

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 23:43:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781813.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_SRR1781813 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781813_1.fastq.gz SRR1781813_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 23:43:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781813.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	300,643,564
Mapped reads	287,133,113 / 95.51%
Unmapped reads	13,510,451 / 4.49%
Mapped paired reads	287,133,113 / 95.51%
Mapped reads, first in pair	147,321,228 / 49%
Mapped reads, second in pair	139,811,885 / 46.5%
Mapped reads, both in pair	278,181,586 / 92.53%
Mapped reads, singletons	8,951,527 / 2.98%
Secondary alignments	0
Supplementary alignments	1,097,182 / 0.36%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	26,592,698 / 8.85%
Duplication rate	8.87%
Clipped reads	24,354,838 / 8.1%

2.2. ACGT Content

Number/percentage of A's	8,123,548,045 / 29.23%
Number/percentage of C's	5,707,939,016 / 20.54%
Number/percentage of T's	8,080,527,029 / 29.08%
Number/percentage of G's	5,795,411,892 / 20.85%
Number/percentage of N's	84,399,187 / 0.3%

GC Percentage	41.39%
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2.3. Coverage

Mean	8.9794
Standard Deviation	10.8317

2.4. Mapping Quality

Mean Mapping Quality	53.73
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2.5. Insert size

Mean	45,782.43
Standard Deviation	2,075,302.94
P25/Median/P75	173 / 211 / 255

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	162,259,499
Insertions	2,510,019
Mapped reads with at least one insertion	0.86%
Deletions	2,475,254
Mapped reads with at least one deletion	0.85%
Homopolymer indels	45.66%

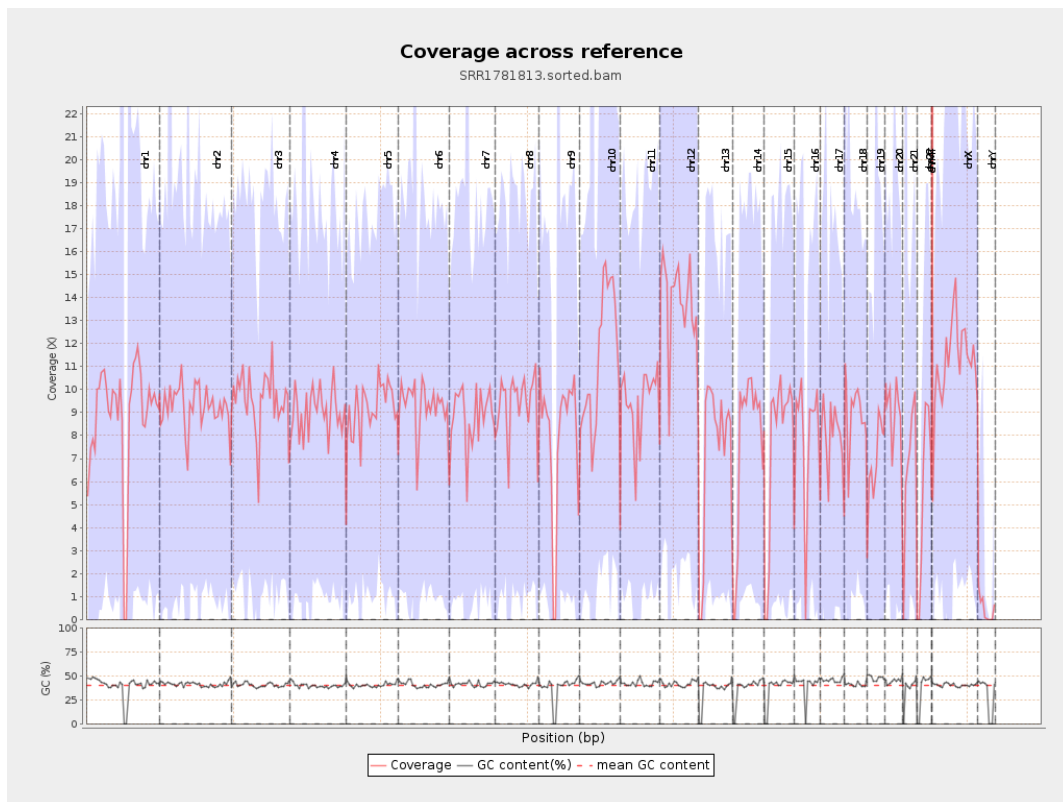
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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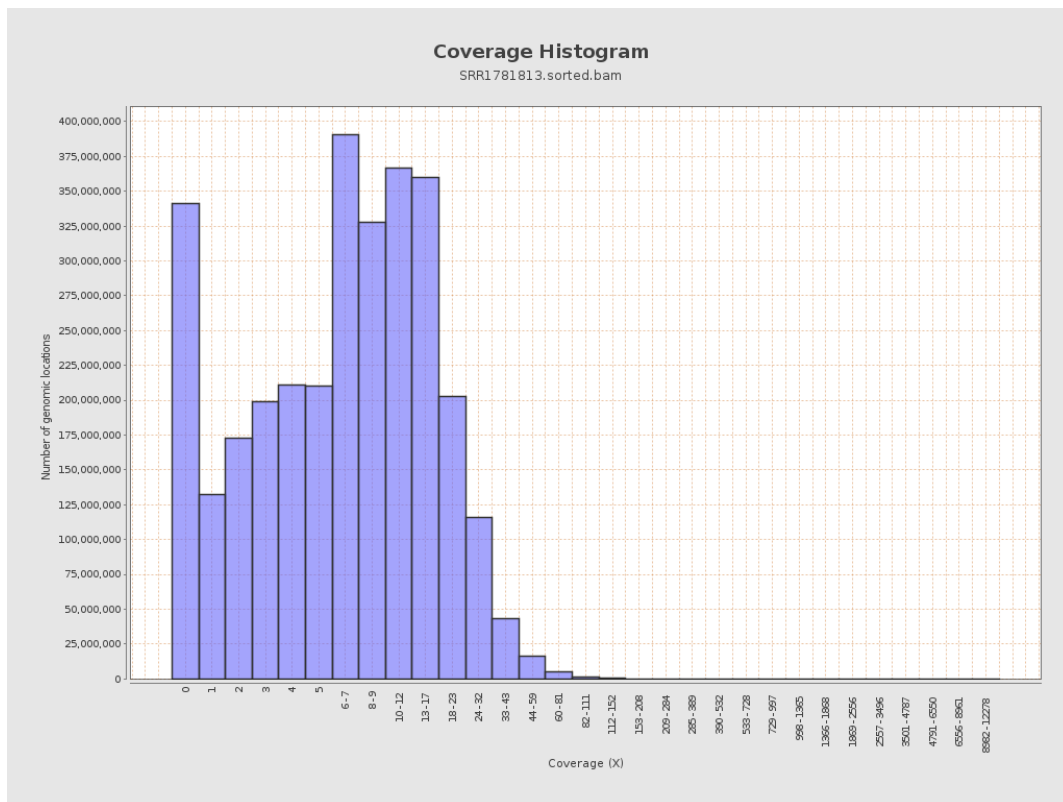
		bases	coverage	deviation
chr1	249250621	2210616626	8.8691	15.9909
chr2	243199373	2255349327	9.2737	10.7686
chr3	198022430	1897755099	9.5835	8.2103
chr4	191154276	1734884594	9.0758	9.8301
chr5	180915260	1663094068	9.1927	7.8297
chr6	171115067	1602497516	9.365	9.3819
chr7	159138663	1403671197	8.8204	9.8581
chr8	146364022	1381040145	9.4357	8.4375
chr9	141213431	1105514098	7.8287	10.8001
chr10	135534747	1552349858	11.4535	16.9664
chr11	135006516	1269376813	9.4023	8.7763
chr12	133851895	1852649055	13.841	11.8843
chr13	115169878	849079162	7.3724	7.6678
chr14	107349540	829189321	7.7242	8.1804
chr15	102531392	776191025	7.5703	8.3008
chr16	90354753	695075080	7.6927	8.6447
chr17	81195210	643945622	7.9308	9.1403
chr18	78077248	705720446	9.0387	12.1736
chr19	59128983	416381461	7.0419	10.9783
chr20	63025520	559214224	8.8728	9.7003
chr21	48129895	330880439	6.8747	14.651
chr22	51304566	285414375	5.5631	7.9308
chrMT	16571	3617105	218.2792	53.666
chrX	155270560	1747296560	11.2532	10.1721

chrY	59373566	26642491	0.4487	5.1918
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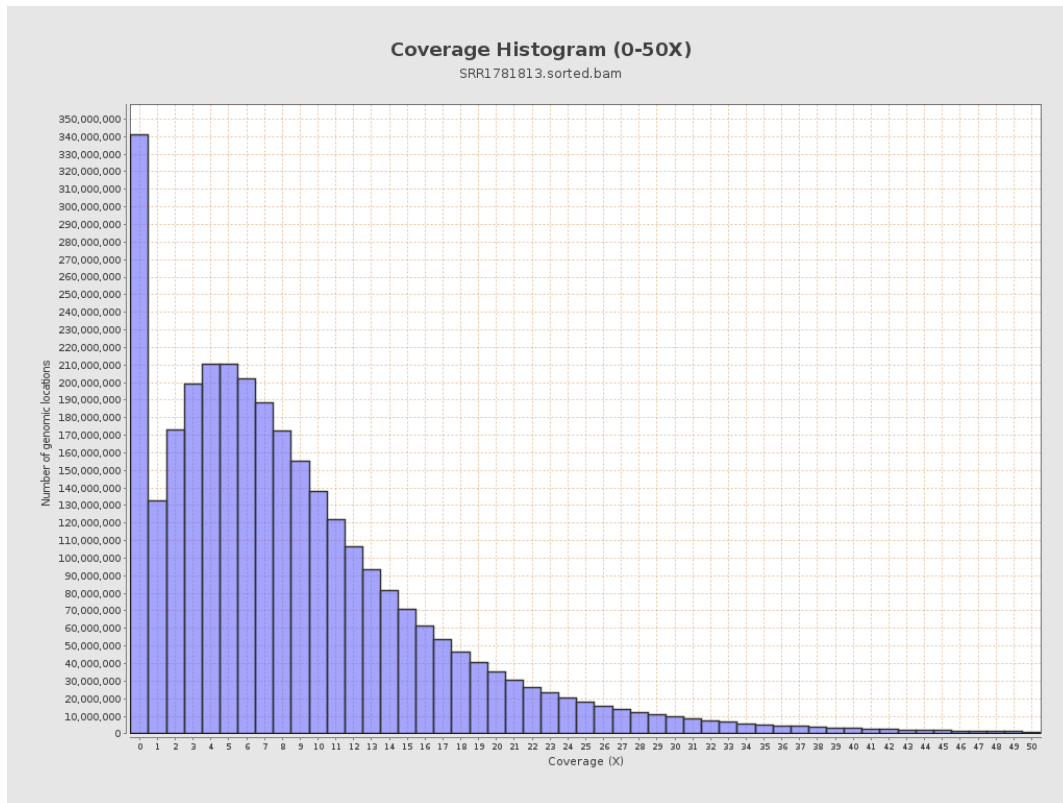
3. Results : Coverage across reference



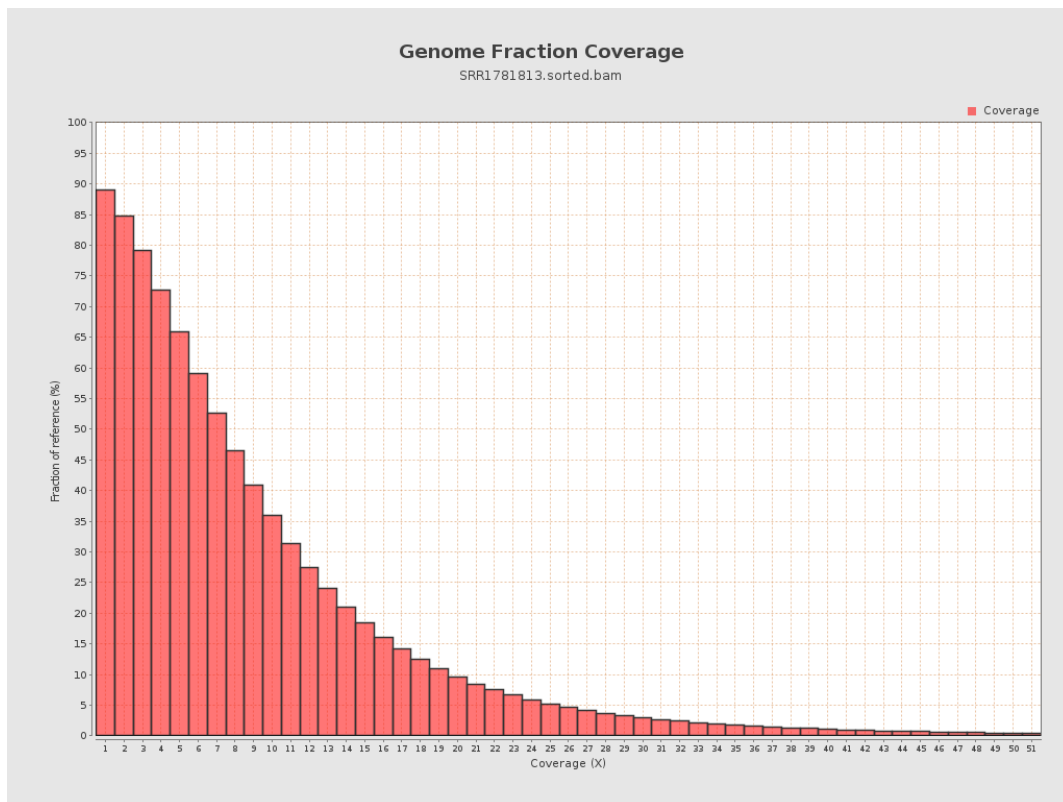
4. Results : Coverage Histogram



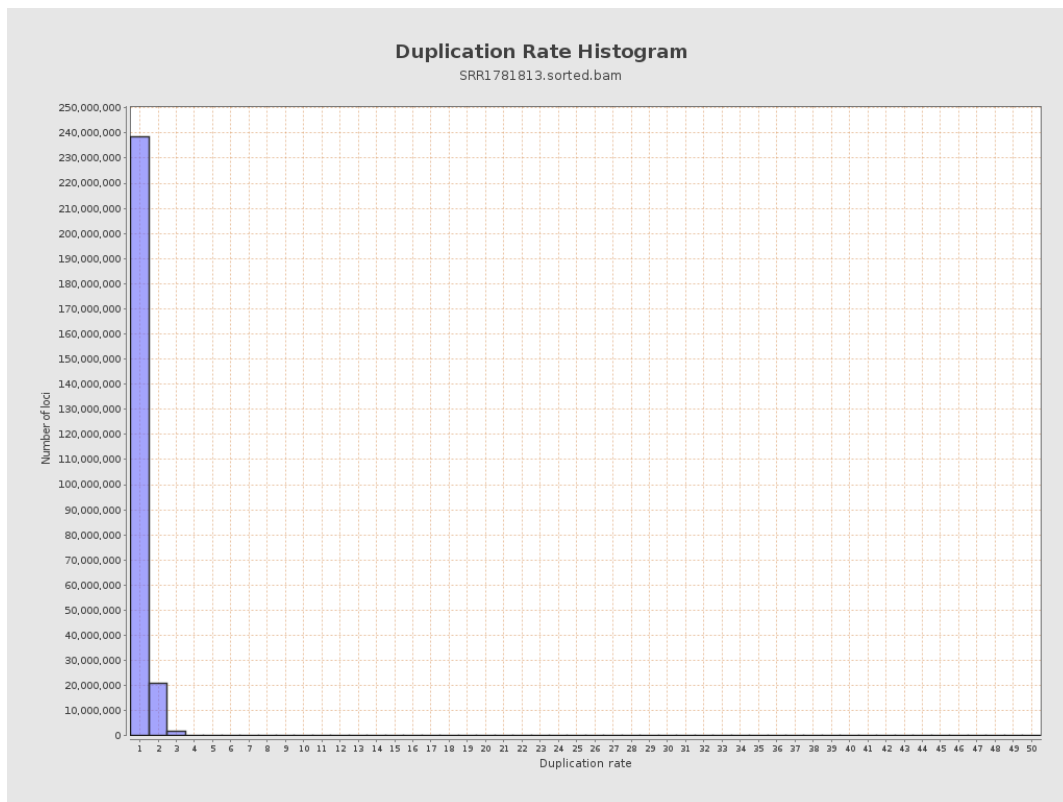
5. Results : Coverage Histogram (0-50X)



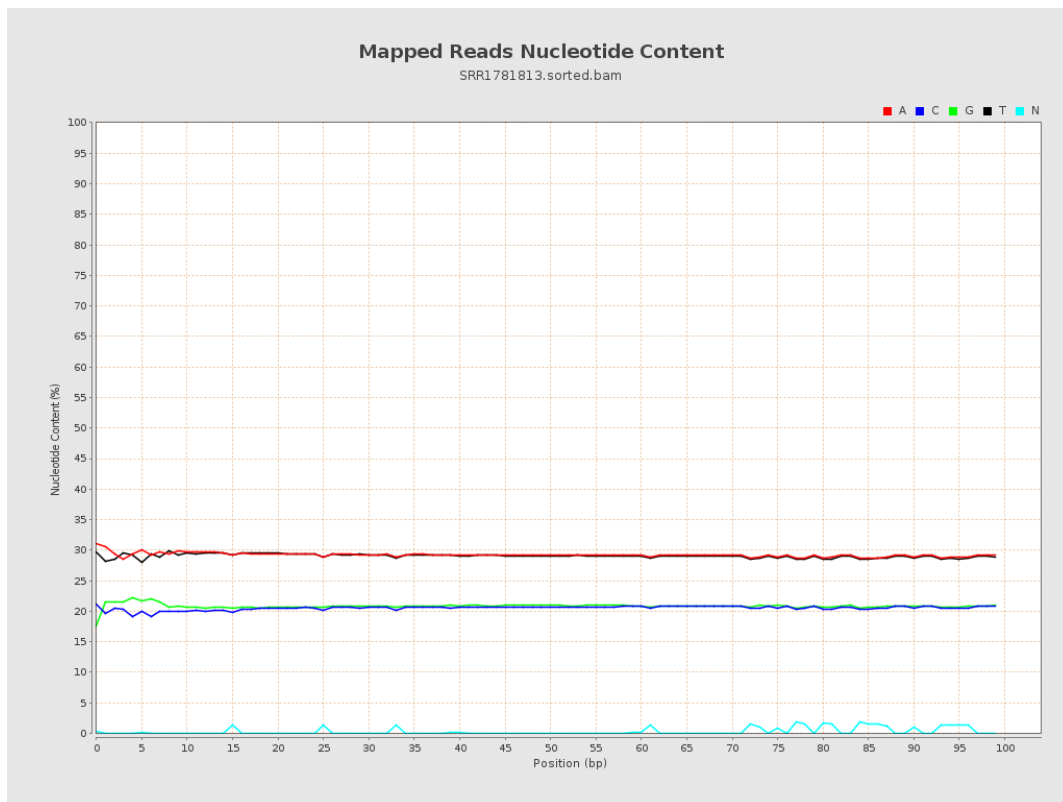
6. Results : Genome Fraction Coverage



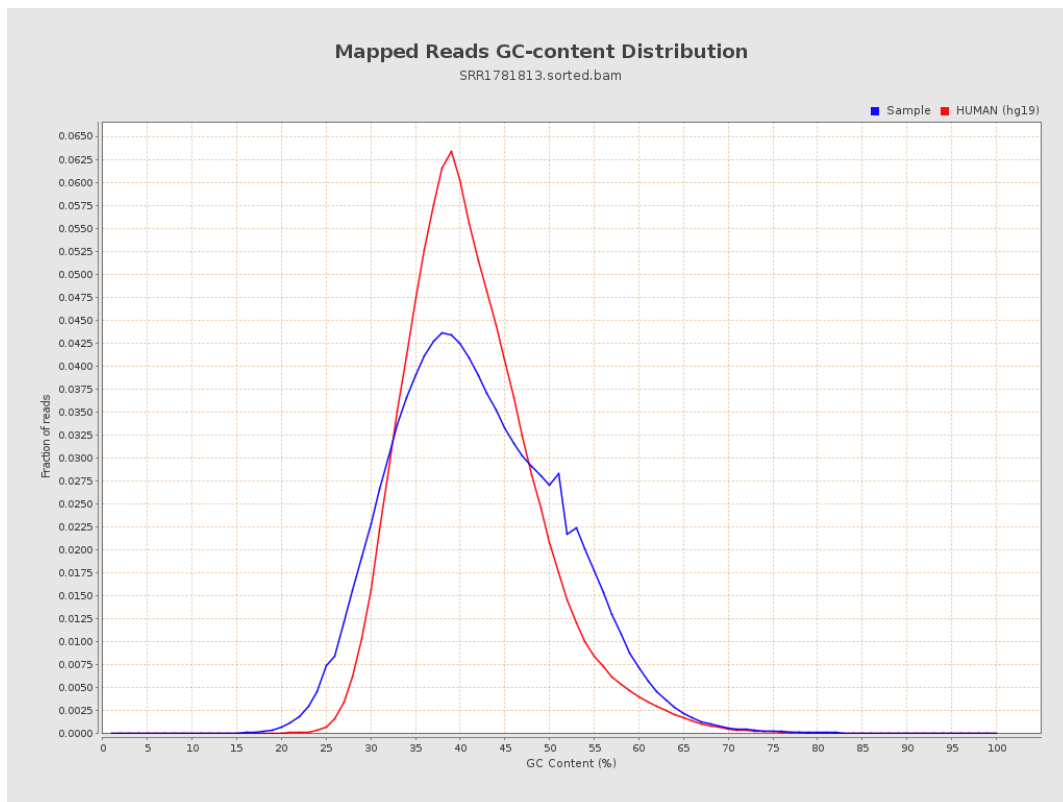
7. Results : Duplication Rate Histogram



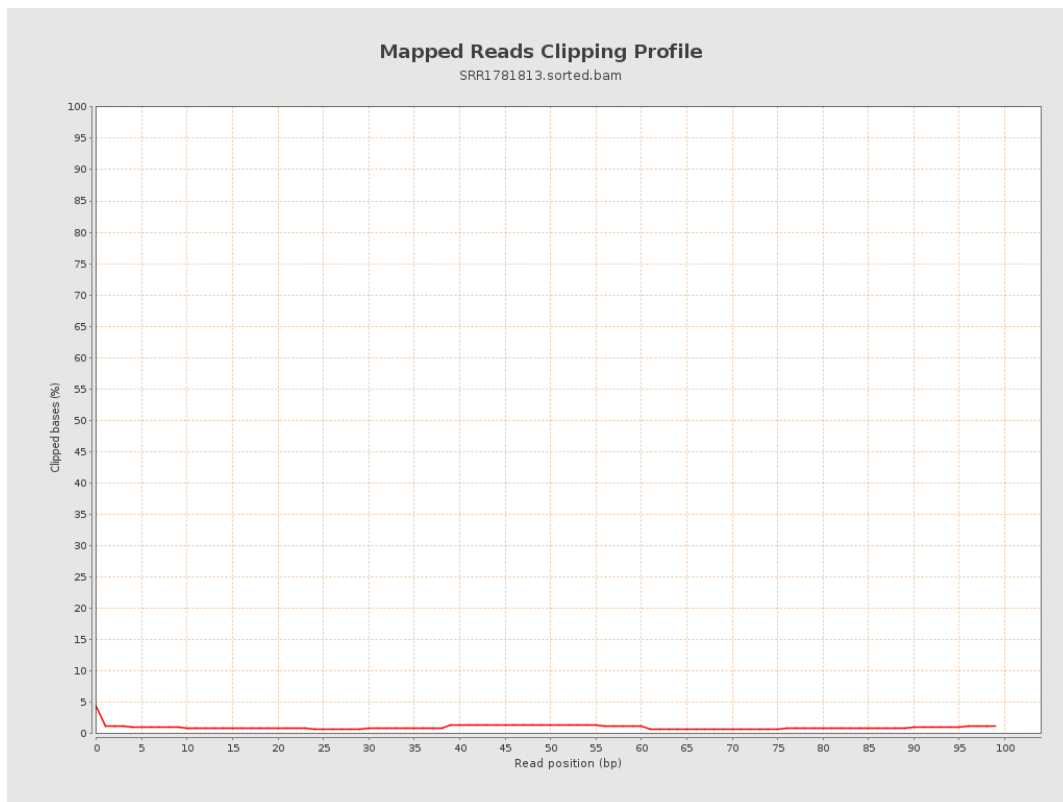
8. Results : Mapped Reads Nucleotide Content



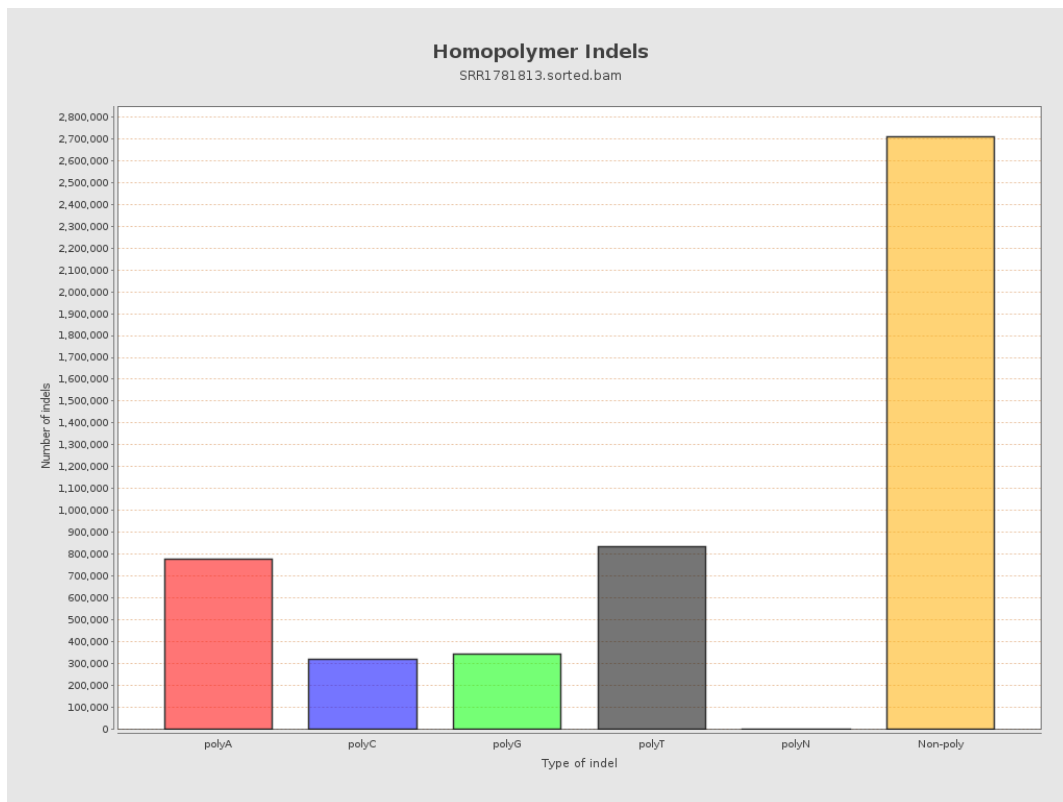
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



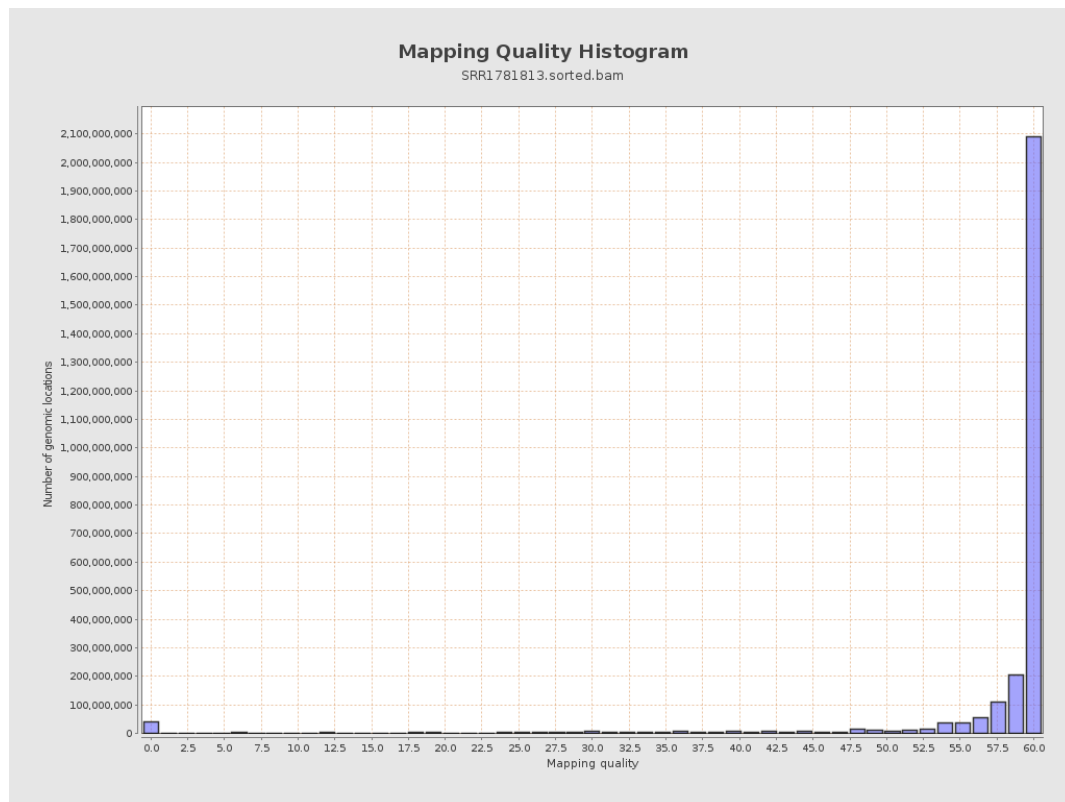
11. Results : Homopolymer Indels



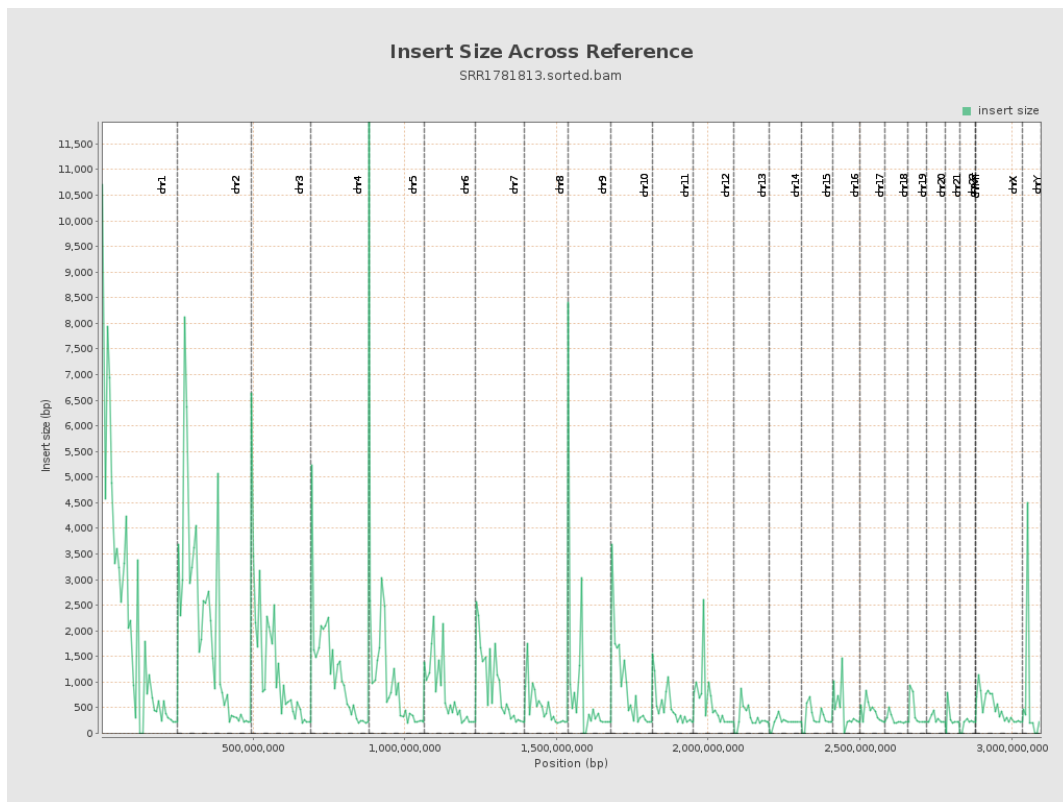
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

