

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 11:02:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781910.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_SRR1781910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781910_1.fastq.gz SRR1781910_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 11:02:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,331,484
Mapped reads	55,856,436 / 97.43%
Unmapped reads	1,475,048 / 2.57%
Mapped paired reads	55,856,436 / 97.43%
Mapped reads, first in pair	28,172,256 / 49.14%
Mapped reads, second in pair	27,684,180 / 48.29%
Mapped reads, both in pair	55,115,418 / 96.13%
Mapped reads, singletons	741,018 / 1.29%
Secondary alignments	0
Supplementary alignments	213,824 / 0.37%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	1,796,599 / 3.13%
Duplication rate	3.08%
Clipped reads	2,340,934 / 4.08%

2.2. ACGT Content

Number/percentage of A's	1,662,743,521 / 30.01%
Number/percentage of C's	1,101,007,139 / 19.87%
Number/percentage of T's	1,660,034,567 / 29.96%
Number/percentage of G's	1,116,751,782 / 20.15%
Number/percentage of N's	972,485 / 0.02%

GC Percentage	40.02%
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2.3. Coverage

Mean	1.7905
Standard Deviation	2.5969

2.4. Mapping Quality

Mean Mapping Quality	53.97
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2.5. Insert size

Mean	52,643.08
Standard Deviation	2,227,235.48
P25/Median/P75	215 / 272 / 351

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	22,570,656
Insertions	634,758
Mapped reads with at least one insertion	1.12%
Deletions	613,959
Mapped reads with at least one deletion	1.08%
Homopolymer indels	48.4%

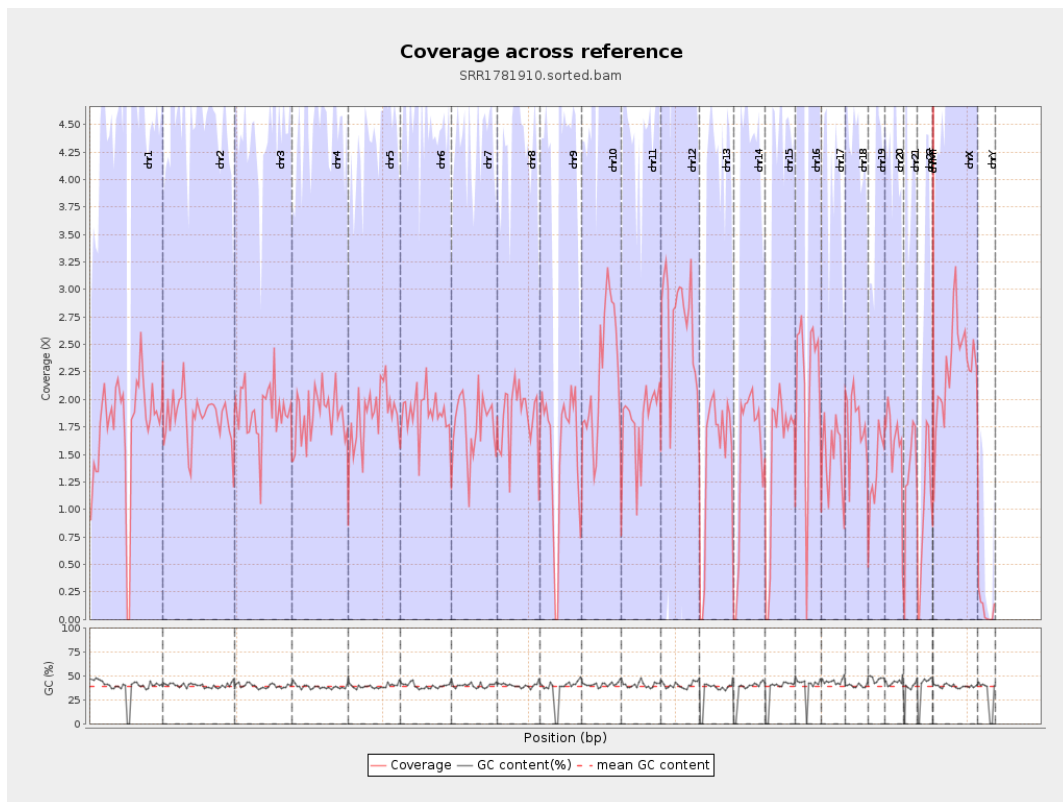
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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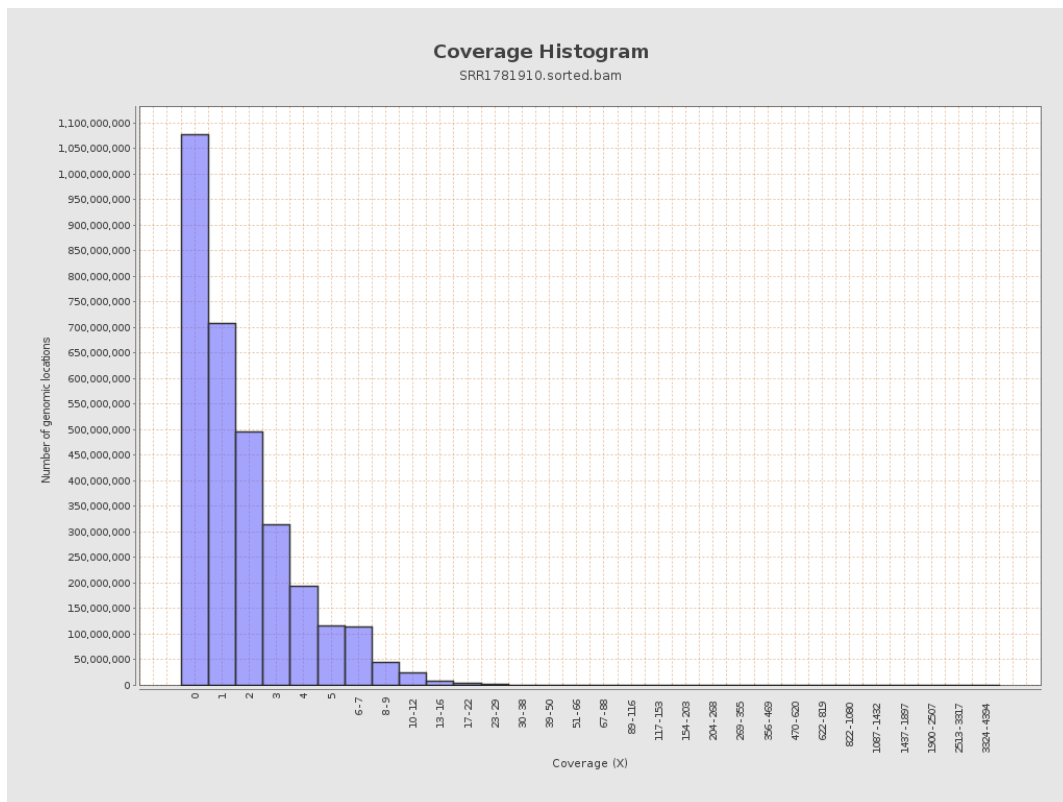
		bases	coverage	deviation
chr1	249250621	435654528	1.7479	2.9828
chr2	243199373	445477459	1.8317	3.9516
chr3	198022430	375270890	1.8951	2.1581
chr4	191154276	355613053	1.8603	2.2675
chr5	180915260	335010850	1.8518	2.1024
chr6	171115067	322316625	1.8836	2.3172
chr7	159138663	279799244	1.7582	2.2158
chr8	146364022	268563011	1.8349	2.1525
chr9	141213431	217519948	1.5404	2.3635
chr10	135534747	304156528	2.2441	3.3401
chr11	135006516	244734641	1.8128	2.1895
chr12	133851895	364598172	2.7239	3.1381
chr13	115169878	170168071	1.4775	1.9551
chr14	107349540	161968890	1.5088	2.0333
chr15	102531392	151353838	1.4762	2.0806
chr16	90354753	190025264	2.1031	2.667
chr17	81195210	122092557	1.5037	2.1332
chr18	78077248	139381077	1.7852	2.321
chr19	59128983	80687796	1.3646	2.4026
chr20	63025520	102981139	1.634	2.2718
chr21	48129895	63919967	1.3281	2.6575
chr22	51304566	51073376	0.9955	1.7621
chrMT	16571	256307	15.4672	5.5404
chrX	155270560	355146258	2.2873	2.618

chrY	59373566	5109730	0.0861	0.8899
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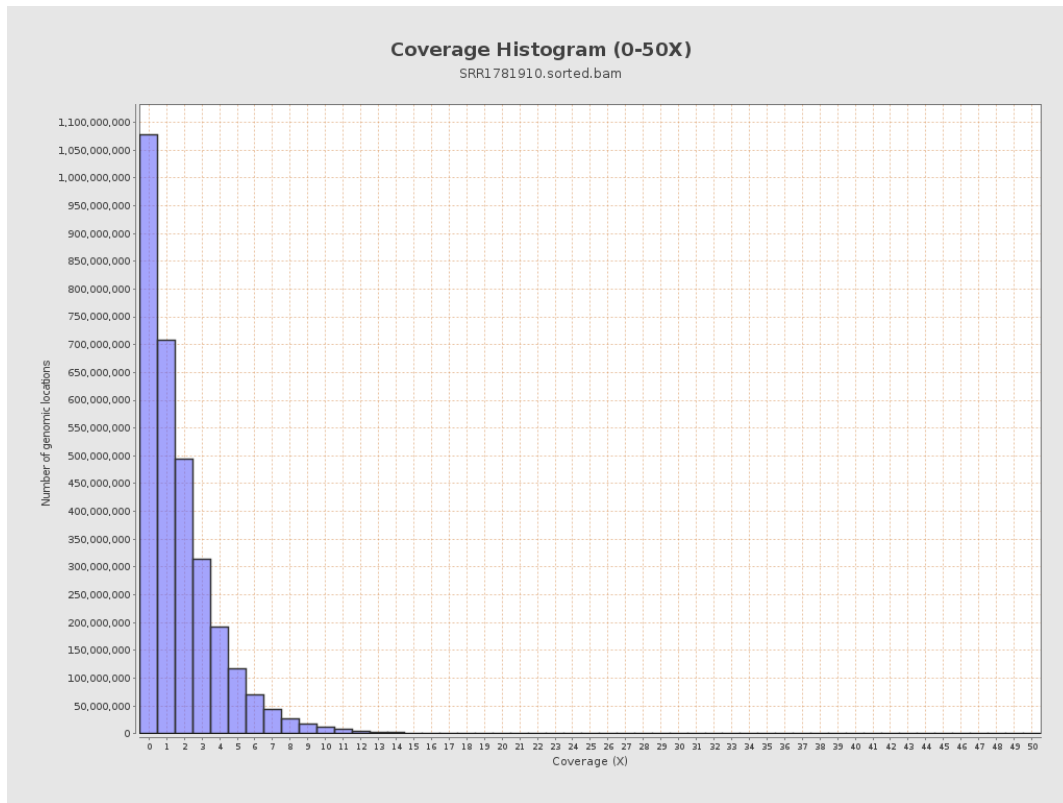
3. Results : Coverage across reference



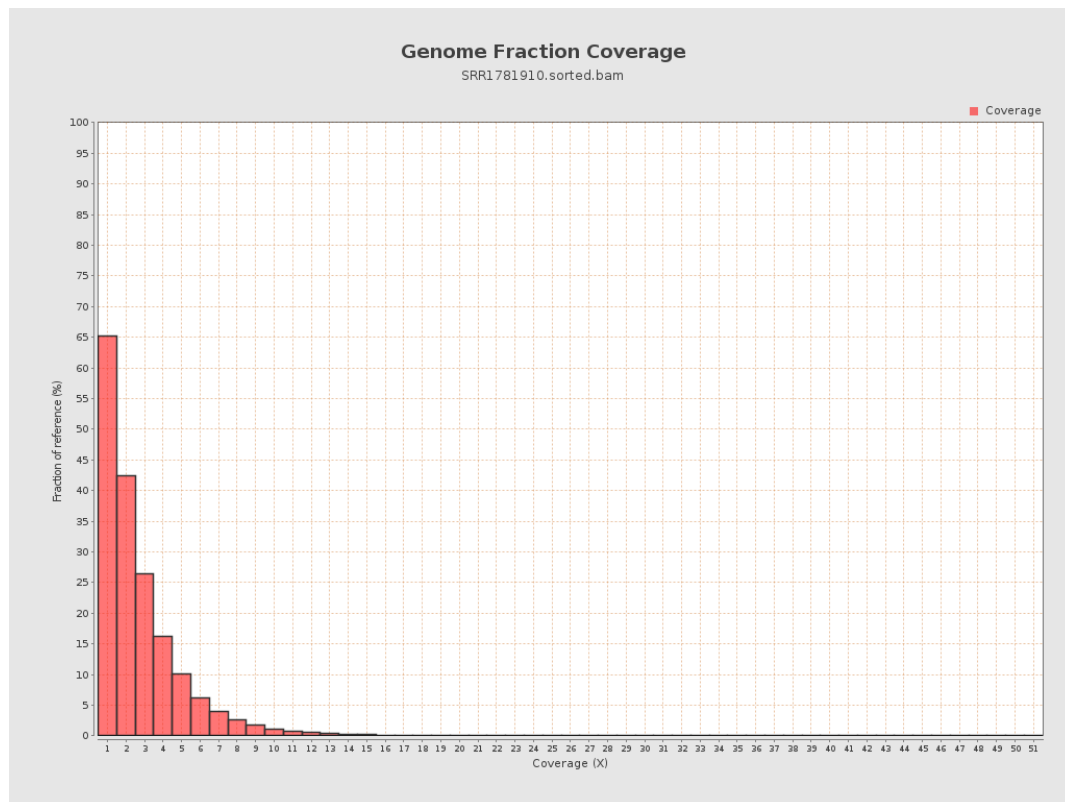
4. Results : Coverage Histogram



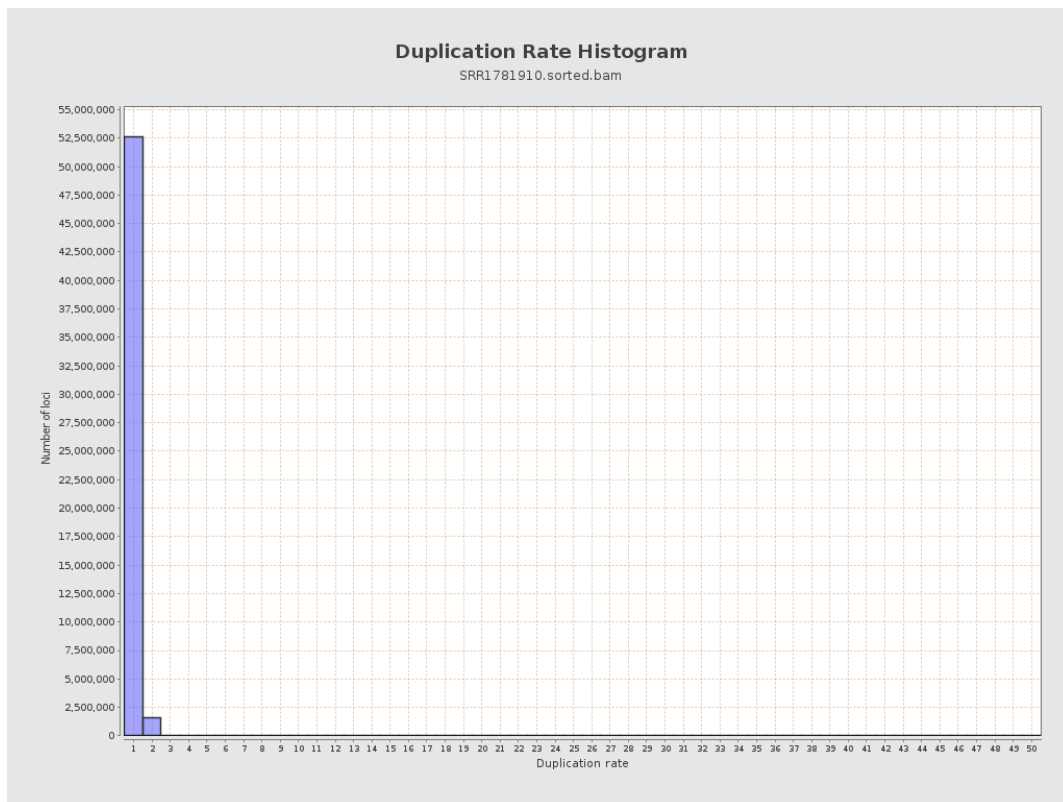
5. Results : Coverage Histogram (0-50X)



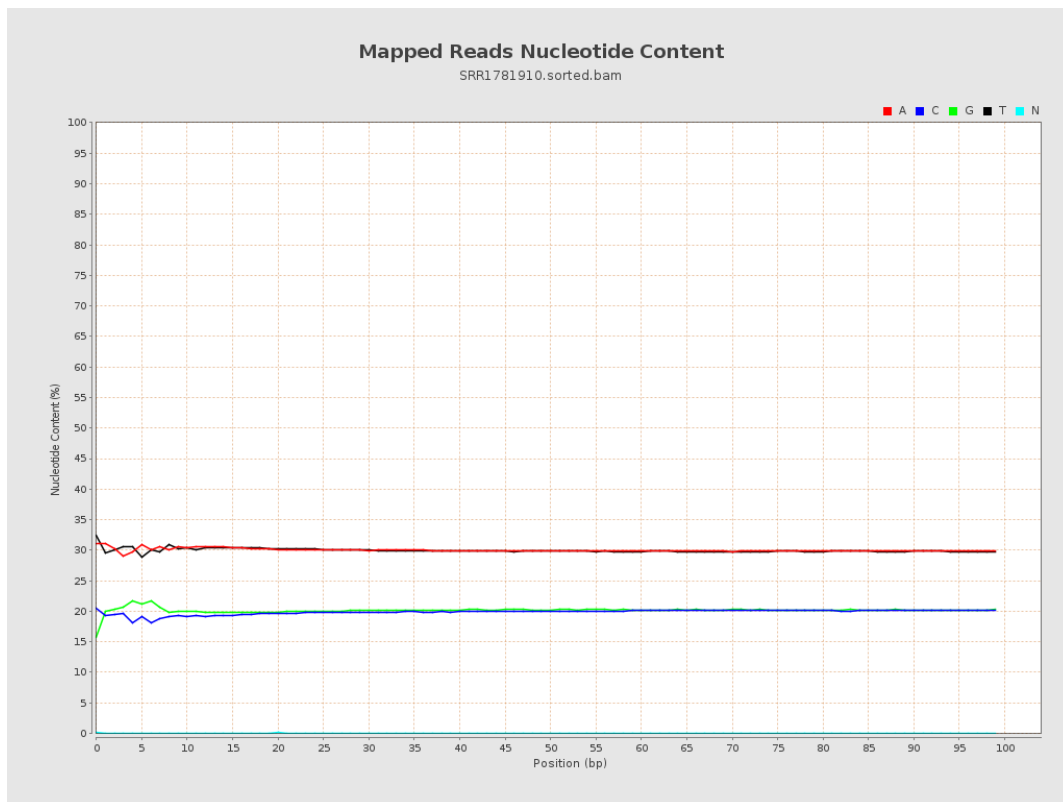
6. Results : Genome Fraction Coverage



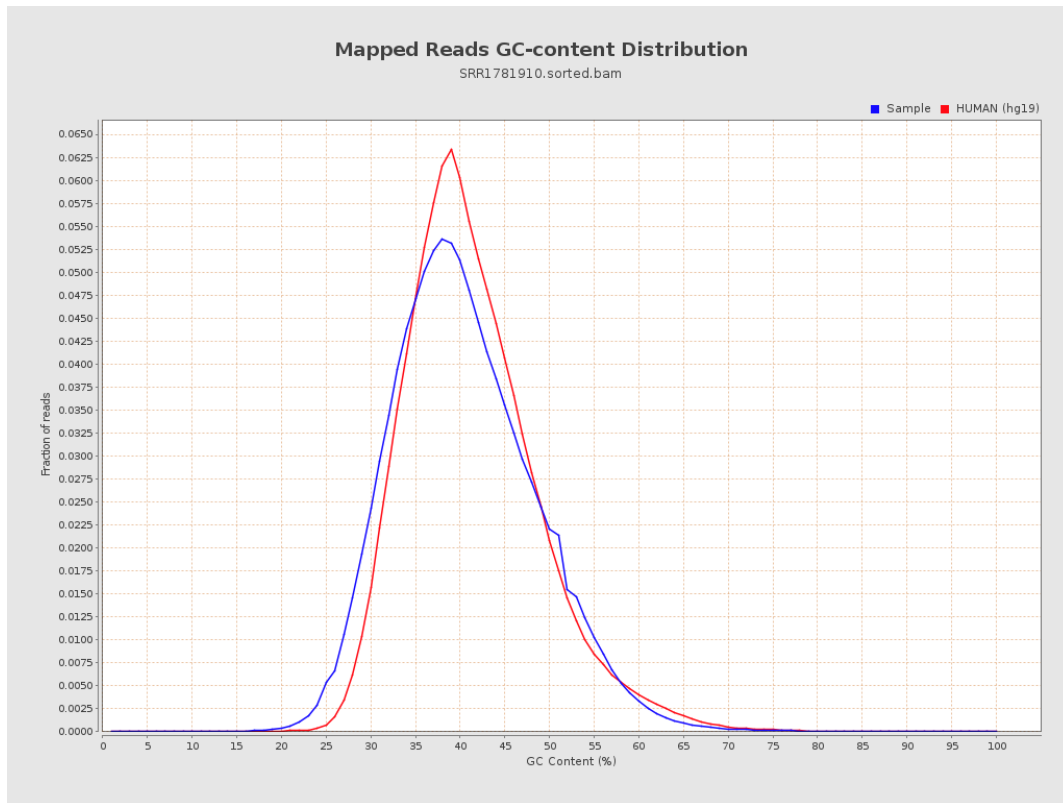
7. Results : Duplication Rate Histogram



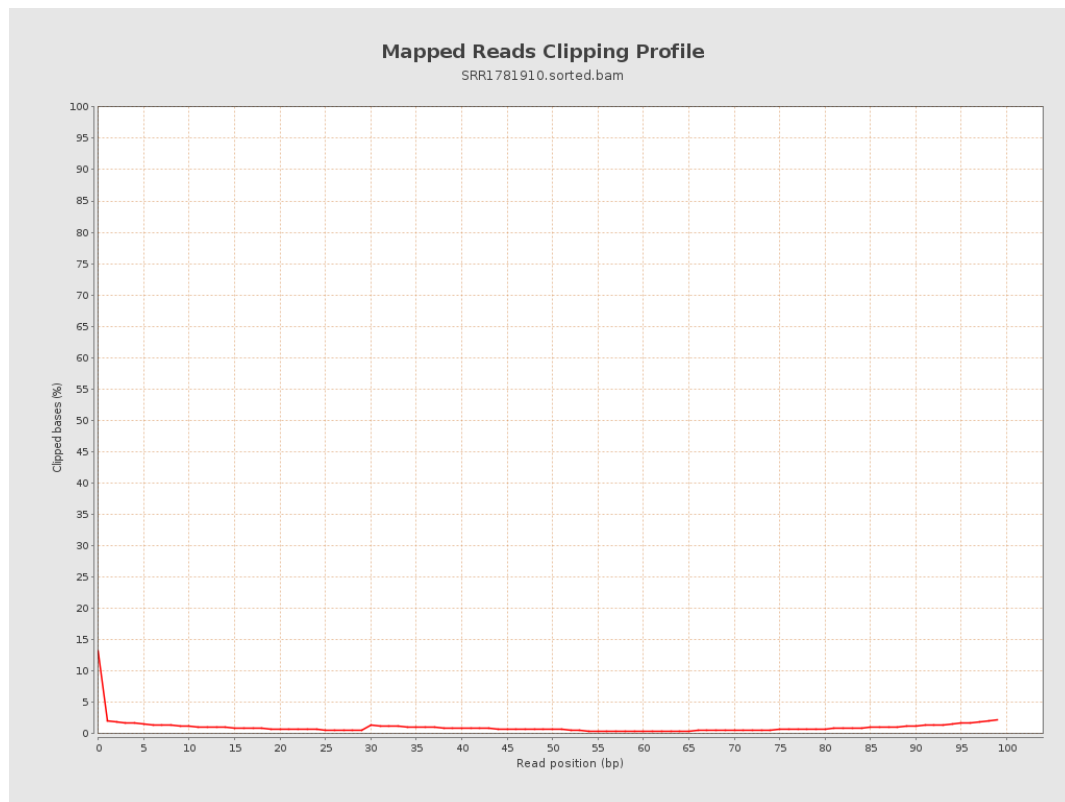
8. Results : Mapped Reads Nucleotide Content



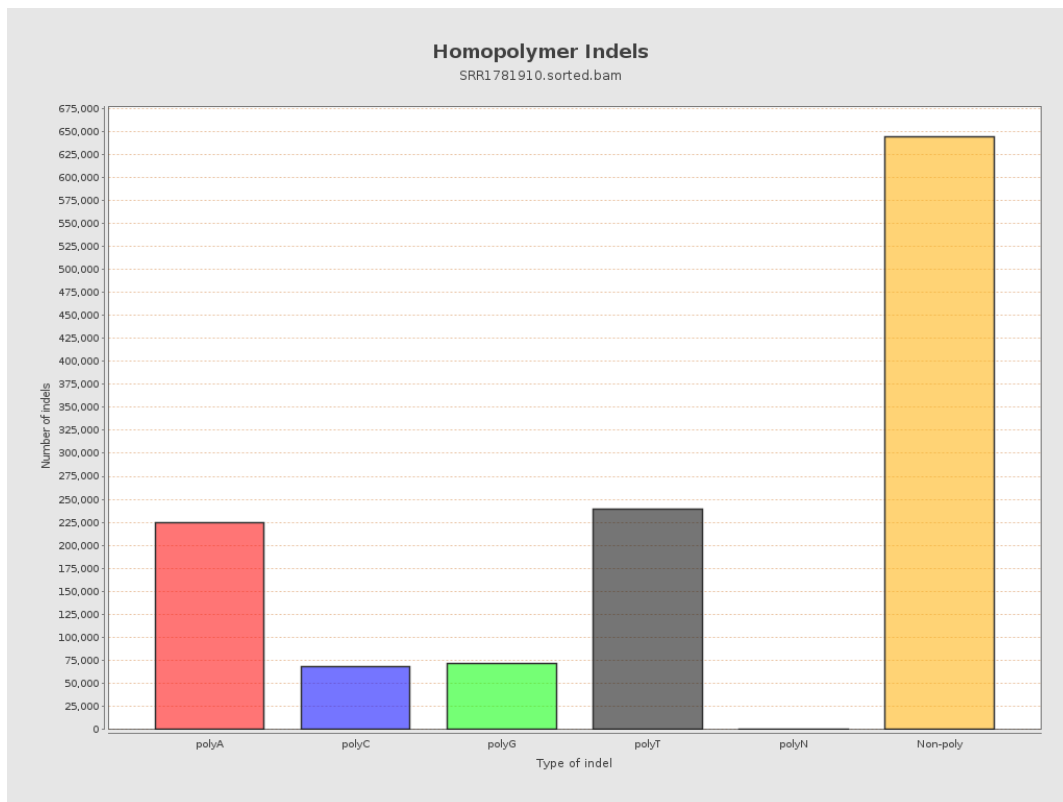
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



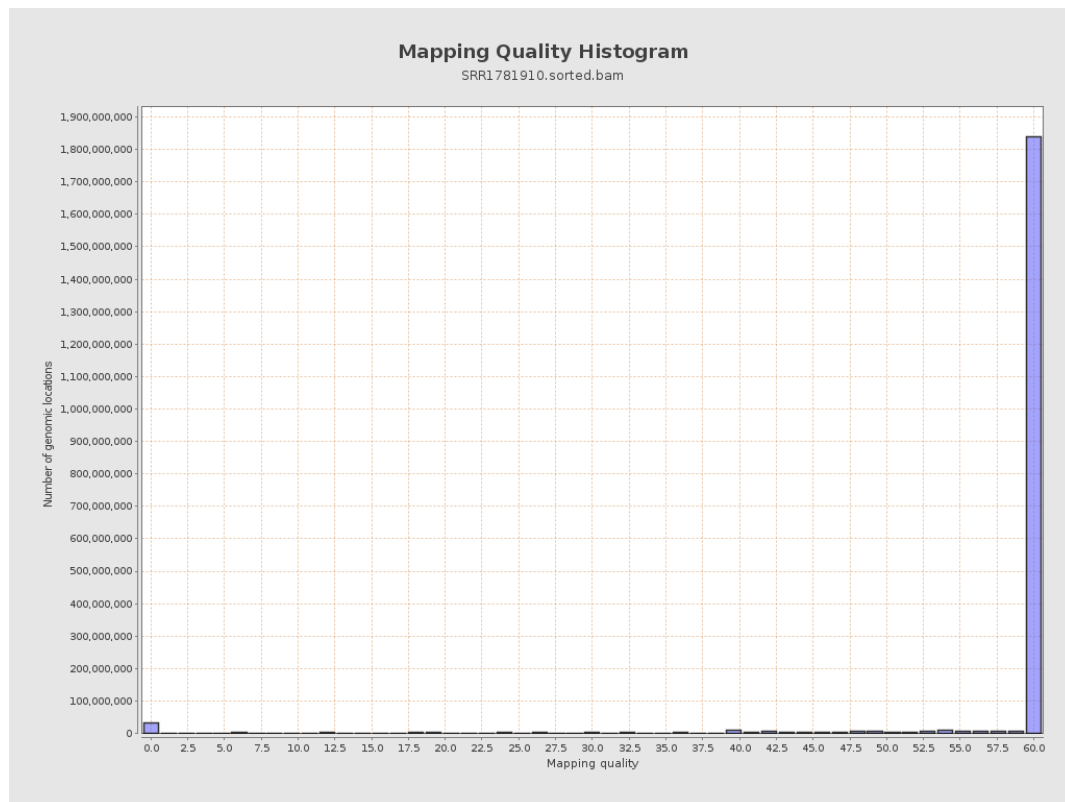
11. Results : Homopolymer Indels



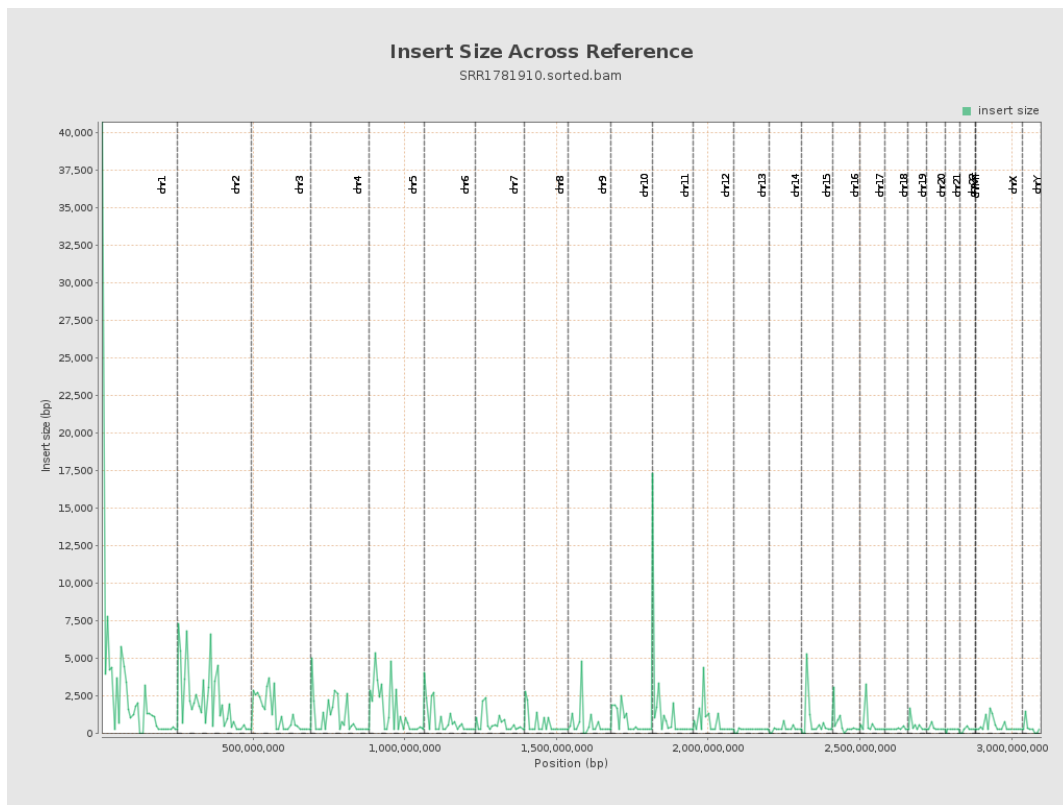
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

