Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:46:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054594.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_SRR054594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:46:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,725,809
Mapped reads	1,923,545 / 70.57%
Unmapped reads	802,264 / 29.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	256,787 / 9.42%
Duplication rate	10.64%
Clipped reads	354,591 / 13.01%

2.2. ACGT Content

Number/percentage of A's	27,686,007 / 31.12%
Number/percentage of C's	17,852,606 / 20.07%
Number/percentage of T's	26,141,773 / 29.39%
Number/percentage of G's	17,277,250 / 19.42%
Number/percentage of N's	1,314 / 0%
GC Percentage	39.49%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.3175

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

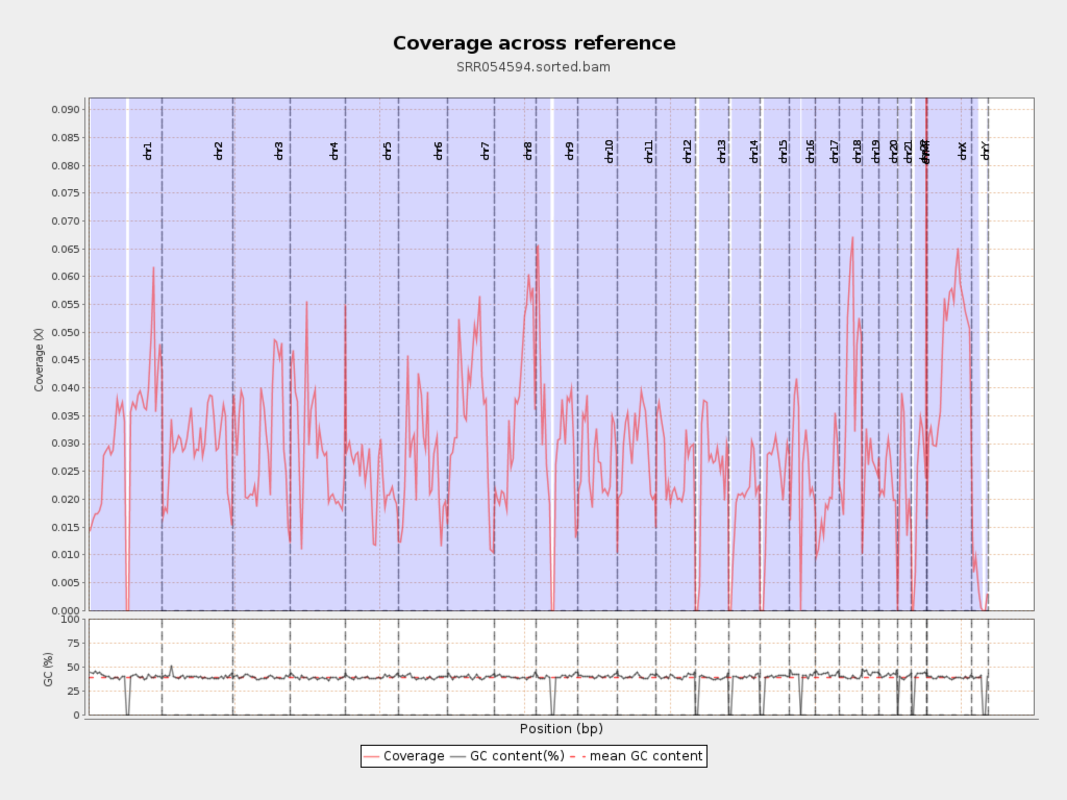
General error rate	0.79%
Mismatches	700,784
Insertions	4,432
Mapped reads with at least one insertion	0.23%
Deletions	12,960
Mapped reads with at least one deletion	0.67%
Homopolymer indels	43.92%

2.6. Chromosome stats

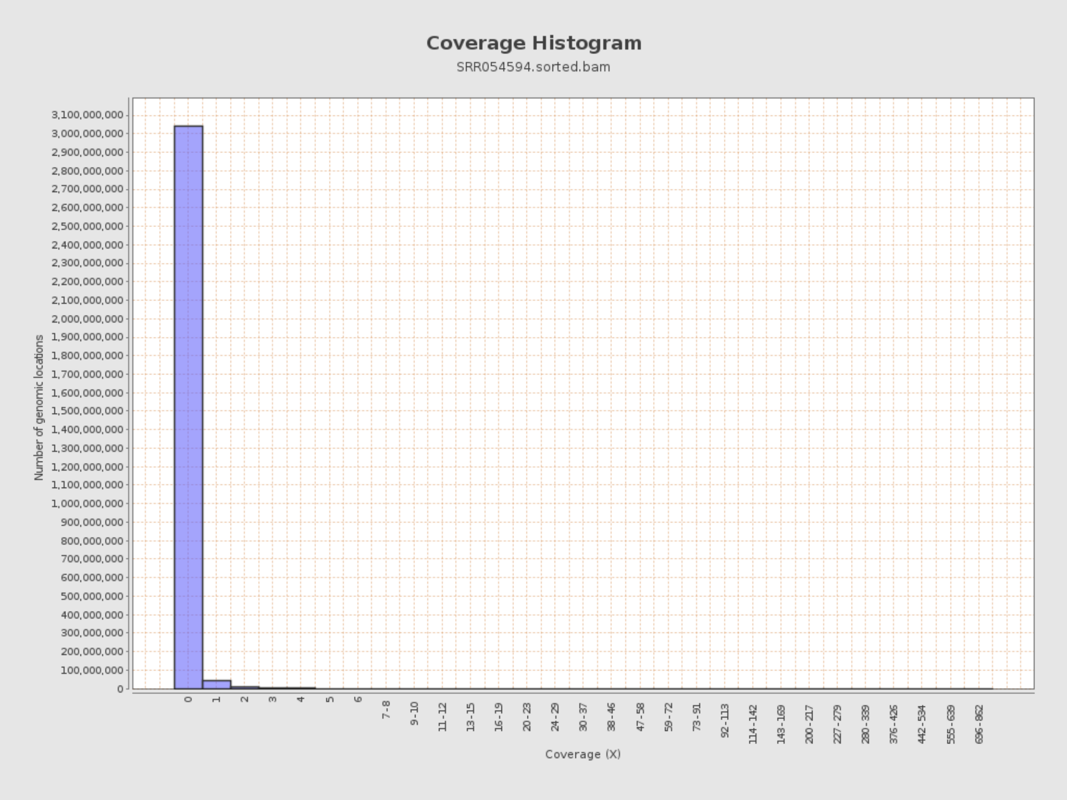
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7807971	0.0313	0.4652
chr2	243199373	7173177	0.0295	0.3816
chr3	198022430	6181120	0.0312	0.2933
chr4	191154276	5585795	0.0292	0.2977
chr5	180915260	4336533	0.024	0.2461
chr6	171115067	4423758	0.0259	0.2798
chr7	159138663	5762513	0.0362	0.3474

chr8	146364022	5294521	0.0362	0.3286
chr9	141213431	4277646	0.0303	0.3134
chr10	135534747	3712608	0.0274	0.2707
chr11	135006516	3935804	0.0292	0.317
chr12	133851895	3469071	0.0259	0.2628
chr13	115169878	2799374	0.0243	0.2489
chr14	107349540	2018294	0.0188	0.2356
chr15	102531392	2260471	0.022	0.237
chr16	90354753	2384130	0.0264	0.2898
chr17	81195210	1609558	0.0198	0.2252
chr18	78077248	3306183	0.0423	0.3687
chr19	59128983	1548603	0.0262	0.2953
chr20	63025520	1450924	0.023	0.2521
chr21	48129895	1074986	0.0223	0.2788
chr22	51304566	1034544	0.0202	0.2278
chrMT	16571	3539	0.2136	0.7569
chrX	155270560	7277728	0.0469	0.4034
chrY	59373566	248586	0.0042	0.1041

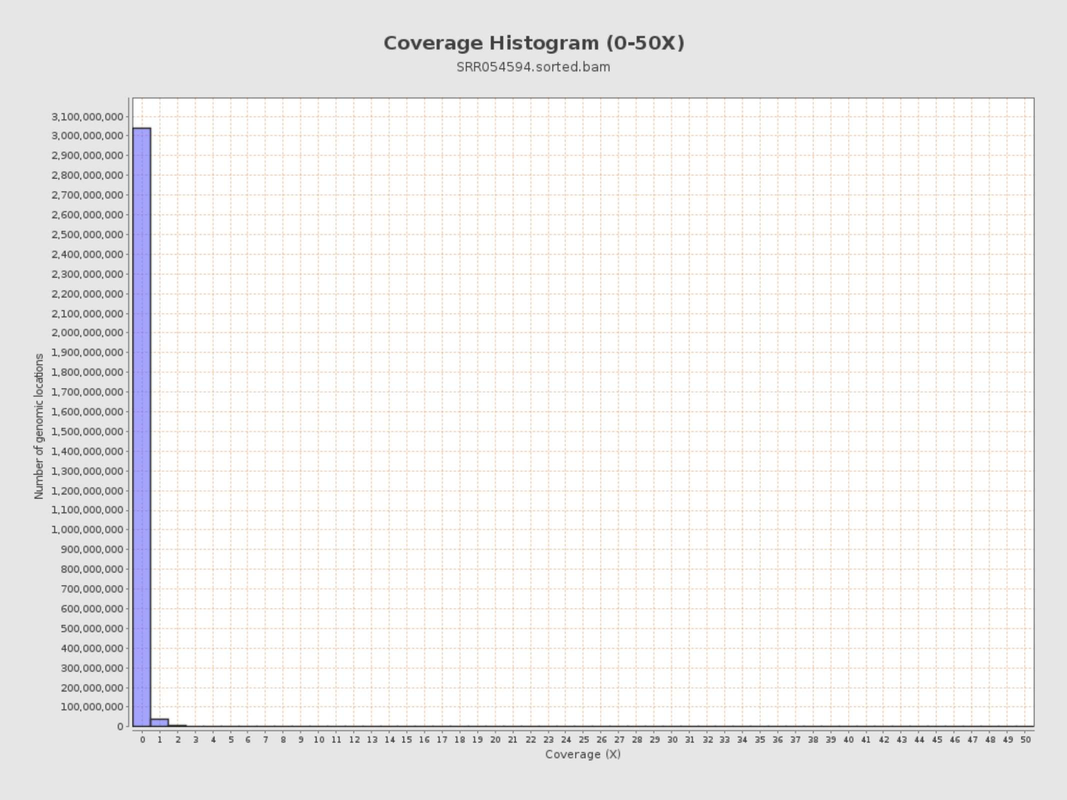
3. Results : Coverage across reference



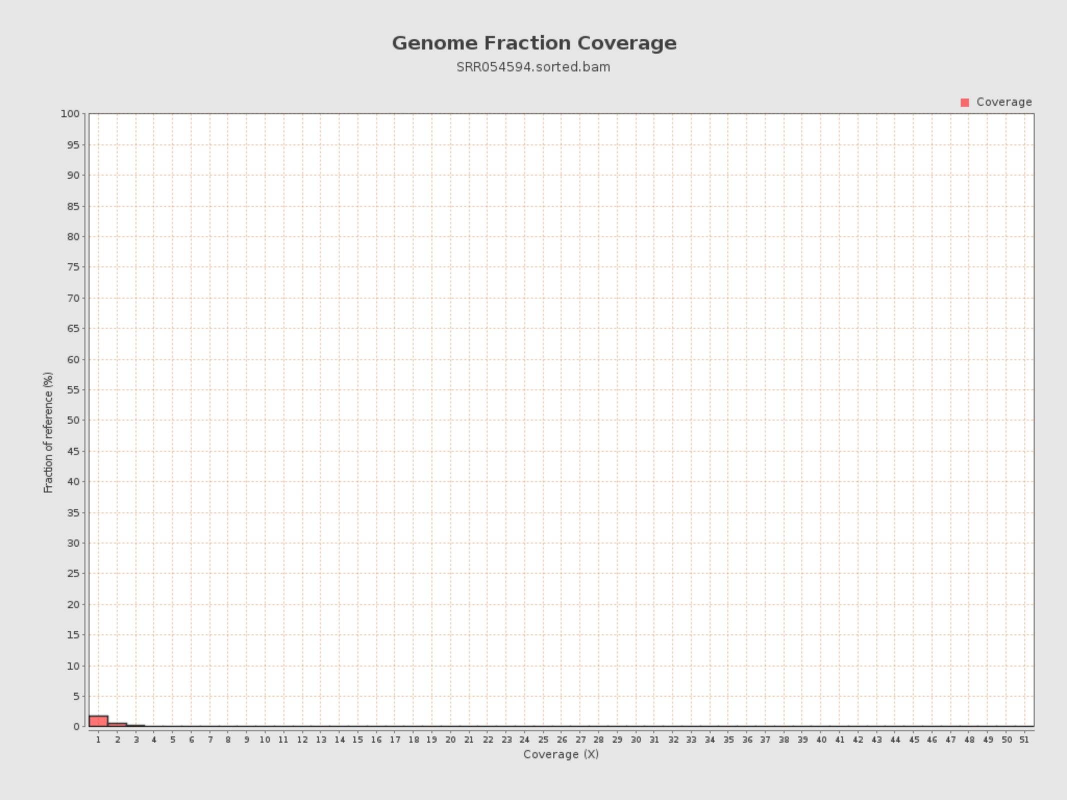
4. Results : Coverage Histogram



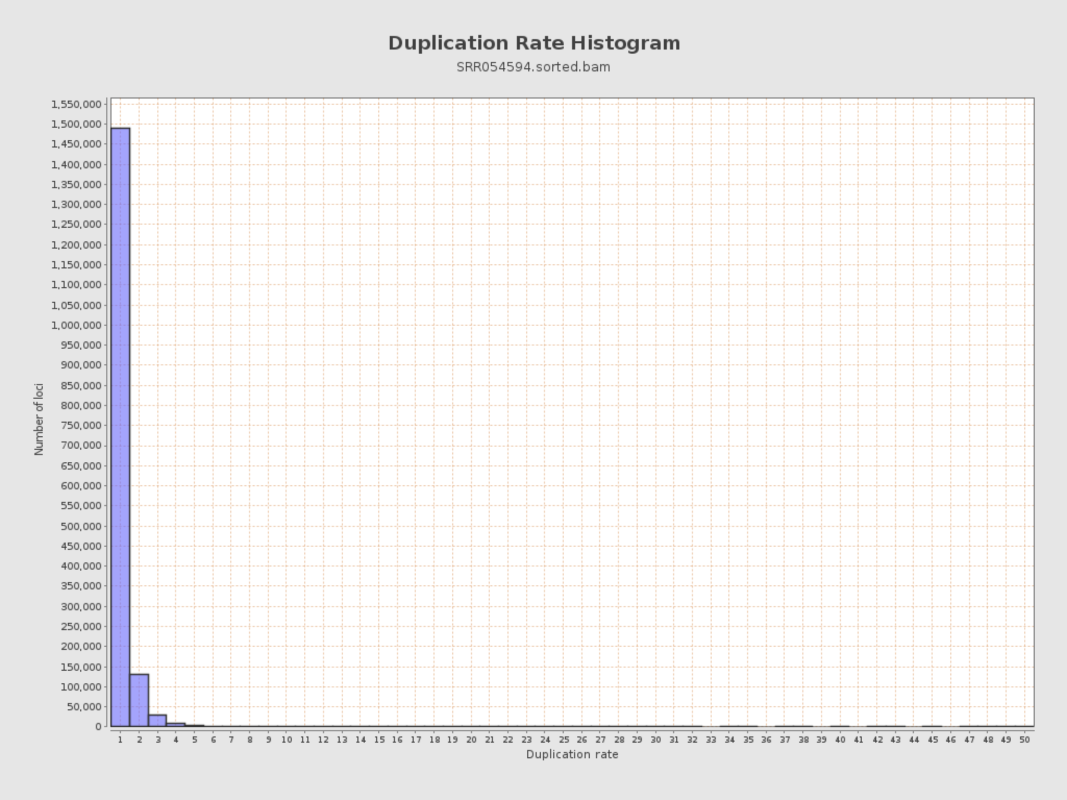
5. Results : Coverage Histogram (0-50X)



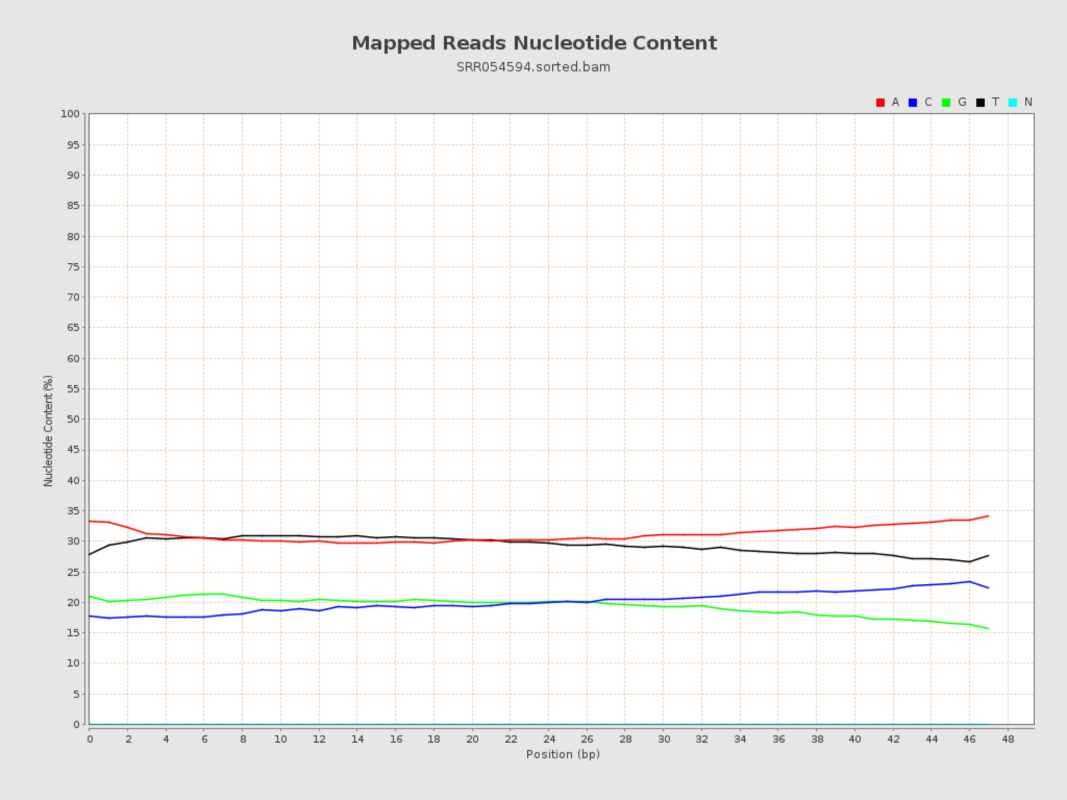
6. Results : Genome Fraction Coverage



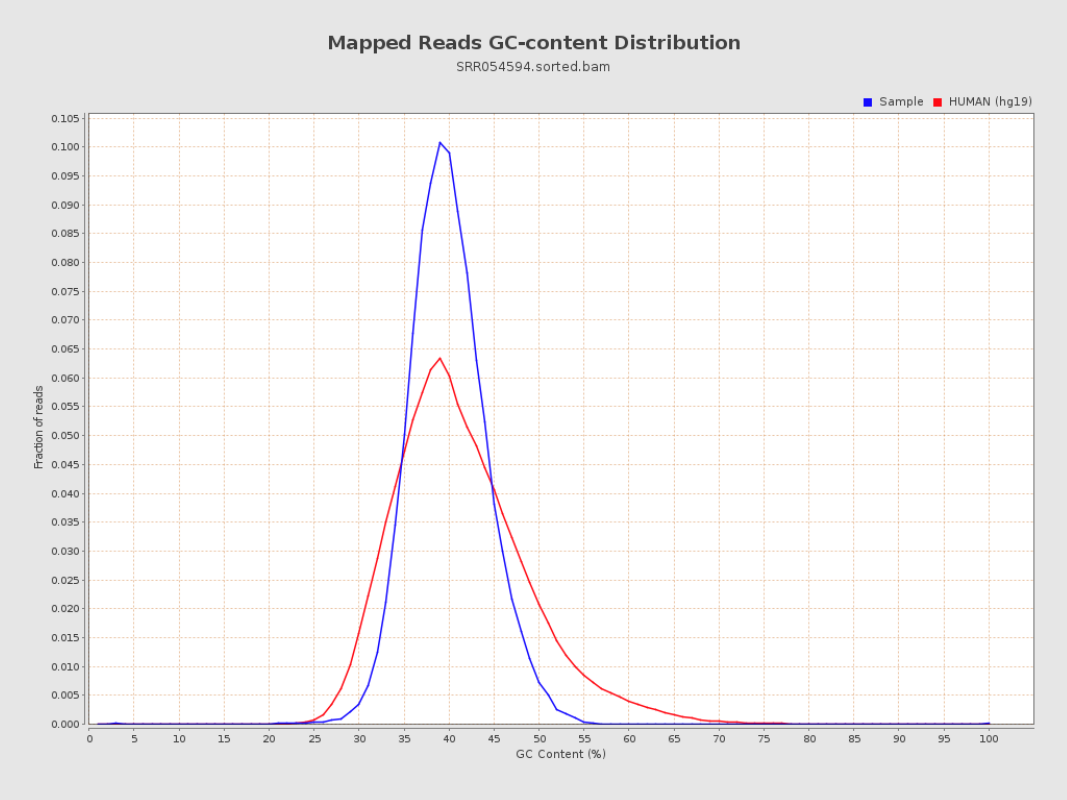
7. Results : Duplication Rate Histogram



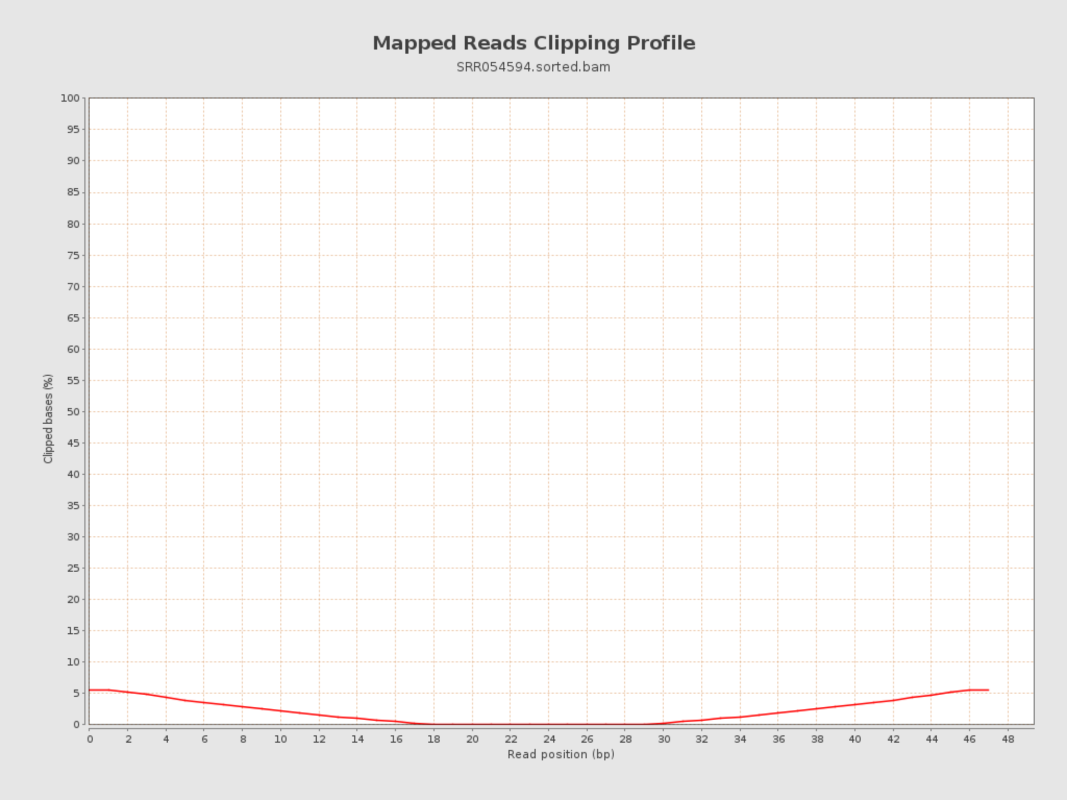
8. Results : Mapped Reads Nucleotide Content



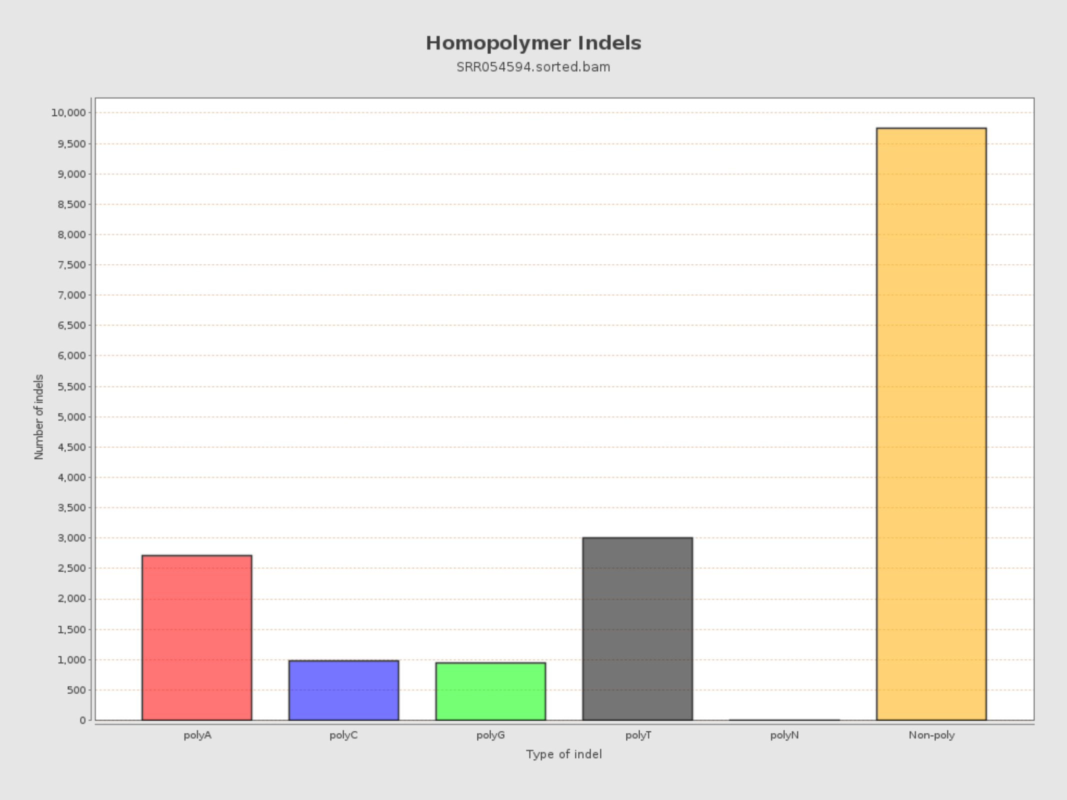
9. Results : Mapped Reads GC-content Distribution



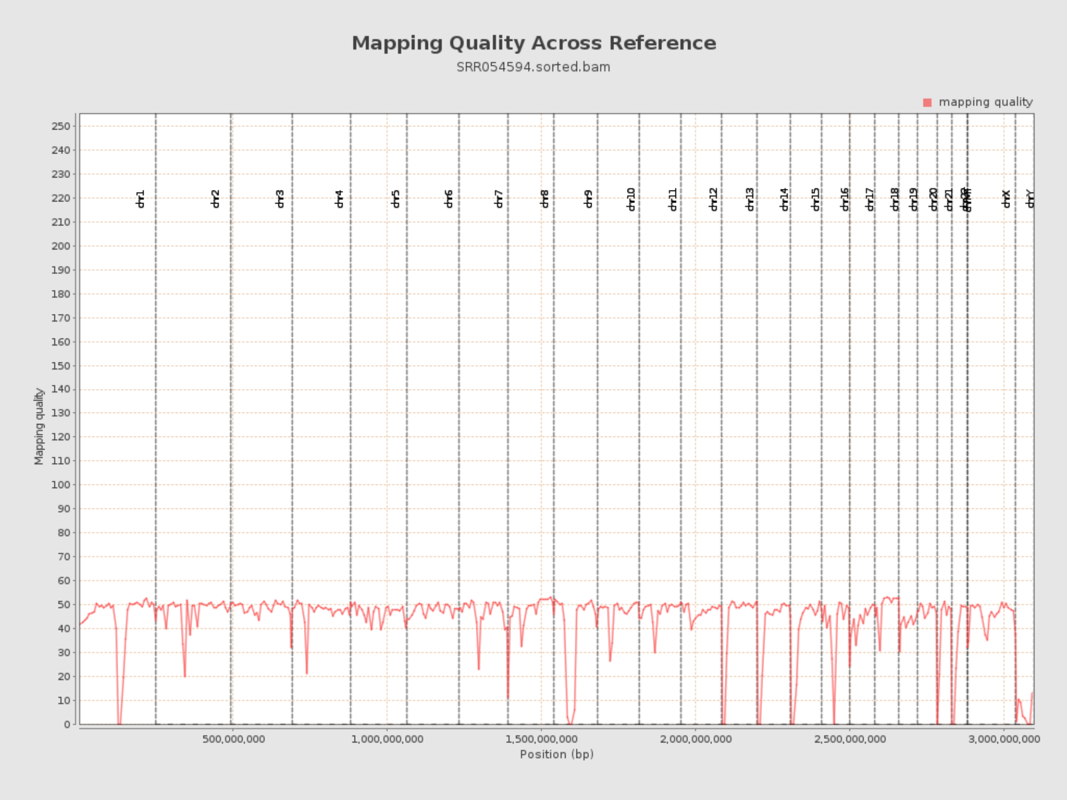
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram