Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 16:16:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926985.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_SRR926985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926985_1.fastq.gz SRR926985_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 16:16:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,274,098
Mapped reads	28,853,277 / 98.56%
Unmapped reads	420,821 / 1.44%
Mapped paired reads	28,853,277 / 98.56%
Mapped reads, first in pair	14,476,106 / 49.45%
Mapped reads, second in pair	14,377,171 / 49.11%
Mapped reads, both in pair	28,635,314 / 97.82%
Mapped reads, singletons	217,963 / 0.74%
Secondary alignments	0
Supplementary alignments	337,216 / 1.15%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	2,056,370 / 7.02%
Duplication rate	5.28%
Clipped reads	6,455,447 / 22.05%

2.2. ACGT Content

Number/percentage of A's	776,861,152 / 28.18%
Number/percentage of C's	572,386,588 / 20.77%
Number/percentage of T's	785,033,993 / 28.48%
Number/percentage of G's	621,886,237 / 22.56%
Number/percentage of N's	249,350 / 0.01%

GC Percentage	43.33%

2.3. Coverage

Mean	0.8911
Standard Deviation	4.2771

2.4. Mapping Quality

Mean Mapping Quality	53.48

2.5. Insert size

Mean	113,729.09
Standard Deviation	3,344,464.45
P25/Median/P75	140 / 175 / 228

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	24,906,980
Insertions	432,155
Mapped reads with at least one insertion	1.47%
Deletions	1,417,304
Mapped reads with at least one deletion	4.79%
Homopolymer indels	52.72%

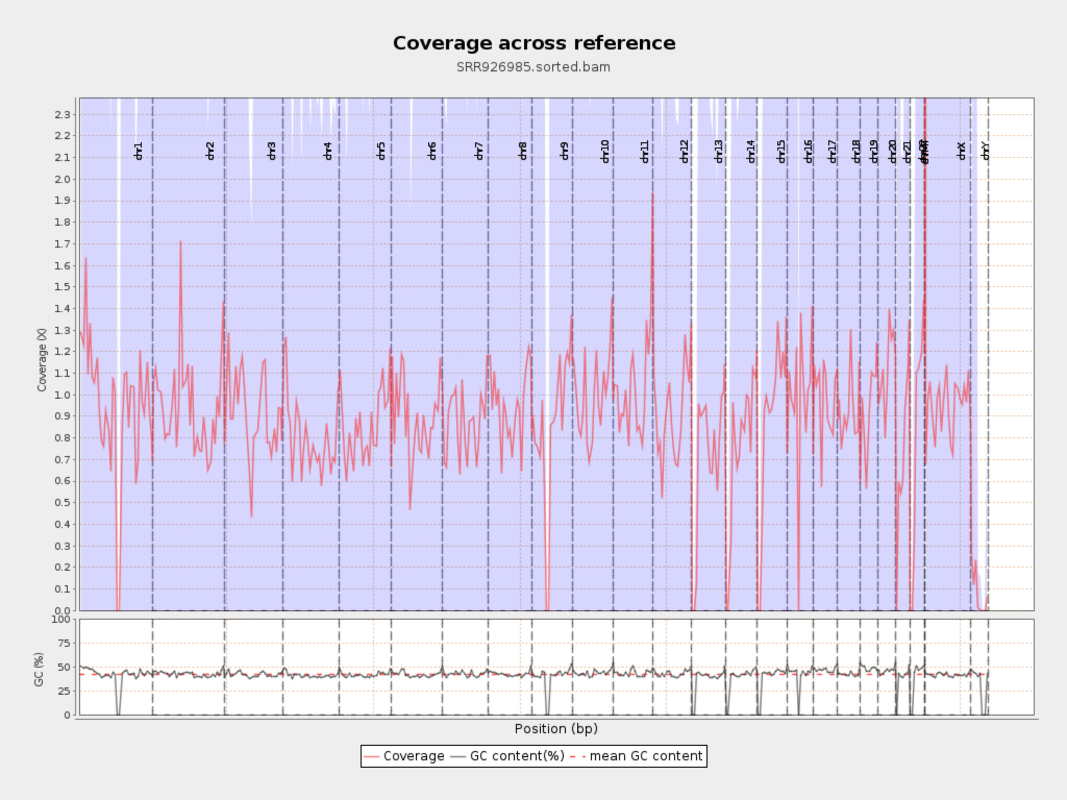
2.7. Chromosome stats

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

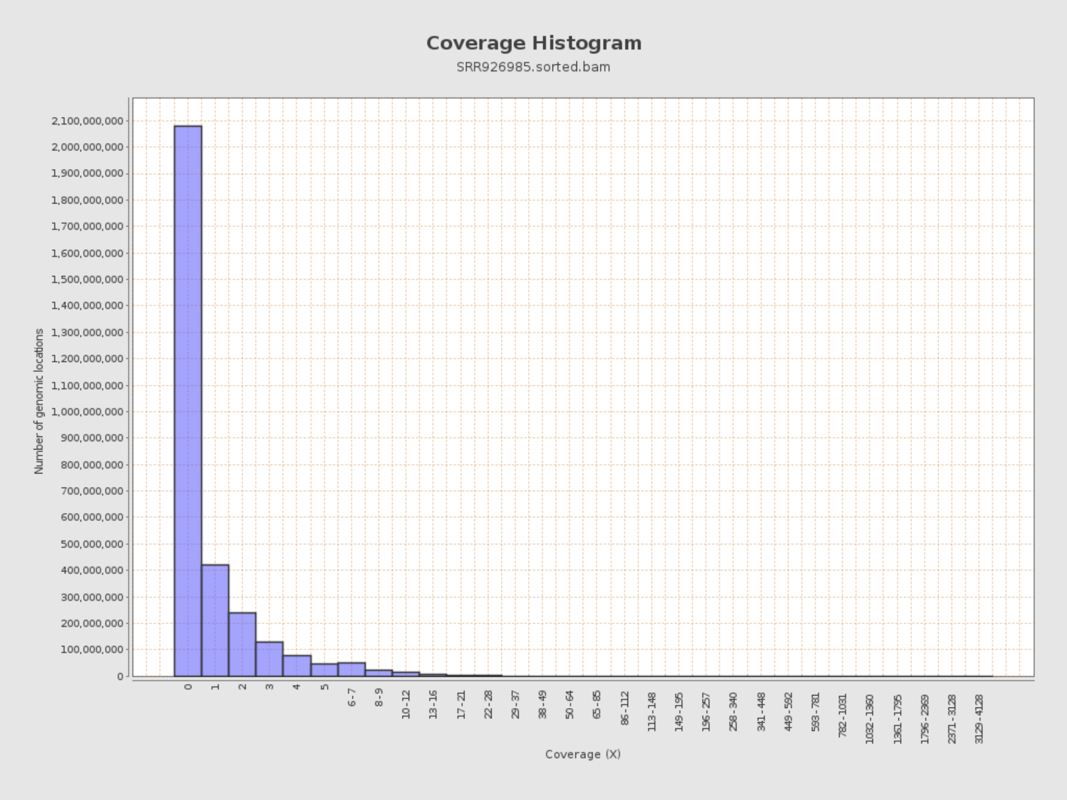
		bases	coverage	deviation
chr1	249250621	234112960	0.9393	4.2331
chr2	243199373	230401401	0.9474	5.6372
chr3	198022430	181367433	0.9159	1.923
chr4	191154276	152736707	0.799	2.6516
chr5	180915260	155200230	0.8579	1.8115
chr6	171115067	152694741	0.8924	3.0034
chr7	159138663	138969632	0.8733	2.4865
chr8	146364022	138764733	0.9481	2.3247
chr9	141213431	120257094	0.8516	4.0438
chr10	135534747	135265202	0.998	4.7357
chr11	135006516	136517229	1.0112	4.7175
chr12	133851895	121167420	0.9052	2.1998
chr13	115169878	80538998	0.6993	1.7112
chr14	107349540	79090538	0.7368	1.7552
chr15	102531392	88620884	0.8643	2.0278
chr16	90354753	89355935	0.9889	4.7573
chr17	81195210	79639573	0.9808	2.6894
chr18	78077248	73156058	0.937	4.2716
chr19	59128983	55140657	0.9325	2.9636
chr20	63025520	70417090	1.1173	2.3824
chr21	48129895	36044474	0.7489	3.1866
chr22	51304566	42413587	0.8267	2.1157
chrMT	16571	15358552	926.8331	660.8766
chrX	155270560	146562513	0.9439	2.4361

chrY	59373566	4653522	0.0784	2.2056

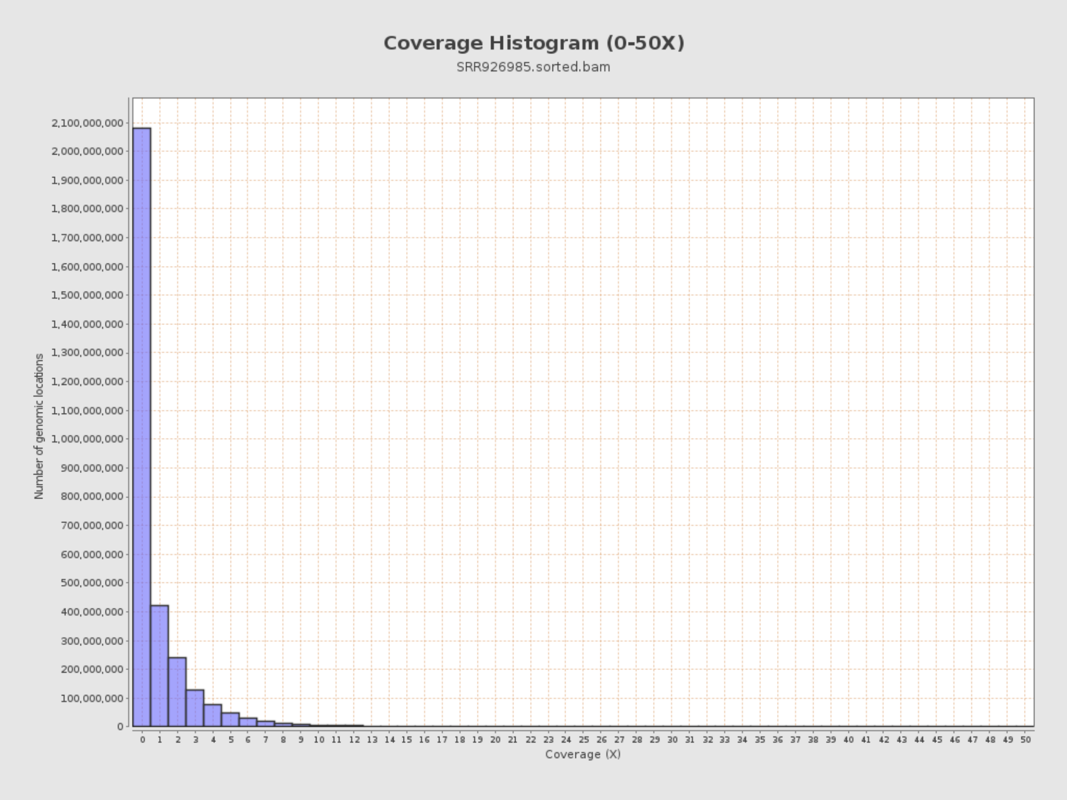
3. Results : Coverage across reference



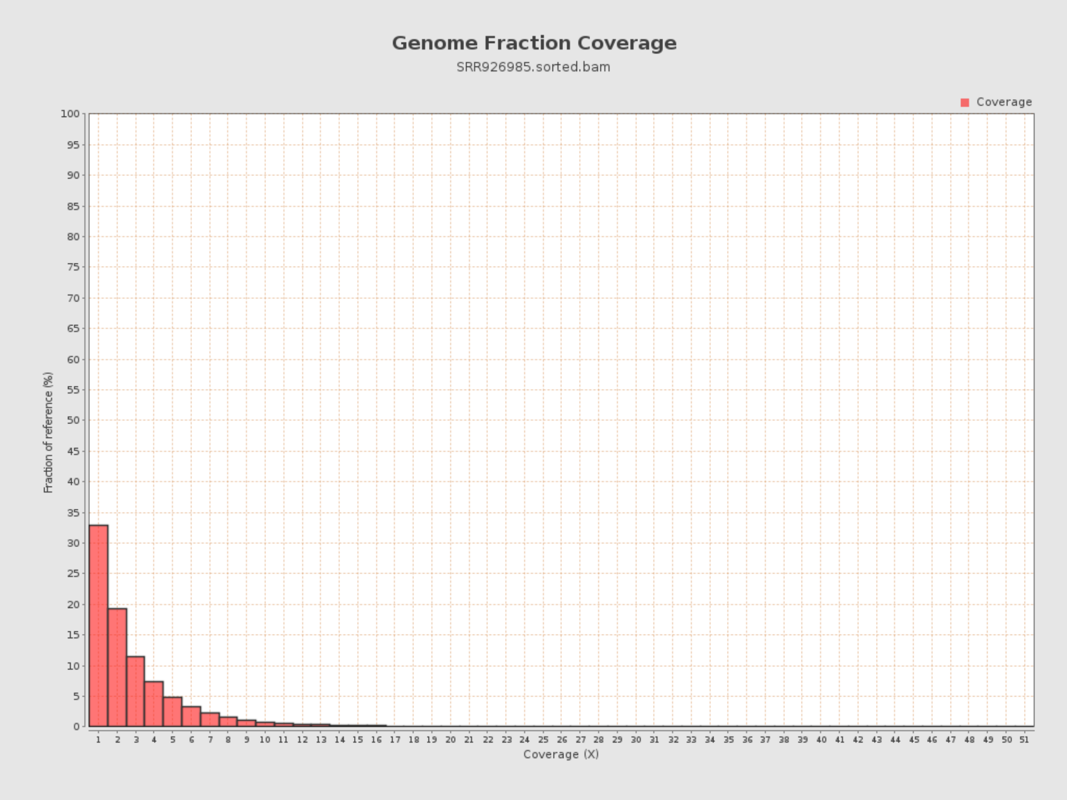
4. Results : Coverage Histogram



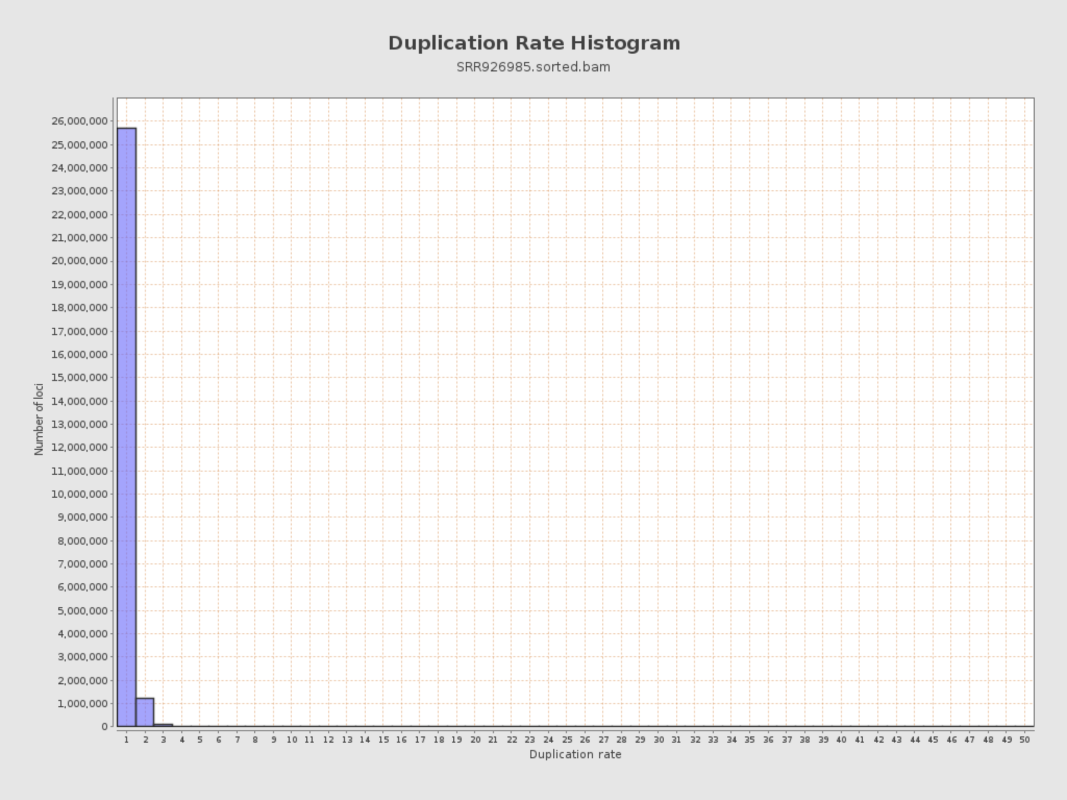
5. Results : Coverage Histogram (0-50X)



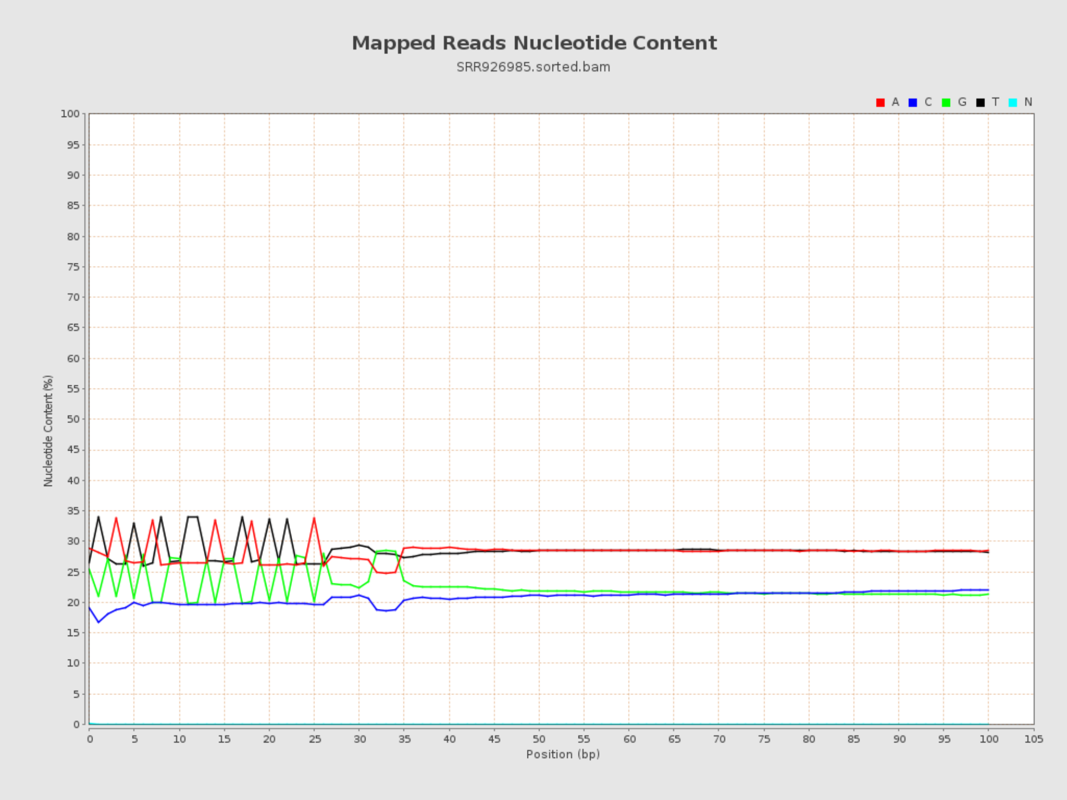
6. Results : Genome Fraction Coverage



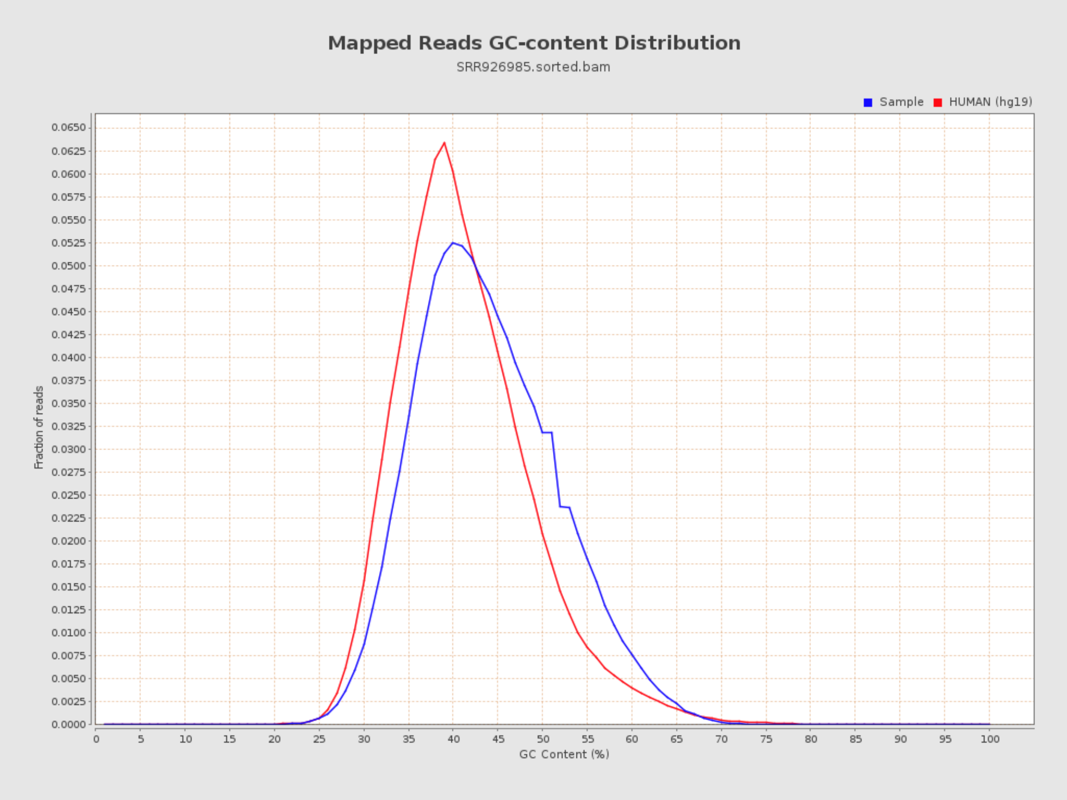
7. Results : Duplication Rate Histogram



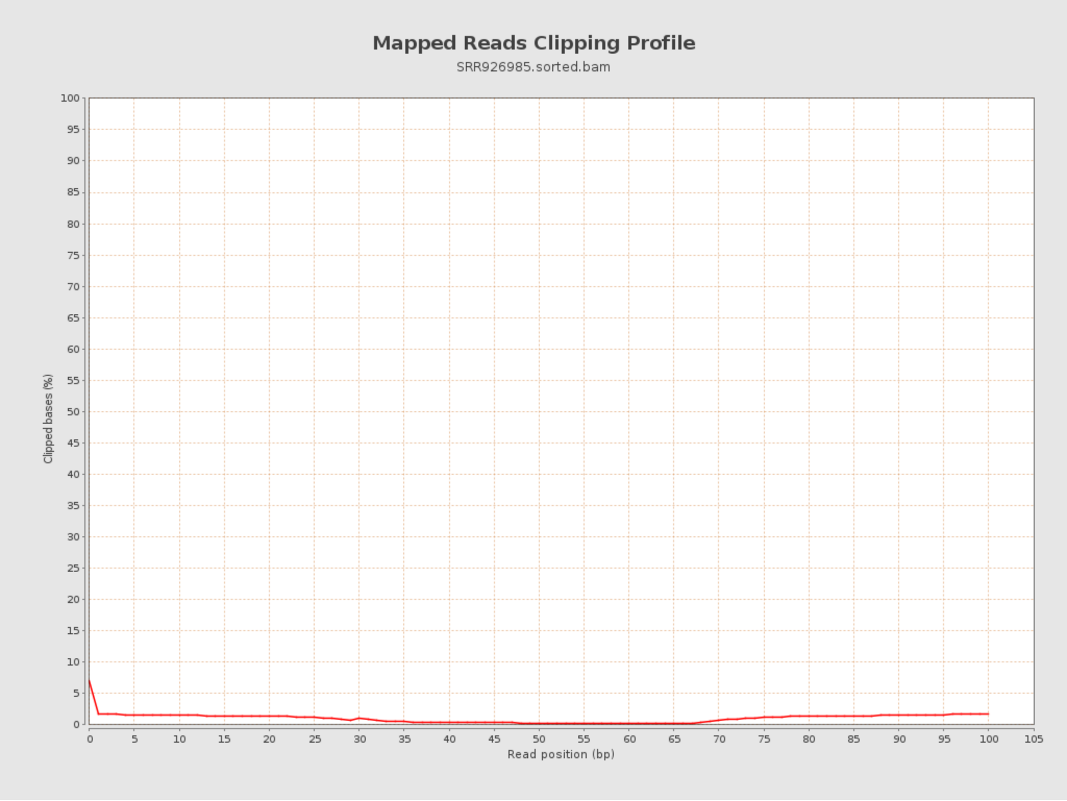
8. Results : Mapped Reads Nucleotide Content



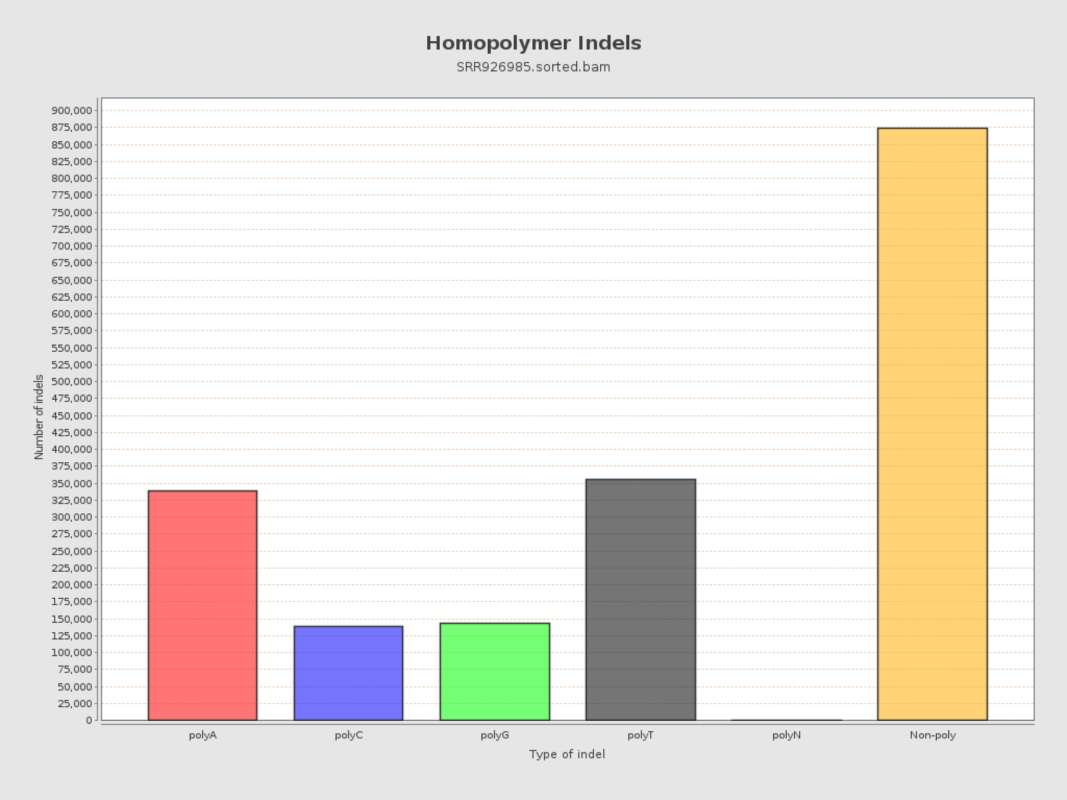
9. Results : Mapped Reads GC-content Distribution



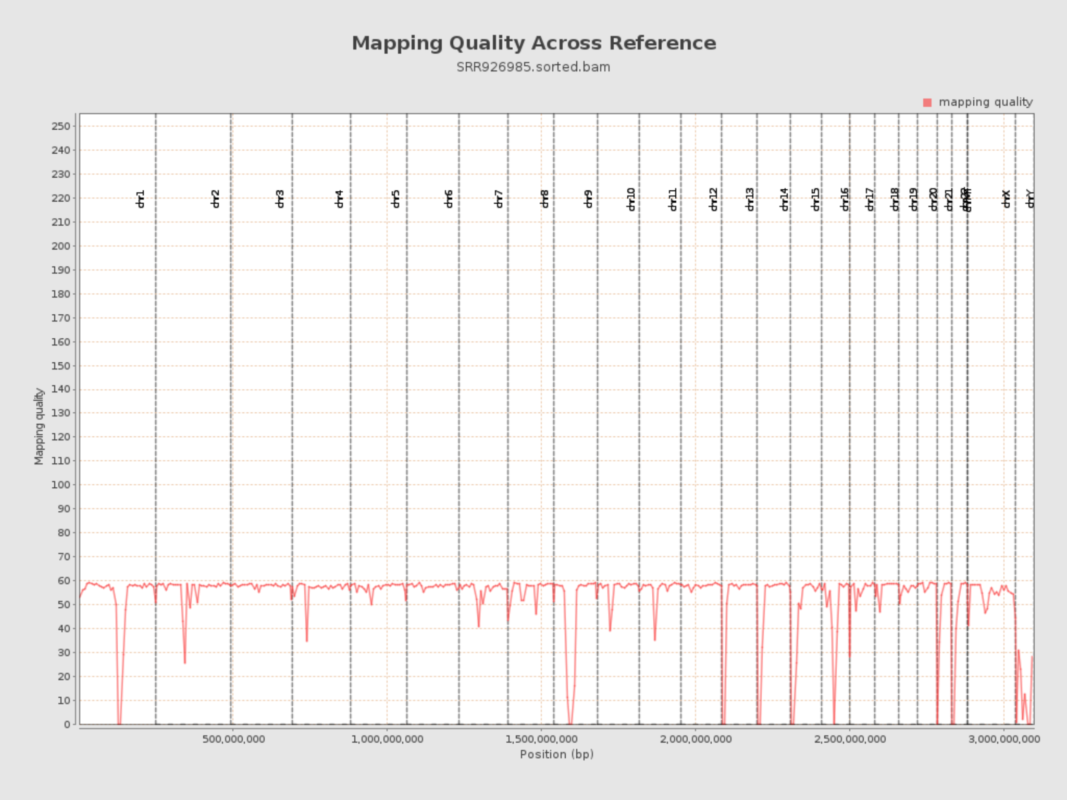
10. Results : Mapped Reads Clipping Profile



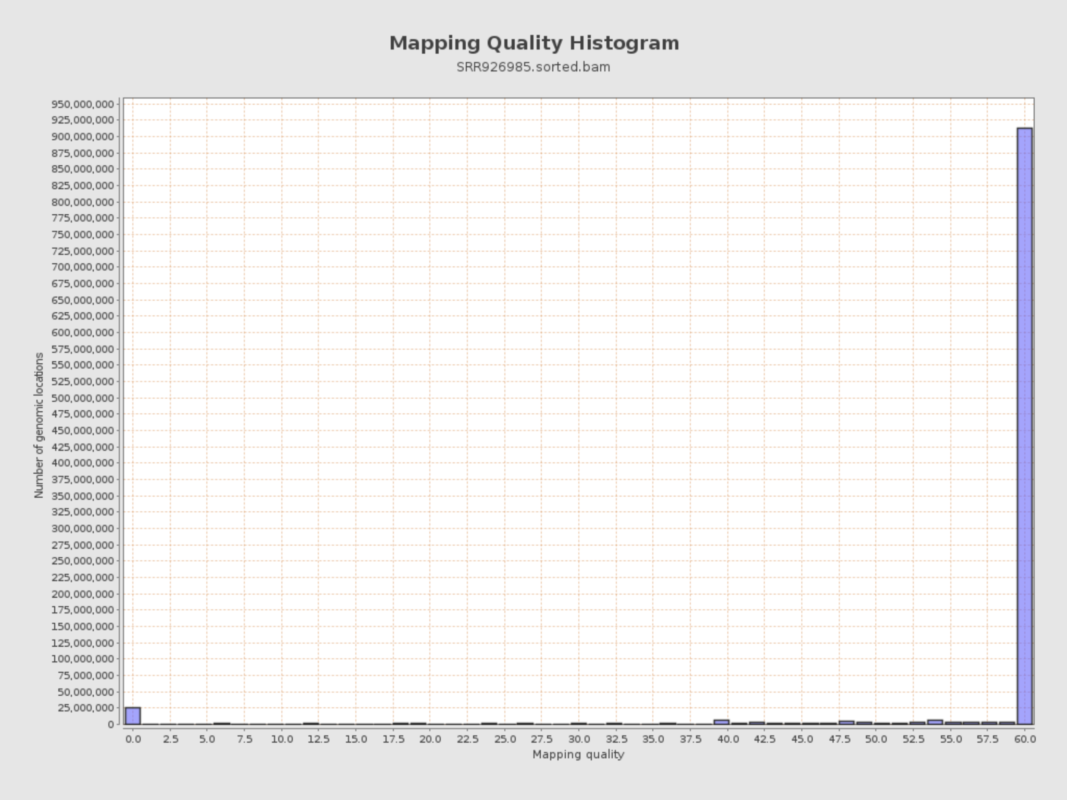
11. Results : Homopolymer Indels



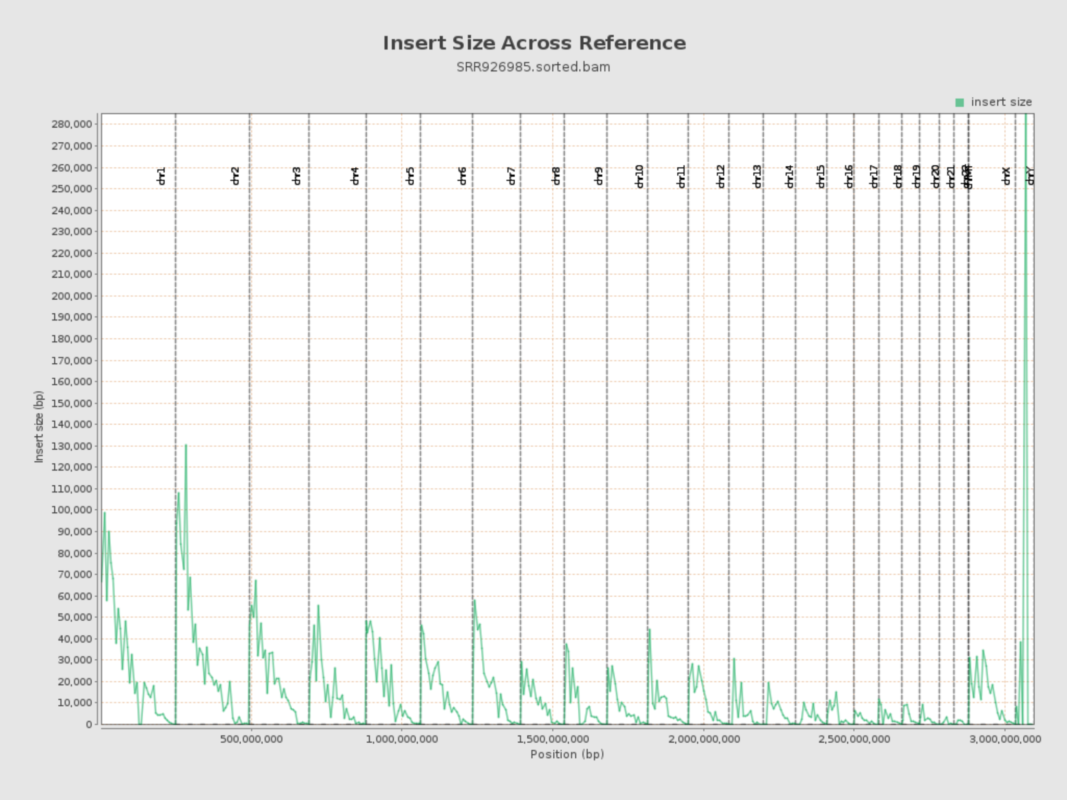
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram