Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 13:04:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926979.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_SRR926979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926979_1.fastq.gz SRR926979_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 13:04:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,902,716
Mapped reads	32,386,897 / 98.43%
Unmapped reads	515,819 / 1.57%
Mapped paired reads	32,386,897 / 98.43%
Mapped reads, first in pair	16,252,652 / 49.4%
Mapped reads, second in pair	16,134,245 / 49.04%
Mapped reads, both in pair	32,099,234 / 97.56%
Mapped reads, singletons	287,663 / 0.87%
Secondary alignments	0
Supplementary alignments	423,401 / 1.29%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	2,783,189 / 8.46%
Duplication rate	6.58%
Clipped reads	9,099,239 / 27.65%

2.2. ACGT Content

Number/percentage of A's	862,407,881 / 28.36%
Number/percentage of C's	612,867,898 / 20.16%
Number/percentage of T's	876,851,360 / 28.84%
Number/percentage of G's	688,004,691 / 22.63%
Number/percentage of N's	275,260 / 0.01%

GC Percentage	42.79%

2.3. Coverage

Mean	0.9829
Standard Deviation	3.8871

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	127,780.96
Standard Deviation	3,474,529.68
P25/Median/P75	142 / 179 / 234

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	28,135,700
Insertions	493,766
Mapped reads with at least one insertion	1.5%
Deletions	1,604,754
Mapped reads with at least one deletion	4.83%
Homopolymer indels	52.74%

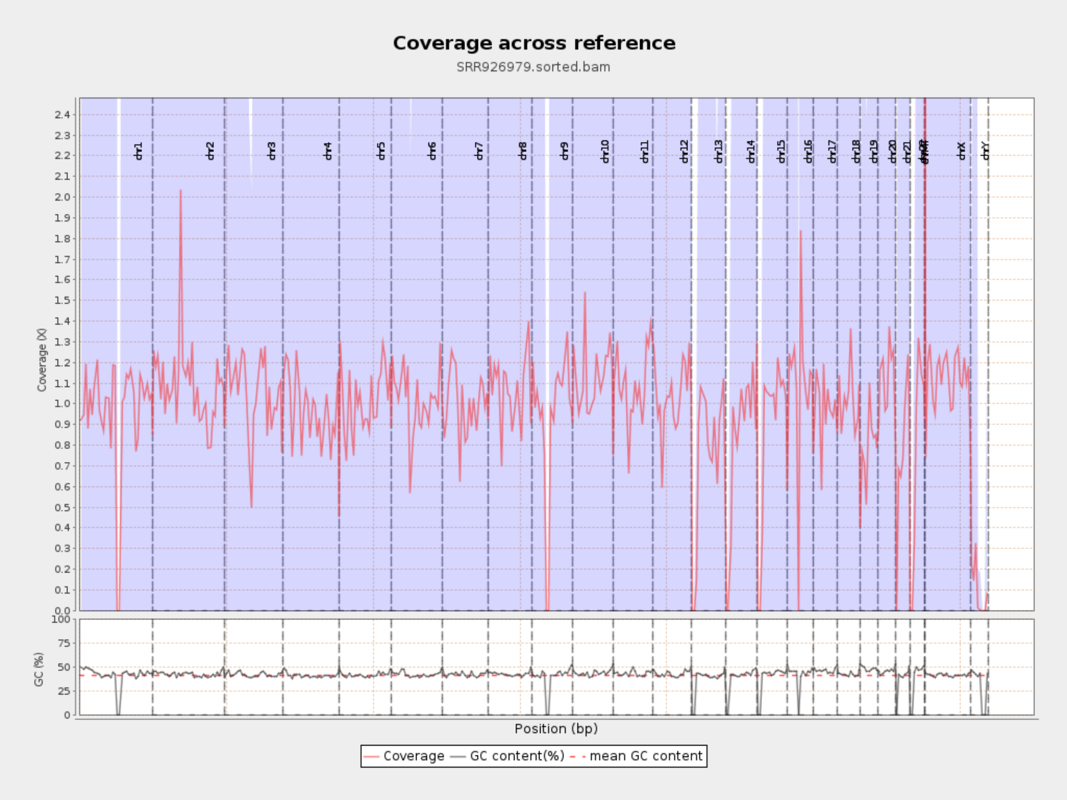
2.7. Chromosome stats

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

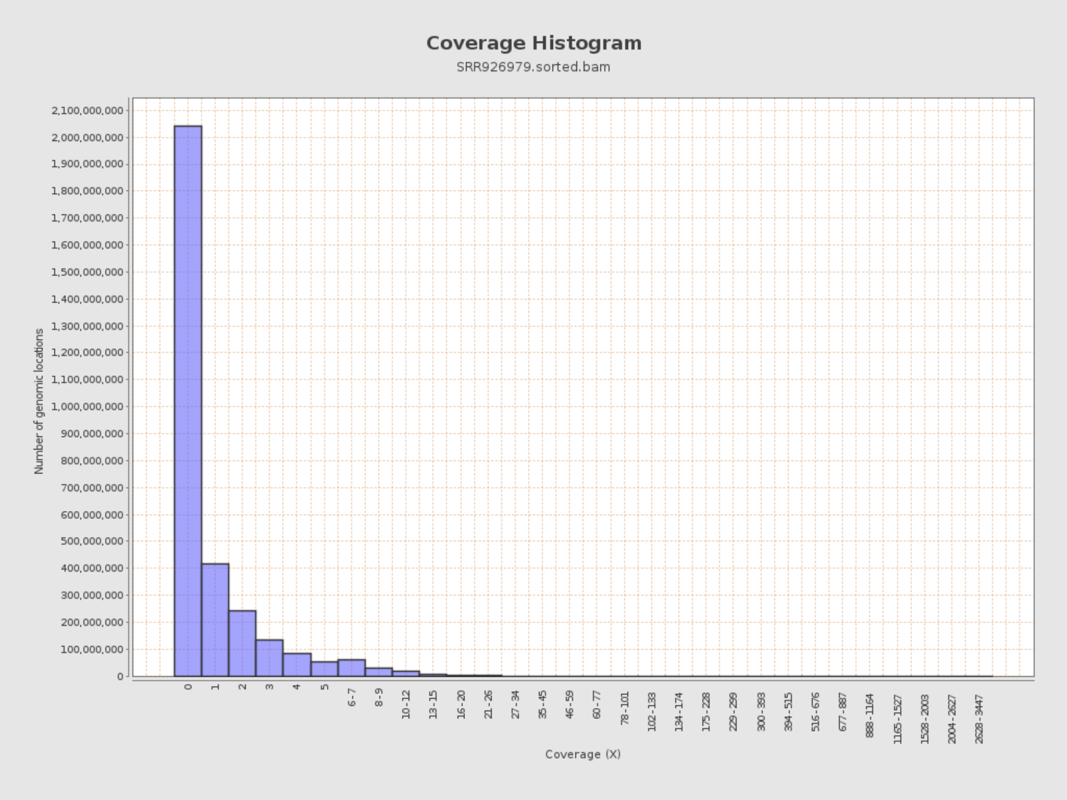
		bases	coverage	deviation
chr1	249250621	239742278	0.9619	4.2783
chr2	243199373	266567005	1.0961	7.1004
chr3	198022430	208928431	1.0551	2.151
chr4	191154276	186307743	0.9746	3.6007
chr5	180915260	184534332	1.02	2.0972
chr6	171115067	175336493	1.0247	2.821
chr7	159138663	158924170	0.9987	2.9087
chr8	146364022	156712438	1.0707	2.6728
chr9	141213431	132299059	0.9369	4.6375
chr10	135534747	154153914	1.1374	6.0337
chr11	135006516	146341598	1.084	3.1116
chr12	133851895	138847903	1.0373	2.4134
chr13	115169878	87202879	0.7572	1.8775
chr14	107349540	86939442	0.8099	1.9402
chr15	102531392	88217307	0.8604	2.0598
chr16	90354753	96988826	1.0734	7.2438
chr17	81195210	79085934	0.974	3.0265
chr18	78077248	80661370	1.0331	5.0122
chr19	59128983	46623891	0.7885	2.9583
chr20	63025520	71112758	1.1283	2.5354
chr21	48129895	38112582	0.7919	2.9011
chr22	51304566	39438146	0.7687	2.0422
chrMT	16571	134229	8.1002	7.4831
chrX	155270560	173904352	1.12	2.5354

chrY	59373566	5584912	0.0941	3.2707

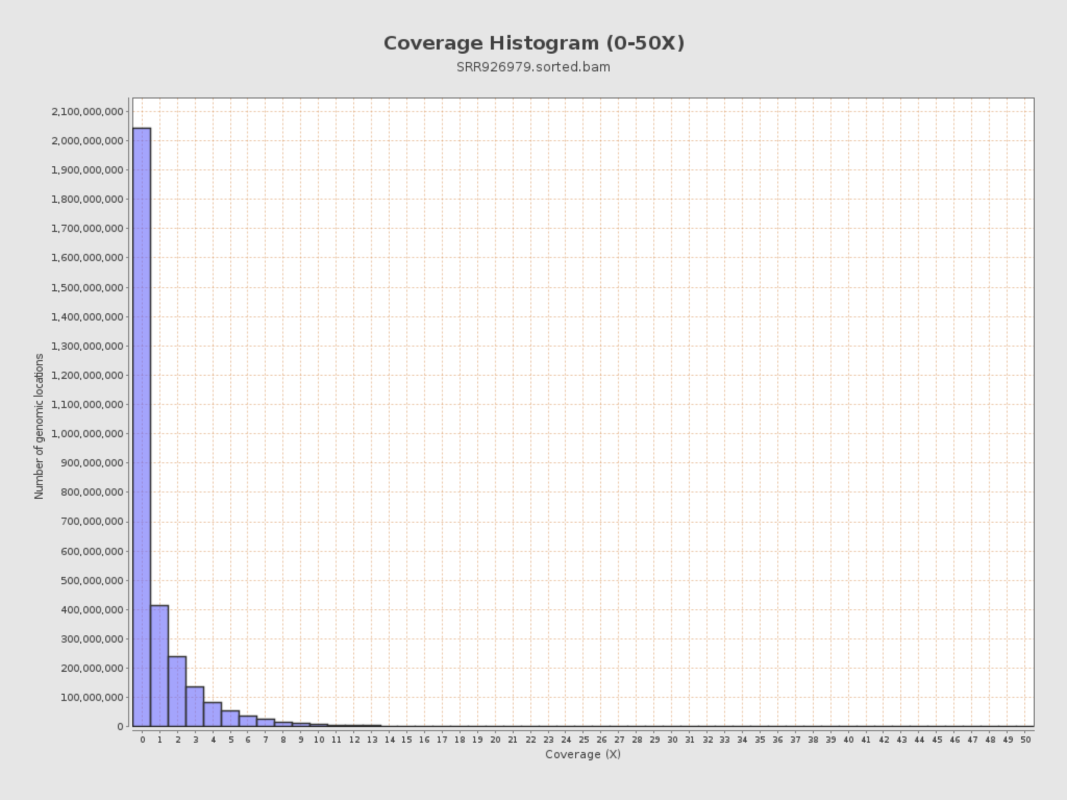
3. Results : Coverage across reference



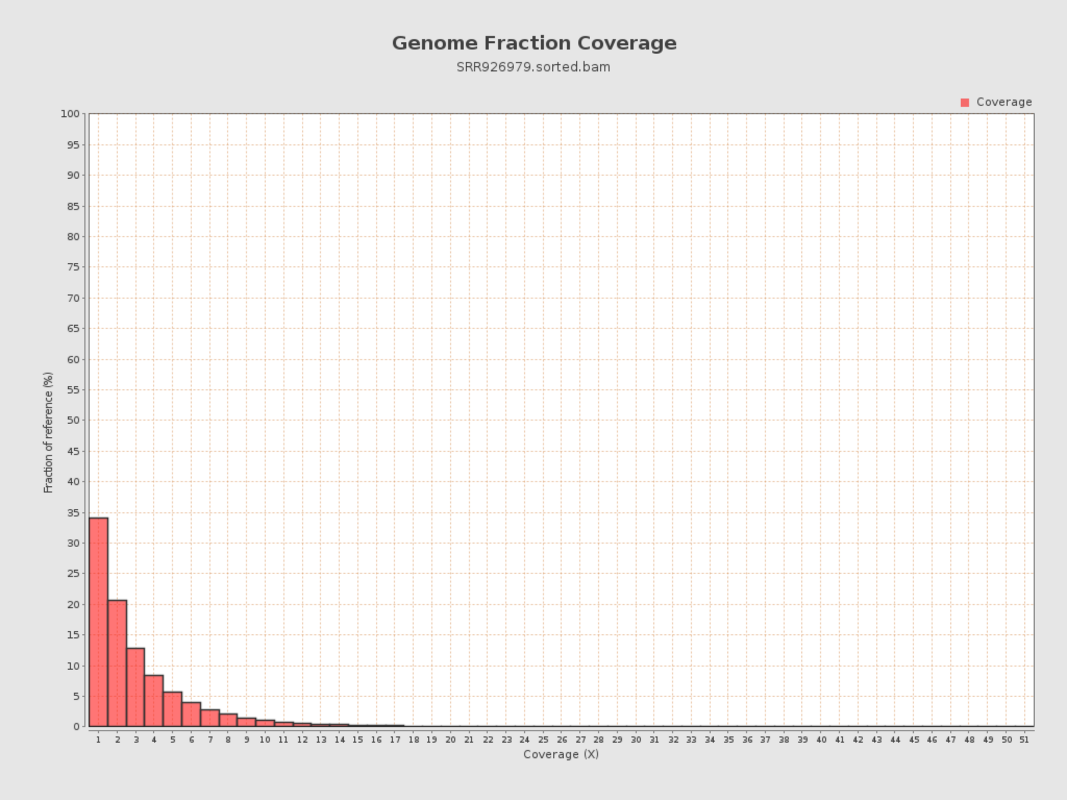
4. Results : Coverage Histogram



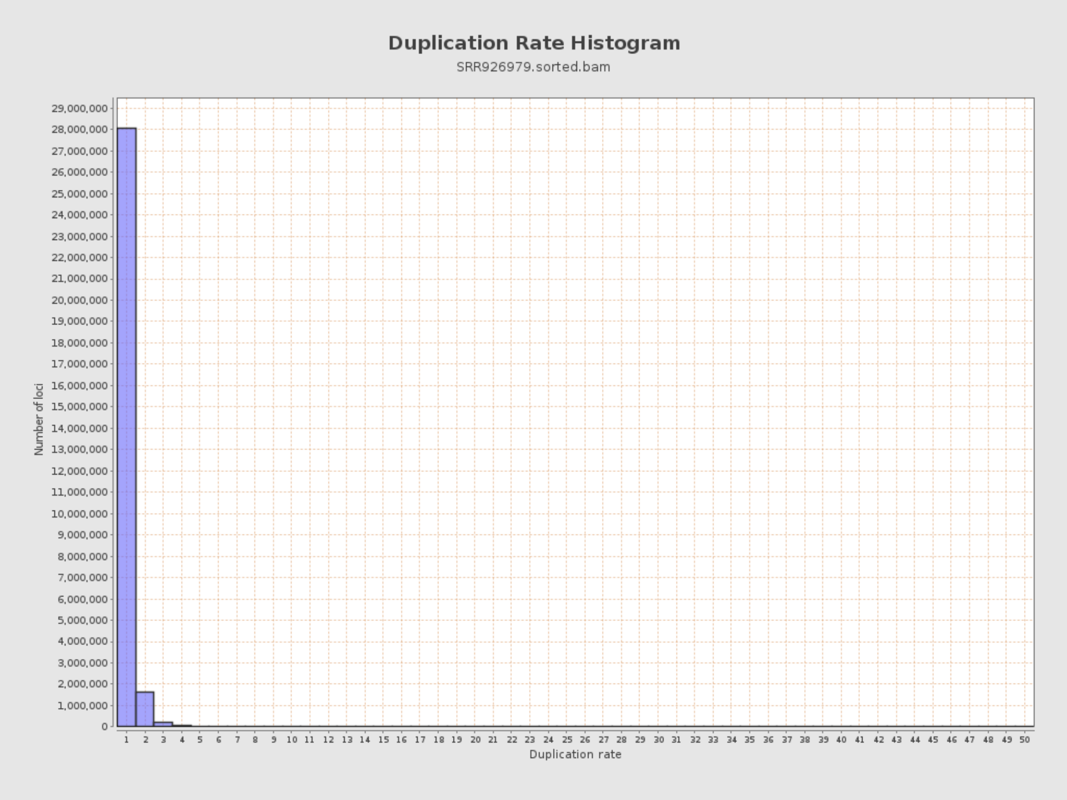
5. Results : Coverage Histogram (0-50X)



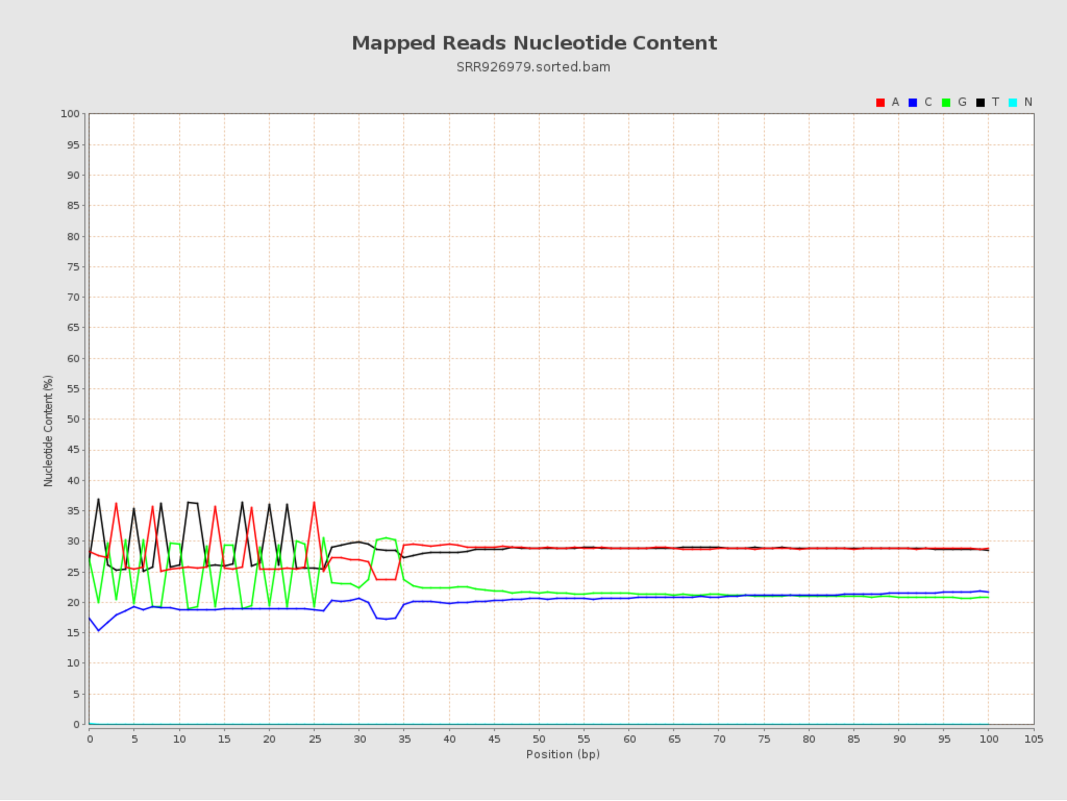
6. Results : Genome Fraction Coverage



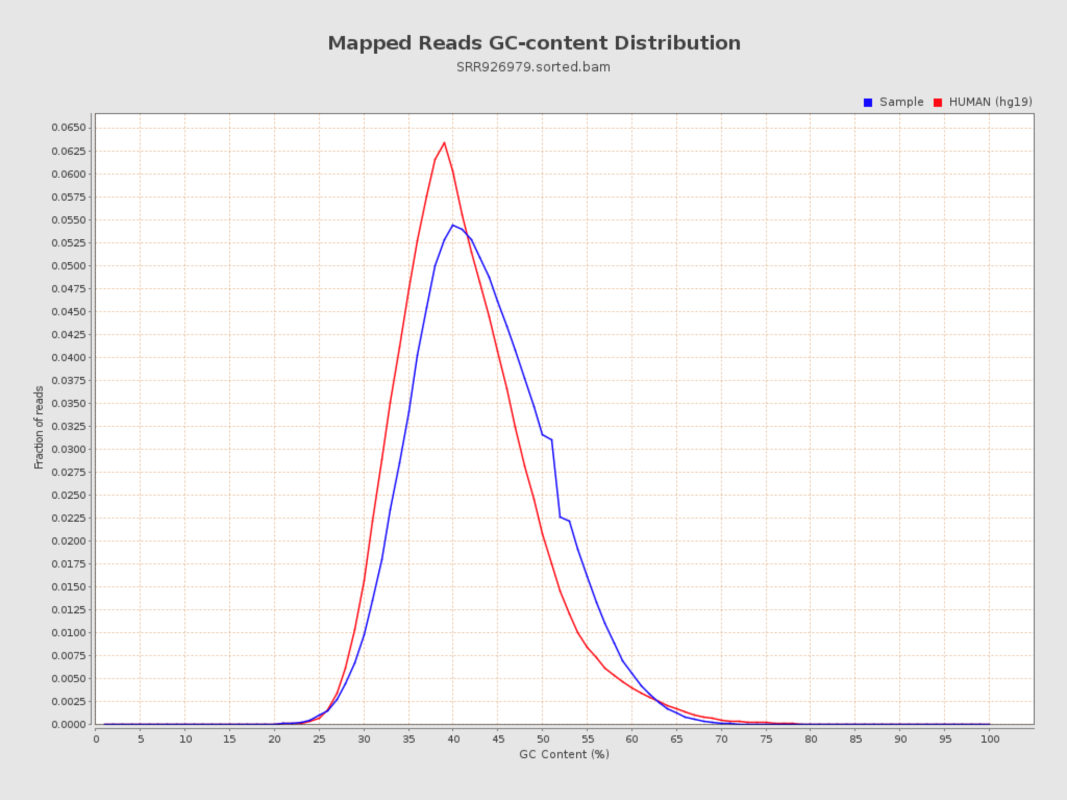
7. Results : Duplication Rate Histogram



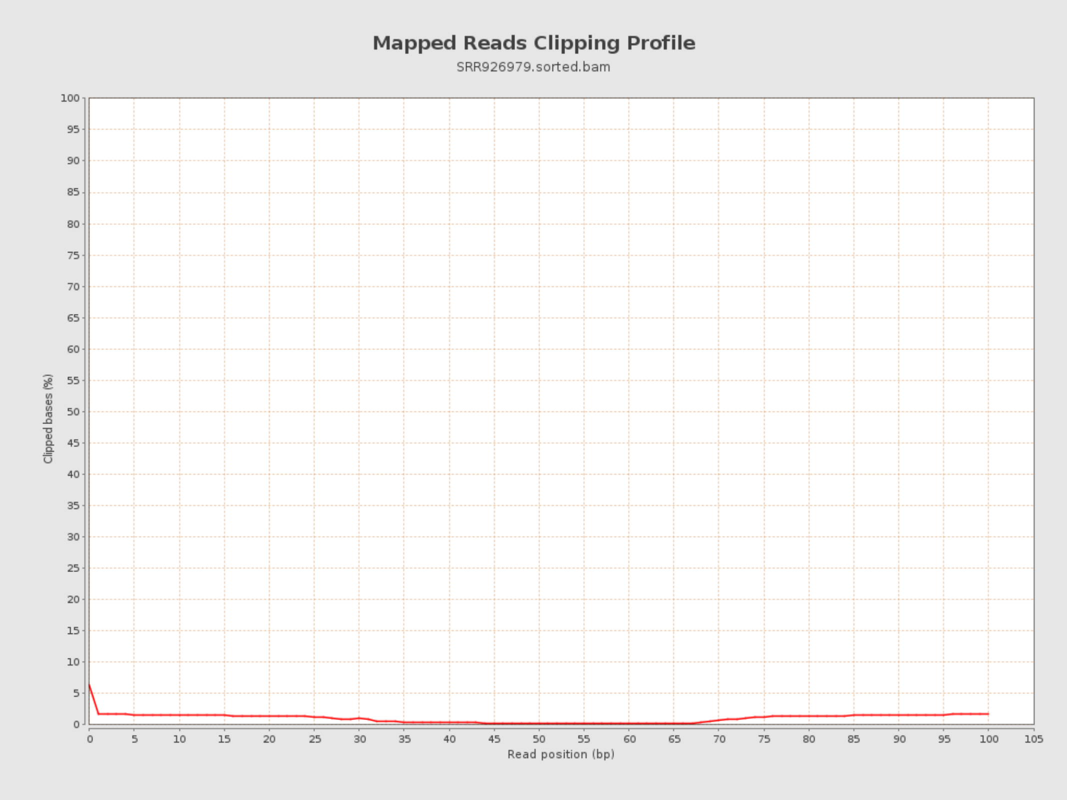
8. Results : Mapped Reads Nucleotide Content



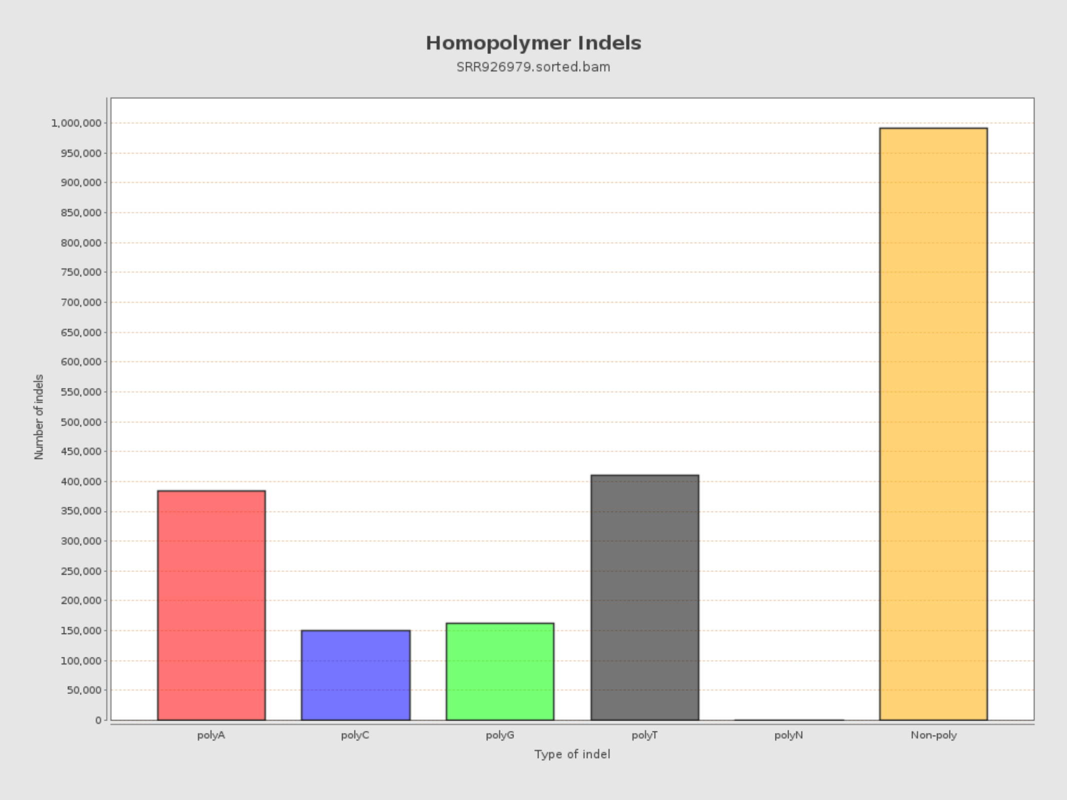
9. Results : Mapped Reads GC-content Distribution



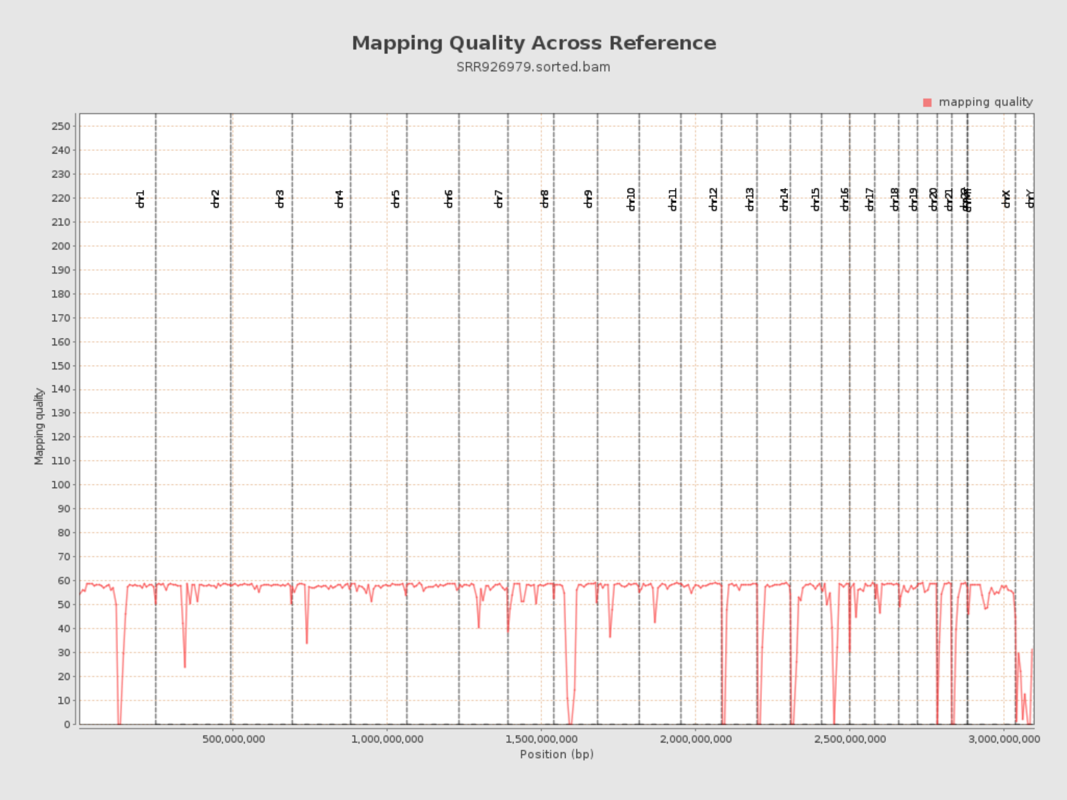
10. Results : Mapped Reads Clipping Profile



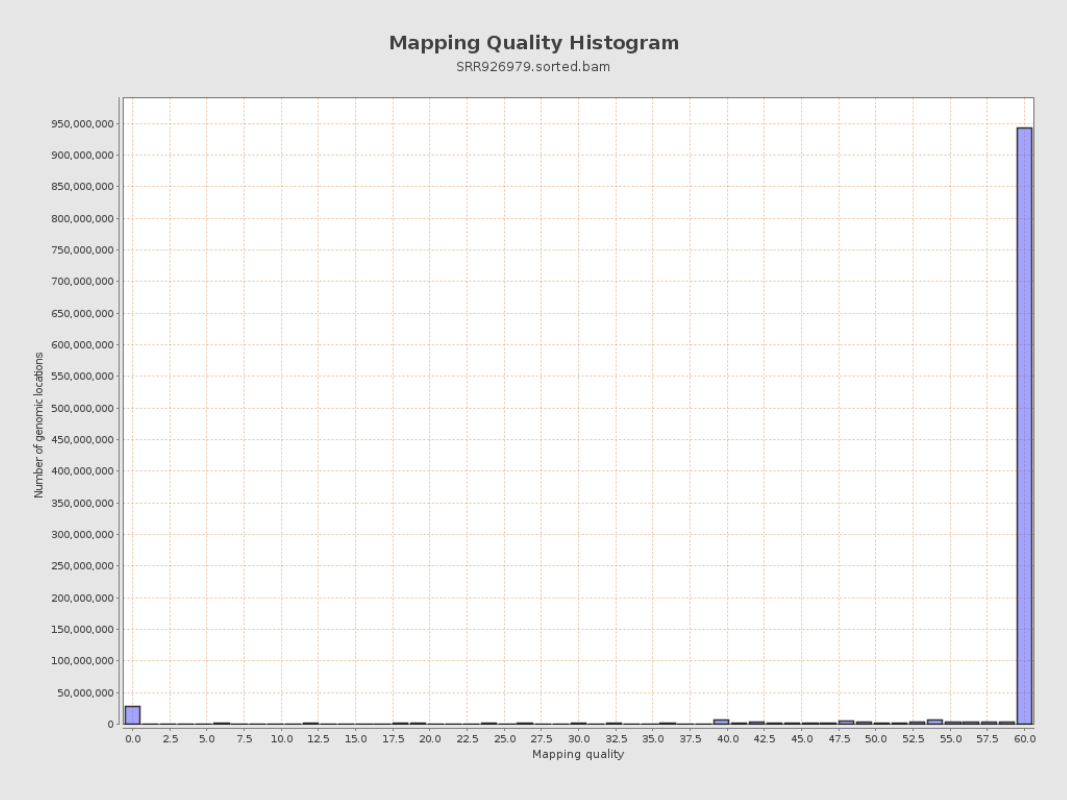
11. Results : Homopolymer Indels



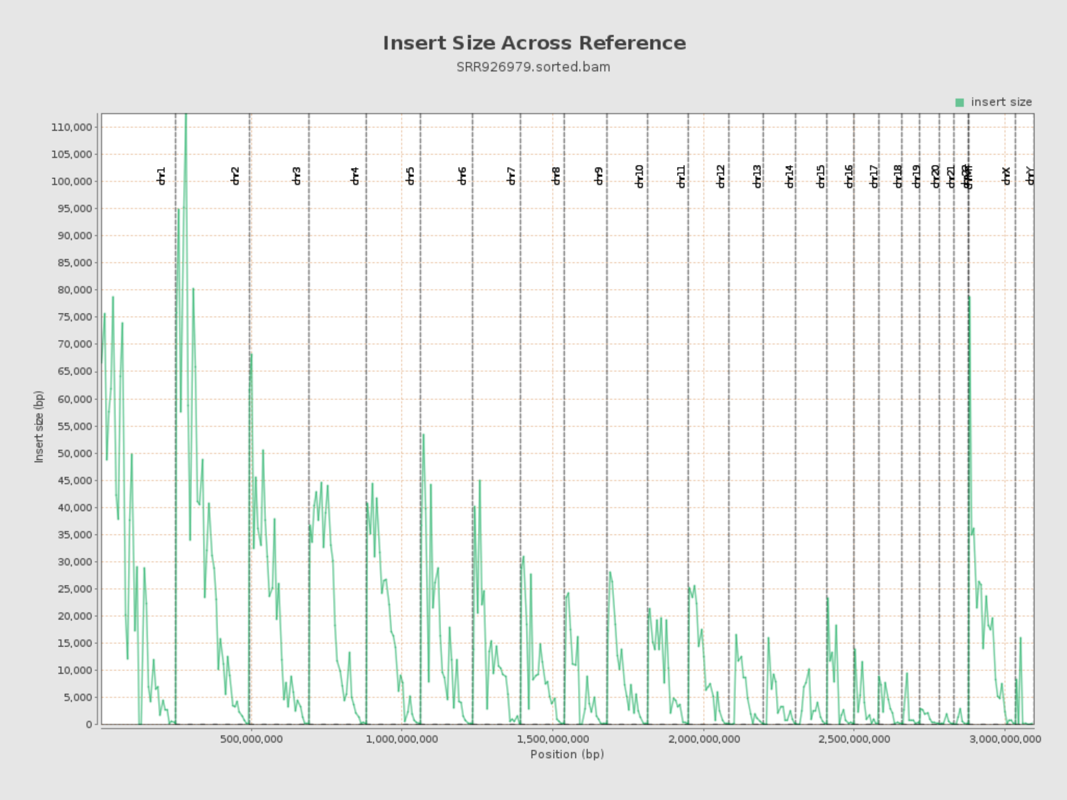
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram