Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 14:44:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926982.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_SRR926982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926982_1.fastq.gz SRR926982_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 14:44:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,515,794
Mapped reads	34,982,910 / 98.5%
Unmapped reads	532,884 / 1.5%
Mapped paired reads	34,982,910 / 98.5%
Mapped reads, first in pair	17,562,289 / 49.45%
Mapped reads, second in pair	17,420,621 / 49.05%
Mapped reads, both in pair	34,668,832 / 97.62%
Mapped reads, singletons	314,078 / 0.88%
Secondary alignments	0
Supplementary alignments	623,763 / 1.76%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	2,973,976 / 8.37%
Duplication rate	6.5%
Clipped reads	9,860,125 / 27.76%

2.2. ACGT Content

Number/percentage of A's	924,030,899 / 28.04%
Number/percentage of C's	677,884,512 / 20.57%
Number/percentage of T's	937,500,557 / 28.45%
Number/percentage of G's	755,518,977 / 22.93%
Number/percentage of N's	294,369 / 0.01%

GC Percentage	43.5%

2.3. Coverage

Mean	1.0652
Standard Deviation	4.2131

2.4. Mapping Quality

Mean Mapping Quality	53.3

2.5. Insert size

Mean	179,089.79
Standard Deviation	4,158,022.18
P25/Median/P75	142 / 178 / 233

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	30,537,065
Insertions	529,654
Mapped reads with at least one insertion	1.49%
Deletions	1,711,108
Mapped reads with at least one deletion	4.77%
Homopolymer indels	52.42%

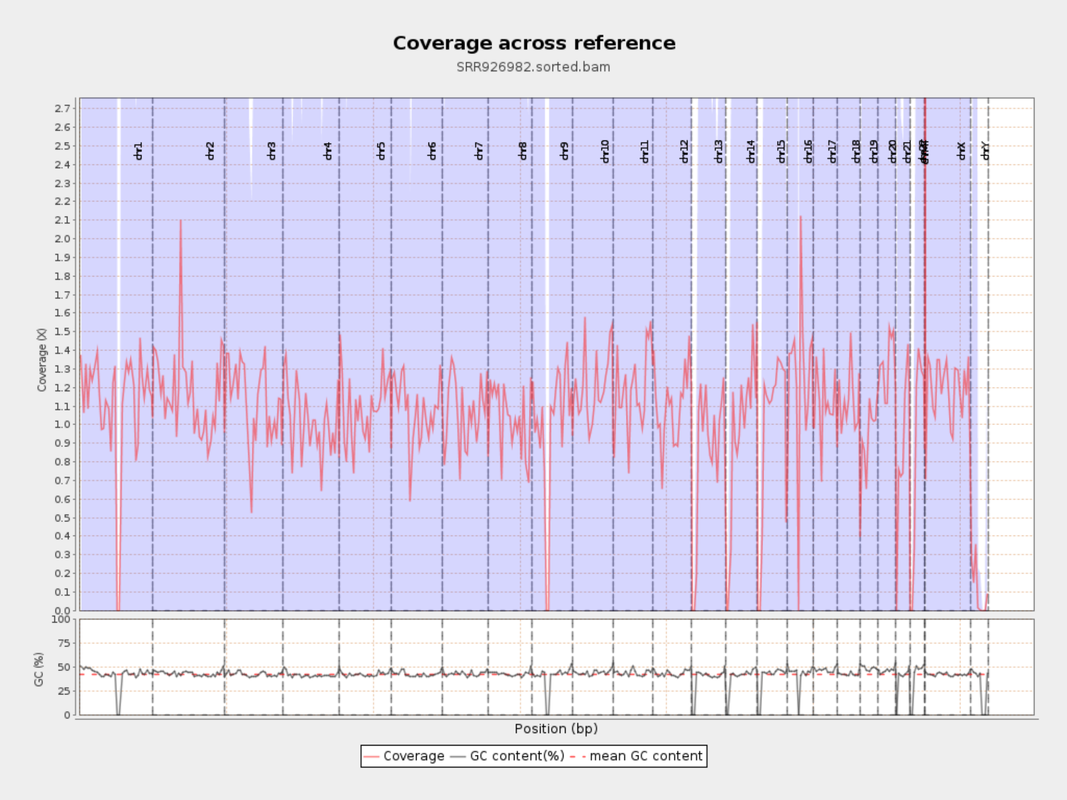
2.7. Chromosome stats

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

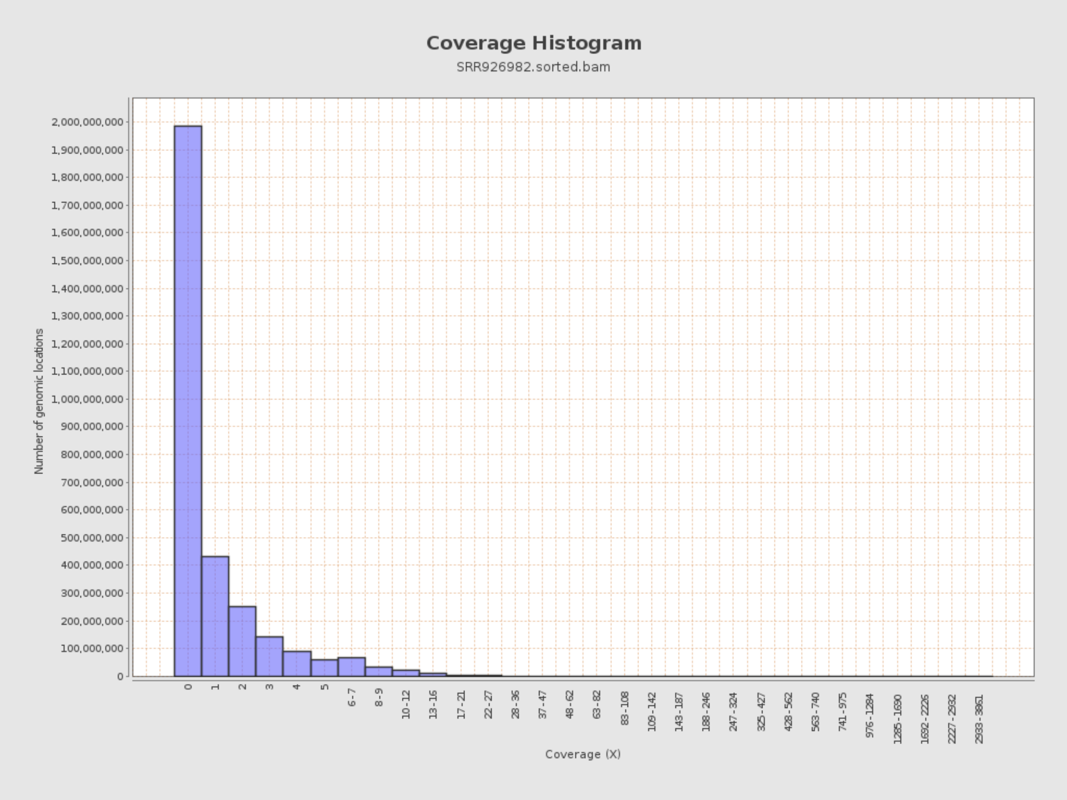
		bases	coverage	deviation
chr1	249250621	276824635	1.1106	4.8234
chr2	243199373	286486346	1.178	7.478
chr3	198022430	222647723	1.1244	2.26
chr4	191154276	194193300	1.0159	3.7343
chr5	180915260	196998001	1.0889	2.2023
chr6	171115067	185198001	1.0823	2.9279
chr7	159138663	169973097	1.0681	3.1231
chr8	146364022	152618365	1.0427	2.6622
chr9	141213431	139470992	0.9877	5.474
chr10	135534747	164009614	1.2101	6.1256
chr11	135006516	159727998	1.1831	3.9416
chr12	133851895	146821118	1.0969	2.5888
chr13	115169878	97682003	0.8482	2.0033
chr14	107349540	98775359	0.9201	2.1587
chr15	102531392	99894698	0.9743	2.2486
chr16	90354753	111705531	1.2363	7.9833
chr17	81195210	89886554	1.107	3.084
chr18	78077248	89166091	1.142	5.8105
chr19	59128983	54925733	0.9289	3.4562
chr20	63025520	83424383	1.3237	2.7559
chr21	48129895	43266886	0.899	3.4273
chr22	51304566	44390826	0.8652	2.2344
chrMT	16571	149896	9.0457	6.9797
chrX	155270560	183262744	1.1803	2.6759

chrY	59373566	6183624	0.1041	3.6084

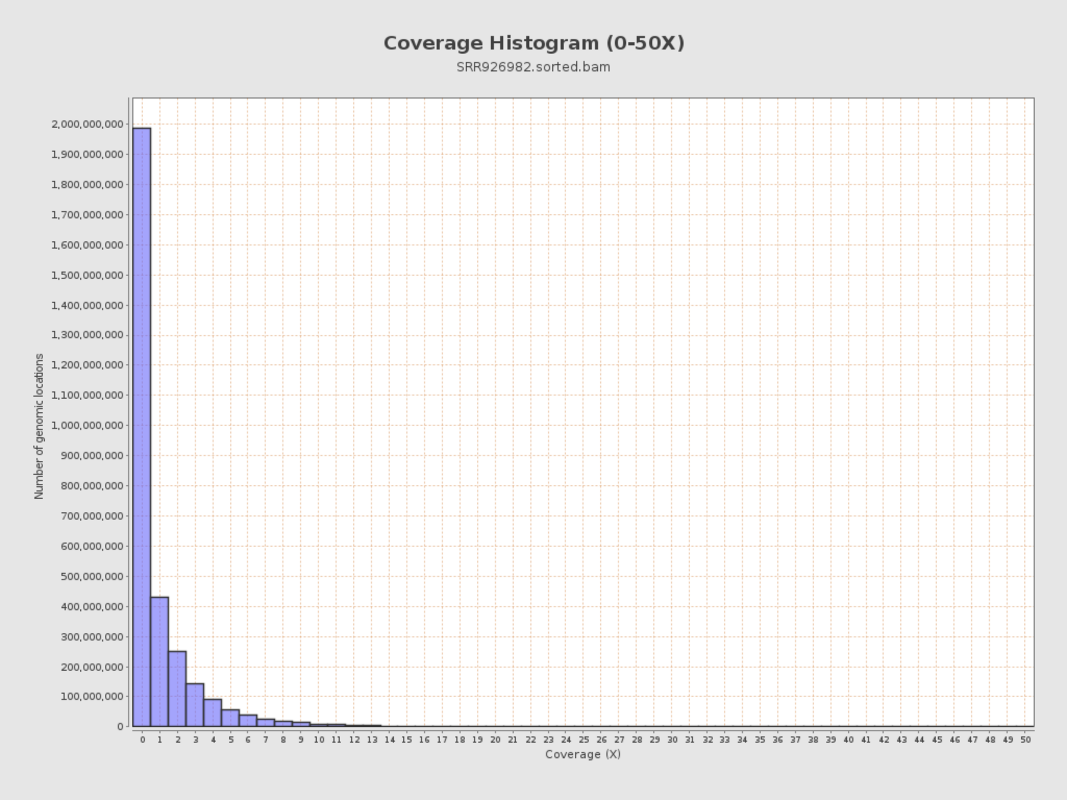
3. Results : Coverage across reference



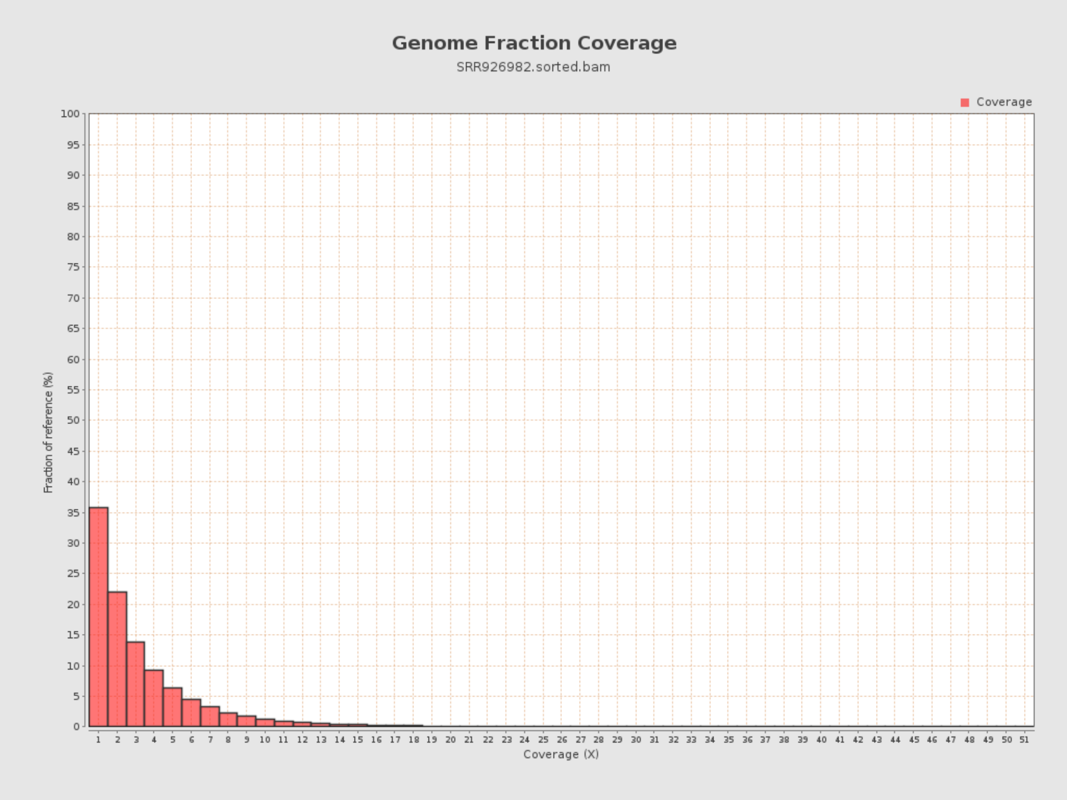
4. Results : Coverage Histogram



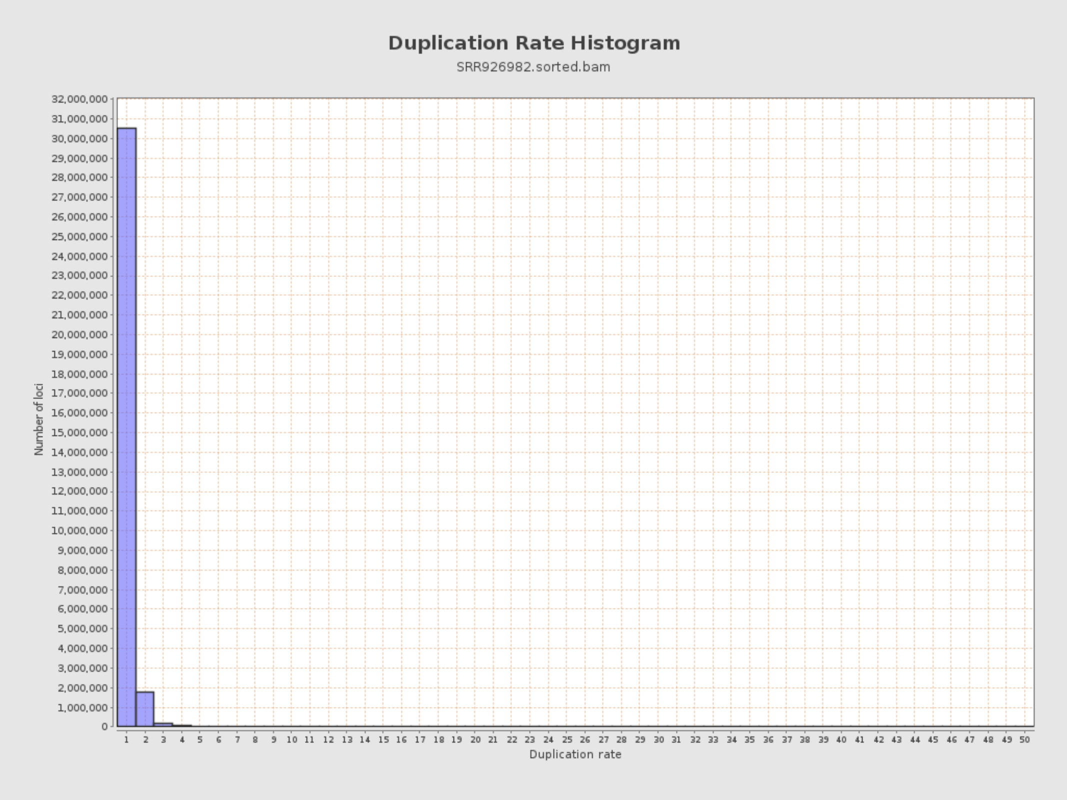
5. Results : Coverage Histogram (0-50X)



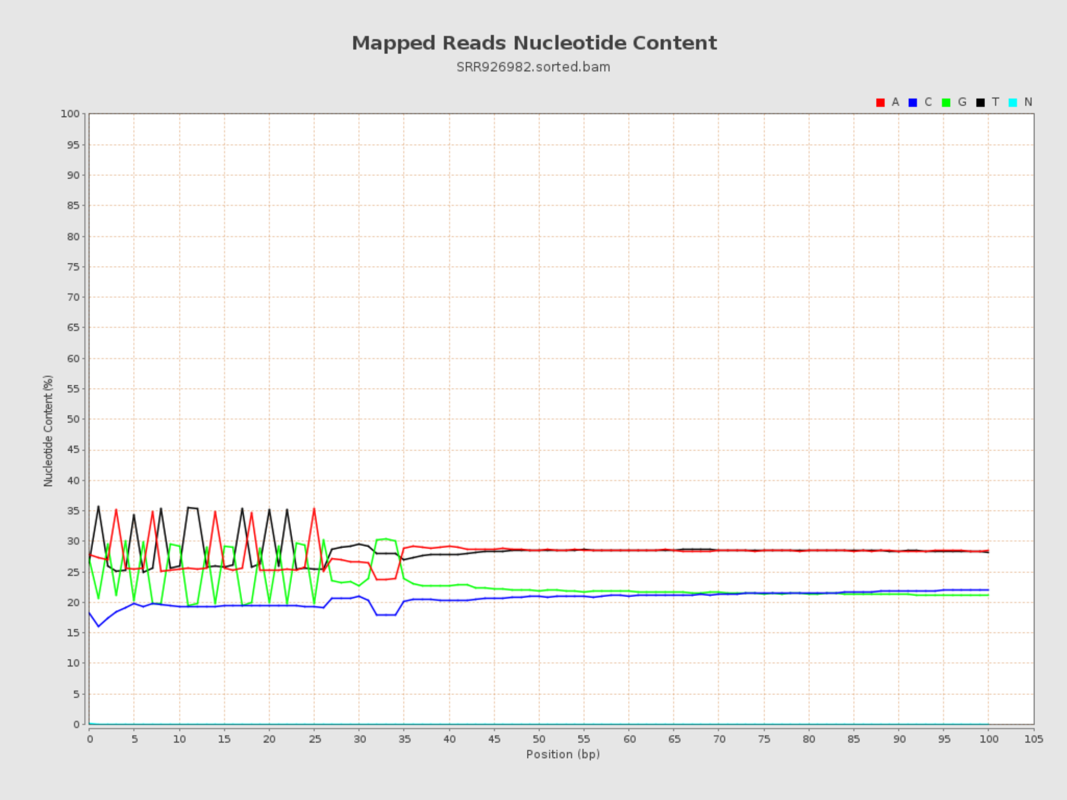
6. Results : Genome Fraction Coverage



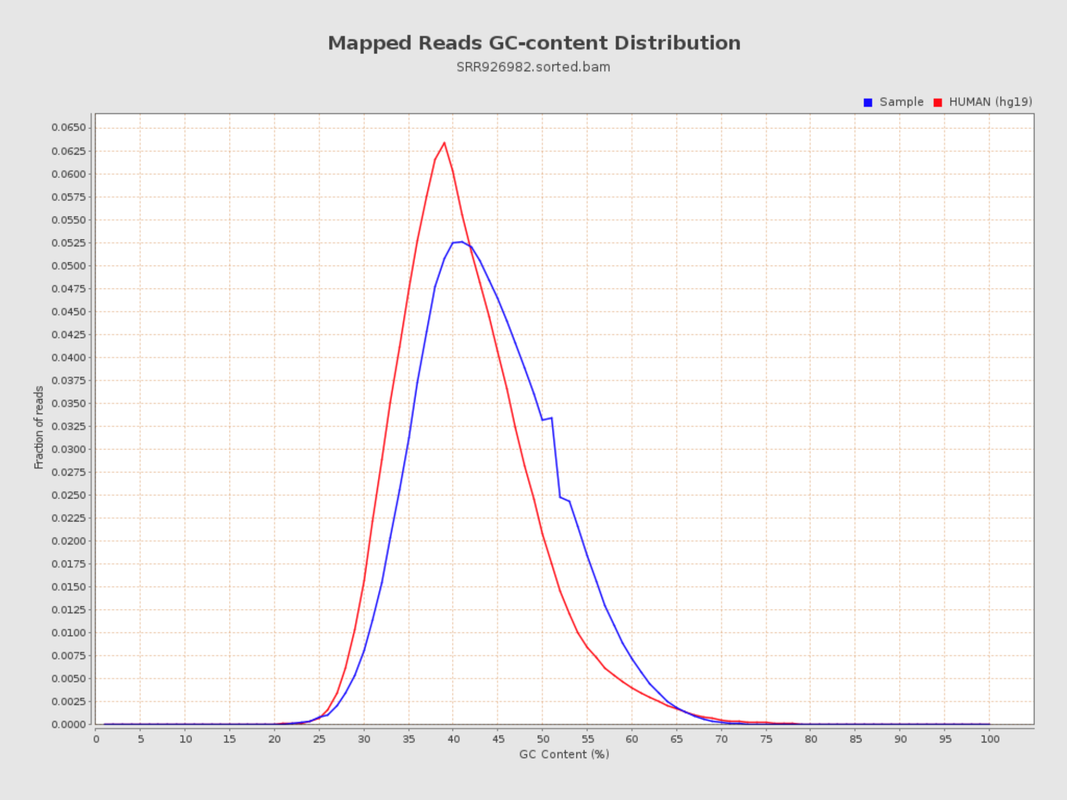
7. Results : Duplication Rate Histogram



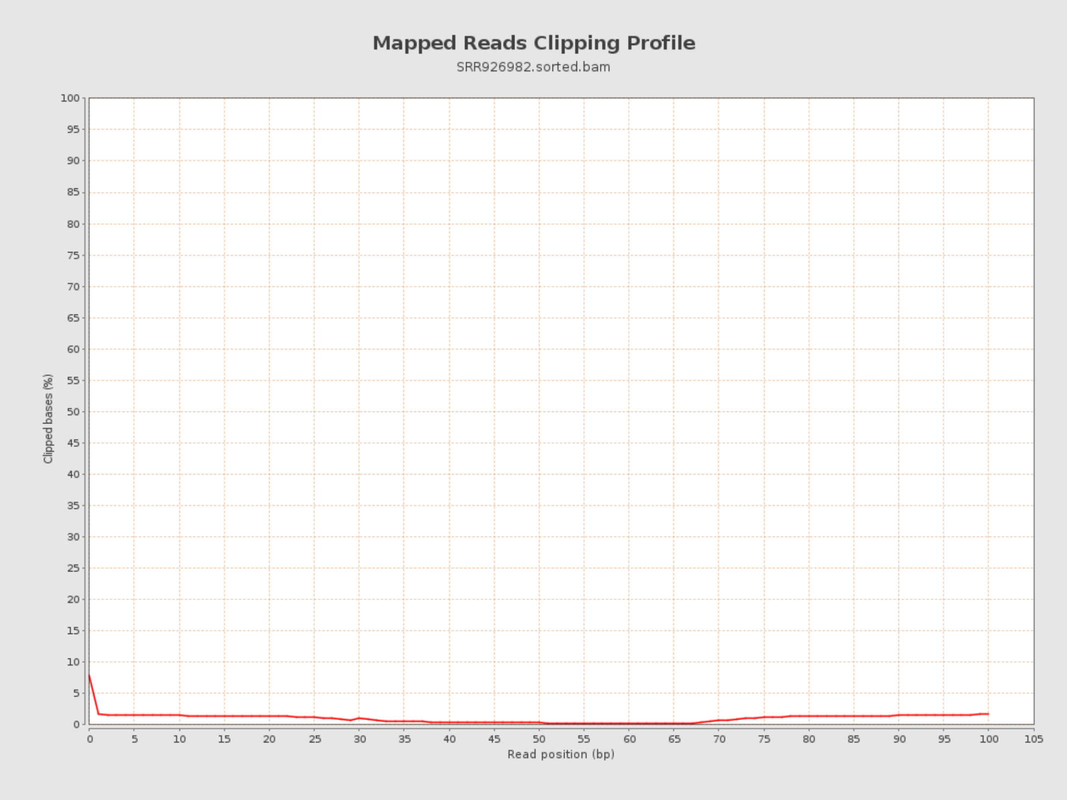
8. Results : Mapped Reads Nucleotide Content



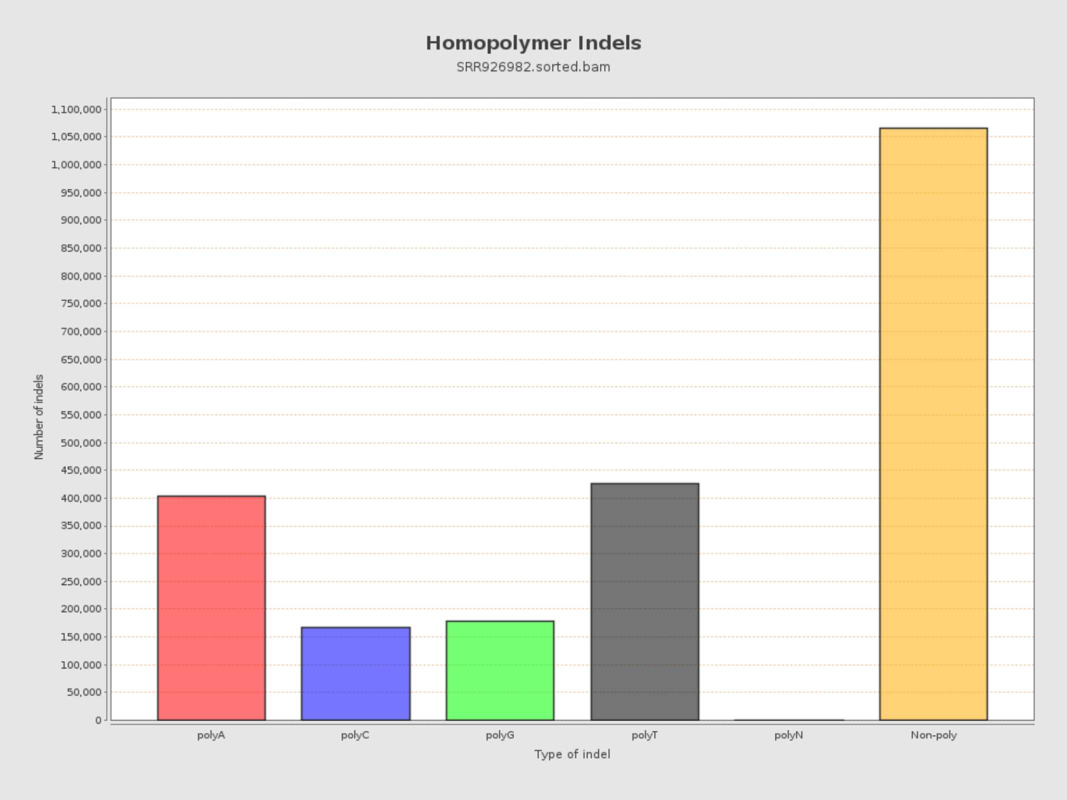
9. Results : Mapped Reads GC-content Distribution



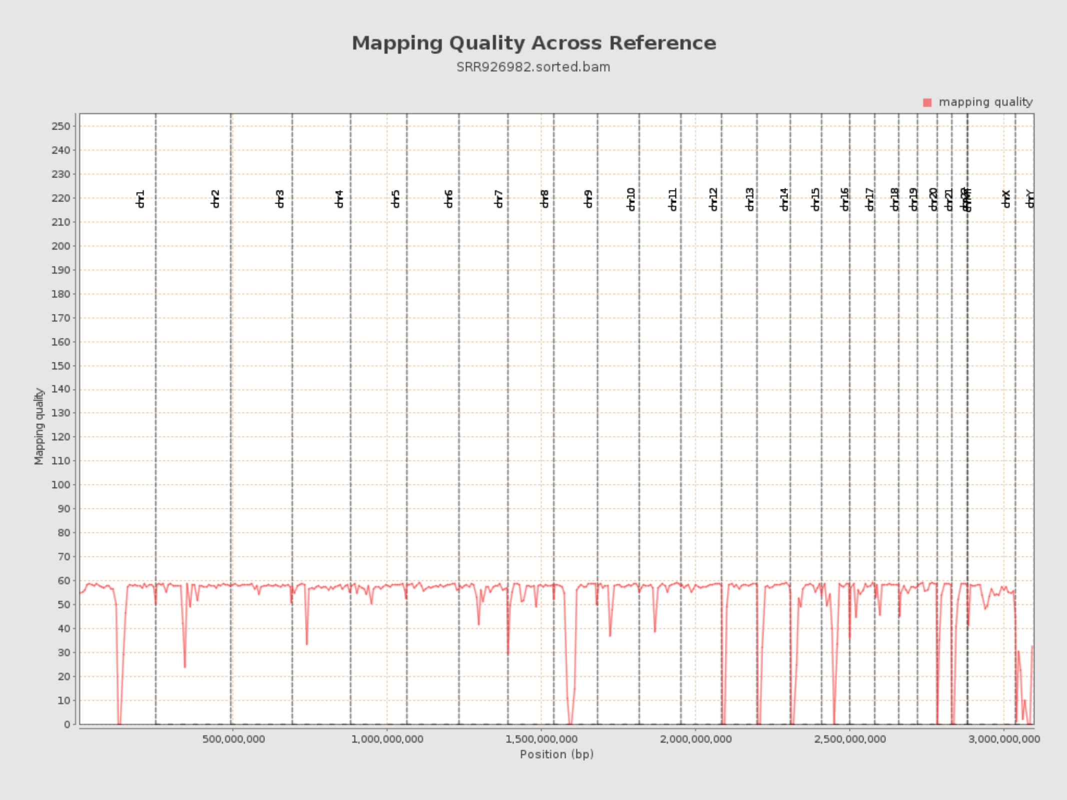
10. Results : Mapped Reads Clipping Profile



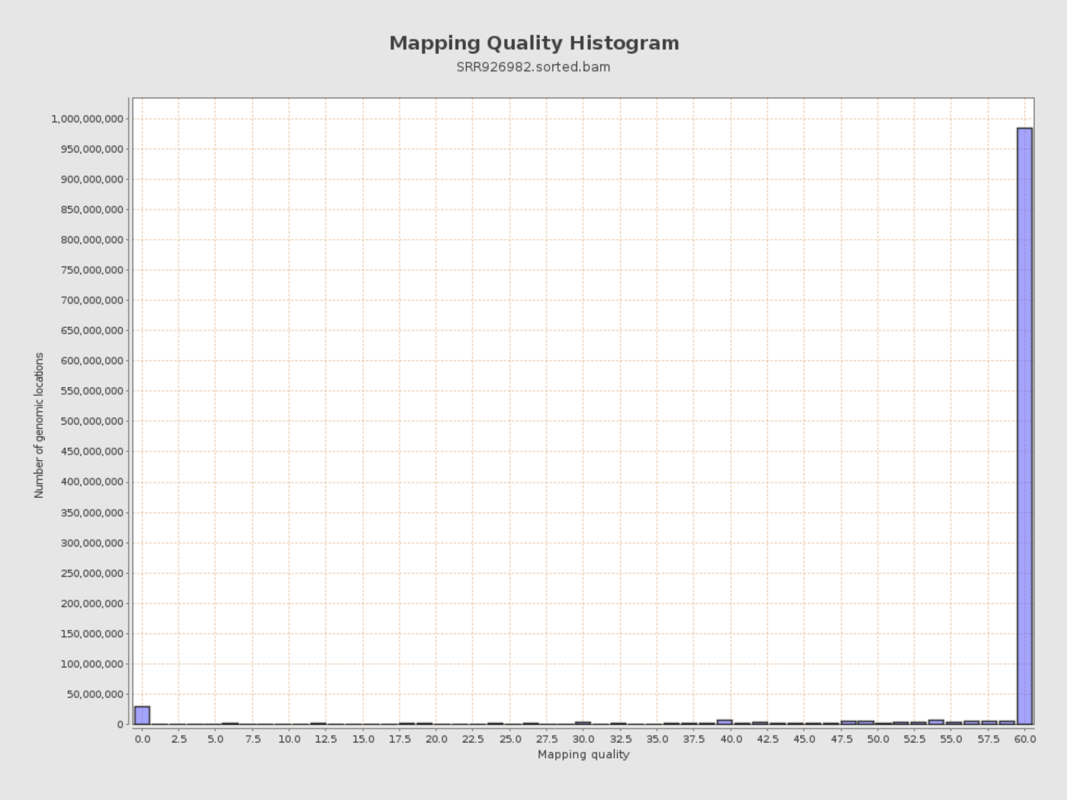
11. Results : Homopolymer Indels



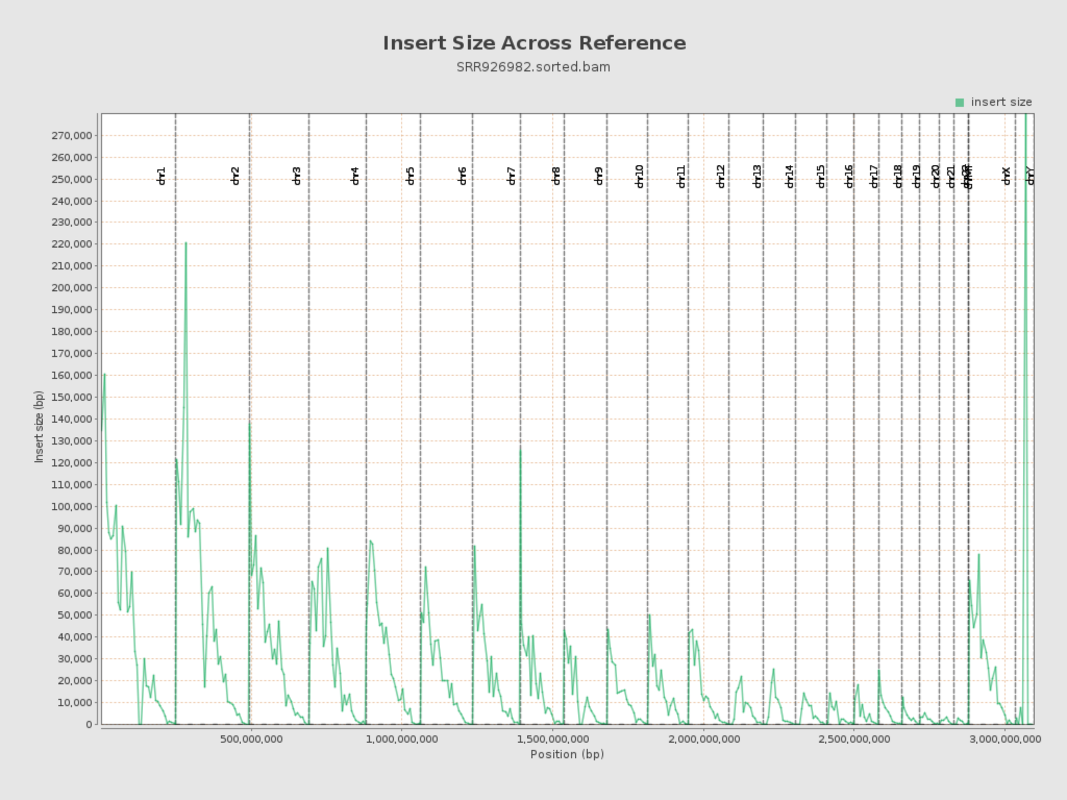
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram