Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:21:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080665.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_SRR3080665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:21:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,264,749
Mapped reads	1,154,560 / 91.29%
Unmapped reads	110,189 / 8.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,954 / 1.1%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	38,701 / 3.06%
Duplication rate	2.94%
Clipped reads	514,632 / 40.69%

2.2. ACGT Content

Number/percentage of A's	21,178,563 / 27.46%
Number/percentage of C's	14,393,816 / 18.66%
Number/percentage of T's	24,226,790 / 31.41%
Number/percentage of G's	17,324,177 / 22.46%
Number/percentage of N's	3,327 / 0%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2025

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

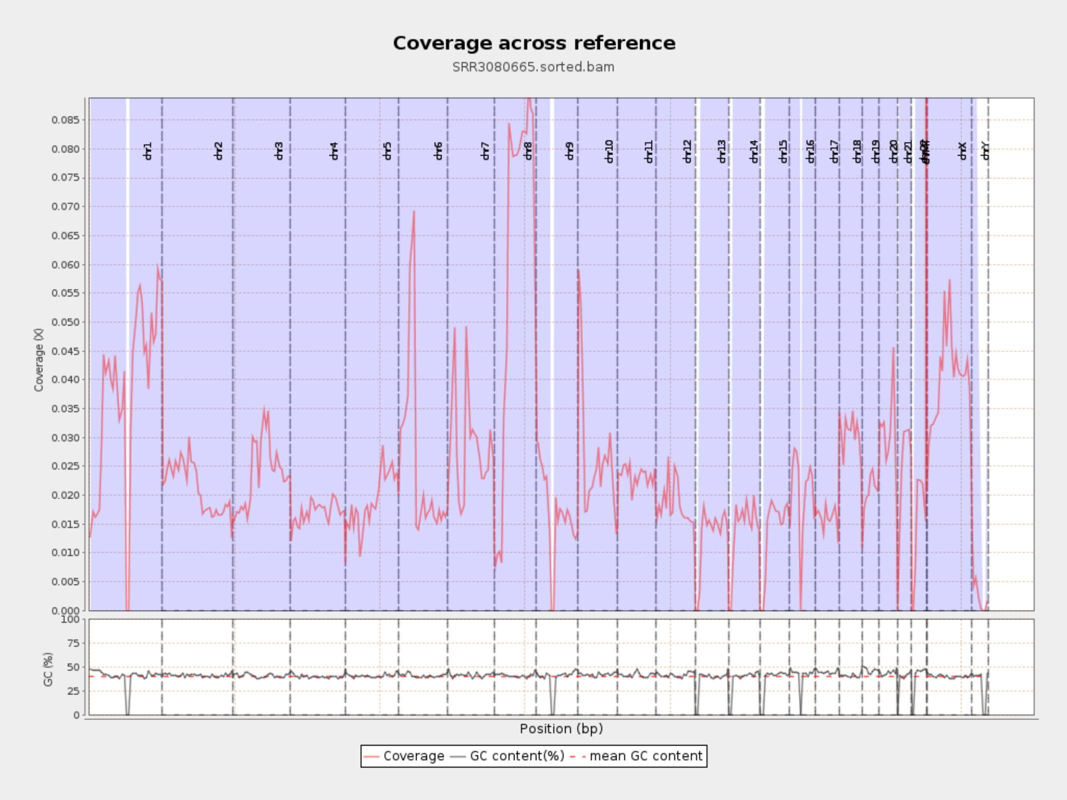
General error rate	0.67%
Mismatches	509,999
Insertions	5,759
Mapped reads with at least one insertion	0.5%
Deletions	17,513
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.84%

2.6. Chromosome stats

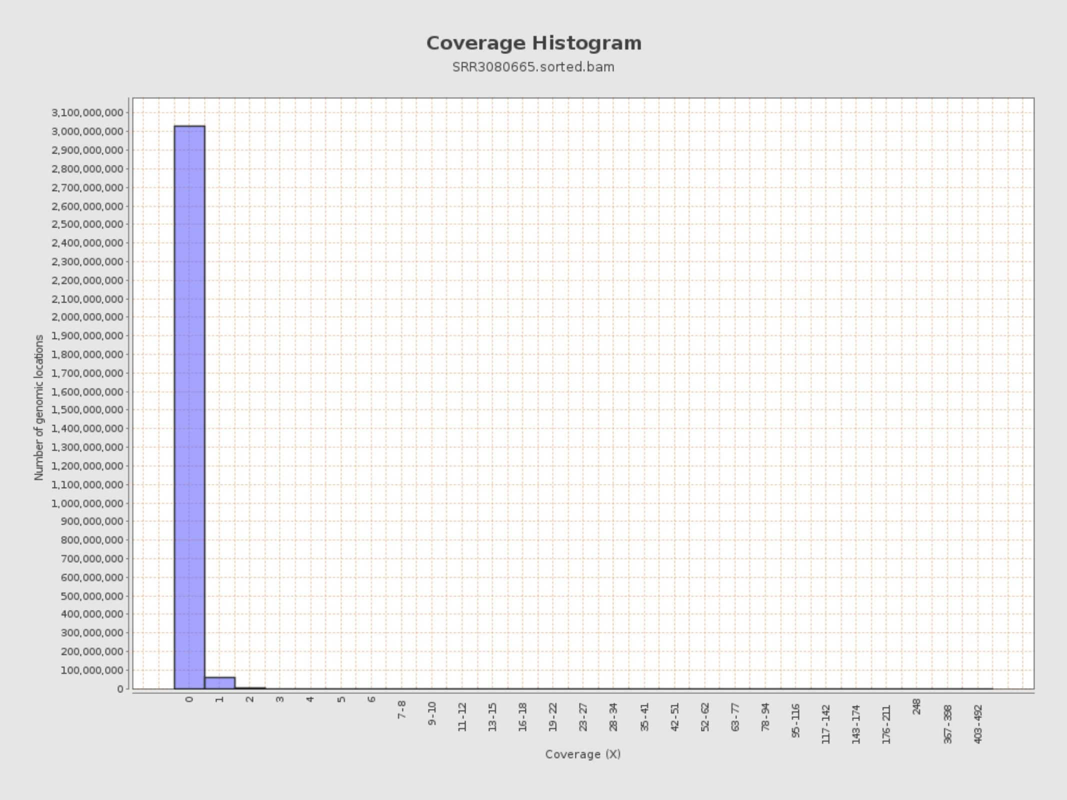
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9312804	0.0374	0.2504
chr2	243199373	5173409	0.0213	0.2679
chr3	198022430	4720730	0.0238	0.1704
chr4	191154276	3255432	0.017	0.1463
chr5	180915260	3469146	0.0192	0.1526
chr6	171115067	4505853	0.0263	0.2038
chr7	159138663	4660617	0.0293	0.3012

chr8	146364022	8991412	0.0614	0.2961
chr9	141213431	2359685	0.0167	0.1633
chr10	135534747	3687779	0.0272	0.1888
chr11	135006516	3139043	0.0233	0.1777
chr12	133851895	2434247	0.0182	0.1496
chr13	115169878	1478545	0.0128	0.1258
chr14	107349540	1489035	0.0139	0.1308
chr15	102531392	1410228	0.0138	0.1336
chr16	90354753	1851361	0.0205	0.1609
chr17	81195210	1299902	0.016	0.1421
chr18	78077248	2402154	0.0308	0.2401
chr19	59128983	1228494	0.0208	0.185
chr20	63025520	1955038	0.031	0.1959
chr21	48129895	1160100	0.0241	0.1733
chr22	51304566	747128	0.0146	0.1322
chrMT	16571	11513	0.6948	0.8982
chrX	155270560	6247188	0.0402	0.2299
chrY	59373566	164167	0.0028	0.0613

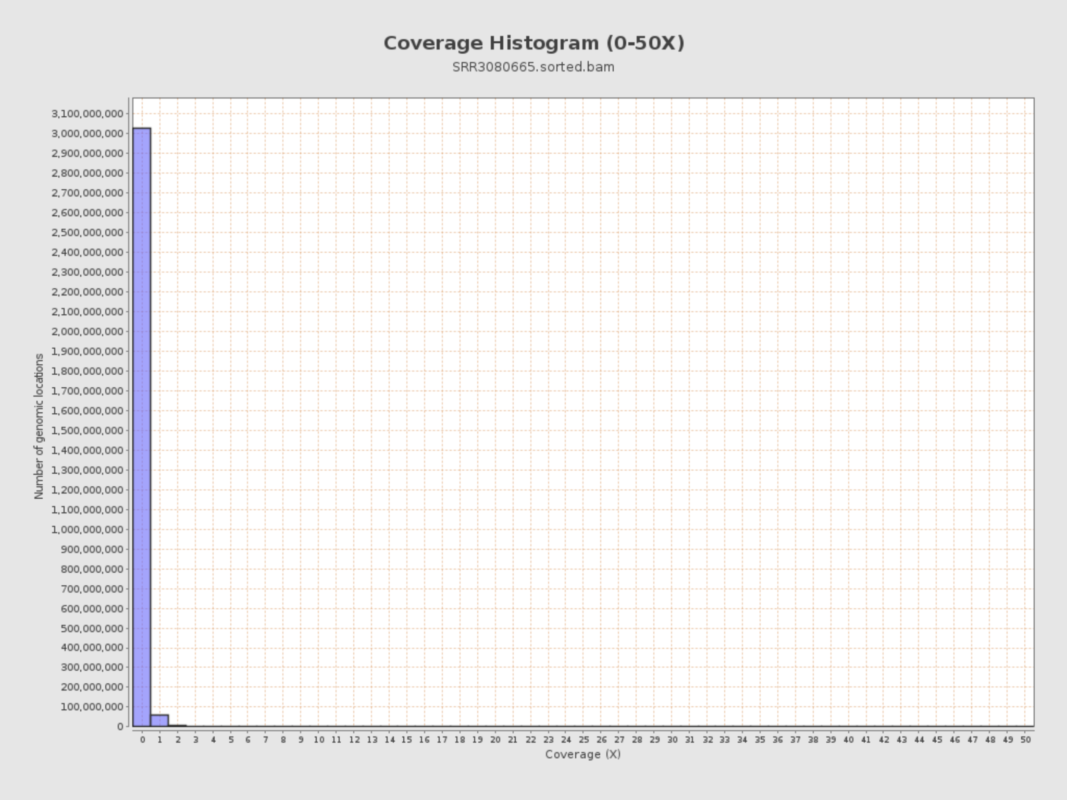
3. Results : Coverage across reference



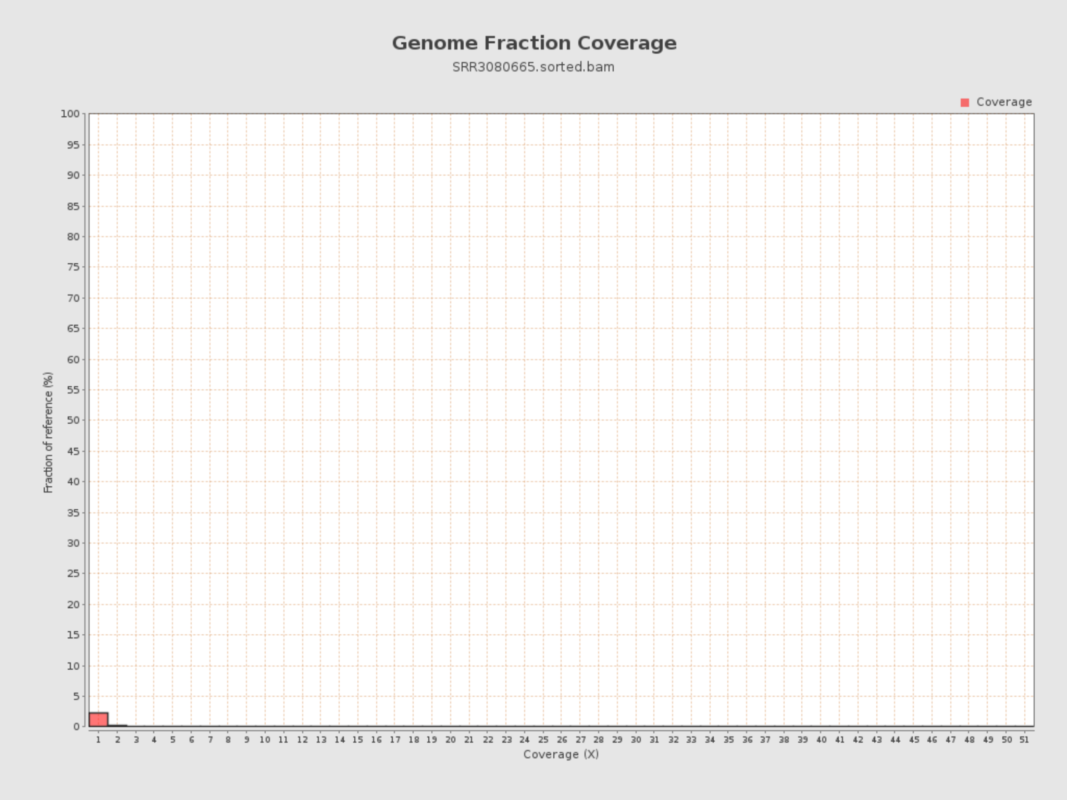
4. Results : Coverage Histogram



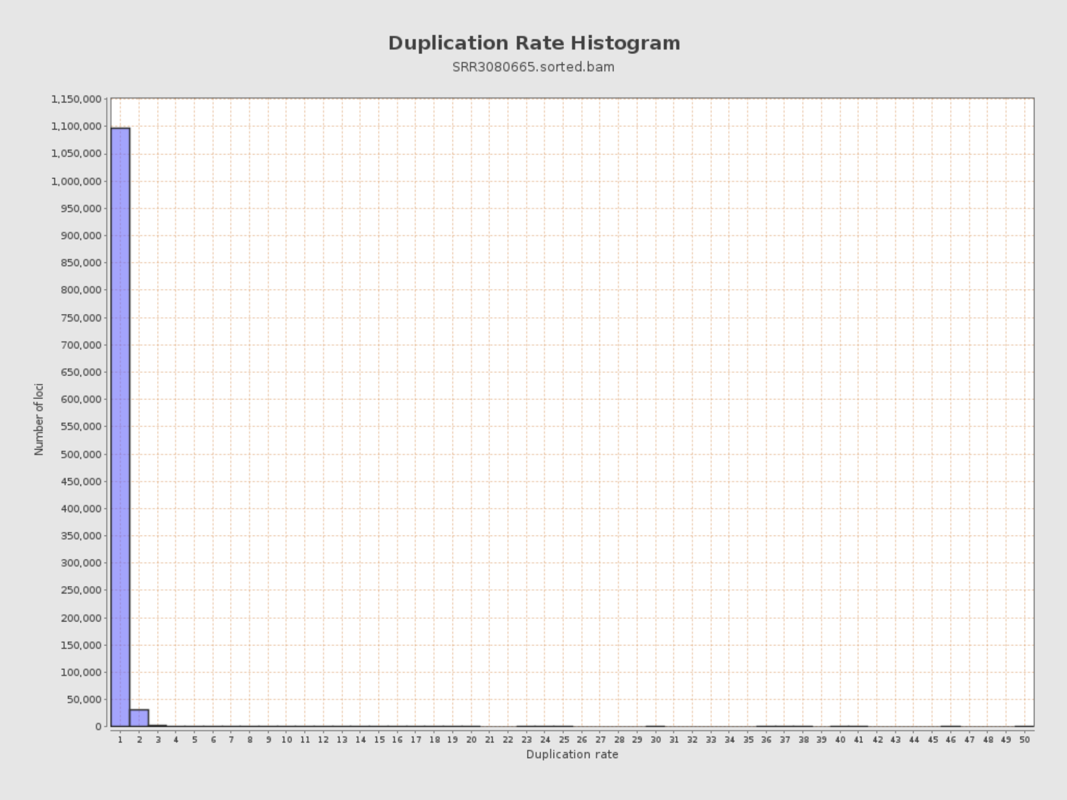
5. Results : Coverage Histogram (0-50X)



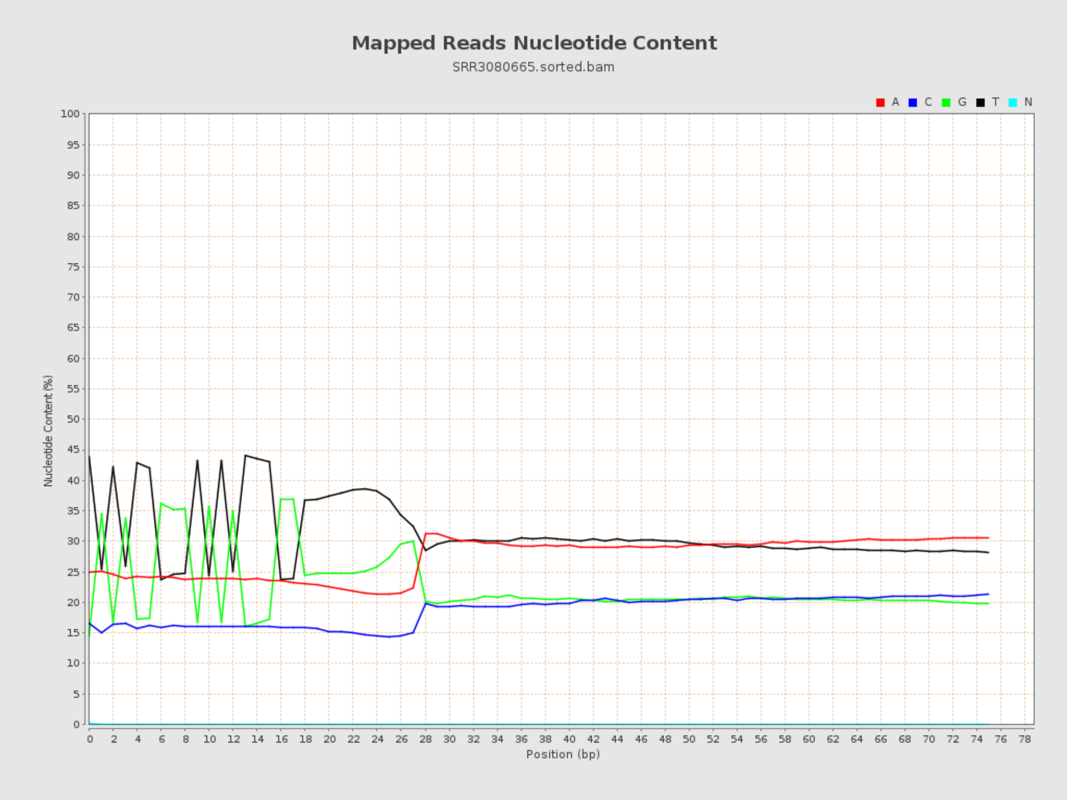
6. Results : Genome Fraction Coverage



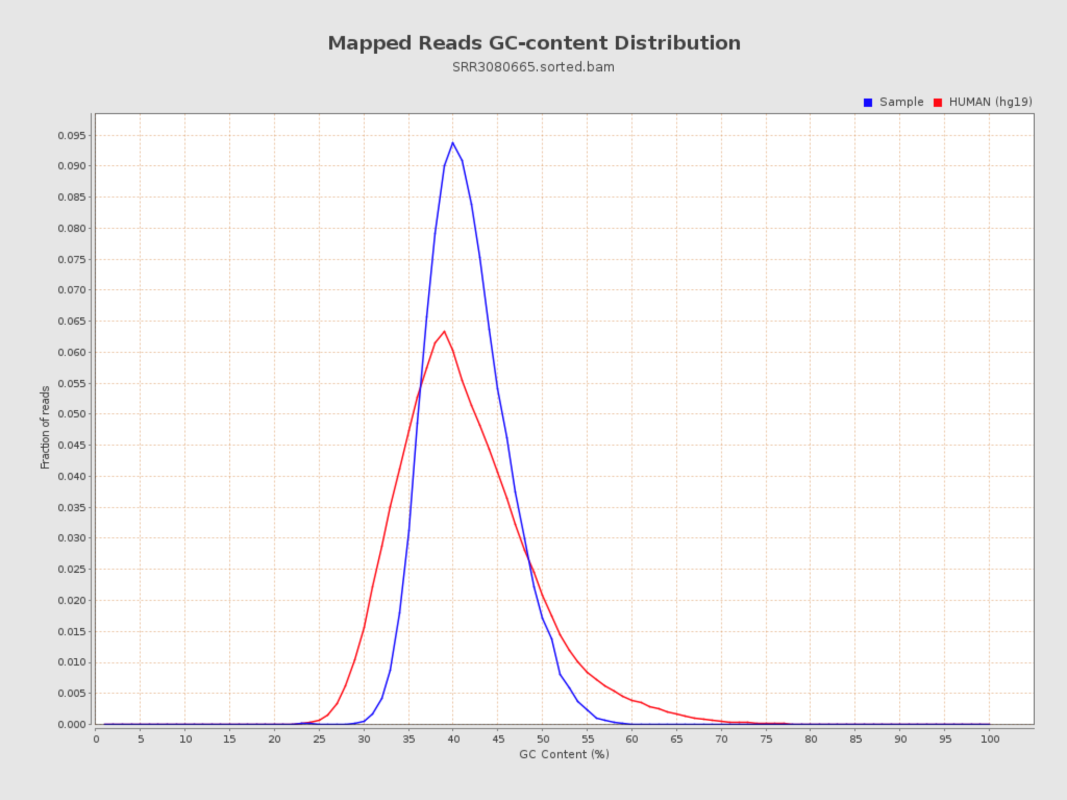
7. Results : Duplication Rate Histogram



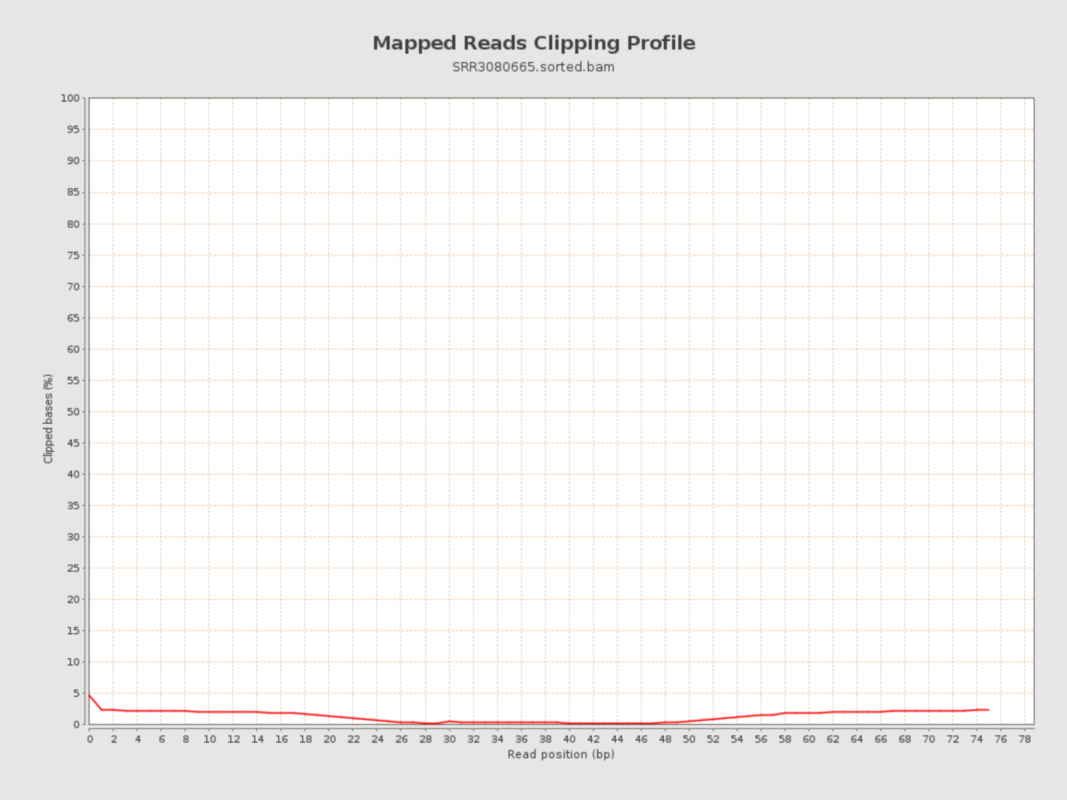
8. Results : Mapped Reads Nucleotide Content



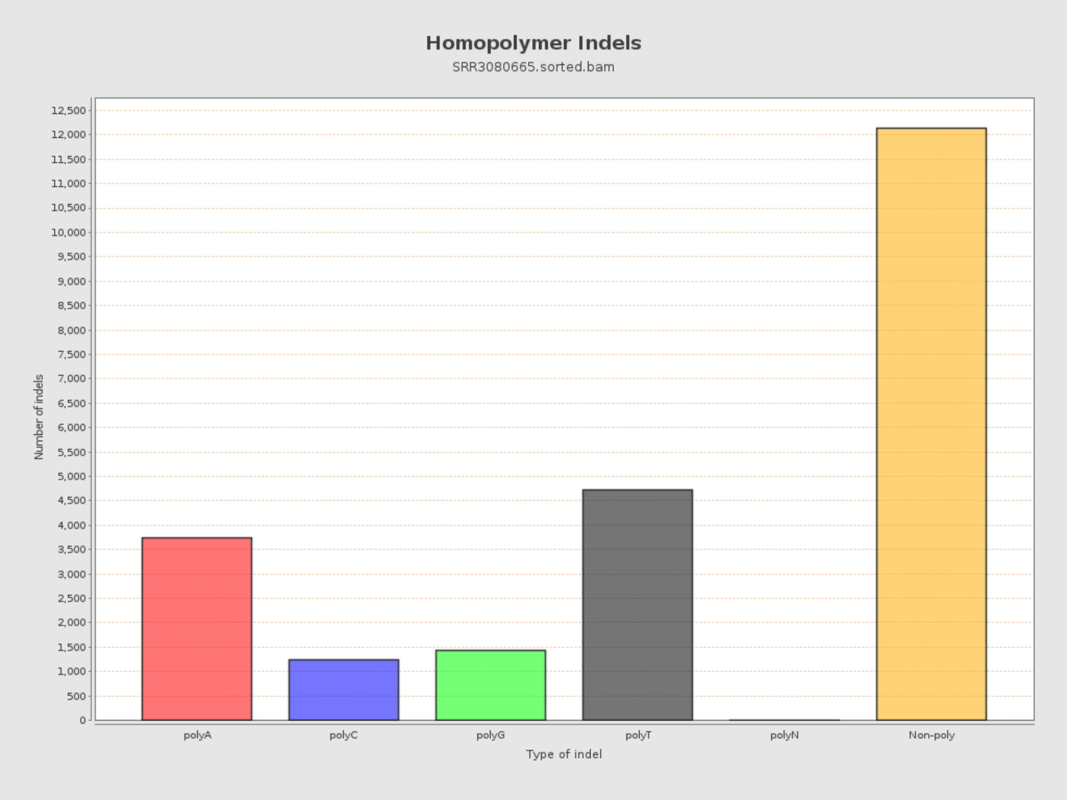
9. Results : Mapped Reads GC-content Distribution



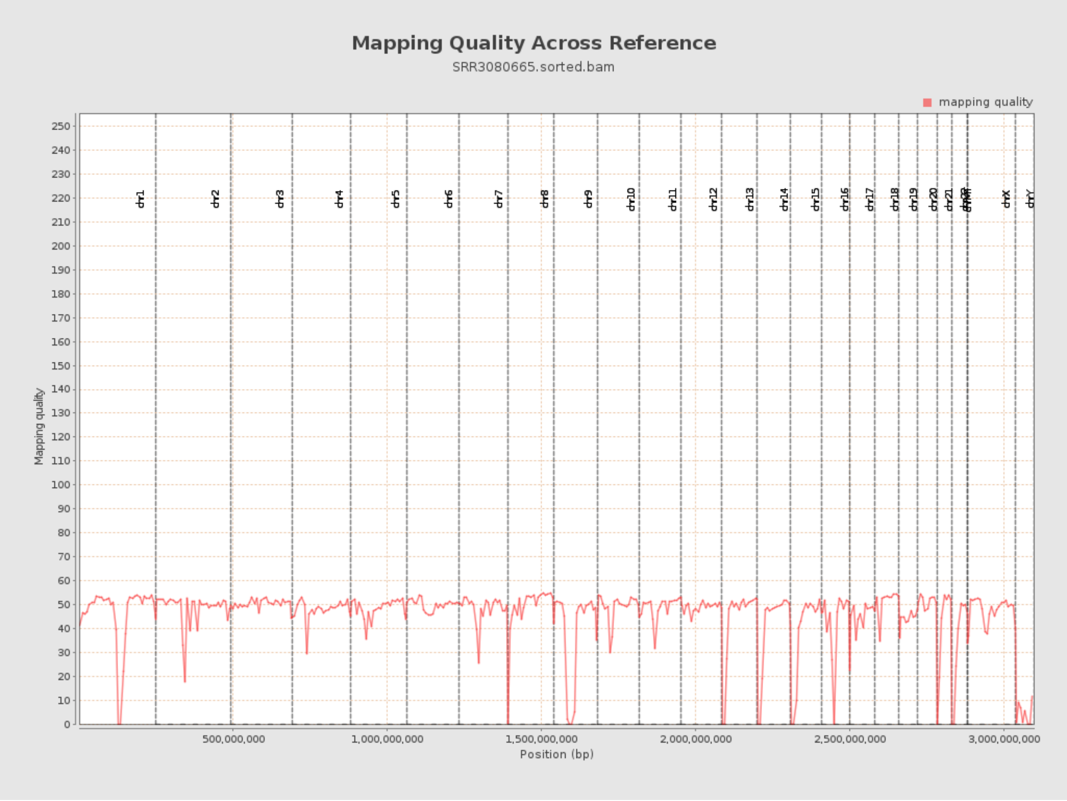
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram