Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:40:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549108.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_SRR1549108 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:40:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,781,019
Mapped reads	9,899,857 / 84.03%
Unmapped reads	1,881,162 / 15.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	410,283 / 3.48%
Duplication rate	2.79%
Clipped reads	621,392 / 5.27%

2.2. ACGT Content

Number/percentage of A's	119,046,288 / 30.34%
Number/percentage of C's	77,551,775 / 19.76%
Number/percentage of T's	118,180,036 / 30.12%
Number/percentage of G's	77,645,370 / 19.79%
Number/percentage of N's	1,491 / 0%
GC Percentage	39.55%

2.3. Coverage

Mean	0.1268
Standard Deviation	1.9686

2.4. Mapping Quality

Mean Mapping Quality	42.86

2.5. Mismatches and indels

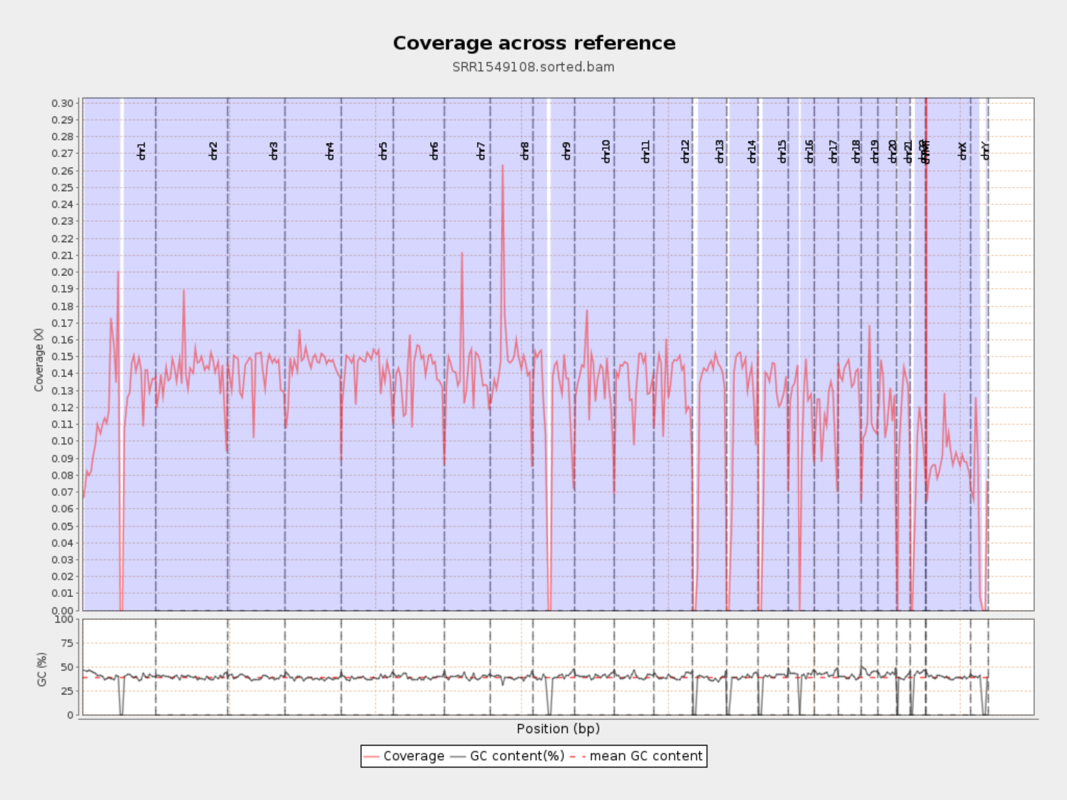
General error rate	0.34%
Mismatches	1,306,926
Insertions	11,699
Mapped reads with at least one insertion	0.12%
Deletions	31,650
Mapped reads with at least one deletion	0.32%
Homopolymer indels	43.14%

2.6. Chromosome stats

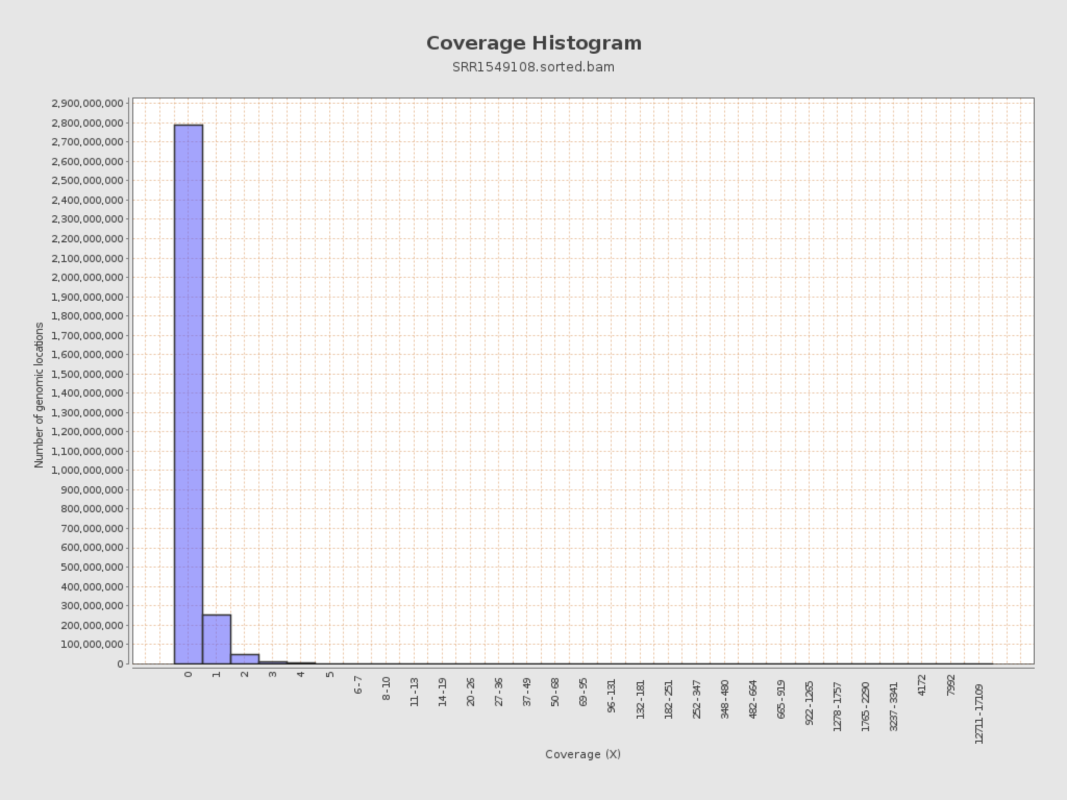
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29022348	0.1164	1.6681
chr2	243199373	34289269	0.141	0.722
chr3	198022430	28041967	0.1416	0.4547
chr4	191154276	27775360	0.1453	0.4991
chr5	180915260	25748628	0.1423	0.4693
chr6	171115067	23989102	0.1402	0.5108
chr7	159138663	22336318	0.1404	1.1394
chr8	146364022	21783787	0.1488	8.3046

chr9	141213431	16791519	0.1189	0.7097
chr10	135534747	18567514	0.137	0.6958
chr11	135006516	18329589	0.1358	0.6842
chr12	133851895	18062336	0.1349	0.4739
chr13	115169878	13554189	0.1177	0.4085
chr14	107349540	12389591	0.1154	0.5829
chr15	102531392	11212112	0.1094	0.3952
chr16	90354753	10030347	0.111	0.4712
chr17	81195210	9230723	0.1137	0.4518
chr18	78077248	10847124	0.1389	1.4259
chr19	59128983	6691764	0.1132	1.4336
chr20	63025520	7632898	0.1211	0.461
chr21	48129895	5224420	0.1085	0.4921
chr22	51304566	3783923	0.0738	0.3912
chrMT	16571	107447	6.484	6.8407
chrX	155270560	13808514	0.0889	0.4836
chrY	59373566	3213943	0.0541	0.4435

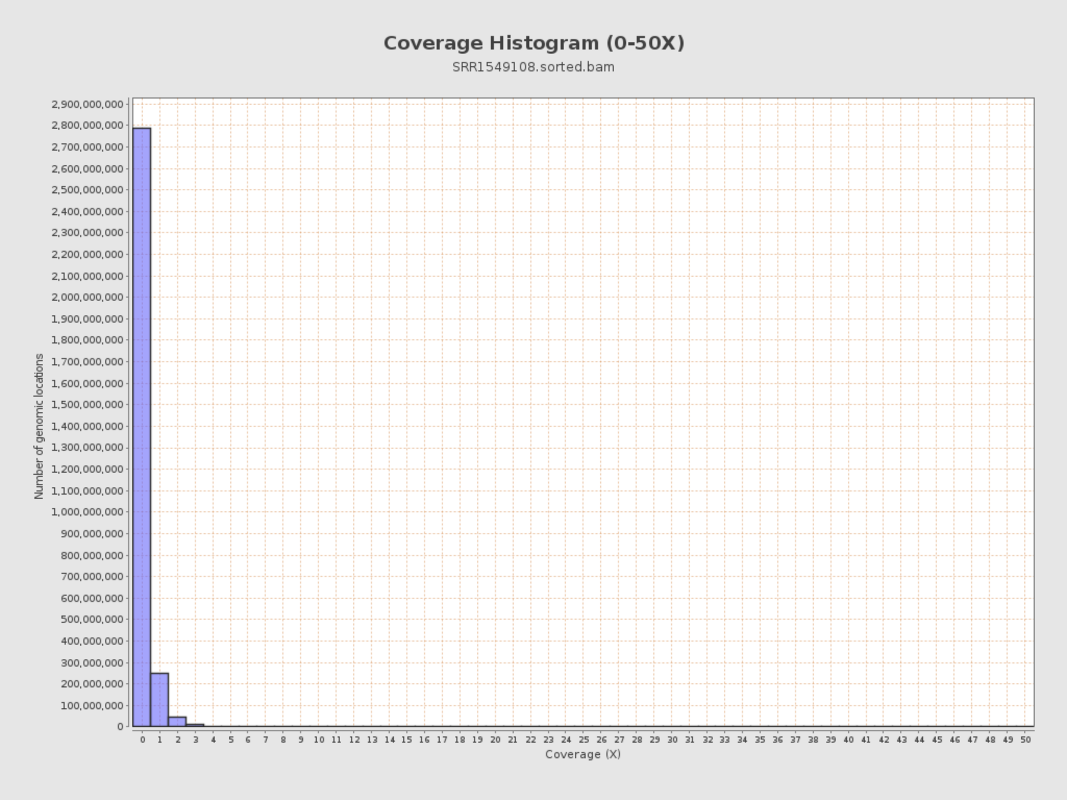
3. Results : Coverage across reference



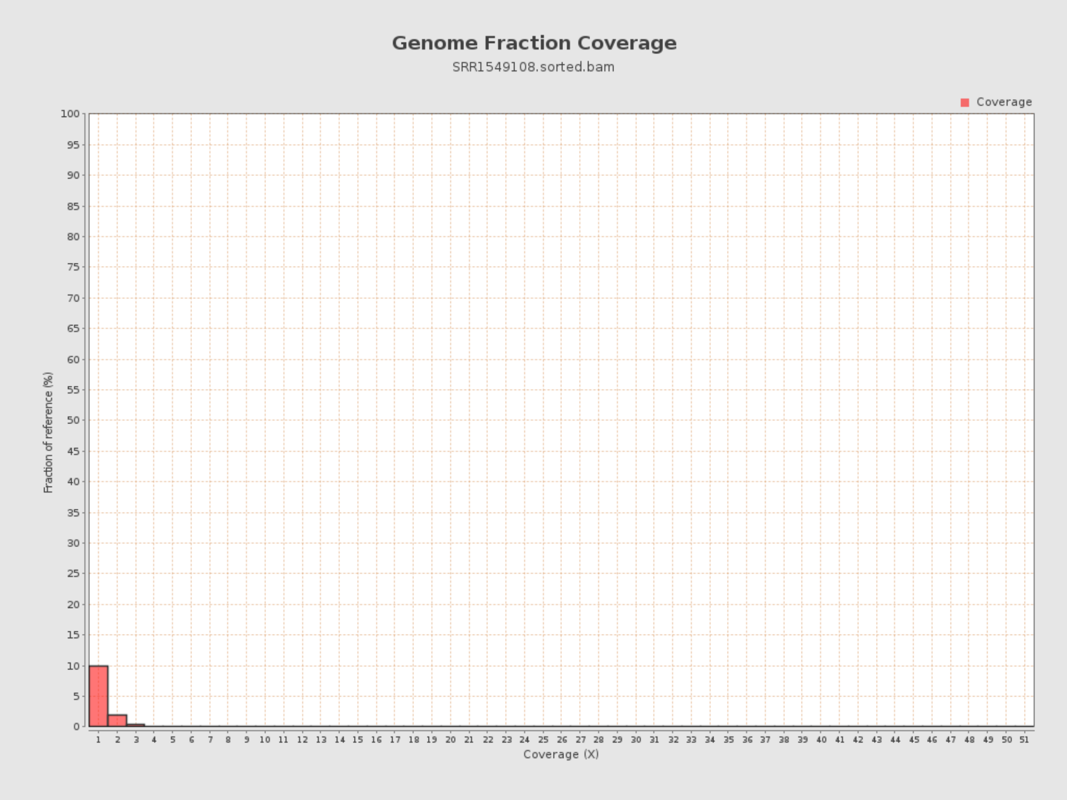
4. Results : Coverage Histogram



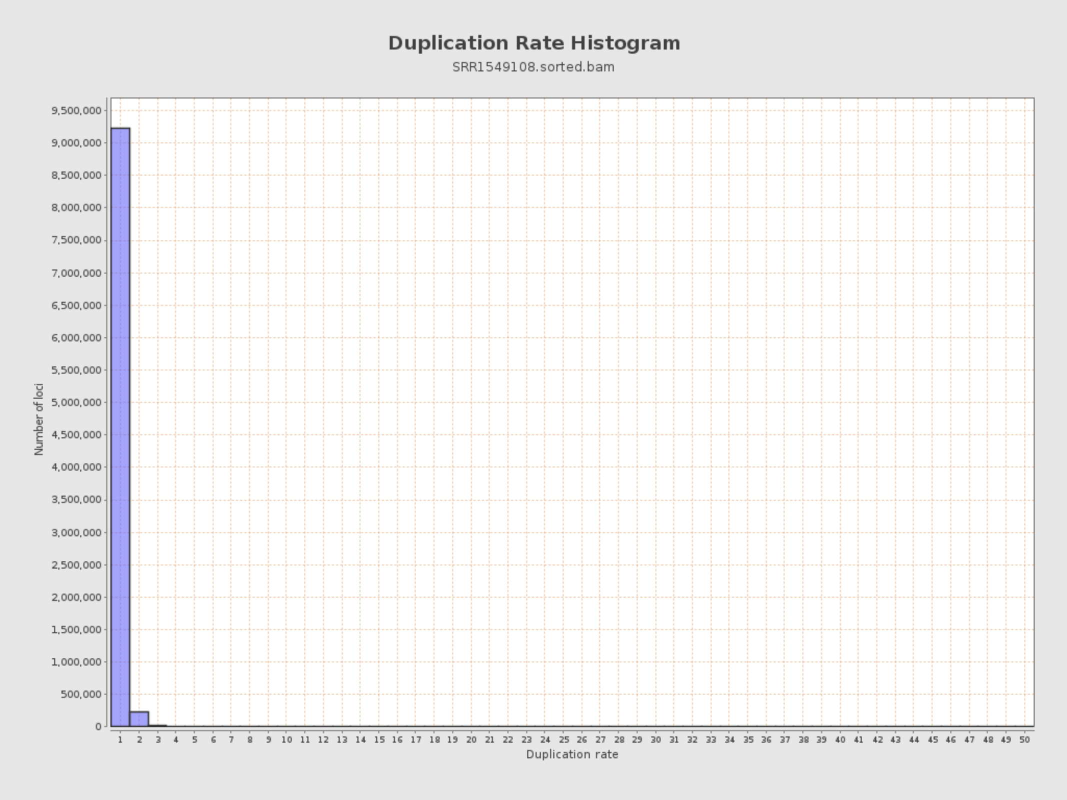
5. Results : Coverage Histogram (0-50X)



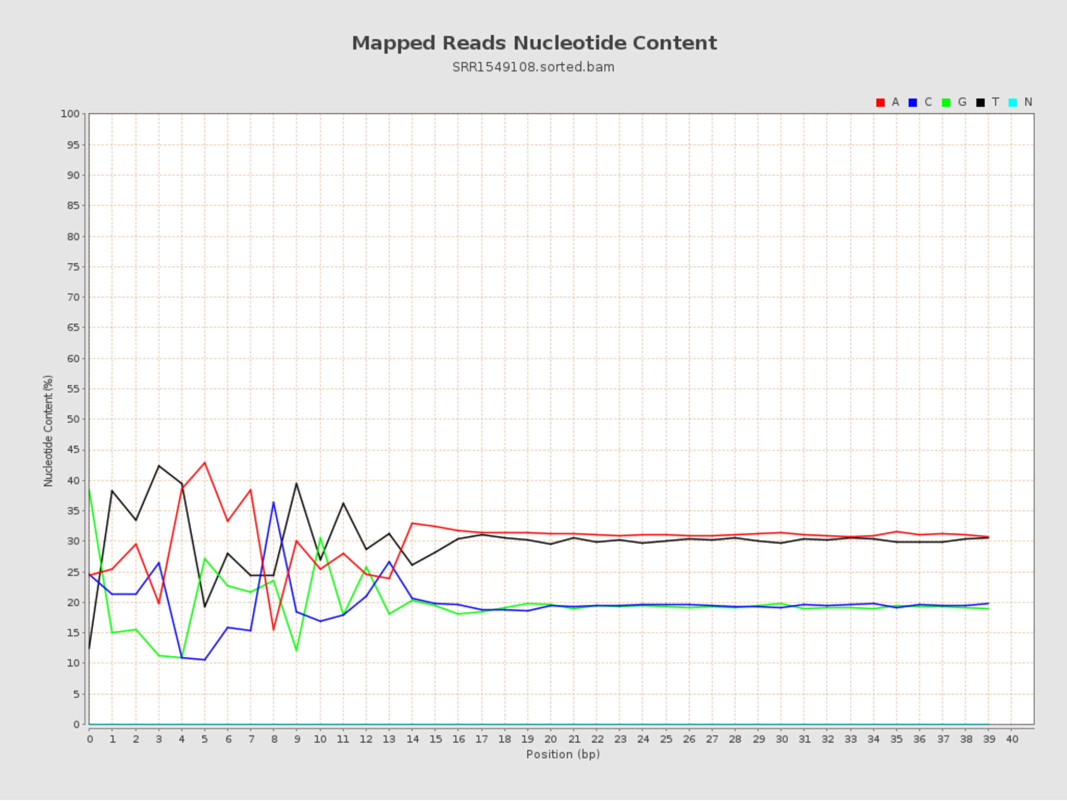
6. Results : Genome Fraction Coverage



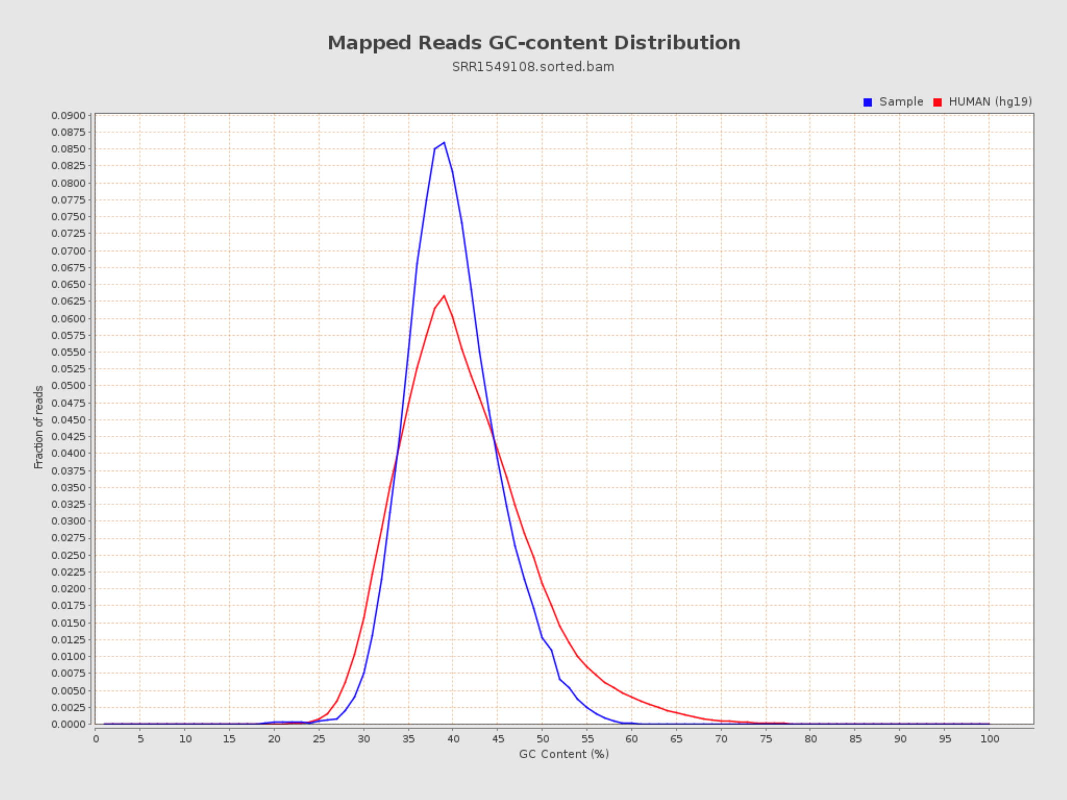
7. Results : Duplication Rate Histogram



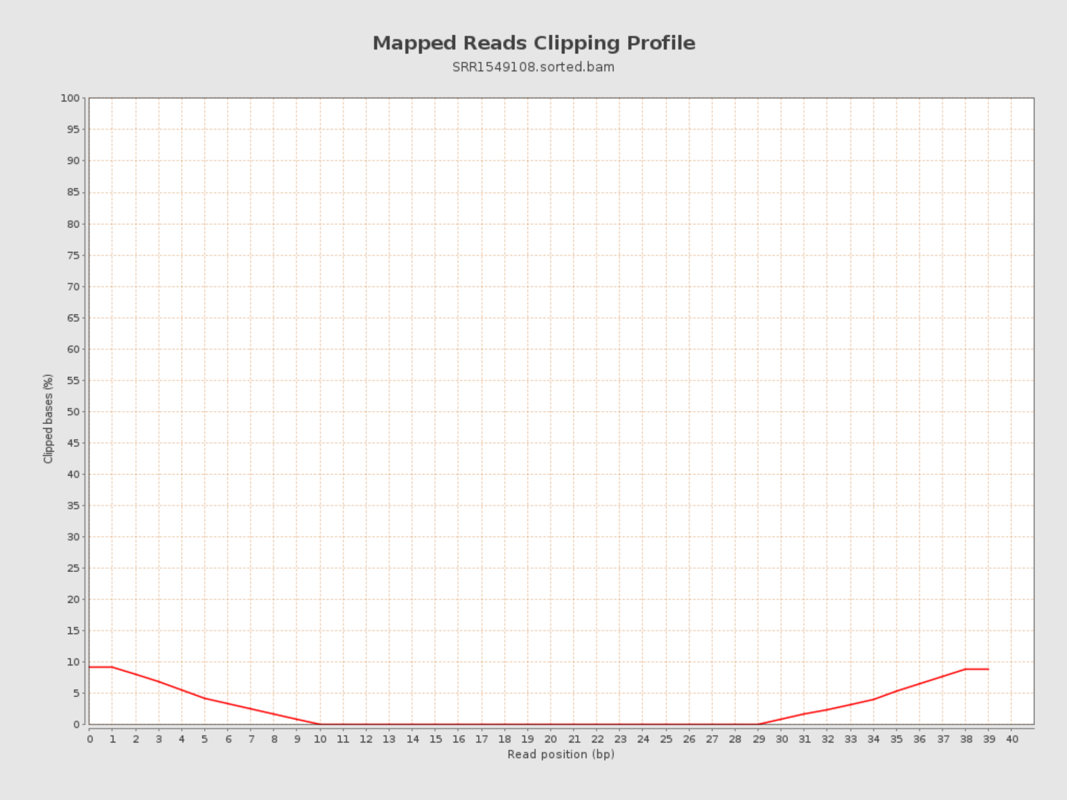
8. Results : Mapped Reads Nucleotide Content



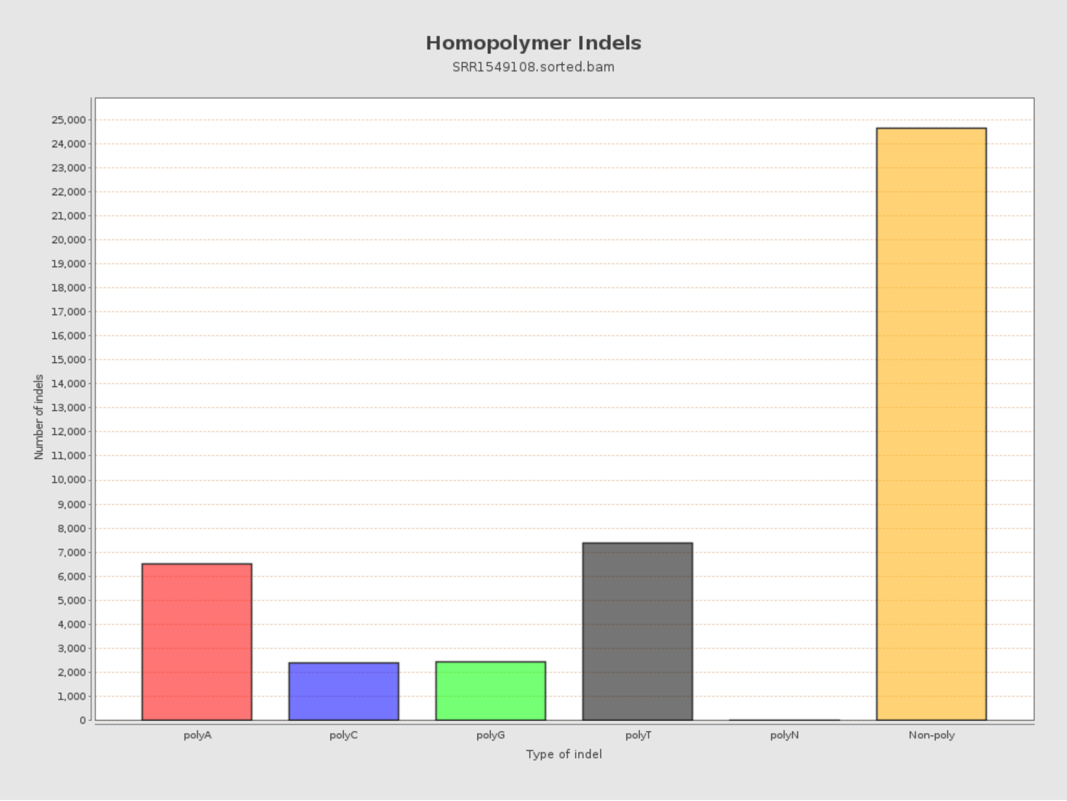
9. Results : Mapped Reads GC-content Distribution



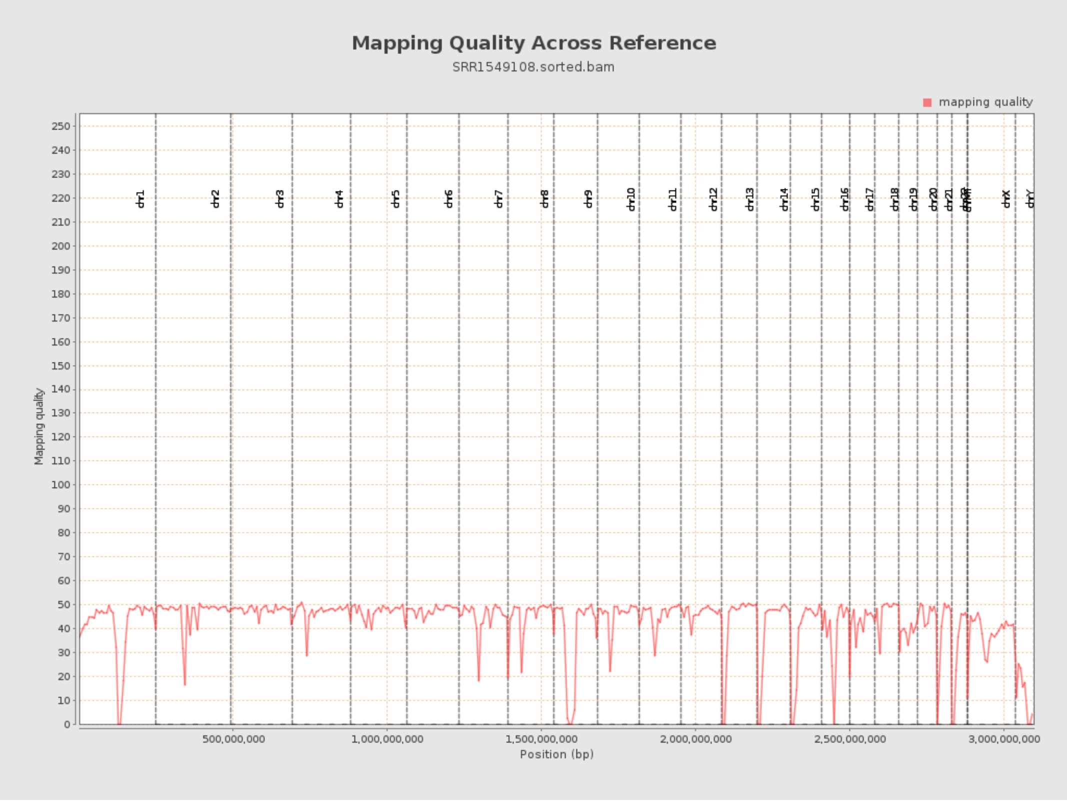
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram