Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 19:38:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926923.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_SRR926923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926923_1.fastq.gz SRR926923_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 19:38:14 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,031,686
Mapped reads	12,761,334 / 90.95%
Unmapped reads	1,270,352 / 9.05%
Mapped paired reads	12,761,334 / 90.95%
Mapped reads, first in pair	6,382,262 / 45.48%
Mapped reads, second in pair	6,379,072 / 45.46%
Mapped reads, both in pair	12,499,304 / 89.08%
Mapped reads, singletons	262,030 / 1.87%
Secondary alignments	0
Supplementary alignments	418,361 / 2.98%
Read min/max/mean length	30 / 101 / 102.23
Duplicated reads (estimated)	959,975 / 6.84%
Duplication rate	6.2%
Clipped reads	6,537,906 / 46.59%

2.2. ACGT Content

Number/percentage of A's	321,538,577 / 28.47%
Number/percentage of C's	213,984,641 / 18.95%
Number/percentage of T's	331,010,219 / 29.31%
Number/percentage of G's	262,794,061 / 23.27%
Number/percentage of N's	54,540 / 0%

GC Percentage	42.22%

2.3. Coverage

Mean	0.3651
Standard Deviation	1.4135

2.4. Mapping Quality

Mean Mapping Quality	52.45

2.5. Insert size

Mean	324,077.93
Standard Deviation	5,569,318.85
P25/Median/P75	136 / 179 / 243

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	10,878,836
Insertions	199,613
Mapped reads with at least one insertion	1.53%
Deletions	607,311
Mapped reads with at least one deletion	4.64%
Homopolymer indels	51.86%

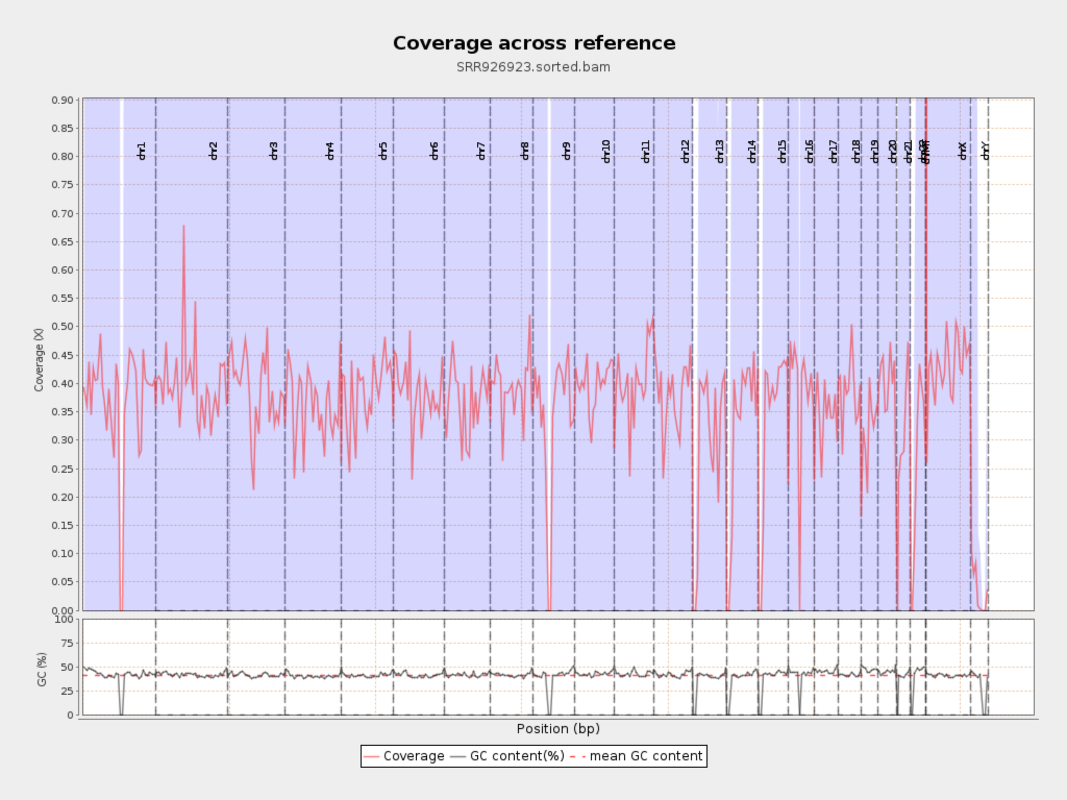
2.7. Chromosome stats

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

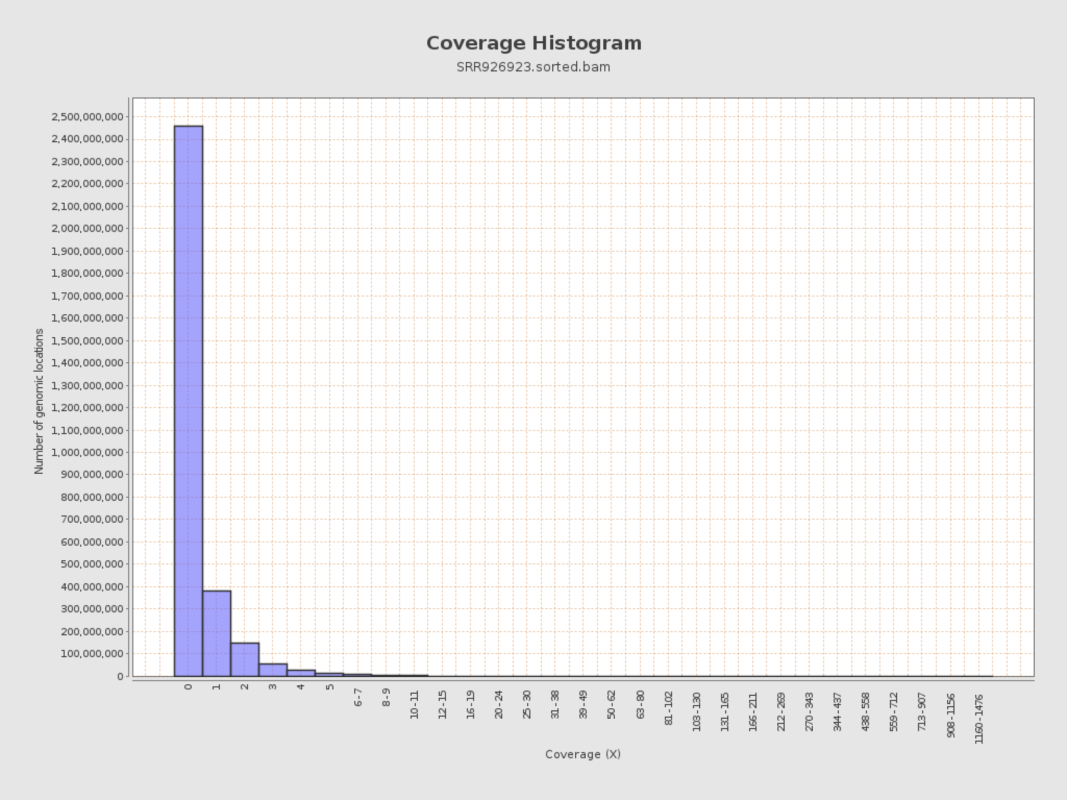
		bases	**coverage**	**deviation**
chr1	249250621	91404067	0.3667	1.4373
chr2	243199373	97215439	0.3997	2.6882
chr3	198022430	76679260	0.3872	0.9547
chr4	191154276	69584427	0.364	1.2174
chr5	180915260	69816072	0.3859	0.9532
chr6	171115067	65559527	0.3831	1.6387
chr7	159138663	58868237	0.3699	1.1936
chr8	146364022	57579467	0.3934	1.0619
chr9	141213431	48007266	0.34	1.6481
chr10	135534747	53962135	0.3981	1.6903
chr11	135006516	54281629	0.4021	1.2398
chr12	133851895	51281067	0.3831	1.0048
chr13	115169878	33590030	0.2917	0.8262
chr14	107349540	34562248	0.322	0.9013
chr15	102531392	33954660	0.3312	0.9085
chr16	90354753	33776193	0.3738	1.6609
chr17	81195210	28443229	0.3503	0.9755
chr18	78077248	30157366	0.3863	1.396
chr19	59128983	18669185	0.3157	1.1922
chr20	63025520	25538651	0.4052	1.032
chr21	48129895	14447580	0.3002	1.1524
chr22	51304566	13272650	0.2587	0.8403
chrMT	16571	901373	54.3946	43.4829
chrX	155270560	66688055	0.4295	1.0694

chrY	59373566	2041980	0.0344	1.103

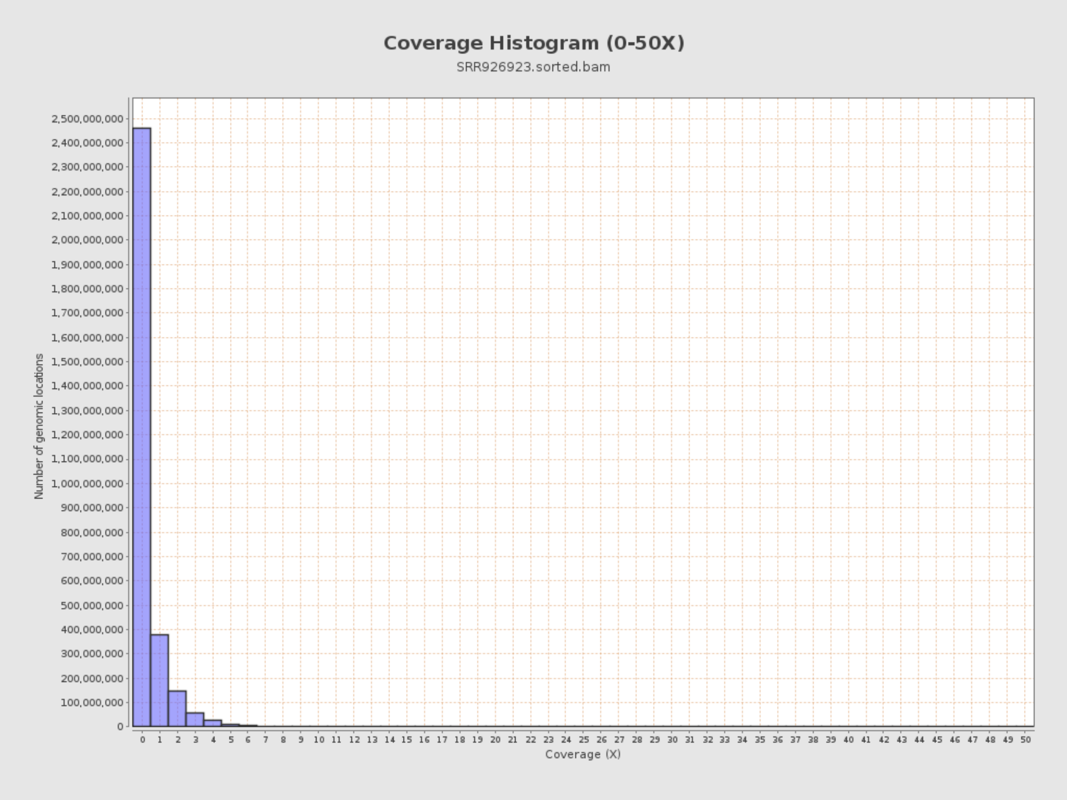
3. Results : Coverage across reference



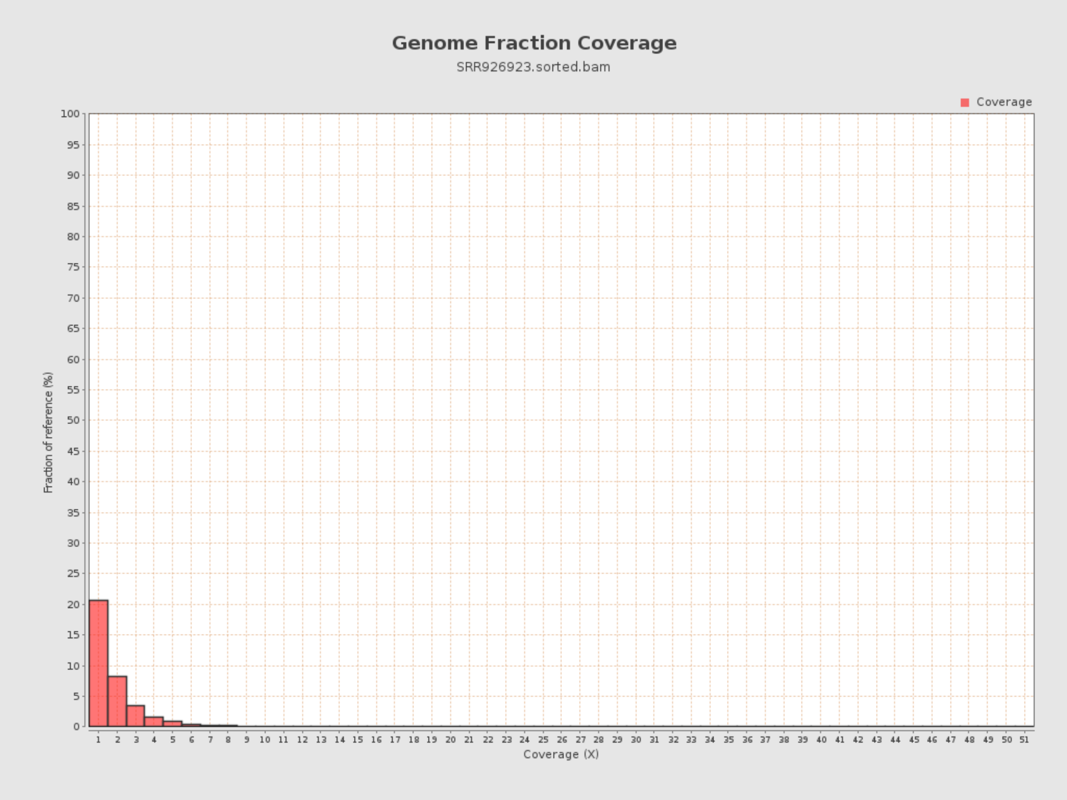
4. Results : Coverage Histogram



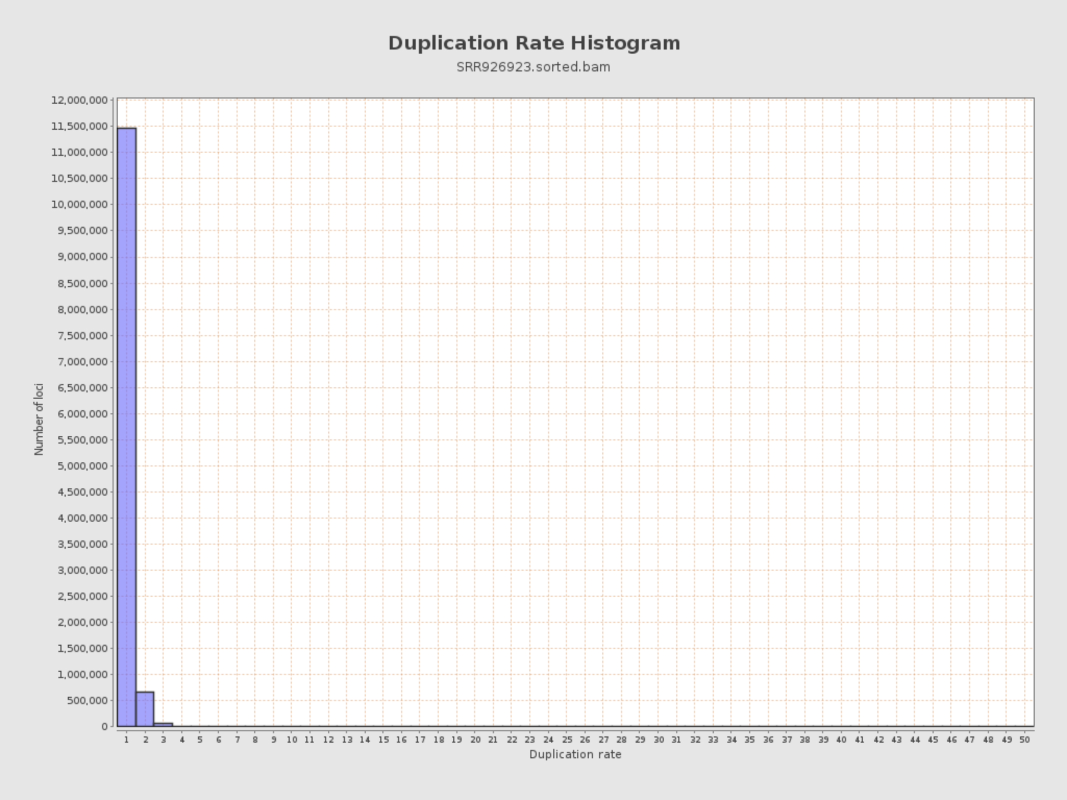
5. Results : Coverage Histogram (0-50X)



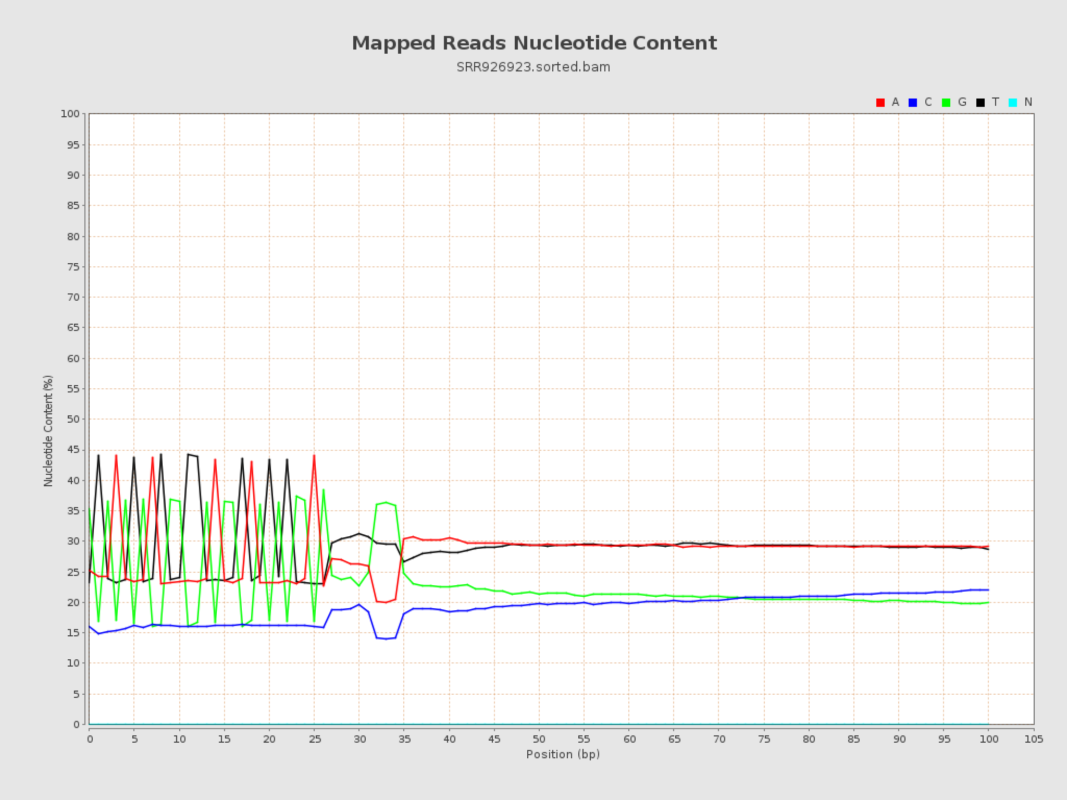
6. Results : Genome Fraction Coverage



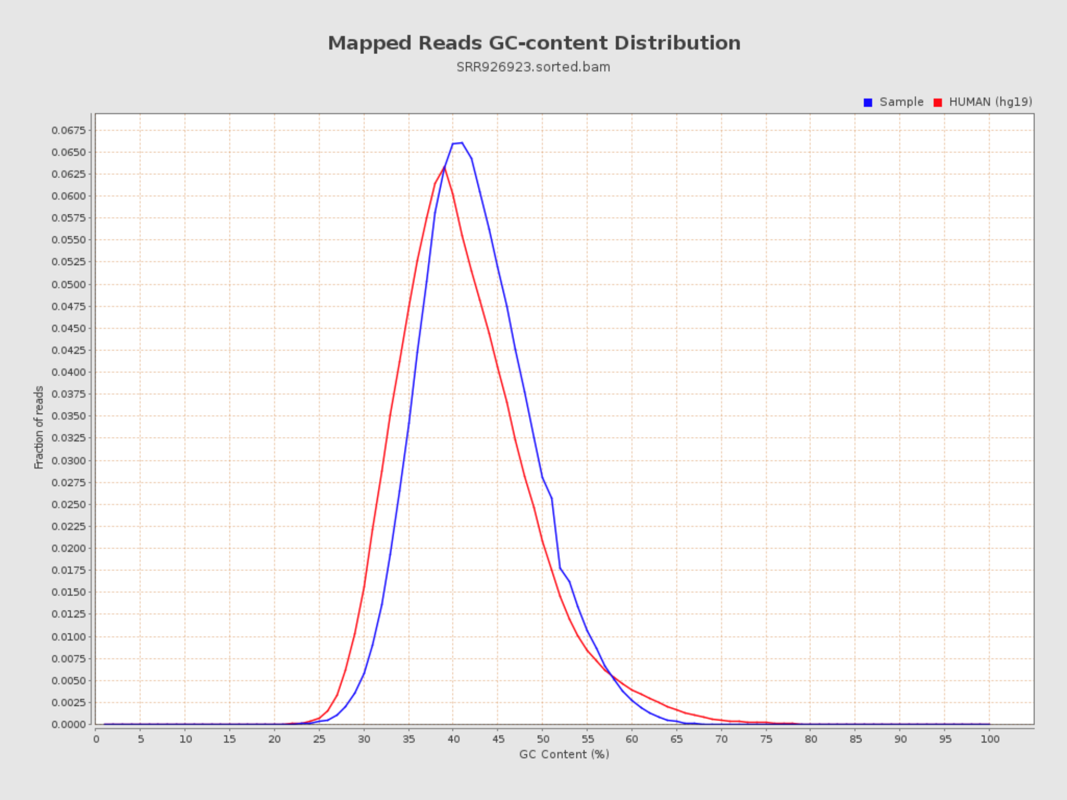
7. Results : Duplication Rate Histogram



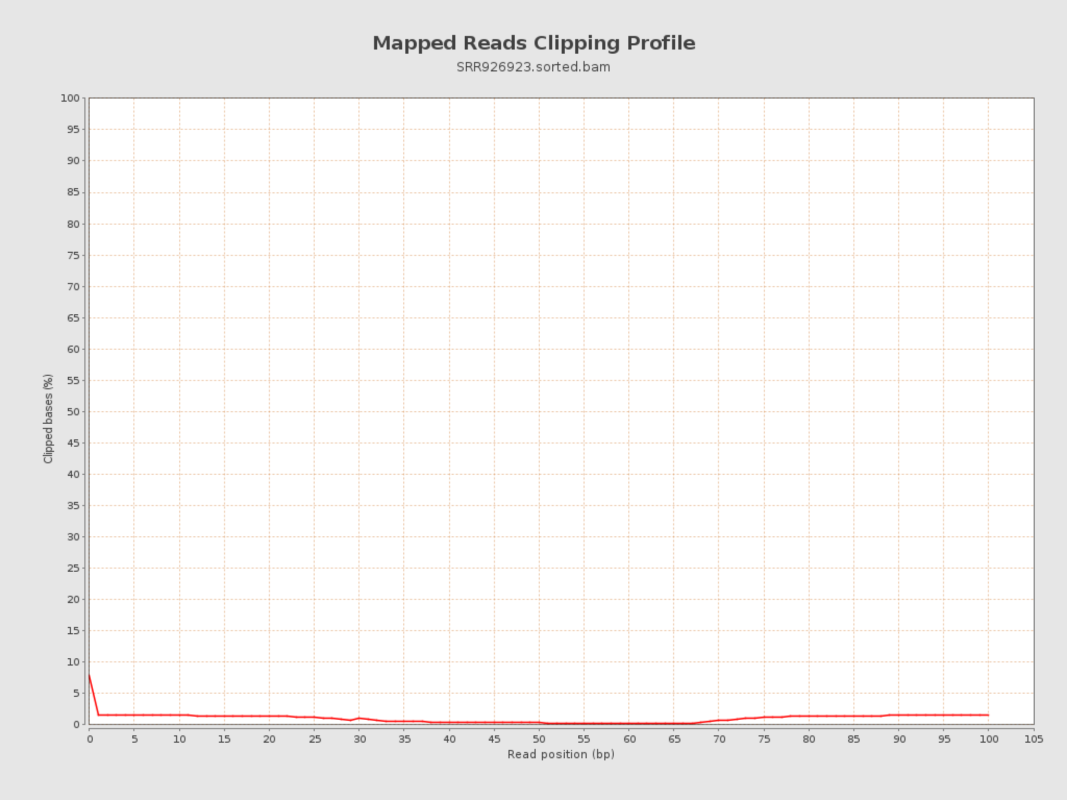
8. Results : Mapped Reads Nucleotide Content



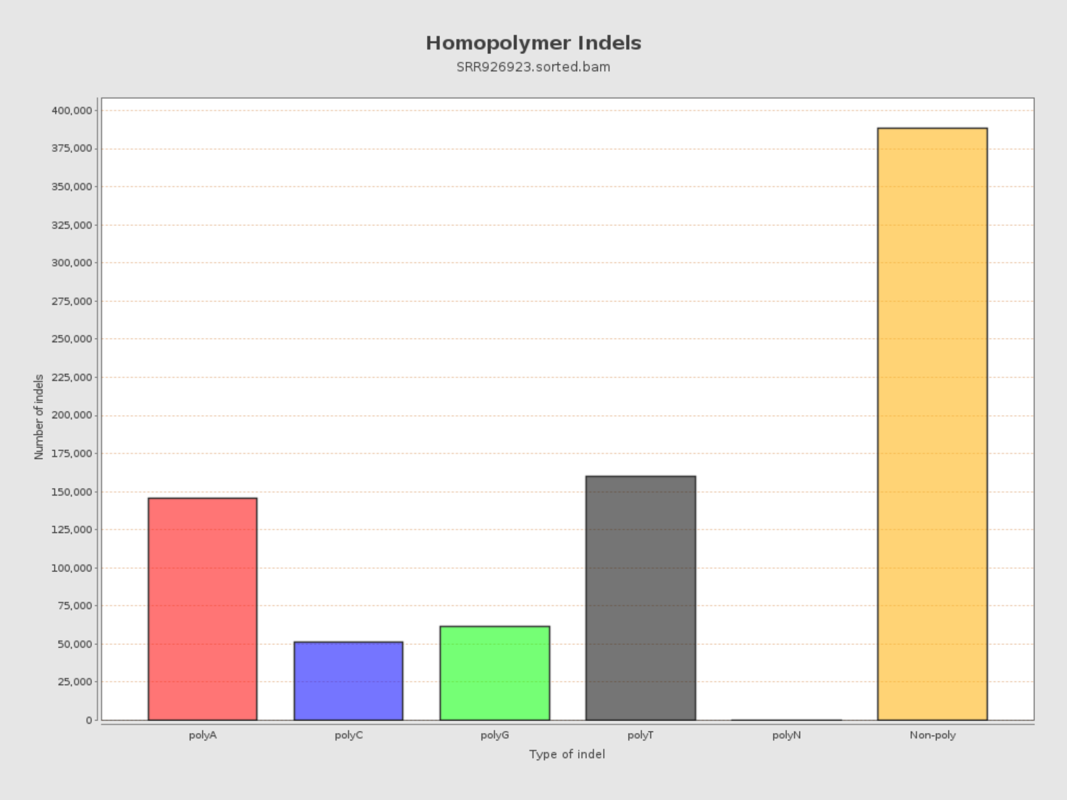
9. Results : Mapped Reads GC-content Distribution



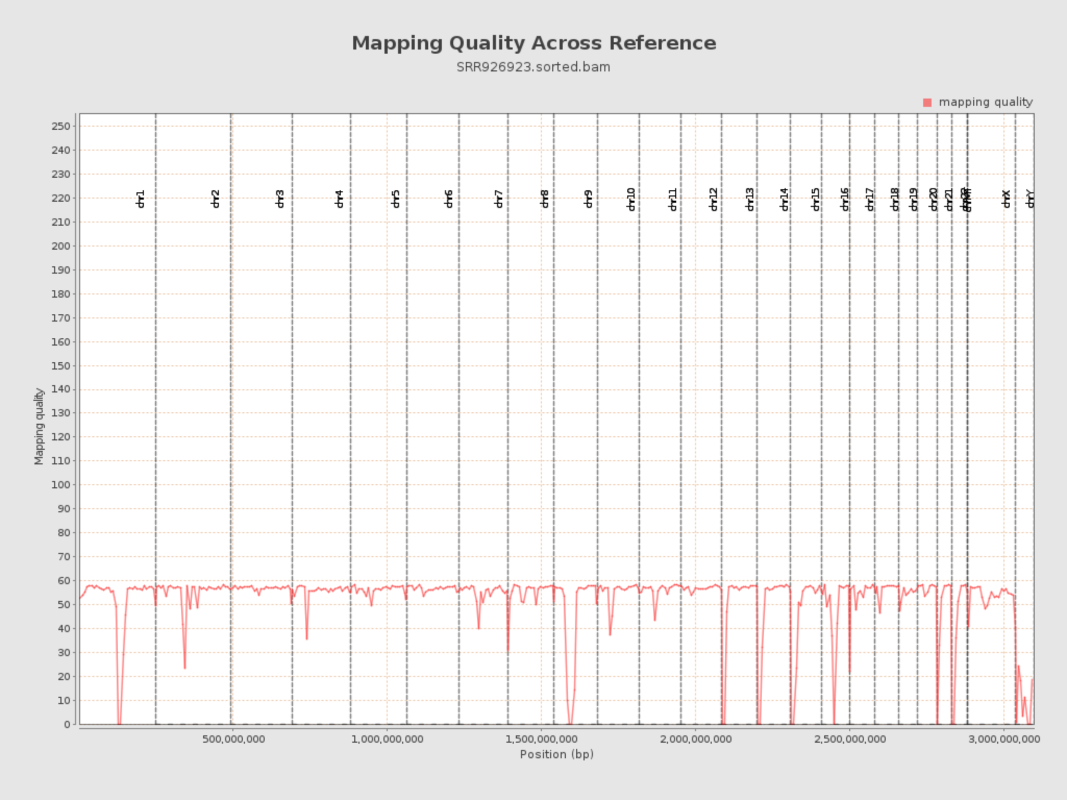
10. Results : Mapped Reads Clipping Profile



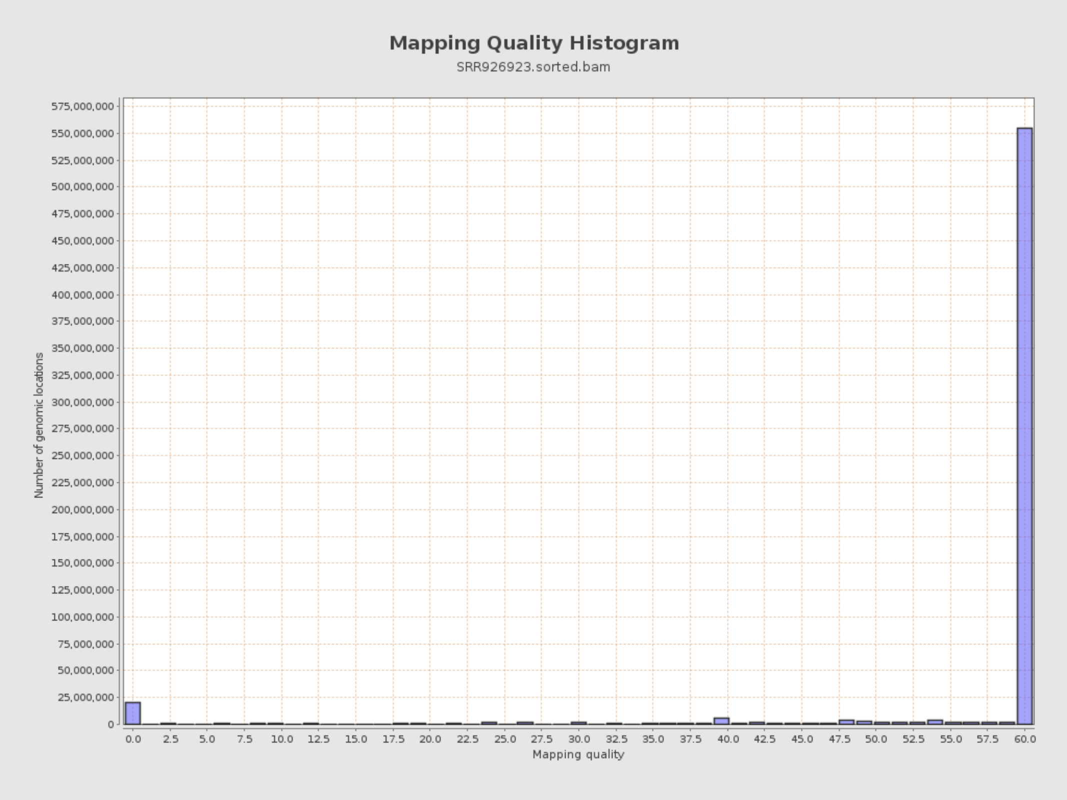
11. Results : Homopolymer Indels



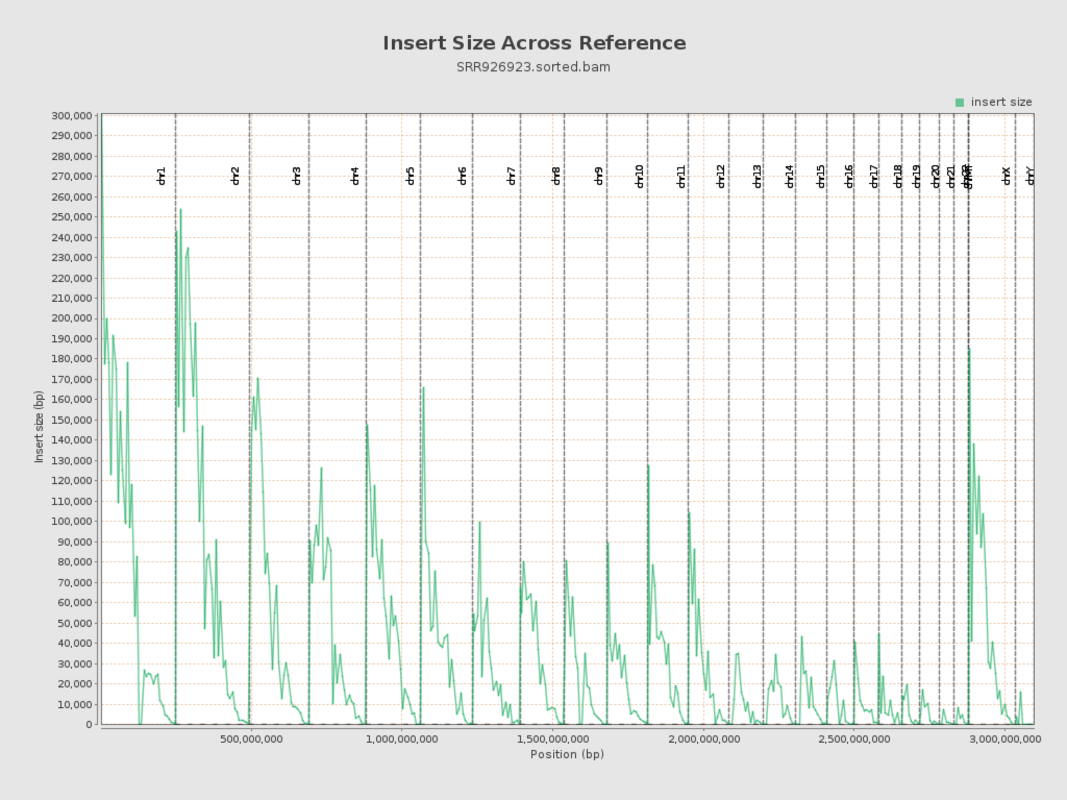
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram