Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:43:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006437.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_SRR1006437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006437.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:43:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,725,866
Mapped reads	1,610,452 / 93.31%
Unmapped reads	115,414 / 6.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,805 / 0.22%
Read min/max/mean length	30 / 59 / 56.28
Duplicated reads (estimated)	30,336 / 1.76%
Duplication rate	1.45%
Clipped reads	208,614 / 12.09%

2.2. ACGT Content

Number/percentage of A's	25,057,356 / 28.2%
Number/percentage of C's	18,918,511 / 21.29%
Number/percentage of T's	24,431,129 / 27.5%
Number/percentage of G's	20,355,025 / 22.91%
Number/percentage of N's	79,028 / 0.09%
GC Percentage	44.21%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2492

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

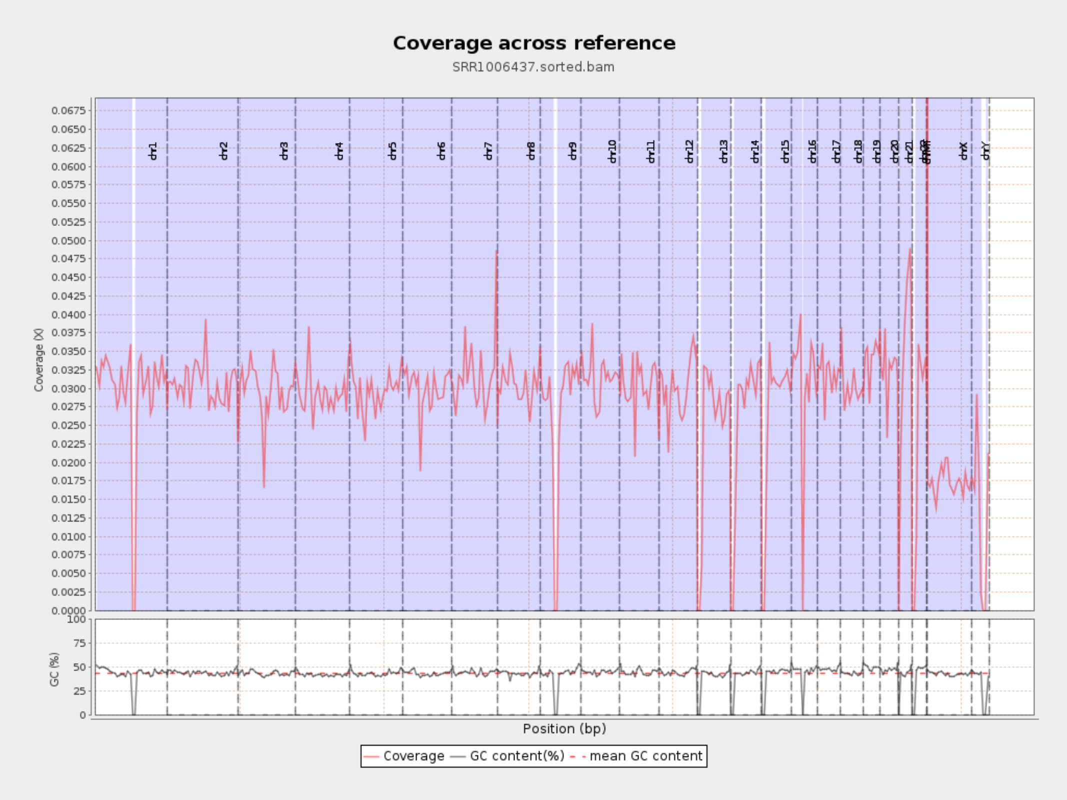
General error rate	0.56%
Mismatches	484,762
Insertions	5,531
Mapped reads with at least one insertion	0.34%
Deletions	15,975
Mapped reads with at least one deletion	0.99%
Homopolymer indels	43.26%

2.6. Chromosome stats

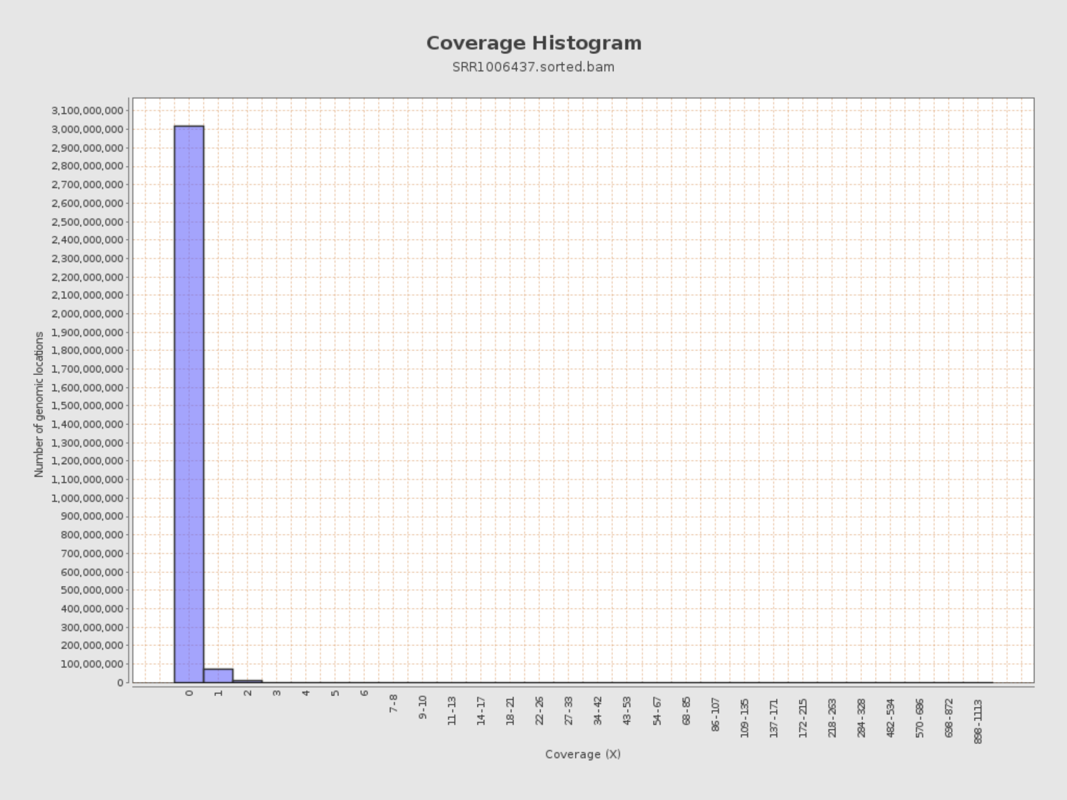
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7337370	0.0294	0.2906
chr2	243199373	7468934	0.0307	0.2205
chr3	198022430	5893031	0.0298	0.1891
chr4	191154276	5648251	0.0295	0.198
chr5	180915260	5358093	0.0296	0.1893
chr6	171115067	5128319	0.03	0.1961
chr7	159138663	5052515	0.0317	0.2383

chr8	146364022	4462794	0.0305	0.6385
chr9	141213431	3760842	0.0266	0.1935
chr10	135534747	4273342	0.0315	0.2277
chr11	135006516	4132050	0.0306	0.208
chr12	133851895	4042371	0.0302	0.1936
chr13	115169878	2809071	0.0244	0.1726
chr14	107349540	2752166	0.0256	0.1804
chr15	102531392	2657527	0.0259	0.1779
chr16	90354753	2738258	0.0303	0.2098
chr17	81195210	2592995	0.0319	0.2078
chr18	78077248	2363451	0.0303	0.2611
chr19	59128983	2010649	0.034	0.2634
chr20	63025520	2041480	0.0324	0.229
chr21	48129895	1650607	0.0343	0.2212
chr22	51304566	1178839	0.023	0.1824
chrMT	16571	49734	3.0013	2.4093
chrX	155270560	2691714	0.0173	0.1477
chrY	59373566	773507	0.013	0.1723

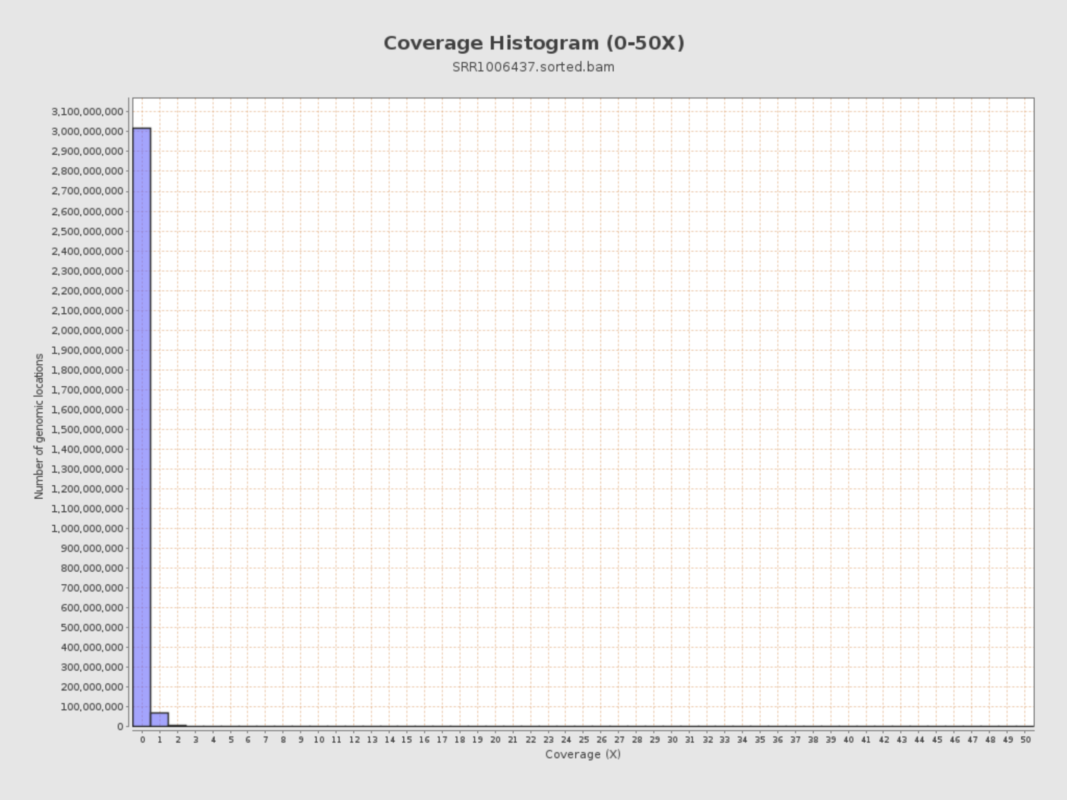
3. Results : Coverage across reference



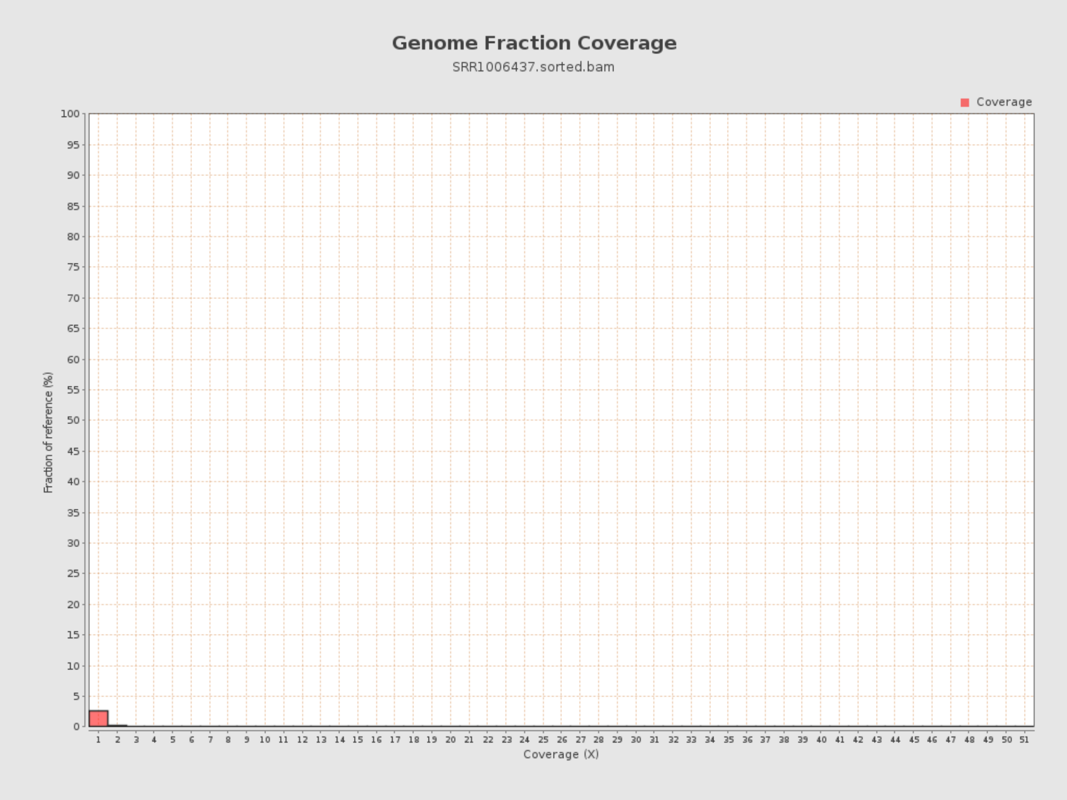
4. Results : Coverage Histogram



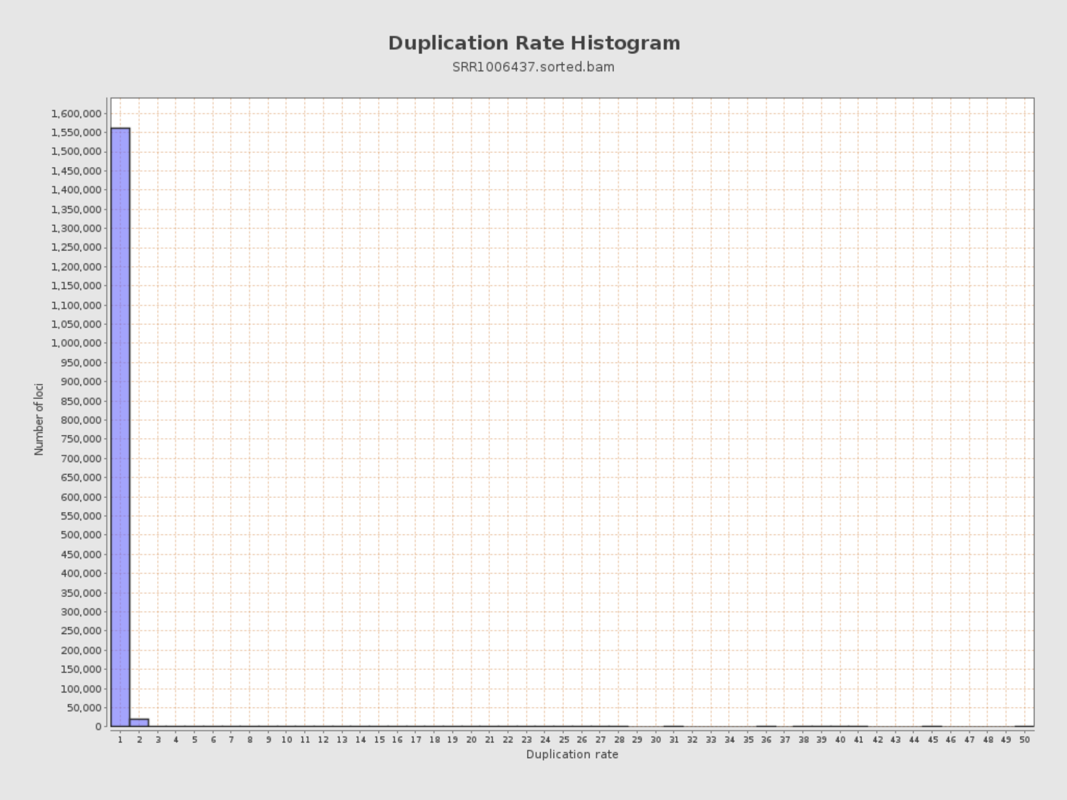
5. Results : Coverage Histogram (0-50X)



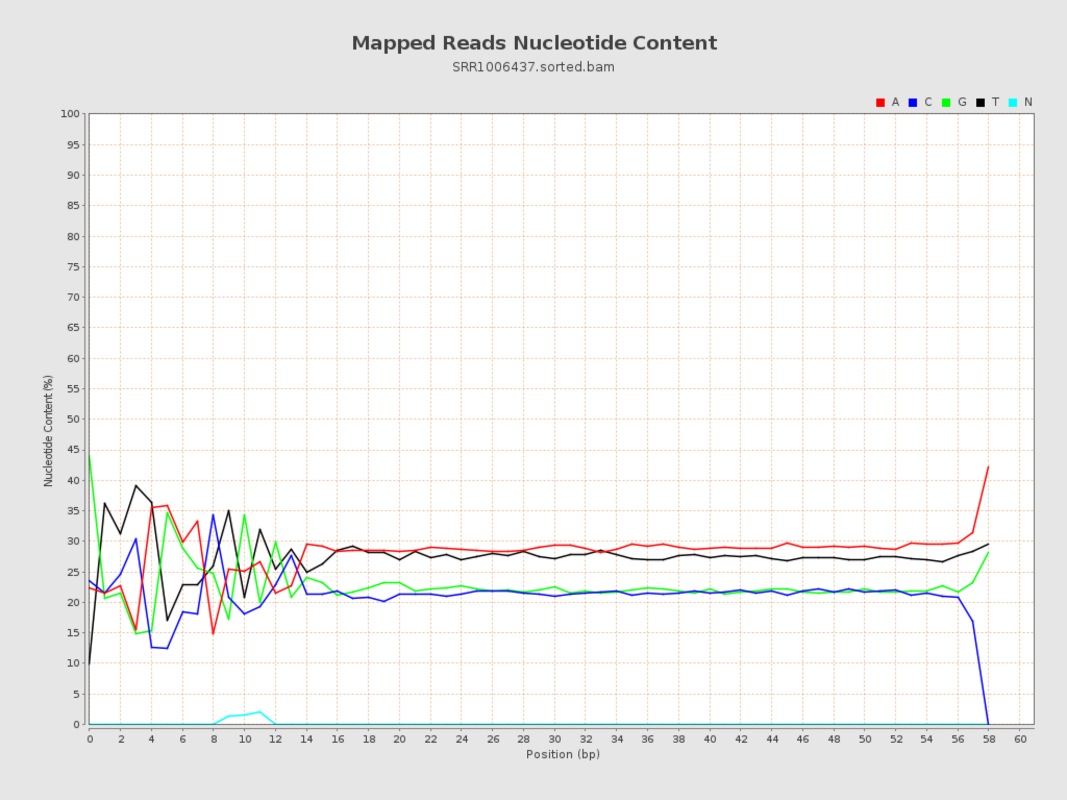
6. Results : Genome Fraction Coverage



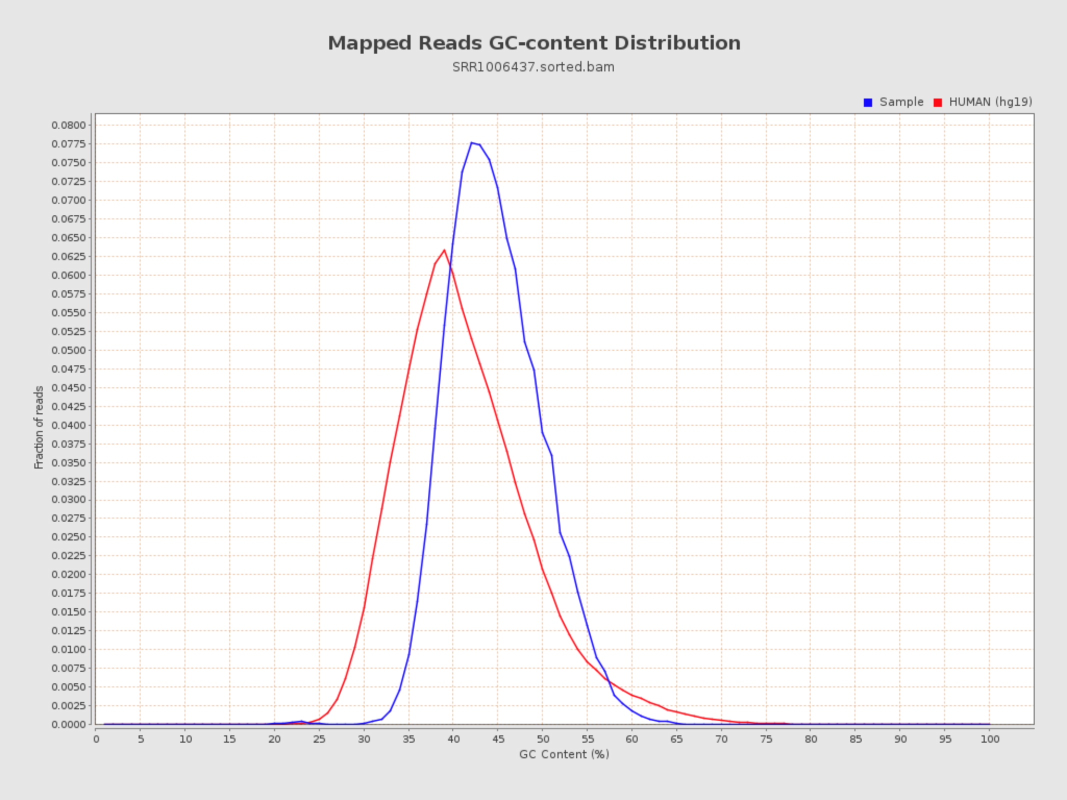
7. Results : Duplication Rate Histogram



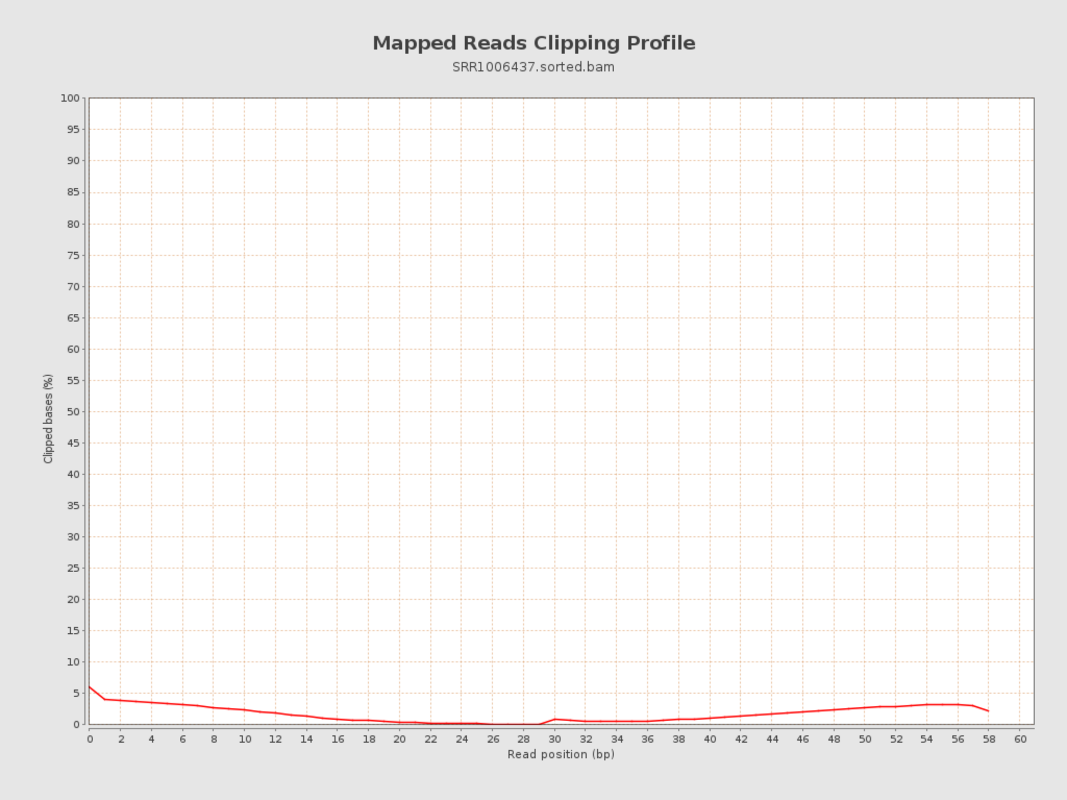
8. Results : Mapped Reads Nucleotide Content



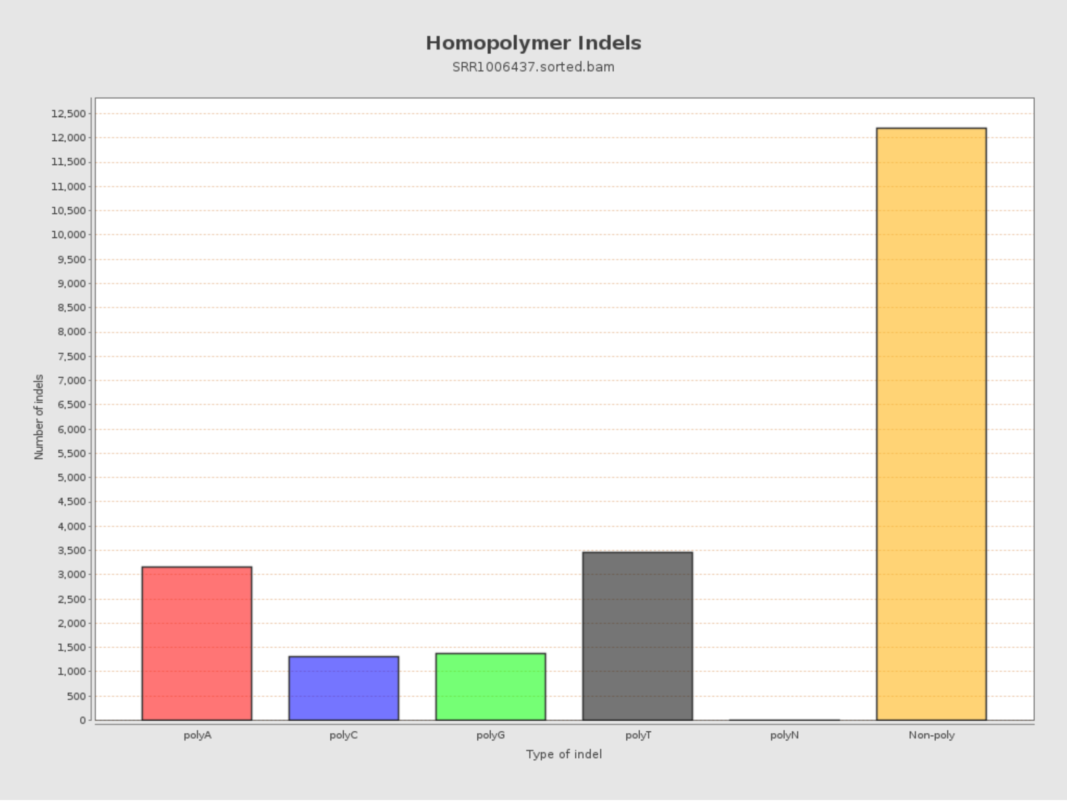
9. Results : Mapped Reads GC-content Distribution



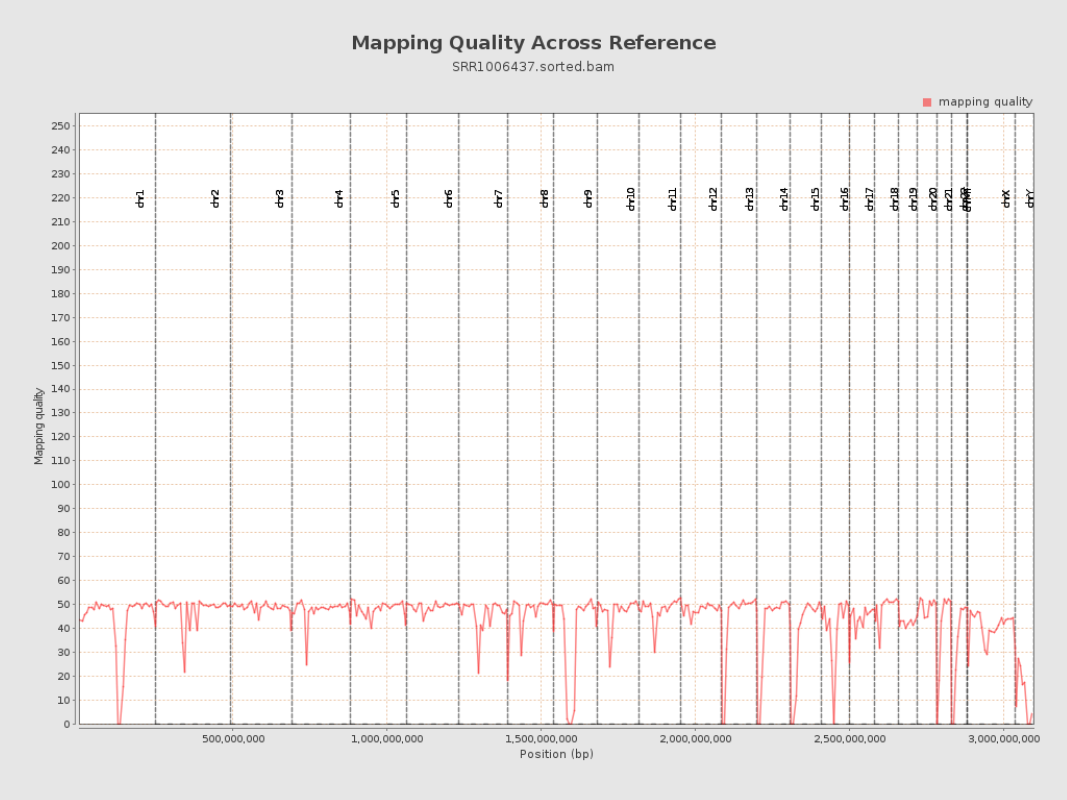
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram