

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 09:30:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781847.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_SRR1781847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781847_1.fastq.gz SRR1781847_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 09:30:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	147,502,694
Mapped reads	139,951,731 / 94.88%
Unmapped reads	7,550,963 / 5.12%
Mapped paired reads	139,951,731 / 94.88%
Mapped reads, first in pair	71,062,657 / 48.18%
Mapped reads, second in pair	68,889,074 / 46.7%
Mapped reads, both in pair	136,722,218 / 92.69%
Mapped reads, singletons	3,229,513 / 2.19%
Secondary alignments	0
Supplementary alignments	462,565 / 0.31%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	8,906,933 / 6.04%
Duplication rate	6.04%
Clipped reads	7,948,594 / 5.39%

2.2. ACGT Content

Number/percentage of A's	4,127,317,273 / 29.81%
Number/percentage of C's	2,786,002,821 / 20.12%
Number/percentage of T's	4,107,633,313 / 29.66%
Number/percentage of G's	2,825,753,699 / 20.41%
Number/percentage of N's	585,760 / 0%

GC Percentage	40.53%
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2.3. Coverage

Mean	4.4741
Standard Deviation	7.1326

2.4. Mapping Quality

Mean Mapping Quality	53.89
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2.5. Insert size

Mean	50,045.31
Standard Deviation	2,173,582.67
P25/Median/P75	163 / 215 / 287

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	55,896,814
Insertions	1,448,812
Mapped reads with at least one insertion	1.02%
Deletions	1,450,570
Mapped reads with at least one deletion	1.02%
Homopolymer indels	47.7%

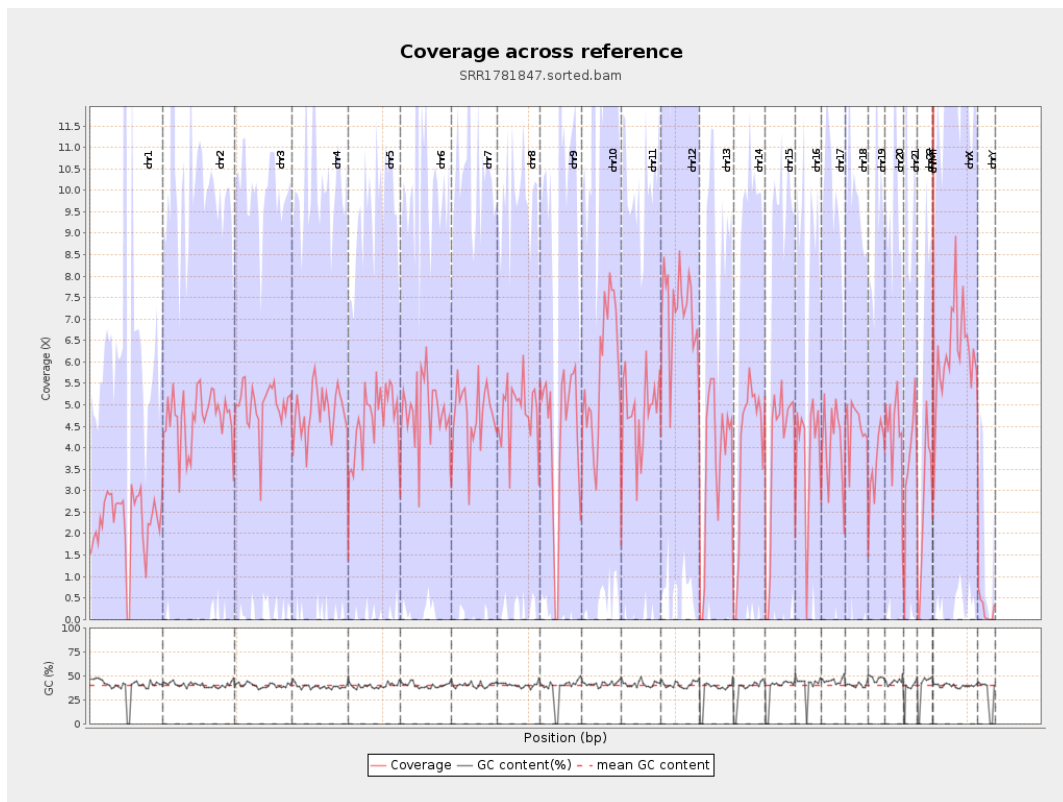
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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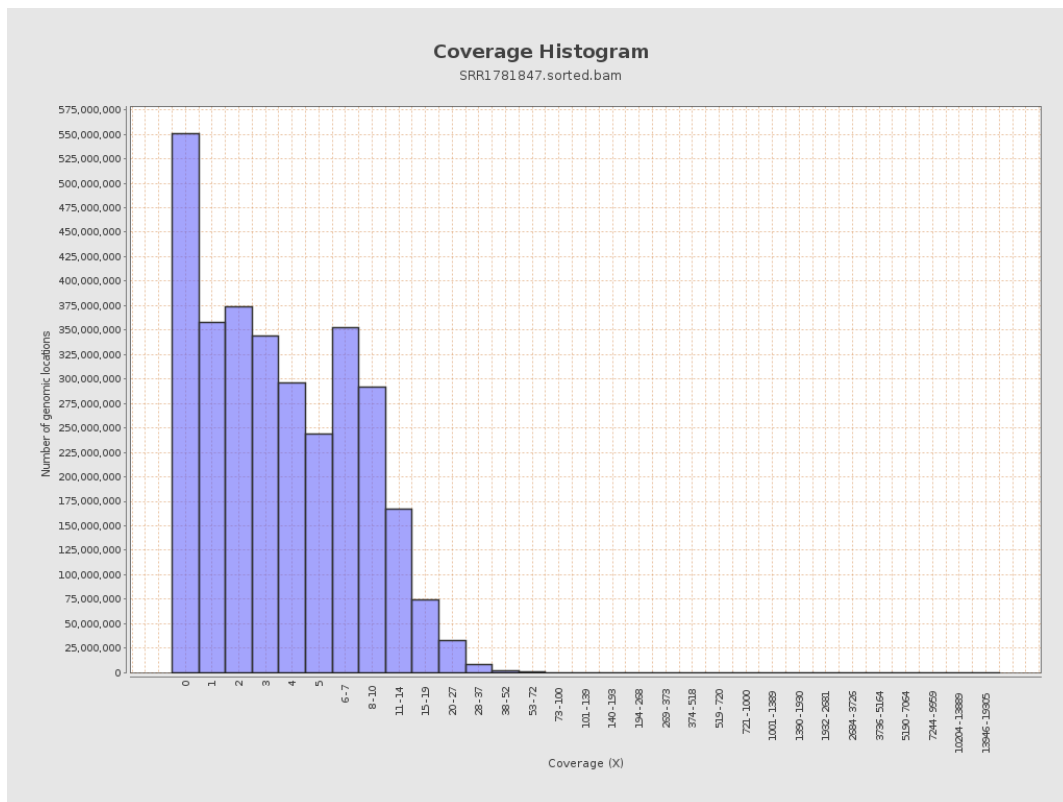
		bases	coverage	deviation
chr1	249250621	569559952	2.2851	6.2639
chr2	243199373	1139597850	4.6859	16.3463
chr3	198022430	987605028	4.9873	4.5531
chr4	191154276	927361622	4.8514	4.8896
chr5	180915260	836066208	4.6213	4.3775
chr6	171115067	834546762	4.8771	5.7004
chr7	159138663	757725018	4.7614	5.3117
chr8	146364022	710767138	4.8562	4.5919
chr9	141213431	610423031	4.3227	5.8952
chr10	135534747	789067966	5.8219	9.6291
chr11	135006516	648688099	4.8049	4.8888
chr12	133851895	967946603	7.2315	7.1123
chr13	115169878	420853890	3.6542	4.1919
chr14	107349540	432845314	4.0321	4.5685
chr15	102531392	398094755	3.8827	4.5562
chr16	90354753	345518266	3.824	4.5306
chr17	81195210	336517184	4.1445	5.5137
chr18	78077248	352721594	4.5176	5.645
chr19	59128983	215725154	3.6484	5.5683
chr20	63025520	276557372	4.388	5.1835
chr21	48129895	177004450	3.6776	6.4497
chr22	51304566	140319614	2.735	4.0739
chrMT	16571	1462510	88.2572	23.8199
chrX	155270560	960226903	6.1842	5.8783

chrY	59373566	13319072	0.2243	2.3821
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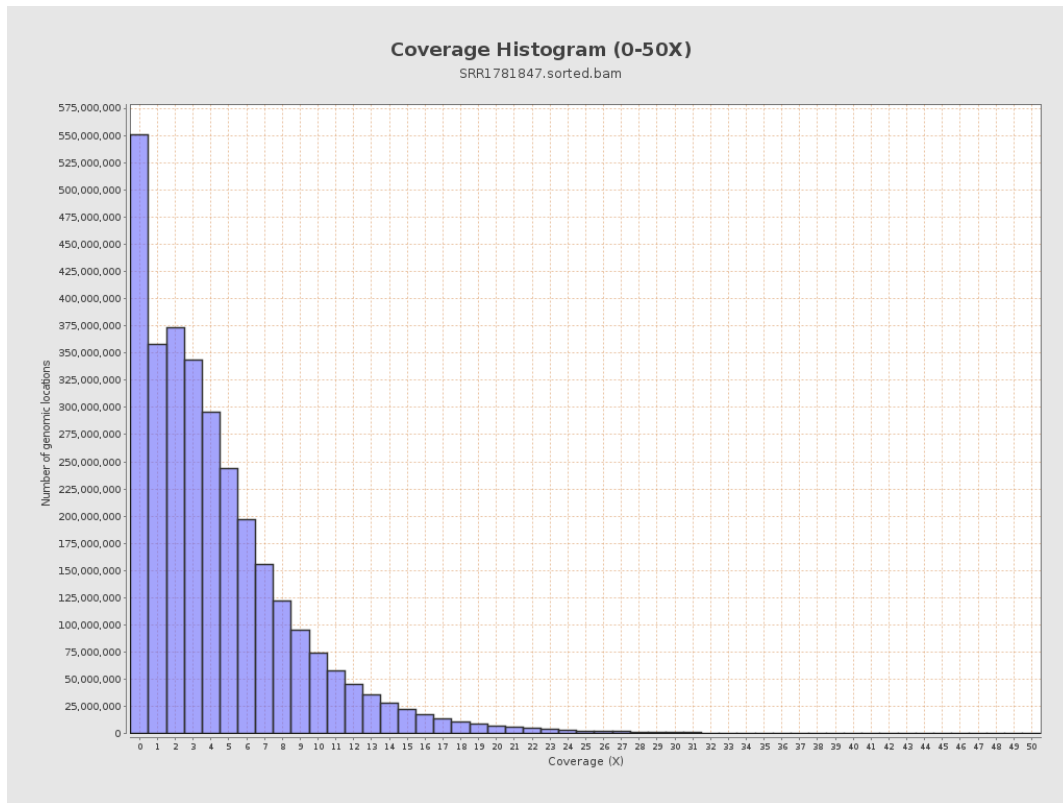
3. Results : Coverage across reference



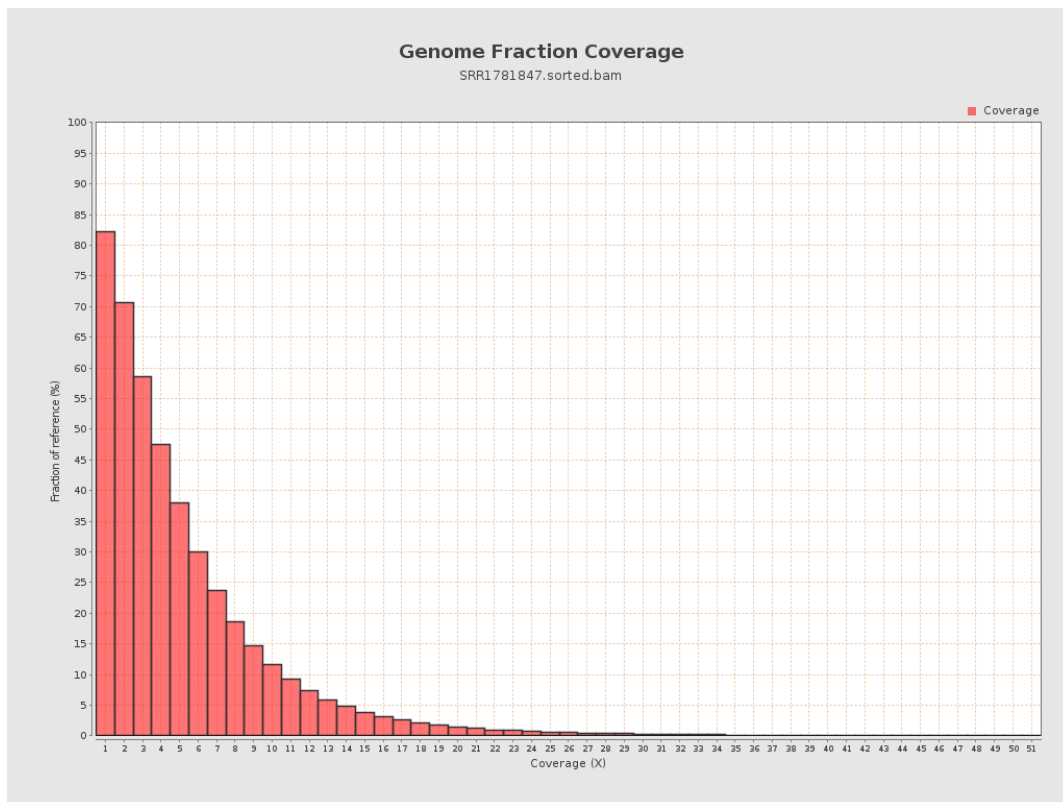
4. Results : Coverage Histogram



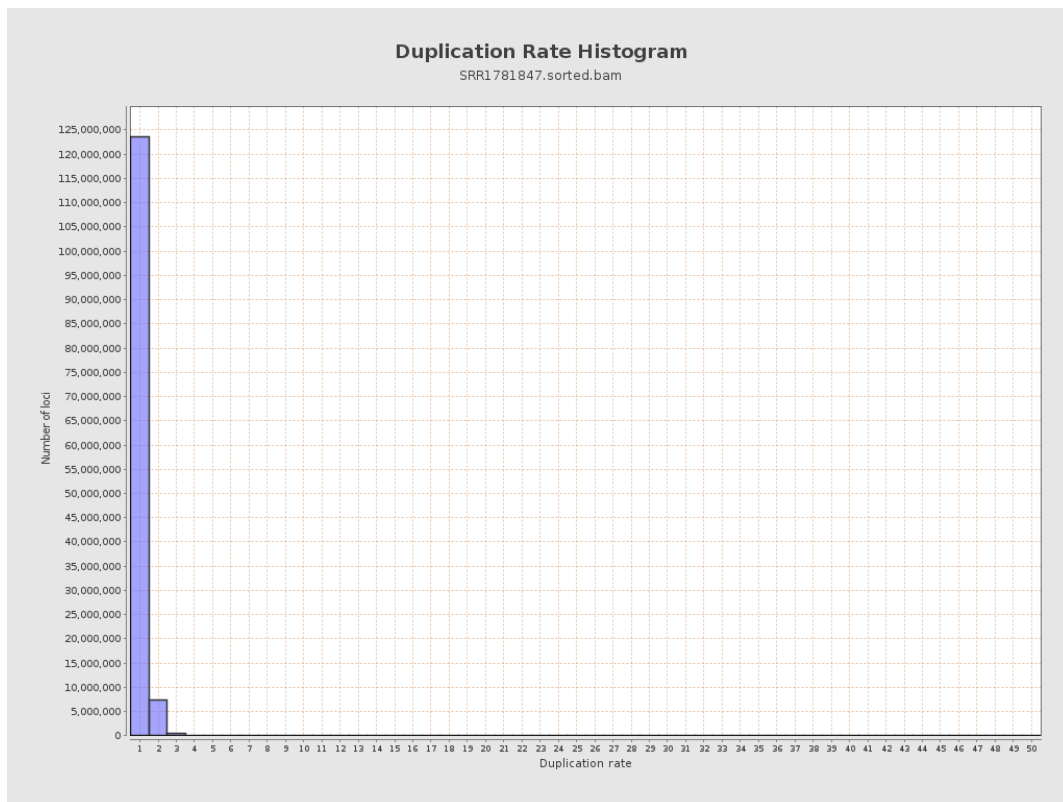
5. Results : Coverage Histogram (0-50X)



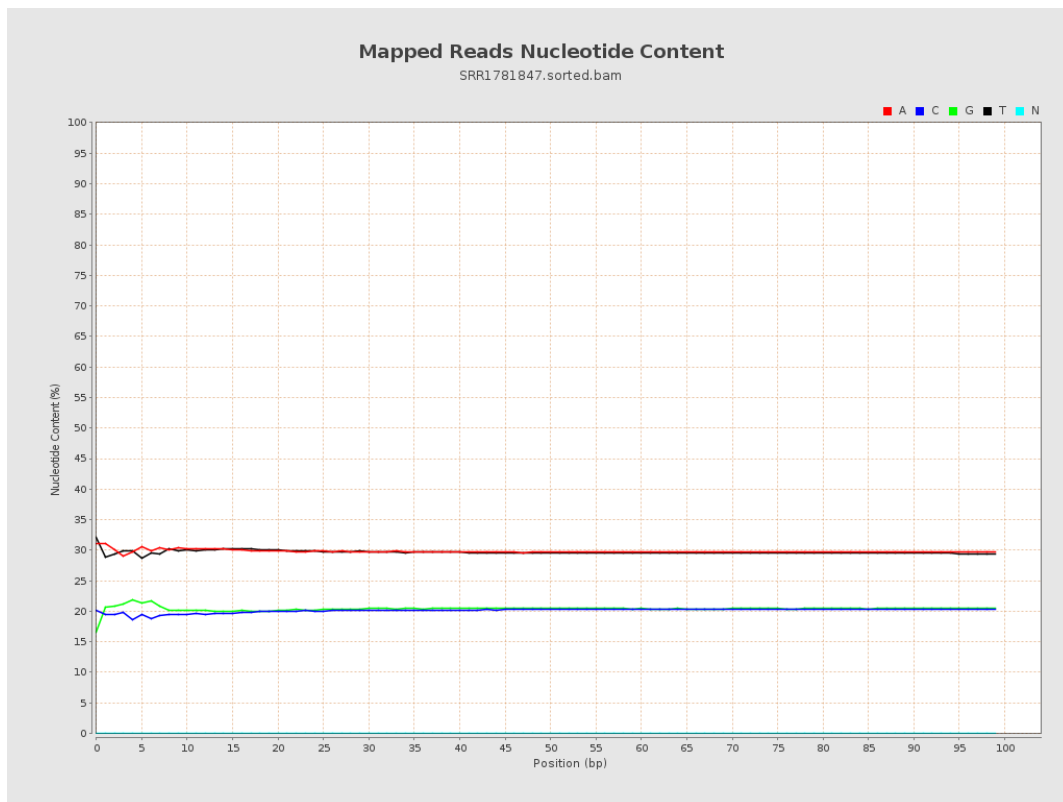
6. Results : Genome Fraction Coverage



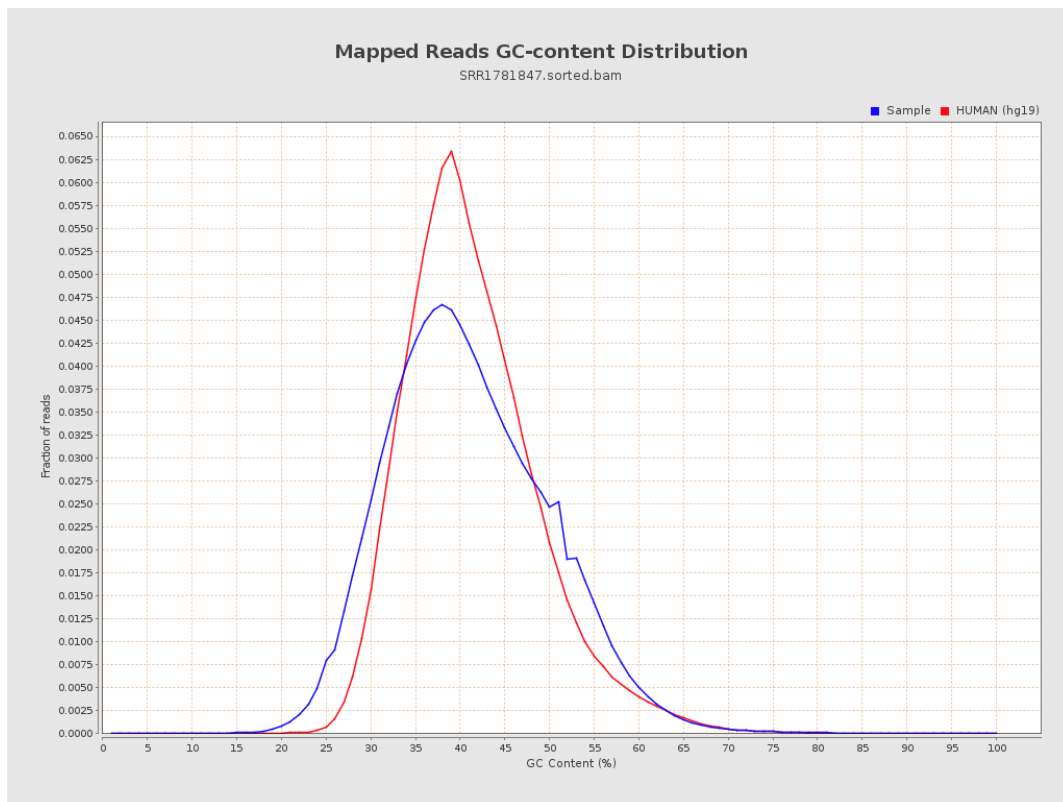
7. Results : Duplication Rate Histogram



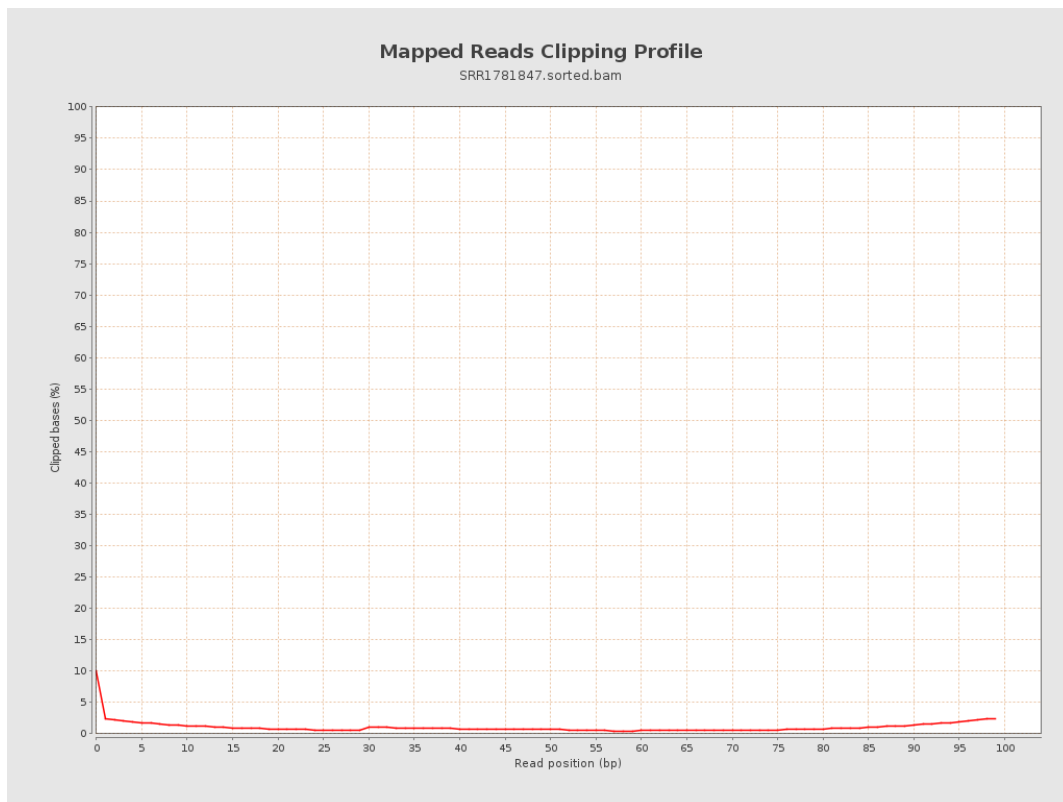
8. Results : Mapped Reads Nucleotide Content



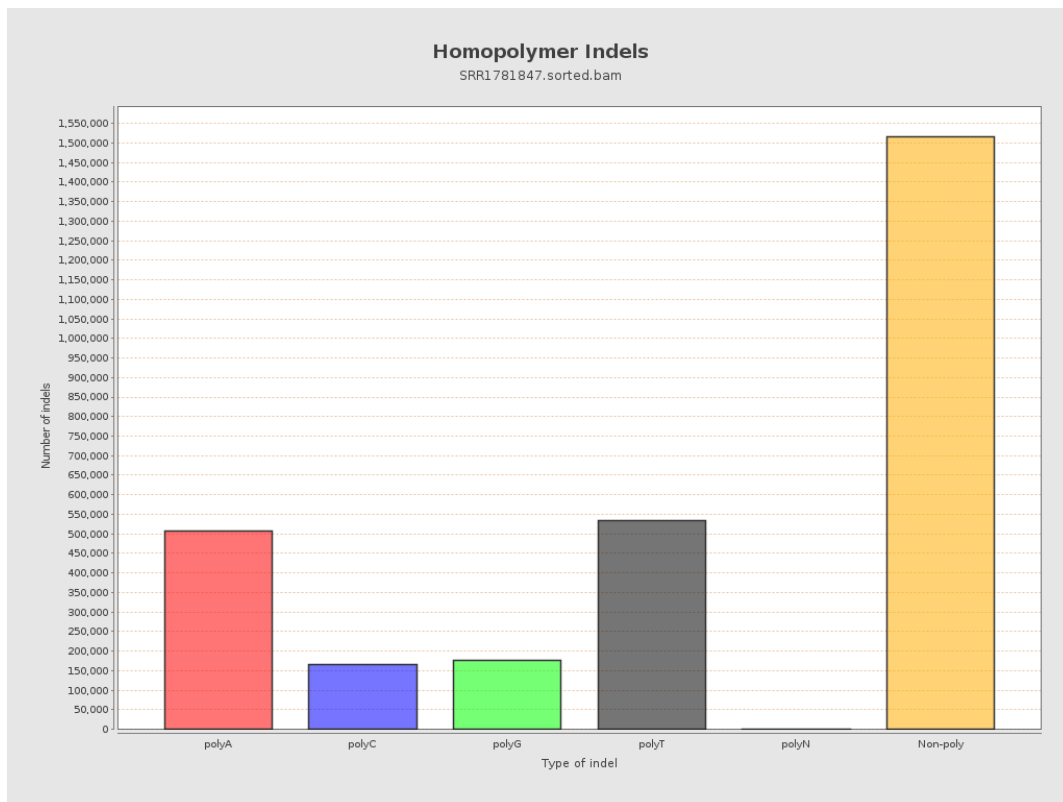
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



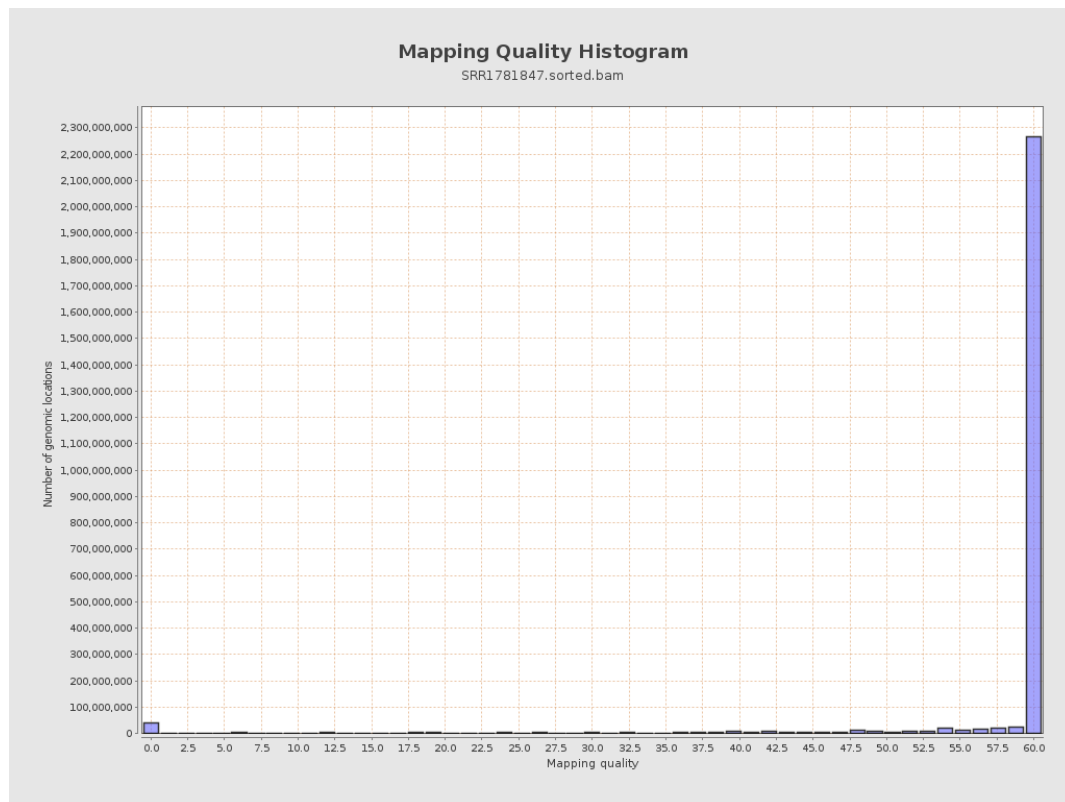
11. Results : Homopolymer Indels



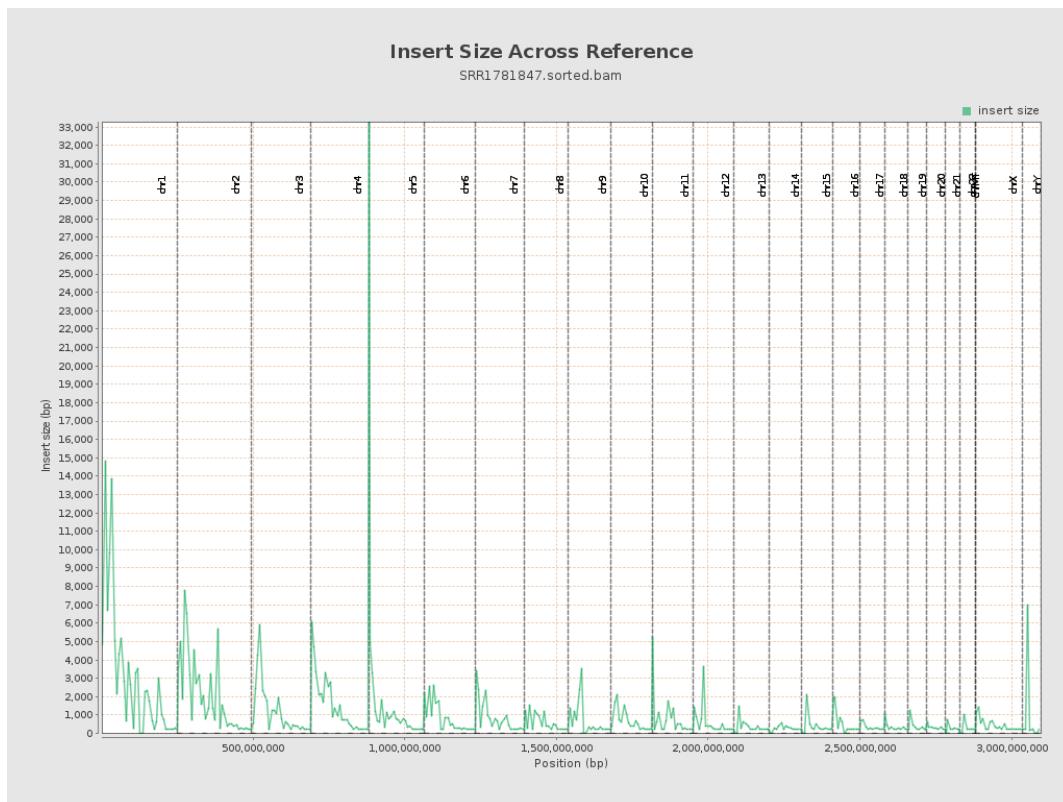
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

