Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:44:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080667.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_SRR3080667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080667.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,662,219
Mapped reads	1,499,214 / 90.19%
Unmapped reads	163,005 / 9.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,415 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	60,049 / 3.61%
Duplication rate	3.34%
Clipped reads	717,678 / 43.18%

2.2. ACGT Content

Number/percentage of A's	26,481,997 / 26.82%
Number/percentage of C's	18,433,953 / 18.67%
Number/percentage of T's	31,040,183 / 31.44%
Number/percentage of G's	22,773,587 / 23.07%
Number/percentage of N's	4,442 / 0%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.2758

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

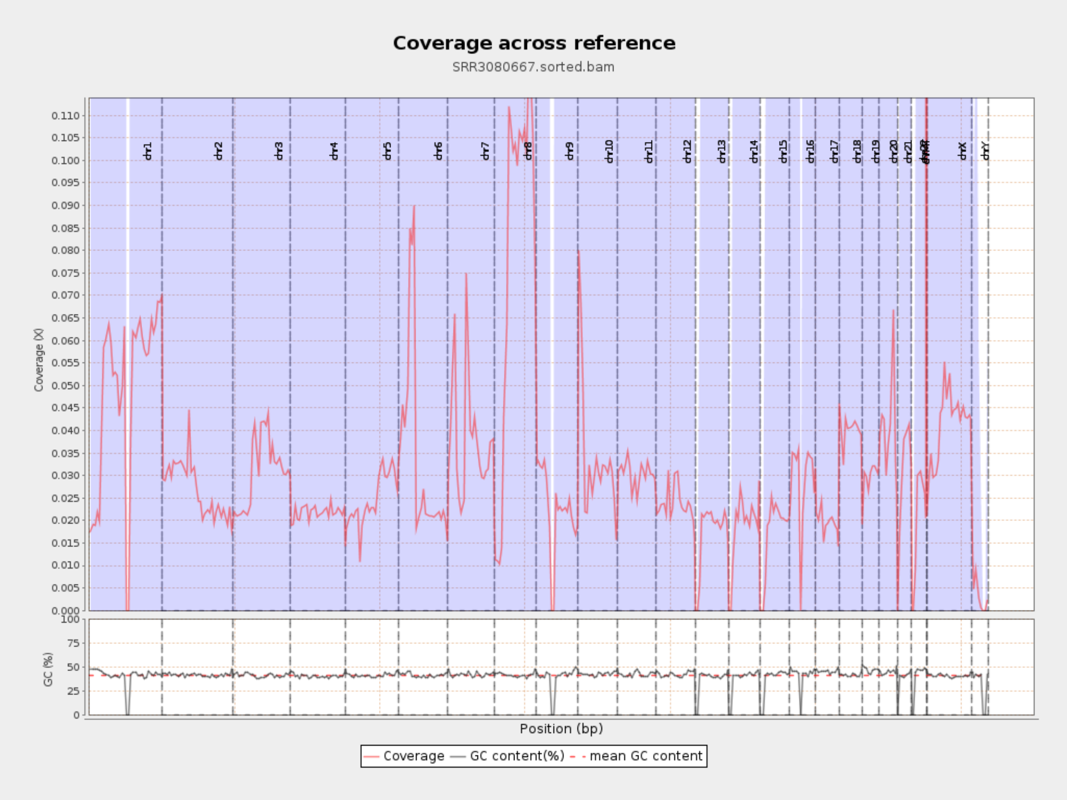
General error rate	0.7%
Mismatches	681,560
Insertions	7,314
Mapped reads with at least one insertion	0.48%
Deletions	22,830
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.17%

2.6. Chromosome stats

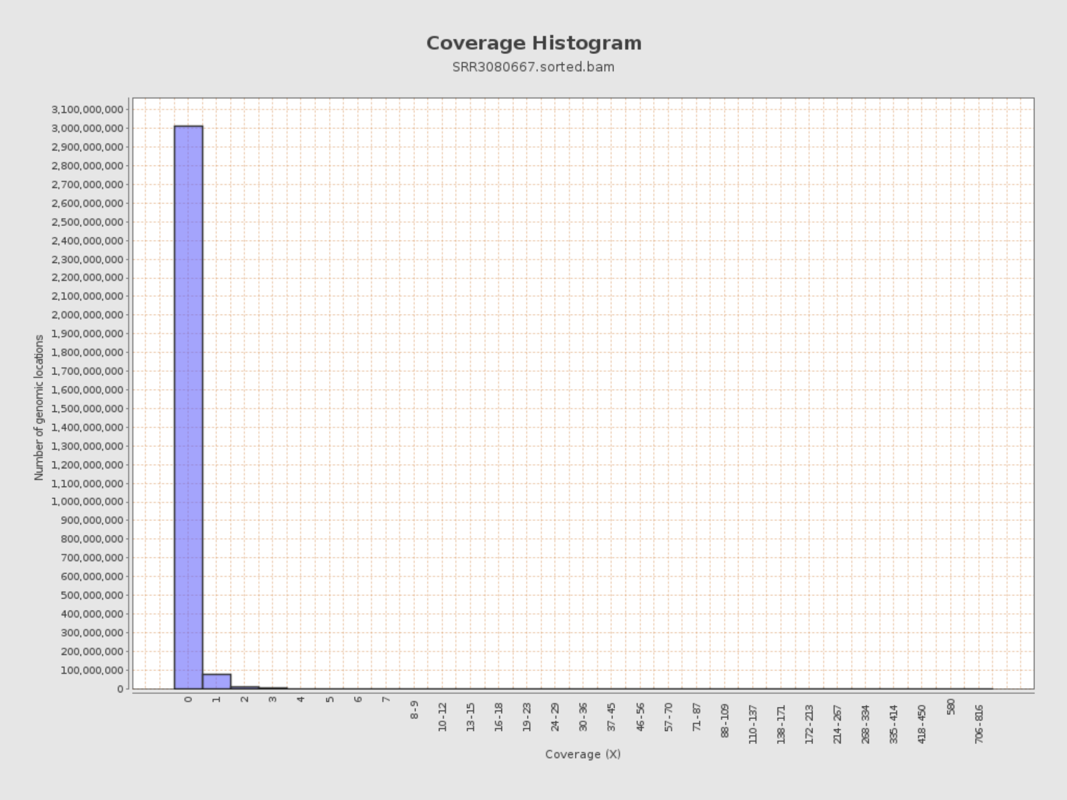
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12046381	0.0483	0.3726
chr2	243199373	6549190	0.0269	0.3964
chr3	198022430	6153808	0.0311	0.1966
chr4	191154276	4173721	0.0218	0.1677
chr5	180915260	4481356	0.0248	0.175
chr6	171115067	5881249	0.0344	0.2673
chr7	159138663	6212137	0.039	0.5629

chr8	146364022	11694782	0.0799	0.3561
chr9	141213431	3133827	0.0222	0.2045
chr10	135534747	4705759	0.0347	0.2292
chr11	135006516	4082309	0.0302	0.2095
chr12	133851895	3184409	0.0238	0.1731
chr13	115169878	1979342	0.0172	0.1469
chr14	107349540	1950733	0.0182	0.156
chr15	102531392	1750084	0.0171	0.1552
chr16	90354753	2619225	0.029	0.1953
chr17	81195210	1582242	0.0195	0.1629
chr18	78077248	3144229	0.0403	0.2946
chr19	59128983	1765119	0.0299	0.2478
chr20	63025520	2580026	0.0409	0.2316
chr21	48129895	1444595	0.03	0.1973
chr22	51304566	1006192	0.0196	0.1549
chrMT	16571	37075	2.2373	1.7815
chrX	155270560	6396070	0.0412	0.2373
chrY	59373566	217127	0.0037	0.0786

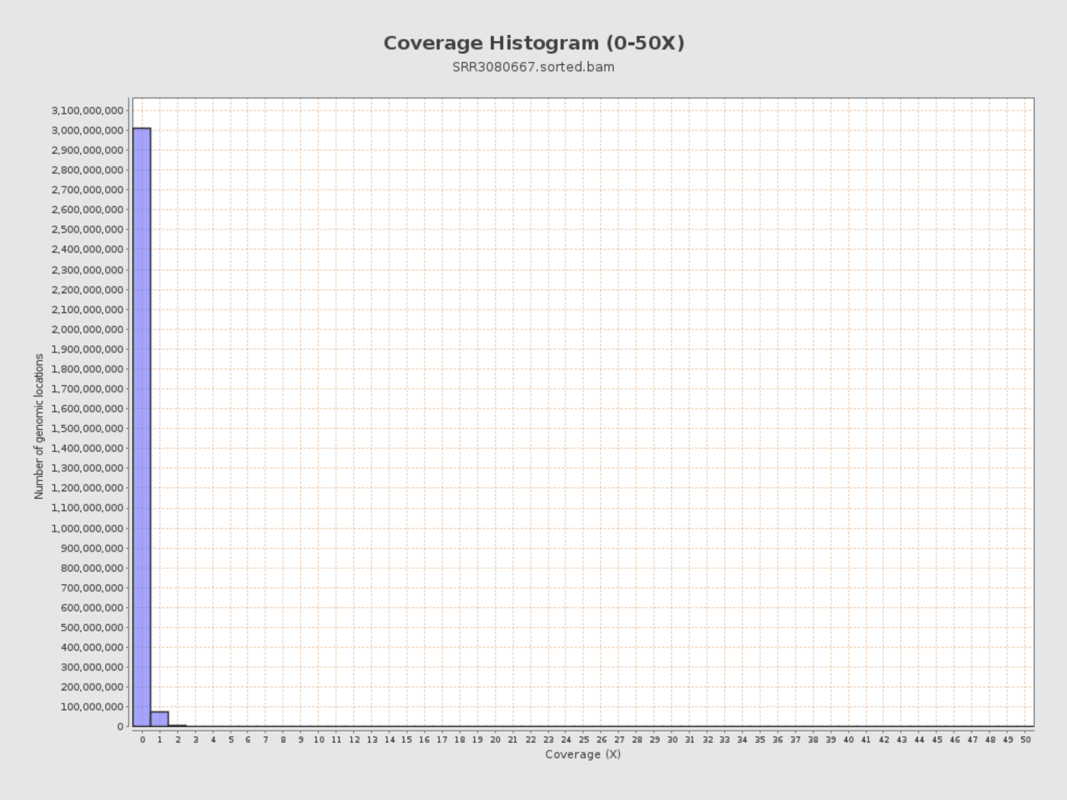
3. Results : Coverage across reference



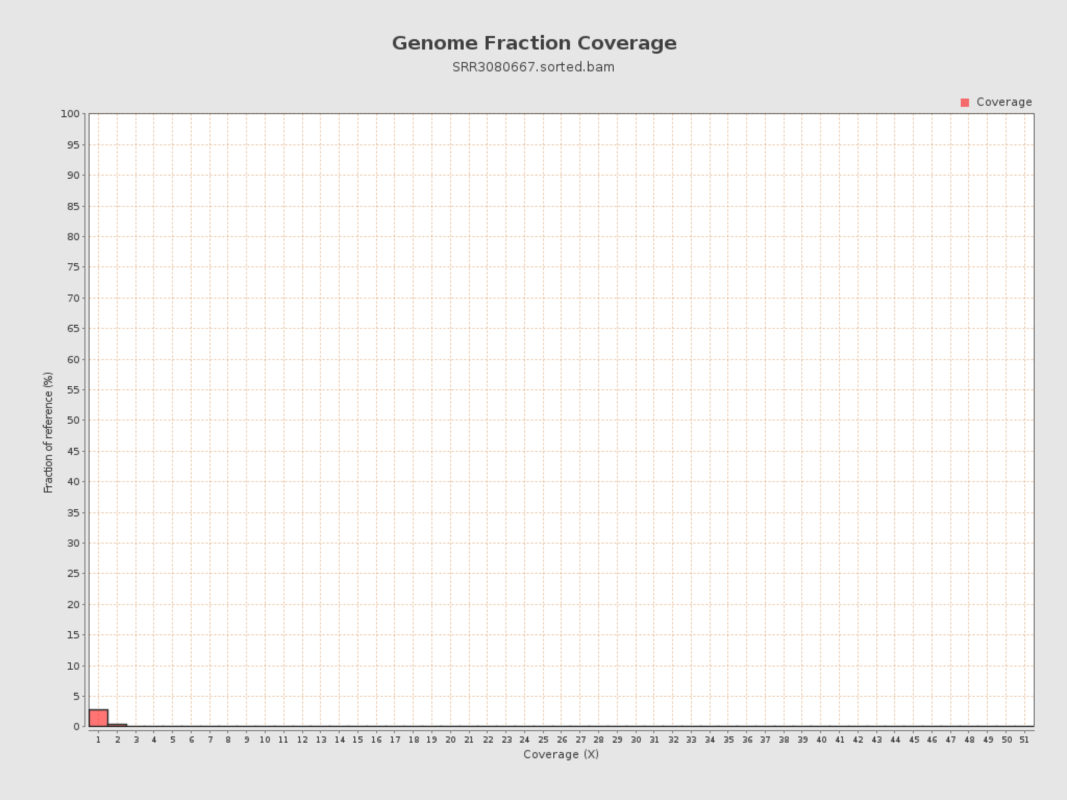
4. Results : Coverage Histogram



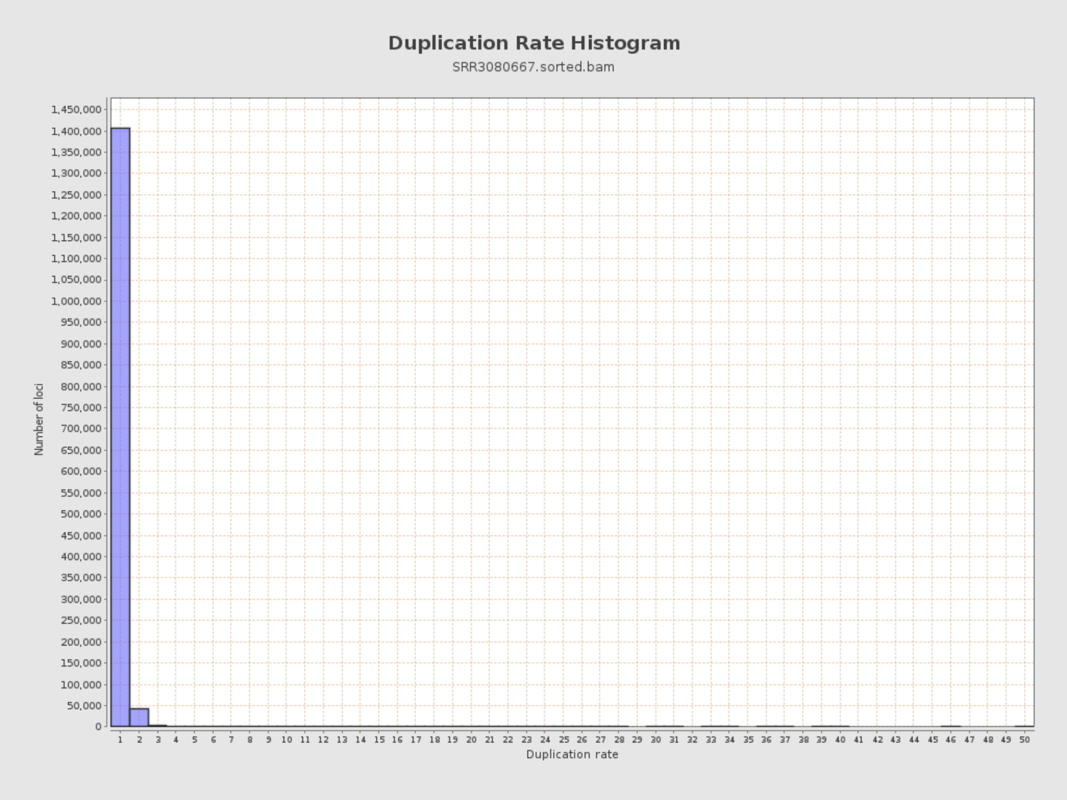
5. Results : Coverage Histogram (0-50X)



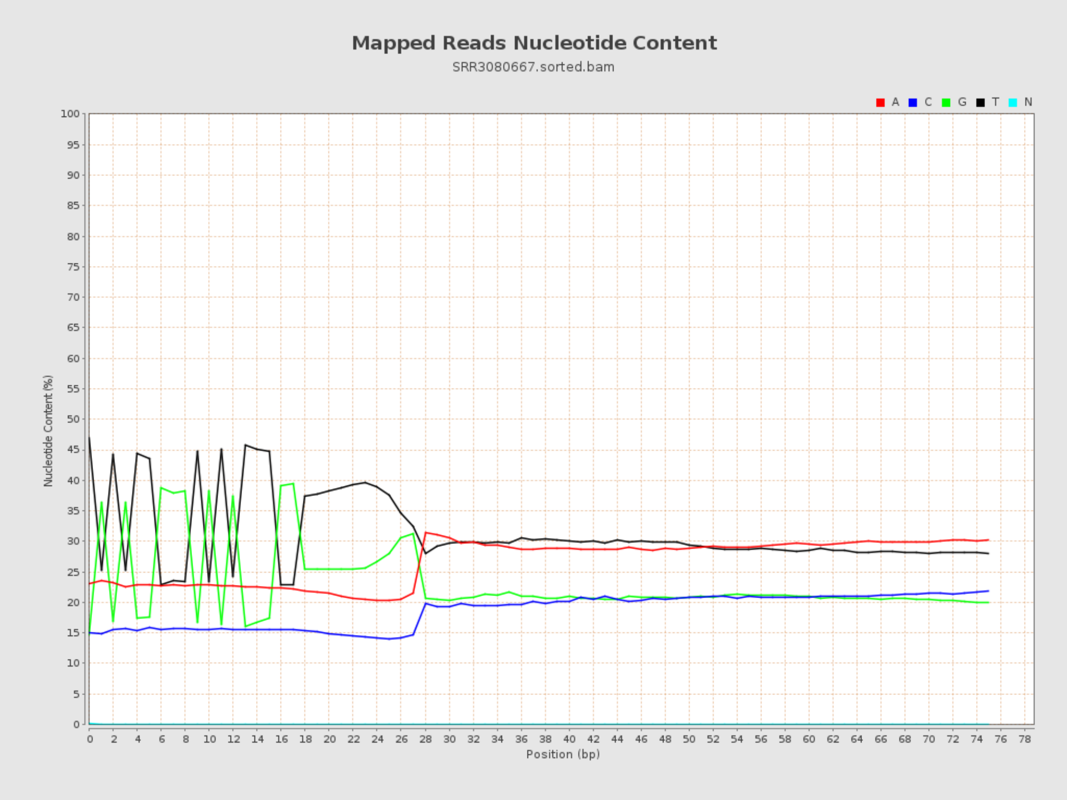
6. Results : Genome Fraction Coverage



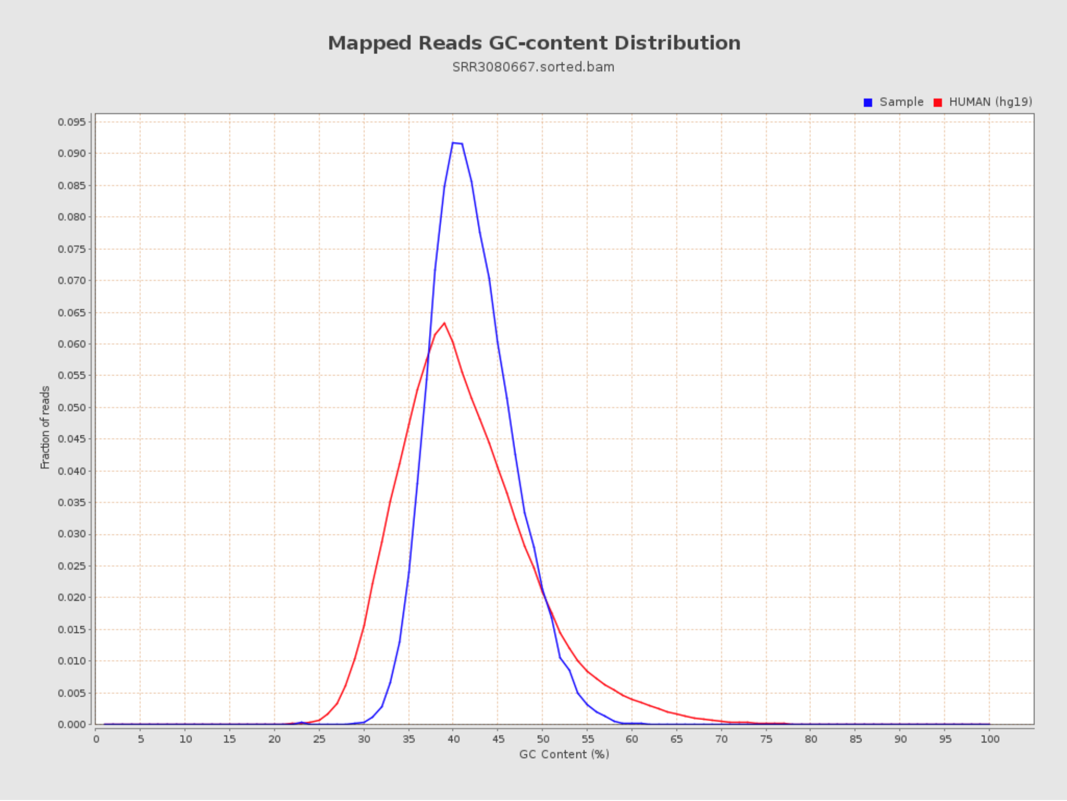
7. Results : Duplication Rate Histogram



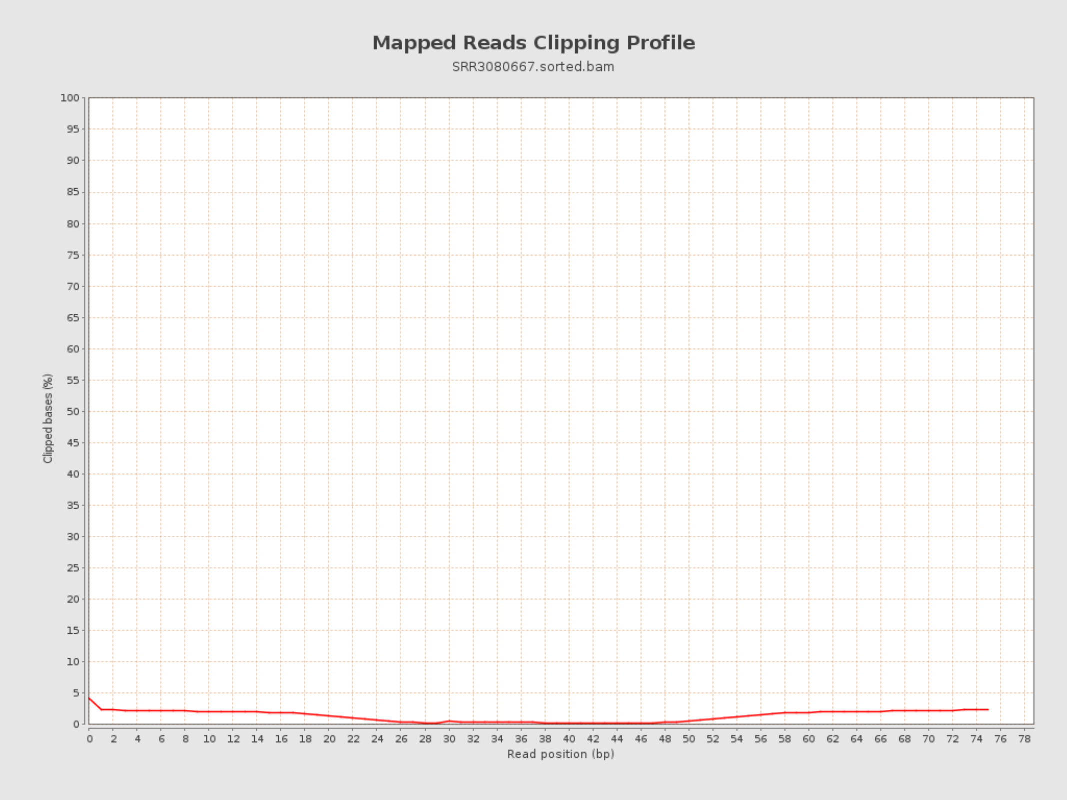
8. Results : Mapped Reads Nucleotide Content



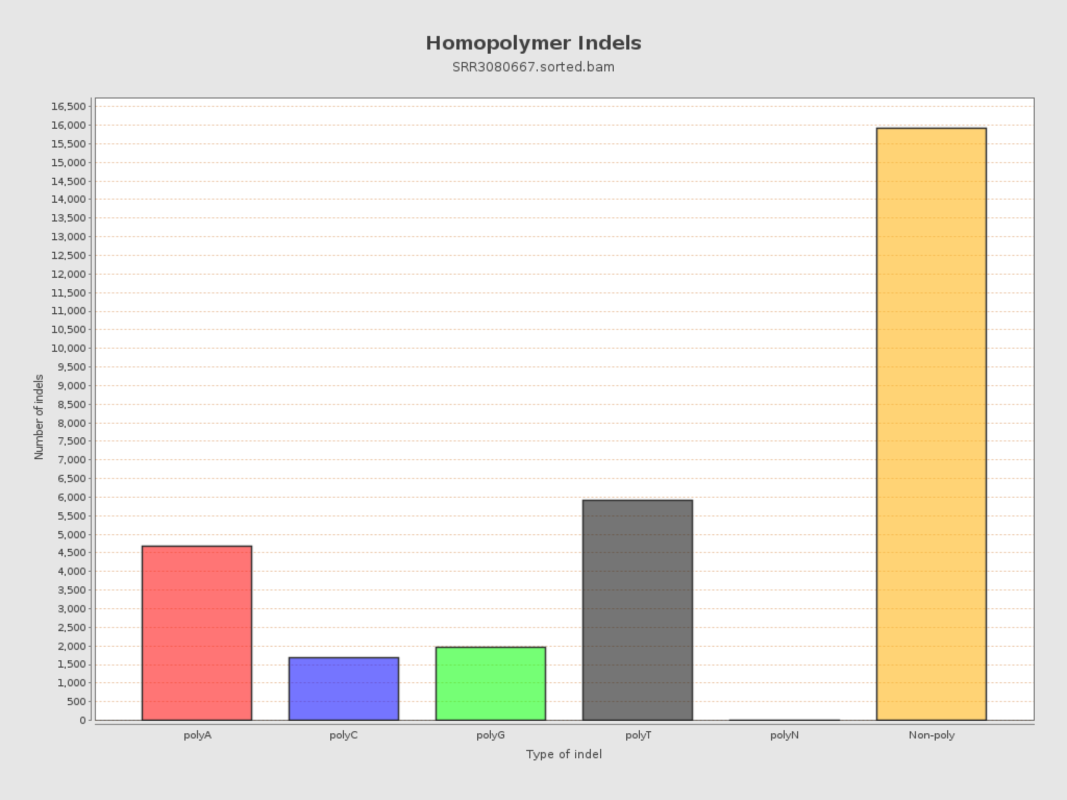
9. Results : Mapped Reads GC-content Distribution



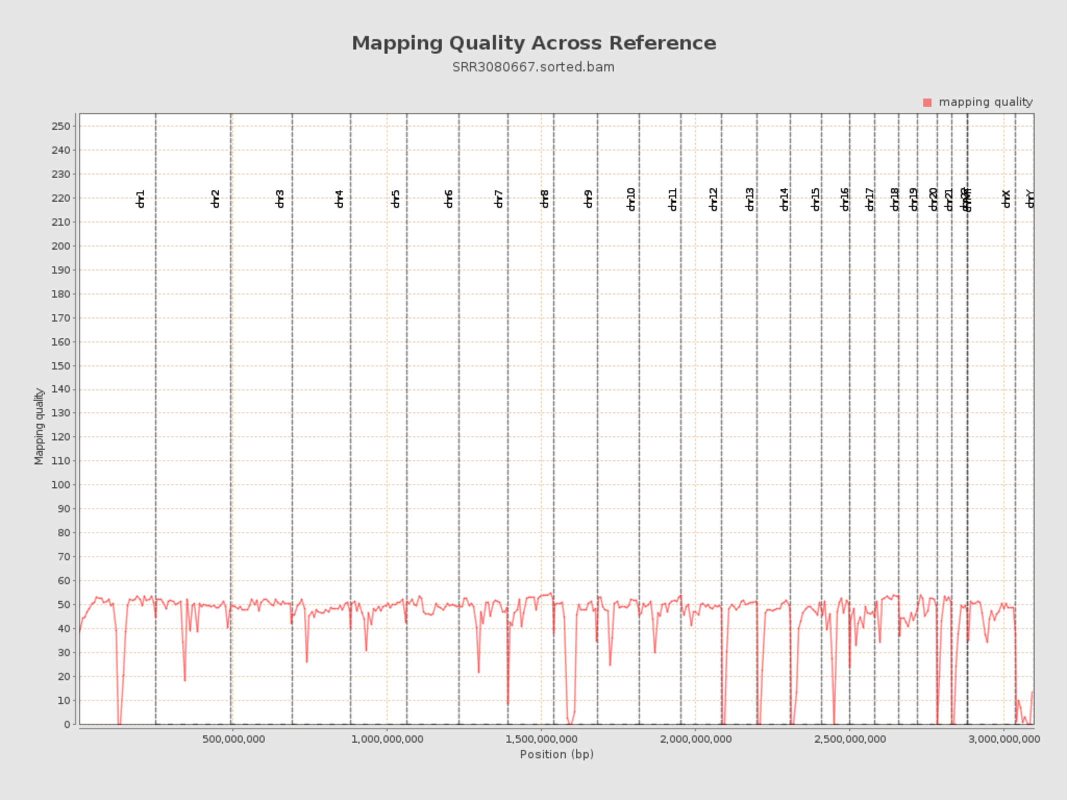
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram