Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 15:11:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926983.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_SRR926983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926983_1.fastq.gz SRR926983_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 15:11:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,447,094
Mapped reads	17,138,564 / 98.23%
Unmapped reads	308,530 / 1.77%
Mapped paired reads	17,138,564 / 98.23%
Mapped reads, first in pair	8,604,566 / 49.32%
Mapped reads, second in pair	8,533,998 / 48.91%
Mapped reads, both in pair	16,954,024 / 97.17%
Mapped reads, singletons	184,540 / 1.06%
Secondary alignments	0
Supplementary alignments	326,225 / 1.87%
Read min/max/mean length	30 / 101 / 101.77
Duplicated reads (estimated)	1,061,433 / 6.08%
Duplication rate	4.86%
Clipped reads	5,330,016 / 30.55%

2.2. ACGT Content

Number/percentage of A's	461,271,250 / 28.79%
Number/percentage of C's	315,874,239 / 19.72%
Number/percentage of T's	468,590,144 / 29.25%
Number/percentage of G's	356,293,919 / 22.24%
Number/percentage of N's	128,773 / 0.01%

GC Percentage	41.95%

2.3. Coverage

Mean	0.5179
Standard Deviation	2.0963

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	194,714.81
Standard Deviation	4,367,736.44
P25/Median/P75	139 / 176 / 231

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	14,874,741
Insertions	272,829
Mapped reads with at least one insertion	1.56%
Deletions	842,457
Mapped reads with at least one deletion	4.79%
Homopolymer indels	52.48%

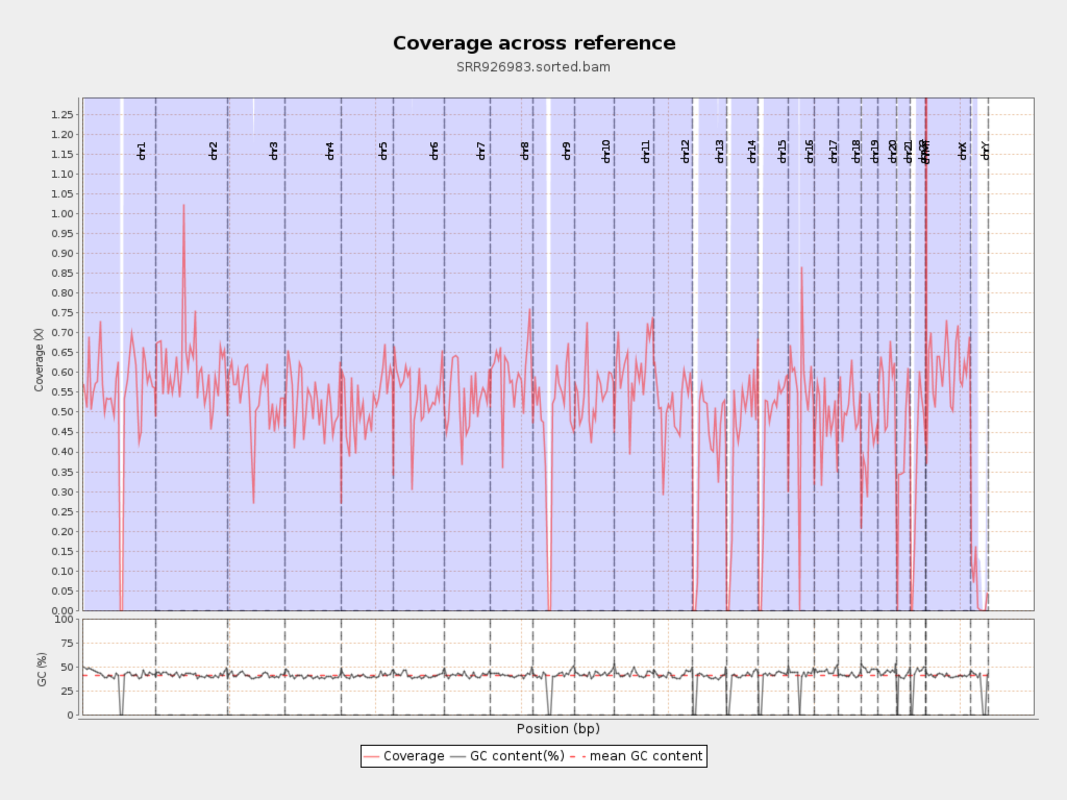
2.7. Chromosome stats

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

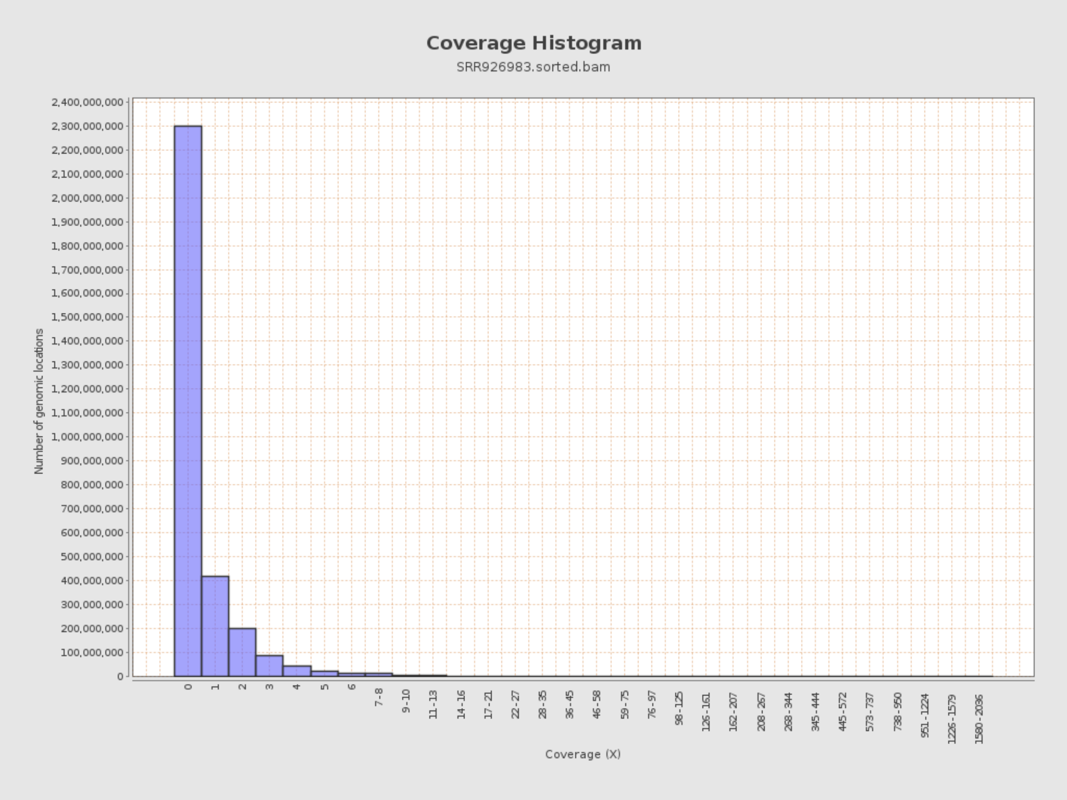
		bases	**coverage**	**deviation**
chr1	249250621	134563174	0.5399	2.5501
chr2	243199373	149393236	0.6143	3.6024
chr3	198022430	105427826	0.5324	1.1834
chr4	191154276	101161402	0.5292	1.9252
chr5	180915260	94558141	0.5227	1.1661
chr6	171115067	93884131	0.5487	1.4997
chr7	159138663	85075679	0.5346	1.7703
chr8	146364022	87497825	0.5978	1.4773
chr9	141213431	66922229	0.4739	2.853
chr10	135534747	73691846	0.5437	2.9213
chr11	135006516	82095627	0.6081	1.946
chr12	133851895	69465766	0.519	1.3993
chr13	115169878	45953140	0.399	1.0823
chr14	107349540	46089677	0.4293	1.1187
chr15	102531392	44809580	0.437	1.1524
chr16	90354753	48777387	0.5398	3.2925
chr17	81195210	39134639	0.482	1.9409
chr18	78077248	40229140	0.5152	2.838
chr19	59128983	24273446	0.4105	1.6385
chr20	63025520	35875494	0.5692	1.3582
chr21	48129895	18986951	0.3945	1.5936
chr22	51304566	18157656	0.3539	1.0345
chrMT	16571	219624	13.2535	11.9382
chrX	155270560	94291450	0.6073	1.4713

chrY	59373566	2842957	0.0479	1.7126

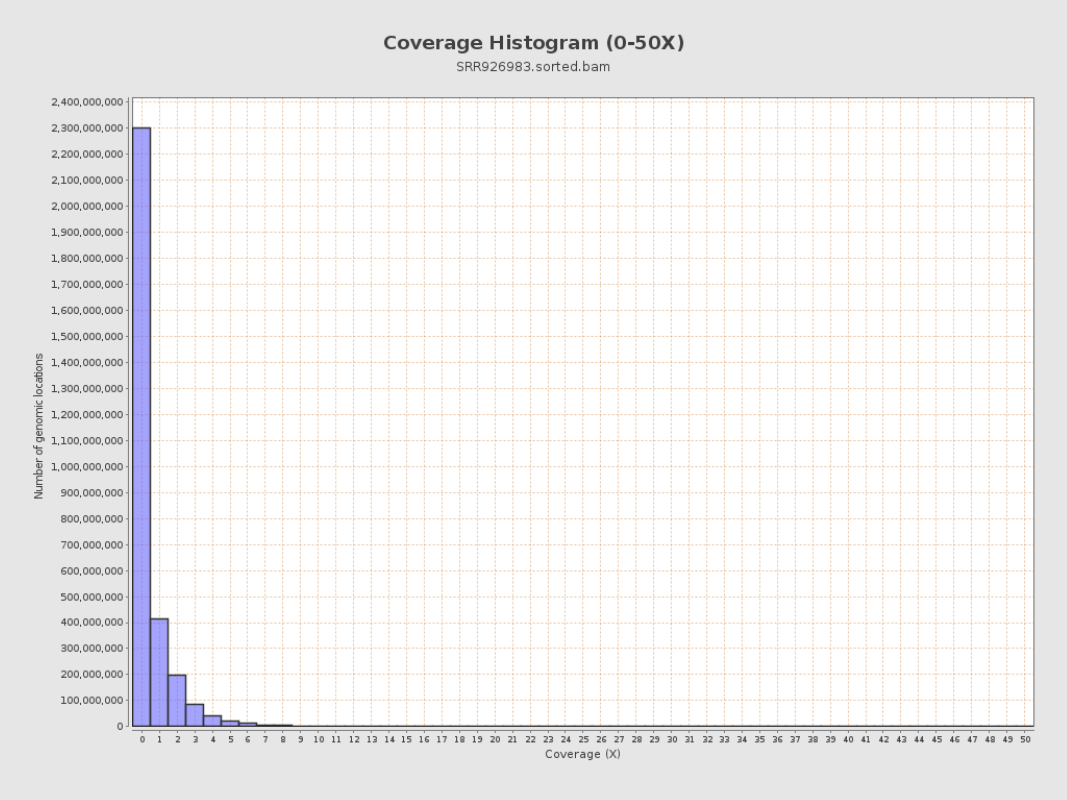
3. Results : Coverage across reference



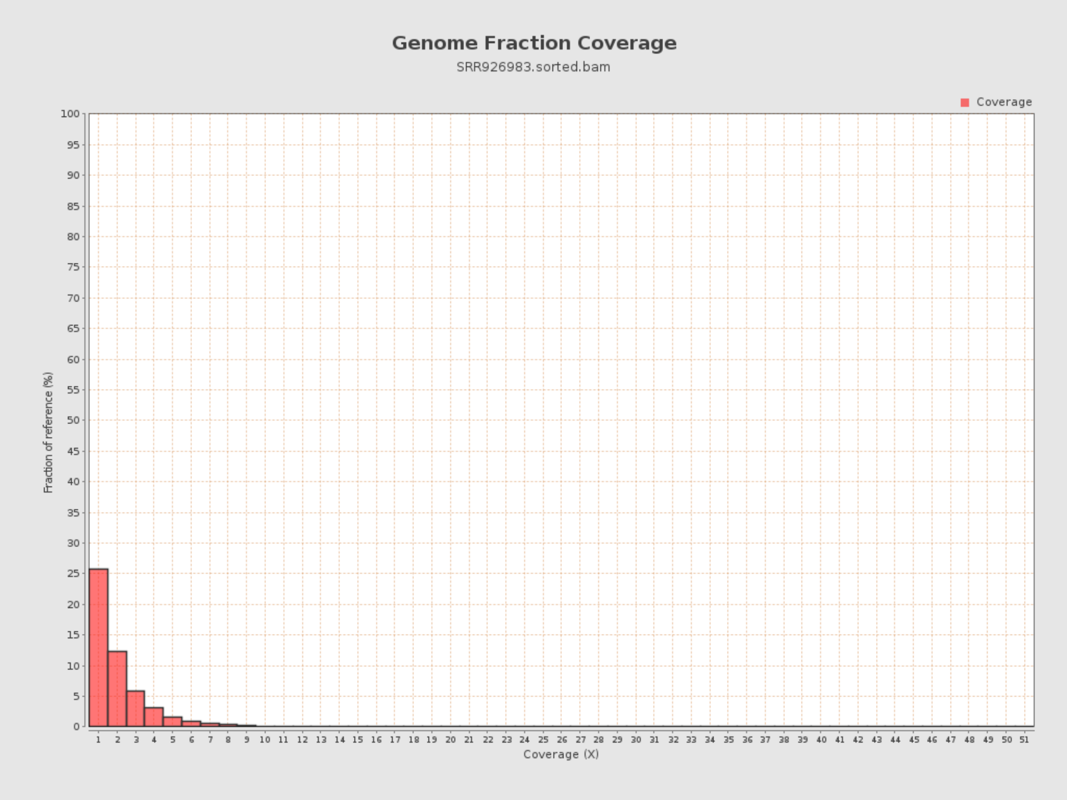
4. Results : Coverage Histogram



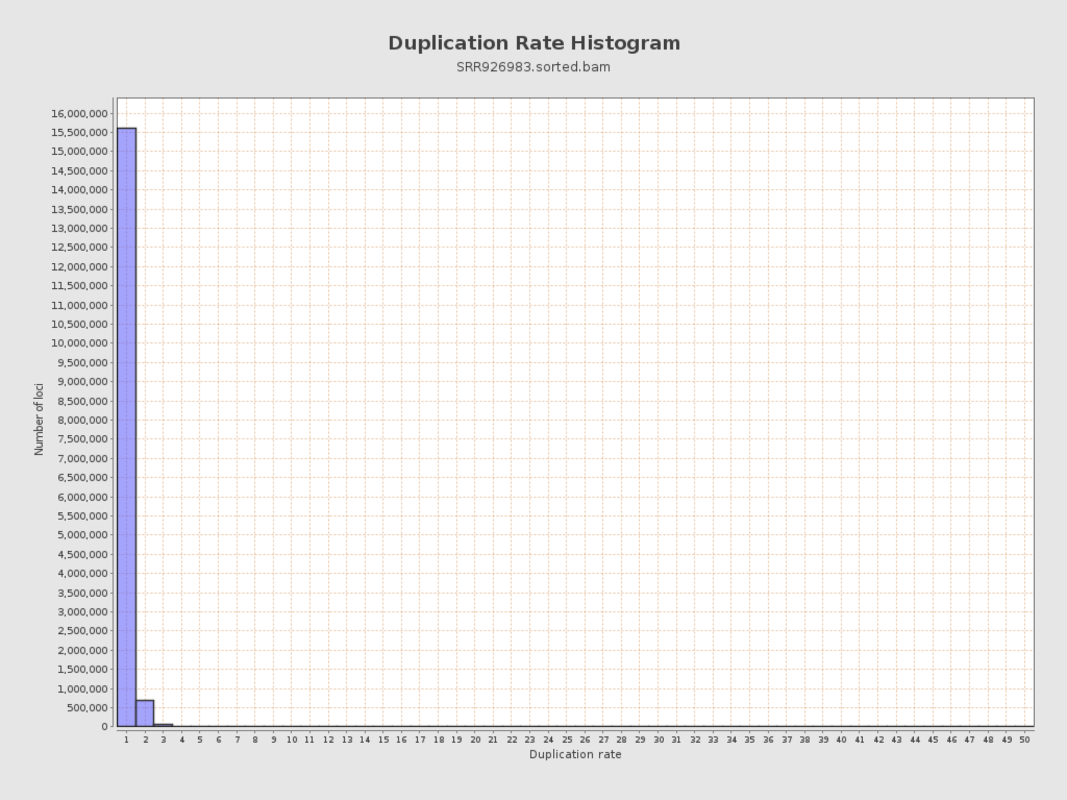
5. Results : Coverage Histogram (0-50X)



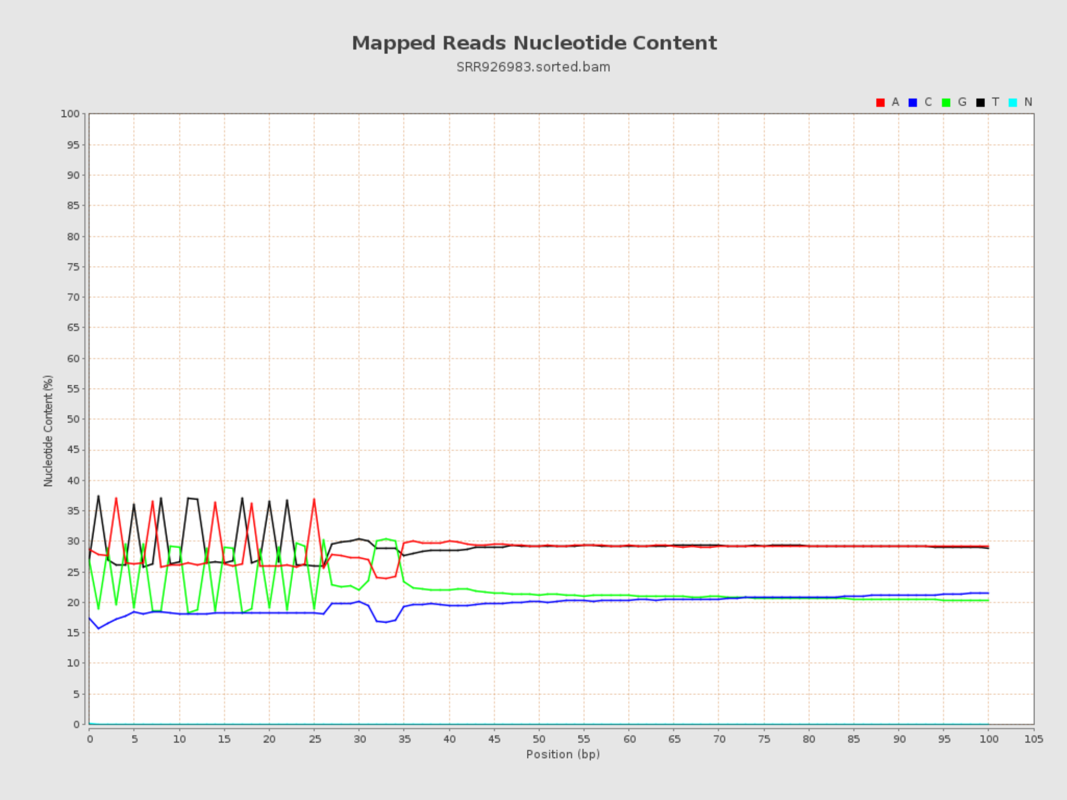
6. Results : Genome Fraction Coverage



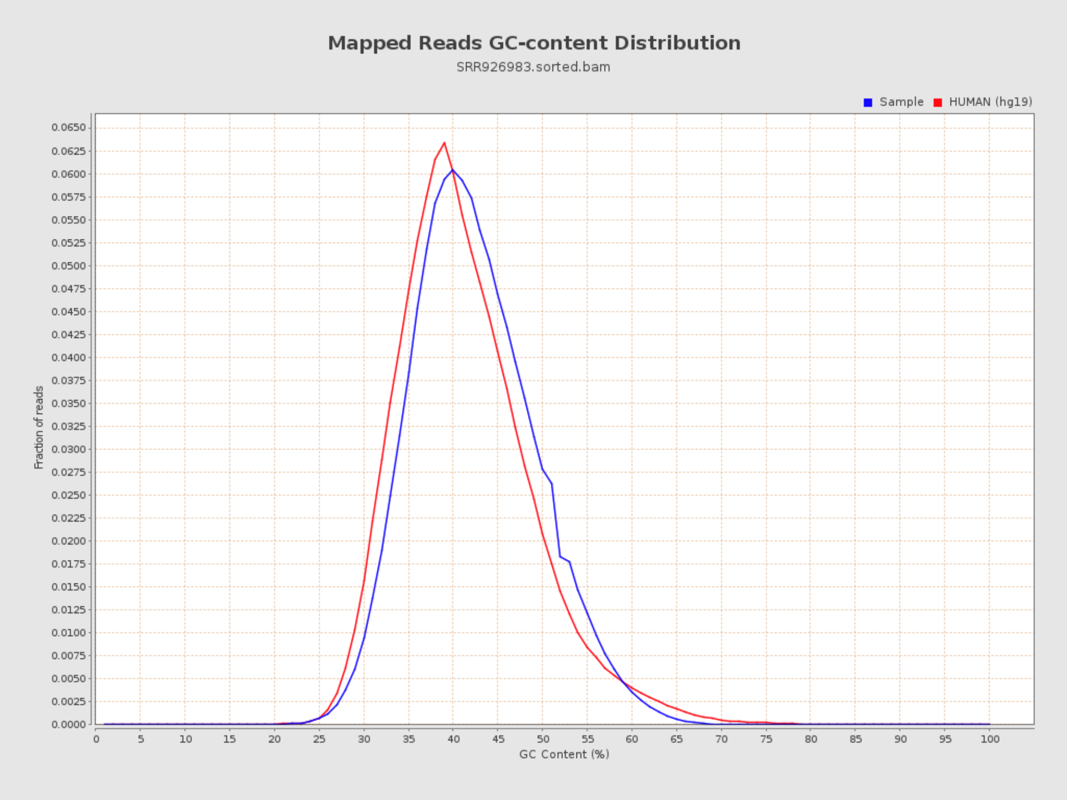
7. Results : Duplication Rate Histogram



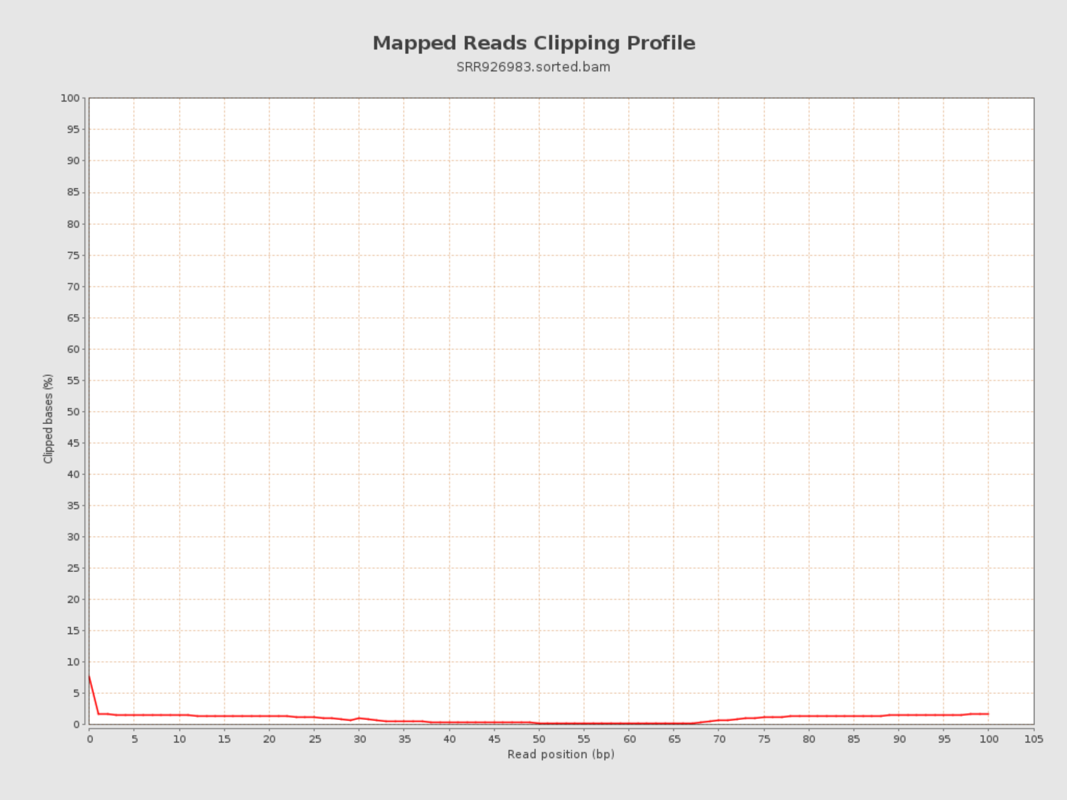
8. Results : Mapped Reads Nucleotide Content



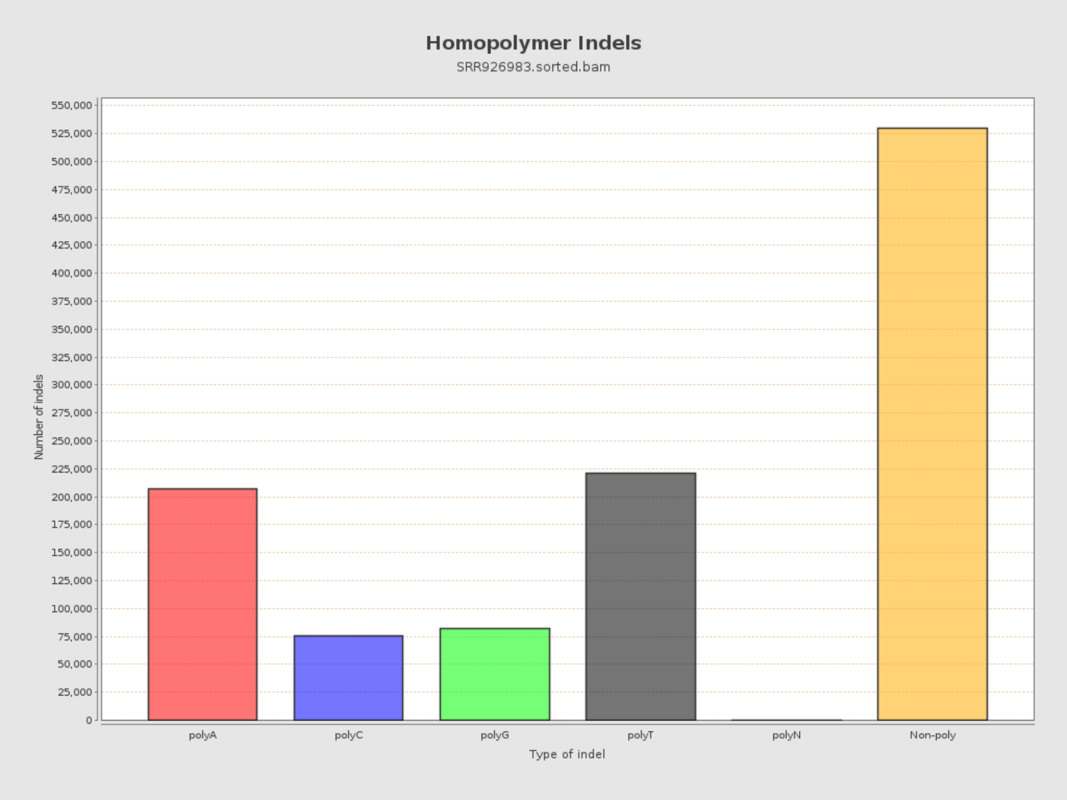
9. Results : Mapped Reads GC-content Distribution



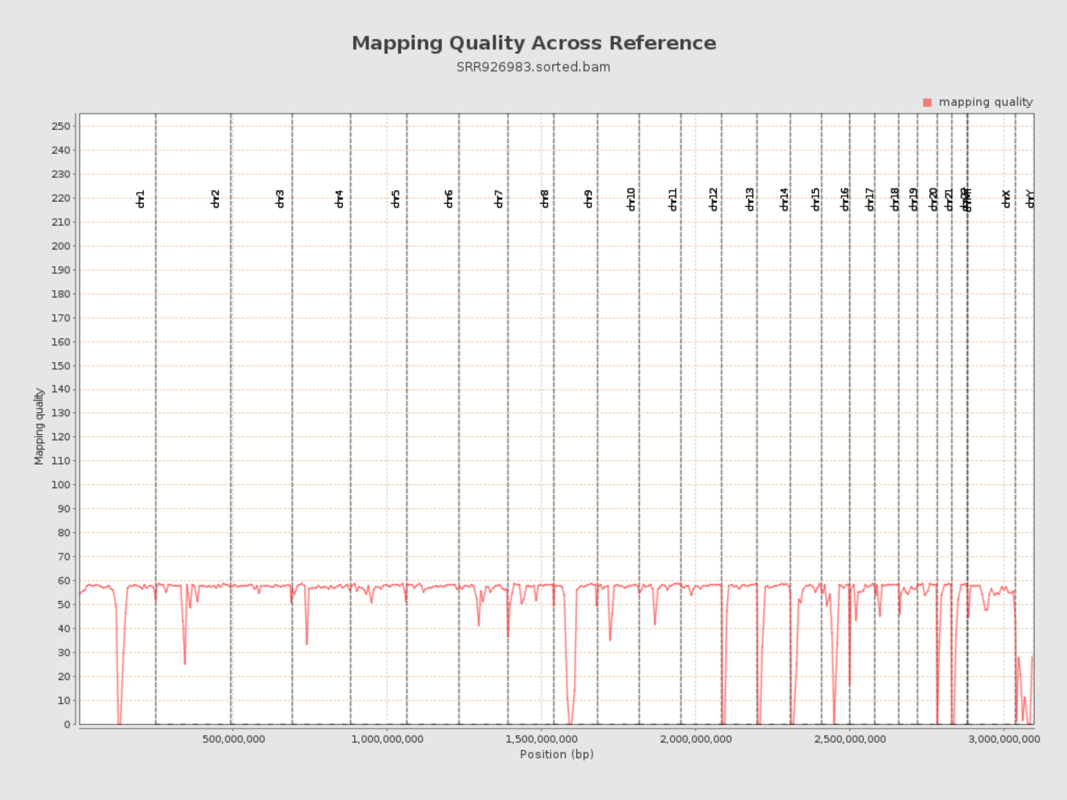
10. Results : Mapped Reads Clipping Profile



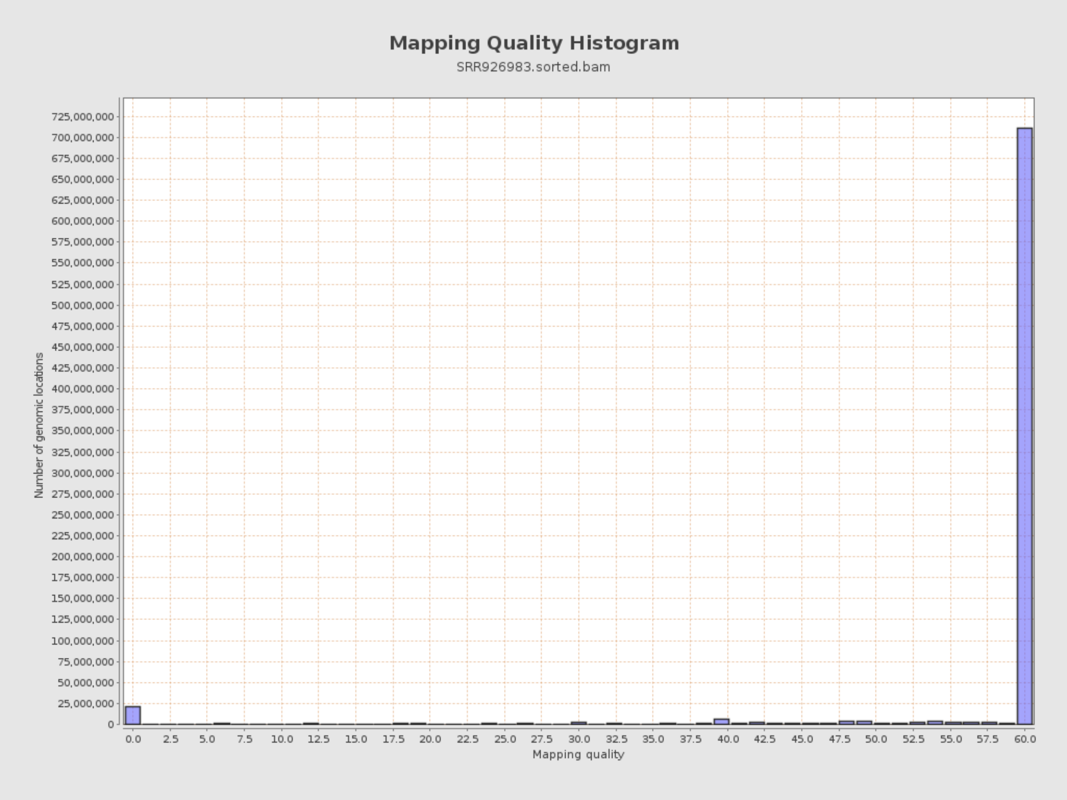
11. Results : Homopolymer Indels



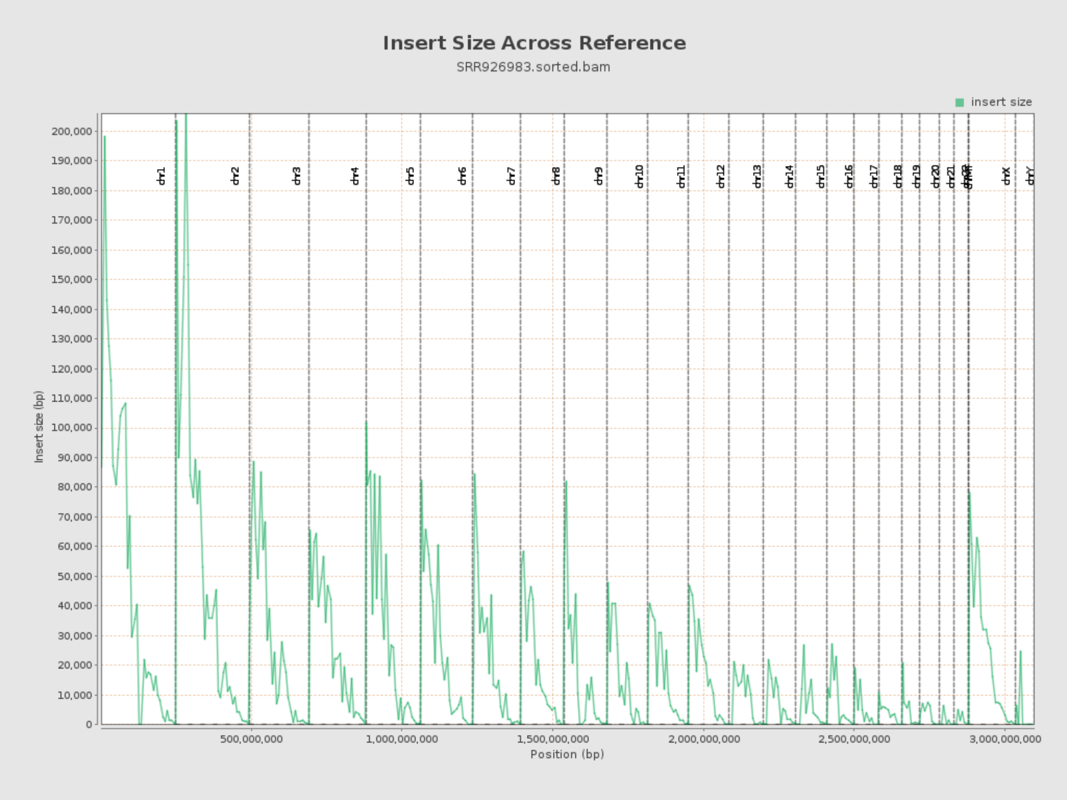
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram