Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 11:43:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926976.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_SRR926976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926976_1.fastq.gz SRR926976_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 11:43:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,175,238
Mapped reads	20,647,297 / 97.51%
Unmapped reads	527,941 / 2.49%
Mapped paired reads	20,647,297 / 97.51%
Mapped reads, first in pair	10,375,414 / 49%
Mapped reads, second in pair	10,271,883 / 48.51%
Mapped reads, both in pair	20,311,232 / 95.92%
Mapped reads, singletons	336,065 / 1.59%
Secondary alignments	0
Supplementary alignments	943,004 / 4.45%
Read min/max/mean length	30 / 101 / 102.84
Duplicated reads (estimated)	2,117,244 / 10%
Duplication rate	8.24%
Clipped reads	10,703,317 / 50.55%

2.2. ACGT Content

Number/percentage of A's	527,955,464 / 28.62%
Number/percentage of C's	354,731,130 / 19.23%
Number/percentage of T's	541,798,365 / 29.37%
Number/percentage of G's	420,230,425 / 22.78%
Number/percentage of N's	130,781 / 0.01%

GC Percentage	42.01%

2.3. Coverage

Mean	0.5964
Standard Deviation	2.3851

2.4. Mapping Quality

Mean Mapping Quality	52.1

2.5. Insert size

Mean	473,776.12
Standard Deviation	6,751,376.7
P25/Median/P75	122 / 159 / 214

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	18,108,647
Insertions	335,481
Mapped reads with at least one insertion	1.6%
Deletions	986,484
Mapped reads with at least one deletion	4.65%
Homopolymer indels	51.47%

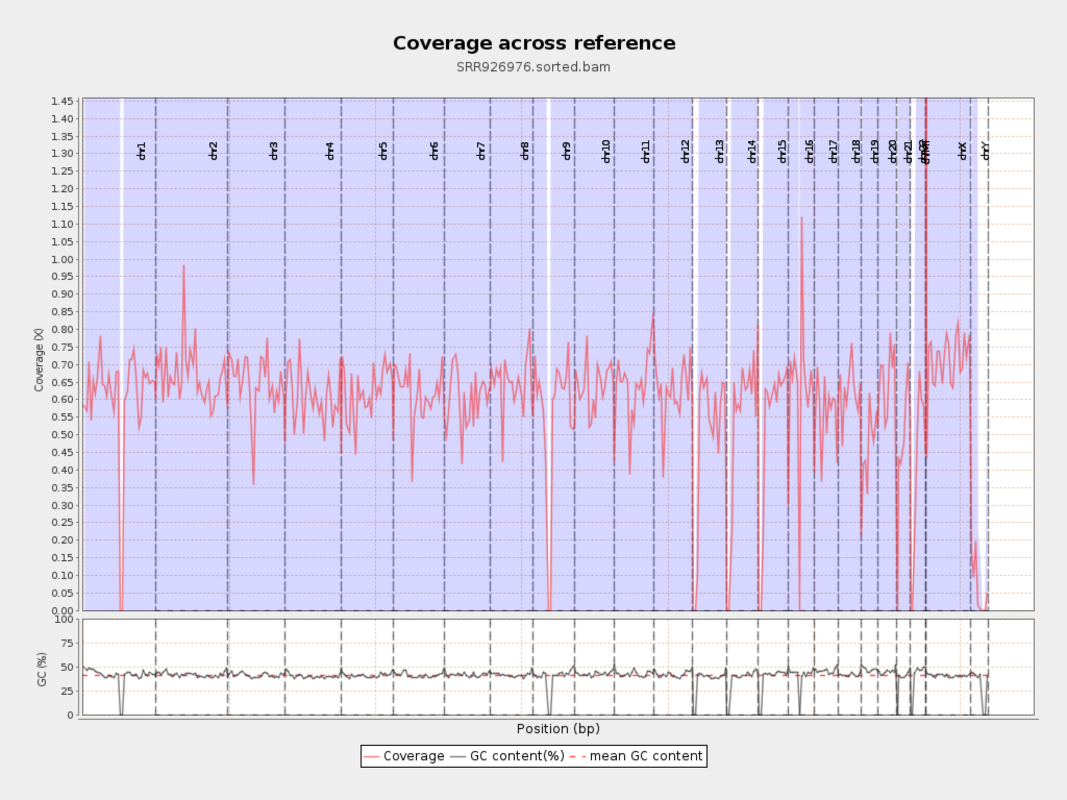
2.7. Chromosome stats

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

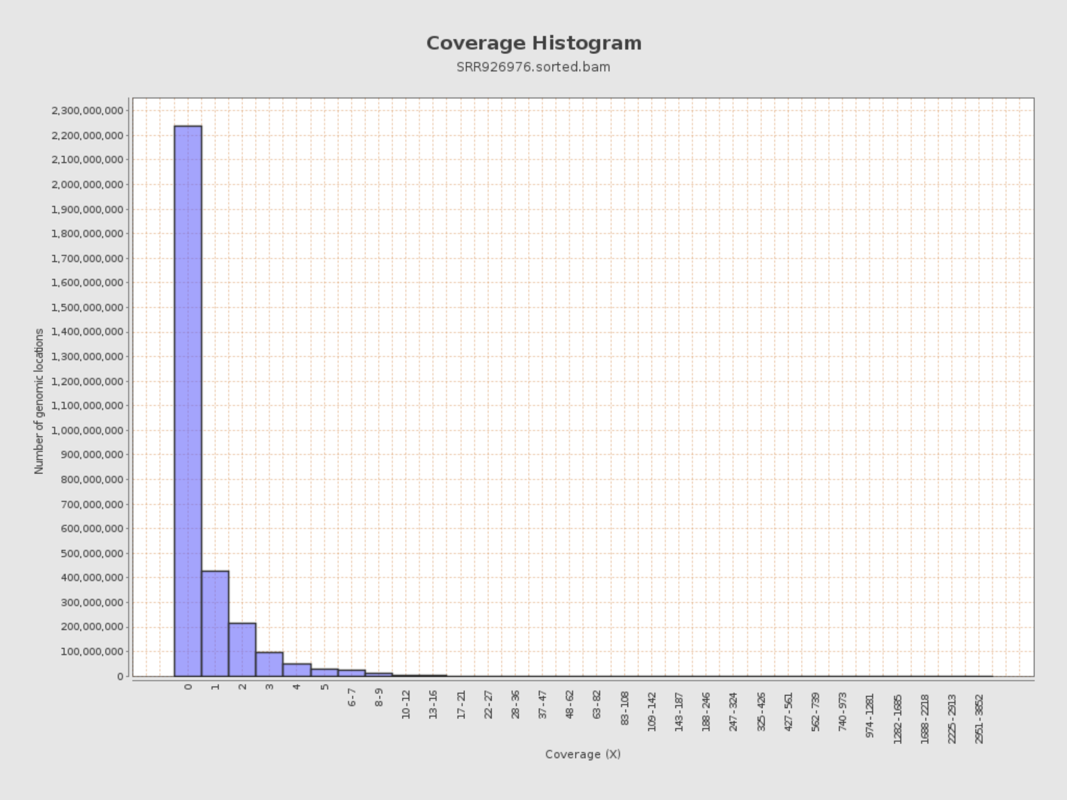
		bases	coverage	deviation
chr1	249250621	150694147	0.6046	2.6243
chr2	243199373	163111874	0.6707	4.2355
chr3	198022430	127407151	0.6434	1.4081
chr4	191154276	117122520	0.6127	2.1547
chr5	180915260	112404300	0.6213	1.3737
chr6	171115067	106205267	0.6207	1.936
chr7	159138663	95416962	0.5996	2.1131
chr8	146364022	95194251	0.6504	1.6897
chr9	141213431	77915189	0.5518	2.9163
chr10	135534747	86477661	0.638	2.9065
chr11	135006516	86635719	0.6417	2.1763
chr12	133851895	84332181	0.63	1.8179
chr13	115169878	56611464	0.4915	1.2948
chr14	107349540	56090949	0.5225	1.37
chr15	102531392	52698435	0.514	1.3686
chr16	90354753	56345460	0.6236	4.4266
chr17	81195210	46119610	0.568	2.0589
chr18	78077248	48544141	0.6217	2.9996
chr19	59128983	27753789	0.4694	1.8162
chr20	63025520	41347744	0.656	1.5315
chr21	48129895	23147164	0.4809	1.8283
chr22	51304566	20648364	0.4025	1.1975
chrMT	16571	216001	13.0349	12.2802
chrX	155270560	110207511	0.7098	1.6921

chrY	59373566	3666885	0.0618	2.061

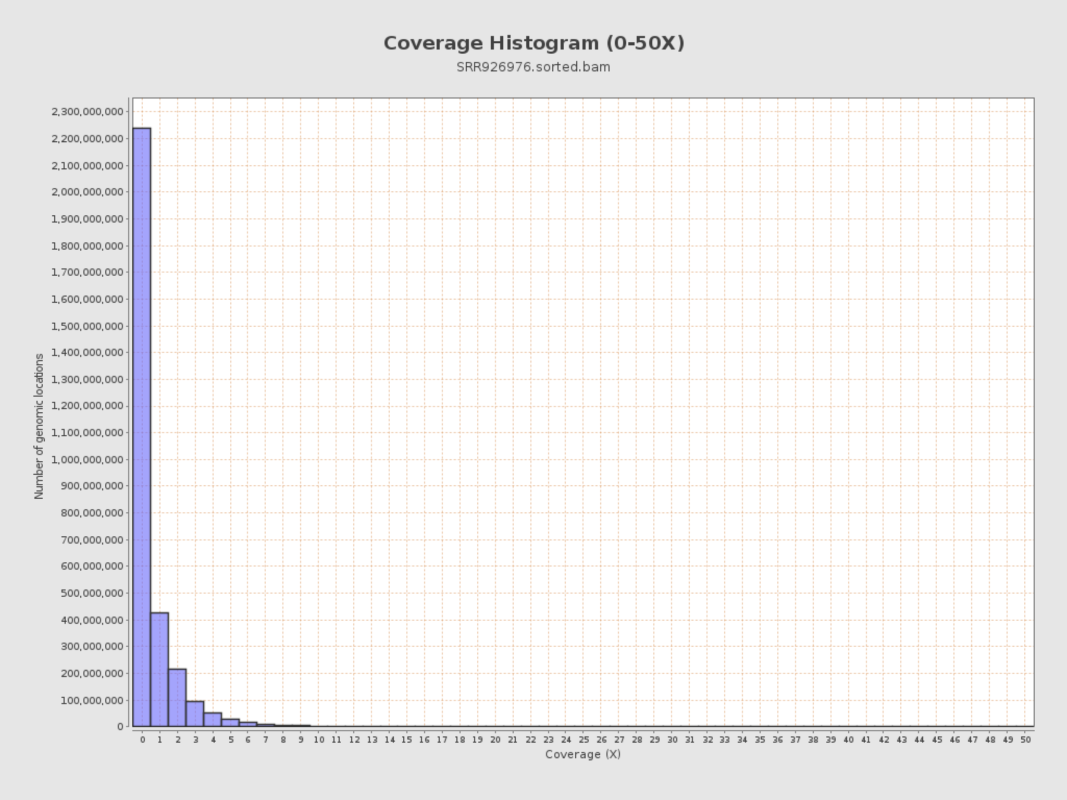
3. Results : Coverage across reference



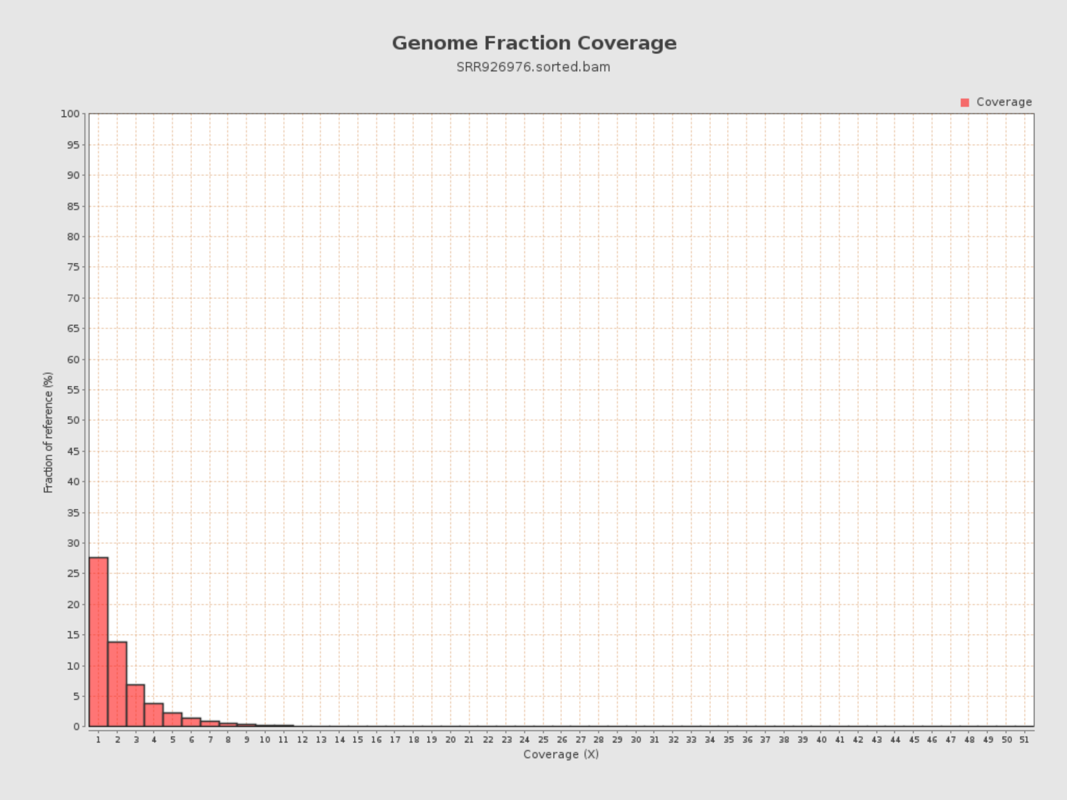
4. Results : Coverage Histogram



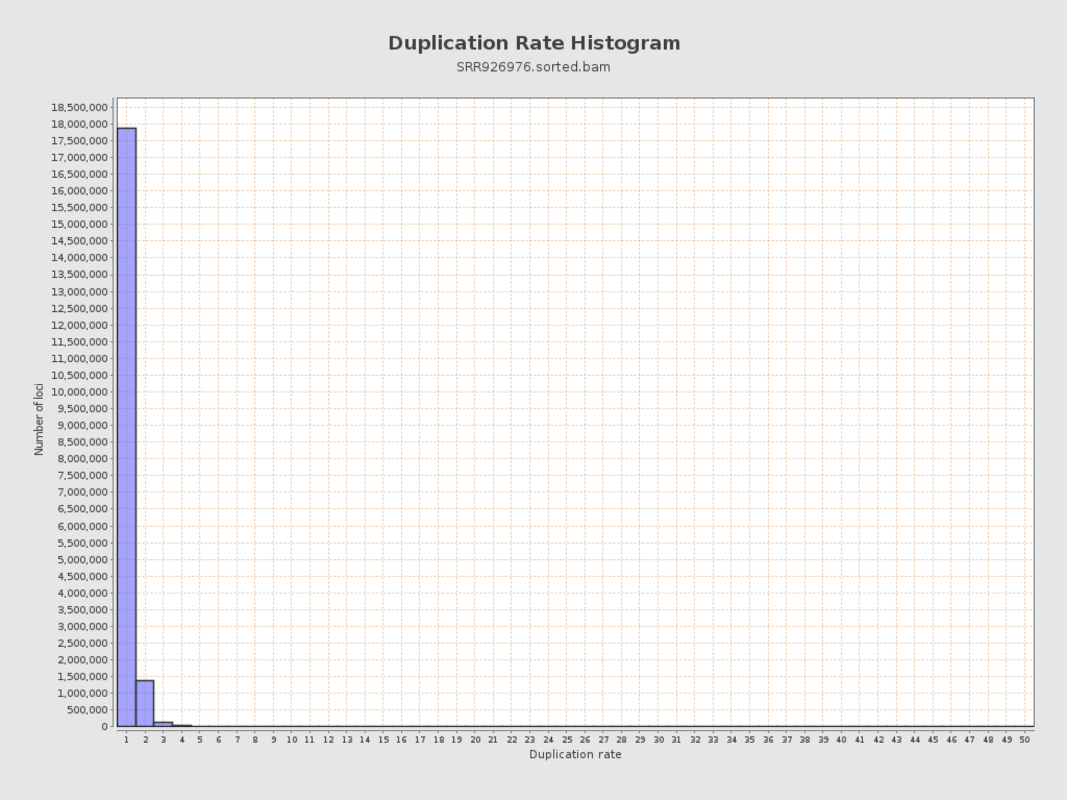
5. Results : Coverage Histogram (0-50X)



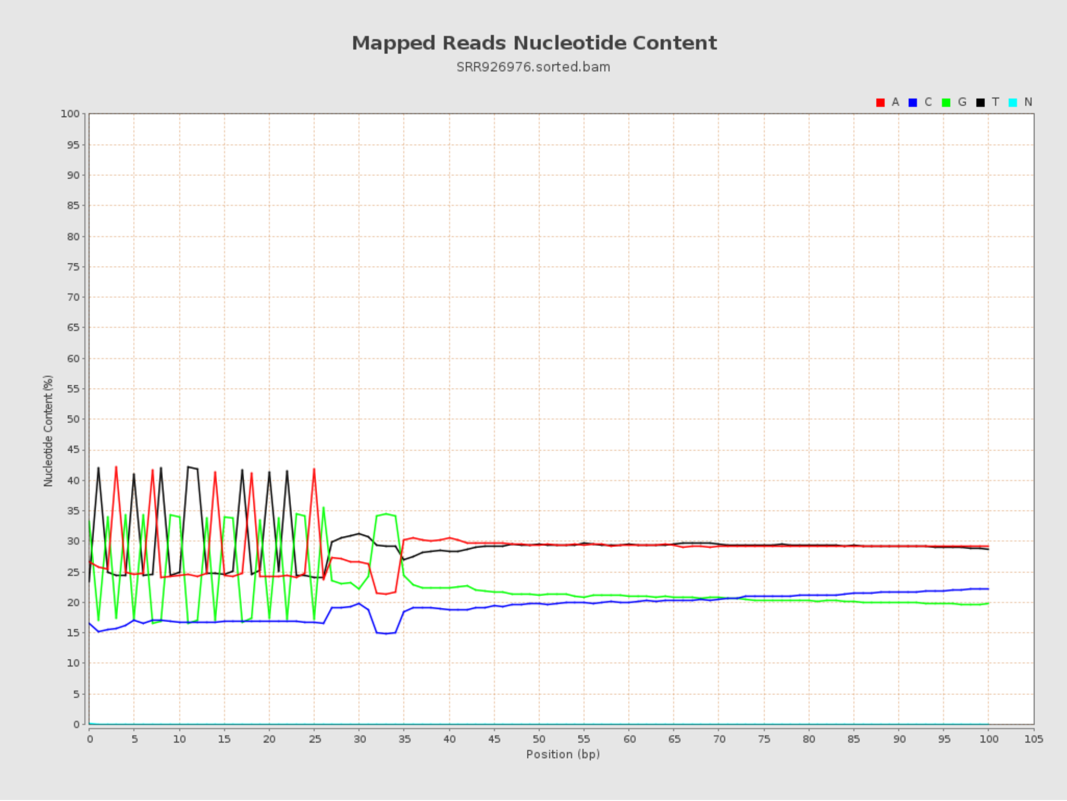
6. Results : Genome Fraction Coverage



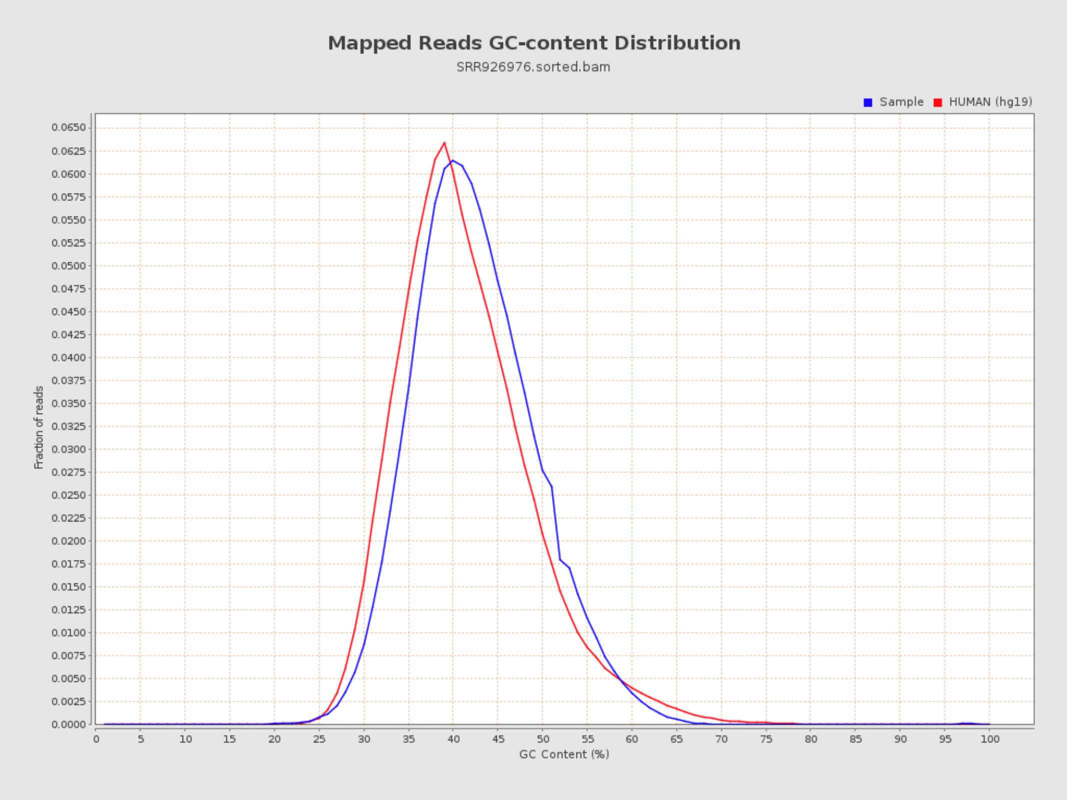
7. Results : Duplication Rate Histogram



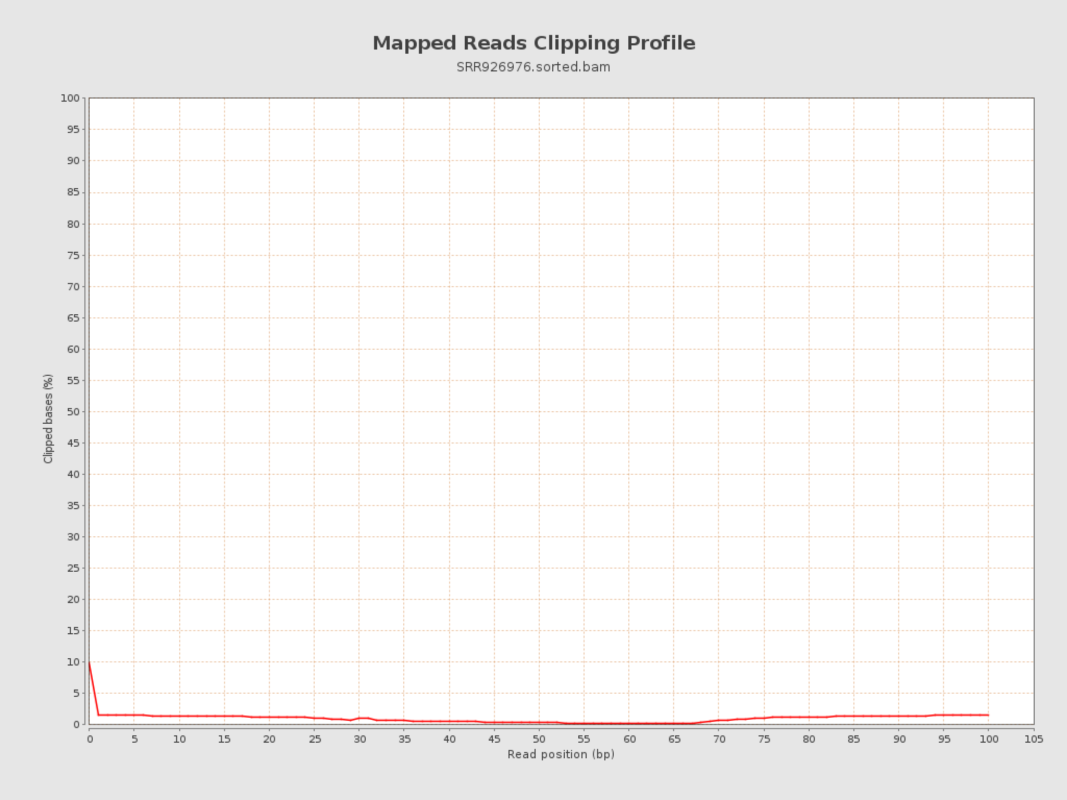
8. Results : Mapped Reads Nucleotide Content



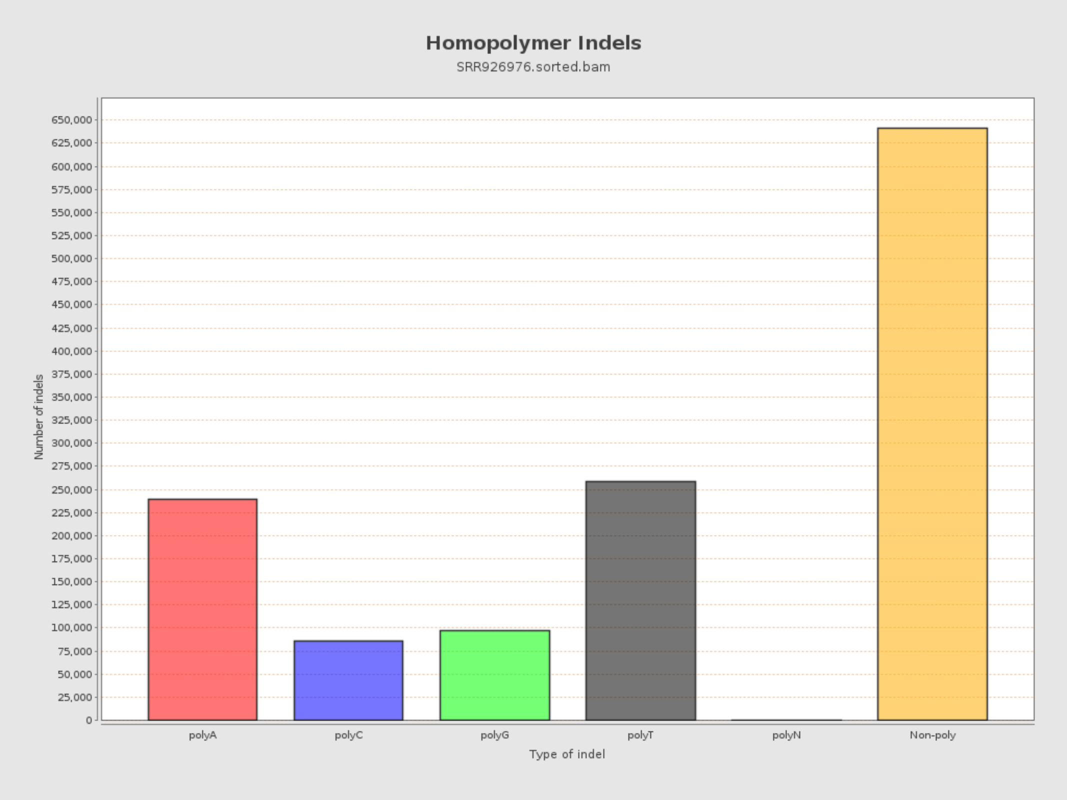
9. Results : Mapped Reads GC-content Distribution



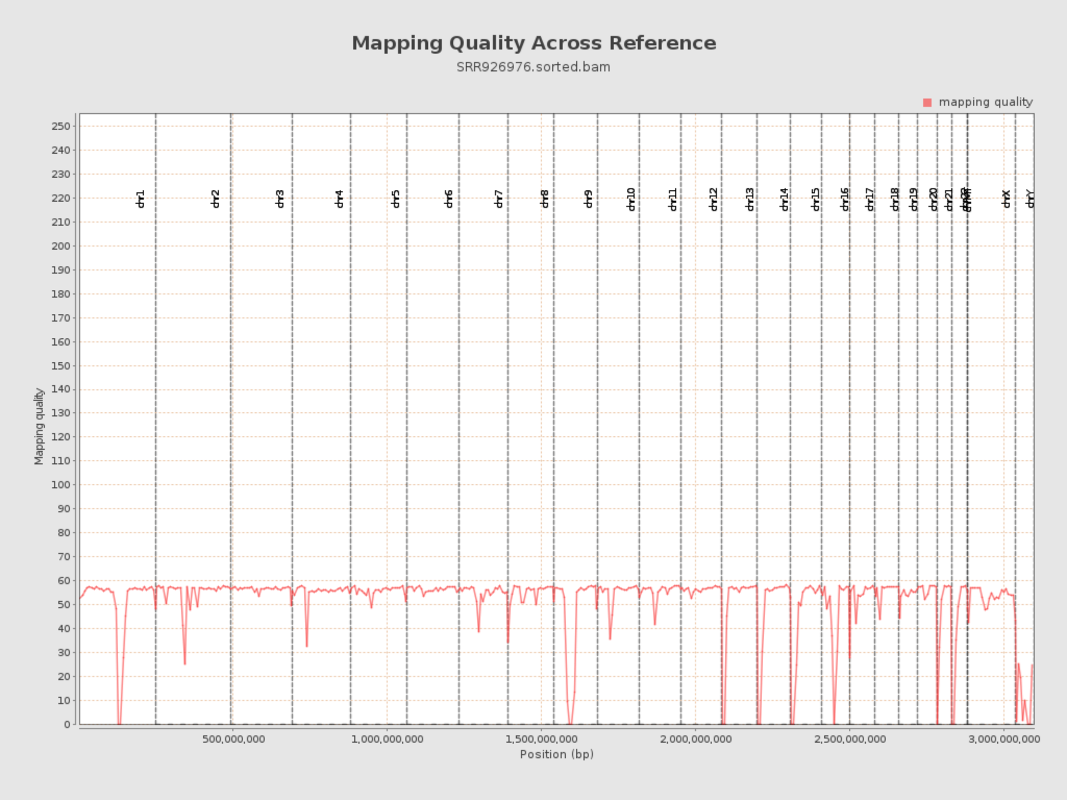
10. Results : Mapped Reads Clipping Profile



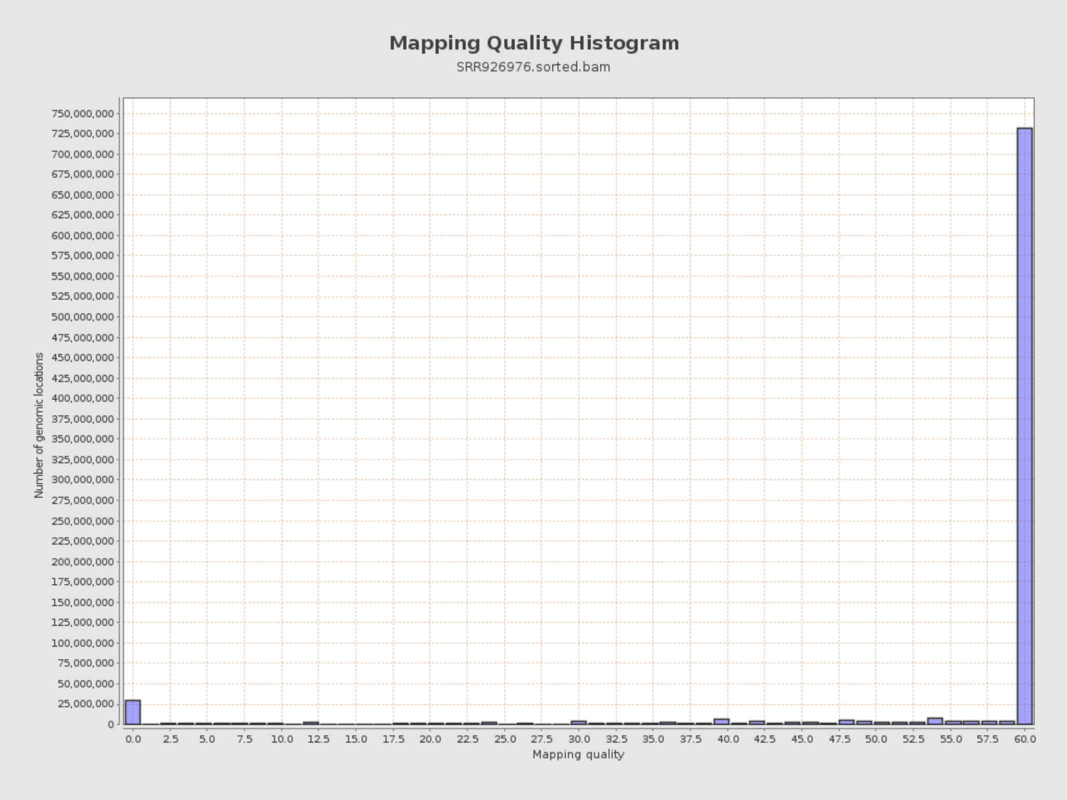
11. Results : Homopolymer Indels



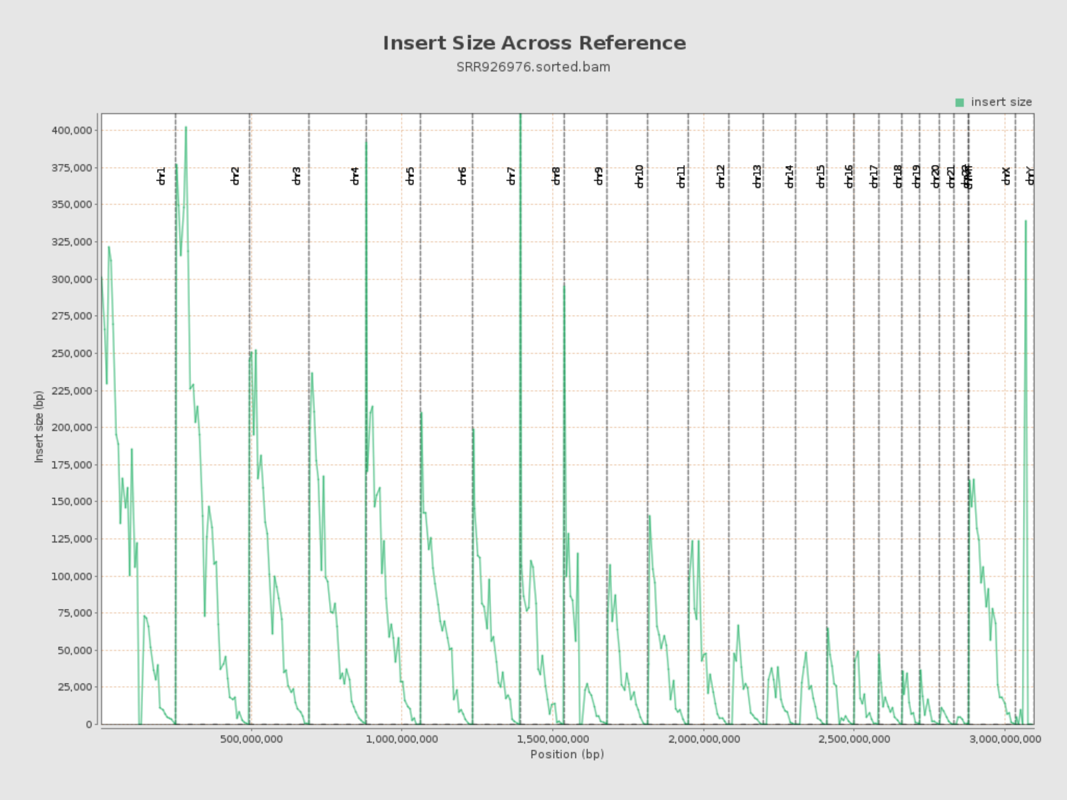
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram