Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 11:22:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781854.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_SRR1781854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781854_1.fastq.gz SRR1781854_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 11:22:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	349,553,126
Mapped reads	340,620,771 / 97.44%
Unmapped reads	8,932,355 / 2.56%
Mapped paired reads	340,620,771 / 97.44%
Mapped reads, first in pair	171,227,299 / 48.98%
Mapped reads, second in pair	169,393,472 / 48.46%
Mapped reads, both in pair	336,662,692 / 96.31%
Mapped reads, singletons	3,958,079 / 1.13%
Secondary alignments	0
Supplementary alignments	863,697 / 0.25%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	40,498,440 / 11.59%
Duplication rate	11.45%
Clipped reads	16,222,331 / 4.64%

2.2. ACGT Content

Number/percentage of A's	10,002,053,078 / 29.58%
Number/percentage of C's	6,899,263,097 / 20.4%
Number/percentage of T's	9,934,791,128 / 29.38%
Number/percentage of G's	6,972,287,965 / 20.62%
Number/percentage of N's	8,627,966 / 0.03%

GC Percentage	41.02%

2.3. Coverage

Mean	10.926
Standard Deviation	12.9033

2.4. Mapping Quality

Mean Mapping Quality	53.98

2.5. Insert size

Mean	24,529.6
Standard Deviation	1,517,278.89
P25/Median/P75	148 / 182 / 223

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	139,412,878
Insertions	3,414,559
Mapped reads with at least one insertion	0.99%
Deletions	2,878,865
Mapped reads with at least one deletion	0.83%
Homopolymer indels	46.37%

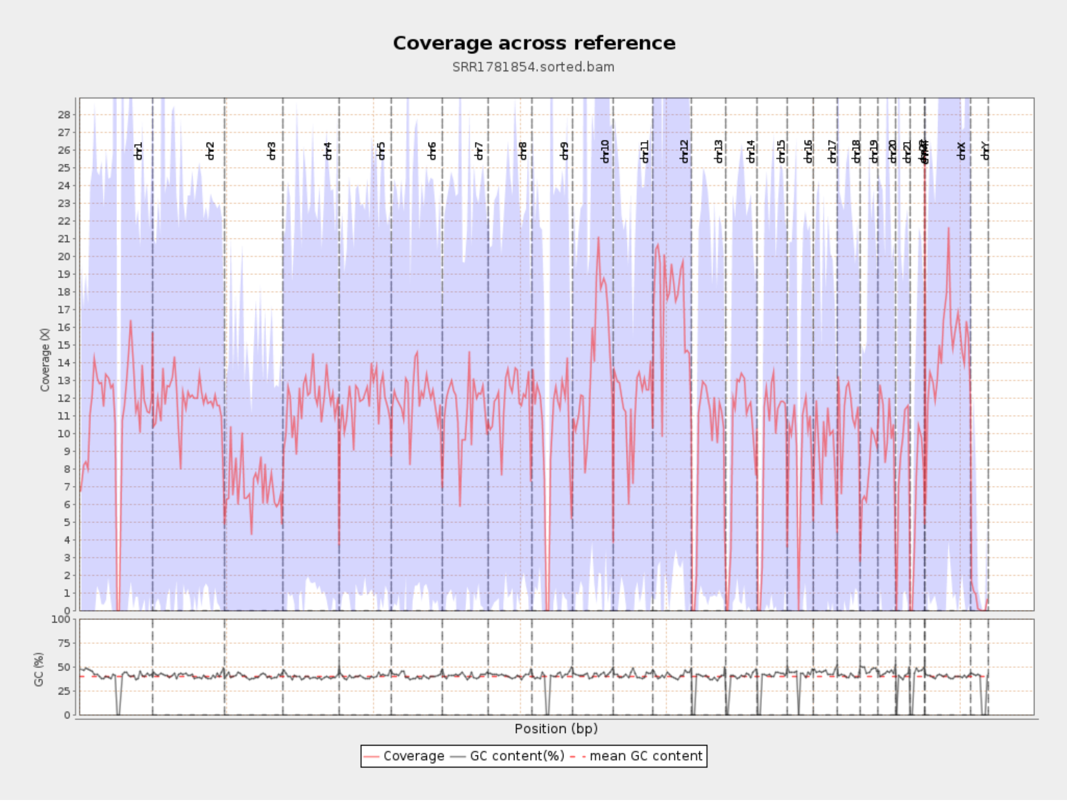
2.7. Chromosome stats

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

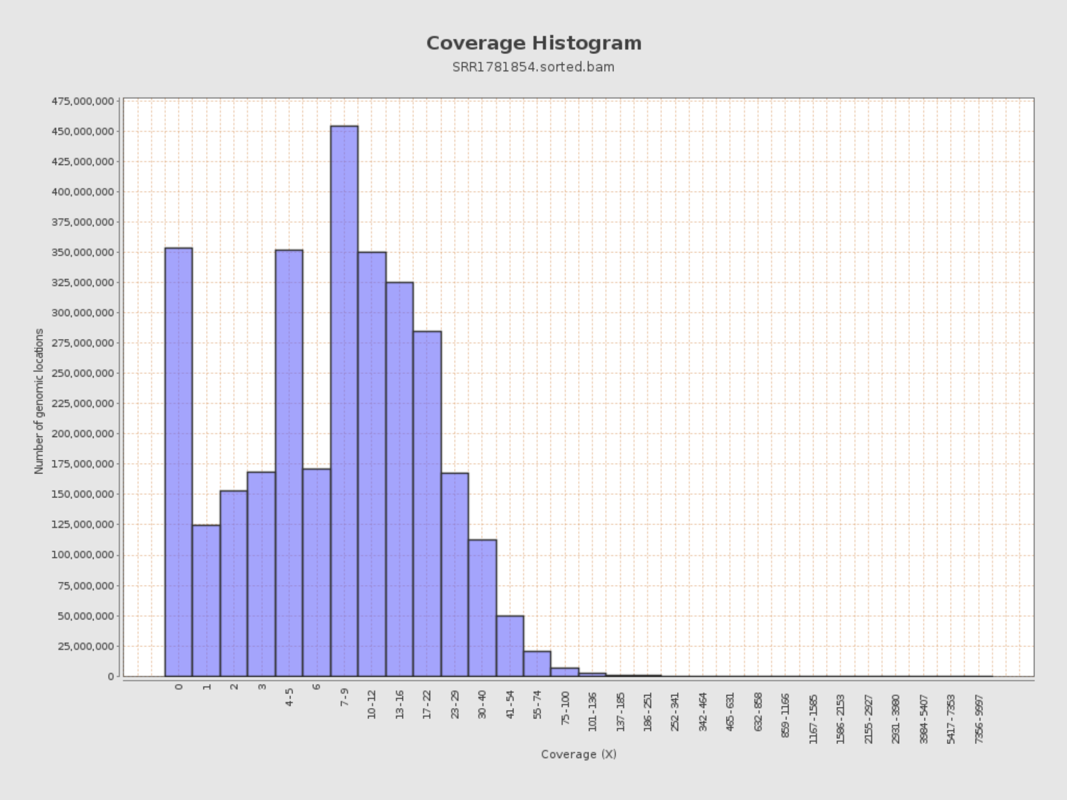
		bases	coverage	deviation
chr1	249250621	2767837294	11.1046	16.2881
chr2	243199373	2863270613	11.7733	13.3366
chr3	198022430	1387158259	7.0051	7.809
chr4	191154276	2255604880	11.7999	11.5301
chr5	180915260	2130484453	11.7761	10.7549
chr6	171115067	2055734860	12.0138	11.7742
chr7	159138663	1791146733	11.2553	12.4125
chr8	146364022	1722113043	11.766	11.1539
chr9	141213431	1392921940	9.8639	13.1993
chr10	135534747	1915133171	14.1302	17.9644
chr11	135006516	1572648885	11.6487	11.7333
chr12	133851895	2339054616	17.4749	16.1755
chr13	115169878	1081502627	9.3905	10.1689
chr14	107349540	1028308723	9.5791	10.9792
chr15	102531392	962473659	9.3871	11.0826
chr16	90354753	791396396	8.7588	10.8557
chr17	81195210	739923377	9.1129	10.7127
chr18	78077248	870094195	11.144	12.0494
chr19	59128983	466980404	7.8977	11.6125
chr20	63025520	649789648	10.3099	12.8576
chr21	48129895	412279565	8.566	14.8084
chr22	51304566	310835121	6.0586	9.3545
chrMT	16571	429959	25.9465	9.3279
chrX	155270560	2286781942	14.7277	14.3717

chrY	59373566	29674657	0.4998	5.2425

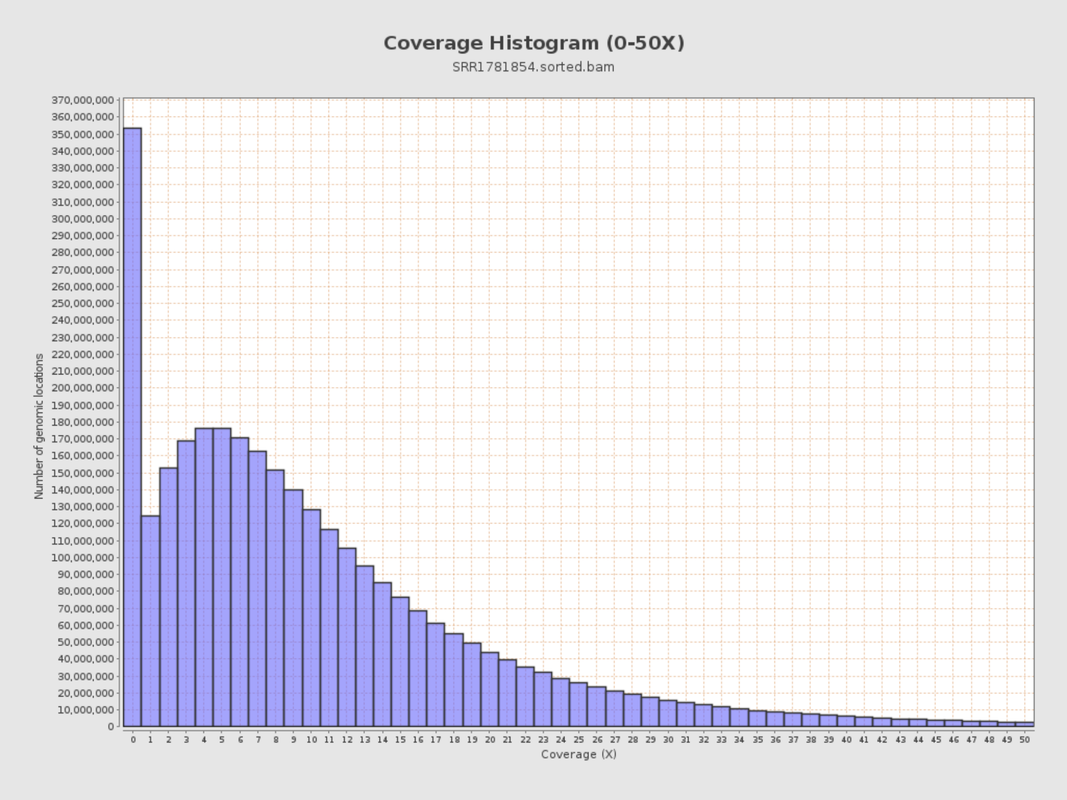
3. Results : Coverage across reference



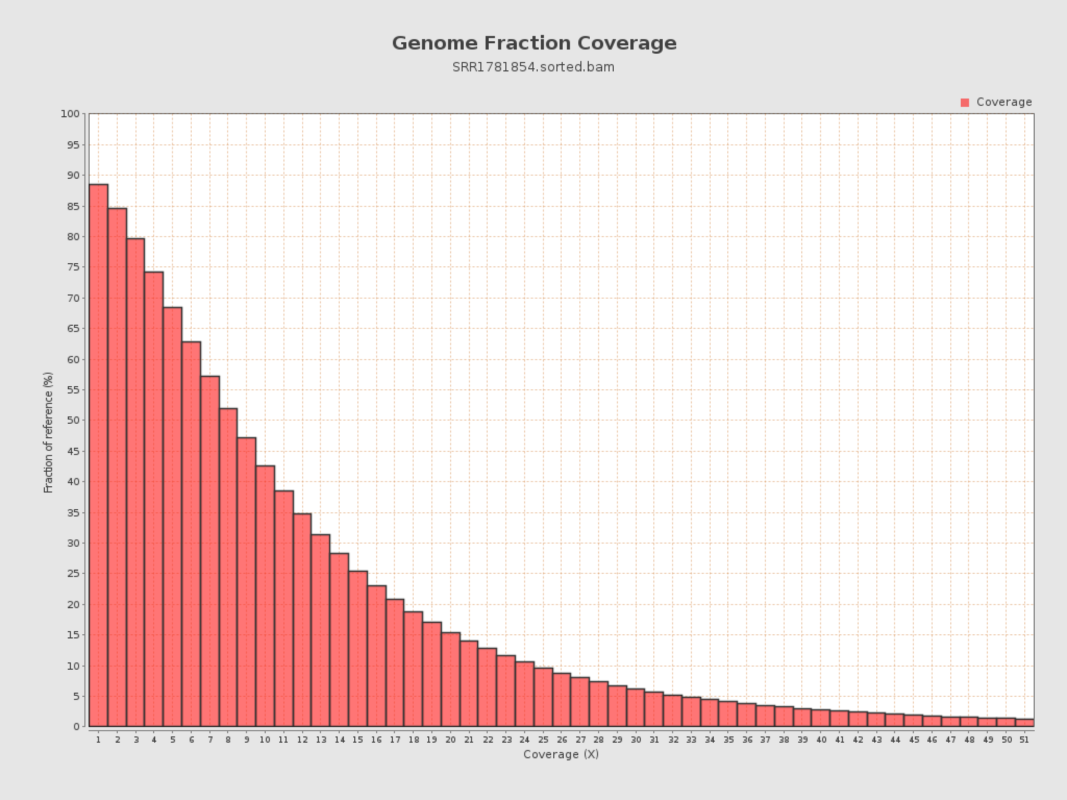
4. Results : Coverage Histogram



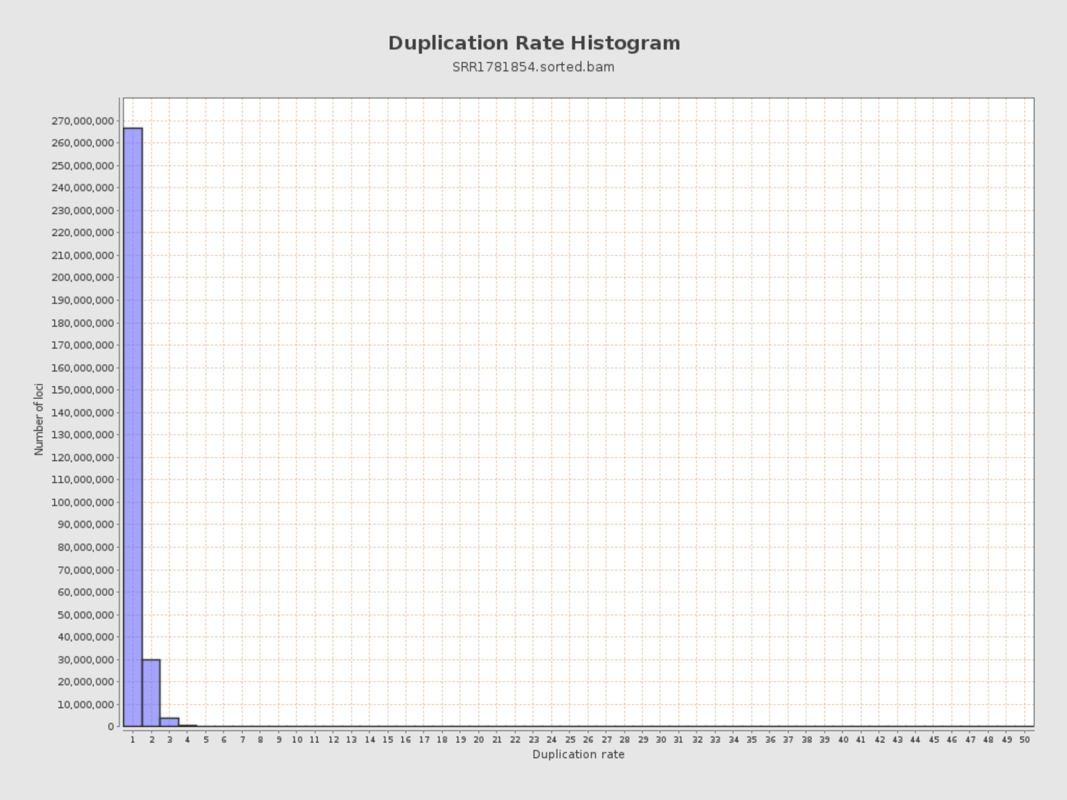
5. Results : Coverage Histogram (0-50X)



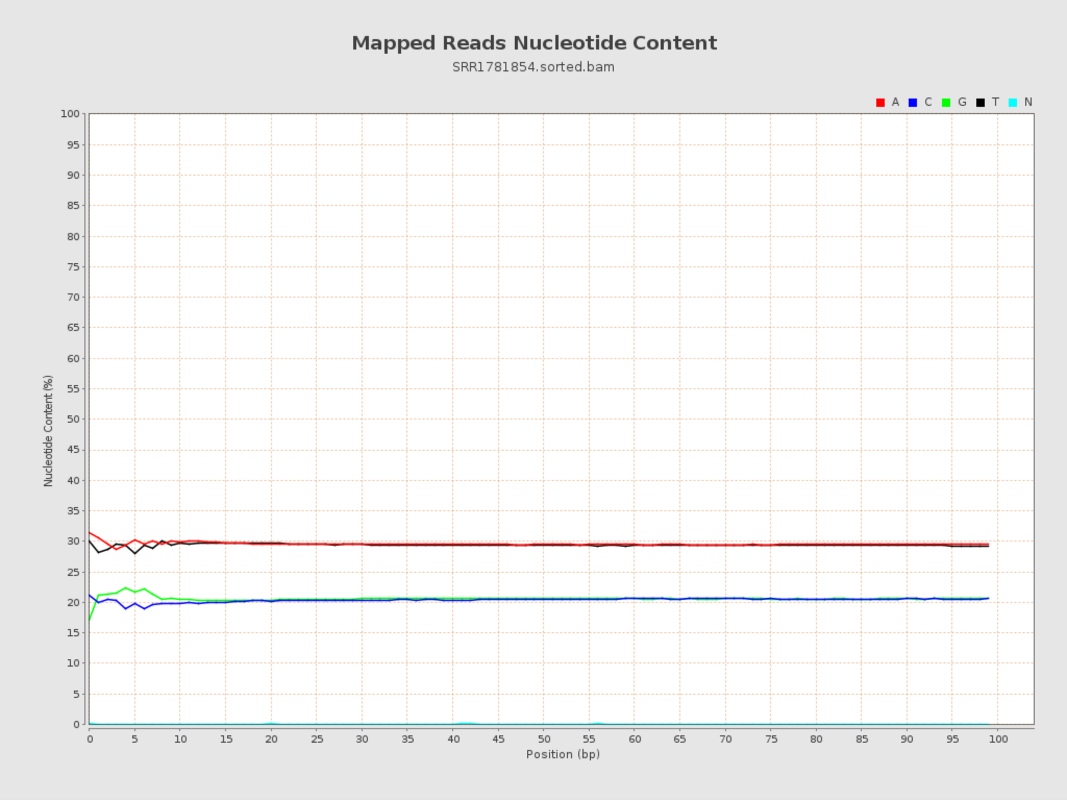
6. Results : Genome Fraction Coverage



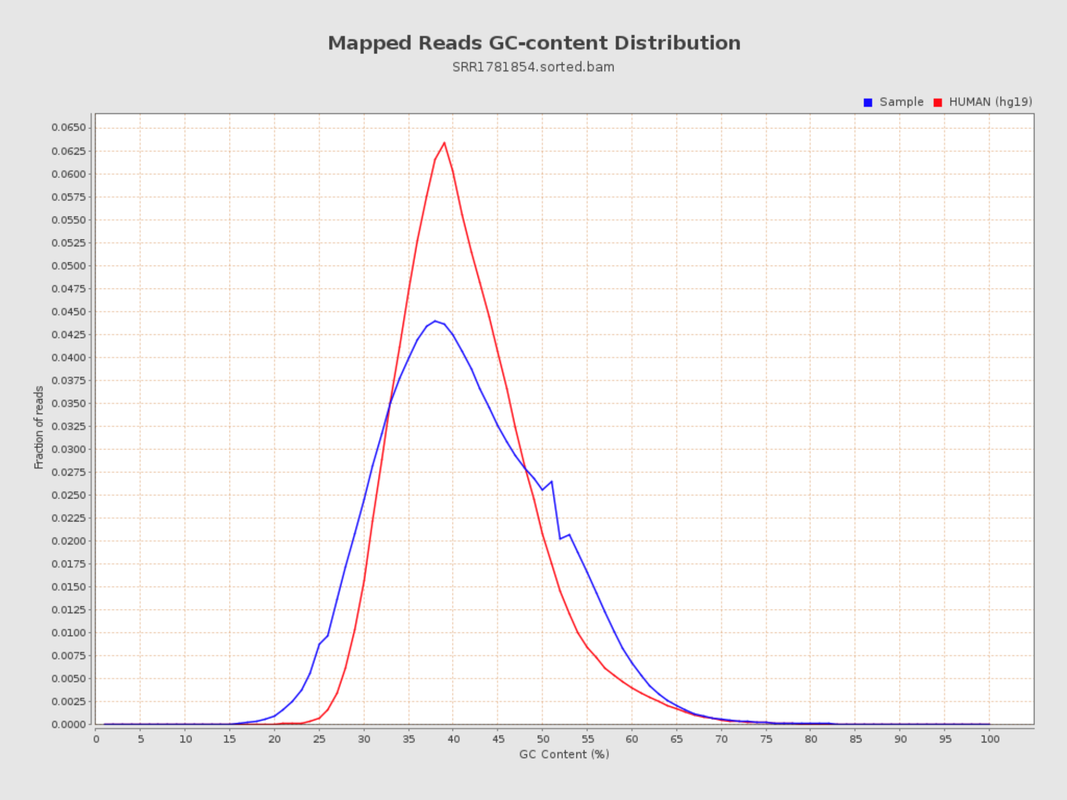
7. Results : Duplication Rate Histogram



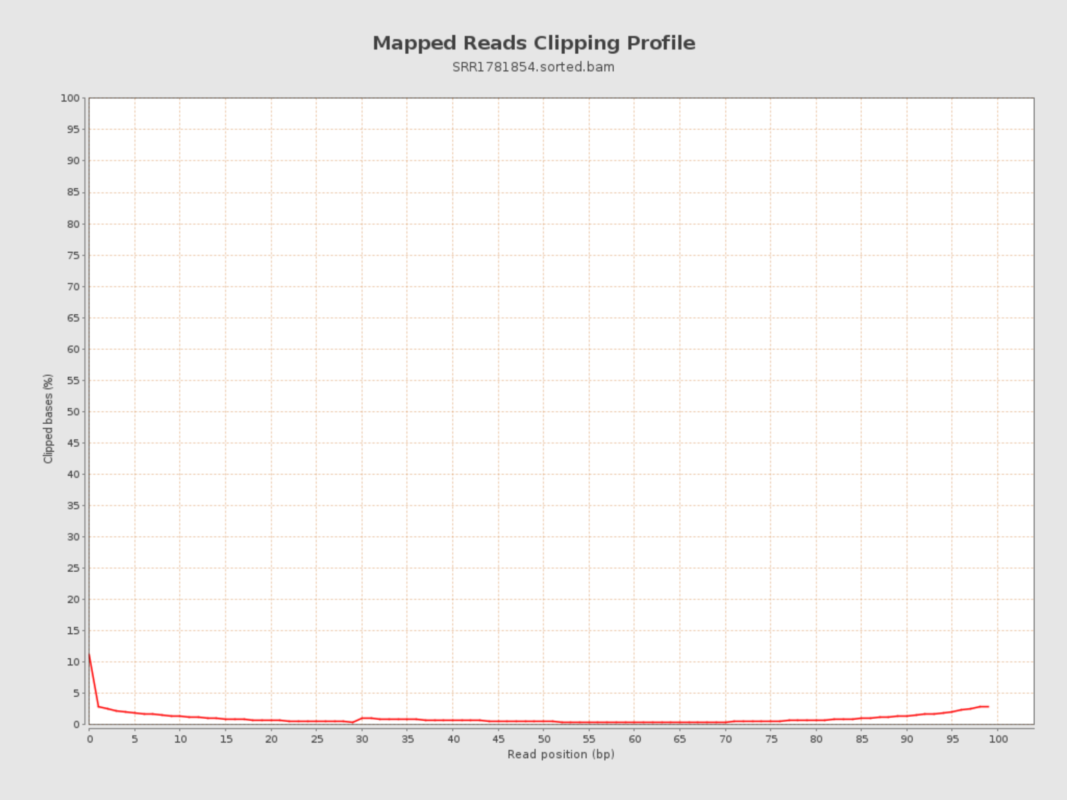
8. Results : Mapped Reads Nucleotide Content



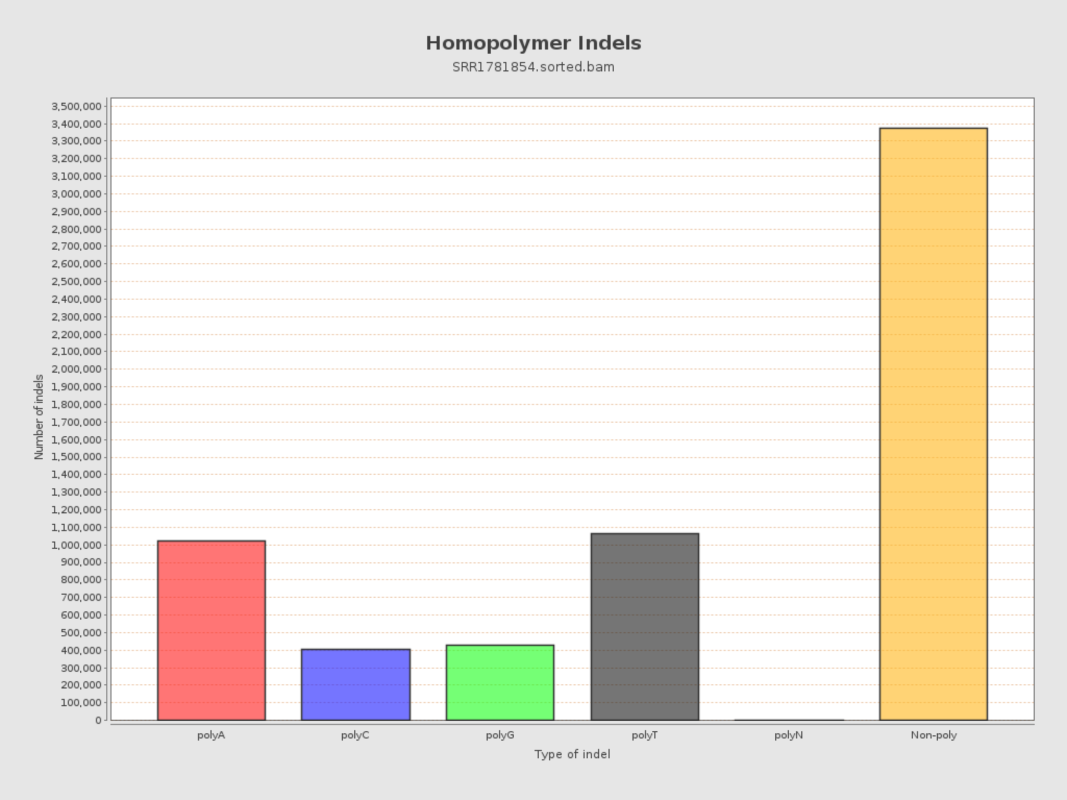
9. Results : Mapped Reads GC-content Distribution



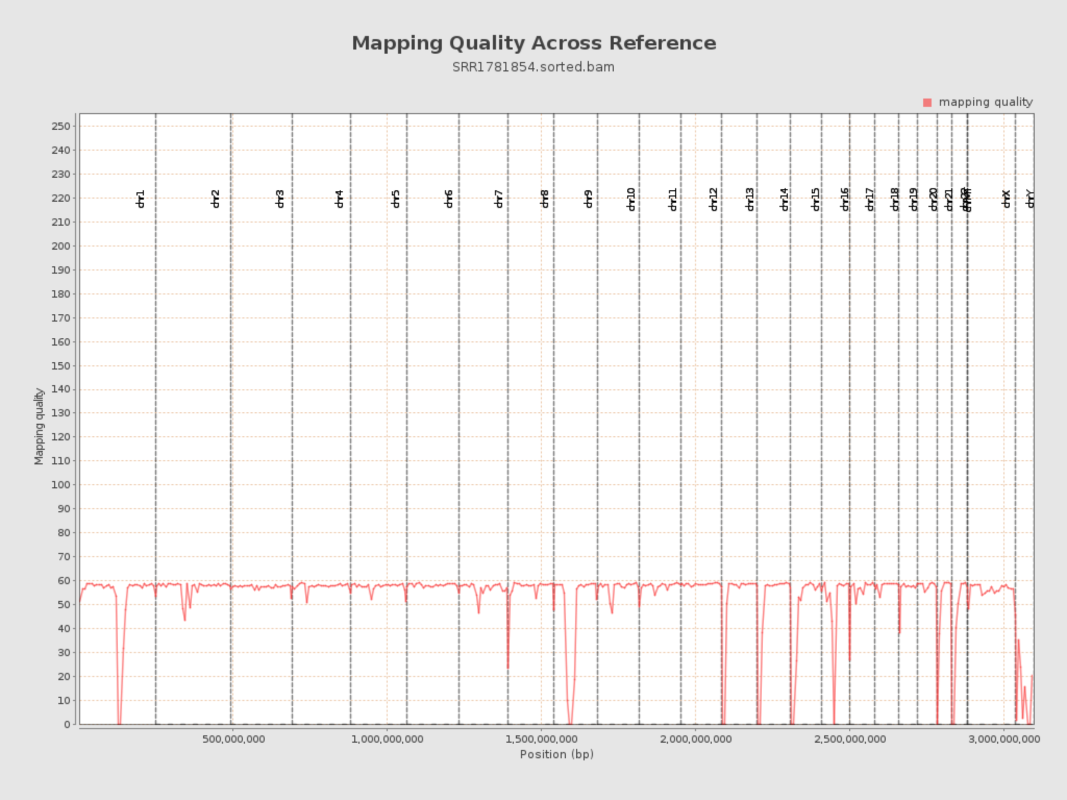
10. Results : Mapped Reads Clipping Profile



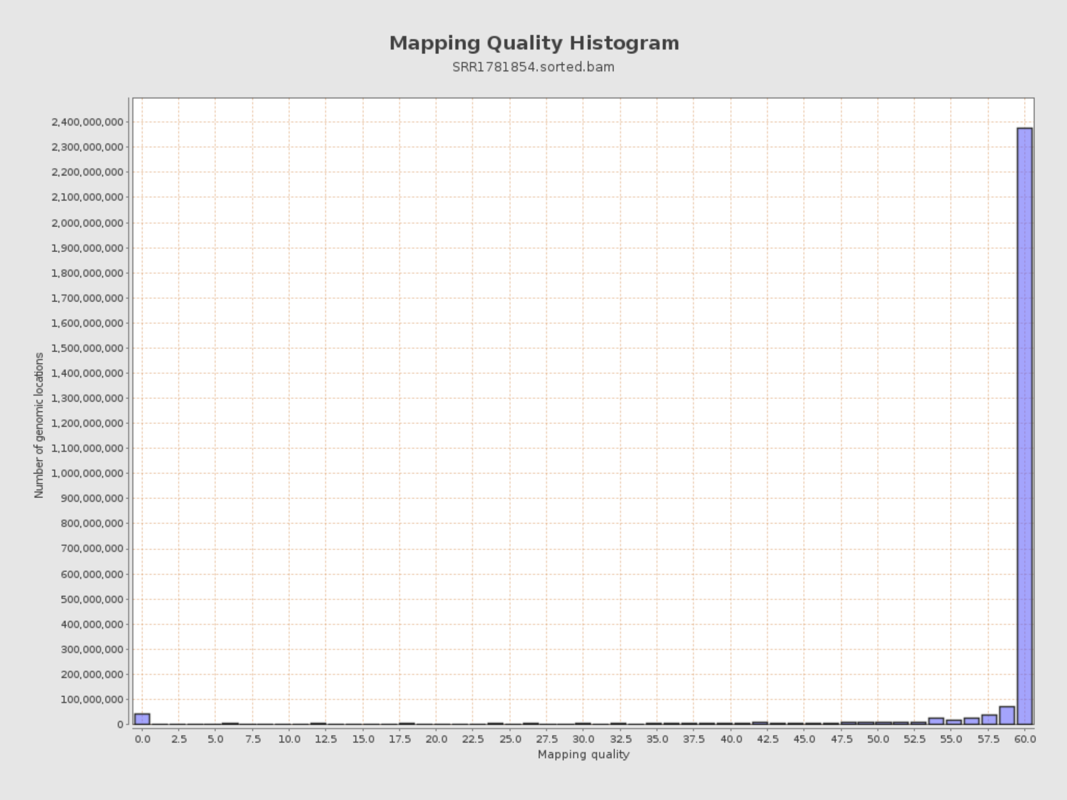
11. Results : Homopolymer Indels



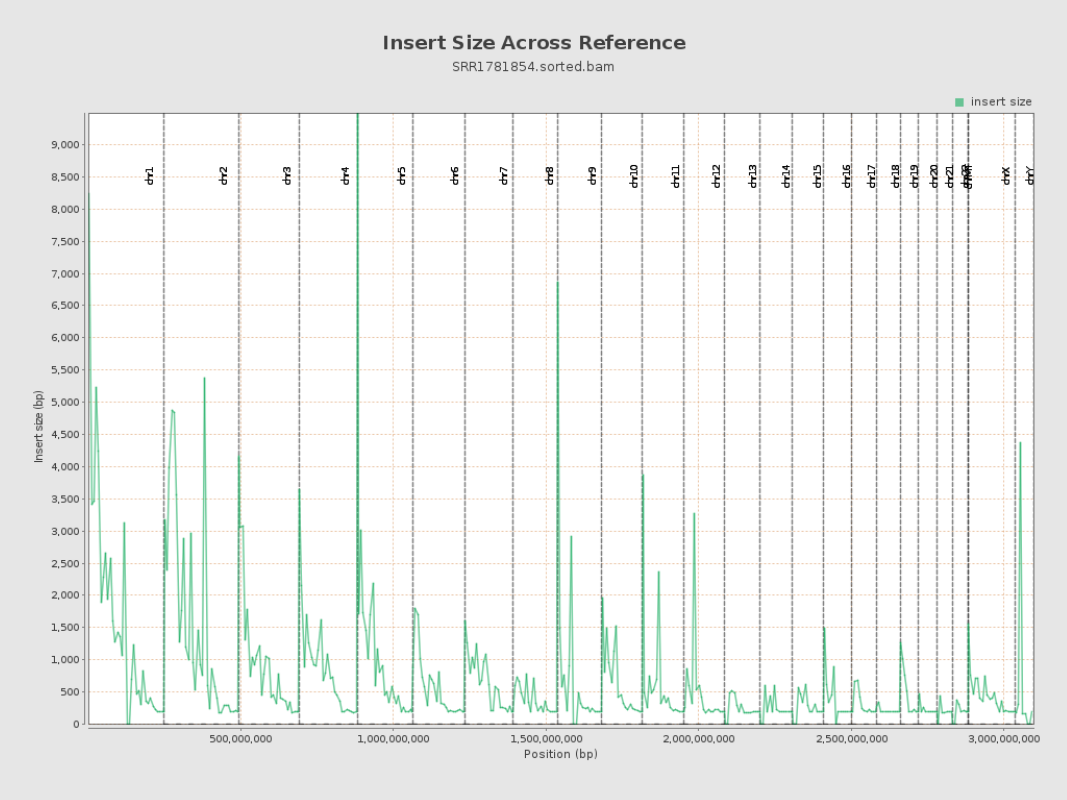
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram