Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:08:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081165.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_SRR3081165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081165.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:08:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081165.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,374,232
Mapped reads	2,131,241 / 89.77%
Unmapped reads	242,991 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,971 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	81,018 / 3.41%
Duplication rate	2.78%
Clipped reads	880,384 / 37.08%

2.2. ACGT Content

Number/percentage of A's	41,392,465 / 28.65%
Number/percentage of C's	26,788,523 / 18.54%
Number/percentage of T's	45,227,950 / 31.3%
Number/percentage of G's	31,048,847 / 21.49%
Number/percentage of N's	43,158 / 0.03%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0467

Standard Deviation	0.4263

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

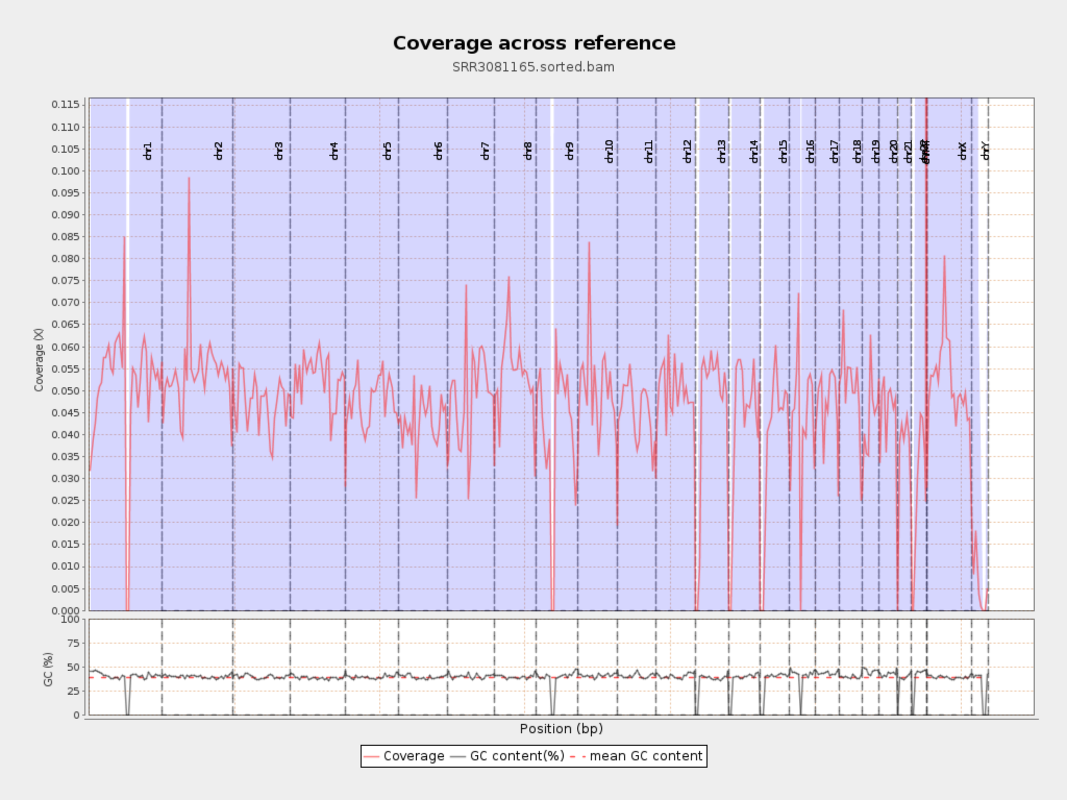
General error rate	0.87%
Mismatches	1,235,908
Insertions	11,887
Mapped reads with at least one insertion	0.55%
Deletions	34,872
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.58%

2.6. Chromosome stats

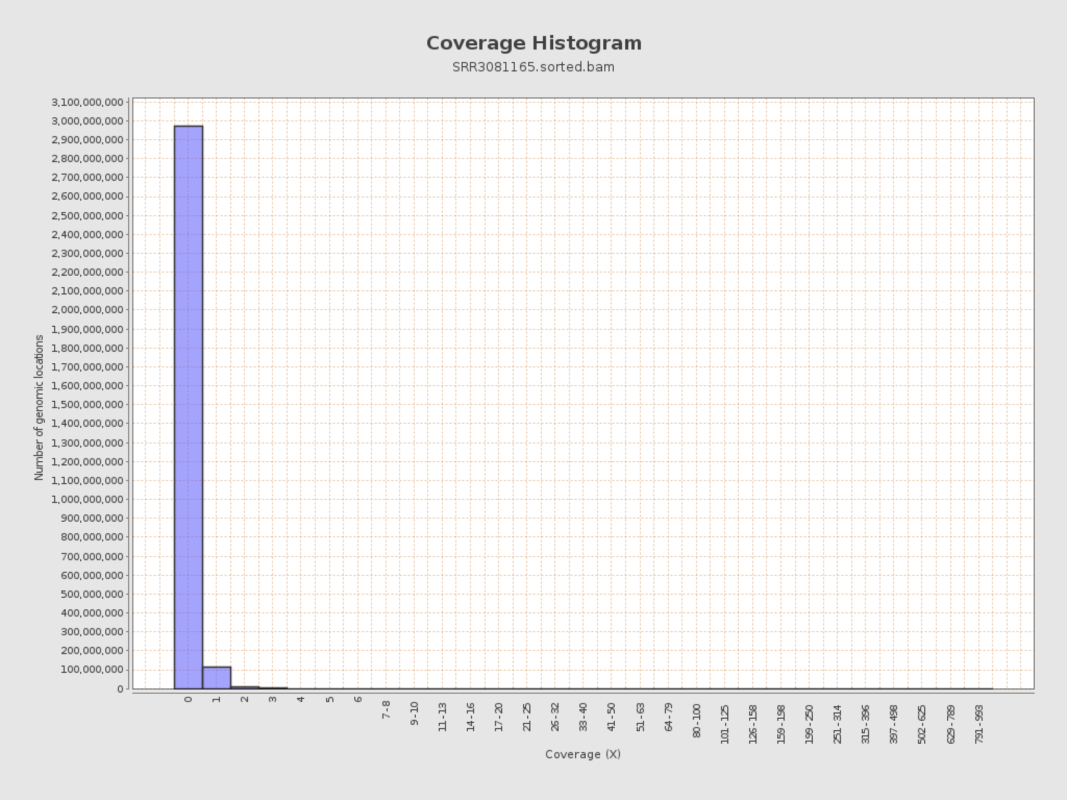
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12631857	0.0507	0.7715
chr2	243199373	13199919	0.0543	0.494
chr3	198022430	9382643	0.0474	0.2405
chr4	191154276	10031073	0.0525	0.2662
chr5	180915260	8672400	0.0479	0.2451
chr6	171115067	7335210	0.0429	0.2976
chr7	159138663	7846622	0.0493	0.5355

chr8	146364022	7865384	0.0537	0.6546
chr9	141213431	5762437	0.0408	0.4019
chr10	135534747	6878670	0.0508	0.4005
chr11	135006516	6067653	0.0449	0.3651
chr12	133851895	6677881	0.0499	0.2538
chr13	115169878	5132477	0.0446	0.2328
chr14	107349540	4491851	0.0418	0.2617
chr15	102531392	3946529	0.0385	0.2235
chr16	90354753	3926091	0.0435	0.2767
chr17	81195210	3789173	0.0467	0.286
chr18	78077248	4027116	0.0516	0.8006
chr19	59128983	2612651	0.0442	0.5652
chr20	63025520	2850246	0.0452	0.2533
chr21	48129895	1679946	0.0349	0.2329
chr22	51304566	1357127	0.0265	0.1781
chrMT	16571	16201	0.9777	1.2059
chrX	155270560	8036385	0.0518	0.2958
chrY	59373566	340660	0.0057	0.13

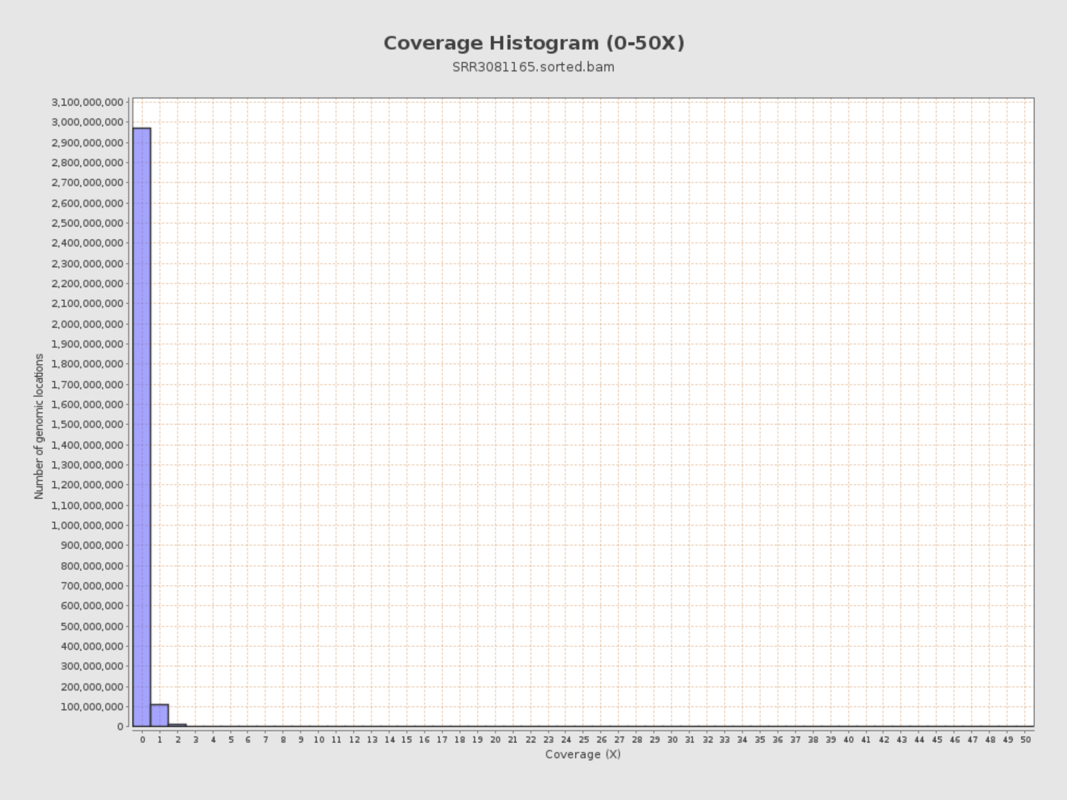
3. Results : Coverage across reference



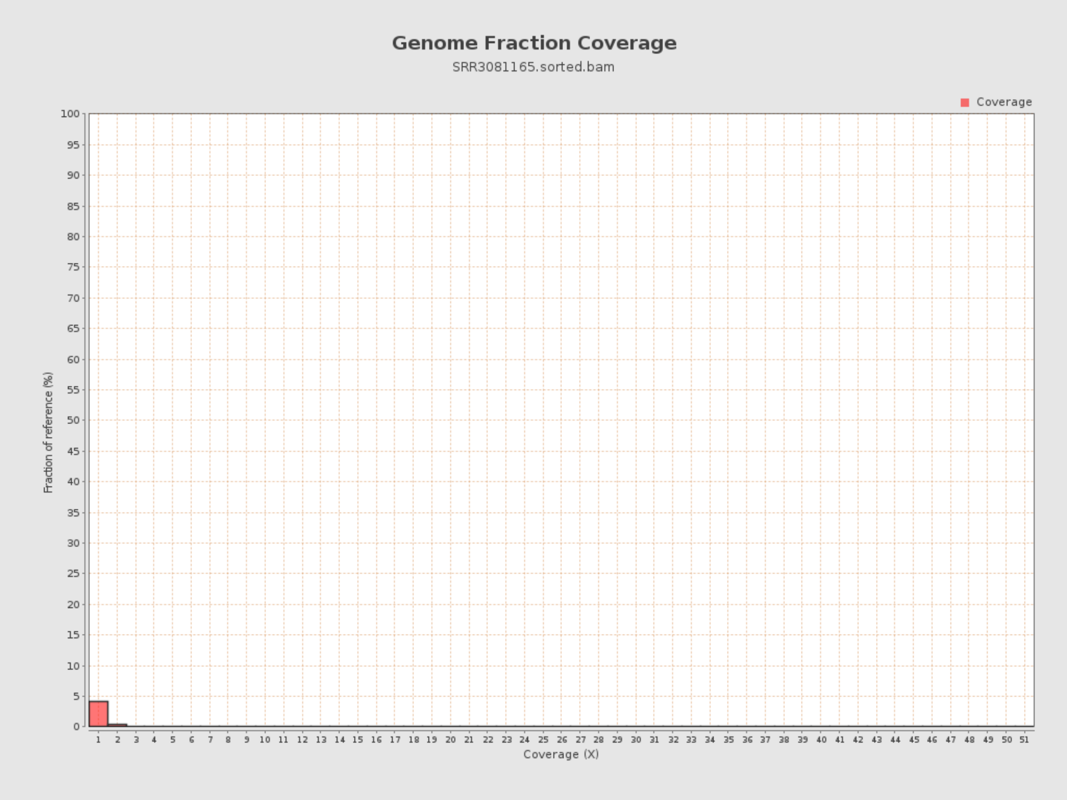
4. Results : Coverage Histogram



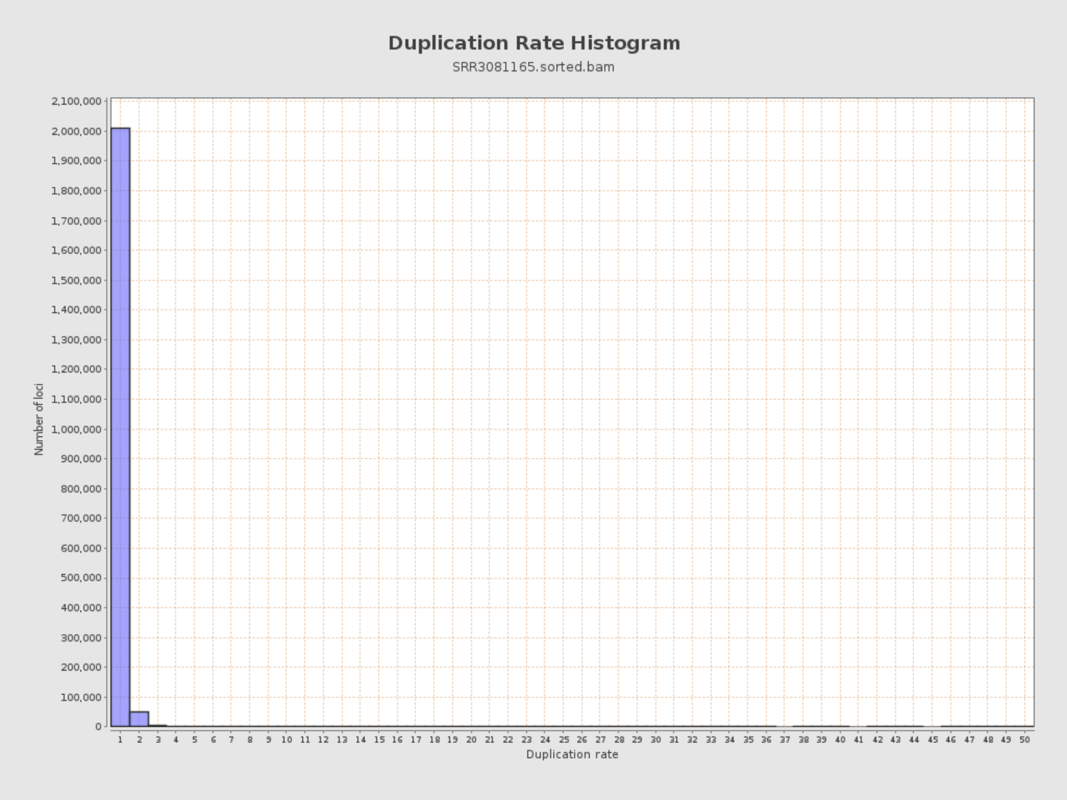
5. Results : Coverage Histogram (0-50X)



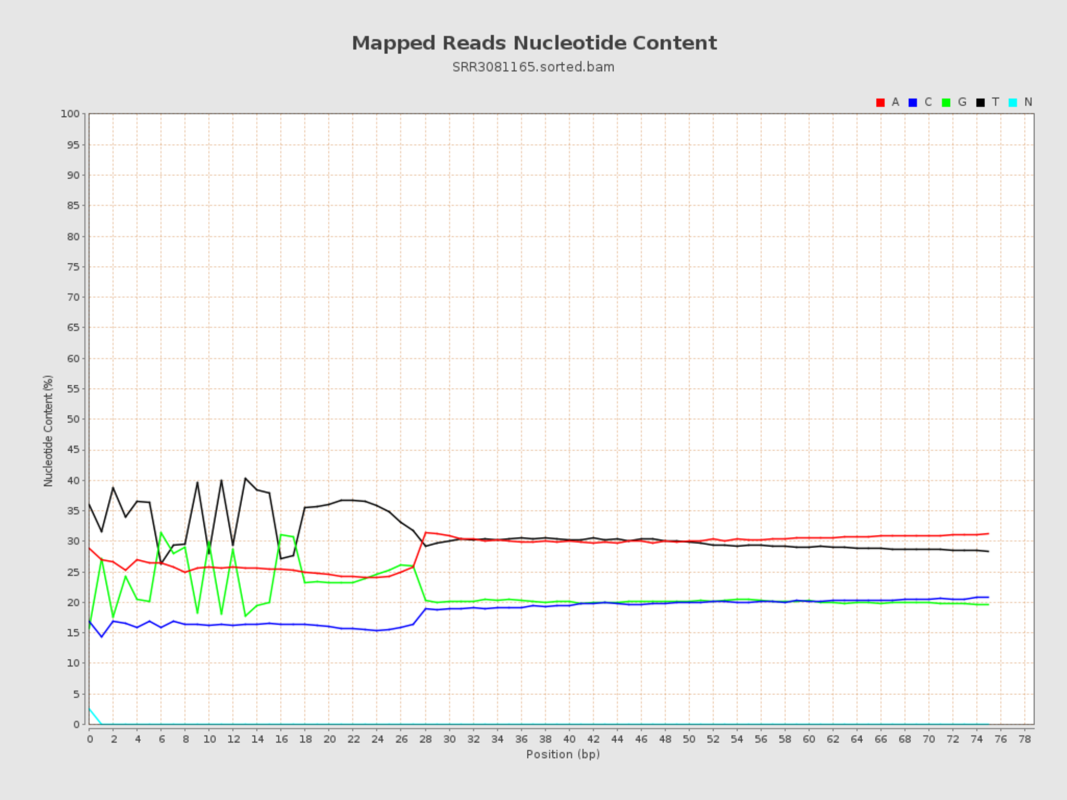
6. Results : Genome Fraction Coverage



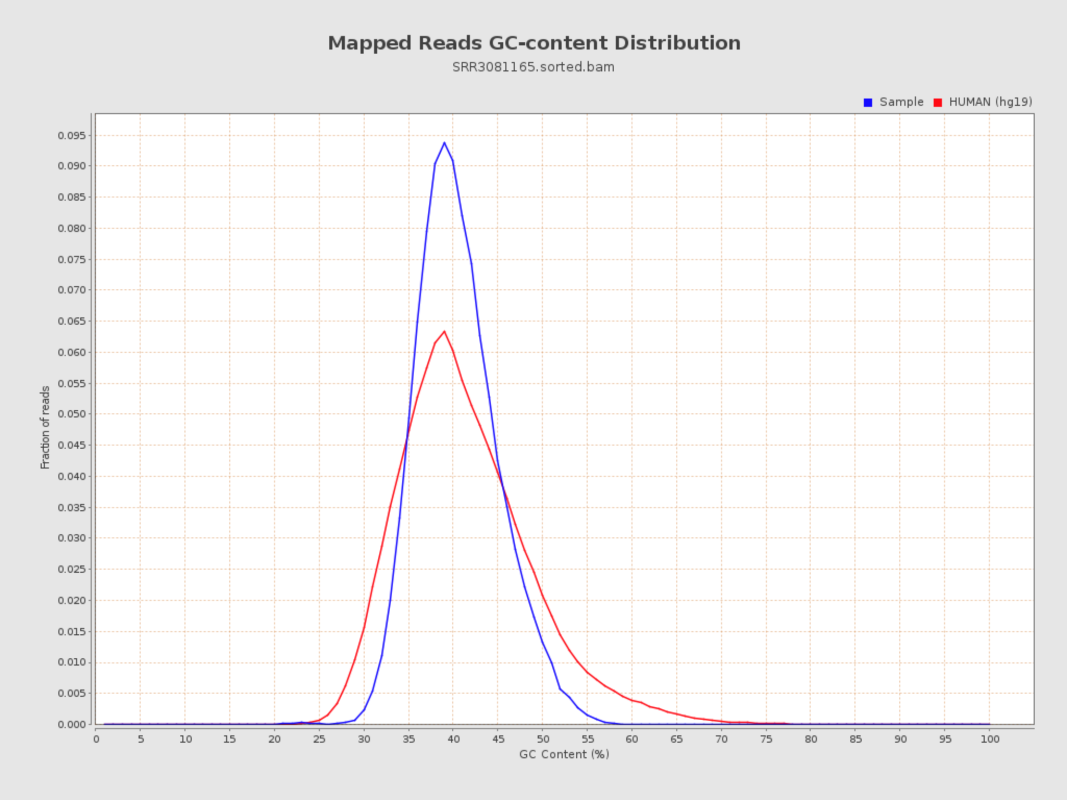
7. Results : Duplication Rate Histogram



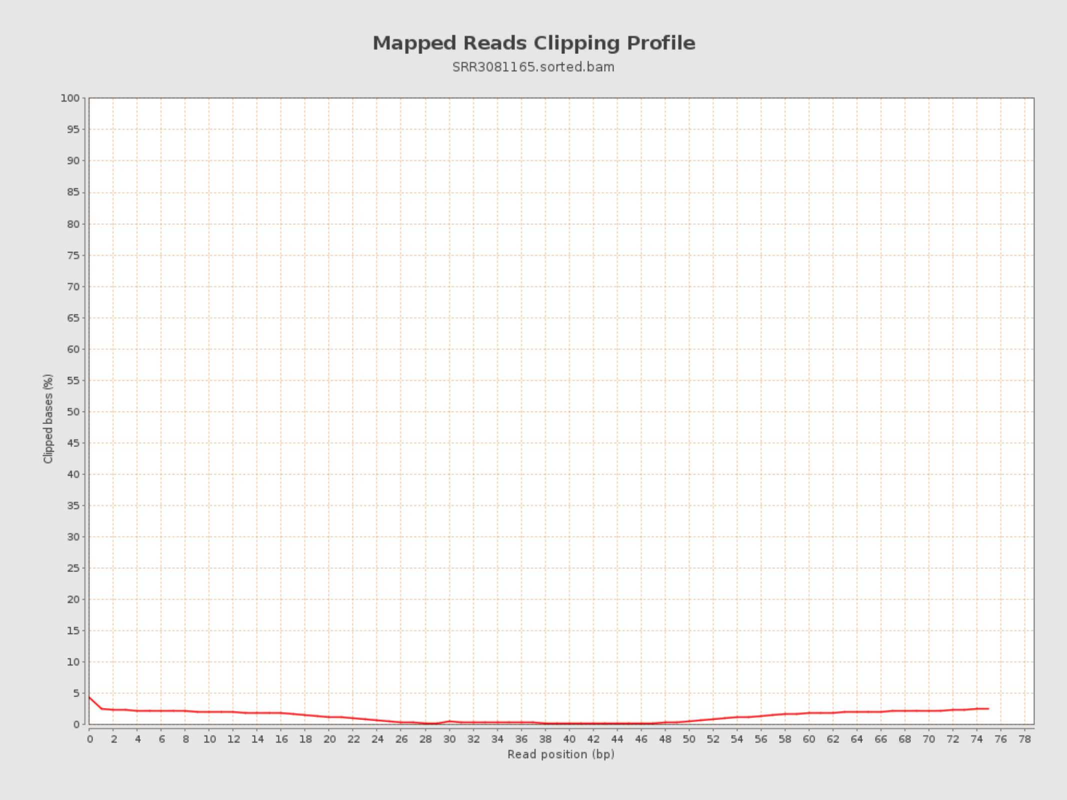
8. Results : Mapped Reads Nucleotide Content



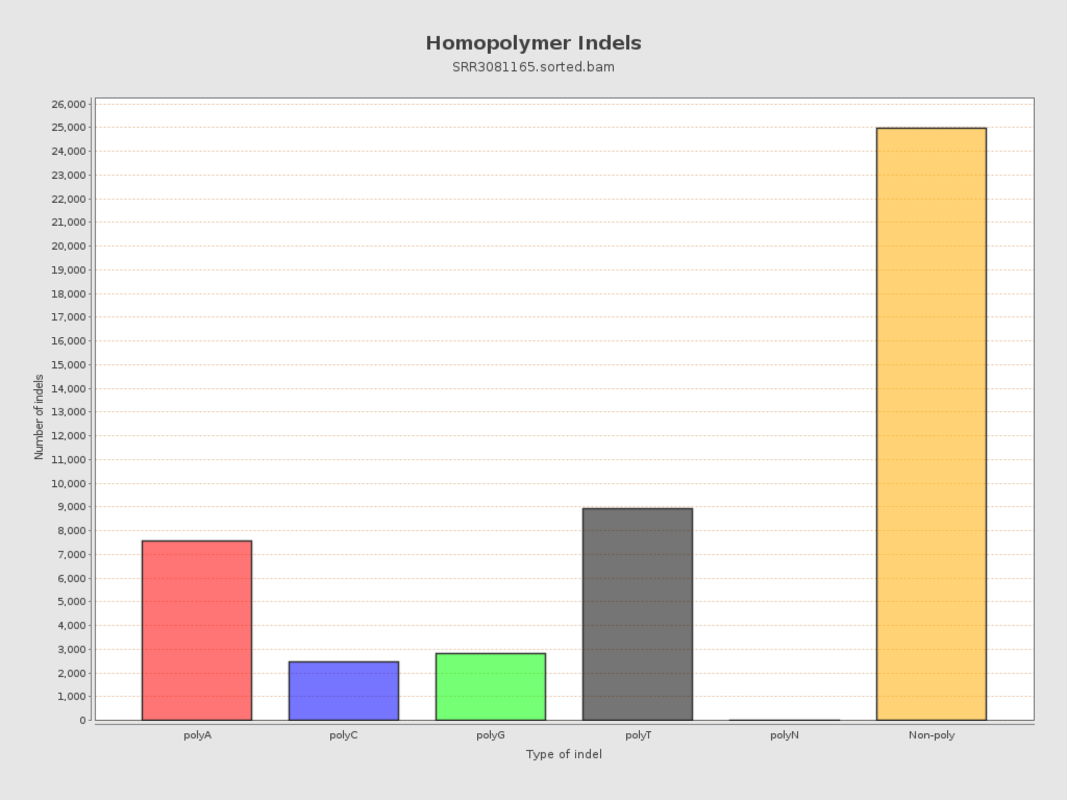
9. Results : Mapped Reads GC-content Distribution



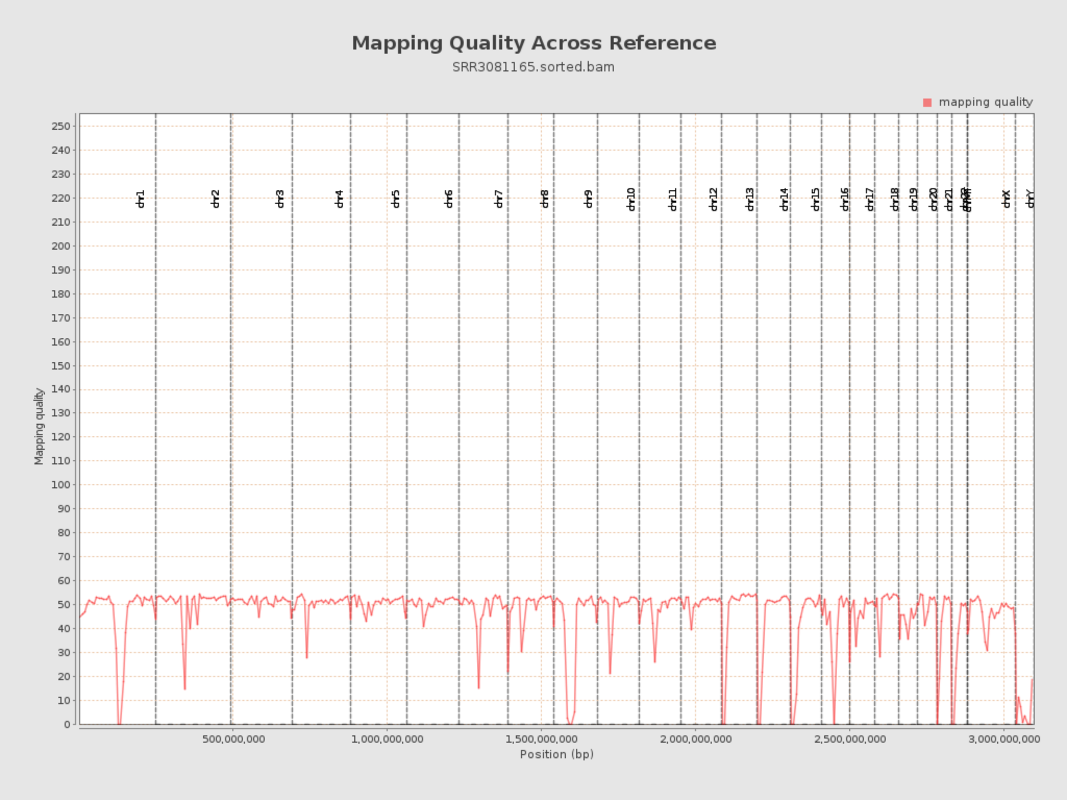
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram