Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 03:28:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926957.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_SRR926957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926957_1.fastq.gz SRR926957_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 03:28:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,992,208
Mapped reads	9,681,779 / 96.89%
Unmapped reads	310,429 / 3.11%
Mapped paired reads	9,681,779 / 96.89%
Mapped reads, first in pair	4,853,821 / 48.58%
Mapped reads, second in pair	4,827,958 / 48.32%
Mapped reads, both in pair	9,526,348 / 95.34%
Mapped reads, singletons	155,431 / 1.56%
Secondary alignments	0
Supplementary alignments	228,189 / 2.28%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	595,086 / 5.96%
Duplication rate	5.13%
Clipped reads	3,896,933 / 39%

2.2. ACGT Content

Number/percentage of A's	250,299,518 / 28.37%
Number/percentage of C's	173,480,313 / 19.66%
Number/percentage of T's	252,633,873 / 28.63%
Number/percentage of G's	205,820,396 / 23.33%
Number/percentage of N's	48,795 / 0.01%

GC Percentage	42.99%

2.3. Coverage

Mean	0.2852
Standard Deviation	1.1819

2.4. Mapping Quality

Mean Mapping Quality	52.99

2.5. Insert size

Mean	244,255.84
Standard Deviation	4,837,467.98
P25/Median/P75	149 / 195 / 265

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	8,840,157
Insertions	148,972
Mapped reads with at least one insertion	1.52%
Deletions	458,348
Mapped reads with at least one deletion	4.61%
Homopolymer indels	52.57%

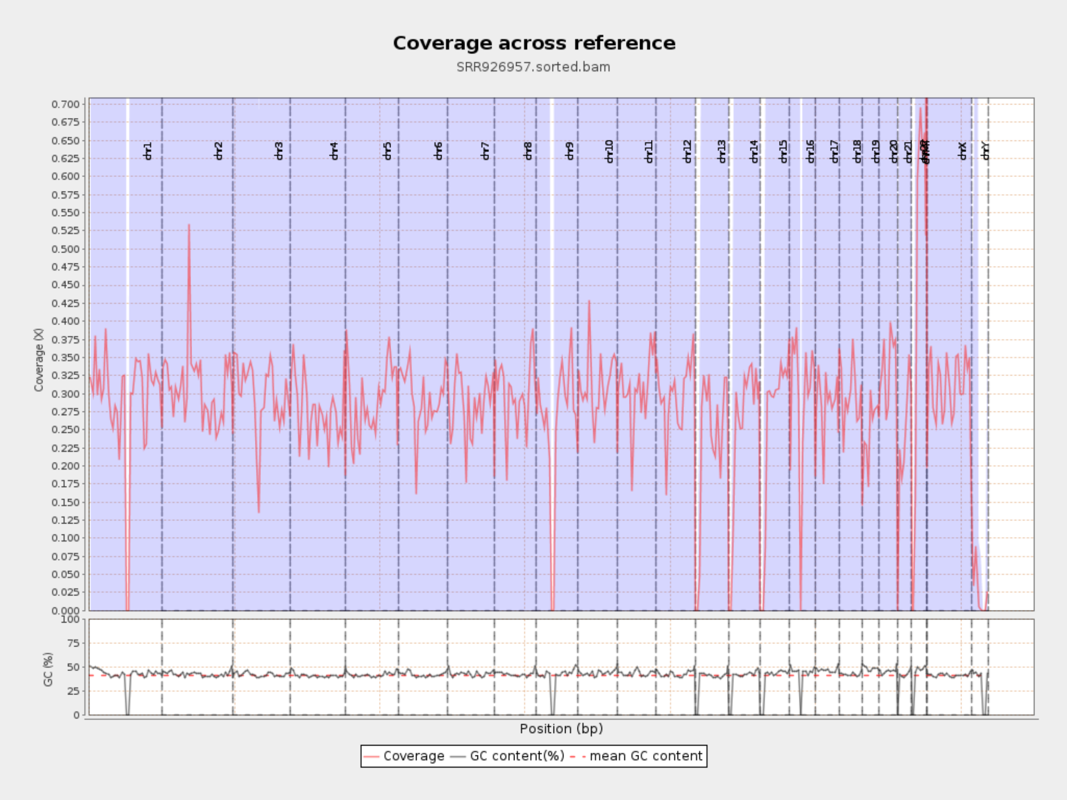
2.7. Chromosome stats

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

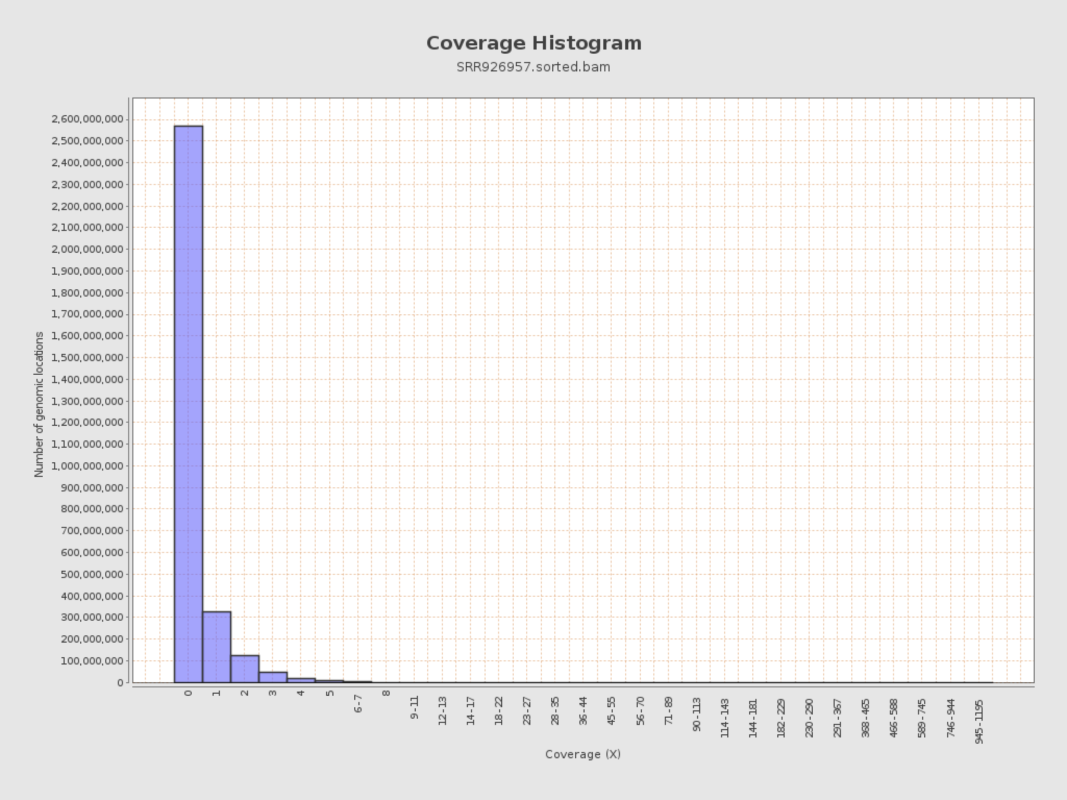
		bases	**coverage**	**deviation**
chr1	249250621	71769125	0.2879	1.4479
chr2	243199373	75477435	0.3104	1.9776
chr3	198022430	58859279	0.2972	0.7942
chr4	191154276	52815330	0.2763	1.2011
chr5	180915260	52410661	0.2897	0.7773
chr6	171115067	50449809	0.2948	0.7983
chr7	159138663	45276017	0.2845	0.9556
chr8	146364022	44193528	0.3019	0.8354
chr9	141213431	36872135	0.2611	1.2076
chr10	135534747	42423345	0.313	2.2209
chr11	135006516	41373370	0.3065	1.0477
chr12	133851895	39932318	0.2983	0.9034
chr13	115169878	26217975	0.2276	0.6886
chr14	107349540	26613726	0.2479	0.7273
chr15	102531392	26002186	0.2536	0.7442
chr16	90354753	26622052	0.2946	0.8889
chr17	81195210	23282151	0.2867	0.8234
chr18	78077248	23416031	0.2999	1.4331
chr19	59128983	14628747	0.2474	1.0045
chr20	63025520	21098495	0.3348	0.8979
chr21	48129895	11189681	0.2325	1.117
chr22	51304566	22224410	0.4332	1.122
chrMT	16571	157788	9.5219	12.6192
chrX	155270560	48082097	0.3097	0.8392

chrY	59373566	1562610	0.0263	0.8419

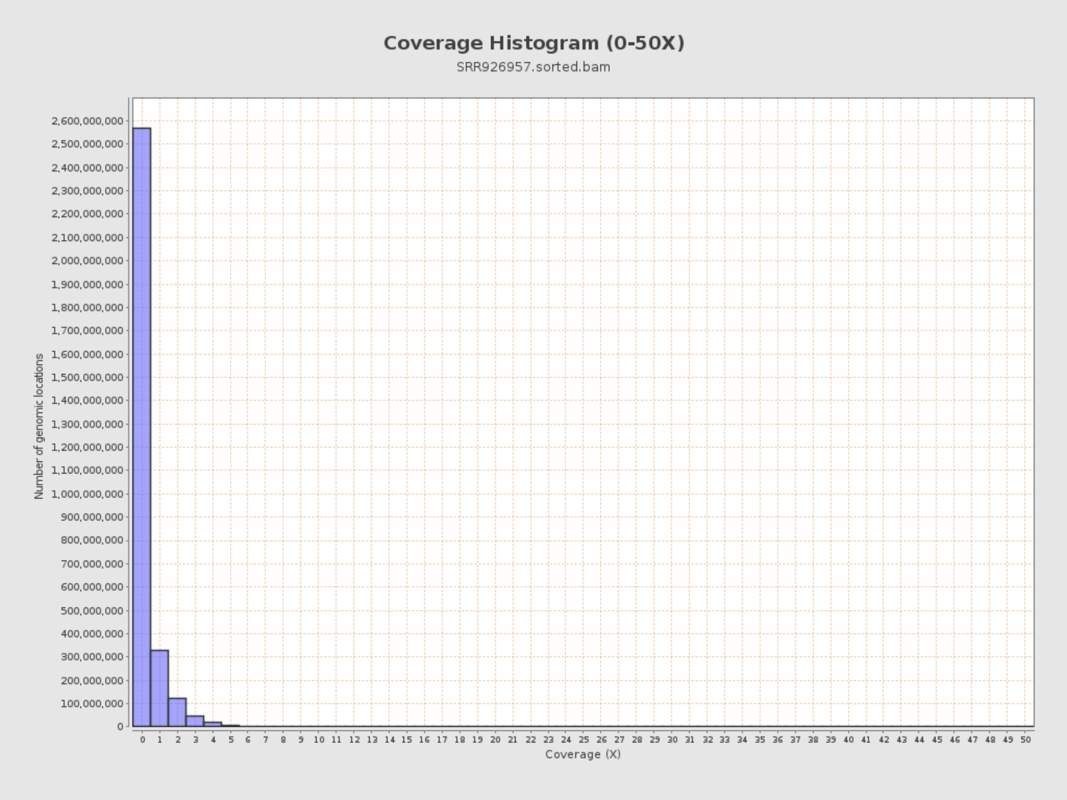
3. Results : Coverage across reference



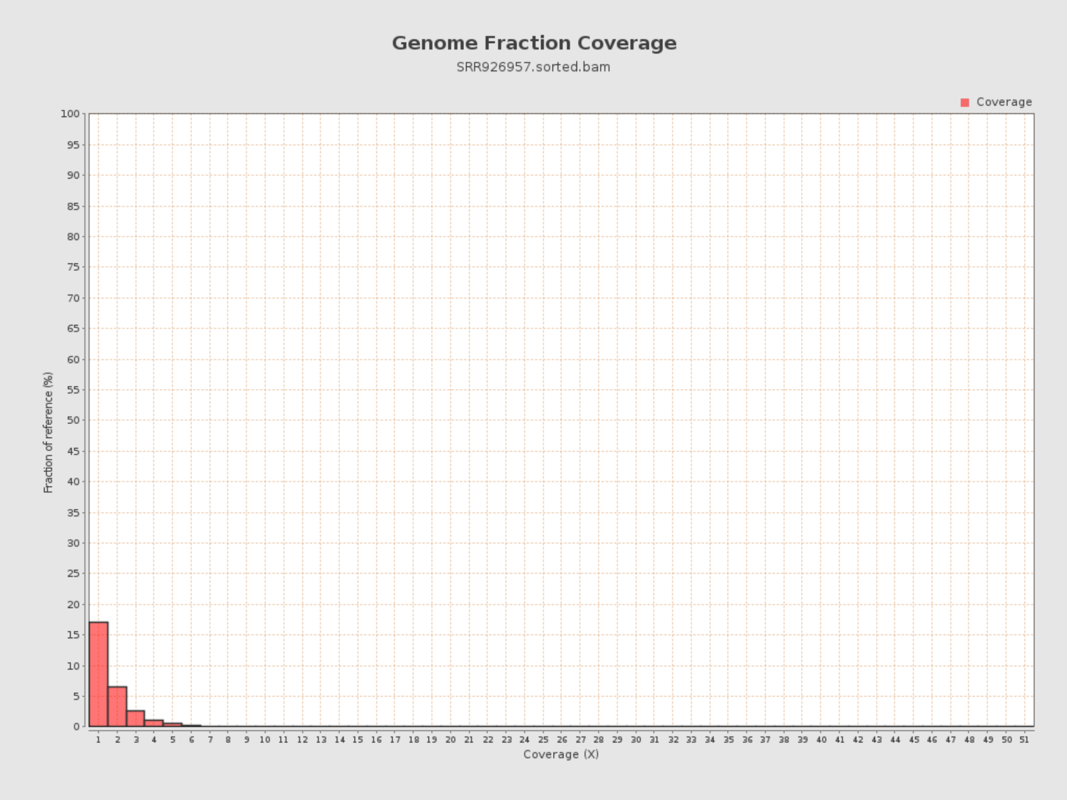
4. Results : Coverage Histogram



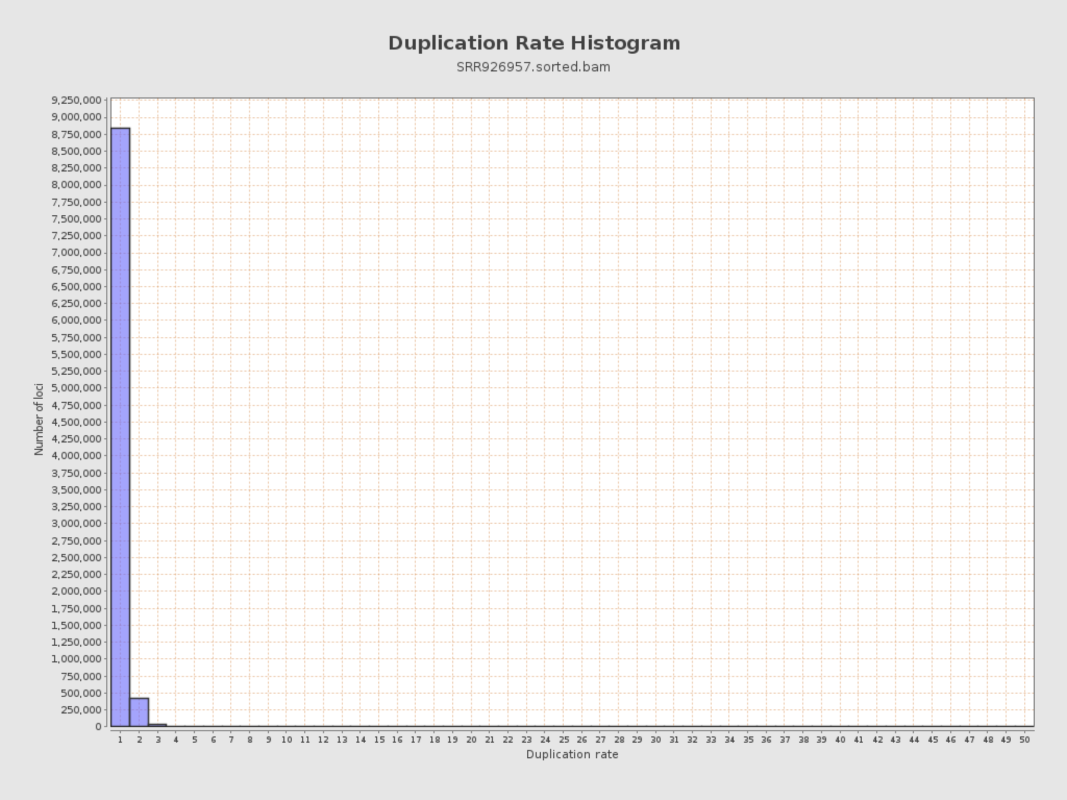
5. Results : Coverage Histogram (0-50X)



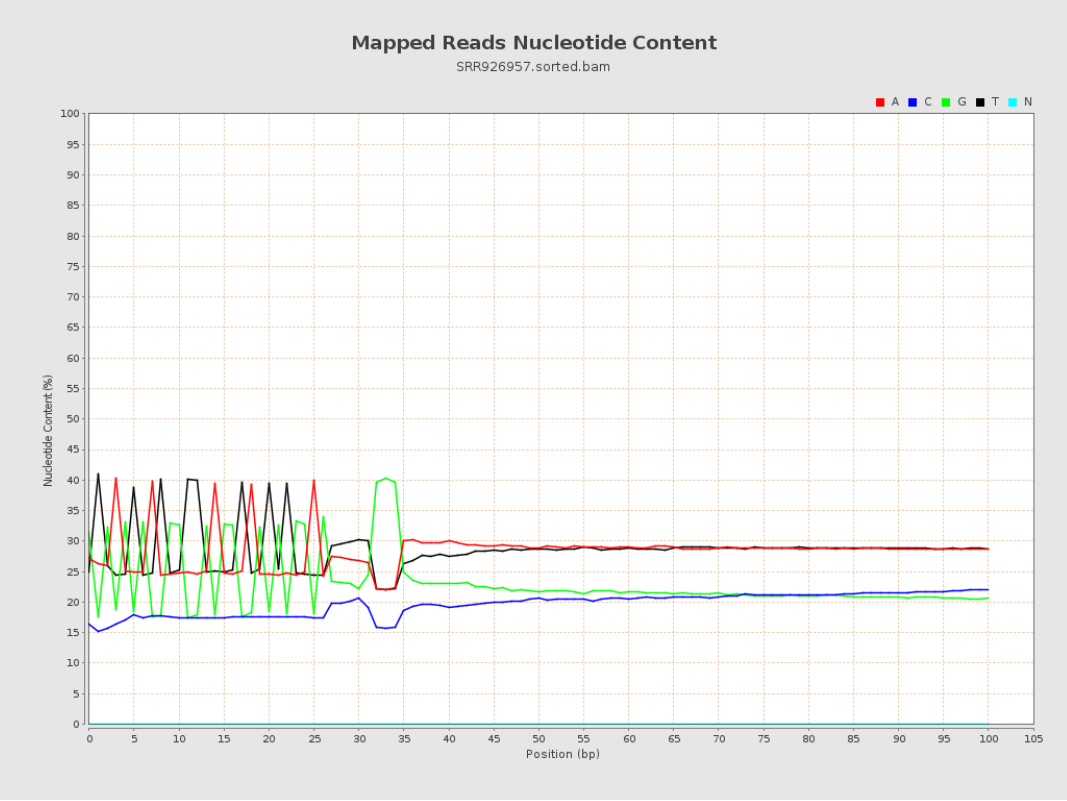
6. Results : Genome Fraction Coverage



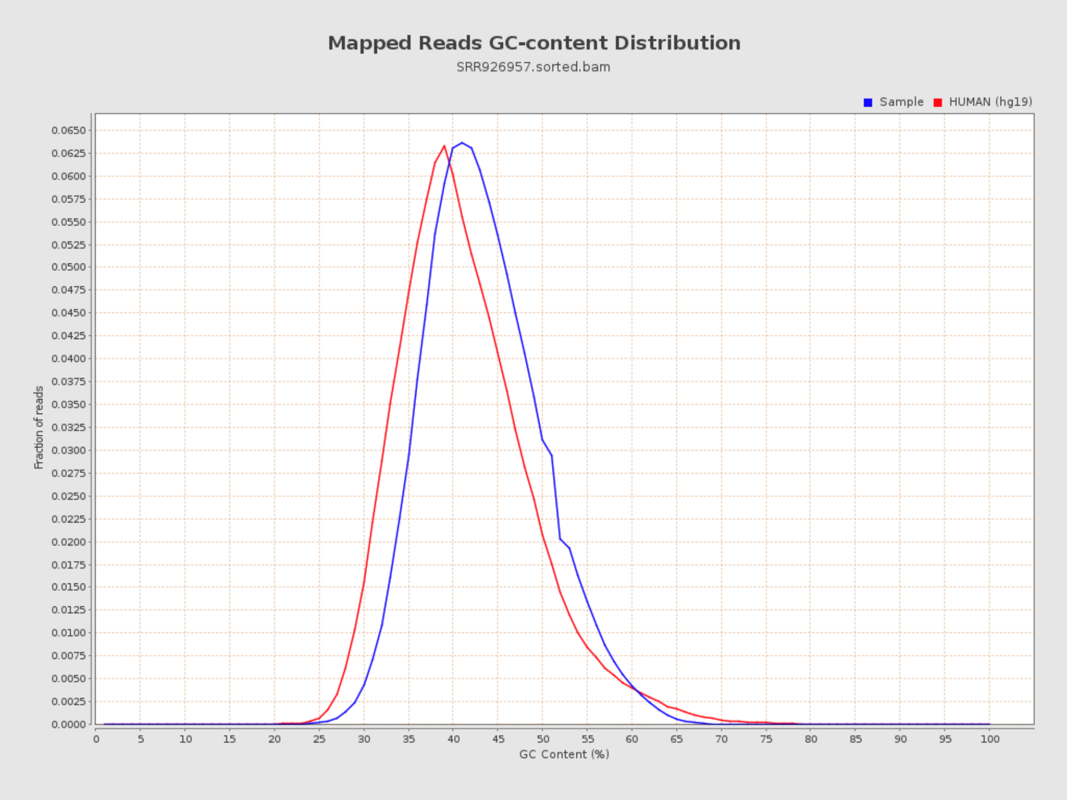
7. Results : Duplication Rate Histogram



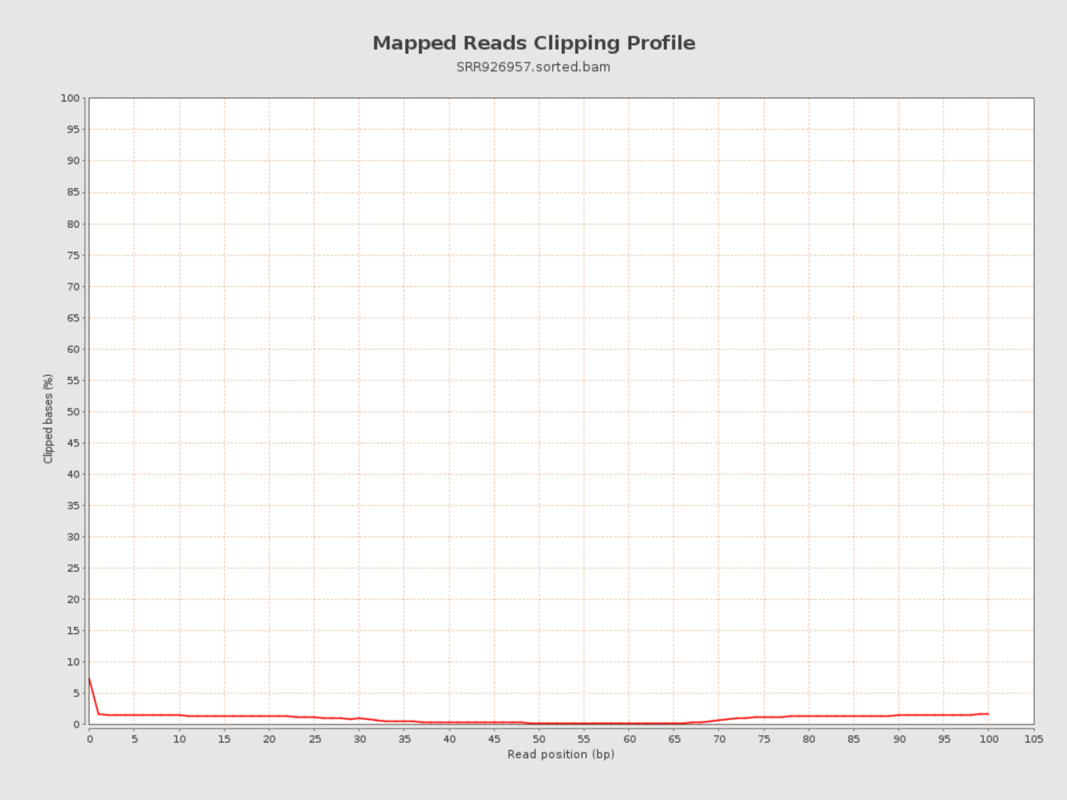
8. Results : Mapped Reads Nucleotide Content



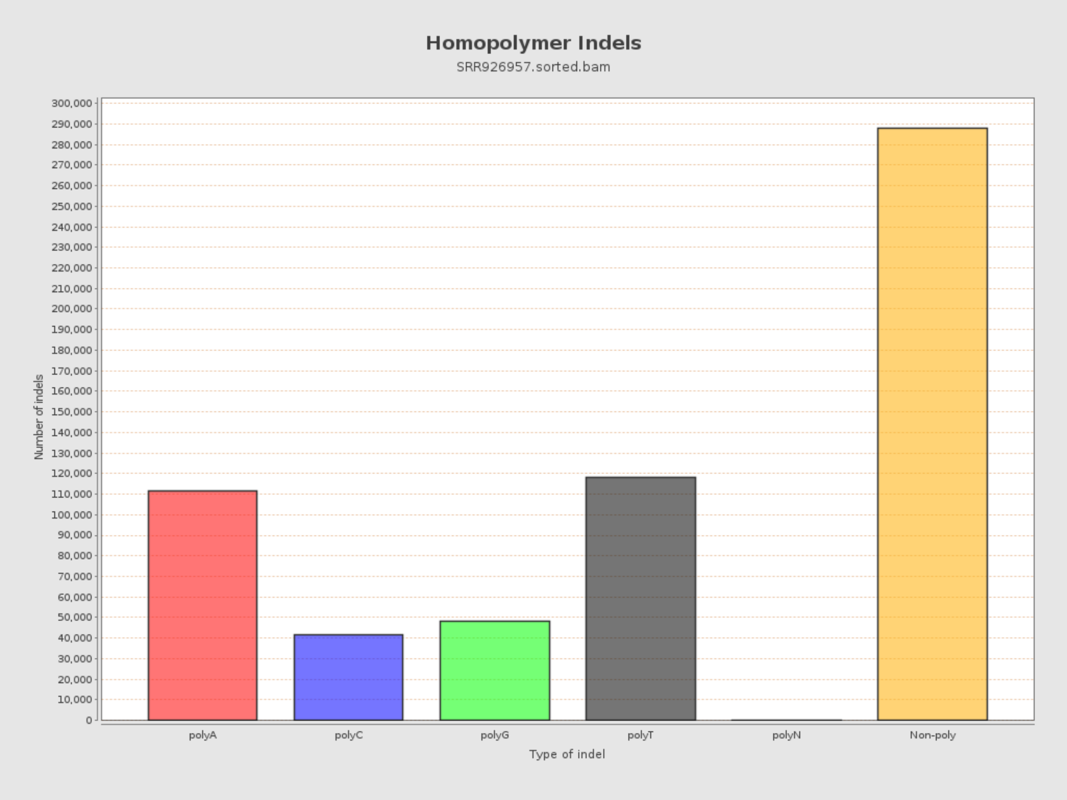
9. Results : Mapped Reads GC-content Distribution



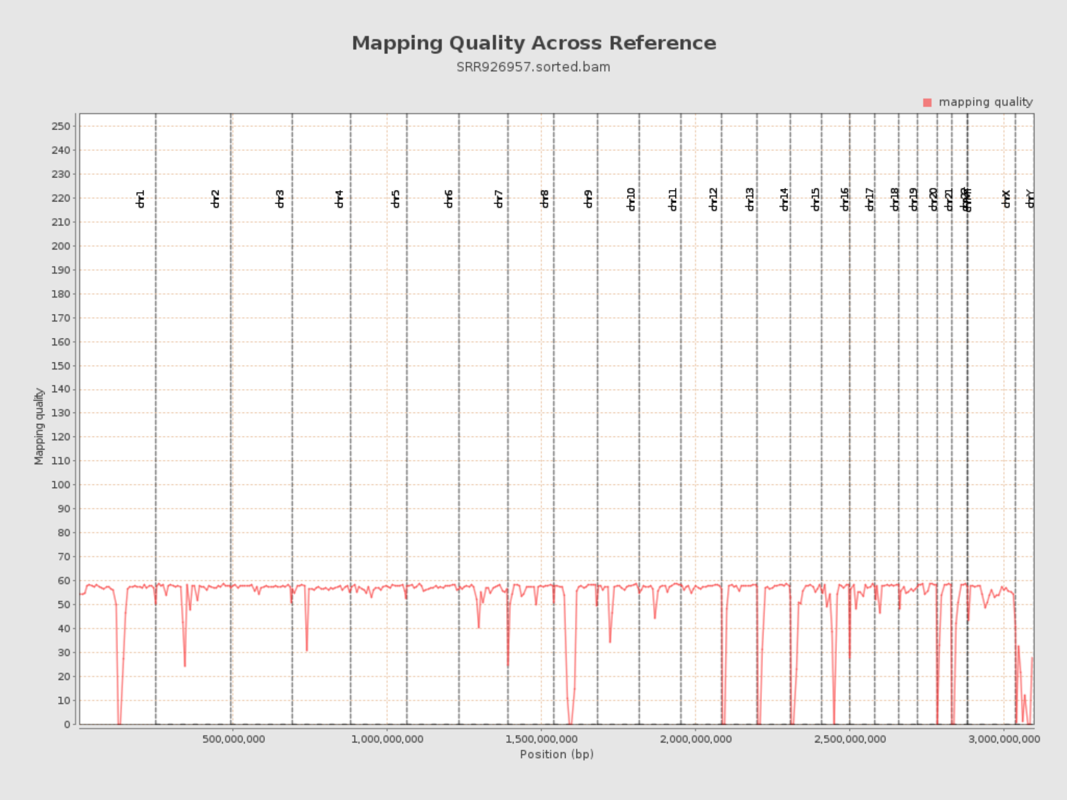
10. Results : Mapped Reads Clipping Profile



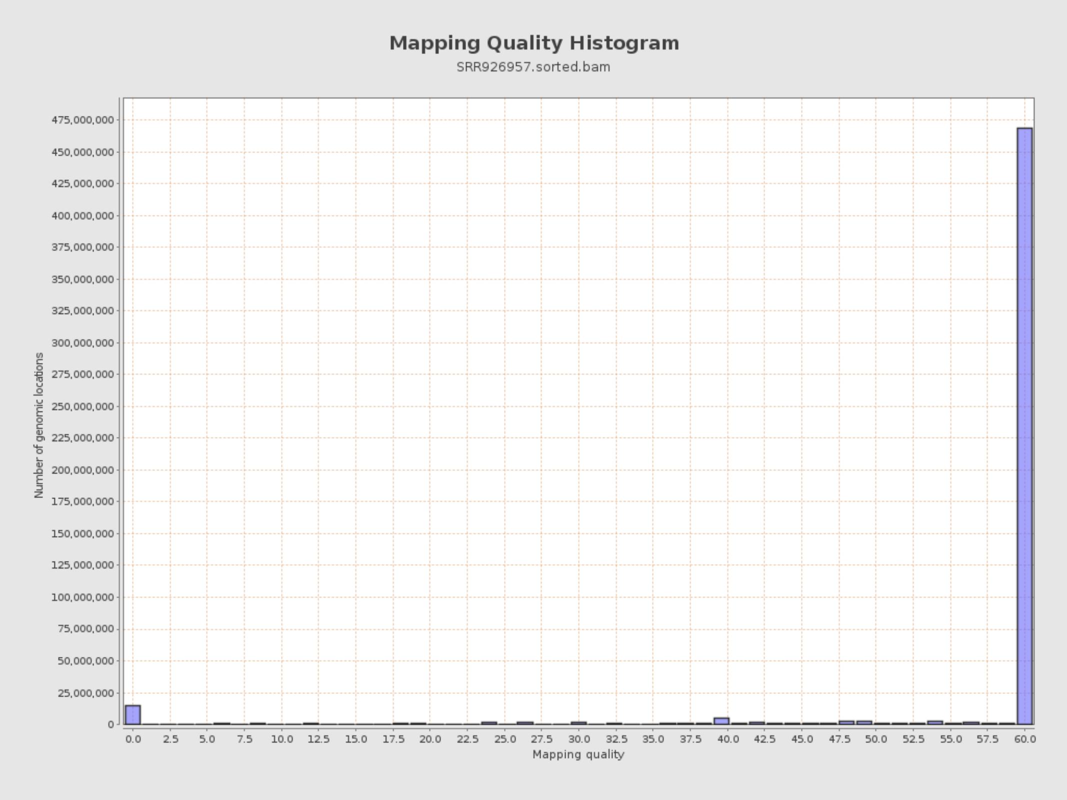
11. Results : Homopolymer Indels



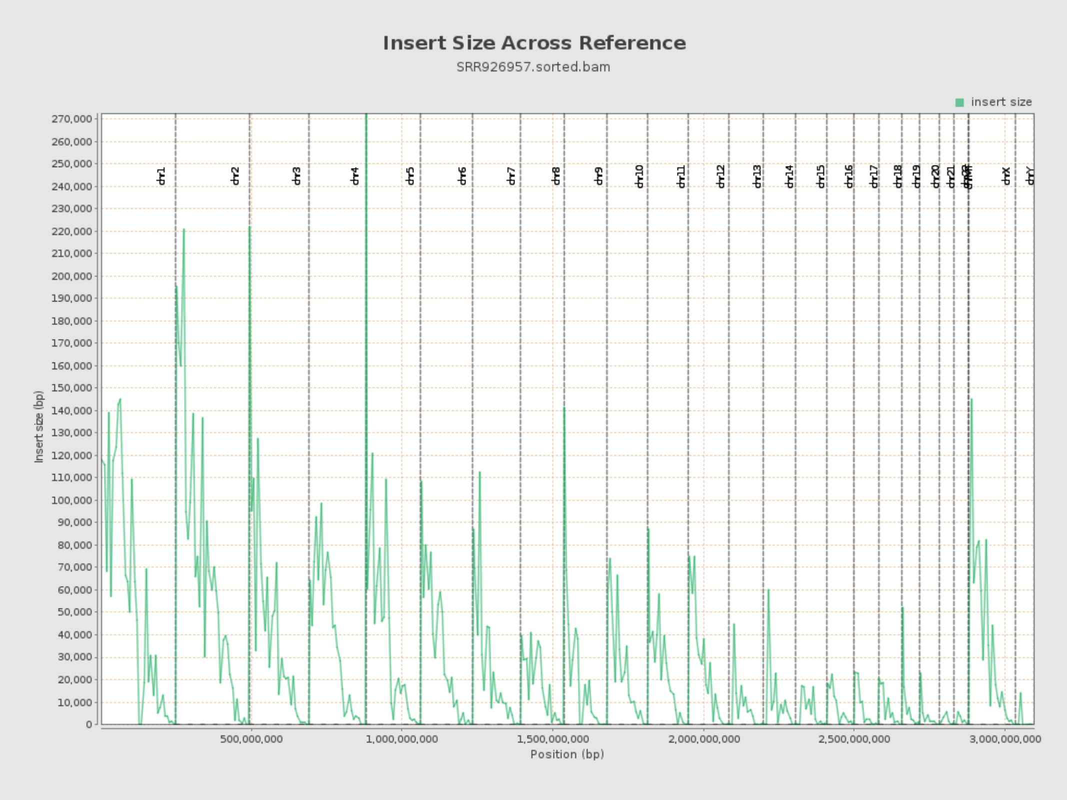
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram