Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:49:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054596.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_SRR054596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:49:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,495,535
Mapped reads	3,426,504 / 76.22%
Unmapped reads	1,069,031 / 23.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	93 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	615,611 / 13.69%
Duplication rate	13.72%
Clipped reads	507,979 / 11.3%

2.2. ACGT Content

Number/percentage of A's	48,703,946 / 30.49%
Number/percentage of C's	32,098,001 / 20.09%
Number/percentage of T's	46,827,295 / 29.32%
Number/percentage of G's	32,100,364 / 20.1%
Number/percentage of N's	1,745 / 0%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4604

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

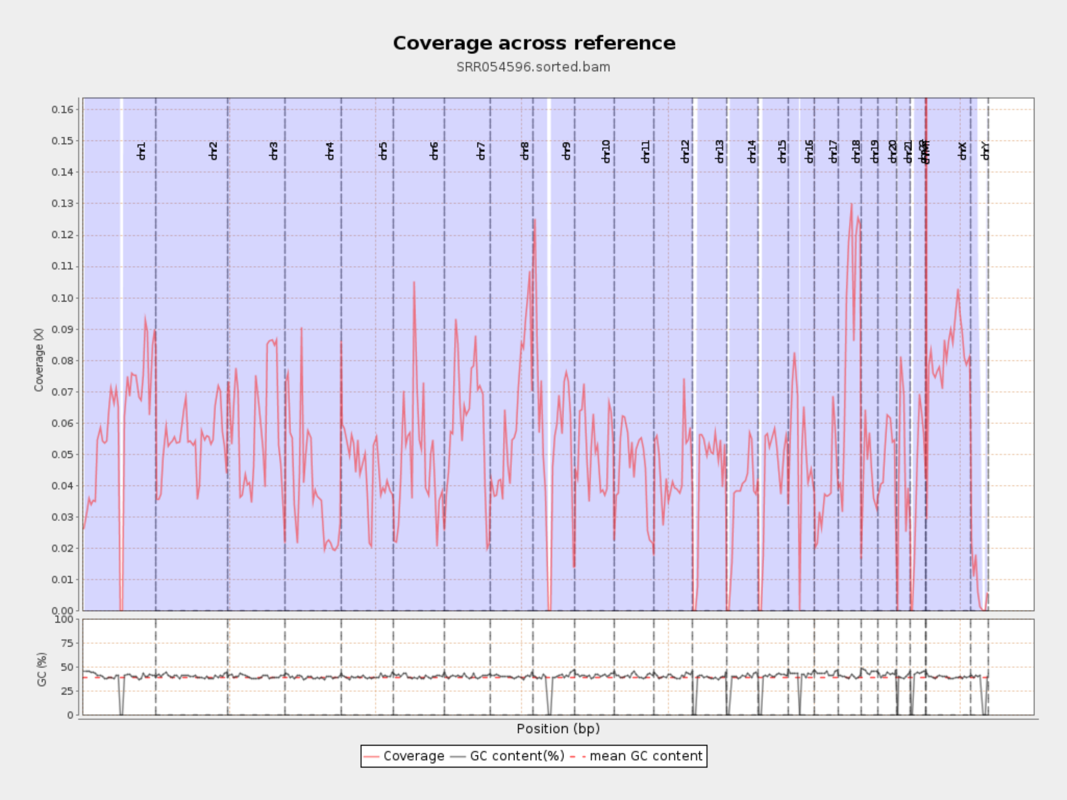
General error rate	0.67%
Mismatches	1,053,973
Insertions	6,942
Mapped reads with at least one insertion	0.2%
Deletions	22,135
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.65%

2.6. Chromosome stats

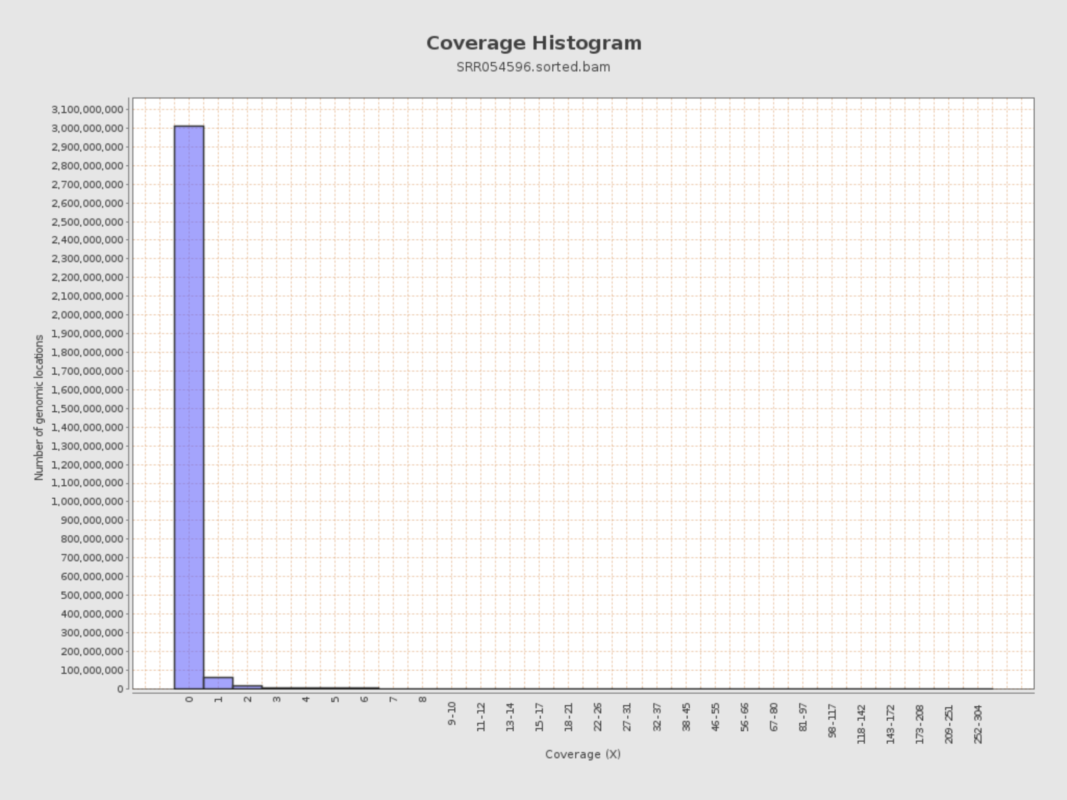
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14618458	0.0586	0.5167
chr2	243199373	13086064	0.0538	0.4975
chr3	198022430	11595479	0.0586	0.4662
chr4	191154276	7666252	0.0401	0.387
chr5	180915260	8171851	0.0452	0.3971
chr6	171115067	8183182	0.0478	0.4508
chr7	159138663	9577362	0.0602	0.5073

chr8	146364022	8960036	0.0612	0.5049
chr9	141213431	7974142	0.0565	0.4807
chr10	135534747	6956400	0.0513	0.4448
chr11	135006516	6119716	0.0453	0.44
chr12	133851895	6106184	0.0456	0.3975
chr13	115169878	4961180	0.0431	0.3913
chr14	107349540	3762524	0.035	0.3813
chr15	102531392	4316291	0.0421	0.3791
chr16	90354753	4619575	0.0511	0.4642
chr17	81195210	3081266	0.0379	0.3572
chr18	78077248	7020917	0.0899	0.6463
chr19	59128983	2625722	0.0444	0.4568
chr20	63025520	3145122	0.0499	0.4279
chr21	48129895	2092088	0.0435	0.4392
chr22	51304566	2053957	0.04	0.3711
chrMT	16571	17560	1.0597	2.1124
chrX	155270560	12616413	0.0813	0.605
chrY	59373566	435961	0.0073	0.1565

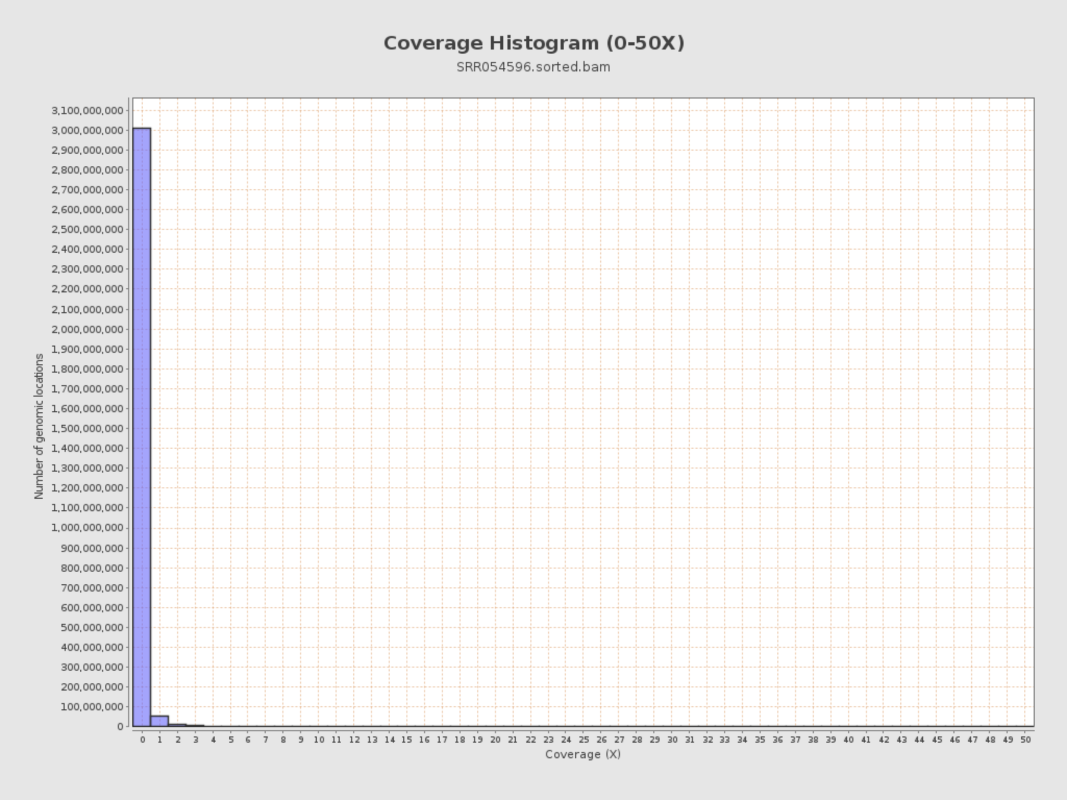
3. Results : Coverage across reference



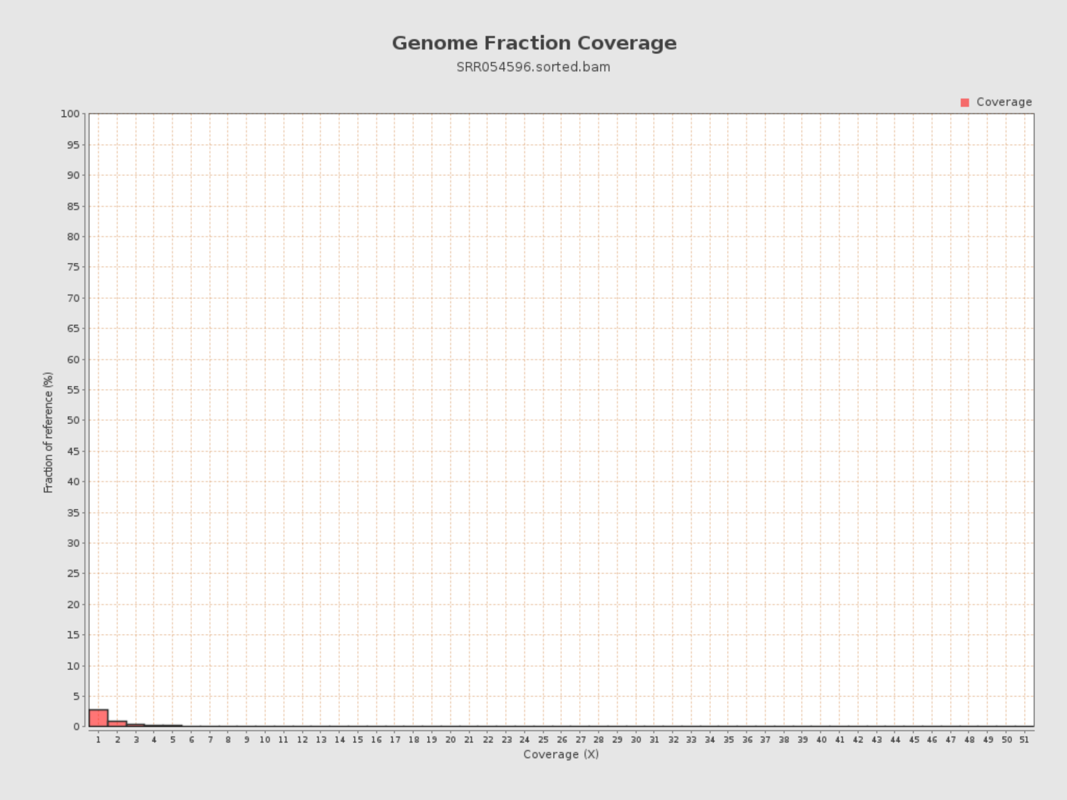
4. Results : Coverage Histogram



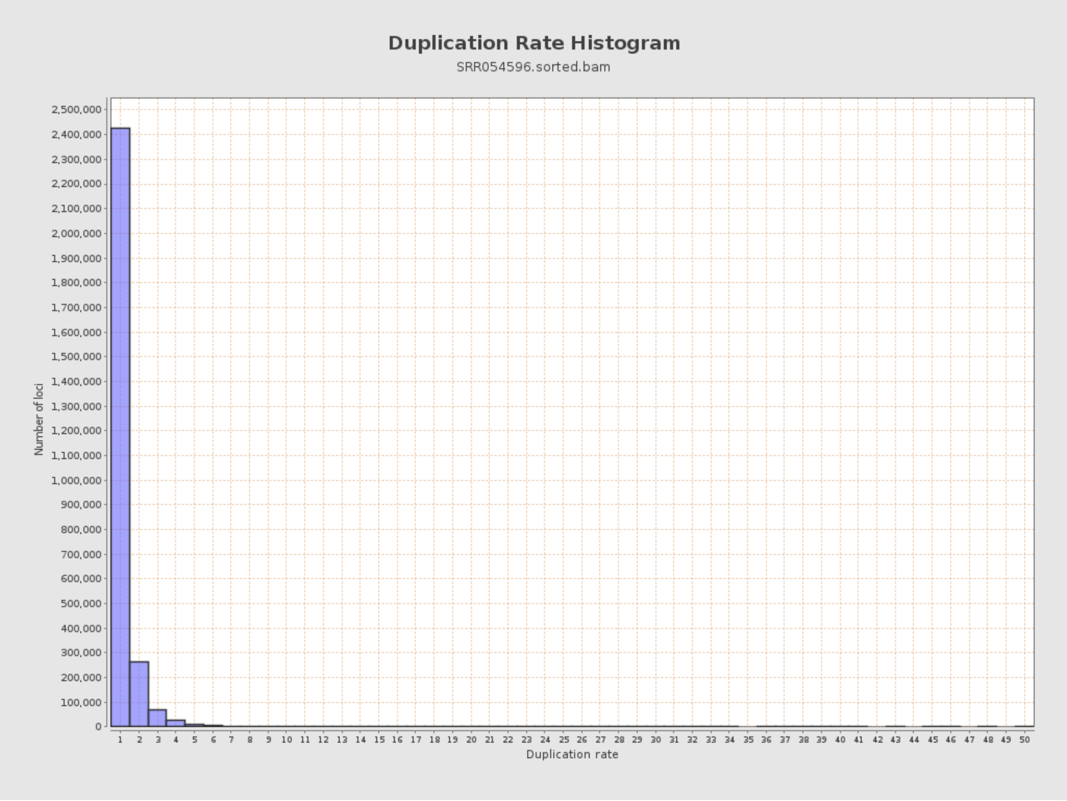
5. Results : Coverage Histogram (0-50X)



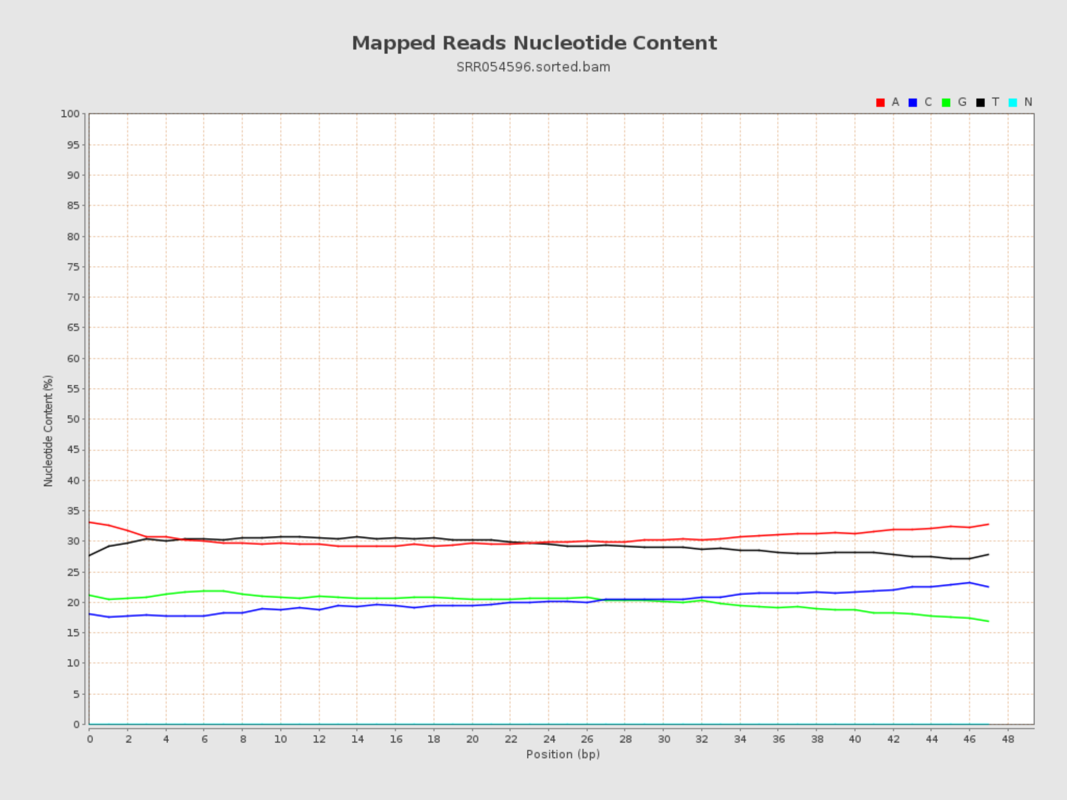
6. Results : Genome Fraction Coverage



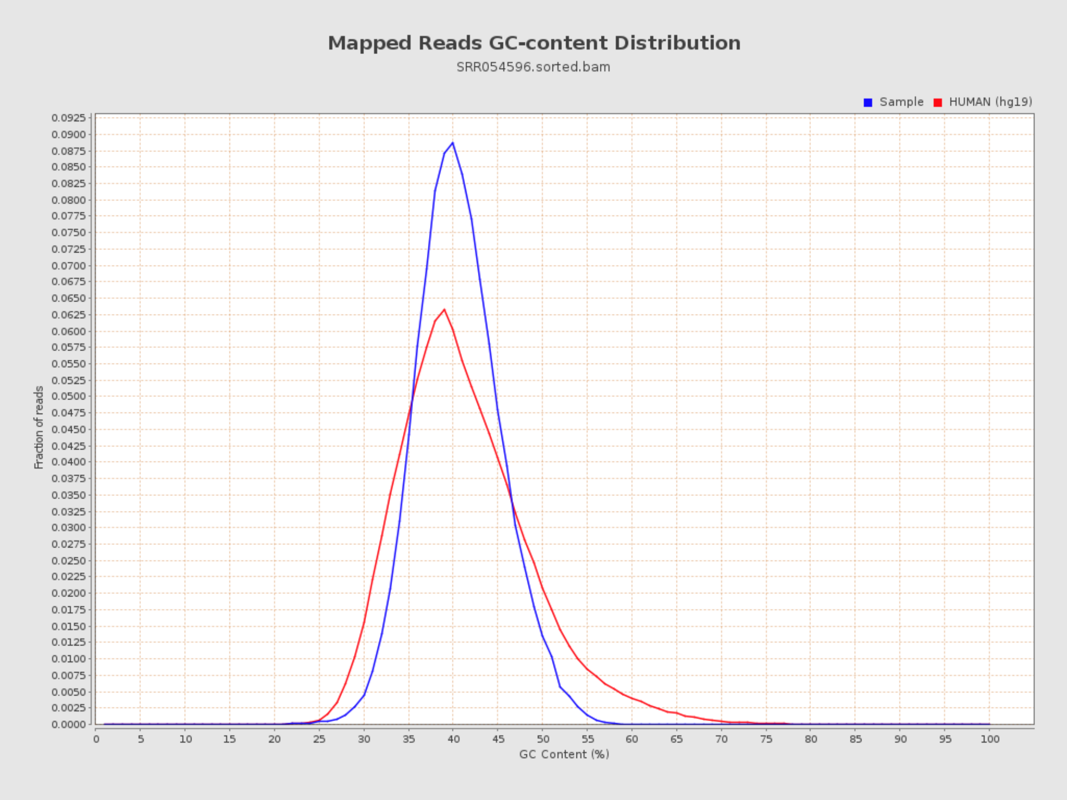
7. Results : Duplication Rate Histogram



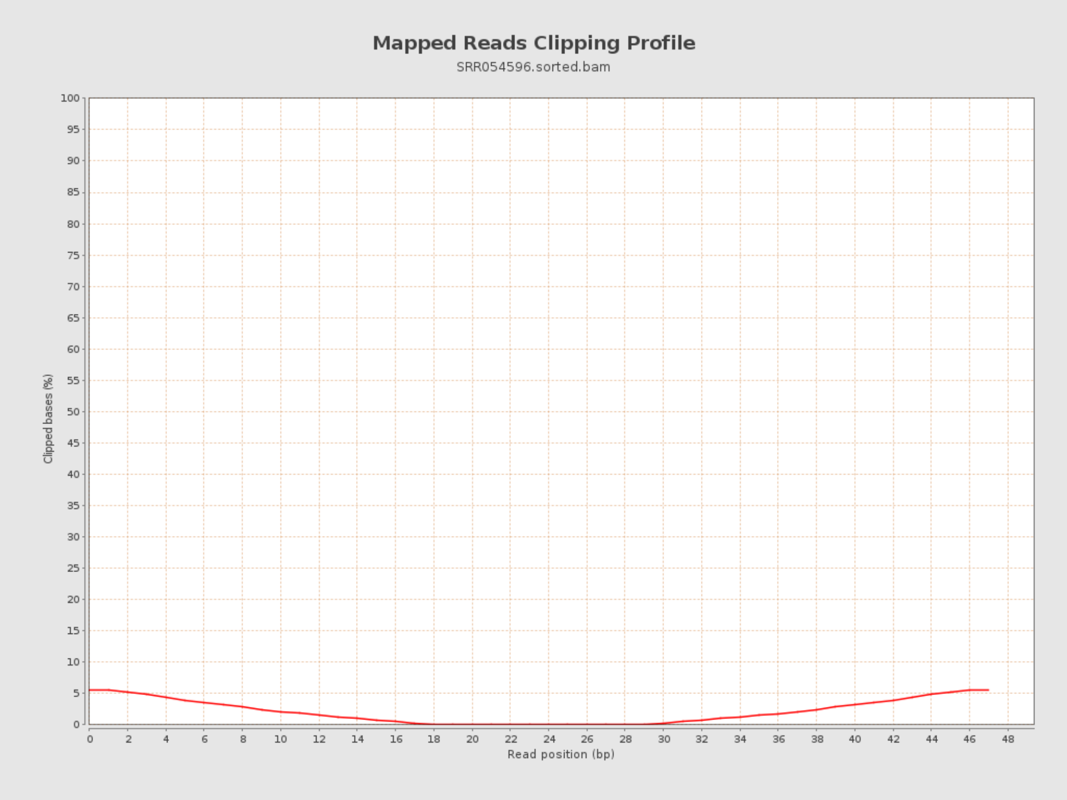
8. Results : Mapped Reads Nucleotide Content



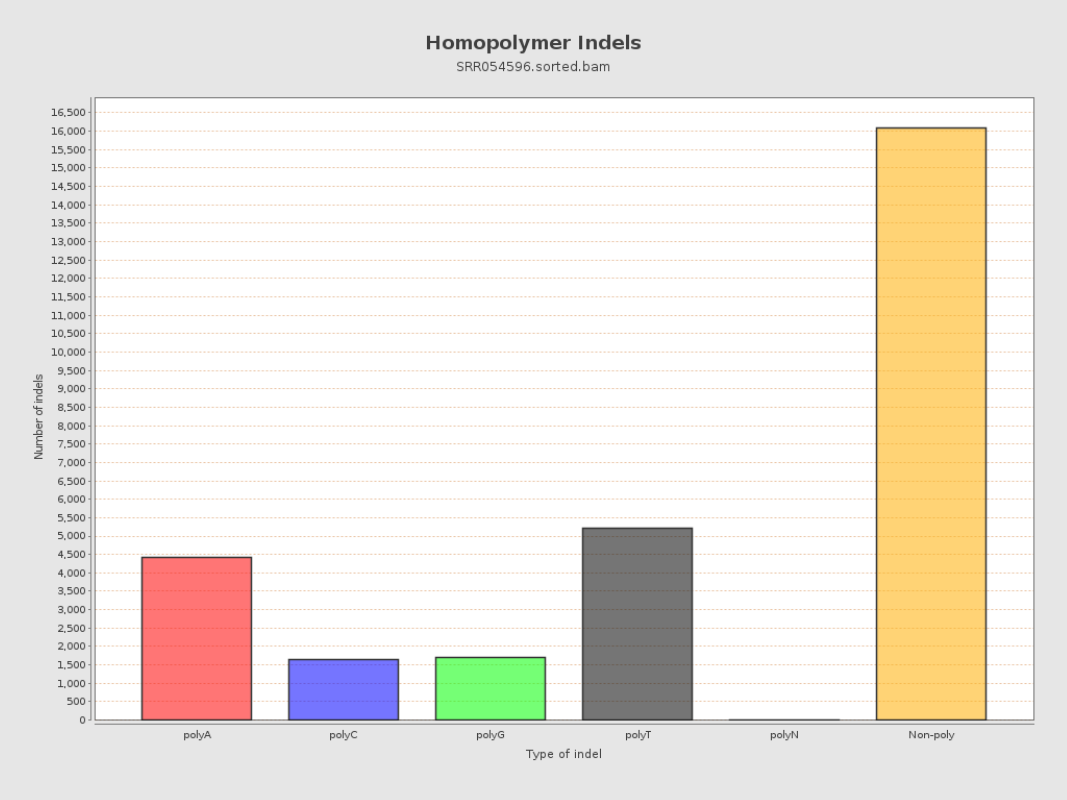
9. Results : Mapped Reads GC-content Distribution



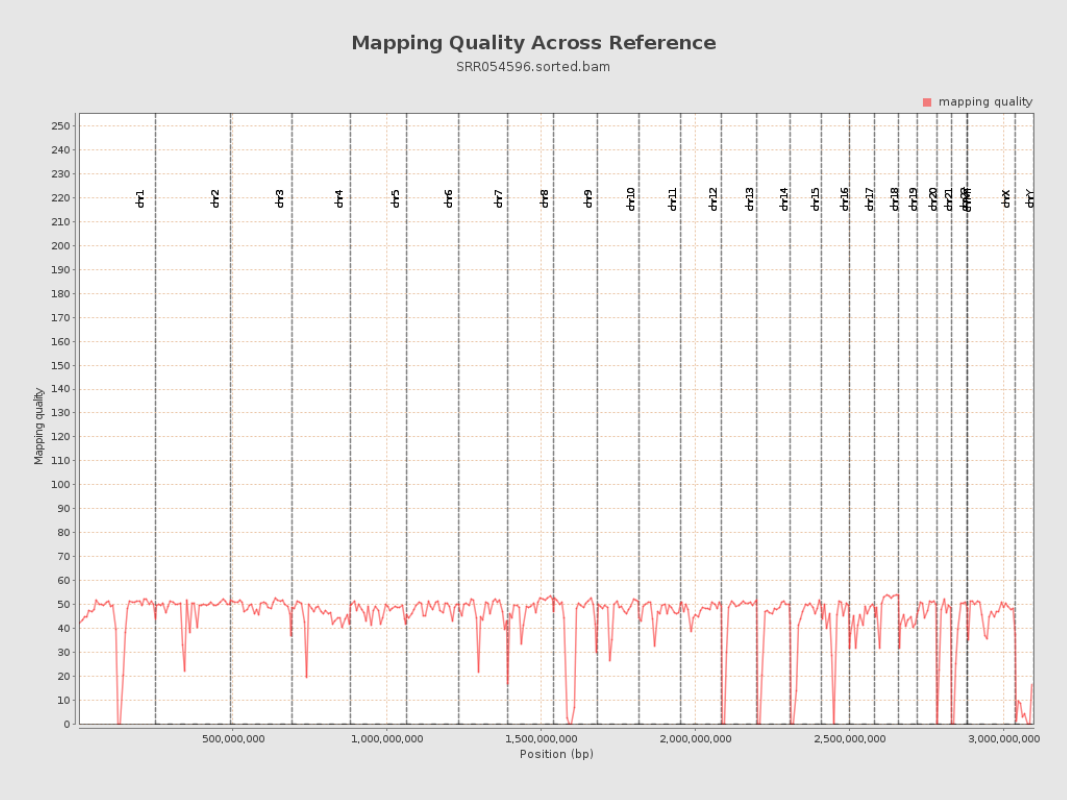
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram