

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 13:30:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781911.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_SRR1781911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781911_1.fastq.gz SRR1781911_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 13:30:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,514,672
Mapped reads	42,745,456 / 98.23%
Unmapped reads	769,216 / 1.77%
Mapped paired reads	42,745,456 / 98.23%
Mapped reads, first in pair	21,553,450 / 49.53%
Mapped reads, second in pair	21,192,006 / 48.7%
Mapped reads, both in pair	42,258,566 / 97.11%
Mapped reads, singletons	486,890 / 1.12%
Secondary alignments	0
Supplementary alignments	180,545 / 0.41%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	1,313,527 / 3.02%
Duplication rate	2.96%
Clipped reads	2,026,734 / 4.66%

2.2. ACGT Content

Number/percentage of A's	1,273,898,619 / 30.05%
Number/percentage of C's	841,339,168 / 19.84%
Number/percentage of T's	1,271,818,002 / 30%
Number/percentage of G's	851,878,535 / 20.09%
Number/percentage of N's	740,931 / 0.02%

GC Percentage	39.94%
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2.3. Coverage

Mean	1.3699
Standard Deviation	2.0504

2.4. Mapping Quality

Mean Mapping Quality	53.92
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2.5. Insert size

Mean	58,103.2
Standard Deviation	2,322,271.09
P25/Median/P75	180 / 241 / 327

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	15,624,271
Insertions	481,188
Mapped reads with at least one insertion	1.11%
Deletions	466,641
Mapped reads with at least one deletion	1.07%
Homopolymer indels	48.32%

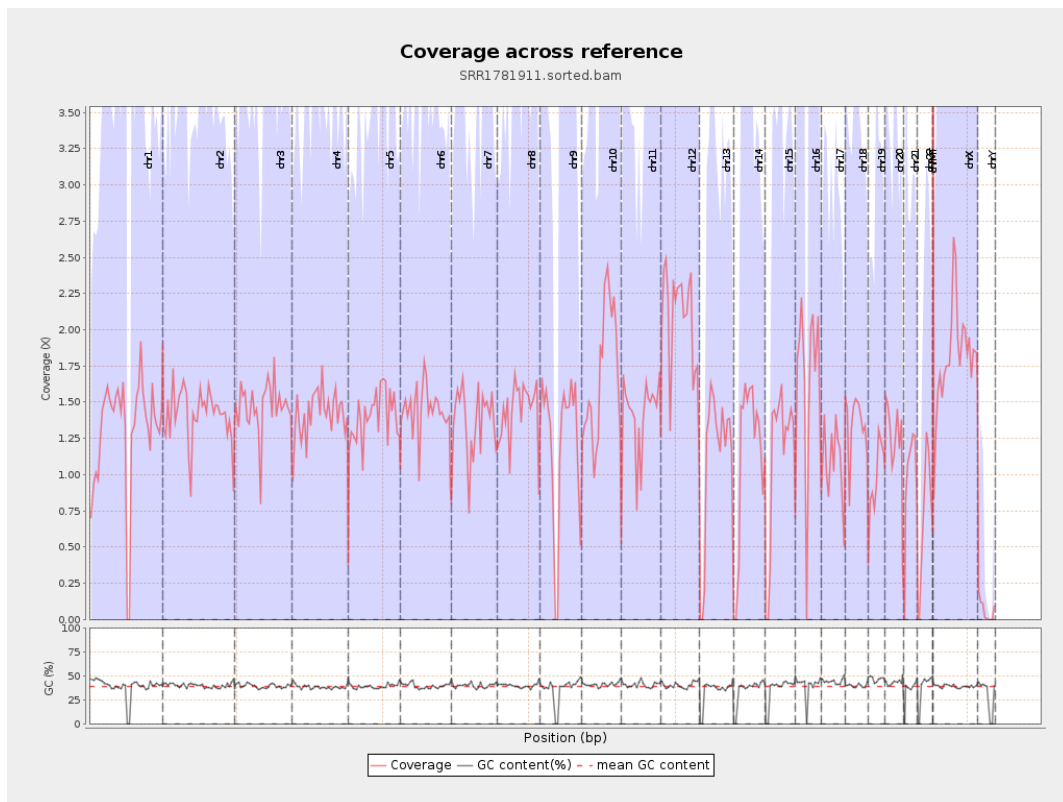
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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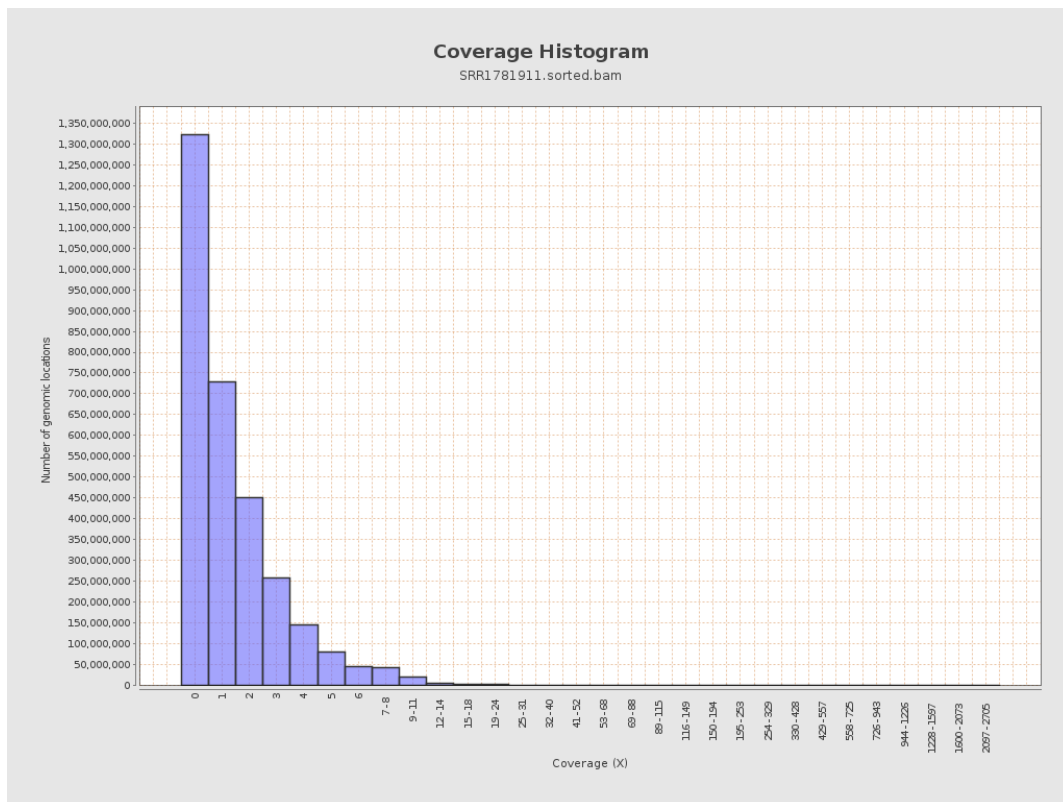
		bases	coverage	deviation
chr1	249250621	325572405	1.3062	2.2873
chr2	243199373	343195295	1.4112	2.7565
chr3	198022430	290187524	1.4654	1.8222
chr4	191154276	272108330	1.4235	1.8388
chr5	180915260	252764611	1.3971	1.7543
chr6	171115067	246928497	1.4431	1.8575
chr7	159138663	215882090	1.3566	1.8357
chr8	146364022	210804028	1.4403	1.819
chr9	141213431	172066589	1.2185	1.9559
chr10	135534747	229559579	1.6937	2.5825
chr11	135006516	190378410	1.4101	1.8344
chr12	133851895	279211312	2.086	2.5513
chr13	115169878	128032185	1.1117	1.5923
chr14	107349540	122979709	1.1456	1.6949
chr15	102531392	114286428	1.1146	1.7092
chr16	90354753	144537089	1.5997	2.1985
chr17	81195210	89306546	1.0999	1.6808
chr18	78077248	104442681	1.3377	1.8805
chr19	59128983	58218187	0.9846	1.8377
chr20	63025520	79641154	1.2636	1.9105
chr21	48129895	47333461	0.9835	1.9259
chr22	51304566	37009435	0.7214	1.3886
chrMT	16571	150669	9.0923	3.8345
chrX	155270560	282445580	1.8191	2.1972

chrY	59373566	3673772	0.0619	0.6853
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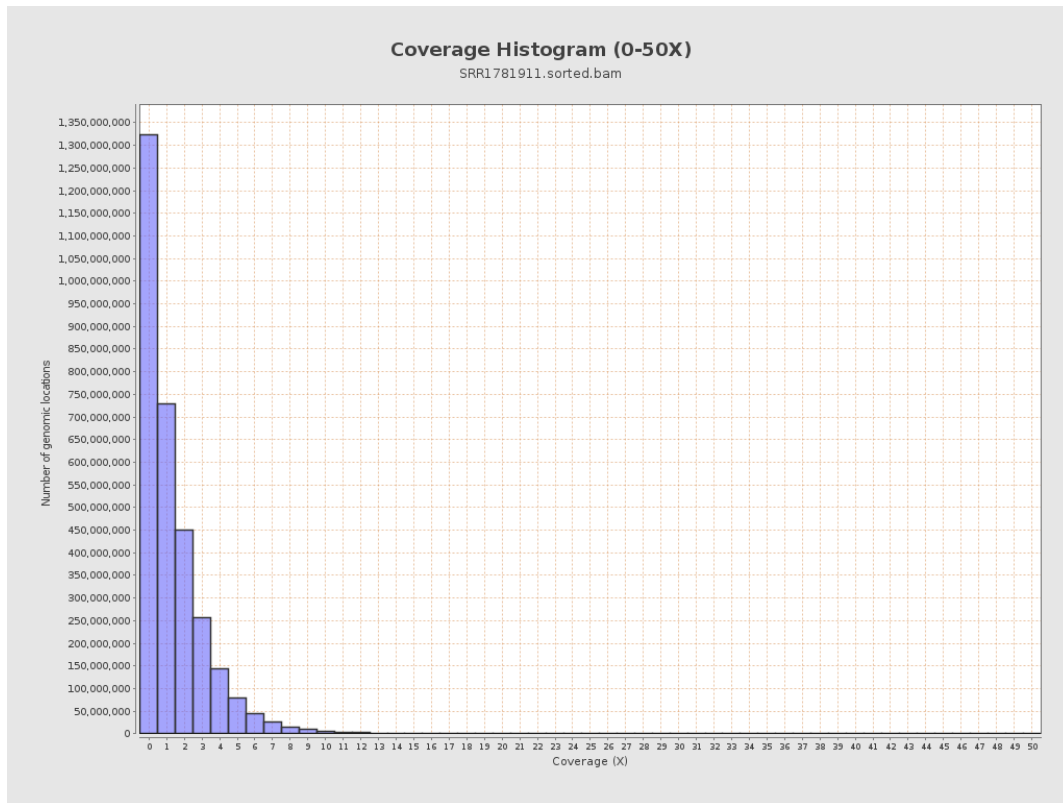
3. Results : Coverage across reference



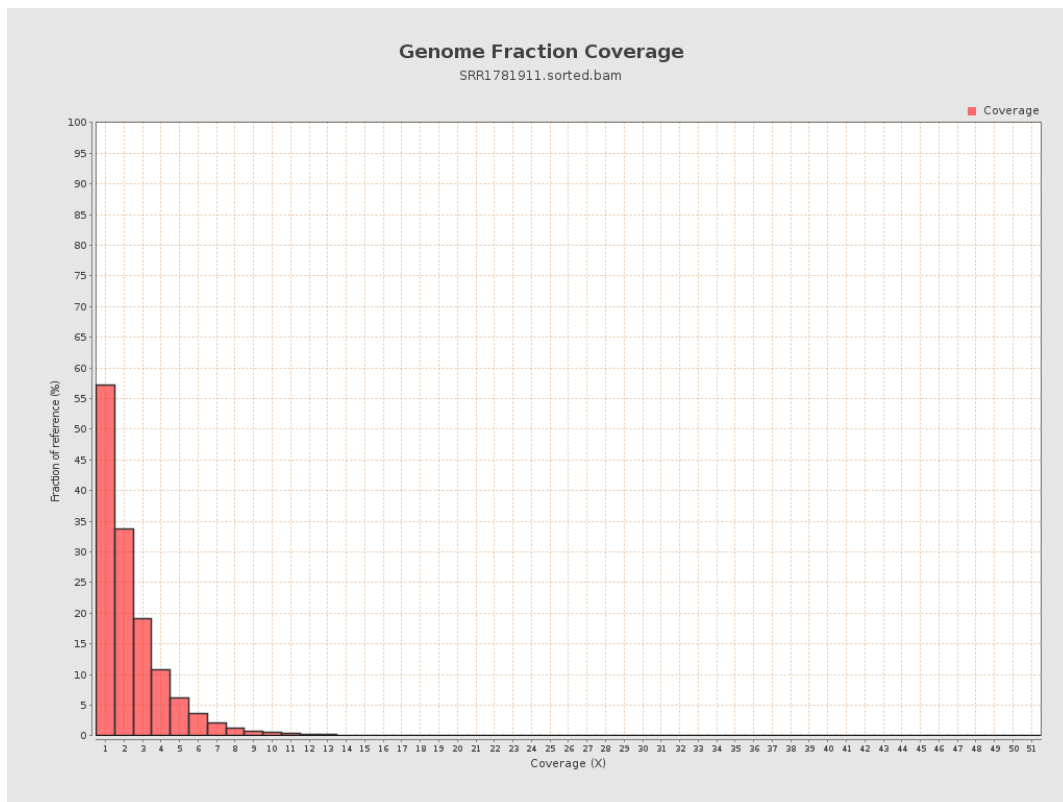
4. Results : Coverage Histogram



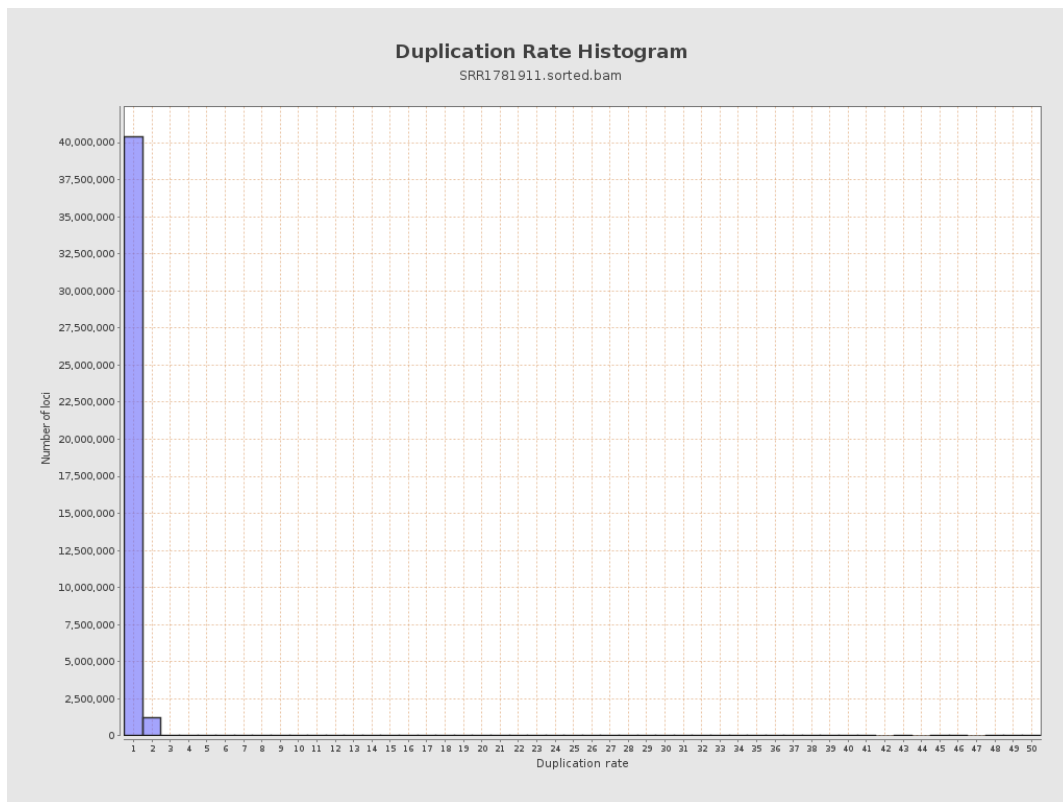
5. Results : Coverage Histogram (0-50X)



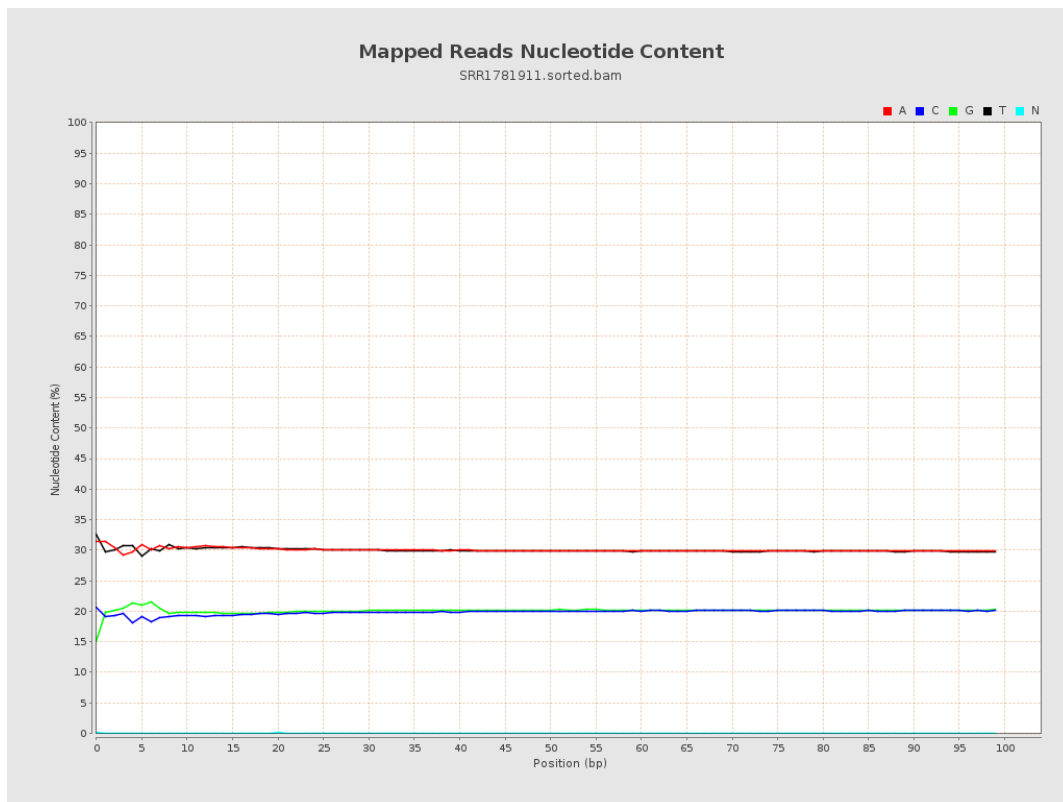
6. Results : Genome Fraction Coverage



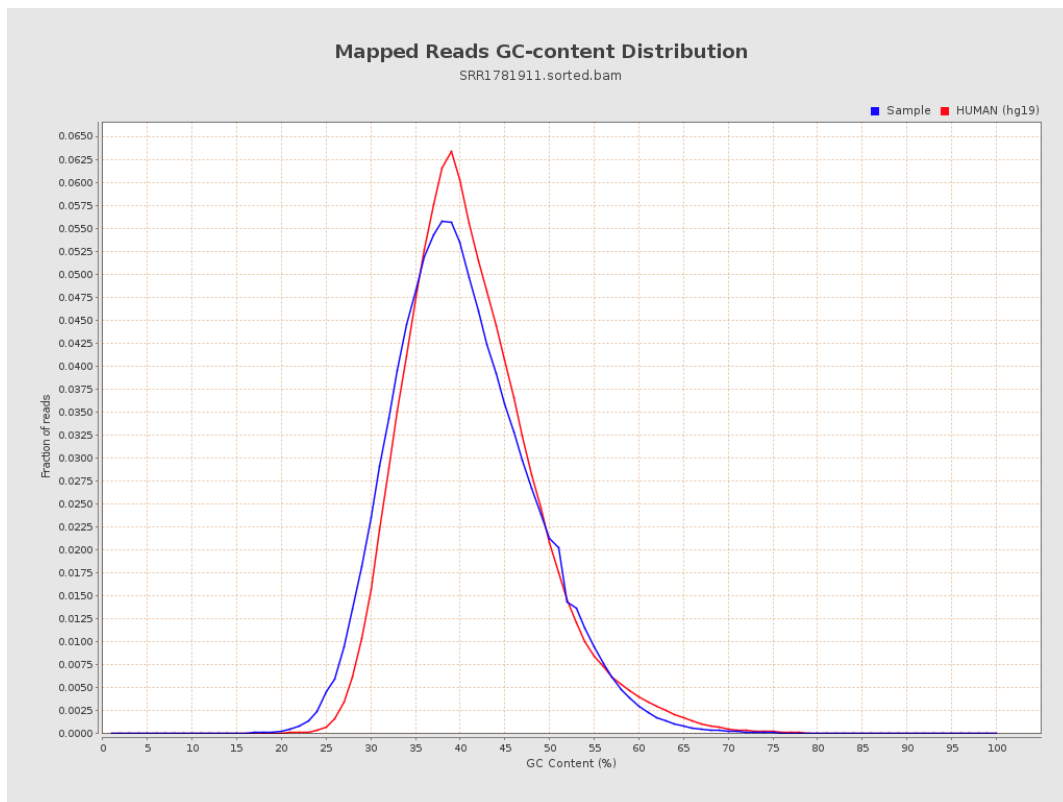
7. Results : Duplication Rate Histogram



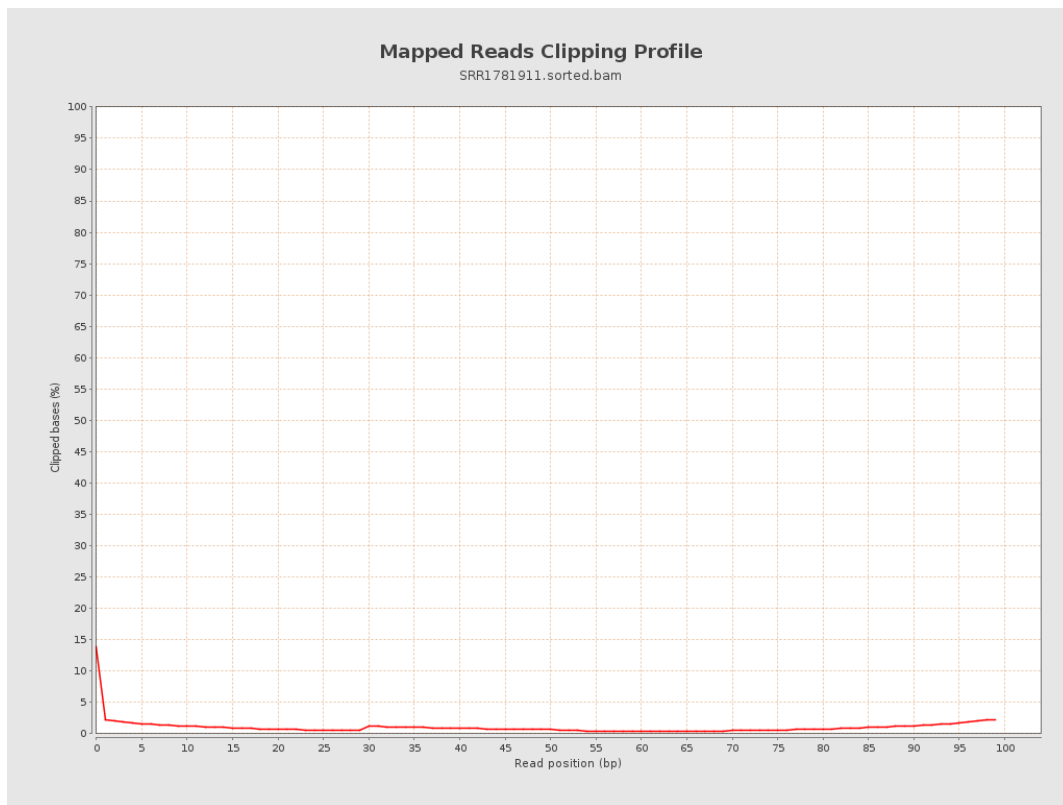
8. Results : Mapped Reads Nucleotide Content



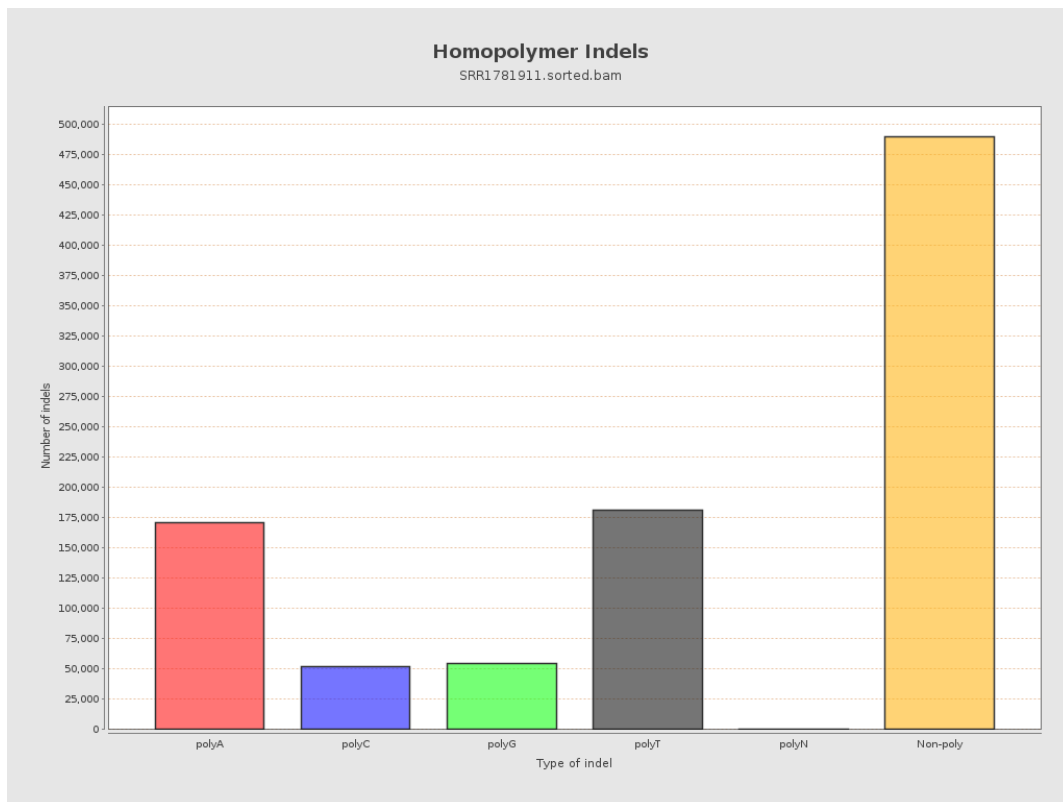
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



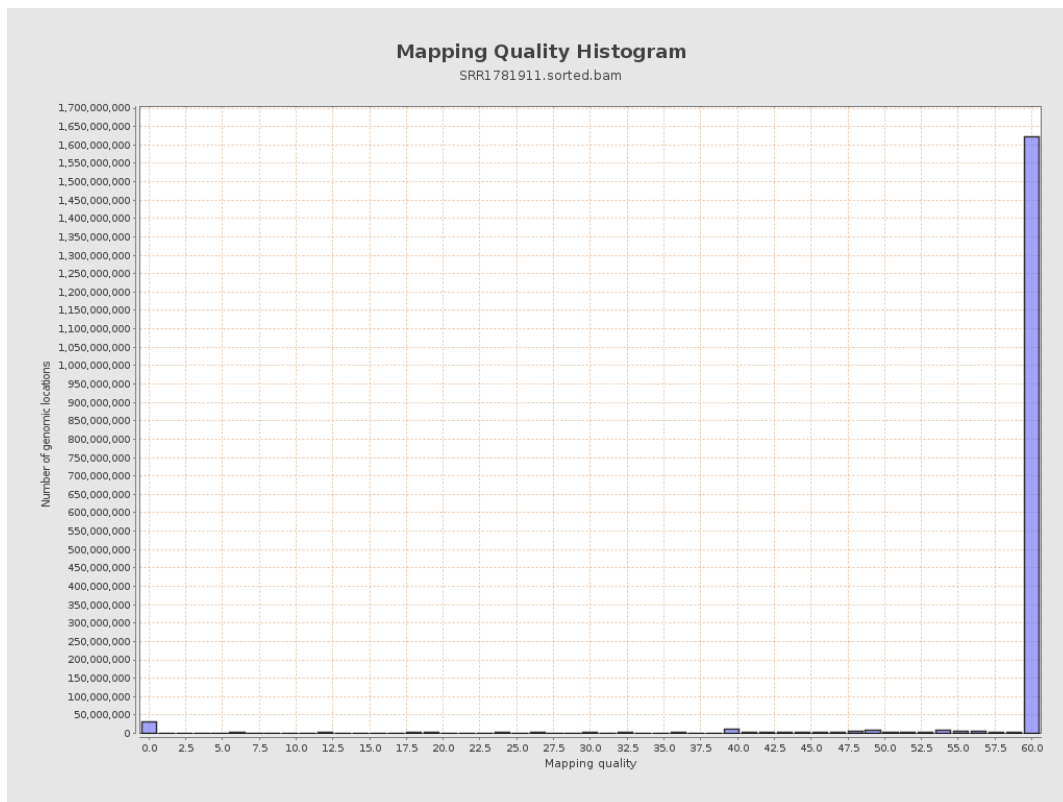
11. Results : Homopolymer Indels



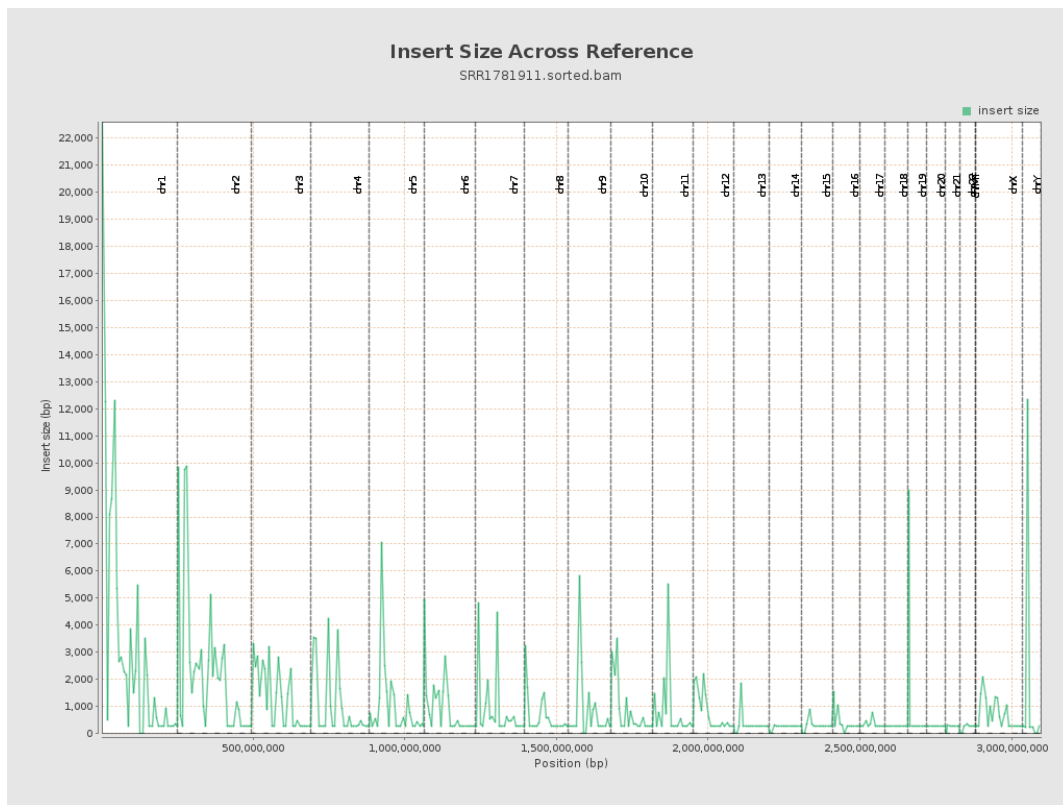
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

