Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:51:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006440.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_SRR1006440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006440.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:51:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,644,701
Mapped reads	4,422,208 / 95.21%
Unmapped reads	222,493 / 4.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,219 / 0.26%
Read min/max/mean length	30 / 59 / 57.3
Duplicated reads (estimated)	170,525 / 3.67%
Duplication rate	3.03%
Clipped reads	538,210 / 11.59%

2.2. ACGT Content

Number/percentage of A's	69,694,800 / 28.13%
Number/percentage of C's	51,984,420 / 20.98%
Number/percentage of T's	71,901,600 / 29.02%
Number/percentage of G's	54,144,324 / 21.86%
Number/percentage of N's	5,112 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.08

Standard Deviation	0.5778

2.4. Mapping Quality

Mean Mapping Quality	45.38

2.5. Mismatches and indels

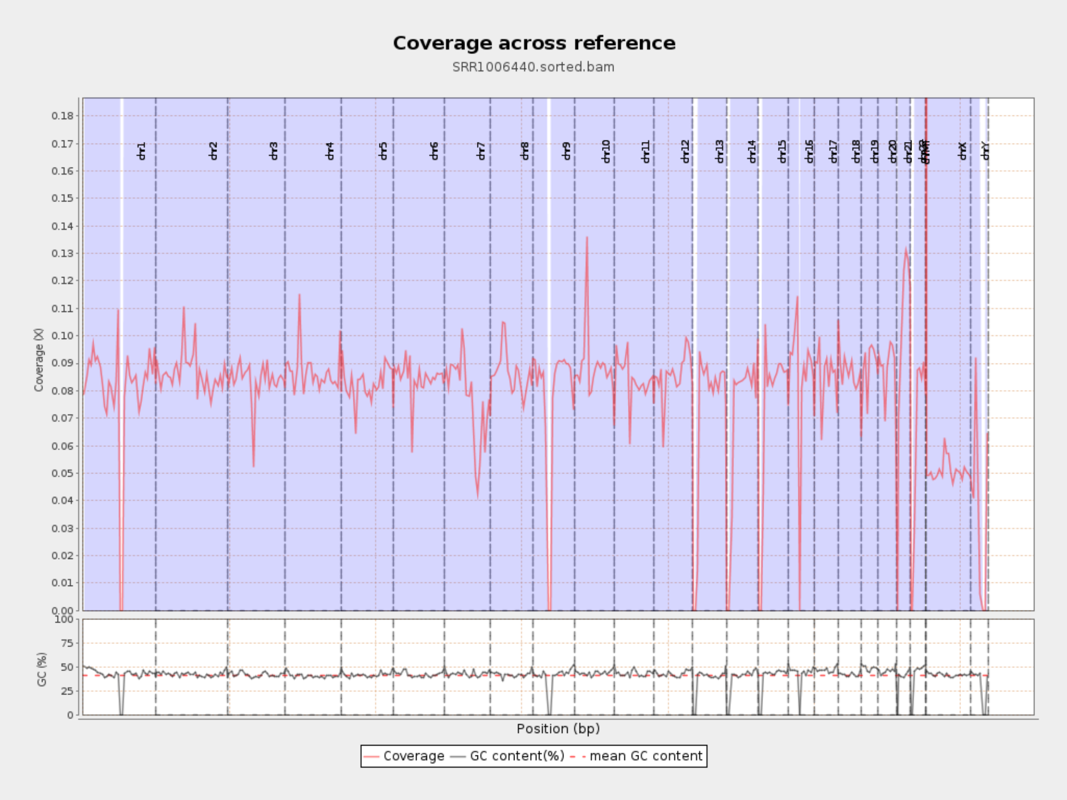
General error rate	0.41%
Mismatches	990,289
Insertions	15,781
Mapped reads with at least one insertion	0.36%
Deletions	46,383
Mapped reads with at least one deletion	1.04%
Homopolymer indels	45.24%

2.6. Chromosome stats

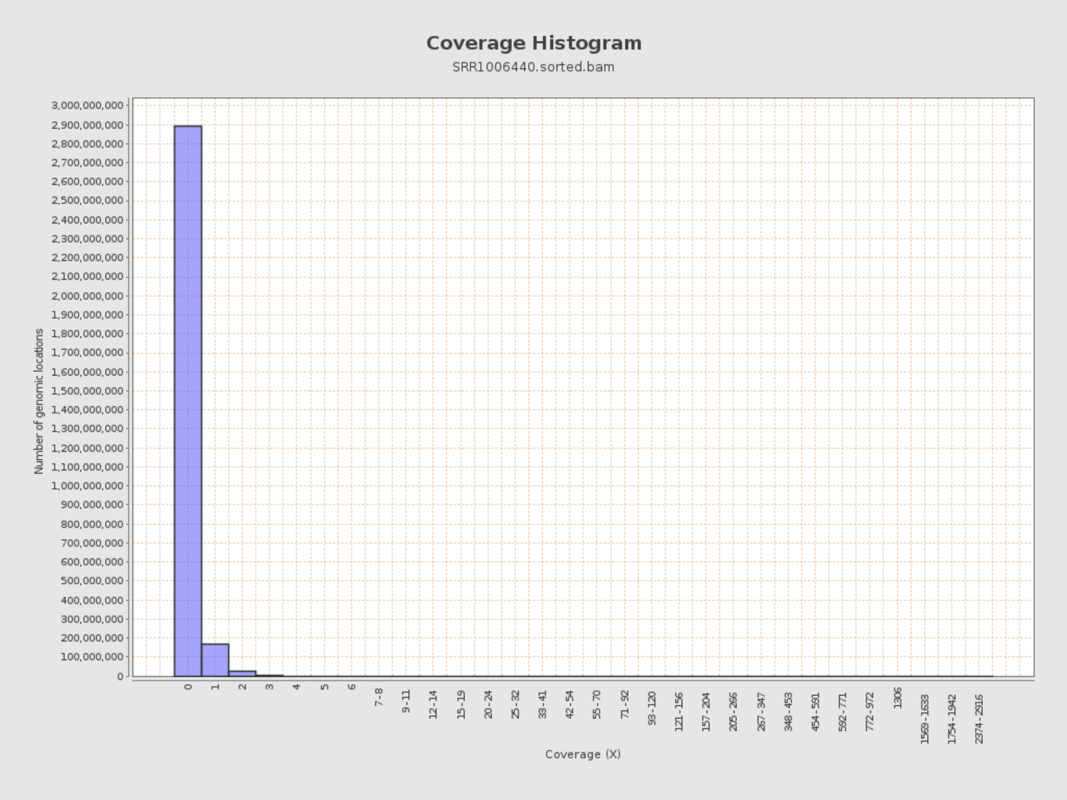
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19968288	0.0801	0.7925
chr2	243199373	21096210	0.0867	0.4776
chr3	198022430	16566723	0.0837	0.336
chr4	191154276	16659873	0.0872	0.3847
chr5	180915260	14953198	0.0827	0.3342
chr6	171115067	14470531	0.0846	0.3658
chr7	159138663	12262410	0.0771	0.5348

chr8	146364022	12640220	0.0864	1.668
chr9	141213431	10757316	0.0762	0.4214
chr10	135534747	12093431	0.0892	0.5537
chr11	135006516	11353307	0.0841	0.4295
chr12	133851895	11541711	0.0862	0.3472
chr13	115169878	8217977	0.0714	0.3094
chr14	107349540	7504926	0.0699	0.3285
chr15	102531392	7375183	0.0719	0.3129
chr16	90354753	7565217	0.0837	0.4196
chr17	81195210	7004360	0.0863	0.3981
chr18	78077248	6802969	0.0871	0.6629
chr19	59128983	5241062	0.0886	0.6187
chr20	63025520	5575182	0.0885	0.358
chr21	48129895	4812312	0.1	0.4423
chr22	51304566	3093055	0.0603	0.3295
chrMT	16571	135145	8.1555	5.5245
chrX	155270560	7923889	0.051	0.2876
chrY	59373566	2192488	0.0369	0.4325

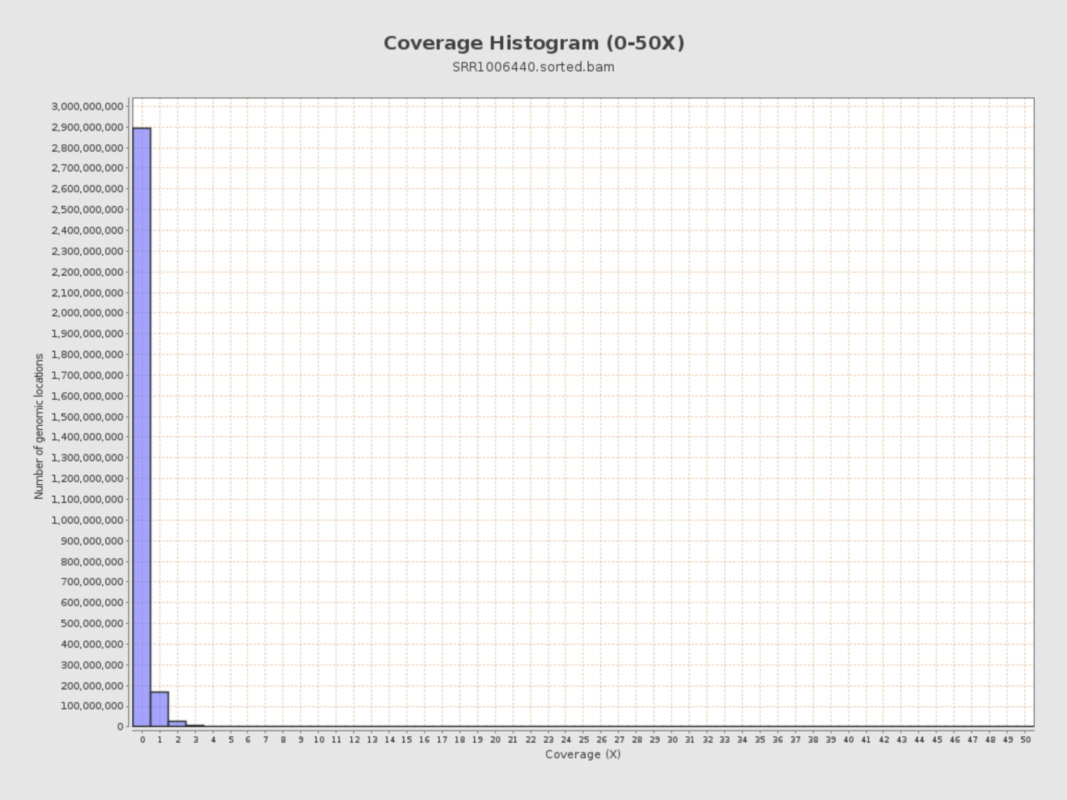
3. Results : Coverage across reference



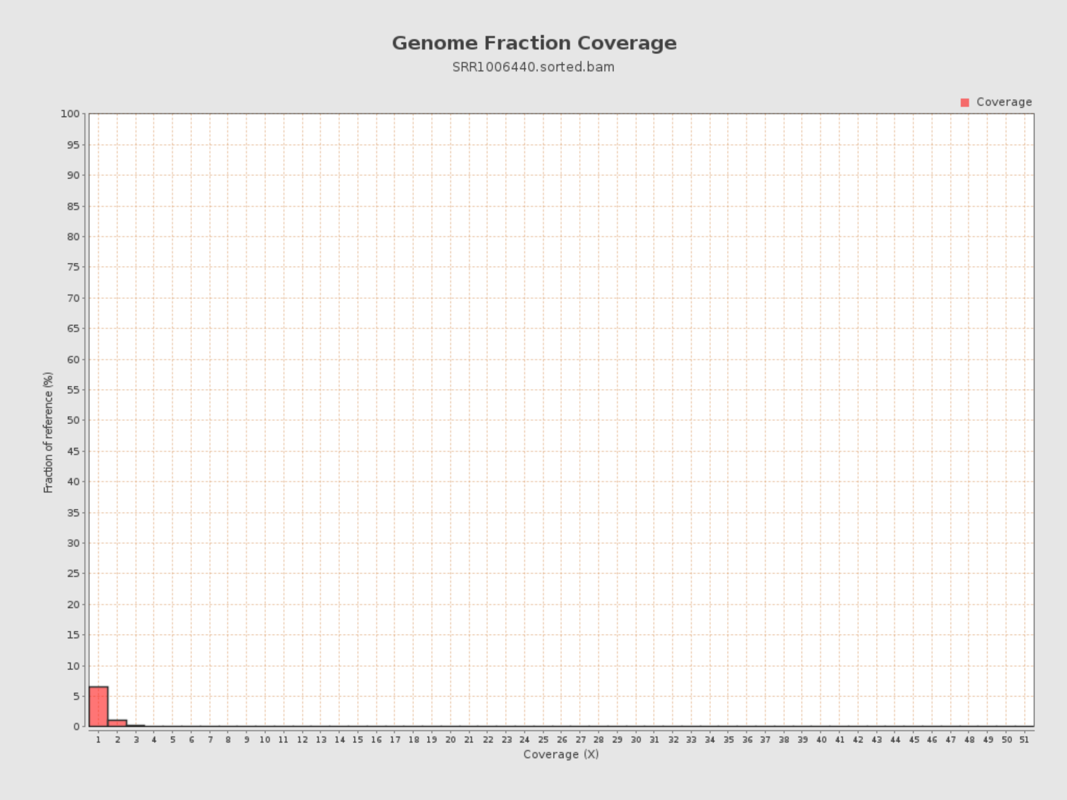
4. Results : Coverage Histogram



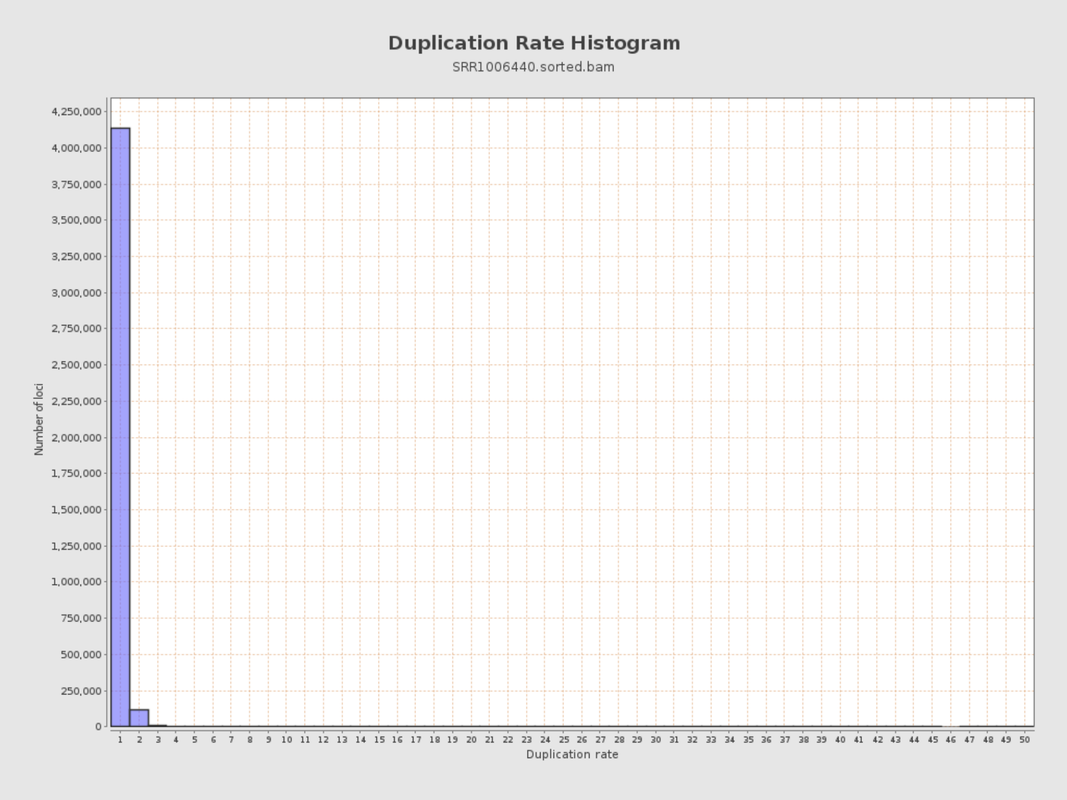
5. Results : Coverage Histogram (0-50X)



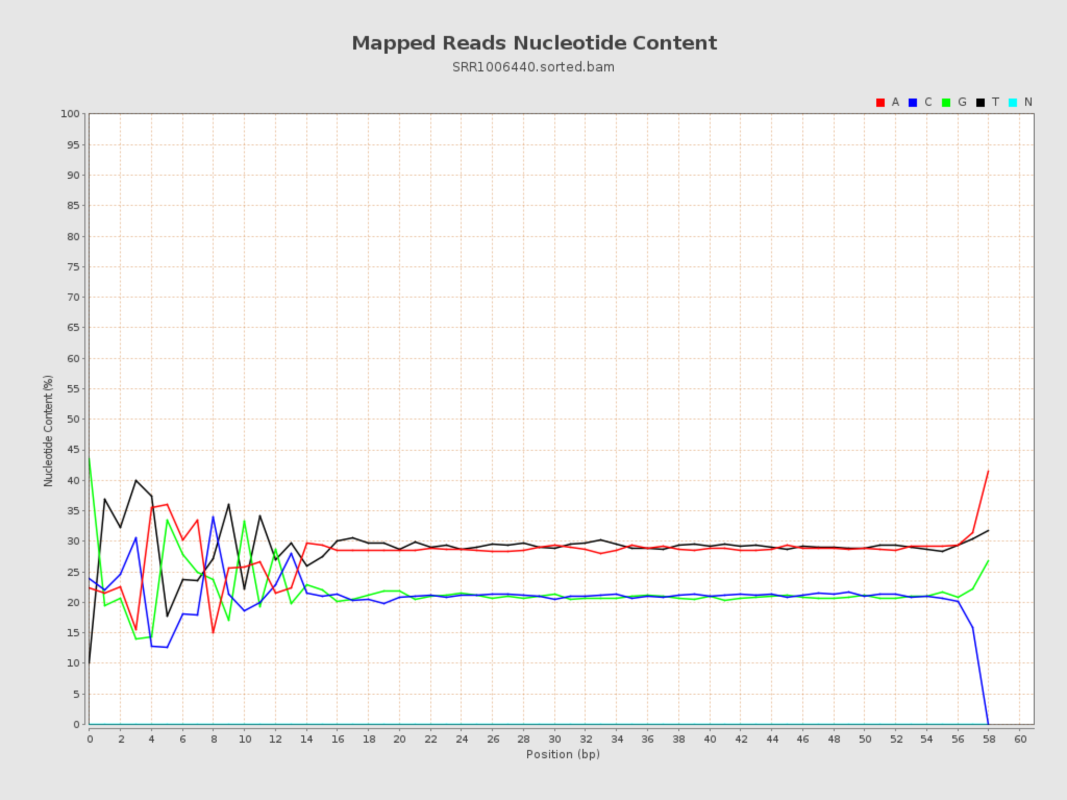
6. Results : Genome Fraction Coverage



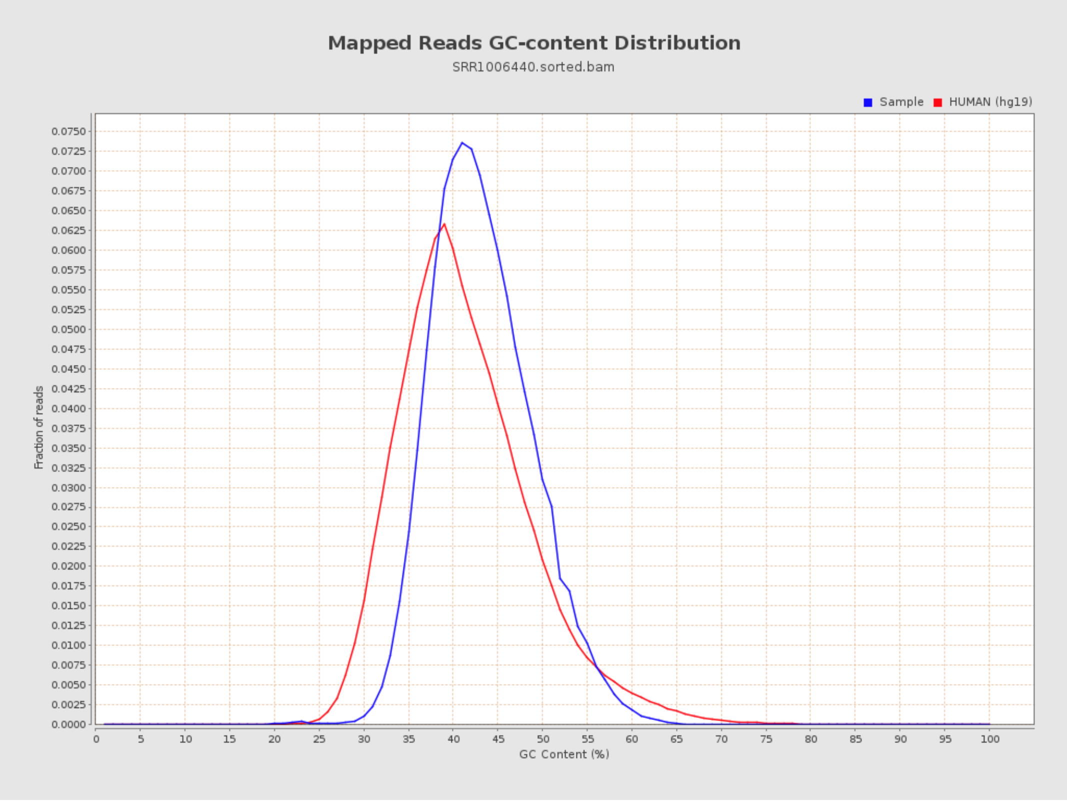
7. Results : Duplication Rate Histogram



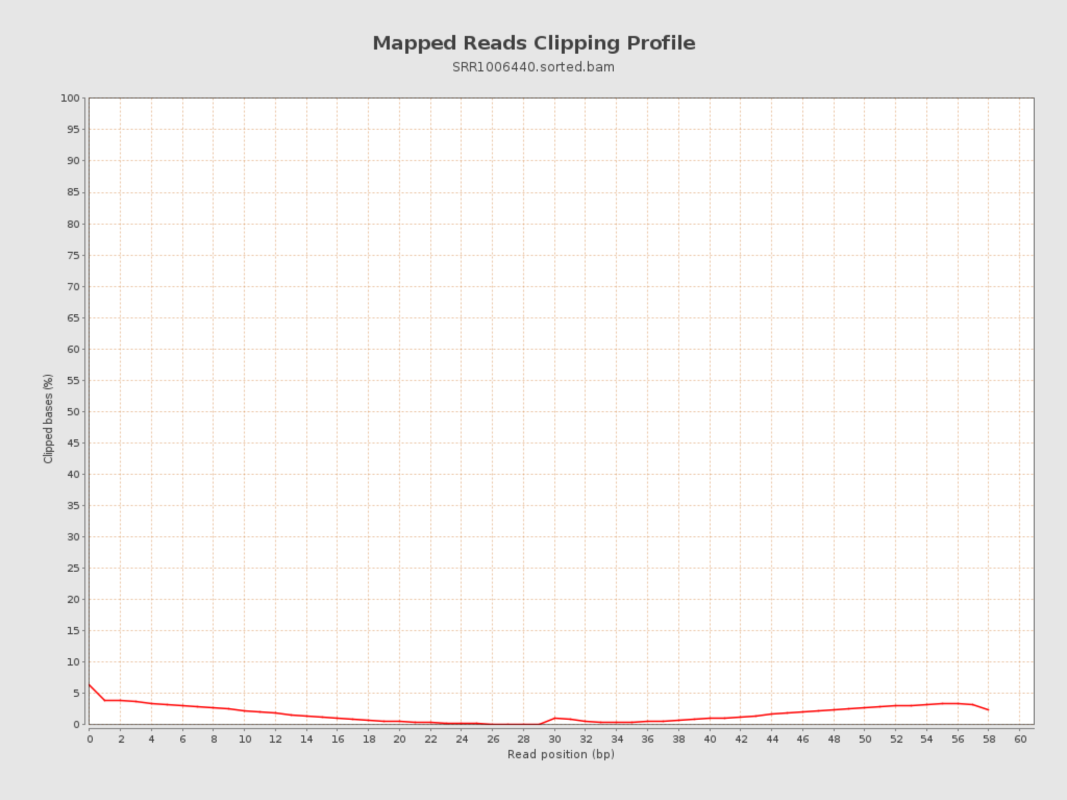
8. Results : Mapped Reads Nucleotide Content



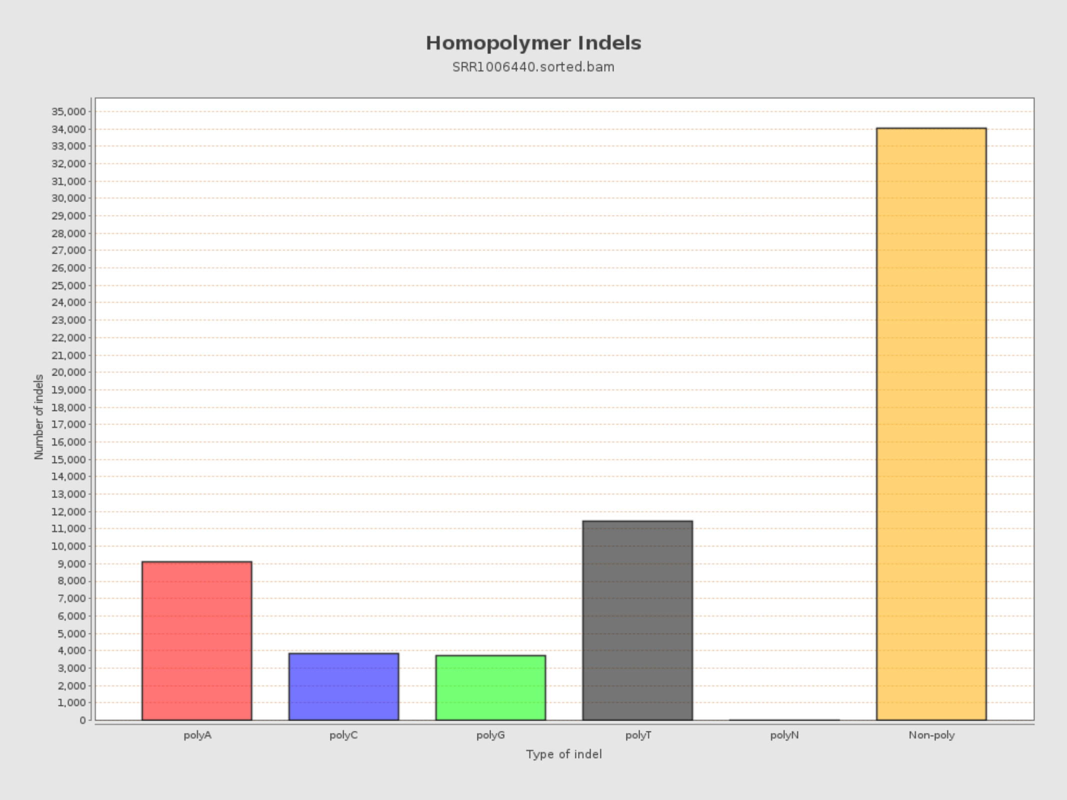
9. Results : Mapped Reads GC-content Distribution



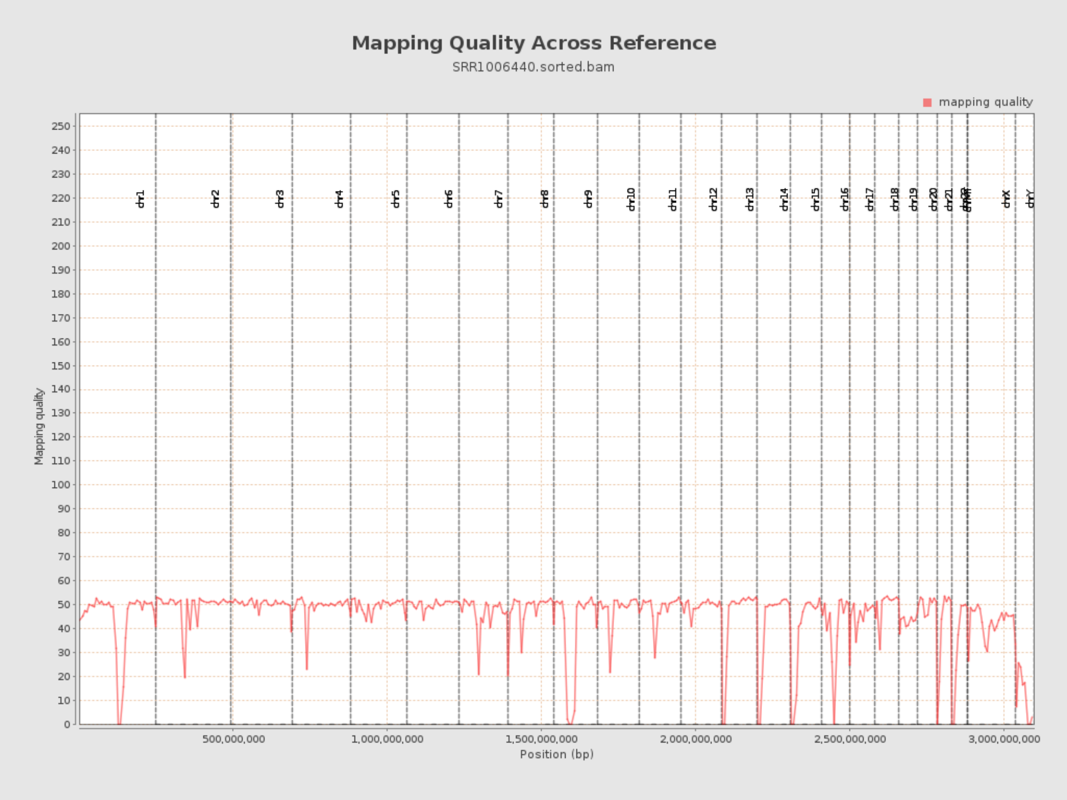
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram