Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 14:27:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781912.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_SRR1781912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781912_1.fastq.gz SRR1781912_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 14:27:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,066,032
Mapped reads	45,239,265 / 96.12%
Unmapped reads	1,826,767 / 3.88%
Mapped paired reads	45,239,265 / 96.12%
Mapped reads, first in pair	22,873,472 / 48.6%
Mapped reads, second in pair	22,365,793 / 47.52%
Mapped reads, both in pair	44,434,592 / 94.41%
Mapped reads, singletons	804,673 / 1.71%
Secondary alignments	0
Supplementary alignments	163,356 / 0.35%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	1,277,077 / 2.71%
Duplication rate	2.72%
Clipped reads	2,025,598 / 4.3%

2.2. ACGT Content

Number/percentage of A's	1,337,497,865 / 29.83%
Number/percentage of C's	898,581,446 / 20.04%
Number/percentage of T's	1,335,495,427 / 29.79%
Number/percentage of G's	911,150,578 / 20.32%
Number/percentage of N's	786,929 / 0.02%

GC Percentage	40.36%

2.3. Coverage

Mean	1.4487
Standard Deviation	2.1874

2.4. Mapping Quality

Mean Mapping Quality	54.03

2.5. Insert size

Mean	63,975.14
Standard Deviation	2,471,111.56
P25/Median/P75	236 / 295 / 376

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	20,689,992
Insertions	523,457
Mapped reads with at least one insertion	1.14%
Deletions	504,024
Mapped reads with at least one deletion	1.09%
Homopolymer indels	48.97%

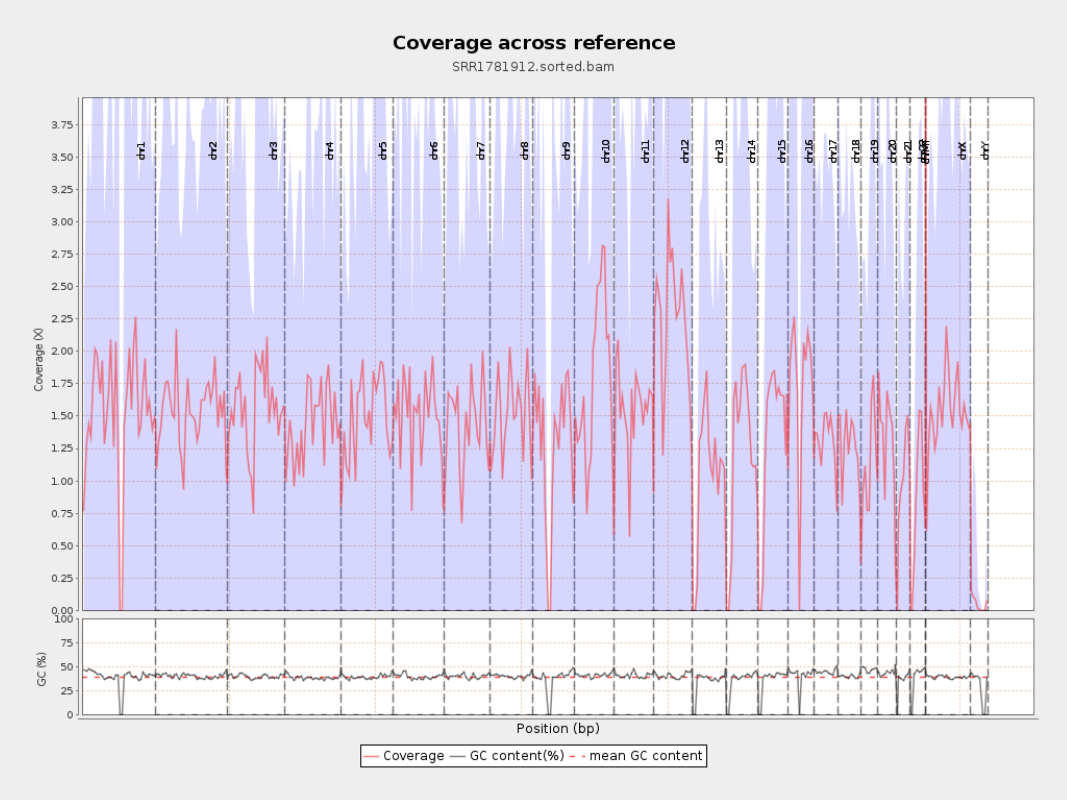
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

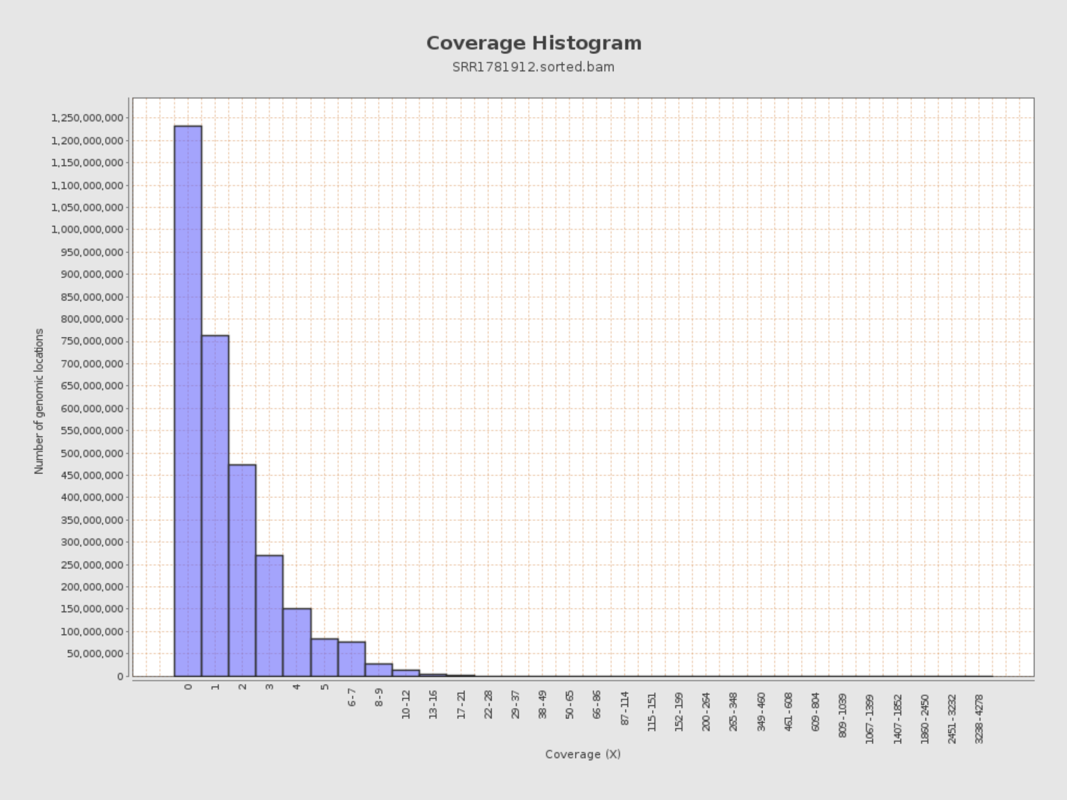
		bases	**coverage**	**deviation**
chr1	249250621	380970603	1.5285	2.2838
chr2	243199373	373907105	1.5375	3.765
chr3	198022430	307081796	1.5507	1.8824
chr4	191154276	273541535	1.431	1.8095
chr5	180915260	269987115	1.4923	1.82
chr6	171115067	260438409	1.522	1.9183
chr7	159138663	226508052	1.4233	1.8606
chr8	146364022	223063551	1.524	1.8821
chr9	141213431	179463077	1.2709	1.8946
chr10	135534747	243952099	1.7999	2.5278
chr11	135006516	209381103	1.5509	1.9236
chr12	133851895	305734742	2.2841	2.8685
chr13	115169878	119923616	1.0413	1.5158
chr14	107349540	133004355	1.239	1.7547
chr15	102531392	130921184	1.2769	1.834
chr16	90354753	154251799	1.7072	2.2071
chr17	81195210	107941630	1.3294	1.7787
chr18	78077248	99784216	1.278	1.7359
chr19	59128983	66299983	1.1213	1.8919
chr20	63025520	84268930	1.3371	1.8889
chr21	48129895	48162578	1.0007	1.7799
chr22	51304566	43936178	0.8564	1.5331
chrMT	16571	93288	5.6296	2.9229
chrX	155270560	239135681	1.5401	1.8838

chrY	59373566	2873964	0.0484	0.5665

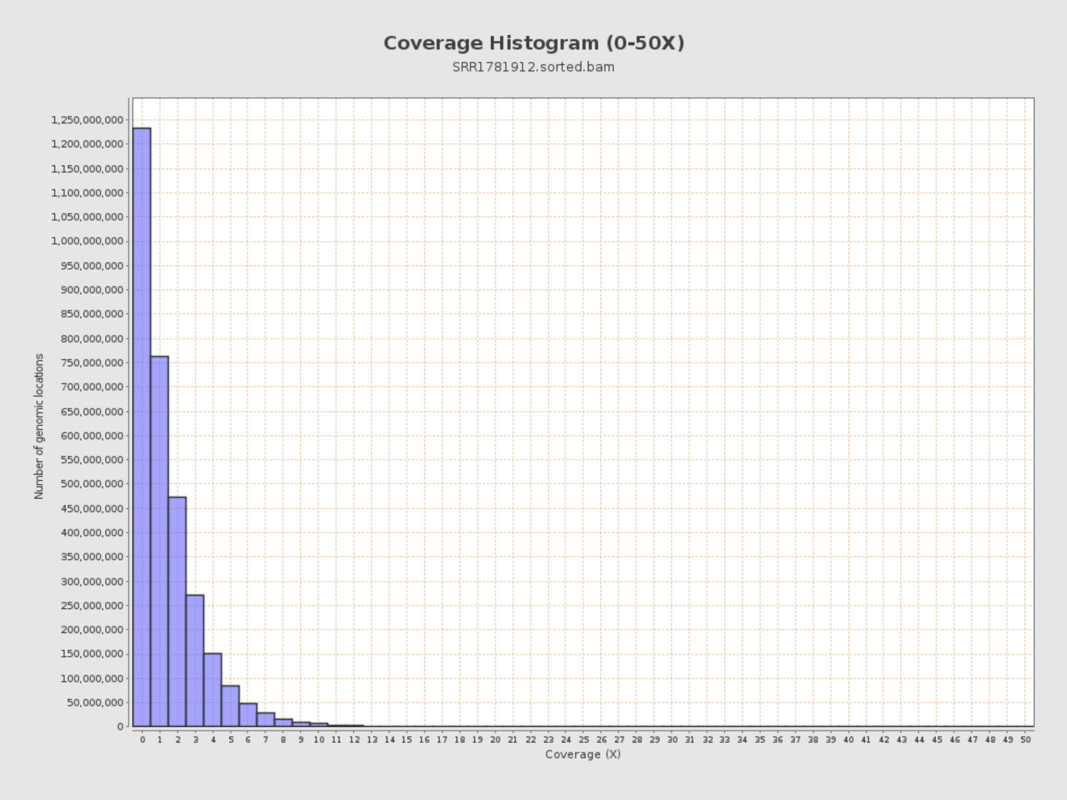
3. Results : Coverage across reference



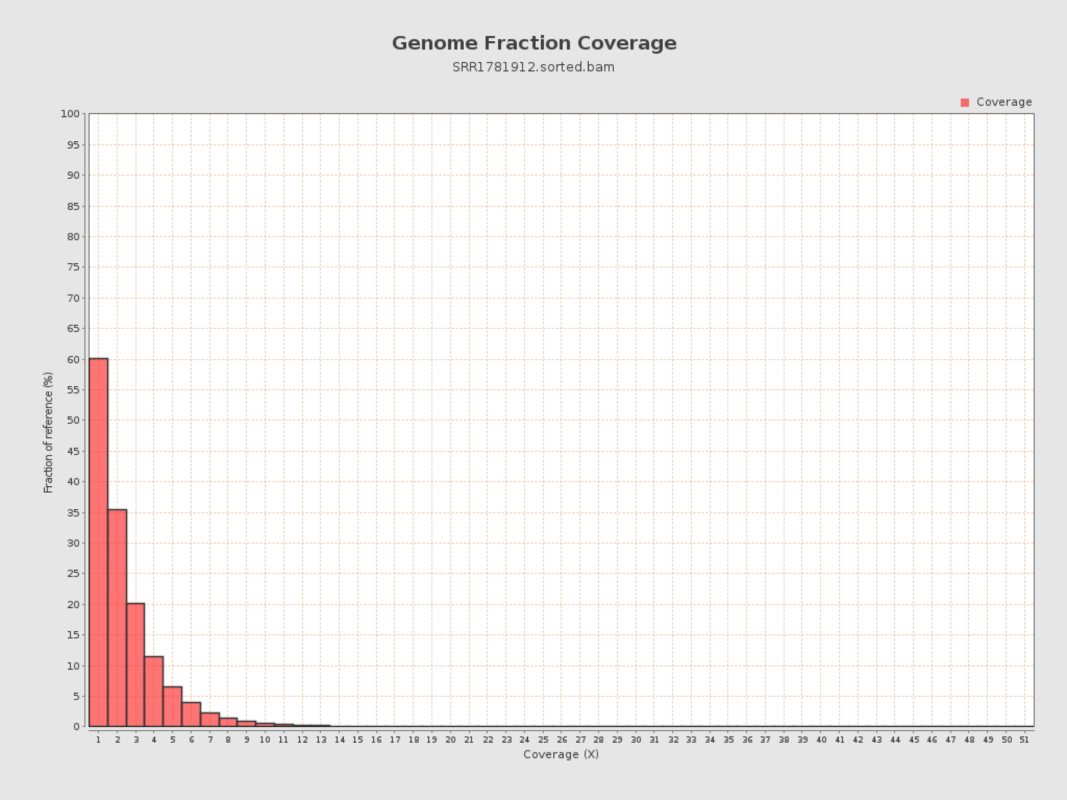
4. Results : Coverage Histogram



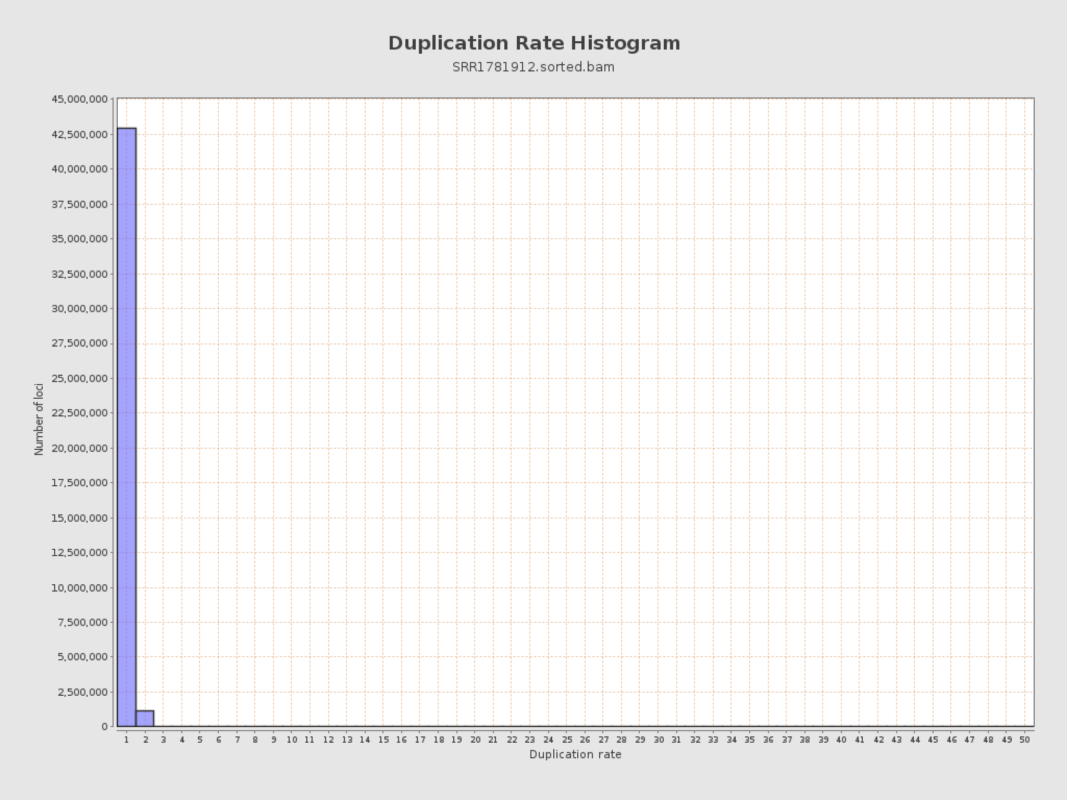
5. Results : Coverage Histogram (0-50X)



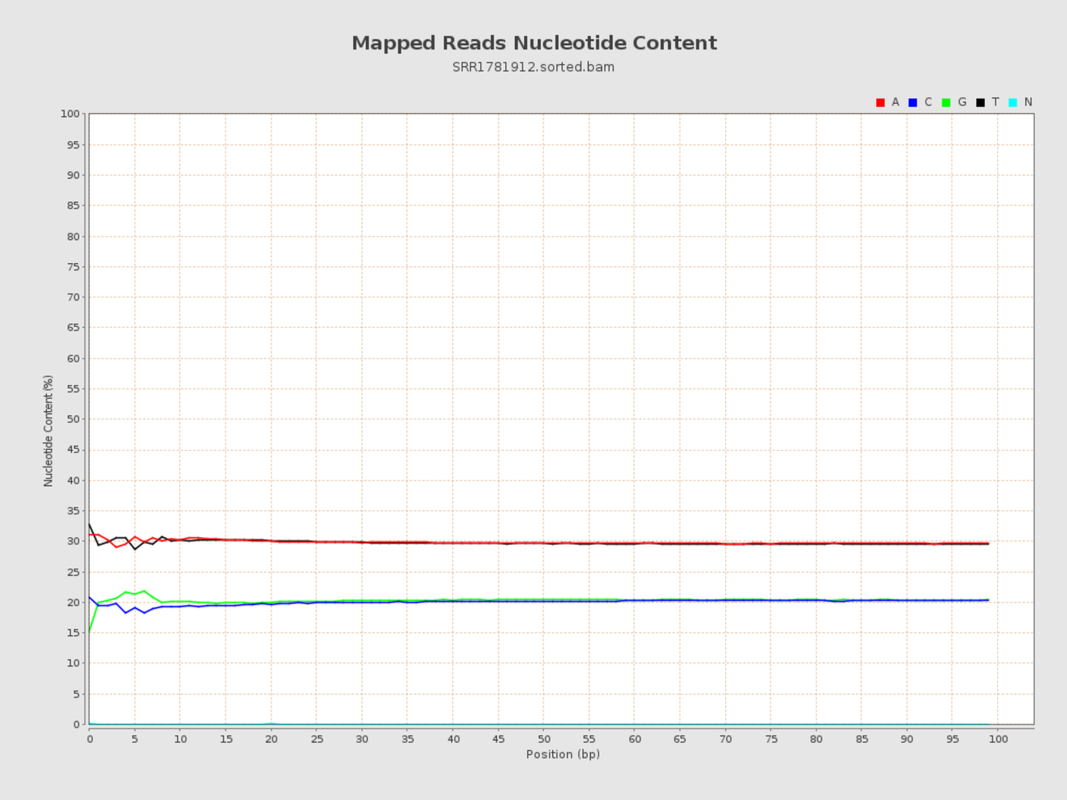
6. Results : Genome Fraction Coverage



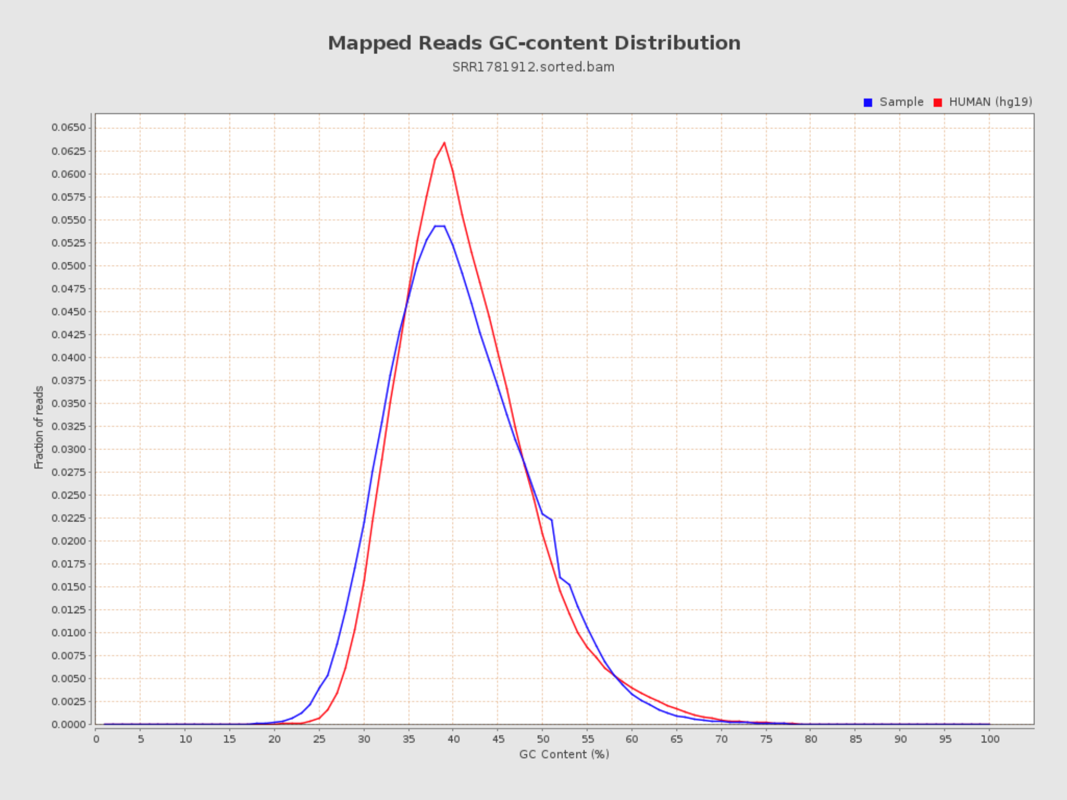
7. Results : Duplication Rate Histogram



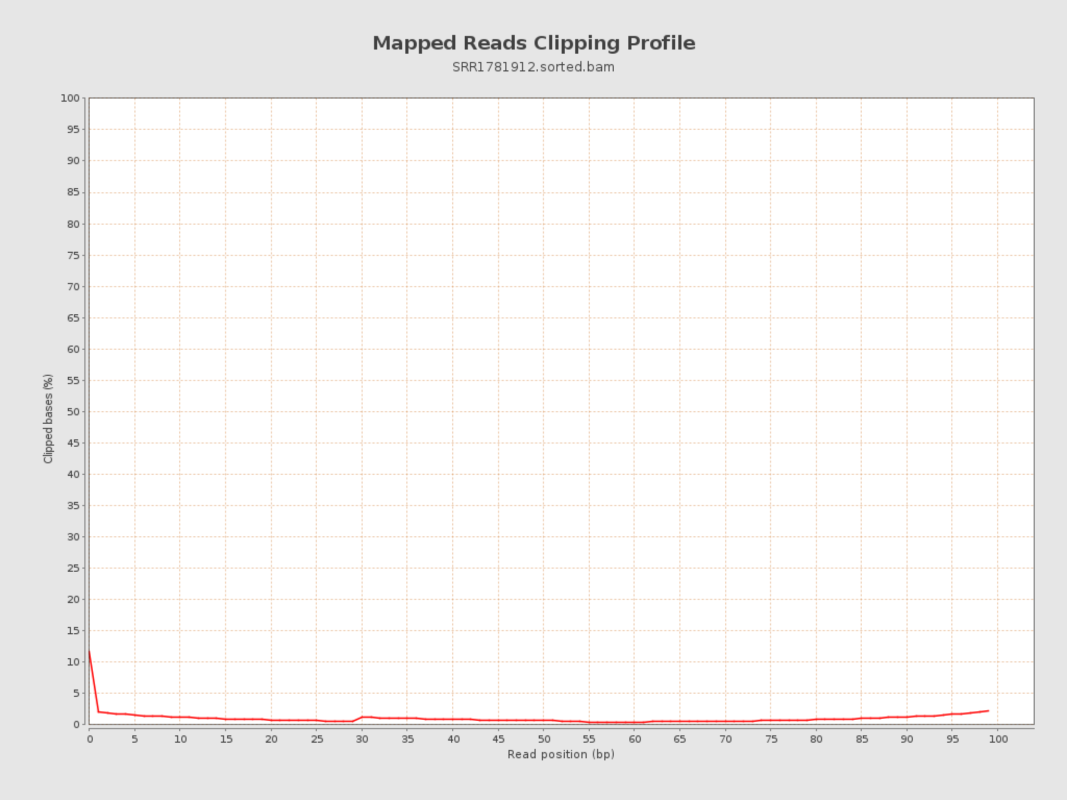
8. Results : Mapped Reads Nucleotide Content



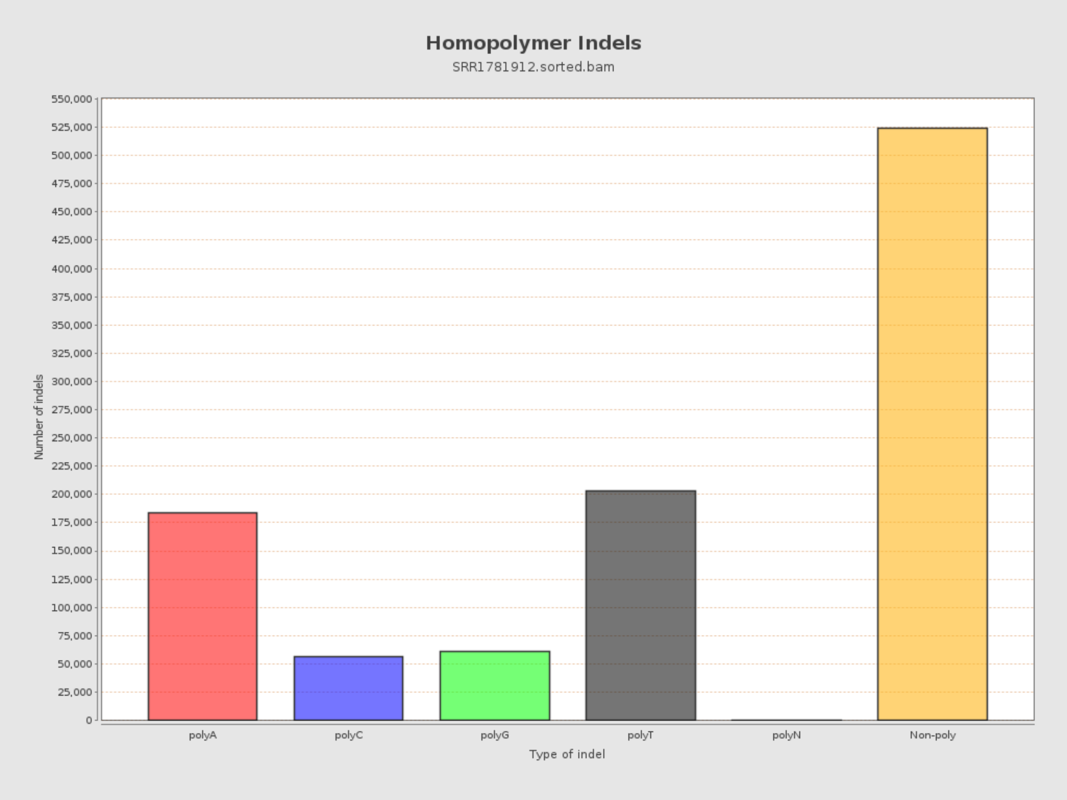
9. Results : Mapped Reads GC-content Distribution



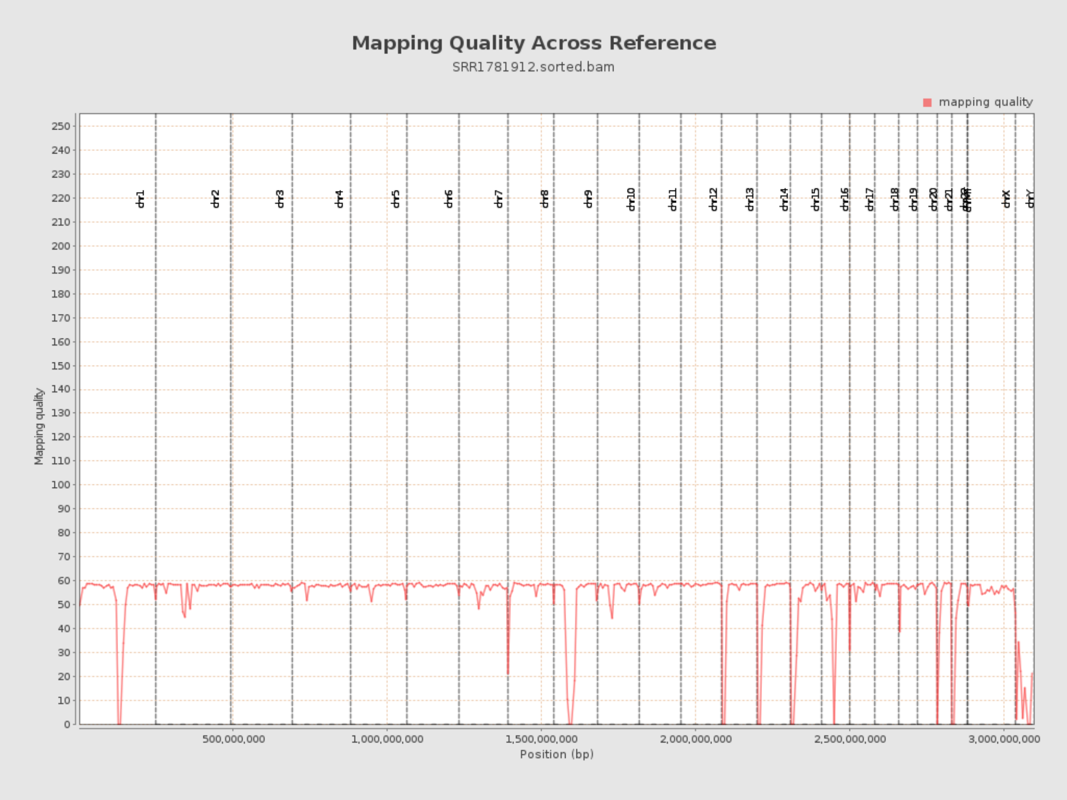
10. Results : Mapped Reads Clipping Profile



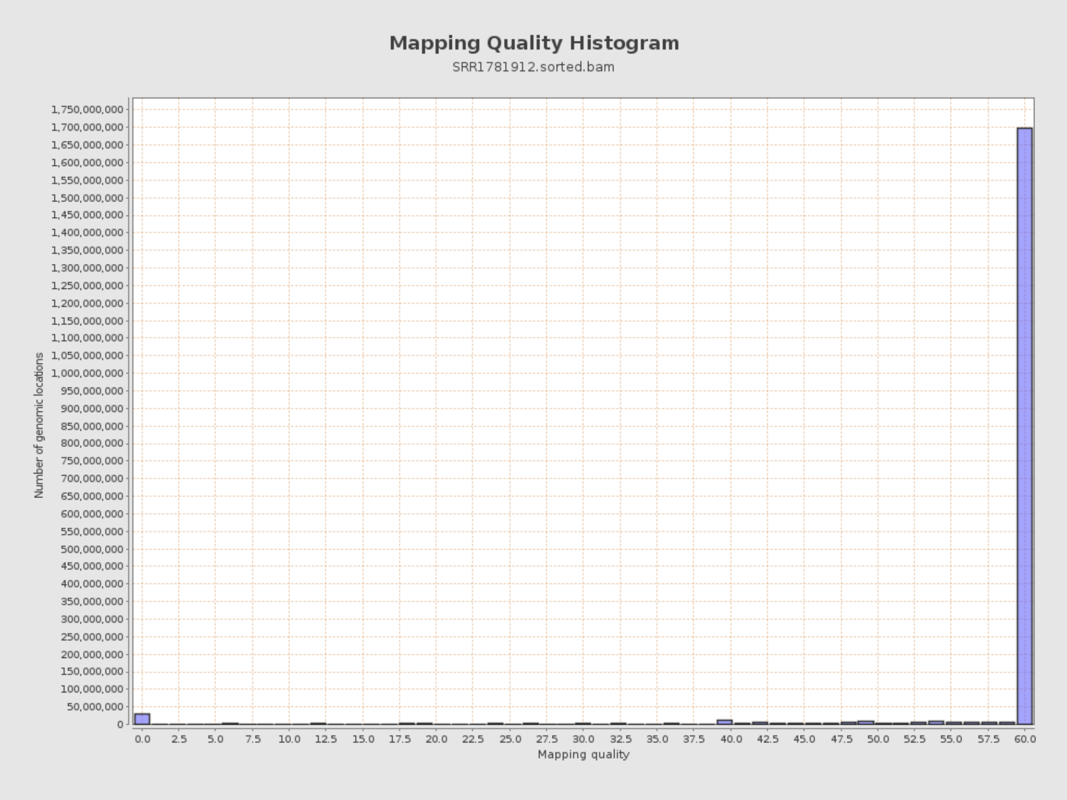
11. Results : Homopolymer Indels



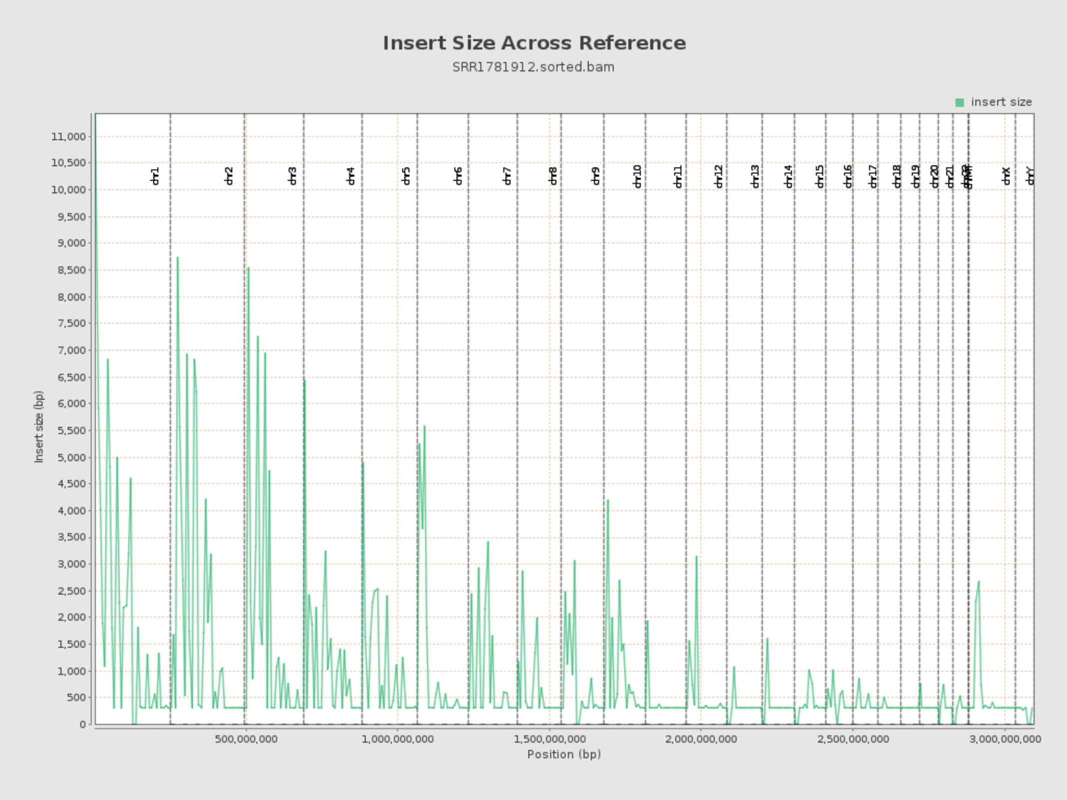
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram