Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 12:32:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926978.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_SRR926978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926978_1.fastq.gz SRR926978_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 12:32:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,312,588
Mapped reads	21,791,789 / 97.67%
Unmapped reads	520,799 / 2.33%
Mapped paired reads	21,791,789 / 97.67%
Mapped reads, first in pair	10,940,986 / 49.04%
Mapped reads, second in pair	10,850,803 / 48.63%
Mapped reads, both in pair	21,487,722 / 96.3%
Mapped reads, singletons	304,067 / 1.36%
Secondary alignments	0
Supplementary alignments	854,532 / 3.83%
Read min/max/mean length	30 / 101 / 102.58
Duplicated reads (estimated)	2,120,503 / 9.5%
Duplication rate	7.72%
Clipped reads	10,657,221 / 47.76%

2.2. ACGT Content

Number/percentage of A's	560,596,864 / 28.68%
Number/percentage of C's	373,016,171 / 19.08%
Number/percentage of T's	575,835,703 / 29.46%
Number/percentage of G's	444,986,335 / 22.77%
Number/percentage of N's	144,794 / 0.01%

GC Percentage	41.85%

2.3. Coverage

Mean	0.6319
Standard Deviation	2.4

2.4. Mapping Quality

Mean Mapping Quality	52.29

2.5. Insert size

Mean	453,030.78
Standard Deviation	6,622,800.33
P25/Median/P75	129 / 167 / 222

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	18,753,855
Insertions	353,220
Mapped reads with at least one insertion	1.59%
Deletions	1,054,157
Mapped reads with at least one deletion	4.71%
Homopolymer indels	51.72%

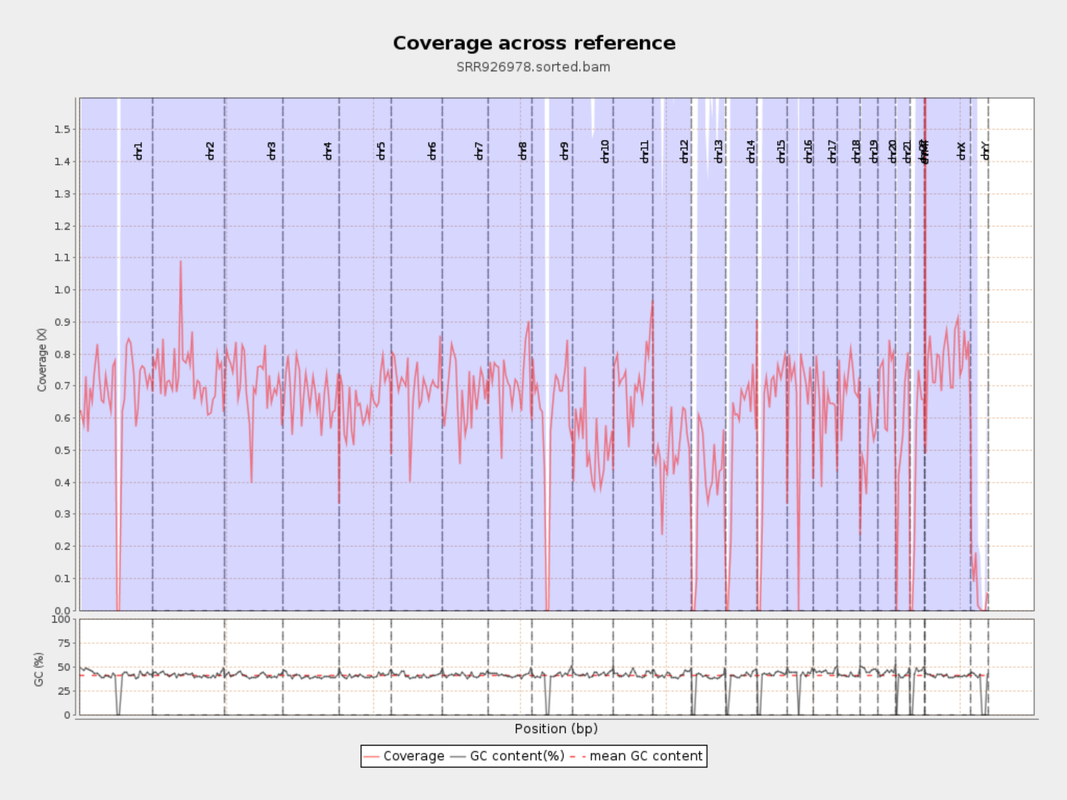
2.7. Chromosome stats

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

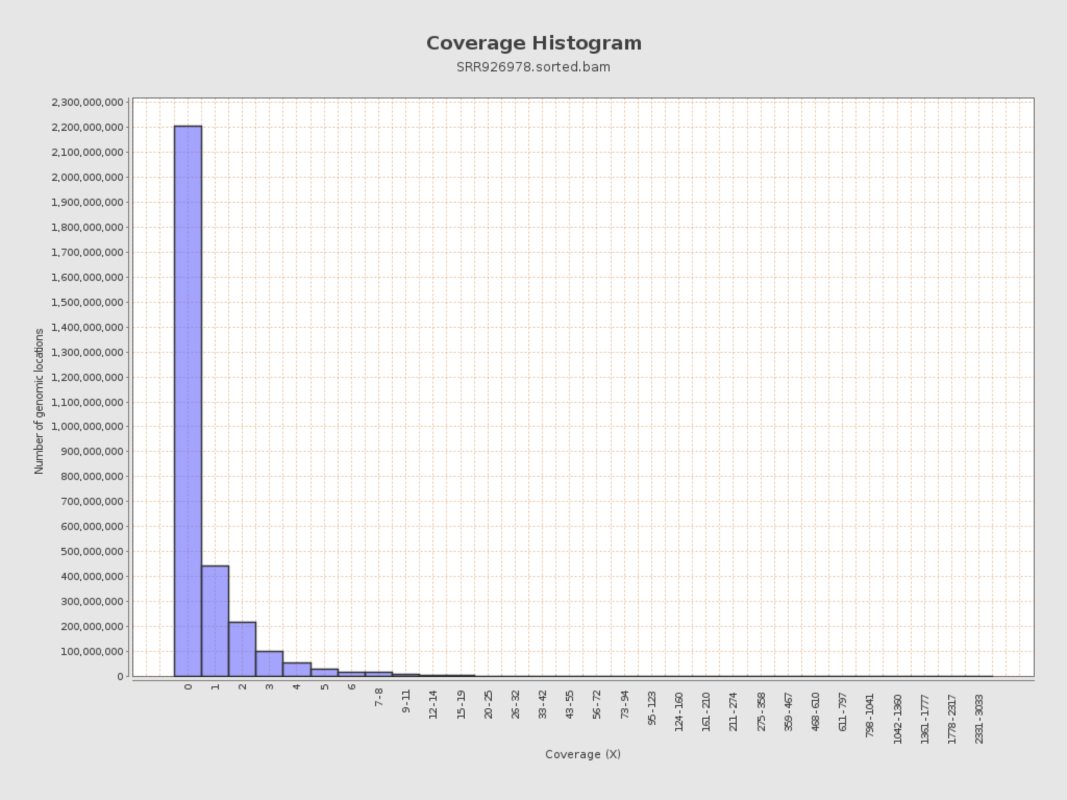
		bases	coverage	deviation
chr1	249250621	164797044	0.6612	2.7907
chr2	243199373	179689789	0.7389	3.9886
chr3	198022430	141289102	0.7135	1.5154
chr4	191154276	128976576	0.6747	2.113
chr5	180915260	117414688	0.649	1.4136
chr6	171115067	120709059	0.7054	2.1411
chr7	159138663	107006245	0.6724	2.3952
chr8	146364022	105479066	0.7207	1.8305
chr9	141213431	83506341	0.5913	3.0053
chr10	135534747	69476547	0.5126	2.8791
chr11	135006516	96616313	0.7156	3.2609
chr12	133851895	66154473	0.4942	1.6362
chr13	115169878	44423901	0.3857	1.1811
chr14	107349540	57999502	0.5403	1.3885
chr15	102531392	60042442	0.5856	1.495
chr16	90354753	58305309	0.6453	2.8444
chr17	81195210	50613102	0.6234	2.1416
chr18	78077248	55549840	0.7115	3.2041
chr19	59128983	30367068	0.5136	1.8336
chr20	63025520	44655413	0.7085	1.6067
chr21	48129895	25788724	0.5358	2.085
chr22	51304566	23100282	0.4503	1.2931
chrMT	16571	338731	20.4412	18.508
chrX	155270560	120262272	0.7745	1.8698

chrY	59373566	3575839	0.0602	1.8828

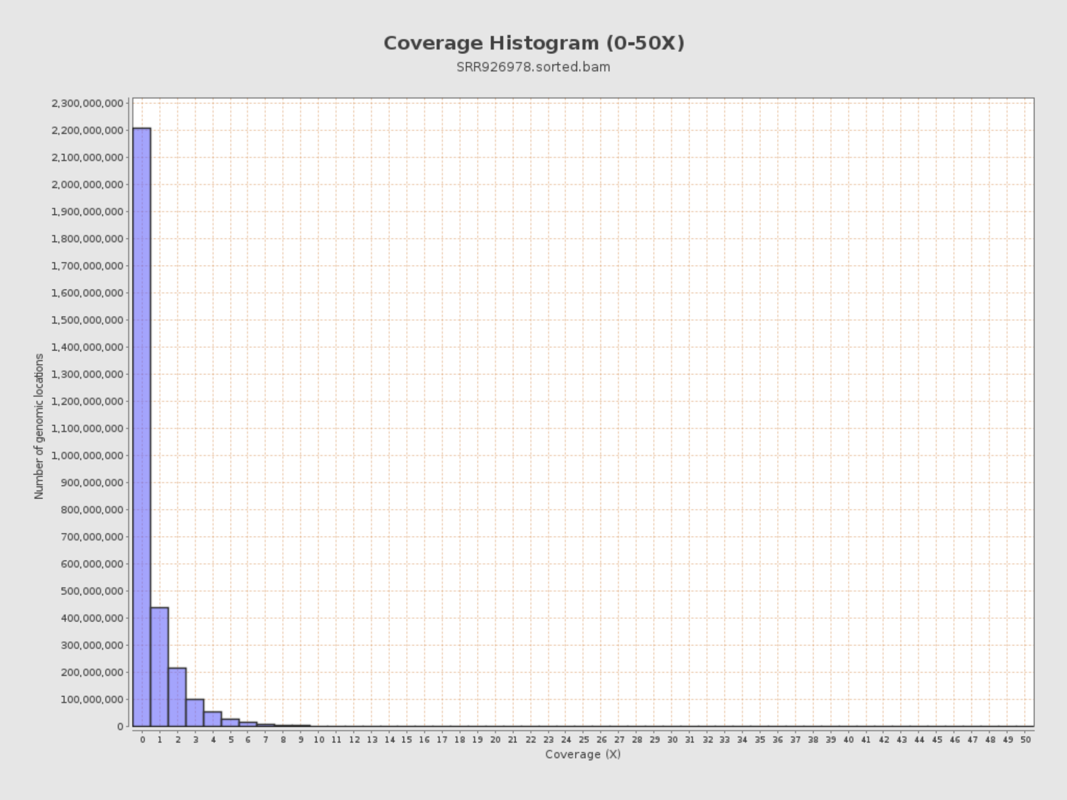
3. Results : Coverage across reference



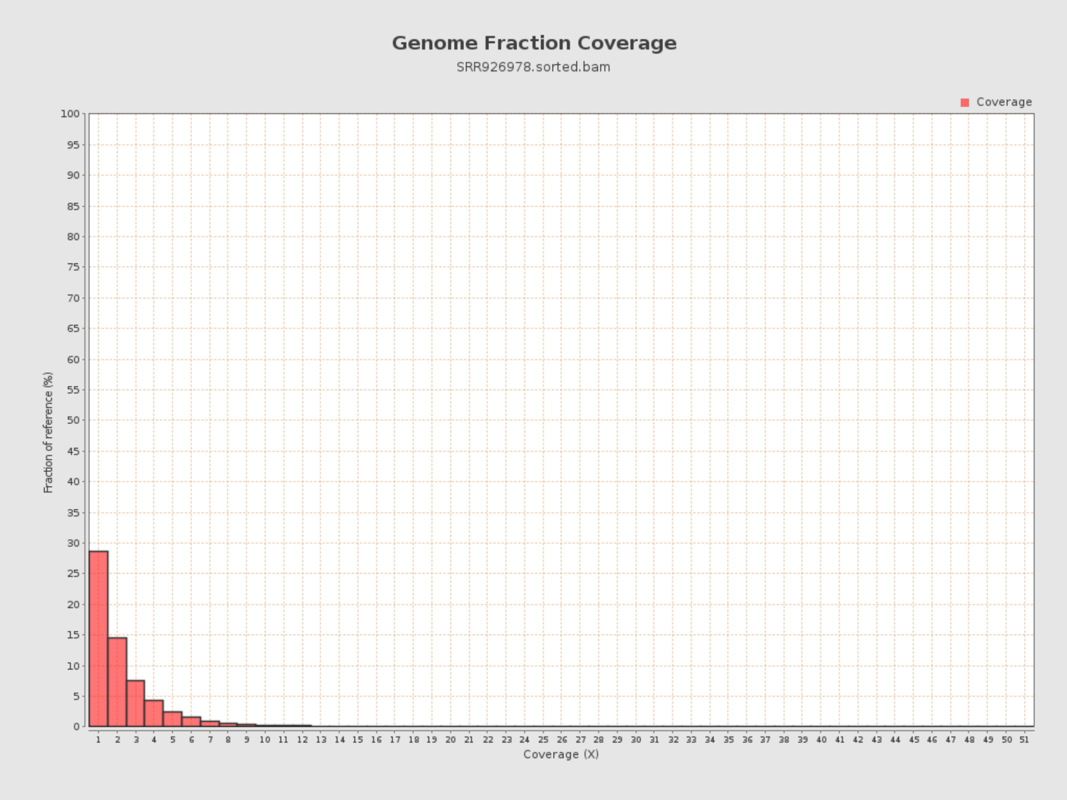
4. Results : Coverage Histogram



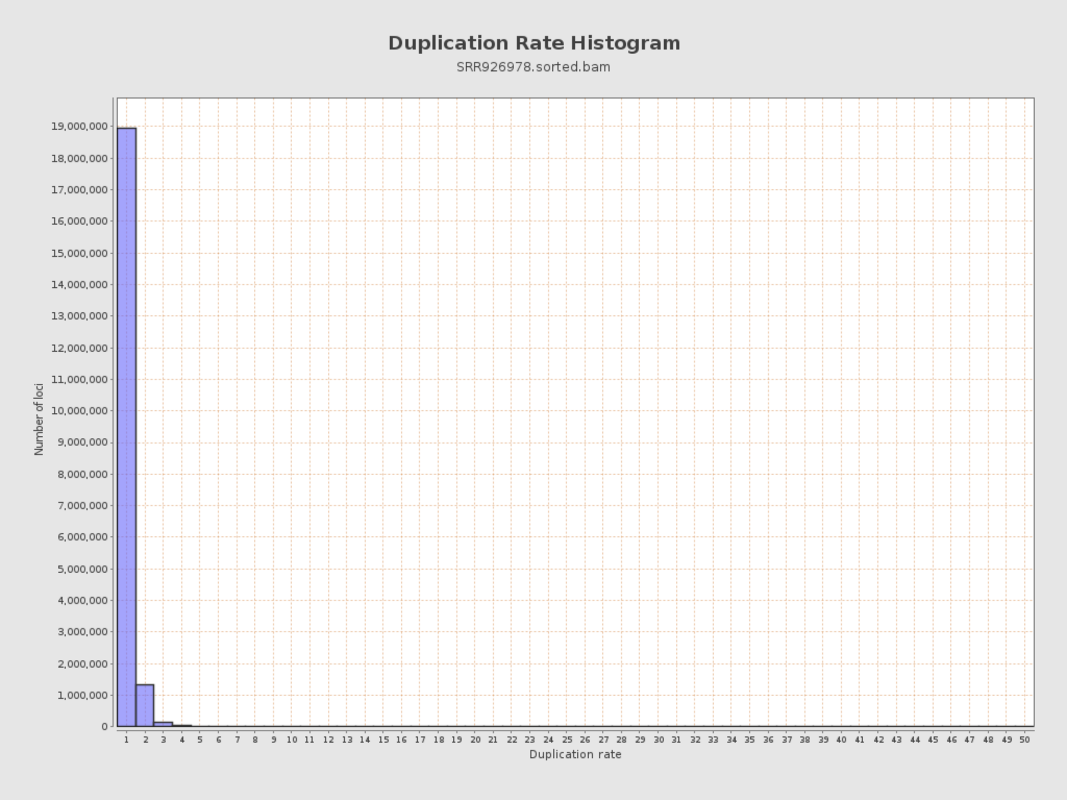
5. Results : Coverage Histogram (0-50X)



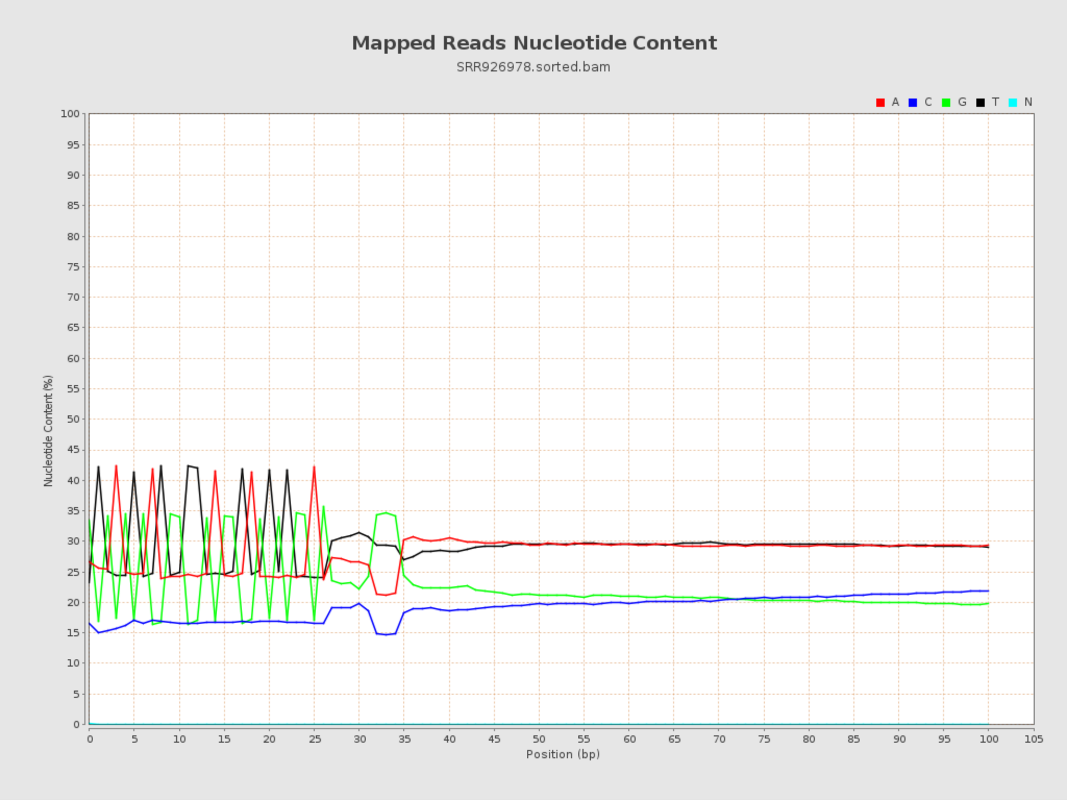
6. Results : Genome Fraction Coverage



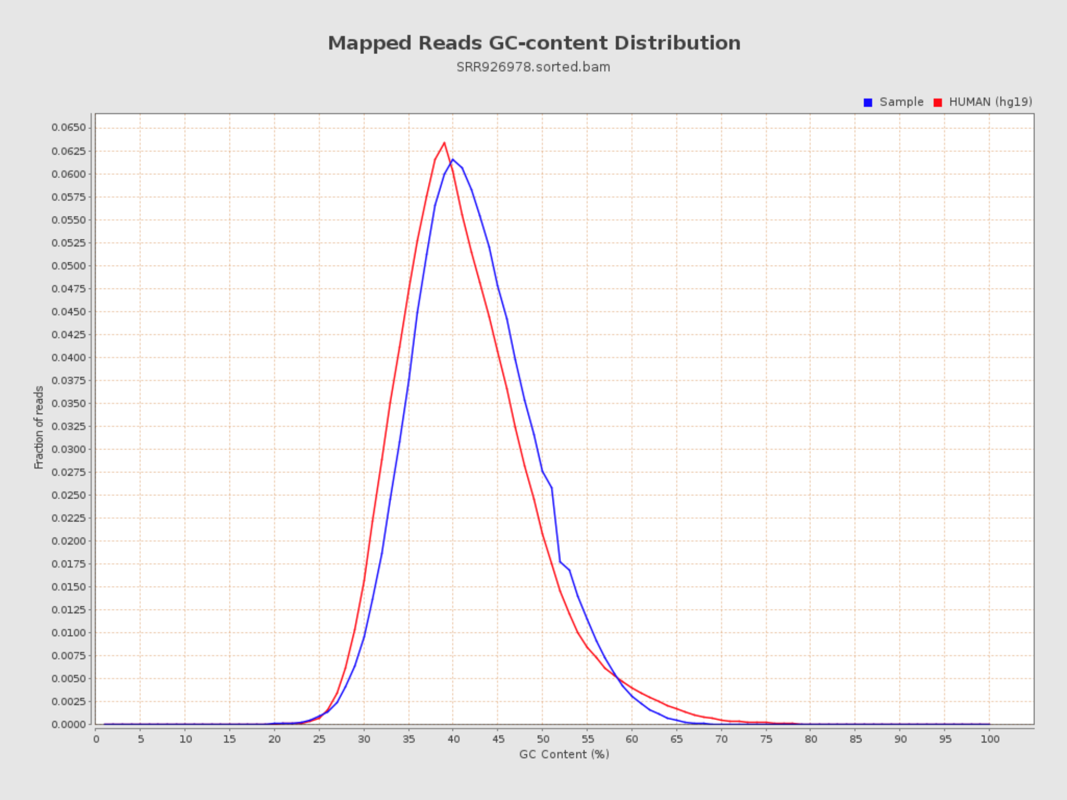
7. Results : Duplication Rate Histogram



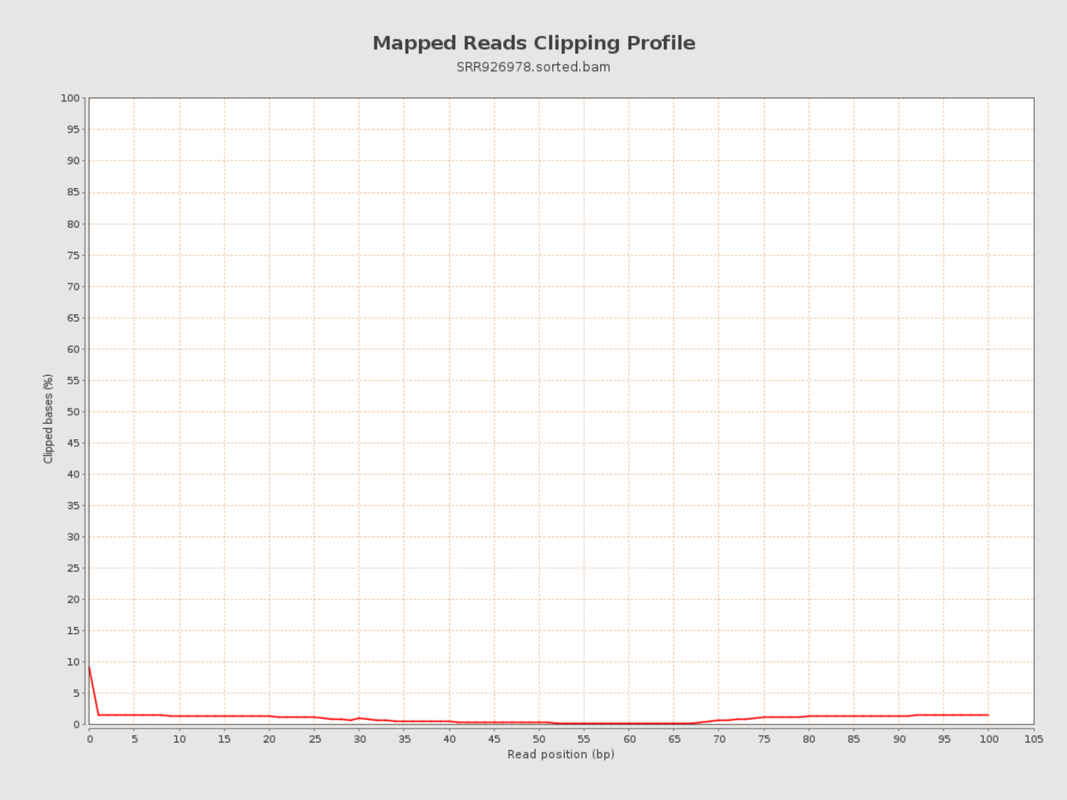
8. Results : Mapped Reads Nucleotide Content



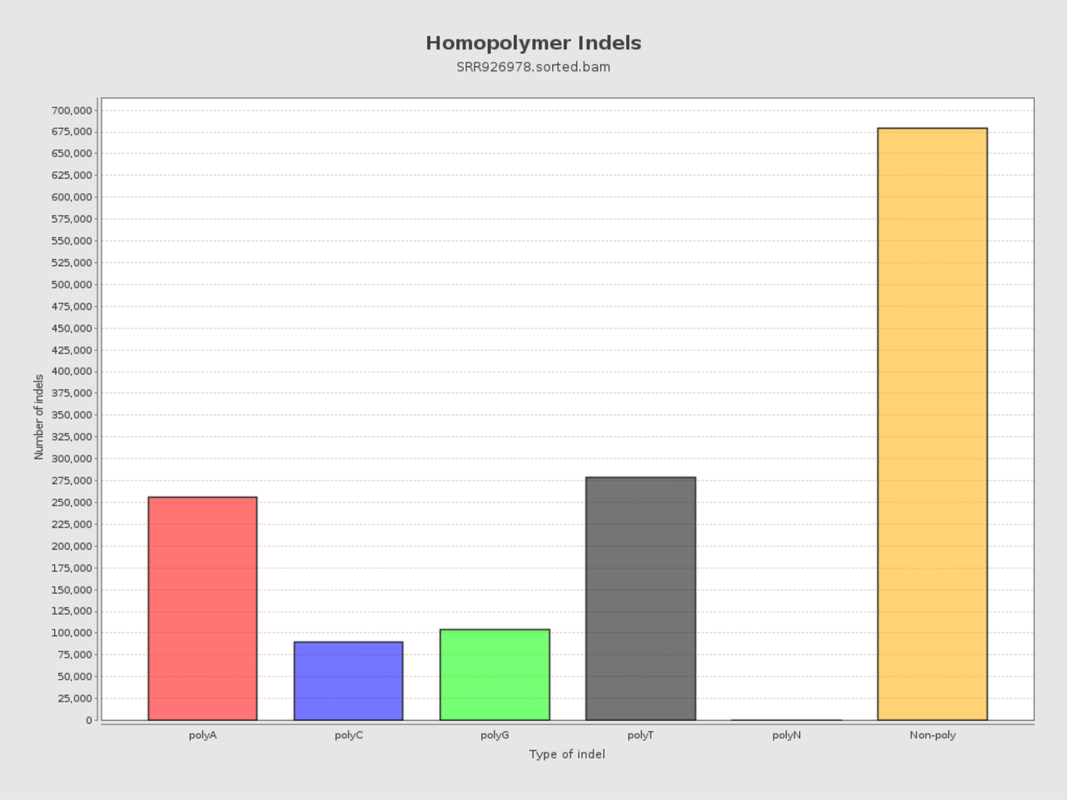
9. Results : Mapped Reads GC-content Distribution



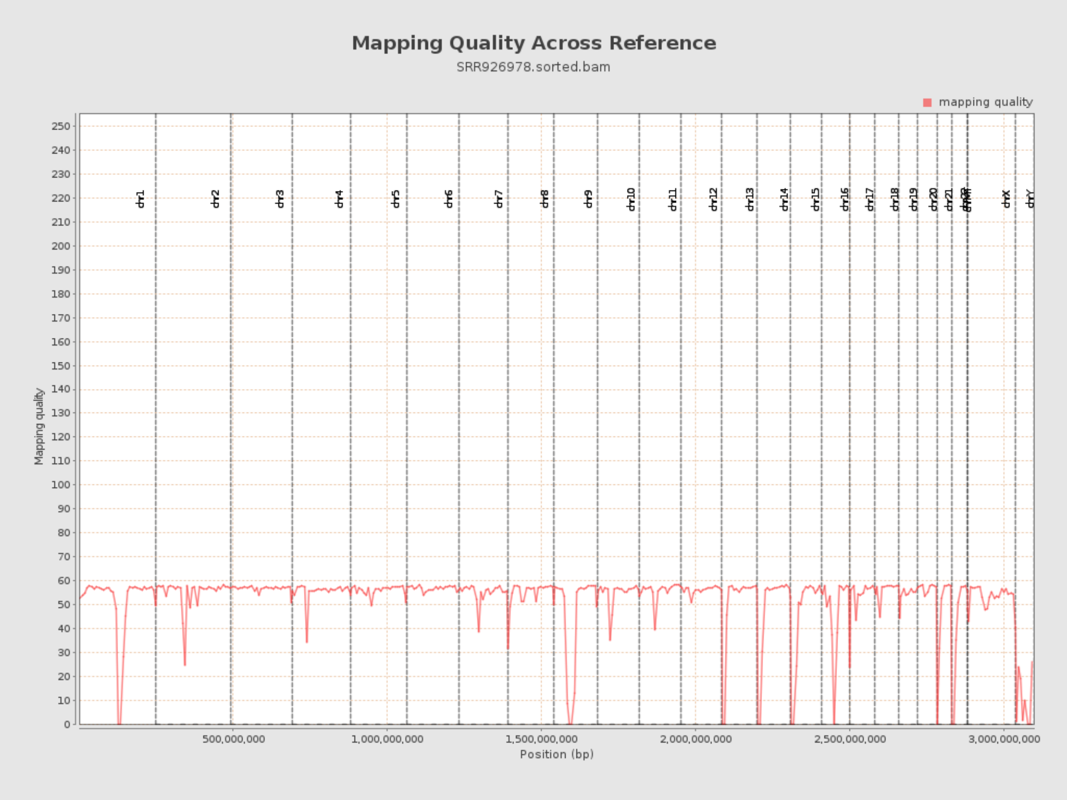
10. Results : Mapped Reads Clipping Profile



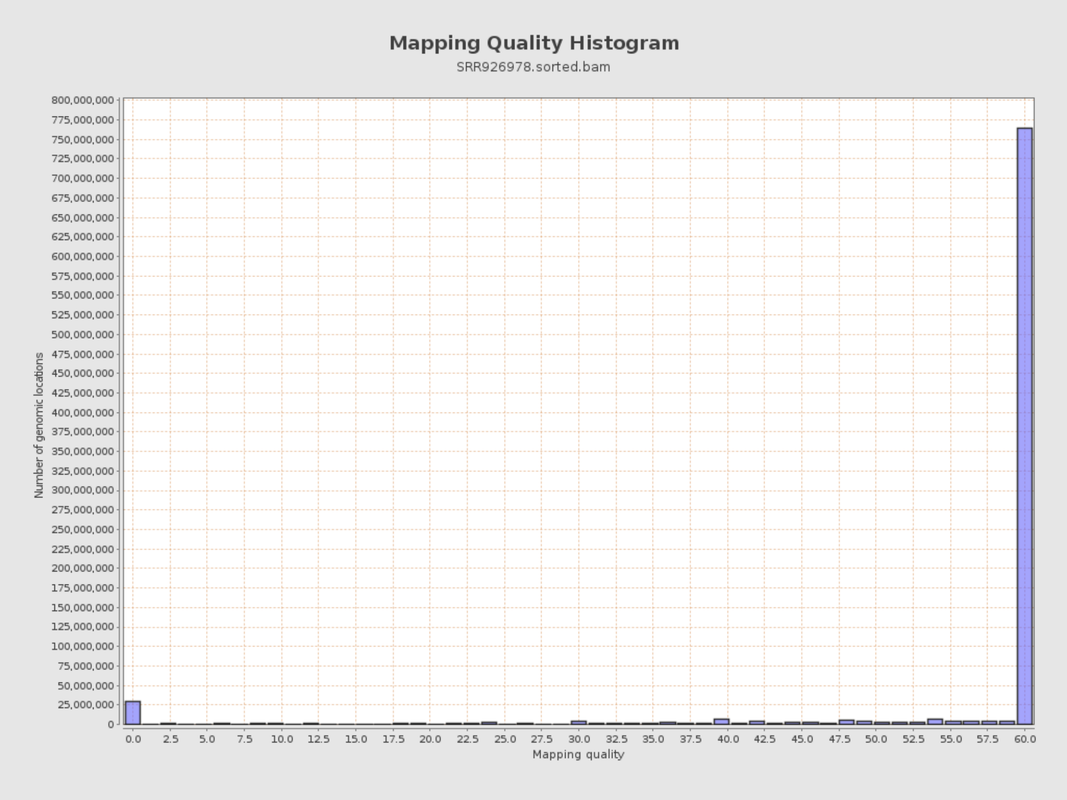
11. Results : Homopolymer Indels



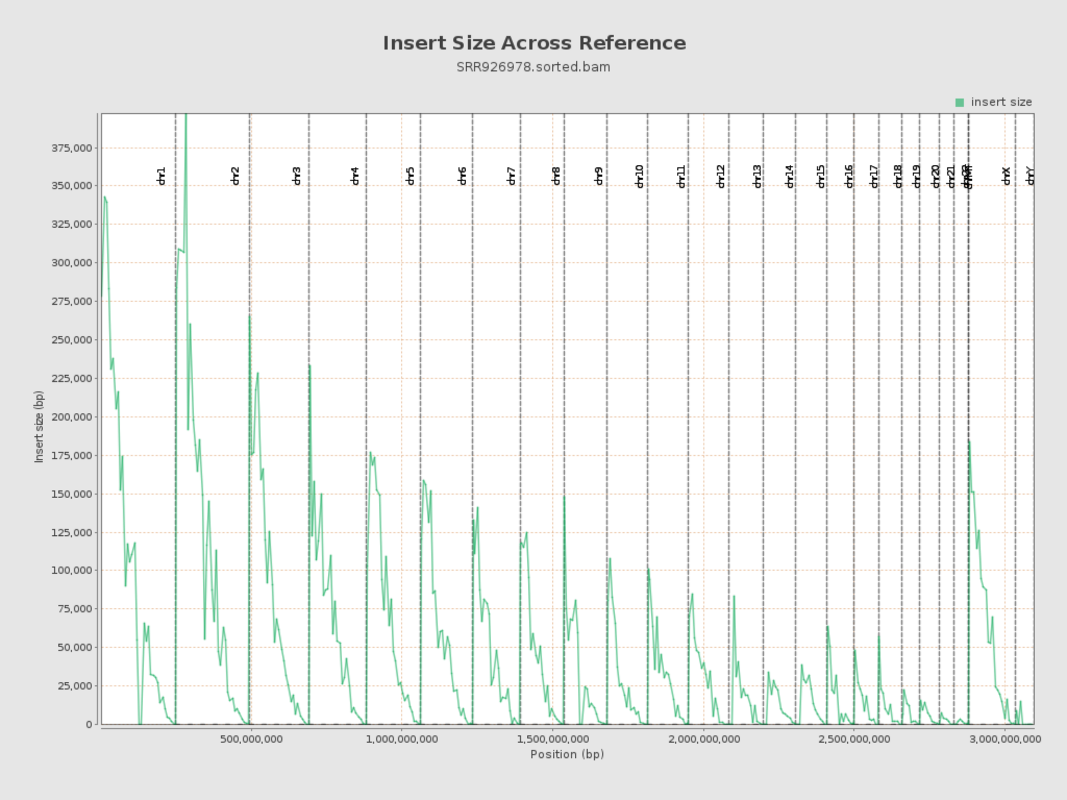
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram