Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:51:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549146.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_SRR1549146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549146.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:51:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,200,525
Mapped reads	11,555,007 / 87.53%
Unmapped reads	1,645,518 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	712,744 / 5.4%
Duplication rate	5.03%
Clipped reads	616,479 / 4.67%

2.2. ACGT Content

Number/percentage of A's	129,144,912 / 28.17%
Number/percentage of C's	98,808,013 / 21.55%
Number/percentage of T's	131,236,499 / 28.62%
Number/percentage of G's	99,246,136 / 21.64%
Number/percentage of N's	92,390 / 0.02%
GC Percentage	43.19%

2.3. Coverage

Mean	0.1481
Standard Deviation	0.8273

2.4. Mapping Quality

Mean Mapping Quality	42.4

2.5. Mismatches and indels

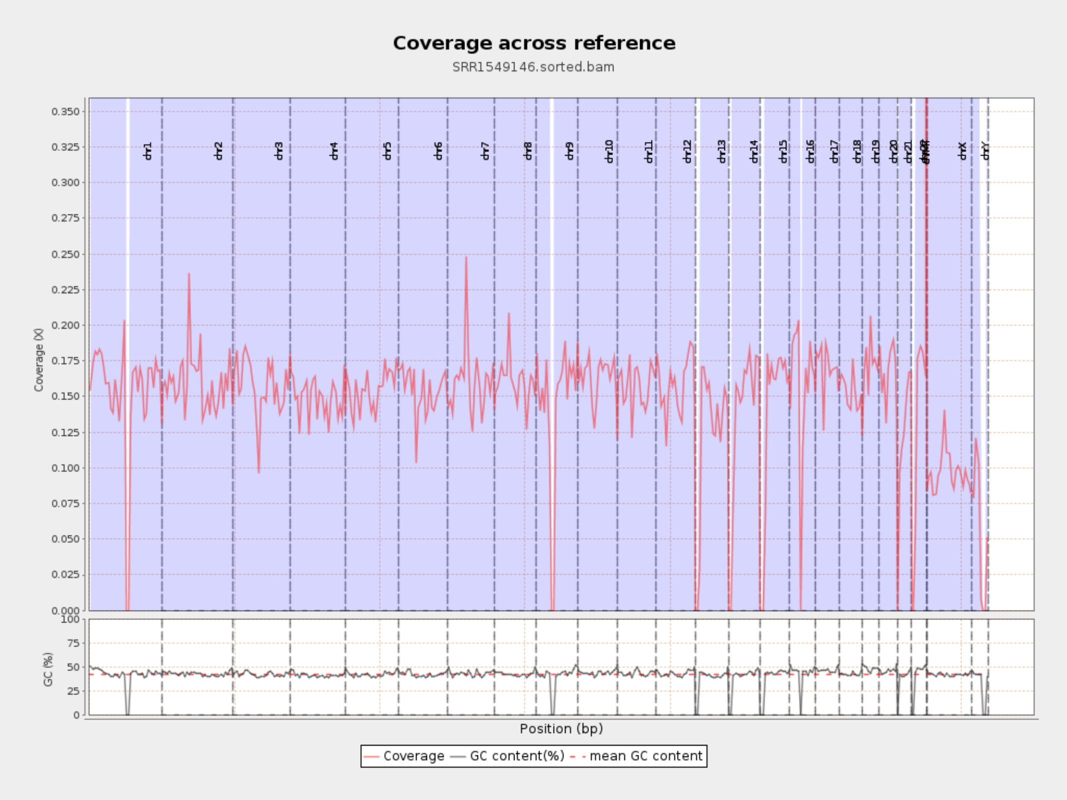
General error rate	0.31%
Mismatches	1,424,764
Insertions	12,152
Mapped reads with at least one insertion	0.11%
Deletions	34,832
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.06%

2.6. Chromosome stats

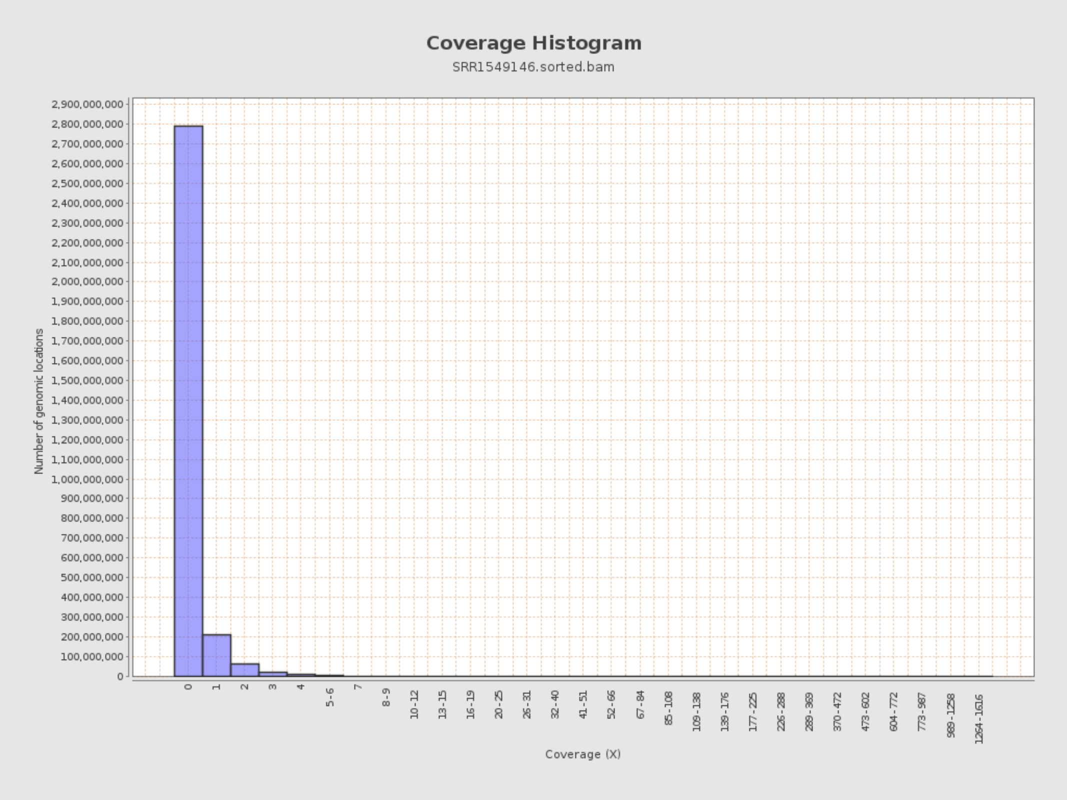
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38009931	0.1525	1.3292
chr2	243199373	38957369	0.1602	0.866
chr3	198022430	31109035	0.1571	0.5597
chr4	191154276	28391255	0.1485	0.5545
chr5	180915260	28061844	0.1551	0.5712
chr6	171115067	26390613	0.1542	0.6328
chr7	159138663	25598545	0.1609	1.2732
chr8	146364022	23503678	0.1606	0.8361

chr9	141213431	19880456	0.1408	0.8332
chr10	135534747	22208427	0.1639	0.7563
chr11	135006516	21155761	0.1567	0.7554
chr12	133851895	21215530	0.1585	0.5924
chr13	115169878	14043928	0.1219	0.4826
chr14	107349540	14550462	0.1355	0.6905
chr15	102531392	14076474	0.1373	0.5234
chr16	90354753	14223459	0.1574	0.6306
chr17	81195210	13840115	0.1705	0.6501
chr18	78077248	12027228	0.154	1.6258
chr19	59128983	10233827	0.1731	1.2379
chr20	63025520	10501487	0.1666	0.6246
chr21	48129895	5893903	0.1225	0.5809
chr22	51304566	6268908	0.1222	0.5385
chrMT	16571	91470	5.5199	8.4835
chrX	155270560	15099938	0.0972	0.5539
chrY	59373566	3237882	0.0545	0.3703

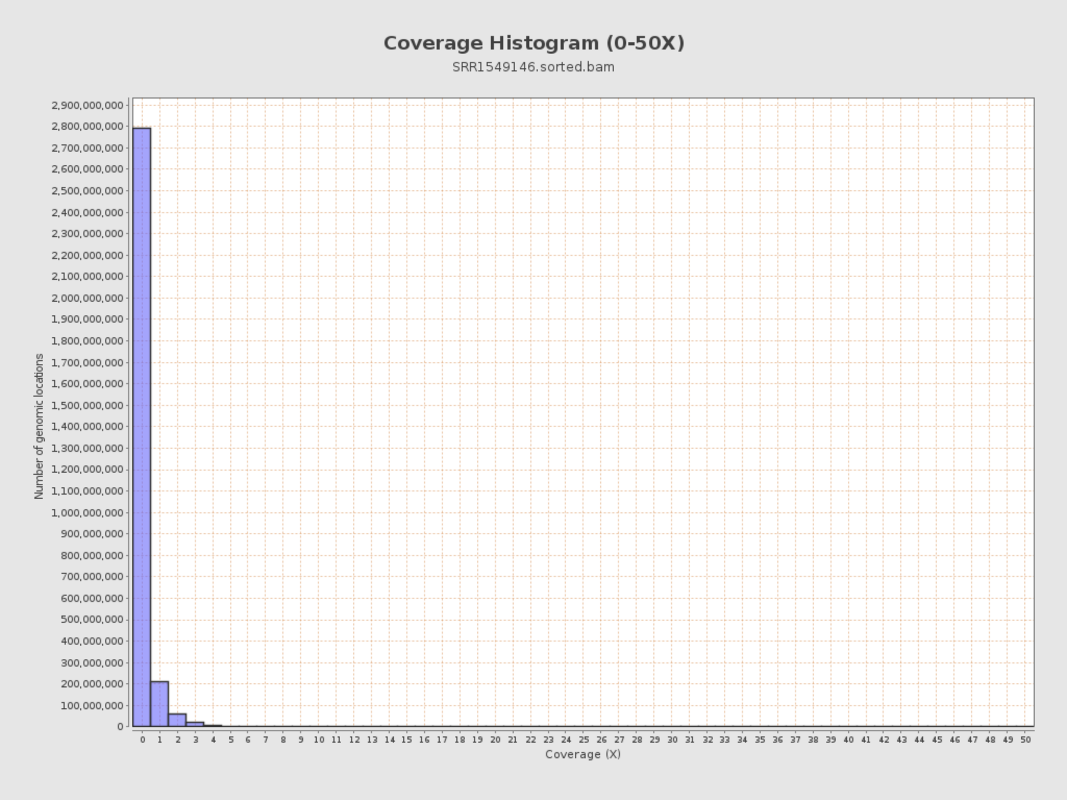
3. Results : Coverage across reference



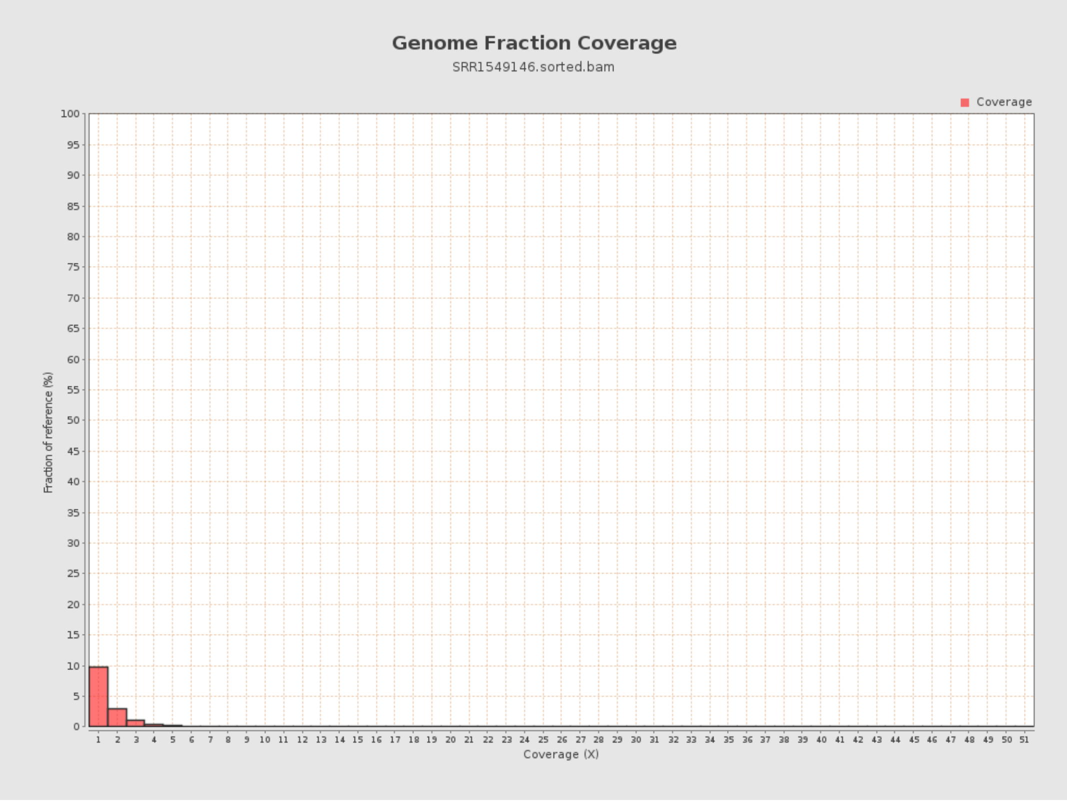
4. Results : Coverage Histogram



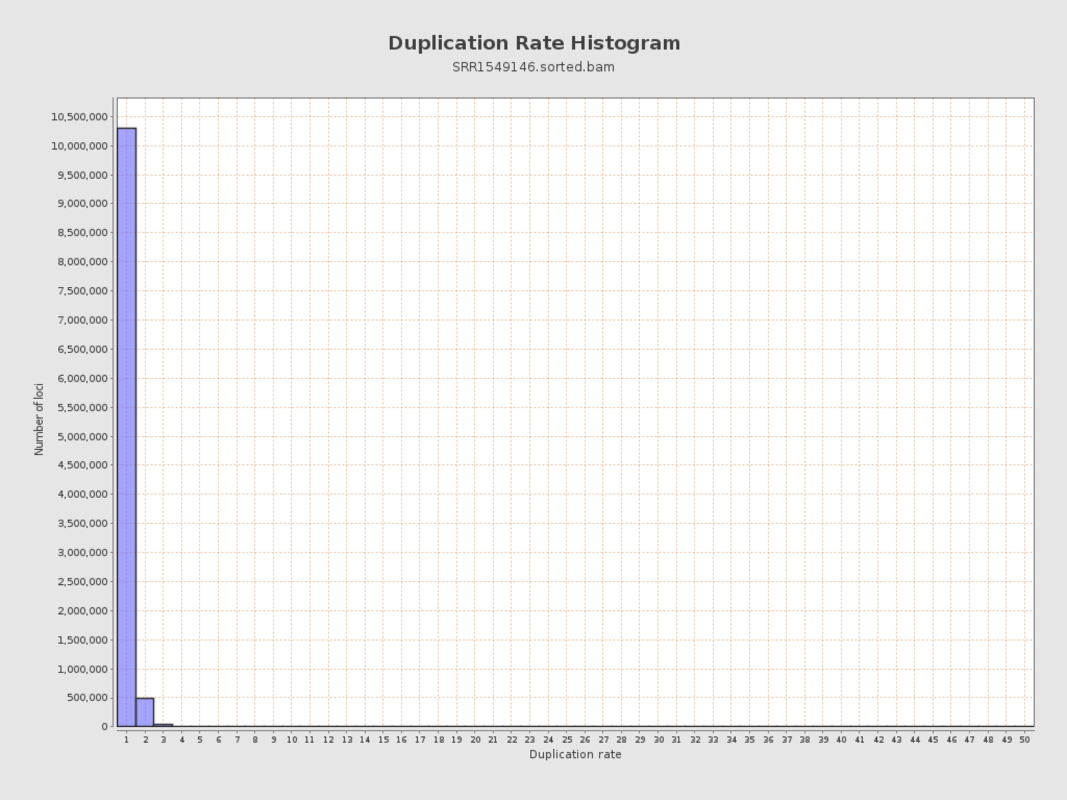
5. Results : Coverage Histogram (0-50X)



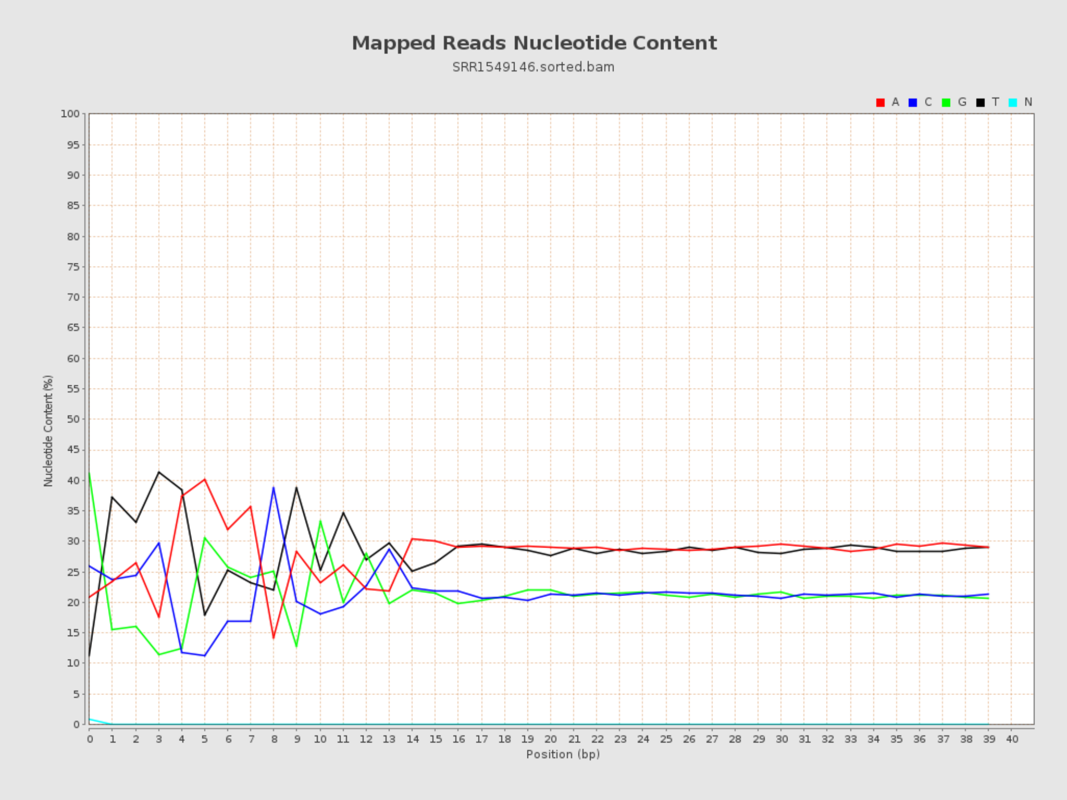
6. Results : Genome Fraction Coverage



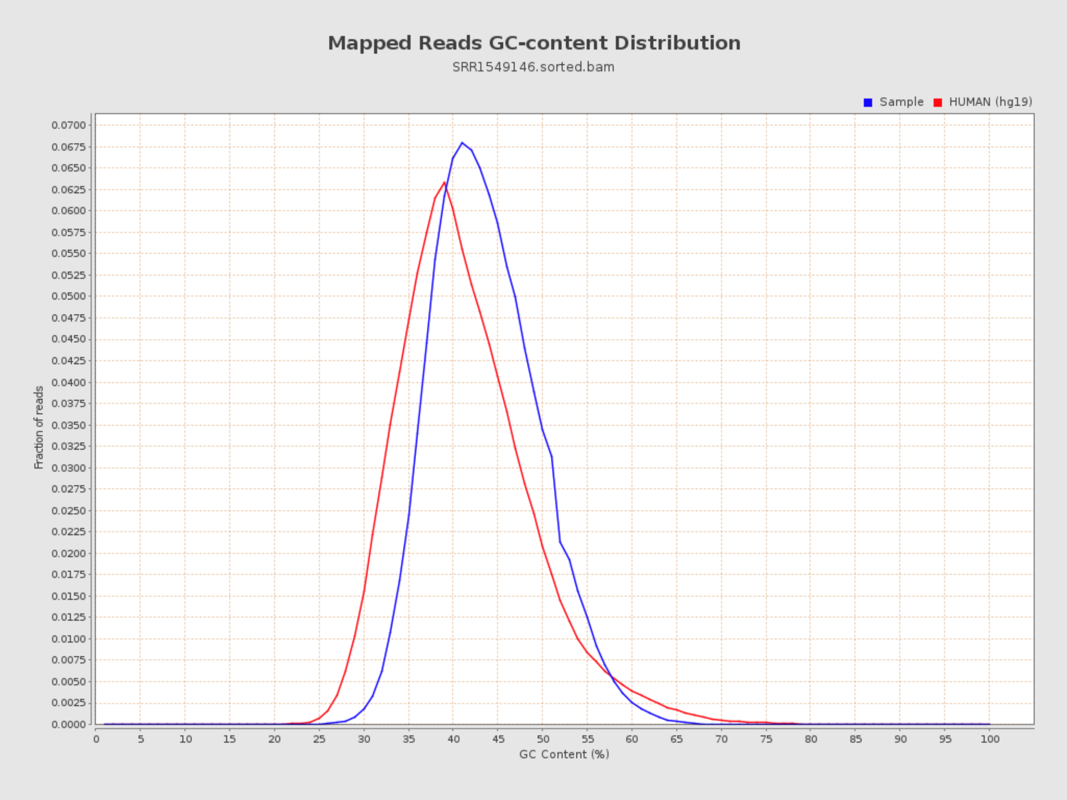
7. Results : Duplication Rate Histogram



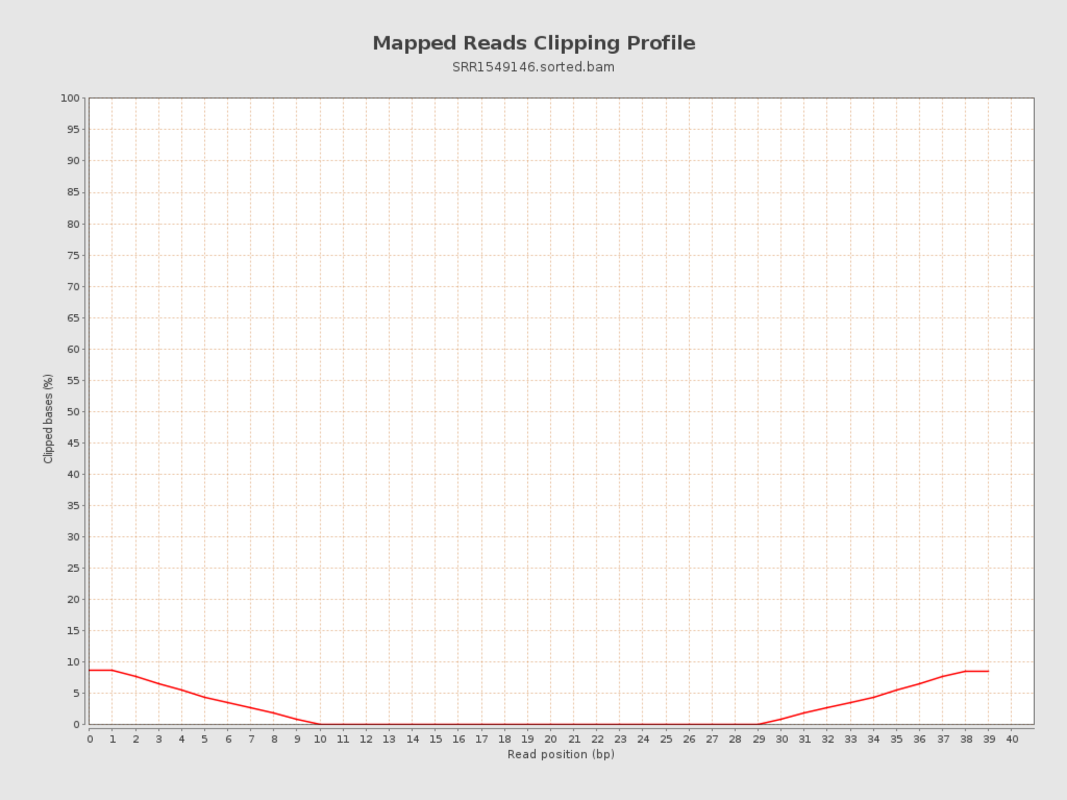
8. Results : Mapped Reads Nucleotide Content



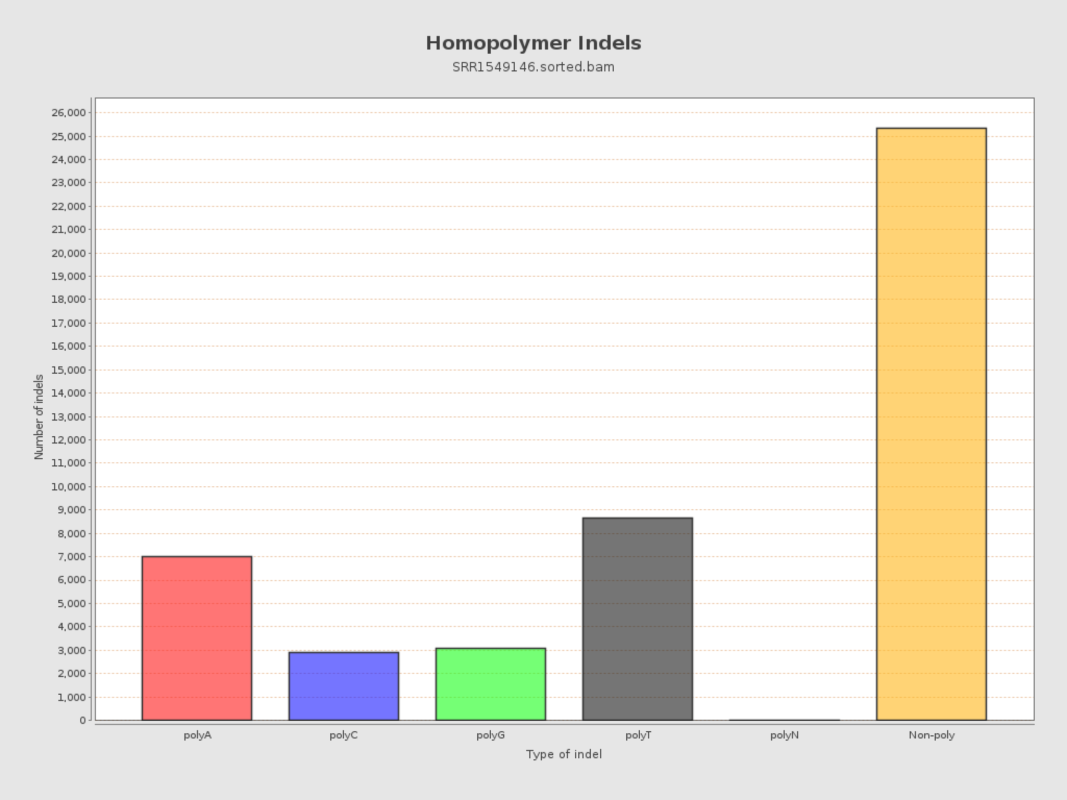
9. Results : Mapped Reads GC-content Distribution



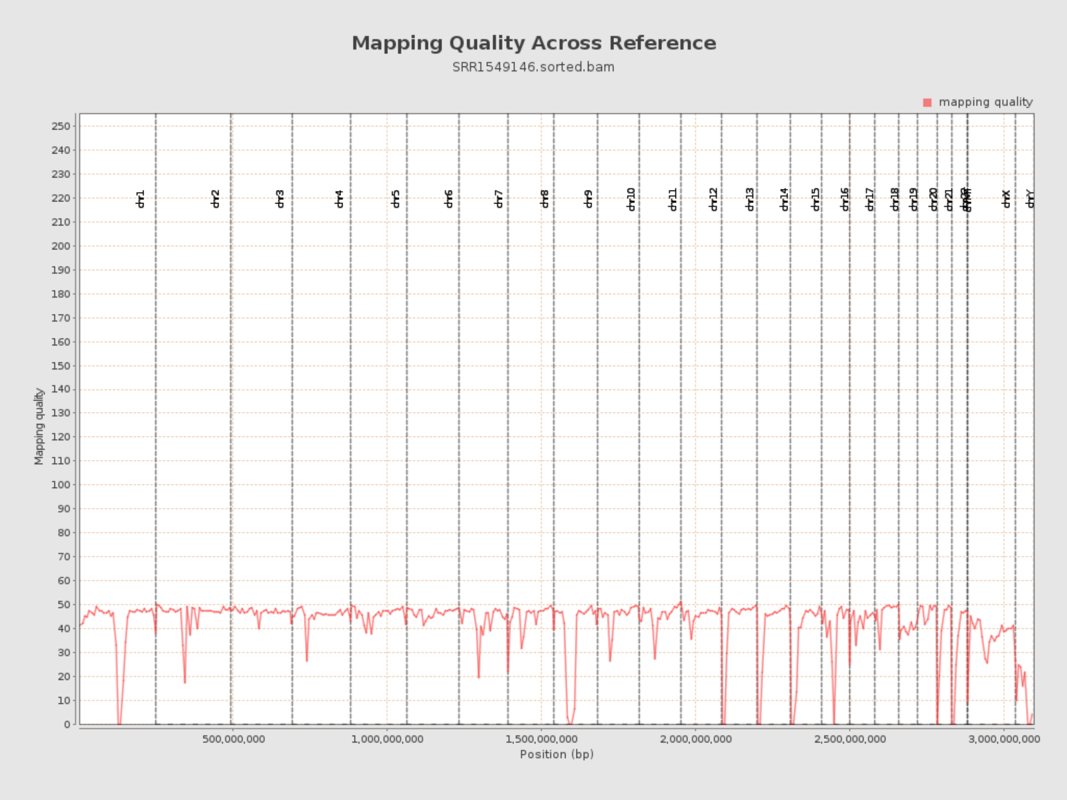
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram