Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:20:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006415.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_SRR1006415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006415_1.fastq.gz SRR1006415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:20:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,239,212
Mapped reads	3,349,772 / 79.02%
Unmapped reads	889,440 / 20.98%
Mapped paired reads	3,349,772 / 79.02%
Mapped reads, first in pair	1,687,809 / 39.81%
Mapped reads, second in pair	1,661,963 / 39.2%
Mapped reads, both in pair	3,069,672 / 72.41%
Mapped reads, singletons	280,100 / 6.61%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	81,226 / 1.92%
Duplication rate	1.96%
Clipped reads	181,999 / 4.29%

2.2. ACGT Content

Number/percentage of A's	36,047,341 / 27.8%
Number/percentage of C's	28,101,153 / 21.67%
Number/percentage of T's	36,595,601 / 28.22%
Number/percentage of G's	28,933,898 / 22.31%
Number/percentage of N's	5,362 / 0%
GC Percentage	43.98%

2.3. Coverage

Mean	0.0419
Standard Deviation	0.275

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Insert size

Mean	72,366.4
Standard Deviation	2,555,803.77
P25/Median/P75	104 / 140 / 186

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	443,871
Insertions	3,593
Mapped reads with at least one insertion	0.11%
Deletions	11,330
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.07%

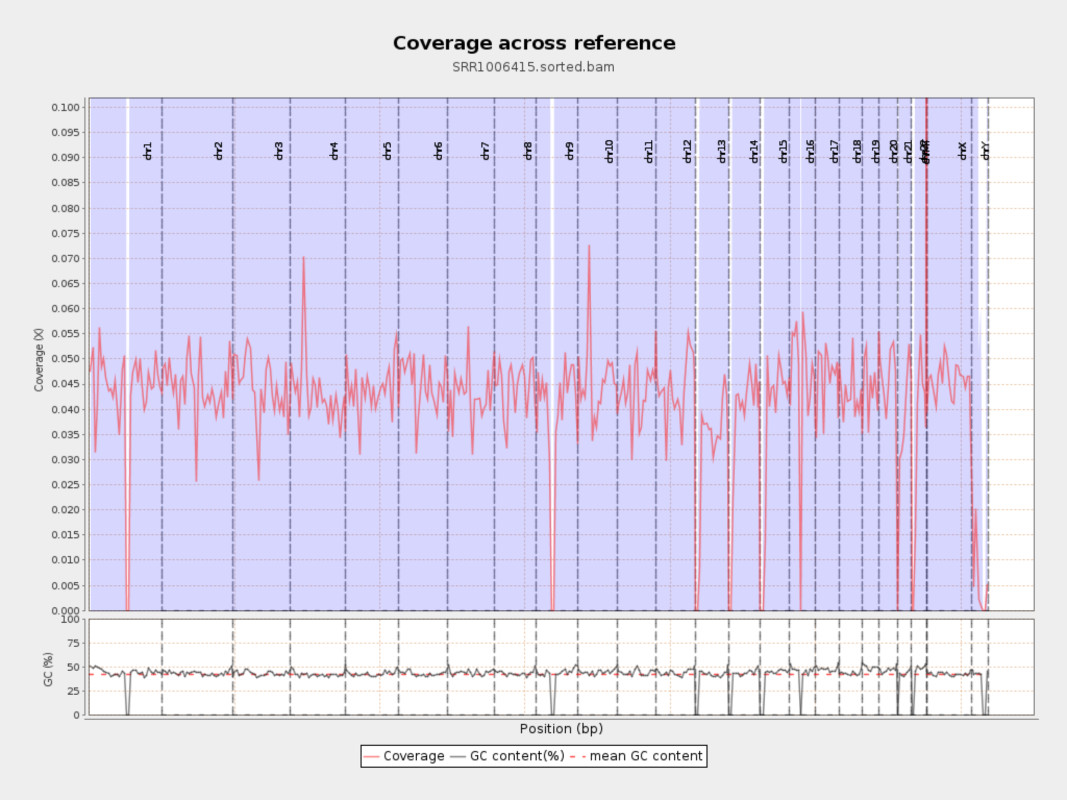
2.7. Chromosome stats

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

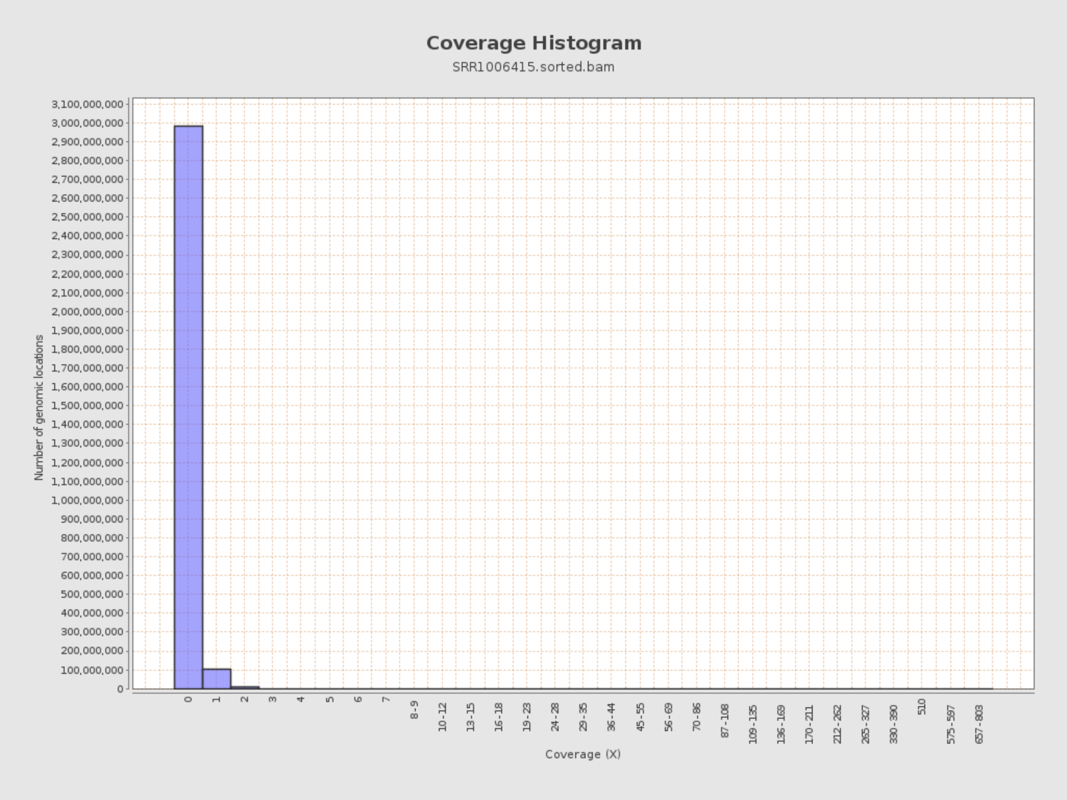
chr1	249250621	10627010	0.0426	0.3554
chr2	243199373	10827068	0.0445	0.2714
chr3	198022430	8745034	0.0442	0.2286
chr4	191154276	8290104	0.0434	0.2588
chr5	180915260	8004381	0.0442	0.2292
chr6	171115067	7728702	0.0452	0.2473
chr7	159138663	6794065	0.0427	0.2902
chr8	146364022	6535329	0.0447	0.4553
chr9	141213431	5417189	0.0384	0.2332
chr10	135534747	6189327	0.0457	0.3286
chr11	135006516	5836093	0.0432	0.2563
chr12	133851895	5896586	0.0441	0.2304
chr13	115169878	3613200	0.0314	0.1924
chr14	107349540	3882132	0.0362	0.2242
chr15	102531392	3739696	0.0365	0.2087
chr16	90354753	4111590	0.0455	0.2752
chr17	81195210	3749021	0.0462	0.2423
chr18	78077248	3359456	0.043	0.3488
chr19	59128983	2648739	0.0448	0.2957
chr20	63025520	2875812	0.0456	0.2379
chr21	48129895	1746133	0.0363	0.2349
chr22	51304566	1613774	0.0315	0.1973
chrMT	16571	3661	0.2209	0.5356
chrX	155270560	7107794	0.0458	0.2445

chrY	59373566	356553	0.006	0.1611

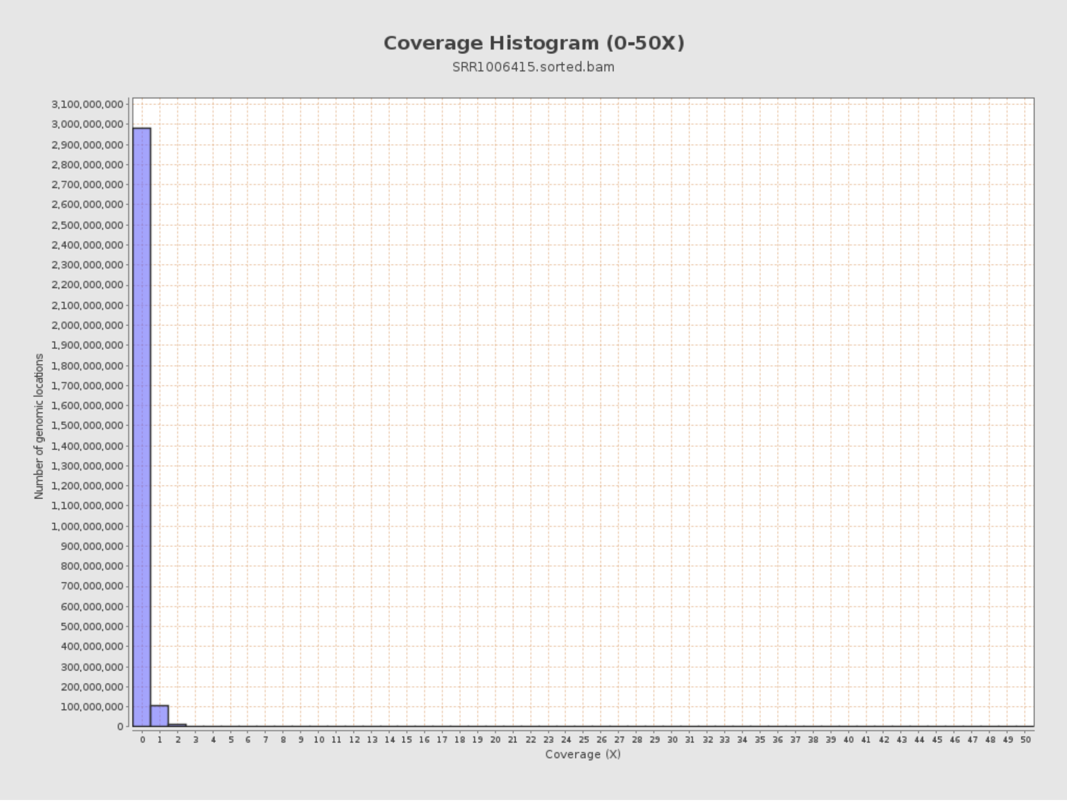
3. Results : Coverage across reference



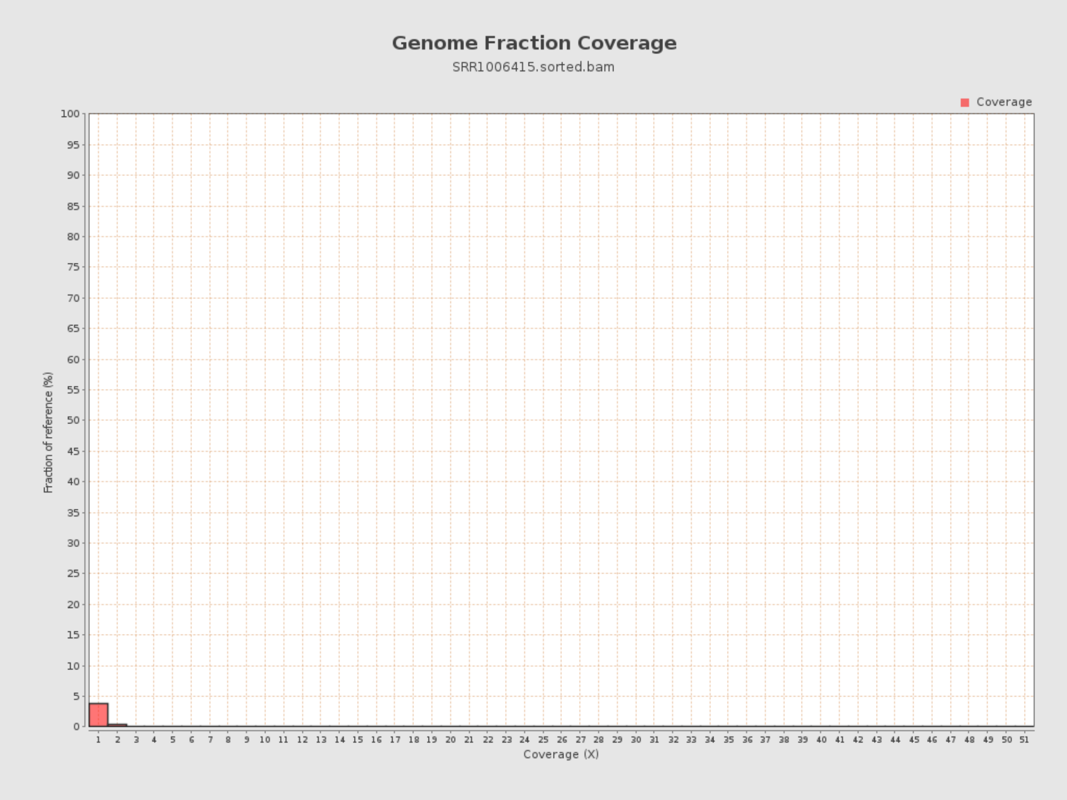
4. Results : Coverage Histogram



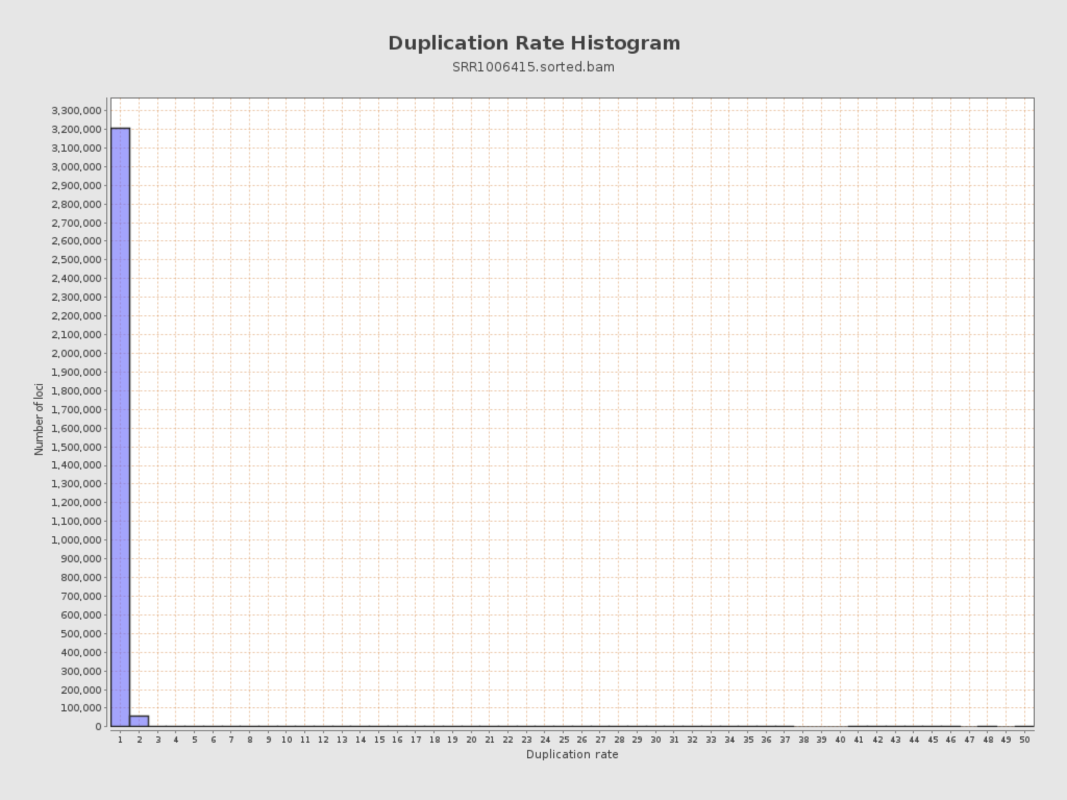
5. Results : Coverage Histogram (0-50X)



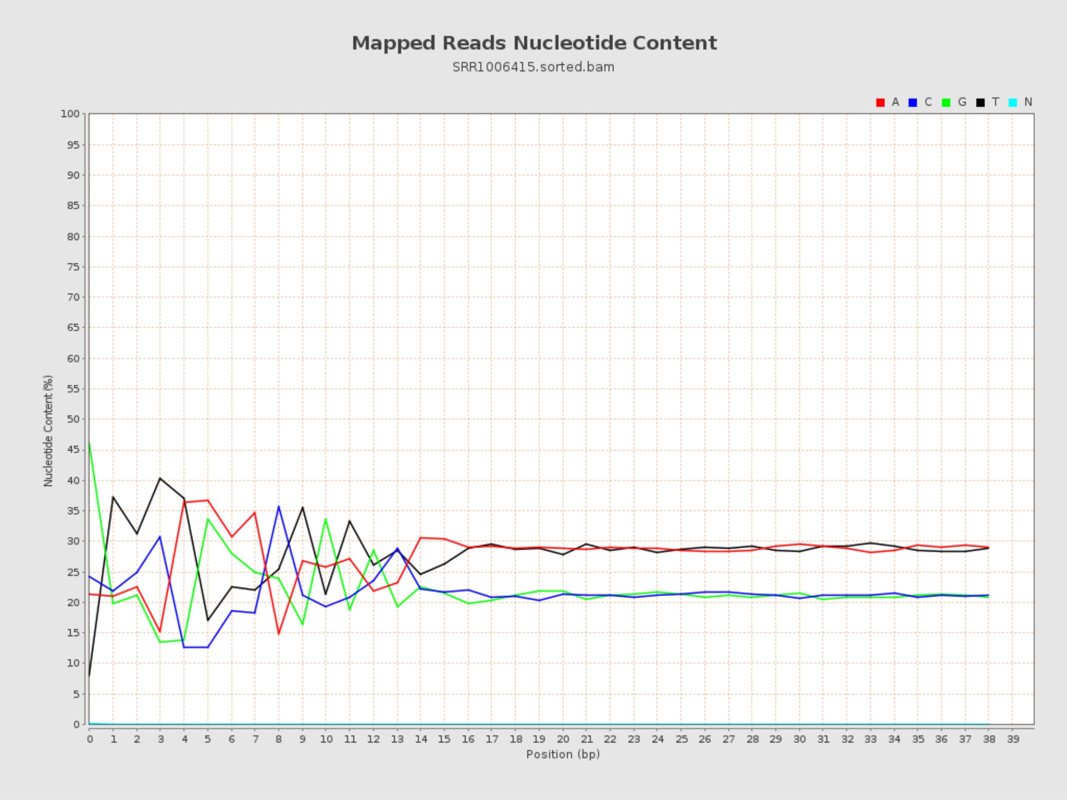
6. Results : Genome Fraction Coverage



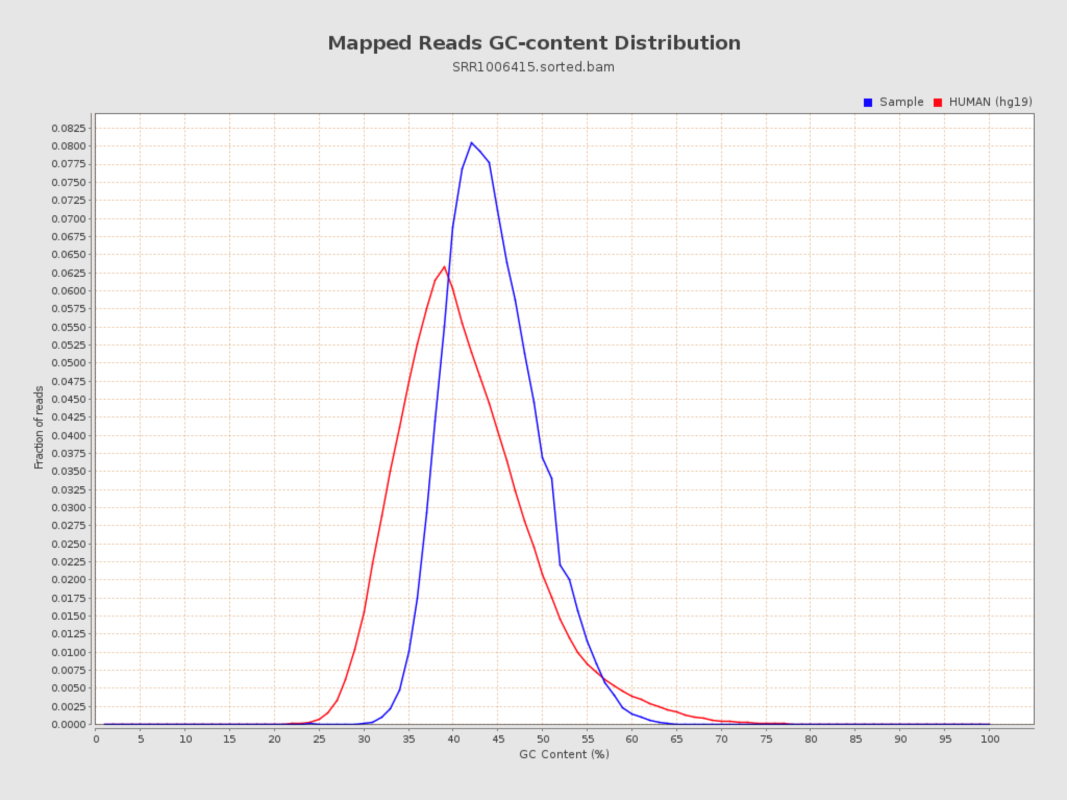
7. Results : Duplication Rate Histogram



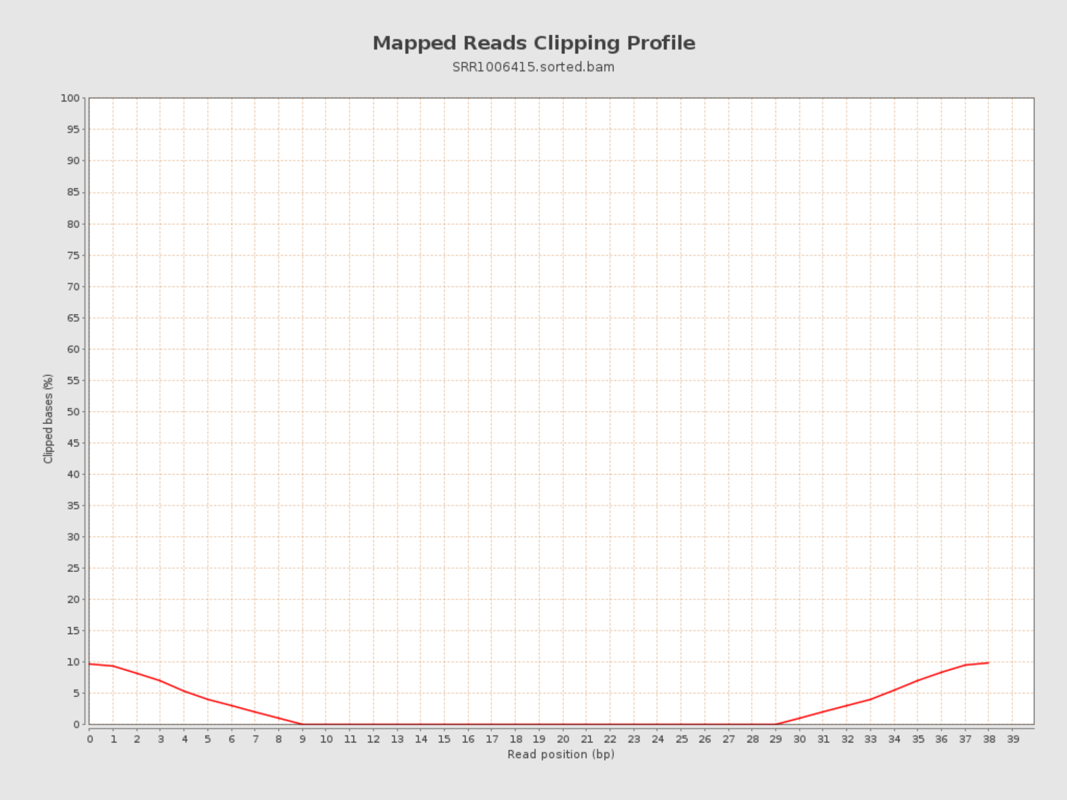
8. Results : Mapped Reads Nucleotide Content



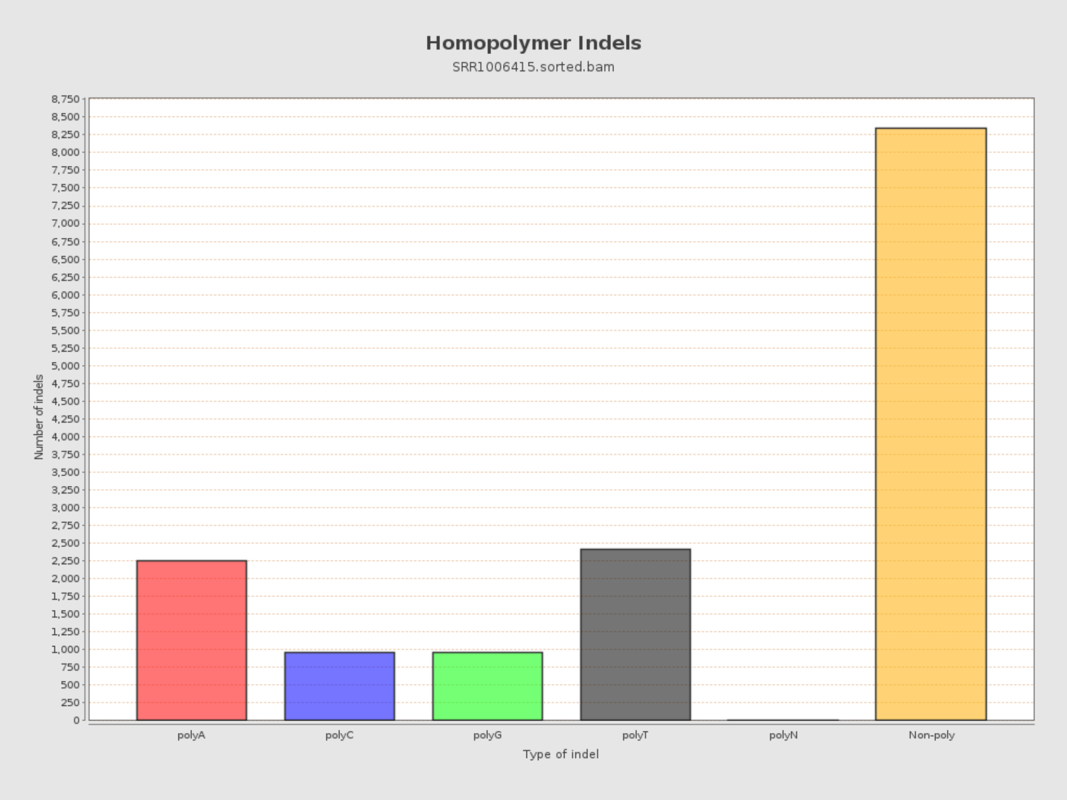
9. Results : Mapped Reads GC-content Distribution



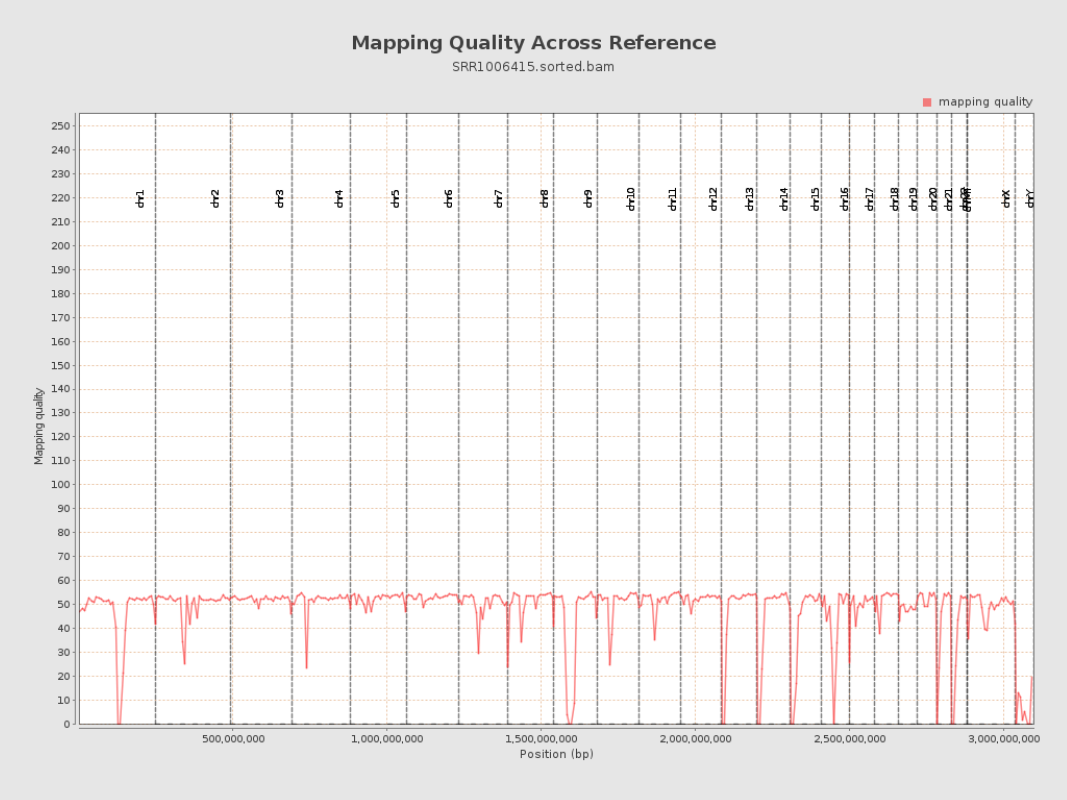
10. Results : Mapped Reads Clipping Profile



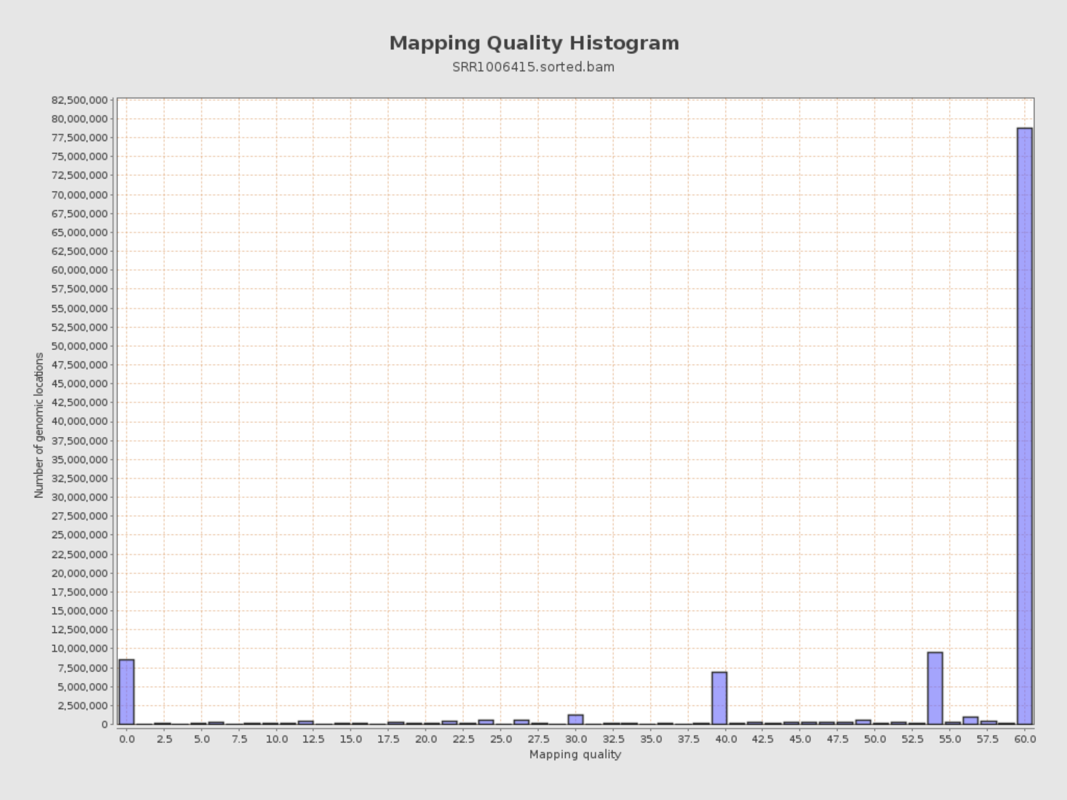
11. Results : Homopolymer Indels



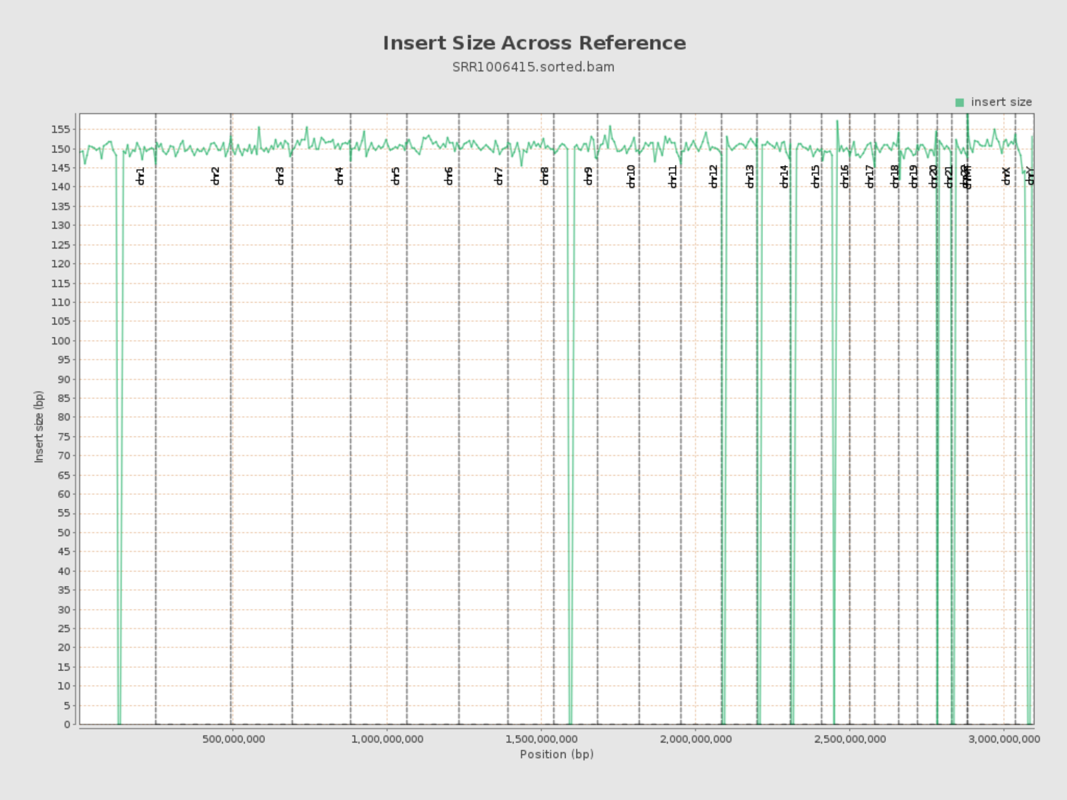
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram