Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 00:02:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781858.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_SRR1781858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781858_1.fastq.gz SRR1781858_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 00:02:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	163,177,316
Mapped reads	158,468,042 / 97.11%
Unmapped reads	4,709,274 / 2.89%
Mapped paired reads	158,468,042 / 97.11%
Mapped reads, first in pair	79,747,060 / 48.87%
Mapped reads, second in pair	78,720,982 / 48.24%
Mapped reads, both in pair	156,670,264 / 96.01%
Mapped reads, singletons	1,797,778 / 1.1%
Secondary alignments	0
Supplementary alignments	486,956 / 0.3%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	10,621,494 / 6.51%
Duplication rate	6.47%
Clipped reads	7,275,560 / 4.46%

2.2. ACGT Content

Number/percentage of A's	4,686,923,859 / 29.79%
Number/percentage of C's	3,167,989,761 / 20.14%
Number/percentage of T's	4,667,951,802 / 29.67%
Number/percentage of G's	3,208,297,429 / 20.39%
Number/percentage of N's	1,582,928 / 0.01%

GC Percentage	40.53%

2.3. Coverage

Mean	5.0832
Standard Deviation	6.4505

2.4. Mapping Quality

Mean Mapping Quality	53.87

2.5. Insert size

Mean	33,060.73
Standard Deviation	1,778,518.4
P25/Median/P75	157 / 193 / 237

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	64,659,712
Insertions	1,750,556
Mapped reads with at least one insertion	1.09%
Deletions	1,440,784
Mapped reads with at least one deletion	0.89%
Homopolymer indels	47.08%

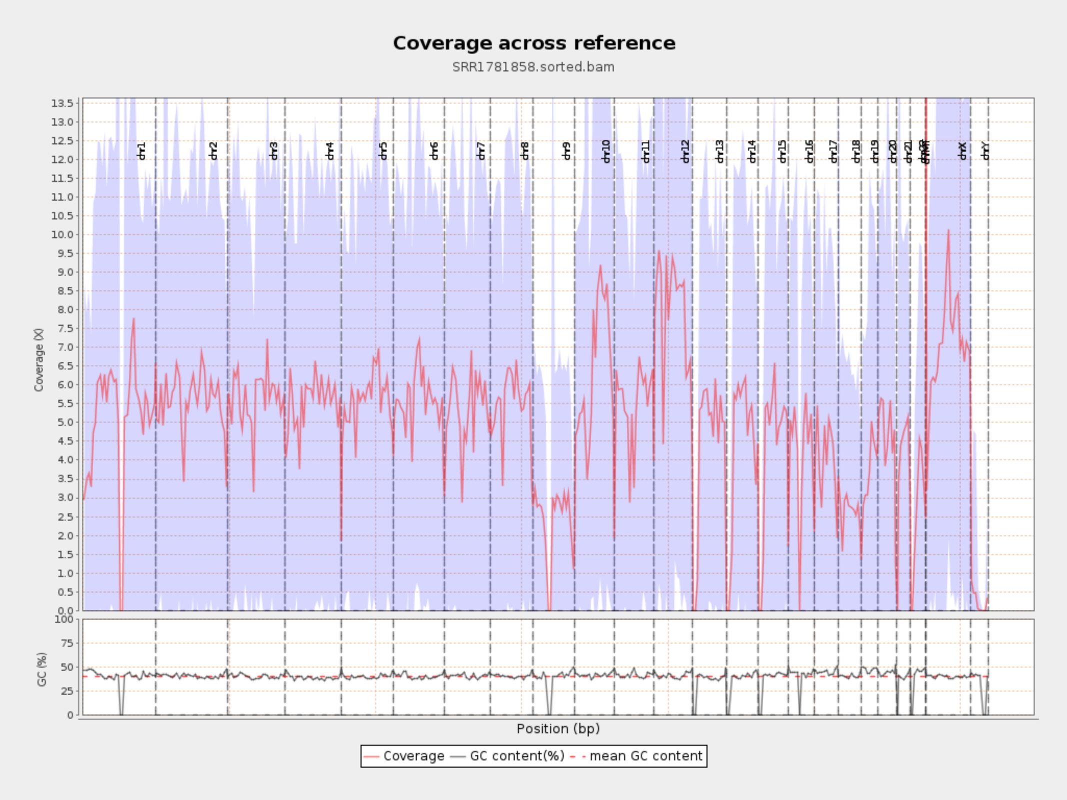
2.7. Chromosome stats

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

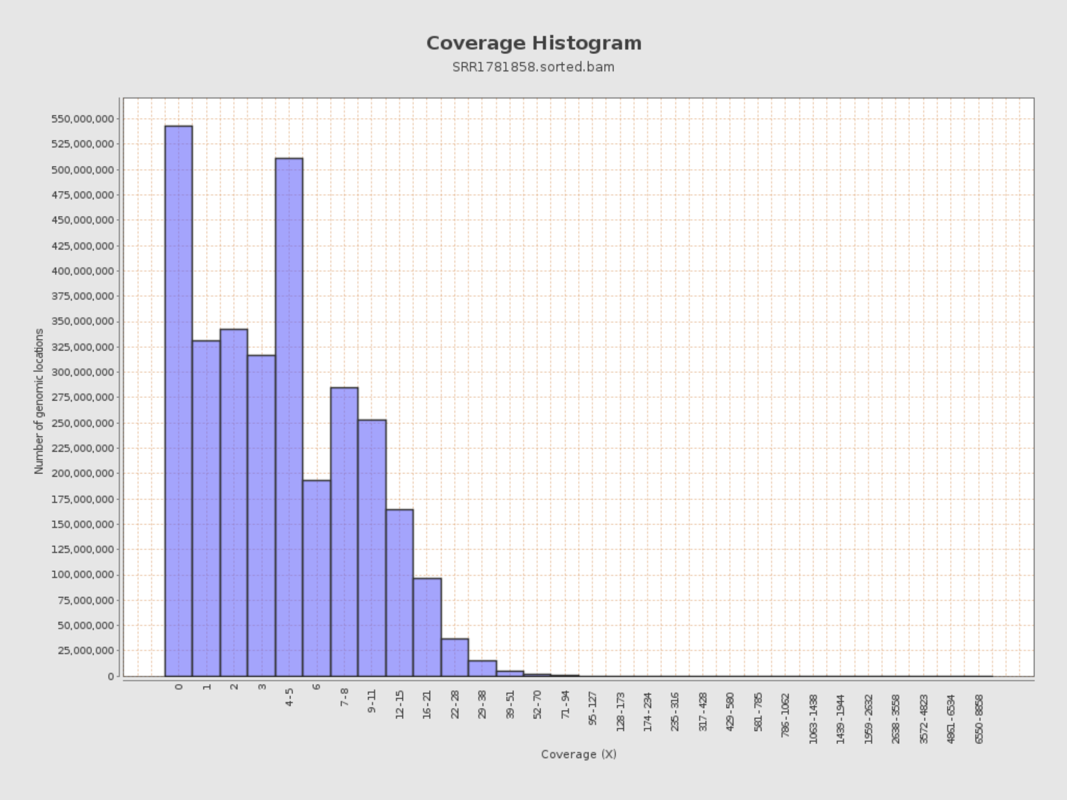
		bases	coverage	deviation
chr1	249250621	1270751718	5.0983	7.3424
chr2	243199373	1353782194	5.5666	9.1091
chr3	198022430	1118430042	5.648	5.617
chr4	191154276	1063058418	5.5613	5.683
chr5	180915260	1012107749	5.5944	5.3559
chr6	171115067	965062025	5.6398	5.7909
chr7	159138663	847419943	5.325	6.0312
chr8	146364022	808745478	5.5256	5.515
chr9	141213431	335374523	2.3749	4.3951
chr10	135534747	874892249	6.4551	8.1456
chr11	135006516	738346453	5.469	5.7634
chr12	133851895	1073713196	8.0217	7.9565
chr13	115169878	505569559	4.3898	5.0236
chr14	107349540	469273172	4.3715	5.3063
chr15	102531392	436741419	4.2596	5.3299
chr16	90354753	366918256	4.0609	5.2489
chr17	81195210	334399549	4.1185	5.205
chr18	78077248	208851767	2.6749	4.2155
chr19	59128983	216973235	3.6695	5.3995
chr20	63025520	296805103	4.7093	6.08
chr21	48129895	190608094	3.9603	6.9832
chr22	51304566	135887469	2.6486	4.2439
chrMT	16571	528330	31.8828	10.906
chrX	155270560	1097442176	7.0679	7.288

chrY	59373566	14289624	0.2407	2.4394

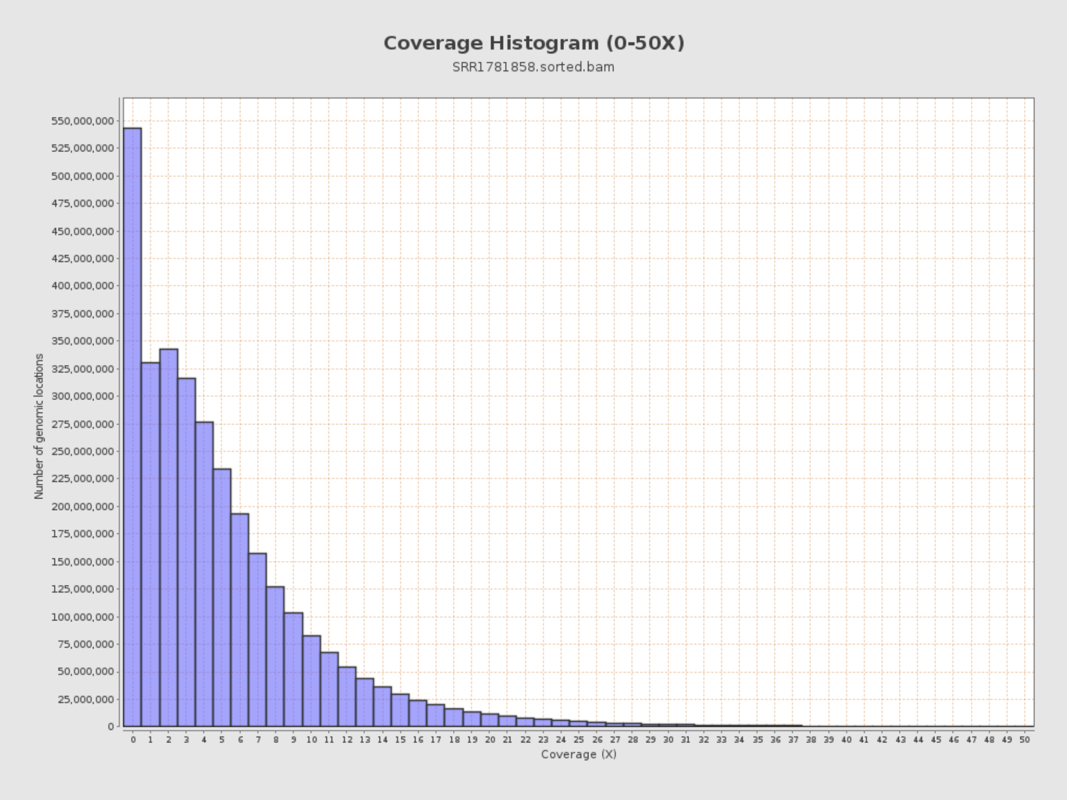
3. Results : Coverage across reference



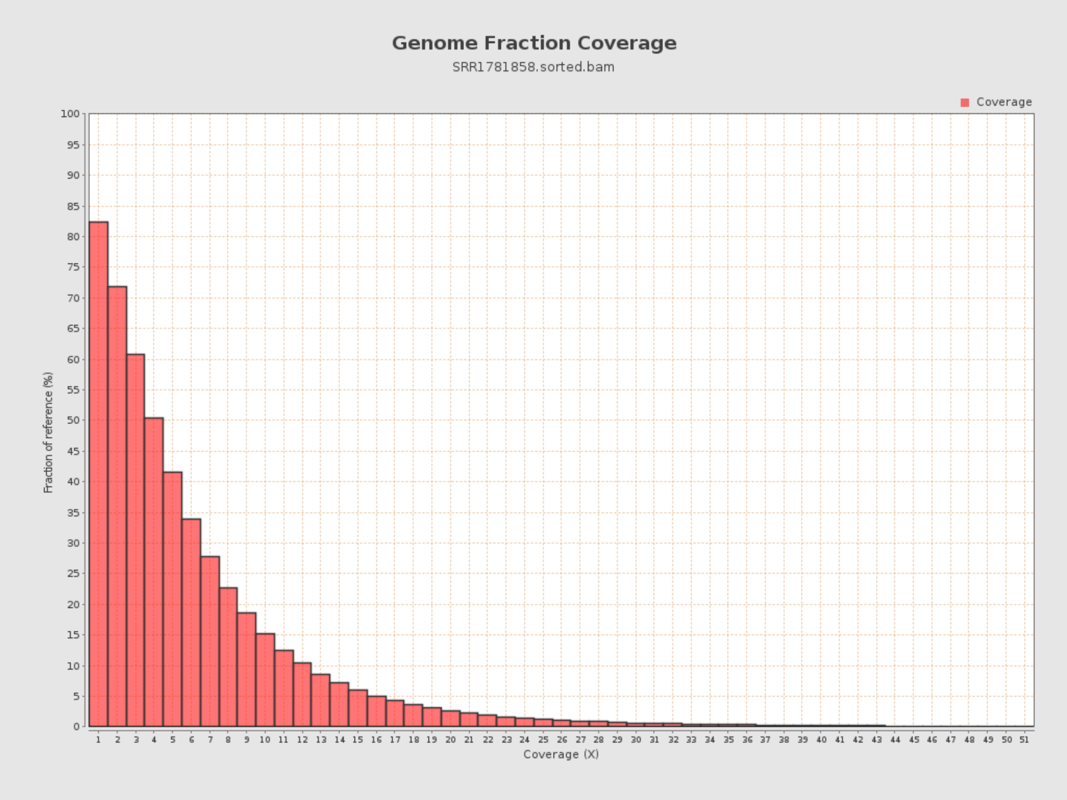
4. Results : Coverage Histogram



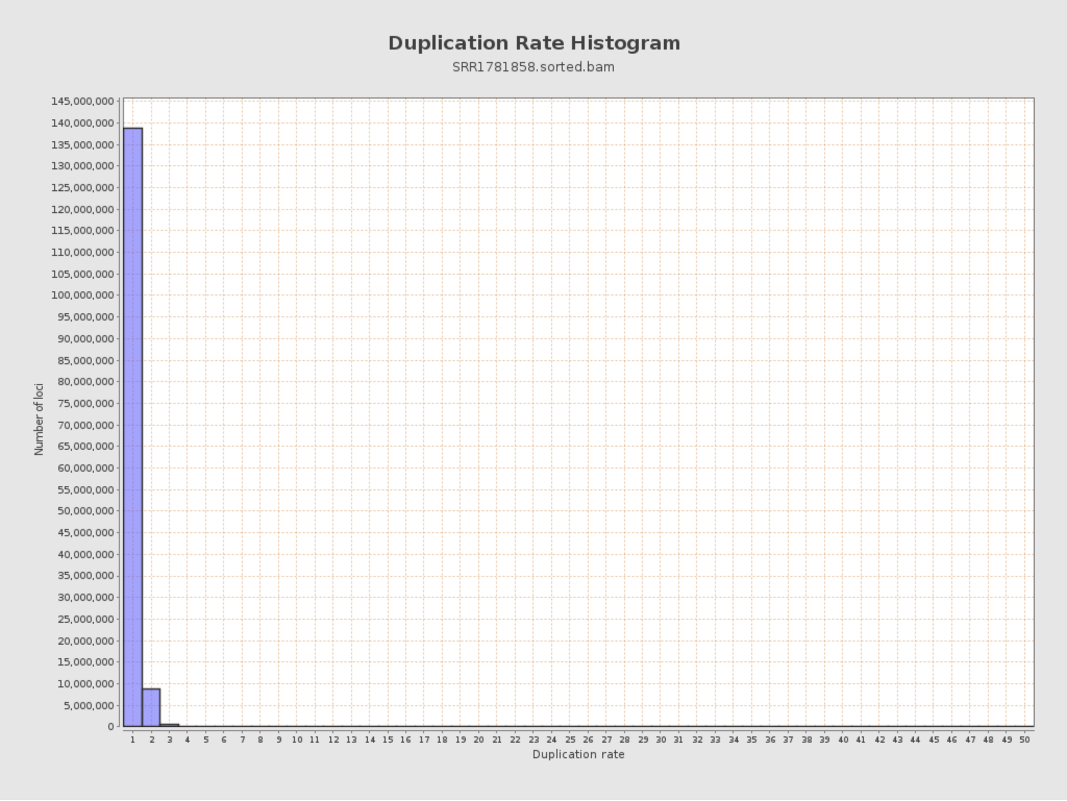
5. Results : Coverage Histogram (0-50X)



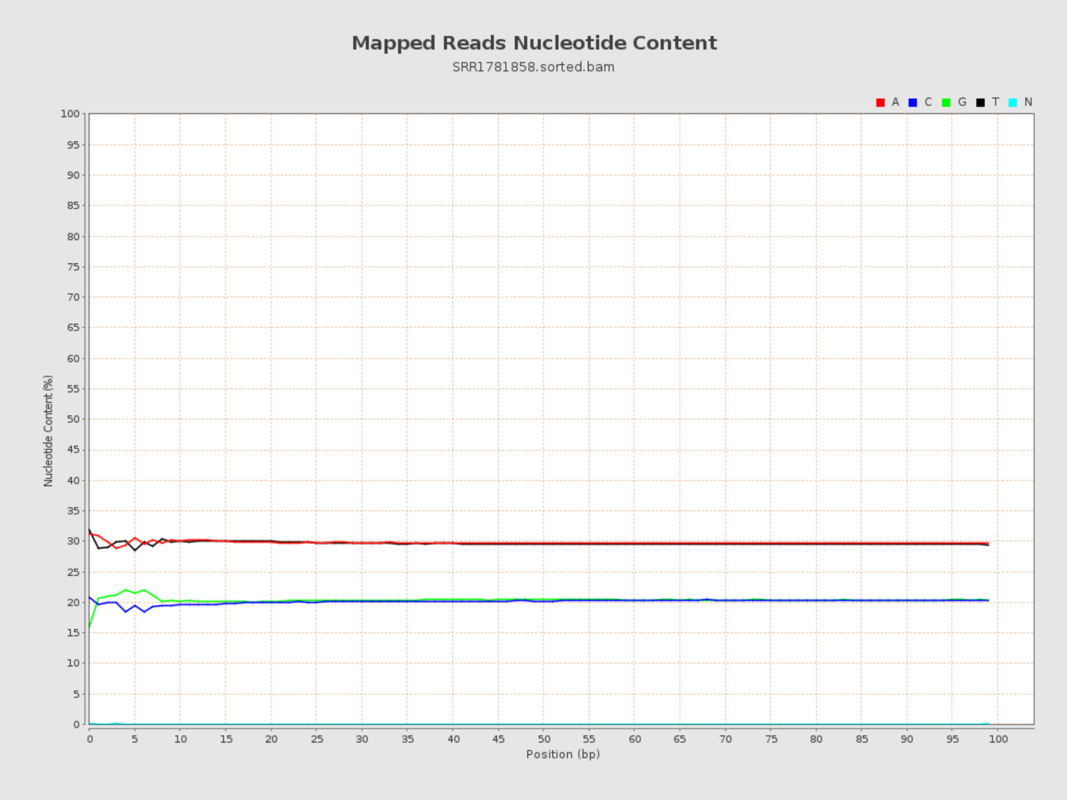
6. Results : Genome Fraction Coverage



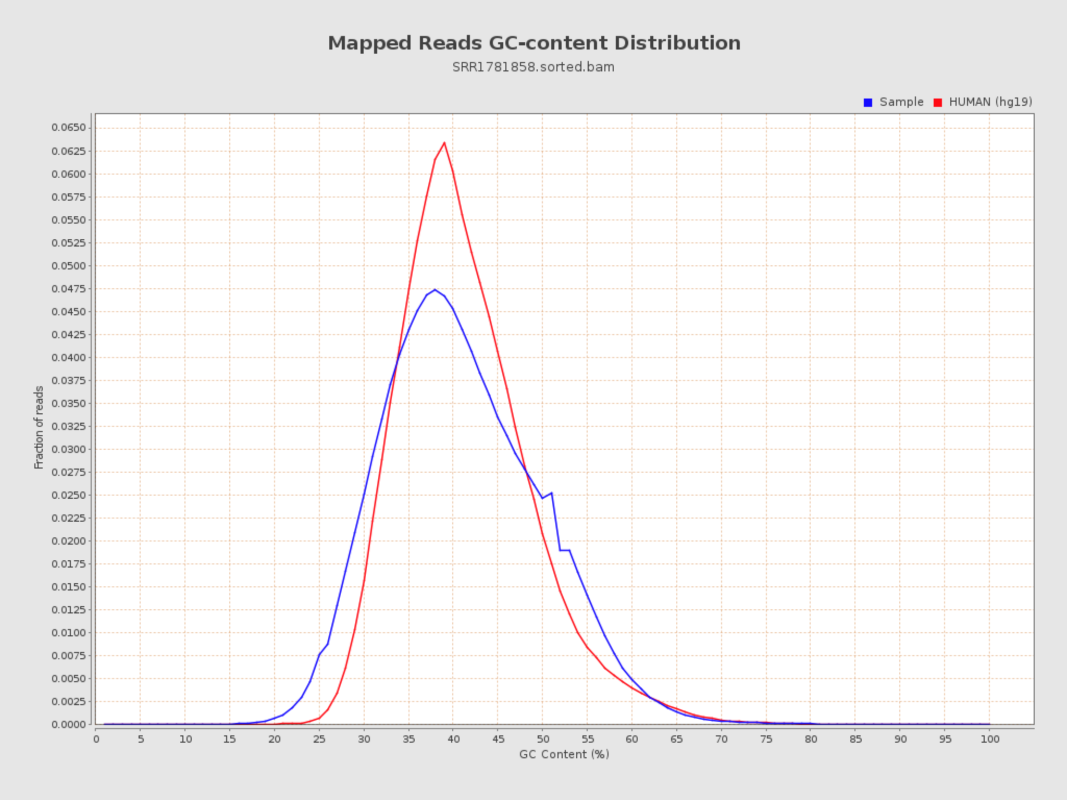
7. Results : Duplication Rate Histogram



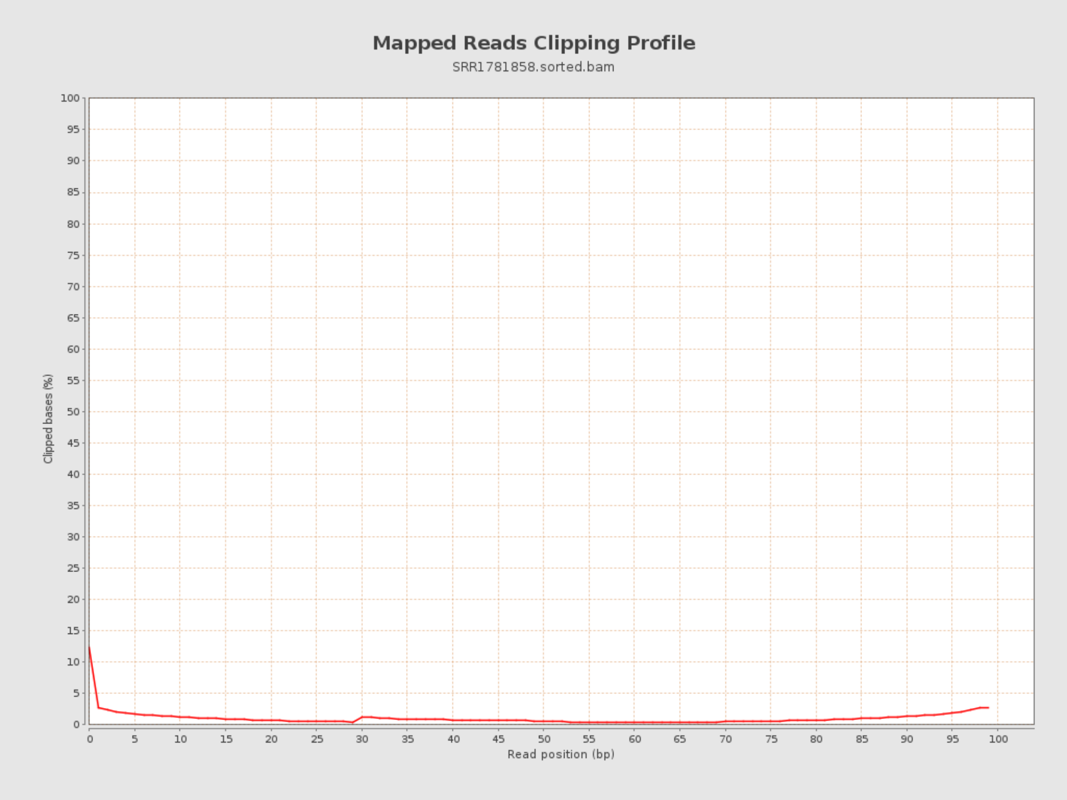
8. Results : Mapped Reads Nucleotide Content



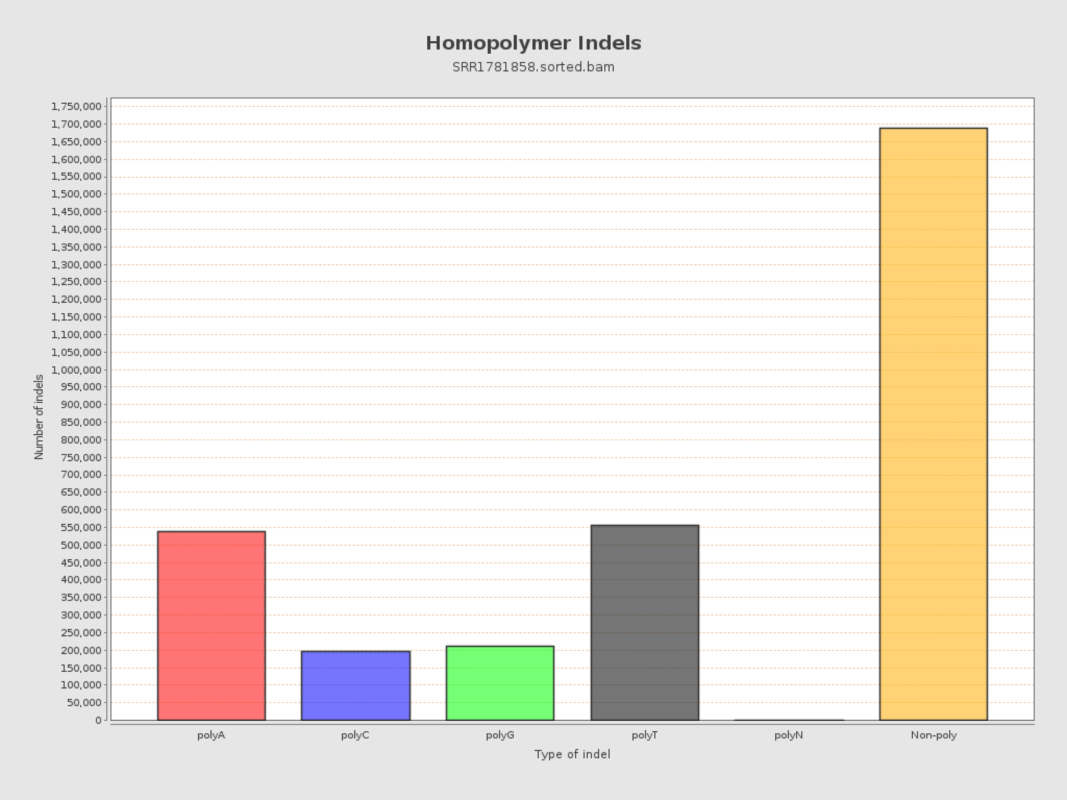
9. Results : Mapped Reads GC-content Distribution



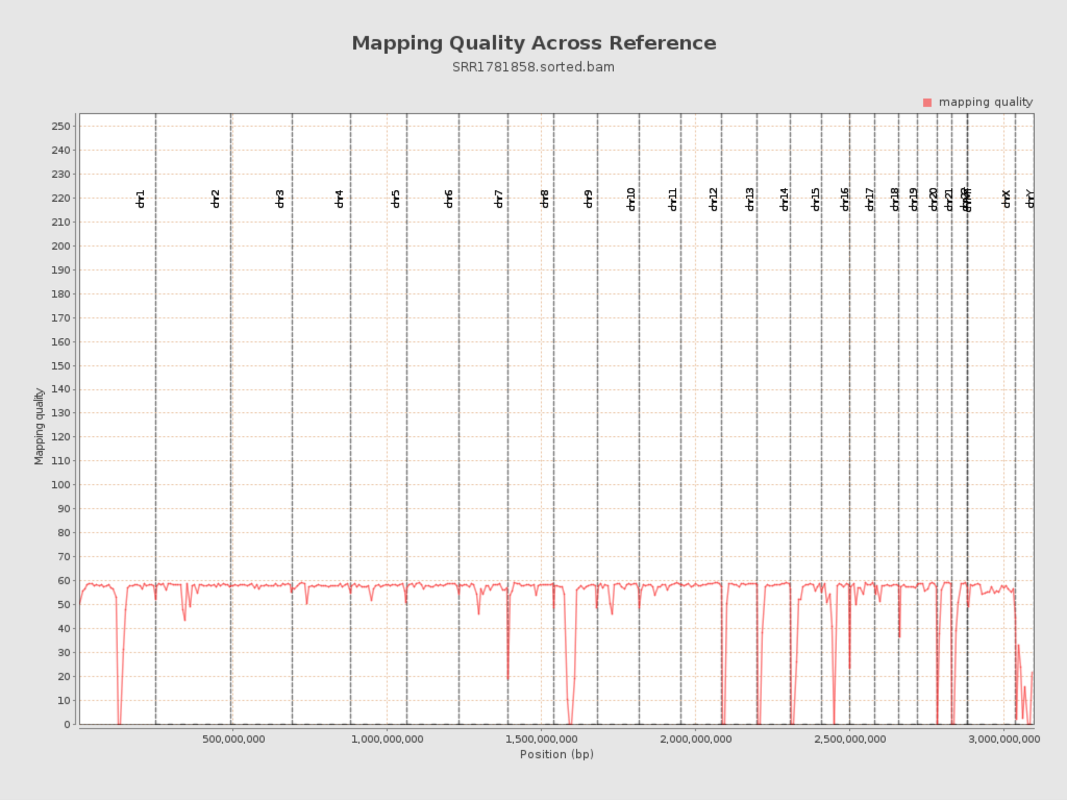
10. Results : Mapped Reads Clipping Profile



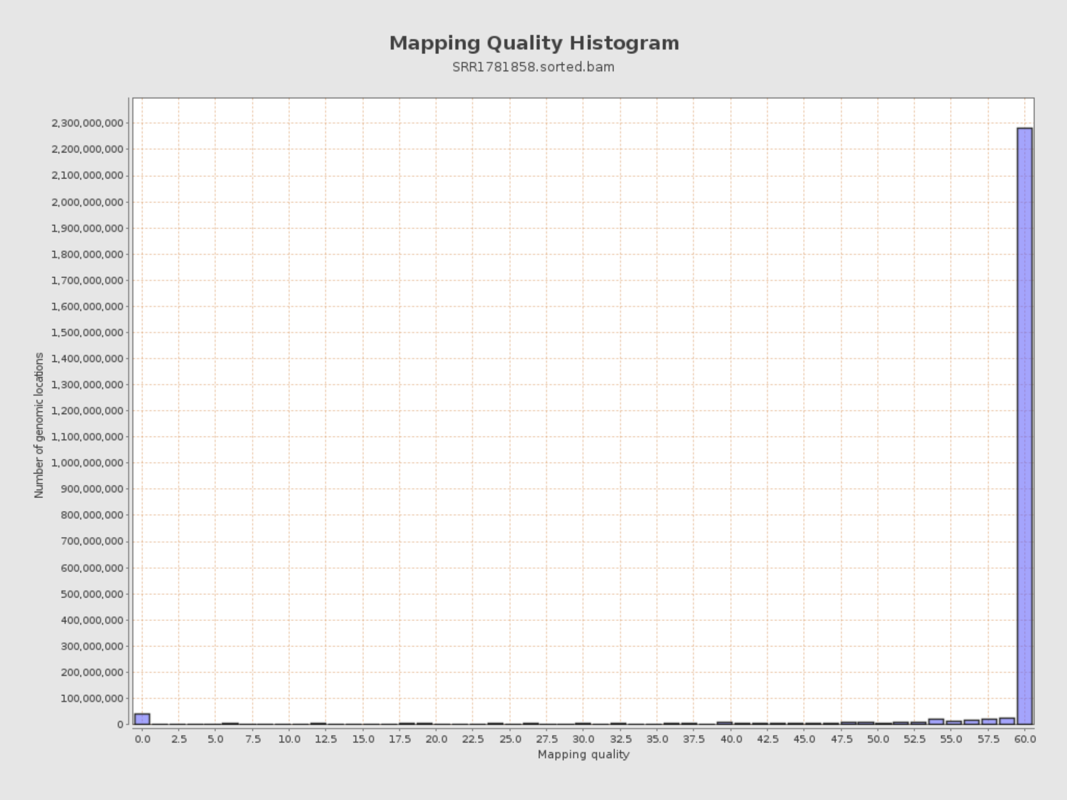
11. Results : Homopolymer Indels



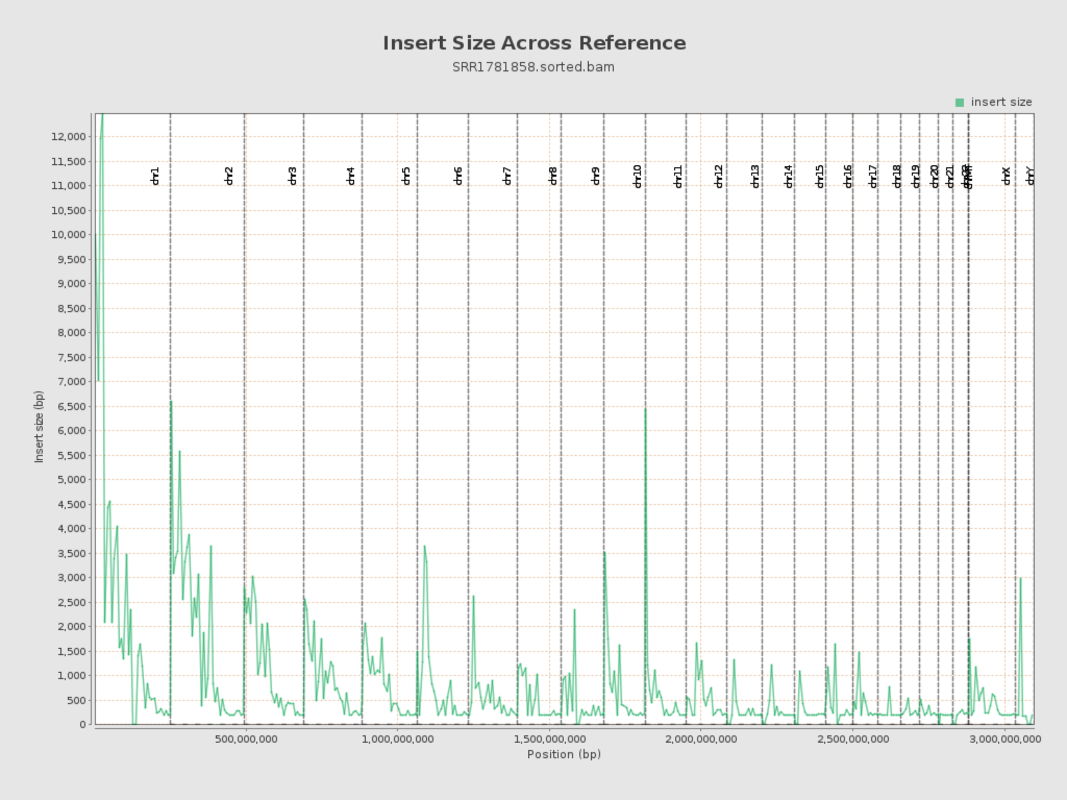
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram