Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:07:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549099.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_SRR1549099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:07:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,836,164
Mapped reads	10,094,183 / 85.28%
Unmapped reads	1,741,981 / 14.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	482,888 / 4.08%
Duplication rate	3.58%
Clipped reads	543,707 / 4.59%

2.2. ACGT Content

Number/percentage of A's	120,720,650 / 30.15%
Number/percentage of C's	78,645,495 / 19.64%
Number/percentage of T's	122,027,179 / 30.48%
Number/percentage of G's	78,978,654 / 19.73%
Number/percentage of N's	1,729 / 0%
GC Percentage	39.37%

2.3. Coverage

Mean	0.1293
Standard Deviation	0.8639

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

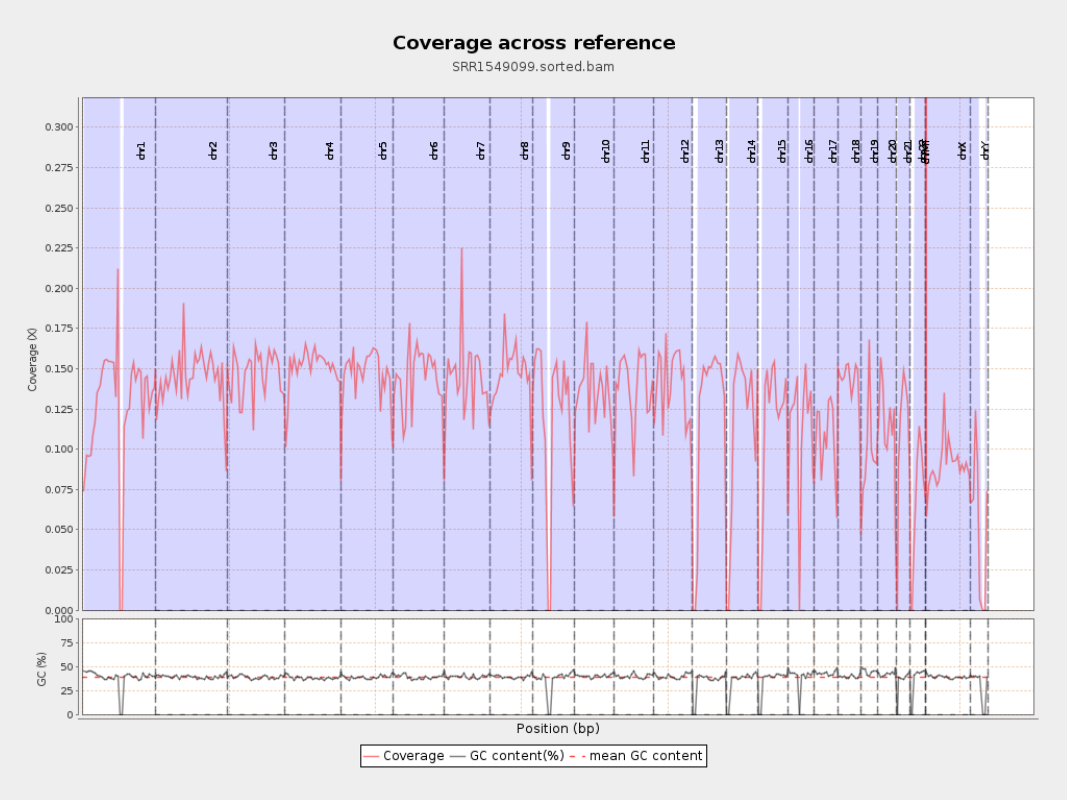
General error rate	0.3%
Mismatches	1,200,789
Insertions	10,086
Mapped reads with at least one insertion	0.1%
Deletions	30,177
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.39%

2.6. Chromosome stats

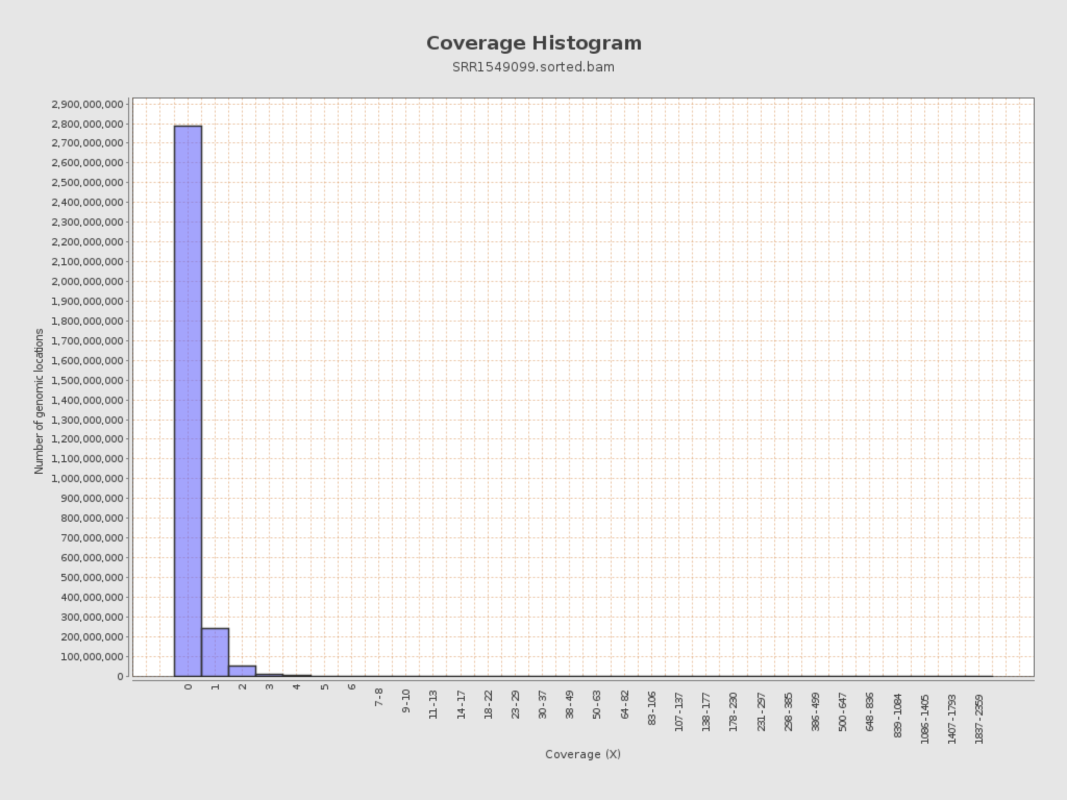
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31442615	0.1261	1.7423
chr2	243199373	35232477	0.1449	0.7564
chr3	198022430	29132939	0.1471	0.4772
chr4	191154276	28859283	0.151	0.5011
chr5	180915260	26472335	0.1463	0.4893
chr6	171115067	24889114	0.1455	0.5574
chr7	159138663	22896064	0.1439	1.2345
chr8	146364022	21428000	0.1464	1.1717

chr9	141213431	17055391	0.1208	0.7334
chr10	135534747	18409447	0.1358	0.7171
chr11	135006516	18728206	0.1387	0.7349
chr12	133851895	18632081	0.1392	0.4968
chr13	115169878	14006480	0.1216	0.4252
chr14	107349540	12382592	0.1153	0.5908
chr15	102531392	11399869	0.1112	0.4083
chr16	90354753	10023572	0.1109	0.4964
chr17	81195210	8791811	0.1083	0.4592
chr18	78077248	11240433	0.144	1.6795
chr19	59128983	5874211	0.0993	1.3586
chr20	63025520	7489546	0.1188	0.4709
chr21	48129895	5269380	0.1095	0.5057
chr22	51304566	3490044	0.068	0.3385
chrMT	16571	95144	5.7416	7.0745
chrX	155270560	13992916	0.0901	0.5076
chrY	59373566	3177262	0.0535	0.4242

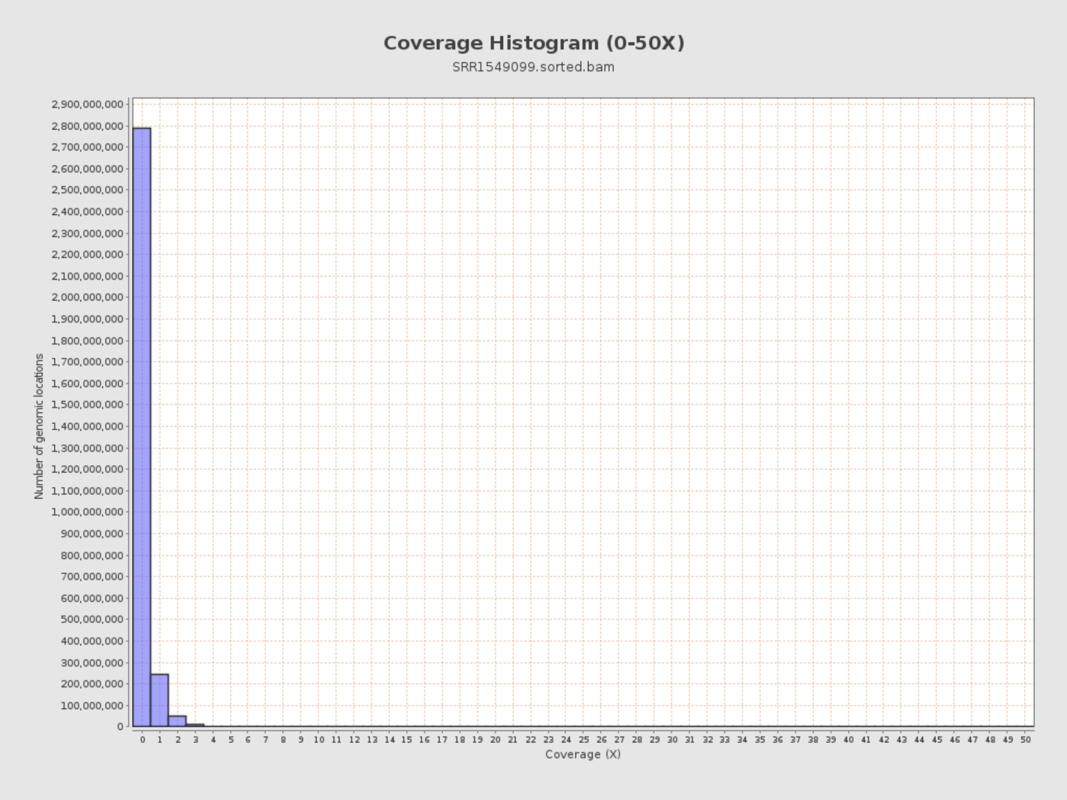
3. Results : Coverage across reference



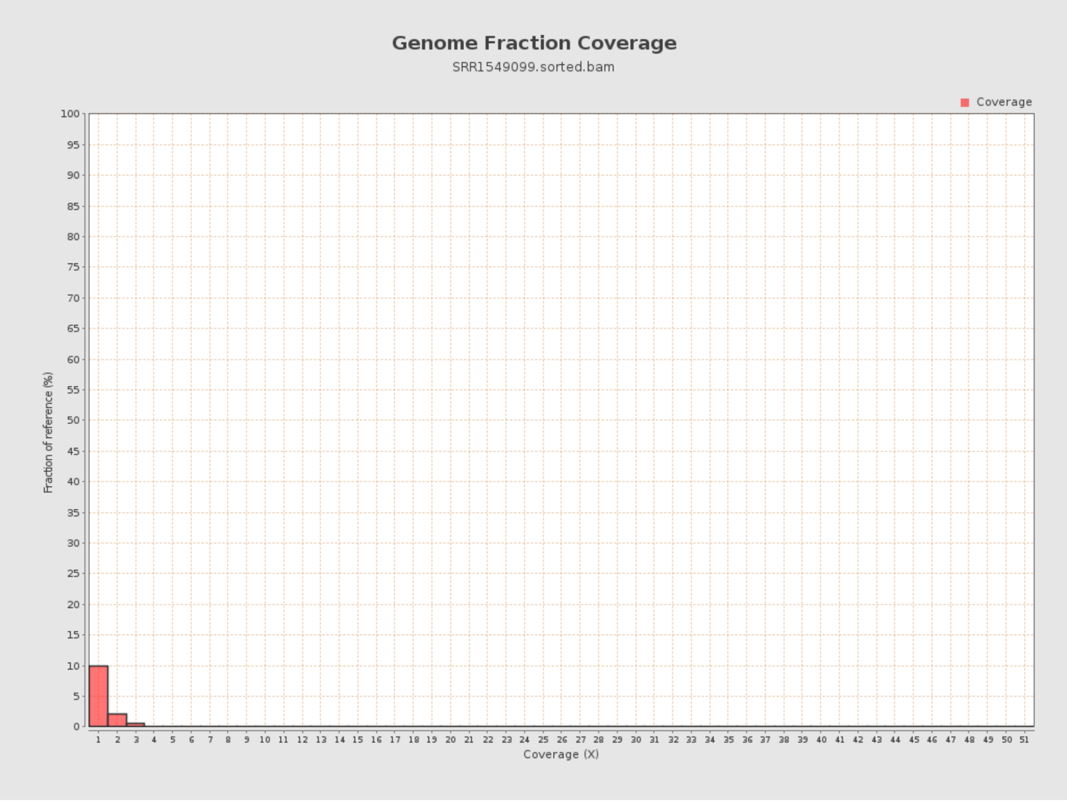
4. Results : Coverage Histogram



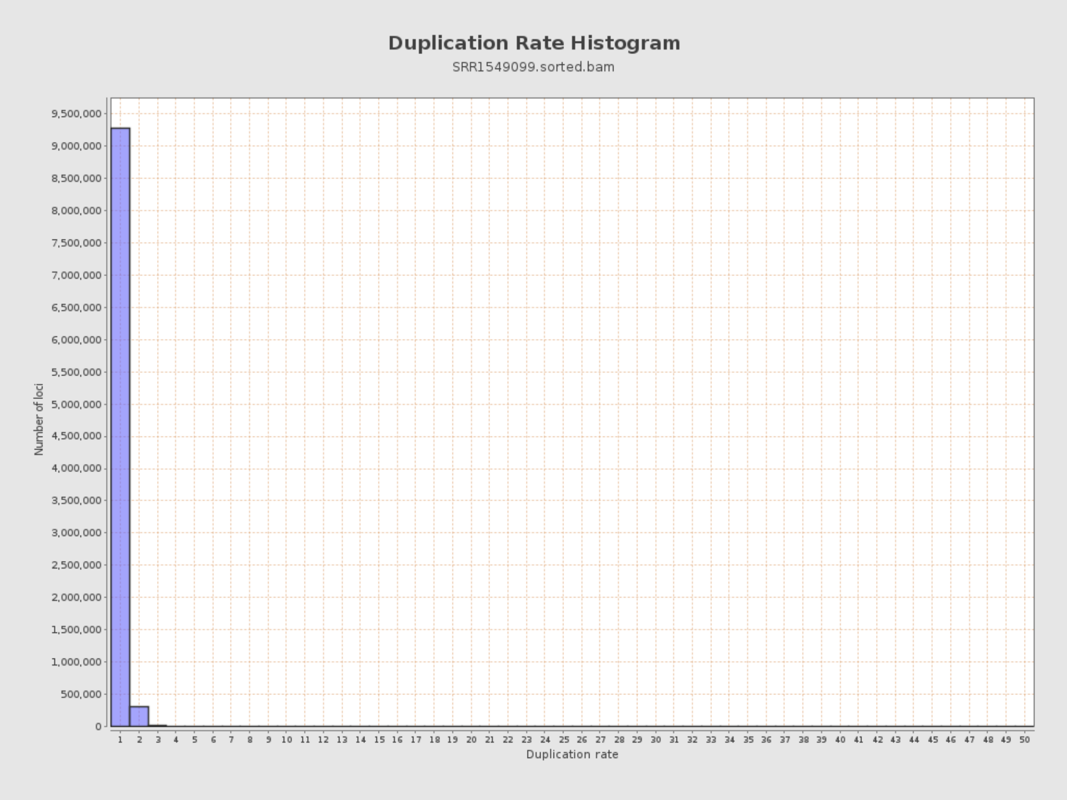
5. Results : Coverage Histogram (0-50X)



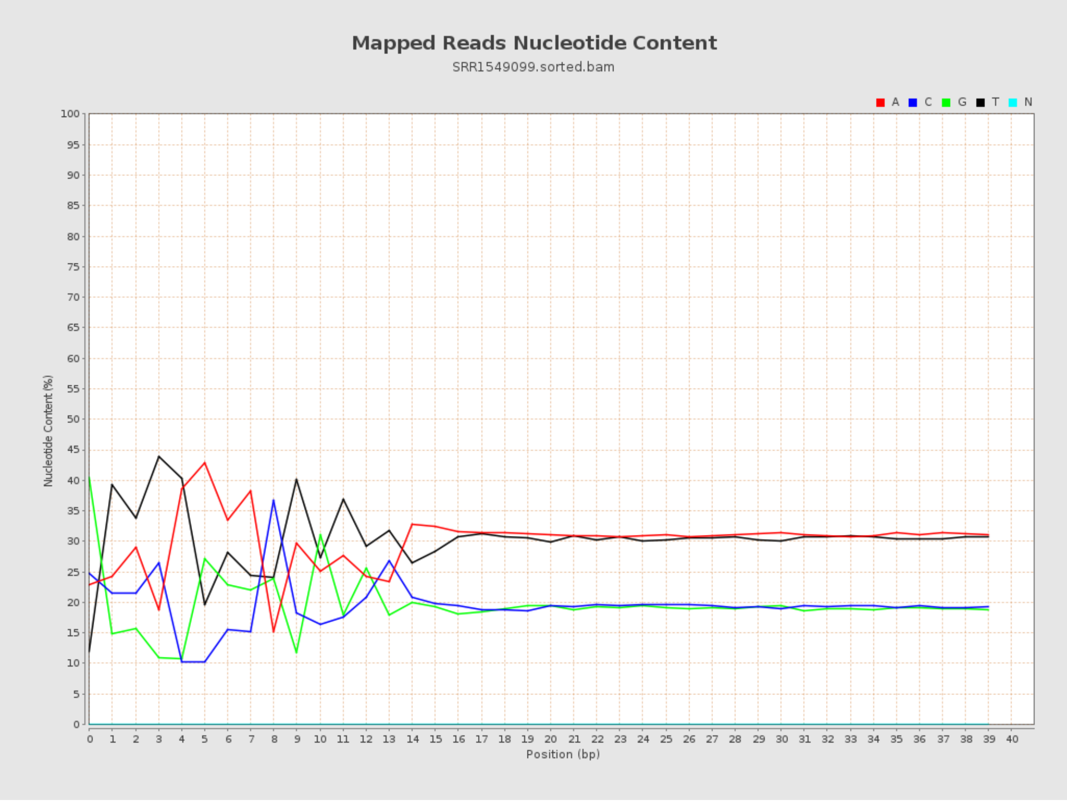
6. Results : Genome Fraction Coverage



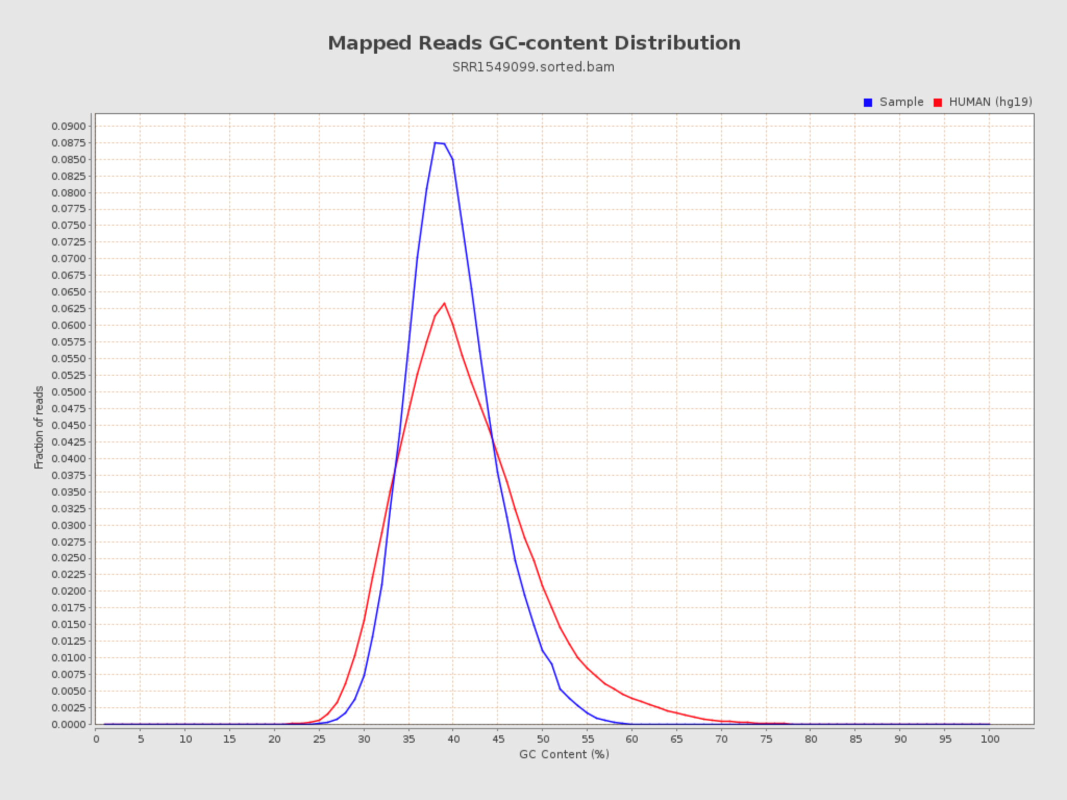
7. Results : Duplication Rate Histogram



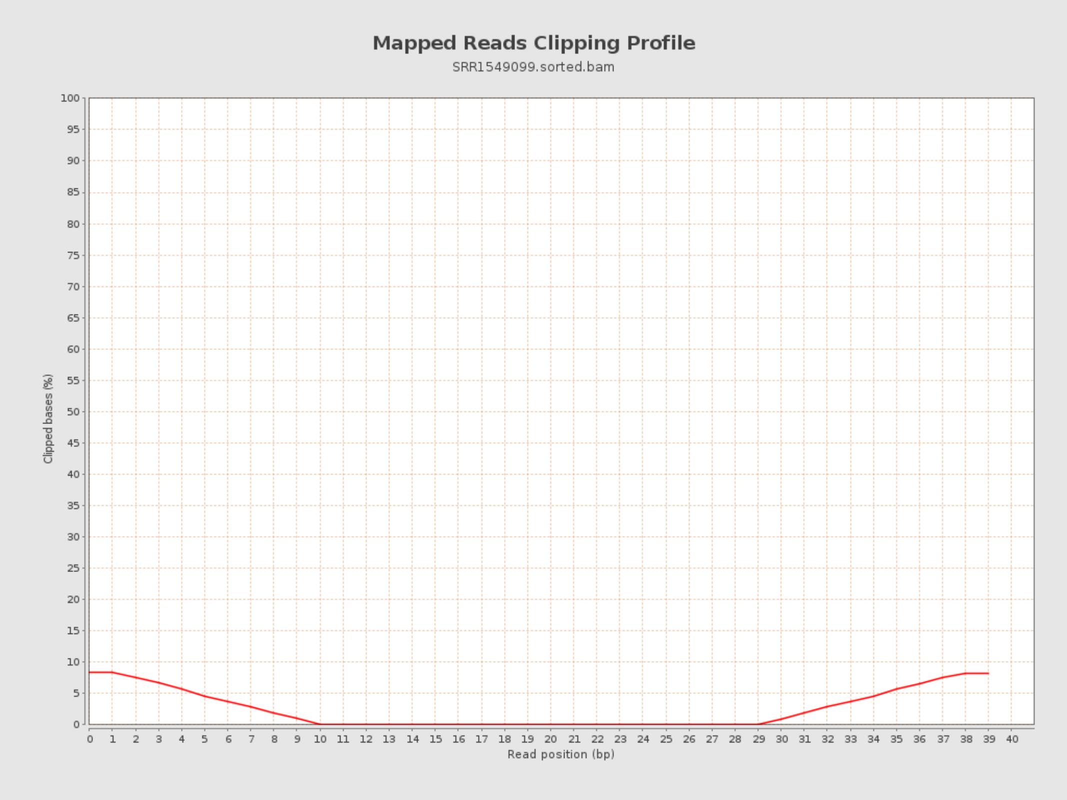
8. Results : Mapped Reads Nucleotide Content



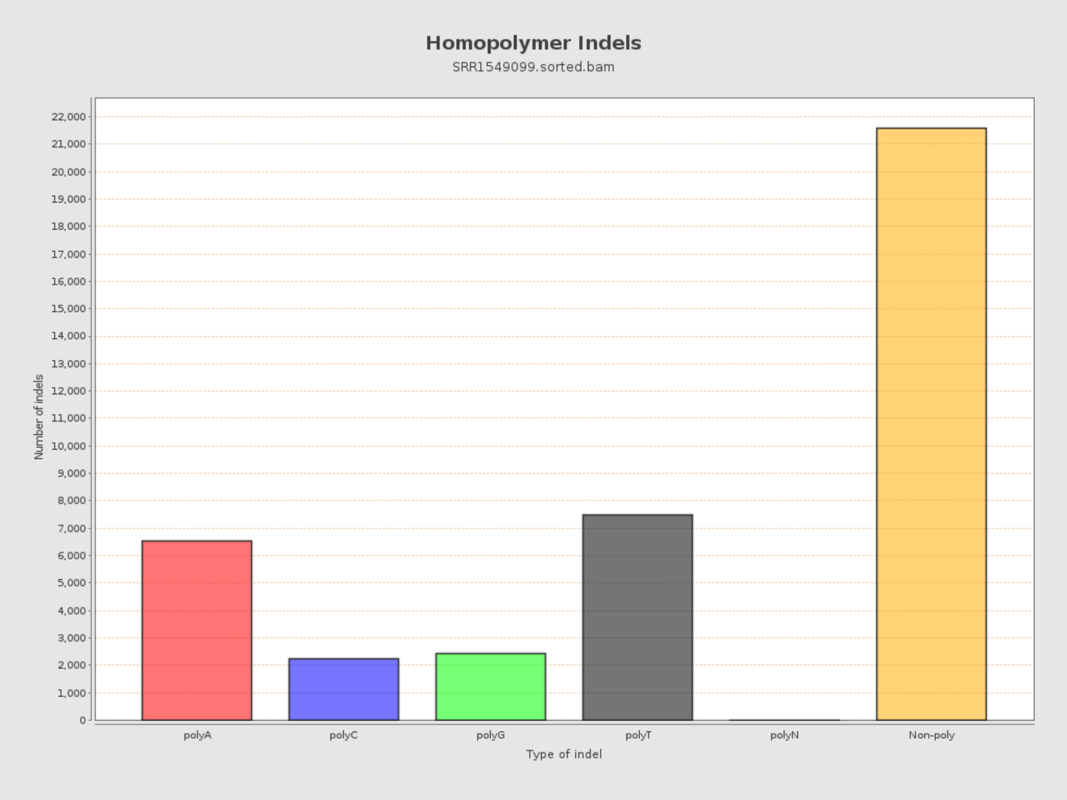
9. Results : Mapped Reads GC-content Distribution



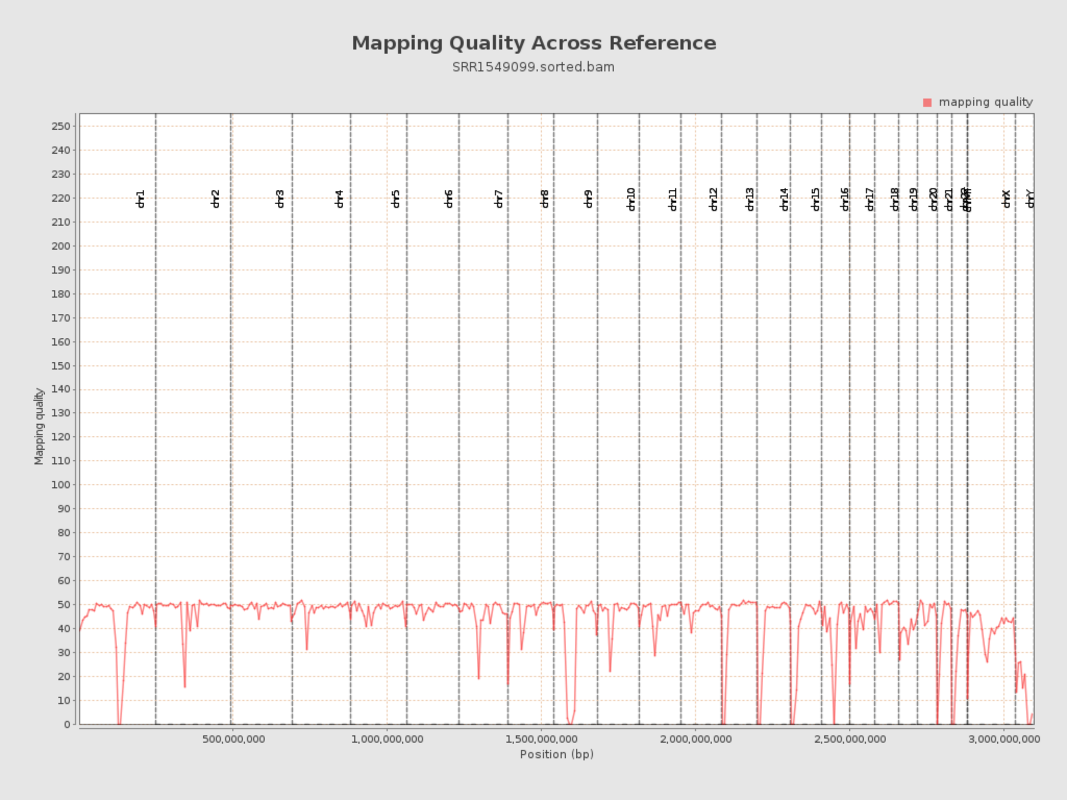
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram