Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 17:08:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926987.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_SRR926987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926987_1.fastq.gz SRR926987_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 17:08:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,221,276
Mapped reads	28,728,370 / 98.31%
Unmapped reads	492,906 / 1.69%
Mapped paired reads	28,728,370 / 98.31%
Mapped reads, first in pair	14,418,642 / 49.34%
Mapped reads, second in pair	14,309,728 / 48.97%
Mapped reads, both in pair	28,456,276 / 97.38%
Mapped reads, singletons	272,094 / 0.93%
Secondary alignments	0
Supplementary alignments	540,242 / 1.85%
Read min/max/mean length	30 / 101 / 101.76
Duplicated reads (estimated)	2,025,974 / 6.93%
Duplication rate	5.35%
Clipped reads	6,802,891 / 23.28%

2.2. ACGT Content

Number/percentage of A's	772,456,806 / 28.12%
Number/percentage of C's	572,529,988 / 20.84%
Number/percentage of T's	779,482,384 / 28.38%
Number/percentage of G's	622,016,779 / 22.65%
Number/percentage of N's	245,830 / 0.01%

GC Percentage	43.49%

2.3. Coverage

Mean	0.8879
Standard Deviation	3.9057

2.4. Mapping Quality

Mean Mapping Quality	53.16

2.5. Insert size

Mean	183,881.91
Standard Deviation	4,240,594.82
P25/Median/P75	144 / 180 / 233

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	26,200,645
Insertions	444,811
Mapped reads with at least one insertion	1.52%
Deletions	1,442,538
Mapped reads with at least one deletion	4.89%
Homopolymer indels	52.67%

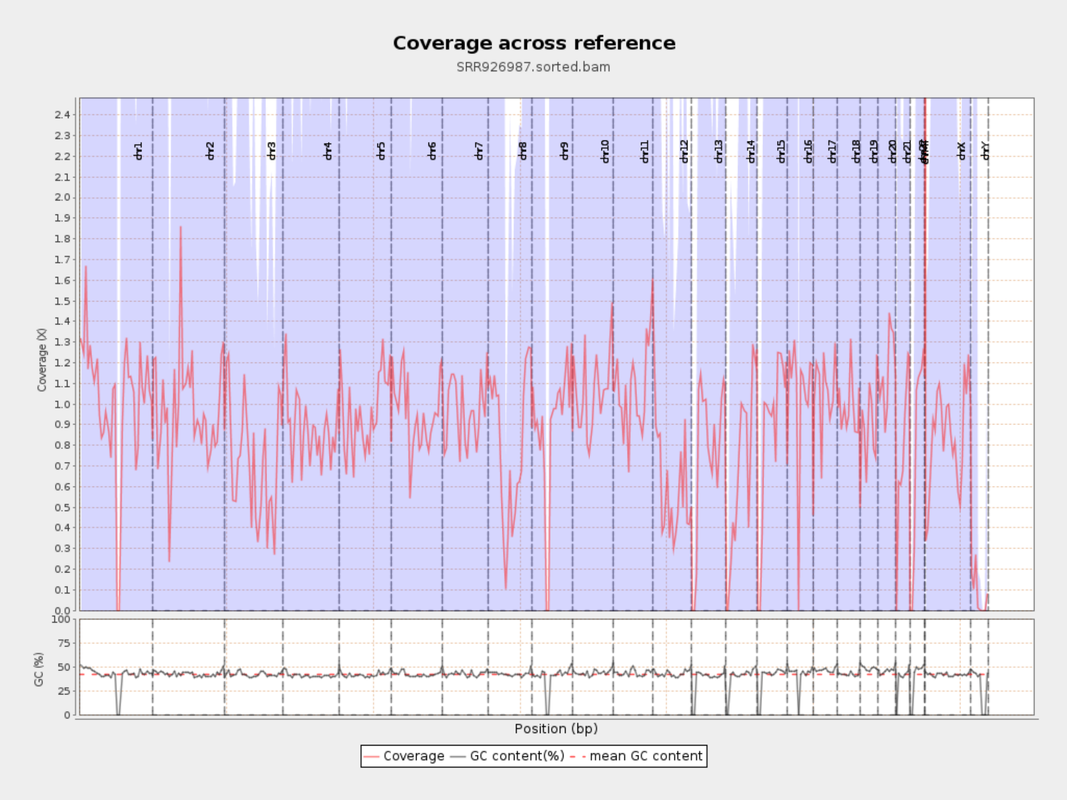
2.7. Chromosome stats

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

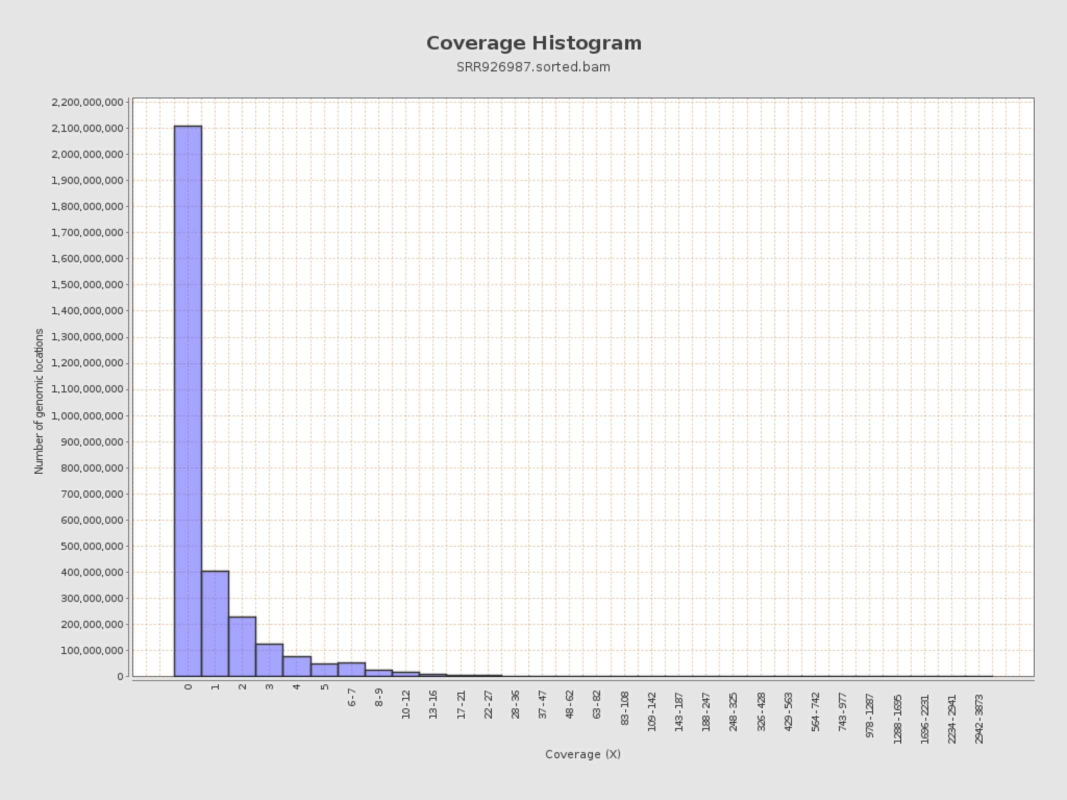
		bases	**coverage**	**deviation**
chr1	249250621	252812184	1.0143	4.7611
chr2	243199373	237380218	0.9761	6.5191
chr3	198022430	144386446	0.7291	1.7733
chr4	191154276	168354033	0.8807	2.83
chr5	180915260	174386745	0.9639	1.9908
chr6	171115067	163433087	0.9551	3.6812
chr7	159138663	153547680	0.9649	3.186
chr8	146364022	114428468	0.7818	2.2479
chr9	141213431	124961346	0.8849	5.5289
chr10	135534747	144127135	1.0634	5.6404
chr11	135006516	143523479	1.0631	3.5565
chr12	133851895	81177255	0.6065	1.9381
chr13	115169878	87700617	0.7615	1.8173
chr14	107349540	70390392	0.6557	1.7866
chr15	102531392	86786683	0.8464	2.017
chr16	90354753	92855458	1.0277	4.2563
chr17	81195210	86615276	1.0668	4.0955
chr18	78077248	77369112	0.9909	6.2169
chr19	59128983	51352554	0.8685	3.1938
chr20	63025520	73094408	1.1598	2.4861
chr21	48129895	37893172	0.7873	3.2798
chr22	51304566	40502817	0.7895	2.1146
chrMT	16571	5506248	332.2822	229.3612
chrX	155270560	131581222	0.8474	2.2917

chrY	59373566	4632357	0.078	2.4652

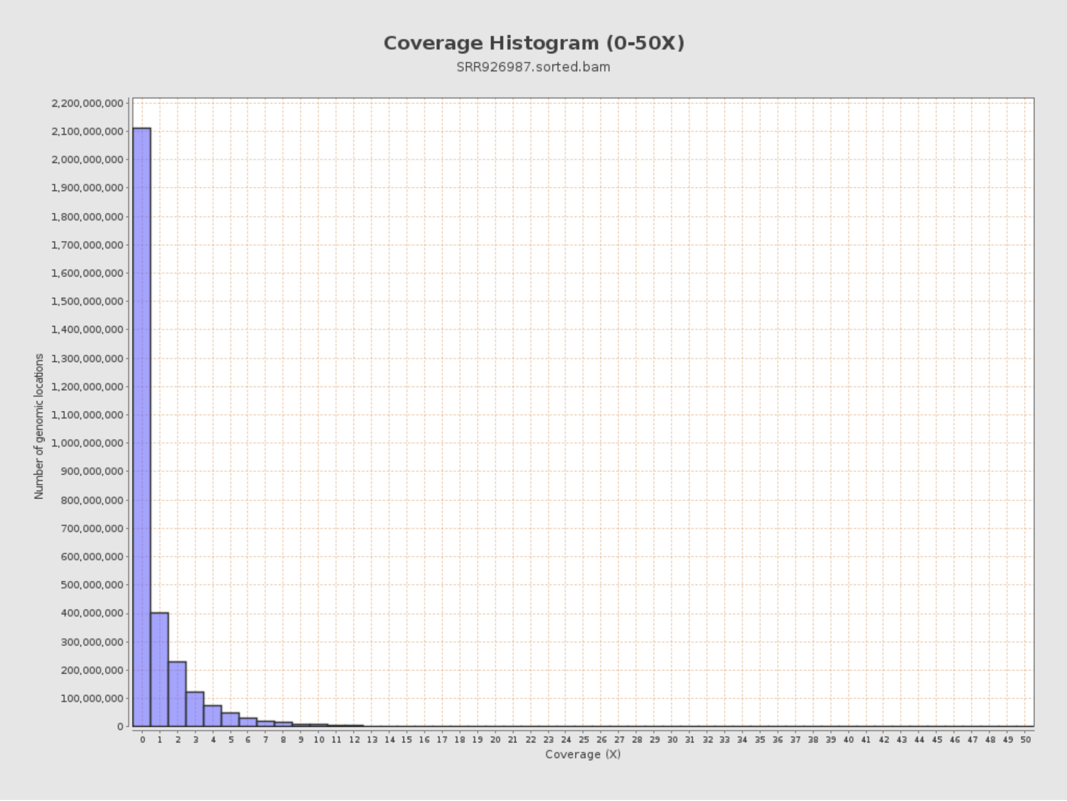
3. Results : Coverage across reference



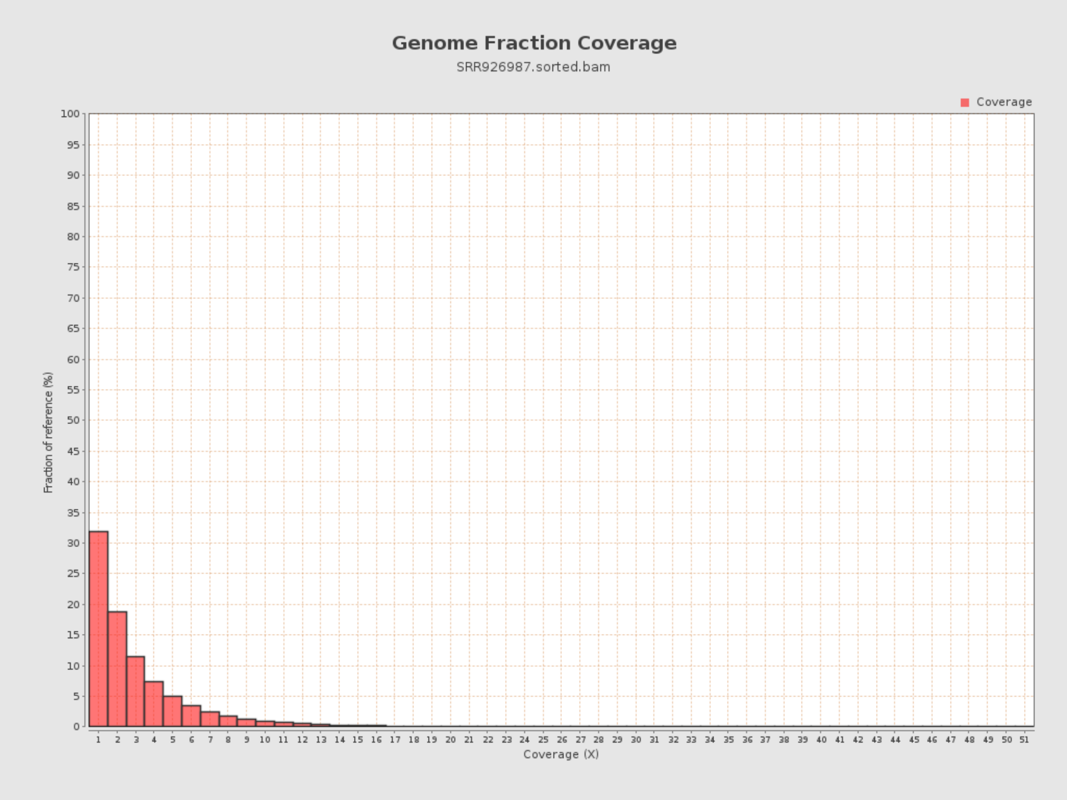
4. Results : Coverage Histogram



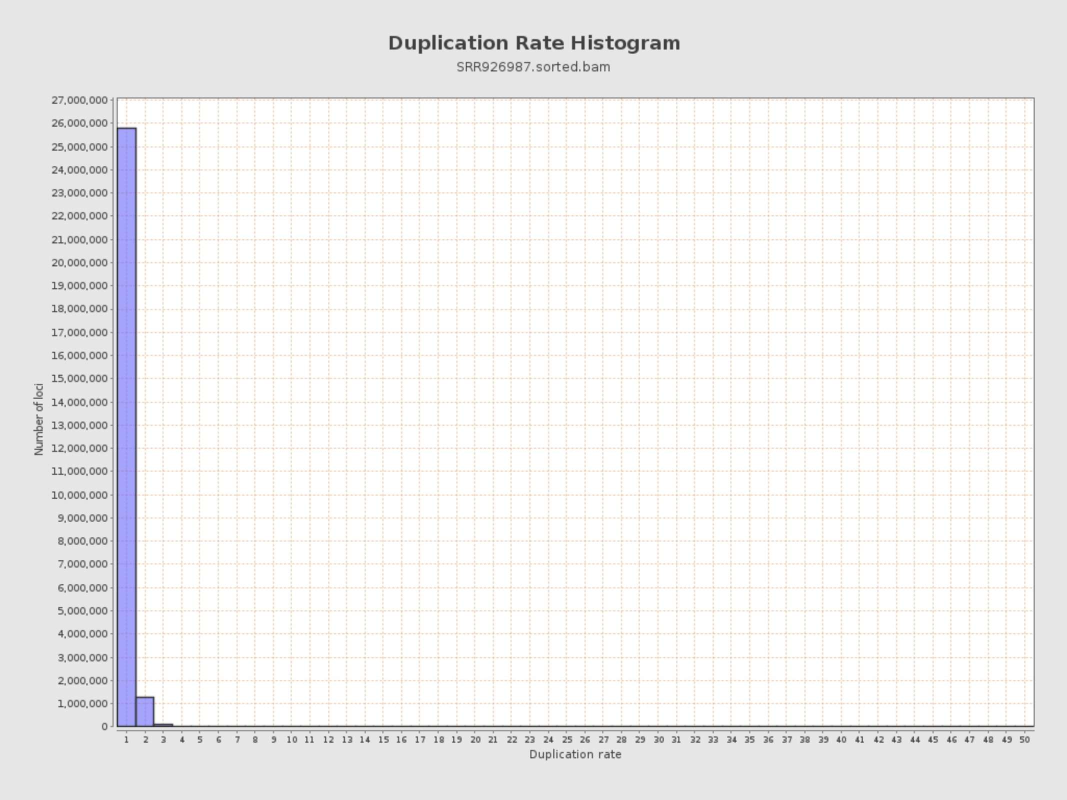
5. Results : Coverage Histogram (0-50X)



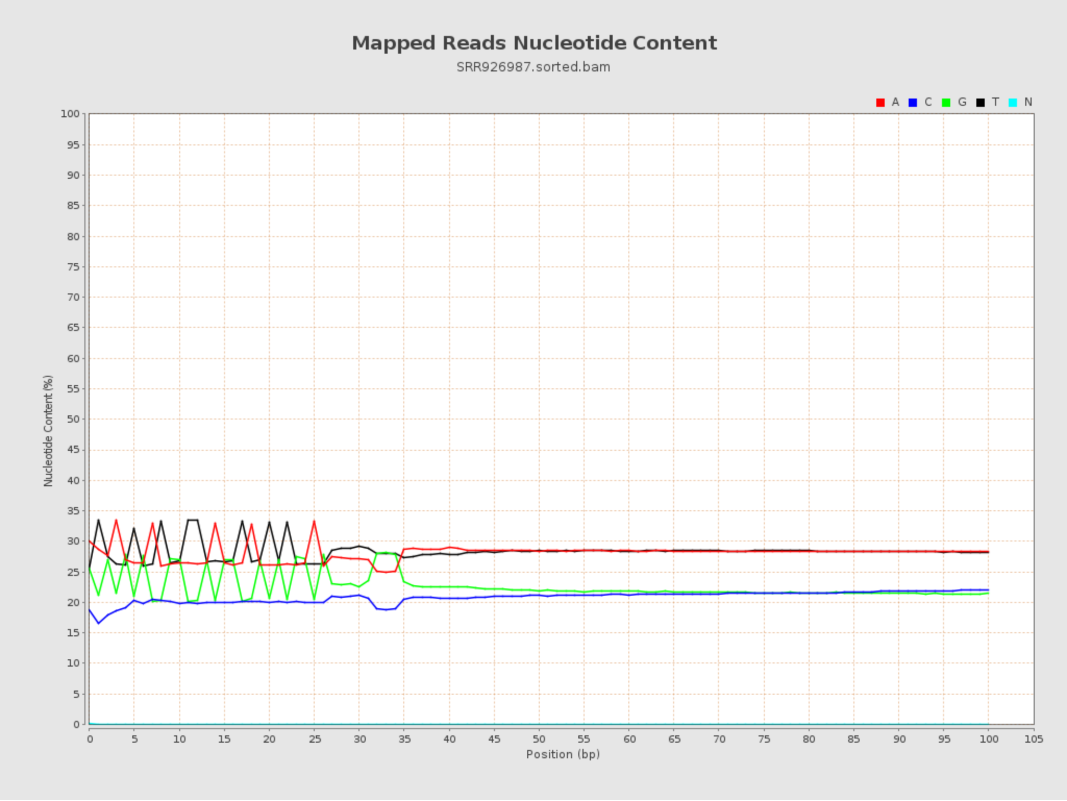
6. Results : Genome Fraction Coverage



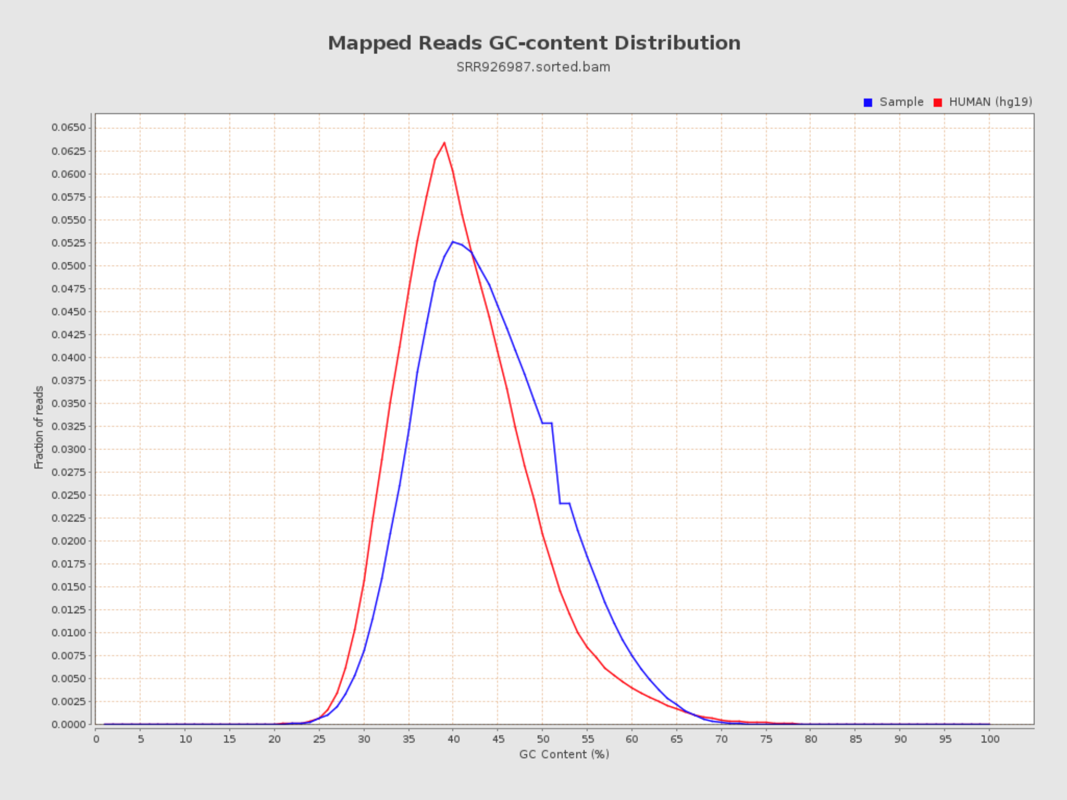
7. Results : Duplication Rate Histogram



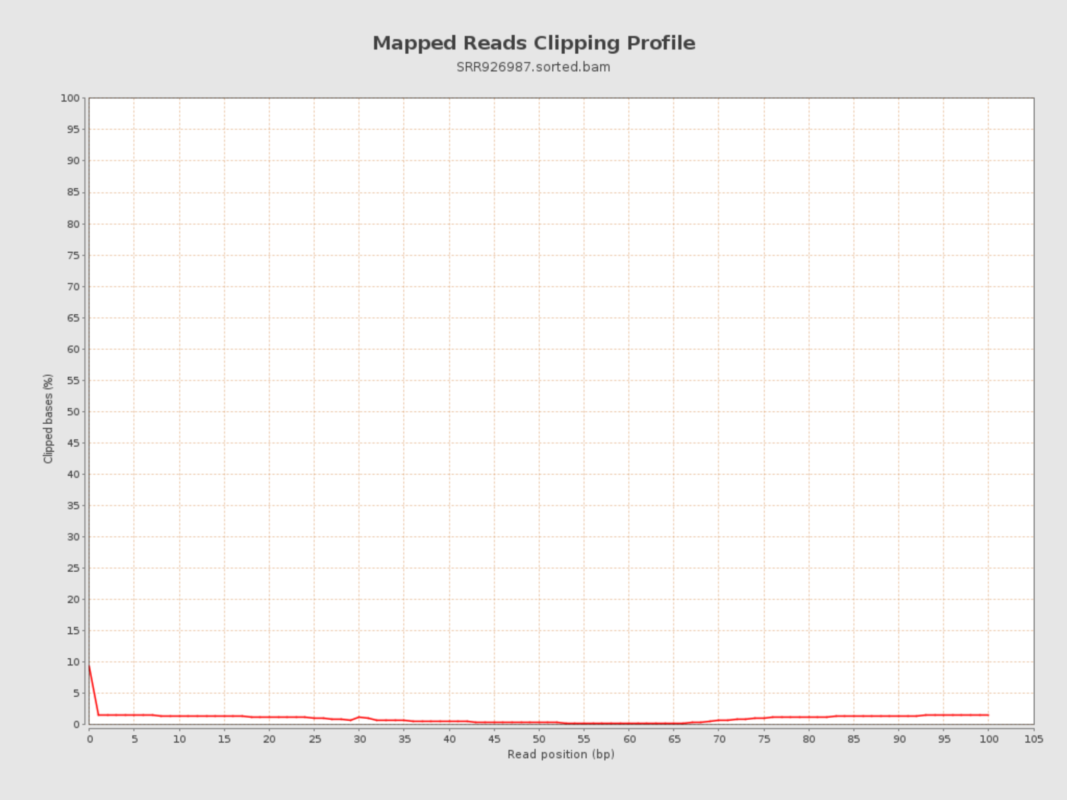
8. Results : Mapped Reads Nucleotide Content



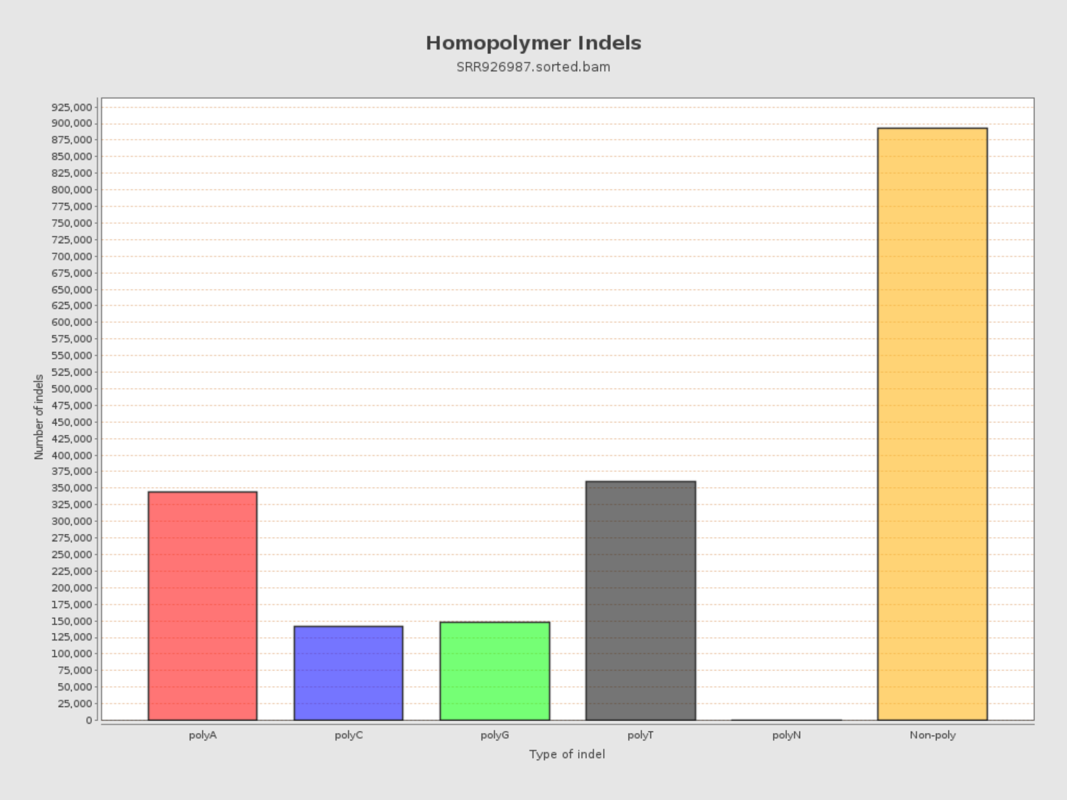
9. Results : Mapped Reads GC-content Distribution



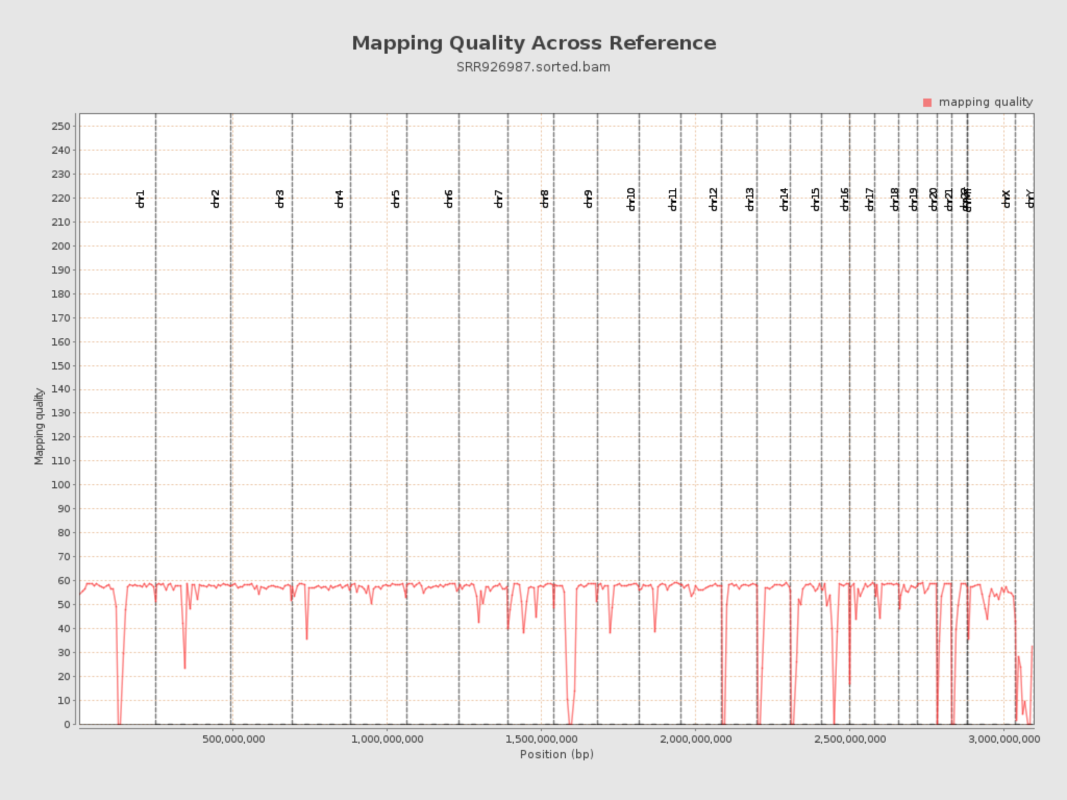
10. Results : Mapped Reads Clipping Profile



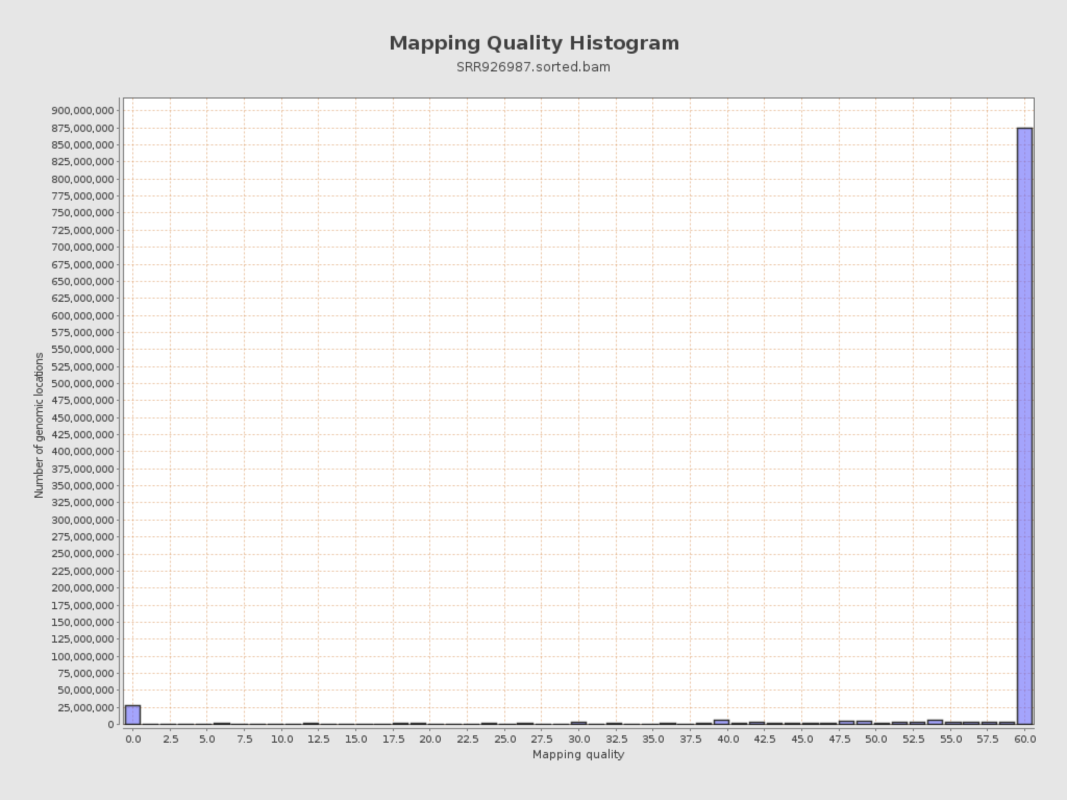
11. Results : Homopolymer Indels



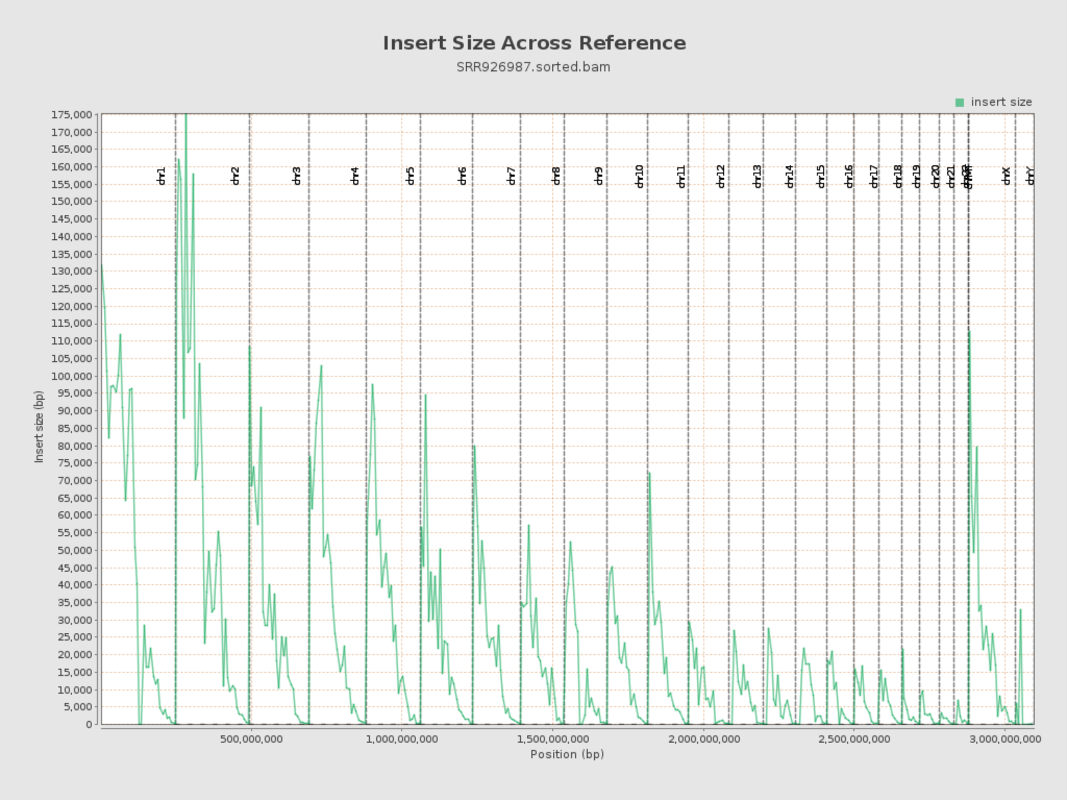
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram