Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:31:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084801.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_SRR3084801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:31:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,587,073
Mapped reads	1,465,223 / 92.32%
Unmapped reads	121,850 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,152 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	59,775 / 3.77%
Duplication rate	3.44%
Clipped reads	574,720 / 36.21%

2.2. ACGT Content

Number/percentage of A's	27,985,989 / 28.14%
Number/percentage of C's	18,175,441 / 18.28%
Number/percentage of T's	31,878,585 / 32.05%
Number/percentage of G's	21,395,901 / 21.51%
Number/percentage of N's	13,921 / 0.01%
GC Percentage	39.79%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.2613

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Mismatches and indels

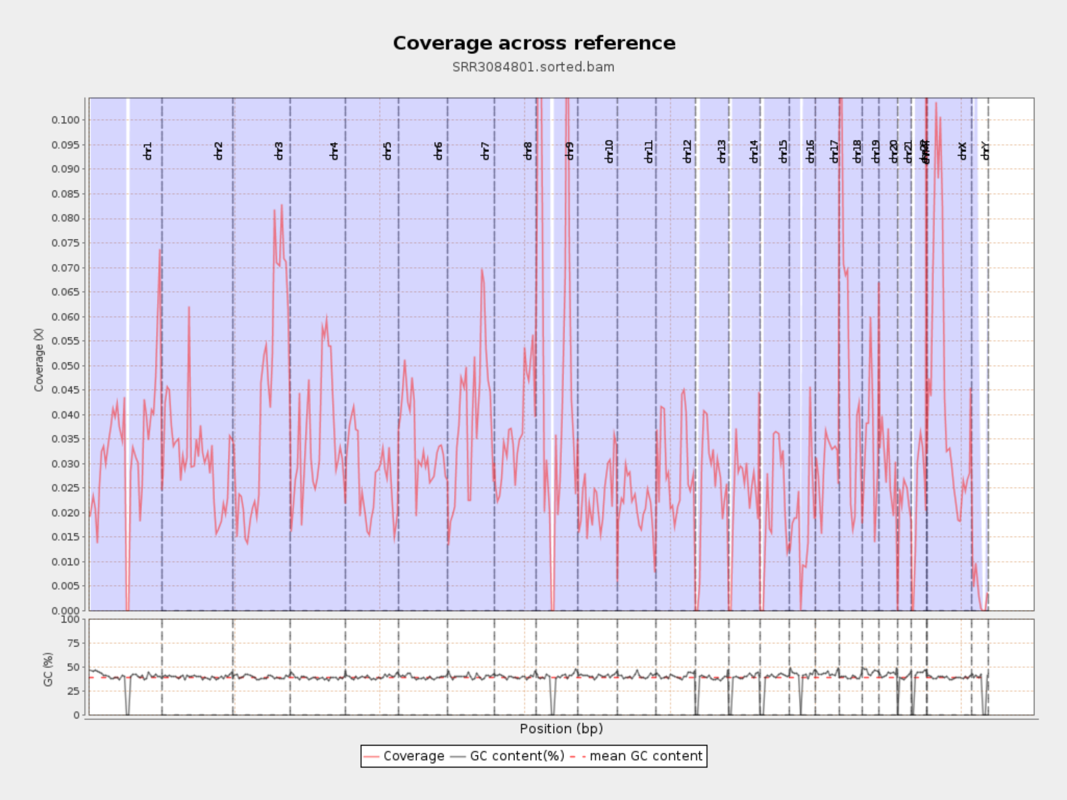
General error rate	0.78%
Mismatches	759,344
Insertions	8,532
Mapped reads with at least one insertion	0.58%
Deletions	23,812
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.83%

2.6. Chromosome stats

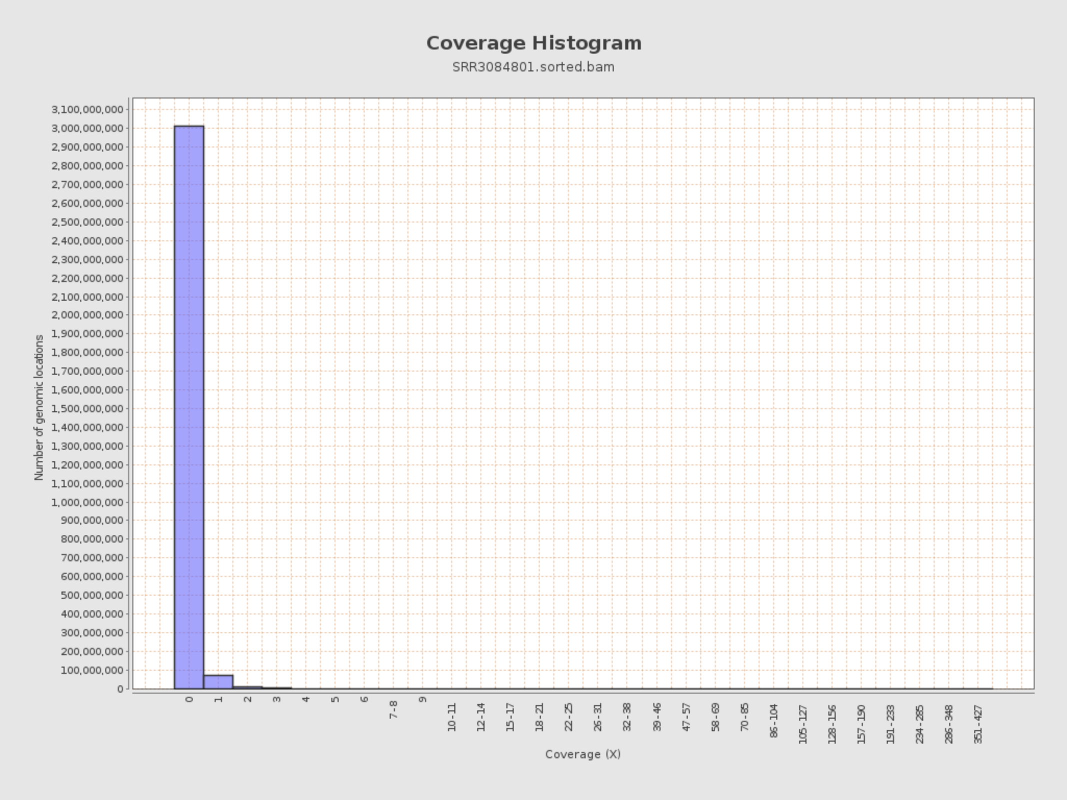
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8224577	0.033	0.344
chr2	243199373	7661861	0.0315	0.3272
chr3	198022430	8314517	0.042	0.2351
chr4	191154276	6763379	0.0354	0.2176
chr5	180915260	4882035	0.027	0.1893
chr6	171115067	5863087	0.0343	0.2243
chr7	159138663	6233992	0.0392	0.3048

chr8	146364022	5363642	0.0366	0.3045
chr9	141213431	7264674	0.0514	0.3387
chr10	135534747	3143802	0.0232	0.1913
chr11	135006516	2815849	0.0209	0.196
chr12	133851895	3948764	0.0295	0.2001
chr13	115169878	2819618	0.0245	0.1789
chr14	107349540	2474926	0.0231	0.1819
chr15	102531392	2188857	0.0213	0.1722
chr16	90354753	1657732	0.0183	0.1669
chr17	81195210	2480150	0.0305	0.2012
chr18	78077248	4061569	0.052	0.5529
chr19	59128983	2130046	0.036	0.2769
chr20	63025520	1857126	0.0295	0.2004
chr21	48129895	1011528	0.021	0.1716
chr22	51304566	1109978	0.0216	0.1651
chrMT	16571	12838	0.7747	1.0412
chrX	155270560	6987390	0.045	0.256
chrY	59373566	217376	0.0037	0.0776

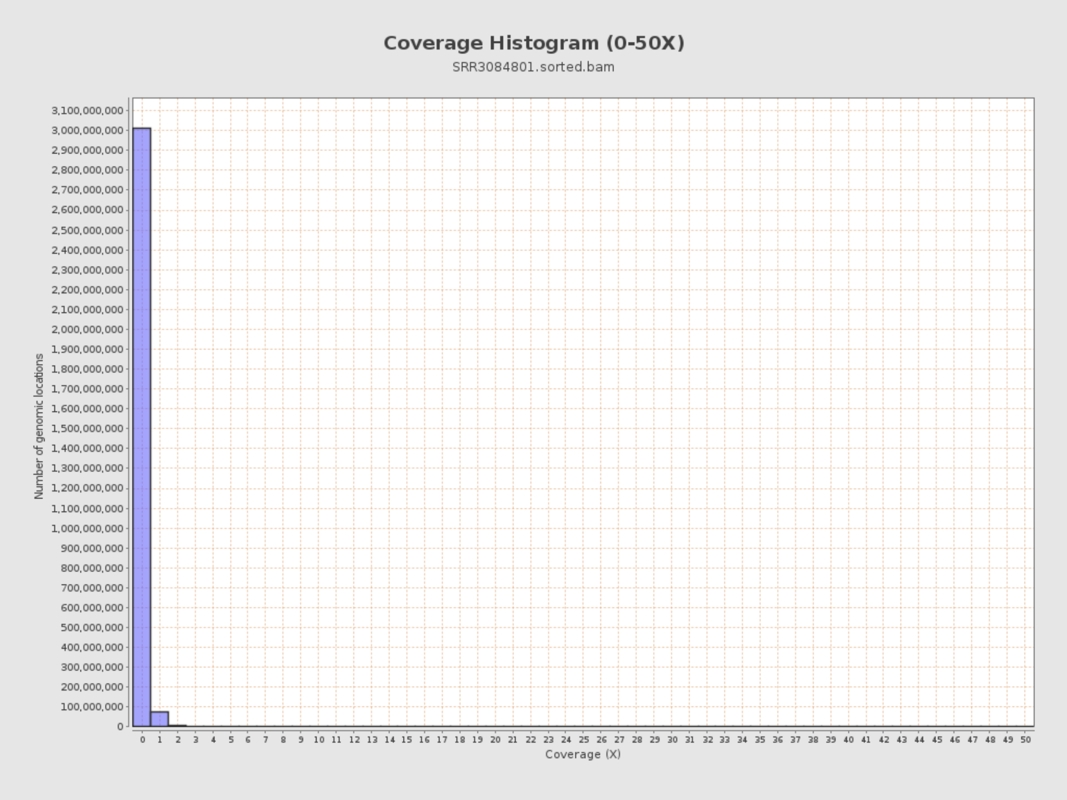
3. Results : Coverage across reference



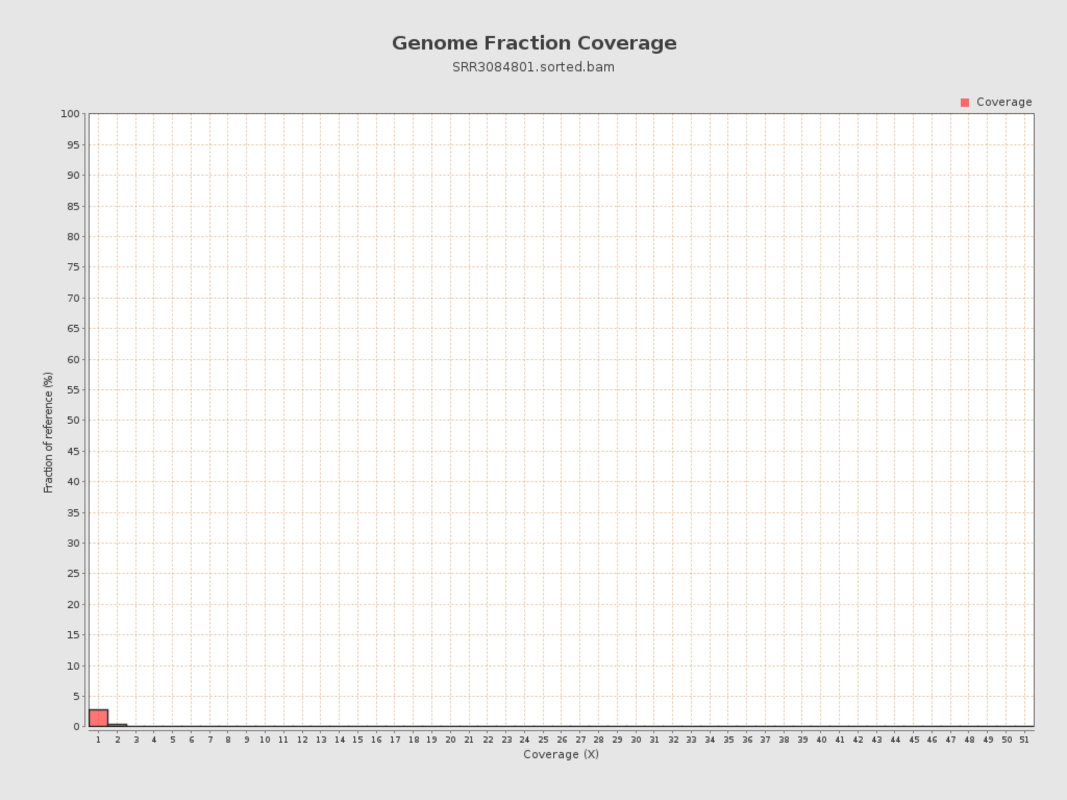
4. Results : Coverage Histogram



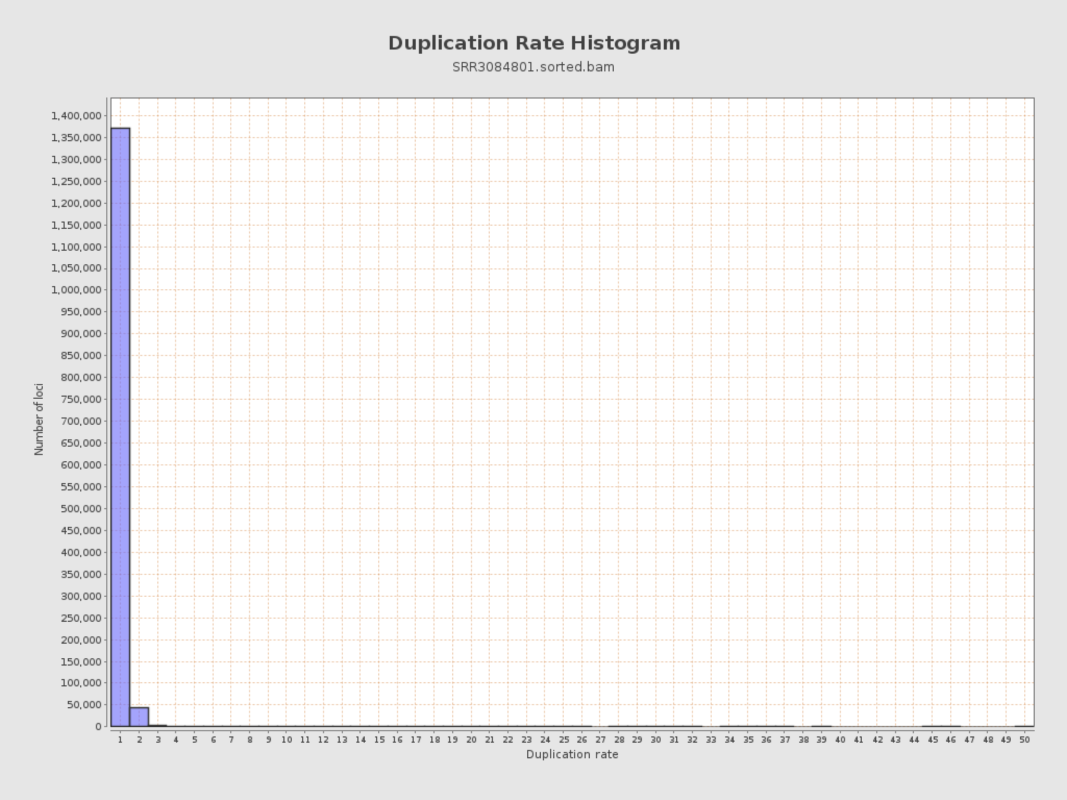
5. Results : Coverage Histogram (0-50X)



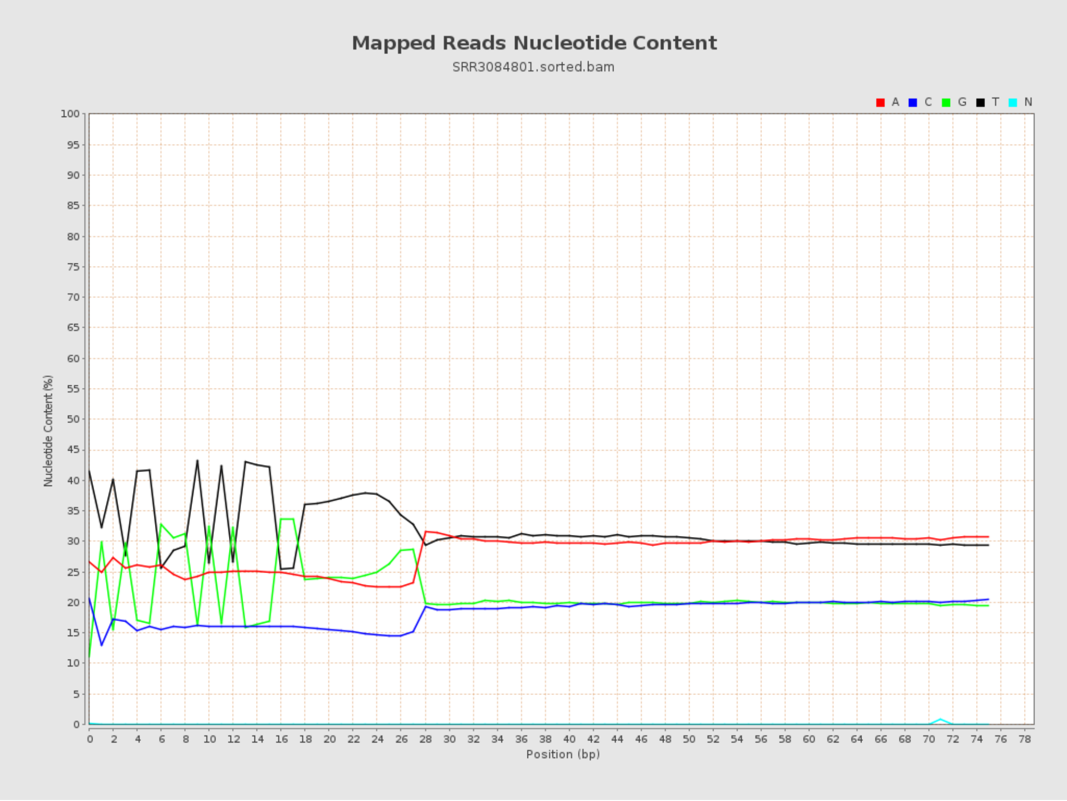
6. Results : Genome Fraction Coverage



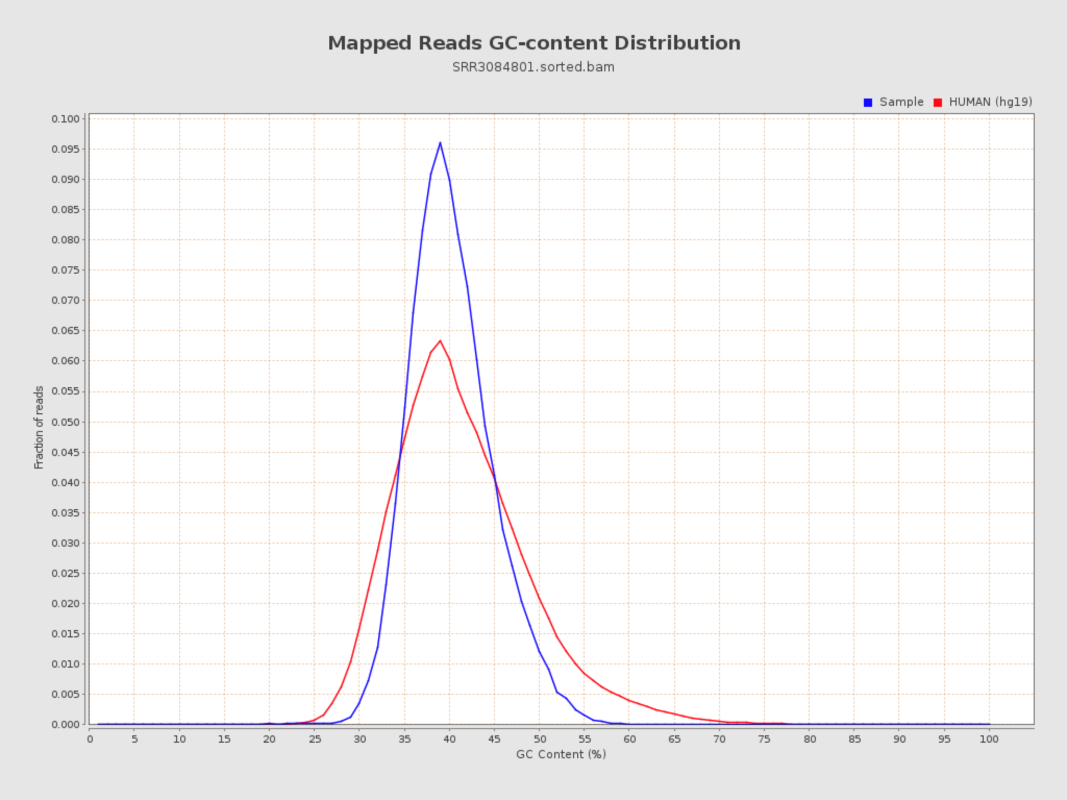
7. Results : Duplication Rate Histogram



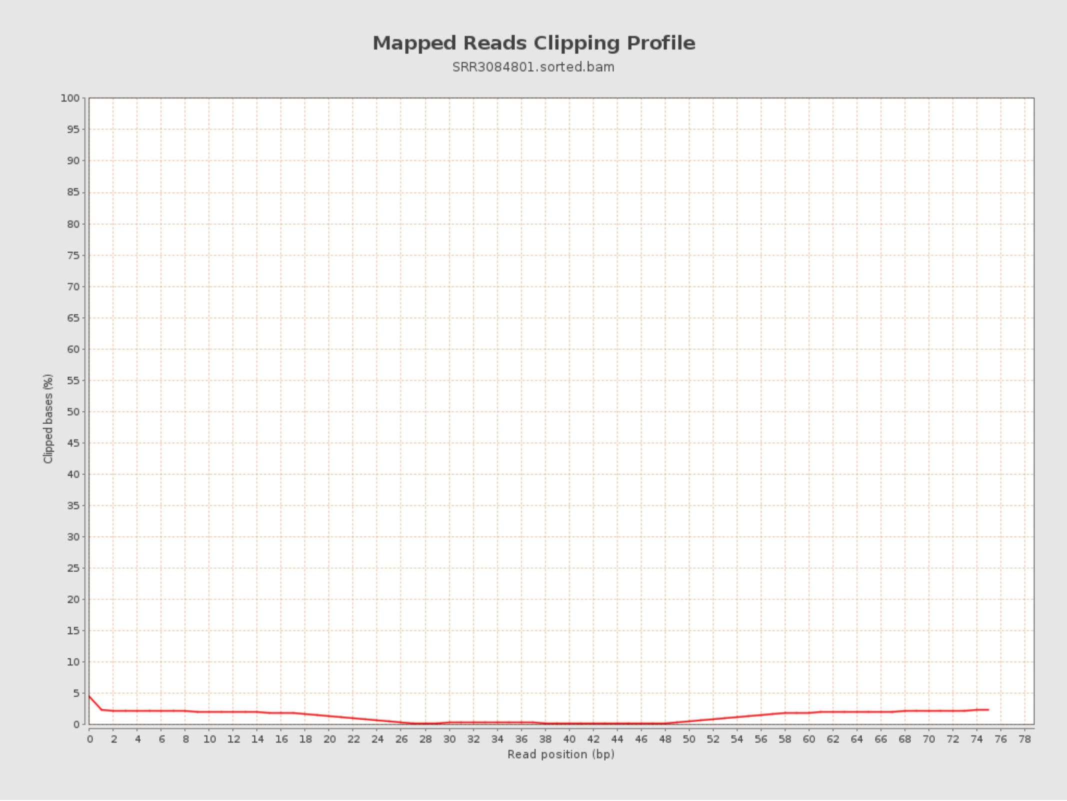
8. Results : Mapped Reads Nucleotide Content



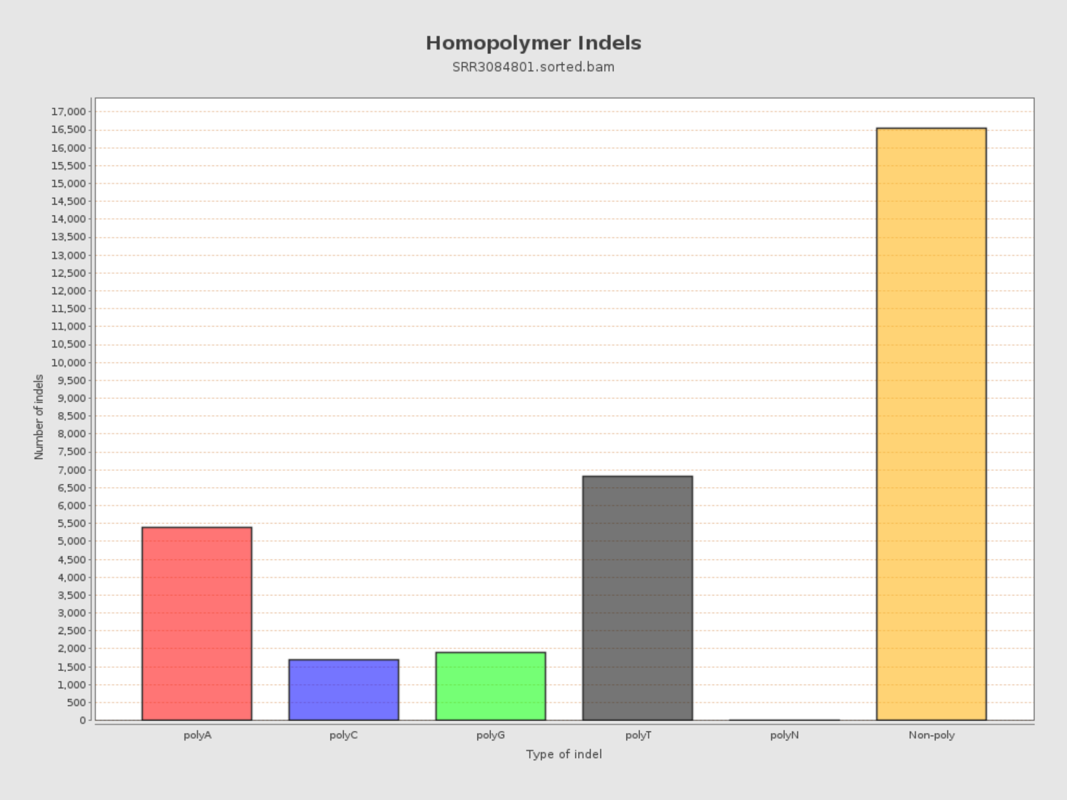
9. Results : Mapped Reads GC-content Distribution



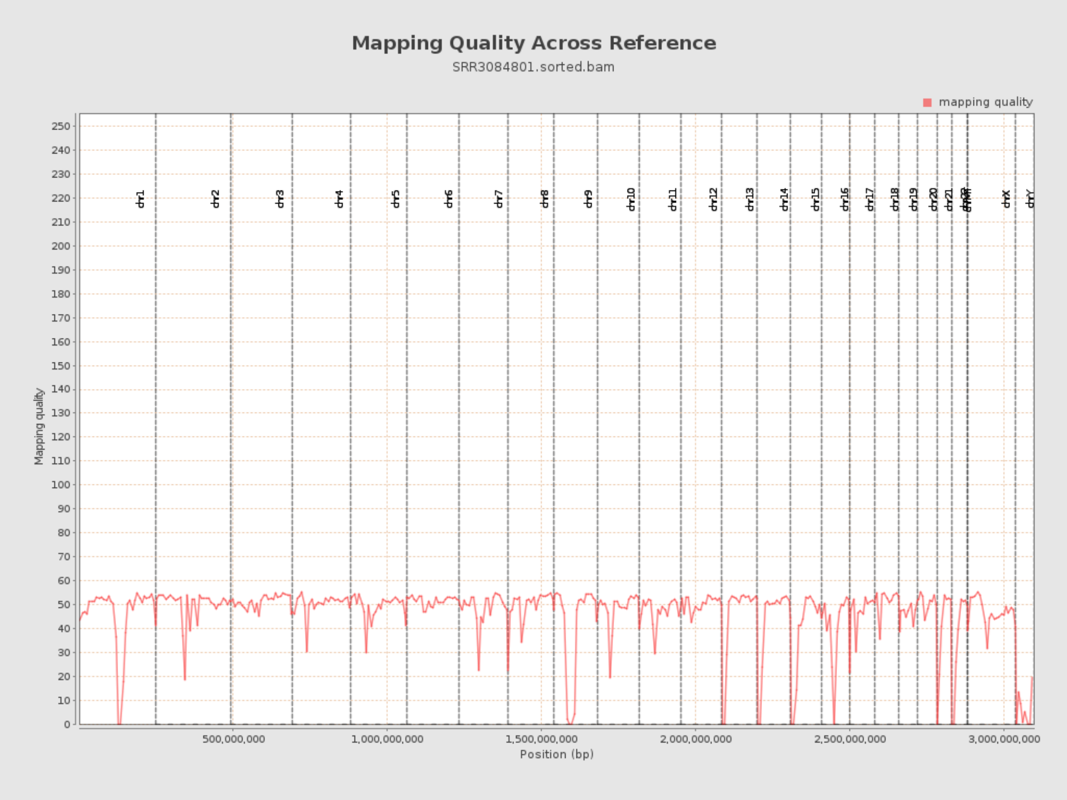
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram