Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:56:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549098.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_SRR1549098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549098.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:56:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,952,344
Mapped reads	10,191,882 / 85.27%
Unmapped reads	1,760,462 / 14.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	486,559 / 4.07%
Duplication rate	3.47%
Clipped reads	495,907 / 4.15%

2.2. ACGT Content

Number/percentage of A's	121,372,485 / 30%
Number/percentage of C's	81,269,062 / 20.09%
Number/percentage of T's	121,307,491 / 29.98%
Number/percentage of G's	80,647,639 / 19.93%
Number/percentage of N's	1,515 / 0%
GC Percentage	40.02%

2.3. Coverage

Mean	0.1307
Standard Deviation	1.1565

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

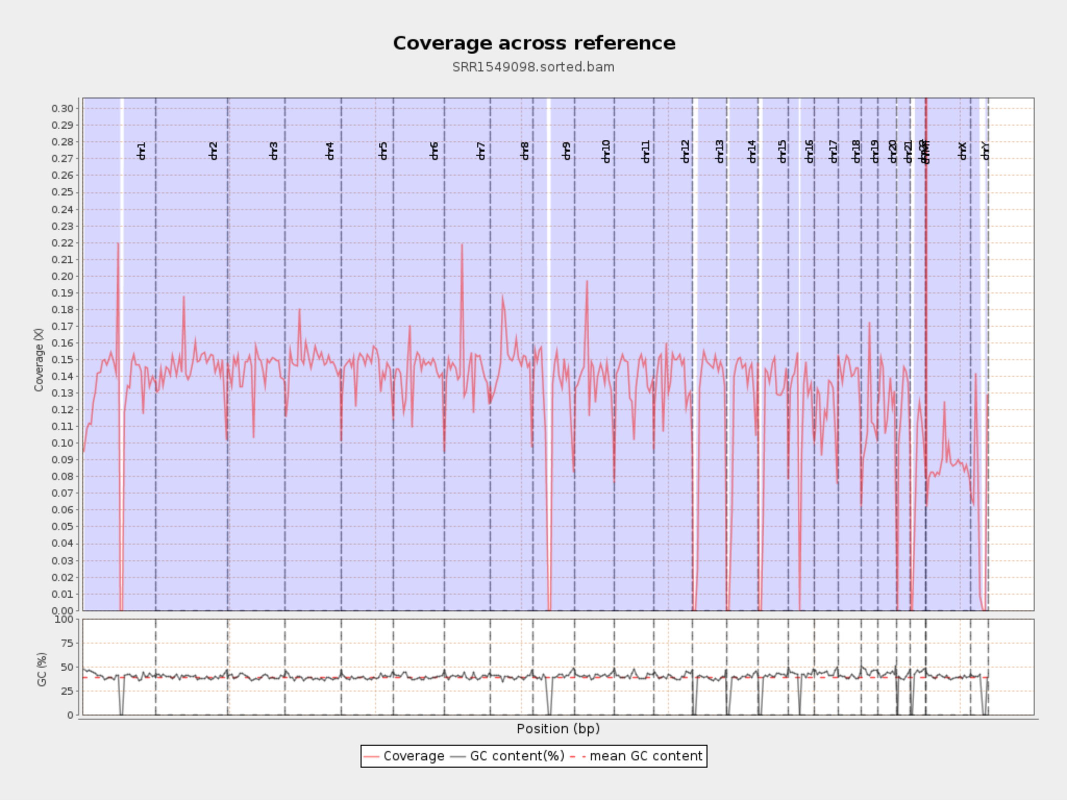
General error rate	0.3%
Mismatches	1,219,597
Insertions	9,860
Mapped reads with at least one insertion	0.1%
Deletions	30,889
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.03%

2.6. Chromosome stats

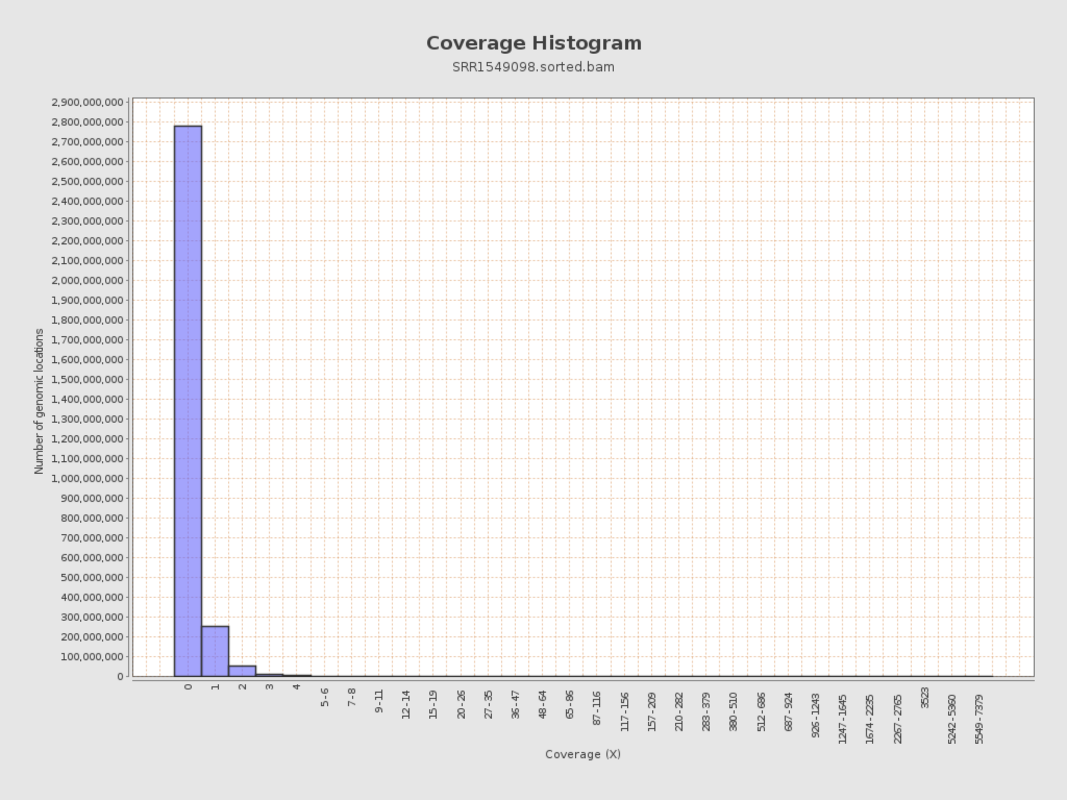
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32516324	0.1305	1.9332
chr2	243199373	35467863	0.1458	0.7155
chr3	198022430	28595187	0.1444	0.4659
chr4	191154276	28508604	0.1491	0.5284
chr5	180915260	26150719	0.1445	0.4775
chr6	171115067	24462244	0.143	0.5403
chr7	159138663	22865030	0.1437	1.1941
chr8	146364022	21678077	0.1481	3.6278

chr9	141213431	17275734	0.1223	0.6781
chr10	135534747	19054913	0.1406	0.777
chr11	135006516	18656768	0.1382	0.7012
chr12	133851895	18665286	0.1394	0.4886
chr13	115169878	13858226	0.1203	0.4186
chr14	107349540	12534266	0.1168	0.578
chr15	102531392	11561977	0.1128	0.4025
chr16	90354753	10614888	0.1175	0.4915
chr17	81195210	9660548	0.119	0.4761
chr18	78077248	11203278	0.1435	1.4461
chr19	59128983	6588284	0.1114	1.4281
chr20	63025520	7994228	0.1268	0.4838
chr21	48129895	5435540	0.1129	0.5154
chr22	51304566	3974208	0.0775	0.3634
chrMT	16571	158945	9.5918	11.596
chrX	155270560	13470212	0.0868	0.4863
chrY	59373566	3686109	0.0621	0.658

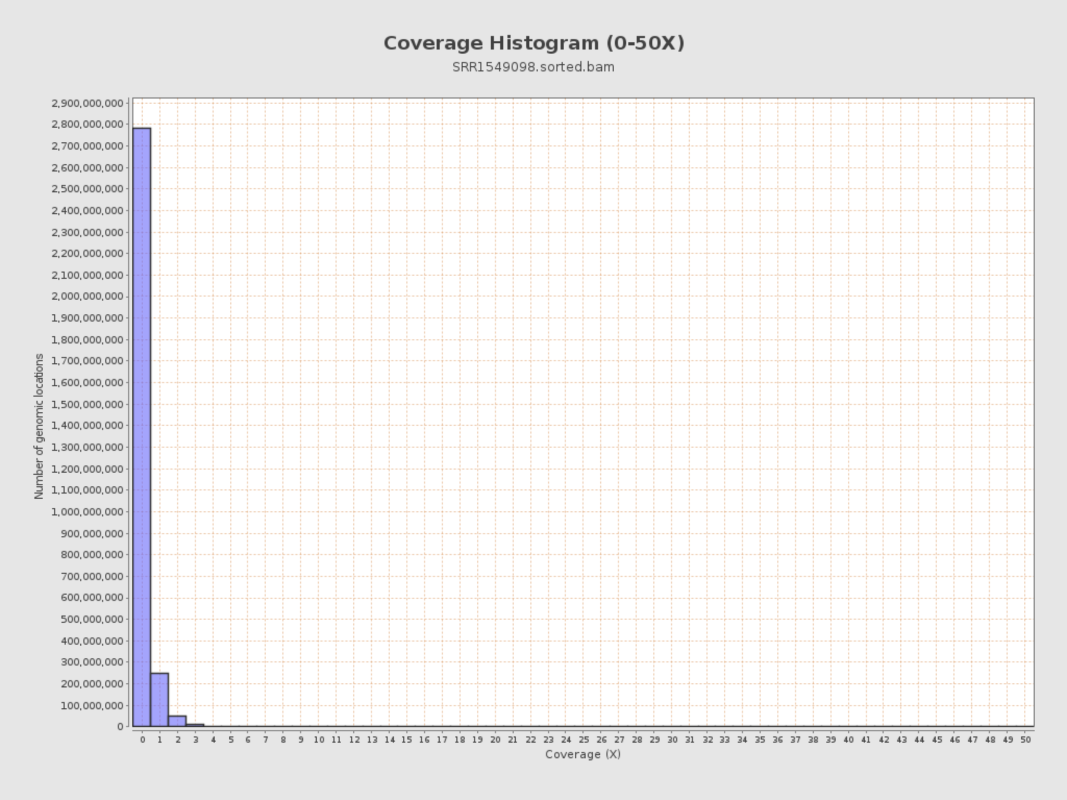
3. Results : Coverage across reference



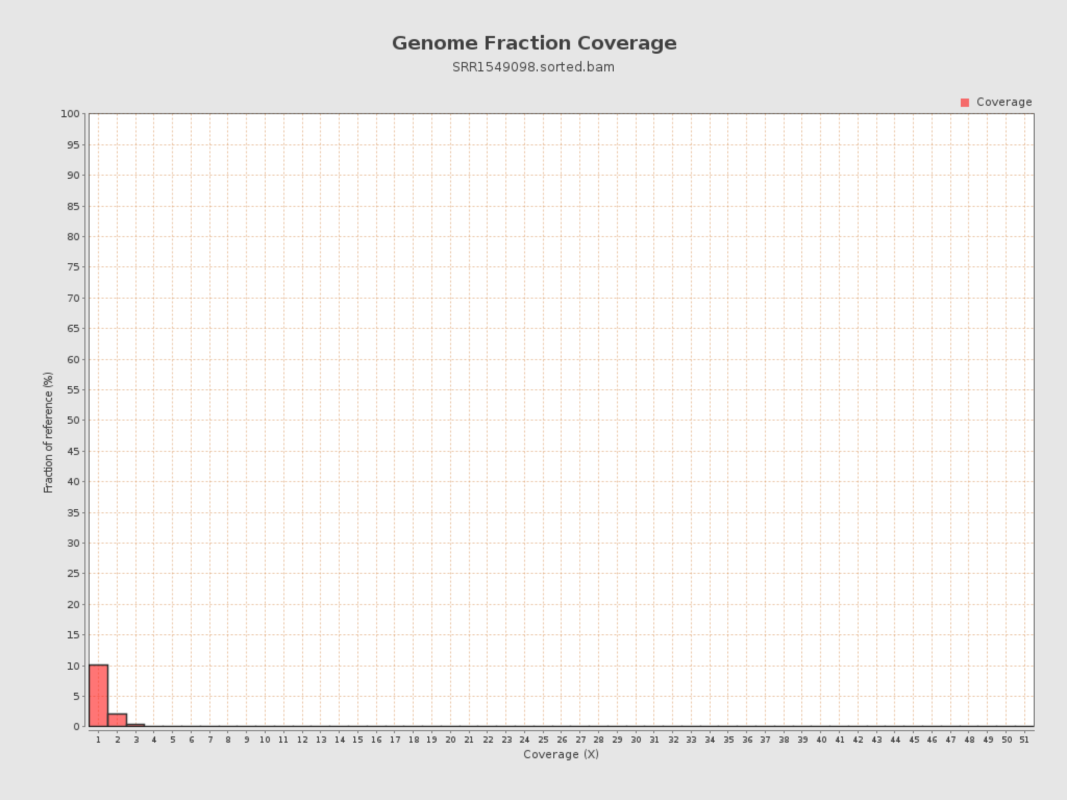
4. Results : Coverage Histogram



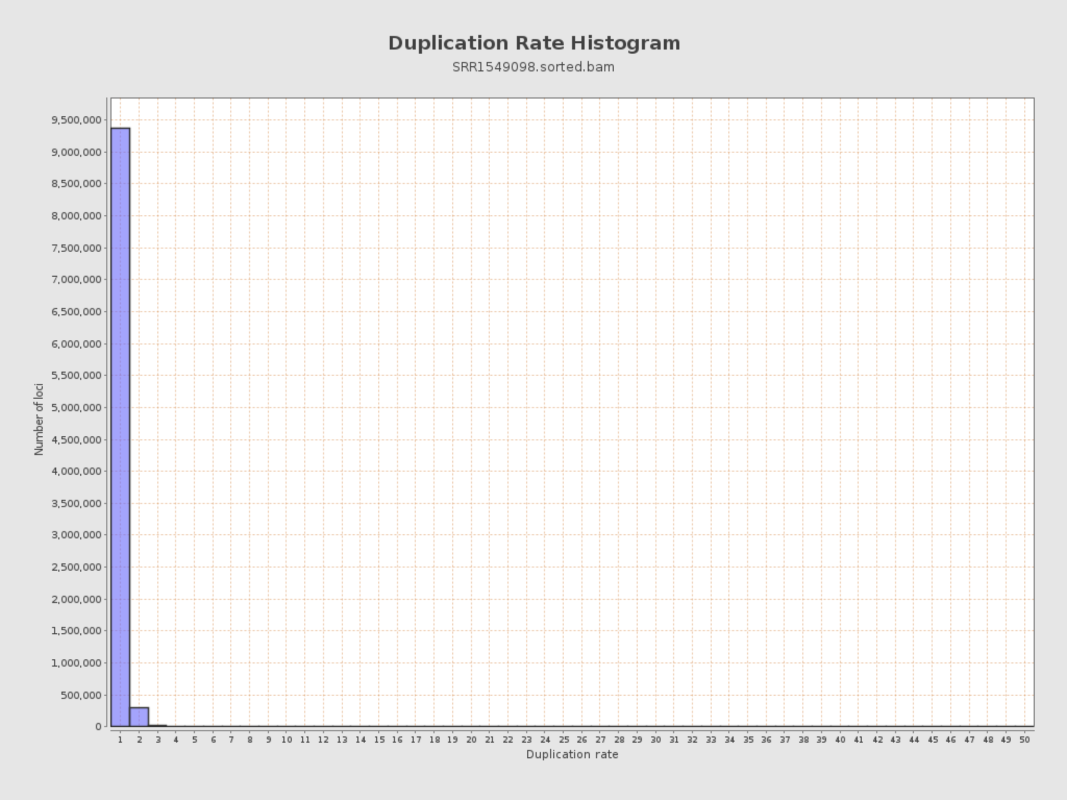
5. Results : Coverage Histogram (0-50X)



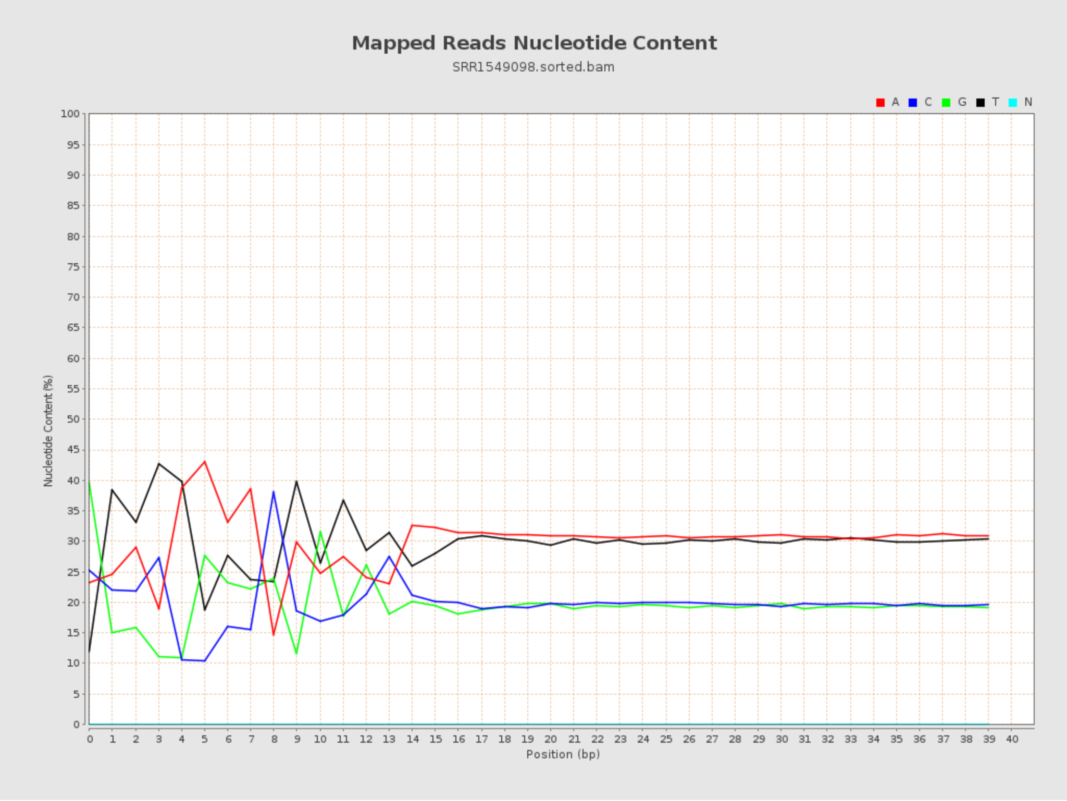
6. Results : Genome Fraction Coverage



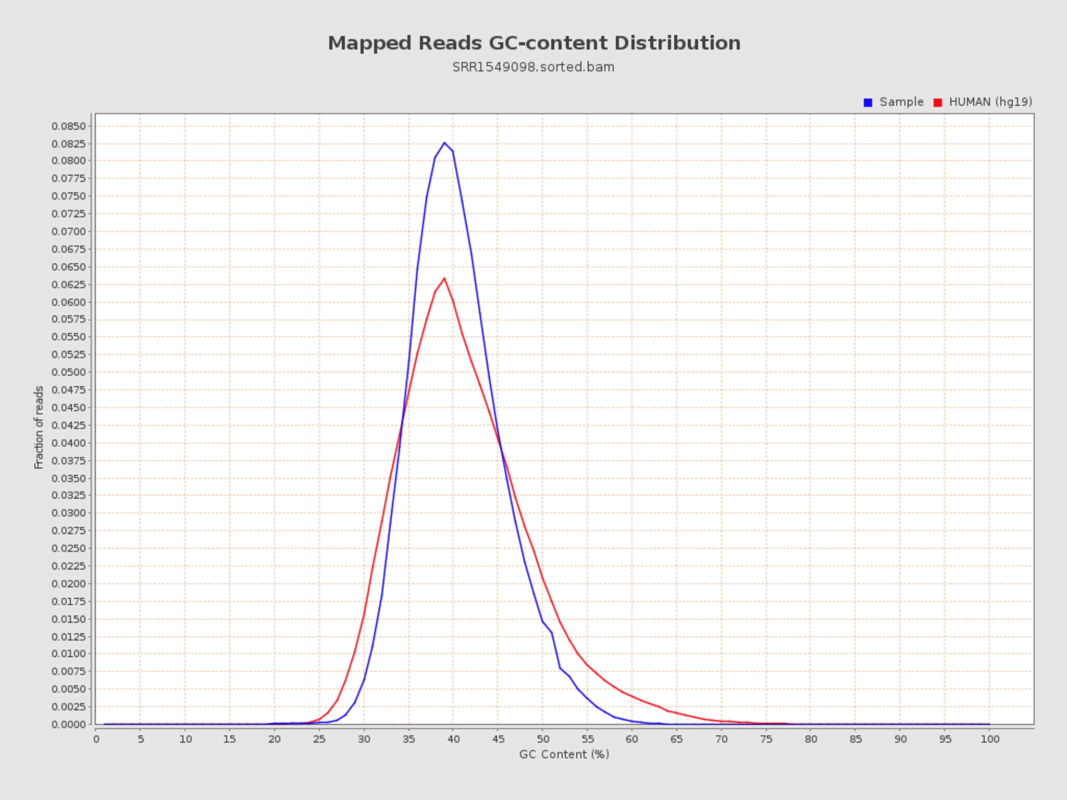
7. Results : Duplication Rate Histogram



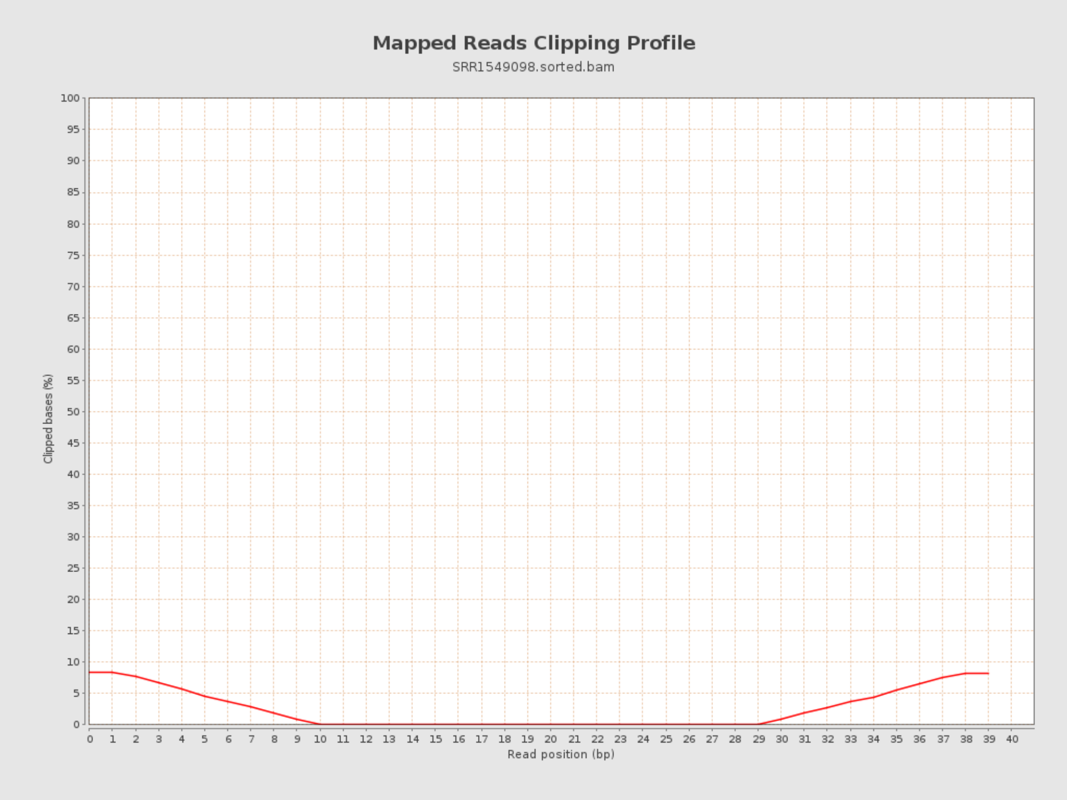
8. Results : Mapped Reads Nucleotide Content



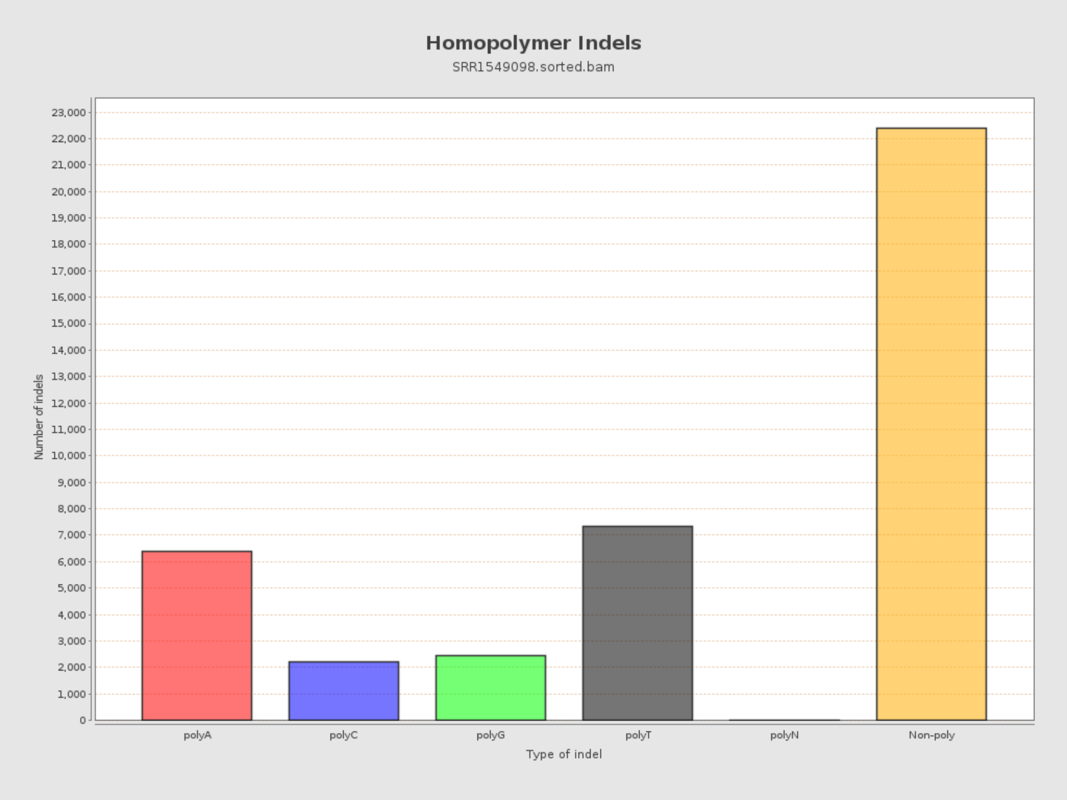
9. Results : Mapped Reads GC-content Distribution



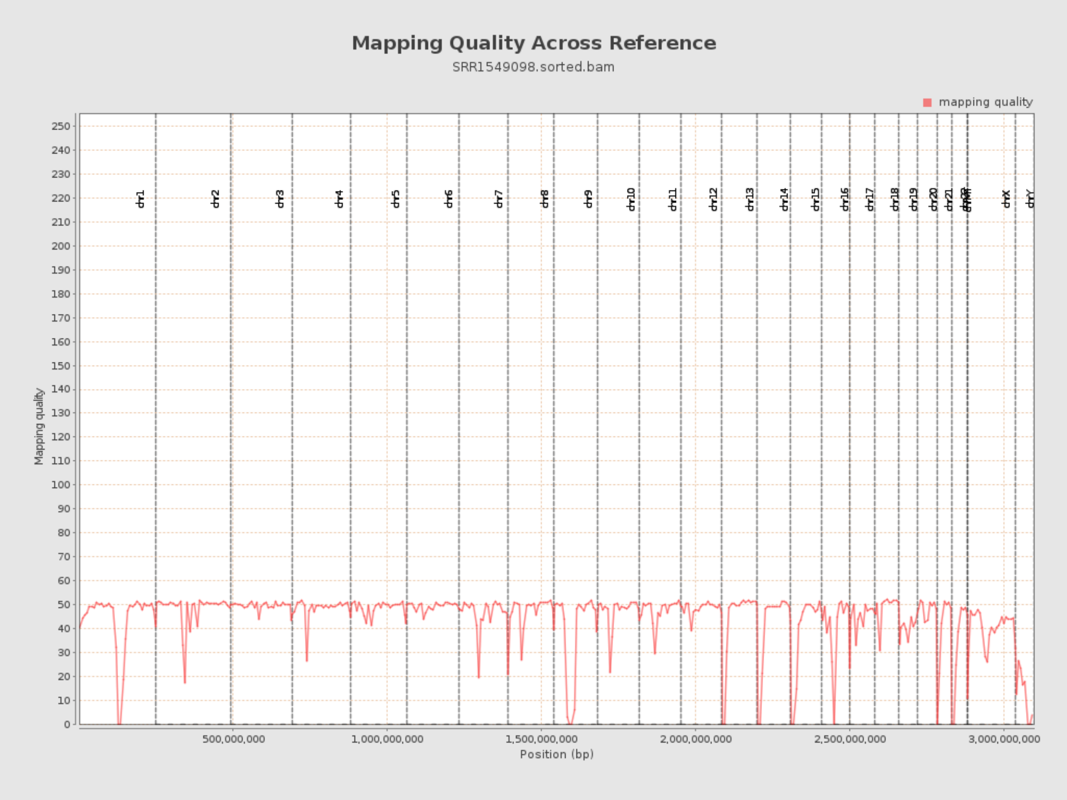
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram