Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:21:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053678.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_SRR053678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:21:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,237,269
Mapped reads	7,125,379 / 86.5%
Unmapped reads	1,111,890 / 13.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	210 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,737,465 / 21.09%
Duplication rate	17.42%
Clipped reads	588,933 / 7.15%

2.2. ACGT Content

Number/percentage of A's	98,688,046 / 29.3%
Number/percentage of C's	67,267,797 / 19.97%
Number/percentage of T's	98,602,777 / 29.27%
Number/percentage of G's	72,253,657 / 21.45%
Number/percentage of N's	11,326 / 0%
GC Percentage	41.42%

2.3. Coverage

Mean	0.1088

Standard Deviation	0.8727

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

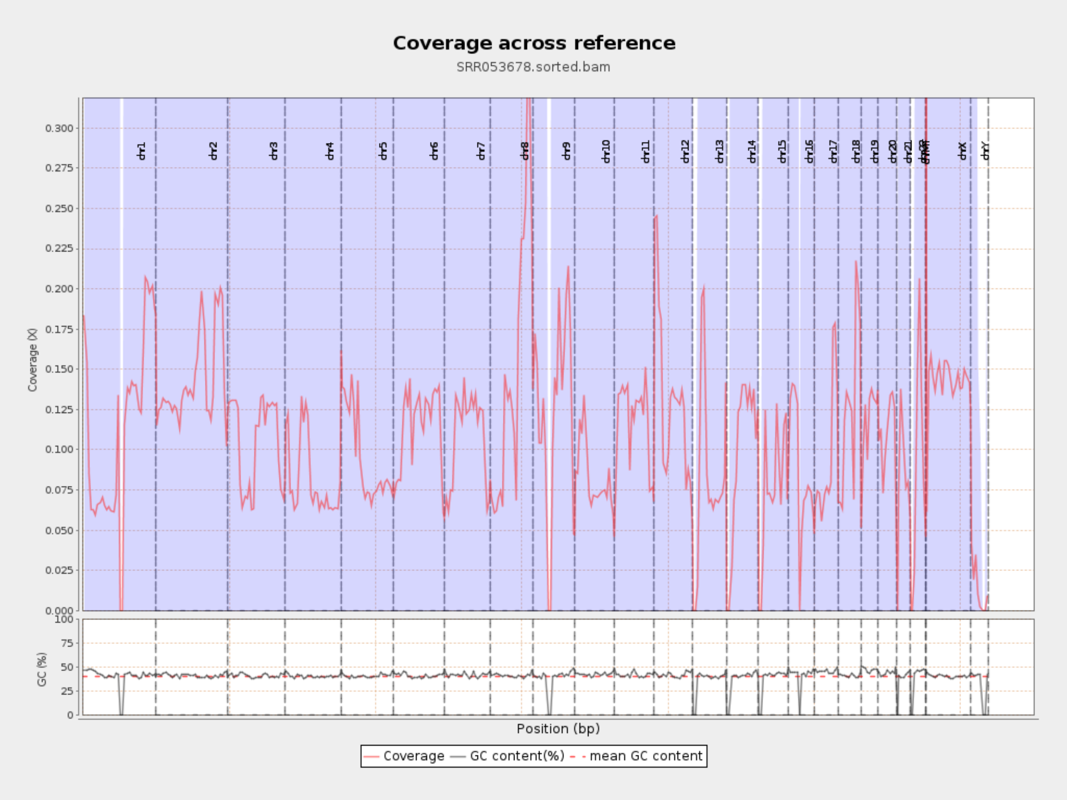
General error rate	0.47%
Mismatches	1,549,816
Insertions	13,026
Mapped reads with at least one insertion	0.18%
Deletions	45,585
Mapped reads with at least one deletion	0.64%
Homopolymer indels	46.85%

2.6. Chromosome stats

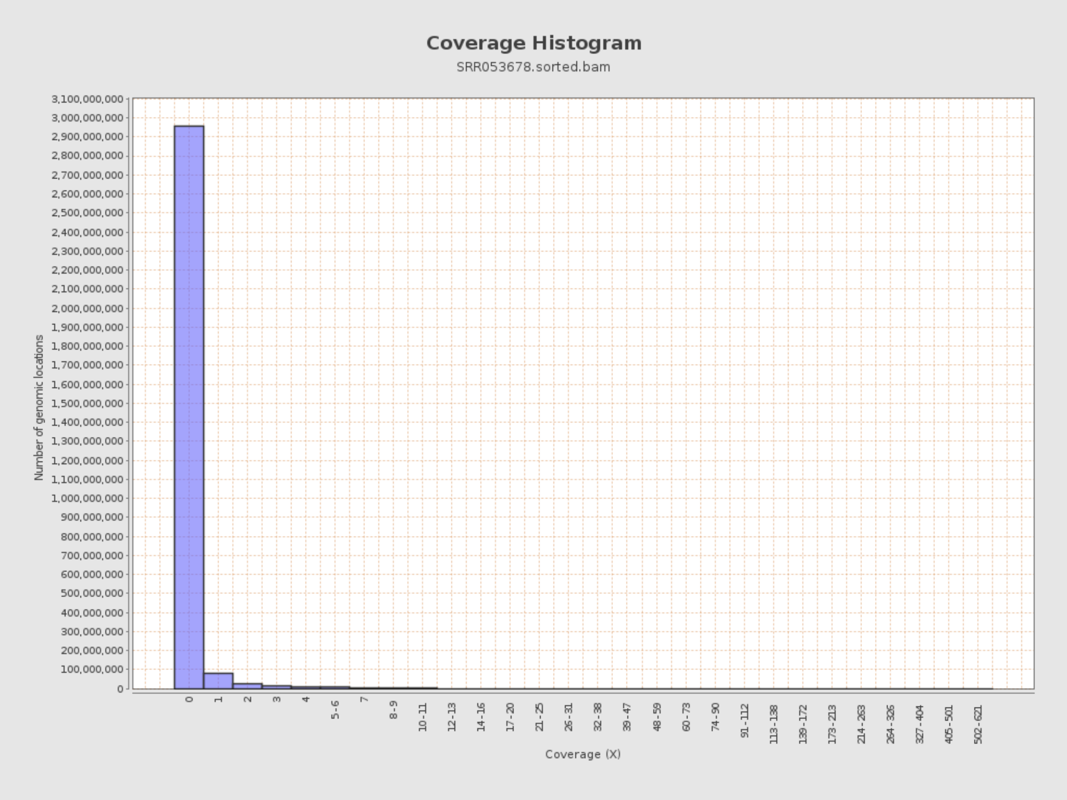
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27788460	0.1115	0.959
chr2	243199373	34866083	0.1434	1.0603
chr3	198022430	20805127	0.1051	0.7965
chr4	191154276	15729951	0.0823	0.7091
chr5	180915260	17209317	0.0951	0.7545
chr6	171115067	19803700	0.1157	0.9133
chr7	159138663	16970581	0.1066	0.849

chr8	146364022	22378200	0.1529	1.0782
chr9	141213431	17837228	0.1263	0.9386
chr10	135534747	11308013	0.0834	0.7623
chr11	135006516	16033673	0.1188	0.9149
chr12	133851895	17830367	0.1332	0.9335
chr13	115169878	9247996	0.0803	0.7101
chr14	107349540	10525446	0.098	0.8546
chr15	102531392	7767389	0.0758	0.6662
chr16	90354753	7724310	0.0855	0.7542
chr17	81195210	7716867	0.095	0.7406
chr18	78077248	9847705	0.1261	0.9602
chr19	59128983	7044431	0.1191	0.9672
chr20	63025520	6969843	0.1106	0.8387
chr21	48129895	3906246	0.0812	0.7553
chr22	51304566	4673627	0.0911	0.7546
chrMT	16571	20668	1.2472	4.5171
chrX	155270560	22090682	0.1423	1.0009
chrY	59373566	796120	0.0134	0.3137

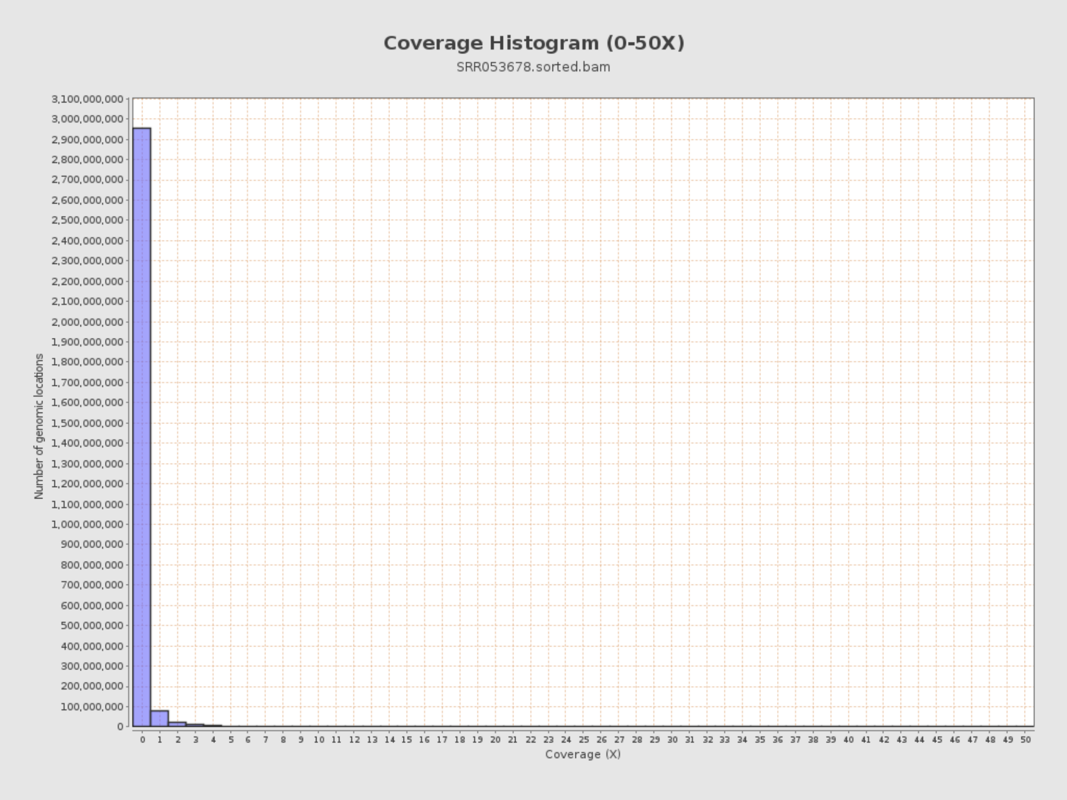
3. Results : Coverage across reference



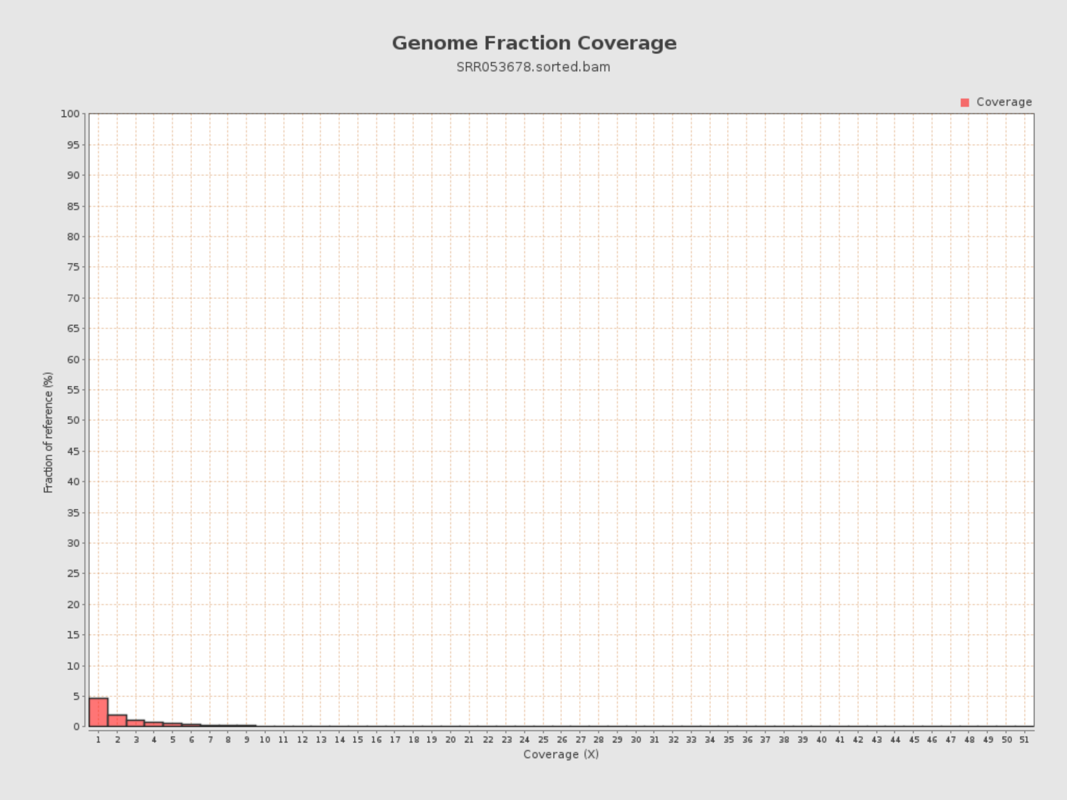
4. Results : Coverage Histogram



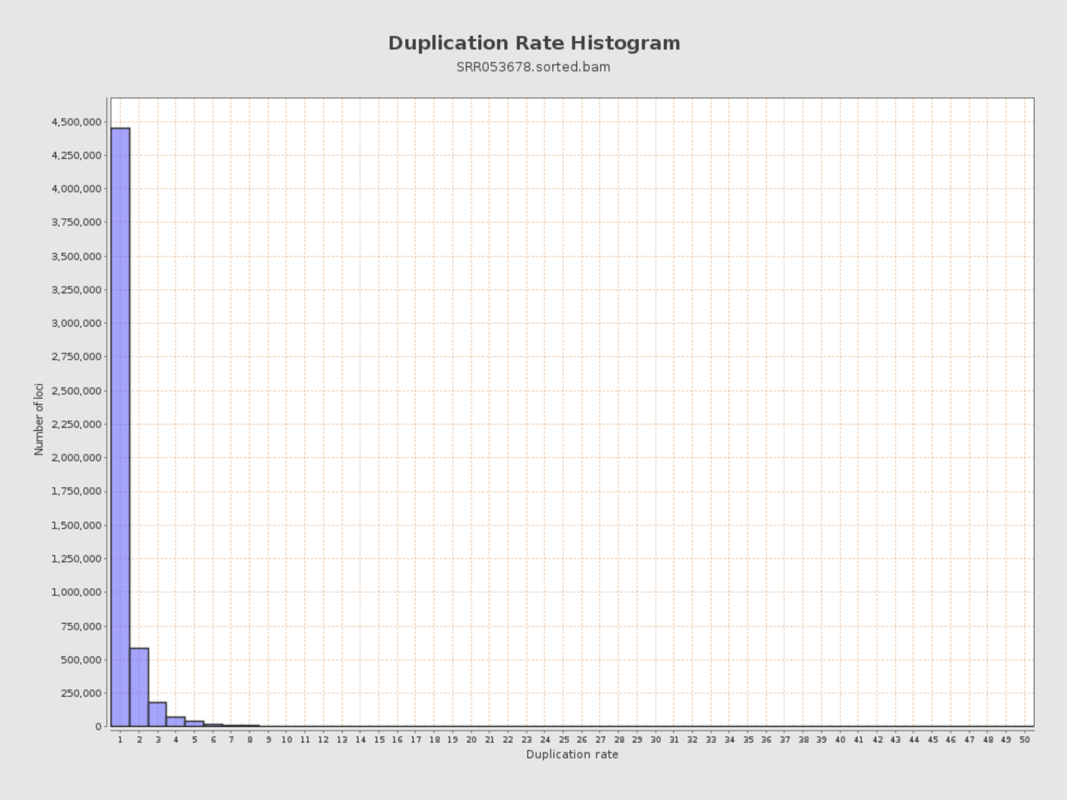
5. Results : Coverage Histogram (0-50X)



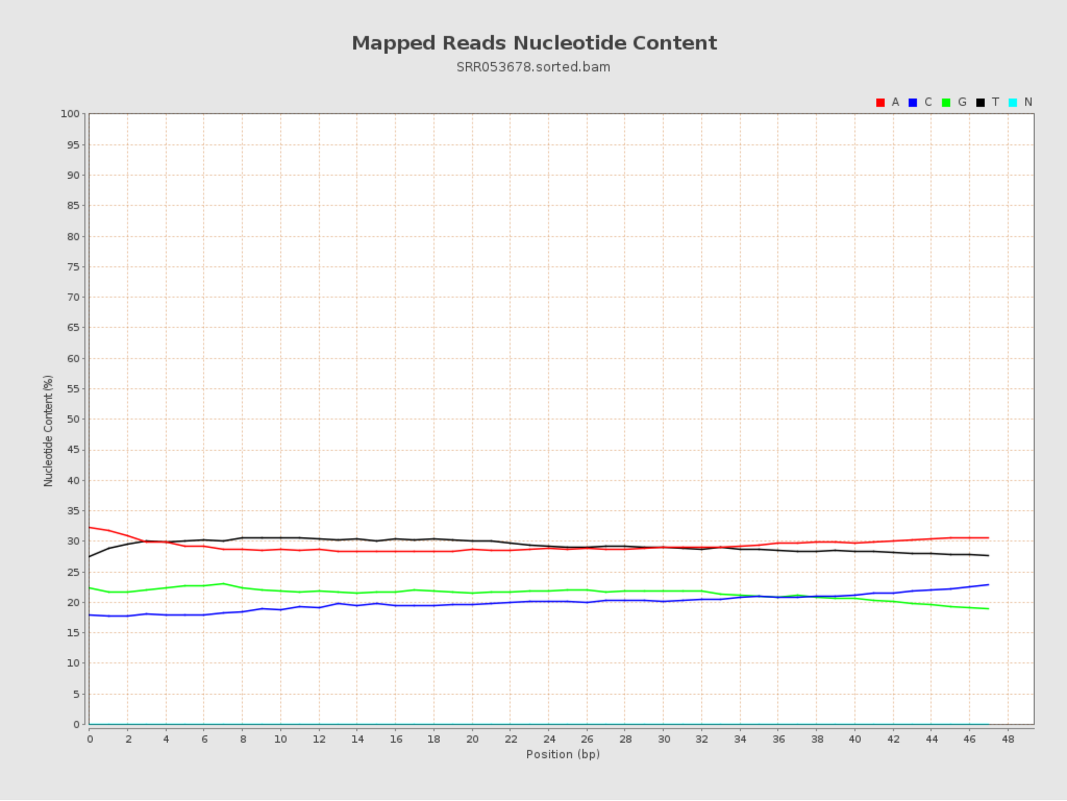
6. Results : Genome Fraction Coverage



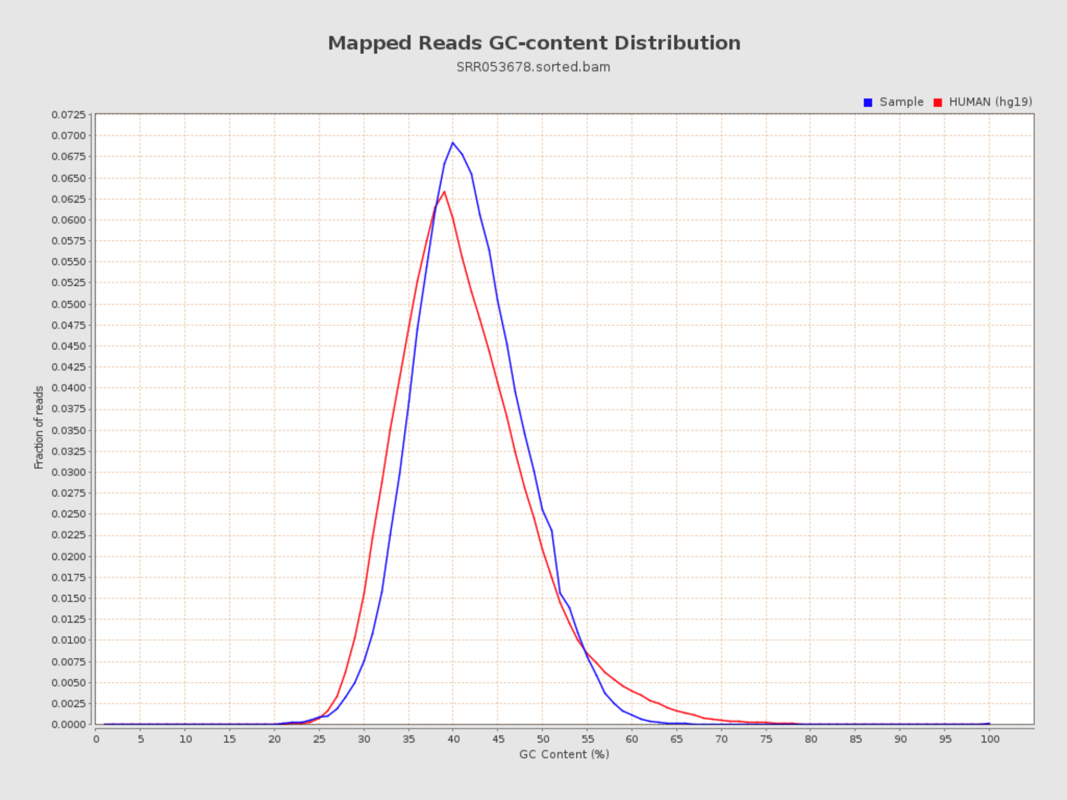
7. Results : Duplication Rate Histogram



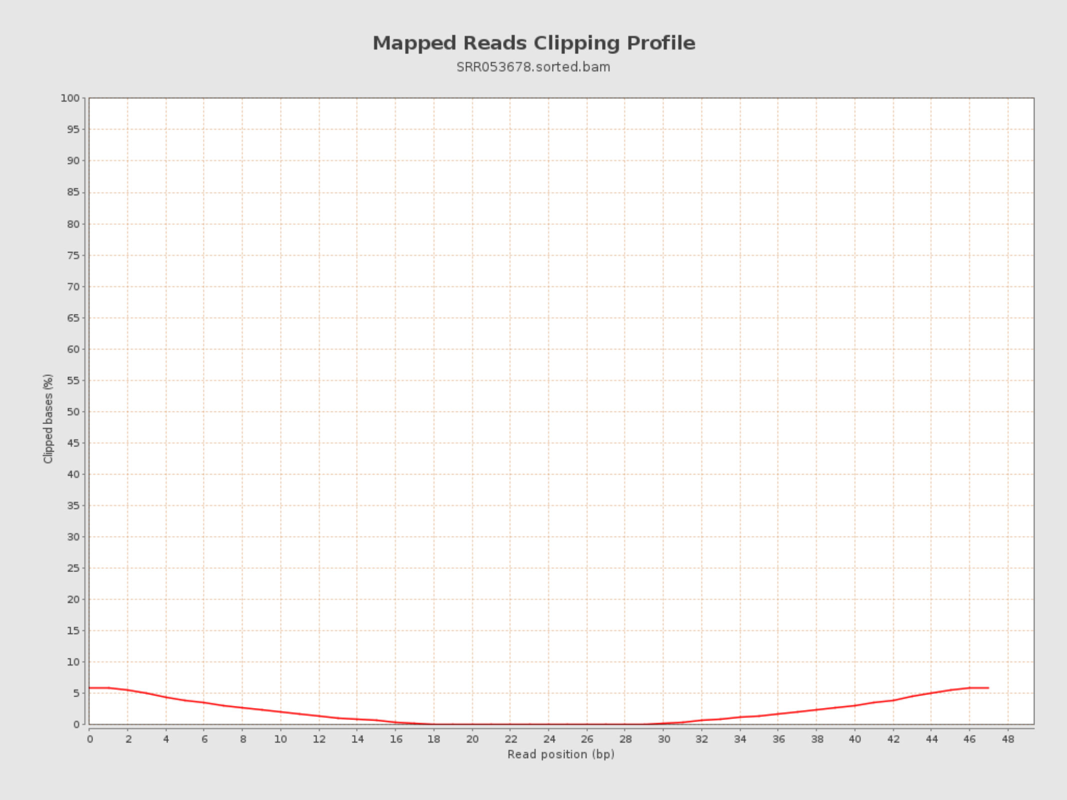
8. Results : Mapped Reads Nucleotide Content



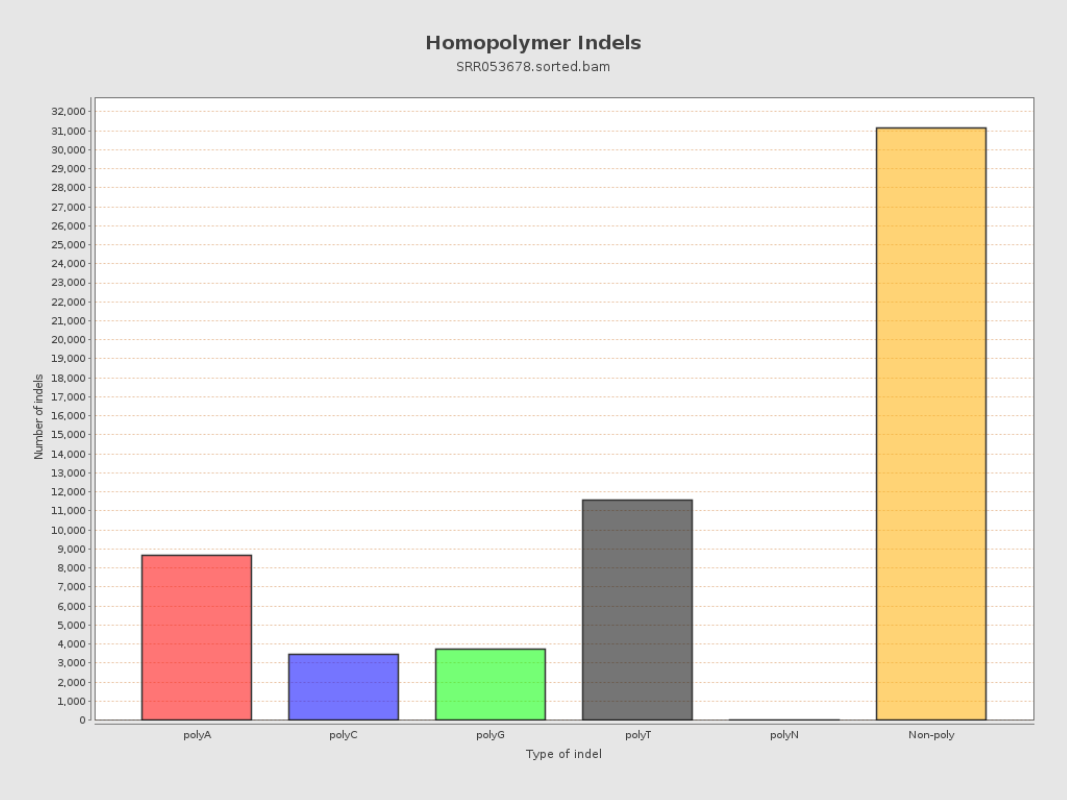
9. Results : Mapped Reads GC-content Distribution



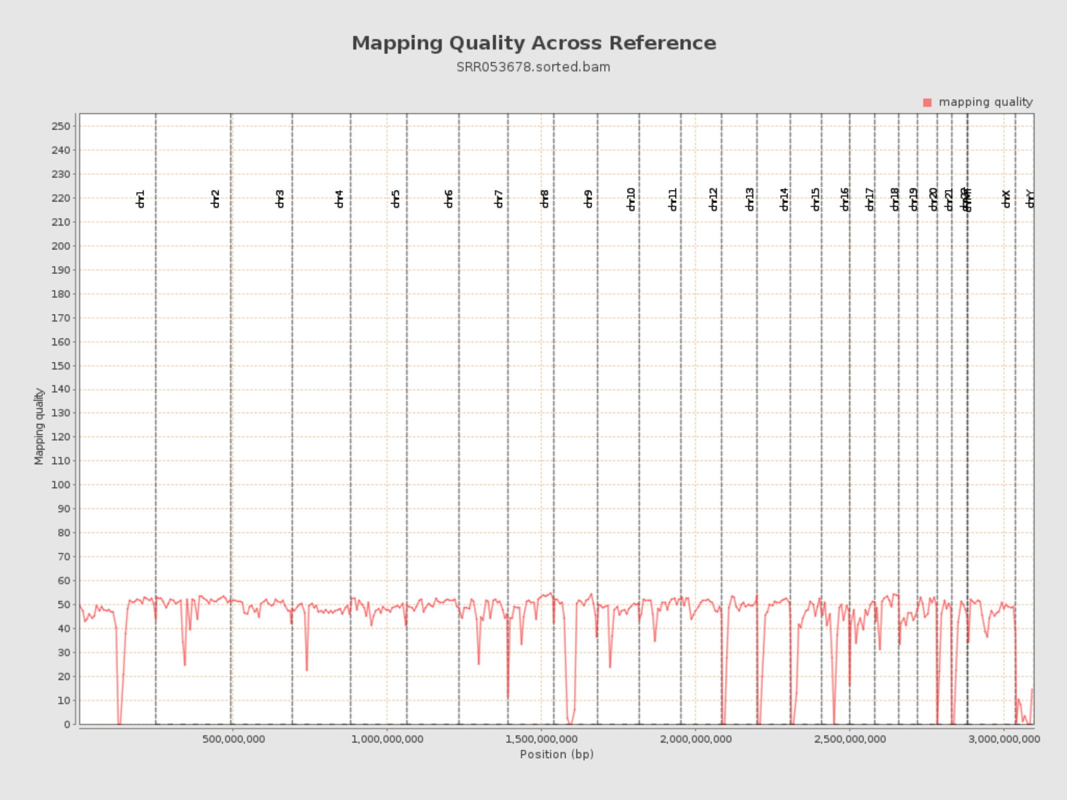
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram