Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 21:13:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926996.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_SRR926996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926996_1.fastq.gz SRR926996_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 21:13:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,811,108
Mapped reads	31,658,816 / 88.41%
Unmapped reads	4,152,292 / 11.59%
Mapped paired reads	31,658,816 / 88.41%
Mapped reads, first in pair	15,841,848 / 44.24%
Mapped reads, second in pair	15,816,968 / 44.17%
Mapped reads, both in pair	31,124,678 / 86.91%
Mapped reads, singletons	534,138 / 1.49%
Secondary alignments	0
Supplementary alignments	877,879 / 2.45%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	2,856,583 / 7.98%
Duplication rate	7.35%
Clipped reads	11,260,757 / 31.44%

2.2. ACGT Content

Number/percentage of A's	836,387,601 / 28.48%
Number/percentage of C's	581,790,476 / 19.81%
Number/percentage of T's	849,051,798 / 28.91%
Number/percentage of G's	669,092,836 / 22.78%
Number/percentage of N's	319,010 / 0.01%

GC Percentage	42.6%

2.3. Coverage

Mean	0.9494
Standard Deviation	3.0076

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	284,000.29
Standard Deviation	5,210,731.27
P25/Median/P75	154 / 200 / 268

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	27,187,612
Insertions	495,008
Mapped reads with at least one insertion	1.54%
Deletions	1,570,461
Mapped reads with at least one deletion	4.83%
Homopolymer indels	52.64%

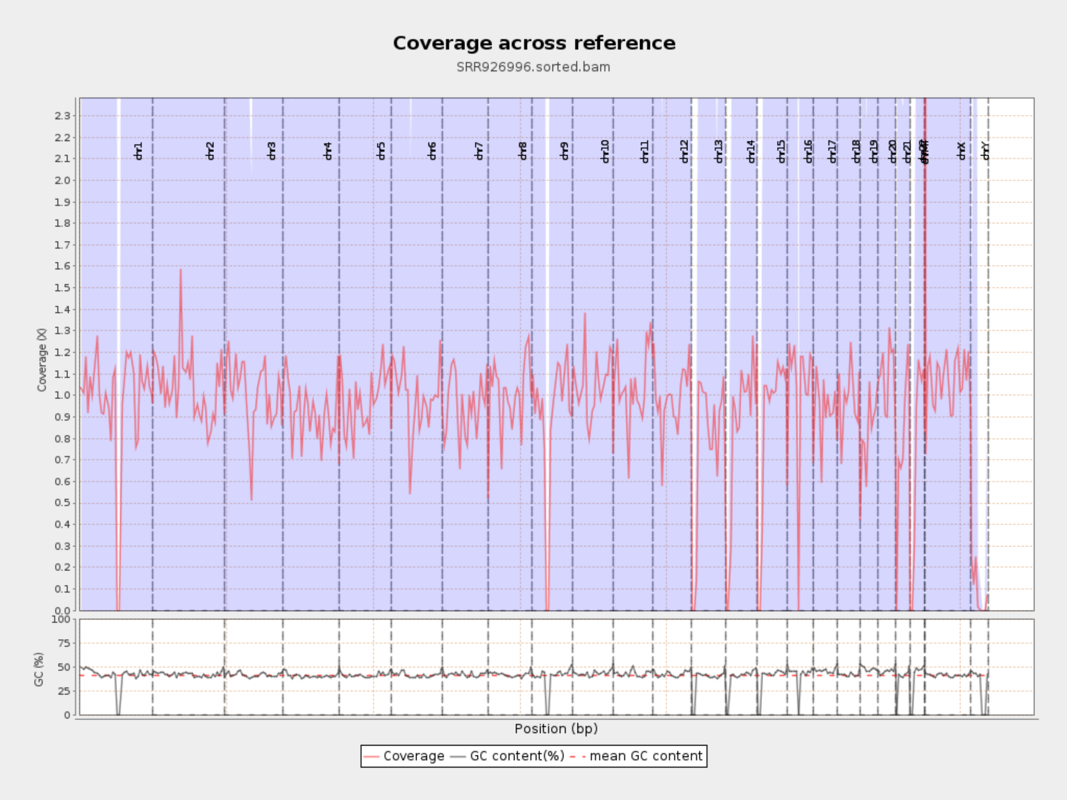
2.7. Chromosome stats

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

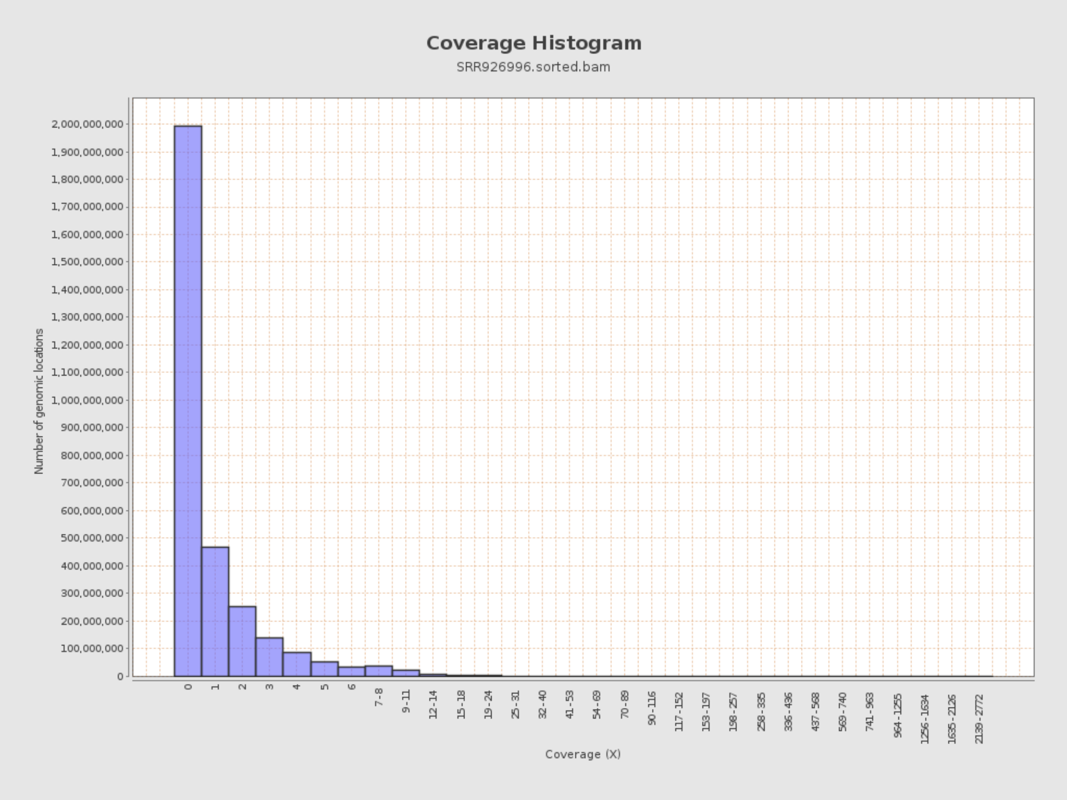
		bases	coverage	deviation
chr1	249250621	242621790	0.9734	3.7234
chr2	243199373	254473535	1.0464	4.8629
chr3	198022430	199455457	1.0072	1.9838
chr4	191154276	176690755	0.9243	2.425
chr5	180915260	177585128	0.9816	1.9313
chr6	171115067	170689472	0.9975	2.3106
chr7	159138663	151323349	0.9509	2.6501
chr8	146364022	149376435	1.0206	2.1476
chr9	141213431	126181609	0.8936	3.6975
chr10	135534747	143146470	1.0562	5.3014
chr11	135006516	140521143	1.0408	2.8948
chr12	133851895	132281491	0.9883	2.0155
chr13	115169878	88372470	0.7673	1.7151
chr14	107349540	88618554	0.8255	1.8344
chr15	102531392	88035078	0.8586	1.9262
chr16	90354753	91196037	1.0093	3.4755
chr17	81195210	75682415	0.9321	2.372
chr18	78077248	78076806	1	3.5611
chr19	59128983	48979532	0.8284	2.6212
chr20	63025520	69361595	1.1005	2.2363
chr21	48129895	38336879	0.7965	3.0037
chr22	51304566	37221407	0.7255	1.8202
chrMT	16571	294767	17.7881	15.1316
chrX	155270560	165557824	1.0663	2.276

chrY	59373566	4834092	0.0814	2.1424

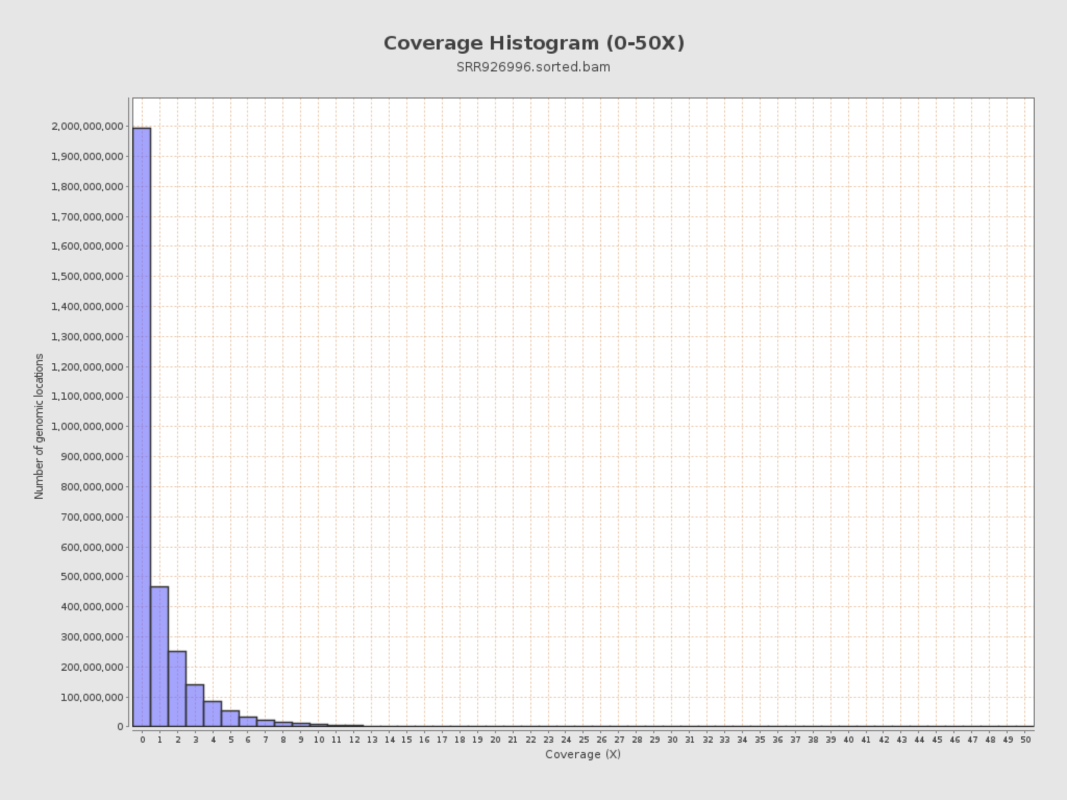
3. Results : Coverage across reference



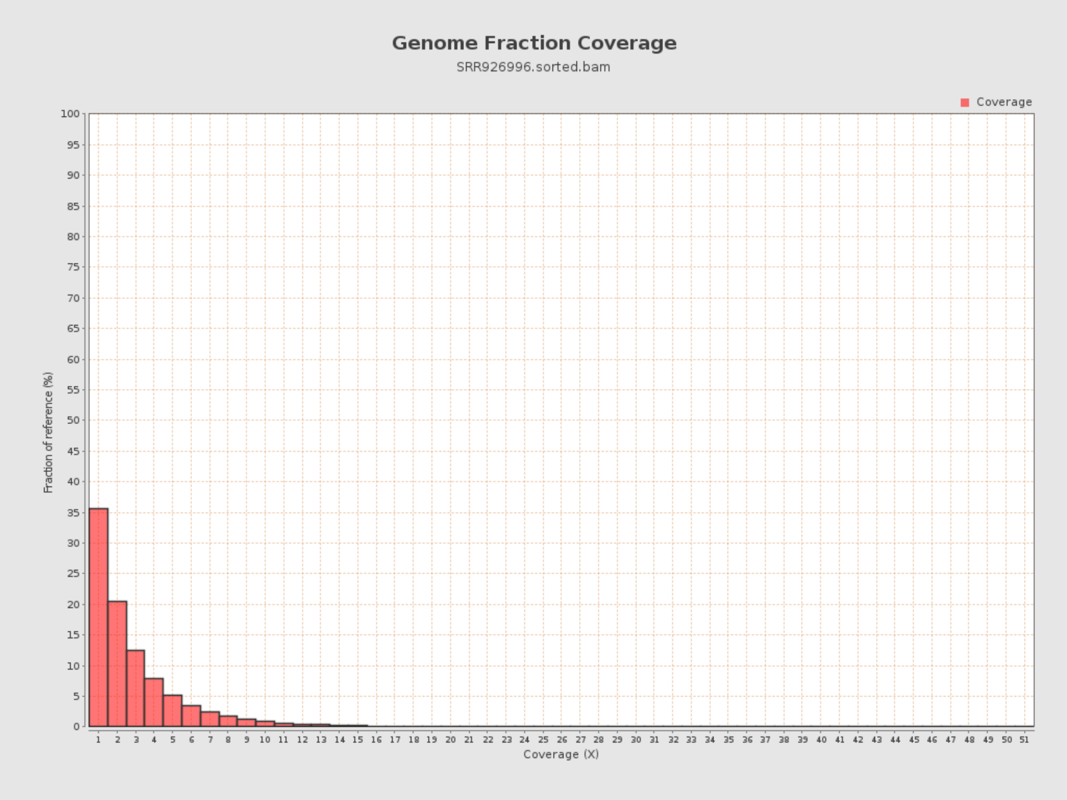
4. Results : Coverage Histogram



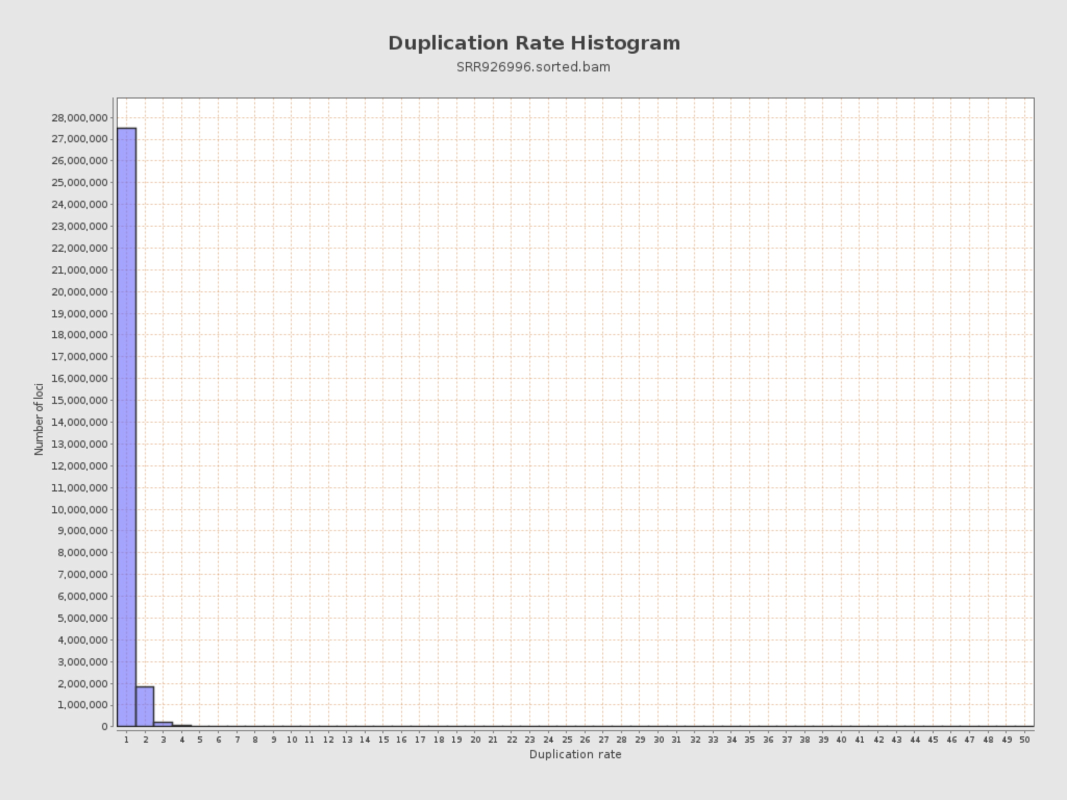
5. Results : Coverage Histogram (0-50X)



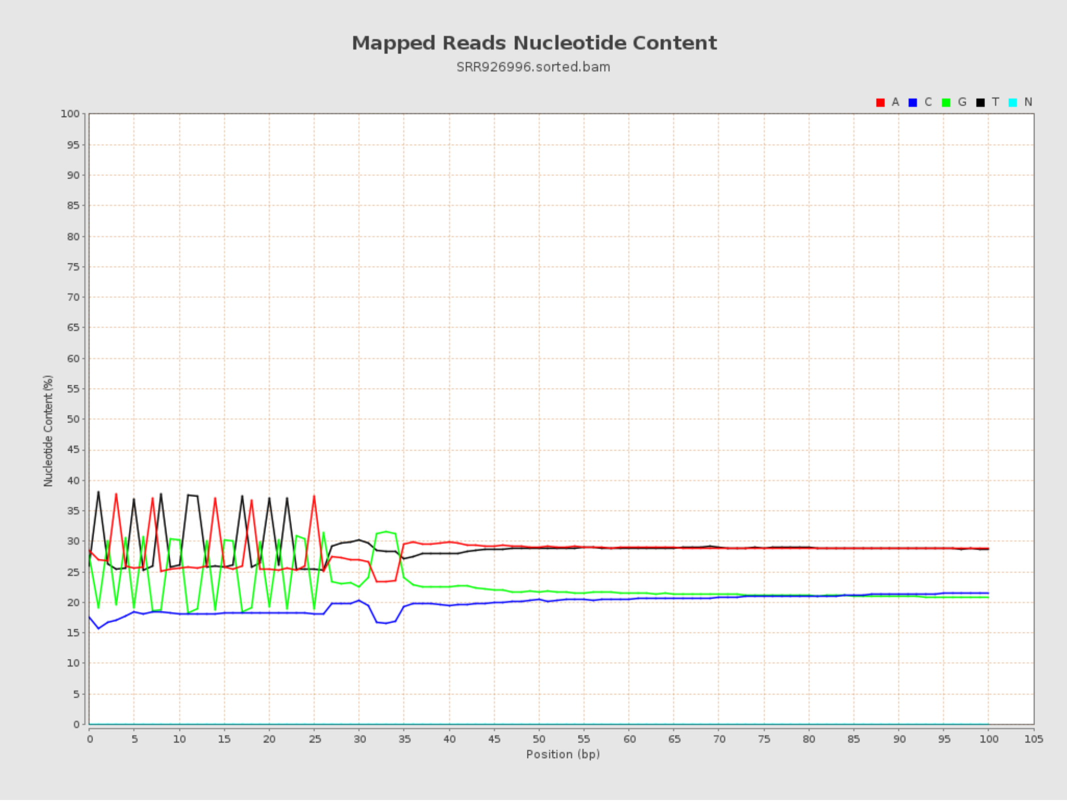
6. Results : Genome Fraction Coverage



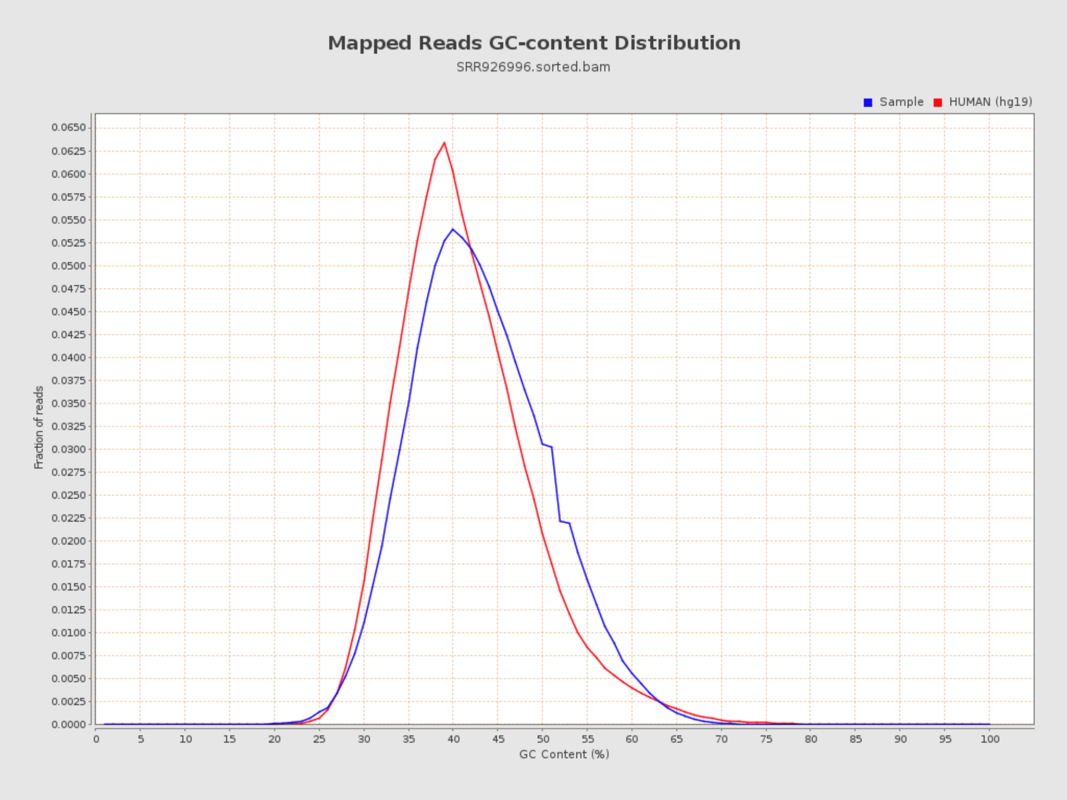
7. Results : Duplication Rate Histogram



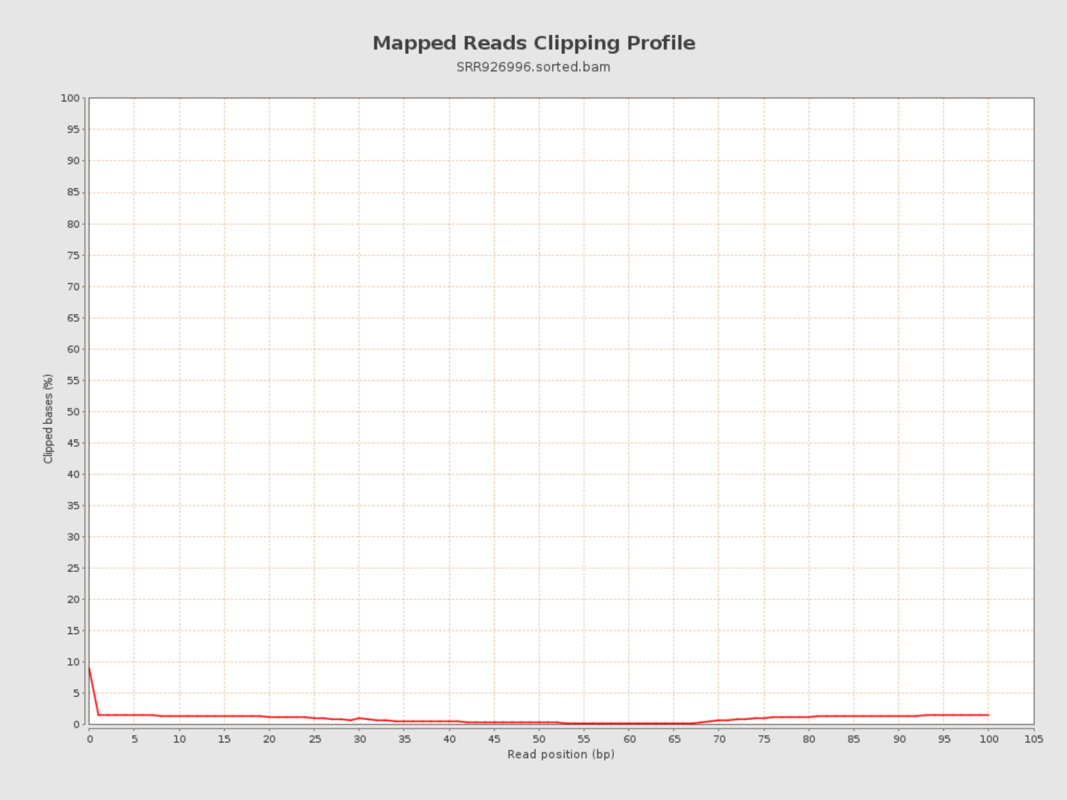
8. Results : Mapped Reads Nucleotide Content



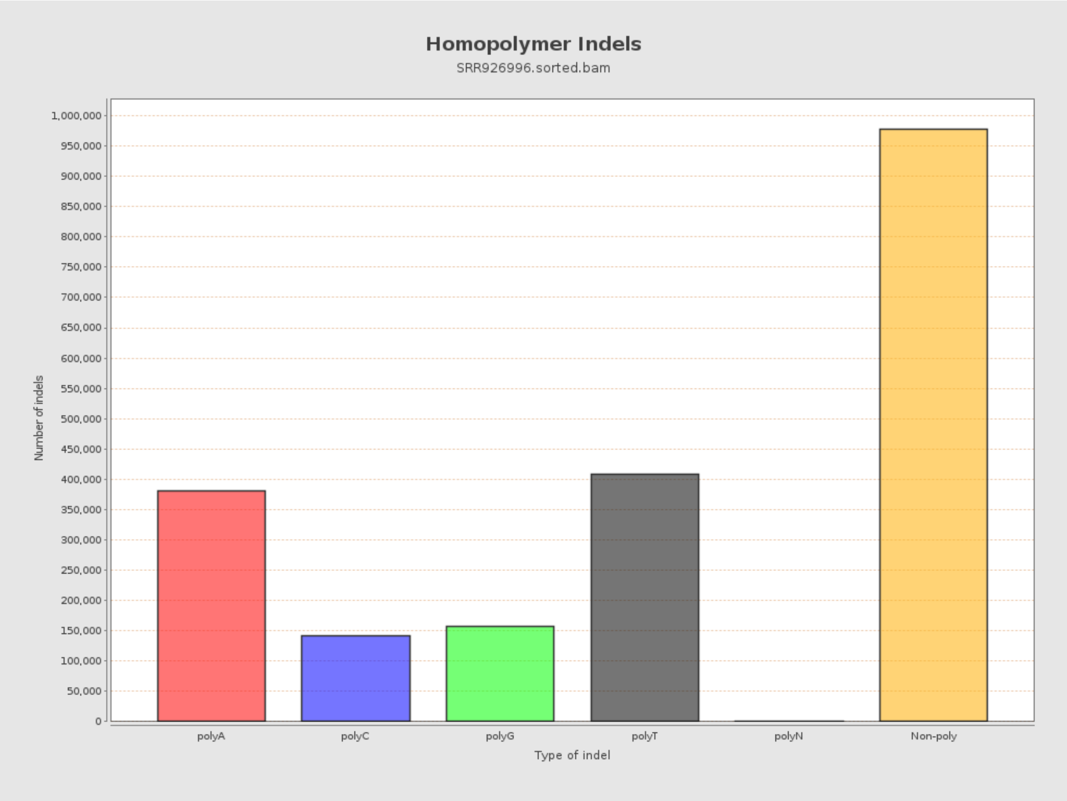
9. Results : Mapped Reads GC-content Distribution



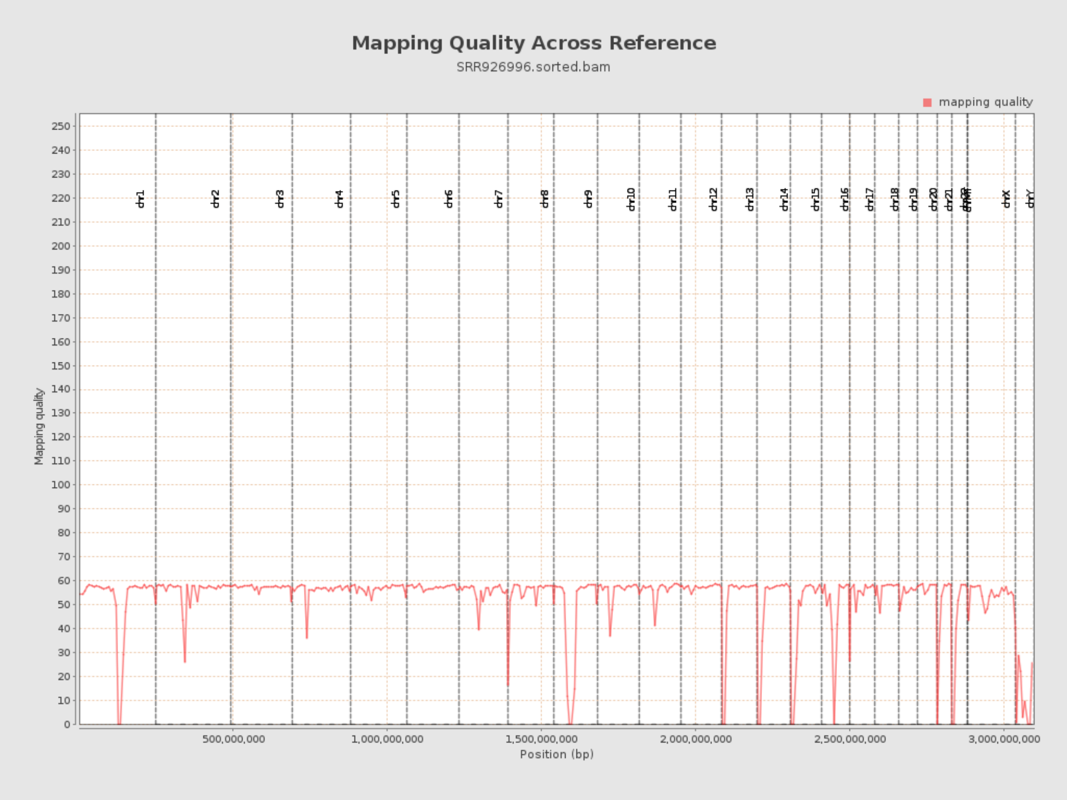
10. Results : Mapped Reads Clipping Profile



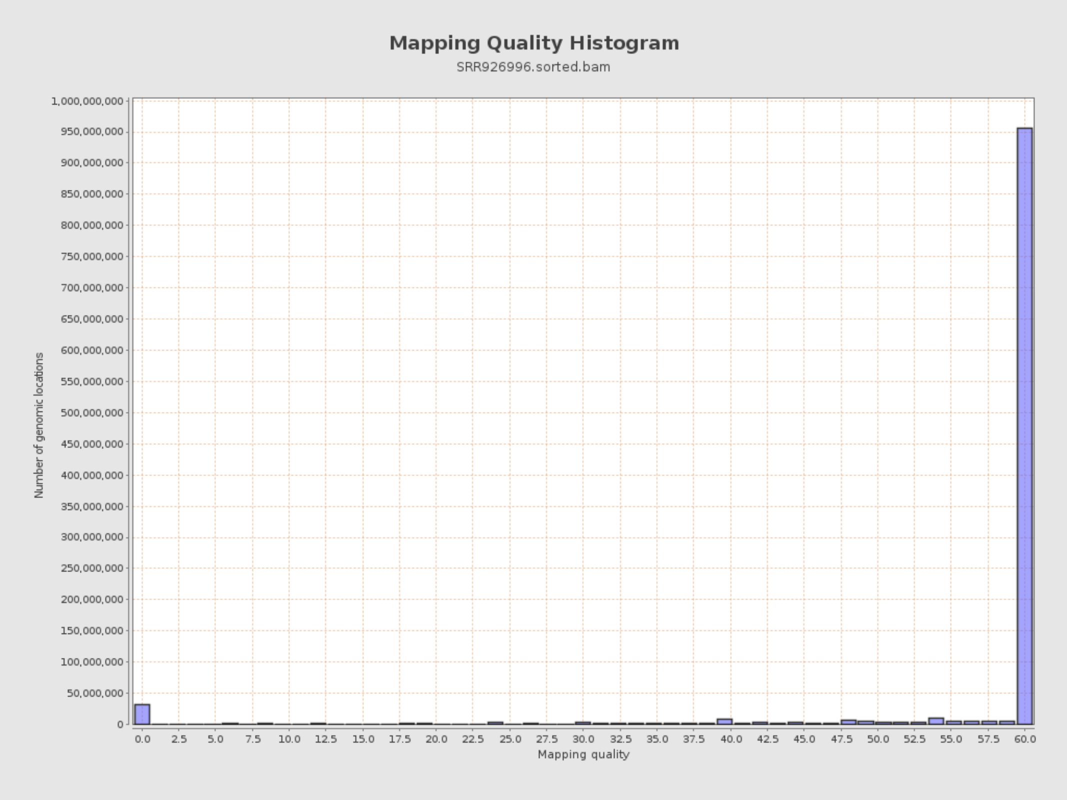
11. Results : Homopolymer Indels



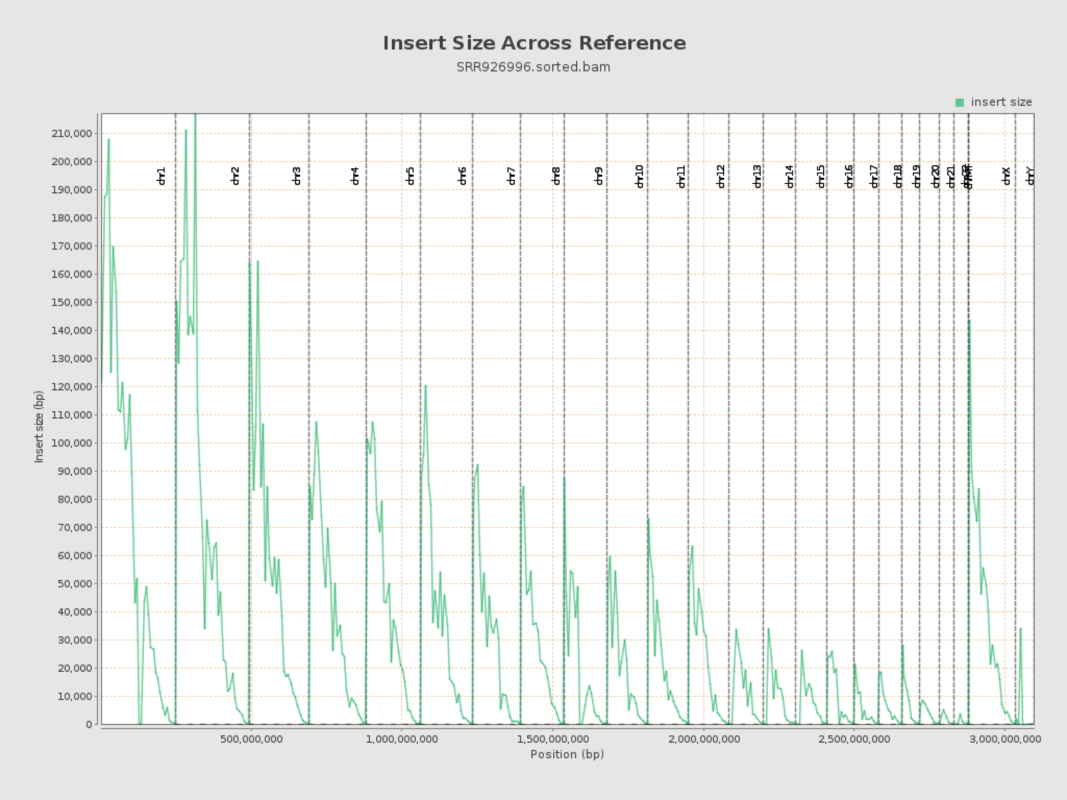
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram