Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 07:44:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926900.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_SRR926900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926900_1.fastq.gz SRR926900_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 07:44:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,698,852
Mapped reads	41,024,737 / 93.88%
Unmapped reads	2,674,115 / 6.12%
Mapped paired reads	41,024,737 / 93.88%
Mapped reads, first in pair	20,577,558 / 47.09%
Mapped reads, second in pair	20,447,179 / 46.79%
Mapped reads, both in pair	40,601,748 / 92.91%
Mapped reads, singletons	422,989 / 0.97%
Secondary alignments	0
Supplementary alignments	583,325 / 1.33%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	3,395,443 / 7.77%
Duplication rate	6.73%
Clipped reads	9,685,605 / 22.16%

2.2. ACGT Content

Number/percentage of A's	1,129,520,693 / 28.83%
Number/percentage of C's	794,285,897 / 20.27%
Number/percentage of T's	1,132,676,552 / 28.91%
Number/percentage of G's	861,542,737 / 21.99%
Number/percentage of N's	270,057 / 0.01%

GC Percentage	42.26%

2.3. Coverage

Mean	1.2667
Standard Deviation	4.8291

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	121,829.16
Standard Deviation	3,435,439.95
P25/Median/P75	135 / 171 / 225

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	36,408,000
Insertions	627,920
Mapped reads with at least one insertion	1.51%
Deletions	2,157,218
Mapped reads with at least one deletion	5.12%
Homopolymer indels	53.24%

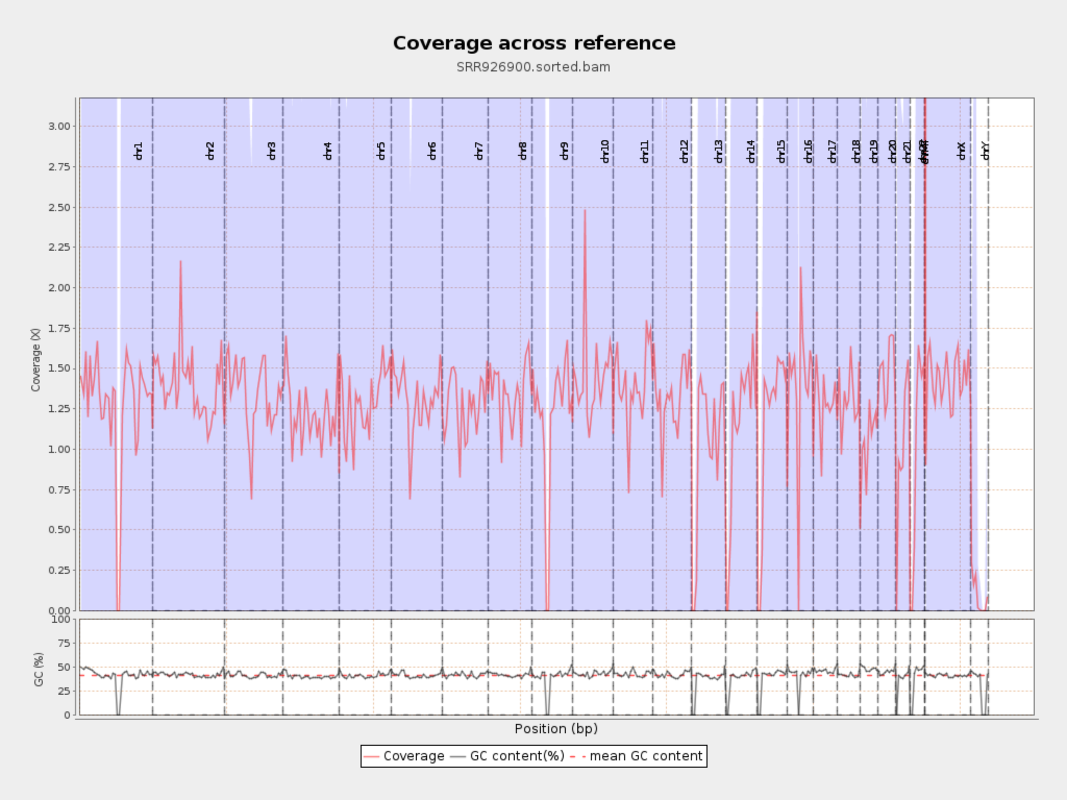
2.7. Chromosome stats

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

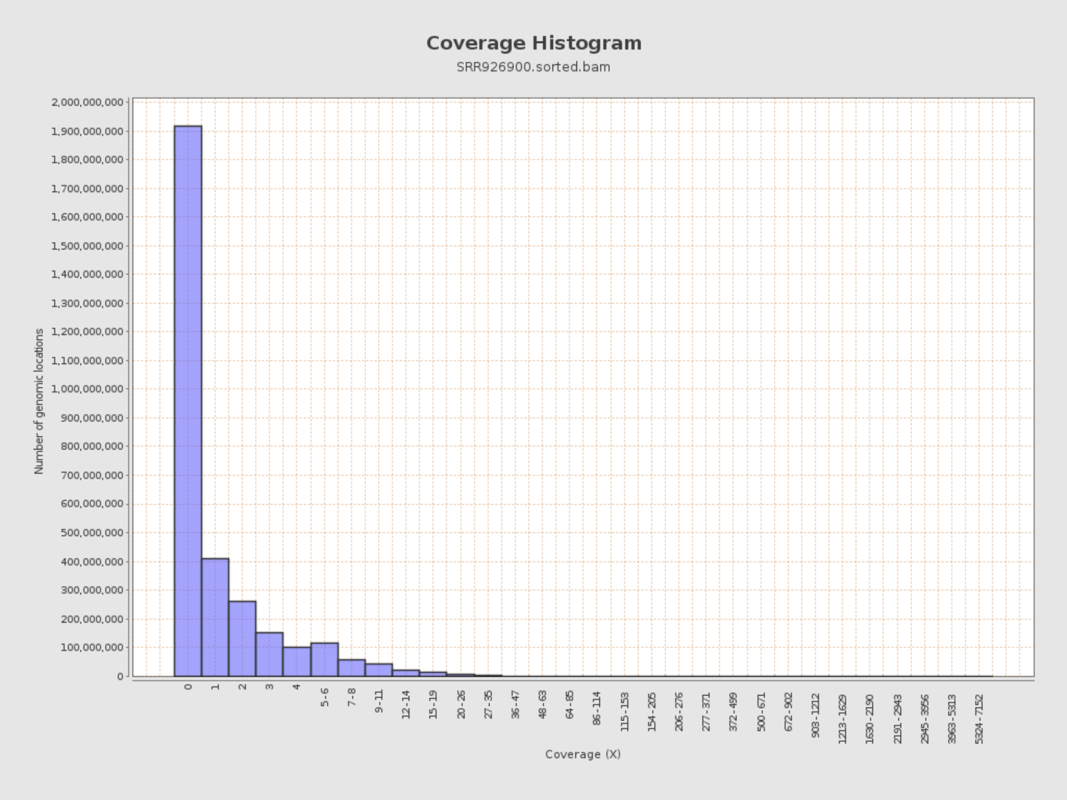
		bases	coverage	deviation
chr1	249250621	317767173	1.2749	4.5013
chr2	243199373	340311652	1.3993	6.8851
chr3	198022430	265233812	1.3394	2.7514
chr4	191154276	233873572	1.2235	2.9009
chr5	180915260	235069895	1.2993	2.5998
chr6	171115067	224865145	1.3141	2.6494
chr7	159138663	201717783	1.2676	3.3568
chr8	146364022	197902185	1.3521	3.0612
chr9	141213431	167318799	1.1849	4.852
chr10	135534747	198333634	1.4633	14.008
chr11	135006516	189439973	1.4032	3.451
chr12	133851895	177871585	1.3289	2.9828
chr13	115169878	116711498	1.0134	2.417
chr14	107349540	120363968	1.1212	2.5209
chr15	102531392	117208319	1.1431	2.6306
chr16	90354753	124877468	1.3821	7.6195
chr17	81195210	104178971	1.2831	3.1762
chr18	78077248	104047031	1.3326	5.1424
chr19	59128983	62430813	1.0558	3.0731
chr20	63025520	94484720	1.4992	3.1346
chr21	48129895	50118705	1.0413	3.9164
chr22	51304566	50398238	0.9823	2.5304
chrMT	16571	629427	37.9836	24.3674
chrX	155270560	220854490	1.4224	3.0143

chrY	59373566	5321890	0.0896	1.7886

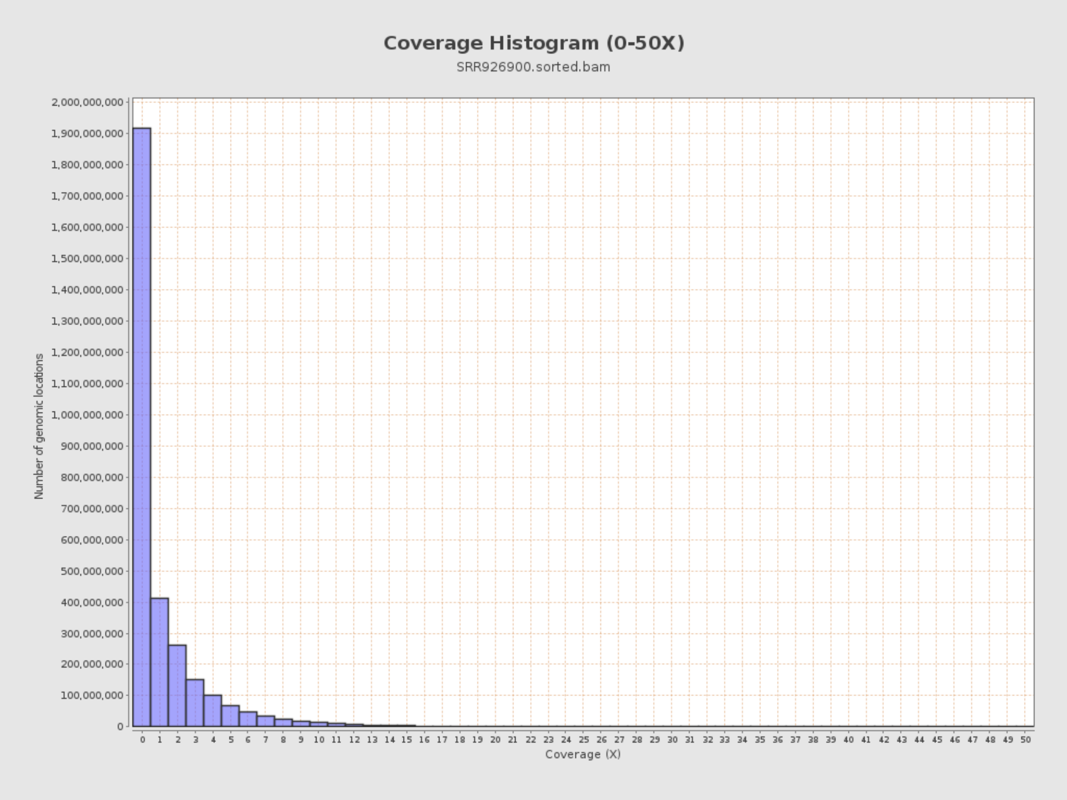
3. Results : Coverage across reference



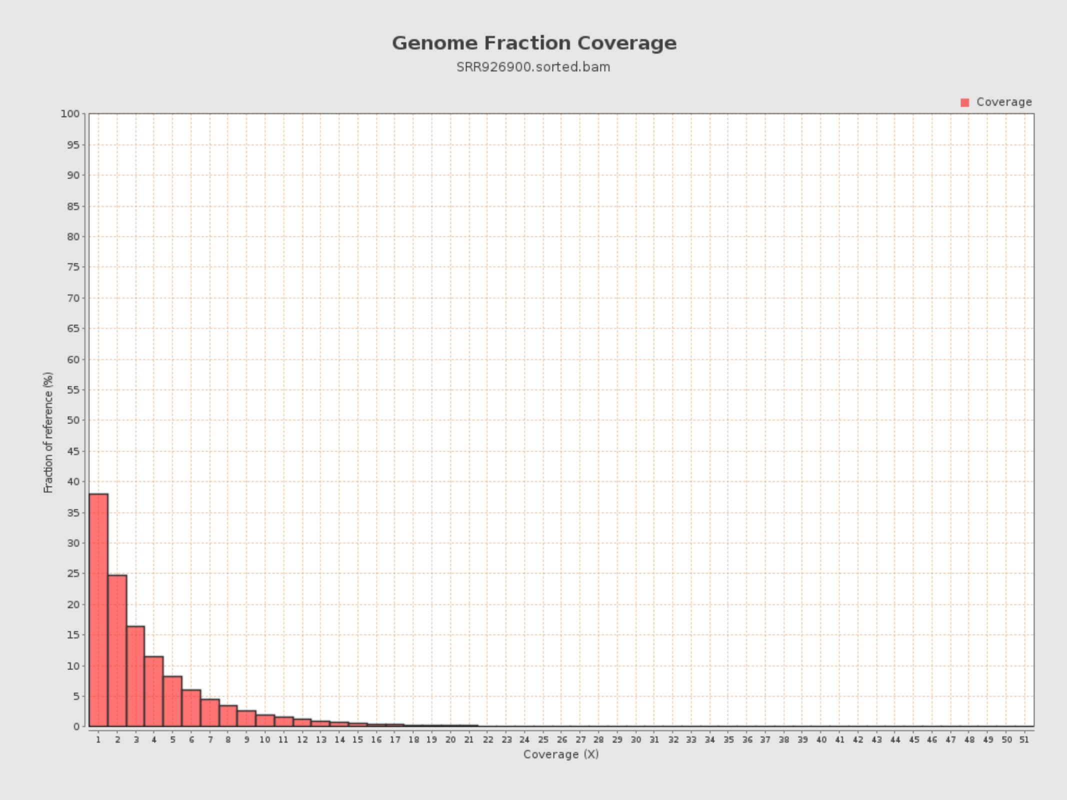
4. Results : Coverage Histogram



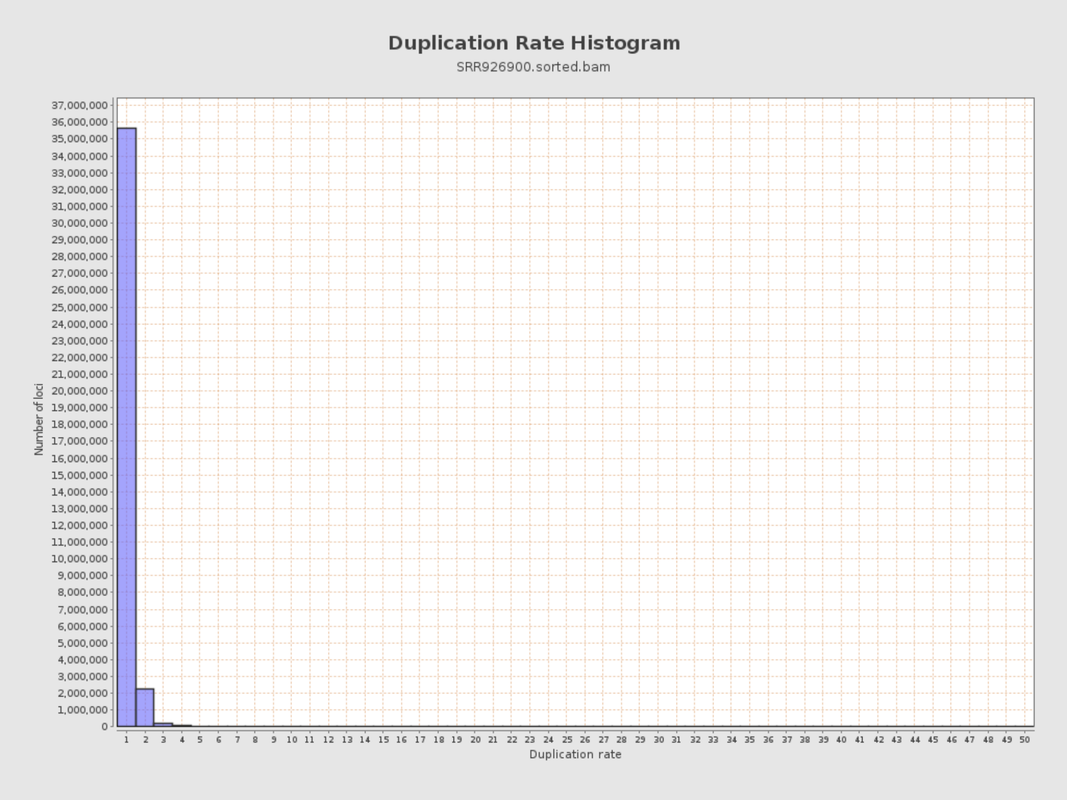
5. Results : Coverage Histogram (0-50X)



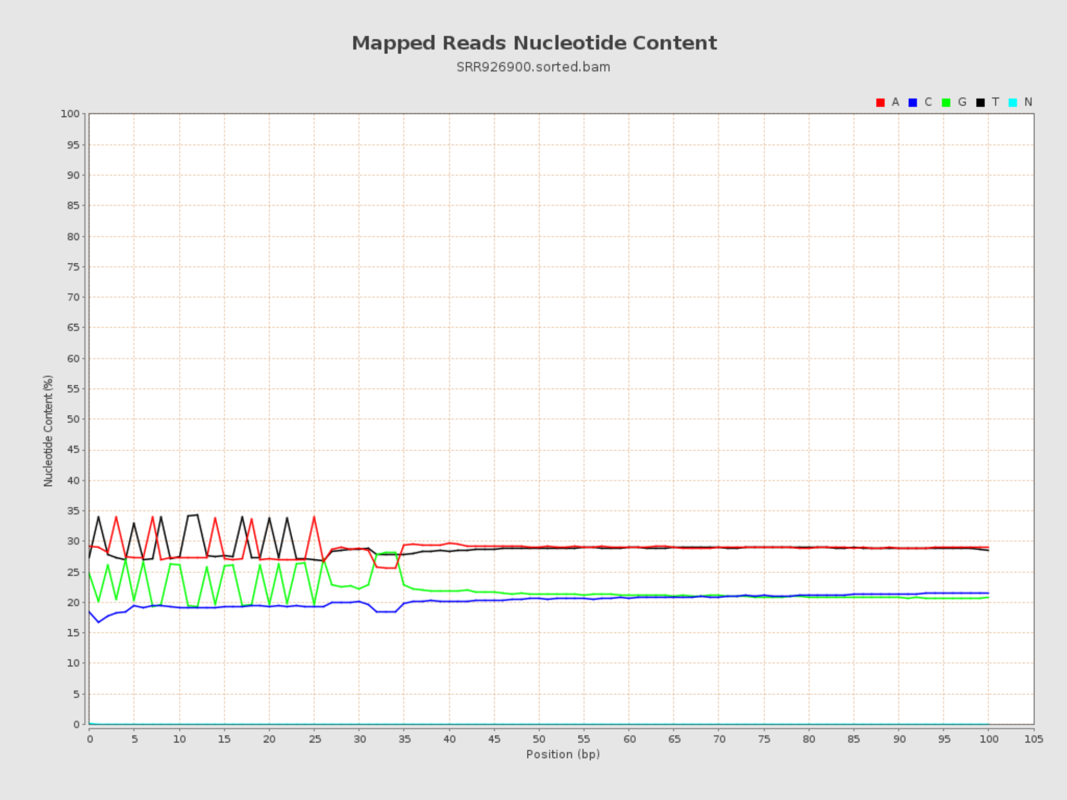
6. Results : Genome Fraction Coverage



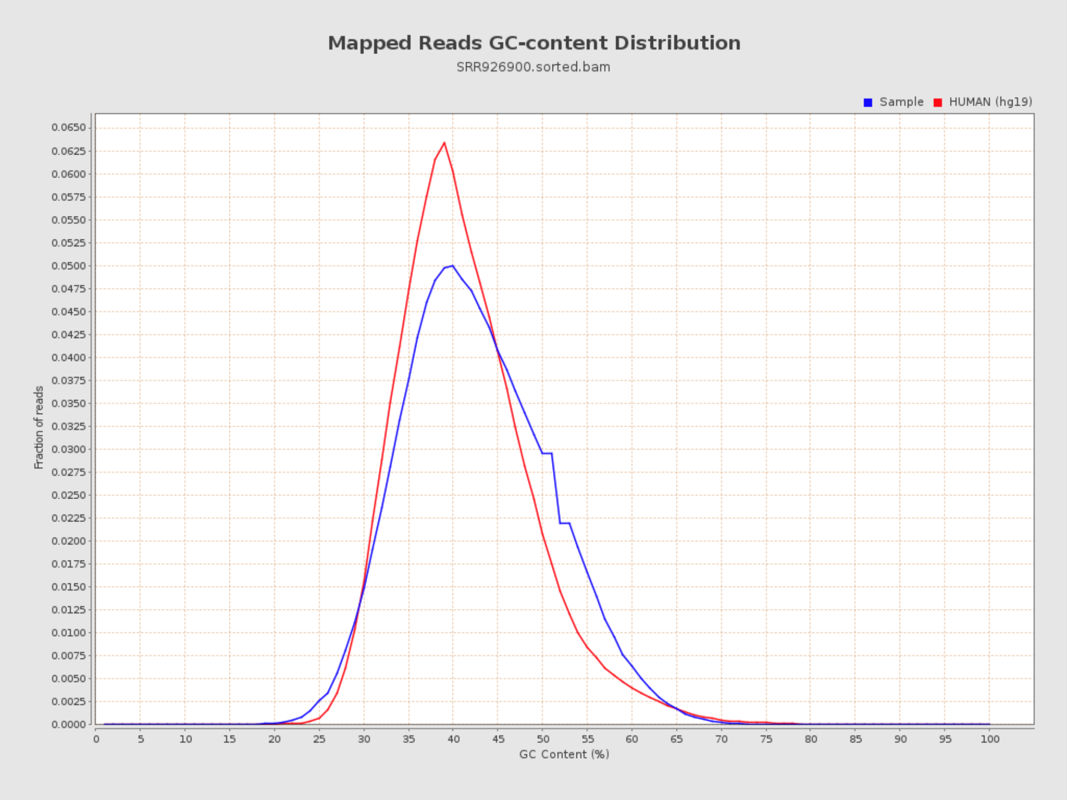
7. Results : Duplication Rate Histogram



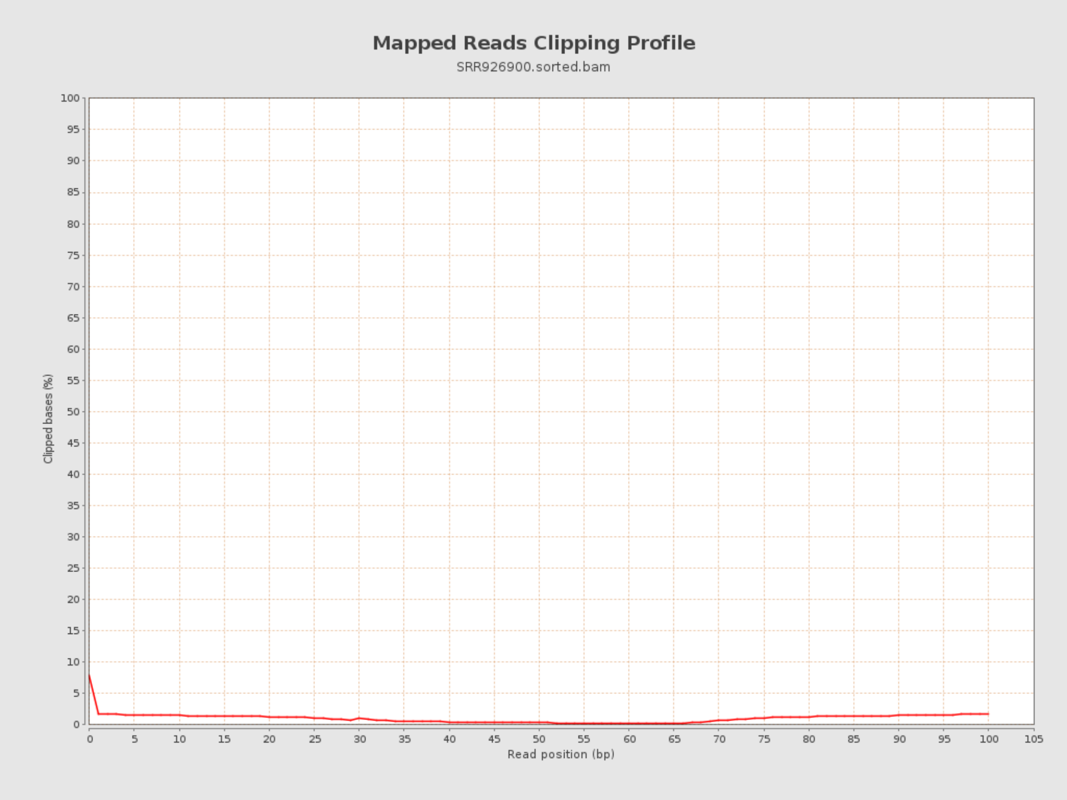
8. Results : Mapped Reads Nucleotide Content



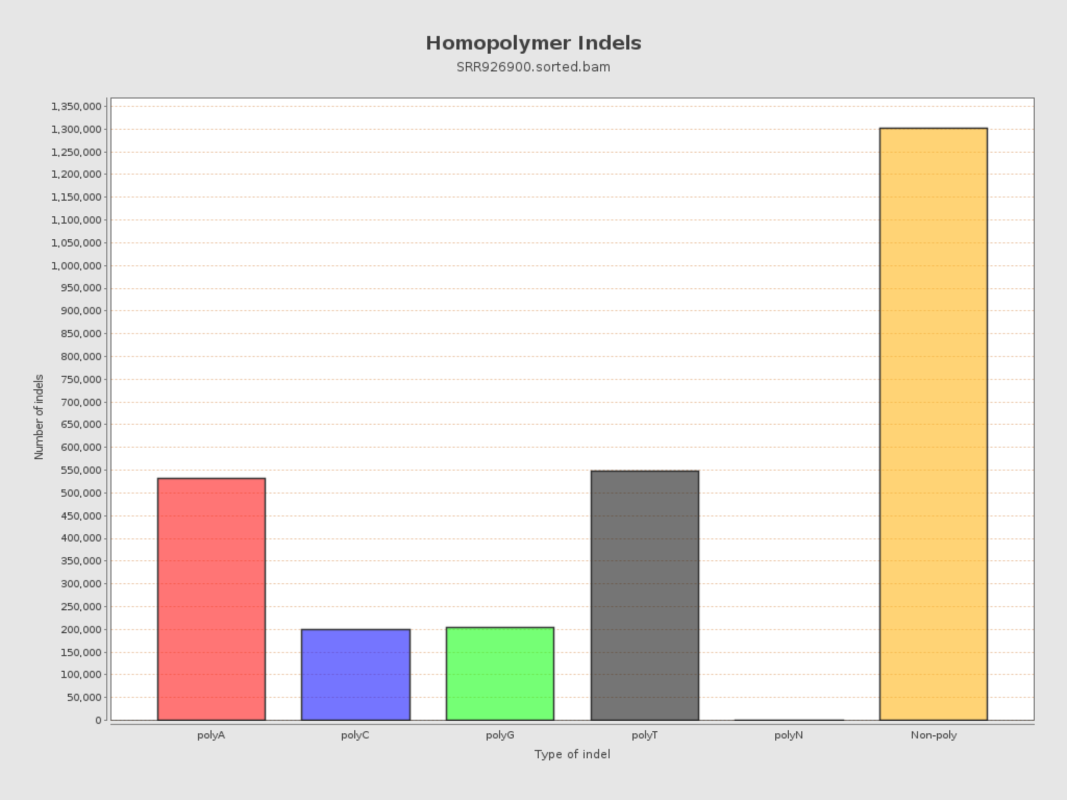
9. Results : Mapped Reads GC-content Distribution



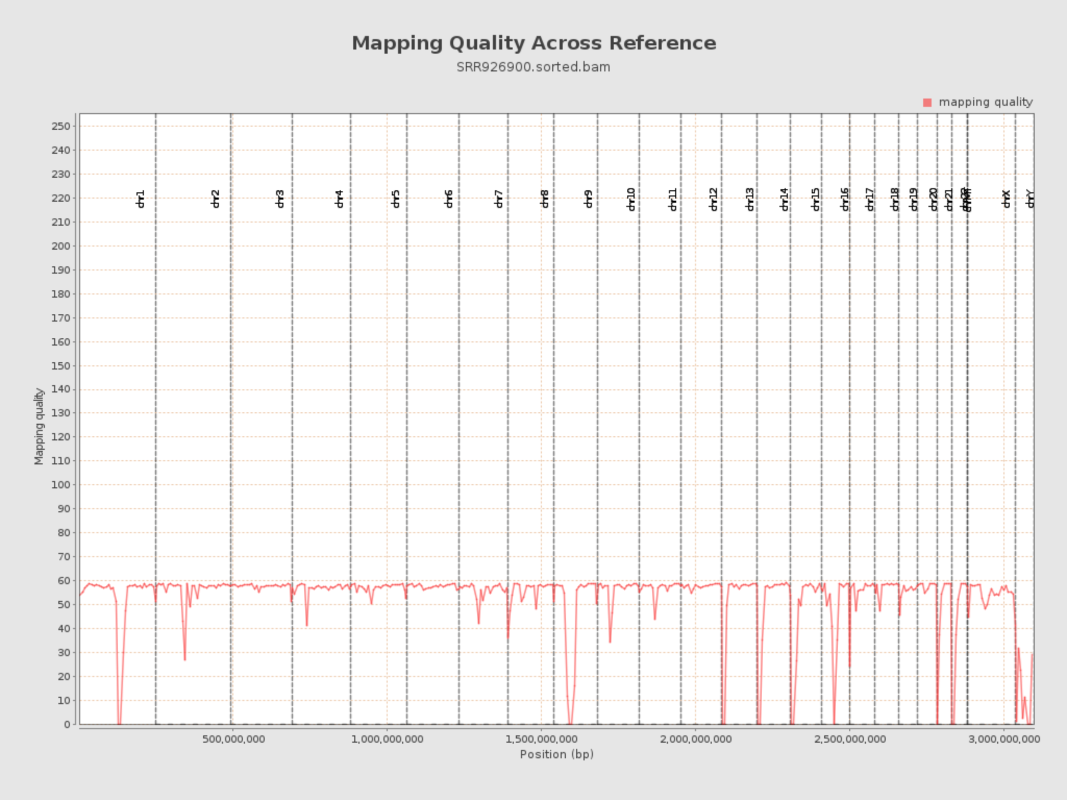
10. Results : Mapped Reads Clipping Profile



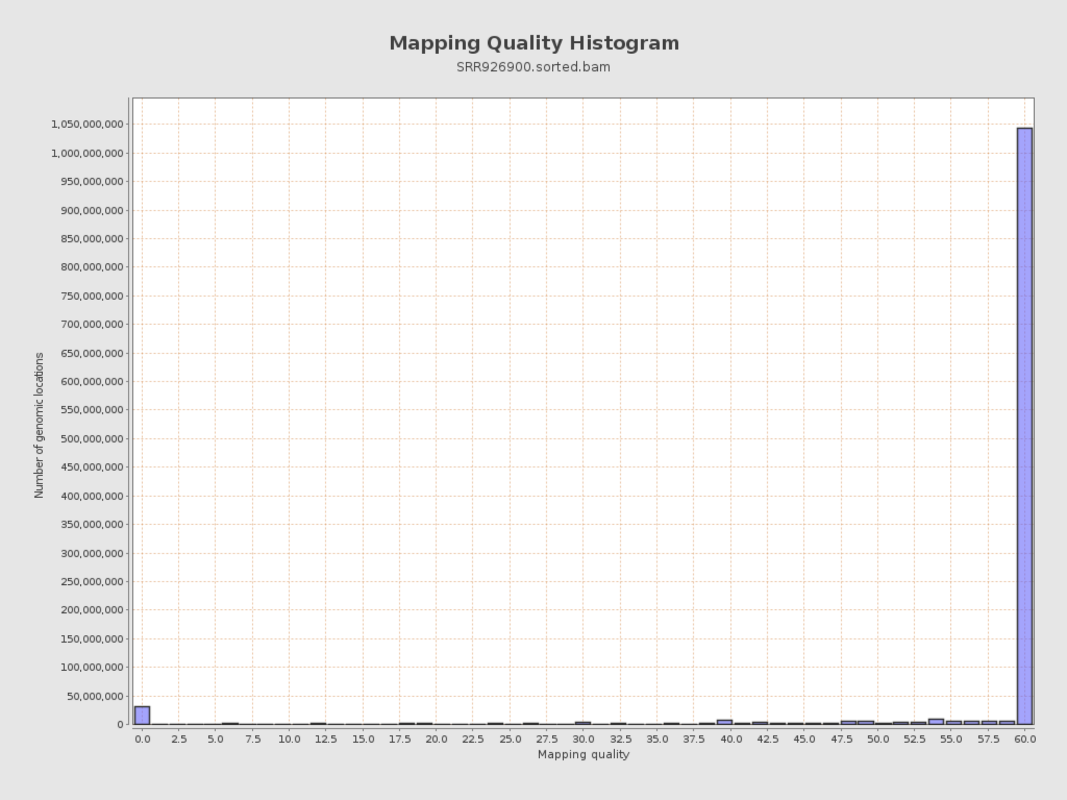
11. Results : Homopolymer Indels



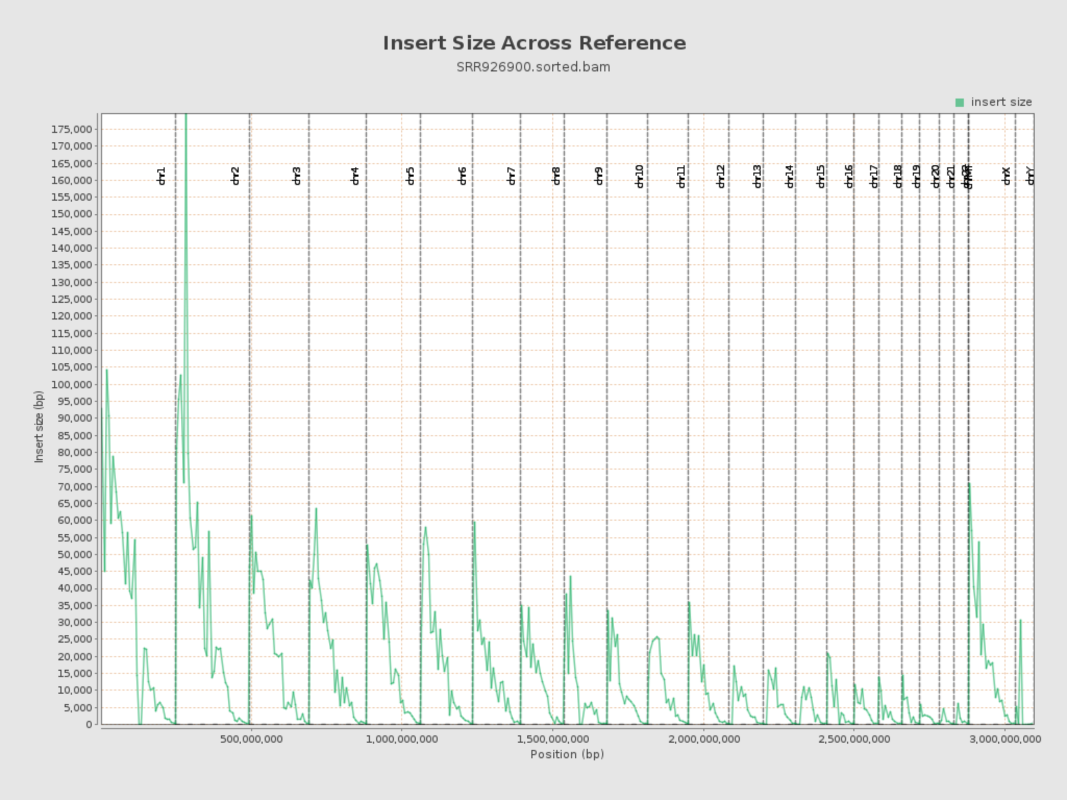
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram