Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 03:52:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926959.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_SRR926959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926959_1.fastq.gz SRR926959_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 03:52:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,499,394
Mapped reads	10,036,278 / 95.59%
Unmapped reads	463,116 / 4.41%
Mapped paired reads	10,036,278 / 95.59%
Mapped reads, first in pair	5,021,551 / 47.83%
Mapped reads, second in pair	5,014,727 / 47.76%
Mapped reads, both in pair	9,817,962 / 93.51%
Mapped reads, singletons	218,316 / 2.08%
Secondary alignments	0
Supplementary alignments	443,968 / 4.23%
Read min/max/mean length	30 / 101 / 102.76
Duplicated reads (estimated)	702,845 / 6.69%
Duplication rate	5.88%
Clipped reads	5,039,575 / 48%

2.2. ACGT Content

Number/percentage of A's	255,209,590 / 28.34%
Number/percentage of C's	176,152,178 / 19.56%
Number/percentage of T's	257,589,695 / 28.6%
Number/percentage of G's	211,673,487 / 23.5%
Number/percentage of N's	46,864 / 0.01%

GC Percentage	43.06%

2.3. Coverage

Mean	0.2912
Standard Deviation	1.1409

2.4. Mapping Quality

Mean Mapping Quality	52.29

2.5. Insert size

Mean	453,196.84
Standard Deviation	6,584,319.96
P25/Median/P75	138 / 183 / 250

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	9,098,350
Insertions	155,287
Mapped reads with at least one insertion	1.52%
Deletions	454,081
Mapped reads with at least one deletion	4.41%
Homopolymer indels	51.9%

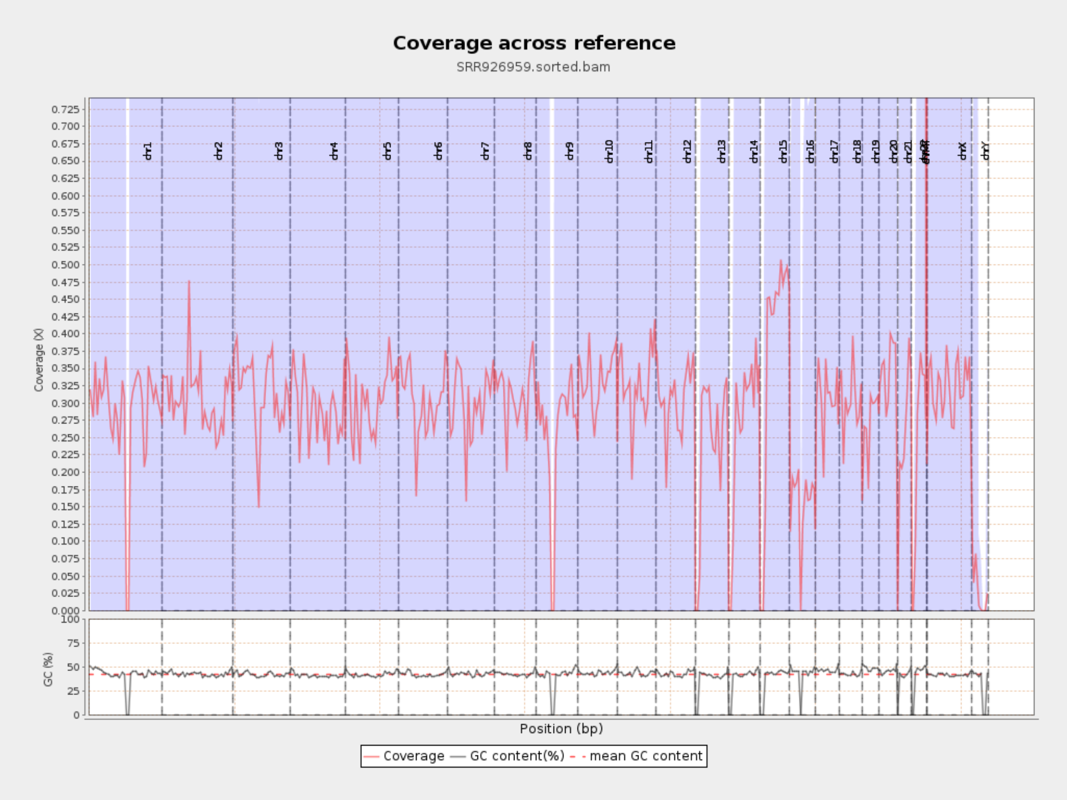
2.7. Chromosome stats

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

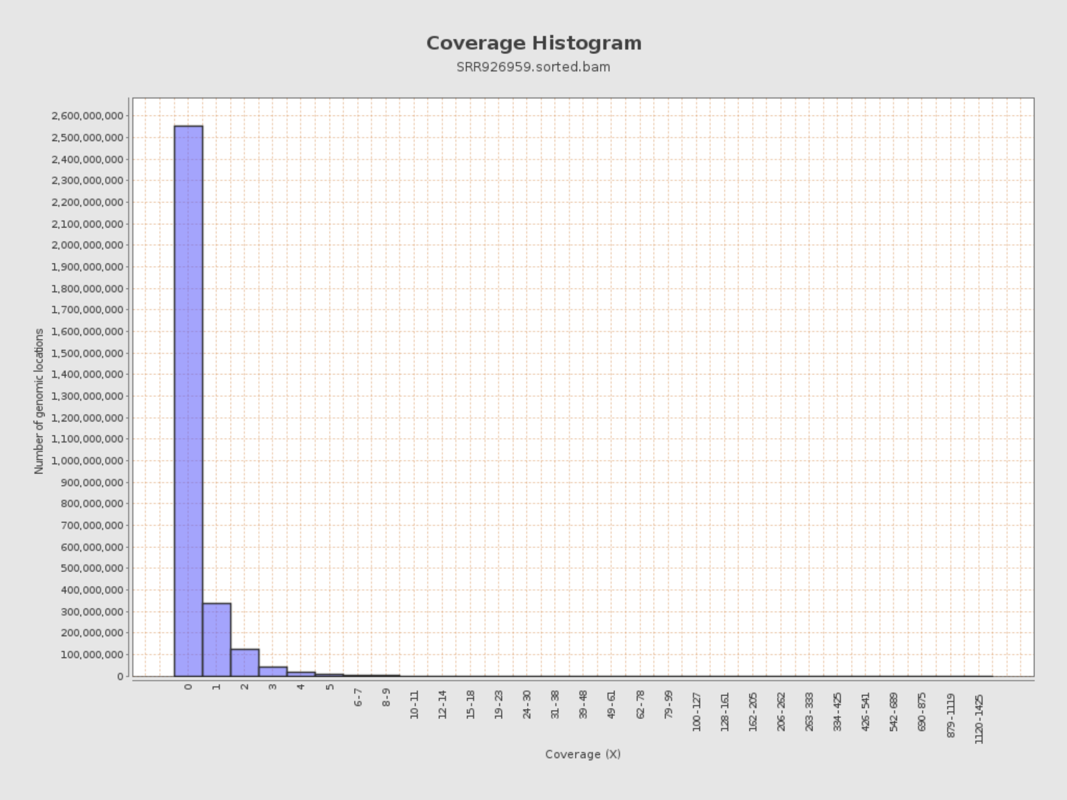
		bases	coverage	deviation
chr1	249250621	70824088	0.2841	1.2257
chr2	243199373	74907707	0.308	2.0135
chr3	198022430	62703537	0.3166	0.8209
chr4	191154276	55738930	0.2916	1.2596
chr5	180915260	55053177	0.3043	0.7978
chr6	171115067	52327851	0.3058	0.8379
chr7	159138663	47503702	0.2985	0.8582
chr8	146364022	45961405	0.314	0.8671
chr9	141213431	36073787	0.2555	1.006
chr10	135534747	45349211	0.3346	1.7867
chr11	135006516	44080032	0.3265	1.1516
chr12	133851895	41023091	0.3065	1.2106
chr13	115169878	27197801	0.2362	0.706
chr14	107349540	28074501	0.2615	0.7587
chr15	102531392	38374119	0.3743	0.9688
chr16	90354753	14186071	0.157	0.8158
chr17	81195210	24937642	0.3071	0.8481
chr18	78077248	23818926	0.3051	1.1099
chr19	59128983	15968879	0.2701	0.9073
chr20	63025520	21824208	0.3463	0.9245
chr21	48129895	12098292	0.2514	1.2358
chr22	51304566	11648077	0.227	0.7073
chrMT	16571	245233	14.7989	17.3087
chrX	155270560	49817106	0.3208	0.851

chrY	59373566	1610968	0.0271	0.9844

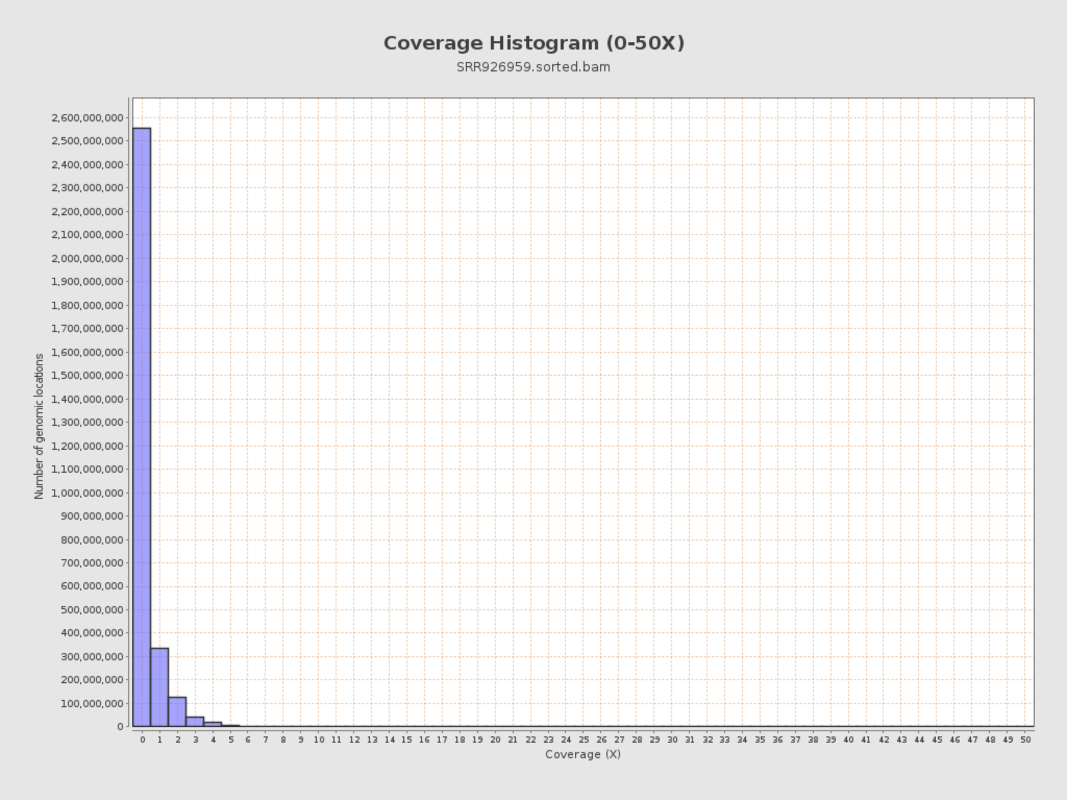
3. Results : Coverage across reference



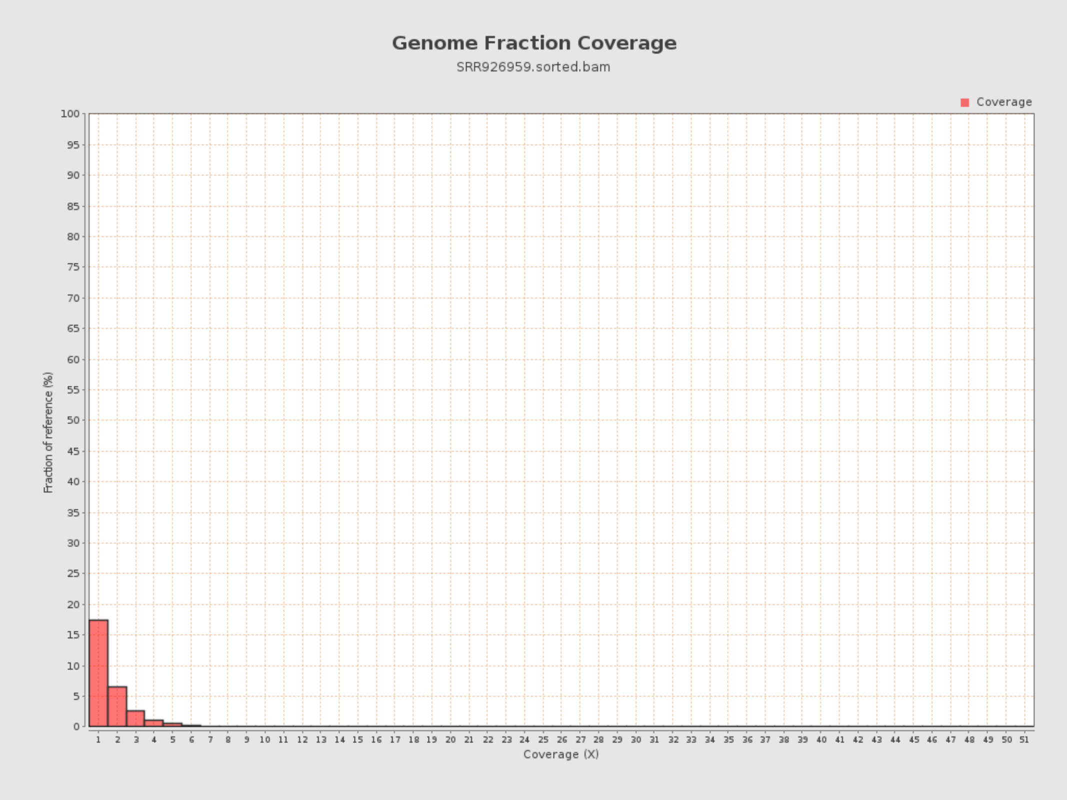
4. Results : Coverage Histogram



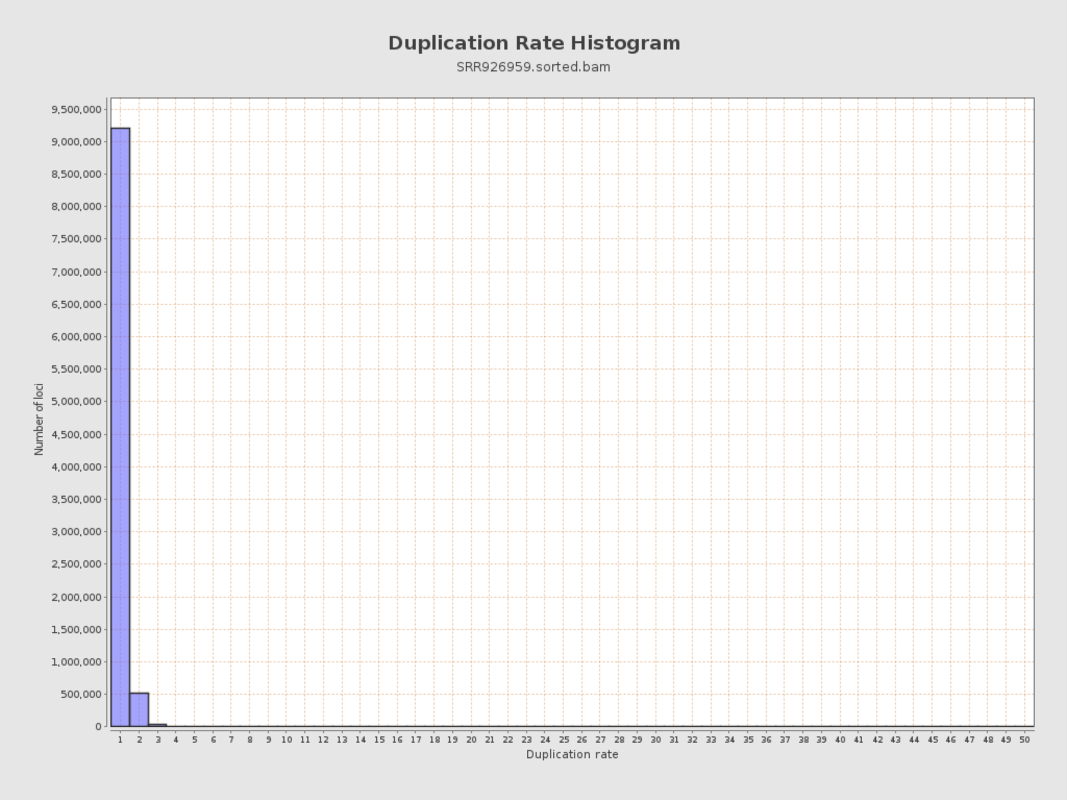
5. Results : Coverage Histogram (0-50X)



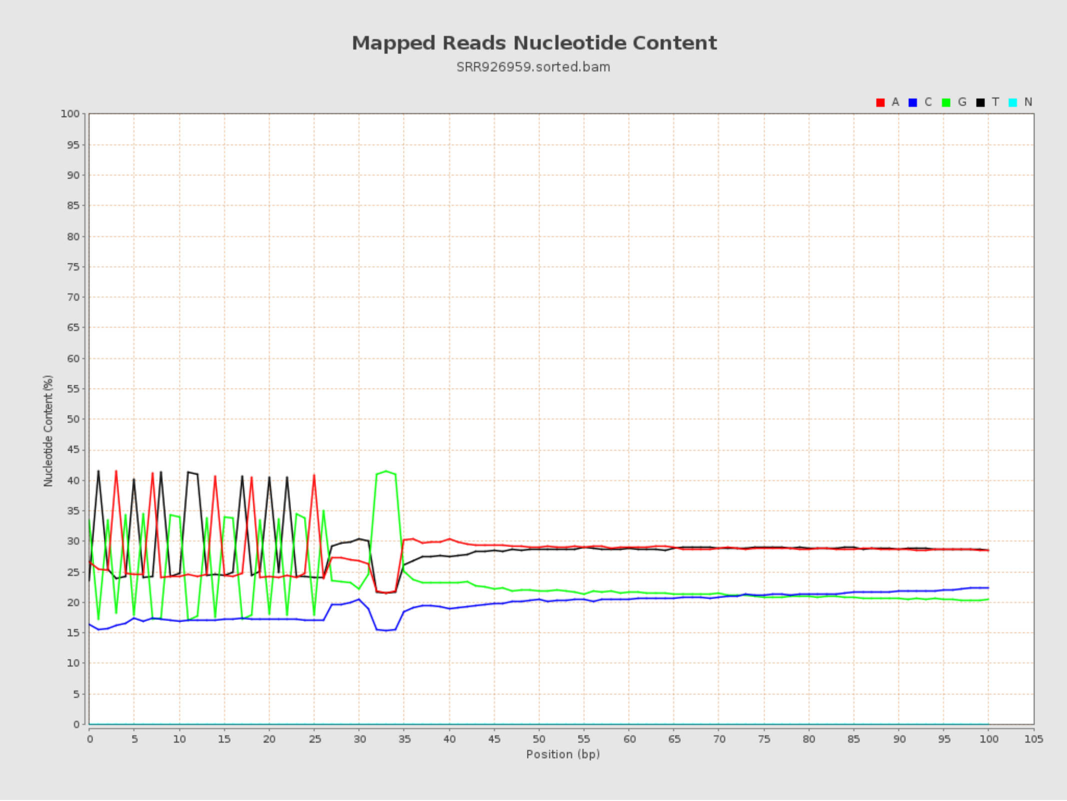
6. Results : Genome Fraction Coverage



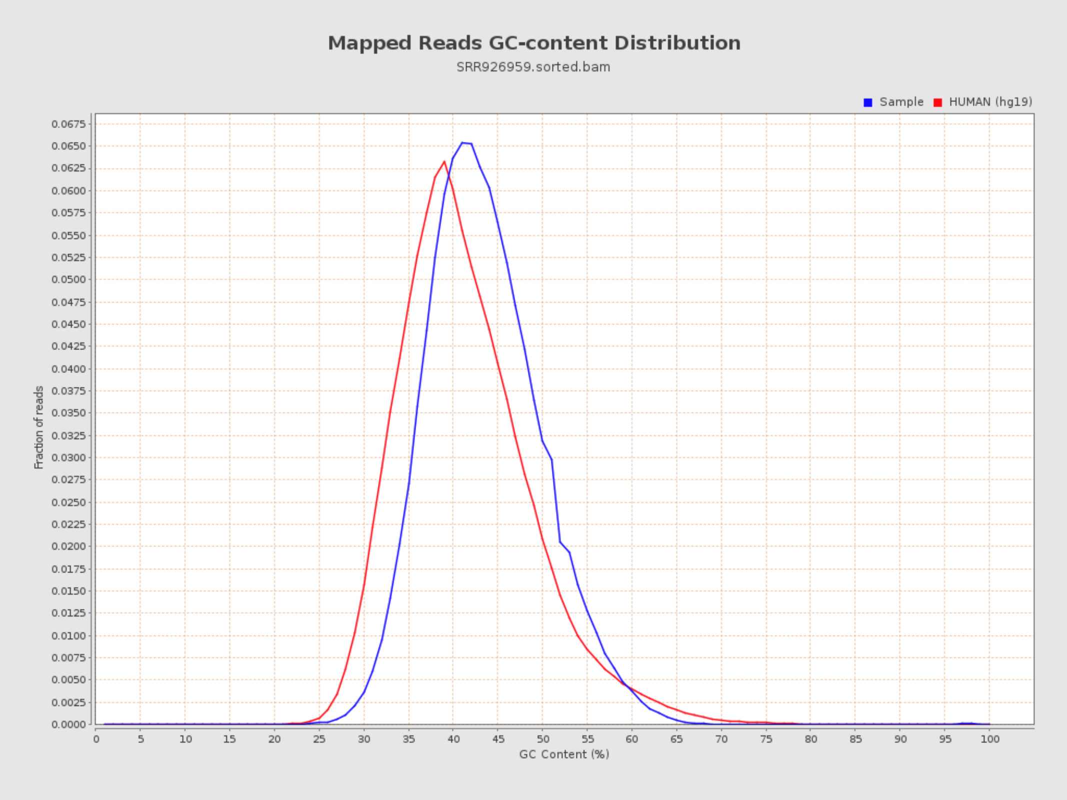
7. Results : Duplication Rate Histogram



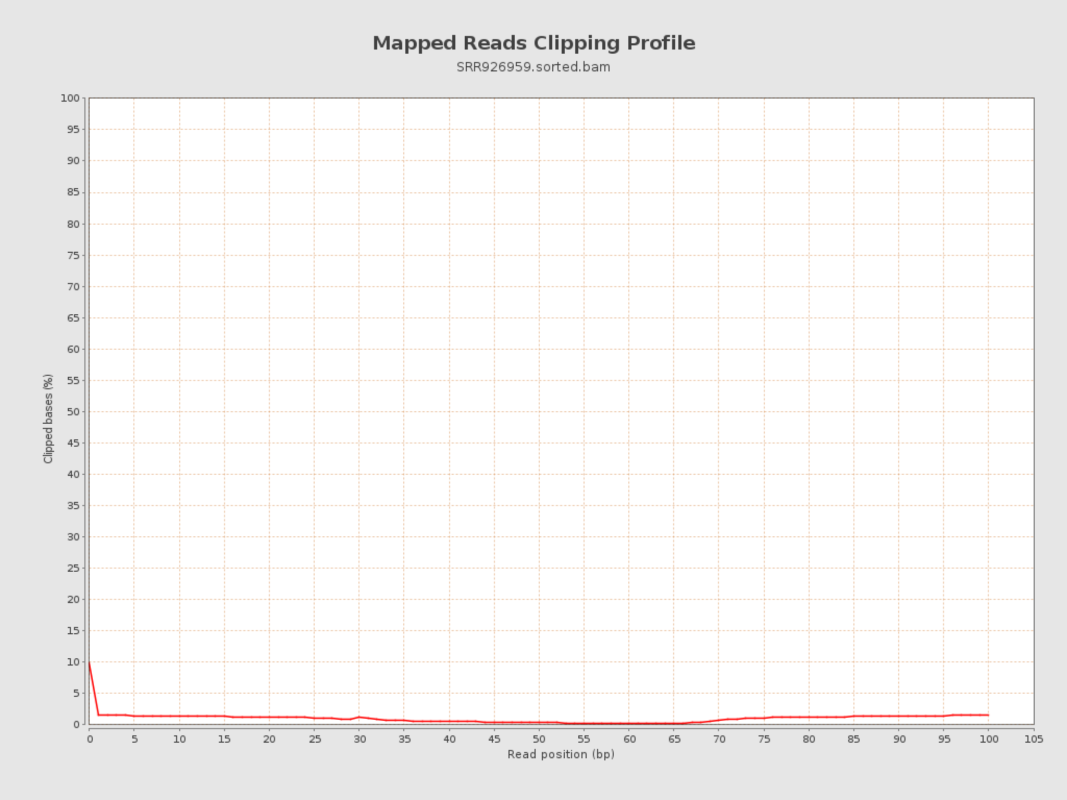
8. Results : Mapped Reads Nucleotide Content



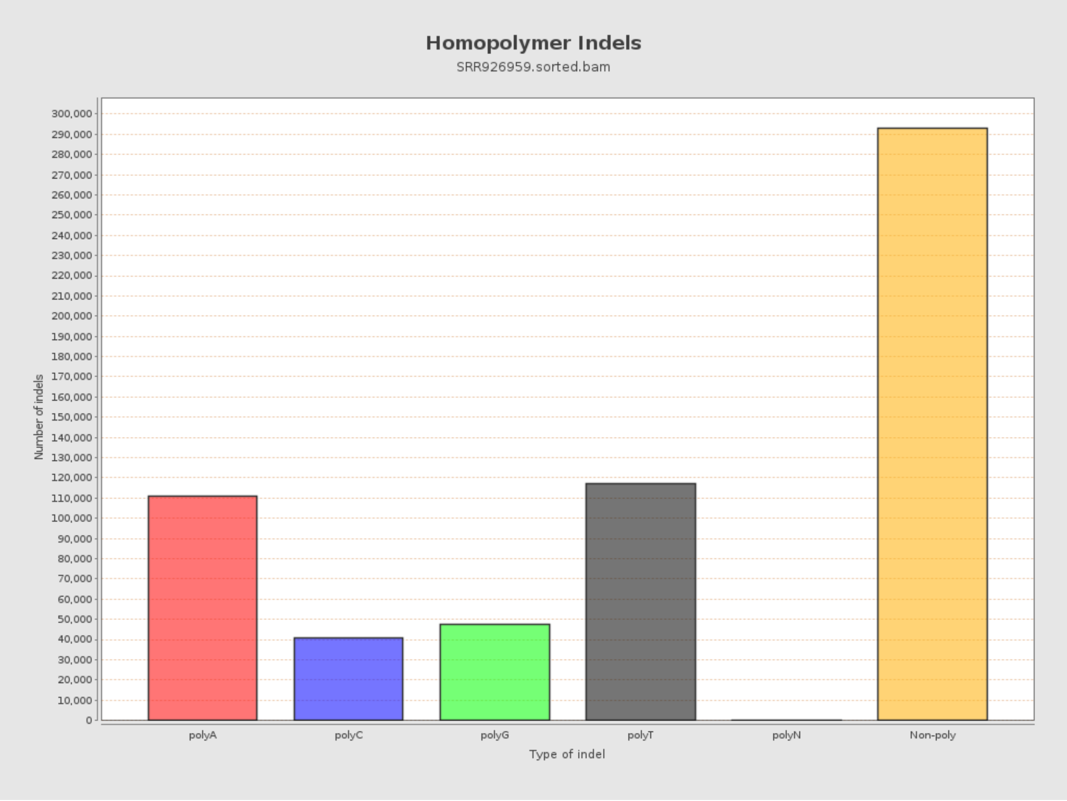
9. Results : Mapped Reads GC-content Distribution



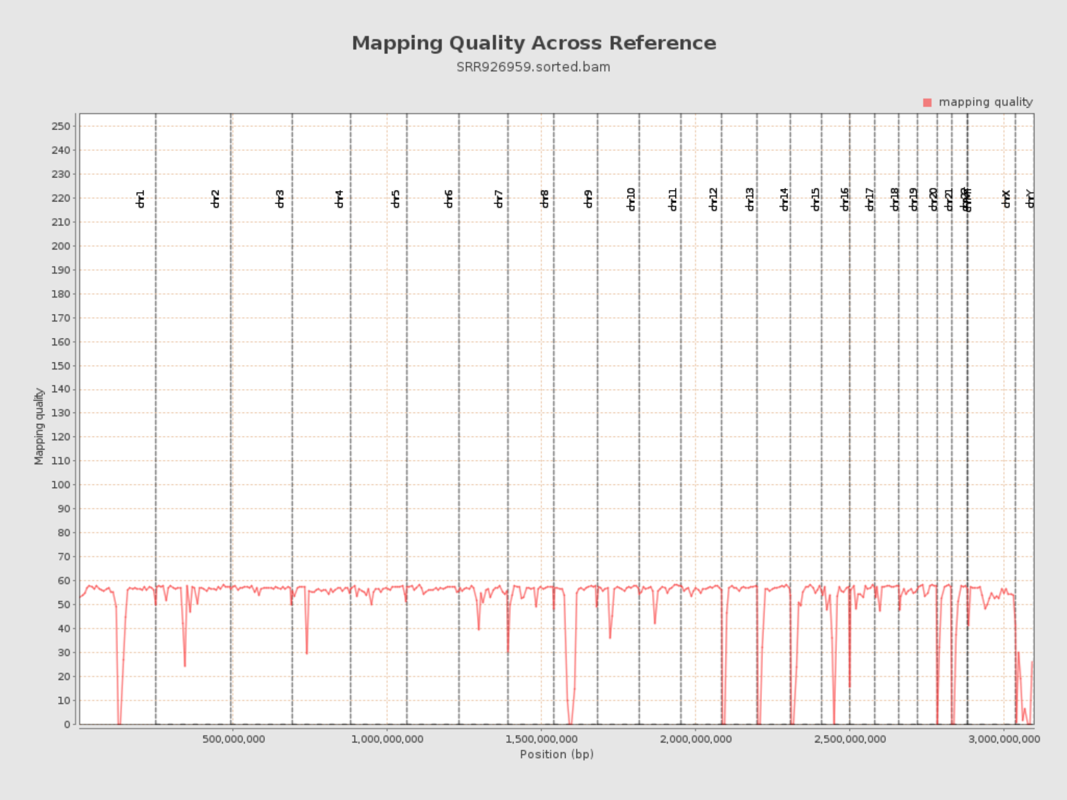
10. Results : Mapped Reads Clipping Profile



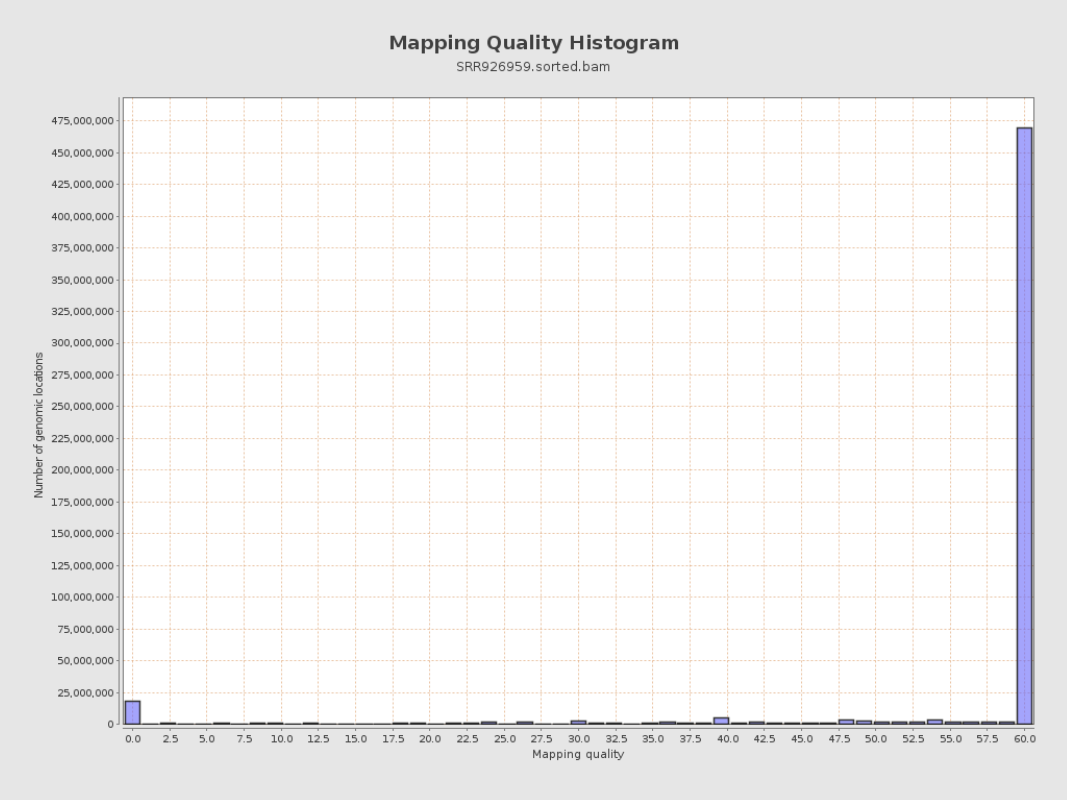
11. Results : Homopolymer Indels



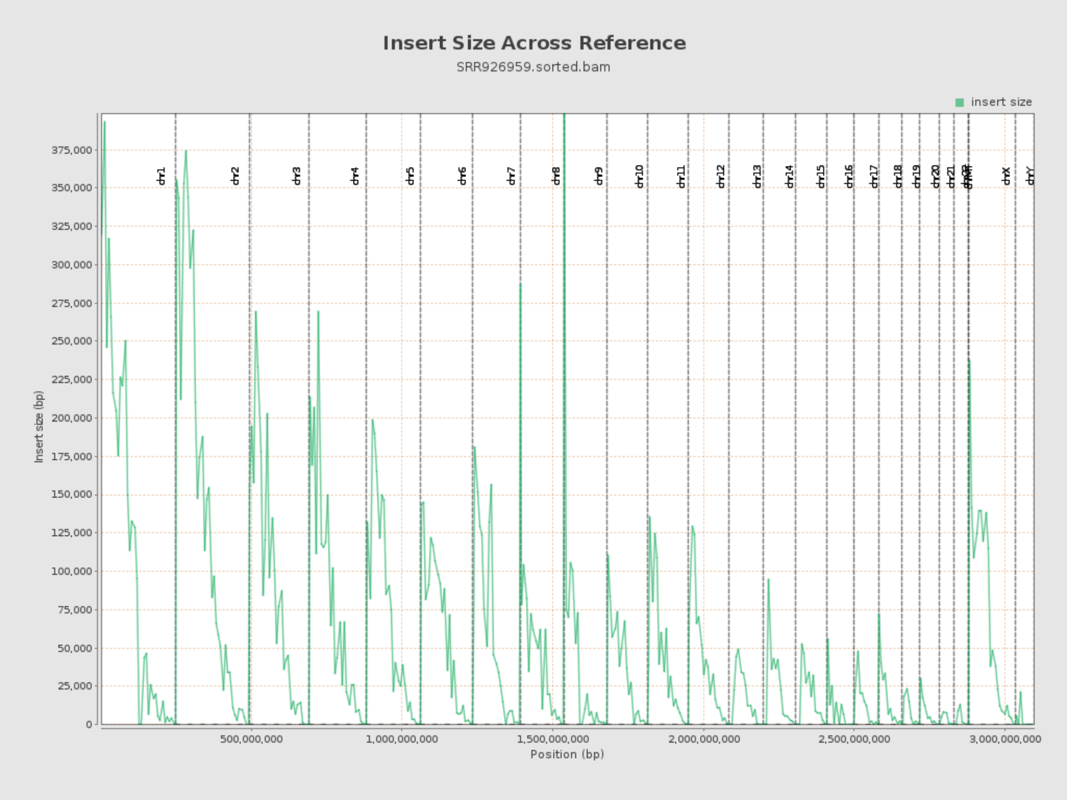
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram