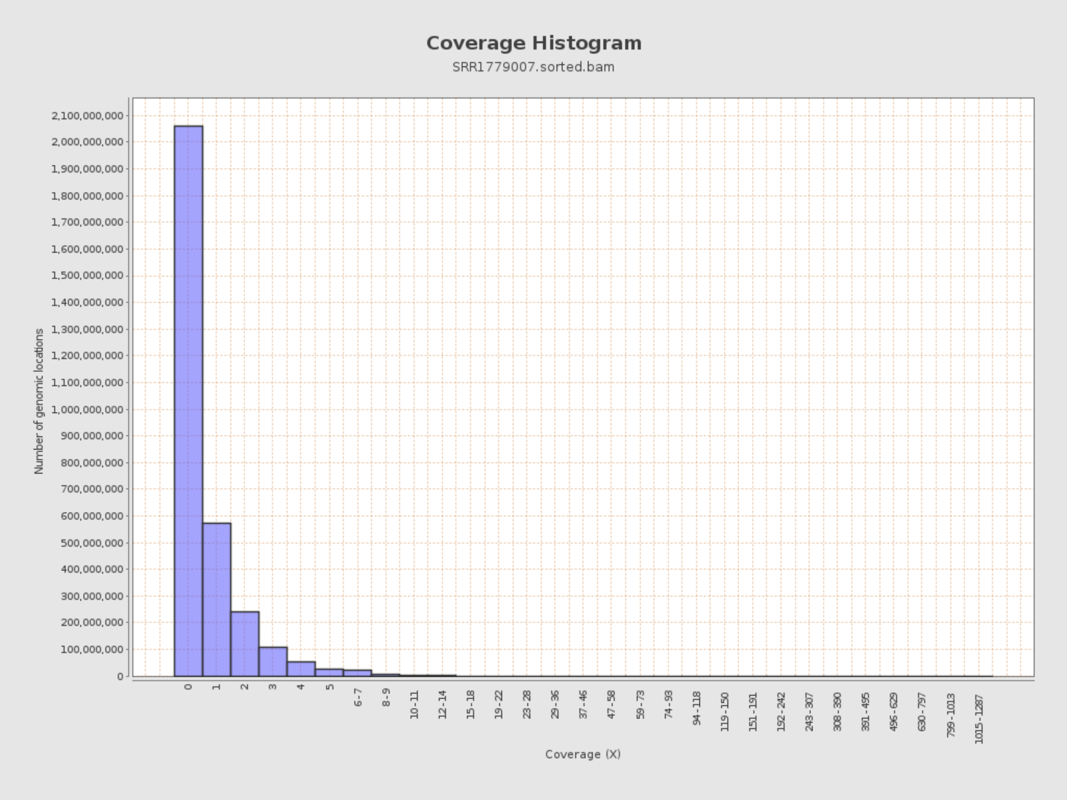
		bases	coverage	deviation
chr1	249250621	149794009	0.601	1.8114
chr2	243199373	160846269	0.6614	1.3884
chr3	198022430	141907277	0.7166	1.2758
chr4	191154276	135341168	0.708	1.2763
chr5	180915260	135029317	0.7464	1.3062
chr6	171115067	122254810	0.7145	1.3089
chr7	159138663	189017067	1.1878	3.9
chr8	146364022	147150495	1.0054	1.5917
chr9	141213431	77663583	0.55	1.2396
chr10	135534747	48787377	0.36	1.903
chr11	135006516	82125757	0.6083	1.1924
chr12	133851895	92248741	0.6892	1.3077
chr13	115169878	64176149	0.5572	1.1536
chr14	107349540	54802191	0.5105	1.114
chr15	102531392	46218619	0.4508	1.0989
chr16	90354753	34039048	0.3767	0.9273
chr17	81195210	32381418	0.3988	1.0635
chr18	78077248	52756238	0.6757	1.2934
chr19	59128983	23392608	0.3956	1.1841
chr20	63025520	40412031	0.6412	1.3093
chr21	48129895	24342792	0.5058	1.1585
chr22	51304566	10216854	0.1991	0.667
chrMT	16571	793	0.0479	0.2481
chrX	155270560	139907994	0.9011	1.5998

chrY	59373566	1310351	0.0221	0.3265

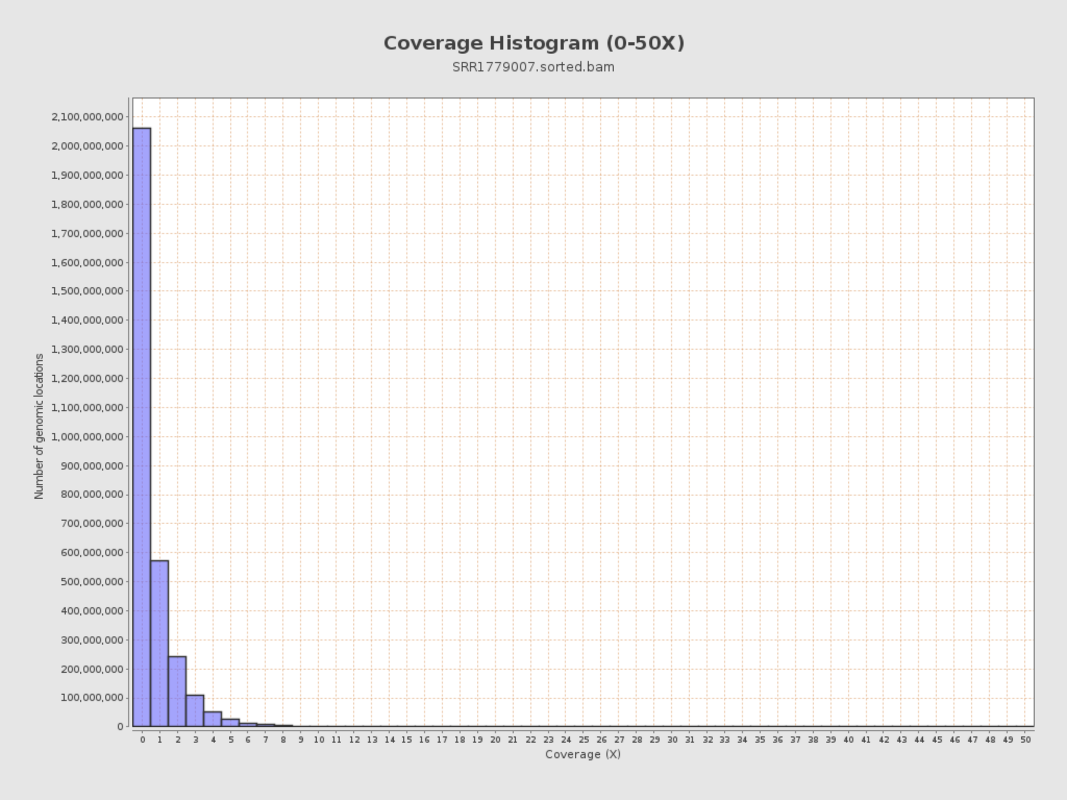
3. Results : Coverage across reference



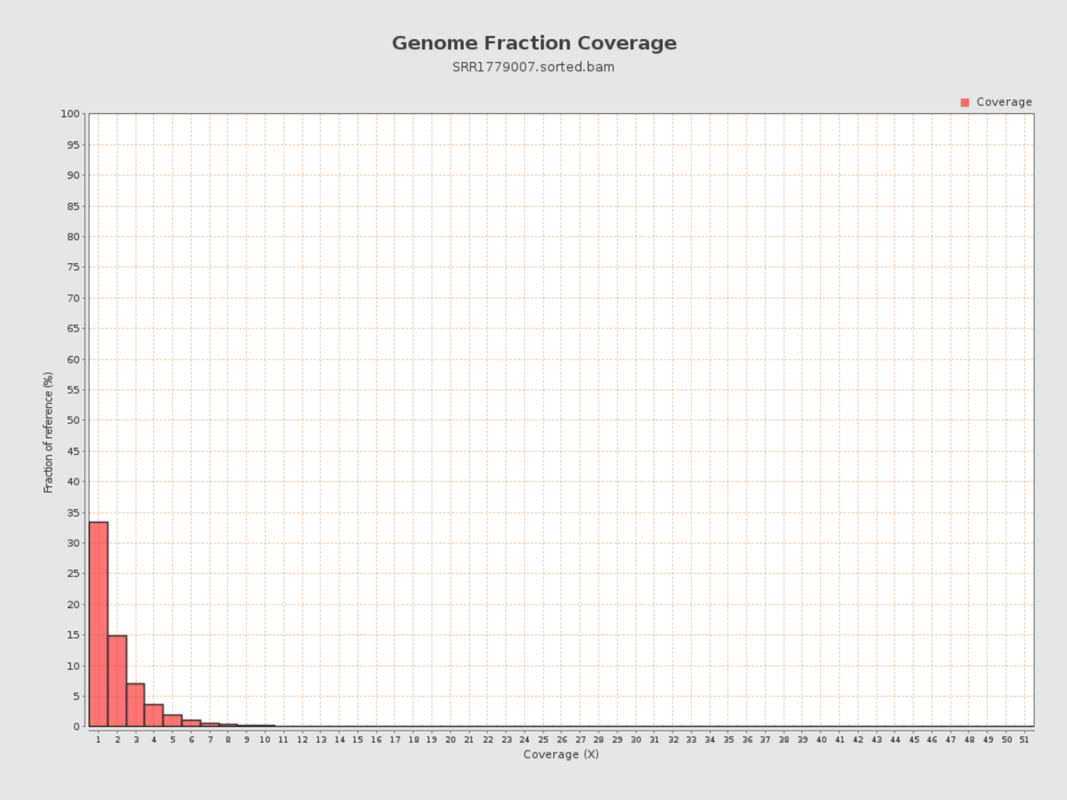
4. Results : Coverage Histogram



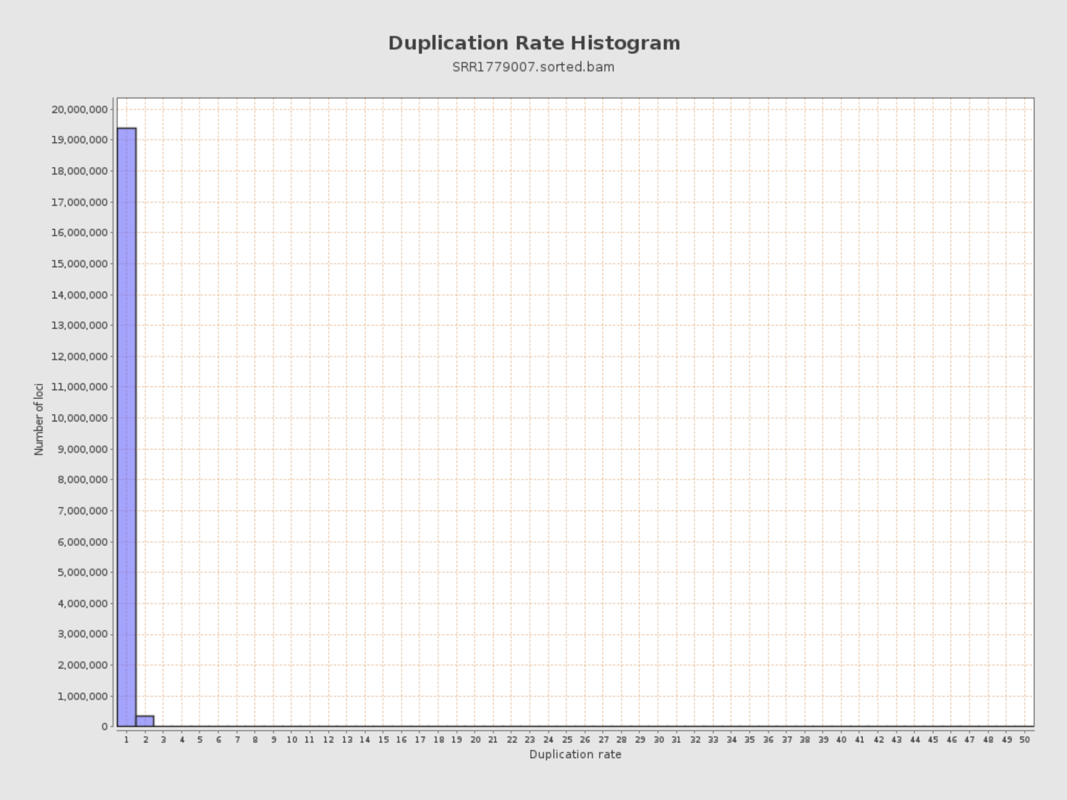
5. Results : Coverage Histogram (0-50X)



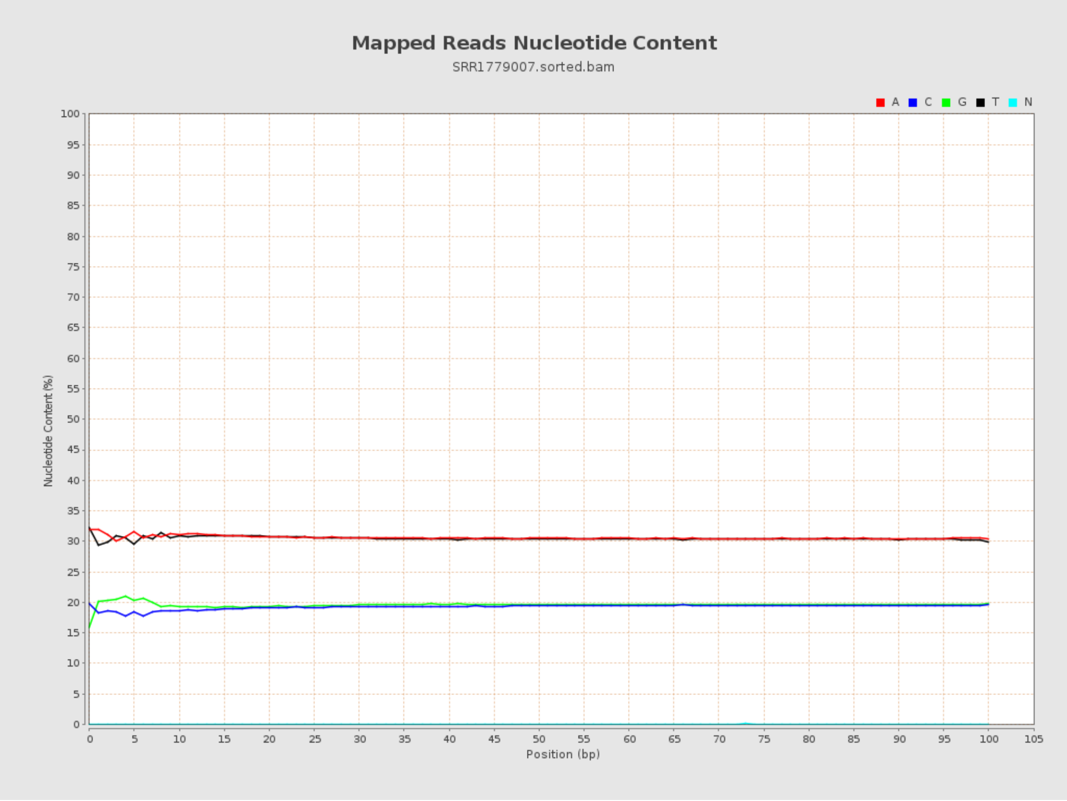
6. Results : Genome Fraction Coverage



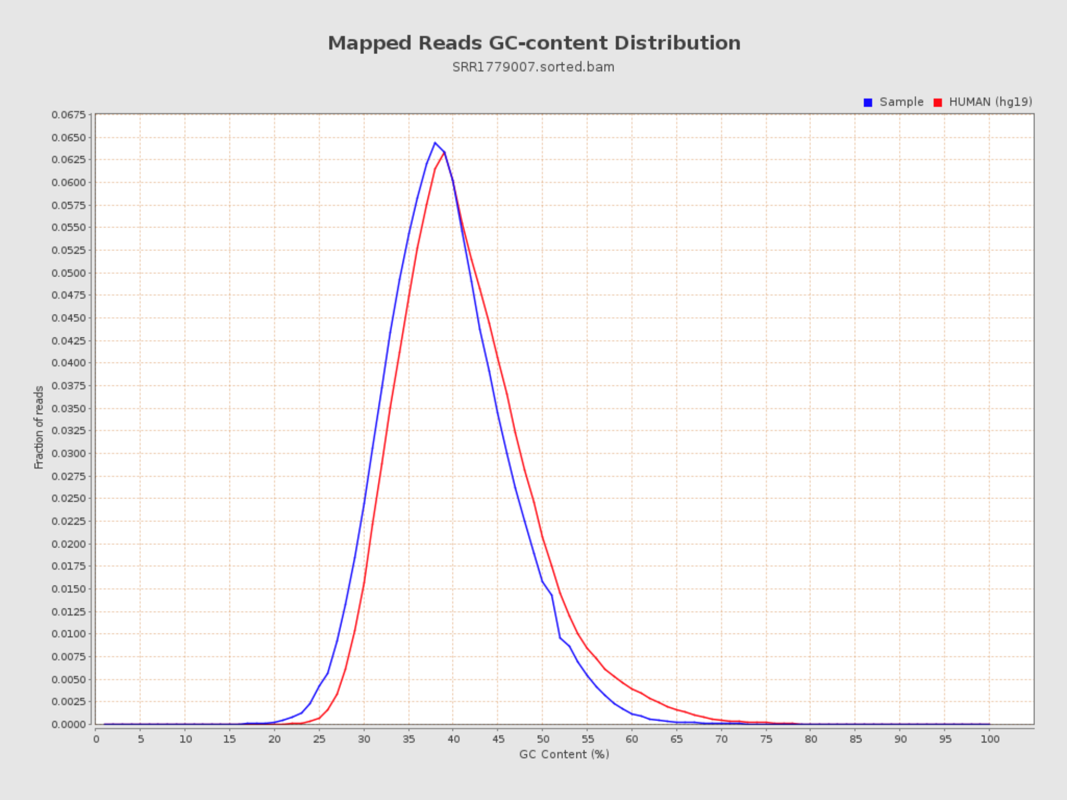
7. Results : Duplication Rate Histogram



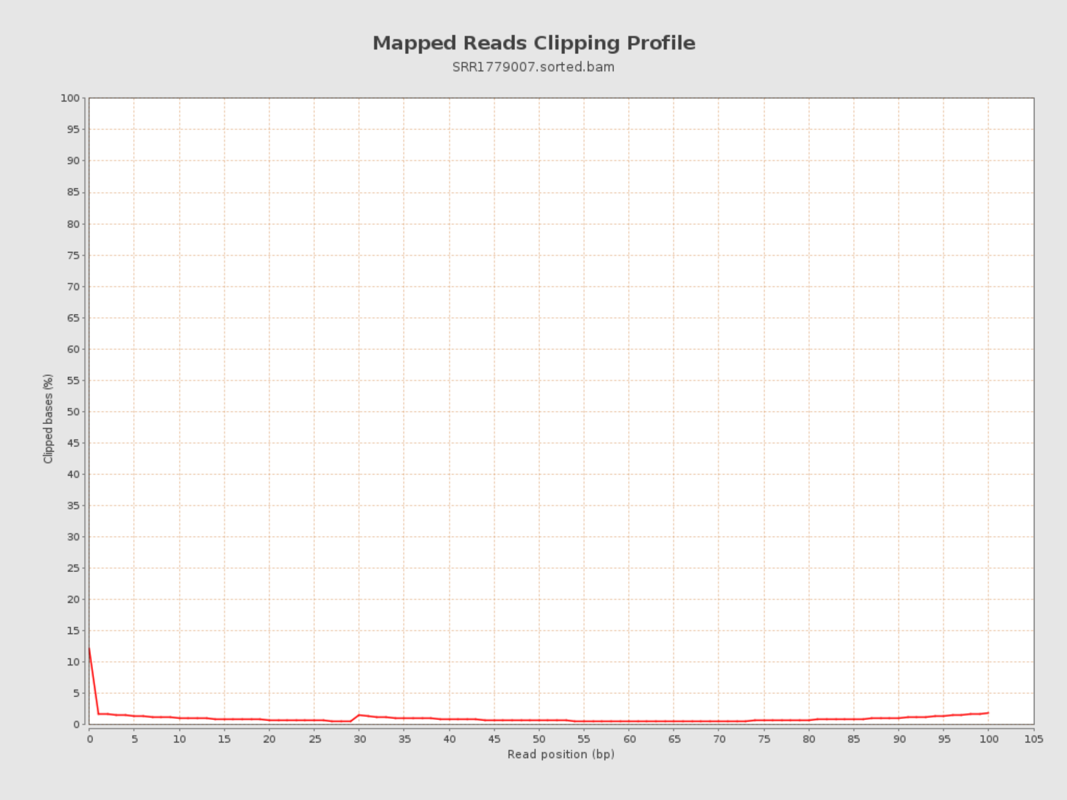
8. Results : Mapped Reads Nucleotide Content



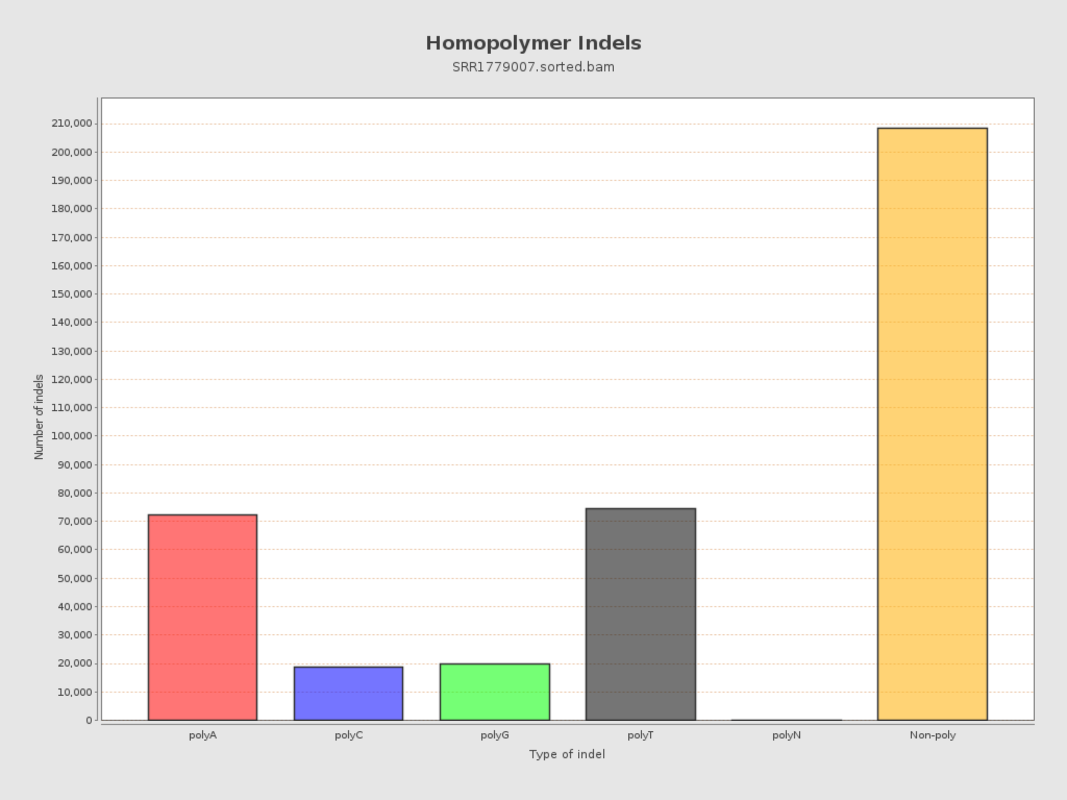
9. Results : Mapped Reads GC-content Distribution



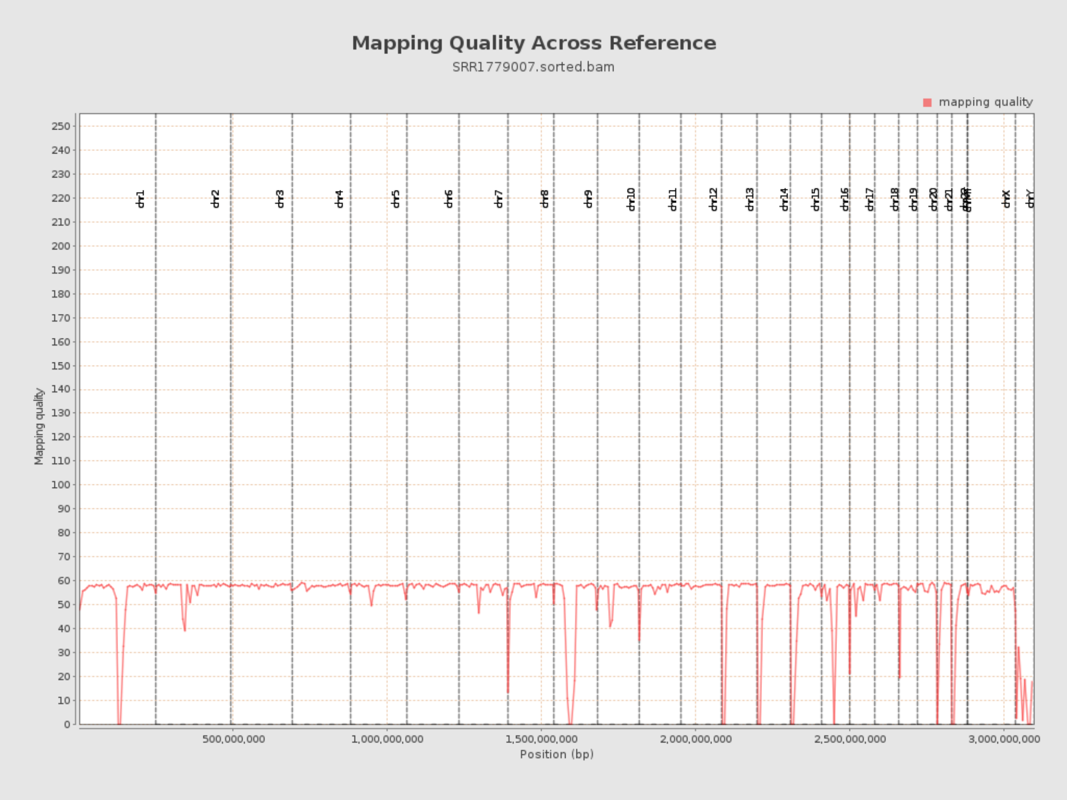
10. Results : Mapped Reads Clipping Profile



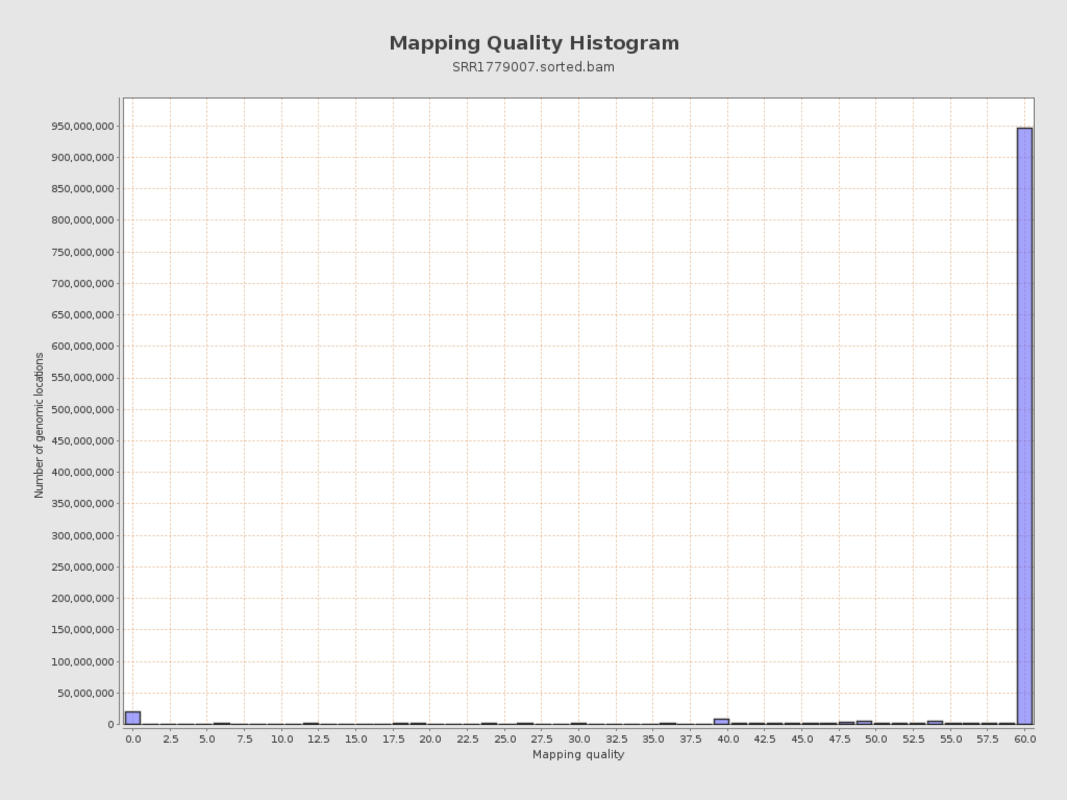
11. Results : Homopolymer Indels



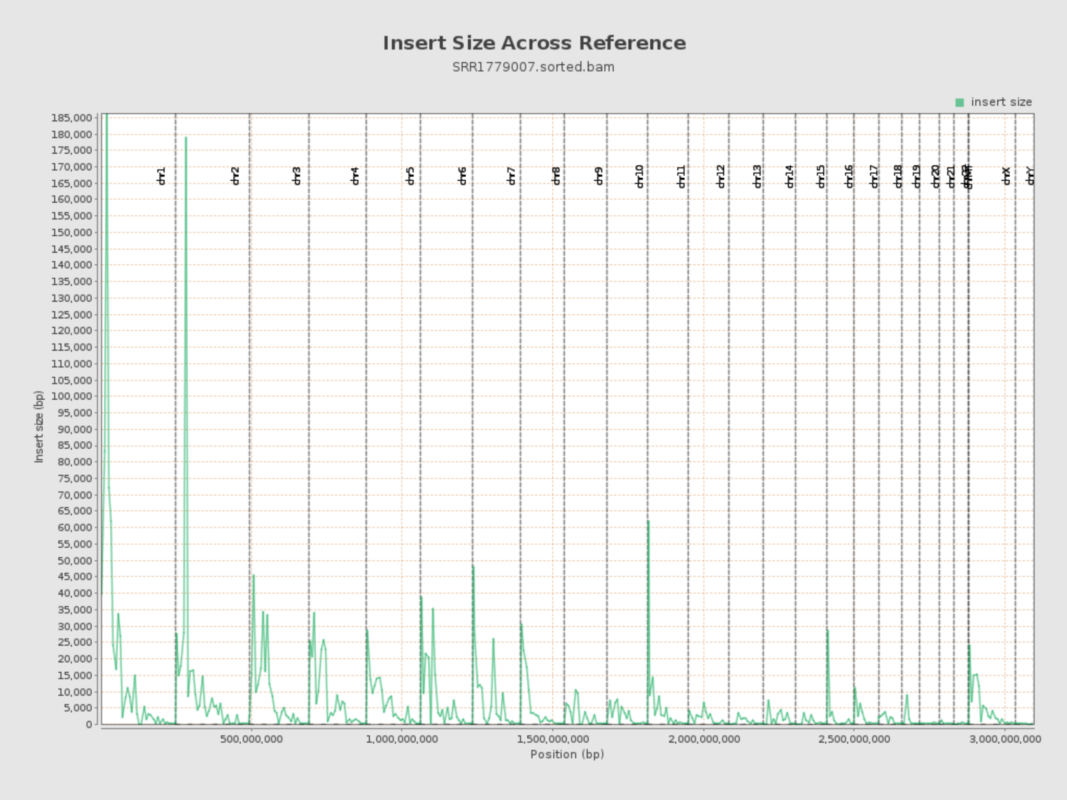
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram