

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 07:02:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781846.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_SRR1781846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781846_1.fastq.gz SRR1781846_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 07:02:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	143,114,406
Mapped reads	135,531,326 / 94.7%
Unmapped reads	7,583,080 / 5.3%
Mapped paired reads	135,531,326 / 94.7%
Mapped reads, first in pair	68,719,912 / 48.02%
Mapped reads, second in pair	66,811,414 / 46.68%
Mapped reads, both in pair	132,759,126 / 92.76%
Mapped reads, singletons	2,772,200 / 1.94%
Secondary alignments	0
Supplementary alignments	447,584 / 0.31%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	8,417,231 / 5.88%
Duplication rate	5.91%
Clipped reads	7,445,859 / 5.2%

2.2. ACGT Content

Number/percentage of A's	3,998,740,342 / 29.81%
Number/percentage of C's	2,695,548,017 / 20.09%
Number/percentage of T's	3,979,536,026 / 29.67%
Number/percentage of G's	2,740,083,048 / 20.43%
Number/percentage of N's	572,346 / 0%

GC Percentage	40.52%
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2.3. Coverage

Mean	4.3343
Standard Deviation	6.8414

2.4. Mapping Quality

Mean Mapping Quality	54.05
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2.5. Insert size

Mean	48,070.03
Standard Deviation	2,171,097.94
P25/Median/P75	165 / 221 / 295

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	46,969,030
Insertions	1,387,987
Mapped reads with at least one insertion	1.01%
Deletions	1,373,167
Mapped reads with at least one deletion	1%
Homopolymer indels	47.61%

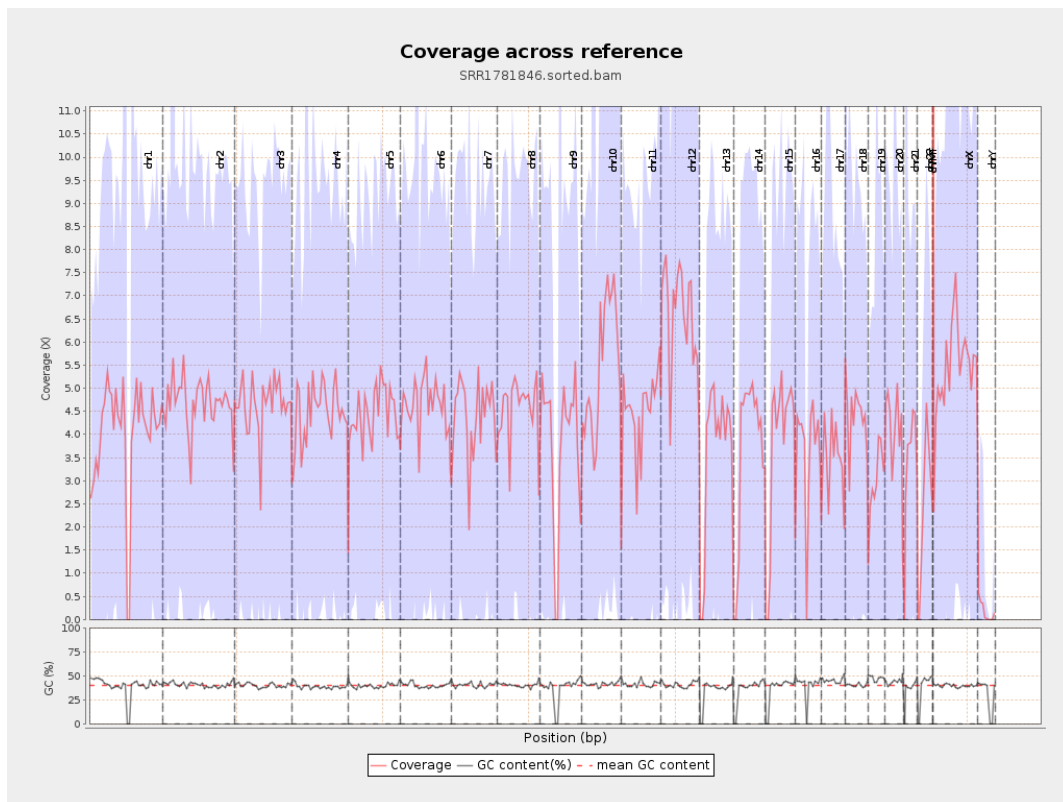
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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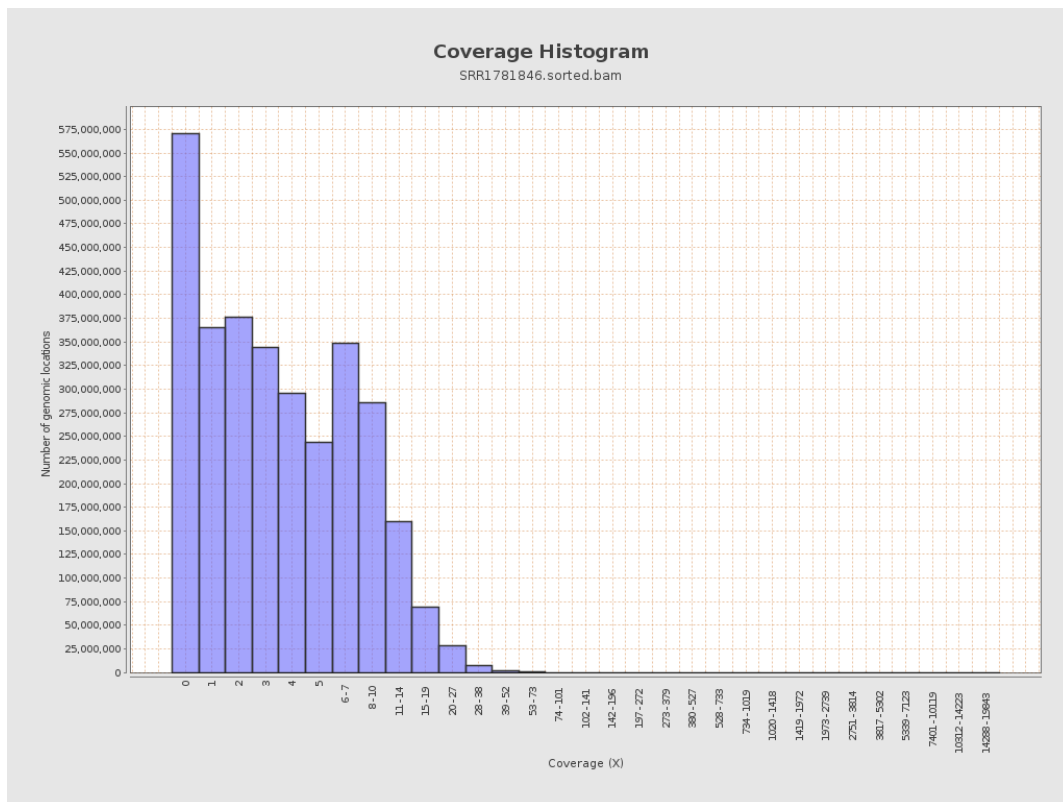
		bases	coverage	deviation
chr1	249250621	1007217716	4.041	6.4258
chr2	243199373	1136062257	4.6713	16.2305
chr3	198022430	918415235	4.6379	4.4047
chr4	191154276	863087272	4.5151	4.7754
chr5	180915260	804129744	4.4448	4.2328
chr6	171115067	797768338	4.6622	4.9888
chr7	159138663	695588754	4.371	4.8156
chr8	146364022	668735449	4.569	4.4234
chr9	141213431	541281717	3.8331	5.2442
chr10	135534747	749795477	5.5321	8.614
chr11	135006516	606483429	4.4923	4.601
chr12	133851895	888601944	6.6387	6.7464
chr13	115169878	413942601	3.5942	3.9863
chr14	107349540	401686173	3.7419	4.3397
chr15	102531392	381325556	3.7191	4.4471
chr16	90354753	320514505	3.5473	4.3924
chr17	81195210	286195345	3.5248	5.2896
chr18	78077248	340934094	4.3666	5.1078
chr19	59128983	180256014	3.0485	5.1249
chr20	63025520	259939626	4.1244	5.067
chr21	48129895	163831259	3.4039	5.9664
chr22	51304566	129356041	2.5213	3.8438
chrMT	16571	2393917	144.4642	38.3975
chrX	155270560	849813369	5.4731	5.3303

chrY	59373566	10184438	0.1715	1.9096
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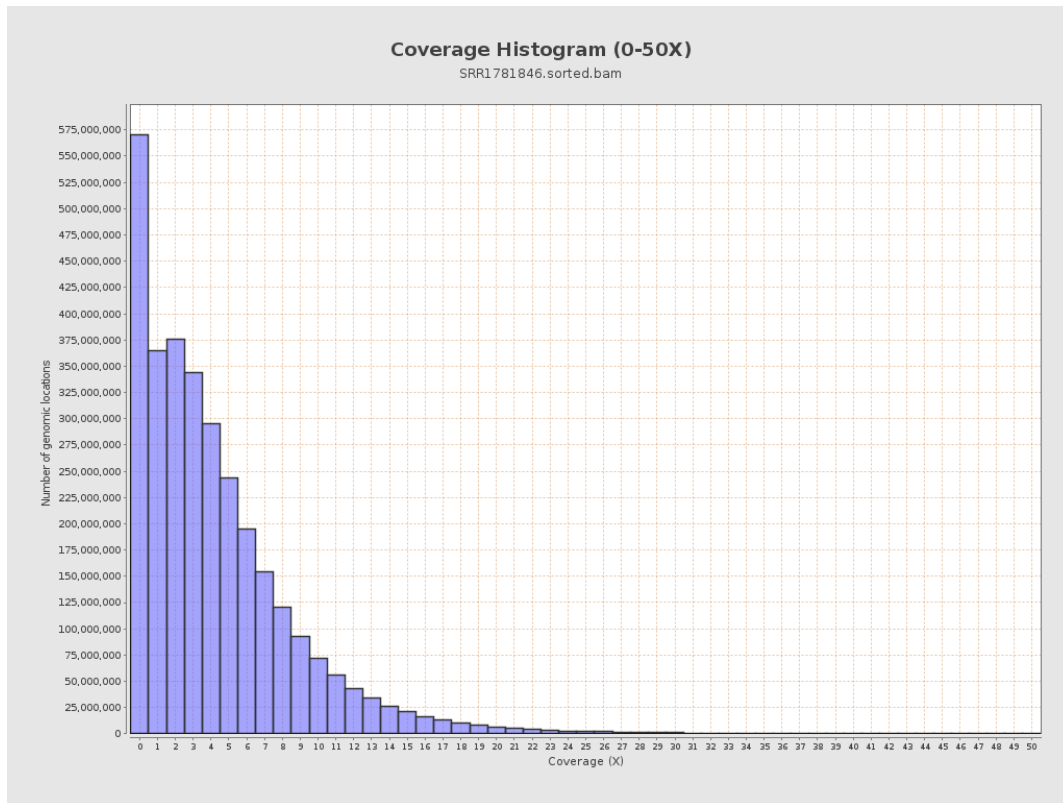
3. Results : Coverage across reference



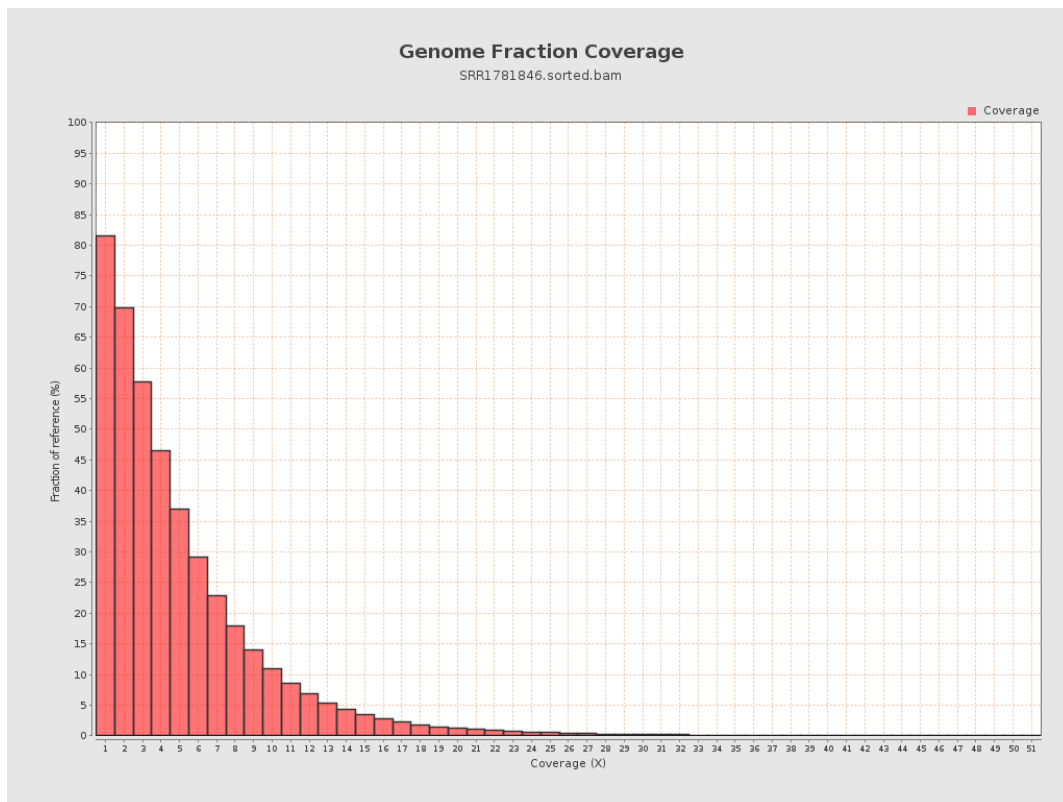
4. Results : Coverage Histogram



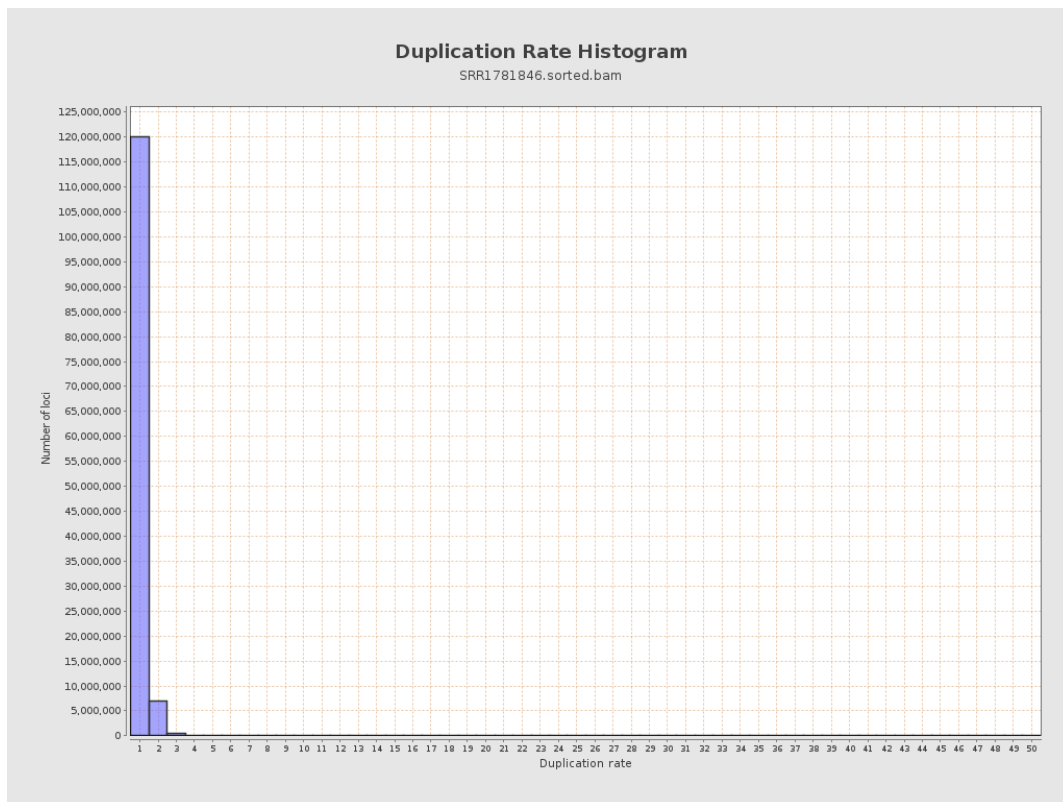
5. Results : Coverage Histogram (0-50X)



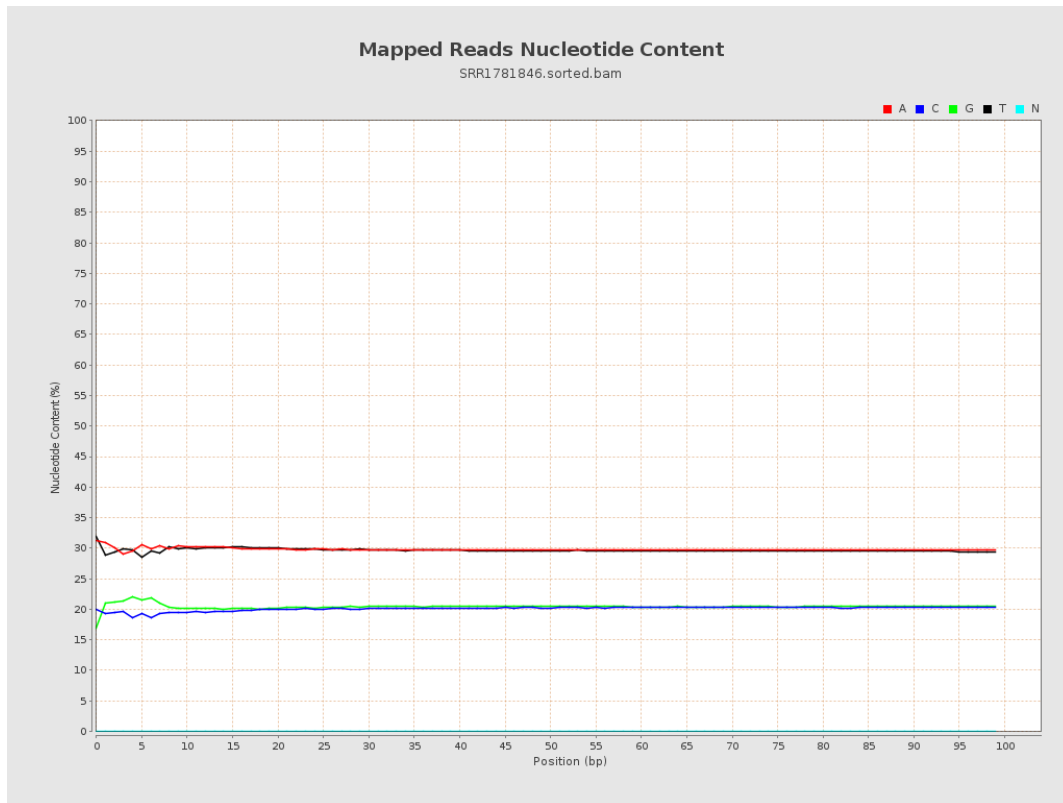
6. Results : Genome Fraction Coverage



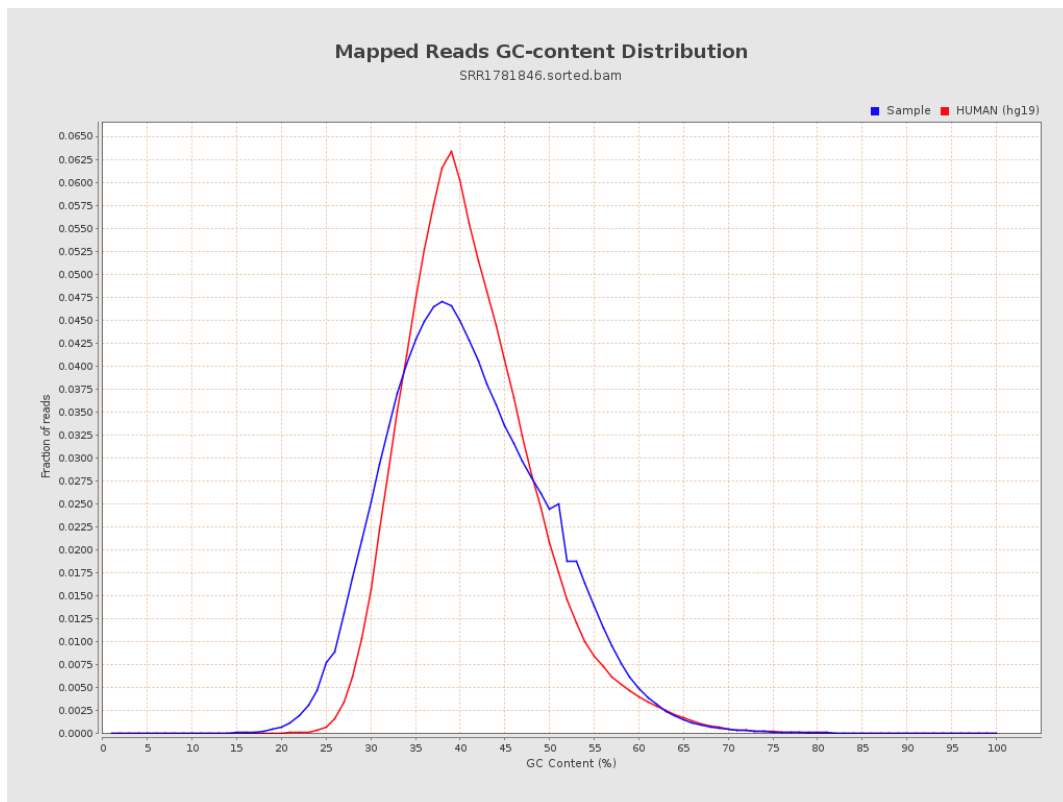
7. Results : Duplication Rate Histogram



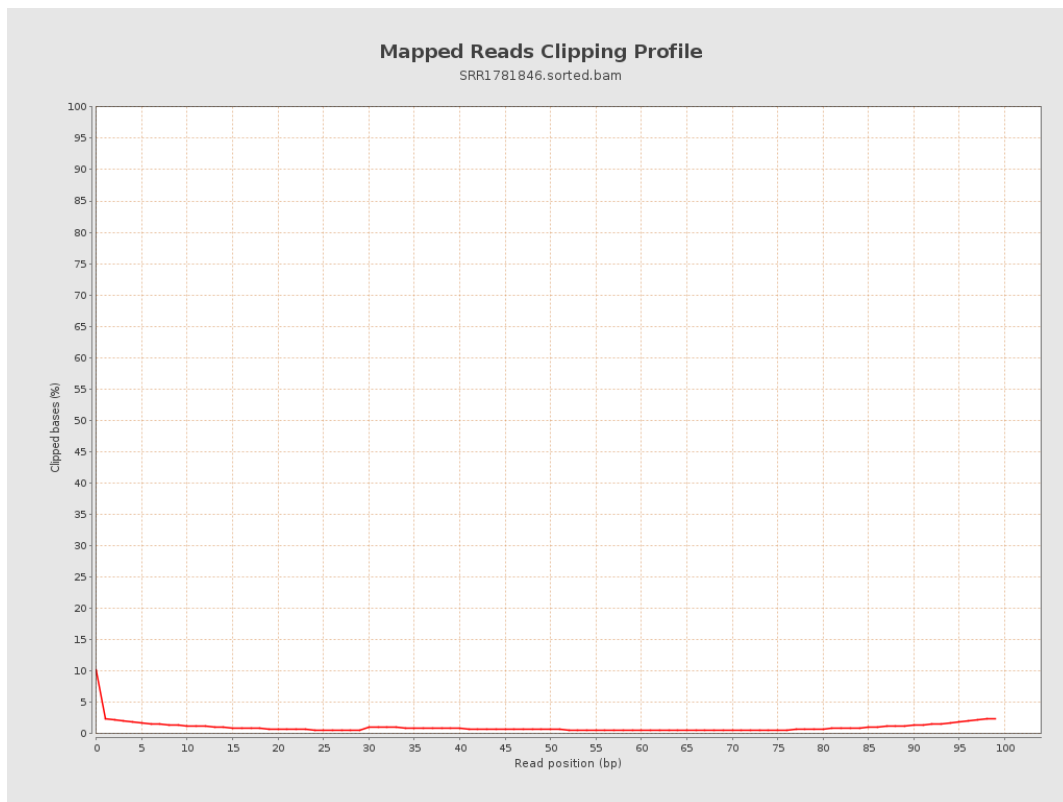
8. Results : Mapped Reads Nucleotide Content



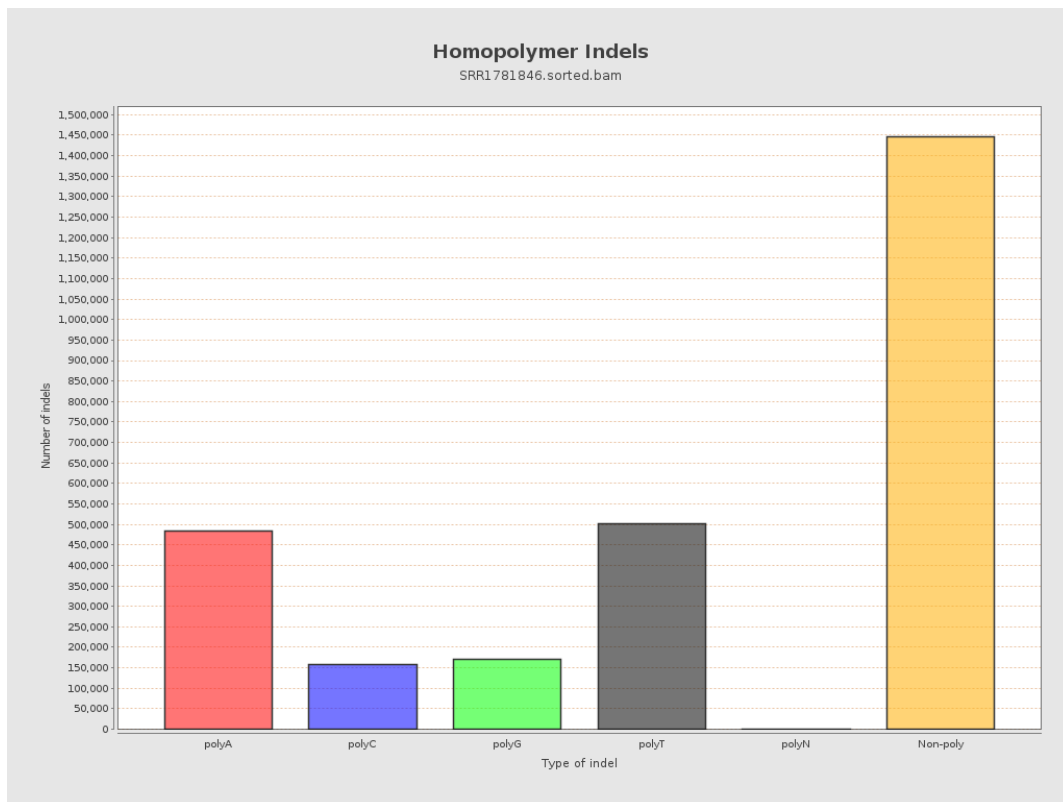
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



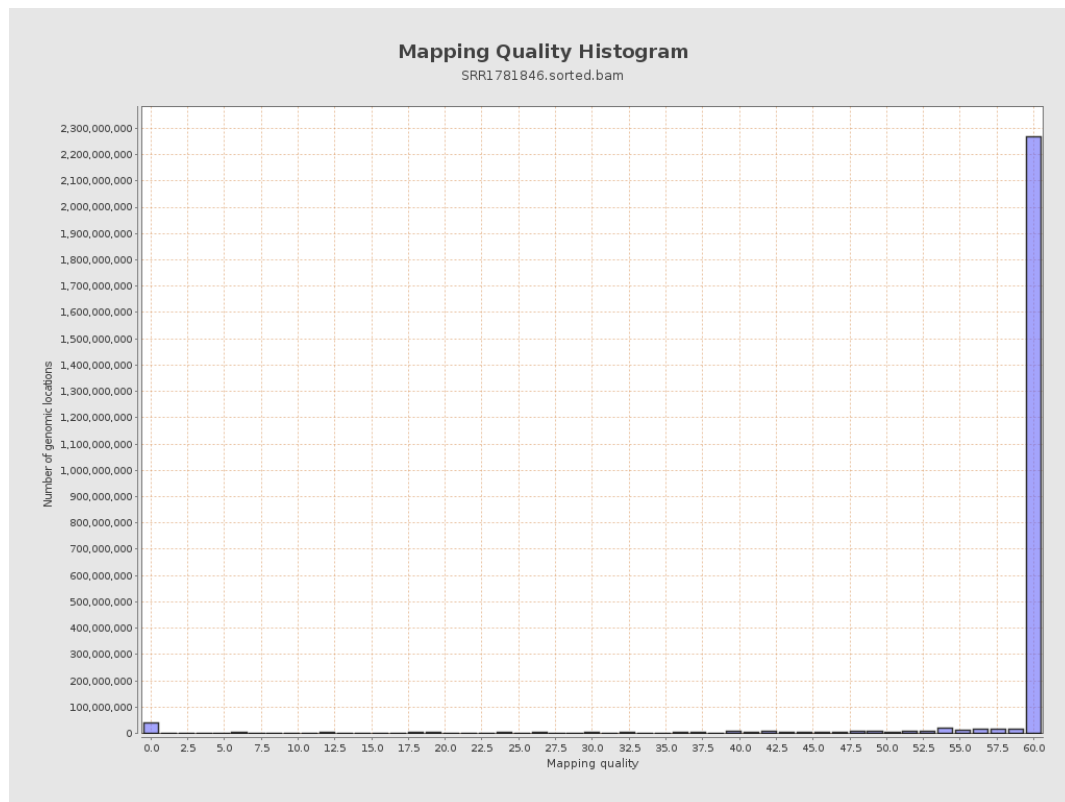
11. Results : Homopolymer Indels



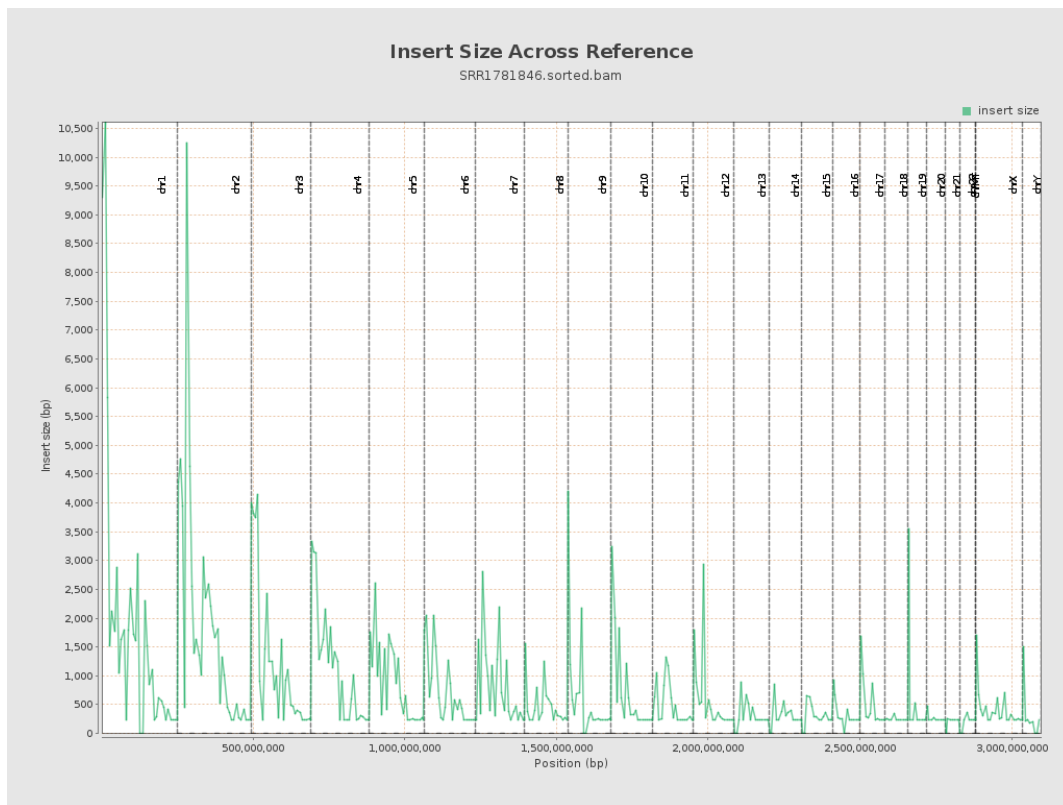
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

