Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 22:31:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR052047.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_SRR052047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR052047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 22:31:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR052047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,888,013
Mapped reads	5,527,951 / 80.25%
Unmapped reads	1,360,062 / 19.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	144 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,547,375 / 22.46%
Duplication rate	20.09%
Clipped reads	699,764 / 10.16%

2.2. ACGT Content

Number/percentage of A's	82,239,279 / 31.74%
Number/percentage of C's	51,470,843 / 19.87%
Number/percentage of T's	70,369,454 / 27.16%
Number/percentage of G's	54,967,760 / 21.22%
Number/percentage of N's	38,861 / 0.01%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0837

Standard Deviation	0.7844

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

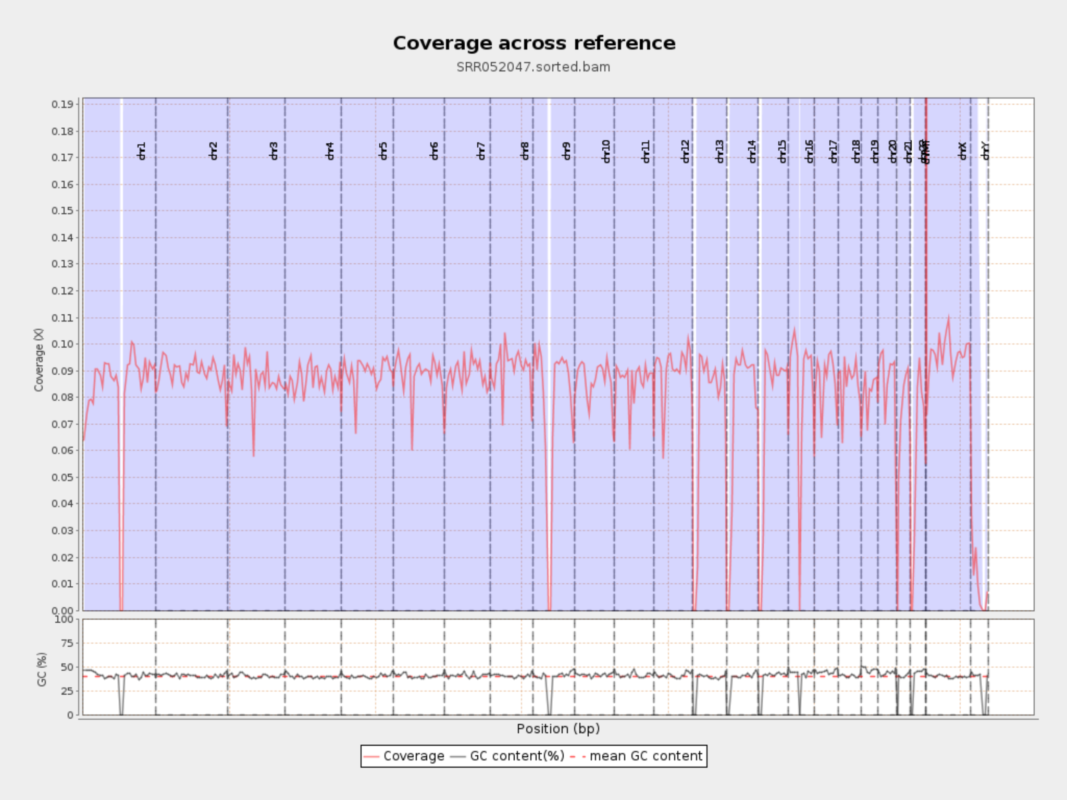
General error rate	0.63%
Mismatches	1,615,602
Insertions	11,232
Mapped reads with at least one insertion	0.2%
Deletions	34,228
Mapped reads with at least one deletion	0.62%
Homopolymer indels	44.25%

2.6. Chromosome stats

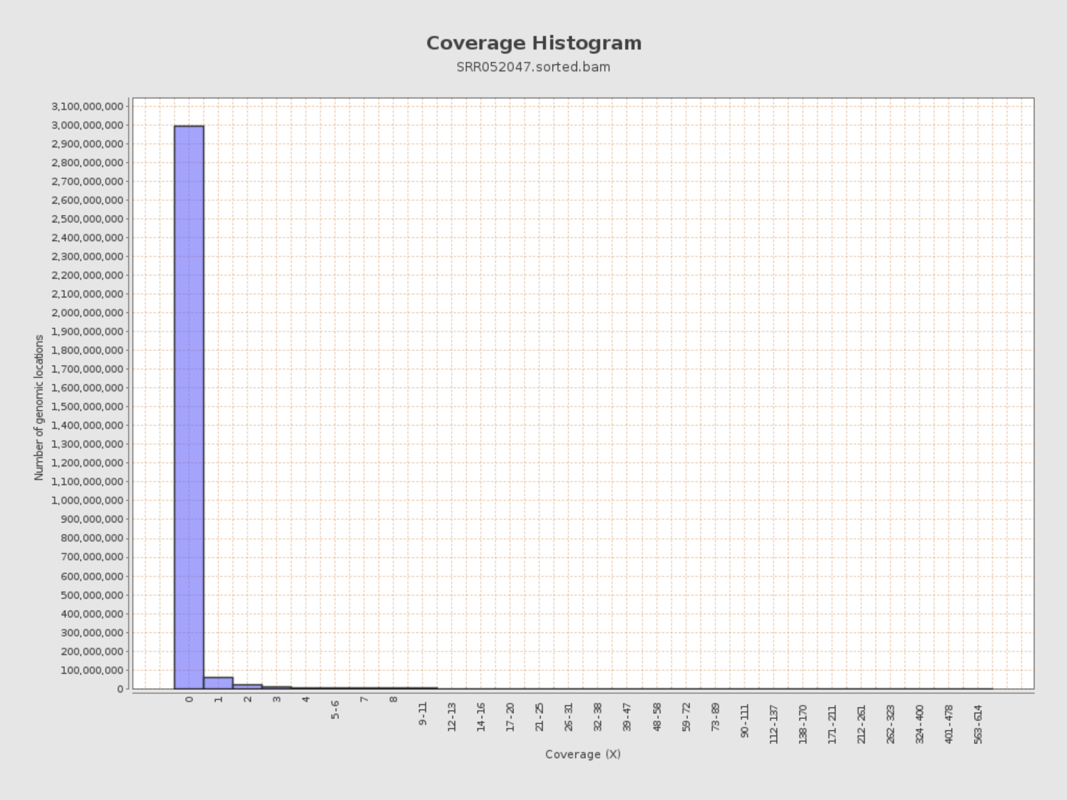
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20493853	0.0822	0.8151
chr2	243199373	21766833	0.0895	0.8414
chr3	198022430	17196038	0.0868	0.7628
chr4	191154276	16667394	0.0872	0.7966
chr5	180915260	16134195	0.0892	0.7801
chr6	171115067	15283531	0.0893	0.839
chr7	159138663	14073053	0.0884	0.8117

chr8	146364022	13339545	0.0911	0.8373
chr9	141213431	10911592	0.0773	0.7619
chr10	135534747	11791274	0.087	0.789
chr11	135006516	11612139	0.086	0.8302
chr12	133851895	12200152	0.0911	0.8112
chr13	115169878	8519486	0.074	0.7172
chr14	107349540	8111669	0.0756	0.7583
chr15	102531392	7526411	0.0734	0.6889
chr16	90354753	7520294	0.0832	0.7983
chr17	81195210	7092458	0.0874	0.745
chr18	78077248	6723663	0.0861	0.7866
chr19	59128983	4828230	0.0817	0.7687
chr20	63025520	5550132	0.0881	0.7747
chr21	48129895	3297982	0.0685	0.7415
chr22	51304566	2926167	0.057	0.5723
chrMT	16571	51811	3.1266	6.9516
chrX	155270560	14907865	0.096	0.8173
chrY	59373566	611530	0.0103	0.2252

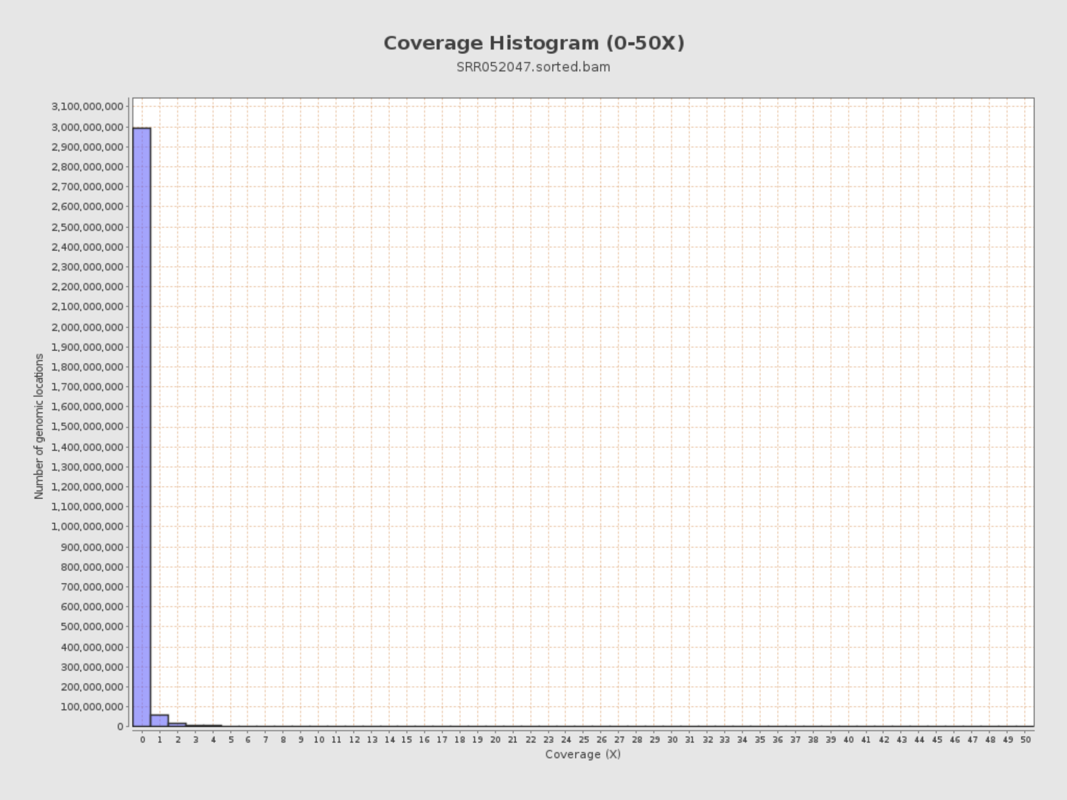
3. Results : Coverage across reference



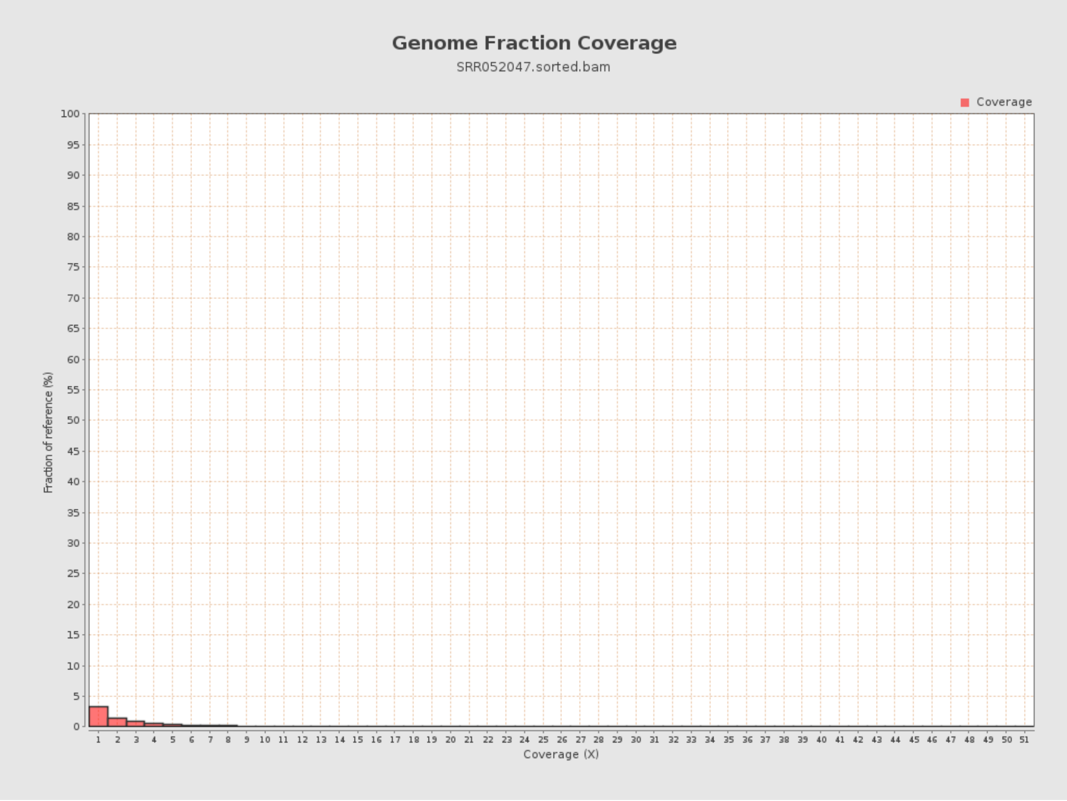
4. Results : Coverage Histogram



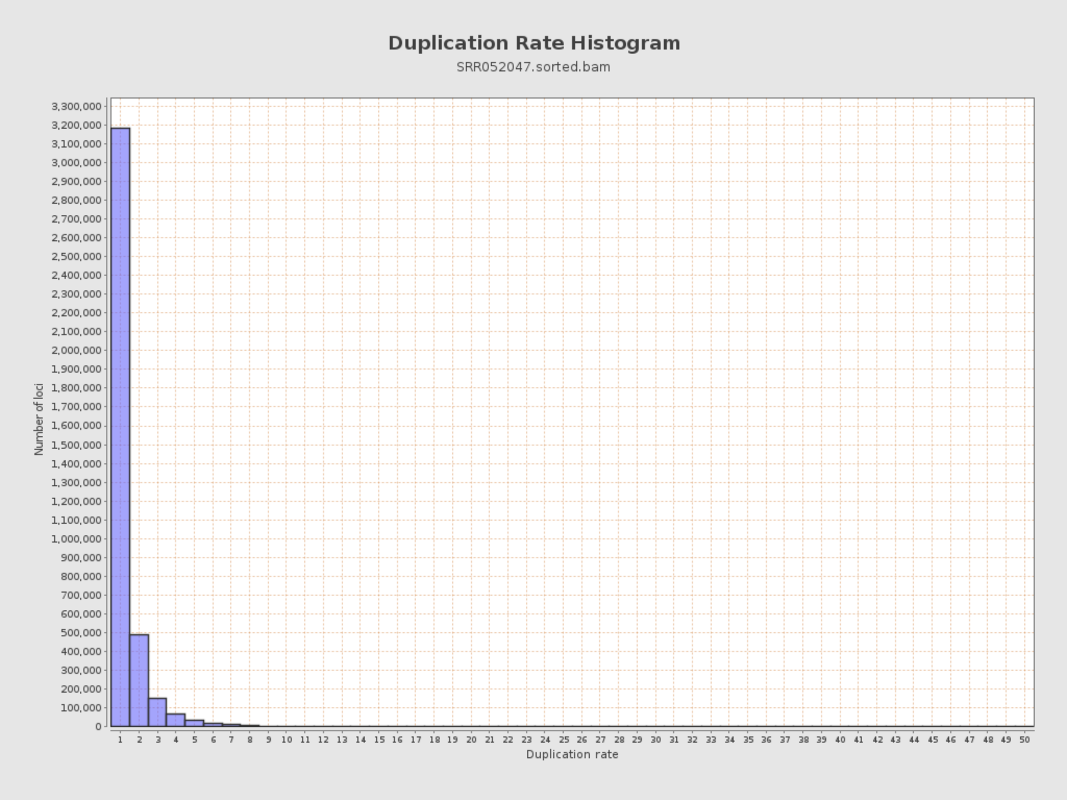
5. Results : Coverage Histogram (0-50X)



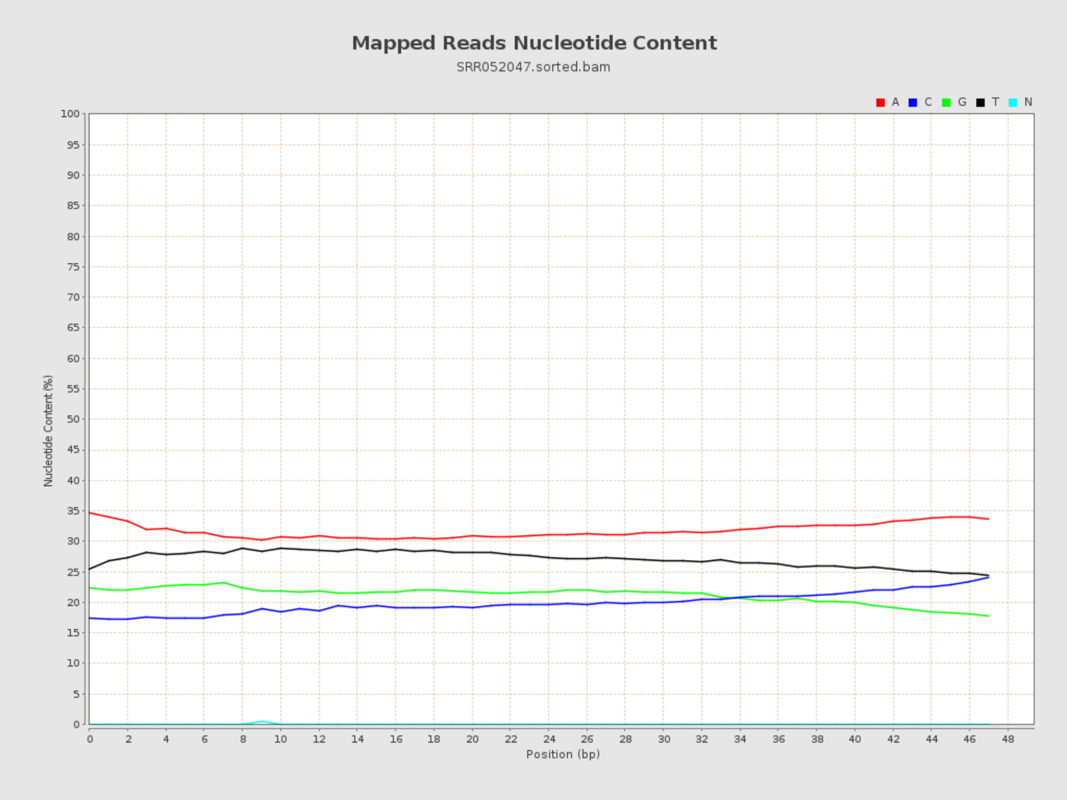
6. Results : Genome Fraction Coverage



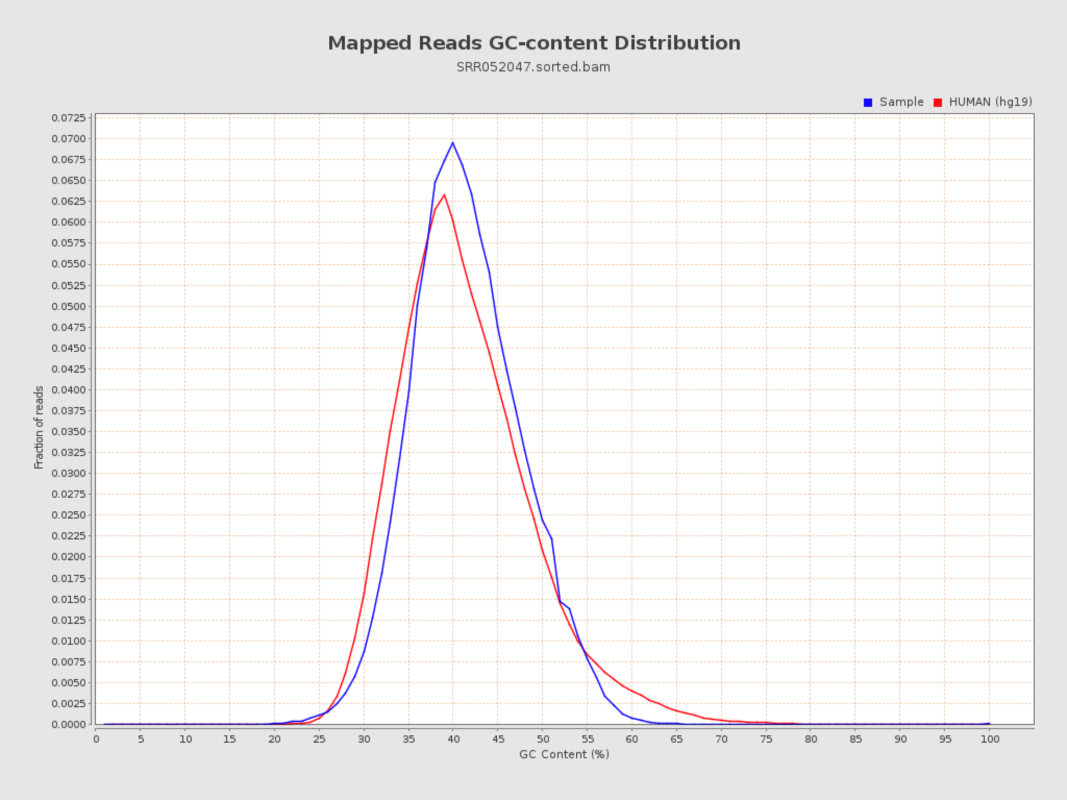
7. Results : Duplication Rate Histogram



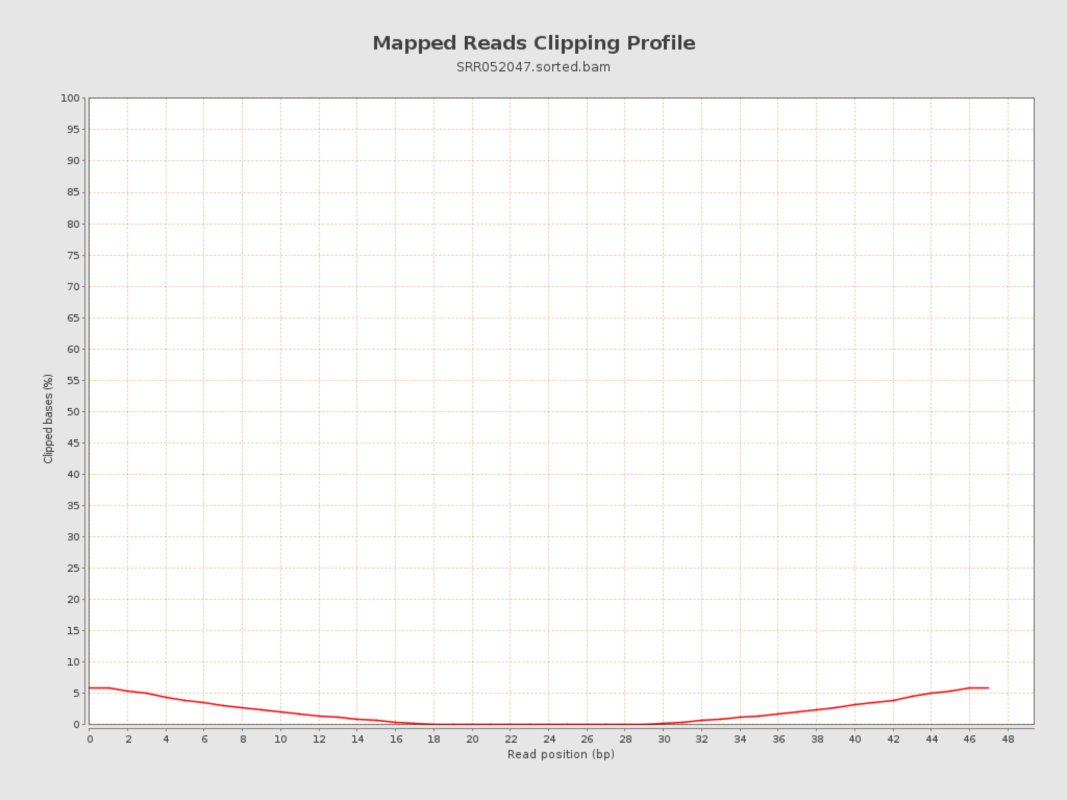
8. Results : Mapped Reads Nucleotide Content



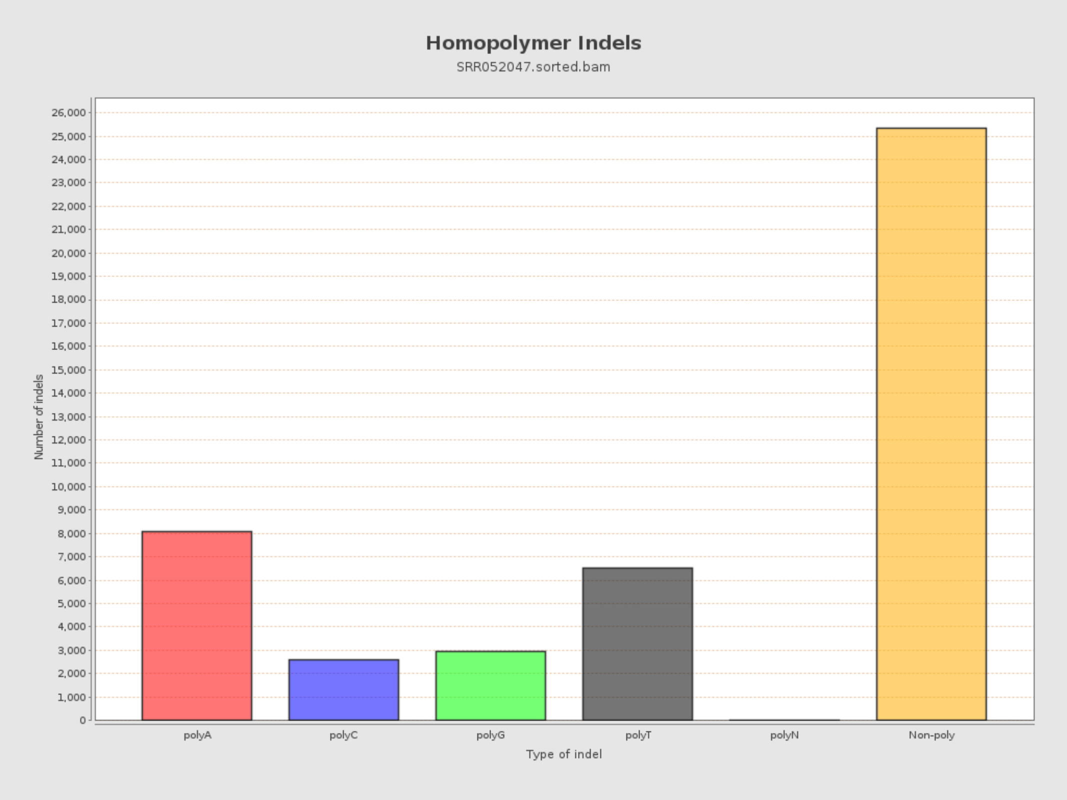
9. Results : Mapped Reads GC-content Distribution



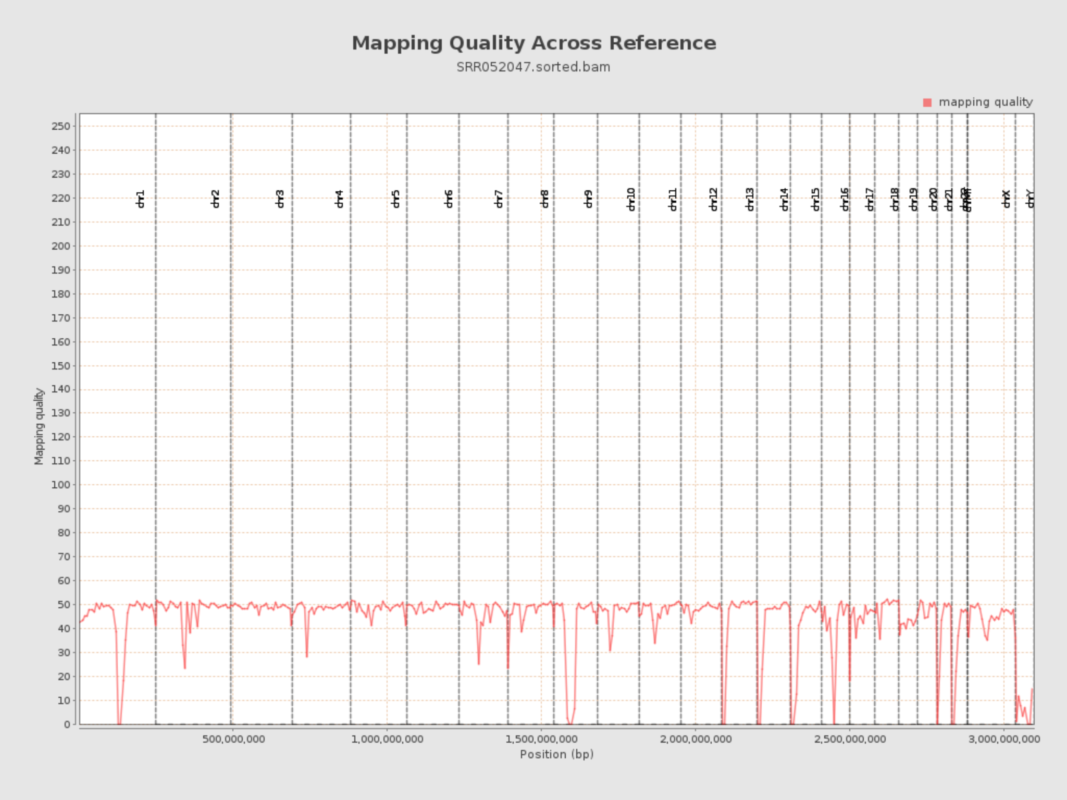
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram