Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:09:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549022.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_SRR1549022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:09:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,829,481
Mapped reads	3,317,644 / 86.63%
Unmapped reads	511,837 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	90,655 / 2.37%
Duplication rate	1.99%
Clipped reads	228,108 / 5.96%

2.2. ACGT Content

Number/percentage of A's	38,347,635 / 29.18%
Number/percentage of C's	27,276,452 / 20.76%
Number/percentage of T's	38,431,044 / 29.25%
Number/percentage of G's	27,350,736 / 20.81%
Number/percentage of N's	1,391 / 0%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0425
Standard Deviation	0.6061

2.4. Mapping Quality

Mean Mapping Quality	42.89

2.5. Mismatches and indels

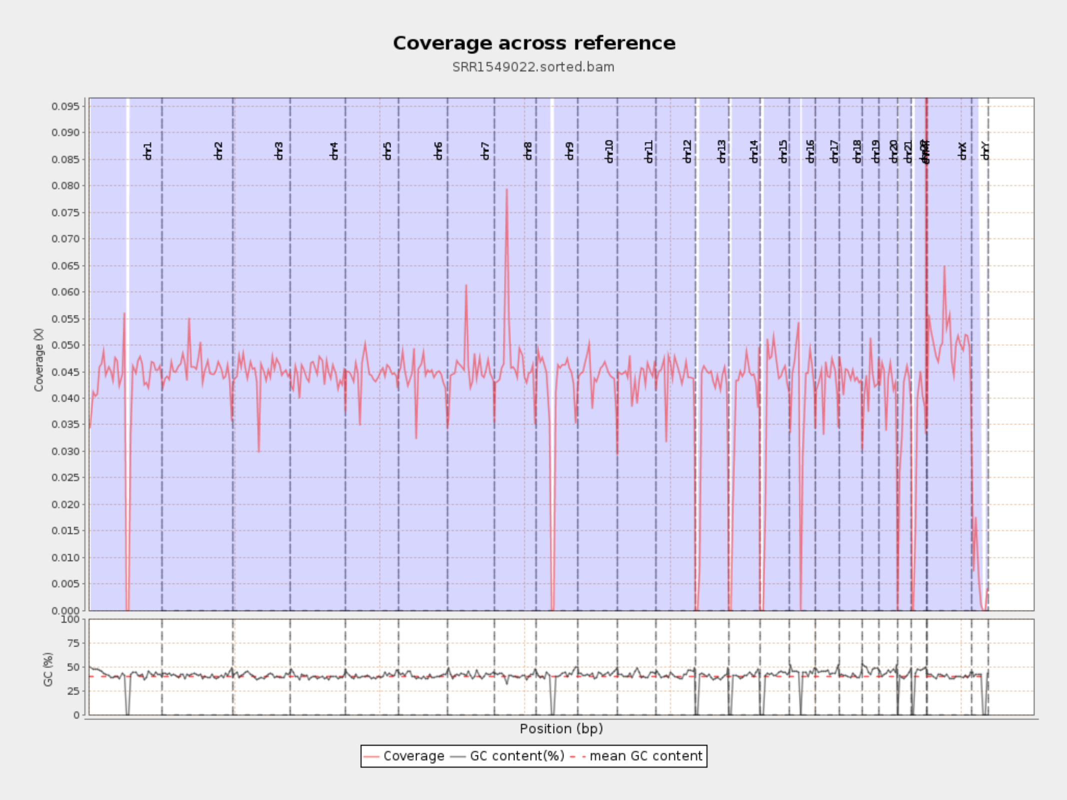
General error rate	0.26%
Mismatches	338,715
Insertions	3,915
Mapped reads with at least one insertion	0.12%
Deletions	10,536
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.2%

2.6. Chromosome stats

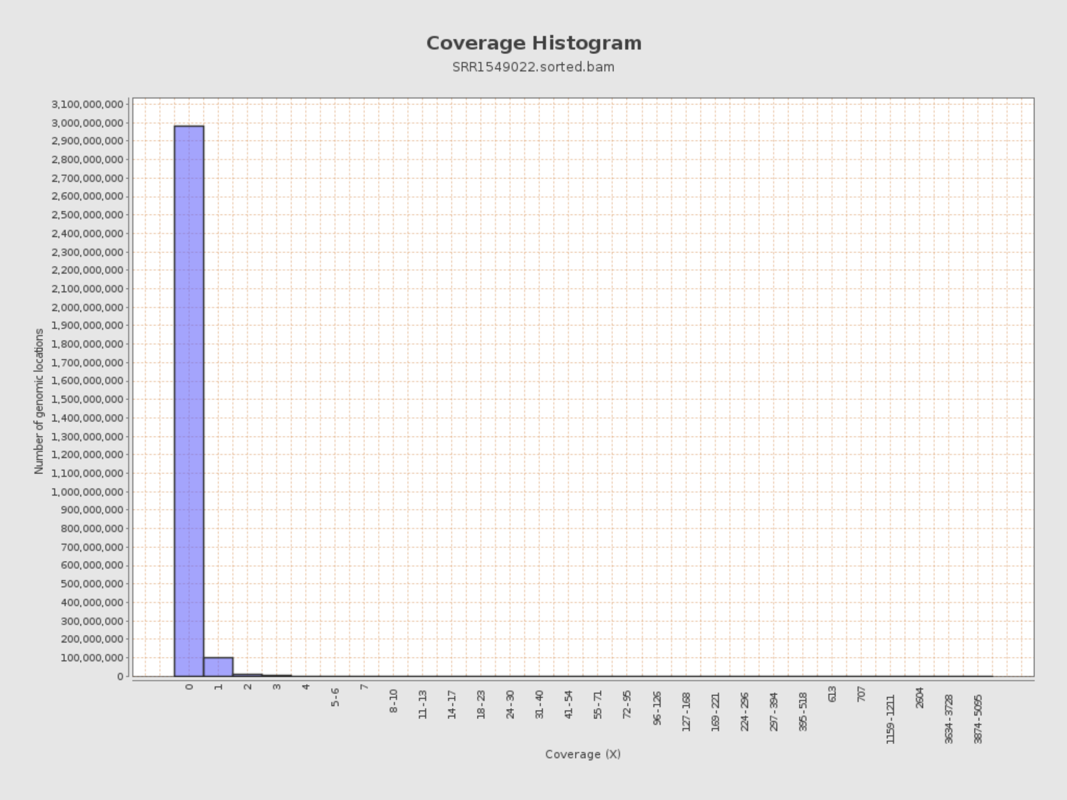
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10424459	0.0418	0.4622
chr2	243199373	11068760	0.0455	0.2843
chr3	198022430	8867553	0.0448	0.2391
chr4	191154276	8524197	0.0446	0.2423
chr5	180915260	8076129	0.0446	0.2396
chr6	171115067	7596399	0.0444	0.2492
chr7	159138663	7274566	0.0457	0.3589
chr8	146364022	6882952	0.047	2.4672

chr9	141213431	5594466	0.0396	0.2644
chr10	135534747	6052254	0.0447	0.2704
chr11	135006516	5929745	0.0439	0.3138
chr12	133851895	5924162	0.0443	0.2404
chr13	115169878	4219748	0.0366	0.2156
chr14	107349540	3960330	0.0369	0.2368
chr15	102531392	3881976	0.0379	0.2187
chr16	90354753	3675462	0.0407	0.2343
chr17	81195210	3463974	0.0427	0.2442
chr18	78077248	3445751	0.0441	0.3909
chr19	59128983	2535358	0.0429	0.4075
chr20	63025520	2664020	0.0423	0.2363
chr21	48129895	1675259	0.0348	0.2205
chr22	51304566	1446578	0.0282	0.211
chrMT	16571	15603	0.9416	1.4263
chrX	155270560	7844106	0.0505	0.2744
chrY	59373566	377211	0.0064	0.1106

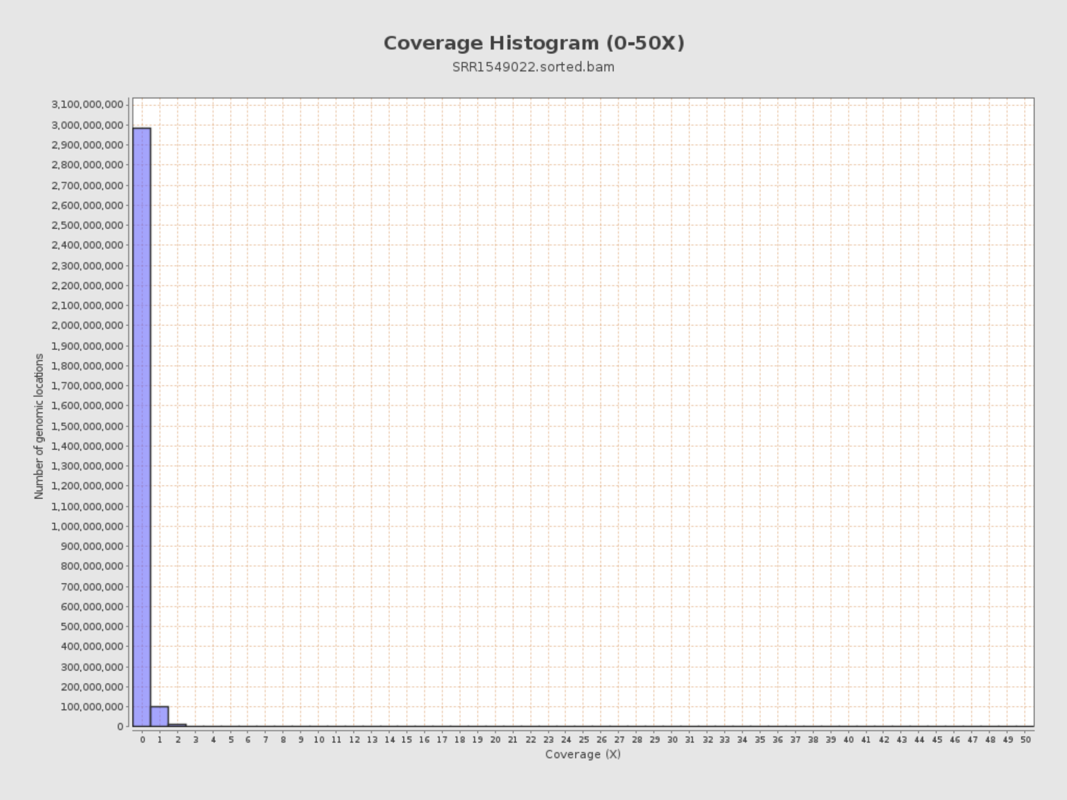
3. Results : Coverage across reference



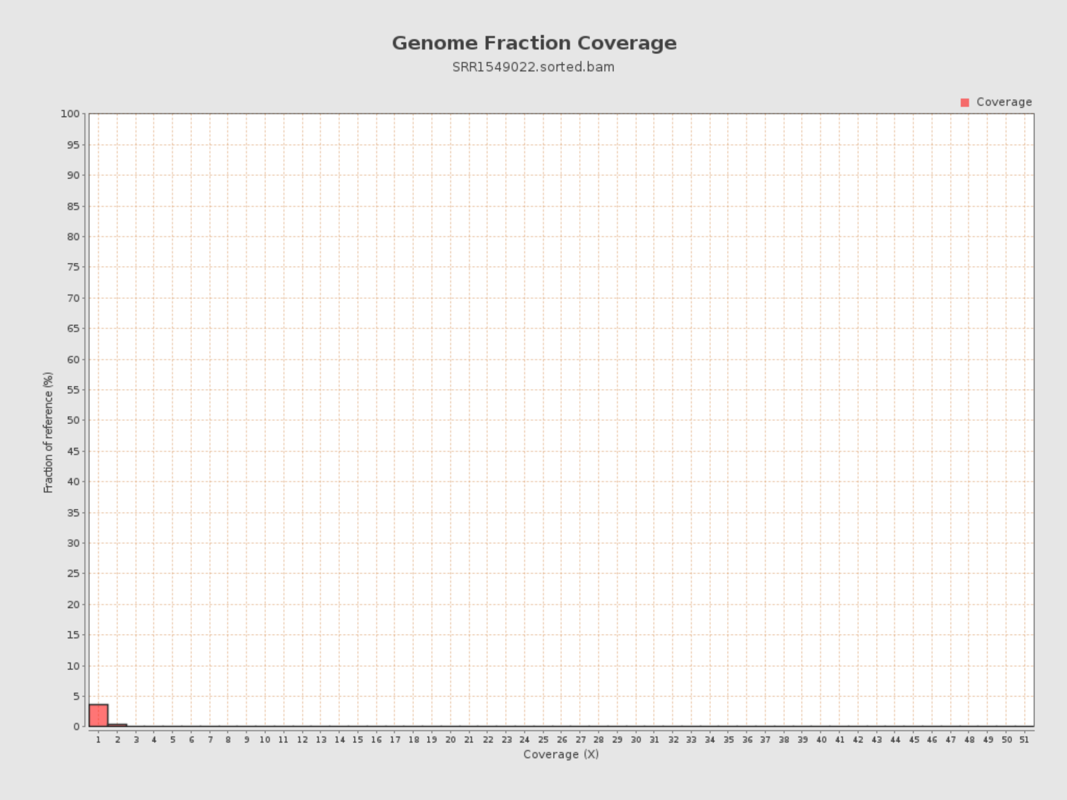
4. Results : Coverage Histogram



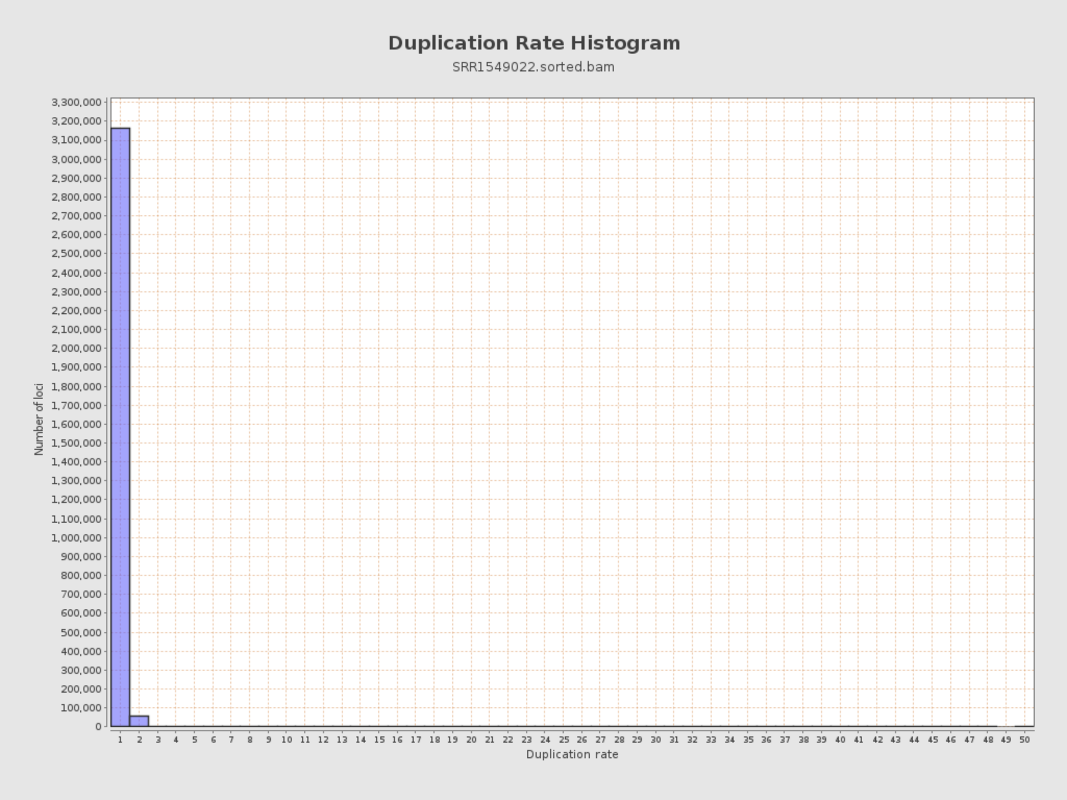
5. Results : Coverage Histogram (0-50X)



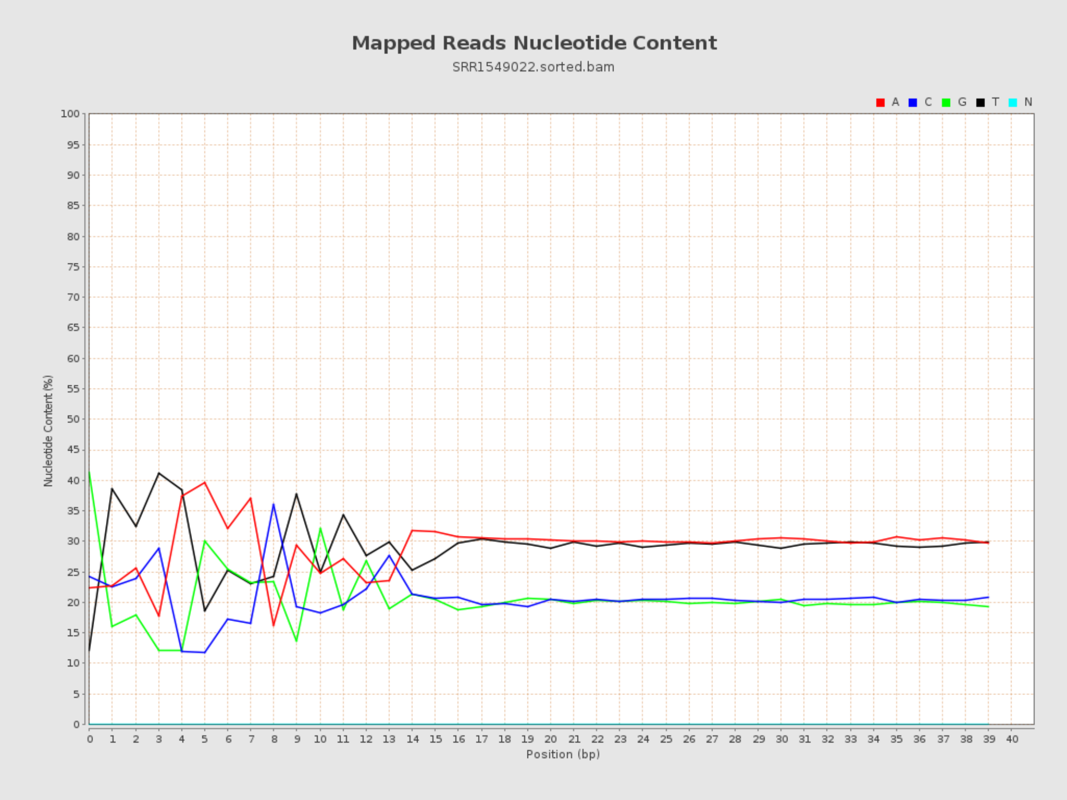
6. Results : Genome Fraction Coverage



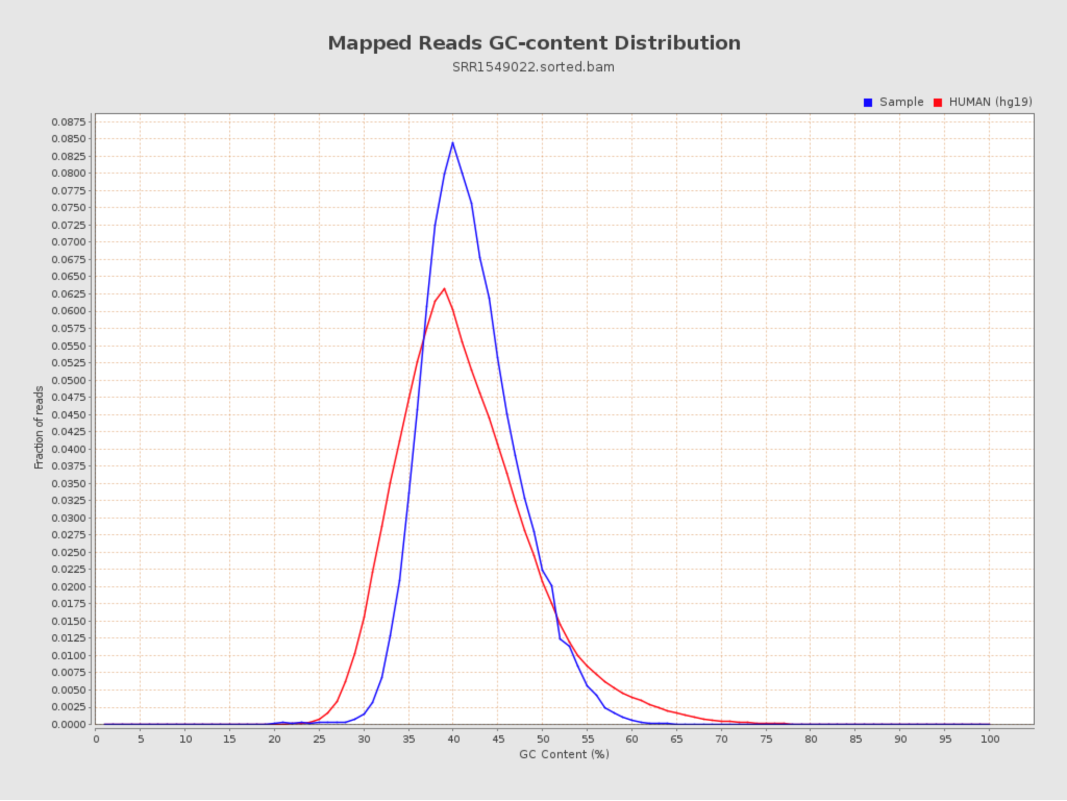
7. Results : Duplication Rate Histogram



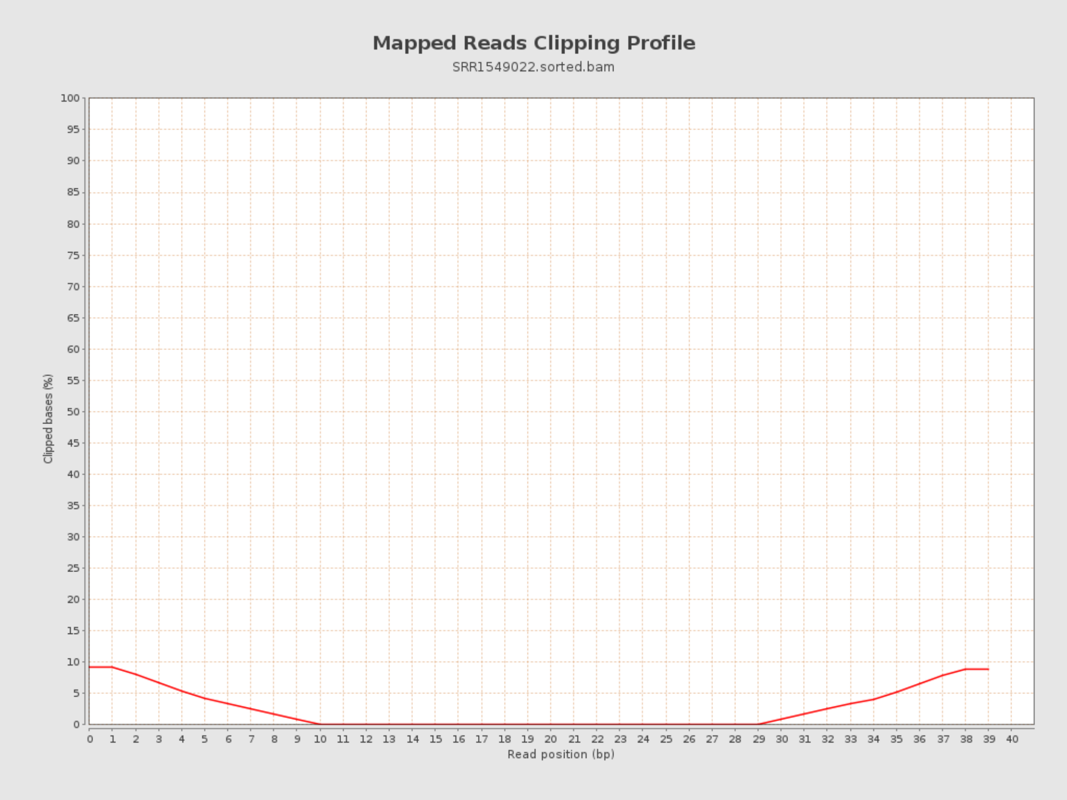
8. Results : Mapped Reads Nucleotide Content



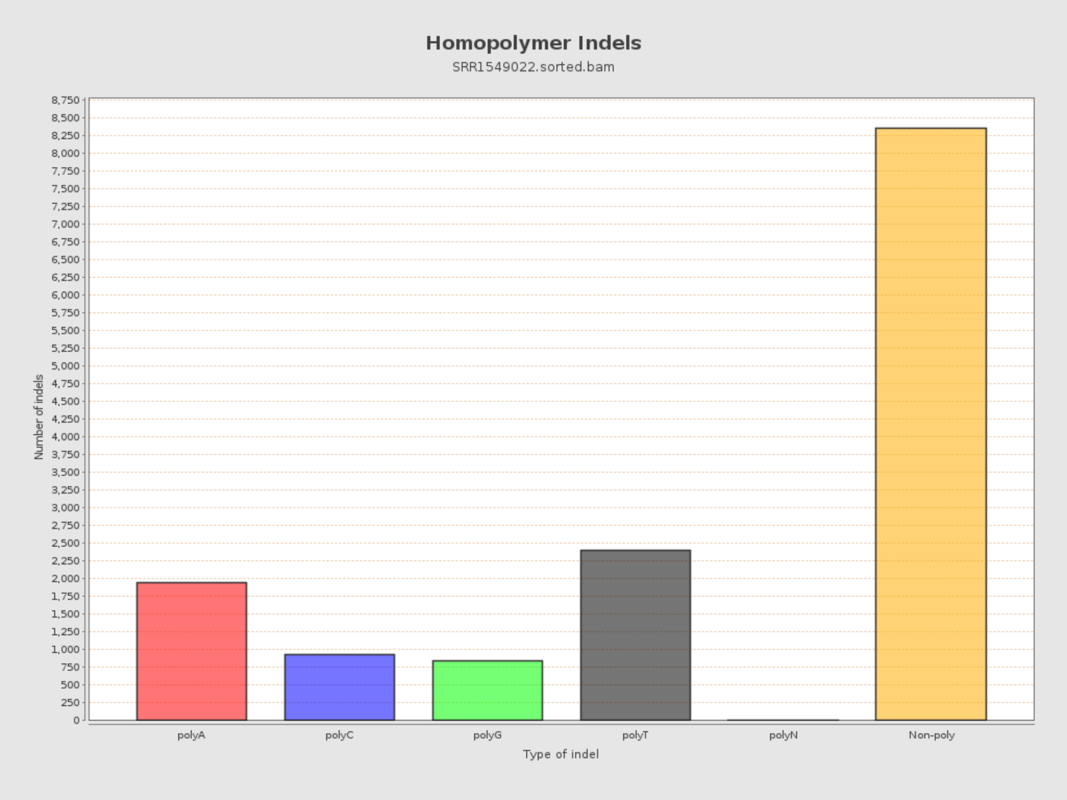
9. Results : Mapped Reads GC-content Distribution



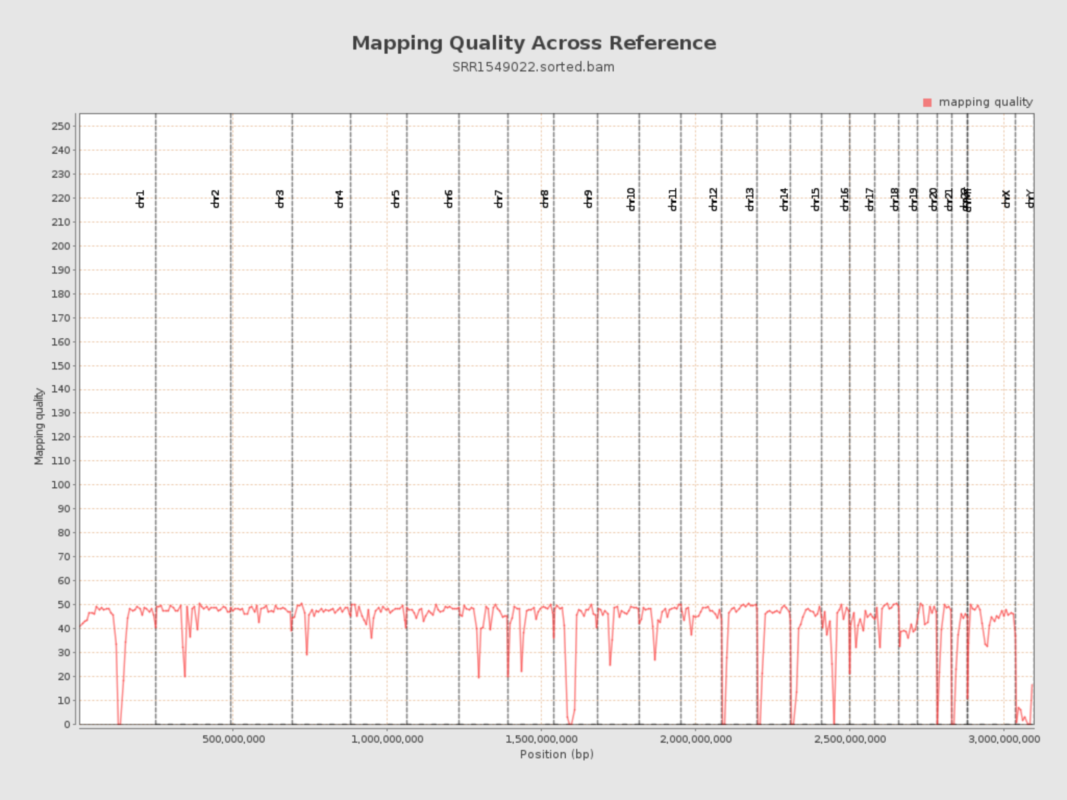
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram