Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 02:09:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926951.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_SRR926951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926951_1.fastq.gz SRR926951_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 02:09:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,841,840
Mapped reads	9,320,968 / 94.71%
Unmapped reads	520,872 / 5.29%
Mapped paired reads	9,320,968 / 94.71%
Mapped reads, first in pair	4,652,606 / 47.27%
Mapped reads, second in pair	4,668,362 / 47.43%
Mapped reads, both in pair	9,087,952 / 92.34%
Mapped reads, singletons	233,016 / 2.37%
Secondary alignments	0
Supplementary alignments	491,875 / 5%
Read min/max/mean length	30 / 101 / 103.08
Duplicated reads (estimated)	665,399 / 6.76%
Duplication rate	5.98%
Clipped reads	4,949,514 / 50.29%

2.2. ACGT Content

Number/percentage of A's	236,204,380 / 28.31%
Number/percentage of C's	163,631,017 / 19.61%
Number/percentage of T's	238,316,757 / 28.56%
Number/percentage of G's	196,257,157 / 23.52%
Number/percentage of N's	42,758 / 0.01%

GC Percentage	43.13%

2.3. Coverage

Mean	0.2698
Standard Deviation	1.1276

2.4. Mapping Quality

Mean Mapping Quality	52.12

2.5. Insert size

Mean	547,584.02
Standard Deviation	7,293,733.68
P25/Median/P75	136 / 179 / 244

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	8,348,275
Insertions	147,227
Mapped reads with at least one insertion	1.55%
Deletions	420,477
Mapped reads with at least one deletion	4.4%
Homopolymer indels	51.68%

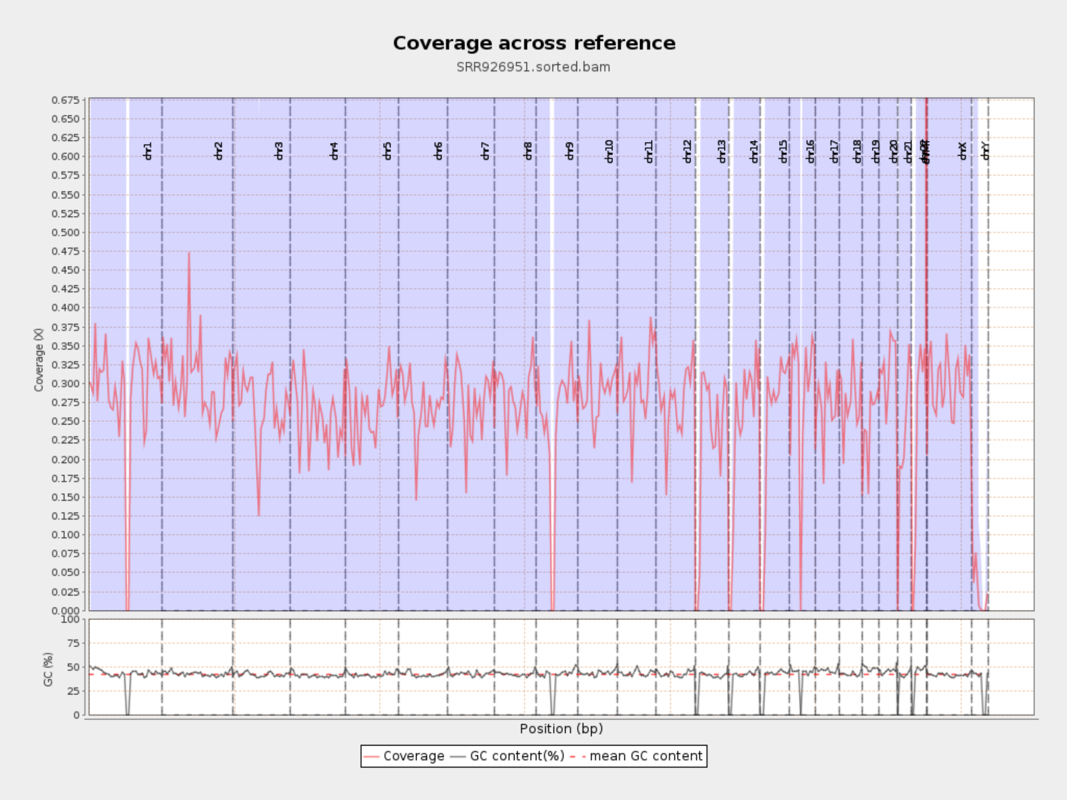
2.7. Chromosome stats

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

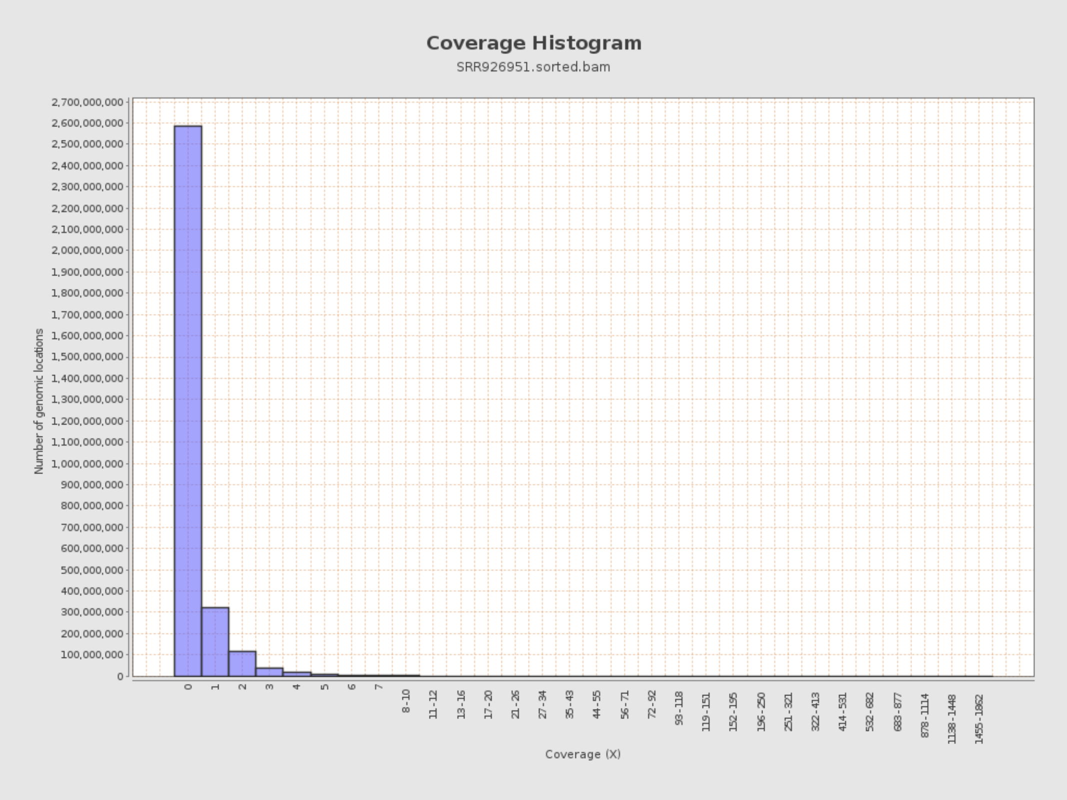
		bases	coverage	deviation
chr1	249250621	71420289	0.2865	1.2252
chr2	243199373	74586533	0.3067	2.1407
chr3	198022430	53953549	0.2725	0.7572
chr4	191154276	49259533	0.2577	1.1725
chr5	180915260	48513823	0.2682	0.7404
chr6	171115067	47005198	0.2747	0.7911
chr7	159138663	43558568	0.2737	0.8117
chr8	146364022	41834115	0.2858	0.8061
chr9	141213431	35171664	0.2491	0.9342
chr10	135534747	39274871	0.2898	1.936
chr11	135006516	40871334	0.3027	1.0457
chr12	133851895	37442598	0.2797	1.0868
chr13	115169878	25691403	0.2231	0.6815
chr14	107349540	25452386	0.2371	0.7127
chr15	102531392	25081295	0.2446	0.7319
chr16	90354753	26365614	0.2918	1.0358
chr17	81195210	22072943	0.2719	0.8107
chr18	78077248	21934293	0.2809	1.0161
chr19	59128983	14619557	0.2472	0.8736
chr20	63025520	20180183	0.3202	0.8669
chr21	48129895	10943772	0.2274	1.143
chr22	51304566	11377939	0.2218	0.7086
chrMT	16571	166646	10.0565	11.6529
chrX	155270560	46776299	0.3013	0.8105

chrY	59373566	1529486	0.0258	0.8363

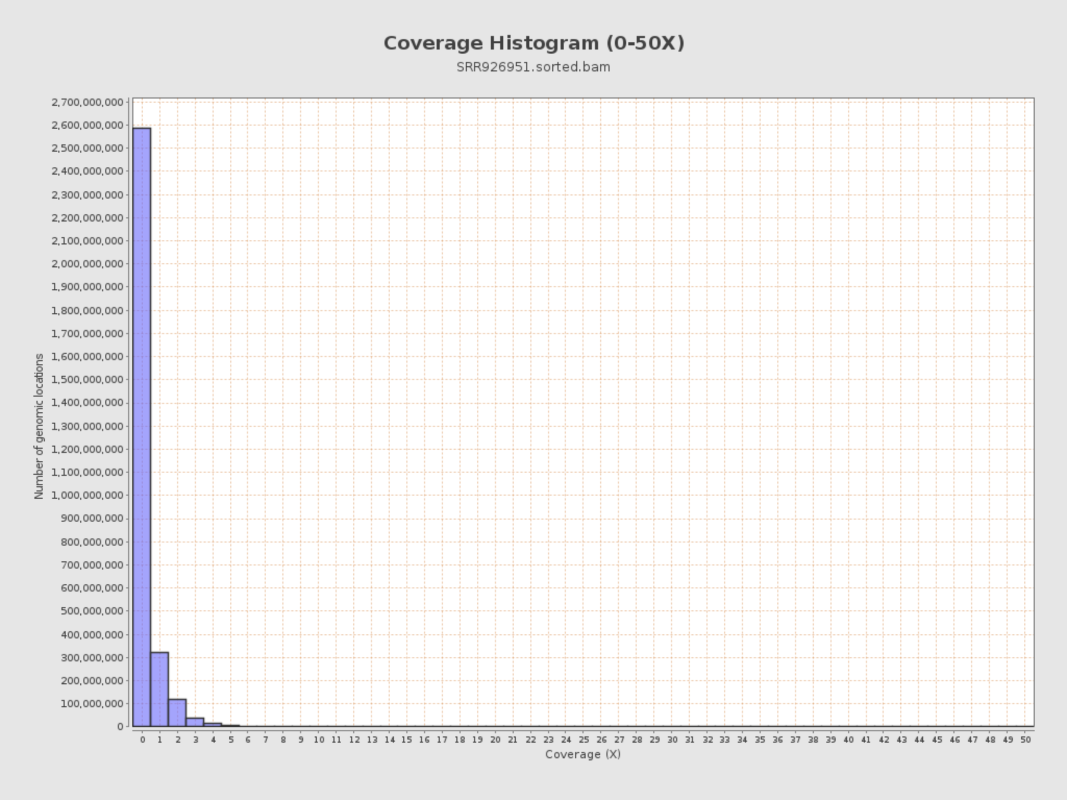
3. Results : Coverage across reference



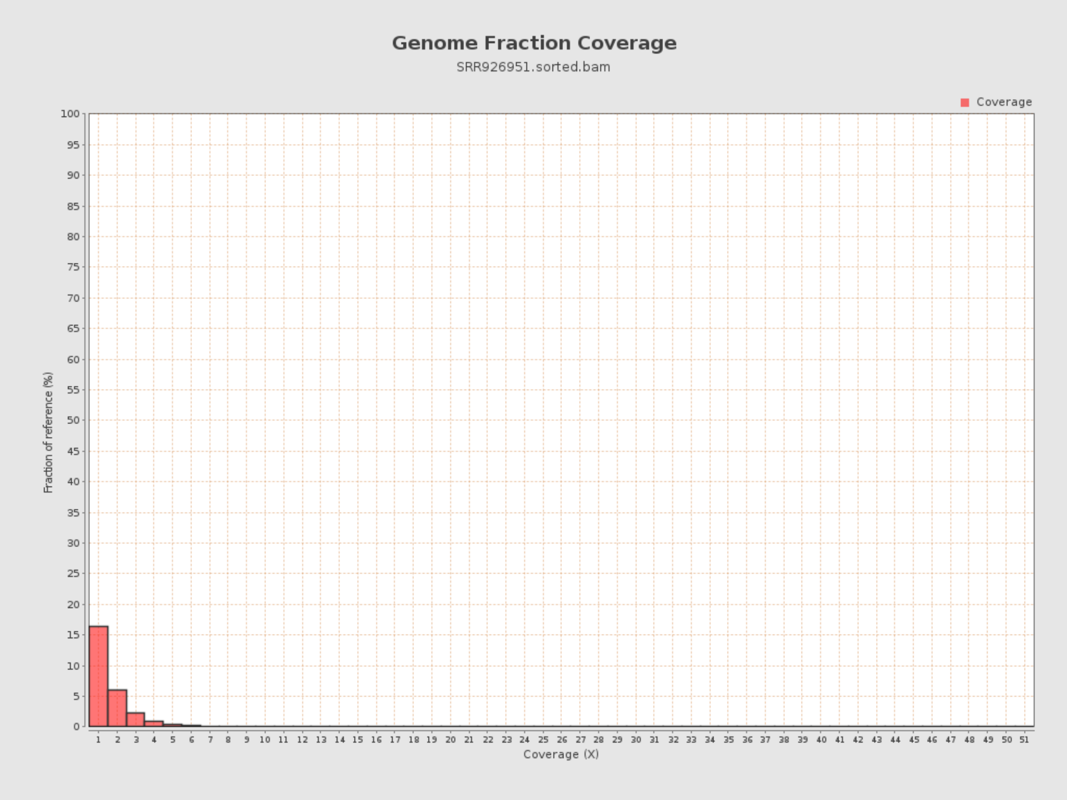
4. Results : Coverage Histogram



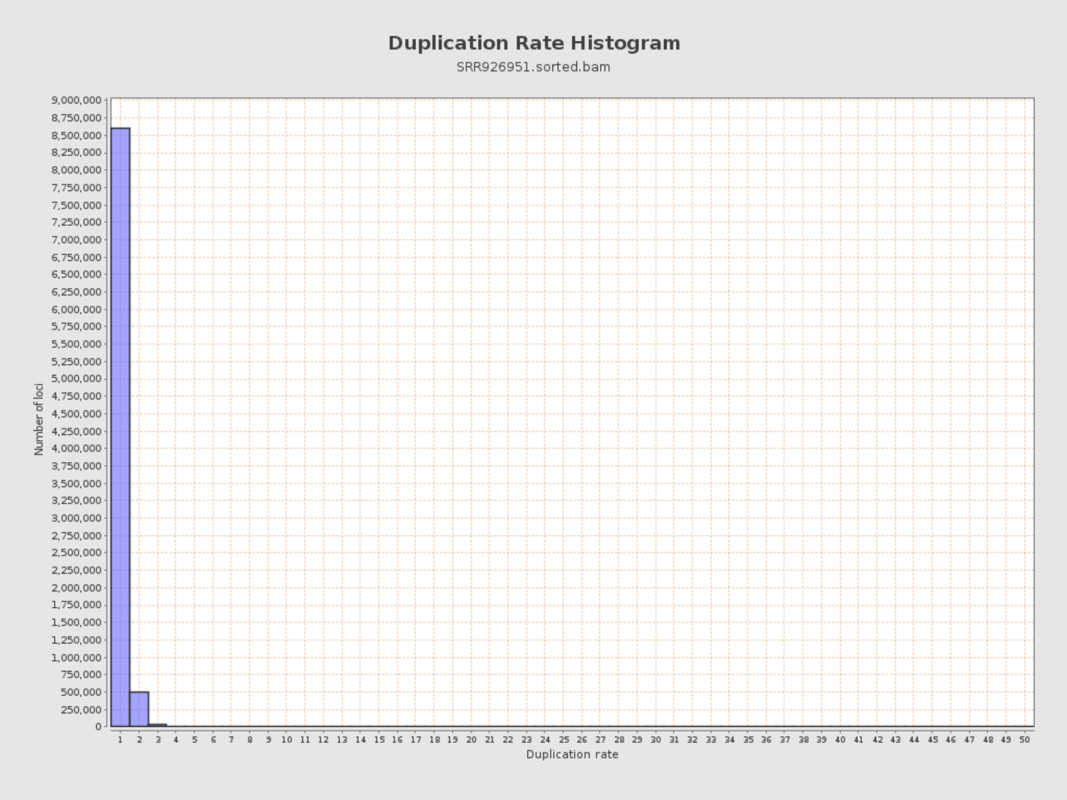
5. Results : Coverage Histogram (0-50X)



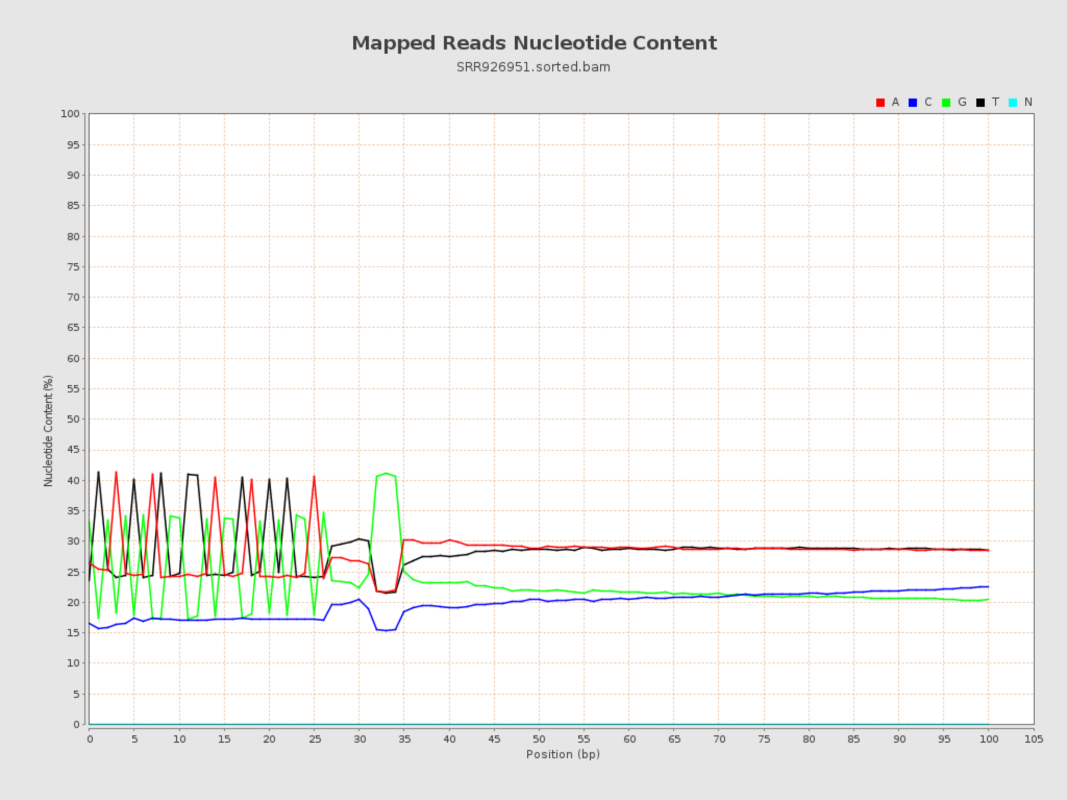
6. Results : Genome Fraction Coverage



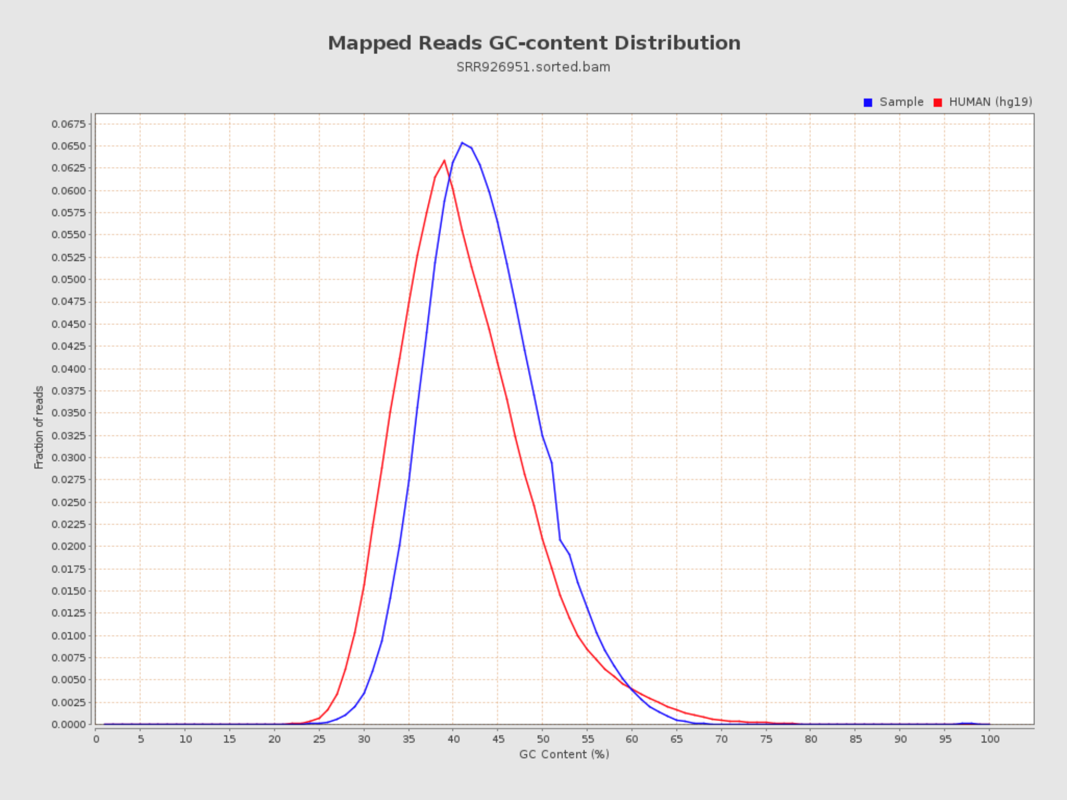
7. Results : Duplication Rate Histogram



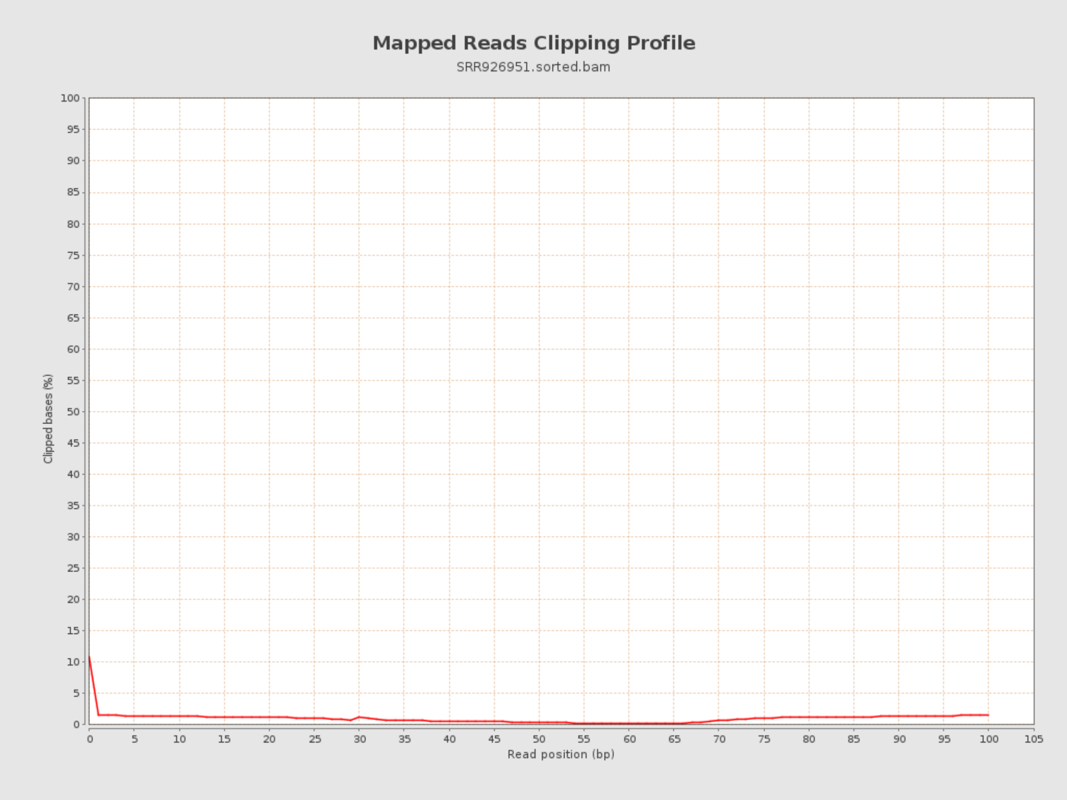
8. Results : Mapped Reads Nucleotide Content



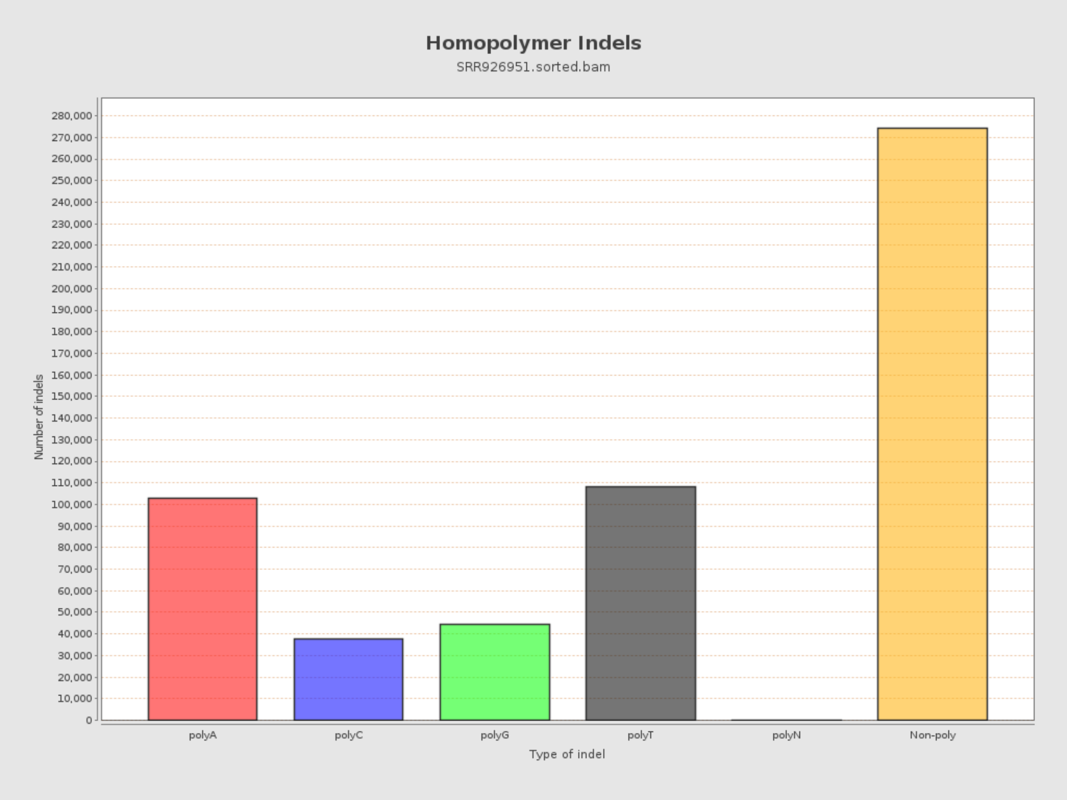
9. Results : Mapped Reads GC-content Distribution



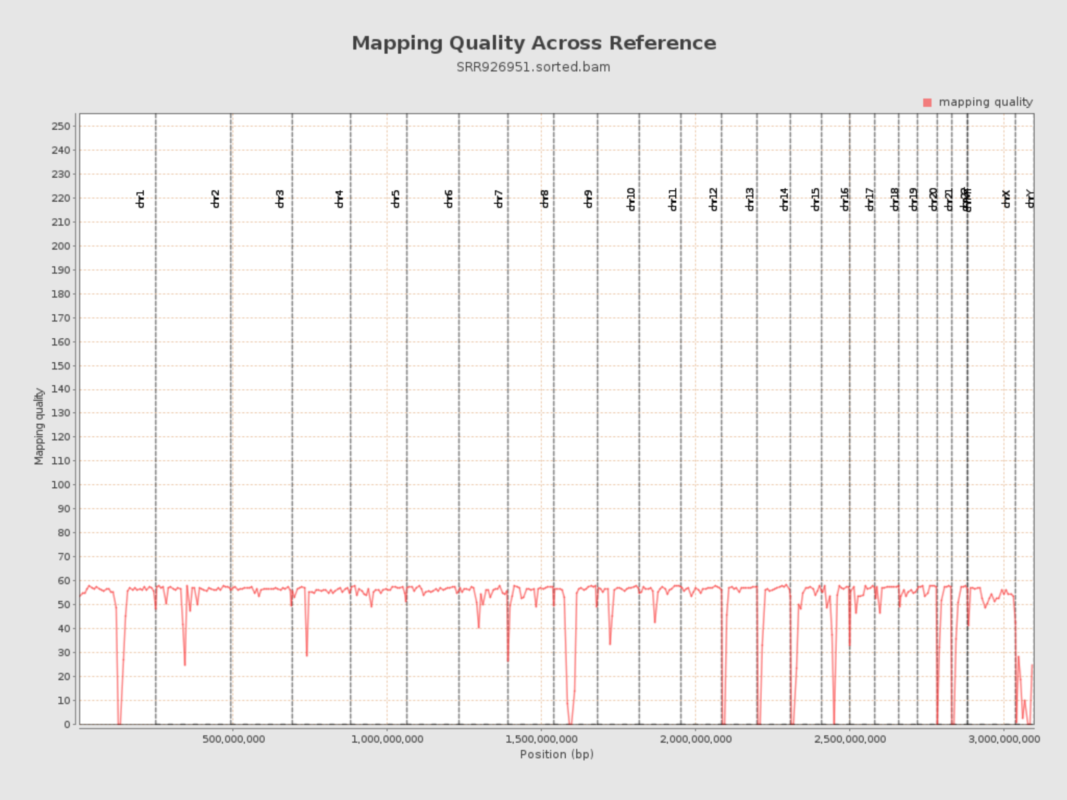
10. Results : Mapped Reads Clipping Profile



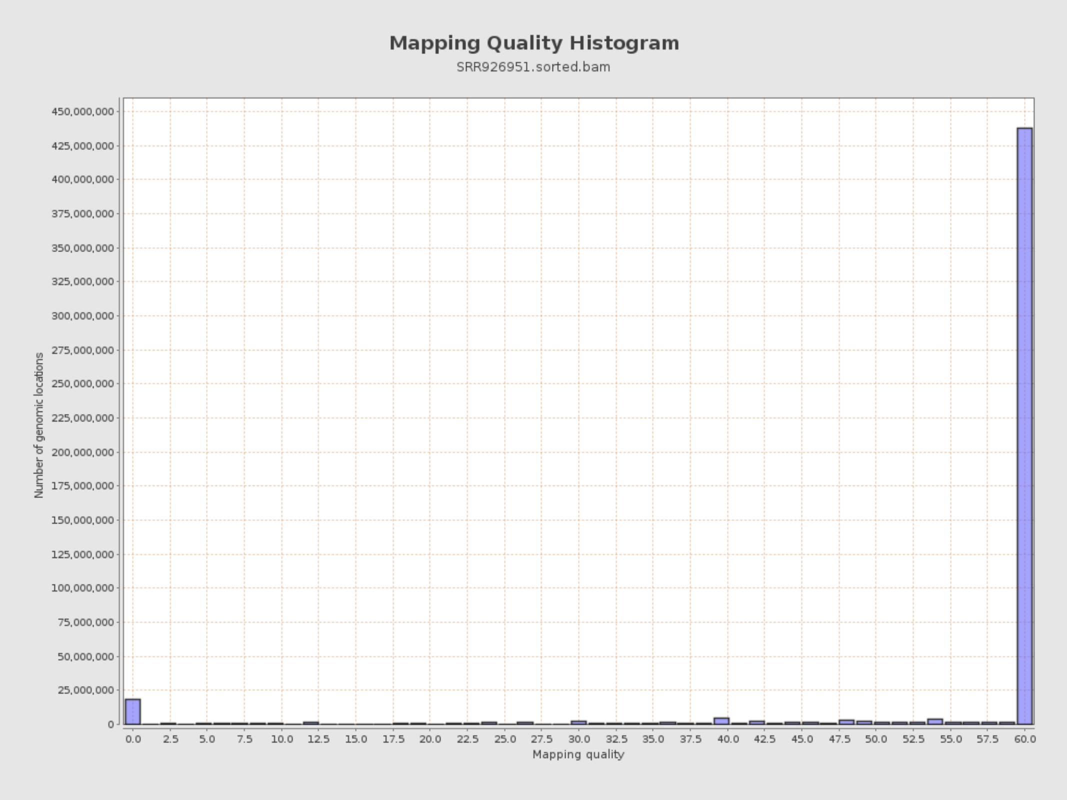
11. Results : Homopolymer Indels



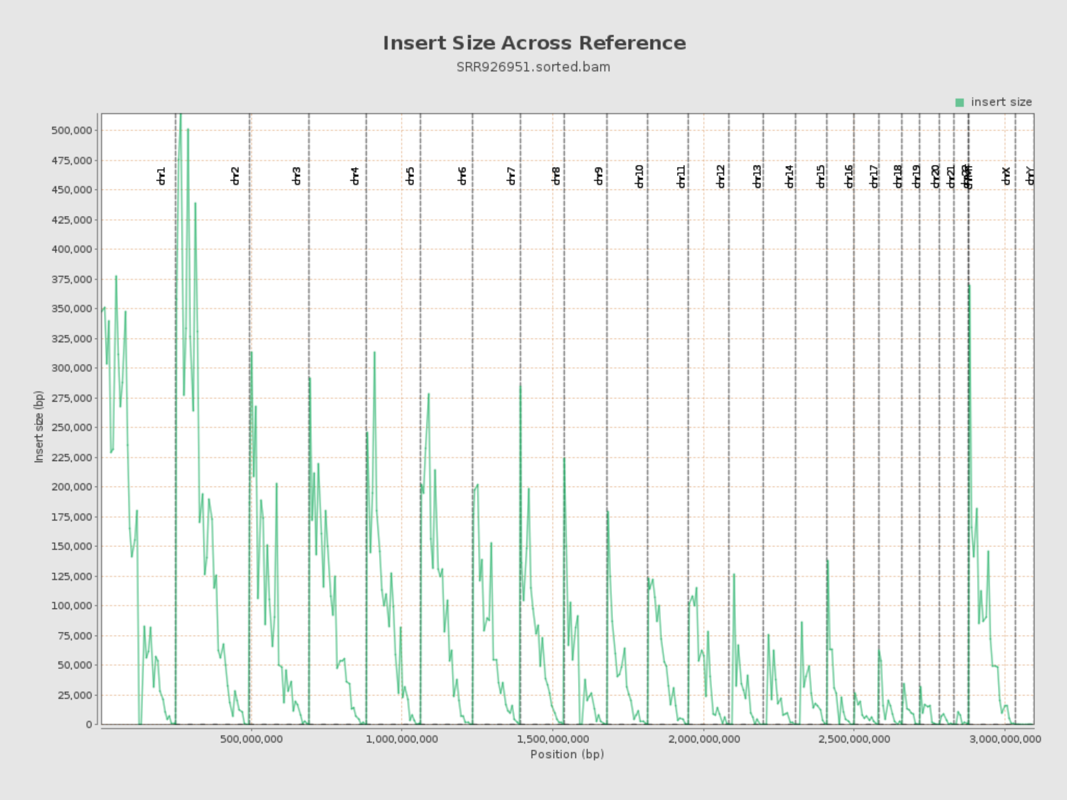
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram