Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 22:10:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926934.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_SRR926934 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926934_1.fastq.gz SRR926934_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 22:10:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,214,250
Mapped reads	15,574,953 / 96.06%
Unmapped reads	639,297 / 3.94%
Mapped paired reads	15,574,953 / 96.06%
Mapped reads, first in pair	7,794,941 / 48.07%
Mapped reads, second in pair	7,780,012 / 47.98%
Mapped reads, both in pair	15,426,646 / 95.14%
Mapped reads, singletons	148,307 / 0.91%
Secondary alignments	0
Supplementary alignments	139,364 / 0.86%
Read min/max/mean length	30 / 101 / 101.35
Duplicated reads (estimated)	893,181 / 5.51%
Duplication rate	4.33%
Clipped reads	4,800,297 / 29.61%

2.2. ACGT Content

Number/percentage of A's	414,354,582 / 28.24%
Number/percentage of C's	300,402,046 / 20.47%
Number/percentage of T's	420,480,615 / 28.65%
Number/percentage of G's	332,156,809 / 22.63%
Number/percentage of N's	63,811 / 0%

GC Percentage	43.11%

2.3. Coverage

Mean	0.4744
Standard Deviation	2.3789

2.4. Mapping Quality

Mean Mapping Quality	53.17

2.5. Insert size

Mean	85,143.94
Standard Deviation	2,901,674.72
P25/Median/P75	145 / 183 / 241

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	13,682,389
Insertions	231,714
Mapped reads with at least one insertion	1.46%
Deletions	752,713
Mapped reads with at least one deletion	4.71%
Homopolymer indels	52.32%

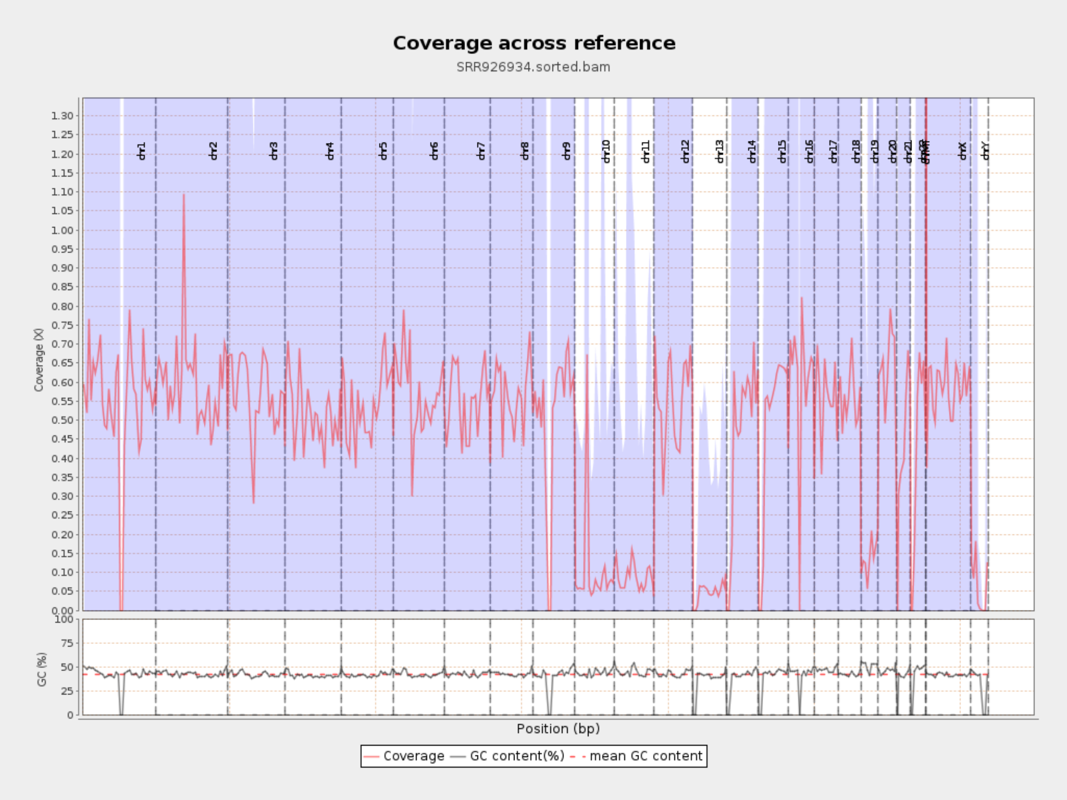
2.7. Chromosome stats

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

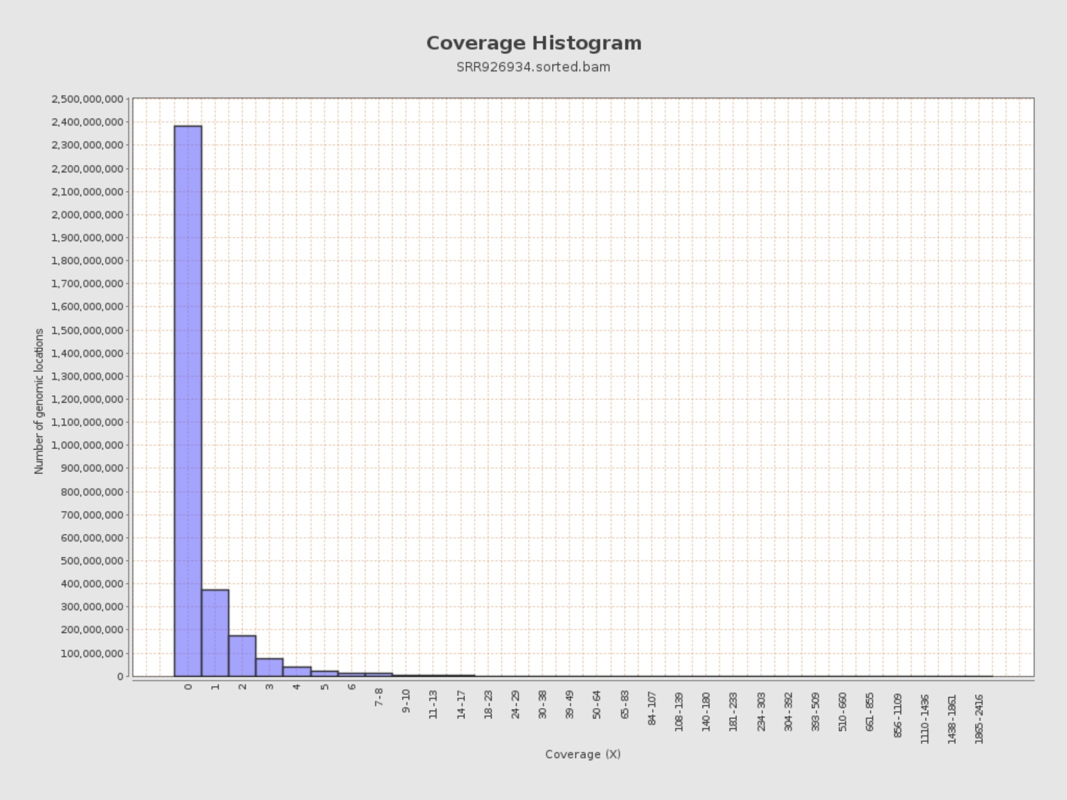
		bases	coverage	deviation
chr1	249250621	137261772	0.5507	2.8722
chr2	243199373	146324094	0.6017	3.8877
chr3	198022430	112098033	0.5661	1.2873
chr4	191154276	99568948	0.5209	2.2385
chr5	180915260	98162190	0.5426	1.2337
chr6	171115067	97679180	0.5708	2.8169
chr7	159138663	87536197	0.5501	1.9238
chr8	146364022	83187776	0.5684	1.5009
chr9	141213431	72269336	0.5118	2.9185
chr10	135534747	13799486	0.1018	4.7054
chr11	135006516	12136386	0.0899	0.9075
chr12	133851895	74696633	0.5581	1.3292
chr13	115169878	5502212	0.0478	0.3835
chr14	107349540	49584545	0.4619	1.1789
chr15	102531392	48971679	0.4776	1.2047
chr16	90354753	53944692	0.597	3.0461
chr17	81195210	45982601	0.5663	1.7935
chr18	78077248	43657769	0.5592	3.0078
chr19	59128983	8302322	0.1404	1.903
chr20	63025520	40963538	0.65	1.6263
chr21	48129895	20901450	0.4343	1.8493
chr22	51304566	21392908	0.417	1.1908
chrMT	16571	91371	5.5139	3.7019
chrX	155270560	90693622	0.5841	1.4073

chrY	59373566	3826728	0.0645	2.0686

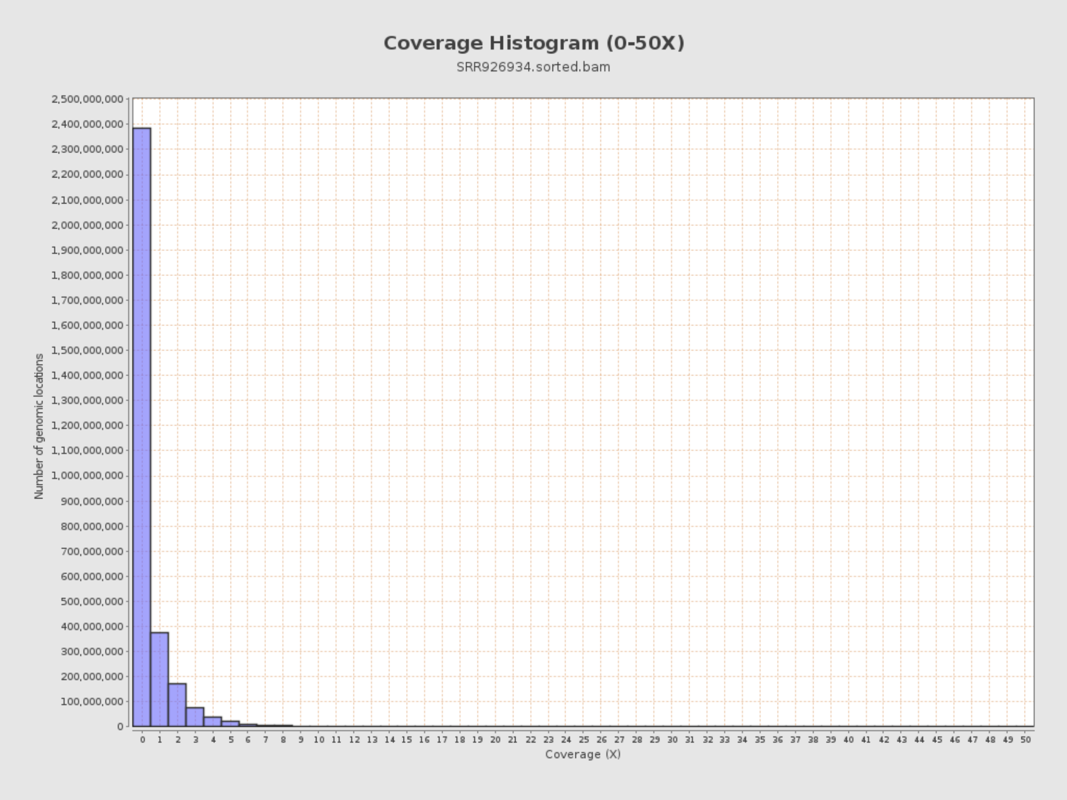
3. Results : Coverage across reference



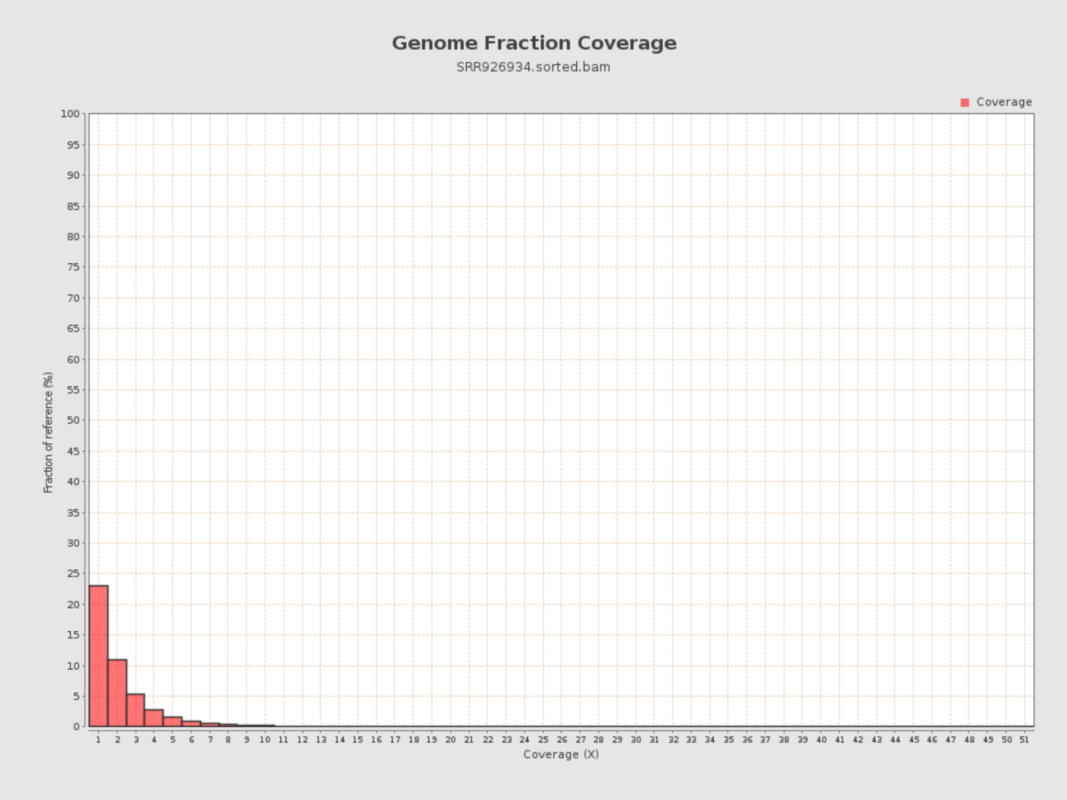
4. Results : Coverage Histogram



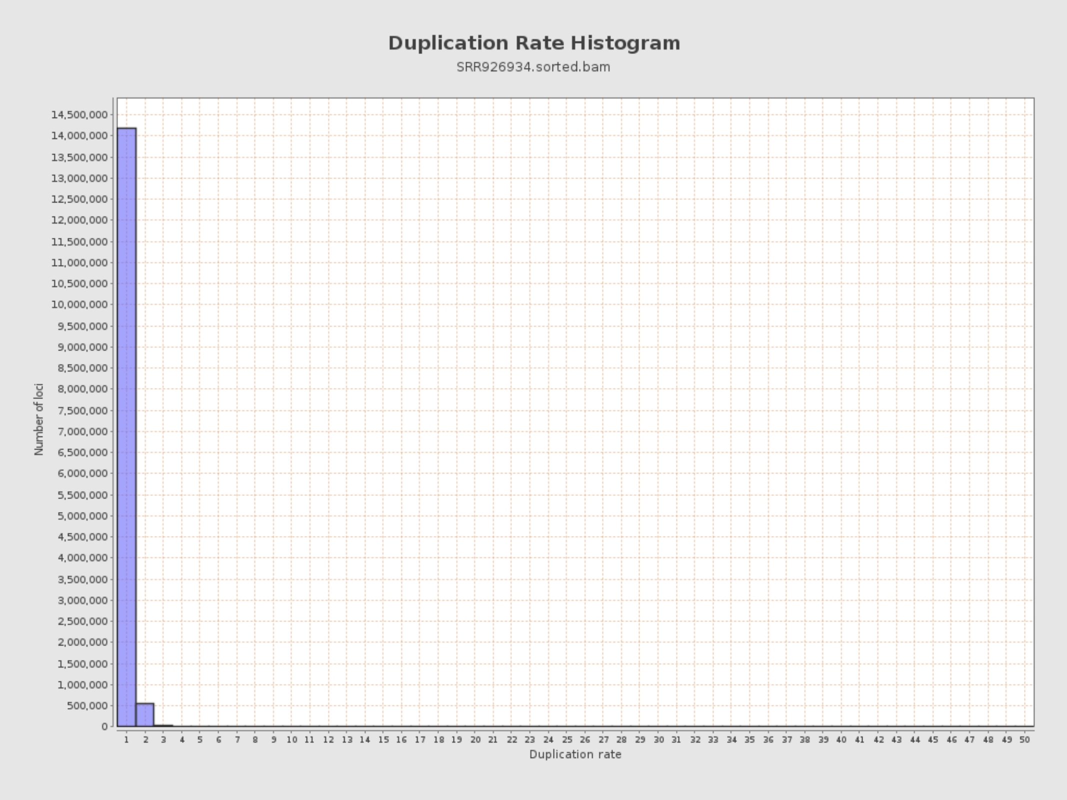
5. Results : Coverage Histogram (0-50X)



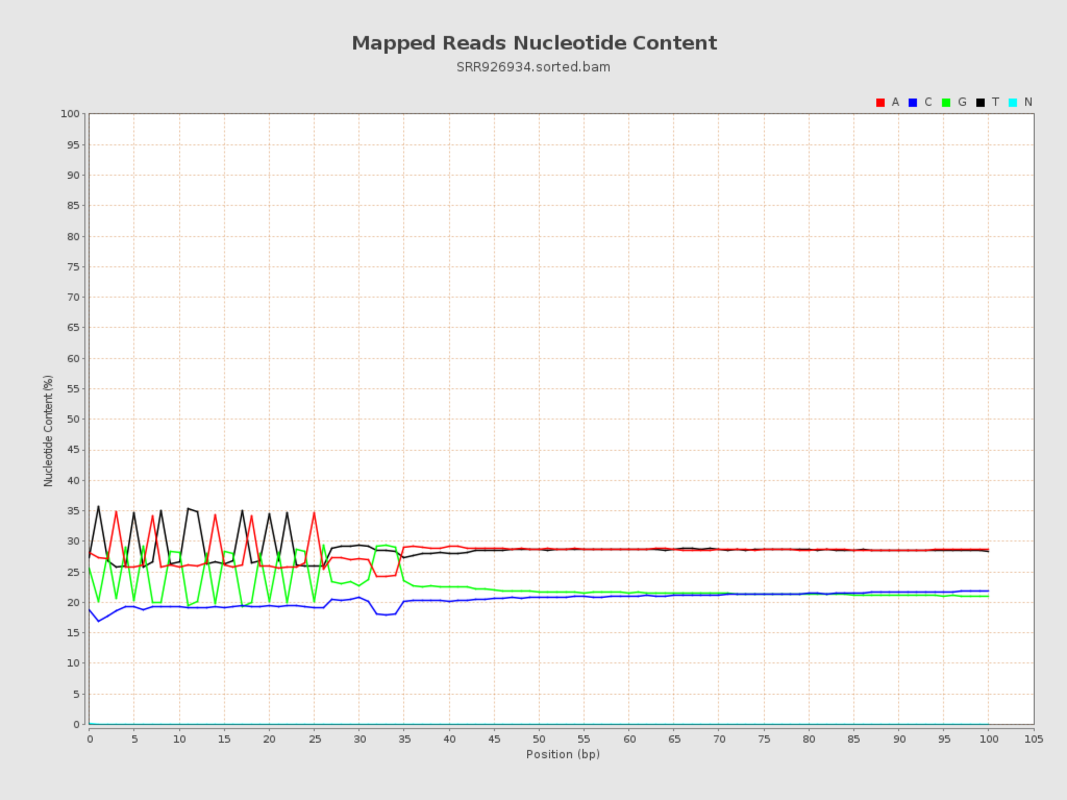
6. Results : Genome Fraction Coverage



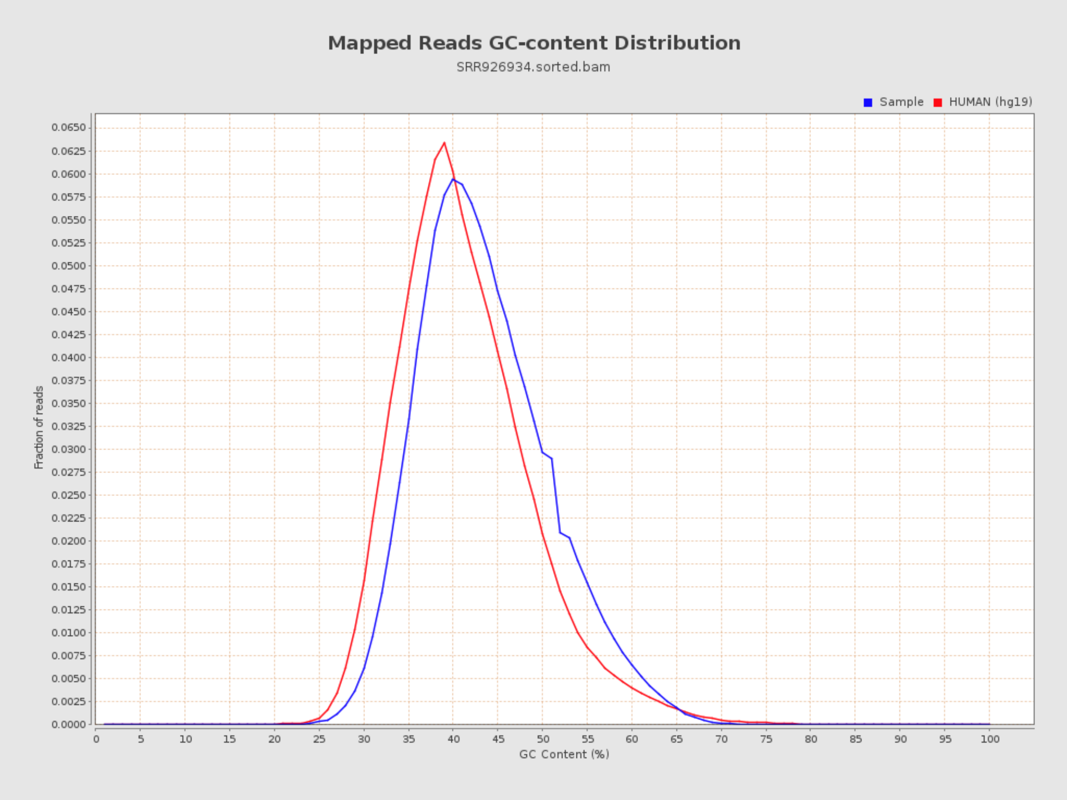
7. Results : Duplication Rate Histogram



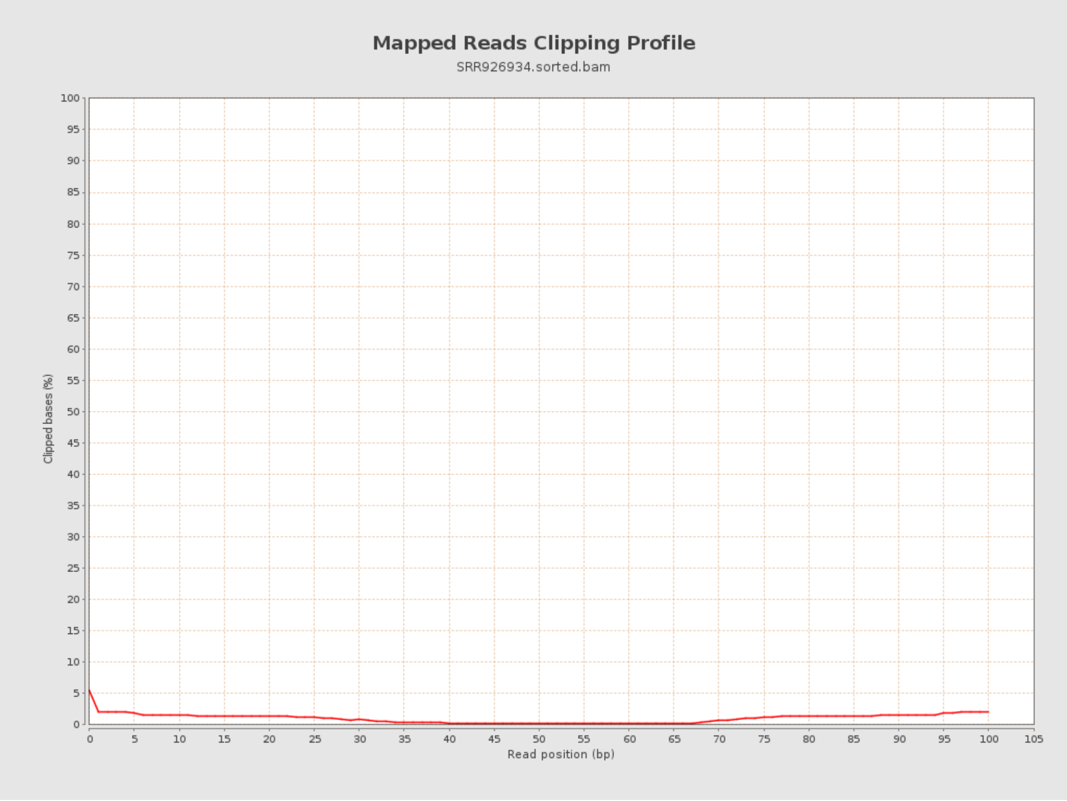
8. Results : Mapped Reads Nucleotide Content



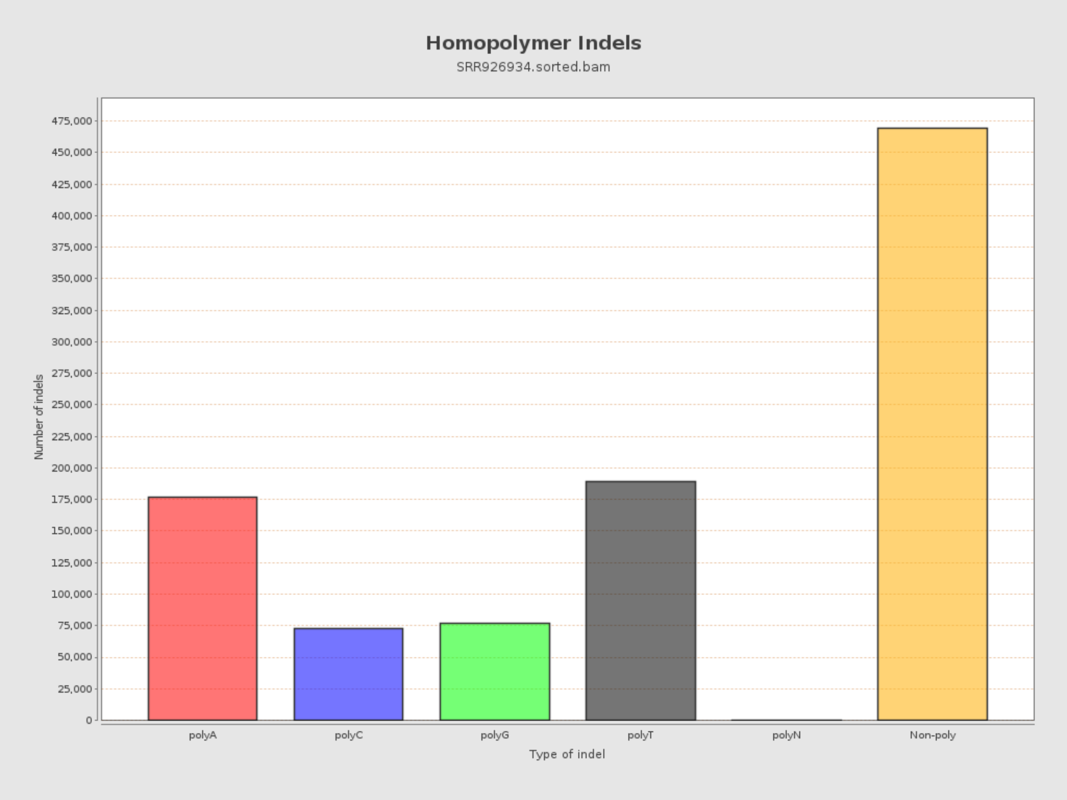
9. Results : Mapped Reads GC-content Distribution



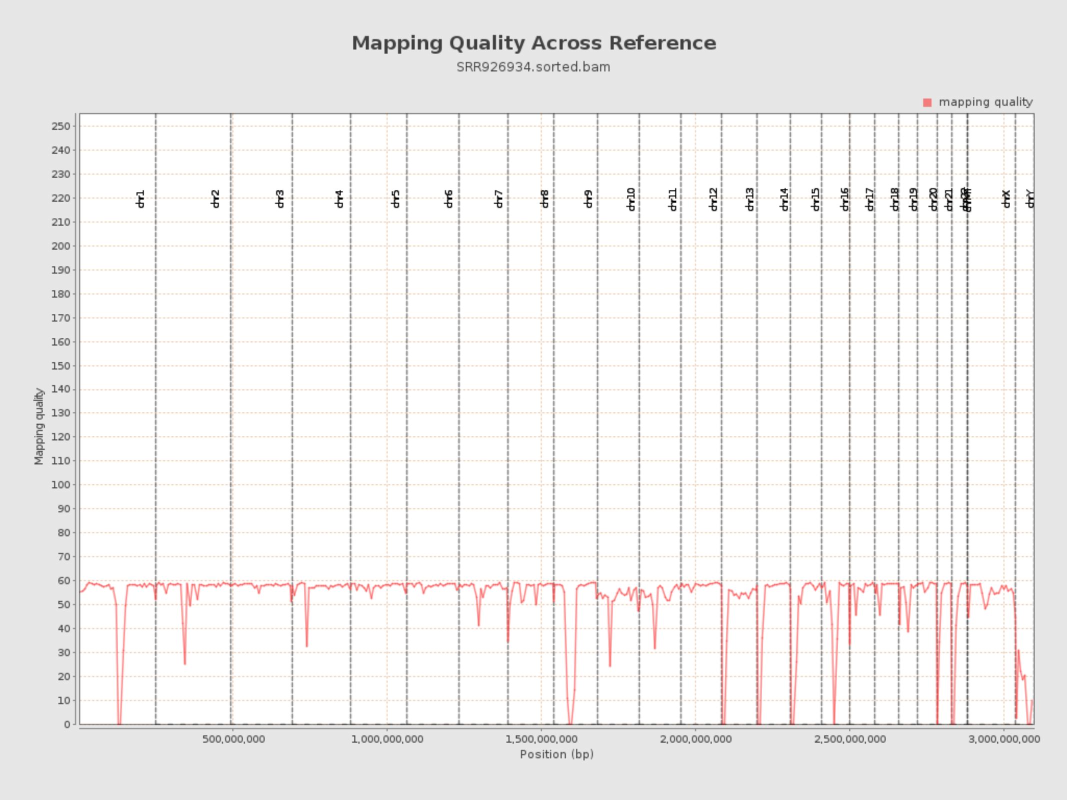
10. Results : Mapped Reads Clipping Profile



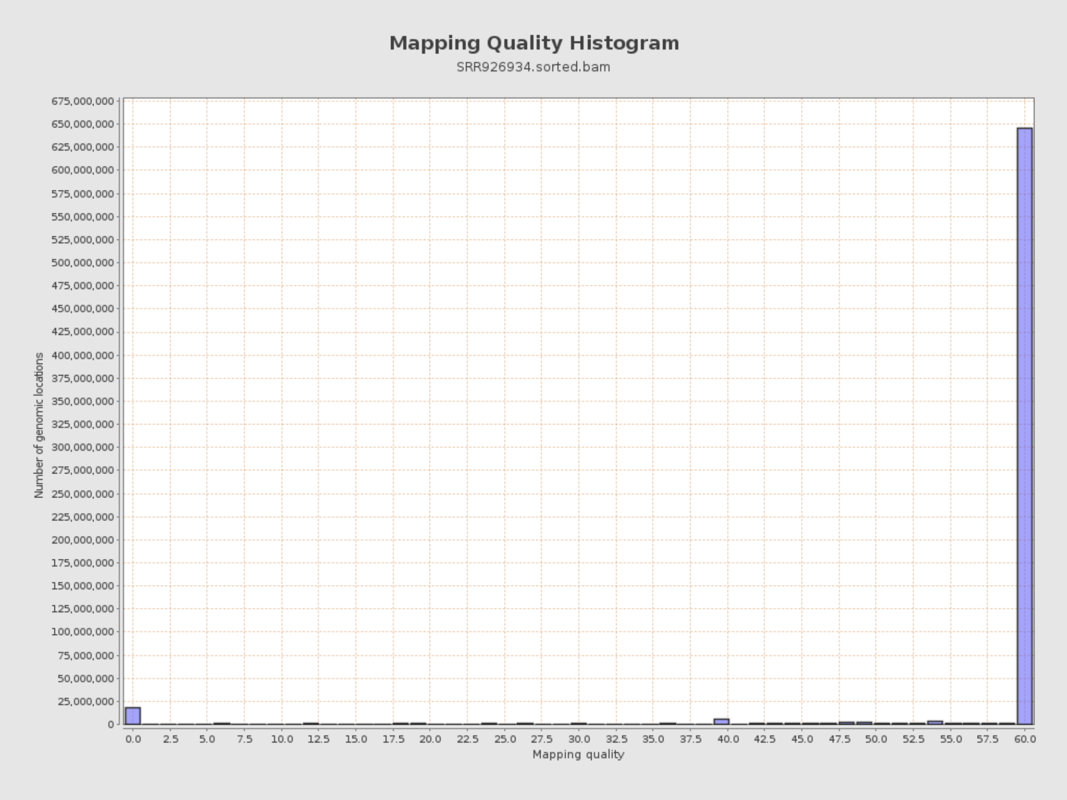
11. Results : Homopolymer Indels



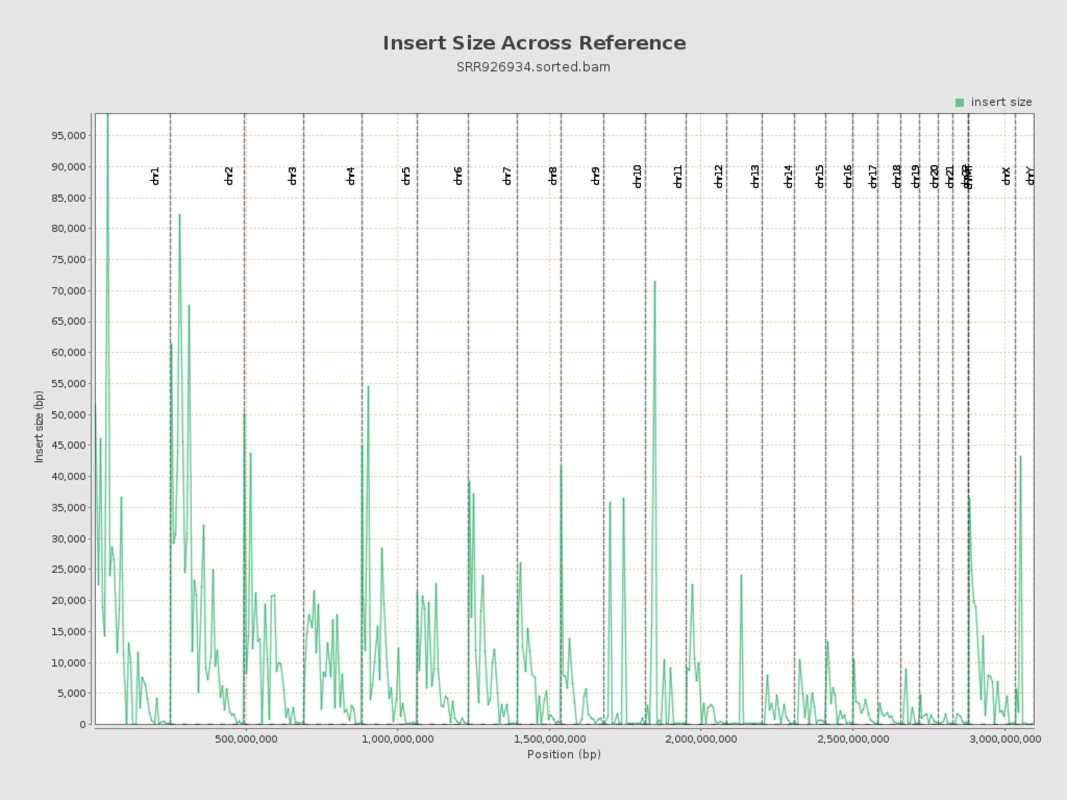
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram