Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:23:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549112.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_SRR1549112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:23:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,318,885
Mapped reads	9,539,972 / 84.28%
Unmapped reads	1,778,913 / 15.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	427,004 / 3.77%
Duplication rate	3.28%
Clipped reads	490,338 / 4.33%

2.2. ACGT Content

Number/percentage of A's	114,685,456 / 30.29%
Number/percentage of C's	73,772,585 / 19.49%
Number/percentage of T's	115,663,351 / 30.55%
Number/percentage of G's	74,456,197 / 19.67%
Number/percentage of N's	1,542 / 0%
GC Percentage	39.15%

2.3. Coverage

Mean	0.1223
Standard Deviation	1.0175

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

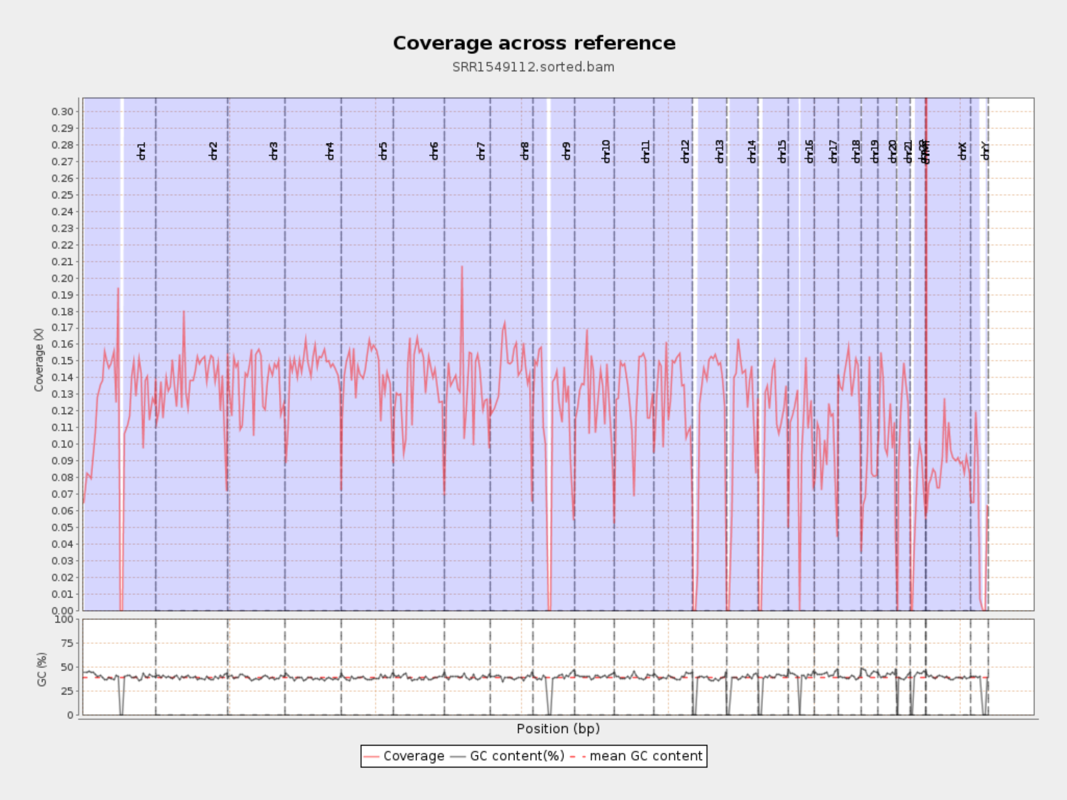
General error rate	0.3%
Mismatches	1,142,385
Insertions	9,722
Mapped reads with at least one insertion	0.1%
Deletions	28,804
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.13%

2.6. Chromosome stats

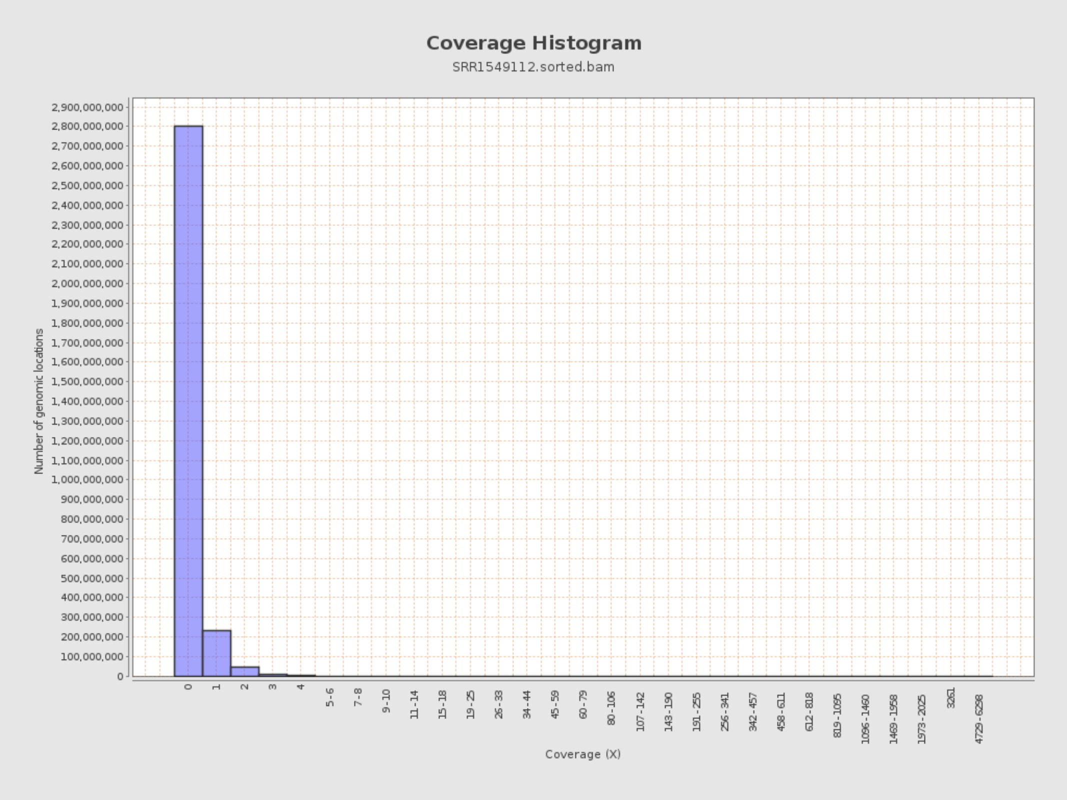
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29468608	0.1182	1.5759
chr2	243199373	33307137	0.137	0.7194
chr3	198022430	27226204	0.1375	0.4584
chr4	191154276	27763776	0.1452	0.4861
chr5	180915260	25536941	0.1412	0.4722
chr6	171115067	23350078	0.1365	0.5342
chr7	159138663	21319746	0.134	1.1405
chr8	146364022	20769676	0.1419	3.1173

chr9	141213431	15942580	0.1129	0.6789
chr10	135534747	17446505	0.1287	0.6575
chr11	135006516	17439672	0.1292	0.6706
chr12	133851895	17380343	0.1298	0.4701
chr13	115169878	13548898	0.1176	0.4183
chr14	107349540	12100454	0.1127	0.5478
chr15	102531392	10566108	0.1031	0.3922
chr16	90354753	9263434	0.1025	0.4728
chr17	81195210	7929977	0.0977	0.4375
chr18	78077248	10988230	0.1407	1.4747
chr19	59128983	5133116	0.0868	1.2499
chr20	63025520	7108779	0.1128	0.4437
chr21	48129895	5113542	0.1062	0.4808
chr22	51304566	3129892	0.061	0.3256
chrMT	16571	93015	5.6131	6.6216
chrX	155270560	13667308	0.088	0.4733
chrY	59373566	3021003	0.0509	0.3811

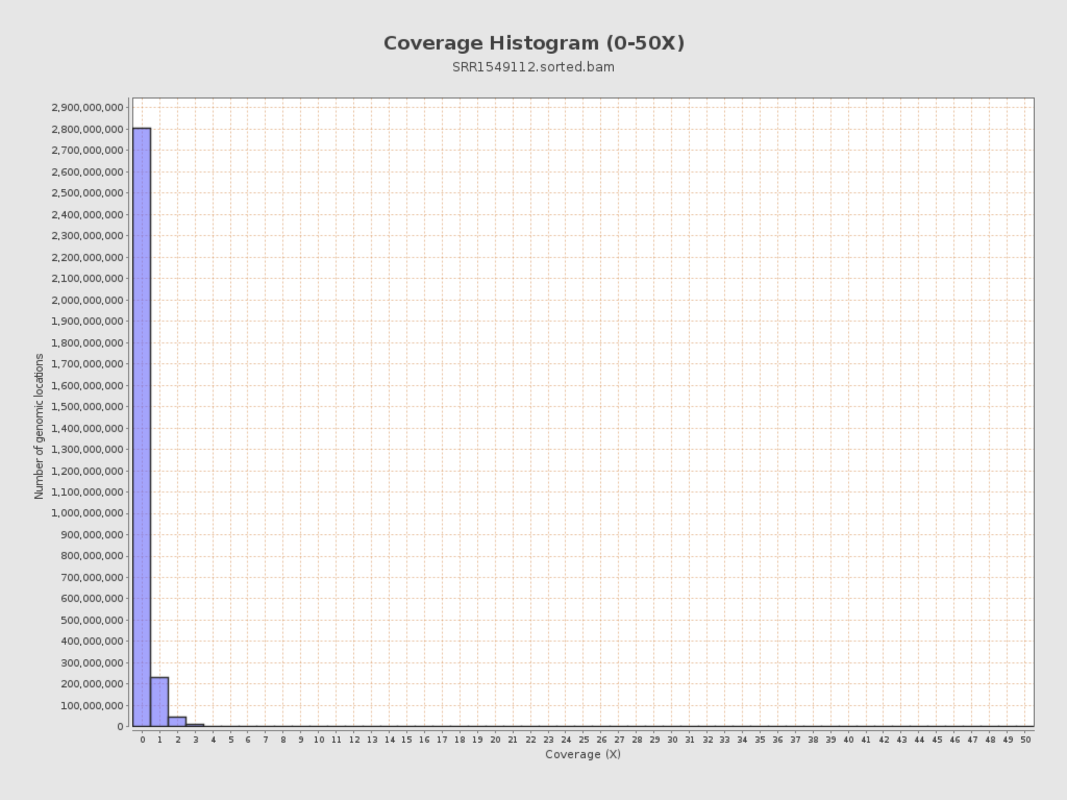
3. Results : Coverage across reference



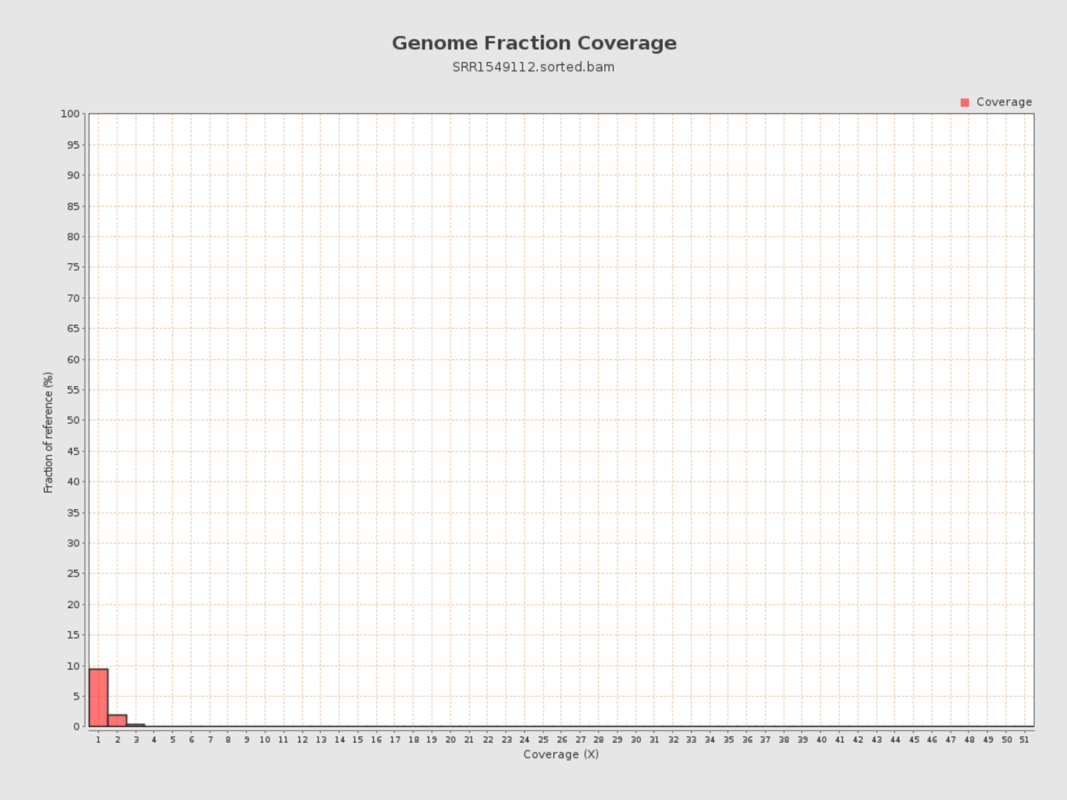
4. Results : Coverage Histogram



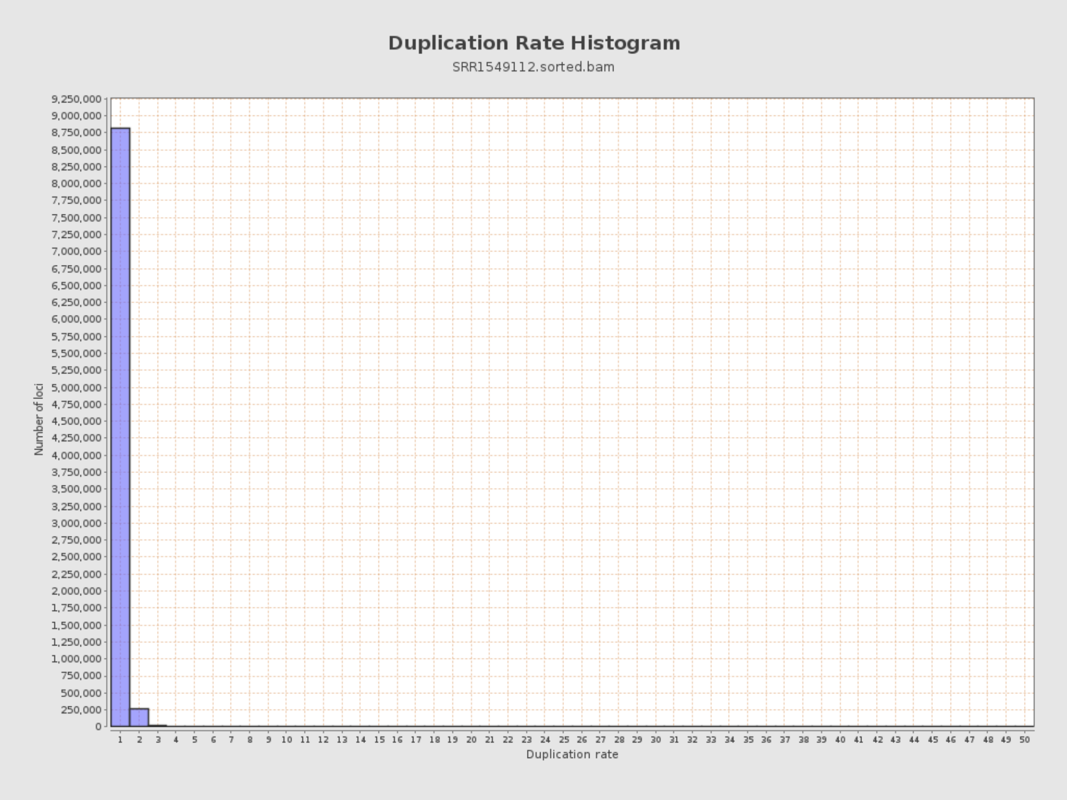
5. Results : Coverage Histogram (0-50X)



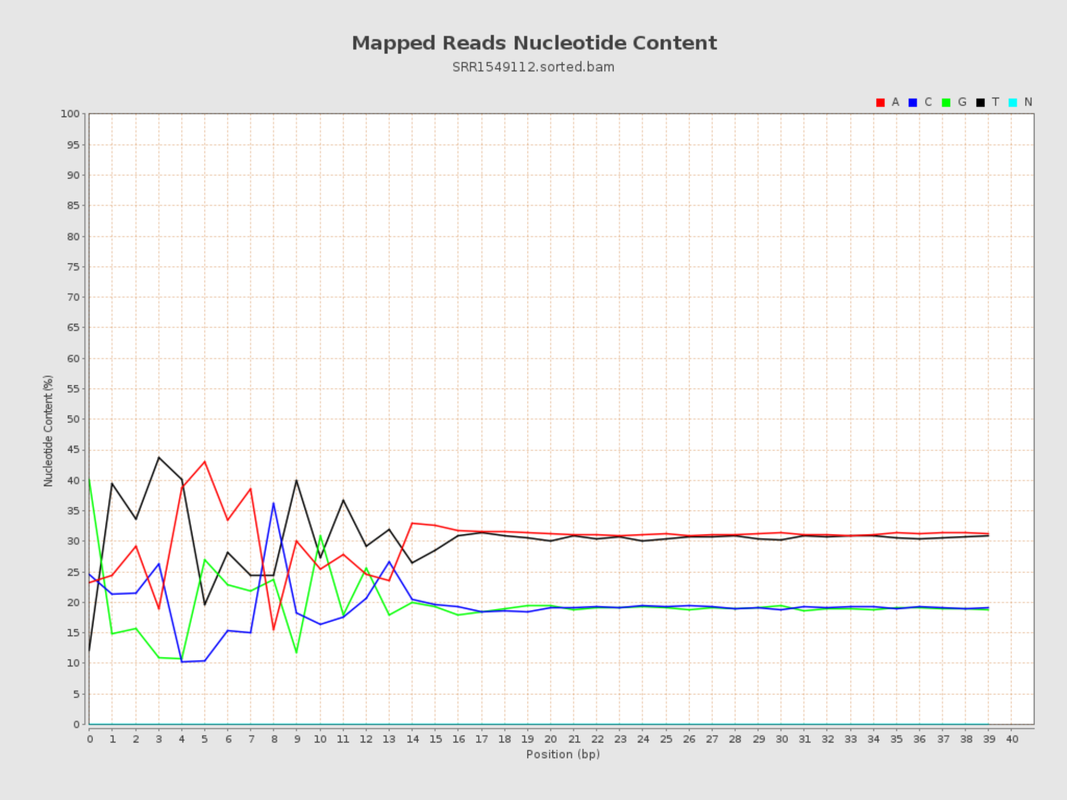
6. Results : Genome Fraction Coverage



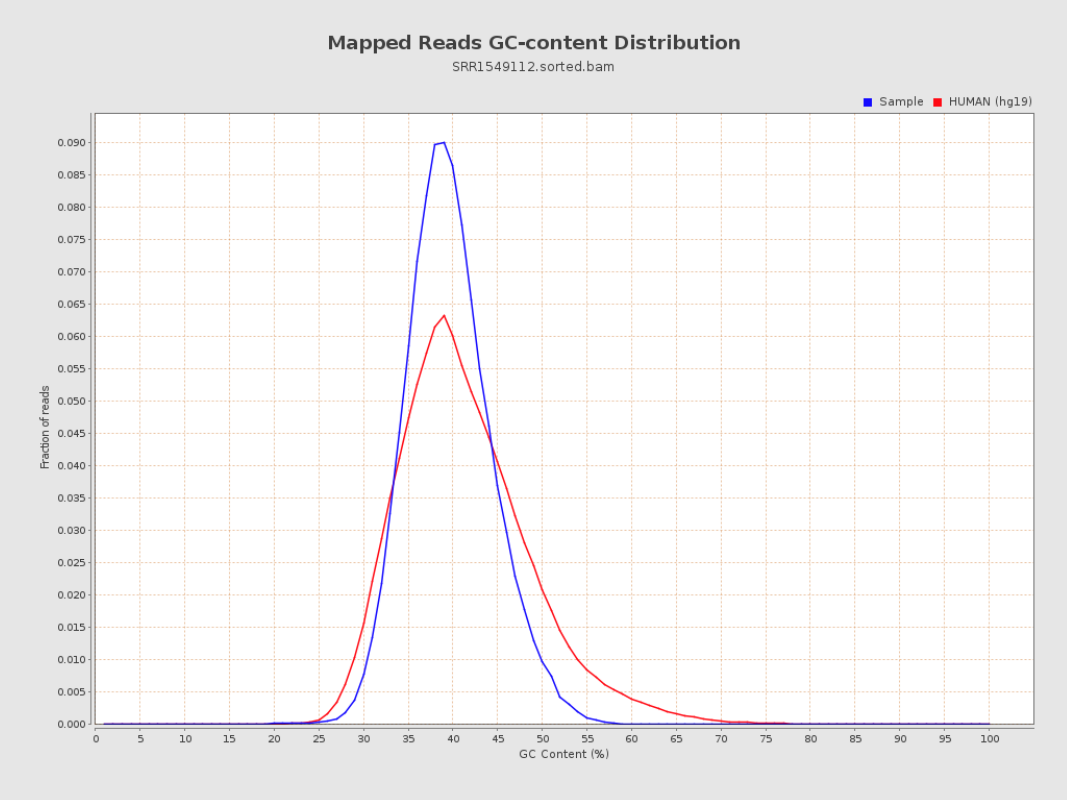
7. Results : Duplication Rate Histogram



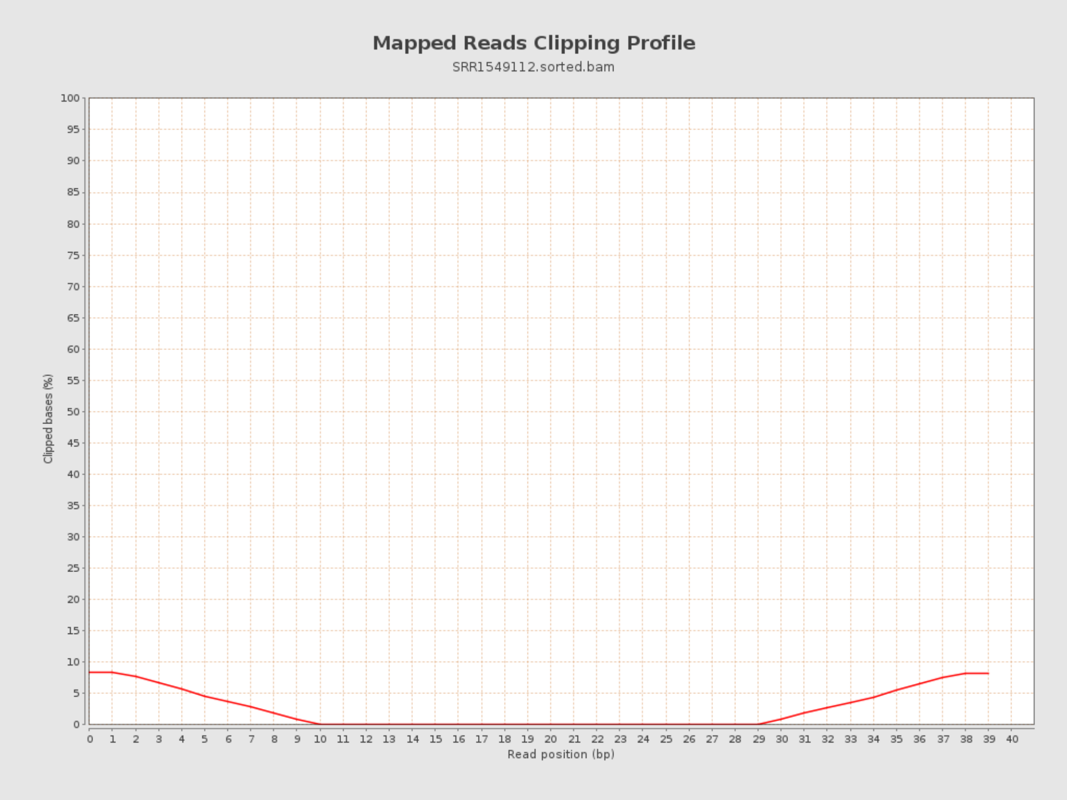
8. Results : Mapped Reads Nucleotide Content



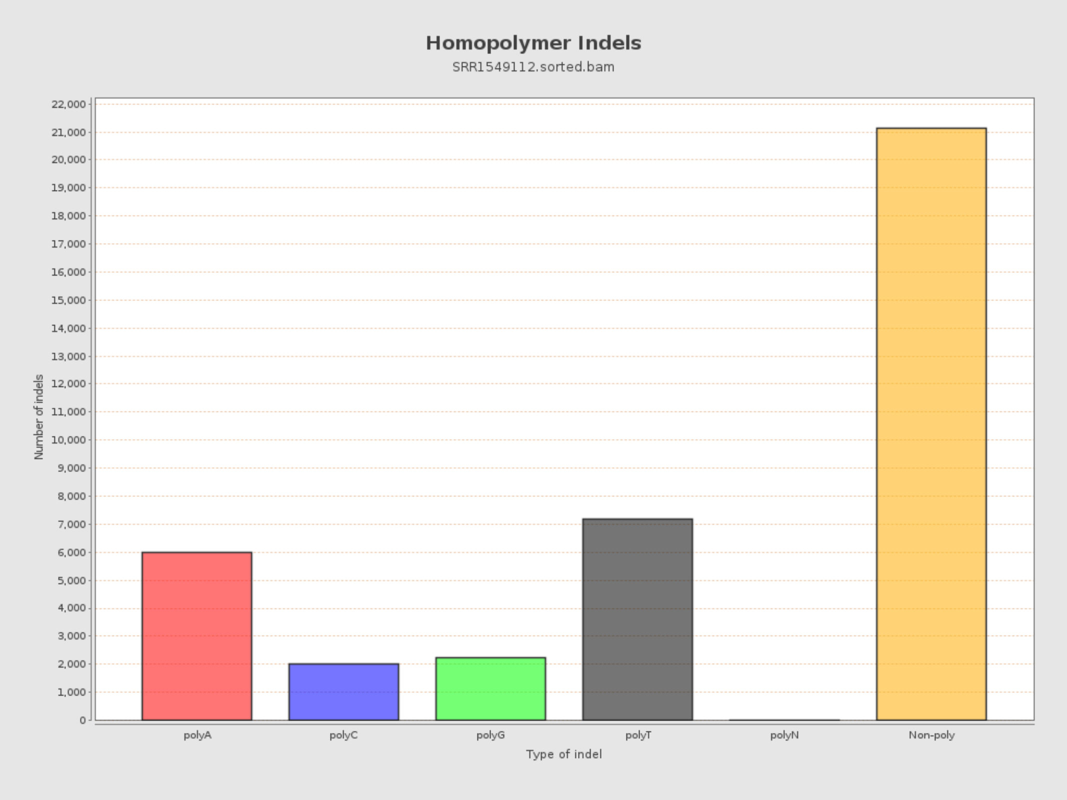
9. Results : Mapped Reads GC-content Distribution



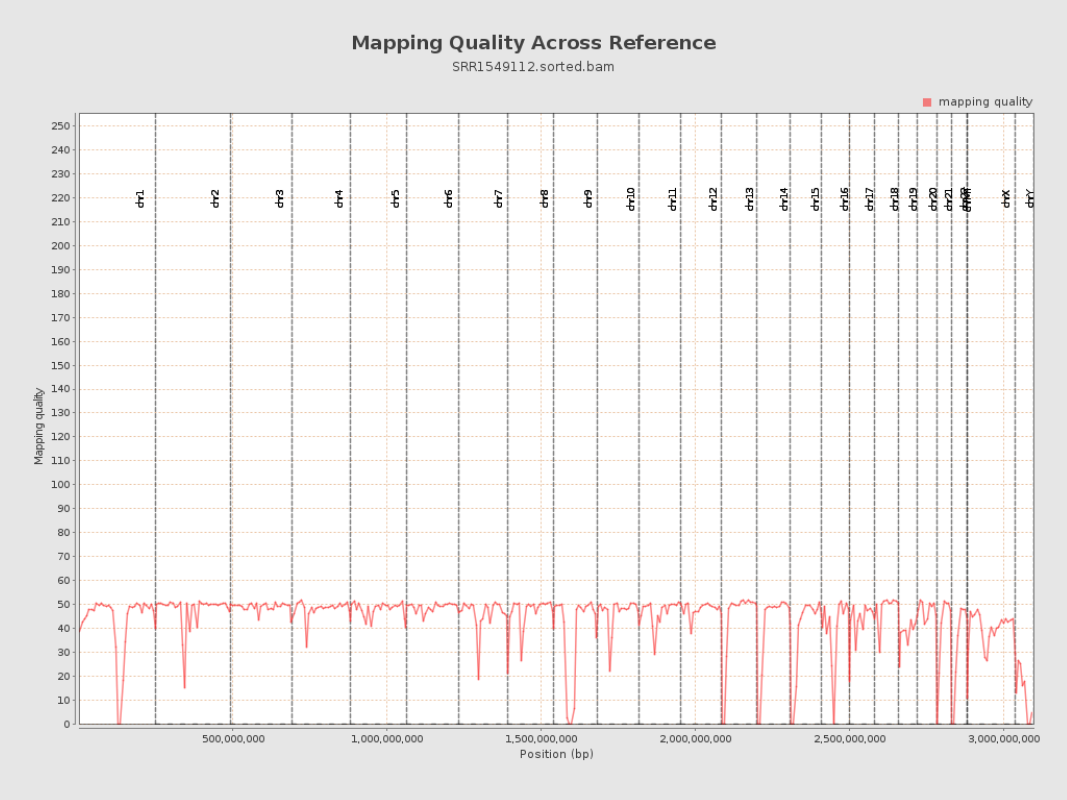
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram