Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:34:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006431.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_SRR1006431 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006431.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:34:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006431.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,373,121
Mapped reads	2,167,204 / 91.32%
Unmapped reads	205,917 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,620 / 0.24%
Read min/max/mean length	30 / 59 / 58.13
Duplicated reads (estimated)	113,042 / 4.76%
Duplication rate	4.54%
Clipped reads	303,419 / 12.79%

2.2. ACGT Content

Number/percentage of A's	34,949,540 / 28.5%
Number/percentage of C's	25,451,497 / 20.75%
Number/percentage of T's	35,295,804 / 28.78%
Number/percentage of G's	26,943,945 / 21.97%
Number/percentage of N's	2,094 / 0%
GC Percentage	42.72%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.3324

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

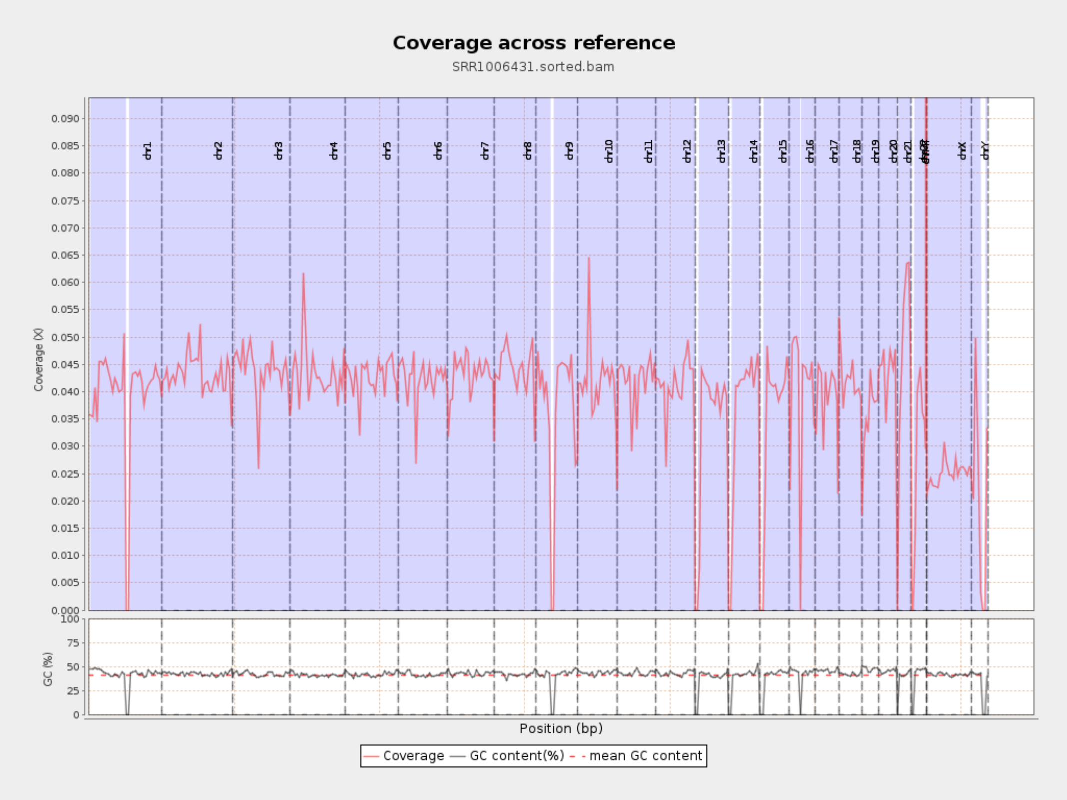
General error rate	0.43%
Mismatches	508,947
Insertions	7,524
Mapped reads with at least one insertion	0.35%
Deletions	21,017
Mapped reads with at least one deletion	0.96%
Homopolymer indels	44.48%

2.6. Chromosome stats

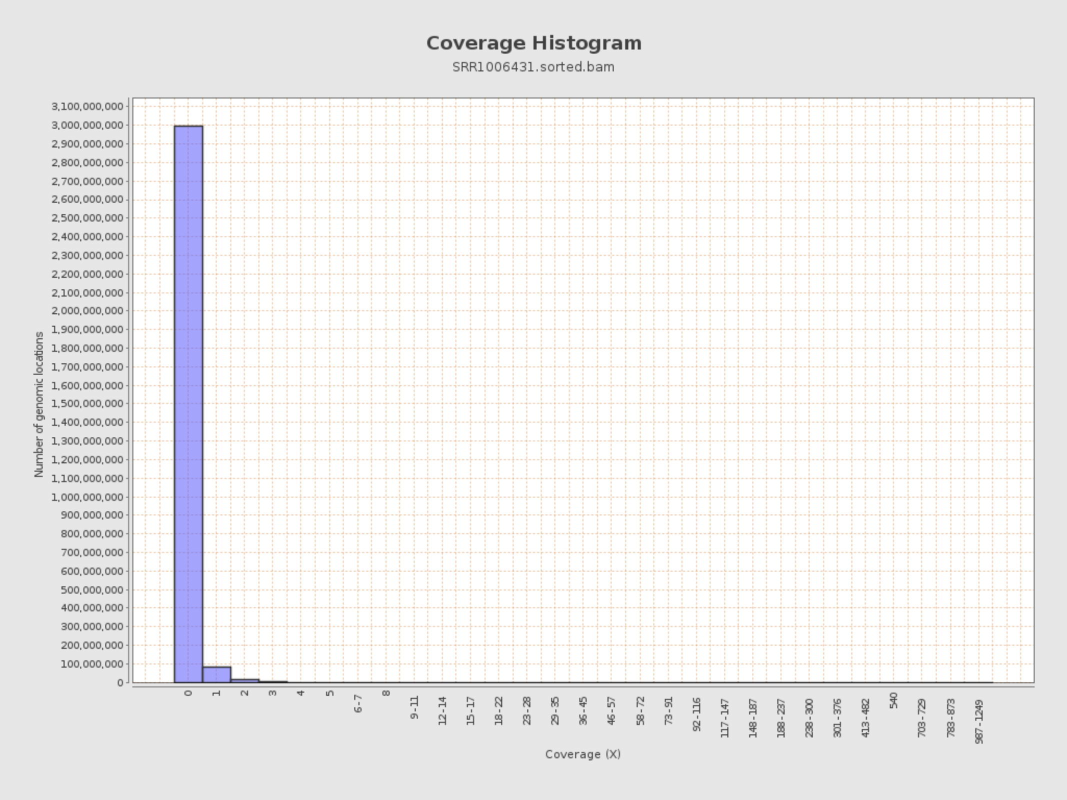
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9795476	0.0393	0.3716
chr2	243199373	10545320	0.0434	0.293
chr3	198022430	8685193	0.0439	0.2459
chr4	191154276	8269493	0.0433	0.2648
chr5	180915260	7710773	0.0426	0.2427
chr6	171115067	7257679	0.0424	0.2557
chr7	159138663	6887125	0.0433	0.3033

chr8	146364022	6455547	0.0441	0.7536
chr9	141213431	5174987	0.0366	0.2621
chr10	135534747	5731474	0.0423	0.323
chr11	135006516	5642387	0.0418	0.262
chr12	133851895	5521891	0.0413	0.2381
chr13	115169878	3841492	0.0334	0.2164
chr14	107349540	3835619	0.0357	0.5771
chr15	102531392	3537960	0.0345	0.2183
chr16	90354753	3604137	0.0399	0.2738
chr17	81195210	3139723	0.0387	0.2516
chr18	78077248	3295305	0.0422	0.3511
chr19	59128983	2139582	0.0362	0.307
chr20	63025520	2725880	0.0433	0.2774
chr21	48129895	2217128	0.0461	0.2808
chr22	51304566	1367220	0.0266	0.2057
chrMT	16571	284398	17.1624	12.373
chrX	155270560	3888958	0.025	0.1903
chrY	59373566	1123615	0.0189	0.2578

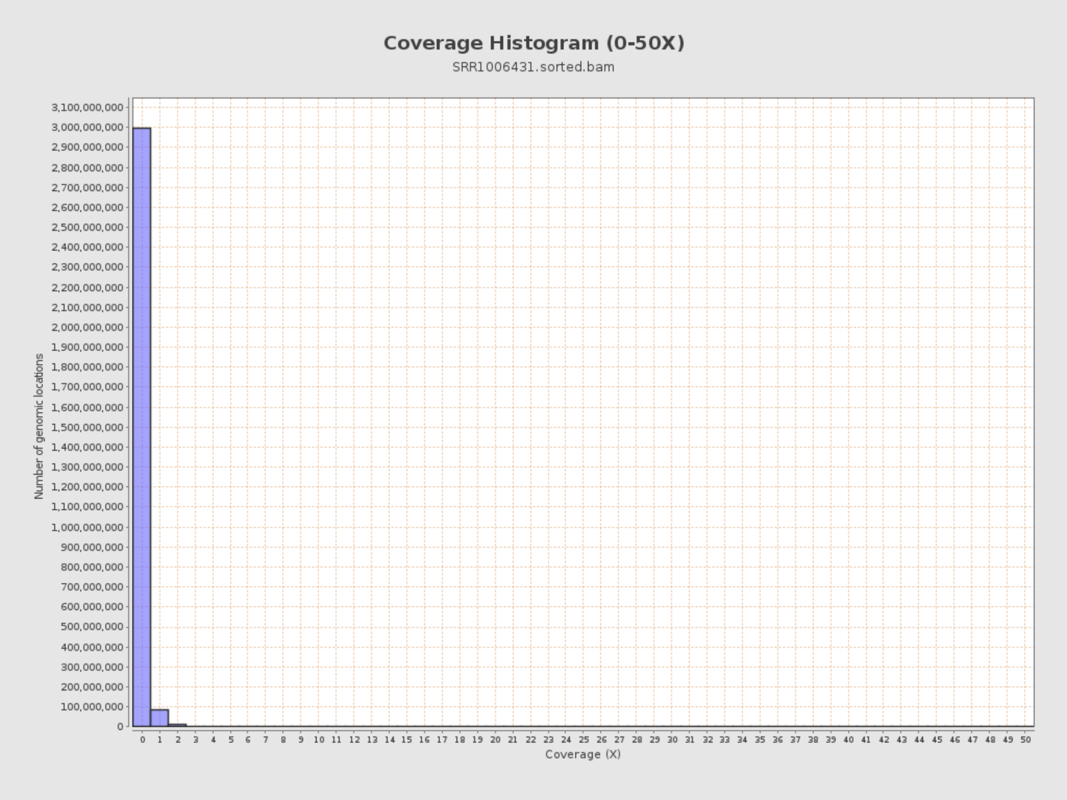
3. Results : Coverage across reference



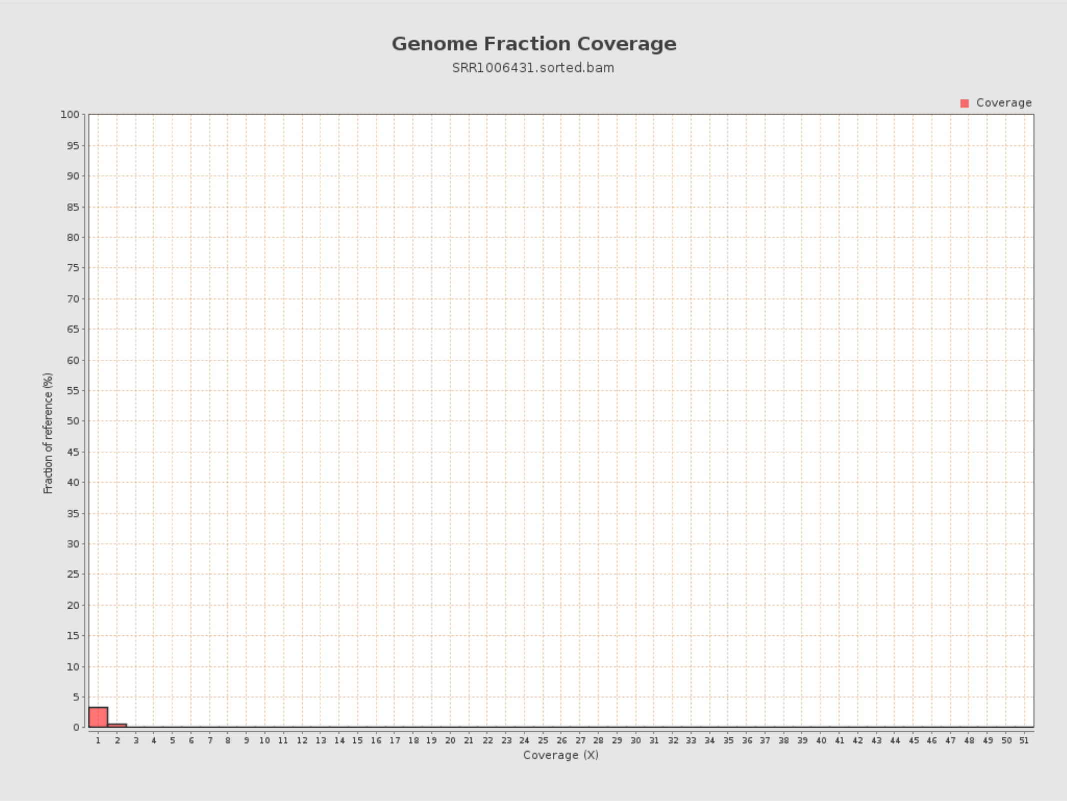
4. Results : Coverage Histogram



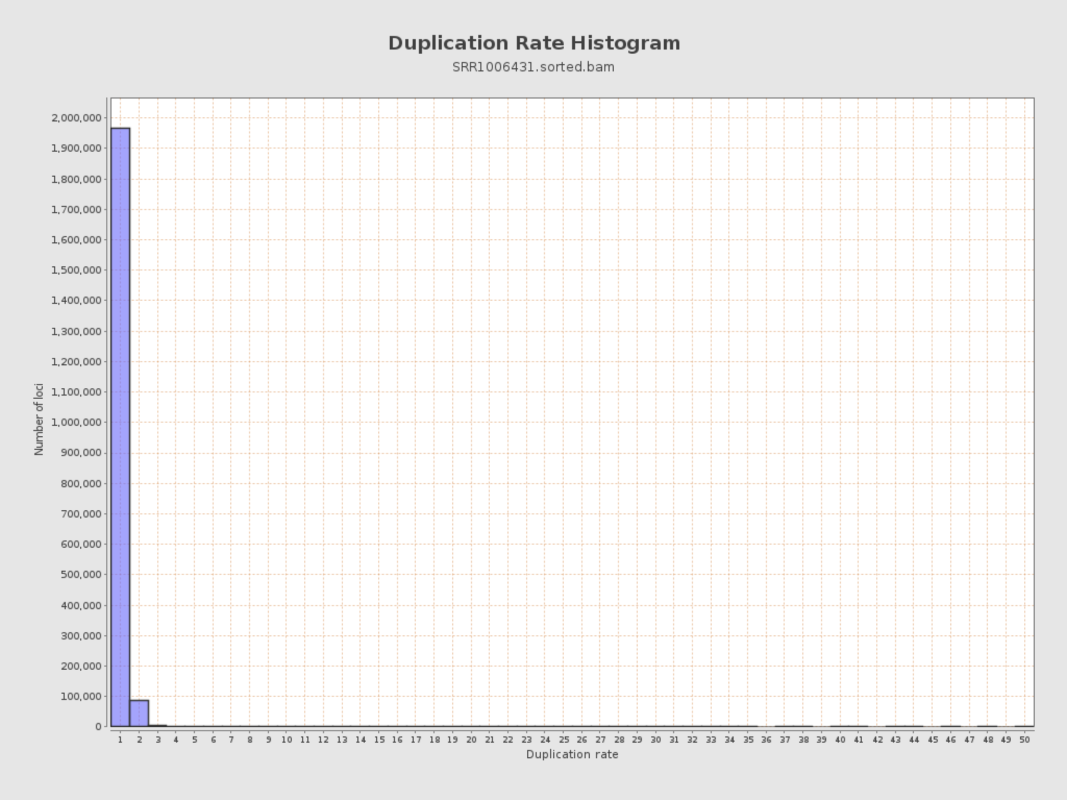
5. Results : Coverage Histogram (0-50X)



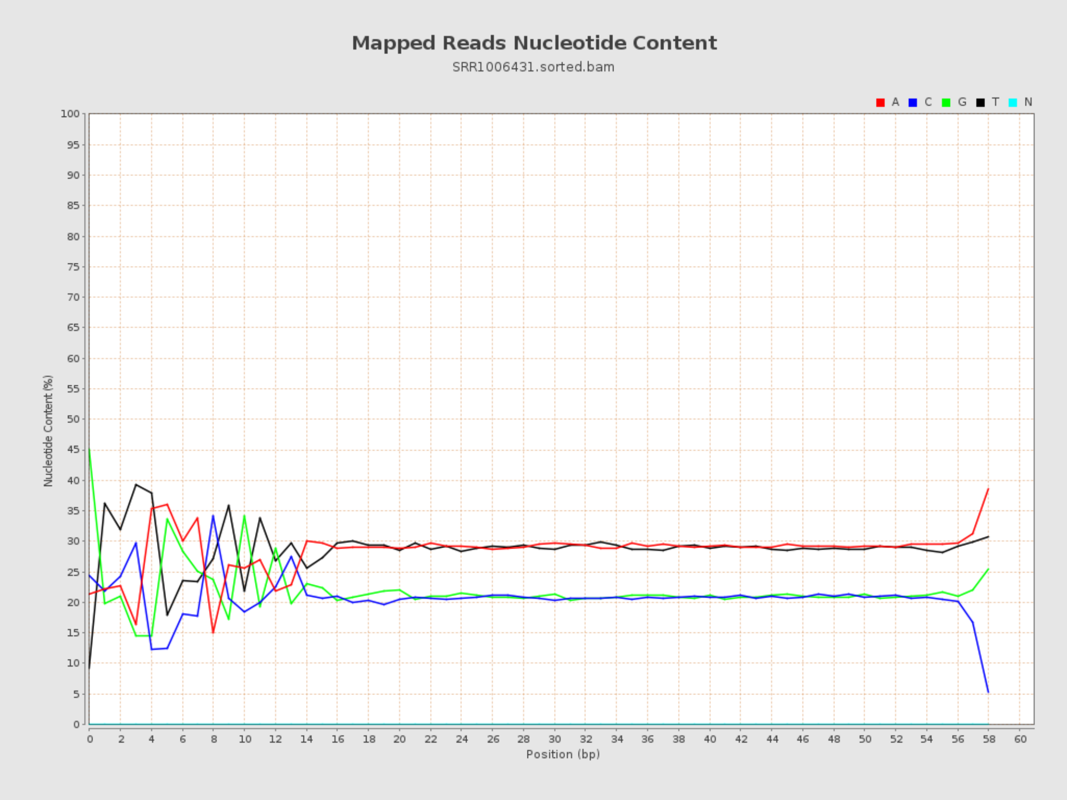
6. Results : Genome Fraction Coverage



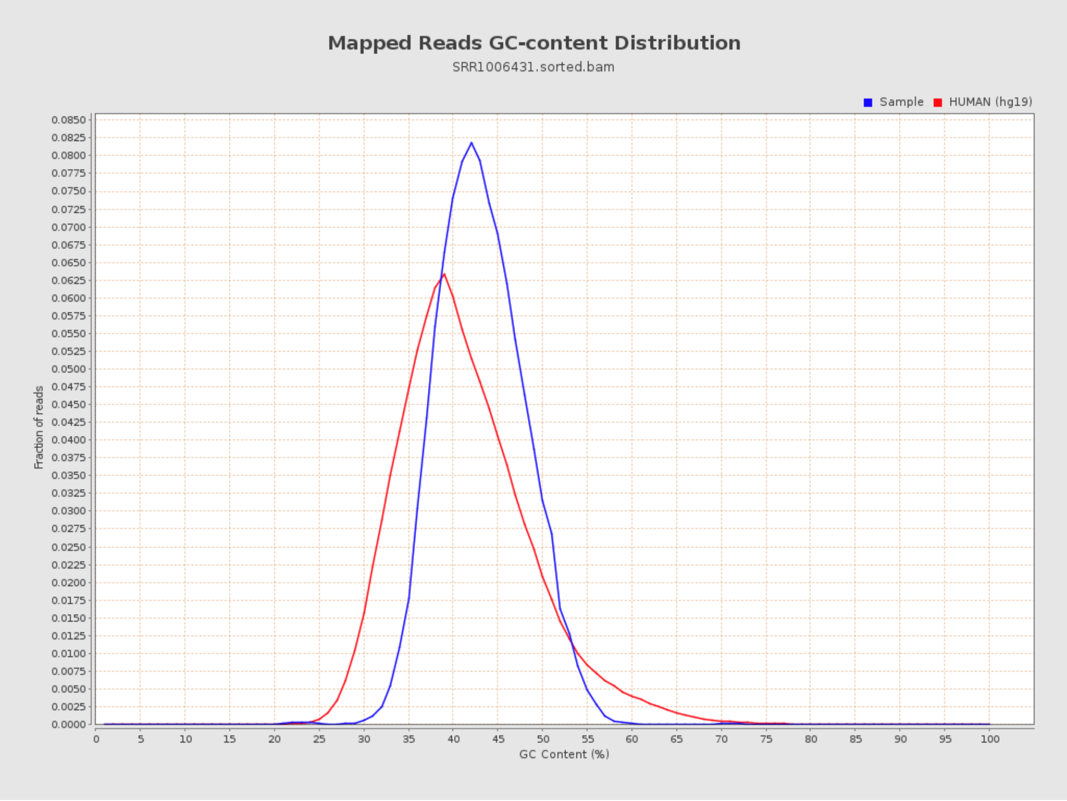
7. Results : Duplication Rate Histogram



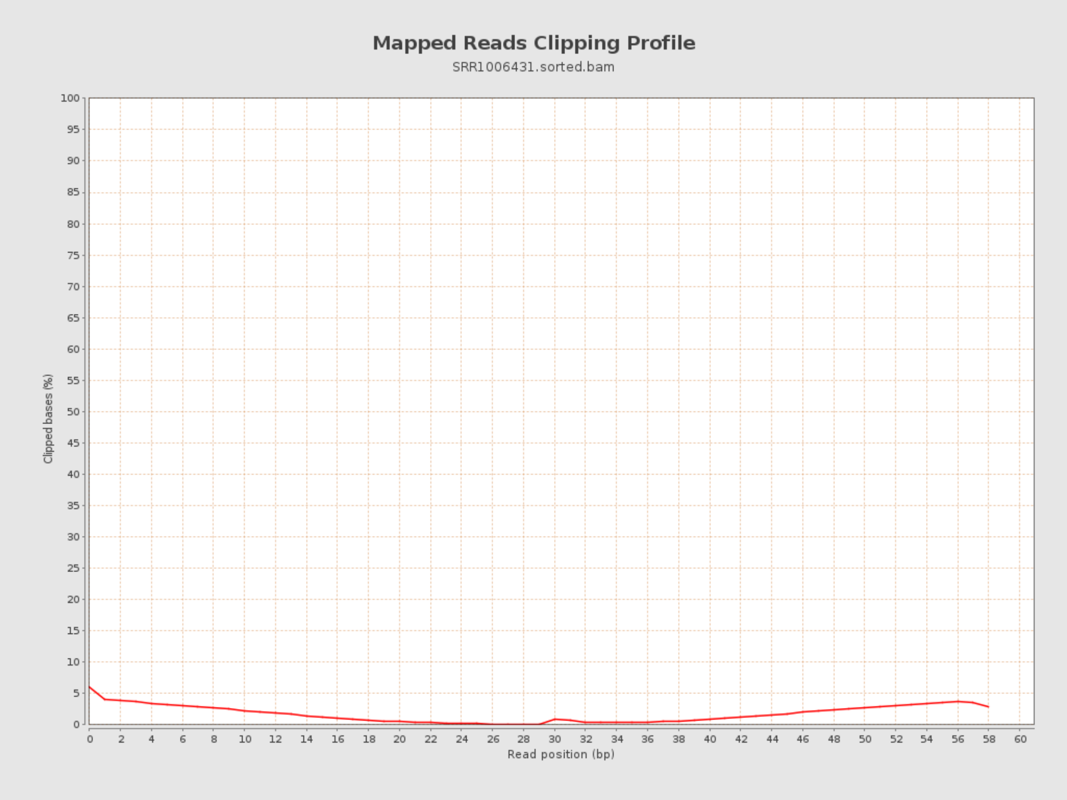
8. Results : Mapped Reads Nucleotide Content



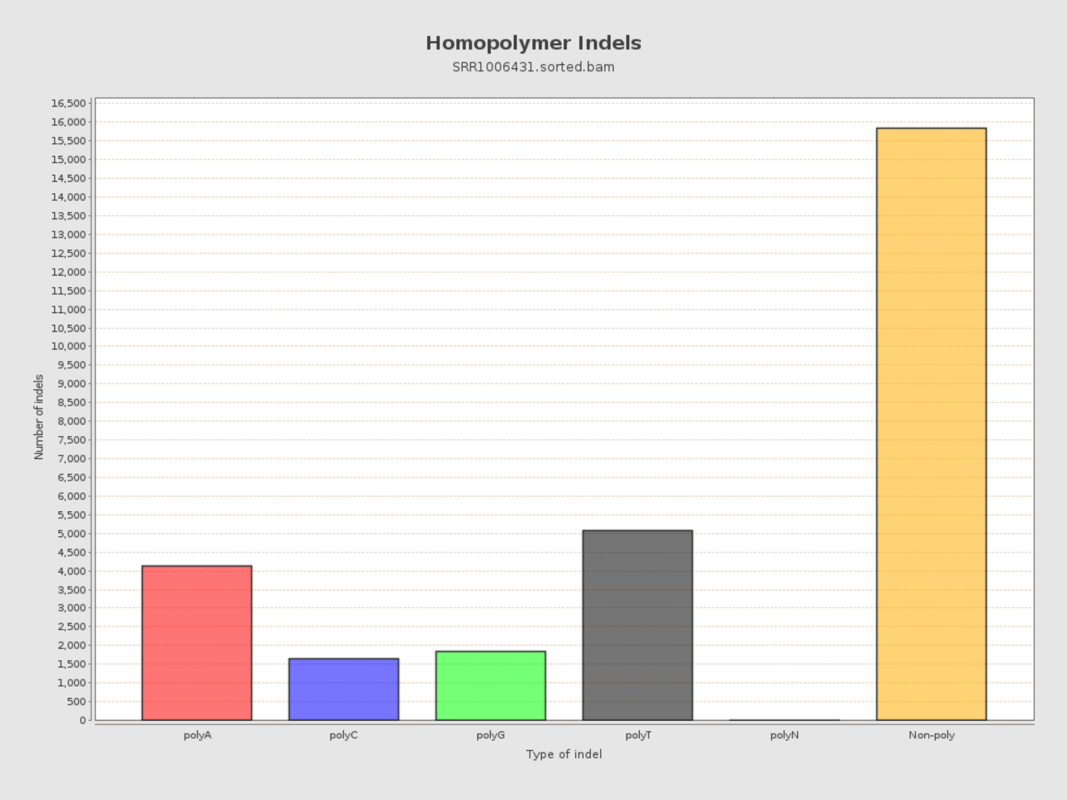
9. Results : Mapped Reads GC-content Distribution



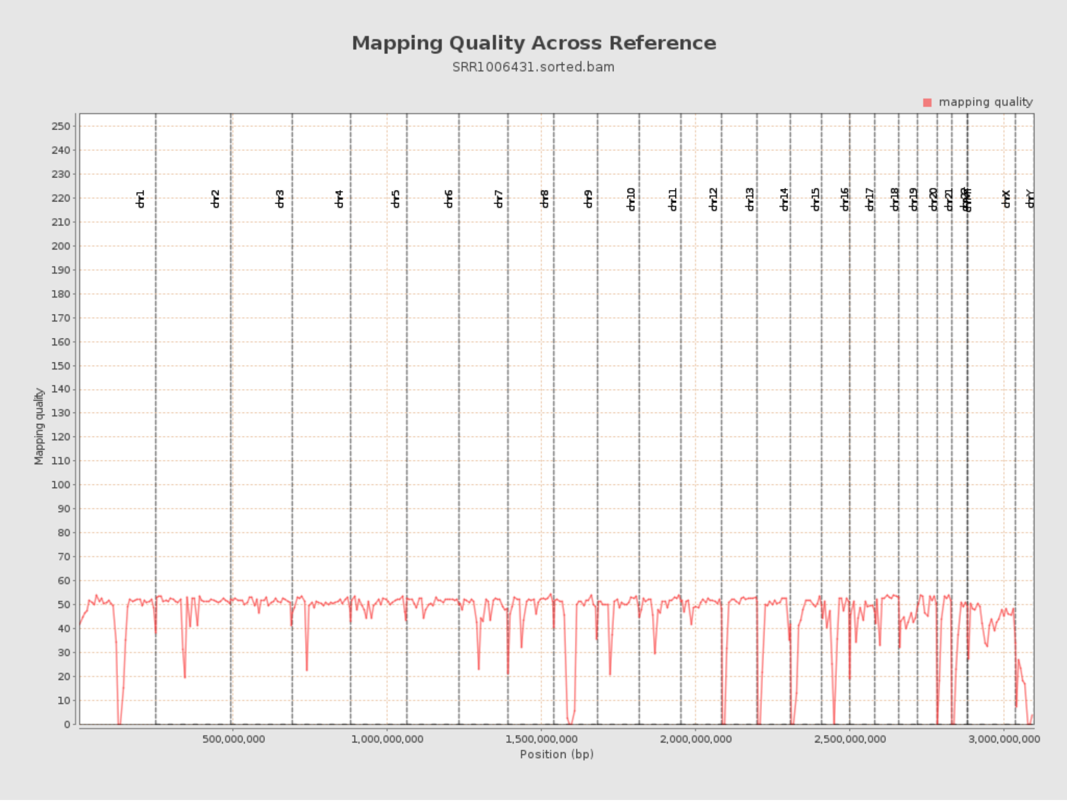
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram