Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:46:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506021.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_SRR1506021 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506021.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:46:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506021.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,626,778
Mapped reads	3,899,973 / 69.31%
Unmapped reads	1,726,805 / 30.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	196 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	263,531 / 4.68%
Duplication rate	5.03%
Clipped reads	727,889 / 12.94%

2.2. ACGT Content

Number/percentage of A's	52,819,232 / 29.33%
Number/percentage of C's	36,883,199 / 20.48%
Number/percentage of T's	52,417,185 / 29.11%
Number/percentage of G's	37,379,392 / 20.76%
Number/percentage of N's	594,473 / 0.33%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.5988

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

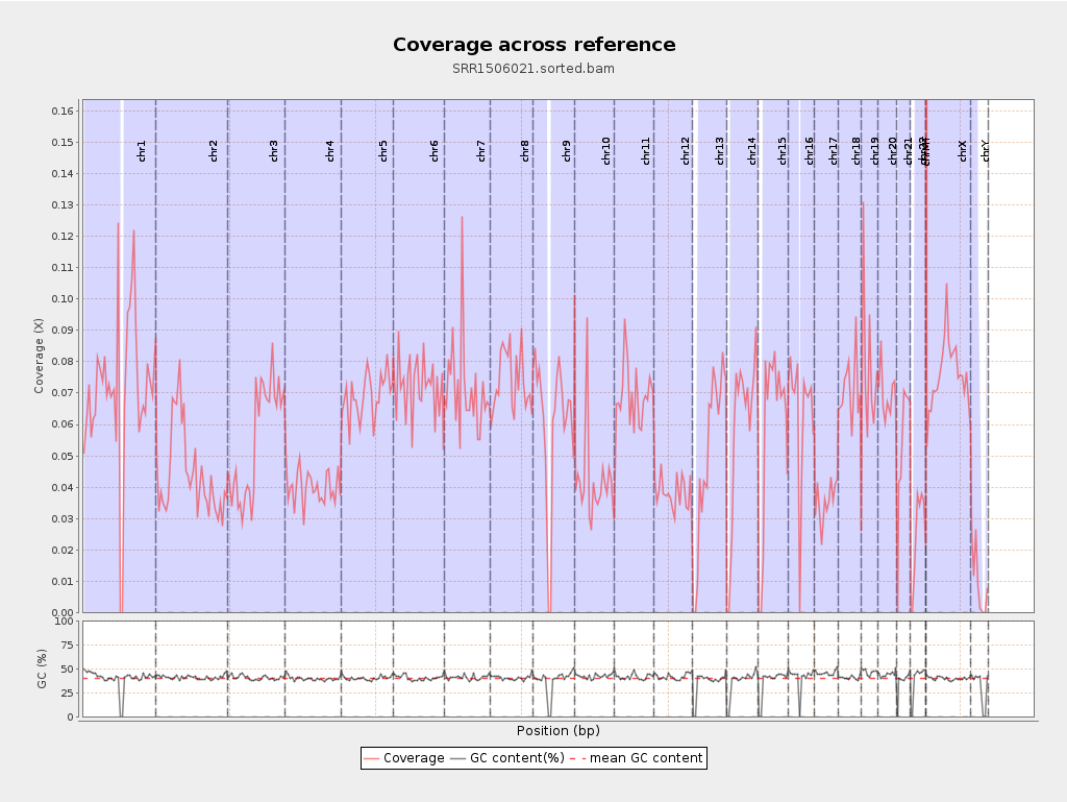
General error rate	0.81%
Mismatches	1,443,912
Insertions	7,740
Mapped reads with at least one insertion	0.2%
Deletions	26,066
Mapped reads with at least one deletion	0.67%
Homopolymer indels	44.5%

2.6. Chromosome stats

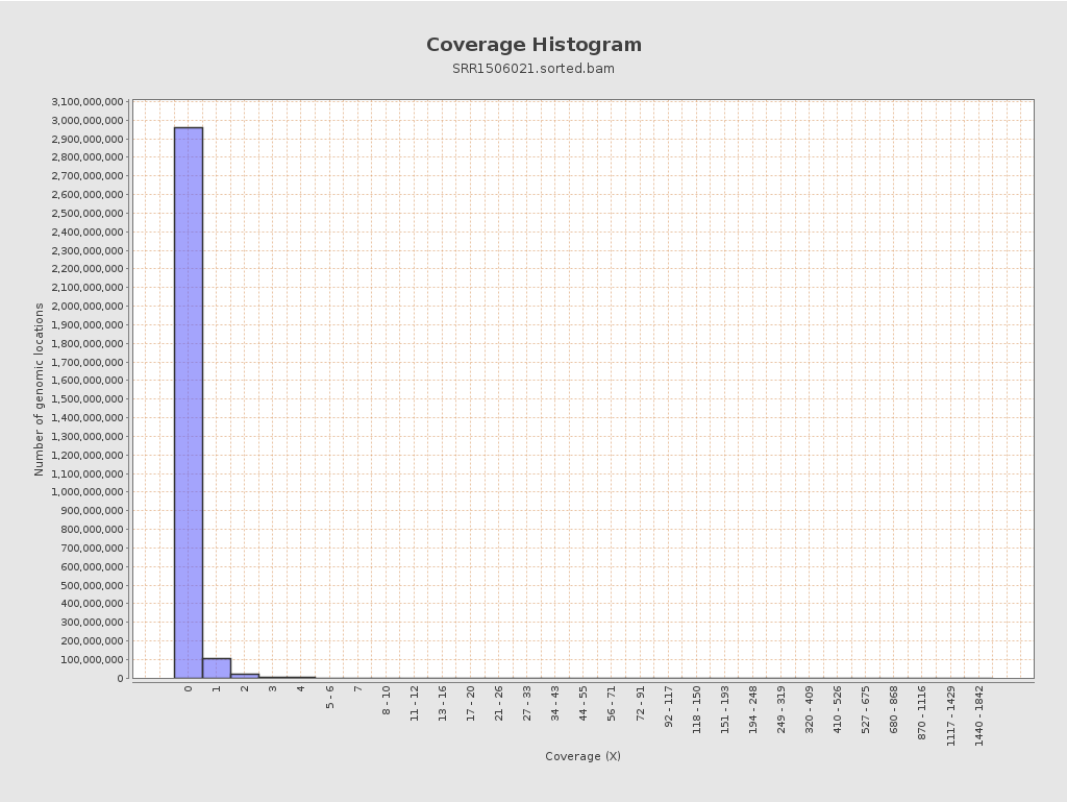
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17747916	0.0712	1.2901
chr2	243199373	10728991	0.0441	0.3983
chr3	198022430	10827269	0.0547	0.2994
chr4	191154276	7615119	0.0398	0.2593
chr5	180915260	12602871	0.0697	0.34
chr6	171115067	12324213	0.072	0.3974
chr7	159138663	11322348	0.0711	0.9913

chr8	146364022	10813753	0.0739	0.6924
chr9	141213431	8497565	0.0602	0.4074
chr10	135534747	5644218	0.0416	0.4908
chr11	135006516	9232095	0.0684	0.4405
chr12	133851895	5070710	0.0379	0.2689
chr13	115169878	5901024	0.0512	0.286
chr14	107349540	6348000	0.0591	0.9509
chr15	102531392	5967636	0.0582	0.3067
chr16	90354753	5716489	0.0633	0.3619
chr17	81195210	2876373	0.0354	0.2569
chr18	78077248	5591772	0.0716	0.6767
chr19	59128983	4548992	0.0769	0.8885
chr20	63025520	4411873	0.07	0.3494
chr21	48129895	2597692	0.054	0.3208
chr22	51304566	1263455	0.0246	0.1974
chrMT	16571	134120	8.0937	6.3453
chrX	155270560	11774814	0.0758	0.4026
chrY	59373566	570230	0.0096	0.165

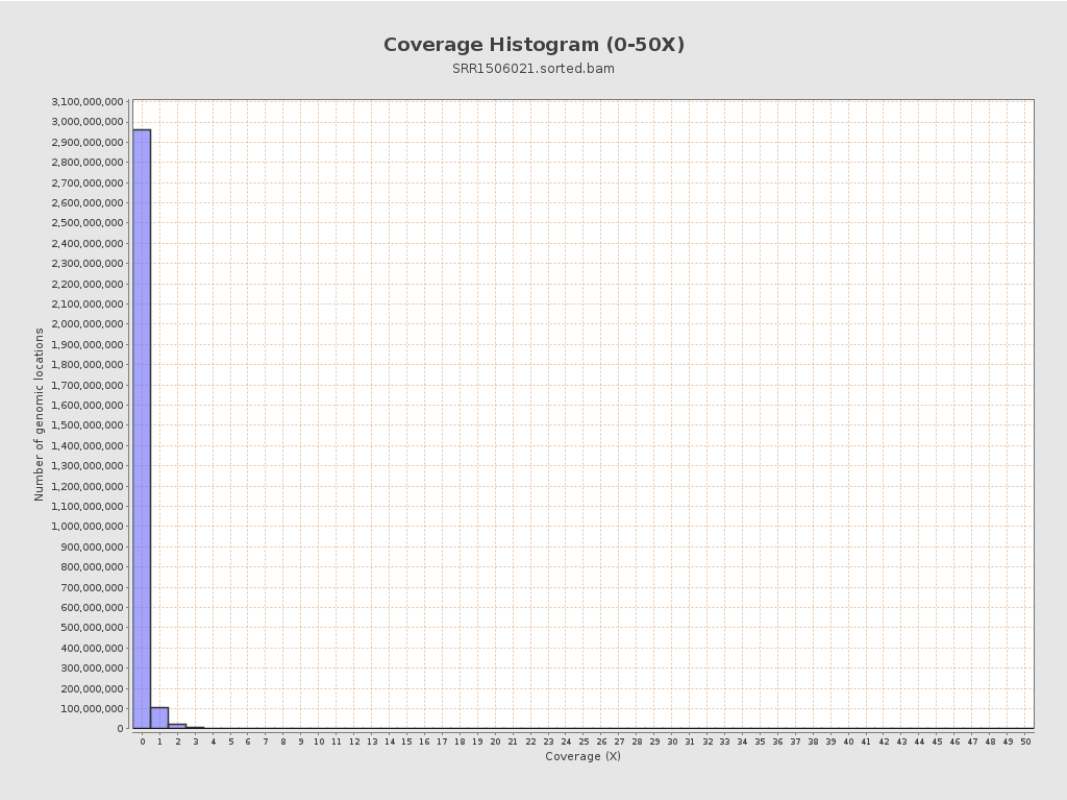
3. Results : Coverage across reference



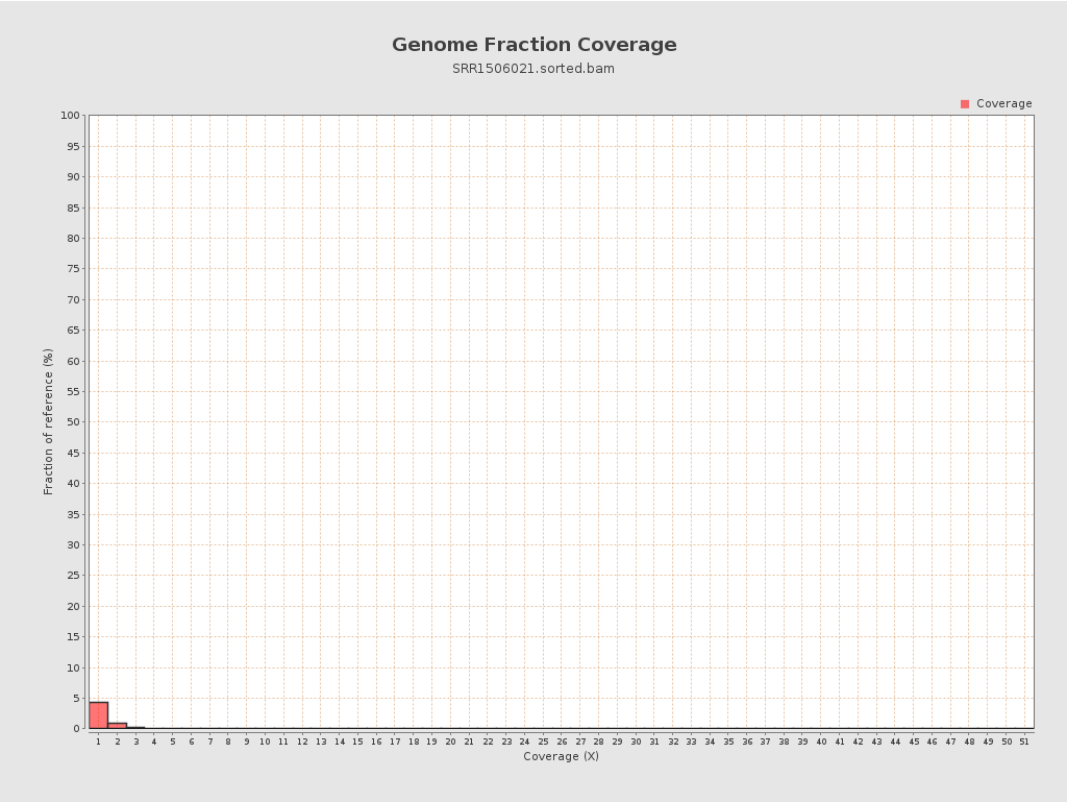
4. Results : Coverage Histogram



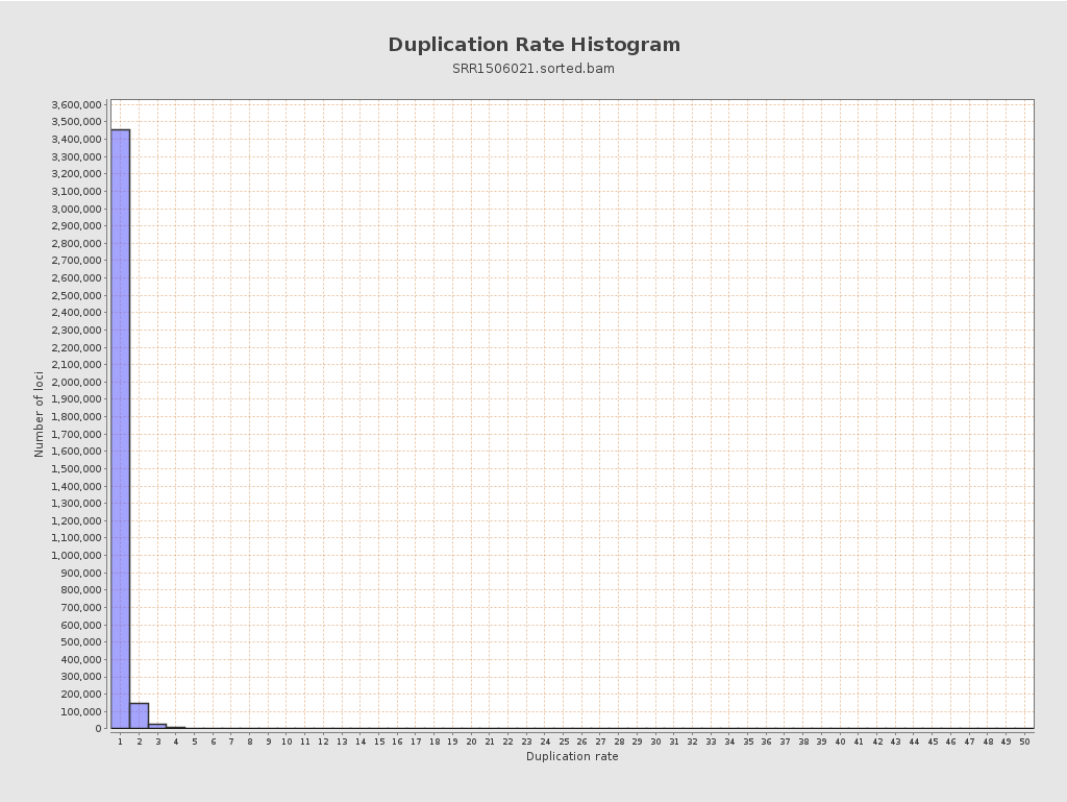
5. Results : Coverage Histogram (0-50X)



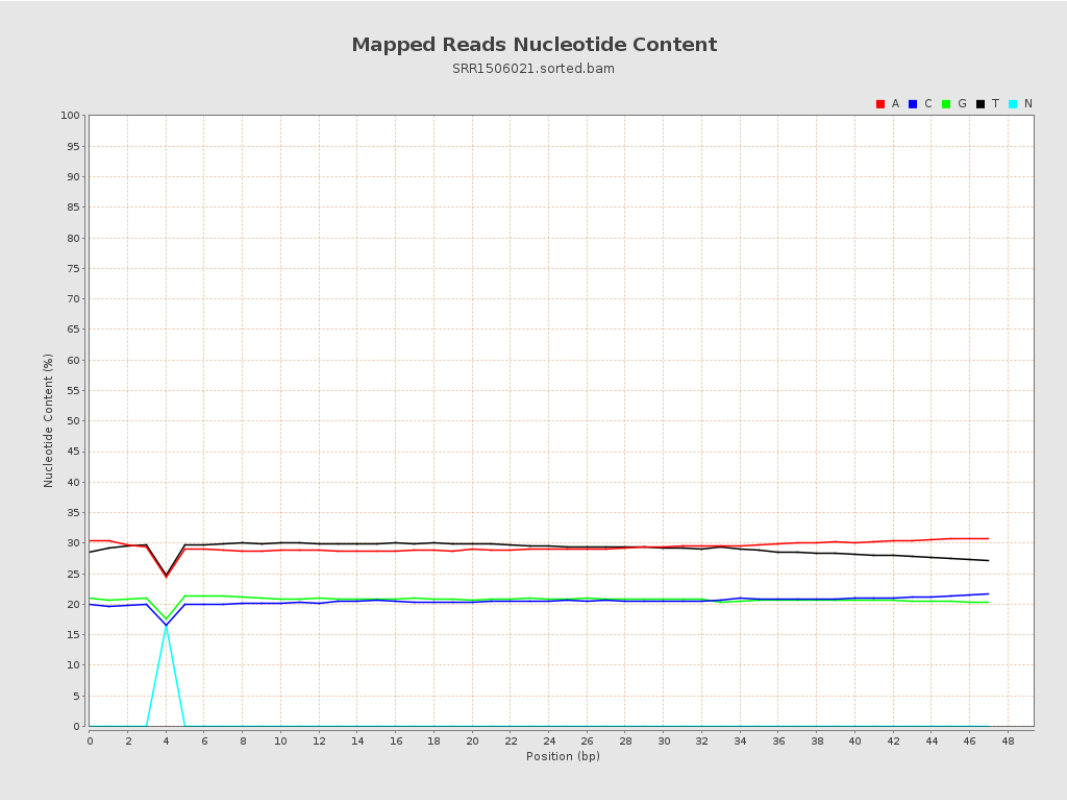
6. Results : Genome Fraction Coverage



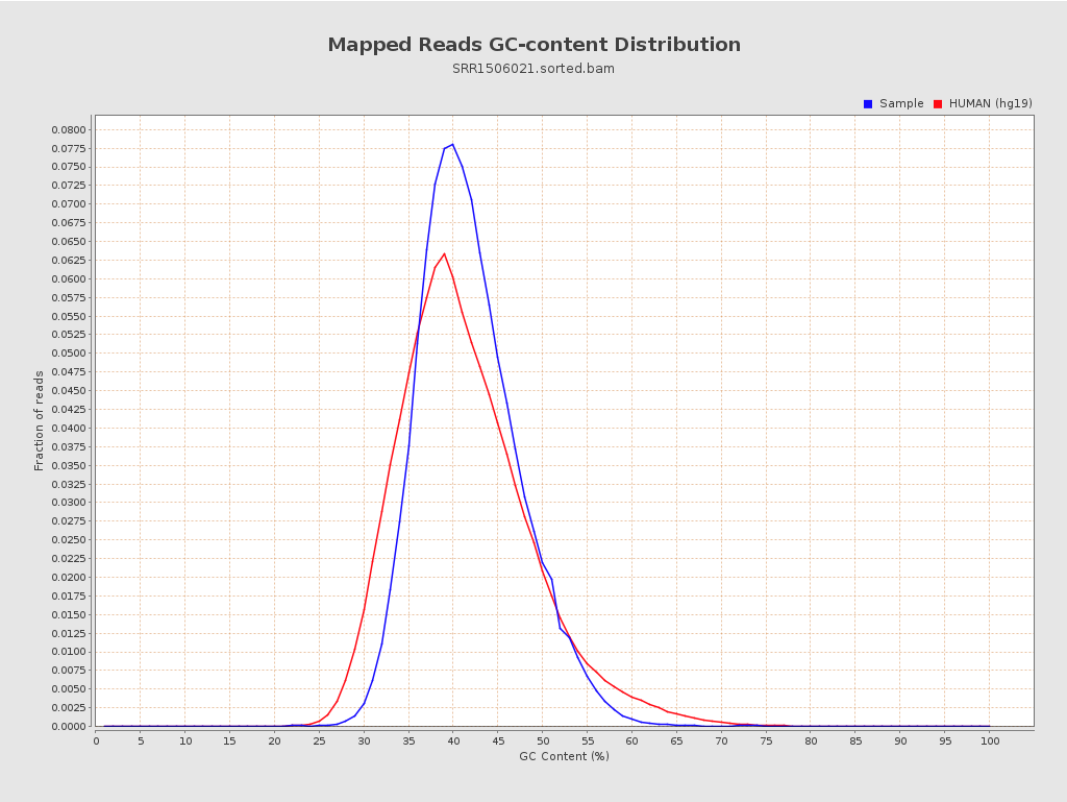
7. Results : Duplication Rate Histogram



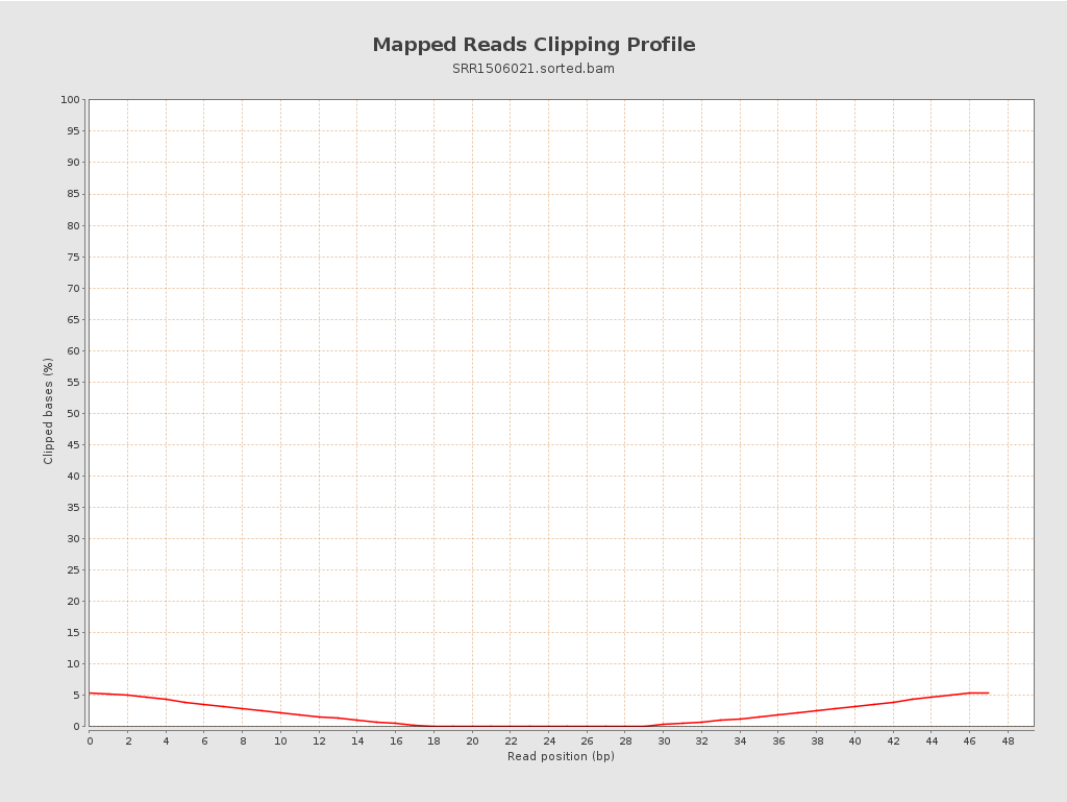
8. Results : Mapped Reads Nucleotide Content



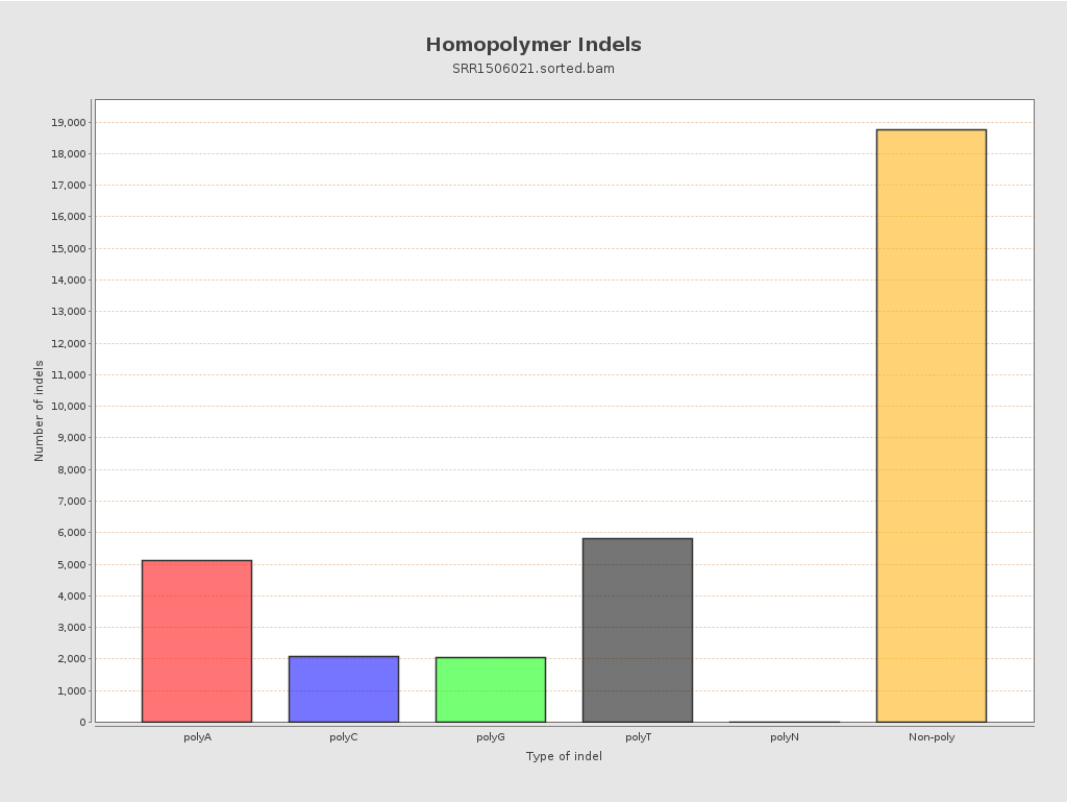
9. Results : Mapped Reads GC-content Distribution



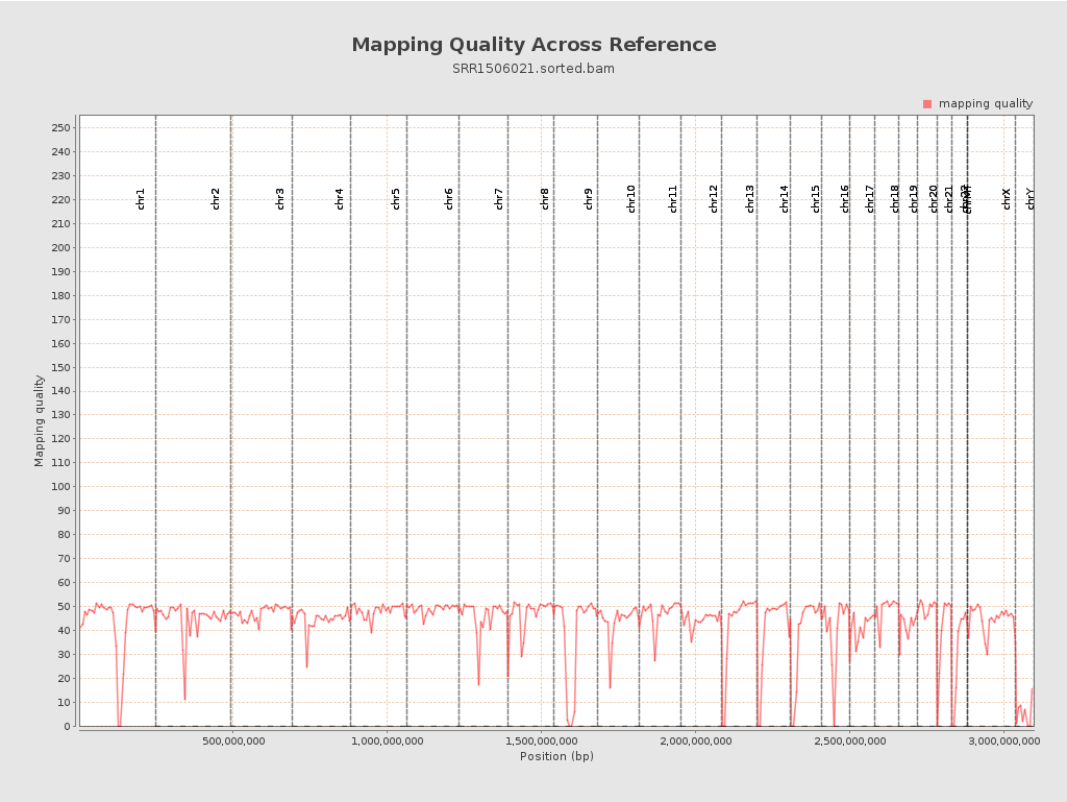
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram