Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 14:33:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926913.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_SRR926913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926913_1.fastq.gz SRR926913_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 14:33:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,728,954
Mapped reads	26,392,500 / 91.87%
Unmapped reads	2,336,454 / 8.13%
Mapped paired reads	26,392,500 / 91.87%
Mapped reads, first in pair	13,250,565 / 46.12%
Mapped reads, second in pair	13,141,935 / 45.74%
Mapped reads, both in pair	26,024,426 / 90.59%
Mapped reads, singletons	368,074 / 1.28%
Secondary alignments	0
Supplementary alignments	386,491 / 1.35%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	1,868,943 / 6.51%
Duplication rate	5.7%
Clipped reads	8,327,082 / 28.98%

2.2. ACGT Content

Number/percentage of A's	690,312,098 / 28.1%
Number/percentage of C's	499,818,591 / 20.34%
Number/percentage of T's	696,922,919 / 28.36%
Number/percentage of G's	569,717,998 / 23.19%
Number/percentage of N's	230,012 / 0.01%

GC Percentage	43.53%

2.3. Coverage

Mean	0.7943
Standard Deviation	2.7676

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	159,283.75
Standard Deviation	3,958,967.97
P25/Median/P75	146 / 188 / 249

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	25,095,430
Insertions	389,410
Mapped reads with at least one insertion	1.45%
Deletions	1,268,003
Mapped reads with at least one deletion	4.68%
Homopolymer indels	52.51%

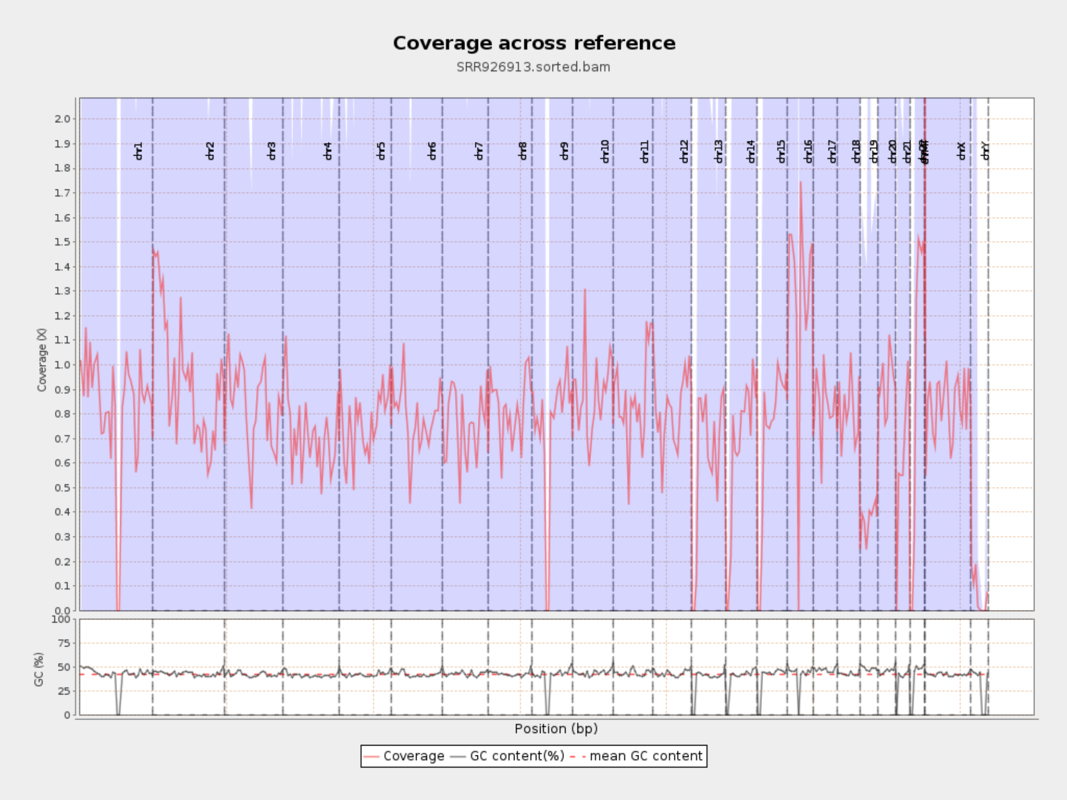
2.7. Chromosome stats

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

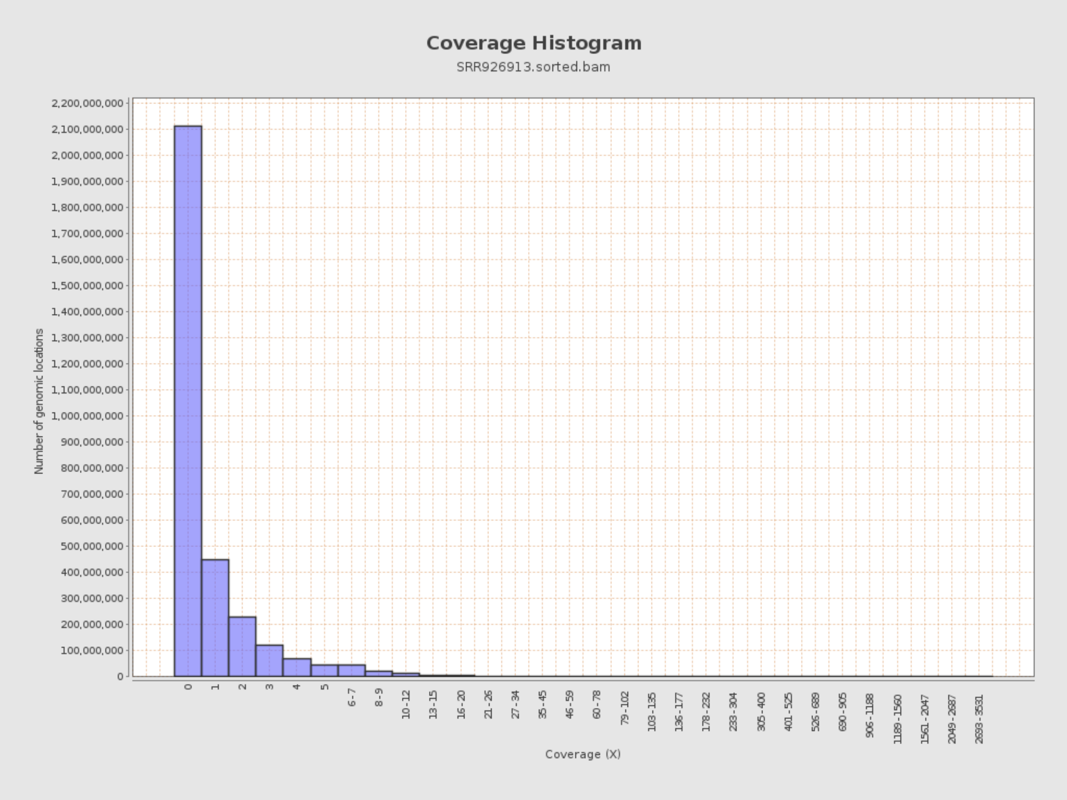
		bases	coverage	deviation
chr1	249250621	206622531	0.829	2.4647
chr2	243199373	229822808	0.945	3.8967
chr3	198022430	166022186	0.8384	1.7594
chr4	191154276	136641312	0.7148	1.7934
chr5	180915260	138874396	0.7676	1.6555
chr6	171115067	134984248	0.7889	1.6784
chr7	159138663	120549945	0.7575	1.8412
chr8	146364022	120914669	0.8261	1.8753
chr9	141213431	105725617	0.7487	3.1461
chr10	135534747	120064567	0.8859	6.9131
chr11	135006516	115694136	0.857	2.0935
chr12	133851895	109445083	0.8177	1.7826
chr13	115169878	71107490	0.6174	1.4825
chr14	107349540	70435710	0.6561	1.585
chr15	102531392	71341642	0.6958	1.6846
chr16	90354753	114499395	1.2672	5.5161
chr17	81195210	67776253	0.8347	1.9779
chr18	78077248	64443188	0.8254	3.2264
chr19	59128983	22239430	0.3761	1.4181
chr20	63025520	58764868	0.9324	1.9794
chr21	48129895	31059623	0.6453	2.3339
chr22	51304566	49035968	0.9558	2.277
chrMT	16571	40942	2.4707	2.6154
chrX	155270560	128744831	0.8292	1.8366

chrY	59373566	3979039	0.067	1.6365

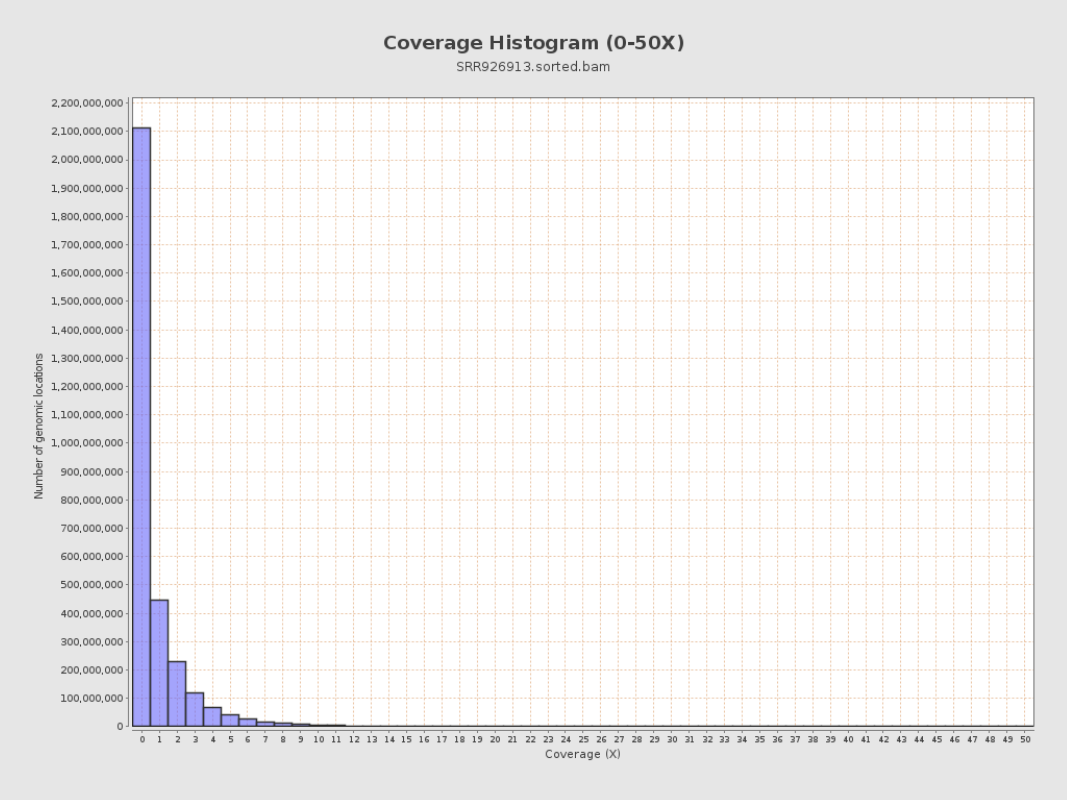
3. Results : Coverage across reference



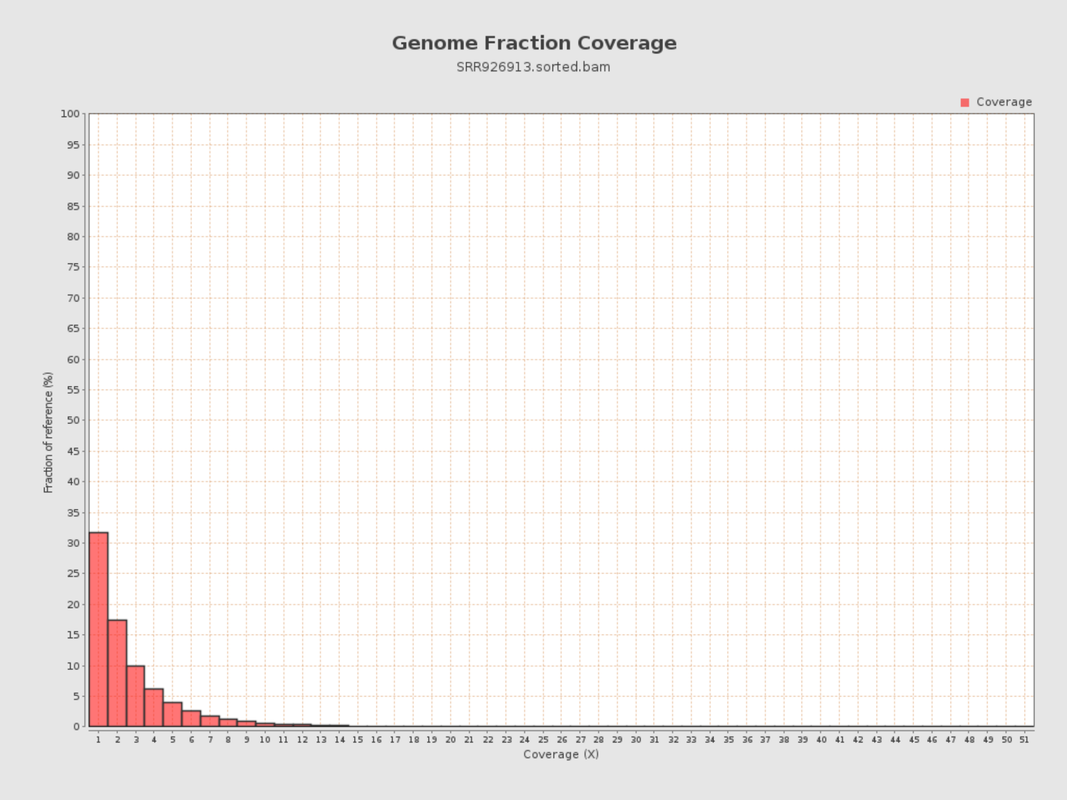
4. Results : Coverage Histogram



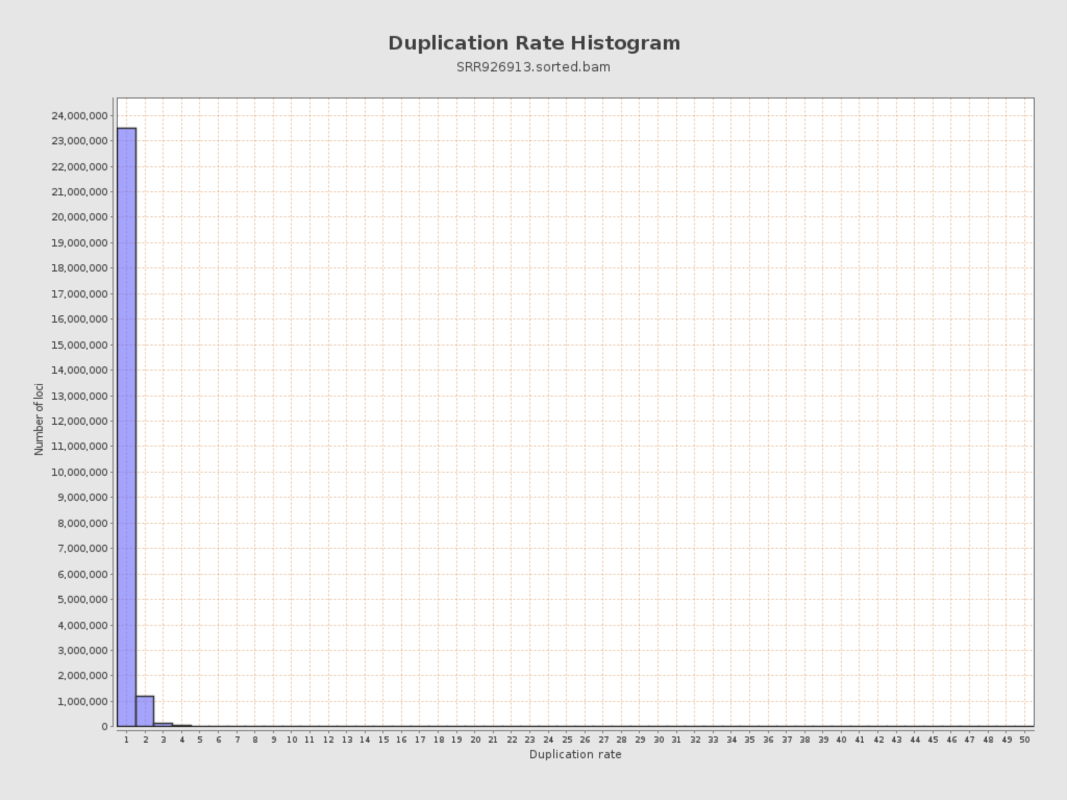
5. Results : Coverage Histogram (0-50X)



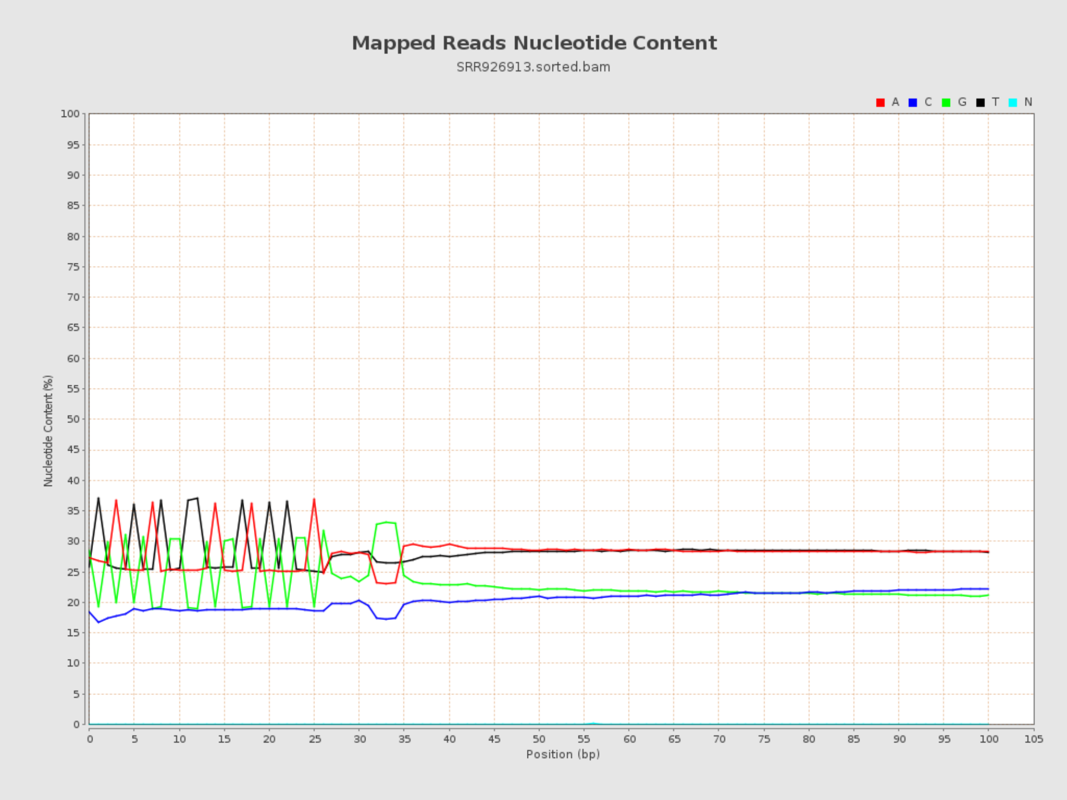
6. Results : Genome Fraction Coverage



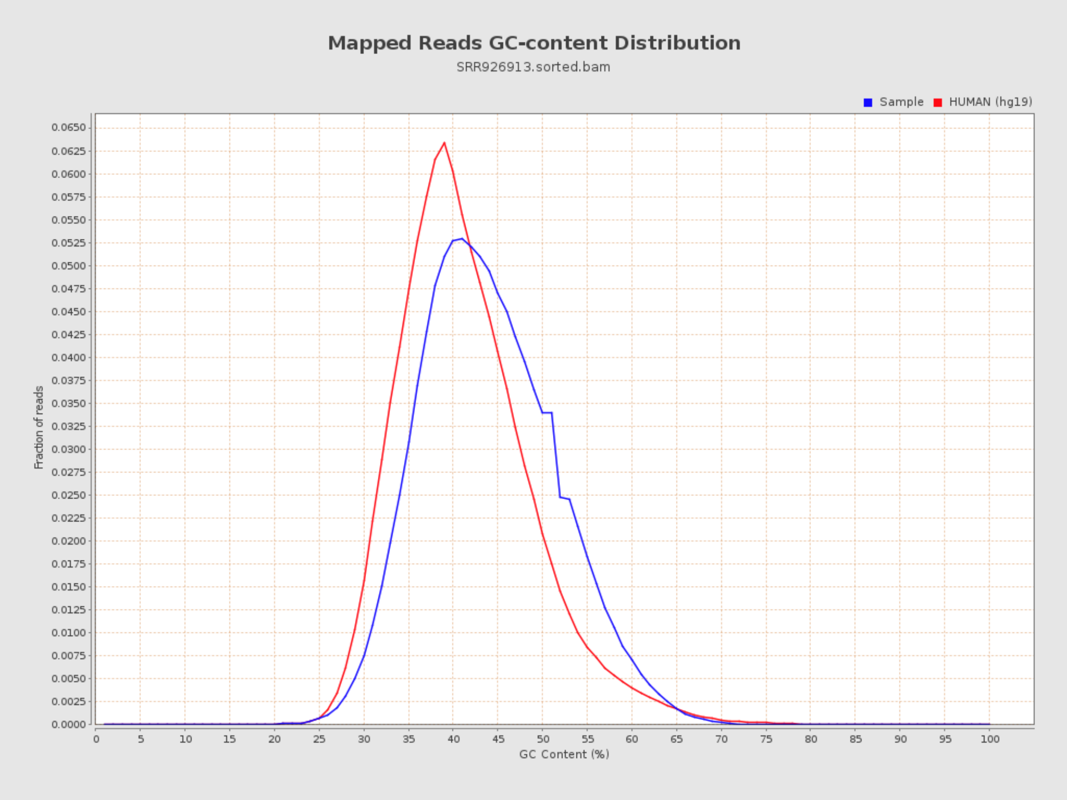
7. Results : Duplication Rate Histogram



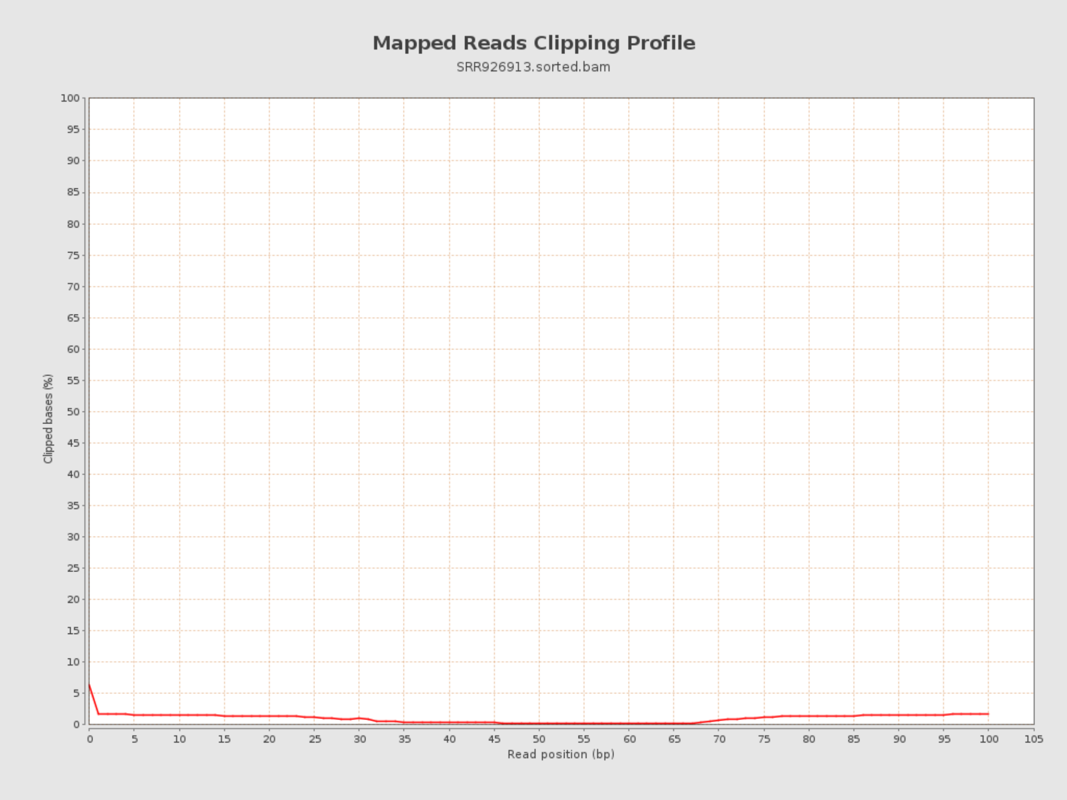
8. Results : Mapped Reads Nucleotide Content



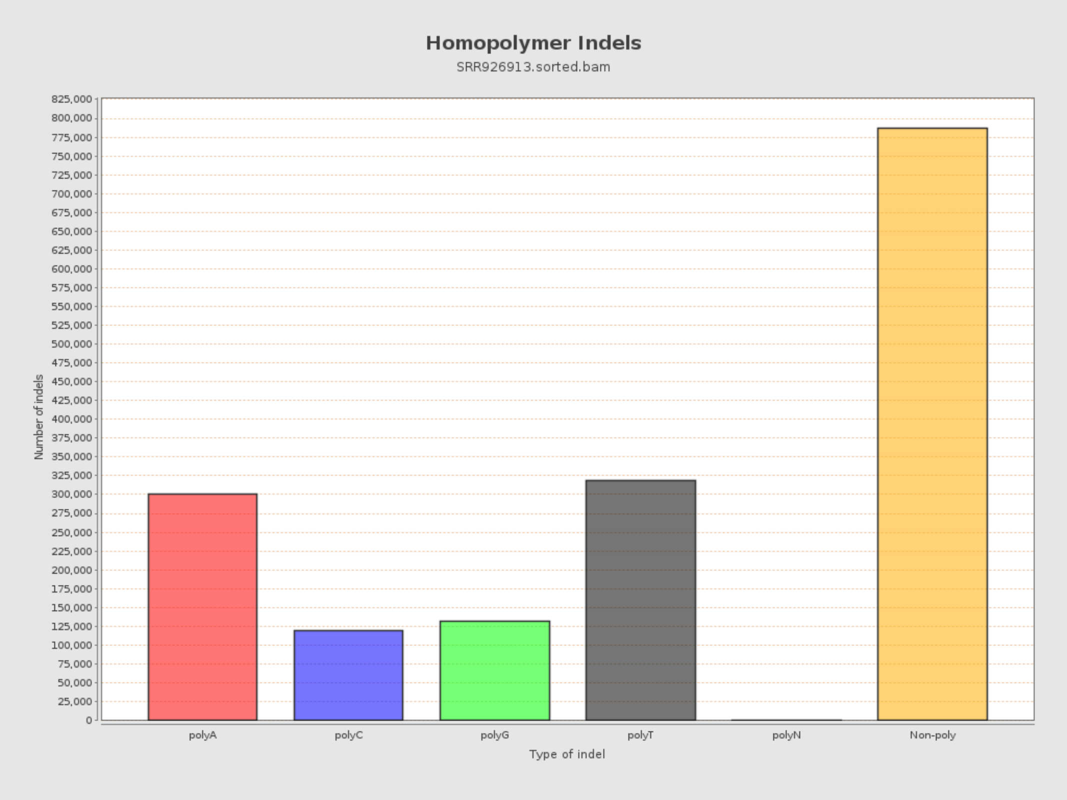
9. Results : Mapped Reads GC-content Distribution



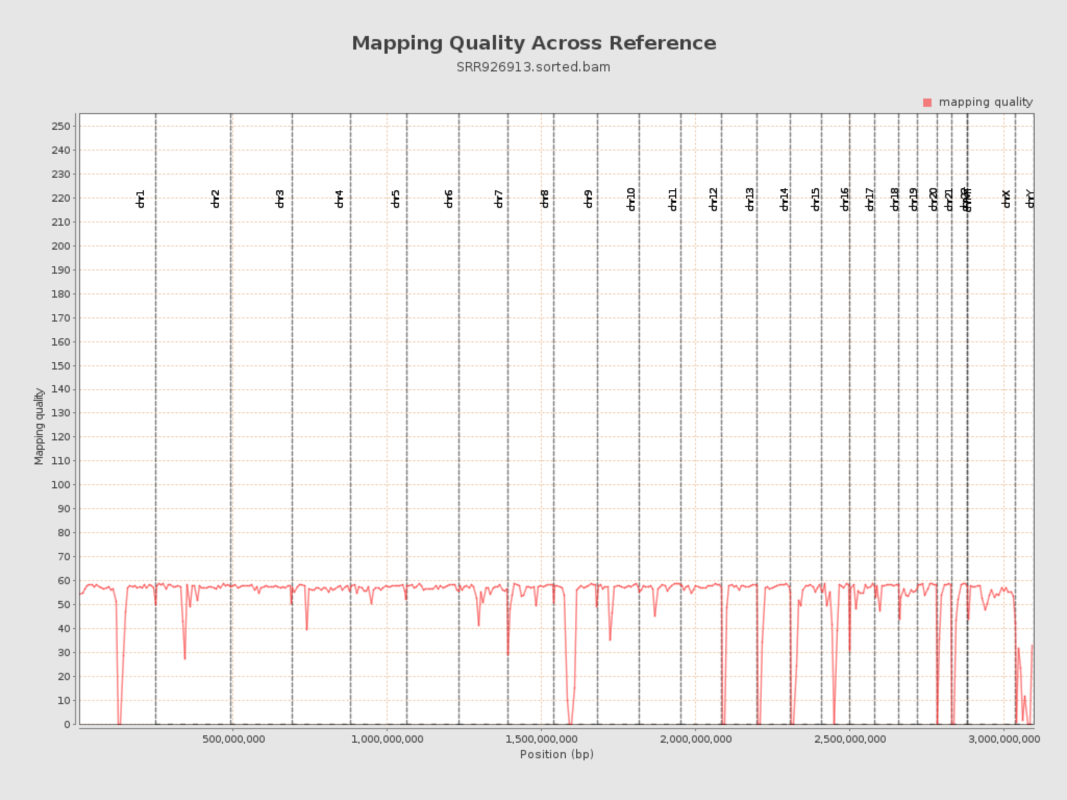
10. Results : Mapped Reads Clipping Profile



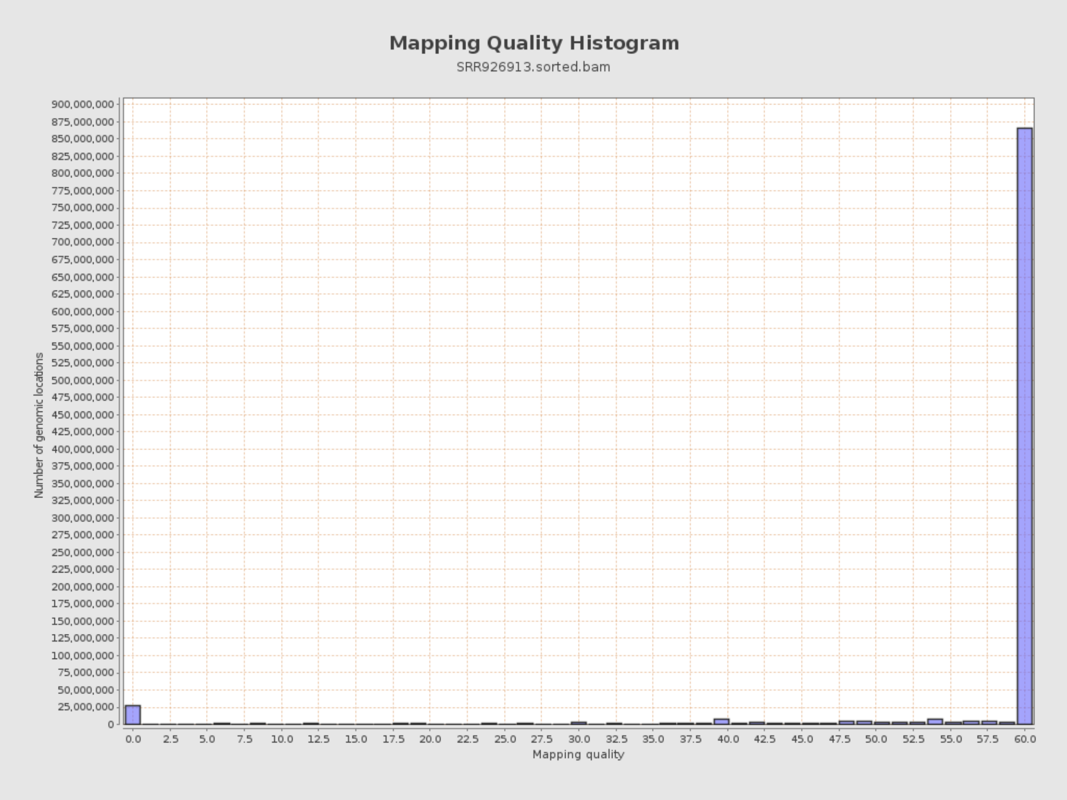
11. Results : Homopolymer Indels



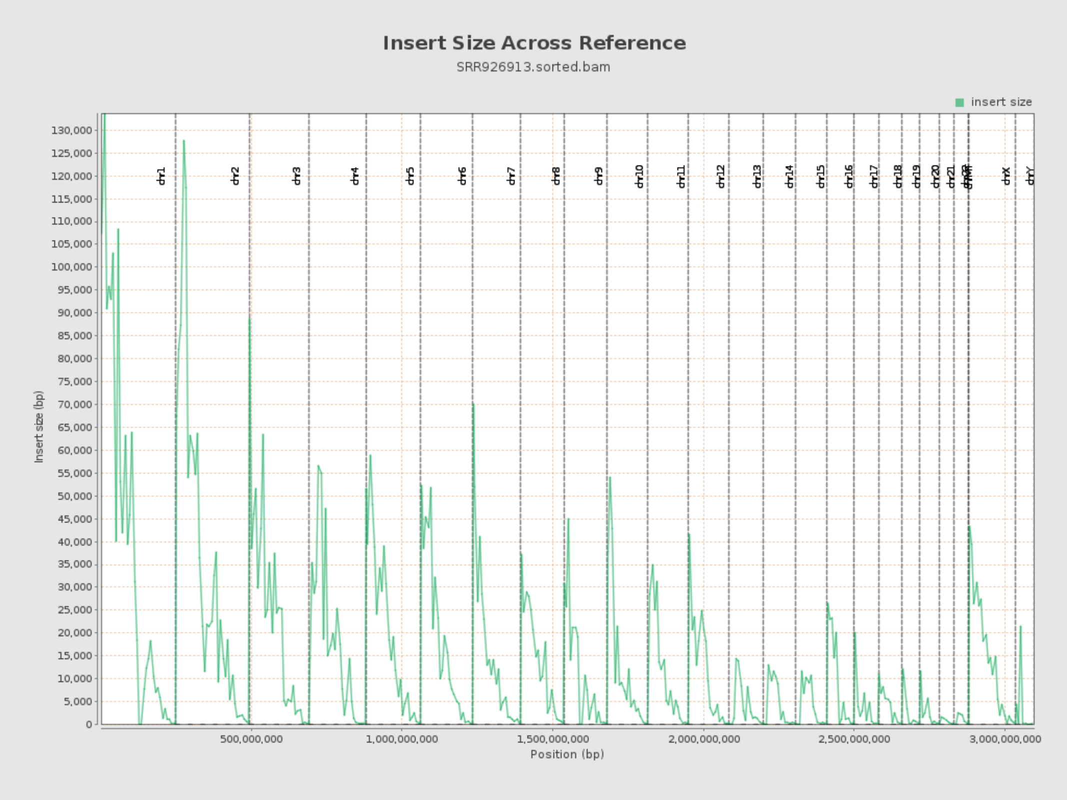
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram