

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046405.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_SRR2046405 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046405_1.fastq.gz SRR2046405_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:07:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046405.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,935,574
Mapped reads	5,845,428 / 98.48%
Unmapped reads	90,146 / 1.52%
Mapped paired reads	5,845,428 / 98.48%
Mapped reads, first in pair	2,956,204 / 49.8%
Mapped reads, second in pair	2,889,224 / 48.68%
Mapped reads, both in pair	5,770,142 / 97.21%
Mapped reads, singletons	75,286 / 1.27%
Secondary alignments	0
Supplementary alignments	12,290 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	3,521,198 / 59.32%
Duplication rate	45.07%
Clipped reads	1,444,345 / 24.33%

2.2. ACGT Content

Number/percentage of A's	161,571,596 / 29.02%
Number/percentage of C's	117,479,059 / 21.1%
Number/percentage of T's	160,357,568 / 28.8%
Number/percentage of G's	117,399,188 / 21.08%
Number/percentage of N's	45,795 / 0.01%

GC Percentage	42.18%
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2.3. Coverage

Mean	0.1799
Standard Deviation	7.432

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	23,258.5
Standard Deviation	1,540,817.9
P25/Median/P75	101 / 128 / 163

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	2,020,104
Insertions	39,085
Mapped reads with at least one insertion	0.65%
Deletions	55,740
Mapped reads with at least one deletion	0.92%
Homopolymer indels	47.06%

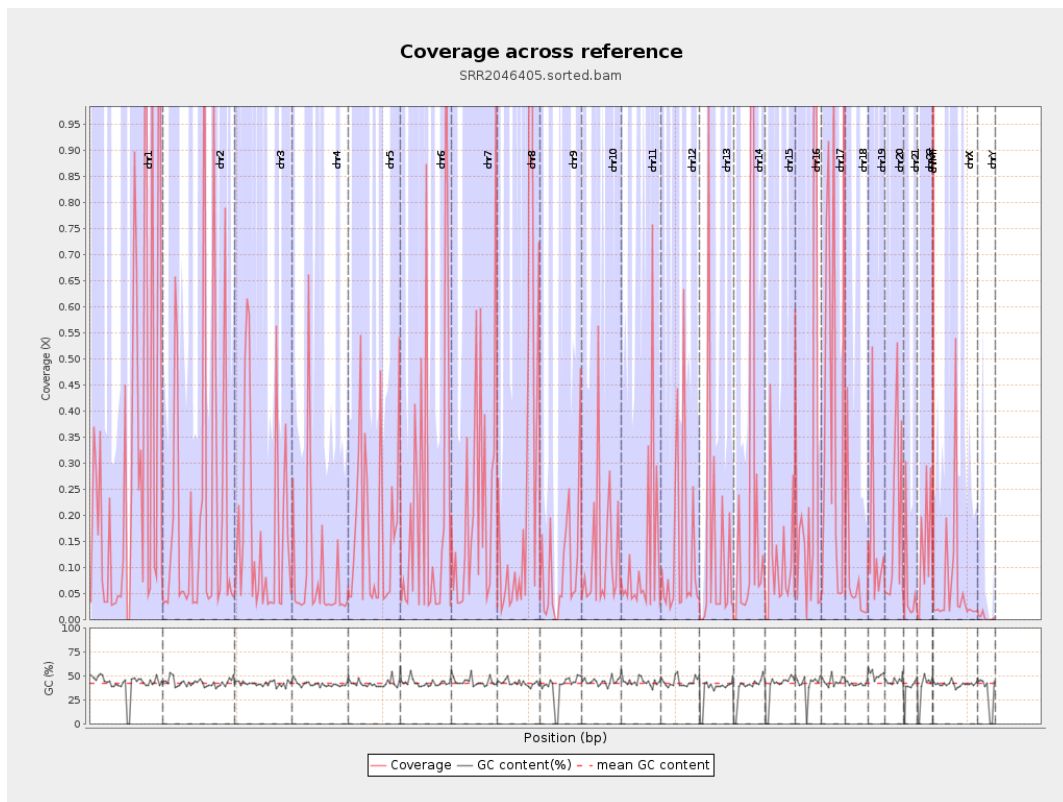
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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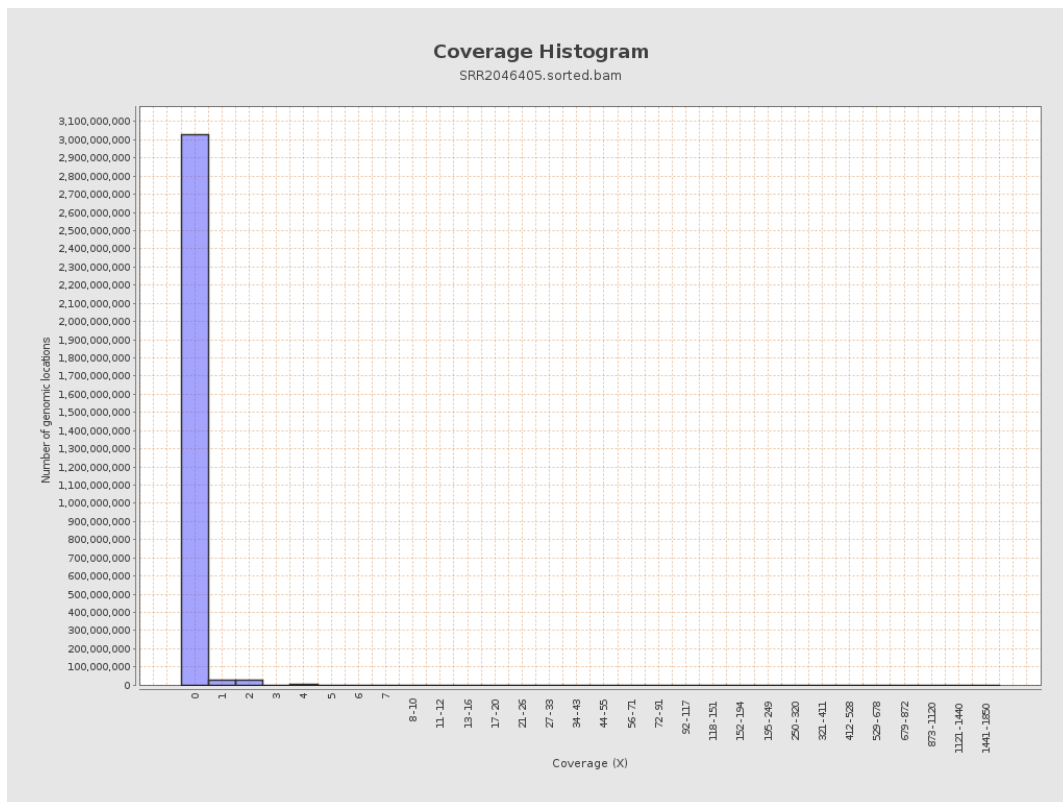
		bases	coverage	deviation
chr1	249250621	73340374	0.2942	9.8857
chr2	243199373	52900199	0.2175	8.4099
chr3	198022430	33294448	0.1681	7.0753
chr4	191154276	16797373	0.0879	3.8057
chr5	180915260	31553571	0.1744	6.8739
chr6	171115067	35932583	0.21	6.9295
chr7	159138663	37505728	0.2357	7.9715
chr8	146364022	48604638	0.3321	12.1894
chr9	141213431	14232143	0.1008	4.5521
chr10	135534747	17022775	0.1256	5.2483
chr11	135006516	16541613	0.1225	4.8696
chr12	133851895	17429705	0.1302	5.1336
chr13	115169878	15437129	0.134	5.7141
chr14	107349540	26979017	0.2513	10.6693
chr15	102531392	11884695	0.1159	5.4554
chr16	90354753	26529355	0.2936	11.599
chr17	81195210	33765596	0.4159	12.1975
chr18	78077248	6109059	0.0782	3.2583
chr19	59128983	8474689	0.1433	4.0377
chr20	63025520	11723365	0.186	8.7649
chr21	48129895	3226407	0.067	5.0055
chr22	51304566	7300602	0.1423	5.804
chrMT	16571	381245	23.0068	7.0518
chrX	155270560	9782011	0.063	3.4622

chrY	59373566	258091	0.0043	0.2218
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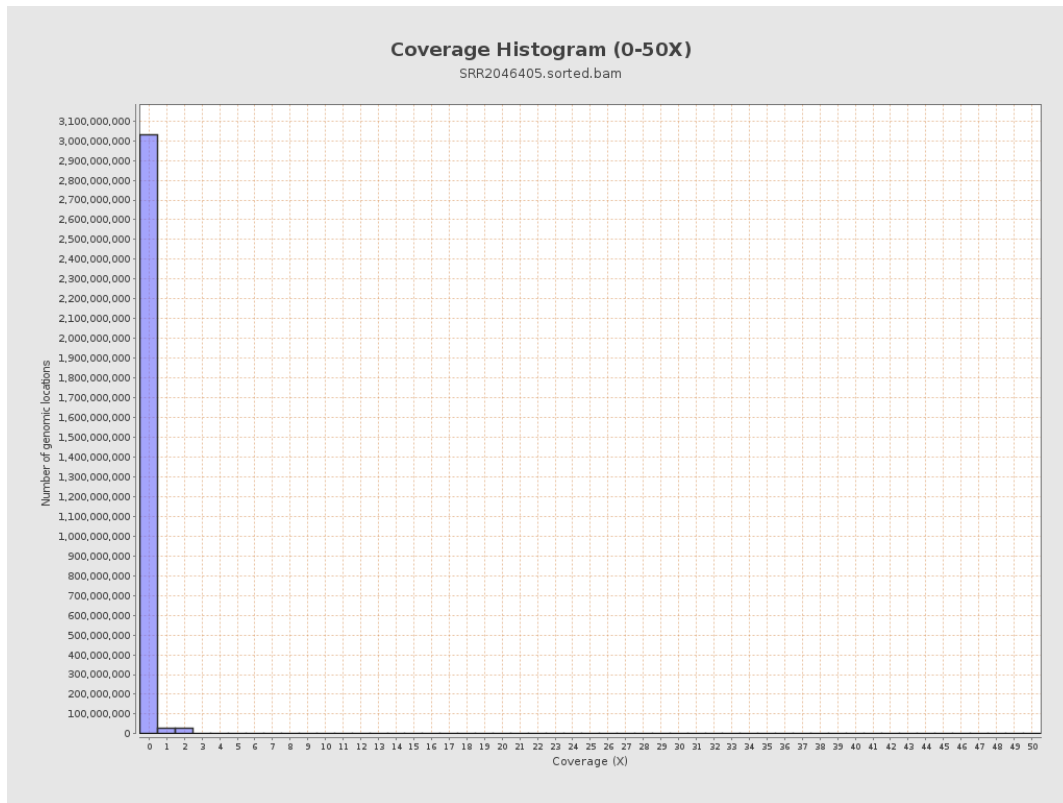
3. Results : Coverage across reference



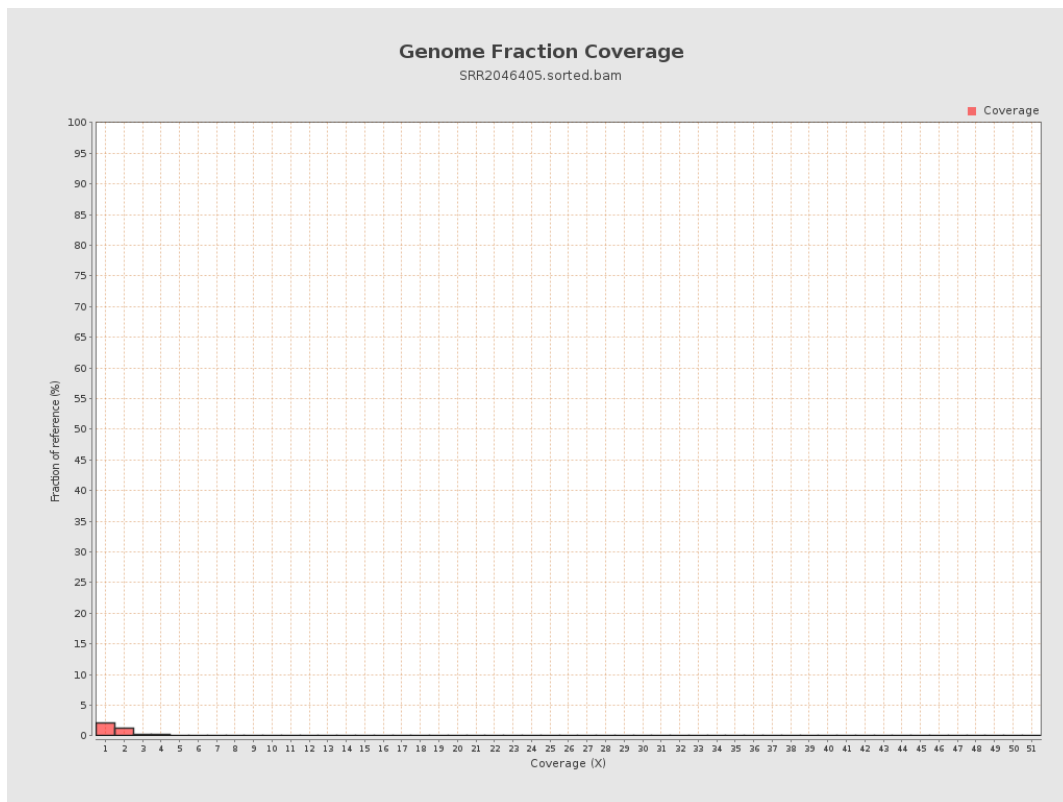
4. Results : Coverage Histogram



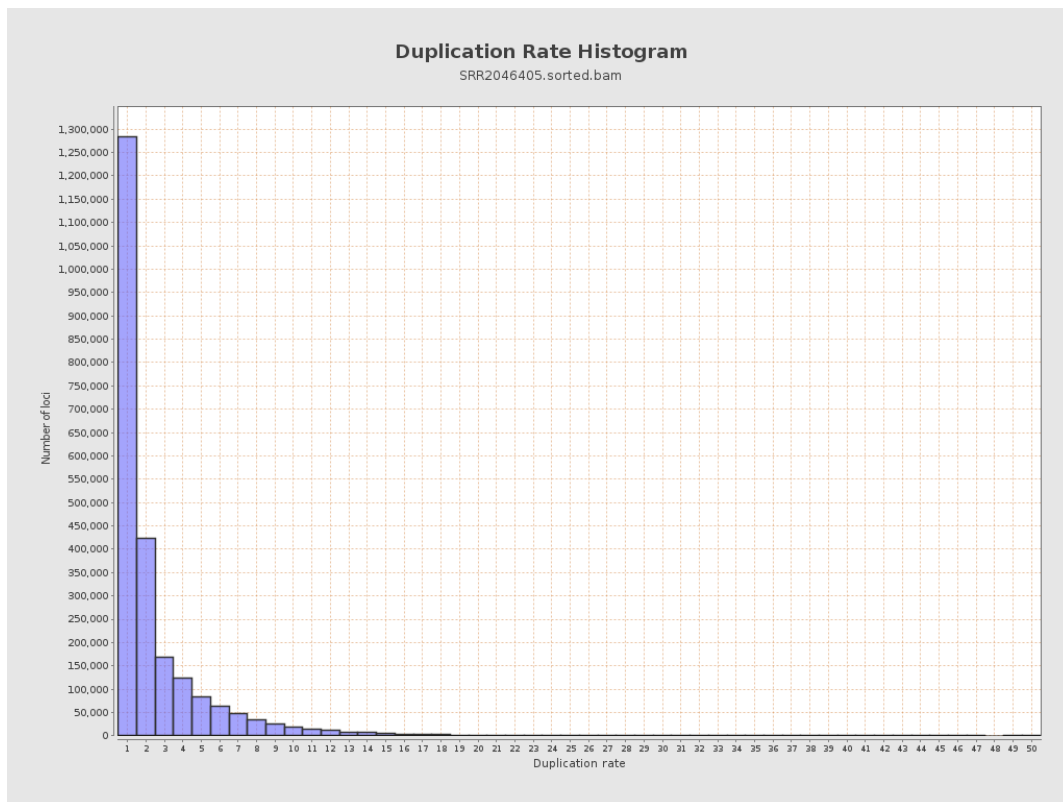
5. Results : Coverage Histogram (0-50X)



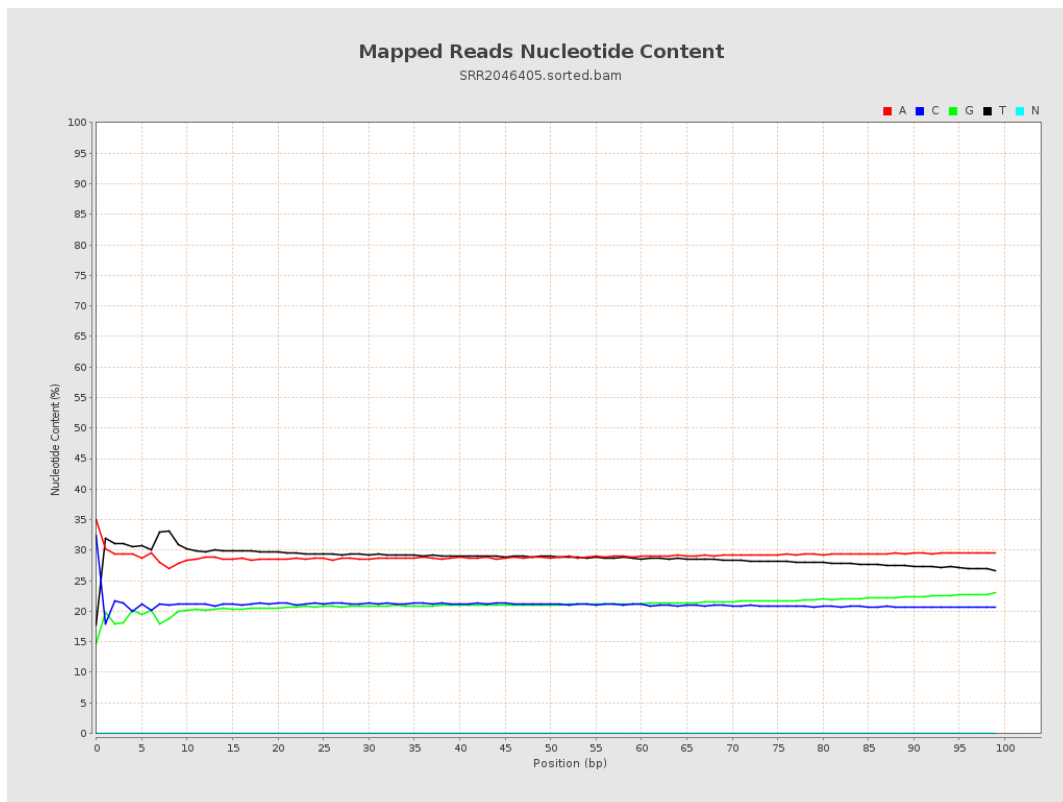
6. Results : Genome Fraction Coverage



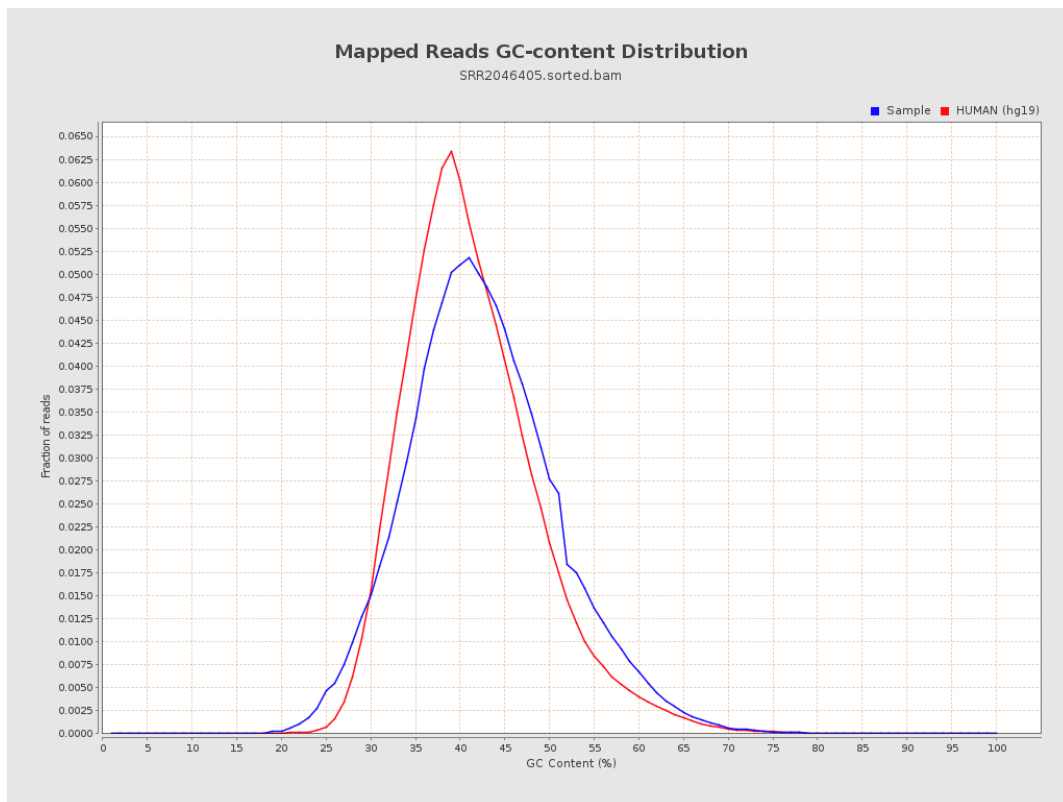
7. Results : Duplication Rate Histogram



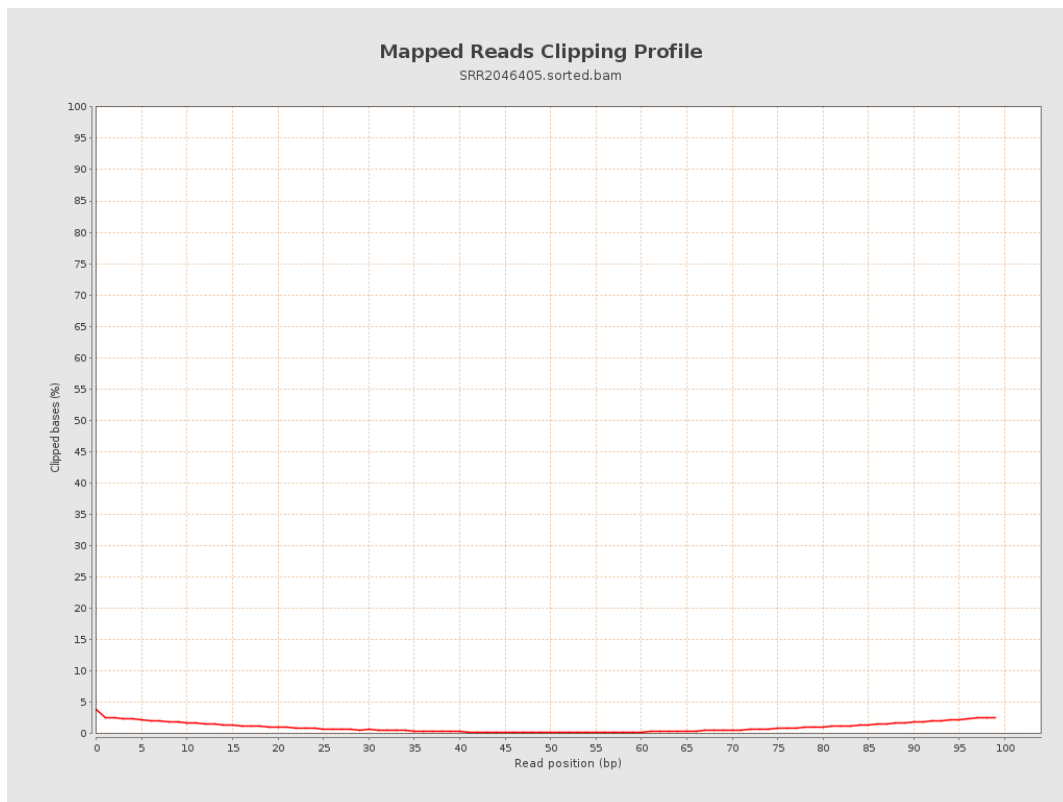
8. Results : Mapped Reads Nucleotide Content



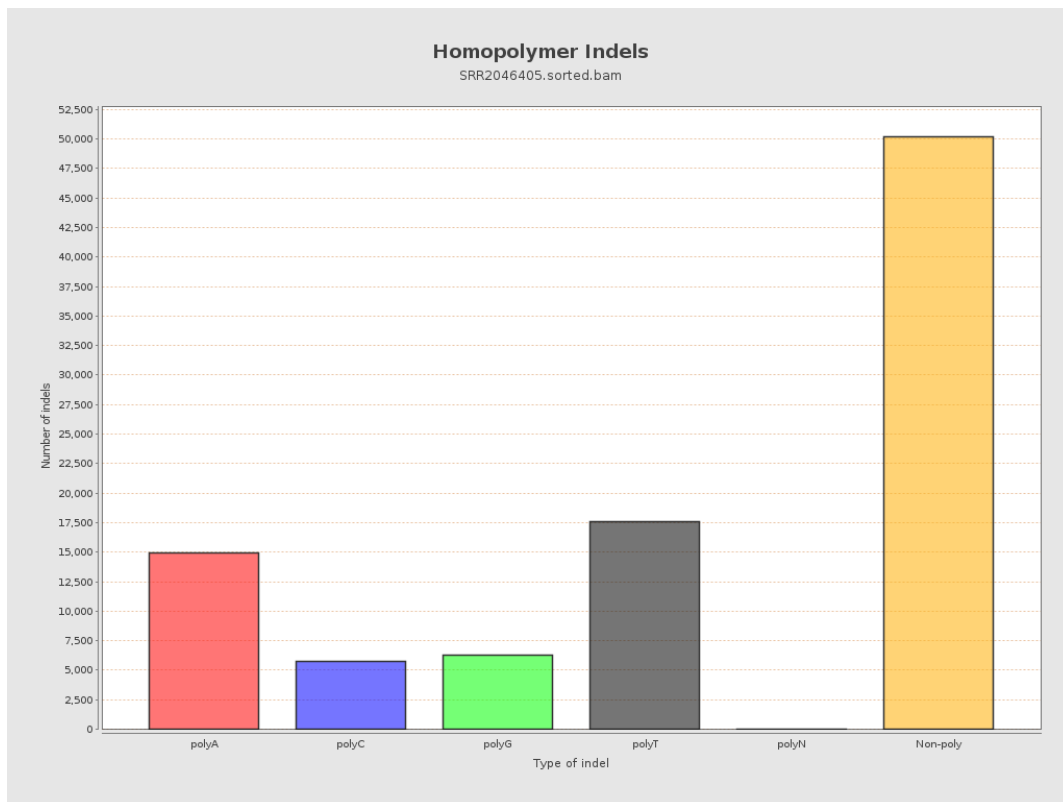
9. Results : Mapped Reads GC-content Distribution



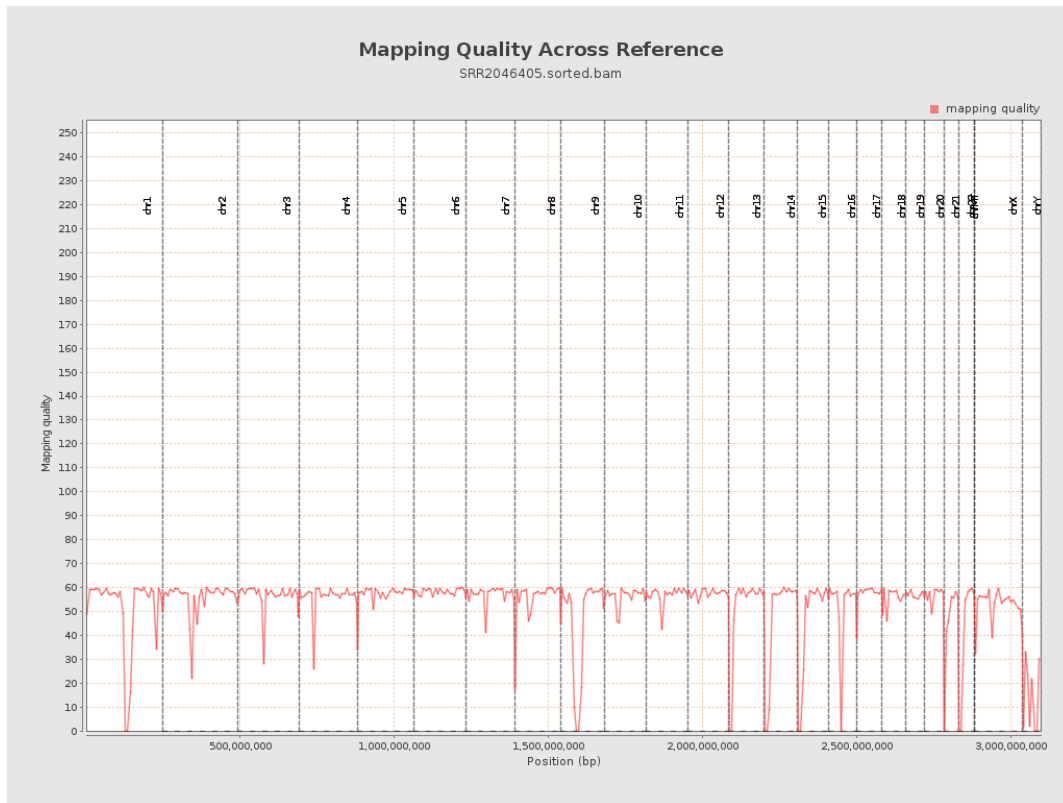
10. Results : Mapped Reads Clipping Profile



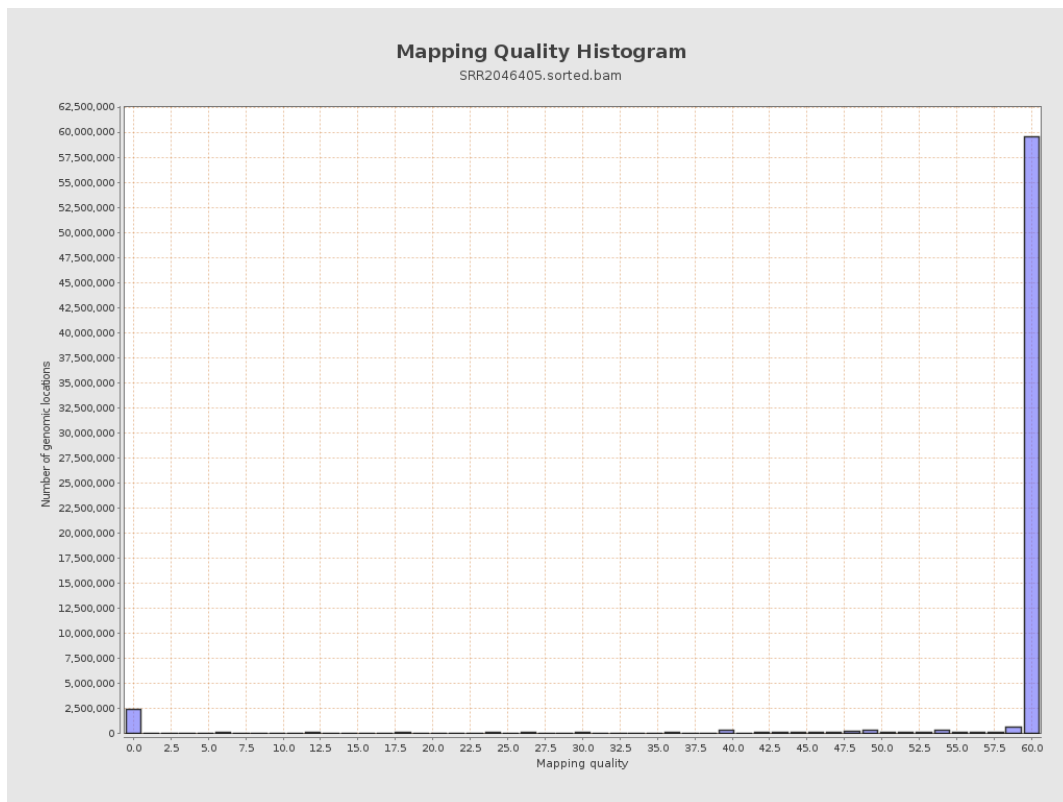
11. Results : Homopolymer Indels



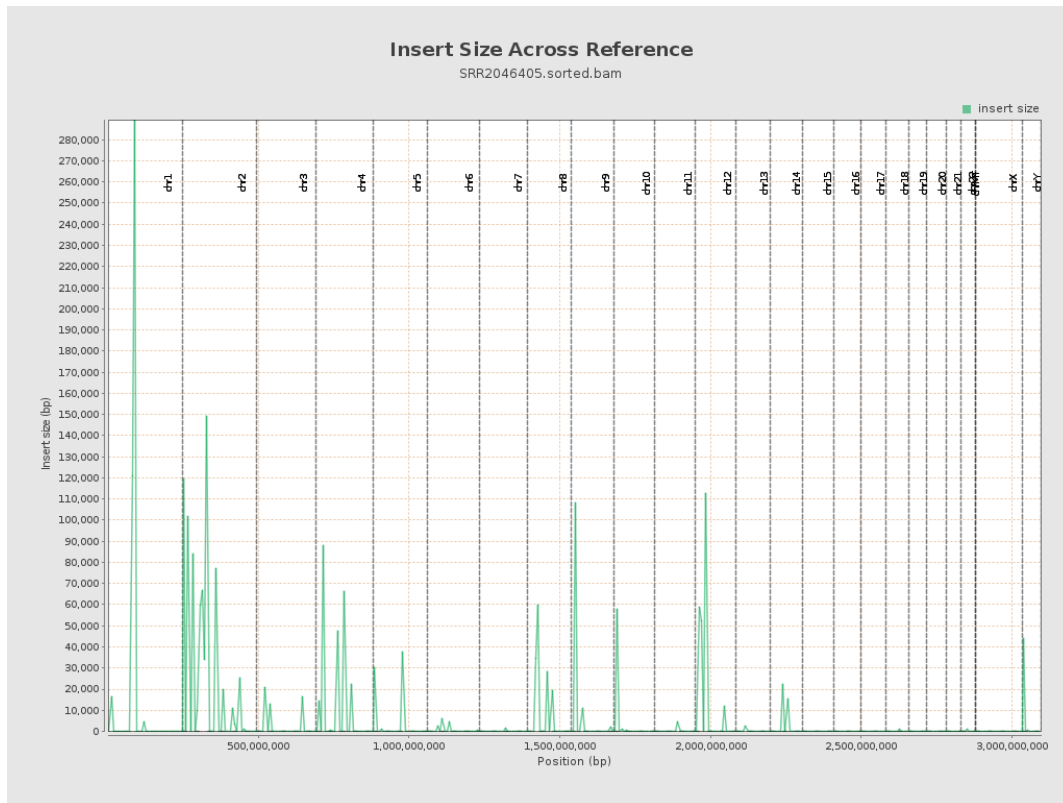
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

