Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 08:37:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781883.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_SRR1781883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781883_1.fastq.gz SRR1781883_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 08:37:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	120,869,322
Mapped reads	118,719,777 / 98.22%
Unmapped reads	2,149,545 / 1.78%
Mapped paired reads	118,719,777 / 98.22%
Mapped reads, first in pair	59,769,116 / 49.45%
Mapped reads, second in pair	58,950,661 / 48.77%
Mapped reads, both in pair	117,533,840 / 97.24%
Mapped reads, singletons	1,185,937 / 0.98%
Secondary alignments	0
Supplementary alignments	406,244 / 0.34%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	5,877,004 / 4.86%
Duplication rate	4.75%
Clipped reads	4,347,132 / 3.6%

2.2. ACGT Content

Number/percentage of A's	3,548,214,923 / 30.09%
Number/percentage of C's	2,333,414,559 / 19.79%
Number/percentage of T's	3,541,198,316 / 30.03%
Number/percentage of G's	2,366,702,530 / 20.07%
Number/percentage of N's	2,080,038 / 0.02%

GC Percentage	39.86%

2.3. Coverage

Mean	3.81
Standard Deviation	4.7242

2.4. Mapping Quality

Mean Mapping Quality	54.01

2.5. Insert size

Mean	48,687.23
Standard Deviation	2,128,747.51
P25/Median/P75	219 / 278 / 358

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	42,001,933
Insertions	1,310,628
Mapped reads with at least one insertion	1.09%
Deletions	1,277,648
Mapped reads with at least one deletion	1.06%
Homopolymer indels	48.45%

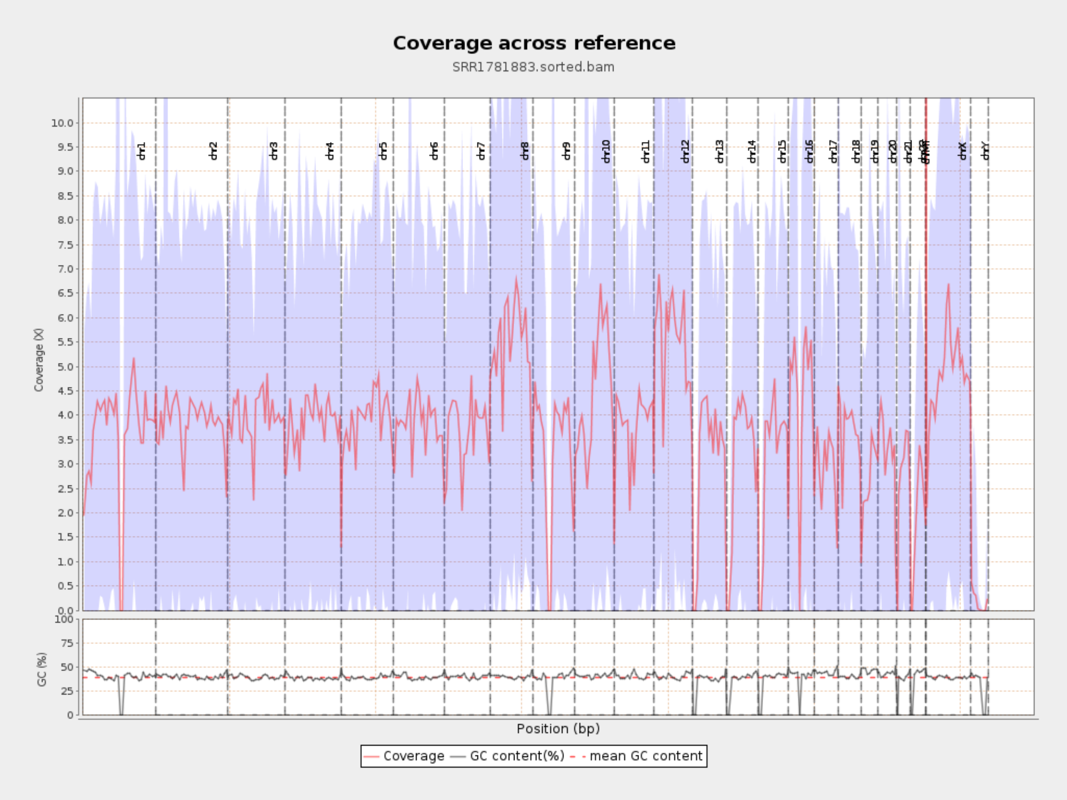
2.7. Chromosome stats

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

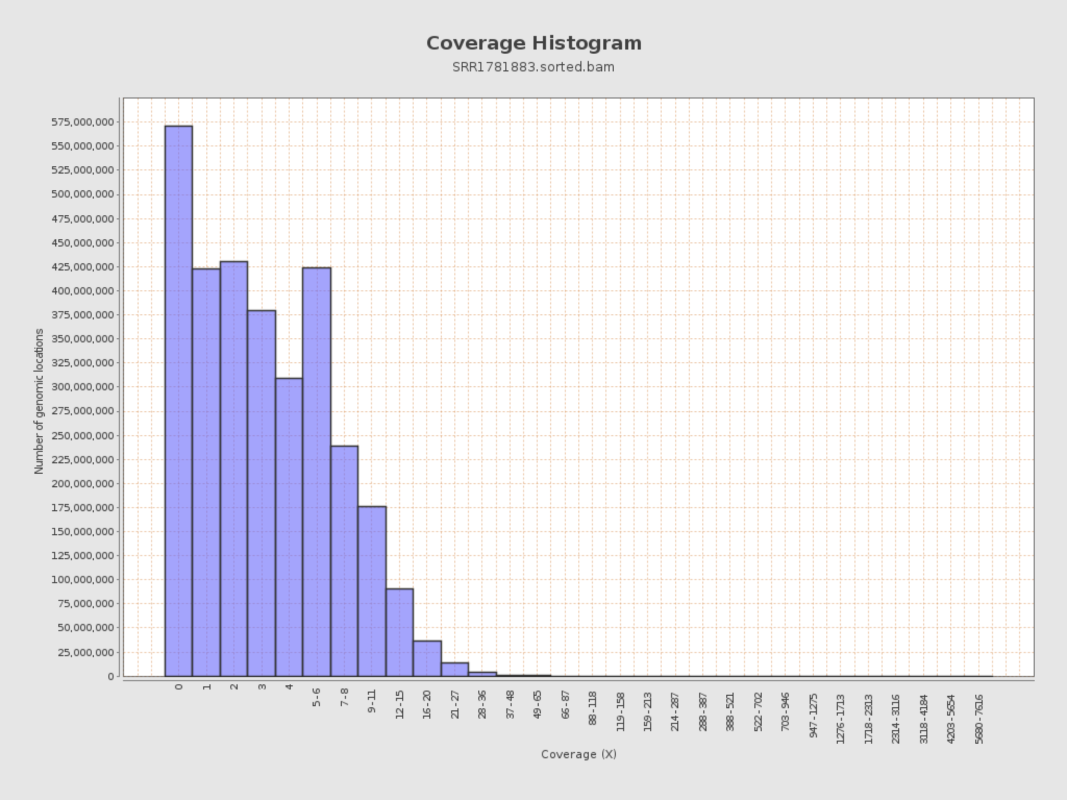
		bases	coverage	deviation
chr1	249250621	906431309	3.6366	5.4642
chr2	243199373	941698577	3.8721	6.8658
chr3	198022430	785861392	3.9685	3.7075
chr4	191154276	745676132	3.9009	3.8723
chr5	180915260	706222235	3.9036	3.6328
chr6	171115067	660903098	3.8623	4.0146
chr7	159138663	582571084	3.6608	3.9925
chr8	146364022	800878891	5.4718	4.969
chr9	141213431	468117293	3.315	4.5458
chr10	135534747	616632107	4.5496	6.4731
chr11	135006516	513630442	3.8045	3.7685
chr12	133851895	755487000	5.6442	5.7592
chr13	115169878	358566785	3.1134	3.4323
chr14	107349540	339868043	3.166	3.6145
chr15	102531392	317183443	3.0935	3.7385
chr16	90354753	389722006	4.3132	4.8286
chr17	81195210	244095803	3.0063	3.627
chr18	78077248	290034756	3.7147	4.0621
chr19	59128983	159444954	2.6966	4.2138
chr20	63025520	214331091	3.4007	4.1897
chr21	48129895	134074725	2.7857	4.7927
chr22	51304566	99160816	1.9328	2.9771
chrMT	16571	400126	24.1462	8.9454
chrX	155270560	753343754	4.8518	4.6146

chrY	59373566	10136470	0.1707	1.727

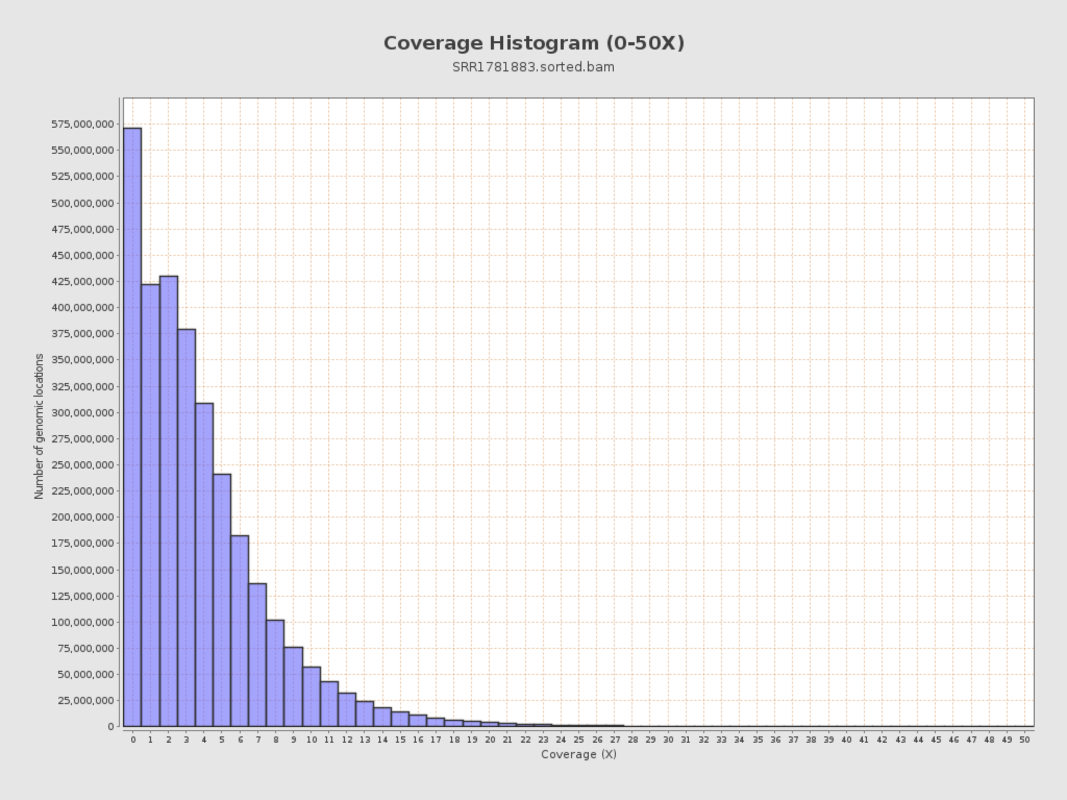
3. Results : Coverage across reference



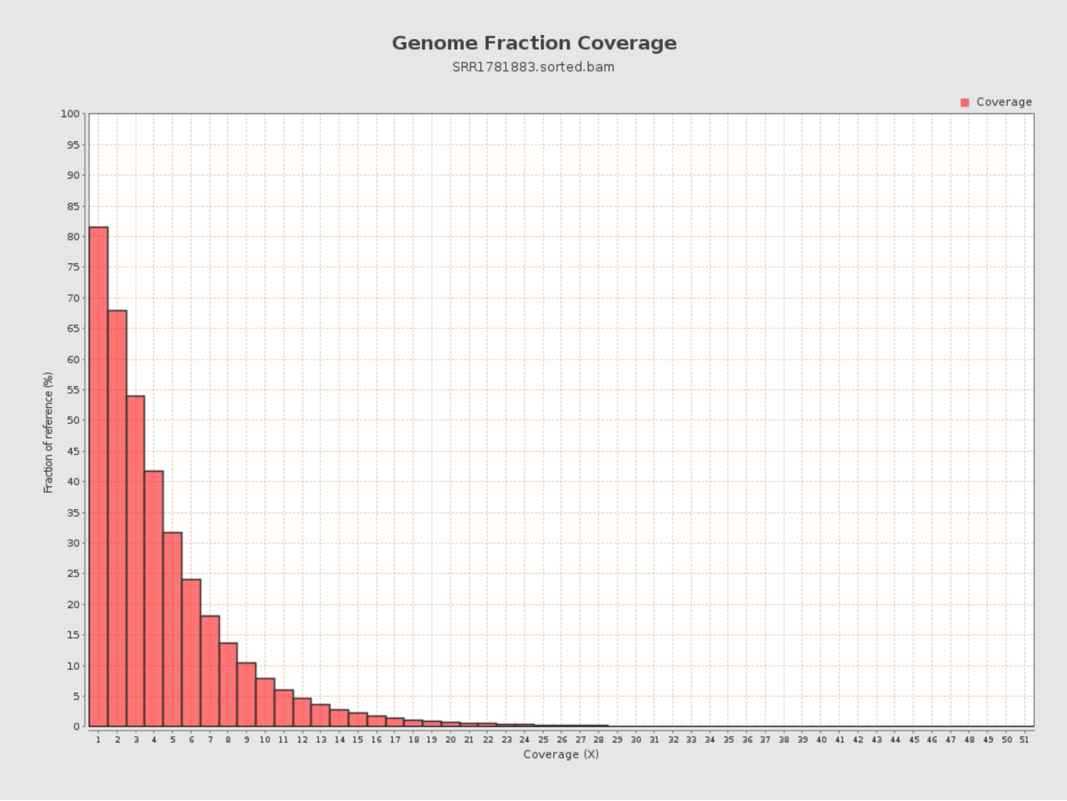
4. Results : Coverage Histogram



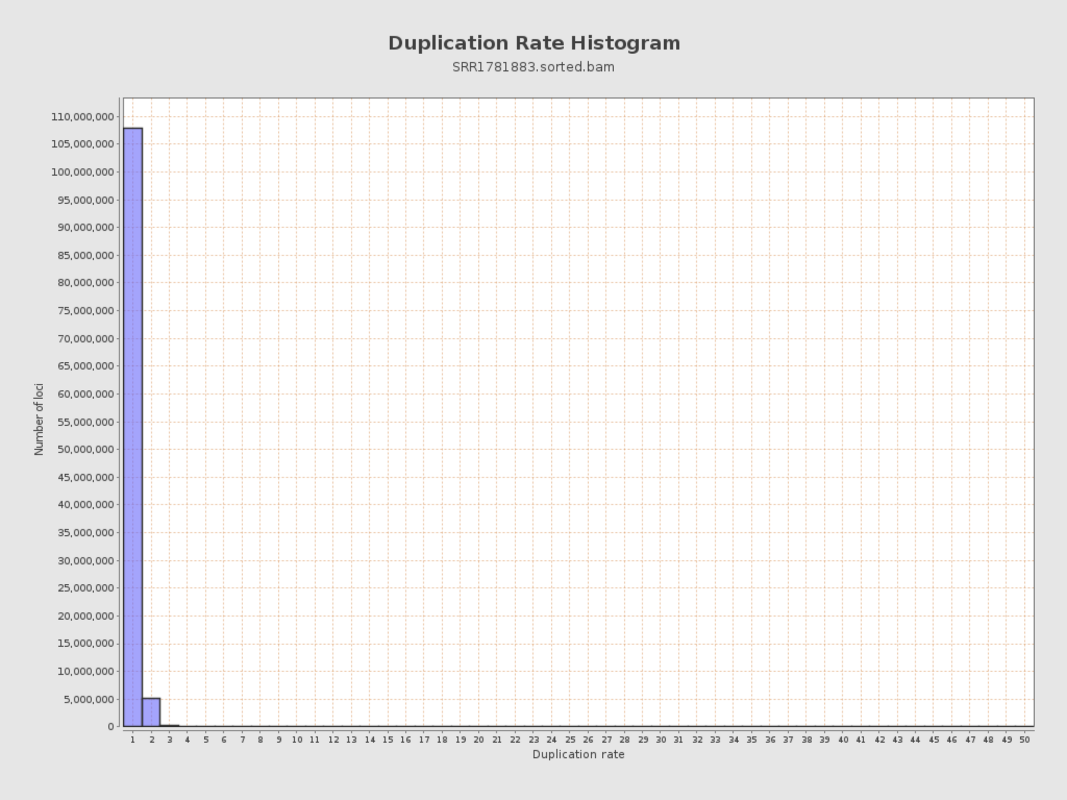
5. Results : Coverage Histogram (0-50X)



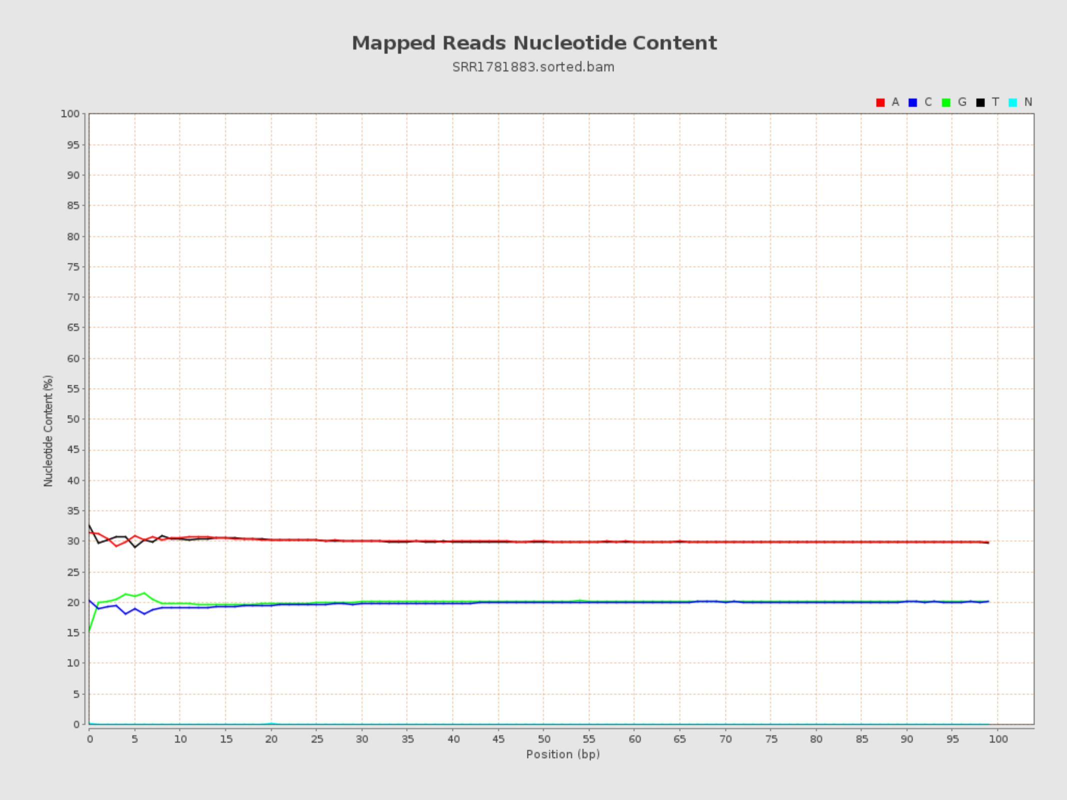
6. Results : Genome Fraction Coverage



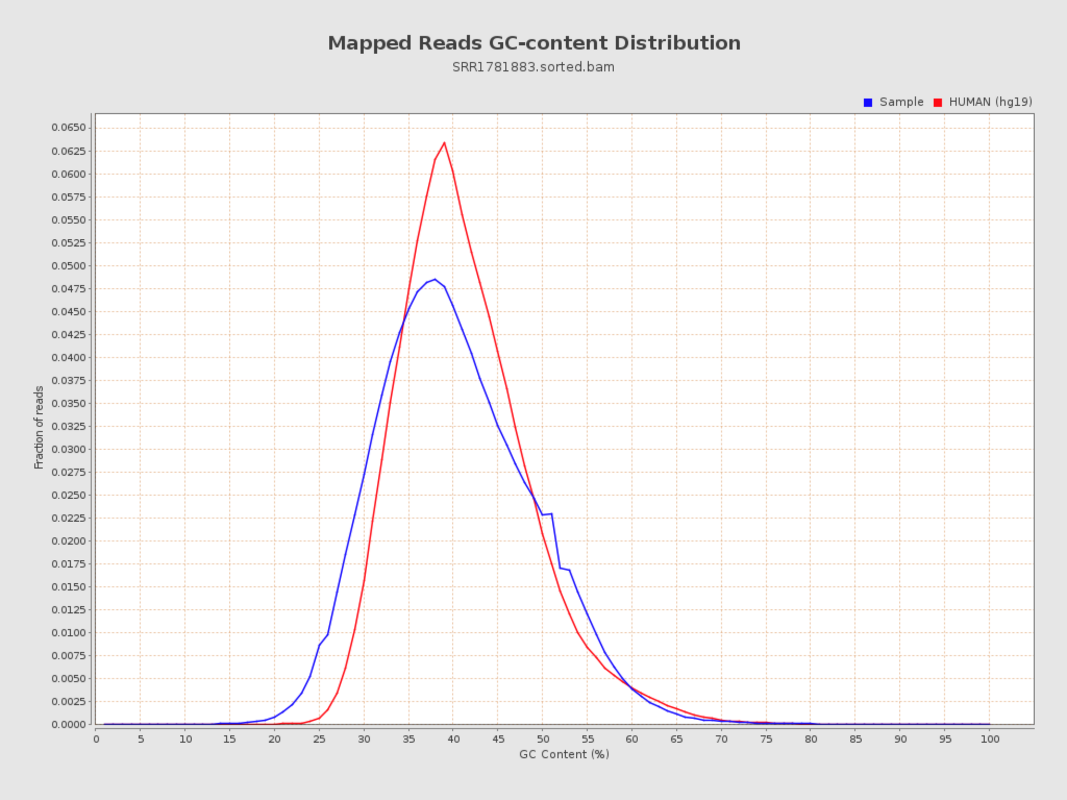
7. Results : Duplication Rate Histogram



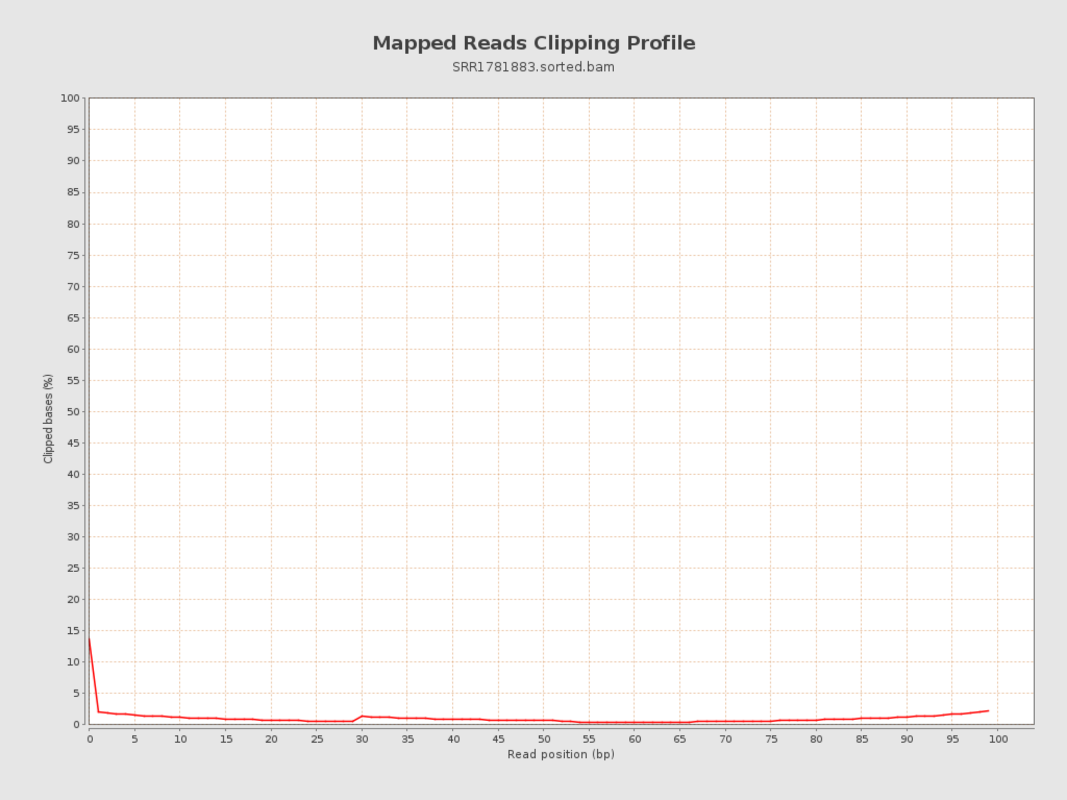
8. Results : Mapped Reads Nucleotide Content



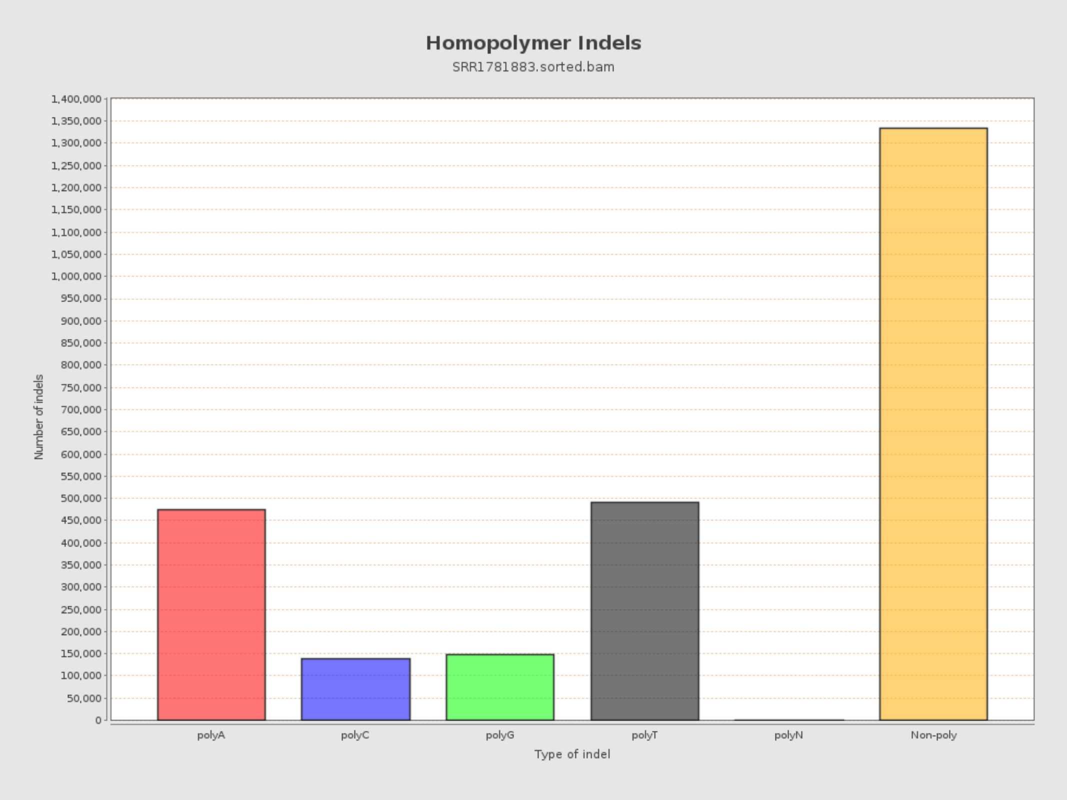
9. Results : Mapped Reads GC-content Distribution



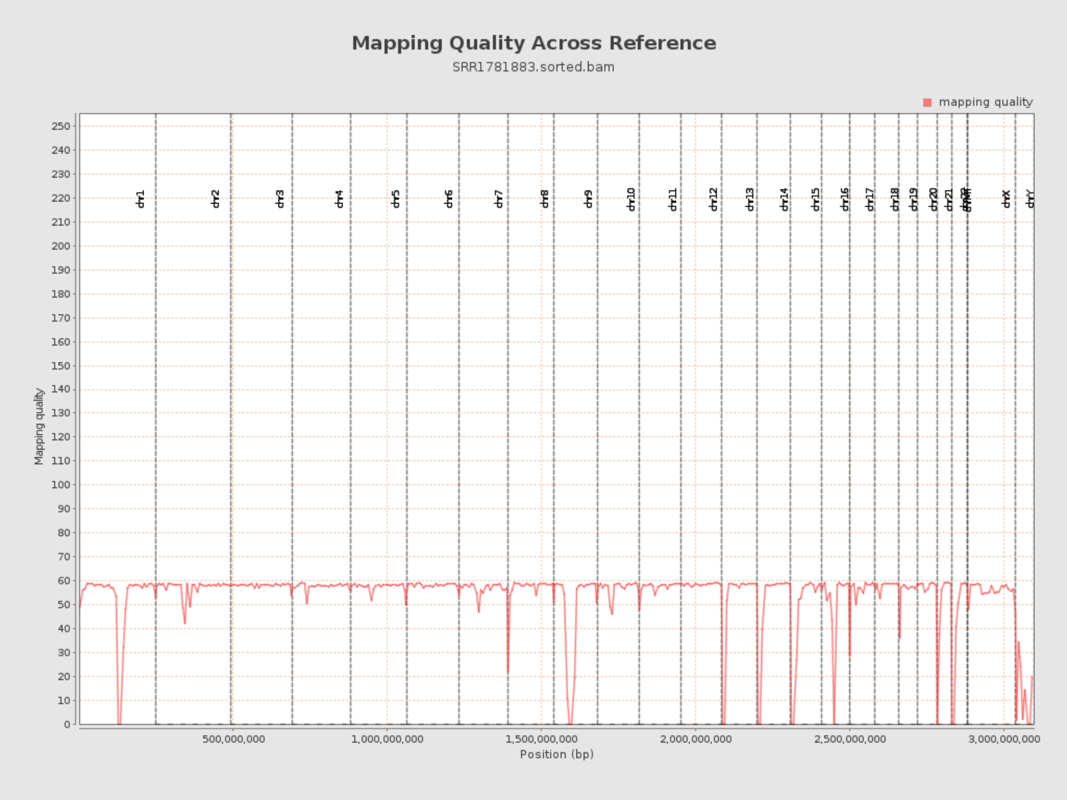
10. Results : Mapped Reads Clipping Profile



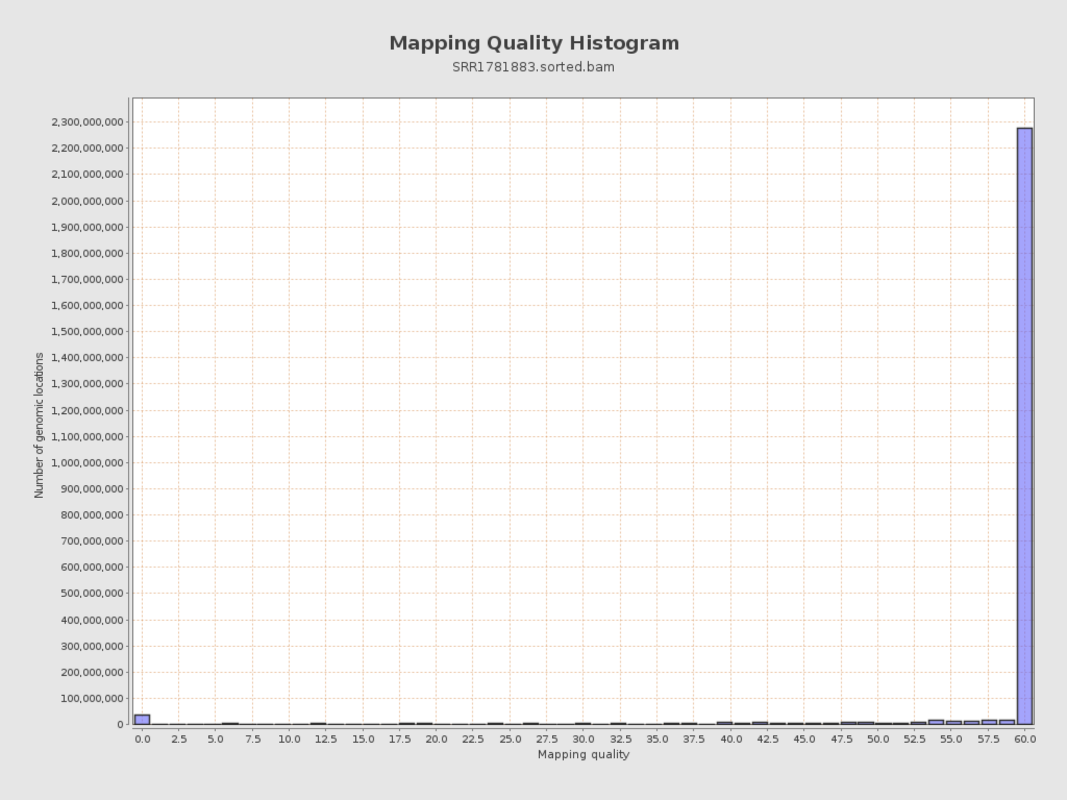
11. Results : Homopolymer Indels



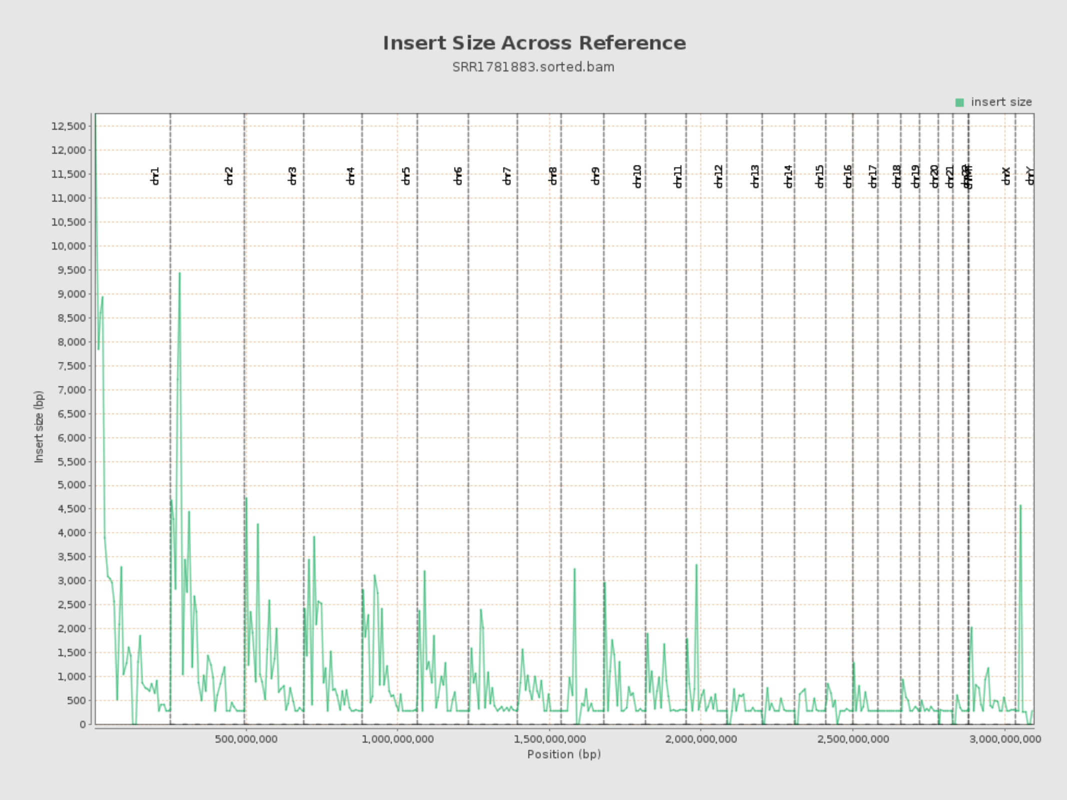
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram