

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 01:37:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006404.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_SRR1006404 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006404_1.fastq.gz SRR1006404_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 01:37:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006404.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,629,344
Mapped reads	8,594,001 / 89.25%
Unmapped reads	1,035,343 / 10.75%
Mapped paired reads	8,594,001 / 89.25%
Mapped reads, first in pair	4,322,727 / 44.89%
Mapped reads, second in pair	4,271,274 / 44.36%
Mapped reads, both in pair	7,953,260 / 82.59%
Mapped reads, singletons	640,741 / 6.65%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	319,421 / 3.32%
Duplication rate	3.11%
Clipped reads	438,264 / 4.55%

2.2. ACGT Content

Number/percentage of A's	92,255,975 / 27.72%
Number/percentage of C's	72,135,333 / 21.67%
Number/percentage of T's	94,062,252 / 28.26%
Number/percentage of G's	74,397,976 / 22.35%
Number/percentage of N's	14,798 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.1075
Standard Deviation	0.538

2.4. Mapping Quality

Mean Mapping Quality	48.27
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2.5. Insert size

Mean	63,835.36
Standard Deviation	2,385,905.79
P25/Median/P75	92 / 138 / 185

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	990,955
Insertions	9,385
Mapped reads with at least one insertion	0.11%
Deletions	31,767
Mapped reads with at least one deletion	0.37%
Homopolymer indels	44.98%

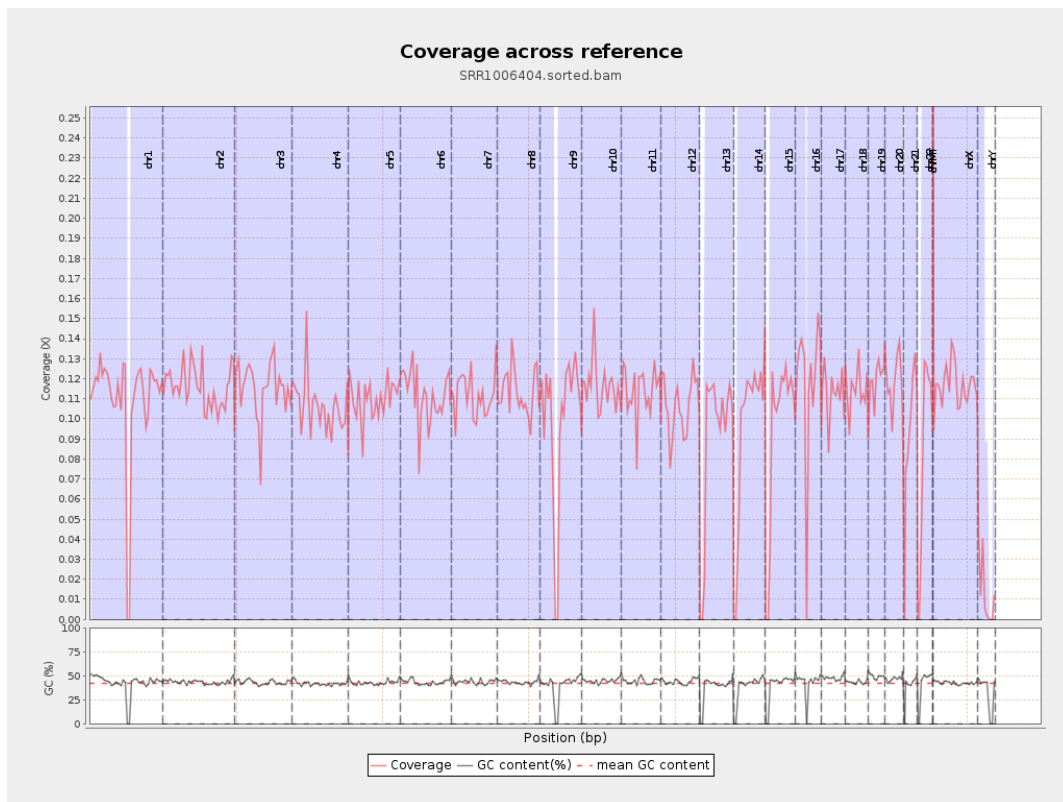
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

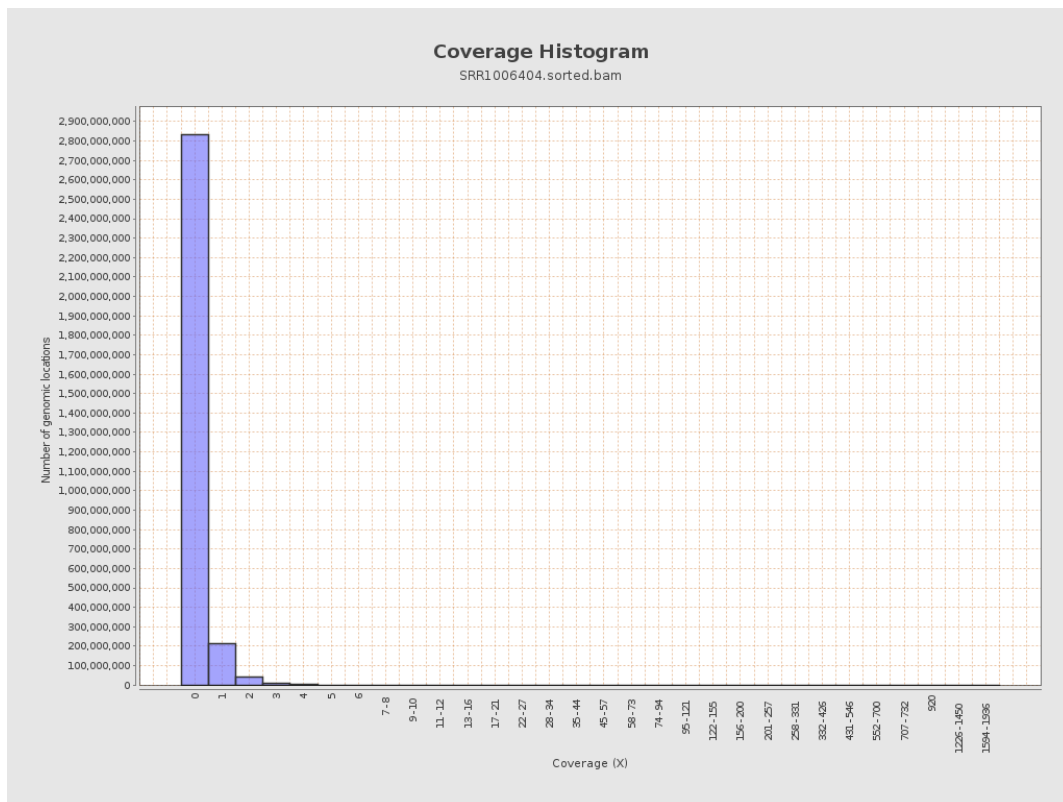
chr1	249250621	27268243	0.1094	0.7447
chr2	243199373	28265846	0.1162	0.5229
chr3	198022430	22801691	0.1151	0.4062
chr4	191154276	20433352	0.1069	0.4371
chr5	180915260	19954792	0.1103	0.3994
chr6	171115067	19027039	0.1112	0.4525
chr7	159138663	17822761	0.112	0.6172
chr8	146364022	16589197	0.1133	1.032
chr9	141213431	14041938	0.0994	0.4529
chr10	135534747	15766351	0.1163	0.5464
chr11	135006516	15371468	0.1139	0.5081
chr12	133851895	14388169	0.1075	0.3981
chr13	115169878	10422412	0.0905	0.3597
chr14	107349540	10277346	0.0957	0.4622
chr15	102531392	9566780	0.0933	0.3692
chr16	90354753	10539915	0.1167	0.4803
chr17	81195210	9224969	0.1136	0.4331
chr18	78077248	8907510	0.1141	0.7268
chr19	59128983	7052744	0.1193	0.5974
chr20	63025520	7449942	0.1182	0.4339
chr21	48129895	4516301	0.0938	0.4426
chr22	51304566	4320013	0.0842	0.3664
chrMT	16571	7243	0.4371	1.4479
chrX	155270560	18115027	0.1167	0.4558

chrY	59373566	777392	0.0131	0.2837
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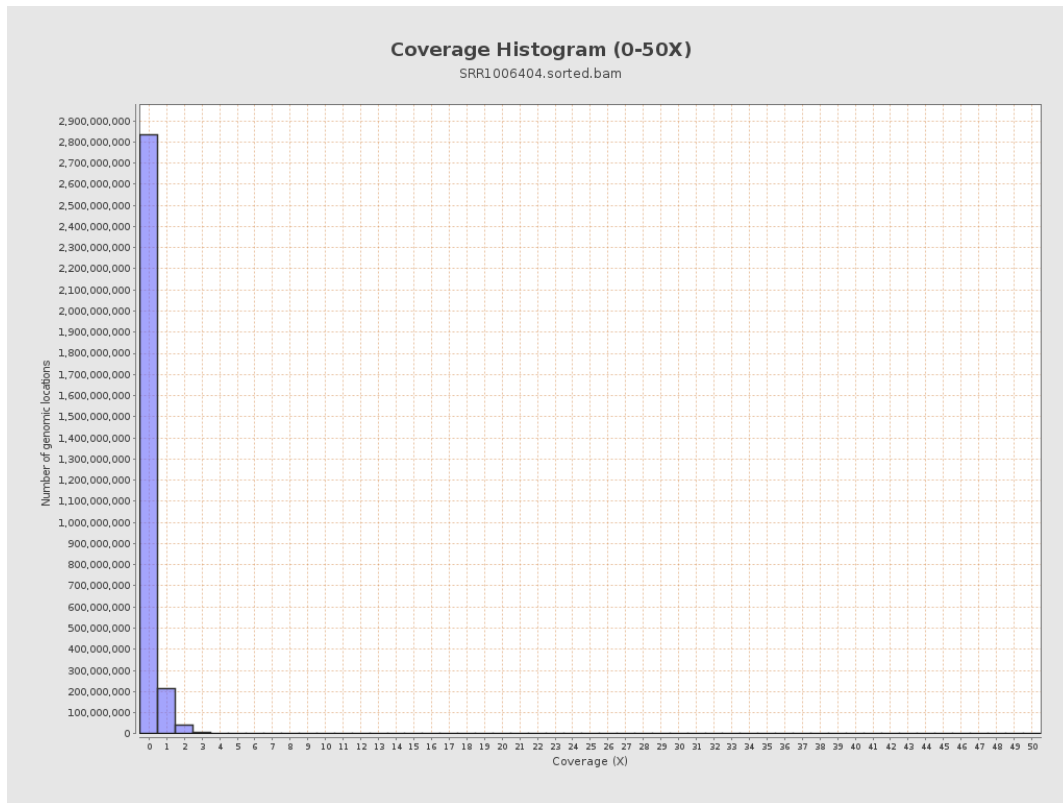
3. Results : Coverage across reference



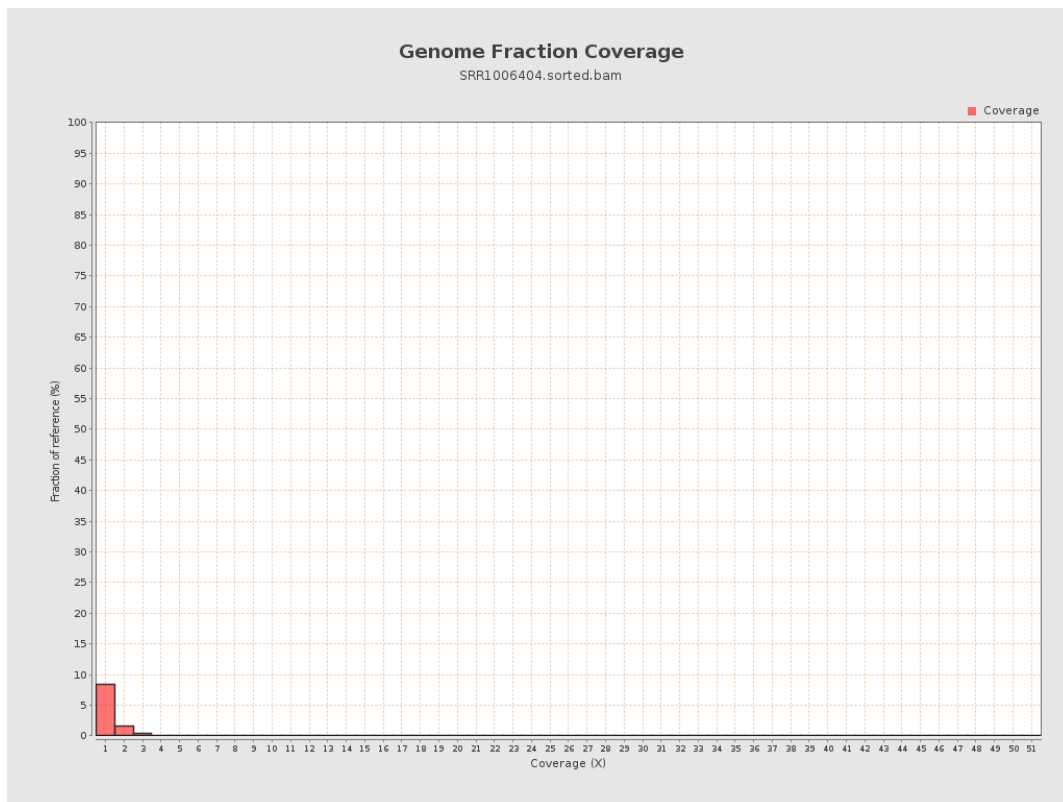
4. Results : Coverage Histogram



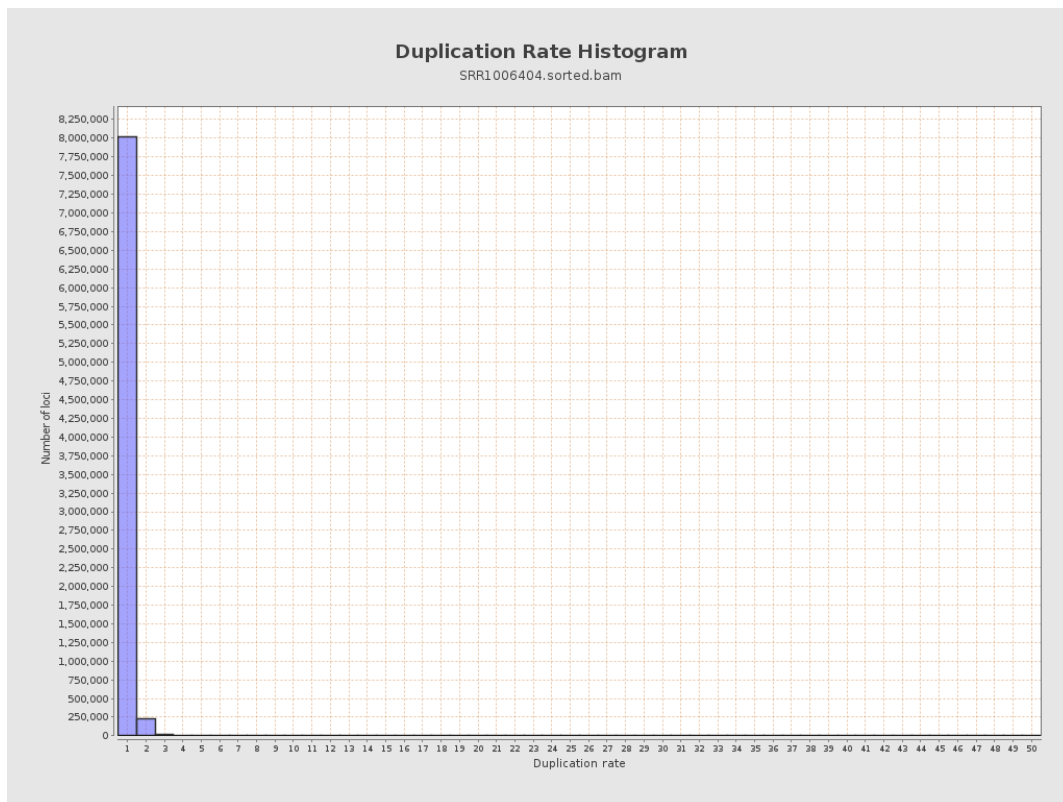
5. Results : Coverage Histogram (0-50X)



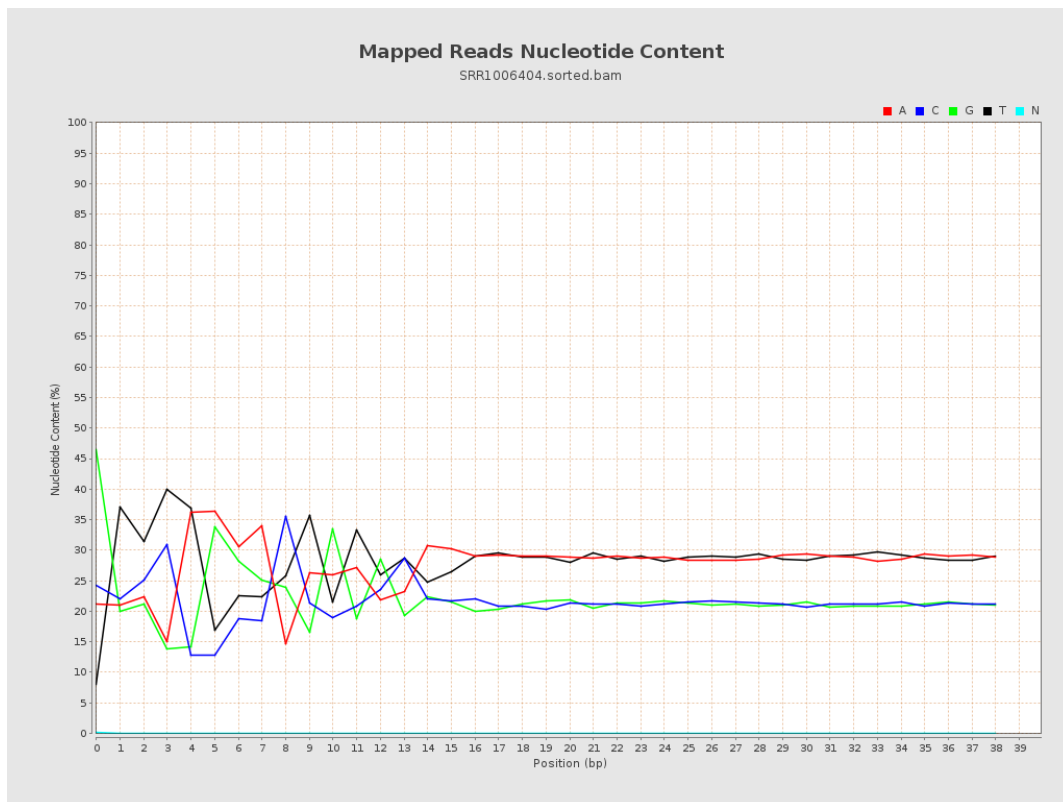
6. Results : Genome Fraction Coverage



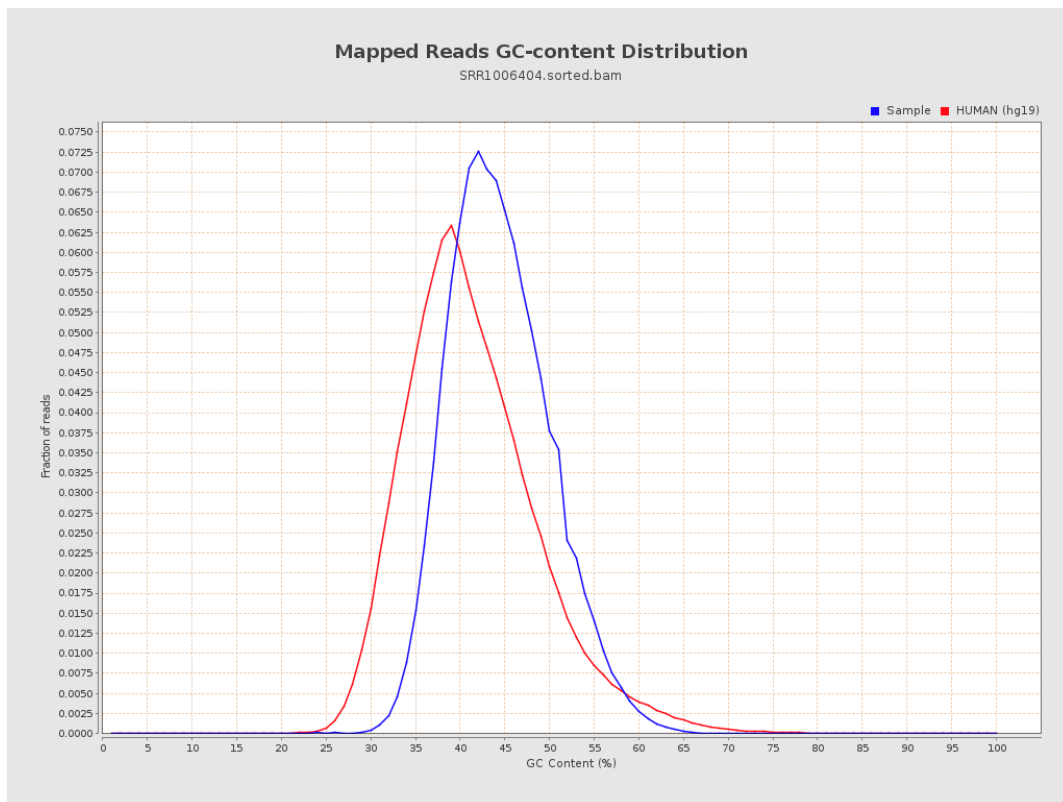
7. Results : Duplication Rate Histogram



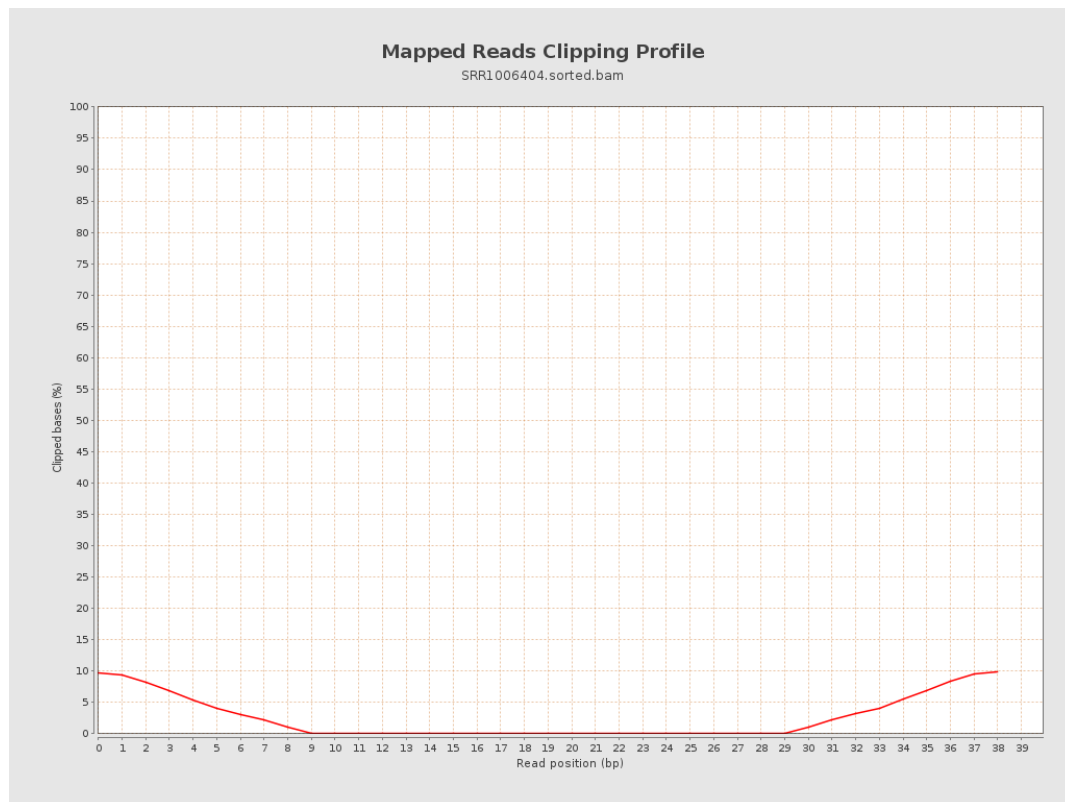
8. Results : Mapped Reads Nucleotide Content



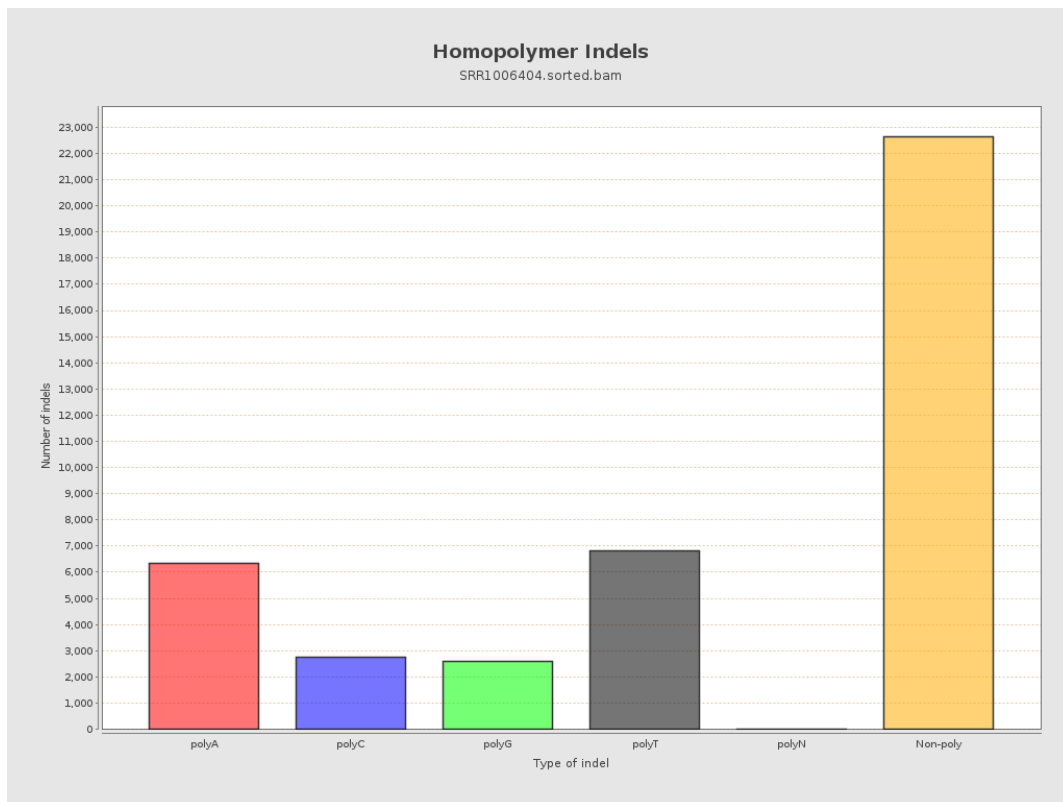
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



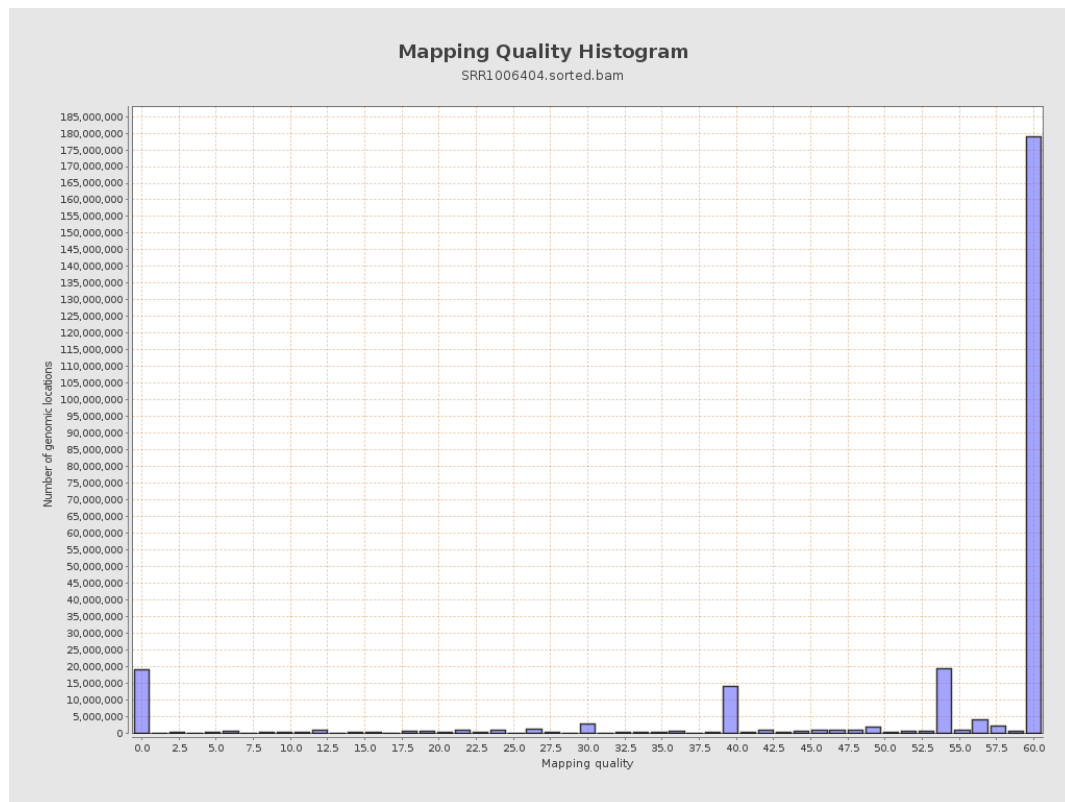
11. Results : Homopolymer Indels



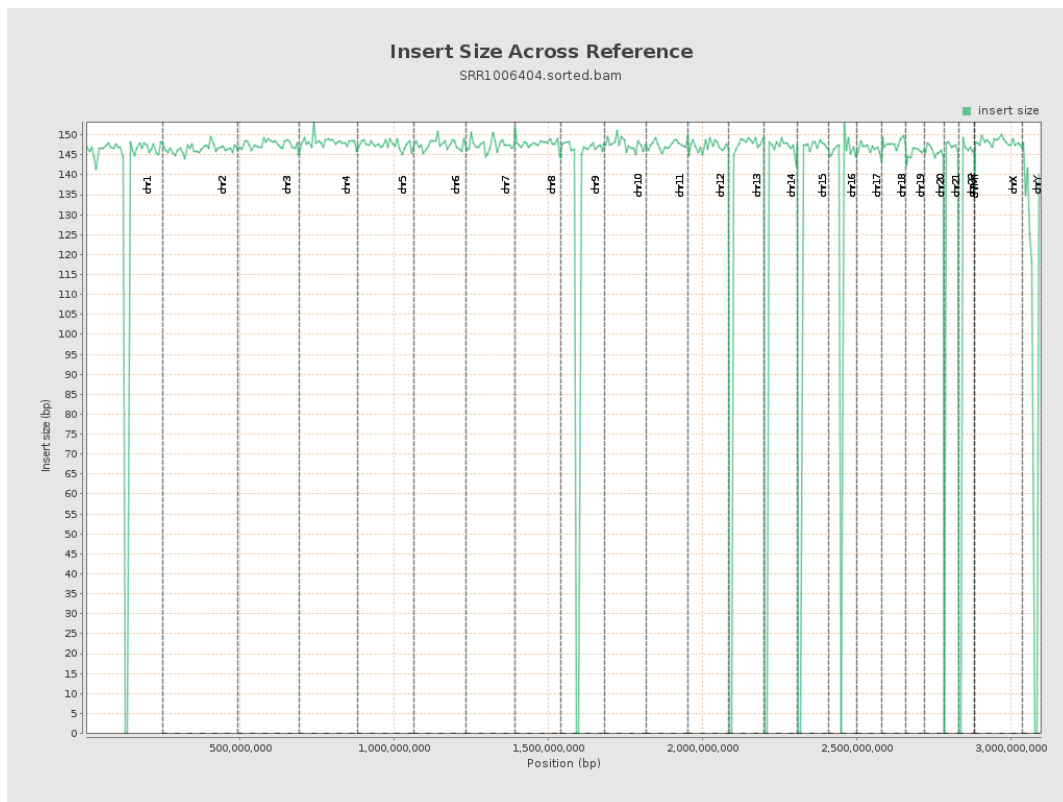
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

