Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:22:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081199.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_SRR3081199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:22:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,280,496
Mapped reads	6,075,906 / 83.45%
Unmapped reads	1,204,590 / 16.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	63,247 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	523,131 / 7.19%
Duplication rate	6.4%
Clipped reads	2,918,322 / 40.08%

2.2. ACGT Content

Number/percentage of A's	110,338,934 / 27.44%
Number/percentage of C's	78,356,834 / 19.49%
Number/percentage of T's	123,635,723 / 30.75%
Number/percentage of G's	89,516,296 / 22.26%
Number/percentage of N's	230,281 / 0.06%
GC Percentage	41.75%

2.3. Coverage

Mean	0.1299

Standard Deviation	1.0999

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

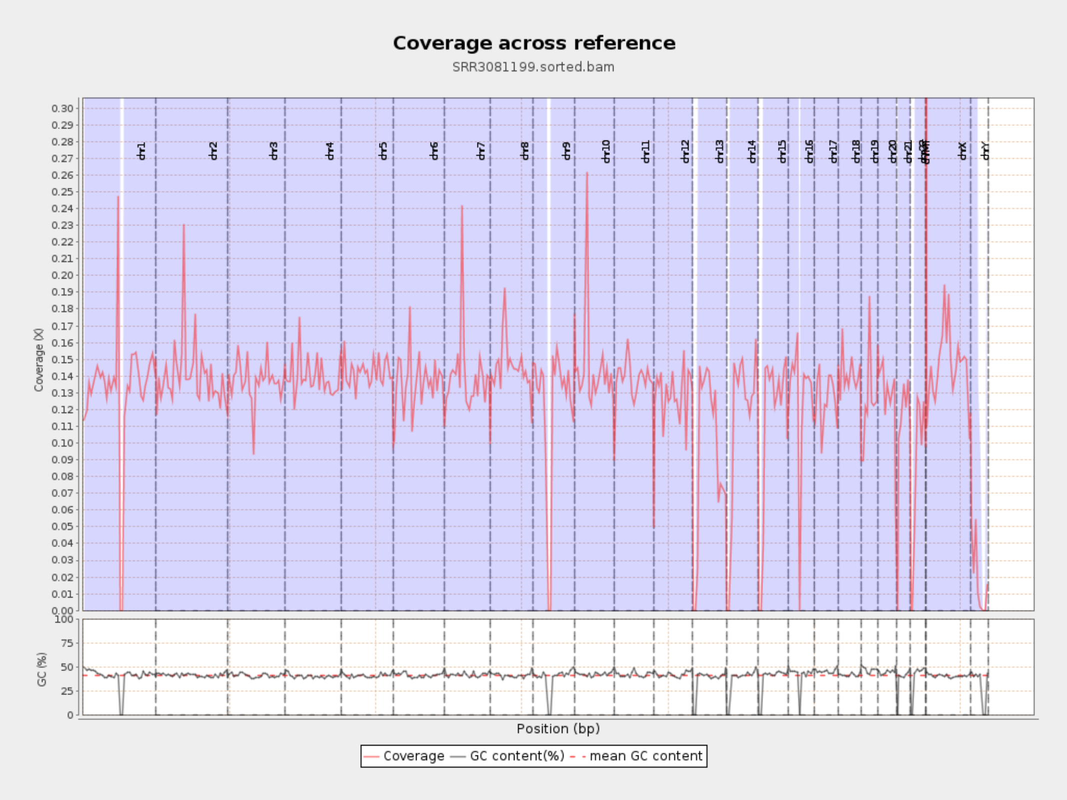
General error rate	1.04%
Mismatches	4,136,534
Insertions	29,688
Mapped reads with at least one insertion	0.48%
Deletions	82,930
Mapped reads with at least one deletion	1.35%
Homopolymer indels	44.57%

2.6. Chromosome stats

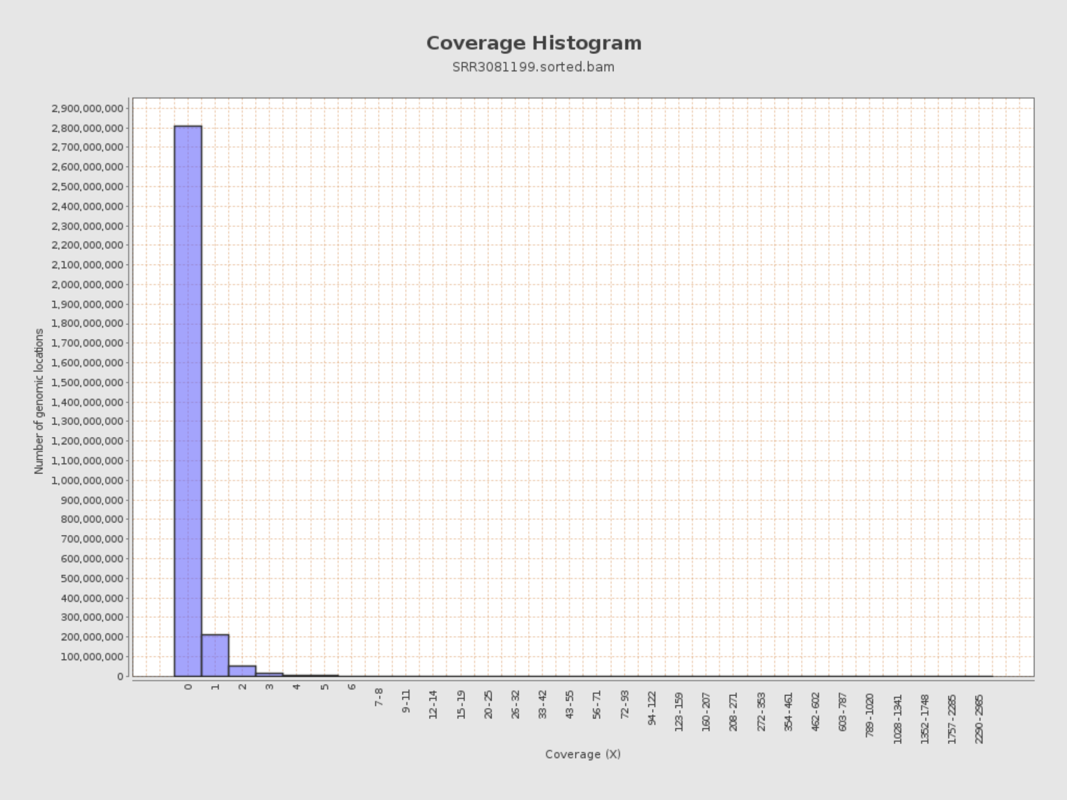
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32790772	0.1316	2.1071
chr2	243199373	34204810	0.1406	0.9539
chr3	198022430	27181248	0.1373	0.497
chr4	191154276	26702867	0.1397	0.5309
chr5	180915260	25619195	0.1416	0.5041
chr6	171115067	23388344	0.1367	0.6249
chr7	159138663	22359691	0.1405	1.6105

chr8	146364022	21286623	0.1454	1.8068
chr9	141213431	17143170	0.1214	0.8587
chr10	135534747	19524159	0.1441	1.2801
chr11	135006516	18645064	0.1381	1.0032
chr12	133851895	17389219	0.1299	0.5089
chr13	115169878	10870864	0.0944	0.402
chr14	107349540	12229164	0.1139	1.3662
chr15	102531392	11267181	0.1099	0.4312
chr16	90354753	11226490	0.1242	0.5625
chr17	81195210	10302391	0.1269	0.6247
chr18	78077248	11021481	0.1412	1.8697
chr19	59128983	7465617	0.1263	1.5379
chr20	63025520	8266061	0.1312	0.5024
chr21	48129895	5257403	0.1092	0.5203
chr22	51304566	4198275	0.0818	0.3782
chrMT	16571	86966	5.2481	3.6194
chrX	155270560	22698498	0.1462	0.6111
chrY	59373566	1082261	0.0182	0.3403

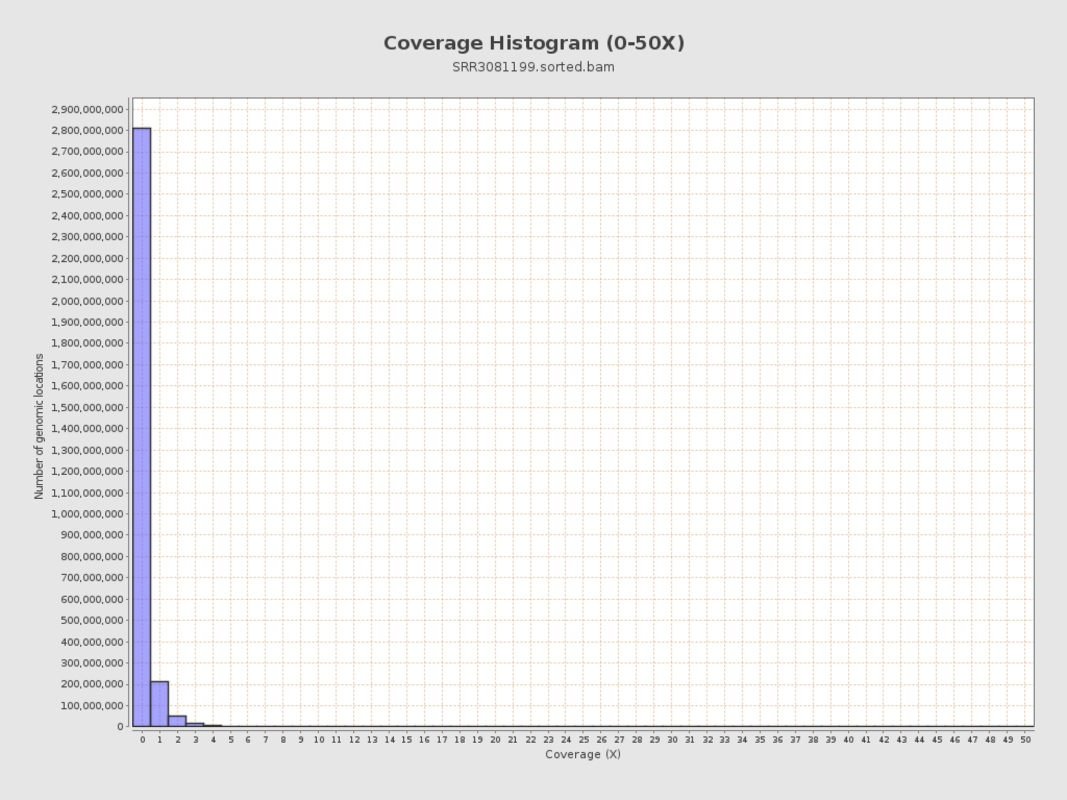
3. Results : Coverage across reference



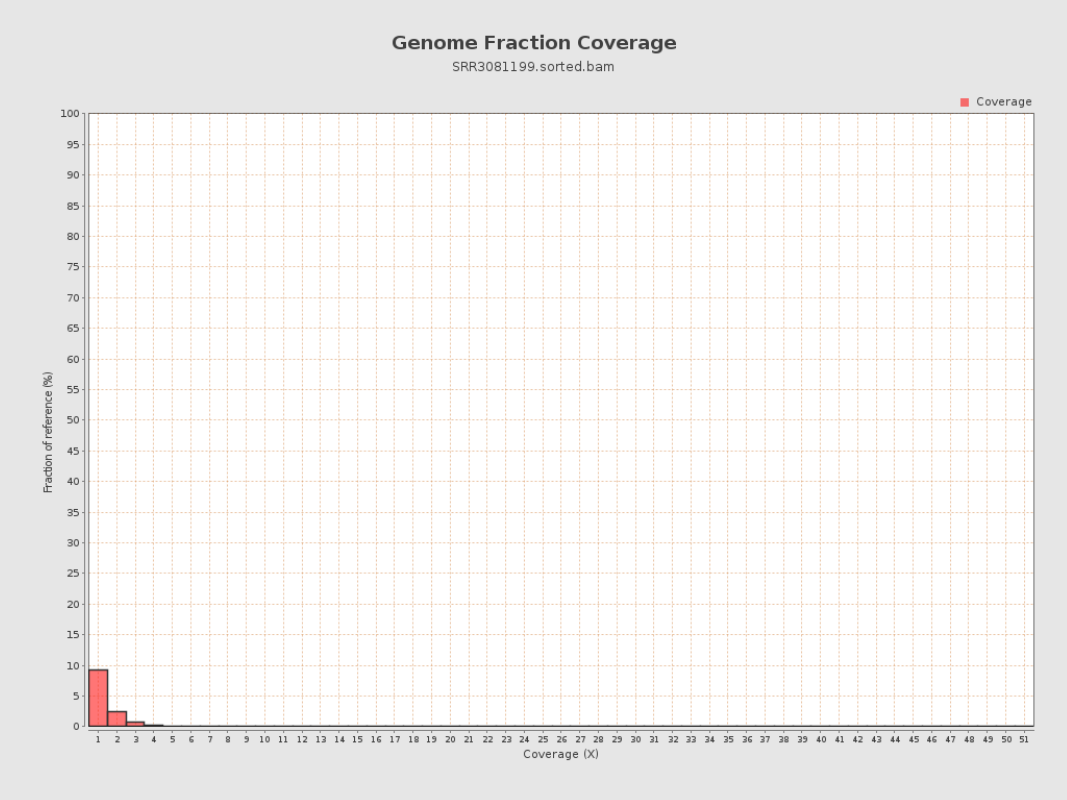
4. Results : Coverage Histogram



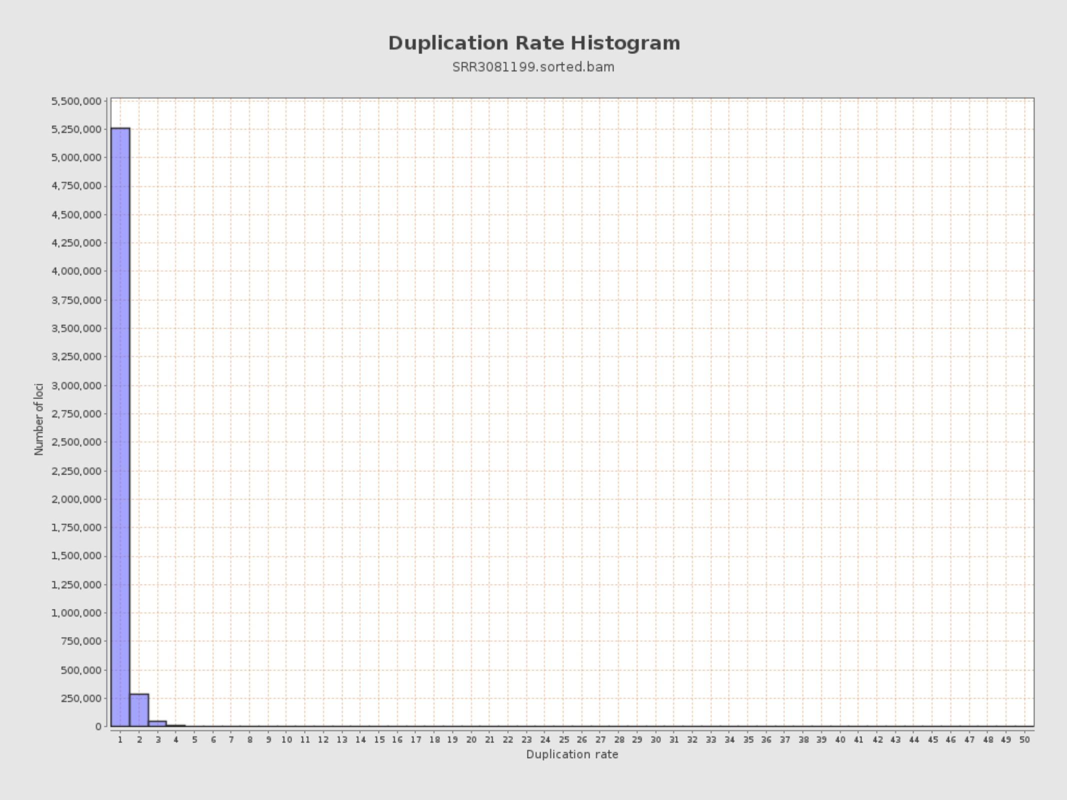
5. Results : Coverage Histogram (0-50X)



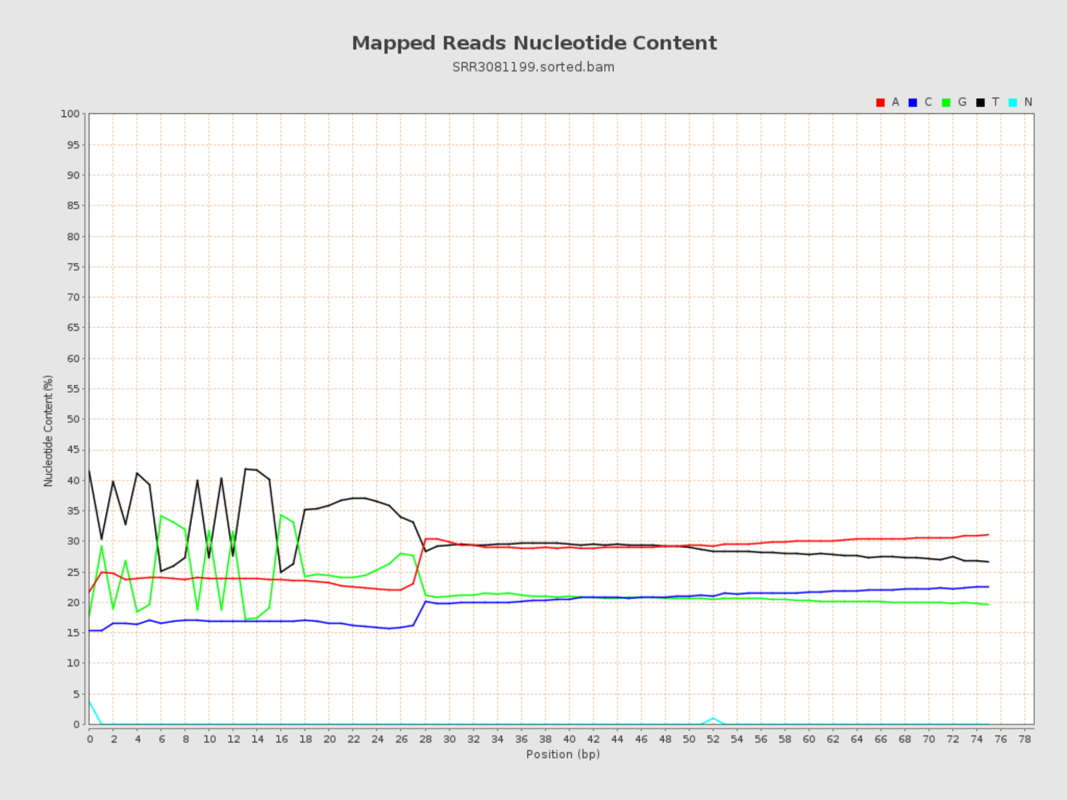
6. Results : Genome Fraction Coverage



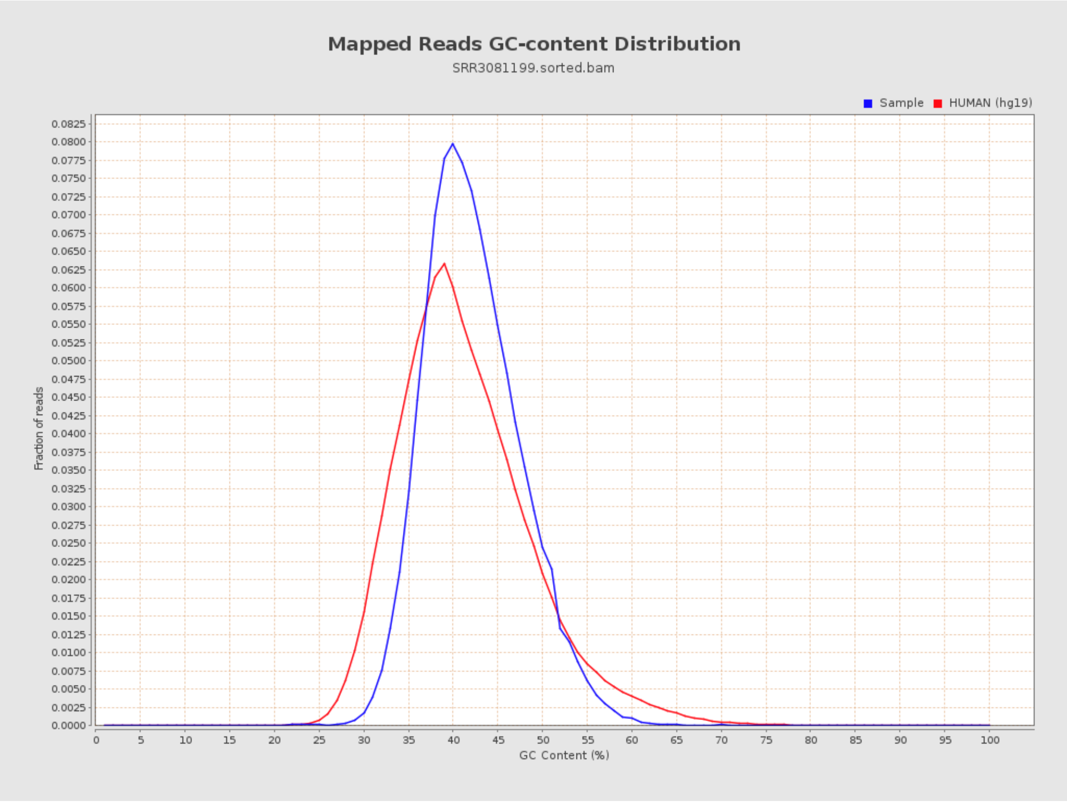
7. Results : Duplication Rate Histogram



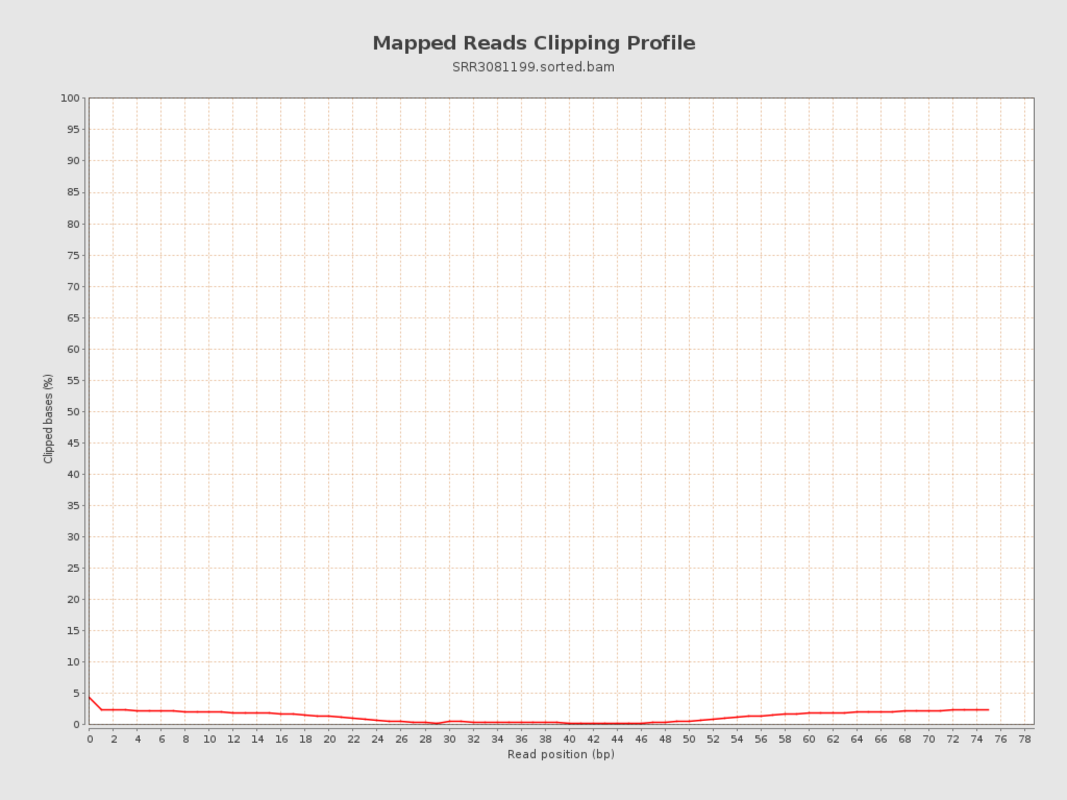
8. Results : Mapped Reads Nucleotide Content



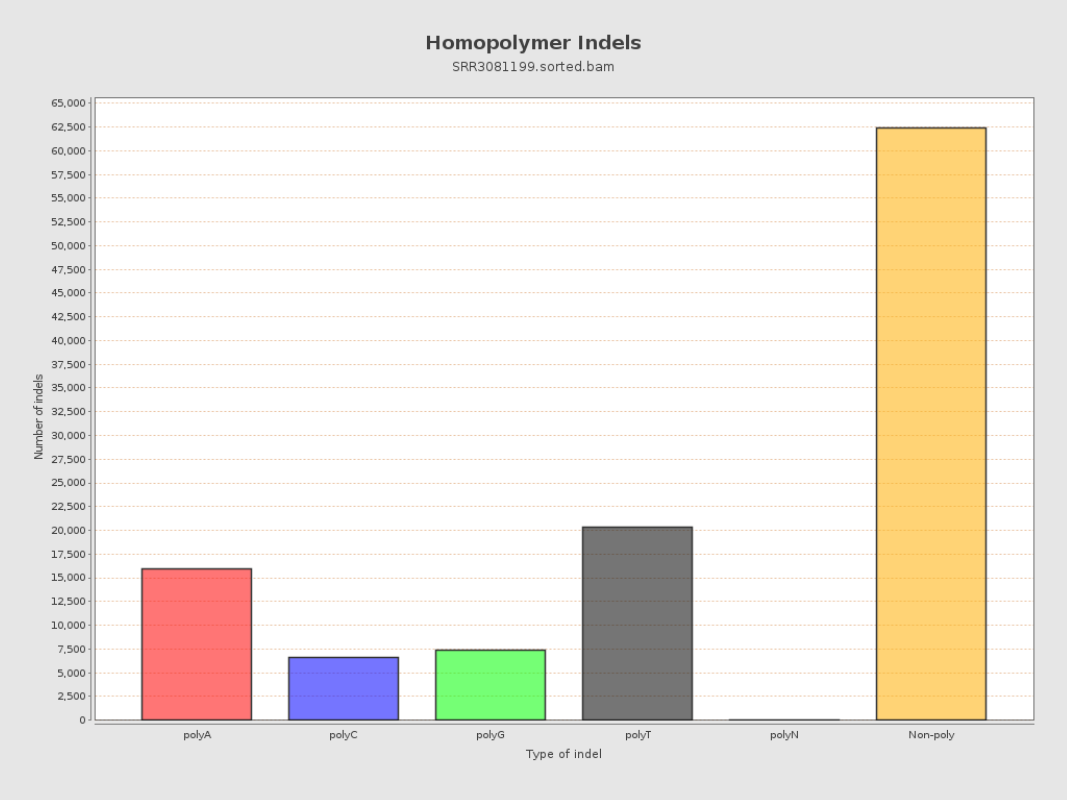
9. Results : Mapped Reads GC-content Distribution



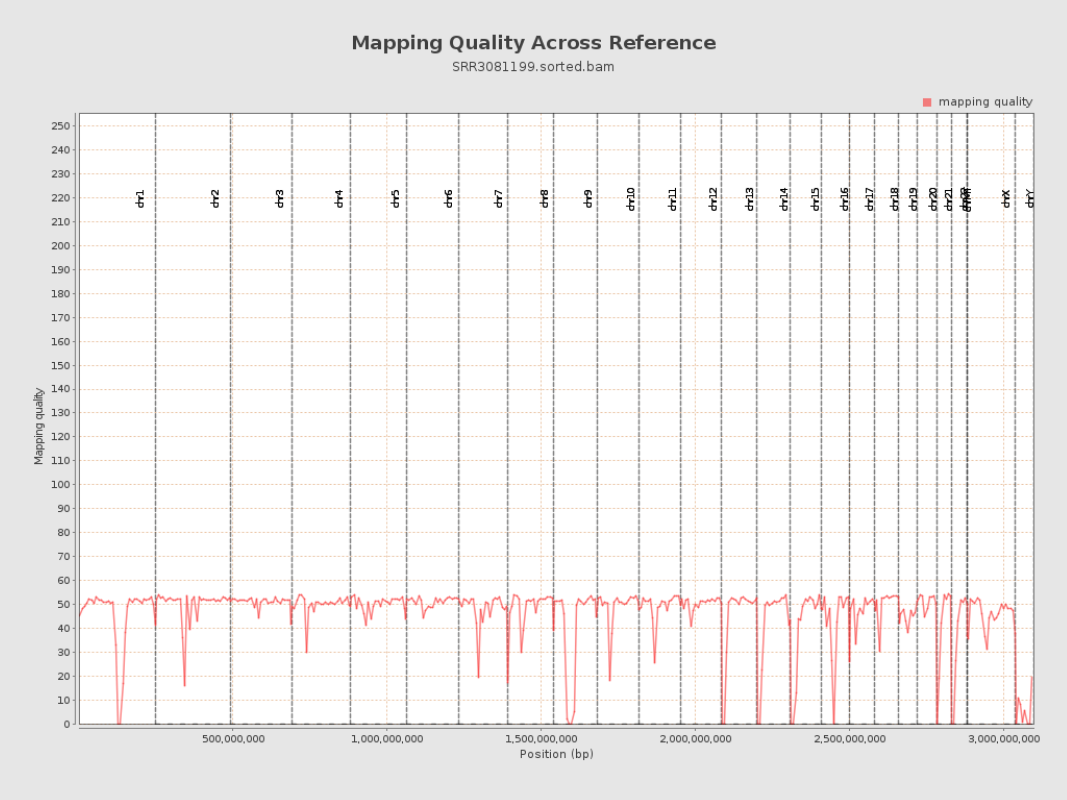
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram