Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 00:12:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926943.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_SRR926943 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926943_1.fastq.gz SRR926943_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 00:12:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,855,356
Mapped reads	11,723,466 / 98.89%
Unmapped reads	131,890 / 1.11%
Mapped paired reads	11,723,466 / 98.89%
Mapped reads, first in pair	5,881,119 / 49.61%
Mapped reads, second in pair	5,842,347 / 49.28%
Mapped reads, both in pair	11,648,958 / 98.26%
Mapped reads, singletons	74,508 / 0.63%
Secondary alignments	0
Supplementary alignments	40,836 / 0.34%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	503,221 / 4.24%
Duplication rate	3.49%
Clipped reads	2,043,368 / 17.24%

2.2. ACGT Content

Number/percentage of A's	322,721,214 / 28.59%
Number/percentage of C's	230,789,719 / 20.44%
Number/percentage of T's	324,680,040 / 28.76%
Number/percentage of G's	250,499,288 / 22.19%
Number/percentage of N's	252,988 / 0.02%

GC Percentage	42.63%

2.3. Coverage

Mean	0.365
Standard Deviation	1.6081

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	41,005.75
Standard Deviation	2,006,025.23
P25/Median/P75	156 / 199 / 263

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	10,058,054
Insertions	172,530
Mapped reads with at least one insertion	1.45%
Deletions	596,855
Mapped reads with at least one deletion	4.96%
Homopolymer indels	53.73%

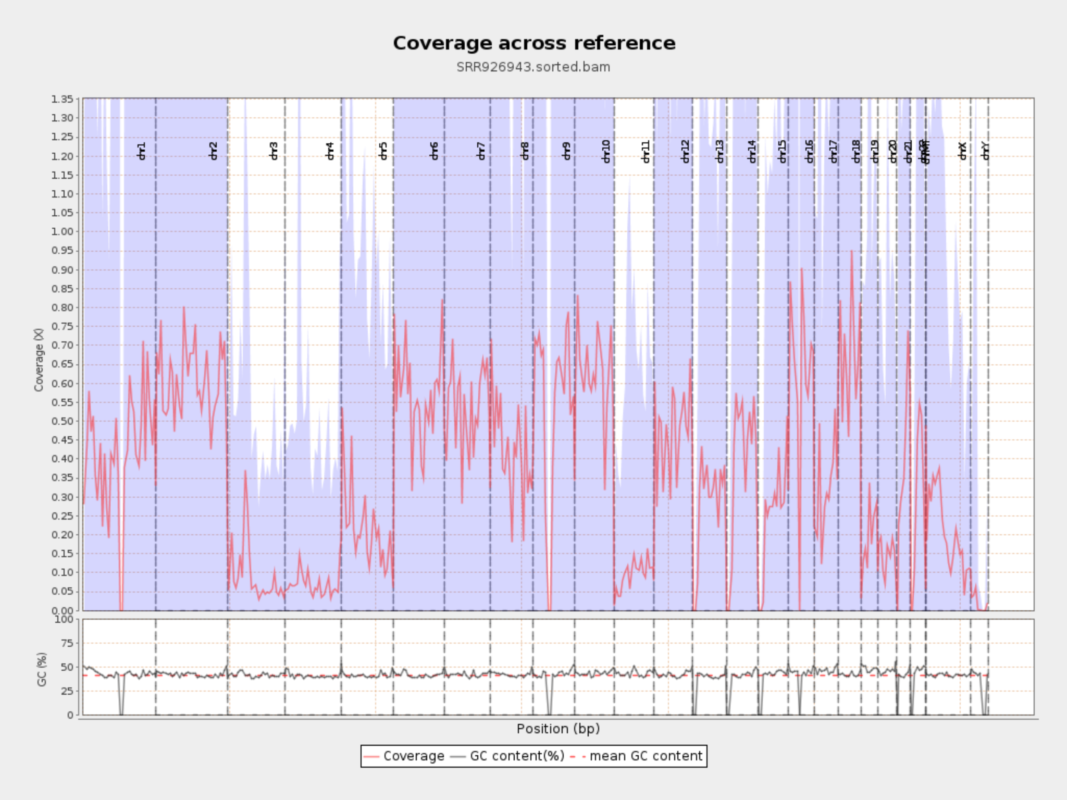
2.7. Chromosome stats

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

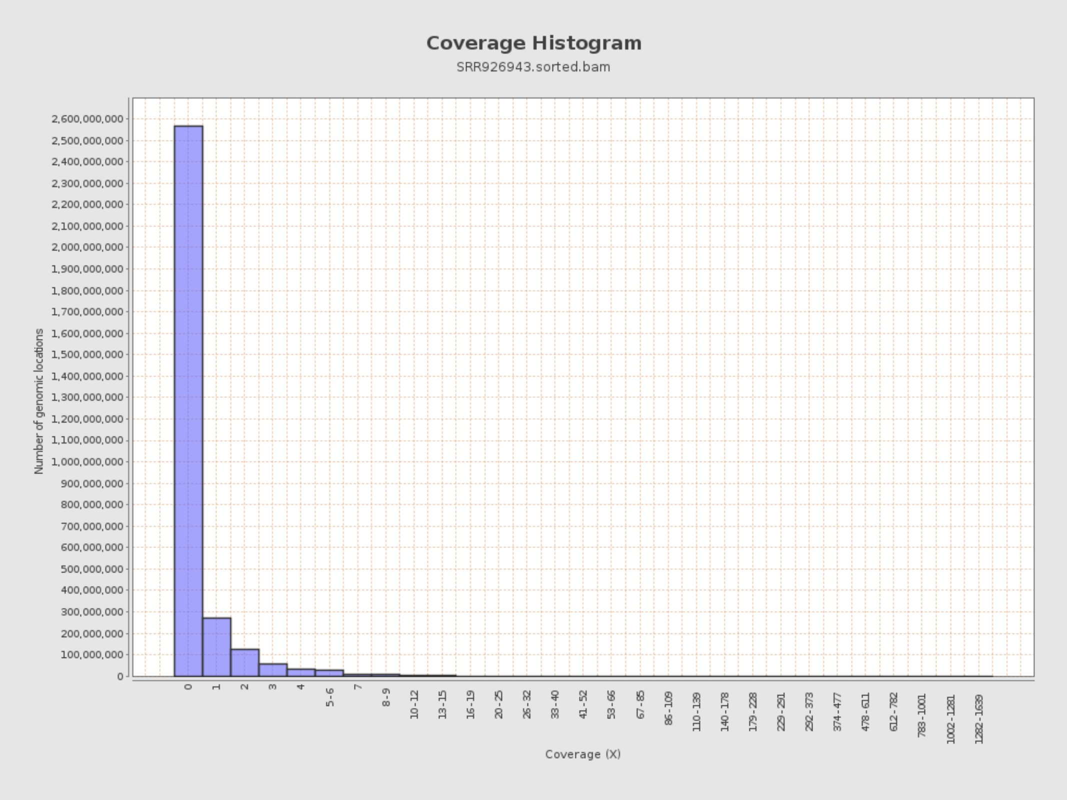
		bases	coverage	deviation
chr1	249250621	103161419	0.4139	1.8017
chr2	243199373	148453722	0.6104	3.0723
chr3	198022430	18402749	0.0929	0.5085
chr4	191154276	13460598	0.0704	0.5751
chr5	180915260	39289825	0.2172	0.7846
chr6	171115067	97558016	0.5701	1.5832
chr7	159138663	85078775	0.5346	1.4272
chr8	146364022	61749984	0.4219	1.2191
chr9	141213431	77051159	0.5456	2.1231
chr10	135534747	85125807	0.6281	2.4072
chr11	135006516	13056797	0.0967	0.5935
chr12	133851895	63501234	0.4744	1.219
chr13	115169878	32514586	0.2823	0.8843
chr14	107349540	42330797	0.3943	1.1351
chr15	102531392	25507897	0.2488	0.8683
chr16	90354753	56315441	0.6233	2.9135
chr17	81195210	26034358	0.3206	1.106
chr18	78077248	52805709	0.6763	2.1957
chr19	59128983	11522000	0.1949	1.136
chr20	63025520	9316395	0.1478	0.7479
chr21	48129895	19198953	0.3989	1.3219
chr22	51304566	15054752	0.2934	1.0288
chrMT	16571	8098	0.4887	1.1012
chrX	155270560	32134741	0.207	0.7846

chrY	59373566	1146828	0.0193	0.6183

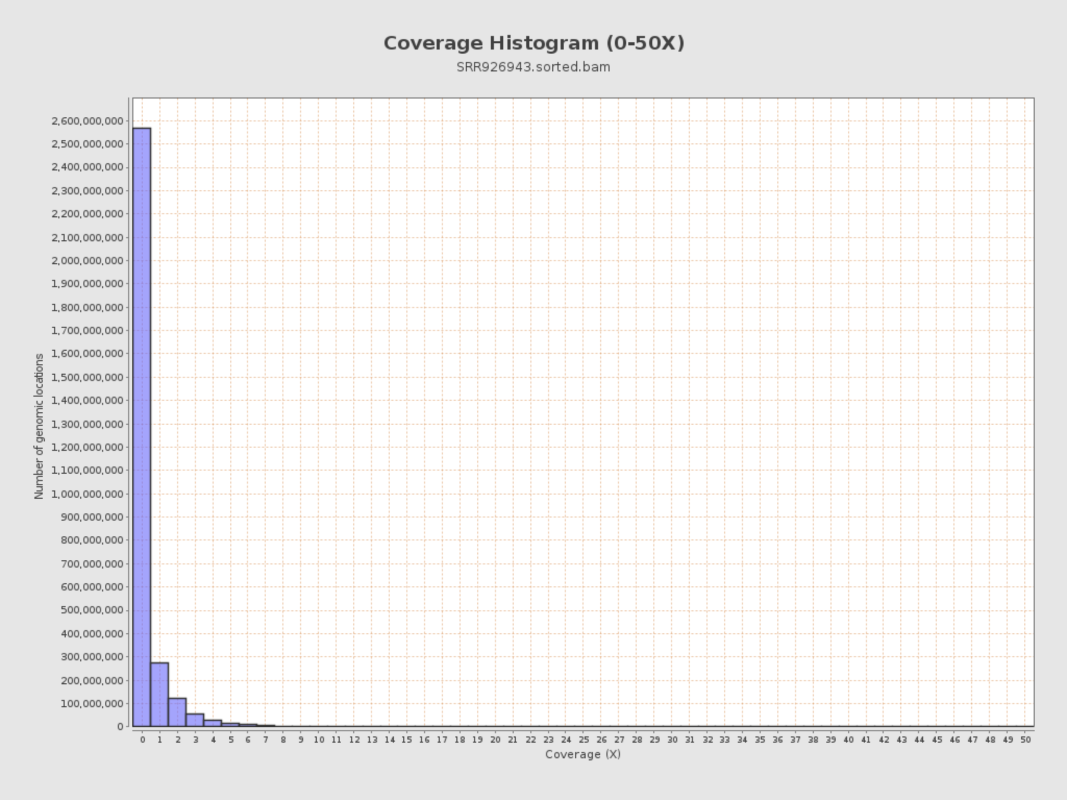
3. Results : Coverage across reference



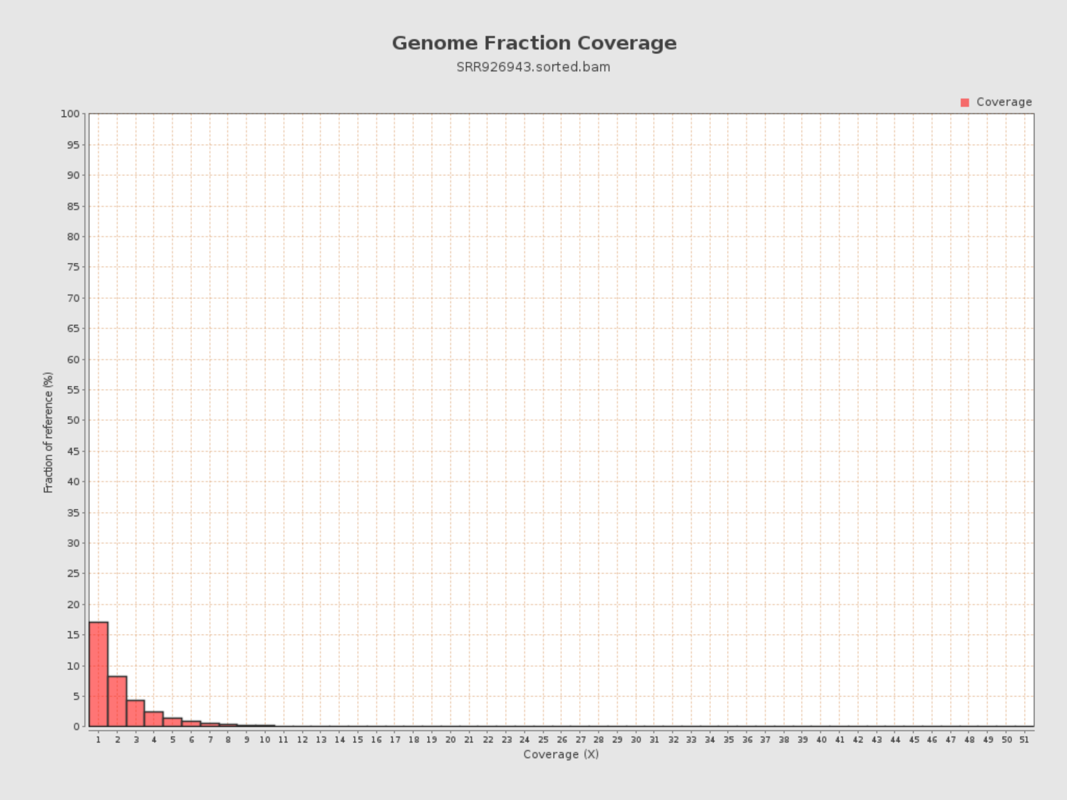
4. Results : Coverage Histogram



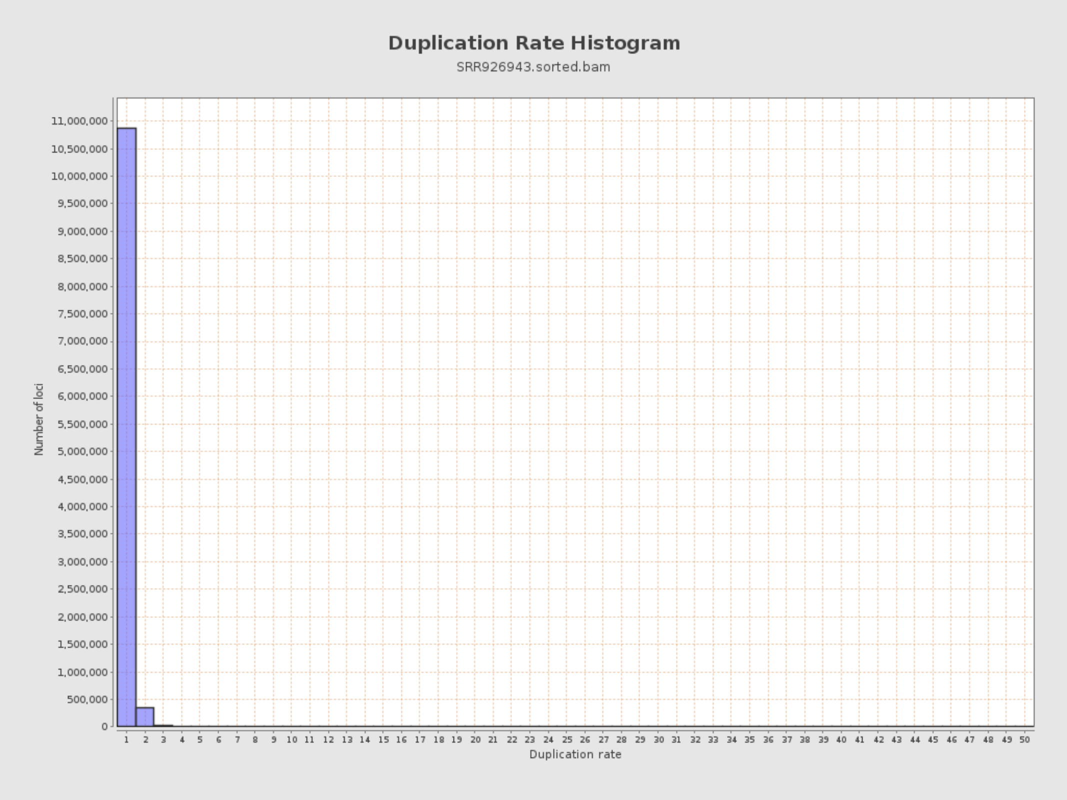
5. Results : Coverage Histogram (0-50X)



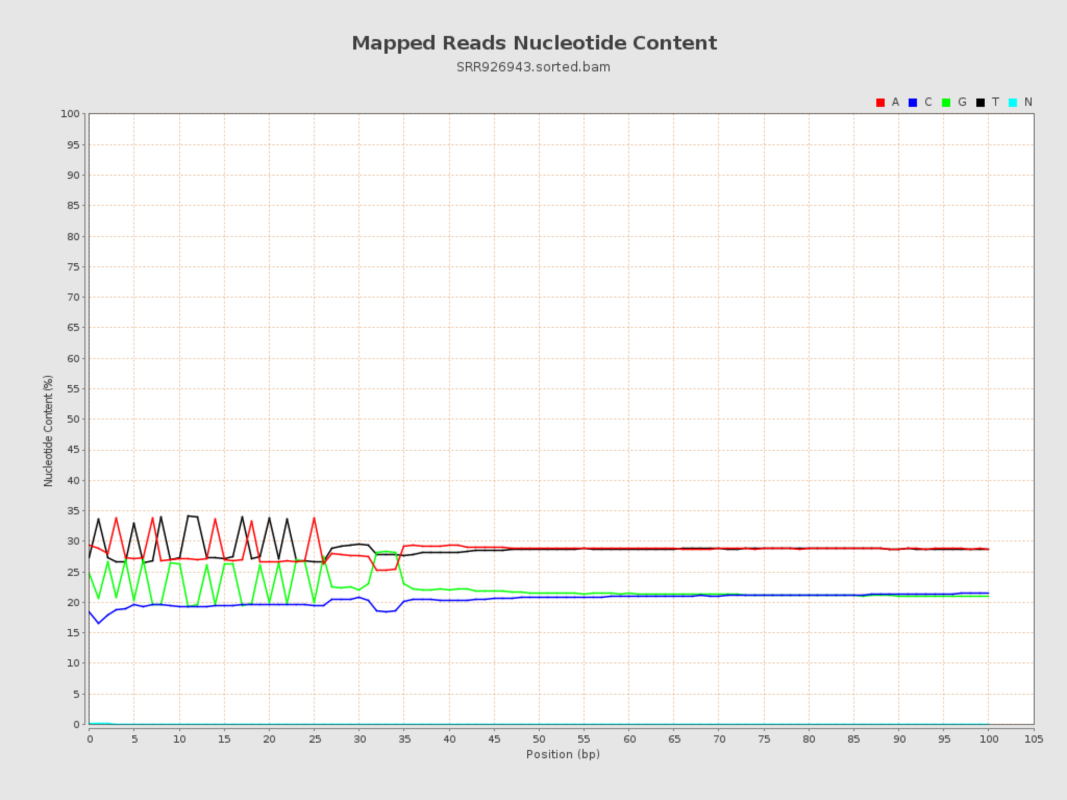
6. Results : Genome Fraction Coverage



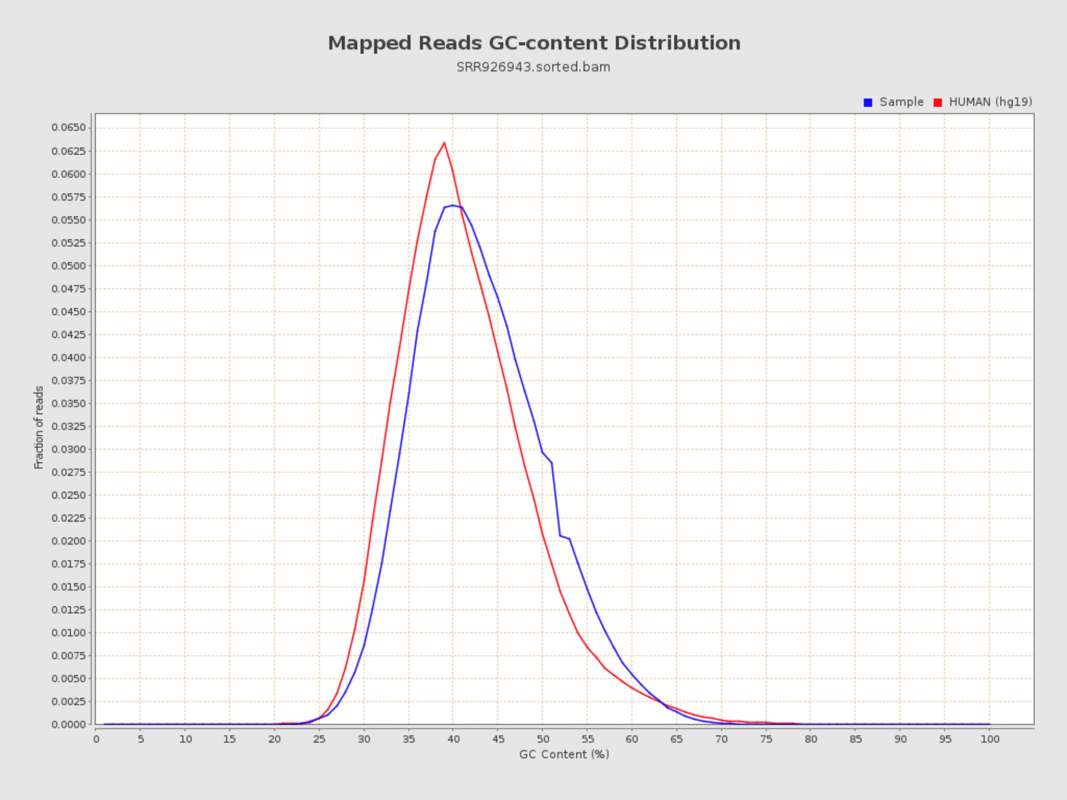
7. Results : Duplication Rate Histogram



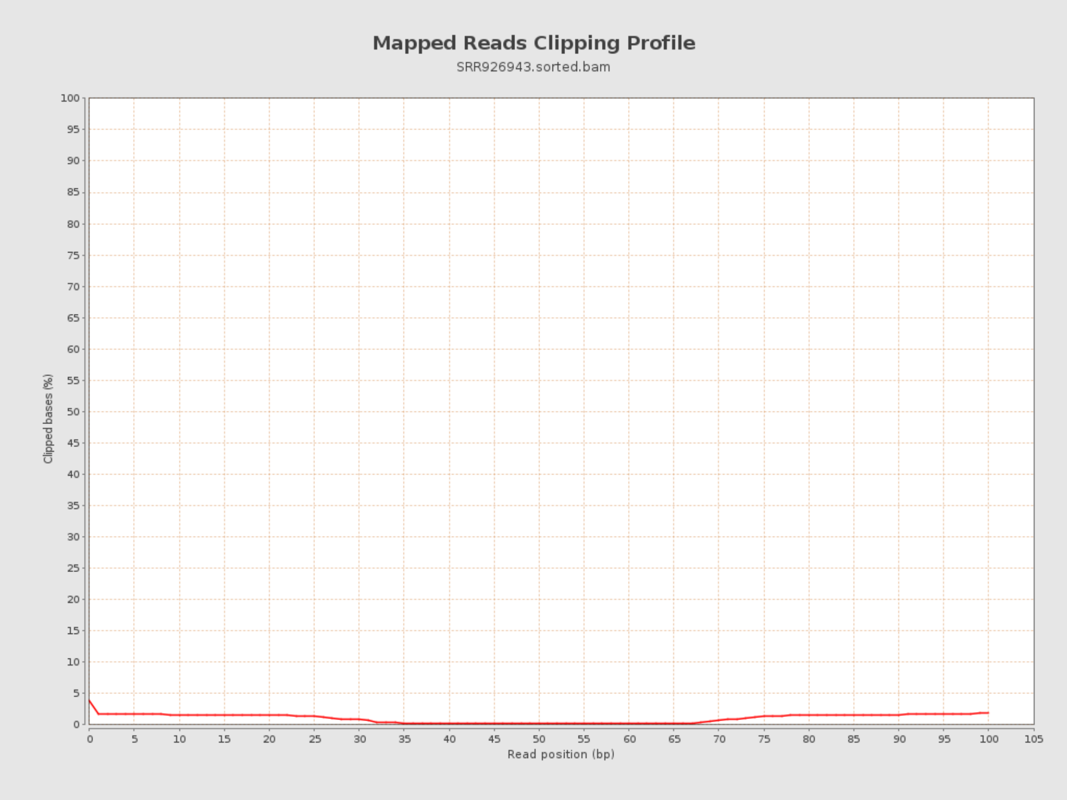
8. Results : Mapped Reads Nucleotide Content



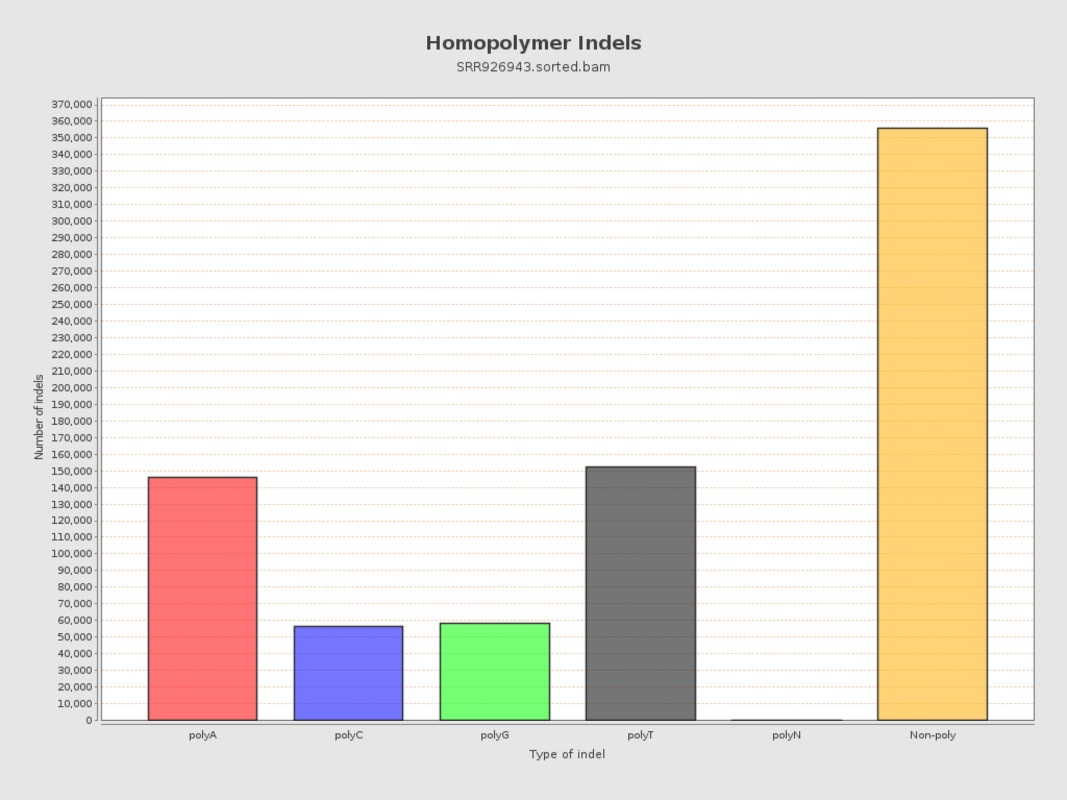
9. Results : Mapped Reads GC-content Distribution



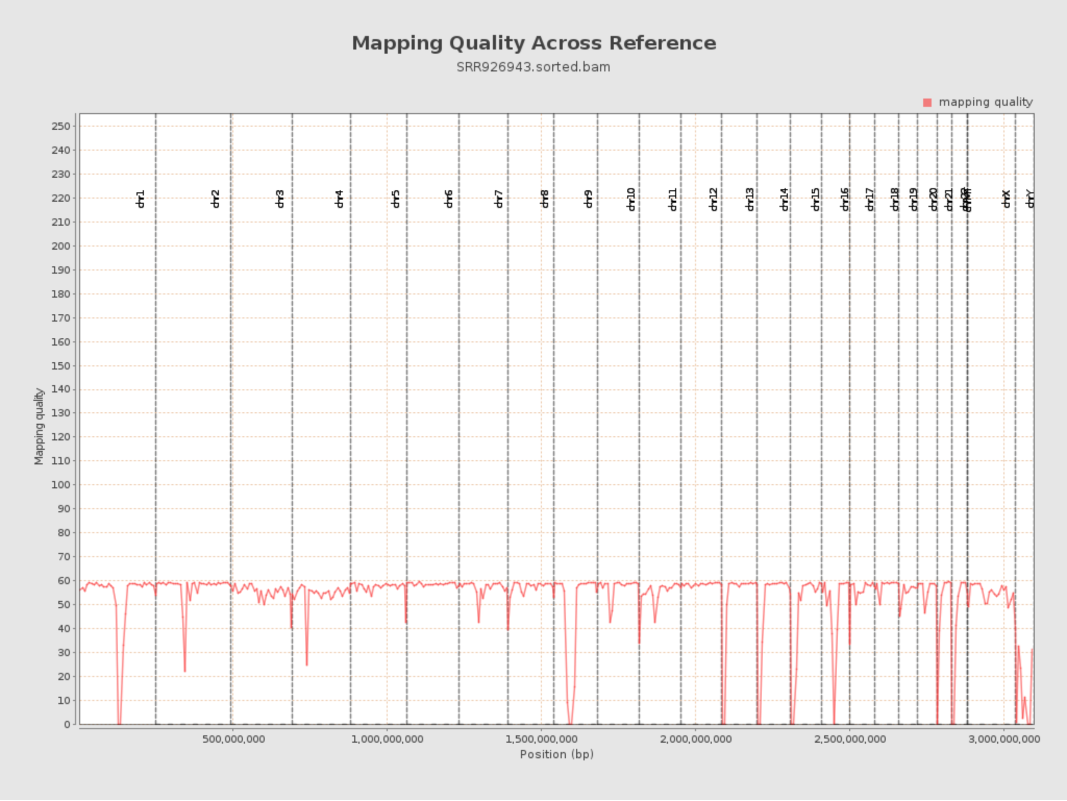
10. Results : Mapped Reads Clipping Profile



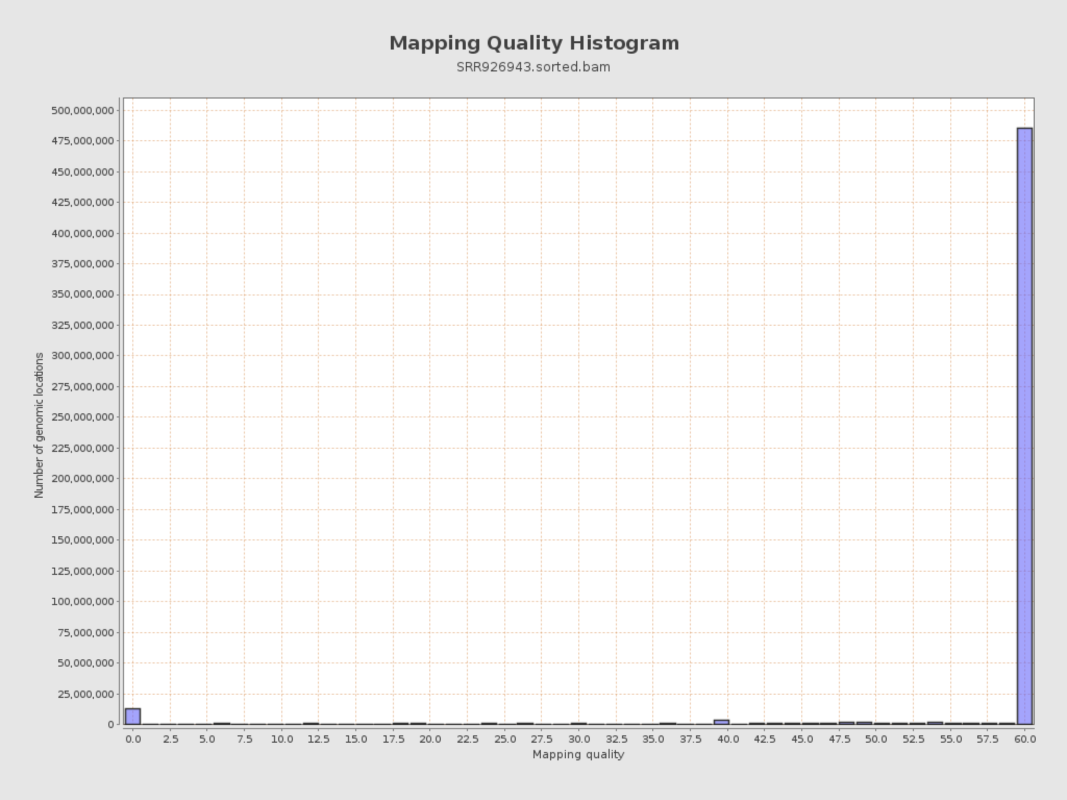
11. Results : Homopolymer Indels



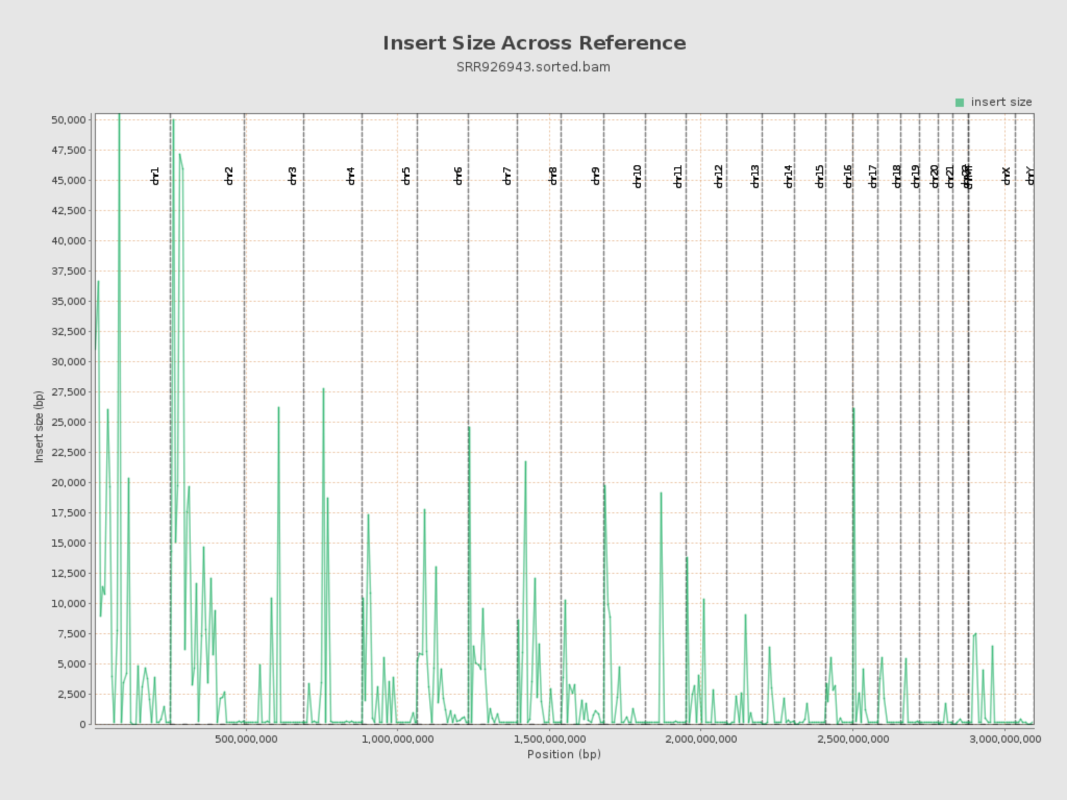
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram