

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 18:33:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781856.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_SRR1781856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781856_1.fastq.gz SRR1781856_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 18:33:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	167,170,460
Mapped reads	163,943,846 / 98.07%
Unmapped reads	3,226,614 / 1.93%
Mapped paired reads	163,943,846 / 98.07%
Mapped reads, first in pair	82,277,120 / 49.22%
Mapped reads, second in pair	81,666,726 / 48.85%
Mapped reads, both in pair	162,837,132 / 97.41%
Mapped reads, singletons	1,106,714 / 0.66%
Secondary alignments	0
Supplementary alignments	628,920 / 0.38%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	10,595,882 / 6.34%
Duplication rate	6.21%
Clipped reads	7,378,541 / 4.41%

2.2. ACGT Content

Number/percentage of A's	4,786,222,727 / 29.4%
Number/percentage of C's	3,331,224,897 / 20.47%
Number/percentage of T's	4,774,151,357 / 29.33%
Number/percentage of G's	3,363,417,120 / 20.66%
Number/percentage of N's	22,200,884 / 0.14%

GC Percentage	41.13%
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2.3. Coverage

Mean	5.2591
Standard Deviation	6.5378

2.4. Mapping Quality

Mean Mapping Quality	53.93
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2.5. Insert size

Mean	37,934.62
Standard Deviation	1,902,032.4
P25/Median/P75	153 / 187 / 229

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	81,320,110
Insertions	1,496,489
Mapped reads with at least one insertion	0.9%
Deletions	1,494,221
Mapped reads with at least one deletion	0.9%
Homopolymer indels	45.64%

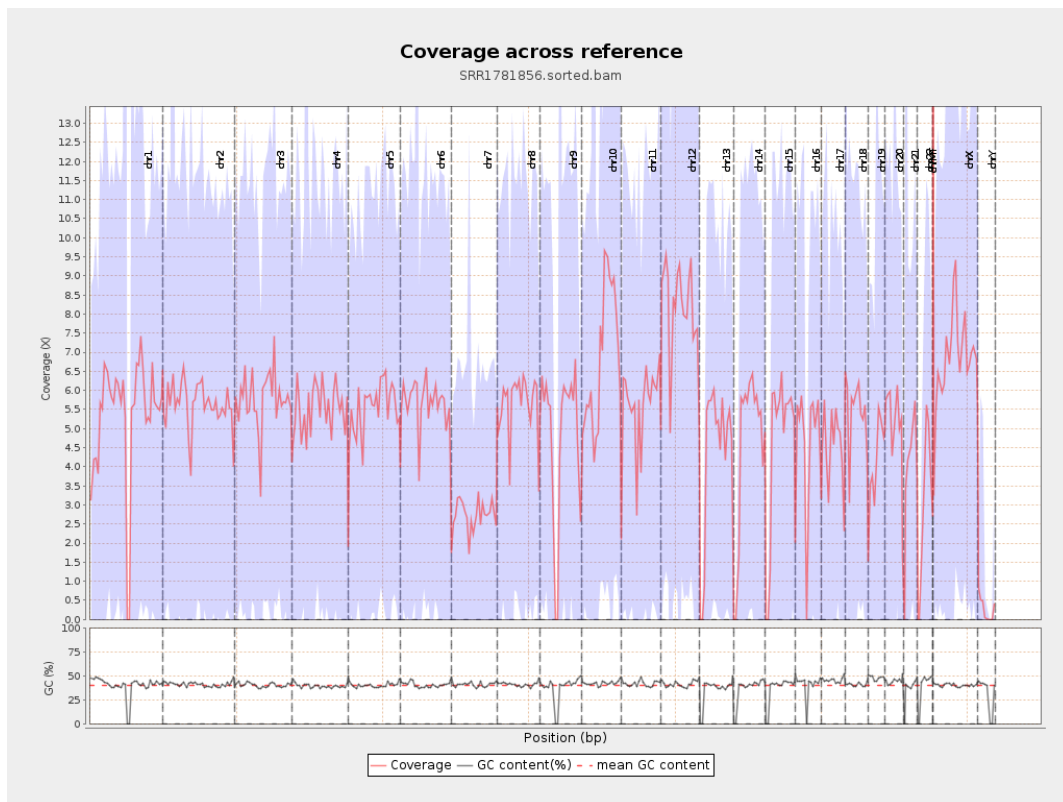
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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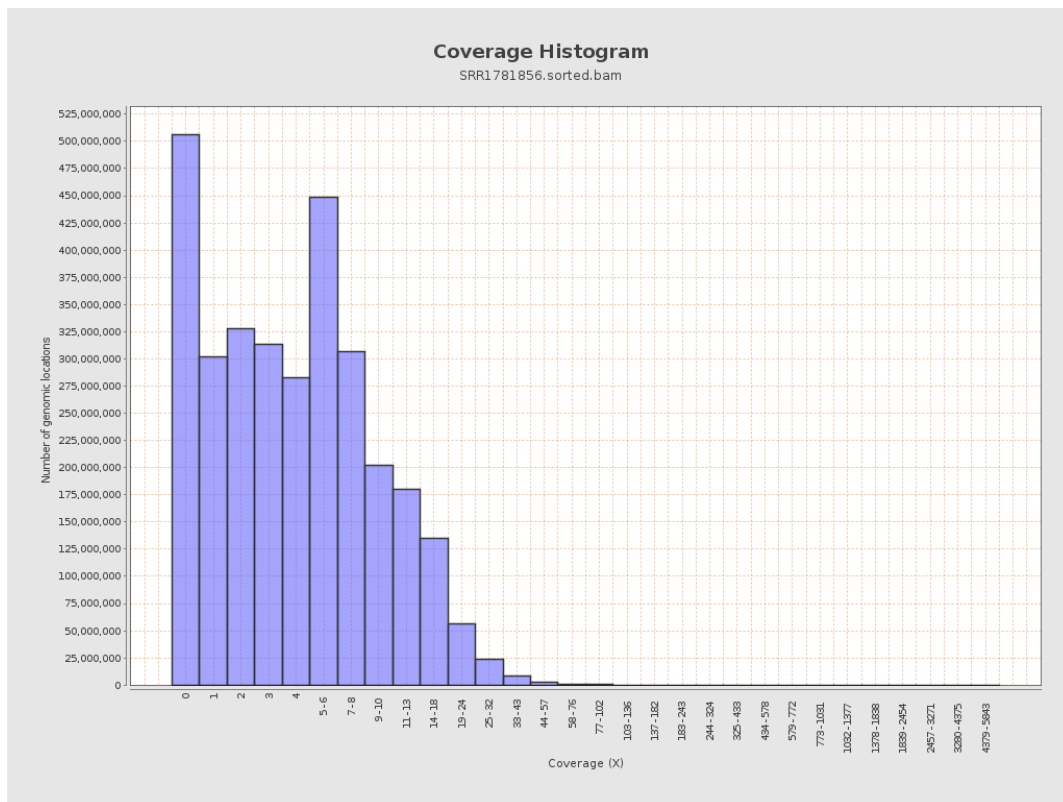
		bases	coverage	deviation
chr1	249250621	1330851721	5.3394	8.7095
chr2	243199373	1366542232	5.619	7.3804
chr3	198022430	1137462402	5.7441	5.3461
chr4	191154276	1062150719	5.5565	5.9995
chr5	180915260	1000354800	5.5294	5.0973
chr6	171115067	972884049	5.6856	5.773
chr7	159138663	434134208	2.728	3.9707
chr8	146364022	824443203	5.6328	5.461
chr9	141213431	680639471	4.8199	6.5742
chr10	135534747	930038037	6.862	10.0624
chr11	135006516	758861603	5.6209	5.6007
chr12	133851895	1103318588	8.2428	7.5842
chr13	115169878	501207235	4.3519	4.8128
chr14	107349540	498472137	4.6434	5.266
chr15	102531392	464983837	4.535	5.3115
chr16	90354753	405283706	4.4855	5.3345
chr17	81195210	373721913	4.6028	5.4608
chr18	78077248	422502324	5.4113	6.5274
chr19	59128983	247055527	4.1782	6.3828
chr20	63025520	328147372	5.2066	6.2235
chr21	48129895	196342747	4.0794	8.3225
chr22	51304566	158668085	3.0927	4.6248
chrMT	16571	595644	35.945	10.3461
chrX	155270560	1066321325	6.8675	6.5336

chrY	59373566	15583472	0.2625	2.8922
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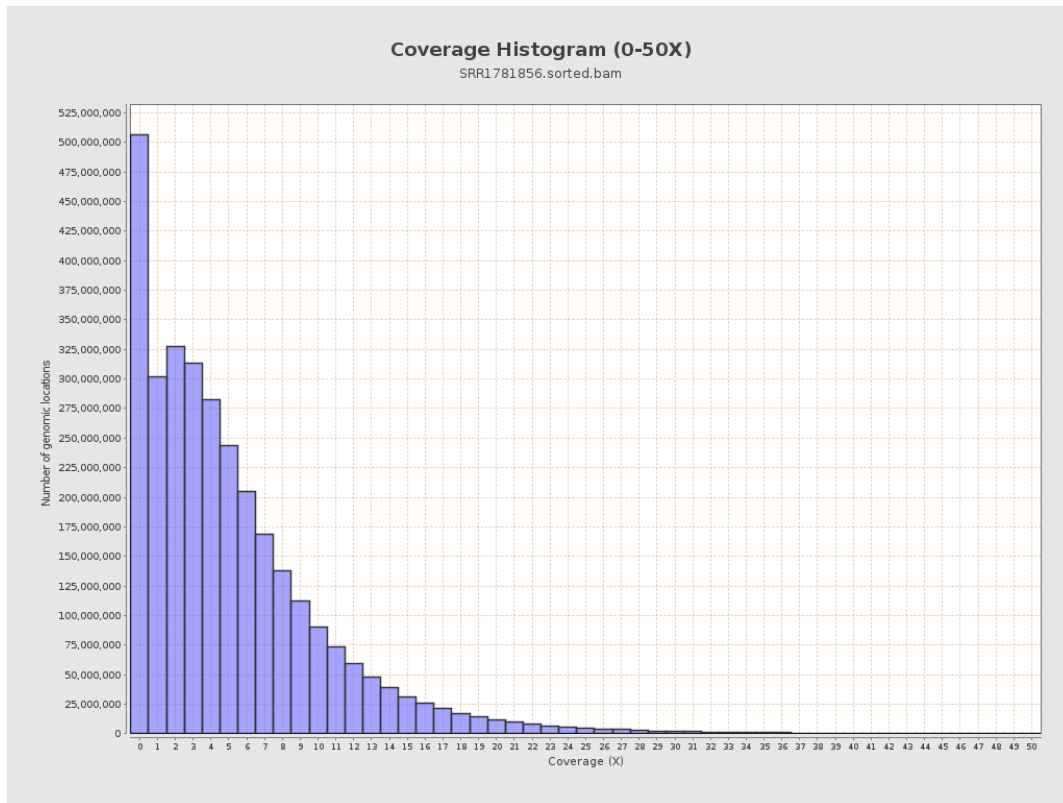
3. Results : Coverage across reference



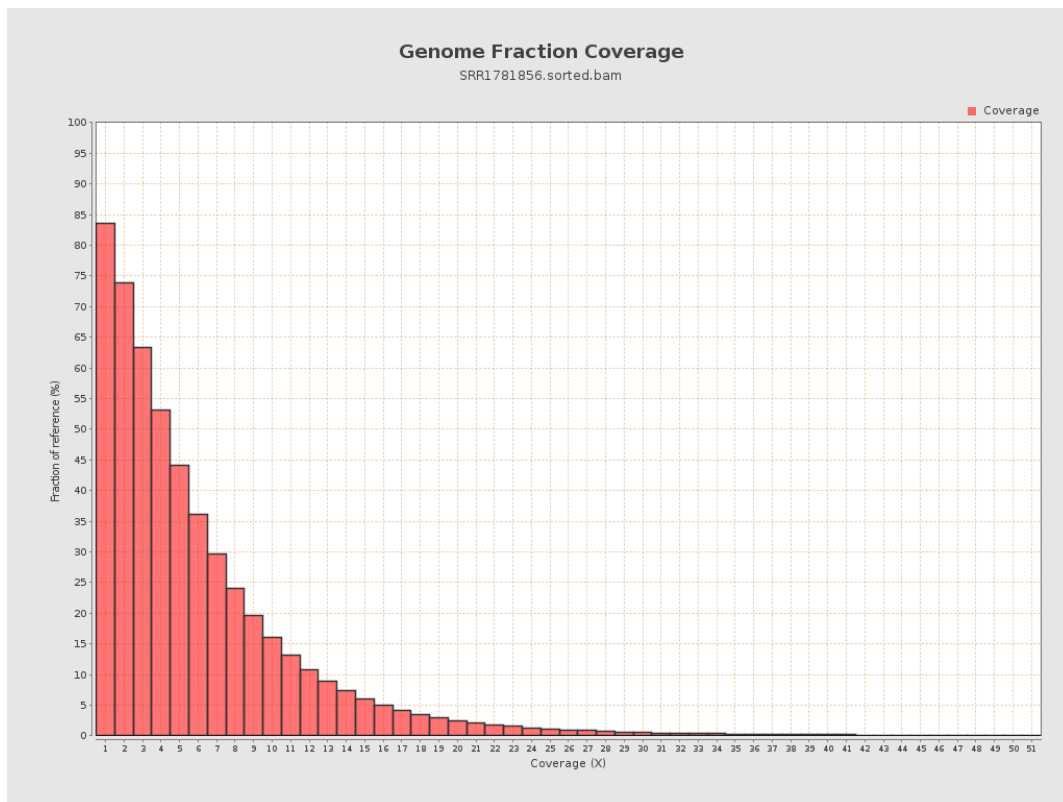
4. Results : Coverage Histogram



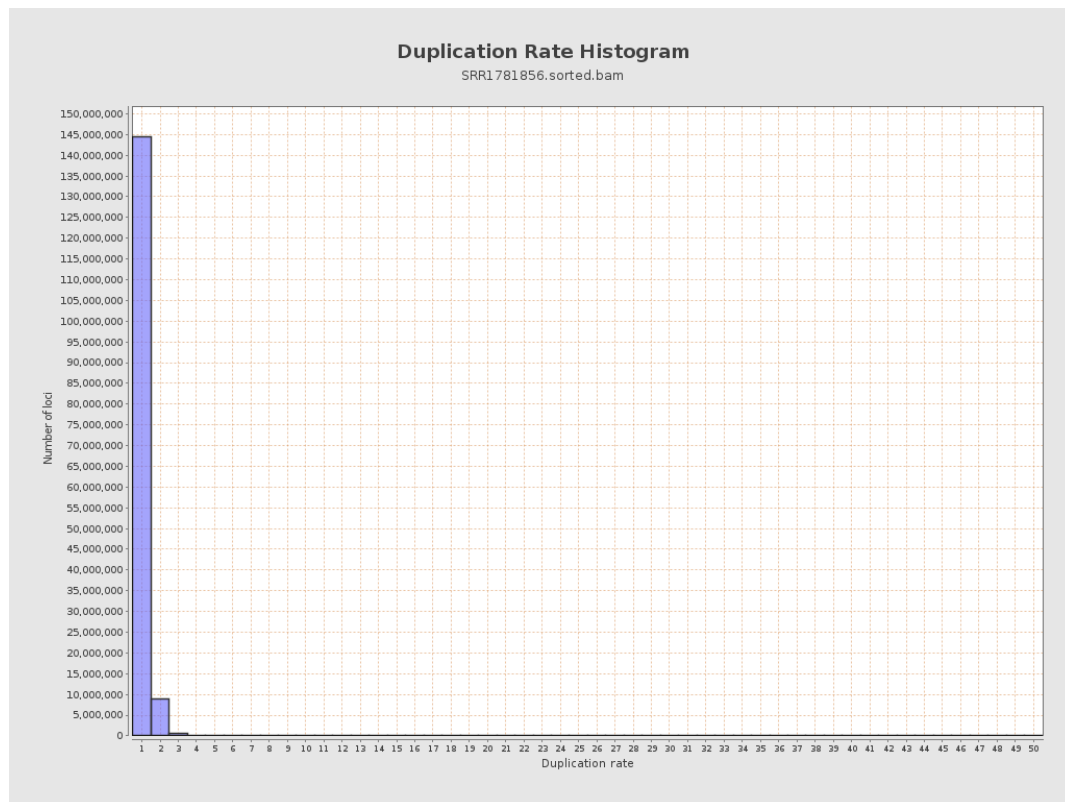
5. Results : Coverage Histogram (0-50X)



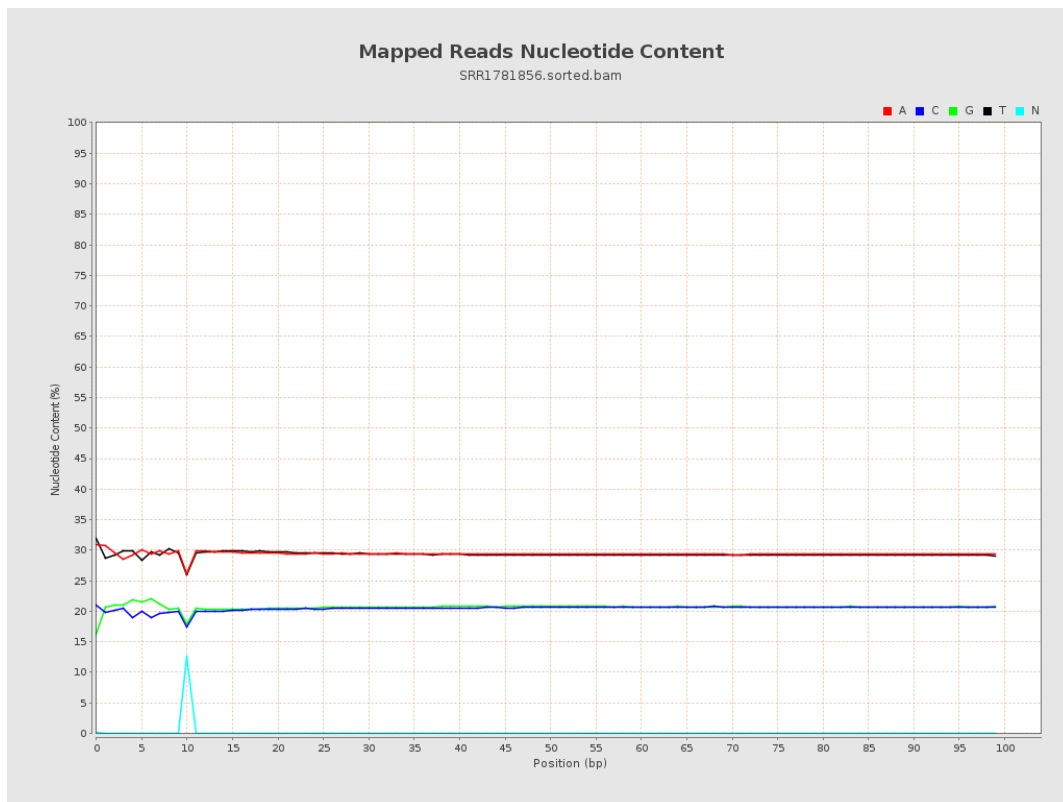
6. Results : Genome Fraction Coverage



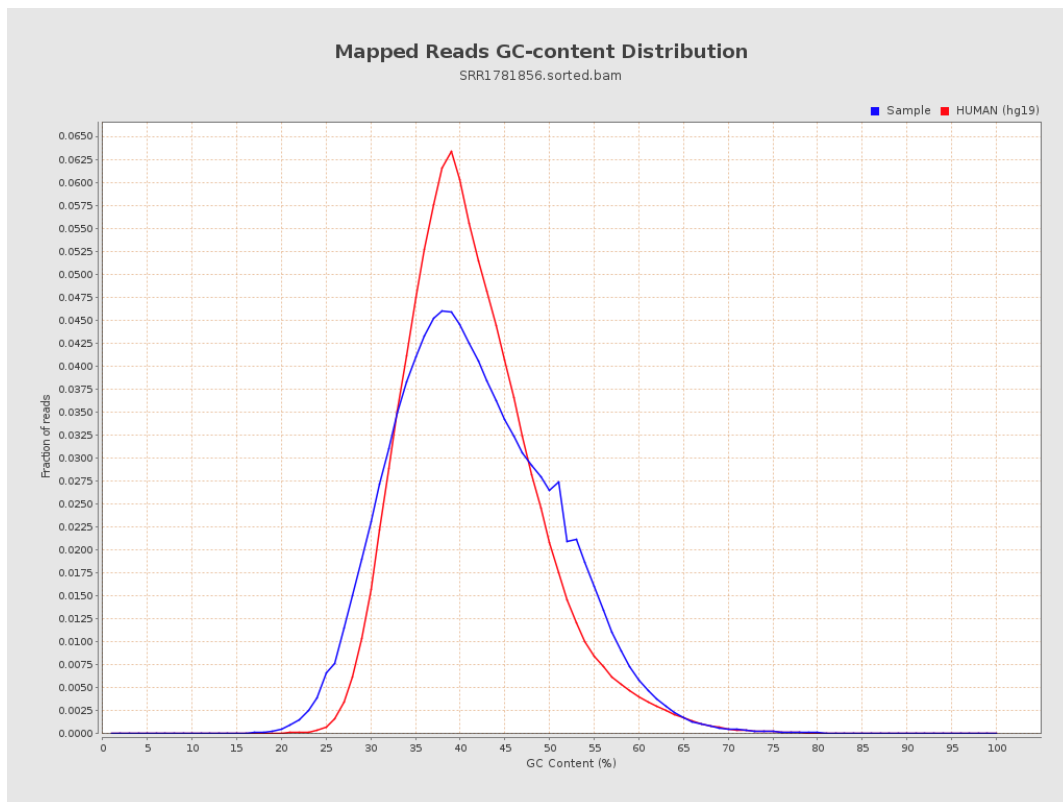
7. Results : Duplication Rate Histogram



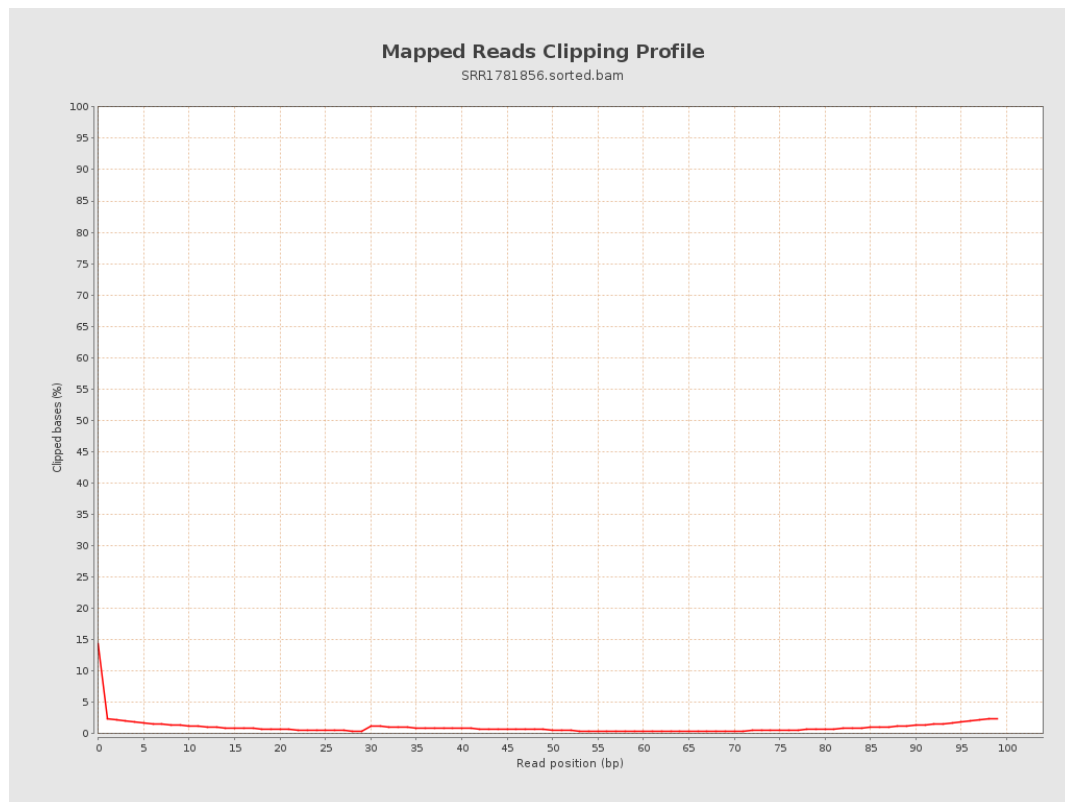
8. Results : Mapped Reads Nucleotide Content



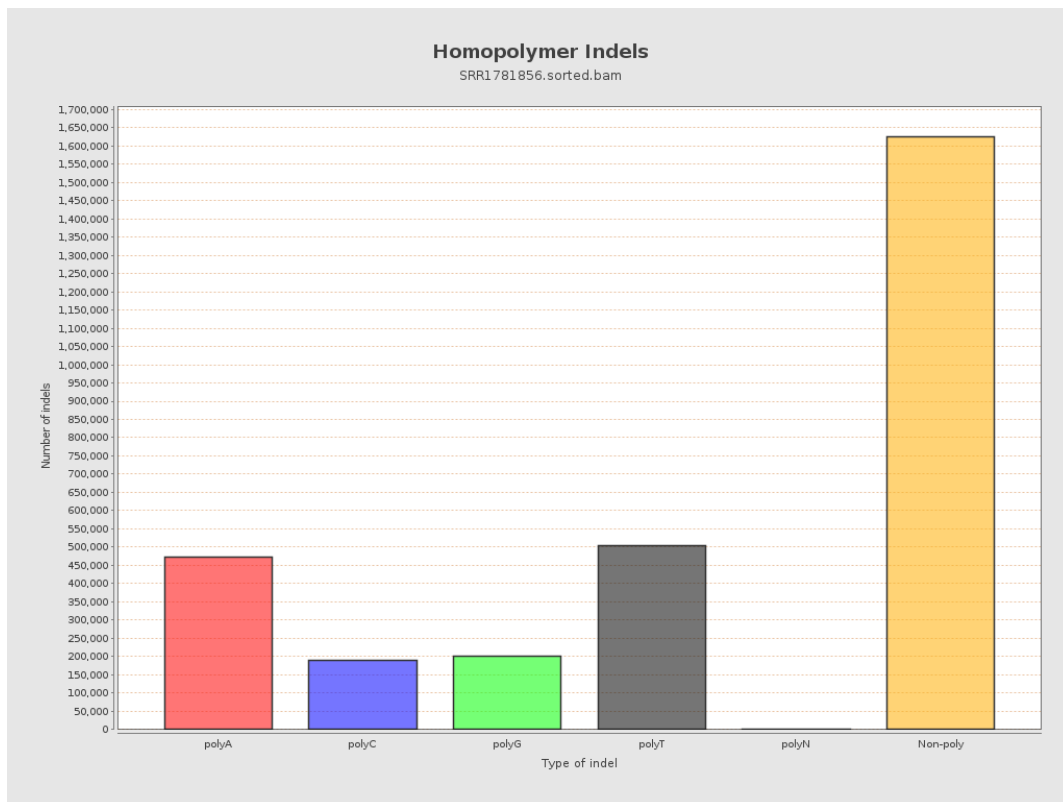
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



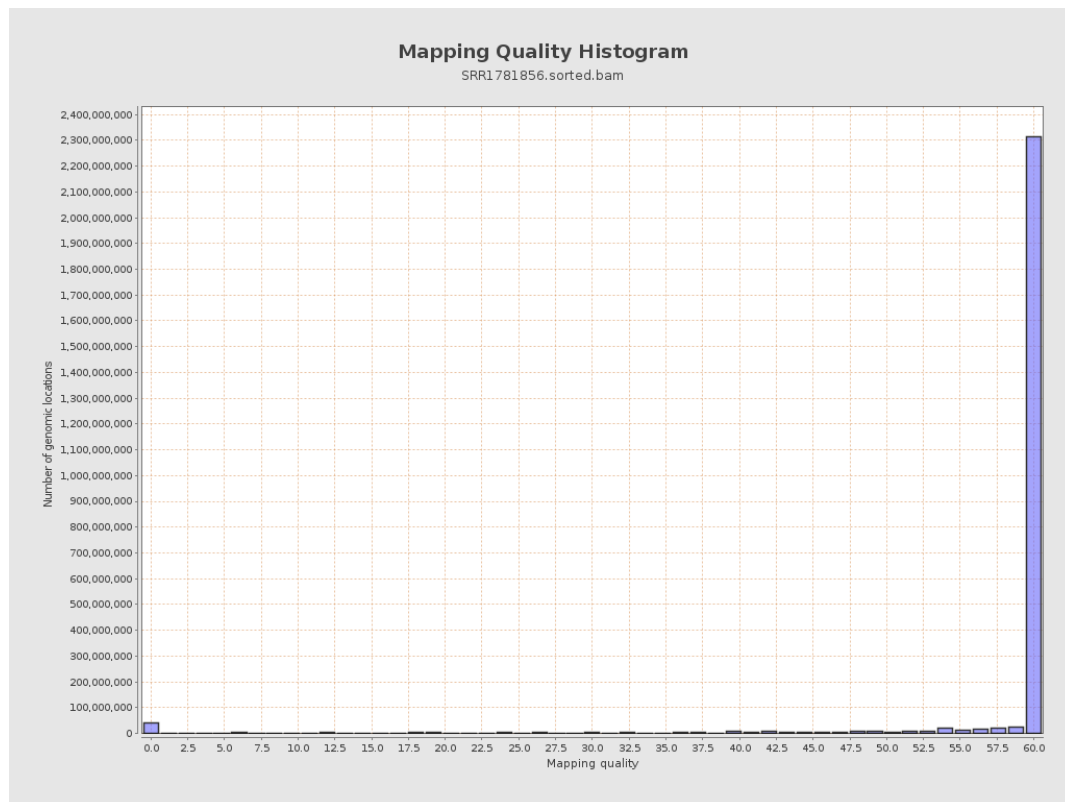
11. Results : Homopolymer Indels



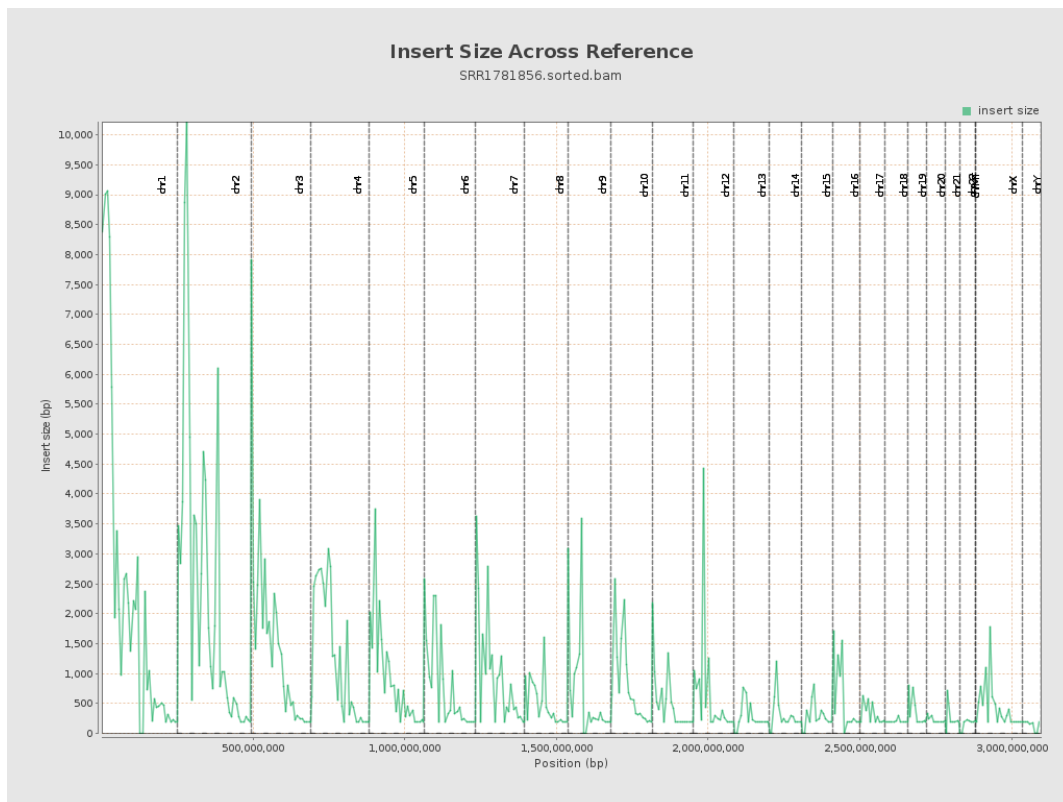
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

