Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/25 05:32:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927063.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_SRR927063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927063_1.fastq.gz SRR927063_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 25 05:32:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,039,588
Mapped reads	20,405,798 / 96.99%
Unmapped reads	633,790 / 3.01%
Mapped paired reads	20,405,798 / 96.99%
Mapped reads, first in pair	10,235,023 / 48.65%
Mapped reads, second in pair	10,170,775 / 48.34%
Mapped reads, both in pair	20,030,588 / 95.2%
Mapped reads, singletons	375,210 / 1.78%
Secondary alignments	0
Supplementary alignments	361,664 / 1.72%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	1,593,765 / 7.58%
Duplication rate	6.25%
Clipped reads	9,024,019 / 42.89%

2.2. ACGT Content

Number/percentage of A's	520,246,617 / 28.25%
Number/percentage of C's	361,188,527 / 19.62%
Number/percentage of T's	531,918,002 / 28.89%
Number/percentage of G's	427,691,643 / 23.23%
Number/percentage of N's	249,435 / 0.01%

GC Percentage	42.84%

2.3. Coverage

Mean	0.5952
Standard Deviation	2.259

2.4. Mapping Quality

Mean Mapping Quality	53.09

2.5. Insert size

Mean	178,594.73
Standard Deviation	4,123,275.51
P25/Median/P75	142 / 183 / 245

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	19,322,710
Insertions	290,849
Mapped reads with at least one insertion	1.4%
Deletions	884,047
Mapped reads with at least one deletion	4.23%
Homopolymer indels	51.64%

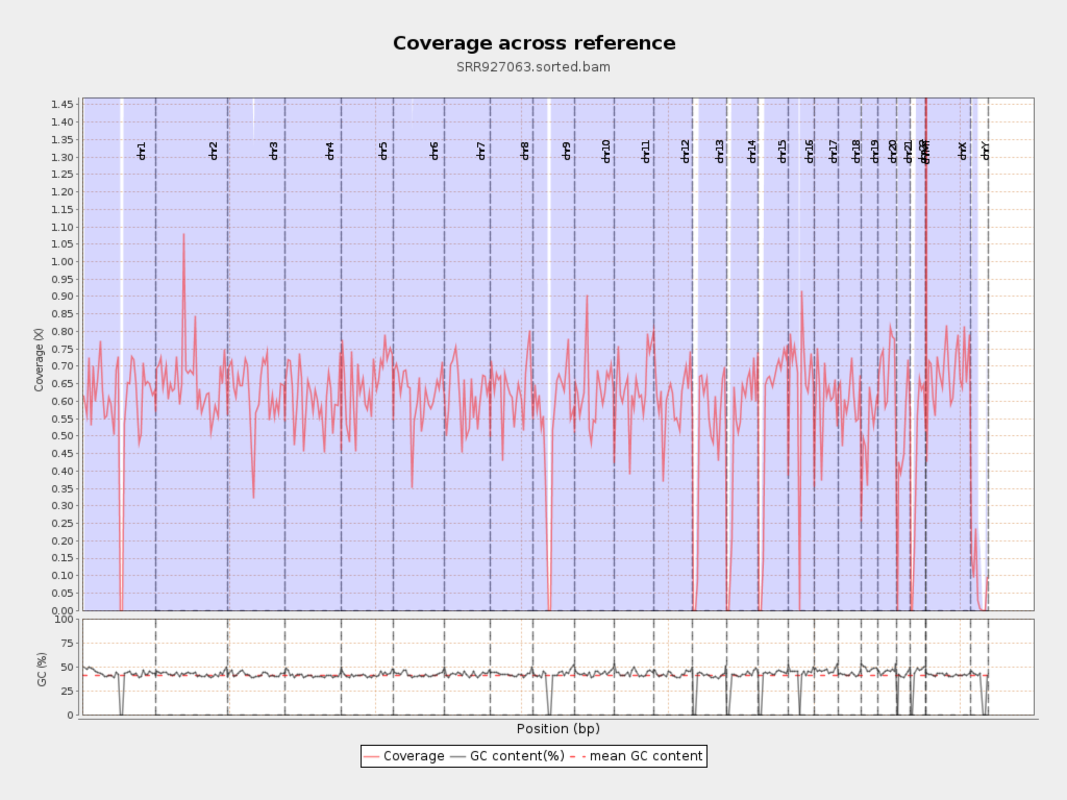
2.7. Chromosome stats

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

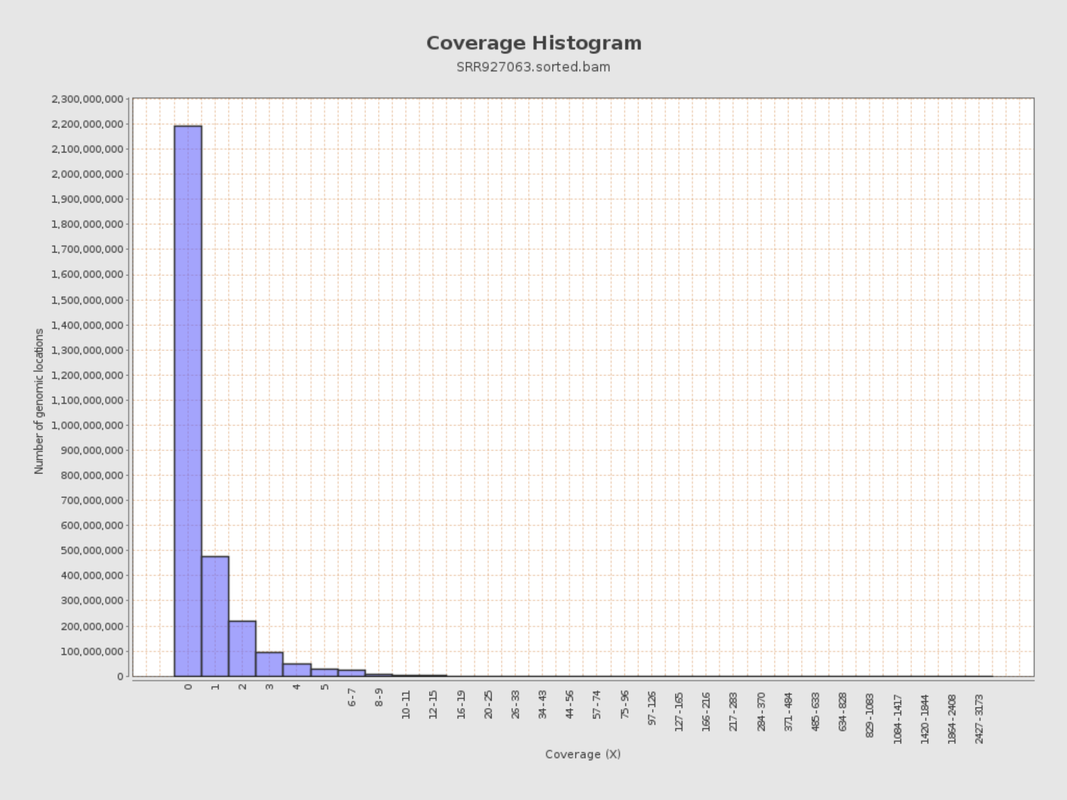
		bases	coverage	deviation
chr1	249250621	146866691	0.5892	3.3987
chr2	243199373	160933725	0.6617	3.6117
chr3	198022430	123301817	0.6227	1.297
chr4	191154276	116773838	0.6109	2.0648
chr5	180915260	117858329	0.6515	1.3368
chr6	171115067	105733565	0.6179	1.3745
chr7	159138663	97328614	0.6116	1.811
chr8	146364022	93007563	0.6355	1.5273
chr9	141213431	75524084	0.5348	2.4861
chr10	135534747	84755382	0.6253	3.7973
chr11	135006516	85991898	0.6369	1.8513
chr12	133851895	81682199	0.6102	1.2953
chr13	115169878	56946908	0.4945	1.1555
chr14	107349540	54769813	0.5102	1.2263
chr15	102531392	56496082	0.551	1.2697
chr16	90354753	58357064	0.6459	3.06
chr17	81195210	49747254	0.6127	1.7587
chr18	78077248	46824873	0.5997	2.6641
chr19	59128983	30558616	0.5168	2.045
chr20	63025520	44537636	0.7067	1.5085
chr21	48129895	22830034	0.4743	1.8612
chr22	51304566	21727597	0.4235	1.1576
chrMT	16571	123522	7.4541	4.4611
chrX	155270560	105582000	0.68	1.5528

chrY	59373566	4319399	0.0727	2.6384

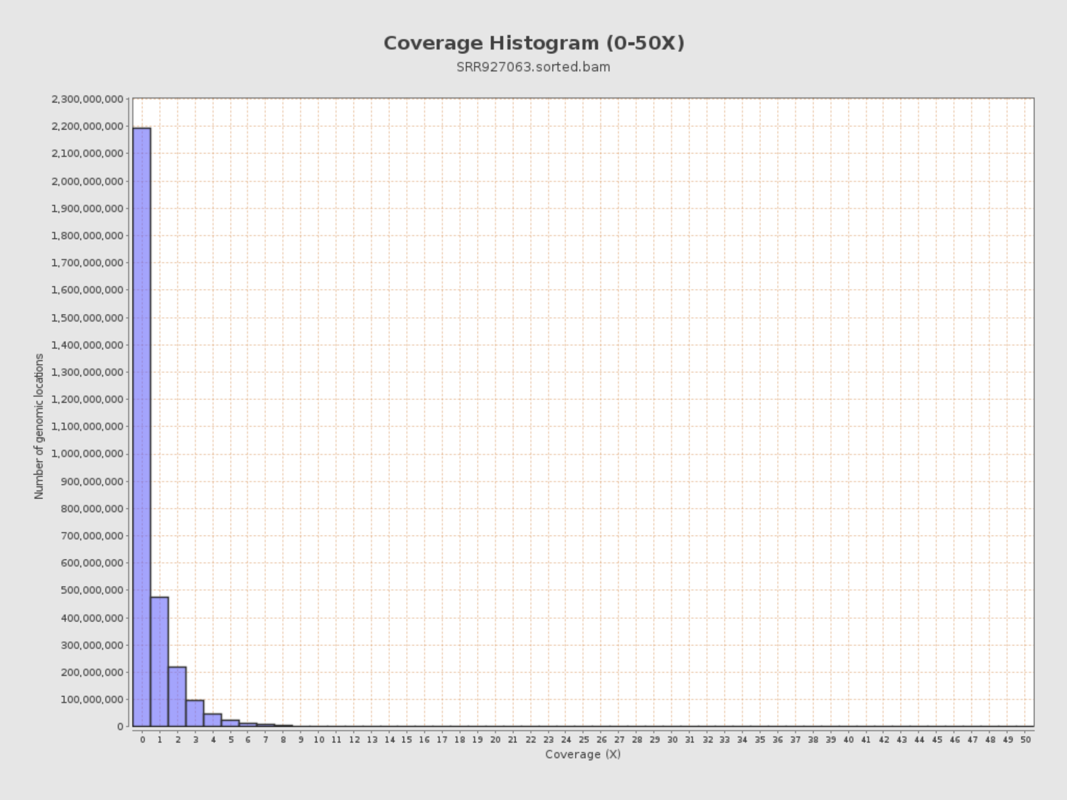
3. Results : Coverage across reference



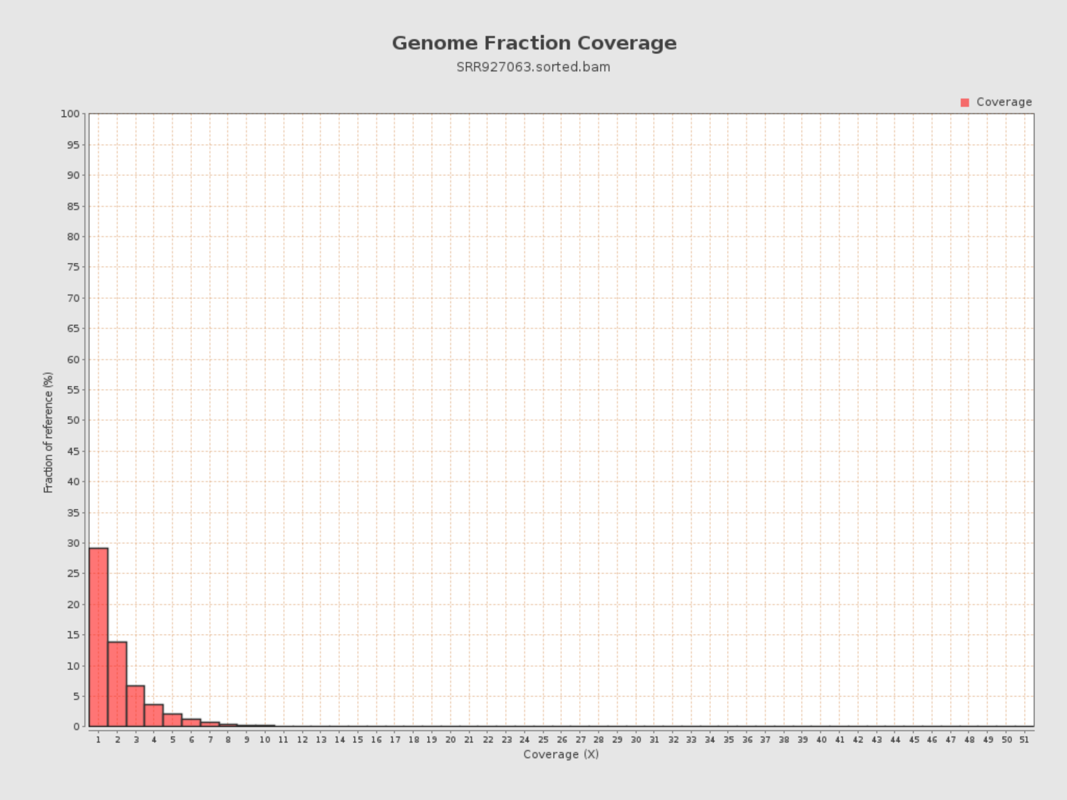
4. Results : Coverage Histogram



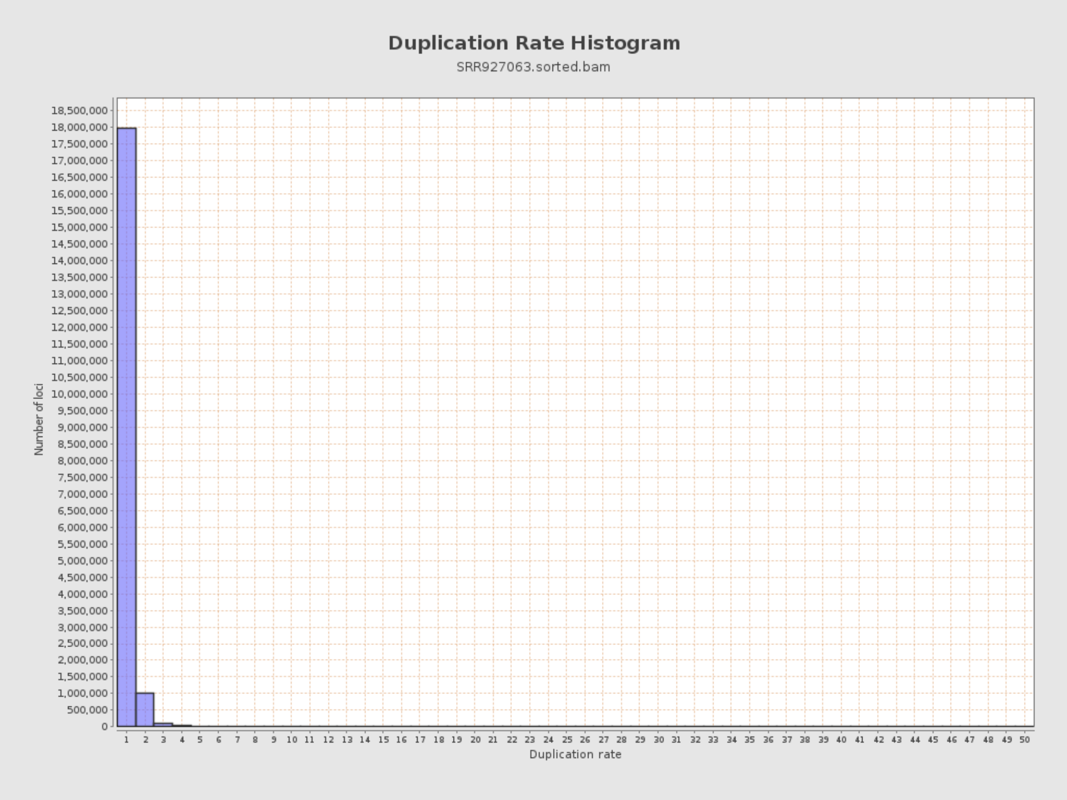
5. Results : Coverage Histogram (0-50X)



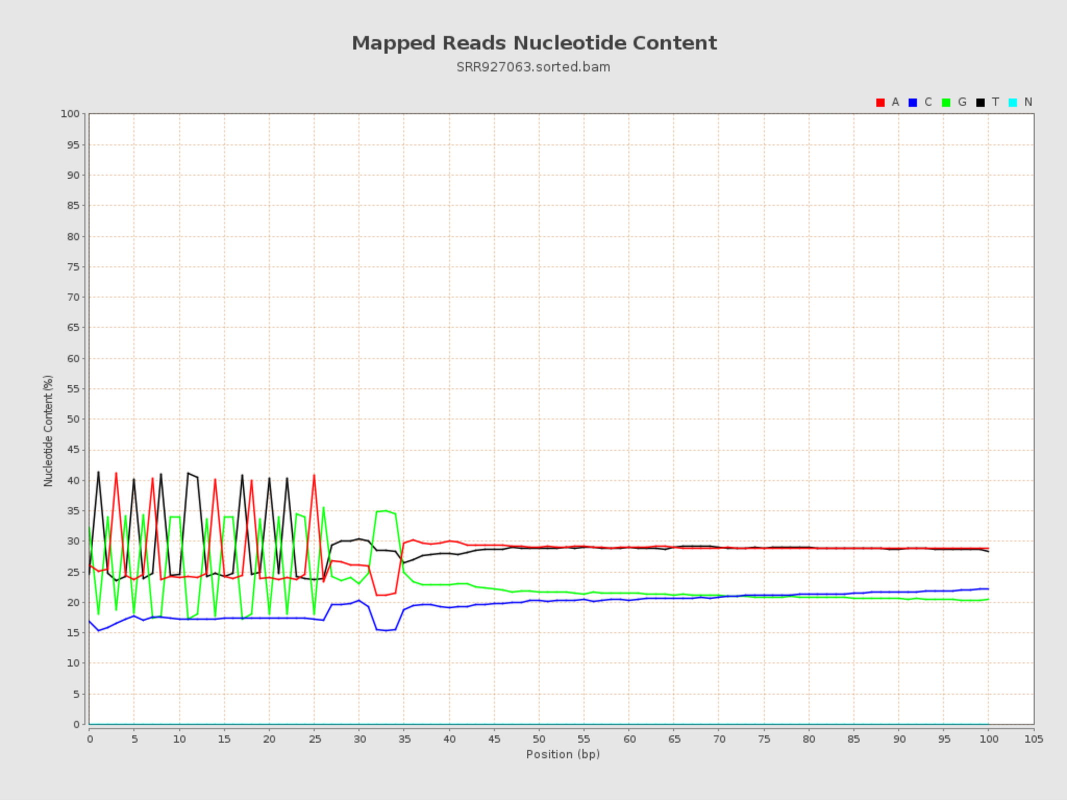
6. Results : Genome Fraction Coverage



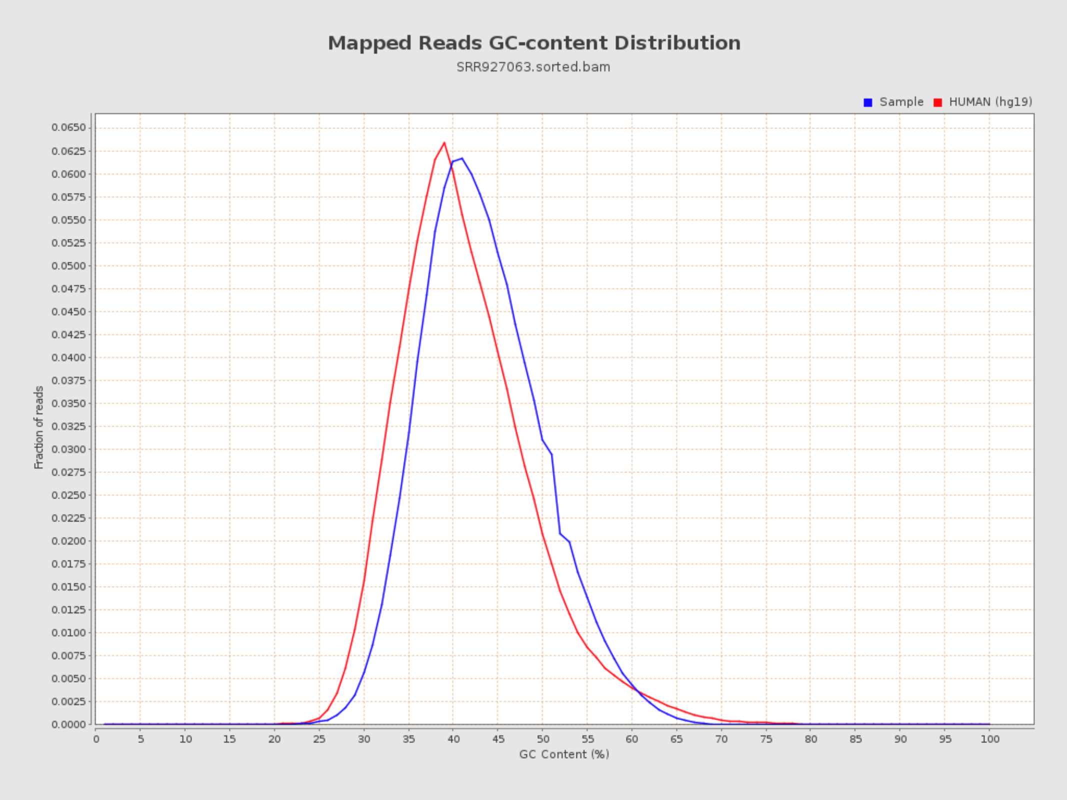
7. Results : Duplication Rate Histogram



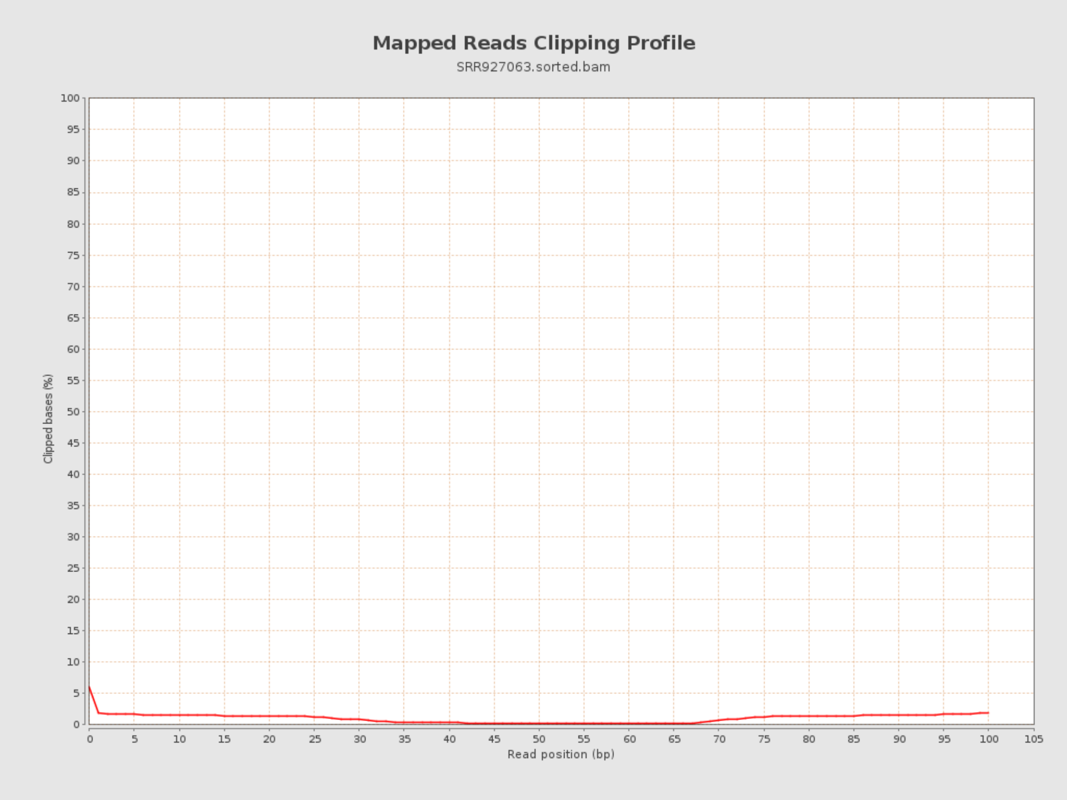
8. Results : Mapped Reads Nucleotide Content



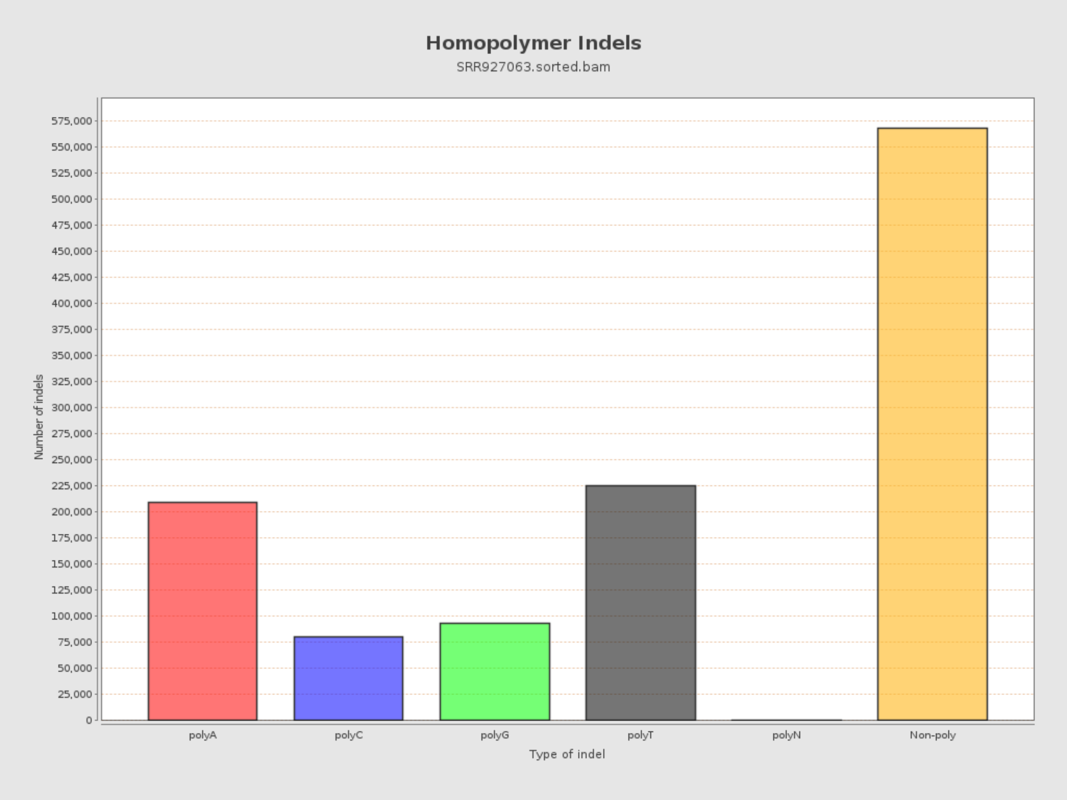
9. Results : Mapped Reads GC-content Distribution



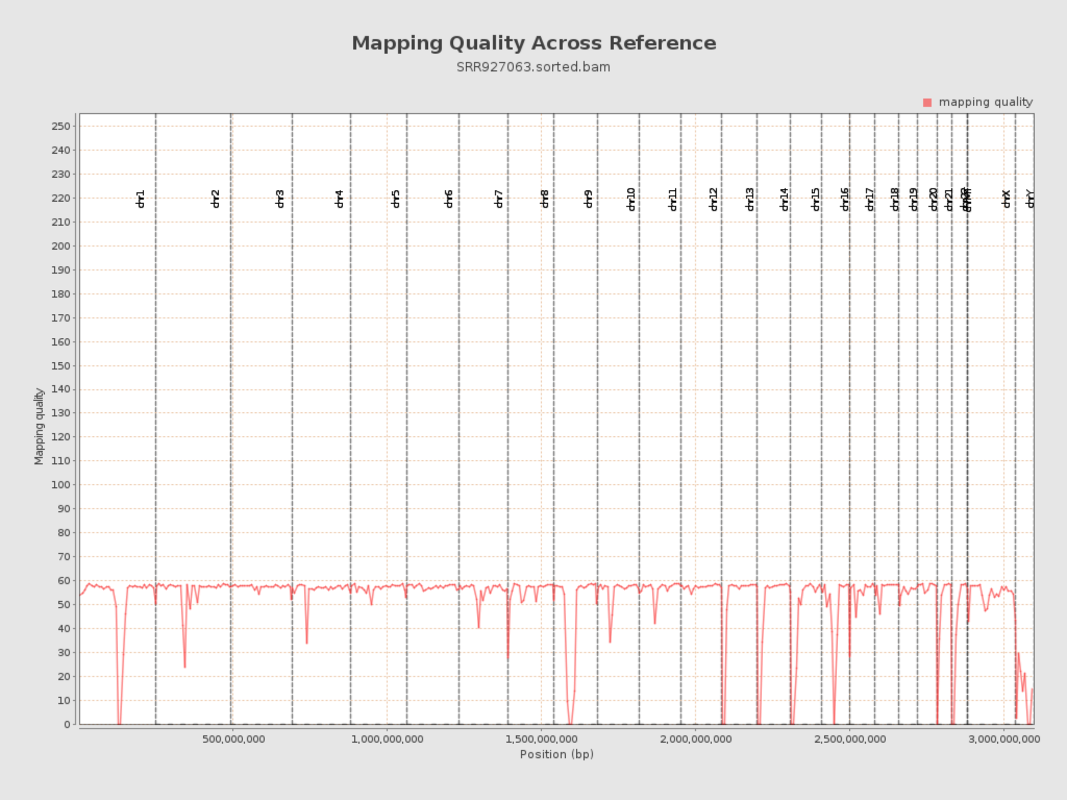
10. Results : Mapped Reads Clipping Profile



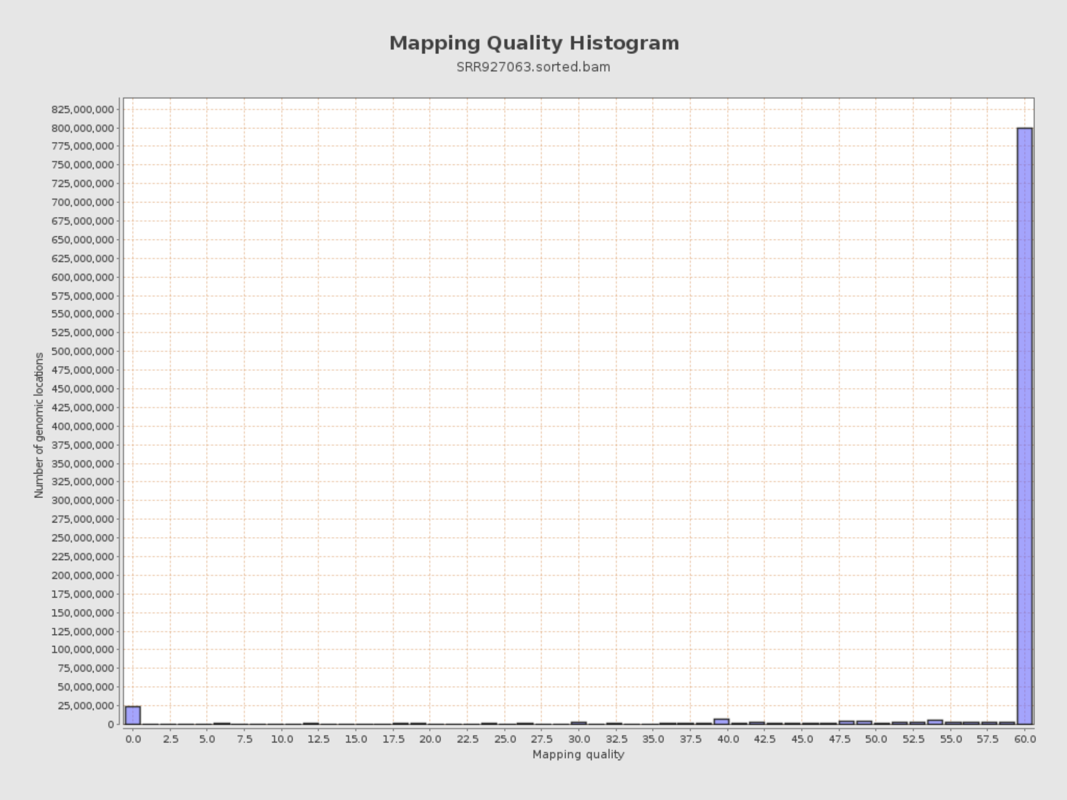
11. Results : Homopolymer Indels



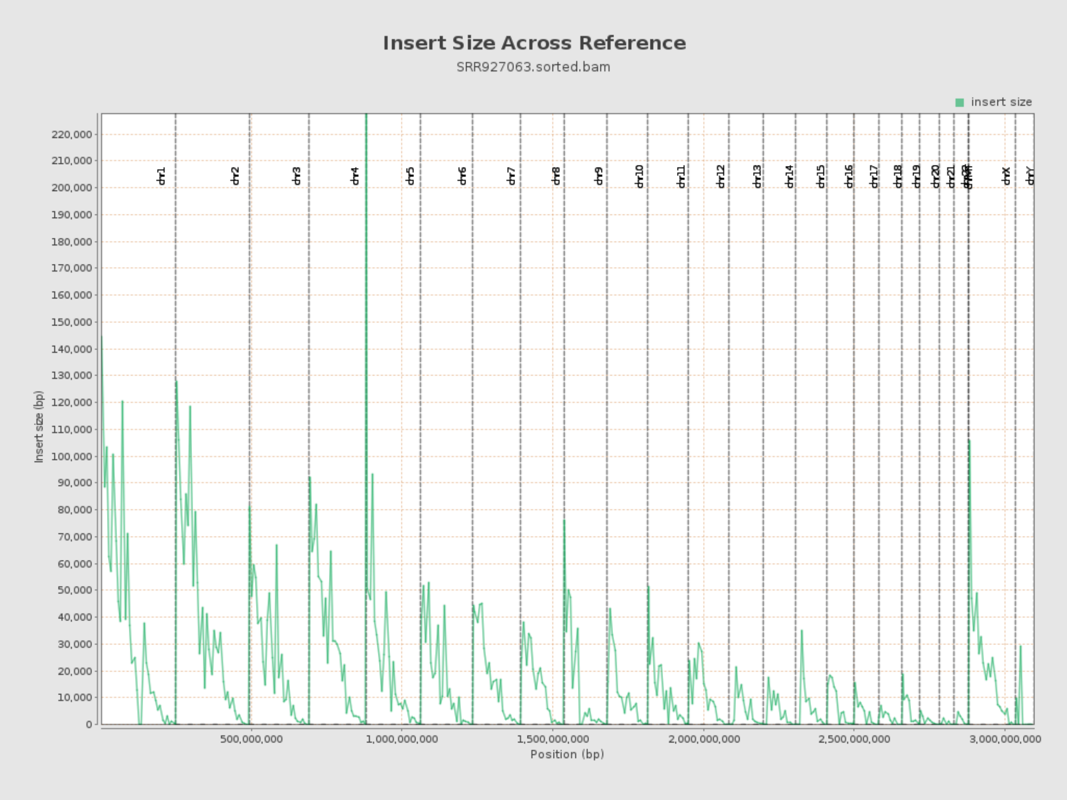
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram