Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 13:38:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926980.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_SRR926980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926980_1.fastq.gz SRR926980_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 13:38:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,470,902
Mapped reads	29,992,708 / 98.43%
Unmapped reads	478,194 / 1.57%
Mapped paired reads	29,992,708 / 98.43%
Mapped reads, first in pair	15,064,918 / 49.44%
Mapped reads, second in pair	14,927,790 / 48.99%
Mapped reads, both in pair	29,727,938 / 97.56%
Mapped reads, singletons	264,770 / 0.87%
Secondary alignments	0
Supplementary alignments	484,889 / 1.59%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	2,280,880 / 7.49%
Duplication rate	5.46%
Clipped reads	7,201,209 / 23.63%

2.2. ACGT Content

Number/percentage of A's	805,971,052 / 28.19%
Number/percentage of C's	592,780,857 / 20.73%
Number/percentage of T's	815,208,857 / 28.51%
Number/percentage of G's	645,185,602 / 22.56%
Number/percentage of N's	256,593 / 0.01%

GC Percentage	43.29%

2.3. Coverage

Mean	0.9244
Standard Deviation	4.6785

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	157,182.41
Standard Deviation	3,922,433.27
P25/Median/P75	140 / 176 / 231

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	26,171,039
Insertions	466,129
Mapped reads with at least one insertion	1.53%
Deletions	1,485,150
Mapped reads with at least one deletion	4.82%
Homopolymer indels	52.65%

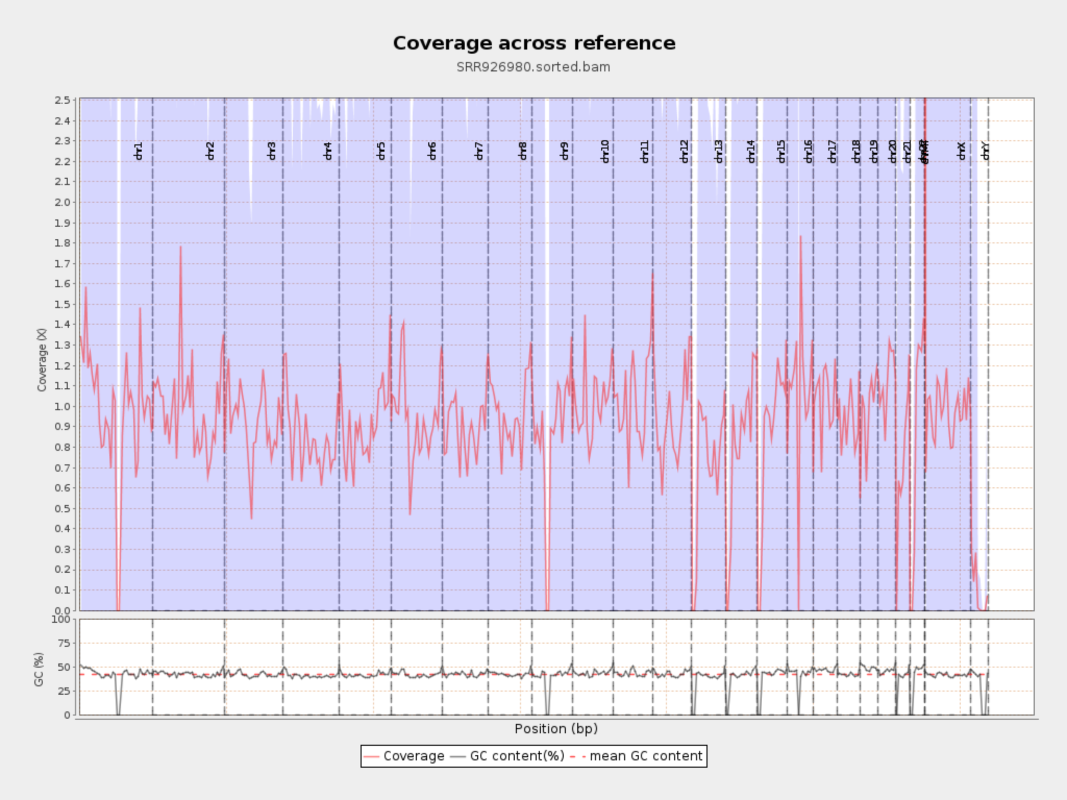
2.7. Chromosome stats

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

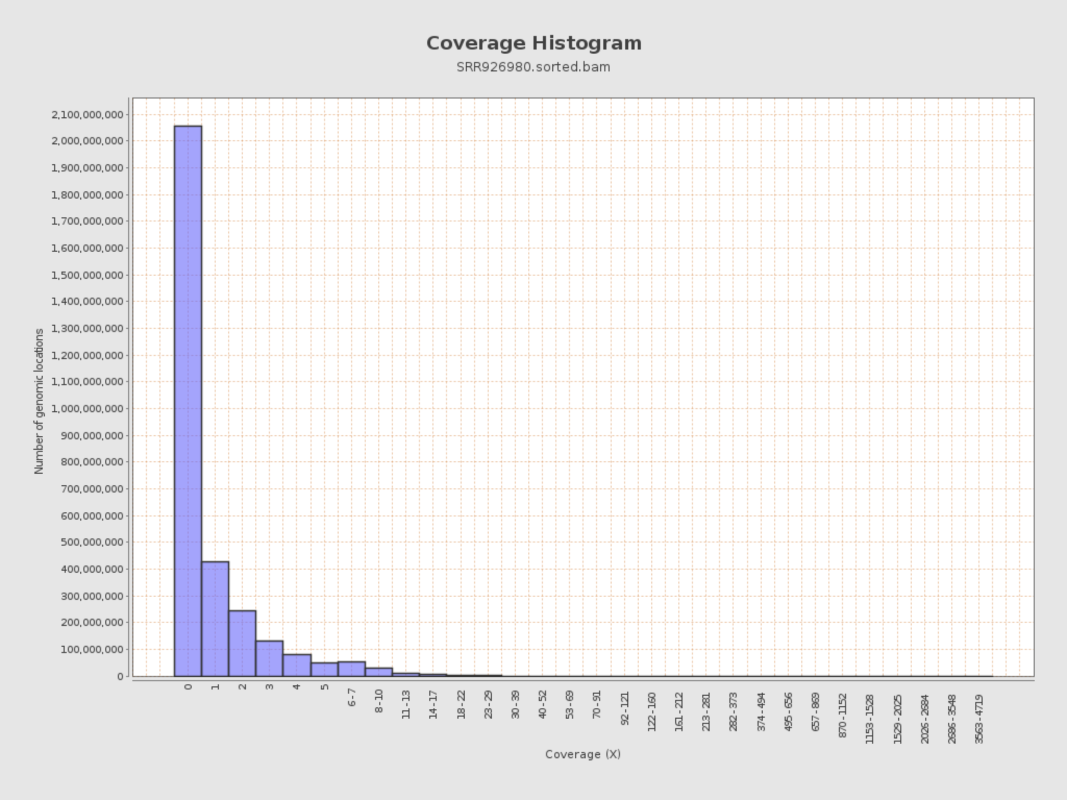
		bases	coverage	deviation
chr1	249250621	243592459	0.9773	4.3624
chr2	243199373	242728016	0.9981	6.4032
chr3	198022430	183422721	0.9263	1.9362
chr4	191154276	161360896	0.8441	3.0741
chr5	180915260	166464488	0.9201	1.9095
chr6	171115067	161693804	0.9449	2.5514
chr7	159138663	143722011	0.9031	2.7269
chr8	146364022	141176442	0.9646	2.3184
chr9	141213431	121746459	0.8621	4.323
chr10	135534747	138785436	1.024	6.1645
chr11	135006516	138453740	1.0255	3.2483
chr12	133851895	126541050	0.9454	2.2845
chr13	115169878	80577710	0.6996	1.7255
chr14	107349540	85573194	0.7971	1.8882
chr15	102531392	86086303	0.8396	2.0148
chr16	90354753	98071962	1.0854	7.4407
chr17	81195210	84814375	1.0446	2.8027
chr18	78077248	73637101	0.9431	4.6457
chr19	59128983	58586922	0.9908	3.164
chr20	63025520	71018533	1.1268	2.4432
chr21	48129895	35459055	0.7367	2.8534
chr22	51304566	44957045	0.8763	2.2764
chrMT	16571	16729894	1,009.5887	714.751
chrX	155270560	150910308	0.9719	2.306

chrY	59373566	5438187	0.0916	3.0236

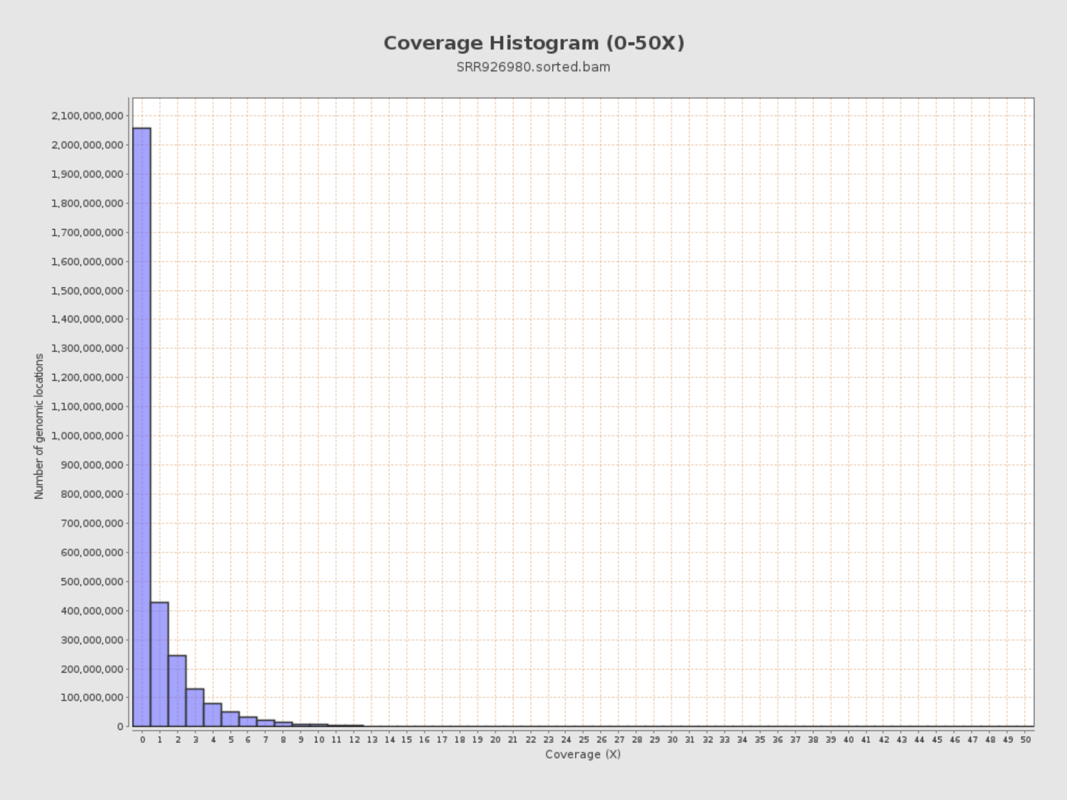
3. Results : Coverage across reference



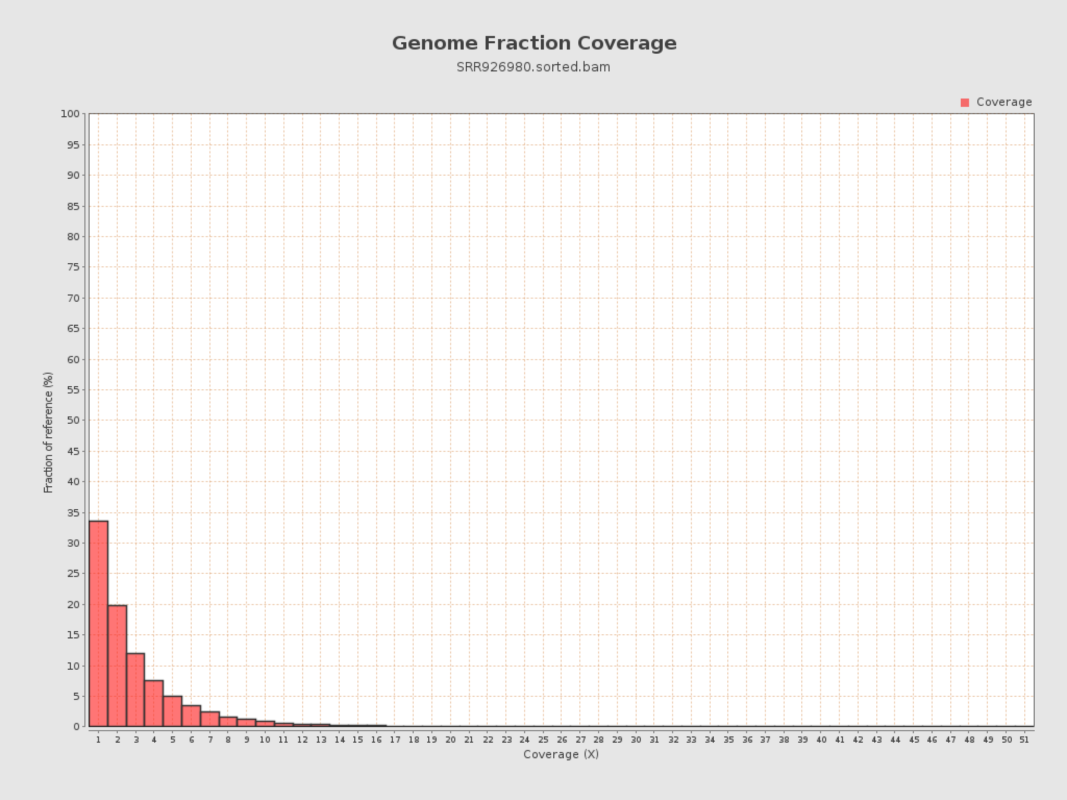
4. Results : Coverage Histogram



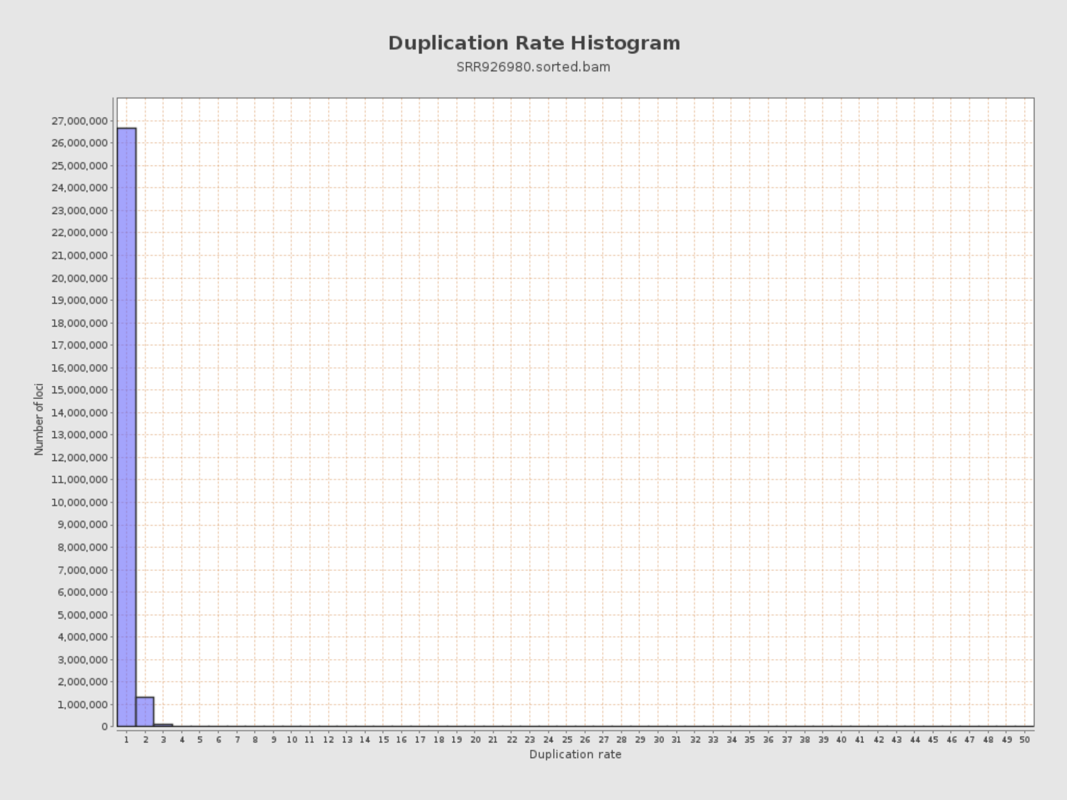
5. Results : Coverage Histogram (0-50X)



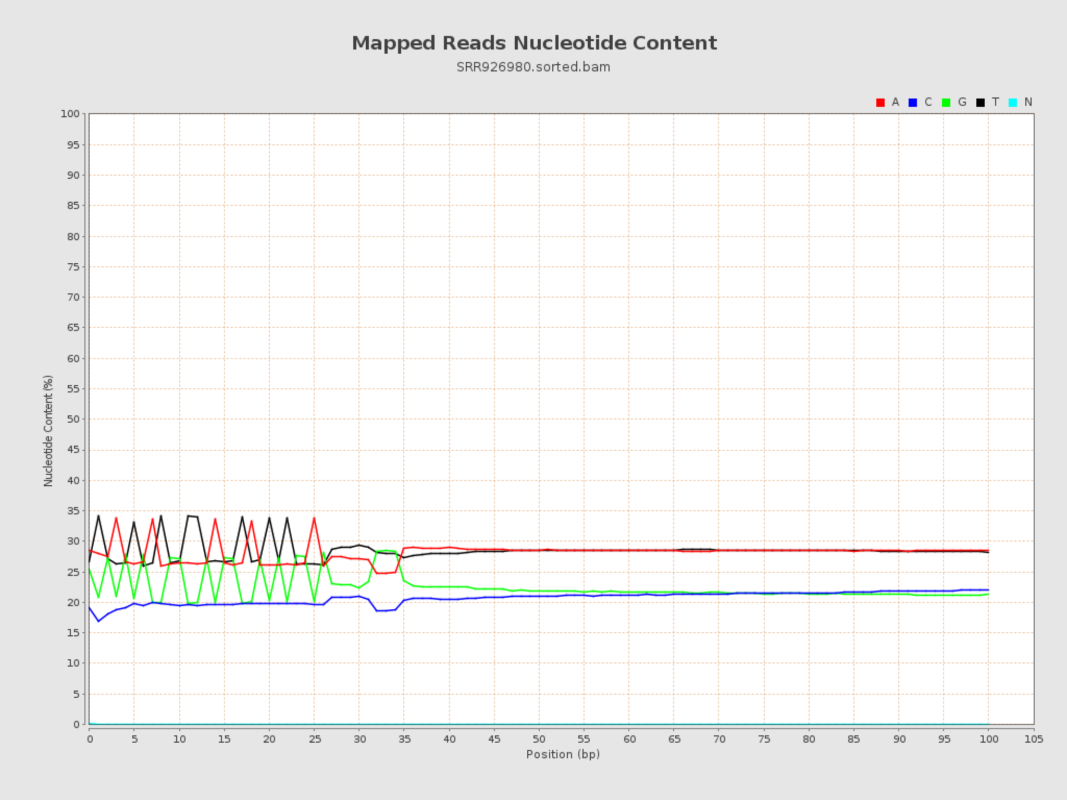
6. Results : Genome Fraction Coverage



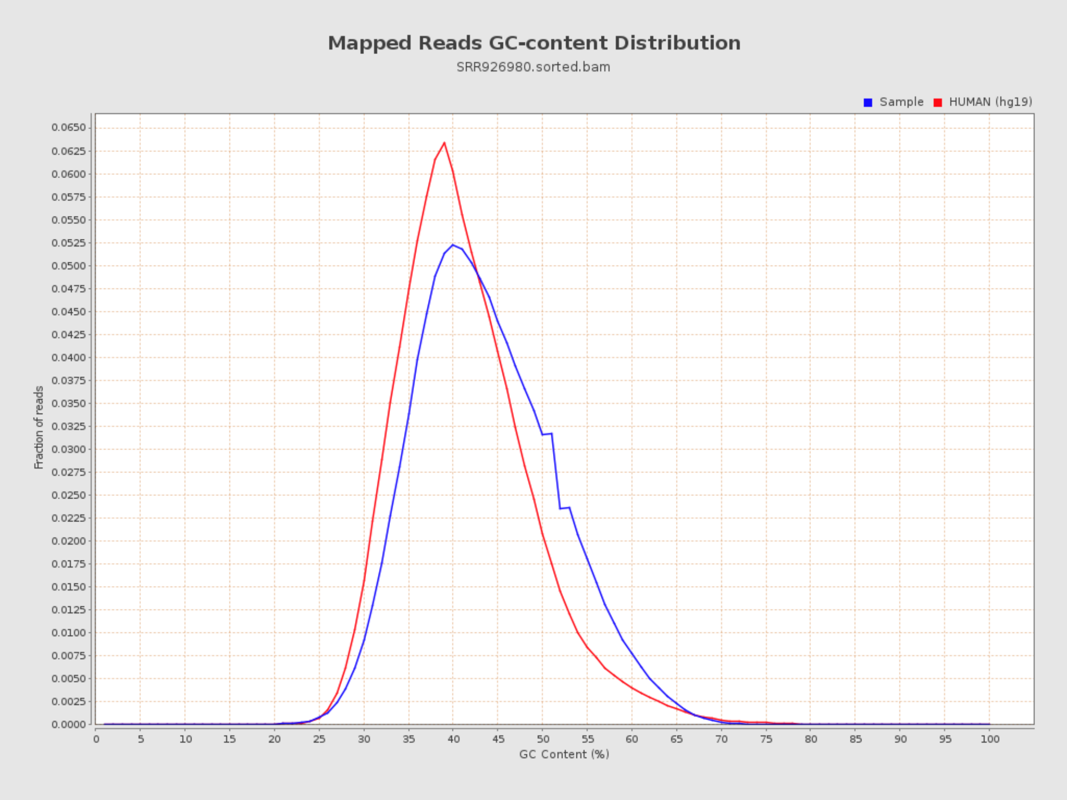
7. Results : Duplication Rate Histogram



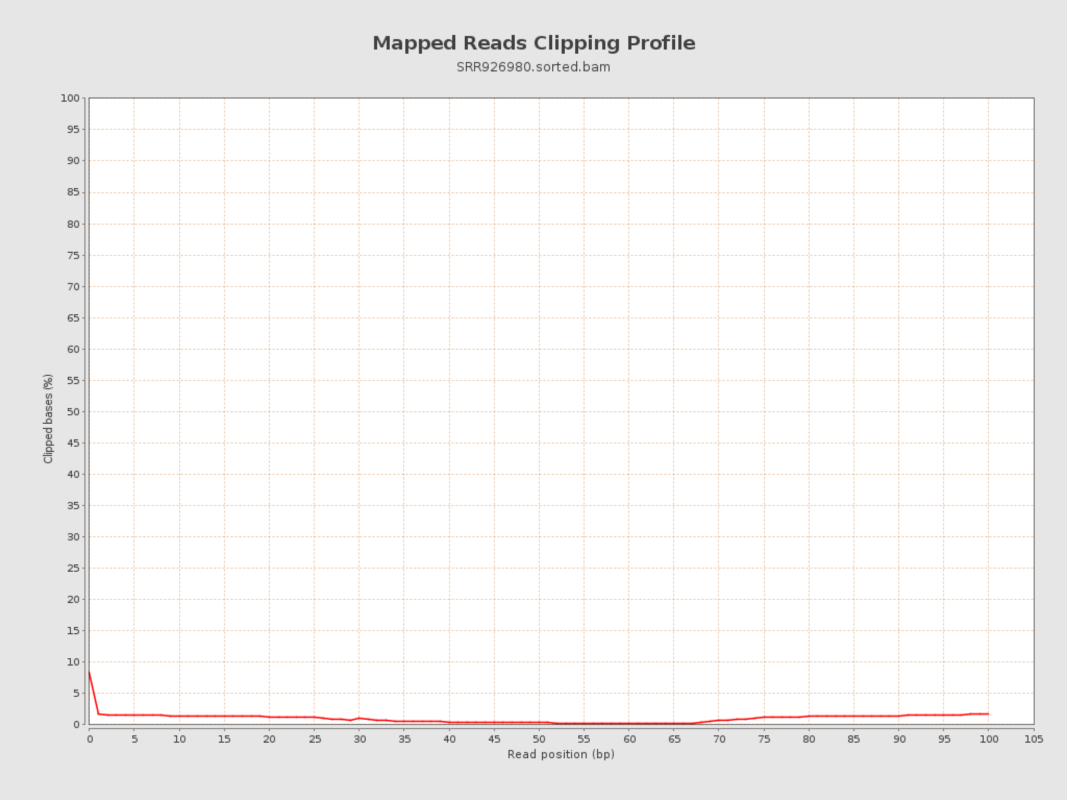
8. Results : Mapped Reads Nucleotide Content



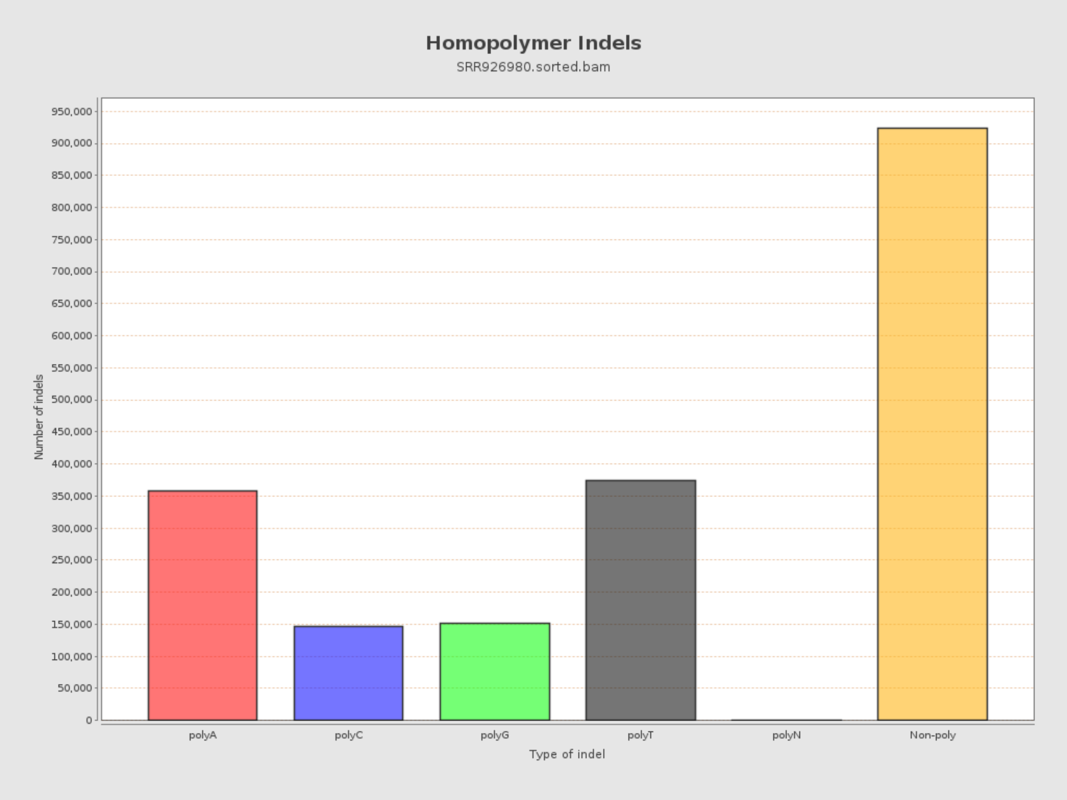
9. Results : Mapped Reads GC-content Distribution



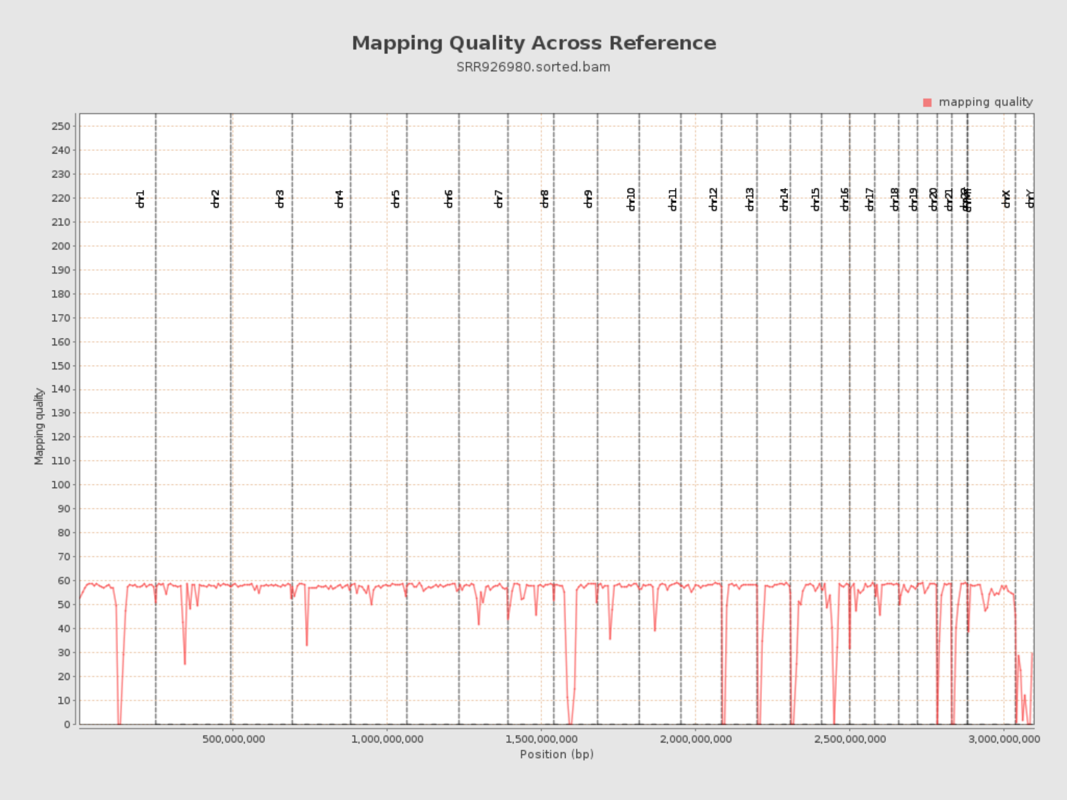
10. Results : Mapped Reads Clipping Profile



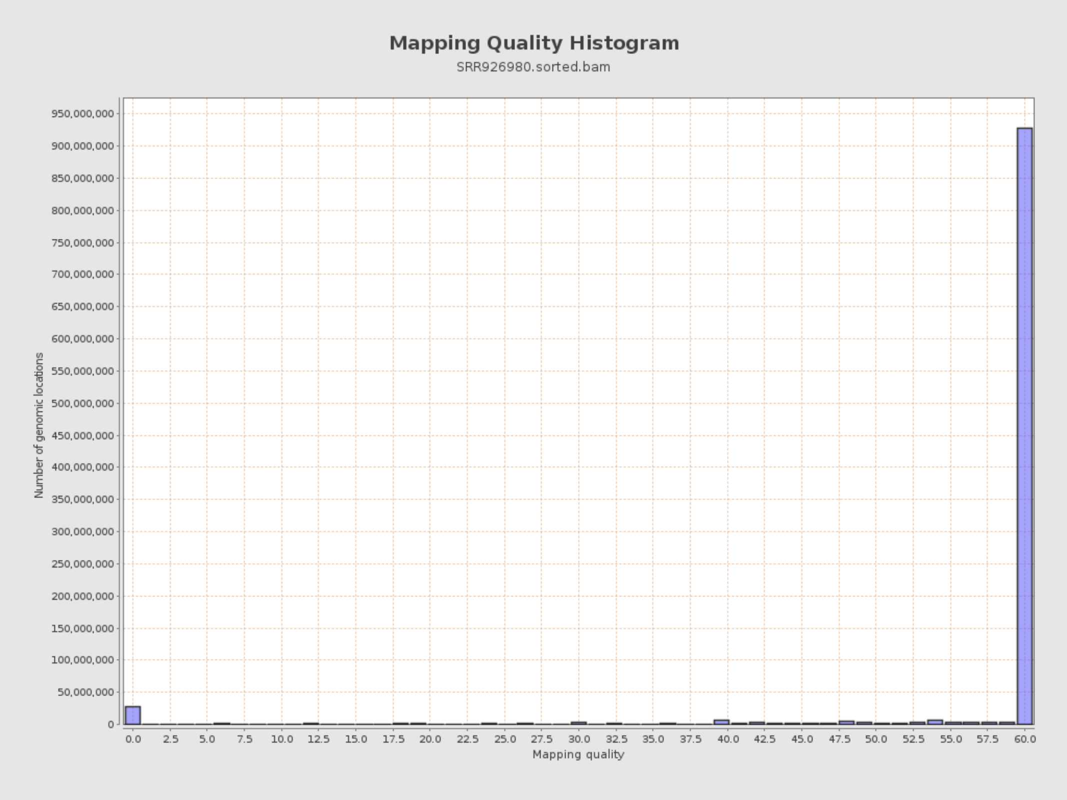
11. Results : Homopolymer Indels



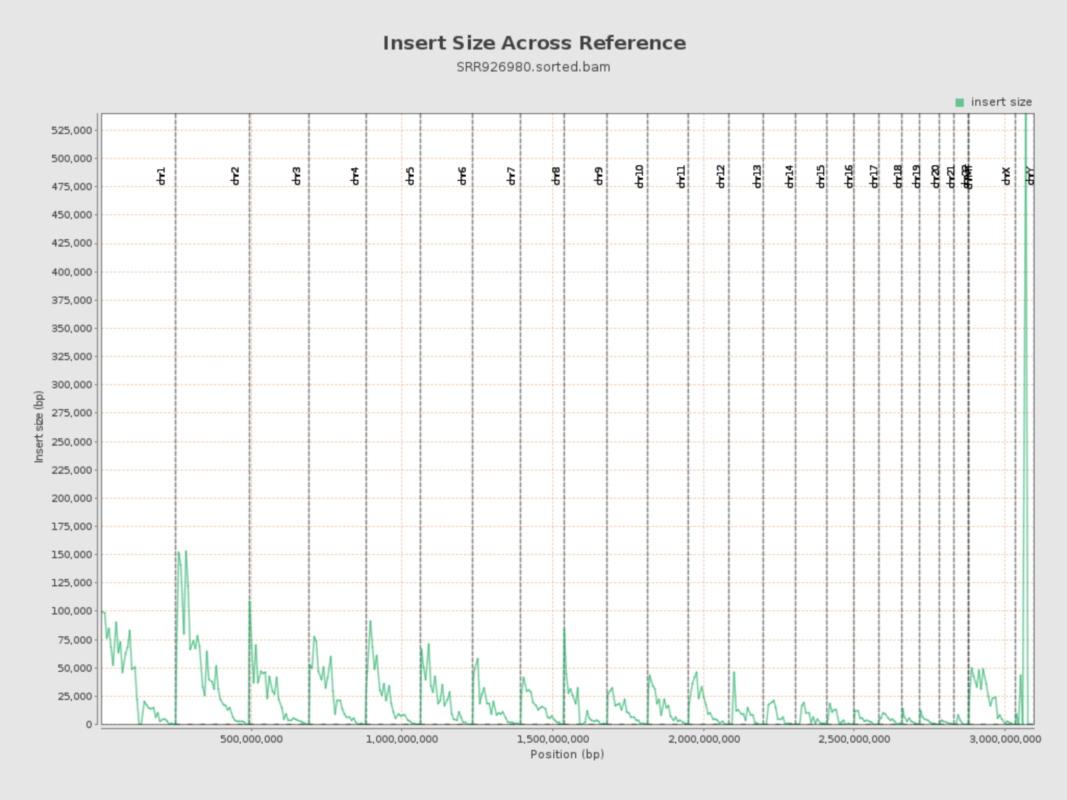
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram