Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:16:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006414.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_SRR1006414 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006414_1.fastq.gz SRR1006414_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:16:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006414.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,418,594
Mapped reads	2,988,807 / 87.43%
Unmapped reads	429,787 / 12.57%
Mapped paired reads	2,988,807 / 87.43%
Mapped reads, first in pair	1,506,995 / 44.08%
Mapped reads, second in pair	1,481,812 / 43.35%
Mapped reads, both in pair	2,732,050 / 79.92%
Mapped reads, singletons	256,757 / 7.51%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	70,755 / 2.07%
Duplication rate	1.96%
Clipped reads	170,407 / 4.98%

2.2. ACGT Content

Number/percentage of A's	32,144,203 / 27.79%
Number/percentage of C's	25,006,966 / 21.62%
Number/percentage of T's	32,740,933 / 28.31%
Number/percentage of G's	25,769,289 / 22.28%
Number/percentage of N's	4,954 / 0%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0374
Standard Deviation	0.2649

2.4. Mapping Quality

Mean Mapping Quality	47.99

2.5. Insert size

Mean	72,049.44
Standard Deviation	2,523,550.47
P25/Median/P75	96 / 144 / 188

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	398,758
Insertions	3,082
Mapped reads with at least one insertion	0.1%
Deletions	11,943
Mapped reads with at least one deletion	0.4%
Homopolymer indels	42.15%

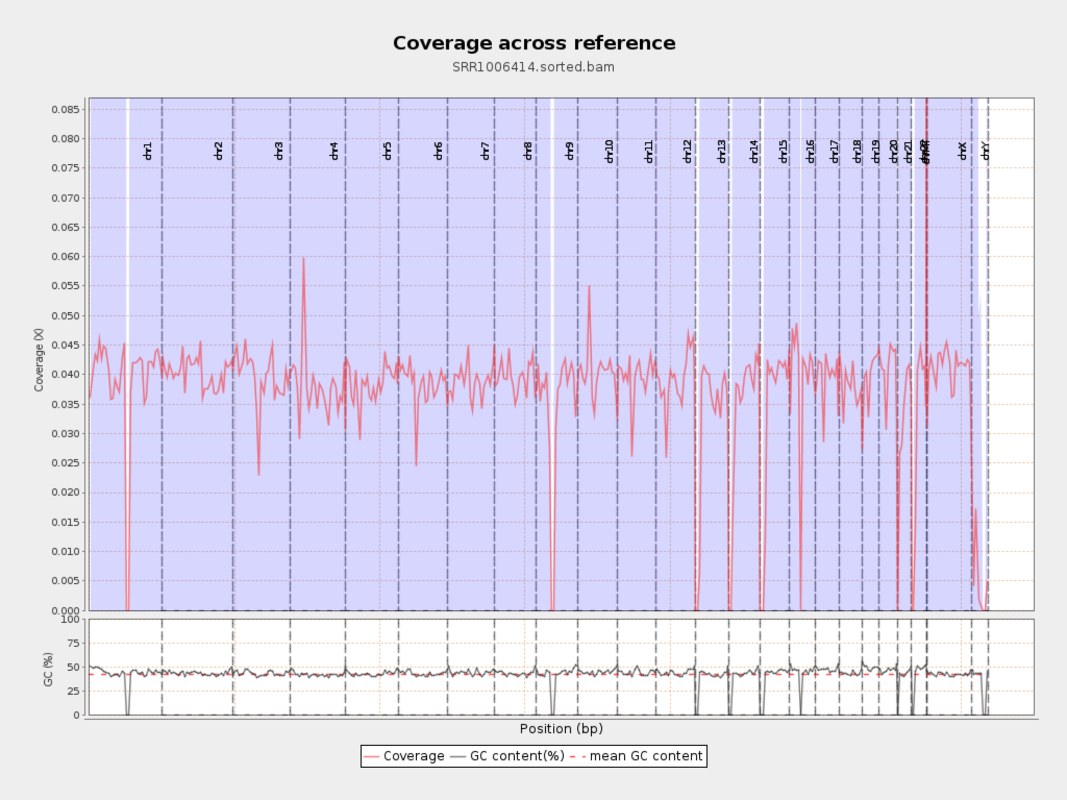
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

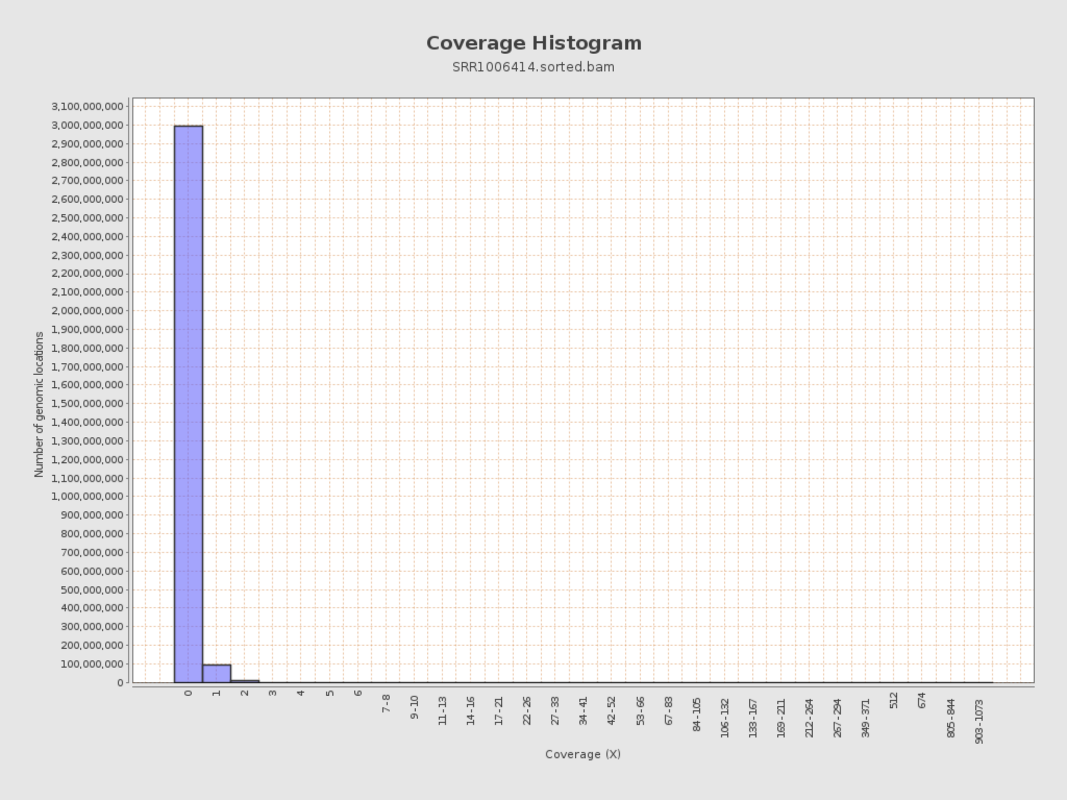
chr1	249250621	9601991	0.0385	0.3154
chr2	243199373	9814187	0.0404	0.2479
chr3	198022430	7822893	0.0395	0.2176
chr4	191154276	7270719	0.038	0.2339
chr5	180915260	6953955	0.0384	0.2156
chr6	171115067	6588230	0.0385	0.2254
chr7	159138663	6166815	0.0388	0.2723
chr8	146364022	5794042	0.0396	0.5674
chr9	141213431	4766737	0.0338	0.2193
chr10	135534747	5500545	0.0406	0.2734
chr11	135006516	5337493	0.0395	0.2383
chr12	133851895	5226996	0.0391	0.2185
chr13	115169878	3620691	0.0314	0.194
chr14	107349540	3527554	0.0329	0.2184
chr15	102531392	3389185	0.0331	0.1998
chr16	90354753	3511279	0.0389	0.2399
chr17	81195210	3208198	0.0395	0.2245
chr18	78077248	2970087	0.038	0.2955
chr19	59128983	2354188	0.0398	0.2682
chr20	63025520	2568713	0.0408	0.2269
chr21	48129895	1514881	0.0315	0.2103
chr22	51304566	1474894	0.0287	0.1916
chrMT	16571	1983	0.1197	0.5063
chrX	155270560	6392062	0.0412	0.2309

chrY	59373566	304405	0.0051	0.1373

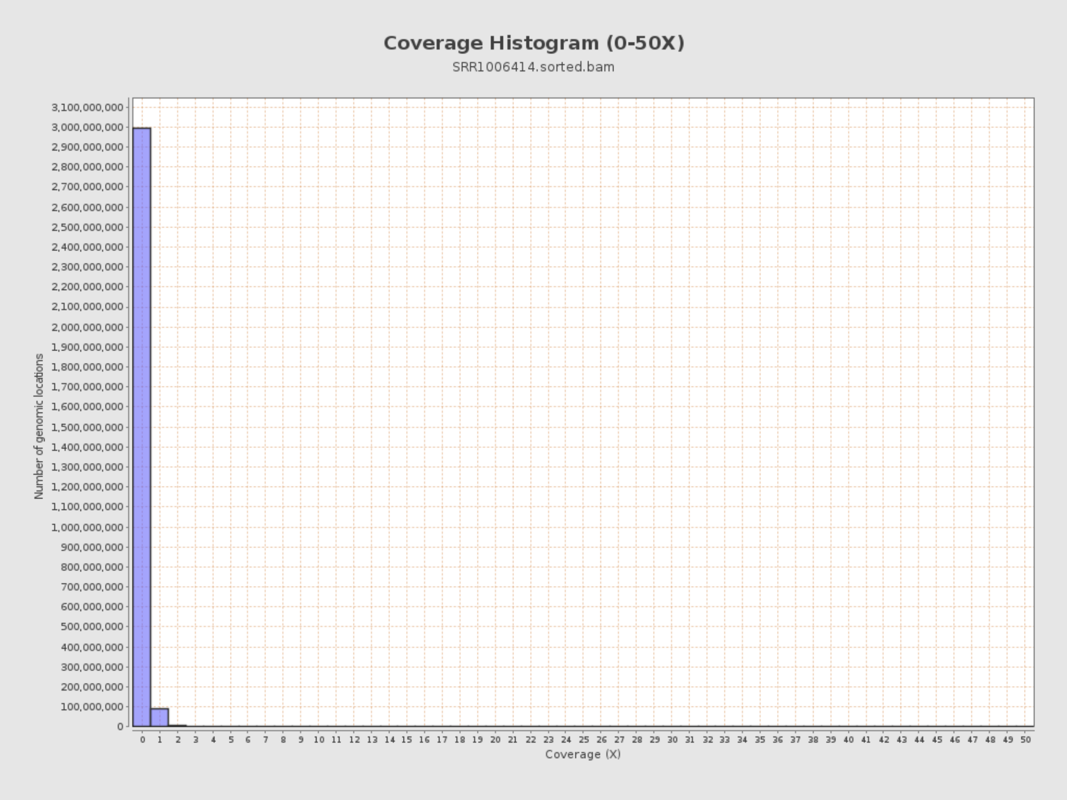
3. Results : Coverage across reference



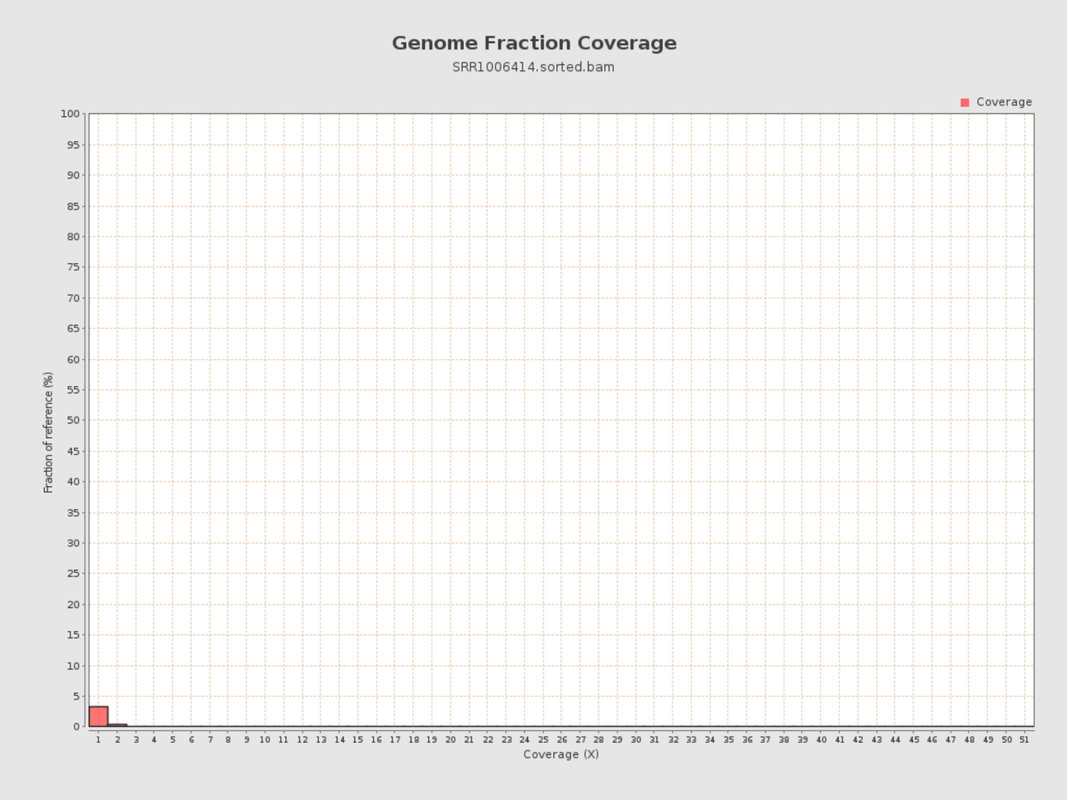
4. Results : Coverage Histogram



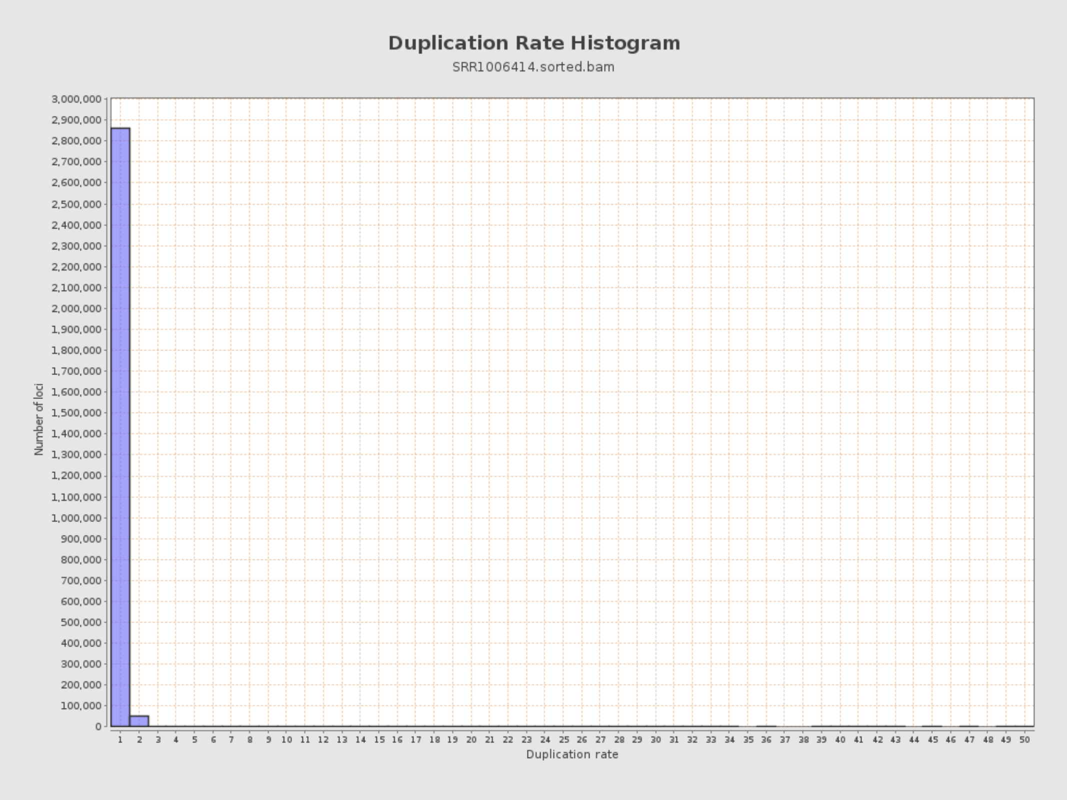
5. Results : Coverage Histogram (0-50X)



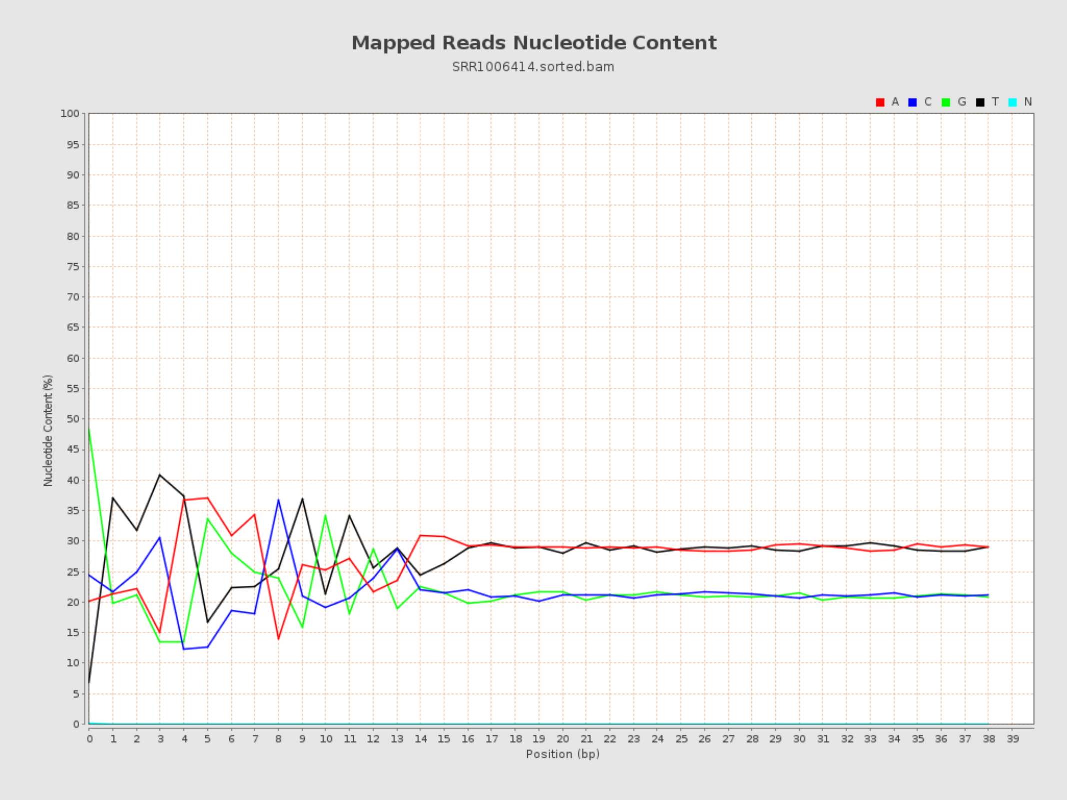
6. Results : Genome Fraction Coverage



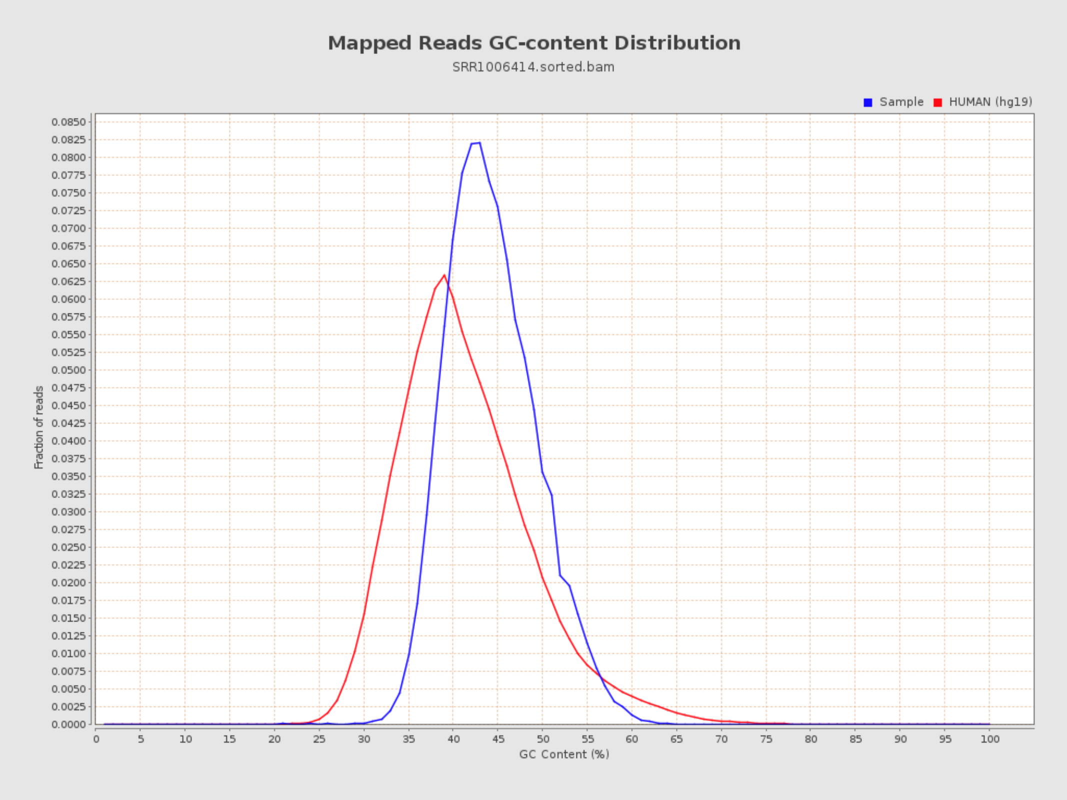
7. Results : Duplication Rate Histogram



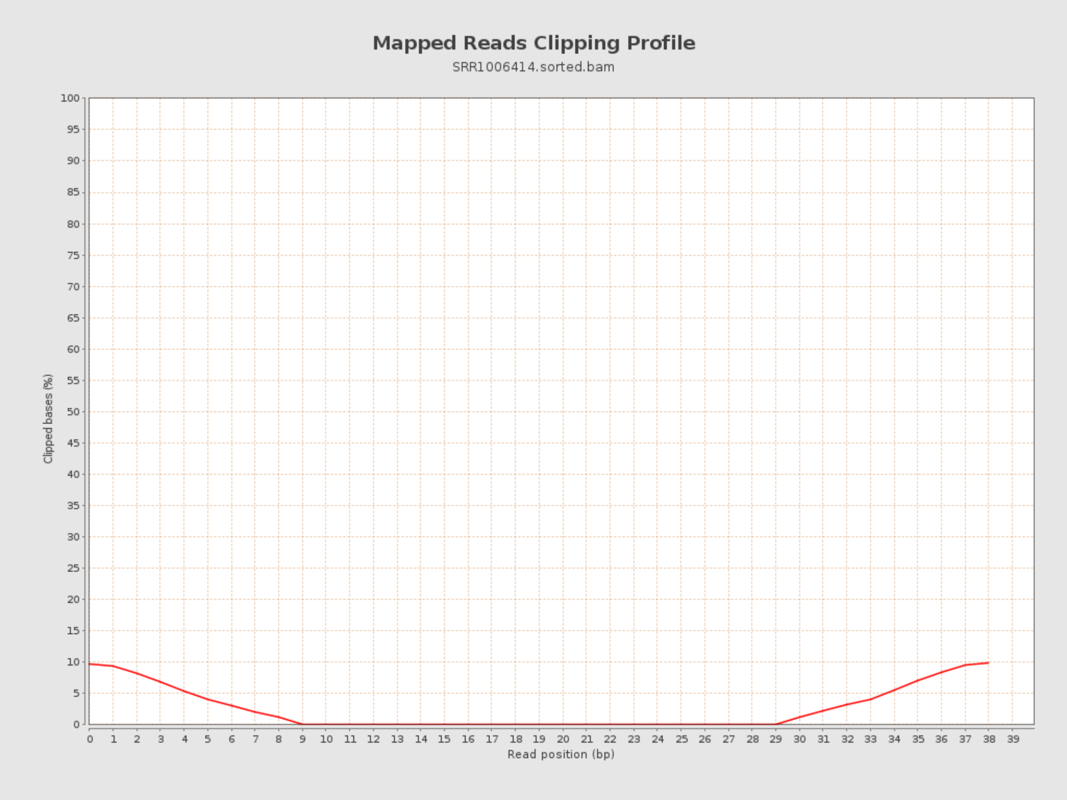
8. Results : Mapped Reads Nucleotide Content



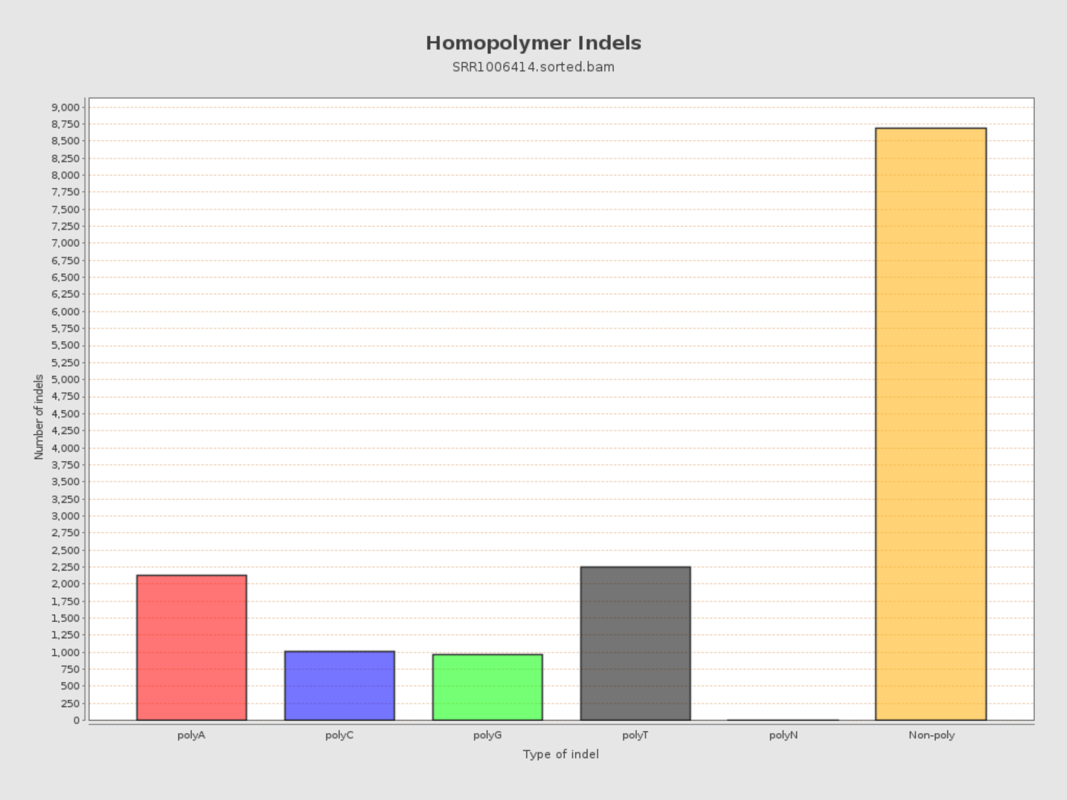
9. Results : Mapped Reads GC-content Distribution



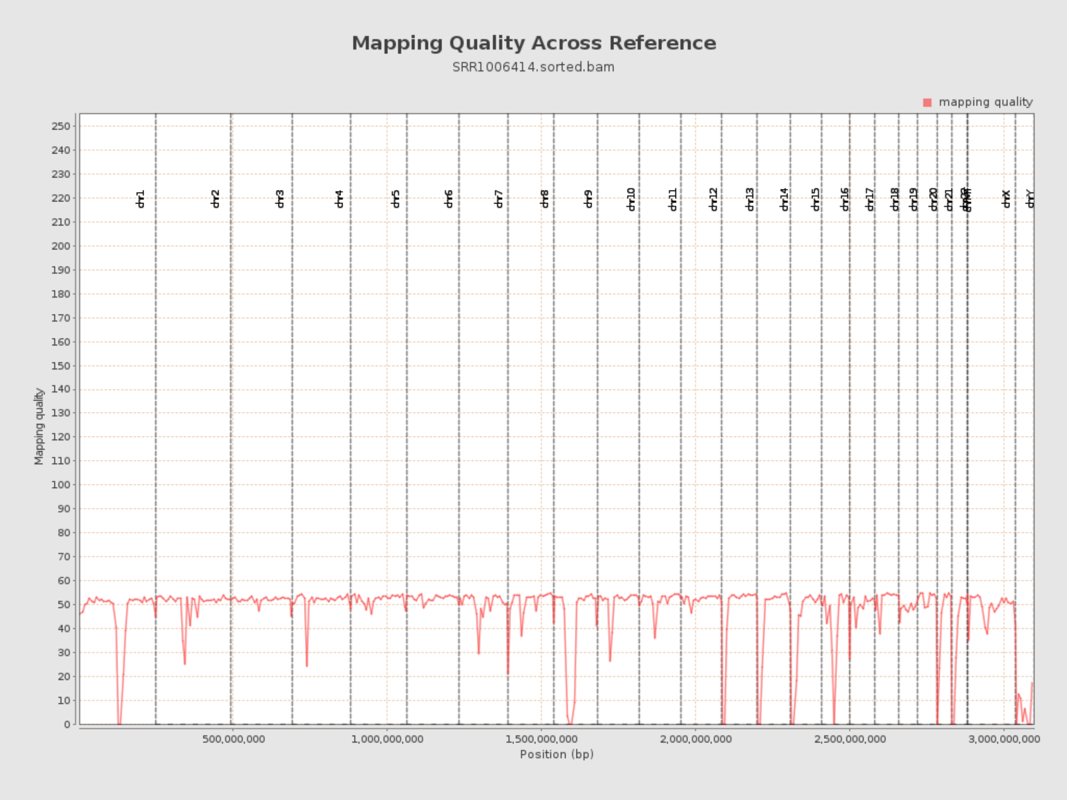
10. Results : Mapped Reads Clipping Profile



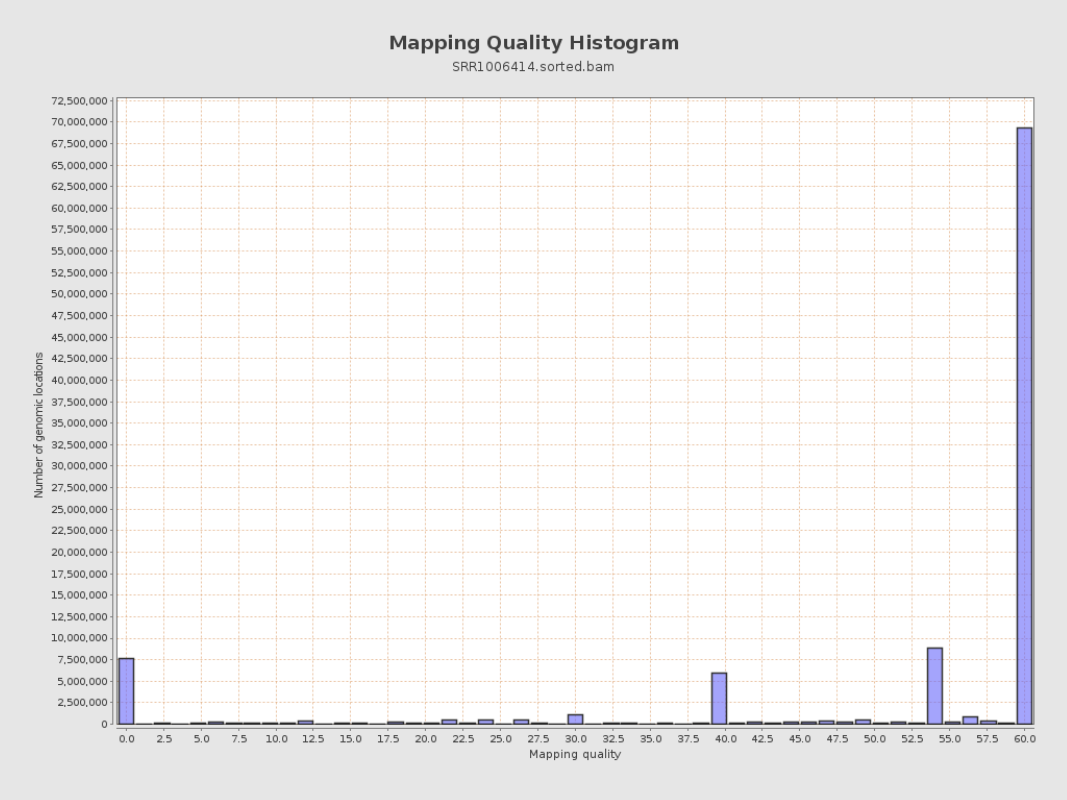
11. Results : Homopolymer Indels



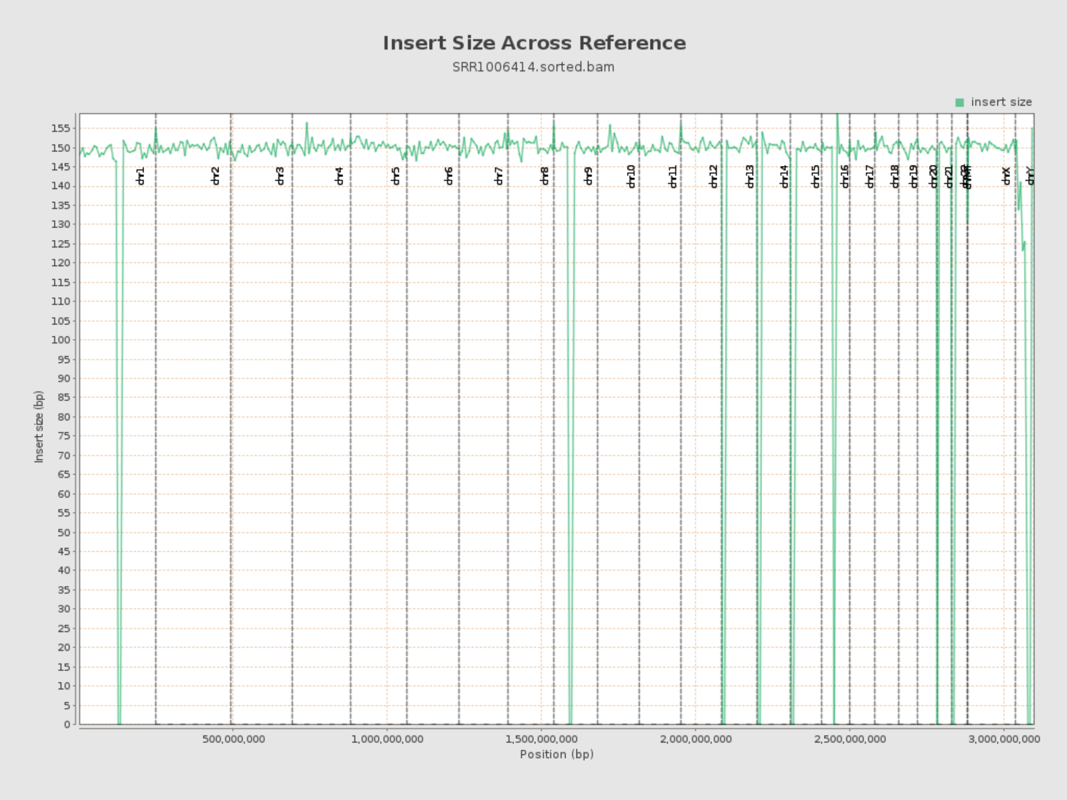
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram