Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 11:17:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926975.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_SRR926975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926975_1.fastq.gz SRR926975_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 11:17:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,704,816
Mapped reads	24,396,698 / 98.75%
Unmapped reads	308,118 / 1.25%
Mapped paired reads	24,396,698 / 98.75%
Mapped reads, first in pair	12,251,591 / 49.59%
Mapped reads, second in pair	12,145,107 / 49.16%
Mapped reads, both in pair	24,220,652 / 98.04%
Mapped reads, singletons	176,046 / 0.71%
Secondary alignments	0
Supplementary alignments	115,093 / 0.47%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	1,778,246 / 7.2%
Duplication rate	5.56%
Clipped reads	4,516,910 / 18.28%

2.2. ACGT Content

Number/percentage of A's	651,300,135 / 27.8%
Number/percentage of C's	494,803,120 / 21.12%
Number/percentage of T's	657,146,269 / 28.05%
Number/percentage of G's	539,417,723 / 23.02%
Number/percentage of N's	209,785 / 0.01%

GC Percentage	44.14%

2.3. Coverage

Mean	0.7574
Standard Deviation	3.7244

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	57,515.21
Standard Deviation	2,463,388.56
P25/Median/P75	158 / 195 / 248

2.6. Mismatches and indels

General error rate	1%
Mismatches	22,705,697
Insertions	374,102
Mapped reads with at least one insertion	1.51%
Deletions	1,268,372
Mapped reads with at least one deletion	5.06%
Homopolymer indels	52.93%

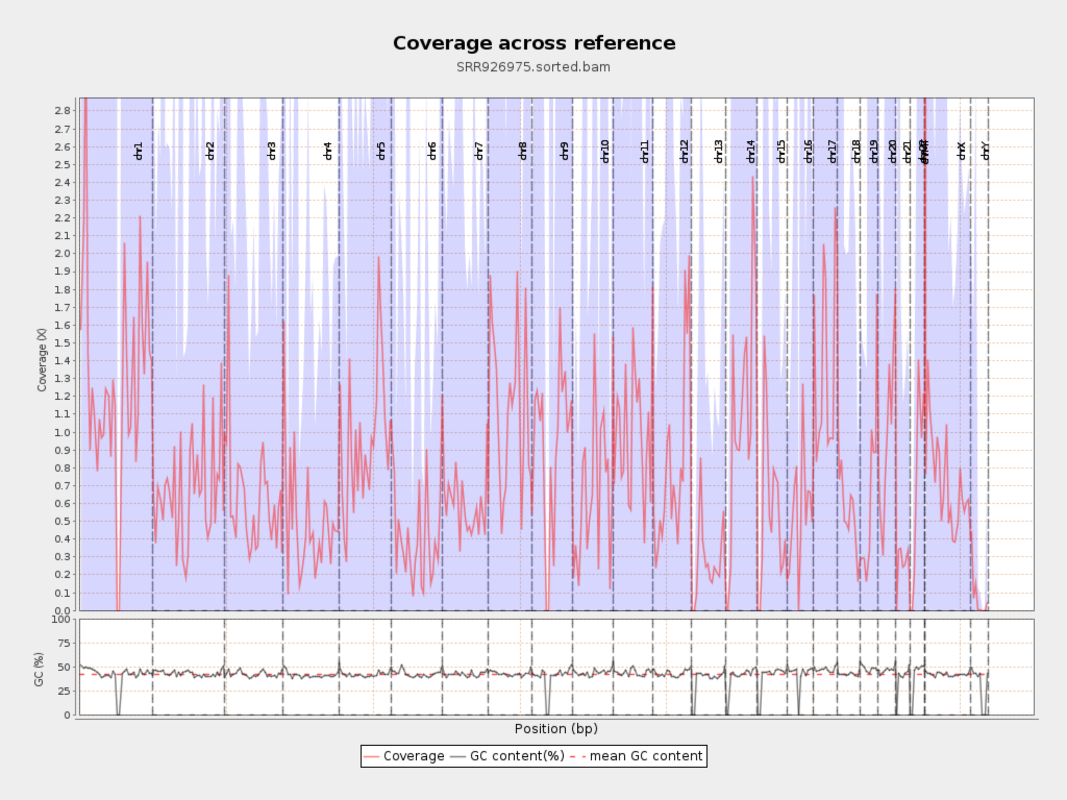
2.7. Chromosome stats

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

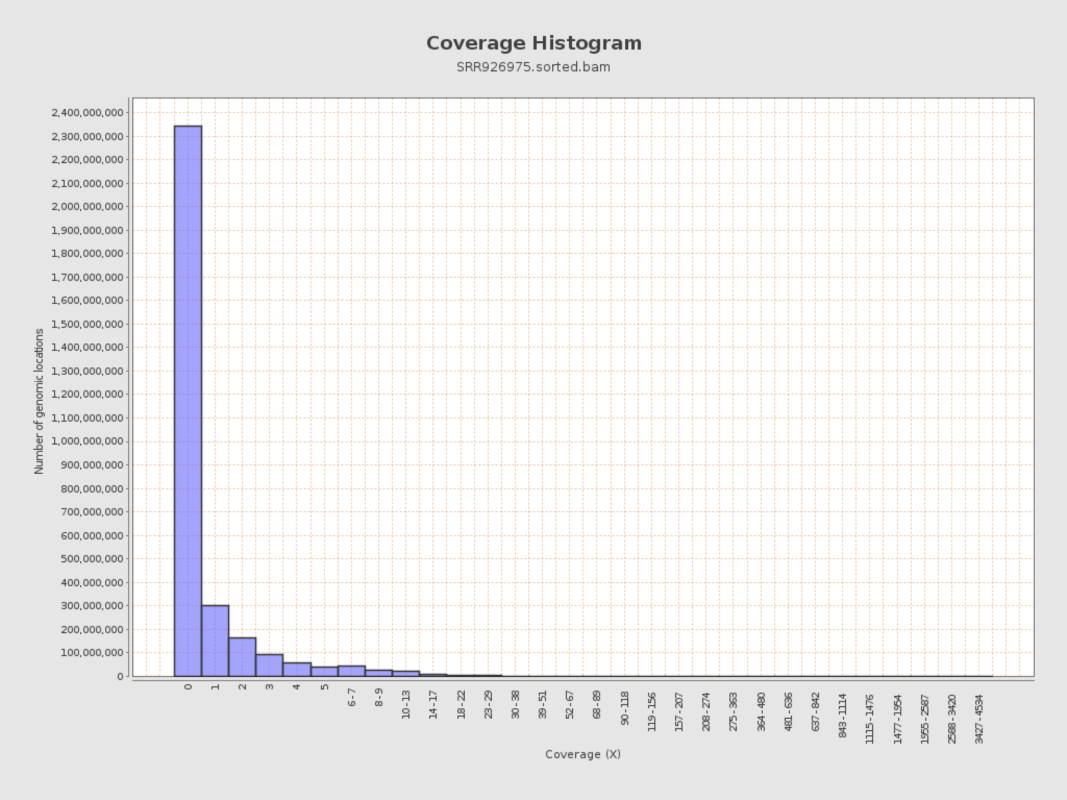
		bases	coverage	deviation
chr1	249250621	323106513	1.2963	5.8078
chr2	243199373	163698219	0.6731	4.3974
chr3	198022430	127163850	0.6422	1.8991
chr4	191154276	92849848	0.4857	1.9109
chr5	180915260	174155311	0.9626	2.2857
chr6	171115067	68682846	0.4014	2.5746
chr7	159138663	95822379	0.6021	2.8609
chr8	146364022	167989977	1.1478	2.9661
chr9	141213431	128346736	0.9089	6.1519
chr10	135534747	88599200	0.6537	5.0764
chr11	135006516	131628152	0.975	4.1446
chr12	133851895	107181412	0.8007	2.3041
chr13	115169878	32856199	0.2853	1.2153
chr14	107349540	115022494	1.0715	2.6784
chr15	102531392	56516113	0.5512	1.8257
chr16	90354753	48541797	0.5372	2.7343
chr17	81195210	113858836	1.4023	5.4755
chr18	78077248	42956250	0.5502	5.8851
chr19	59128983	34491389	0.5833	3.4137
chr20	63025520	60570644	0.961	2.6455
chr21	48129895	12926719	0.2686	2.349
chr22	51304566	37400267	0.729	2.203
chrMT	16571	4553292	274.7747	210.8231
chrX	155270560	111389652	0.7174	2.2398

chrY	59373566	4342362	0.0731	1.2896

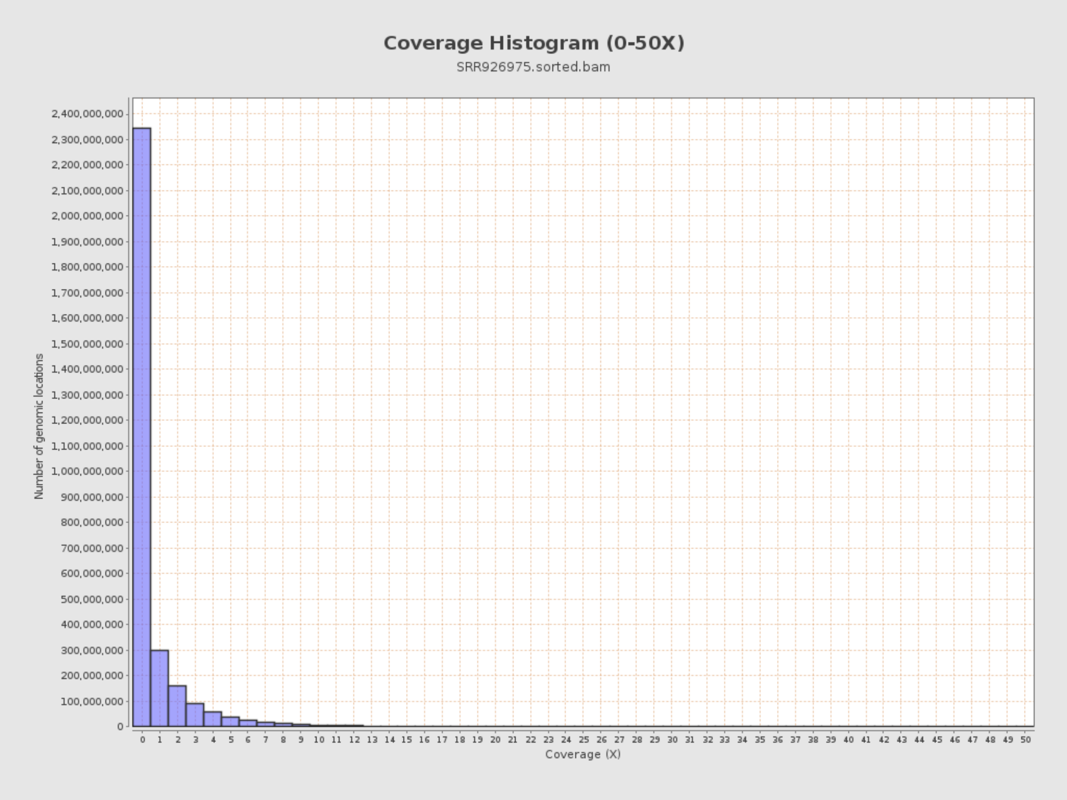
3. Results : Coverage across reference



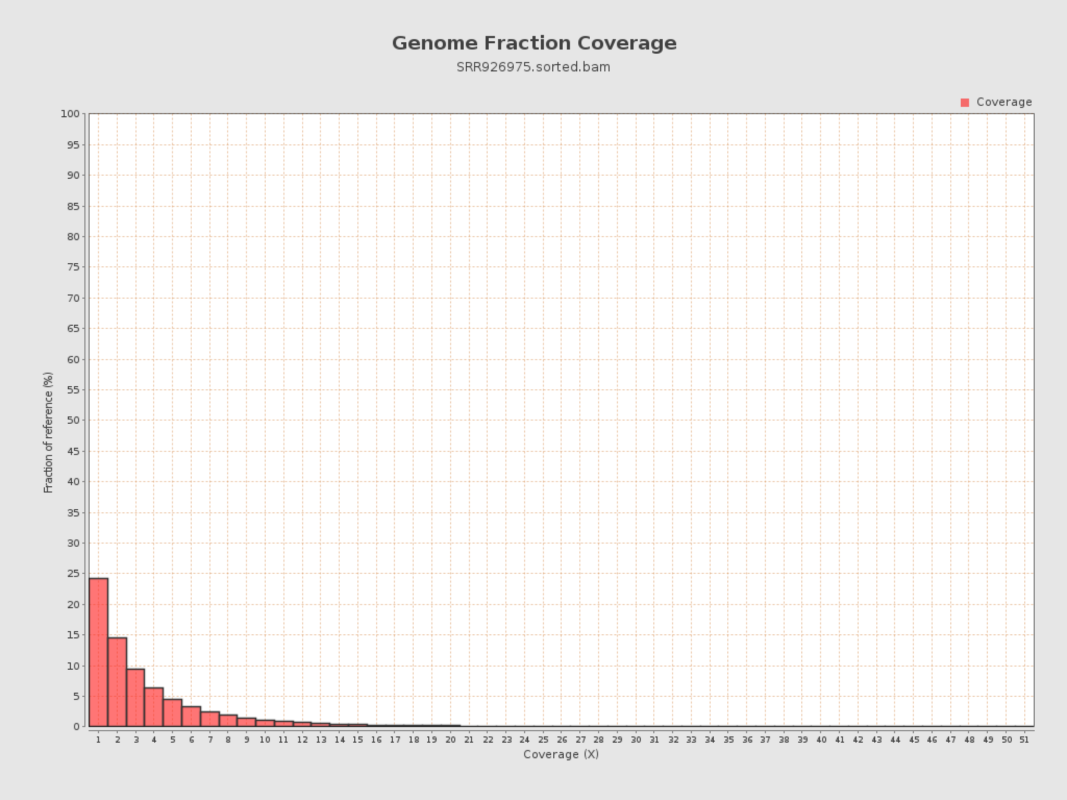
4. Results : Coverage Histogram



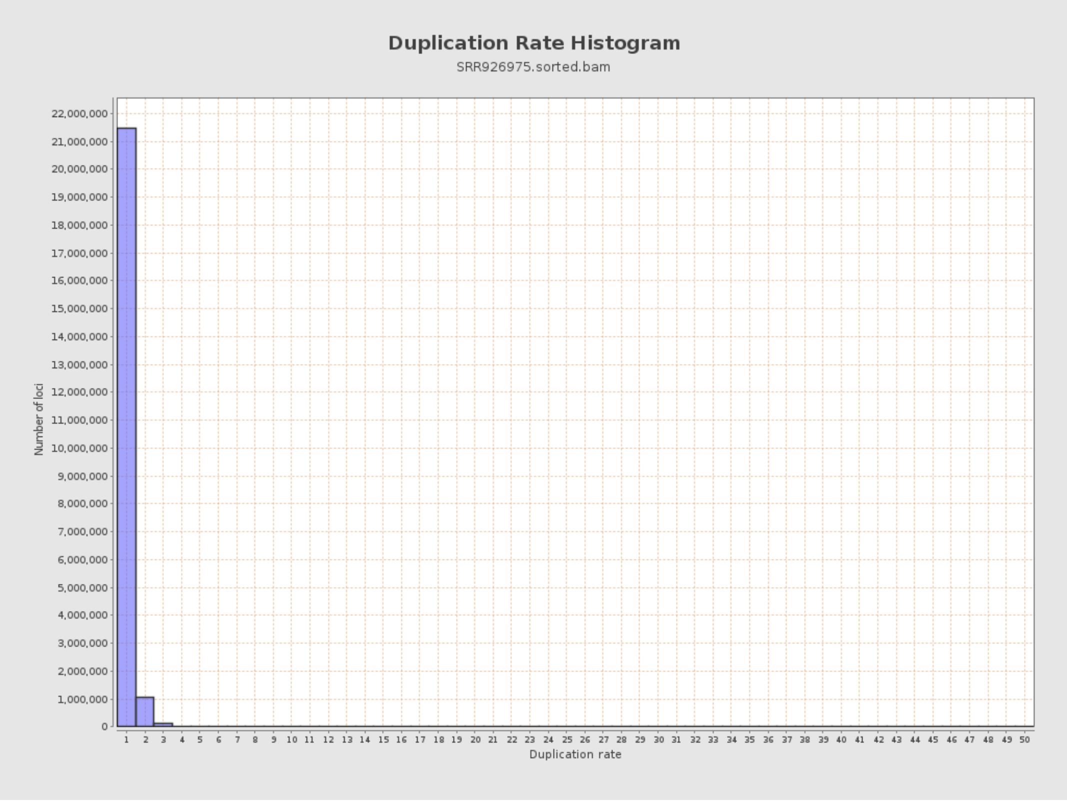
5. Results : Coverage Histogram (0-50X)



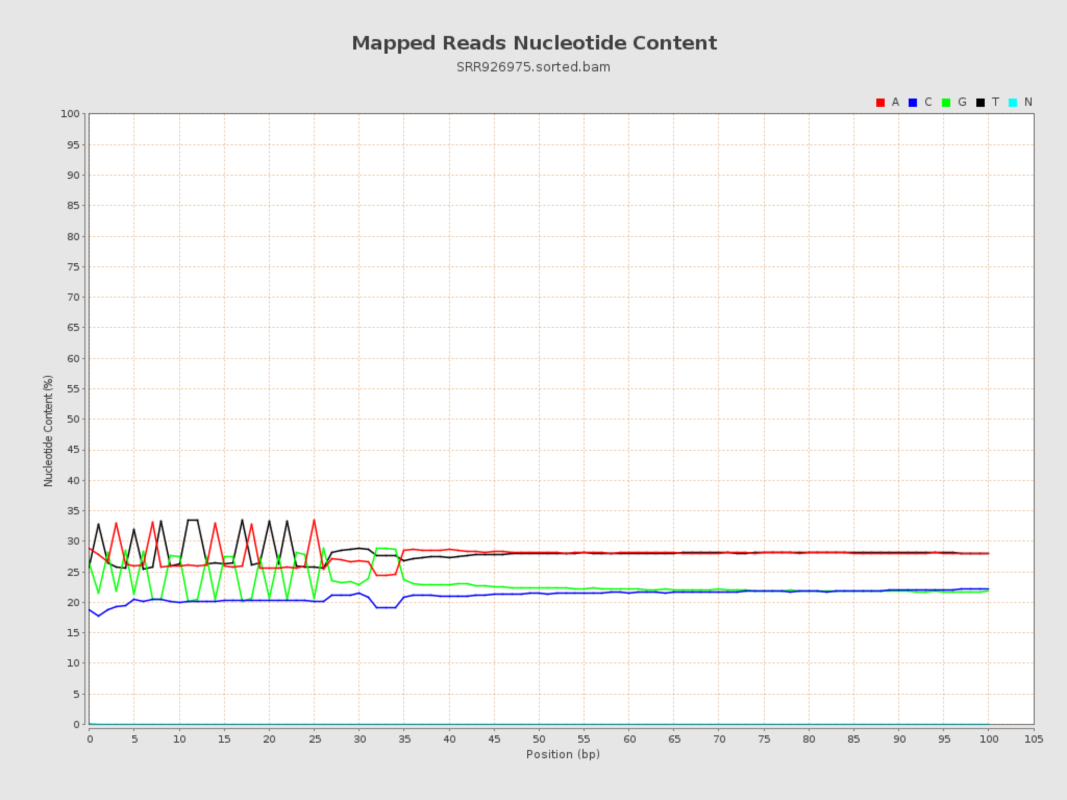
6. Results : Genome Fraction Coverage



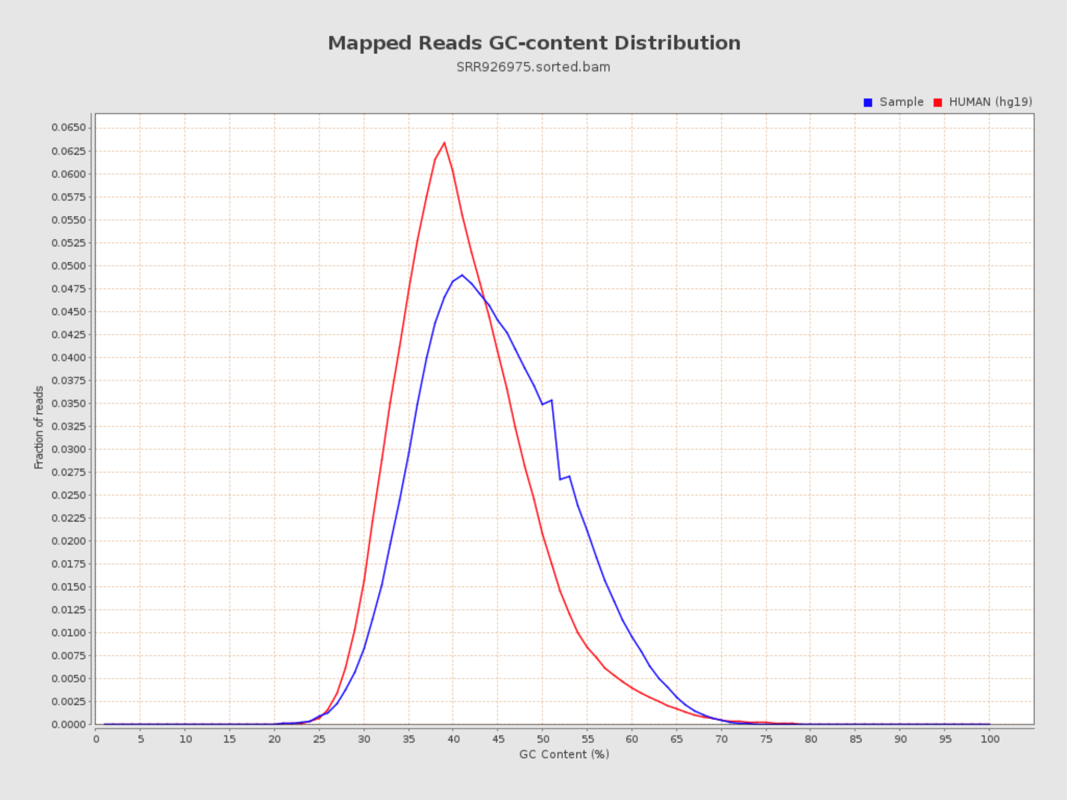
7. Results : Duplication Rate Histogram



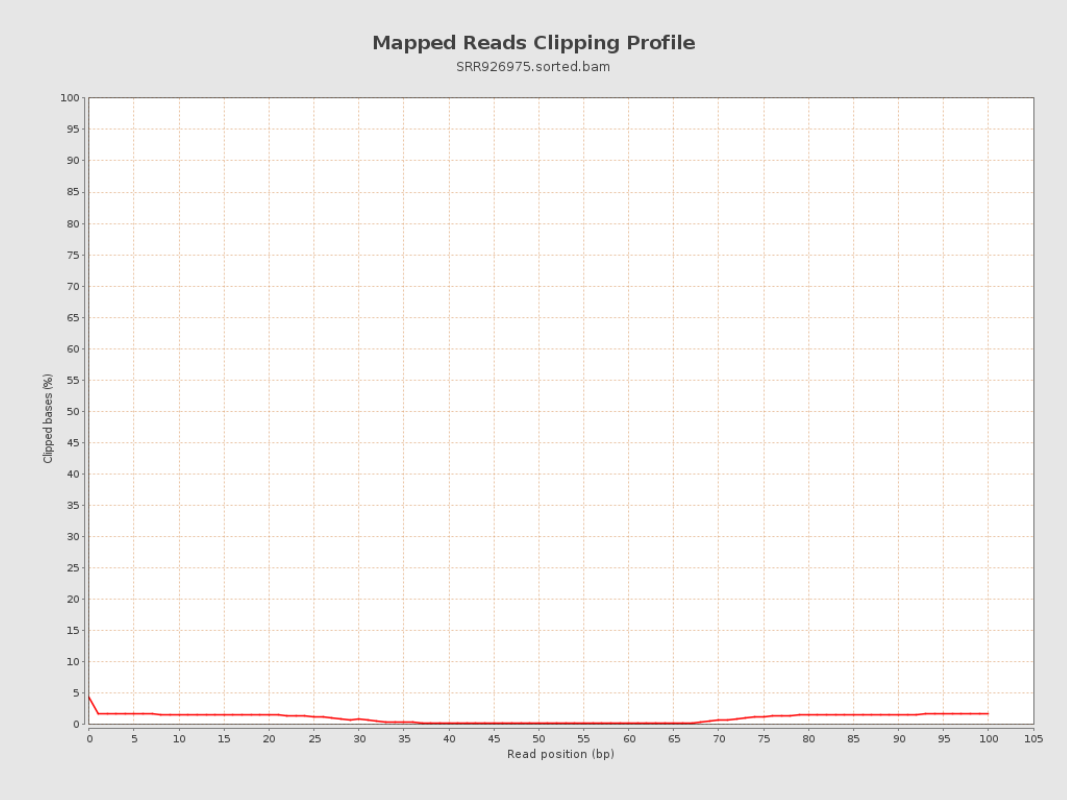
8. Results : Mapped Reads Nucleotide Content



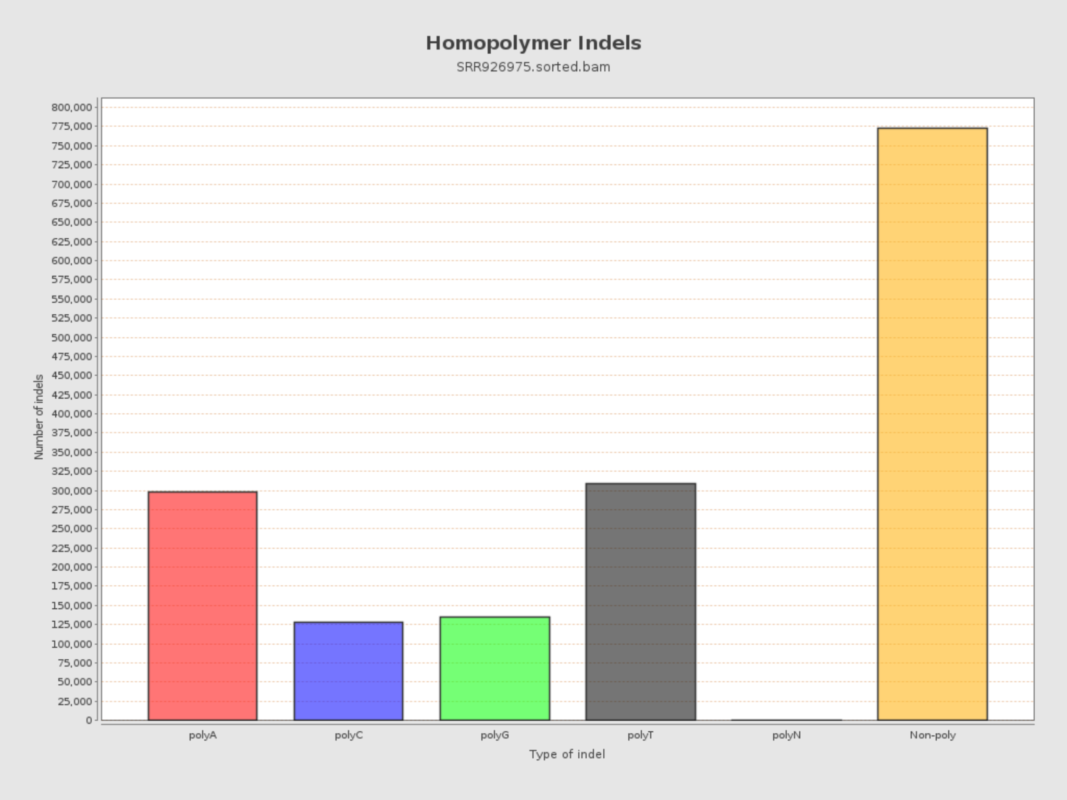
9. Results : Mapped Reads GC-content Distribution



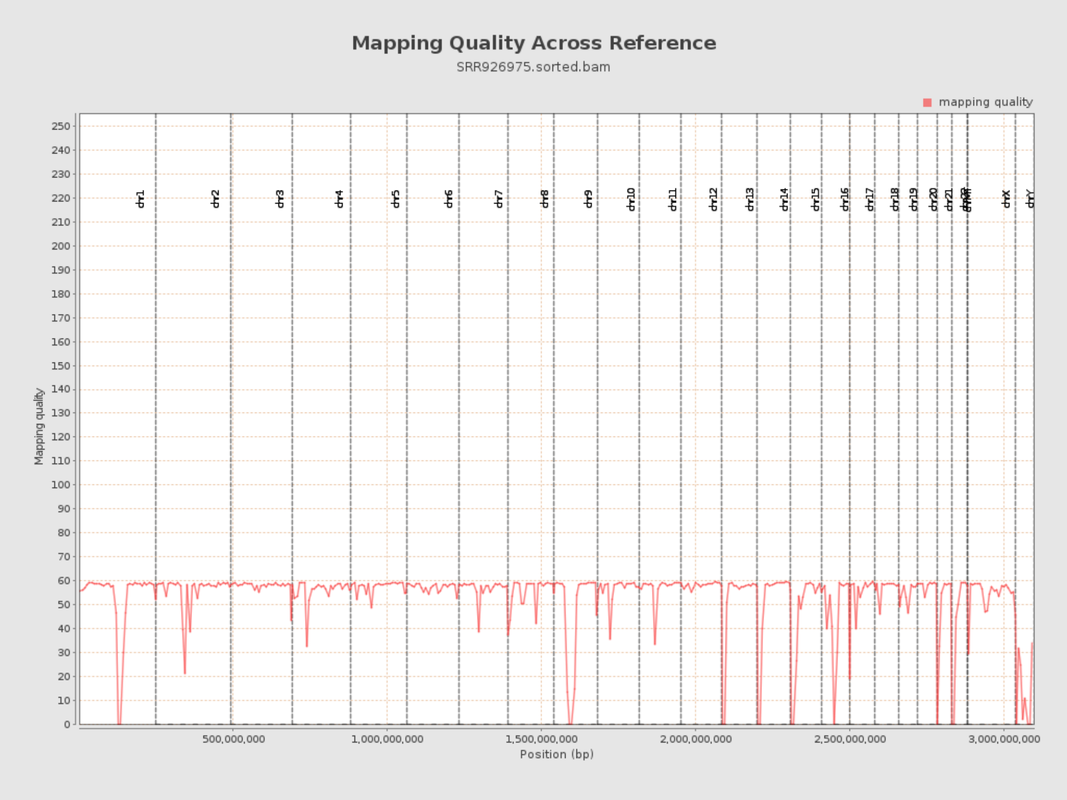
10. Results : Mapped Reads Clipping Profile



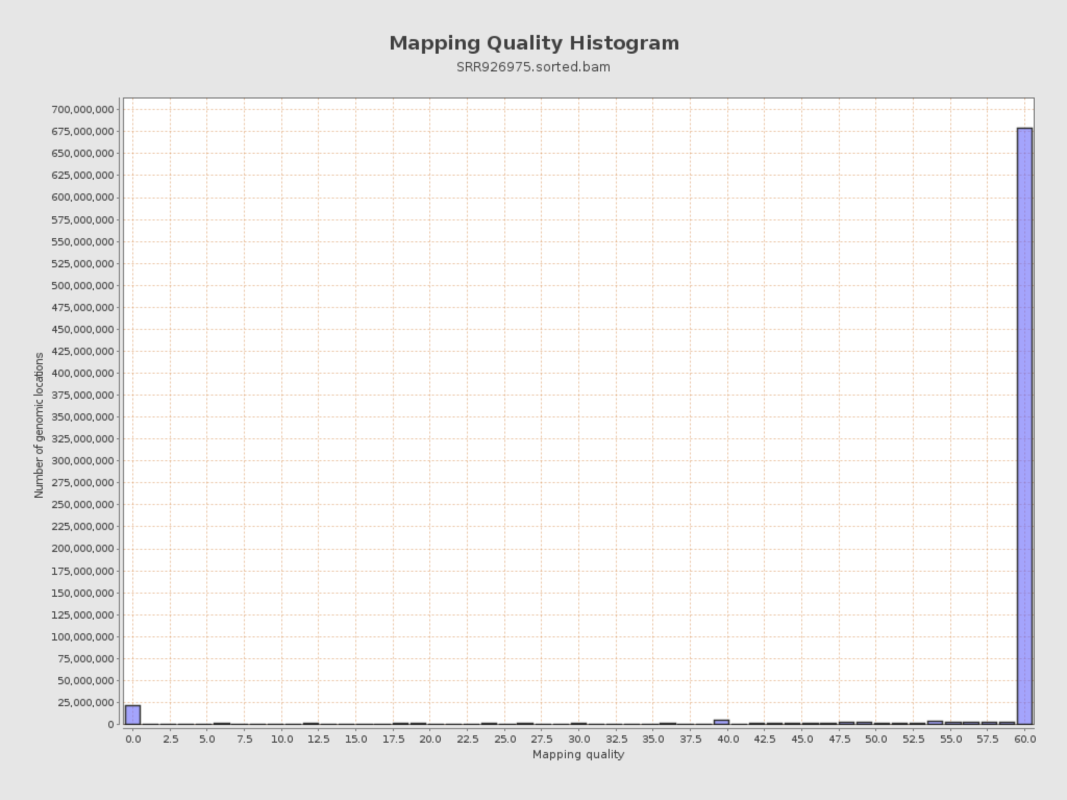
11. Results : Homopolymer Indels



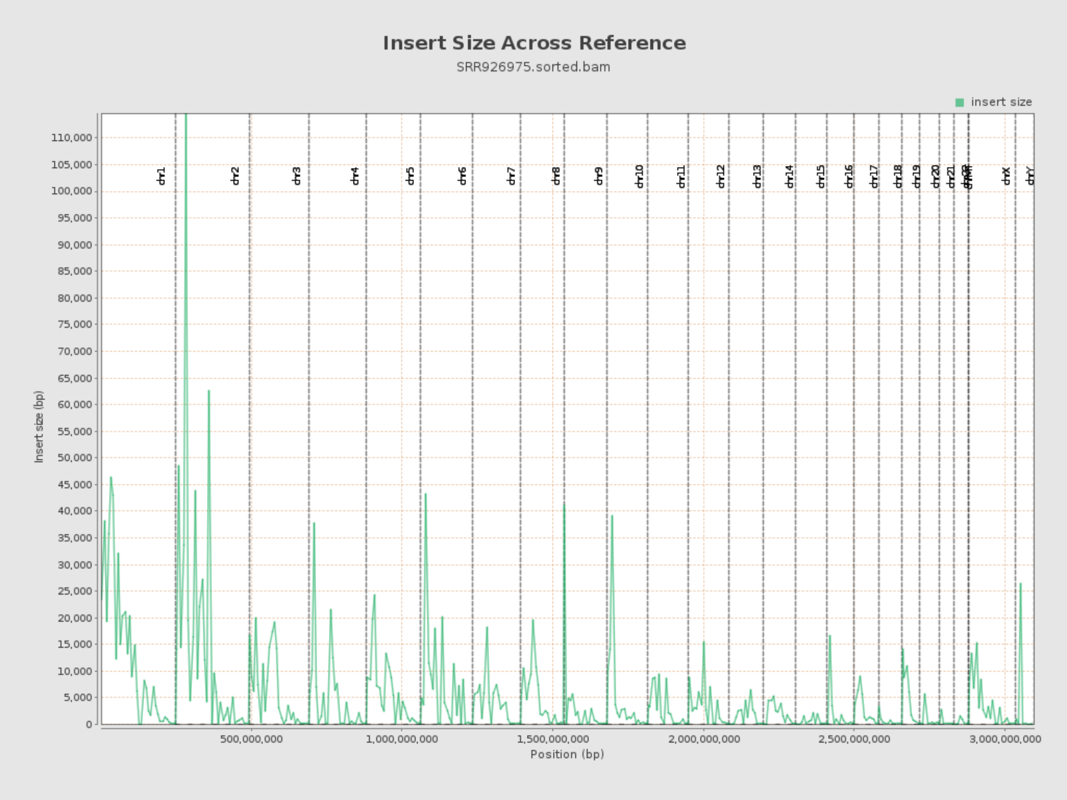
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram