Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:27:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053679.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_SRR053679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:27:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,226,145
Mapped reads	6,783,497 / 82.46%
Unmapped reads	1,442,648 / 17.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	401 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,086,228 / 13.2%
Duplication rate	12%
Clipped reads	738,075 / 8.97%

2.2. ACGT Content

Number/percentage of A's	95,380,300 / 29.94%
Number/percentage of C's	60,917,945 / 19.12%
Number/percentage of T's	96,523,194 / 30.3%
Number/percentage of G's	65,742,671 / 20.64%
Number/percentage of N's	15,557 / 0%
GC Percentage	39.76%

2.3. Coverage

Mean	0.1029

Standard Deviation	0.6781

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

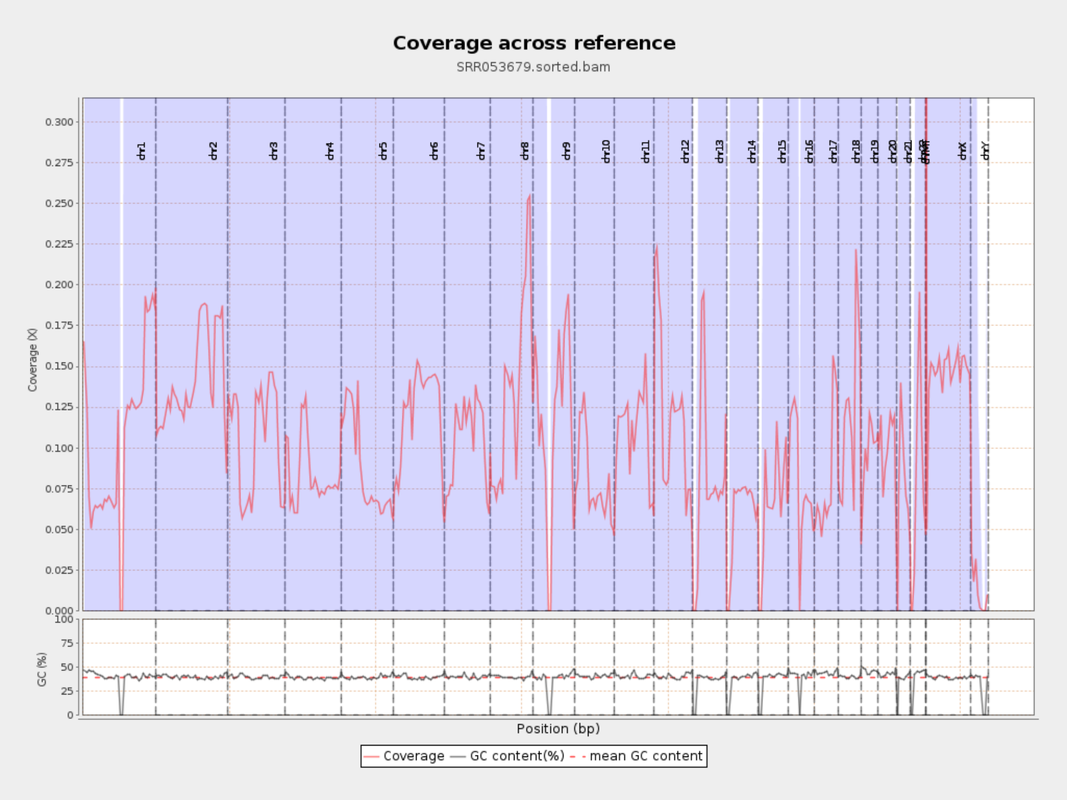
General error rate	0.48%
Mismatches	1,501,988
Insertions	13,844
Mapped reads with at least one insertion	0.2%
Deletions	46,520
Mapped reads with at least one deletion	0.68%
Homopolymer indels	46.69%

2.6. Chromosome stats

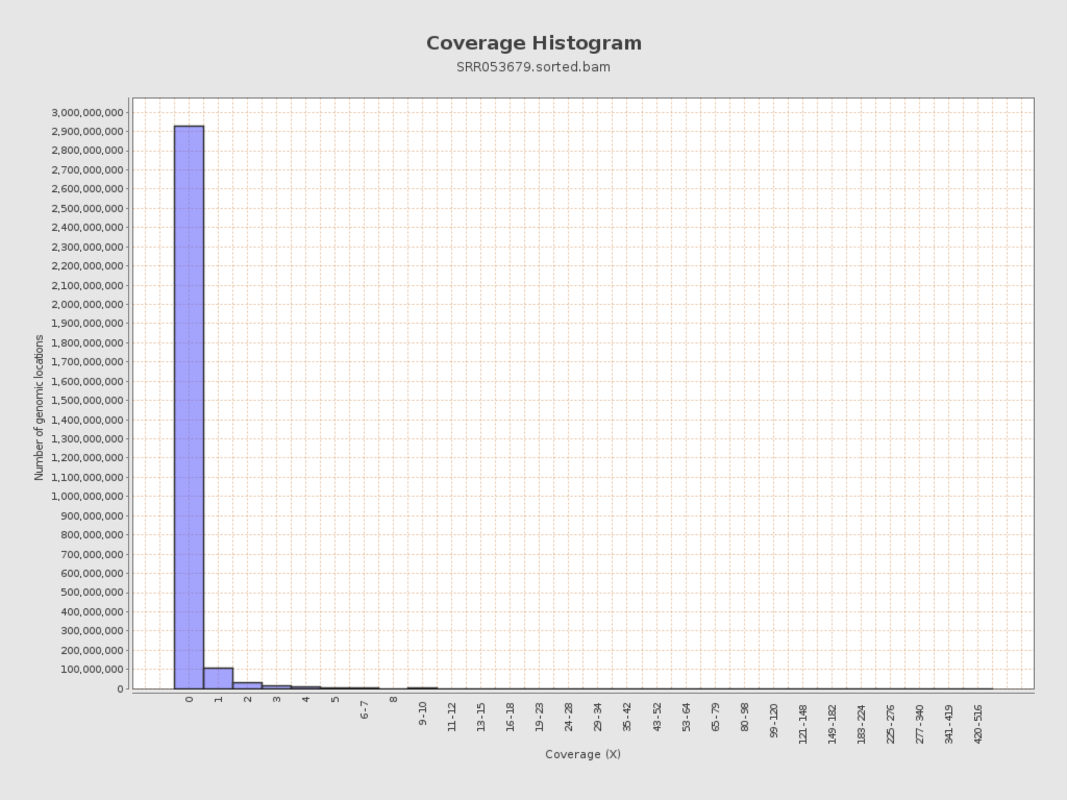
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26077473	0.1046	0.7885
chr2	243199373	34520529	0.1419	0.8234
chr3	198022430	20863522	0.1054	0.6313
chr4	191154276	16101005	0.0842	0.5715
chr5	180915260	15776863	0.0872	0.5534
chr6	171115067	21239632	0.1241	0.7542
chr7	159138663	16426697	0.1032	0.6884

chr8	146364022	20106294	0.1374	0.7955
chr9	141213431	16652474	0.1179	0.711
chr10	135534747	10774535	0.0795	0.67
chr11	135006516	14950033	0.1107	0.6867
chr12	133851895	16463464	0.123	0.7013
chr13	115169878	9109615	0.0791	0.5483
chr14	107349540	6359659	0.0592	0.5076
chr15	102531392	6753095	0.0659	0.4745
chr16	90354753	7048985	0.078	0.5564
chr17	81195210	6586799	0.0811	0.5368
chr18	78077248	9532172	0.1221	0.8014
chr19	59128983	5803347	0.0981	0.7192
chr20	63025520	6420553	0.1019	0.6326
chr21	48129895	3579456	0.0744	0.5627
chr22	51304566	4194868	0.0818	0.5584
chrMT	16571	37178	2.2436	3.5316
chrX	155270560	22546622	0.1452	0.8031
chrY	59373566	724458	0.0122	0.2357

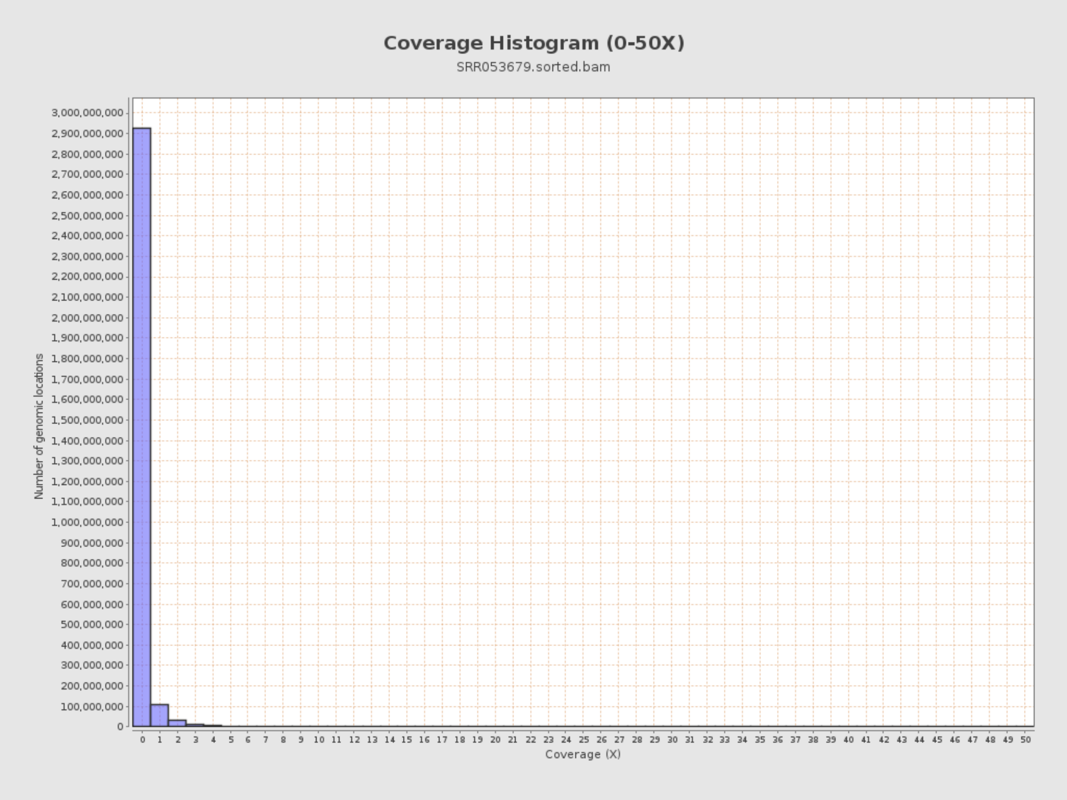
3. Results : Coverage across reference



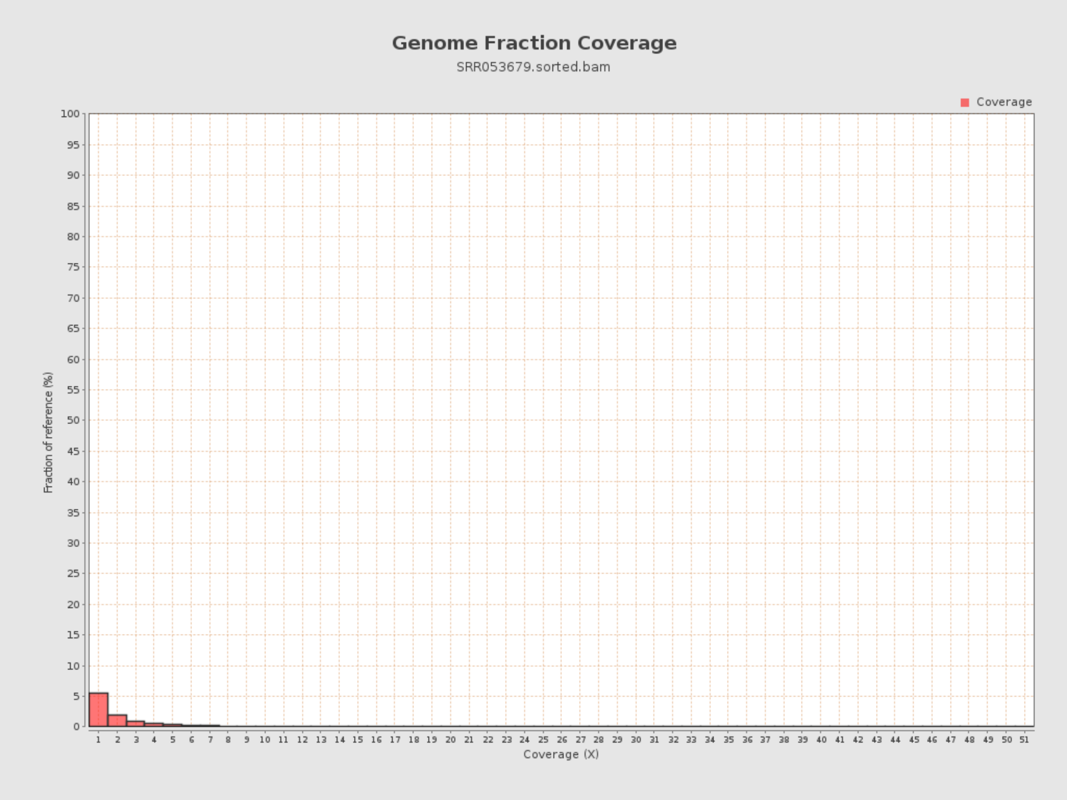
4. Results : Coverage Histogram



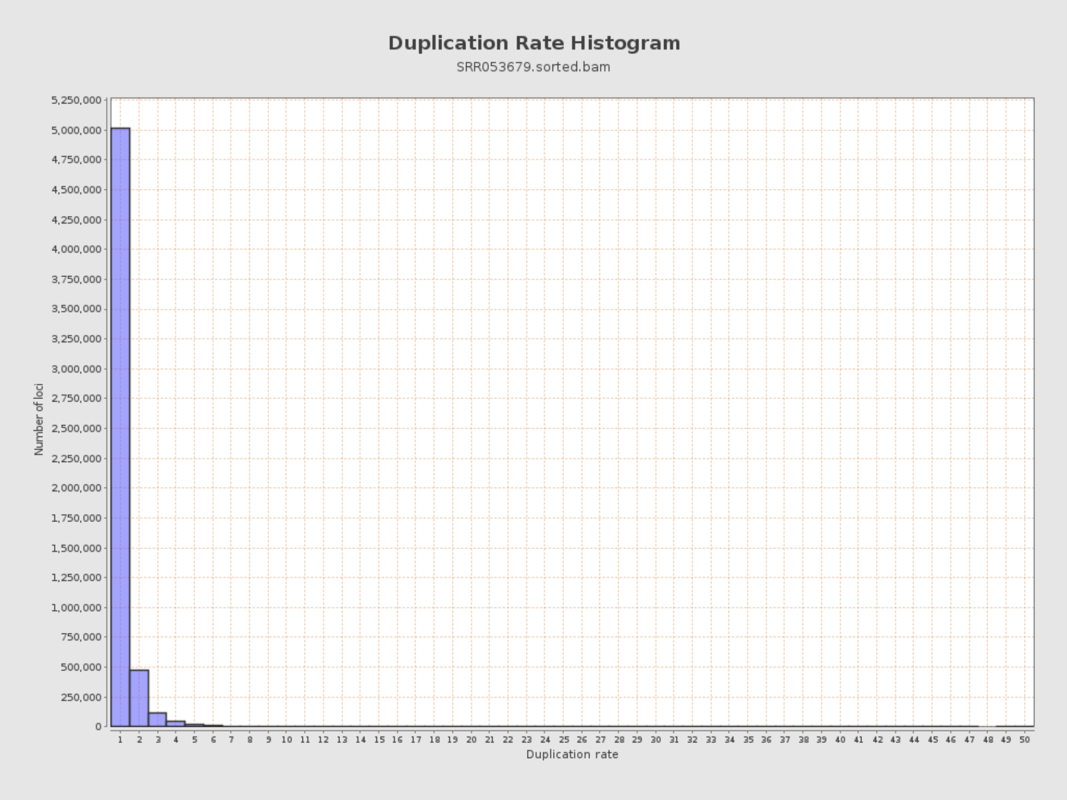
5. Results : Coverage Histogram (0-50X)



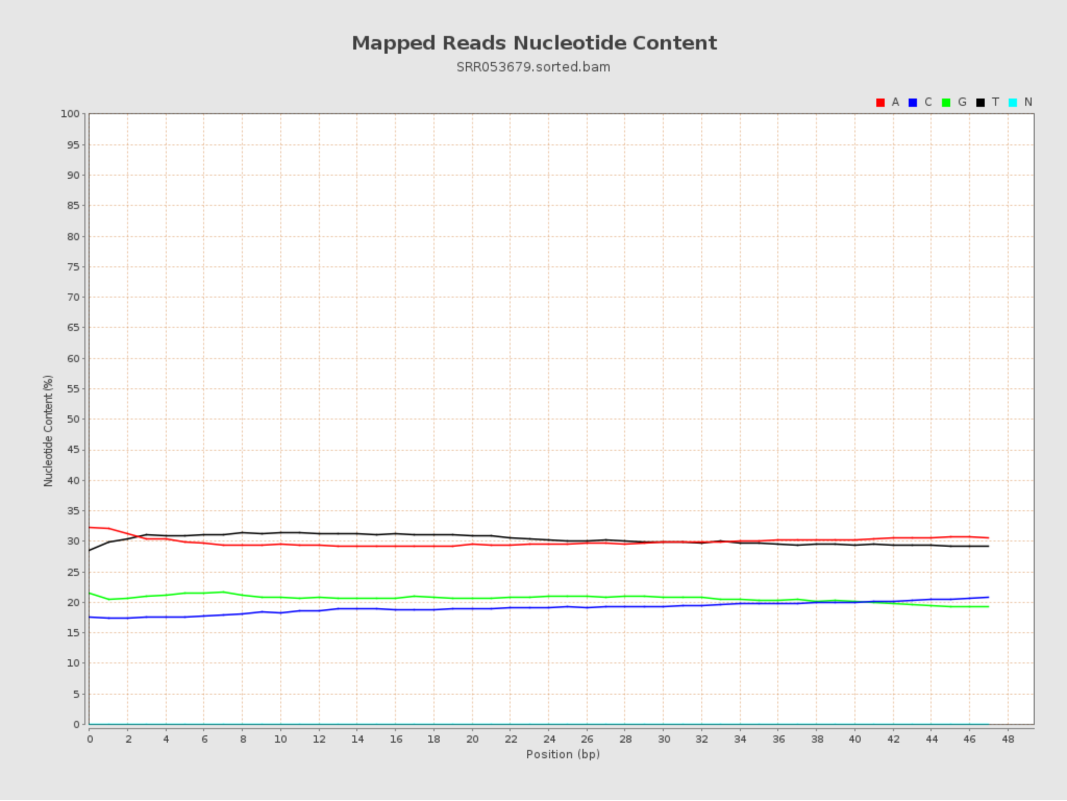
6. Results : Genome Fraction Coverage



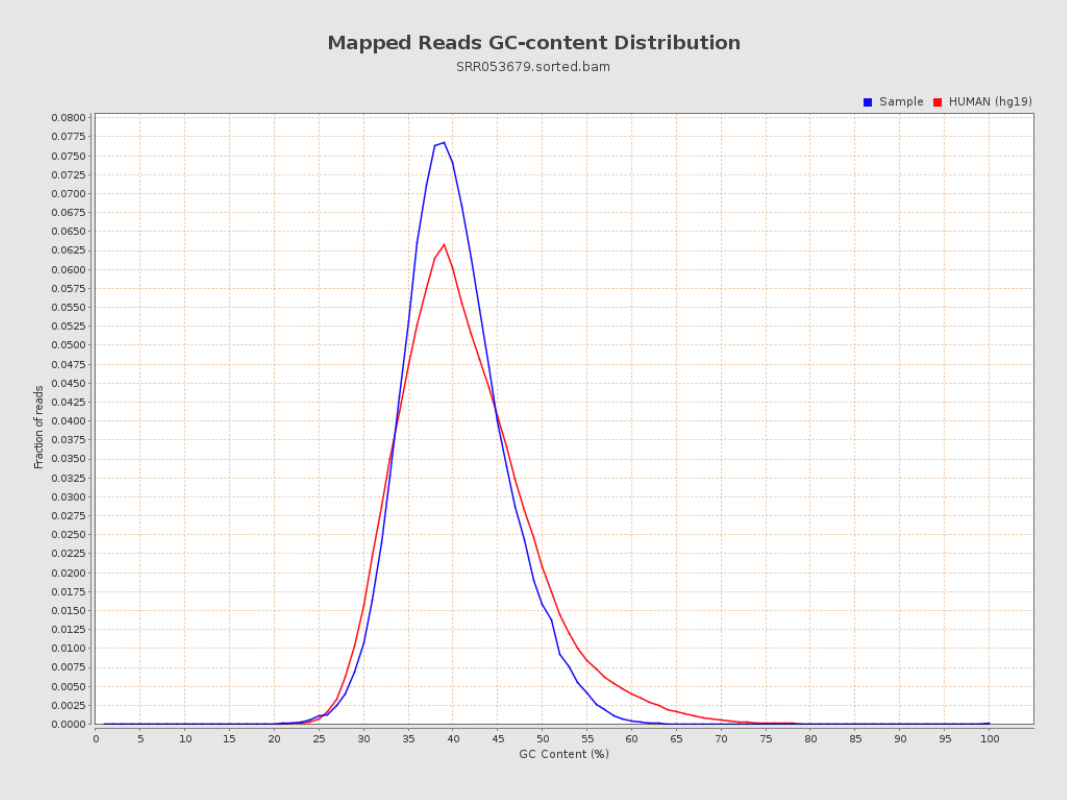
7. Results : Duplication Rate Histogram



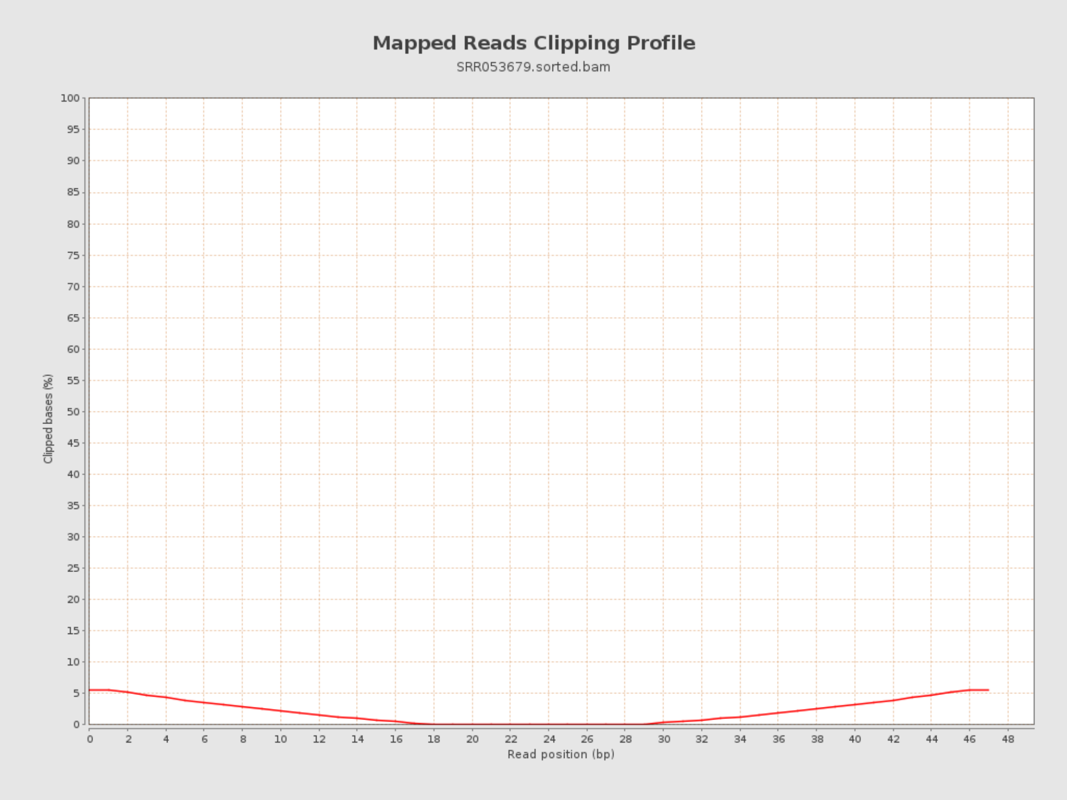
8. Results : Mapped Reads Nucleotide Content



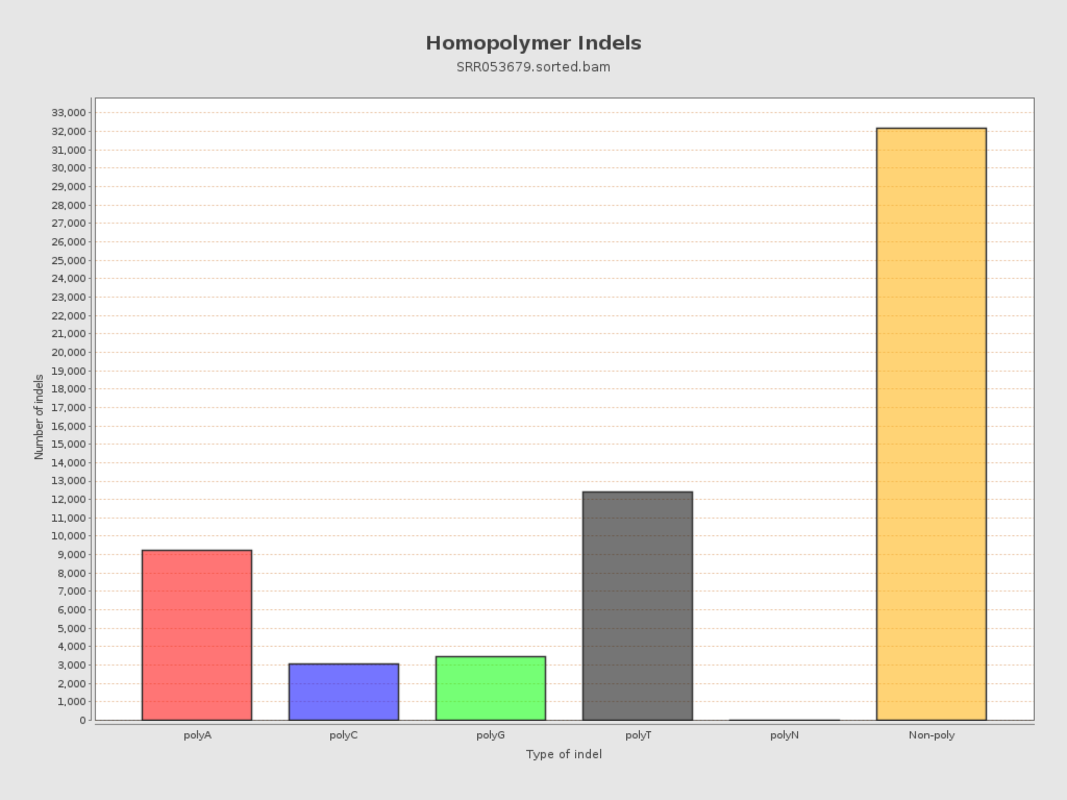
9. Results : Mapped Reads GC-content Distribution



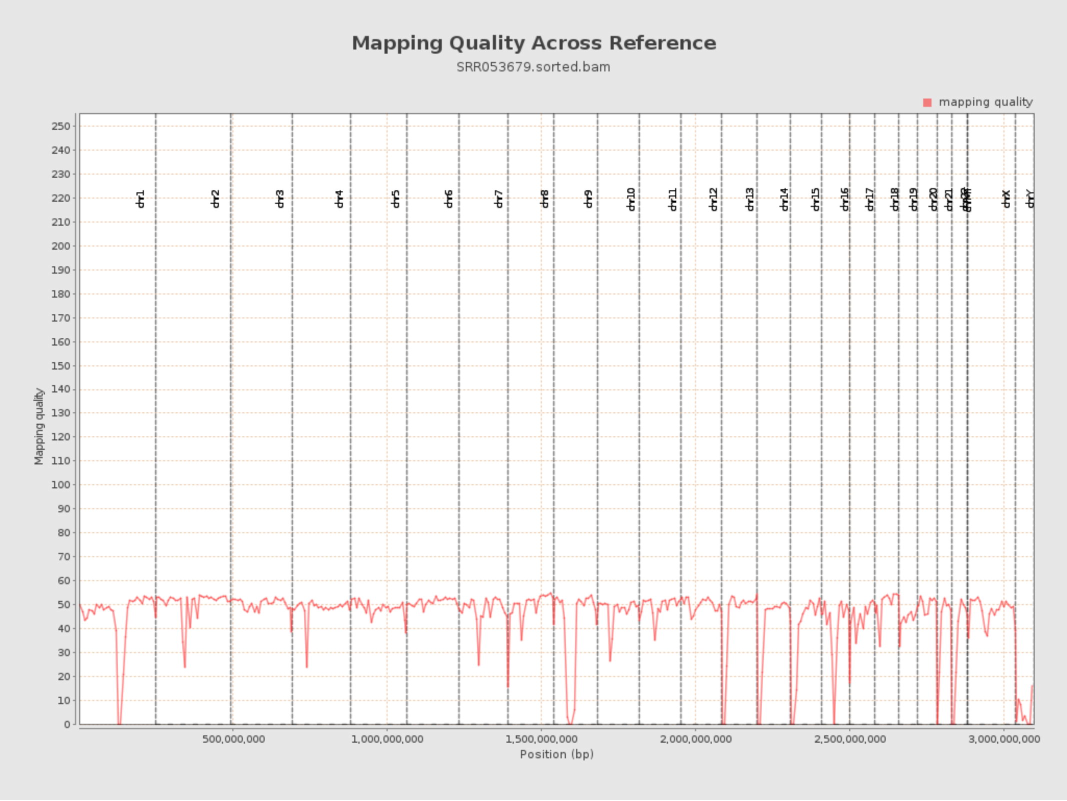
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram