Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:15:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053677.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_SRR053677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:15:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,600,071
Mapped reads	6,318,289 / 83.13%
Unmapped reads	1,281,782 / 16.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	180 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,235,231 / 16.25%
Duplication rate	15.01%
Clipped reads	545,556 / 7.18%

2.2. ACGT Content

Number/percentage of A's	88,198,821 / 29.54%
Number/percentage of C's	57,594,825 / 19.29%
Number/percentage of T's	89,487,528 / 29.97%
Number/percentage of G's	63,062,063 / 21.12%
Number/percentage of N's	228,747 / 0.08%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0965

Standard Deviation	0.6893

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

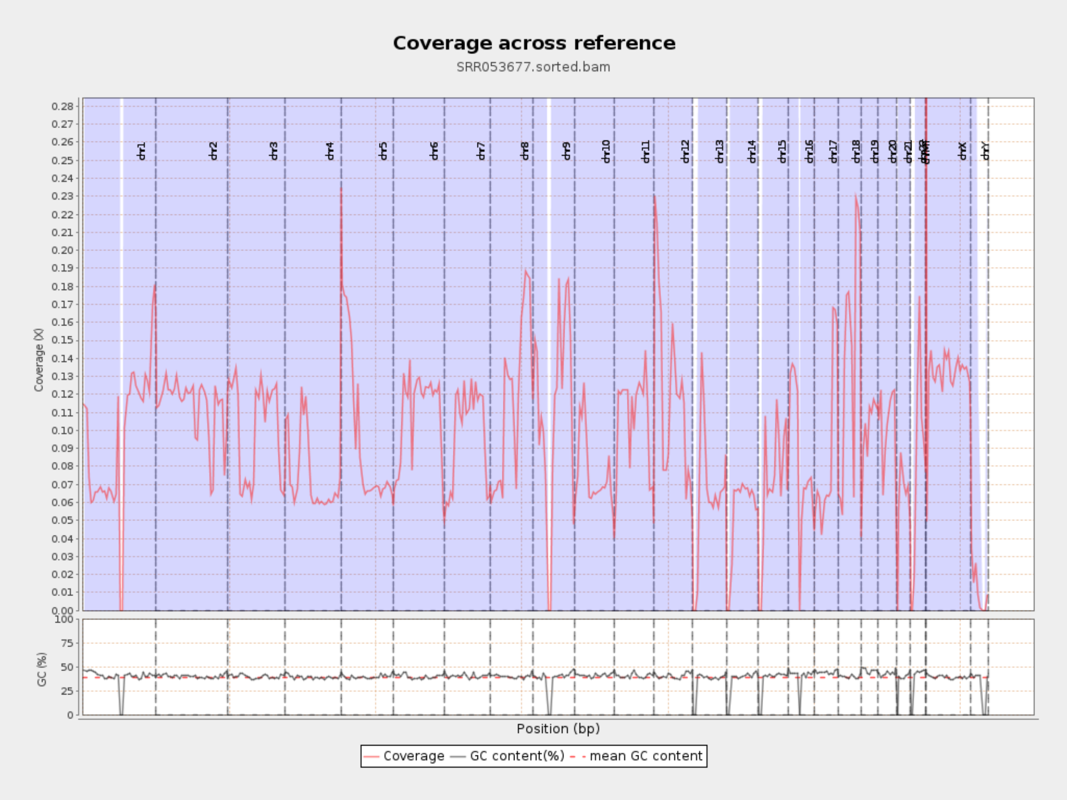
General error rate	0.61%
Mismatches	1,793,985
Insertions	12,489
Mapped reads with at least one insertion	0.2%
Deletions	42,683
Mapped reads with at least one deletion	0.67%
Homopolymer indels	47.11%

2.6. Chromosome stats

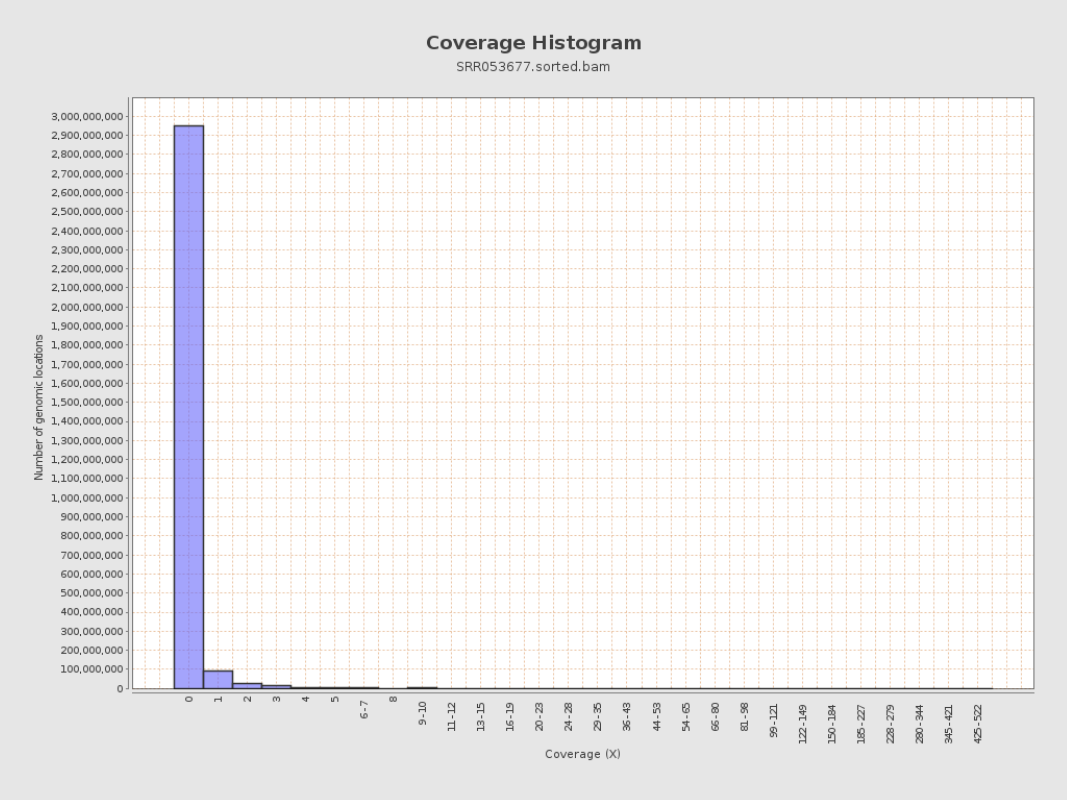
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23572731	0.0946	0.755
chr2	243199373	27476094	0.113	0.7932
chr3	198022430	20083086	0.1014	0.657
chr4	191154276	14398560	0.0753	0.5641
chr5	180915260	17343407	0.0959	0.6394
chr6	171115067	18917680	0.1106	0.7681
chr7	159138663	15596369	0.098	0.723

chr8	146364022	17258894	0.1179	0.7675
chr9	141213431	15854542	0.1123	0.731
chr10	135534747	10428226	0.0769	0.6443
chr11	135006516	14536871	0.1077	0.7145
chr12	133851895	16699344	0.1248	0.7528
chr13	115169878	7279694	0.0632	0.5079
chr14	107349540	5845638	0.0545	0.5308
chr15	102531392	7158076	0.0698	0.5248
chr16	90354753	7463534	0.0826	0.6126
chr17	81195210	6965674	0.0858	0.6037
chr18	78077248	11089074	0.142	0.8633
chr19	59128983	6023671	0.1019	0.7288
chr20	63025520	6567006	0.1042	0.6885
chr21	48129895	2930656	0.0609	0.5459
chr22	51304566	4190953	0.0817	0.6065
chrMT	16571	21548	1.3003	2.3847
chrX	155270560	20282263	0.1306	0.8009
chrY	59373566	652730	0.011	0.2137

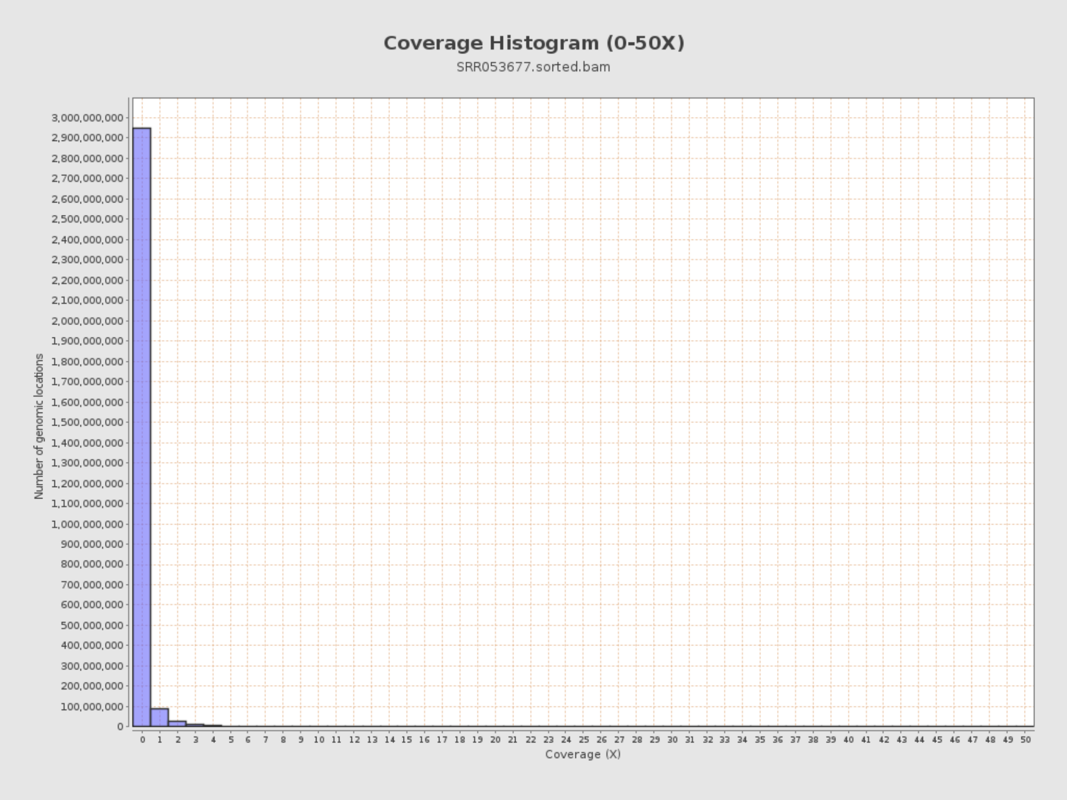
3. Results : Coverage across reference



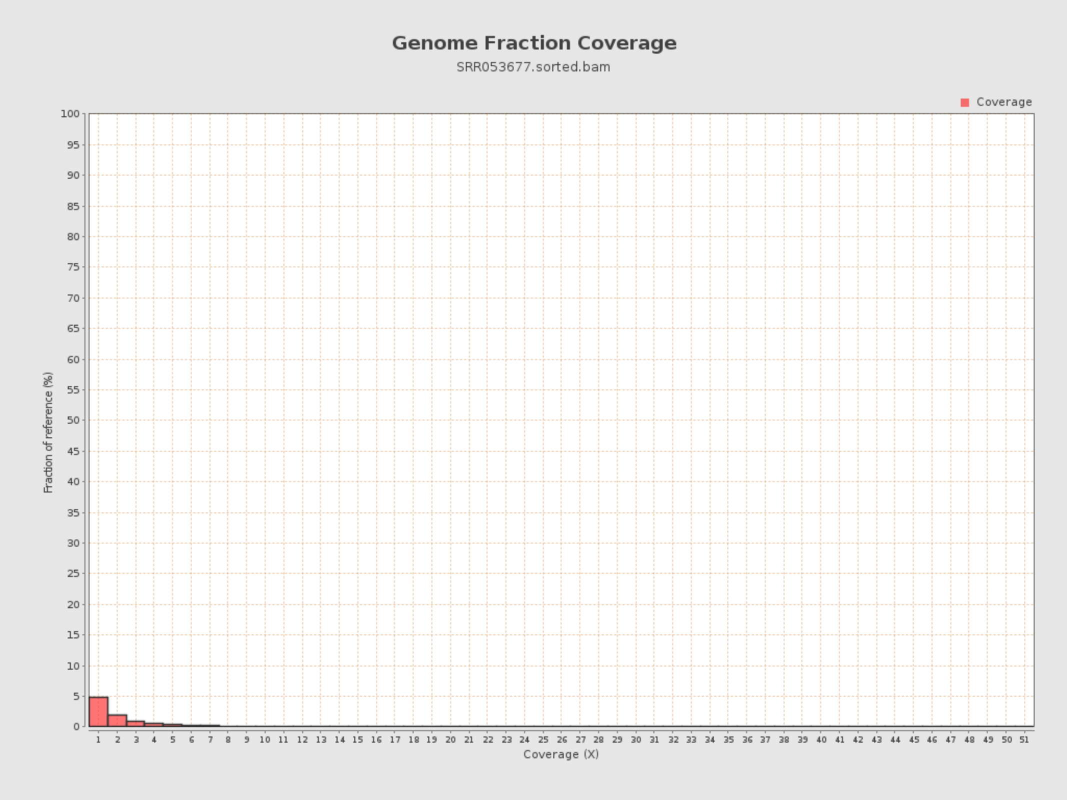
4. Results : Coverage Histogram



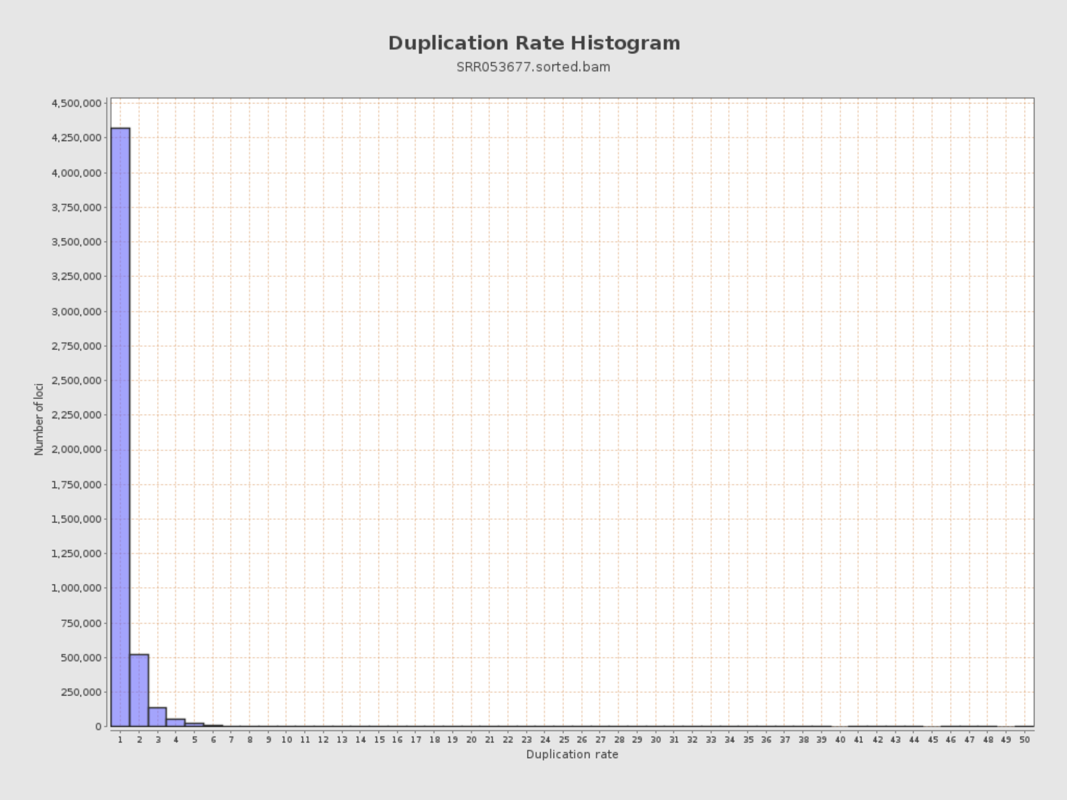
5. Results : Coverage Histogram (0-50X)



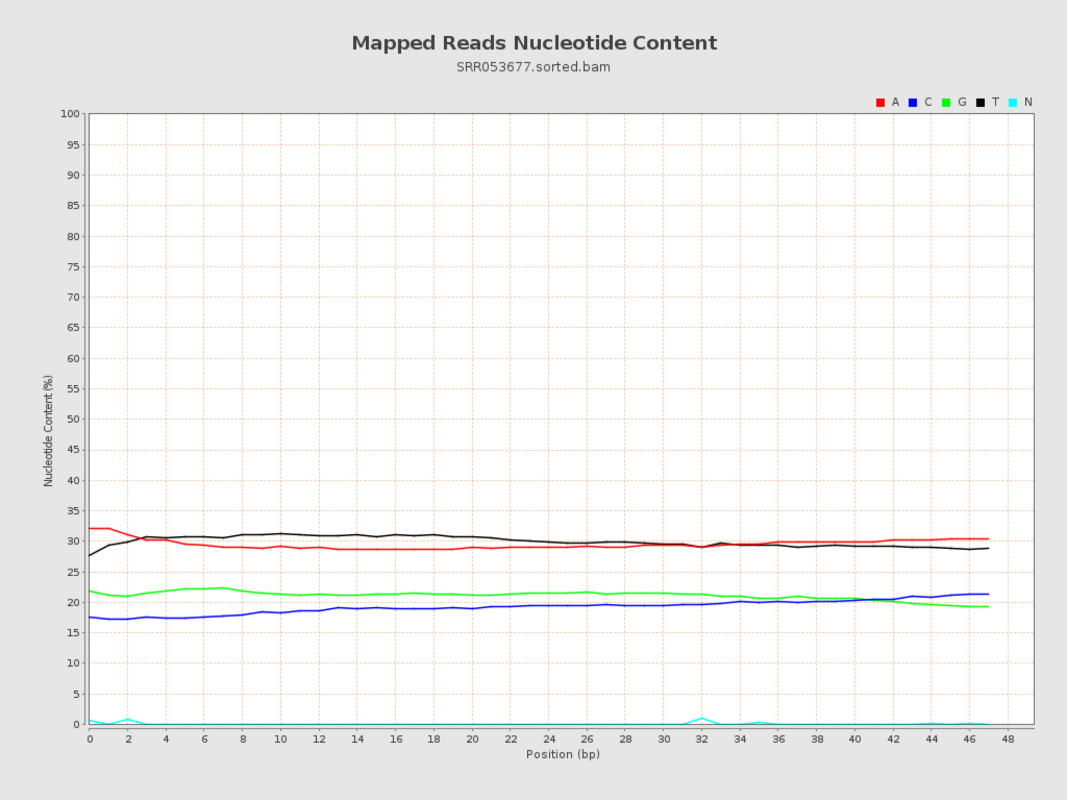
6. Results : Genome Fraction Coverage



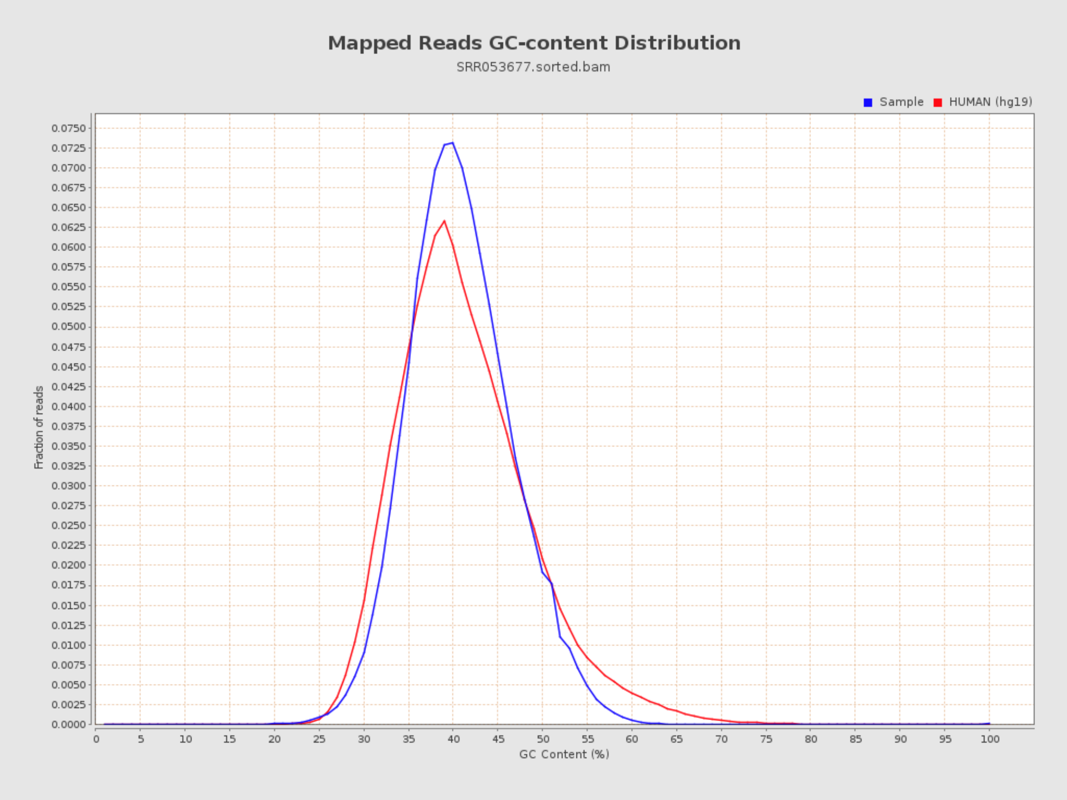
7. Results : Duplication Rate Histogram



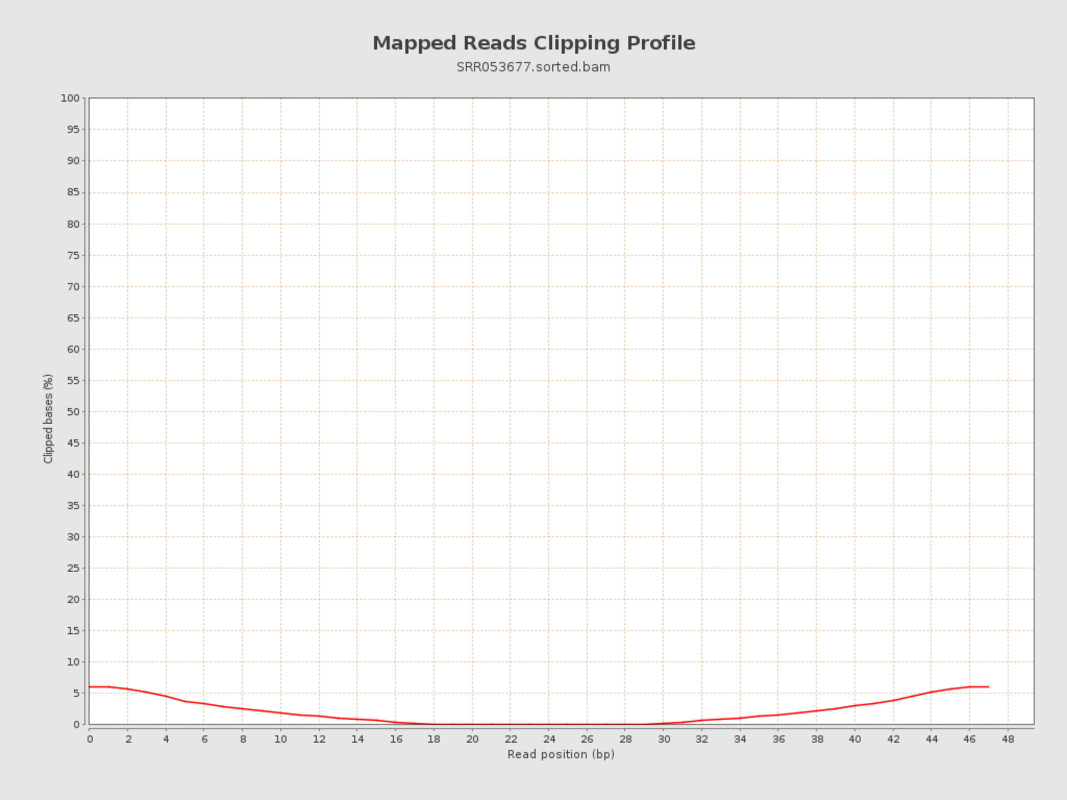
8. Results : Mapped Reads Nucleotide Content



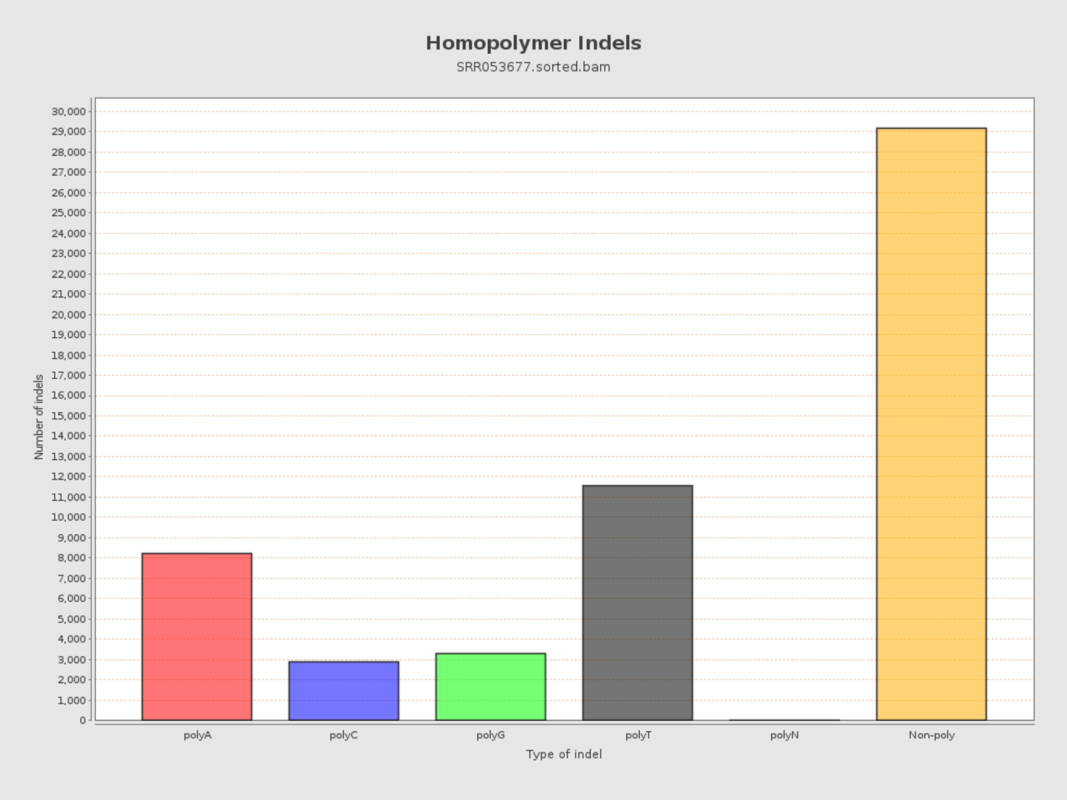
9. Results : Mapped Reads GC-content Distribution



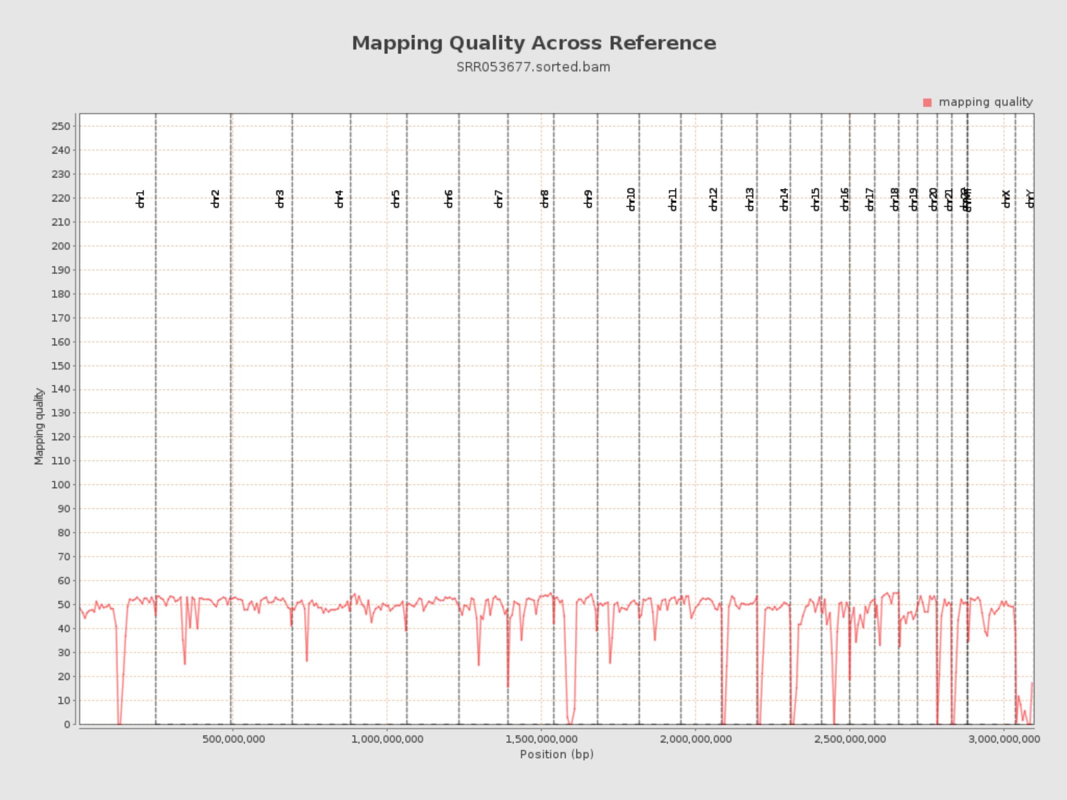
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram