Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 00:04:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053619.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_SRR053619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053619.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 00:04:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053619.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,285,180
Mapped reads	5,116,034 / 81.4%
Unmapped reads	1,169,146 / 18.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	180 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	873,396 / 13.9%
Duplication rate	13.04%
Clipped reads	461,906 / 7.35%

2.2. ACGT Content

Number/percentage of A's	69,799,628 / 28.93%
Number/percentage of C's	47,560,048 / 19.71%
Number/percentage of T's	71,116,234 / 29.48%
Number/percentage of G's	52,764,191 / 21.87%
Number/percentage of N's	9,345 / 0%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0779

Standard Deviation	0.5692

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

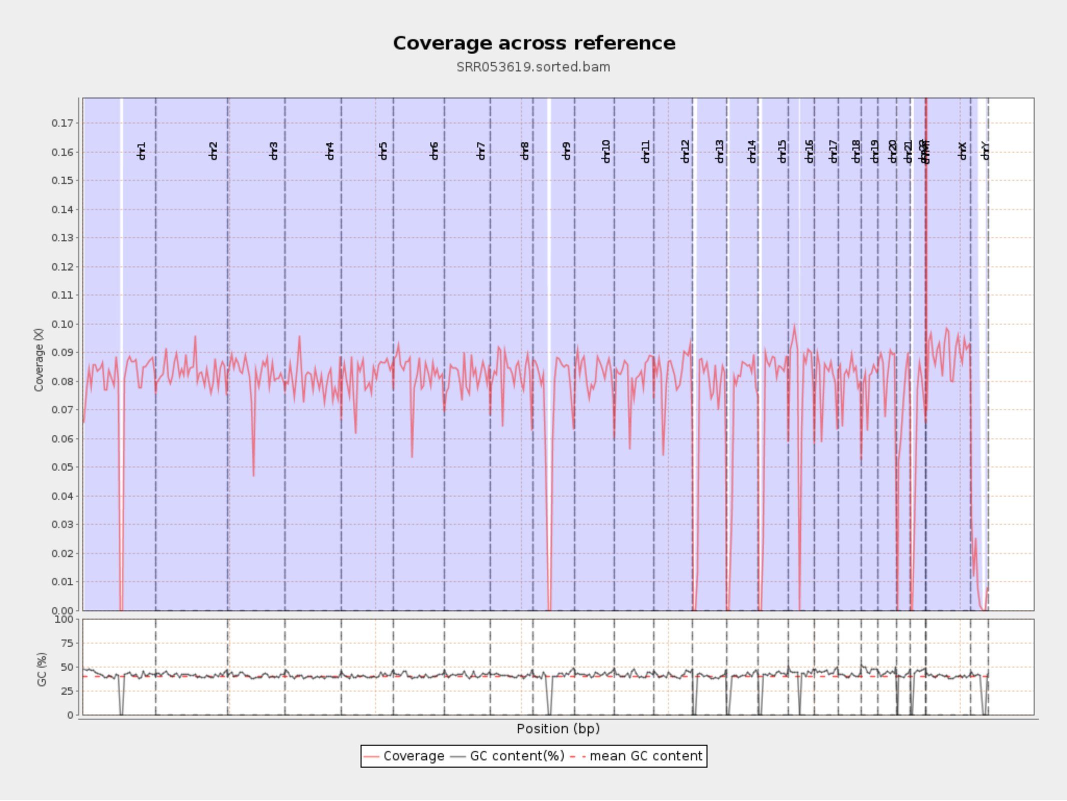
General error rate	0.5%
Mismatches	1,200,396
Insertions	9,545
Mapped reads with at least one insertion	0.19%
Deletions	31,971
Mapped reads with at least one deletion	0.62%
Homopolymer indels	46.44%

2.6. Chromosome stats

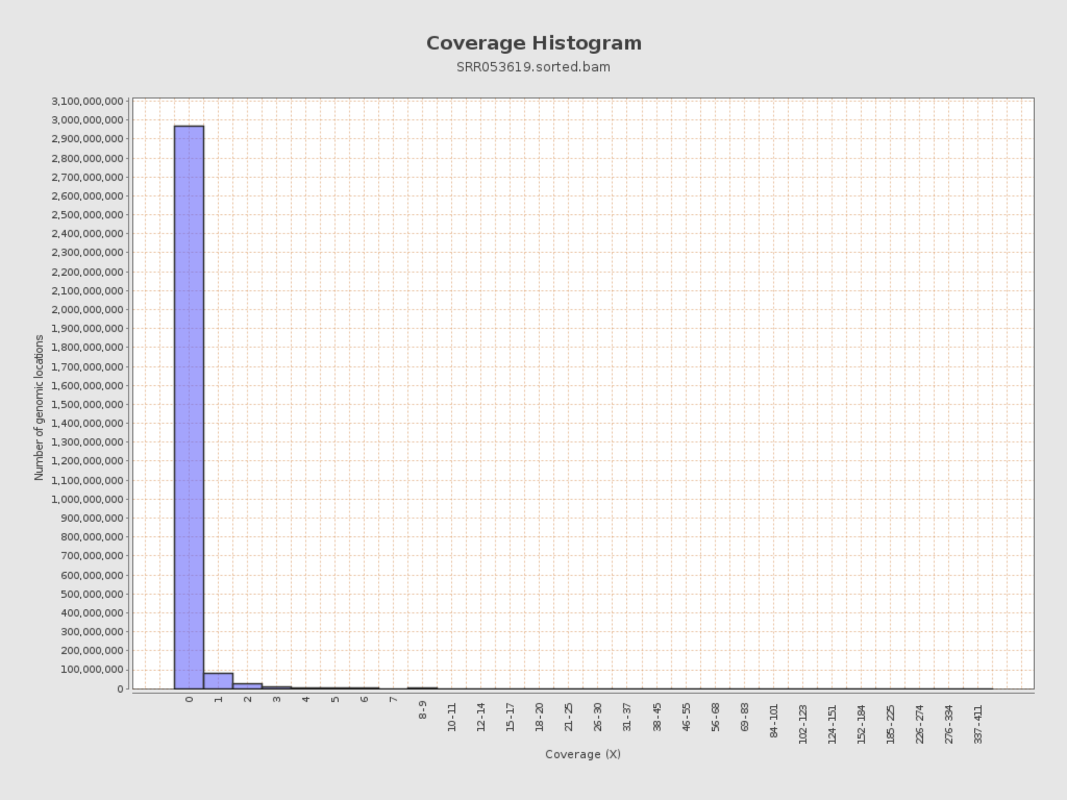
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19368081	0.0777	0.6119
chr2	243199373	20250283	0.0833	0.6536
chr3	198022430	16211027	0.0819	0.5423
chr4	191154276	15426600	0.0807	0.5662
chr5	180915260	14795165	0.0818	0.5459
chr6	171115067	14132735	0.0826	0.5718
chr7	159138663	12980370	0.0816	0.5768

chr8	146364022	12049707	0.0823	0.5725
chr9	141213431	9993271	0.0708	0.5264
chr10	135534747	11258787	0.0831	0.6204
chr11	135006516	10998393	0.0815	0.597
chr12	133851895	11071771	0.0827	0.5551
chr13	115169878	7793115	0.0677	0.5011
chr14	107349540	7450069	0.0694	0.5425
chr15	102531392	7127413	0.0695	0.4913
chr16	90354753	7057781	0.0781	0.564
chr17	81195210	6536966	0.0805	0.5408
chr18	78077248	6361980	0.0815	0.5991
chr19	59128983	4646233	0.0786	0.6064
chr20	63025520	5271024	0.0836	0.5651
chr21	48129895	3142653	0.0653	0.5696
chr22	51304566	2808586	0.0547	0.4572
chrMT	16571	36824	2.2222	3.626
chrX	155270560	13942957	0.0898	0.6022
chrY	59373566	586064	0.0099	0.2546

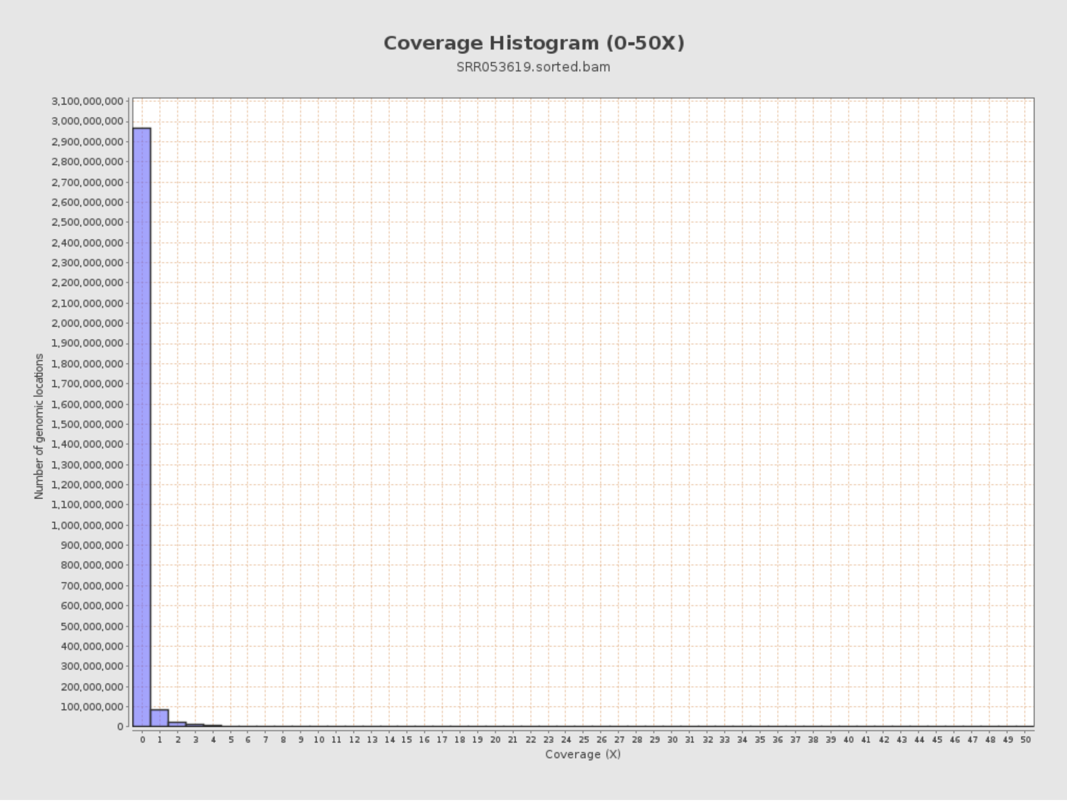
3. Results : Coverage across reference



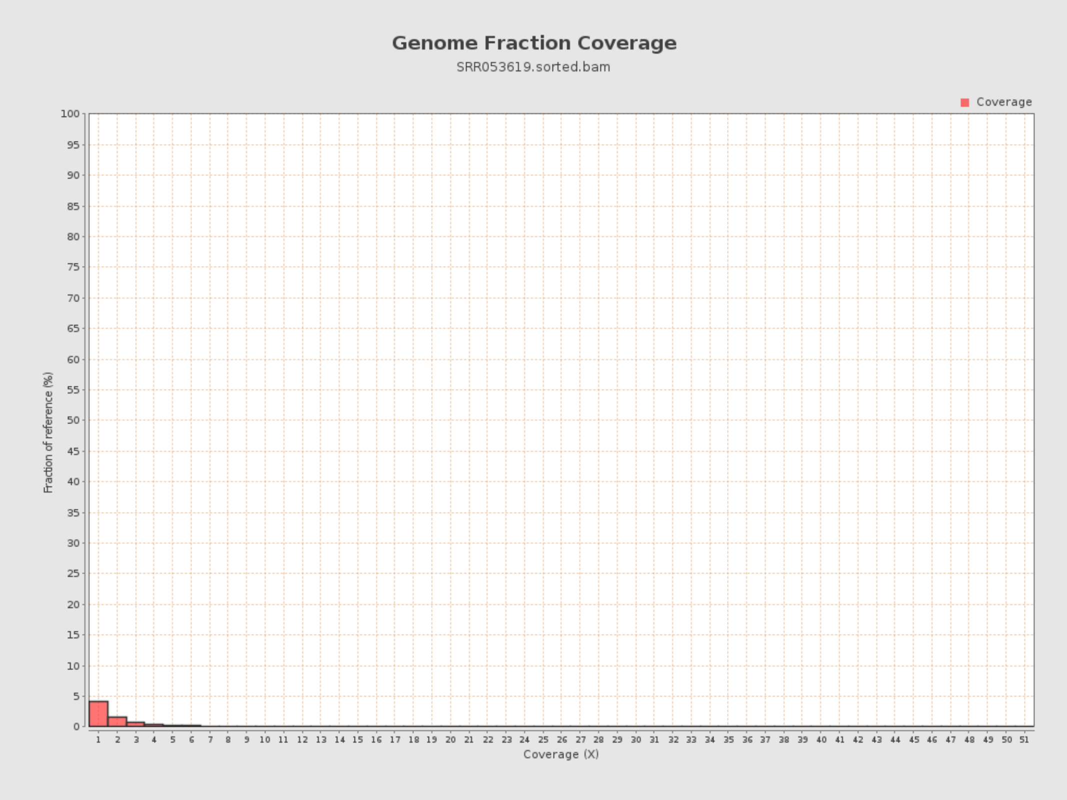
4. Results : Coverage Histogram



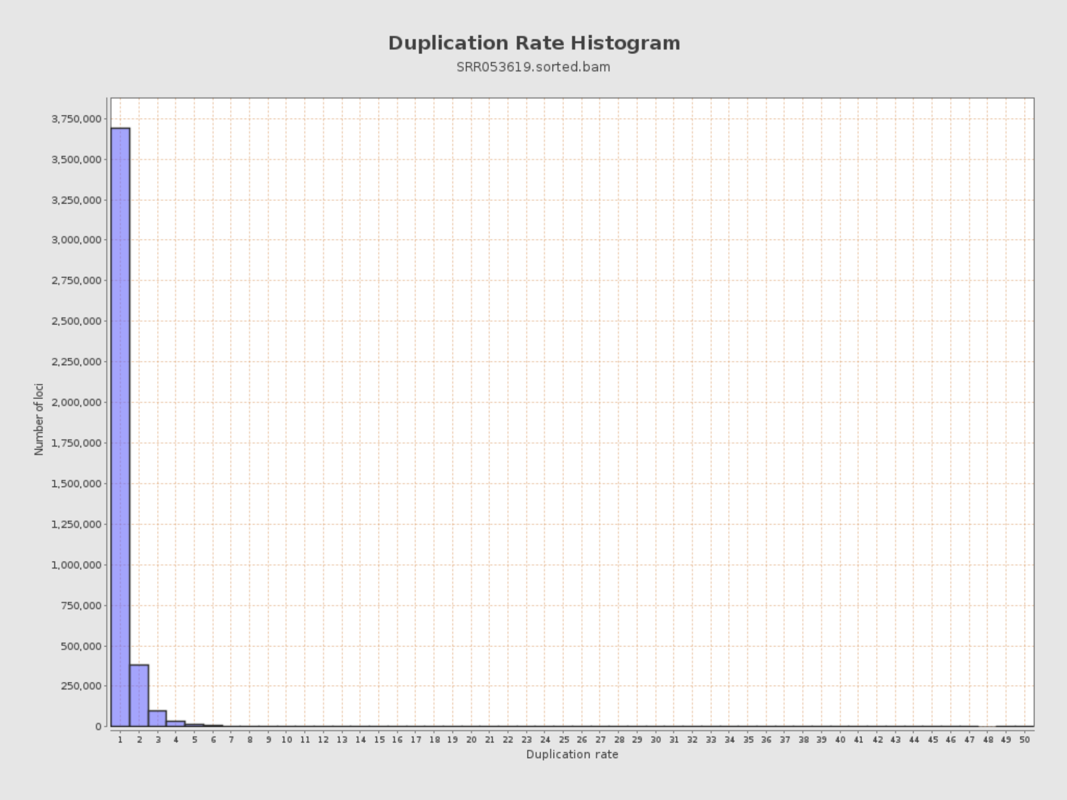
5. Results : Coverage Histogram (0-50X)



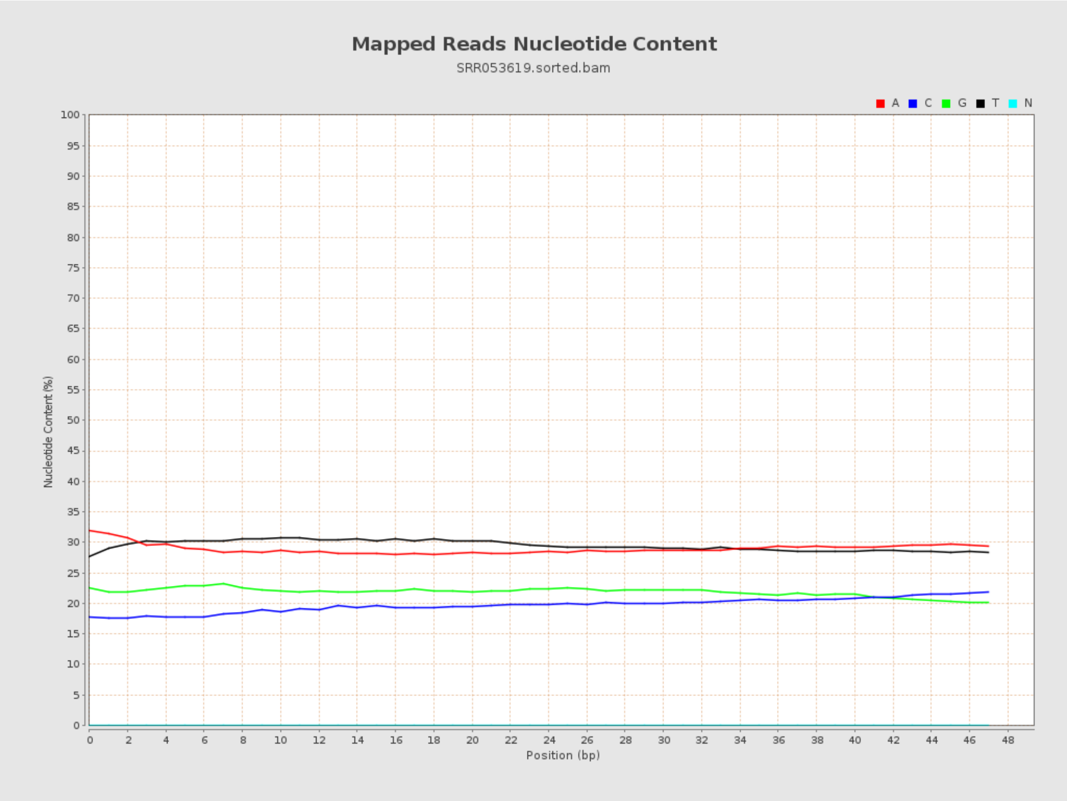
6. Results : Genome Fraction Coverage



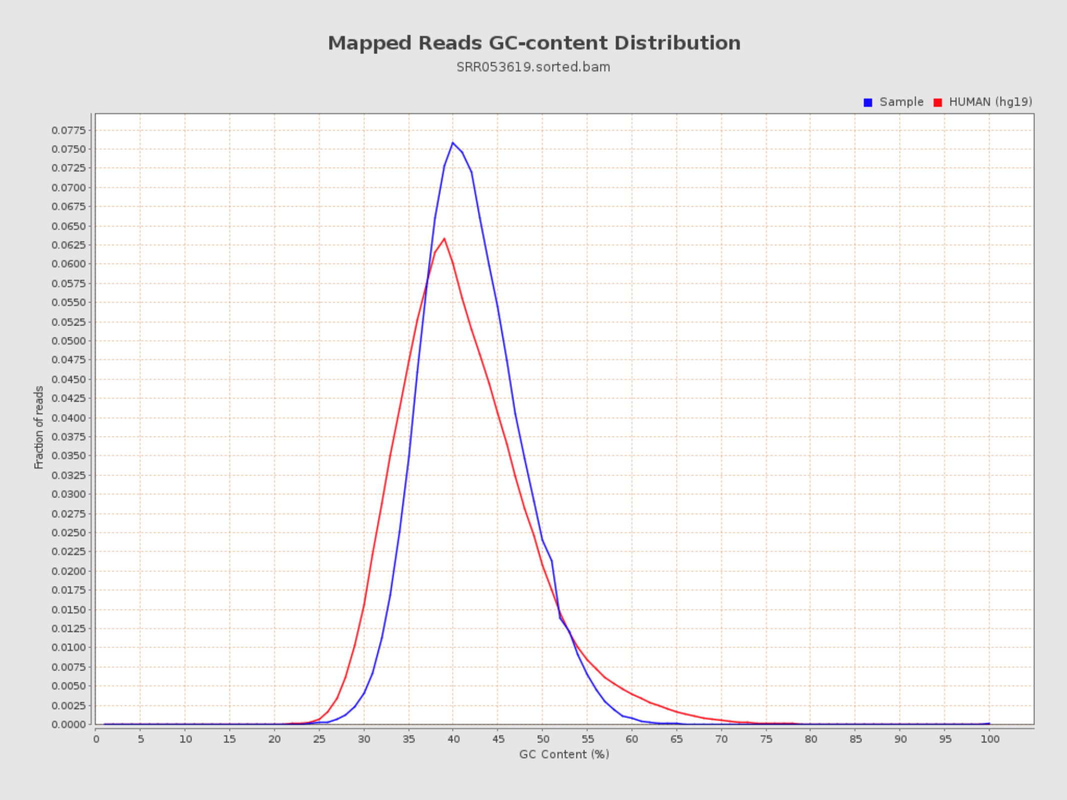
7. Results : Duplication Rate Histogram



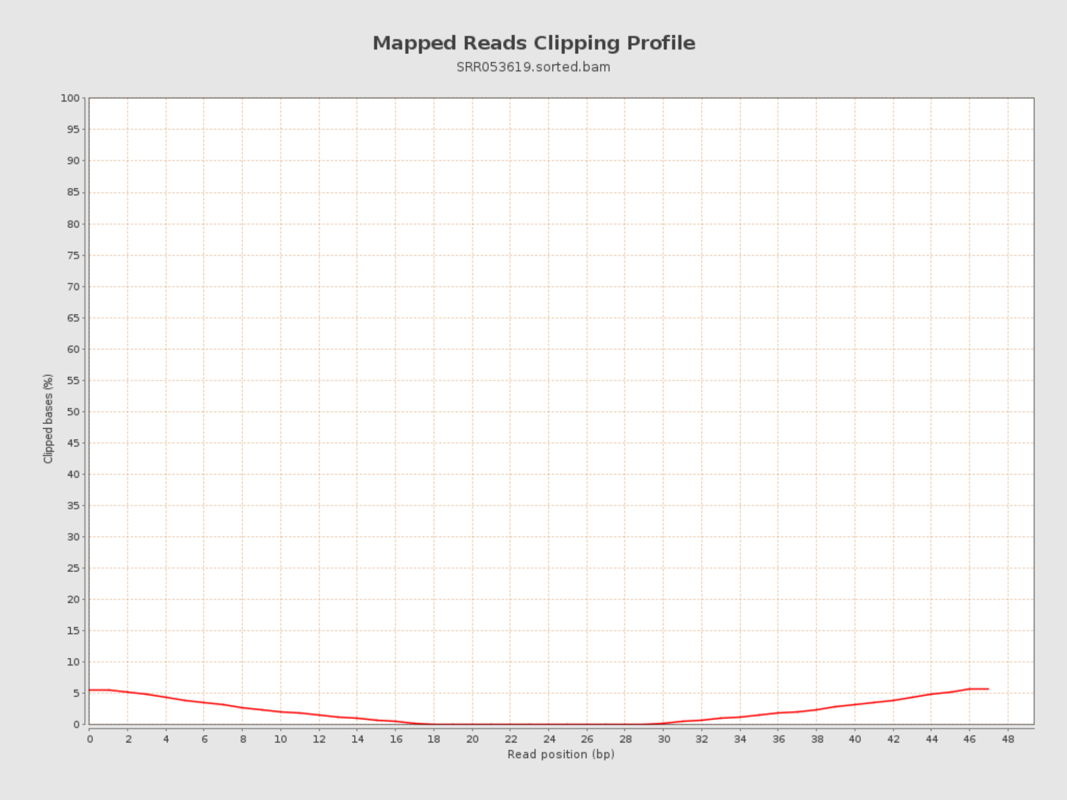
8. Results : Mapped Reads Nucleotide Content



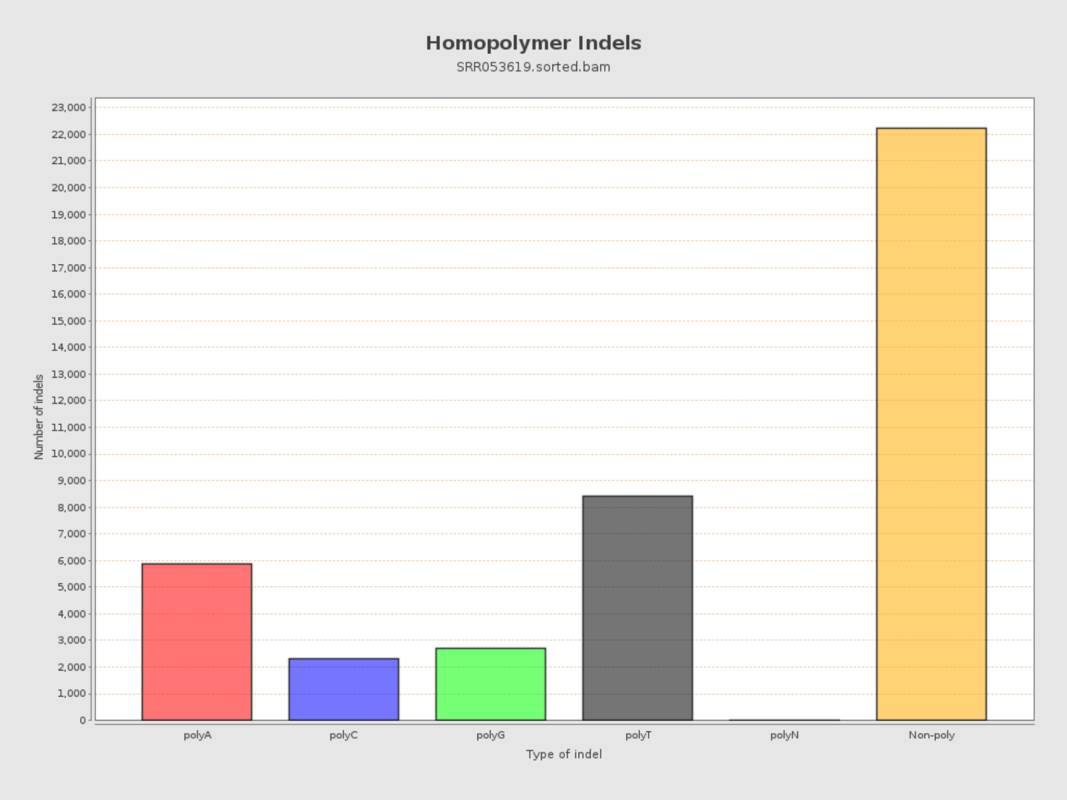
9. Results : Mapped Reads GC-content Distribution



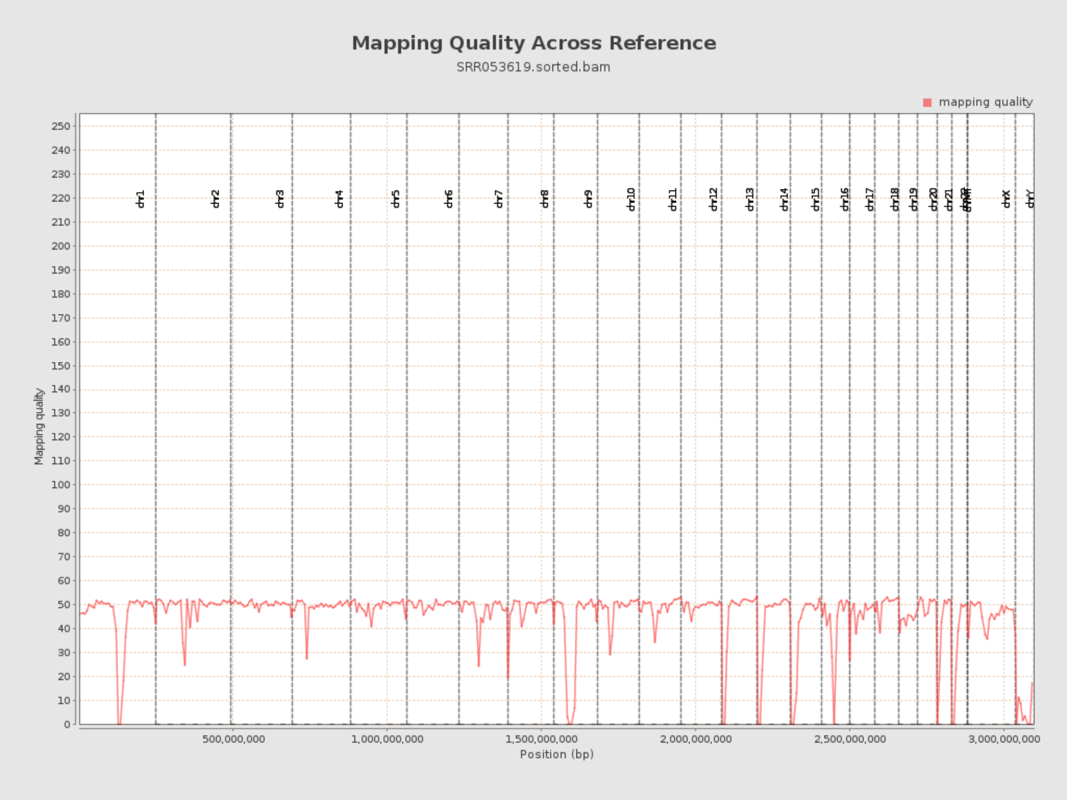
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram