Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 05:25:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926963.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_SRR926963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926963_1.fastq.gz SRR926963_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 05:25:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,444,214
Mapped reads	27,036,325 / 98.51%
Unmapped reads	407,889 / 1.49%
Mapped paired reads	27,036,325 / 98.51%
Mapped reads, first in pair	13,534,376 / 49.32%
Mapped reads, second in pair	13,501,949 / 49.2%
Mapped reads, both in pair	26,829,808 / 97.76%
Mapped reads, singletons	206,517 / 0.75%
Secondary alignments	0
Supplementary alignments	286,483 / 1.04%
Read min/max/mean length	30 / 101 / 101.43
Duplicated reads (estimated)	1,727,304 / 6.29%
Duplication rate	5.07%
Clipped reads	6,455,965 / 23.52%

2.2. ACGT Content

Number/percentage of A's	727,211,909 / 28.31%
Number/percentage of C's	526,554,541 / 20.5%
Number/percentage of T's	735,842,327 / 28.65%
Number/percentage of G's	578,921,464 / 22.54%
Number/percentage of N's	298,660 / 0.01%

GC Percentage	43.03%

2.3. Coverage

Mean	0.8304
Standard Deviation	3.1

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	100,273.67
Standard Deviation	3,116,764.53
P25/Median/P75	144 / 180 / 235

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	24,593,828
Insertions	411,686
Mapped reads with at least one insertion	1.5%
Deletions	1,340,399
Mapped reads with at least one deletion	4.83%
Homopolymer indels	52.78%

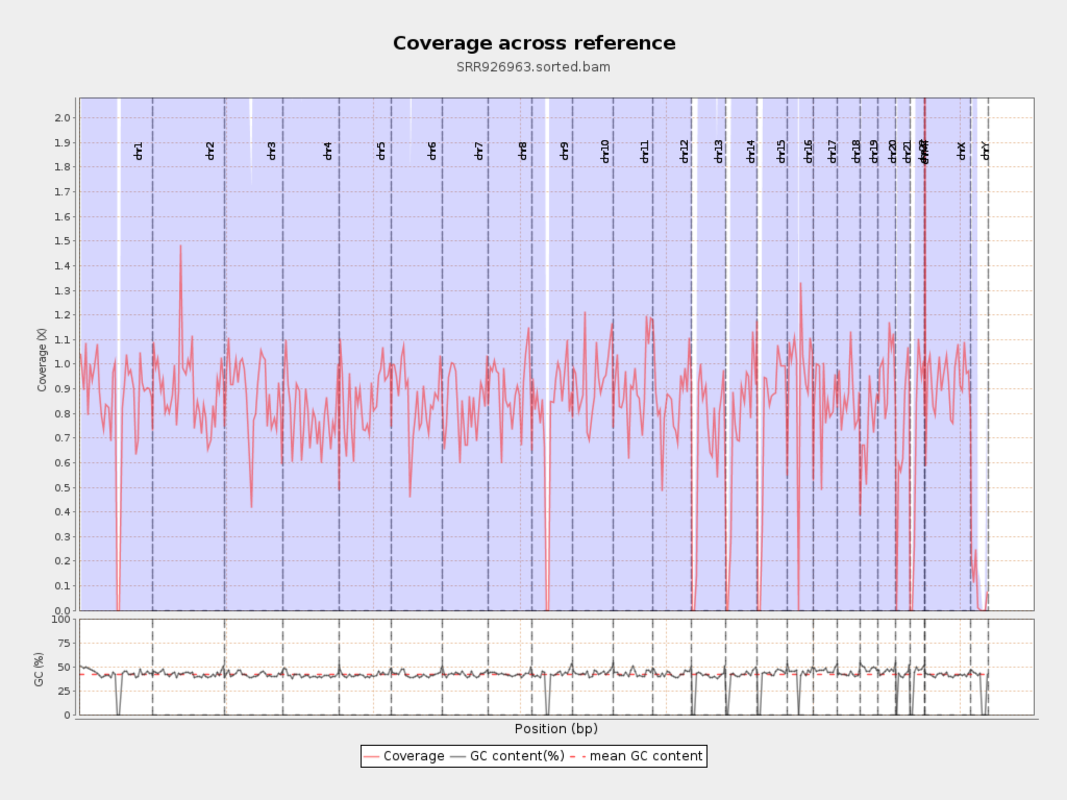
2.7. Chromosome stats

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

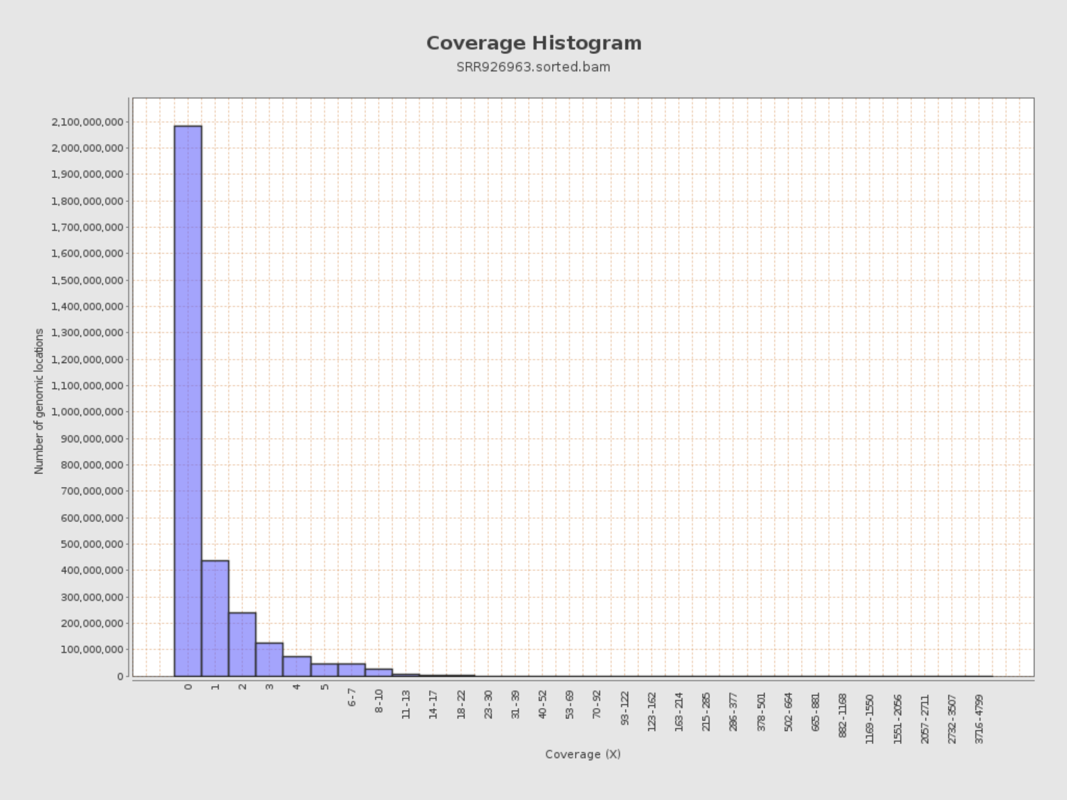
		bases	coverage	deviation
chr1	249250621	210318909	0.8438	3.8649
chr2	243199373	219073945	0.9008	5.5066
chr3	198022430	173556876	0.8765	1.7654
chr4	191154276	151802467	0.7941	2.5342
chr5	180915260	155076270	0.8572	1.7345
chr6	171115067	147438545	0.8616	2.307
chr7	159138663	131971497	0.8293	2.3313
chr8	146364022	131471318	0.8982	2.1286
chr9	141213431	111142829	0.7871	3.7945
chr10	135534747	126430909	0.9328	4.5314
chr11	135006516	123505516	0.9148	3.0714
chr12	133851895	114025539	0.8519	1.7842
chr13	115169878	77848008	0.6759	1.5482
chr14	107349540	77134363	0.7185	1.656
chr15	102531392	77838277	0.7592	1.7358
chr16	90354753	84584557	0.9361	4.5947
chr17	81195210	68852177	0.848	3.3226
chr18	78077248	68427522	0.8764	4.3406
chr19	59128983	43299139	0.7323	2.5633
chr20	63025520	61430428	0.9747	2.0692
chr21	48129895	33462303	0.6952	2.4536
chr22	51304566	33891325	0.6606	1.7101
chrMT	16571	46446	2.8028	3.0388
chrX	155270560	143555210	0.9245	2.1306

chrY	59373566	4565780	0.0769	2.2476

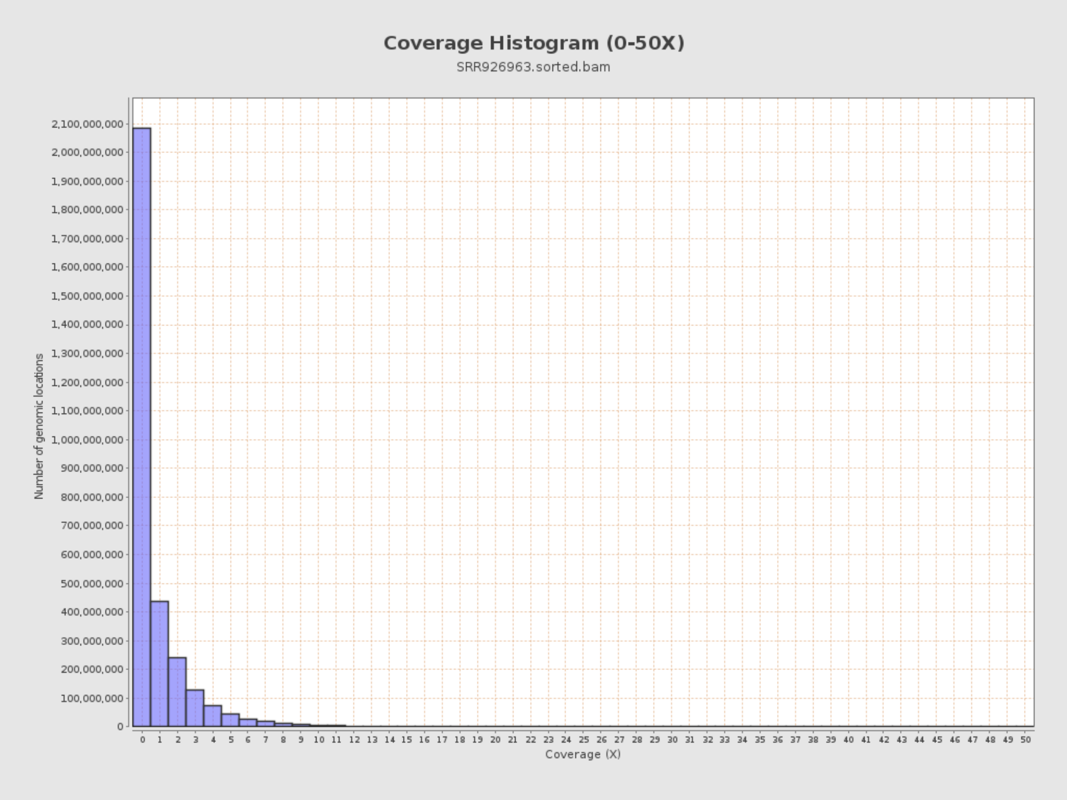
3. Results : Coverage across reference



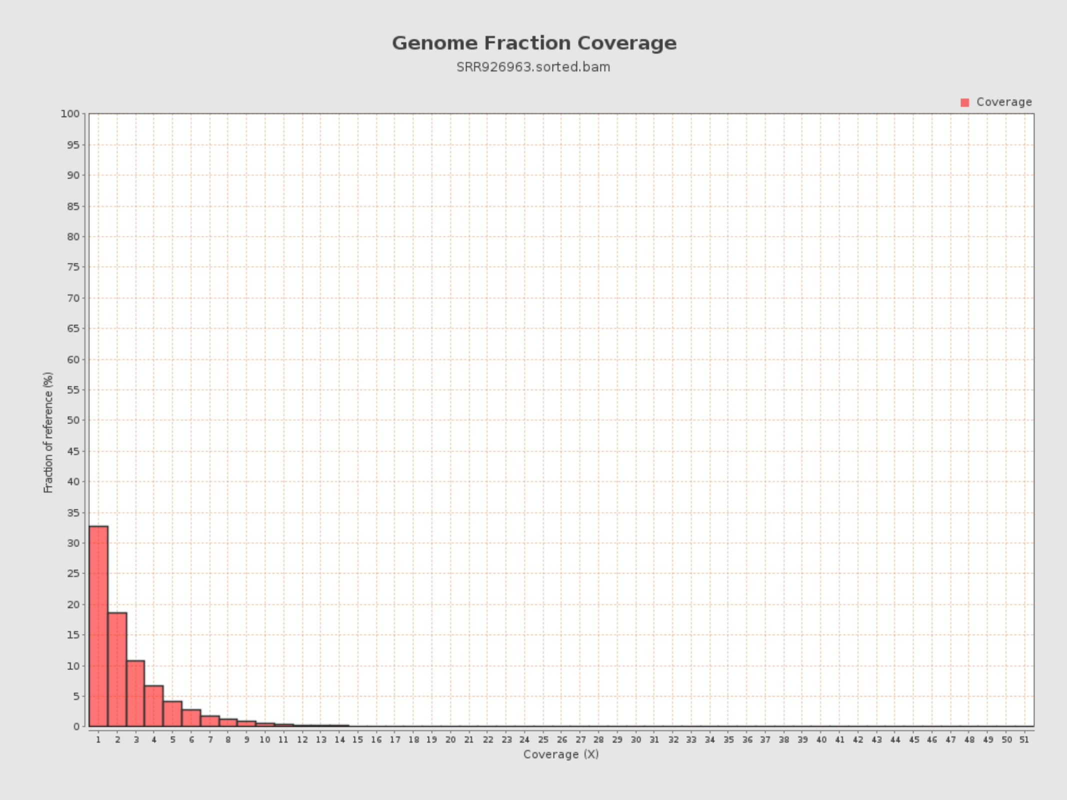
4. Results : Coverage Histogram



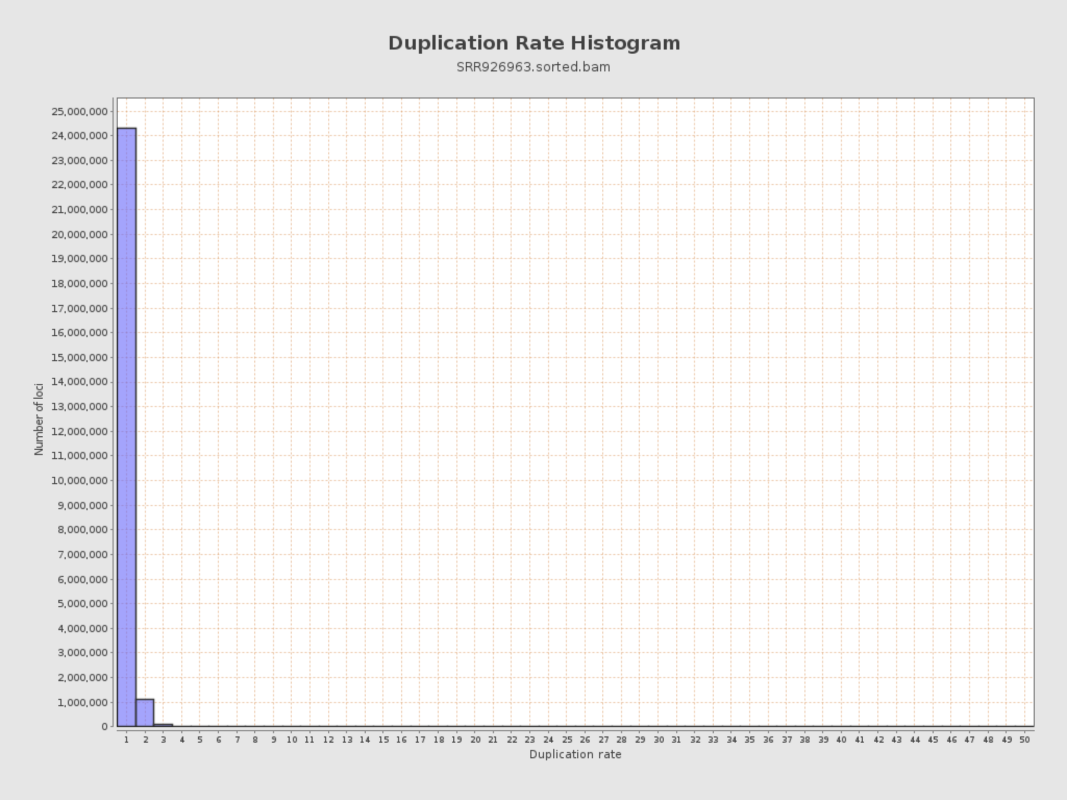
5. Results : Coverage Histogram (0-50X)



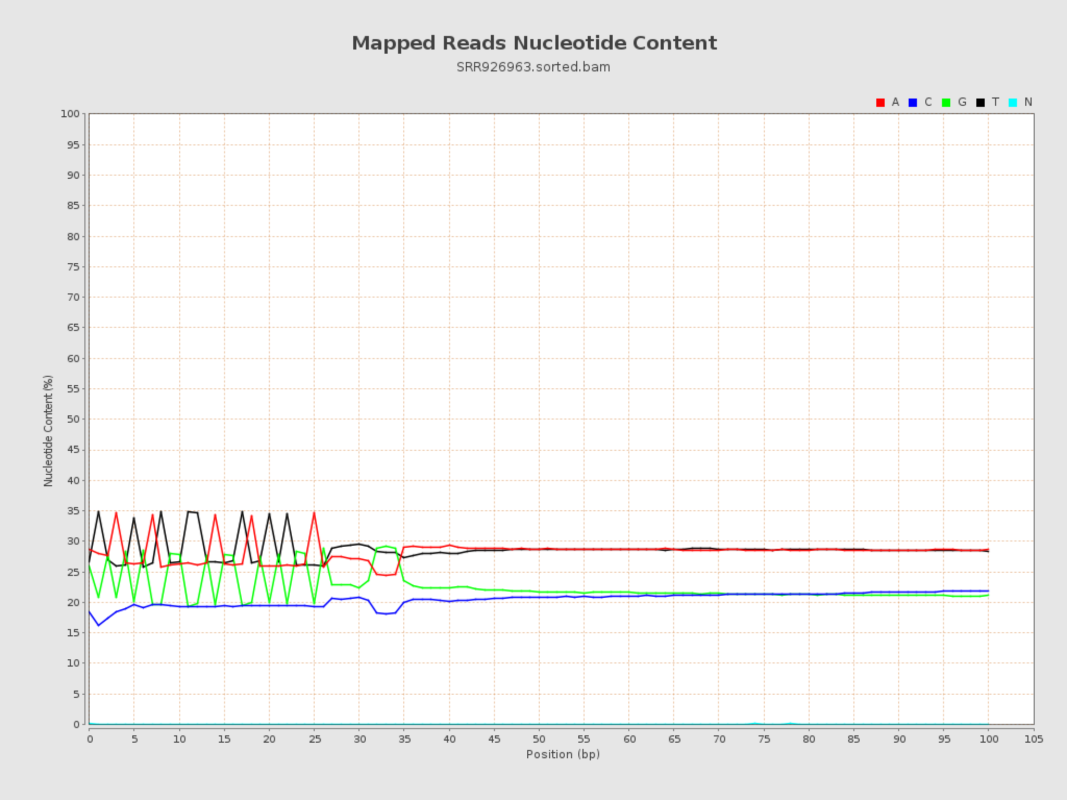
6. Results : Genome Fraction Coverage



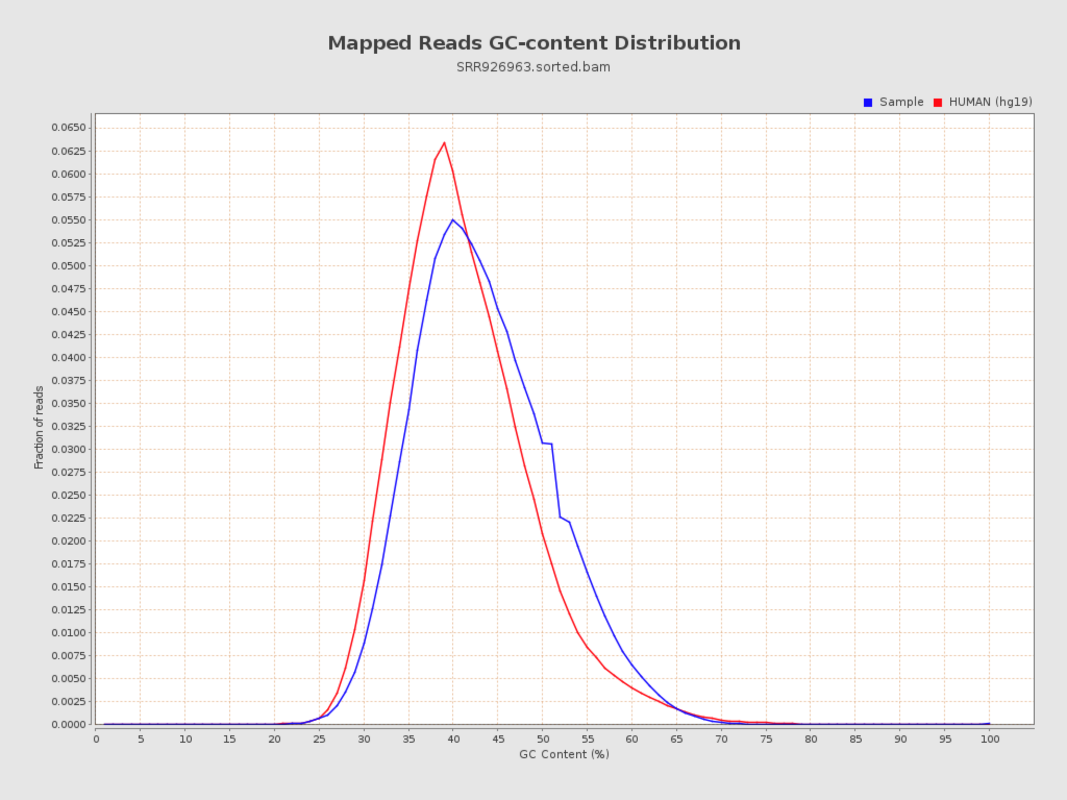
7. Results : Duplication Rate Histogram



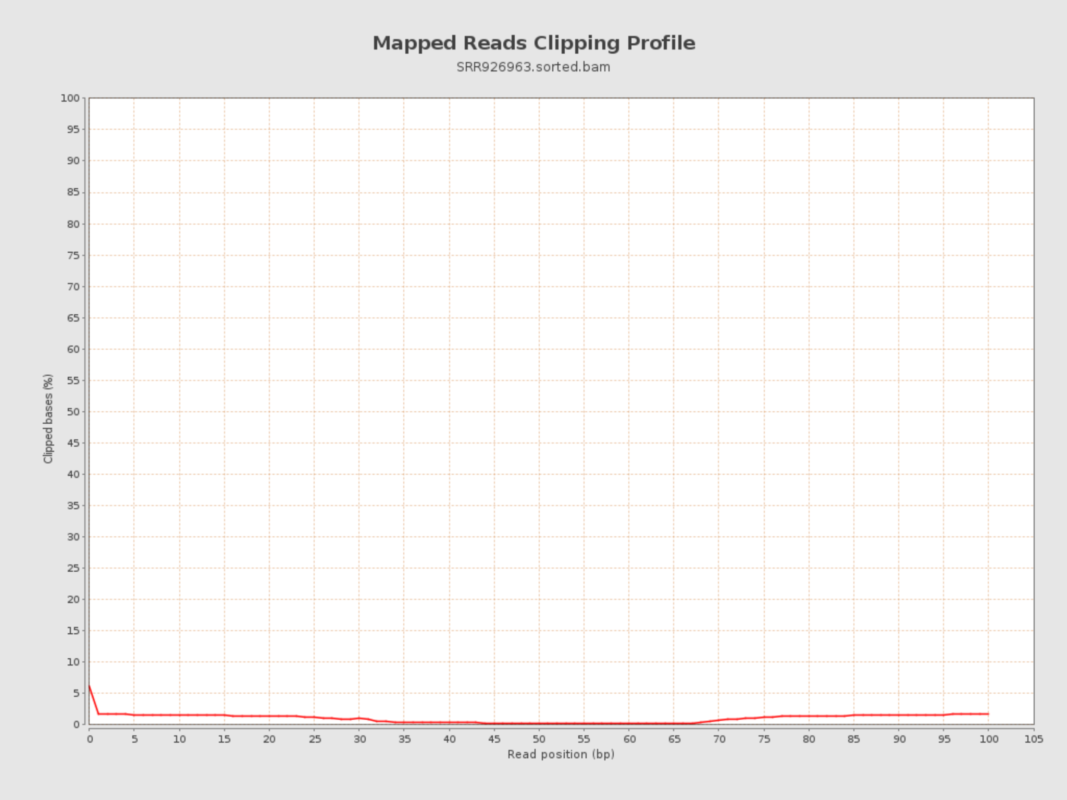
8. Results : Mapped Reads Nucleotide Content



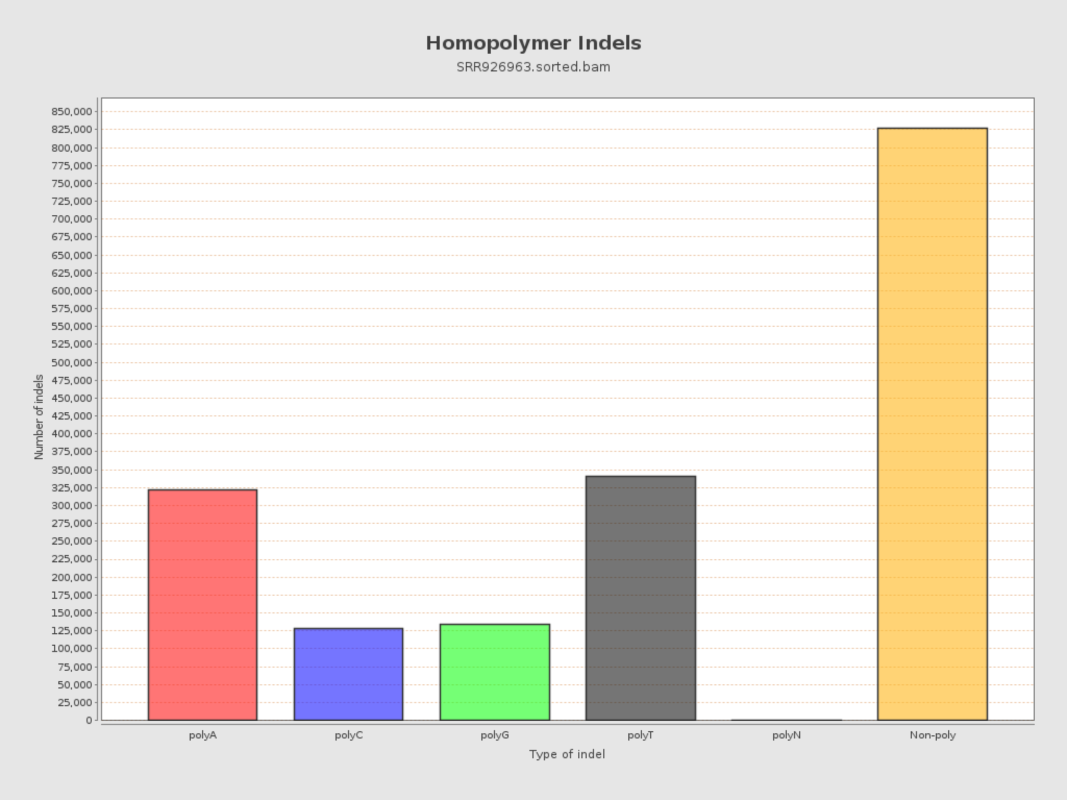
9. Results : Mapped Reads GC-content Distribution



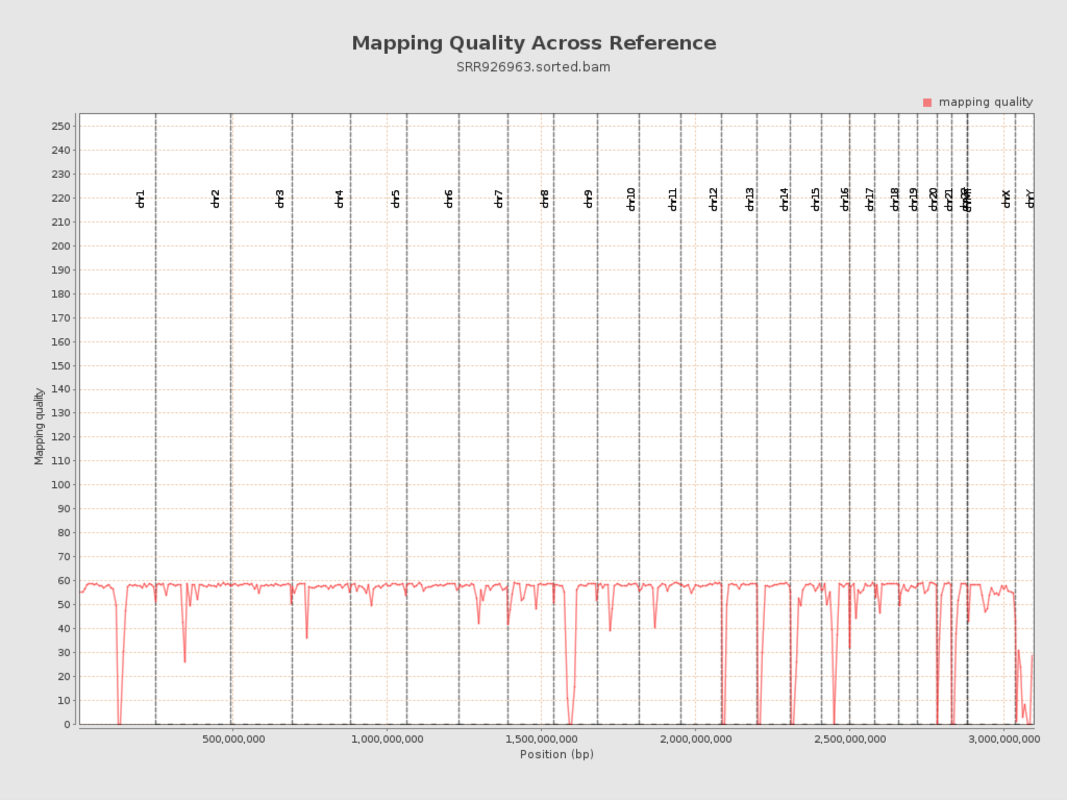
10. Results : Mapped Reads Clipping Profile



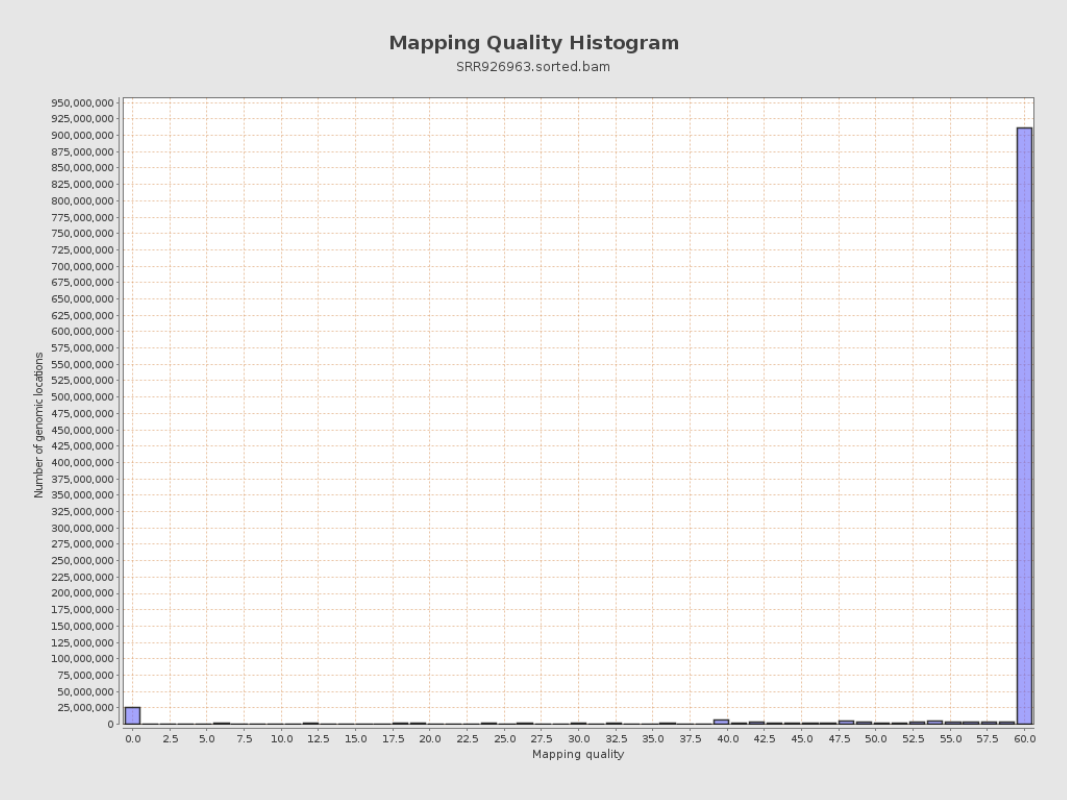
11. Results : Homopolymer Indels



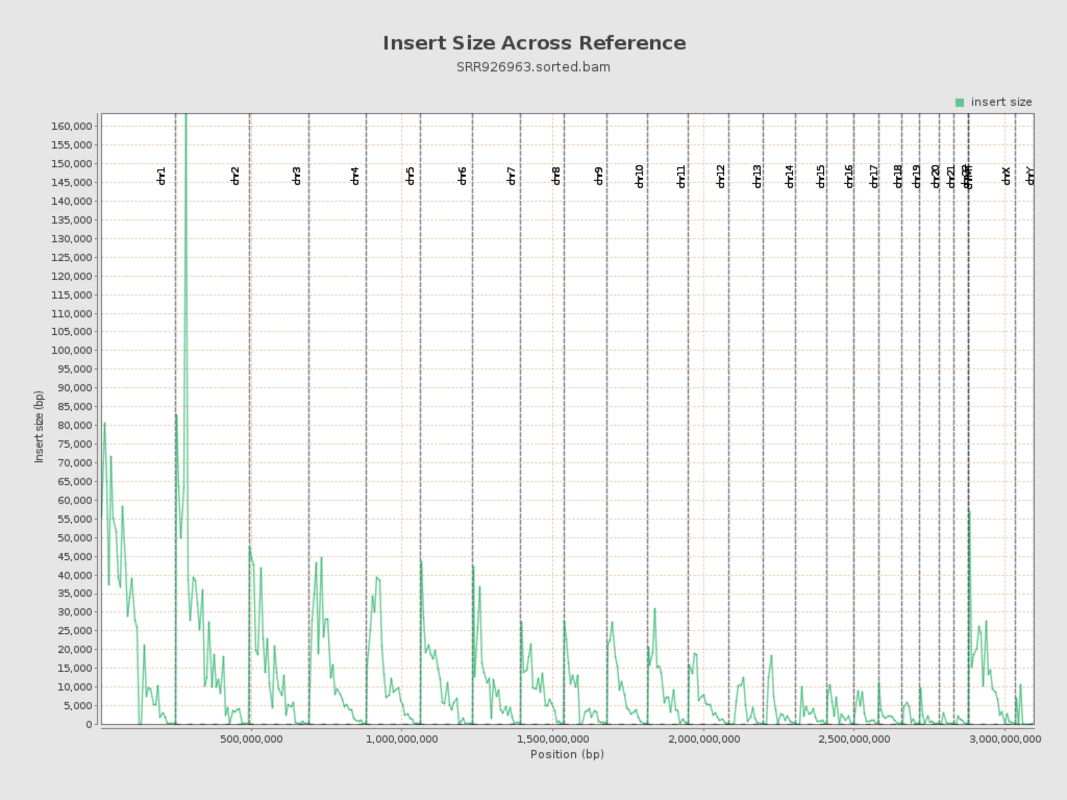
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram