Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 10:53:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080655.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_SRR3080655 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080655.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 10:53:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080655.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,756,609
Mapped reads	1,591,790 / 90.62%
Unmapped reads	164,819 / 9.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,911 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	64,771 / 3.69%
Duplication rate	3.5%
Clipped reads	751,452 / 42.78%

2.2. ACGT Content

Number/percentage of A's	28,033,995 / 26.7%
Number/percentage of C's	19,642,606 / 18.71%
Number/percentage of T's	32,943,784 / 31.37%
Number/percentage of G's	24,381,555 / 23.22%
Number/percentage of N's	4,536 / 0%
GC Percentage	41.93%

2.3. Coverage

Mean	0.0339

Standard Deviation	0.2686

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

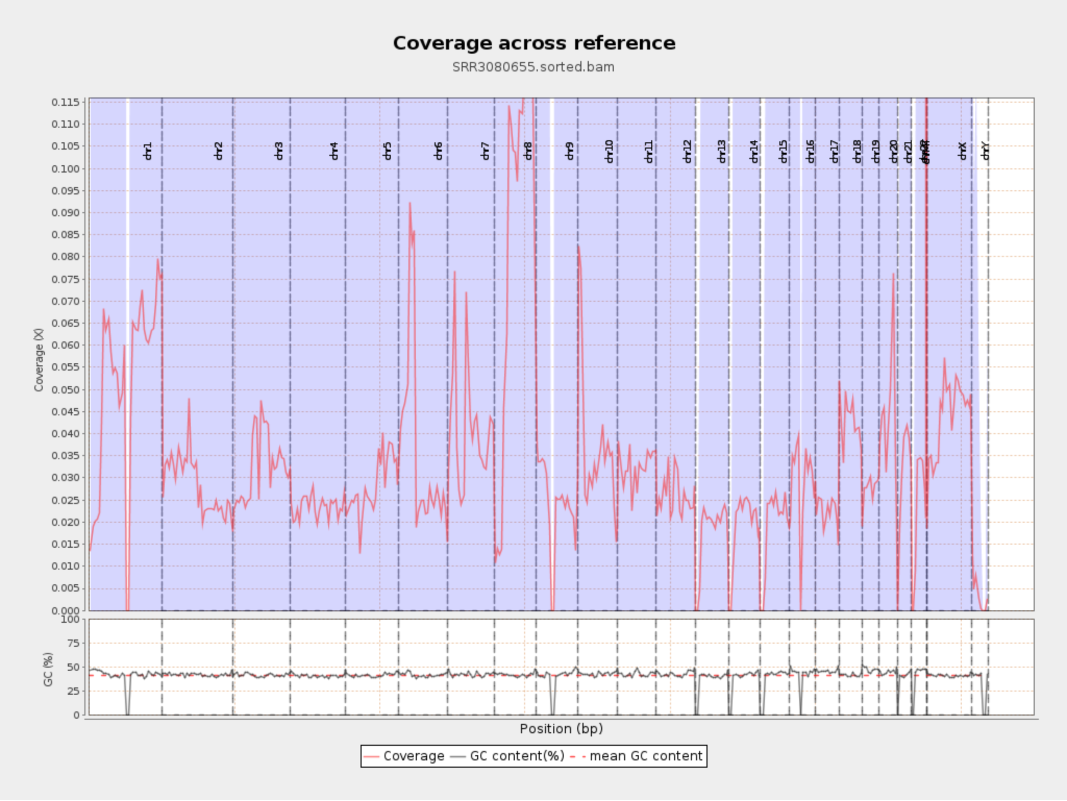
General error rate	0.69%
Mismatches	714,715
Insertions	7,857
Mapped reads with at least one insertion	0.49%
Deletions	23,991
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.83%

2.6. Chromosome stats

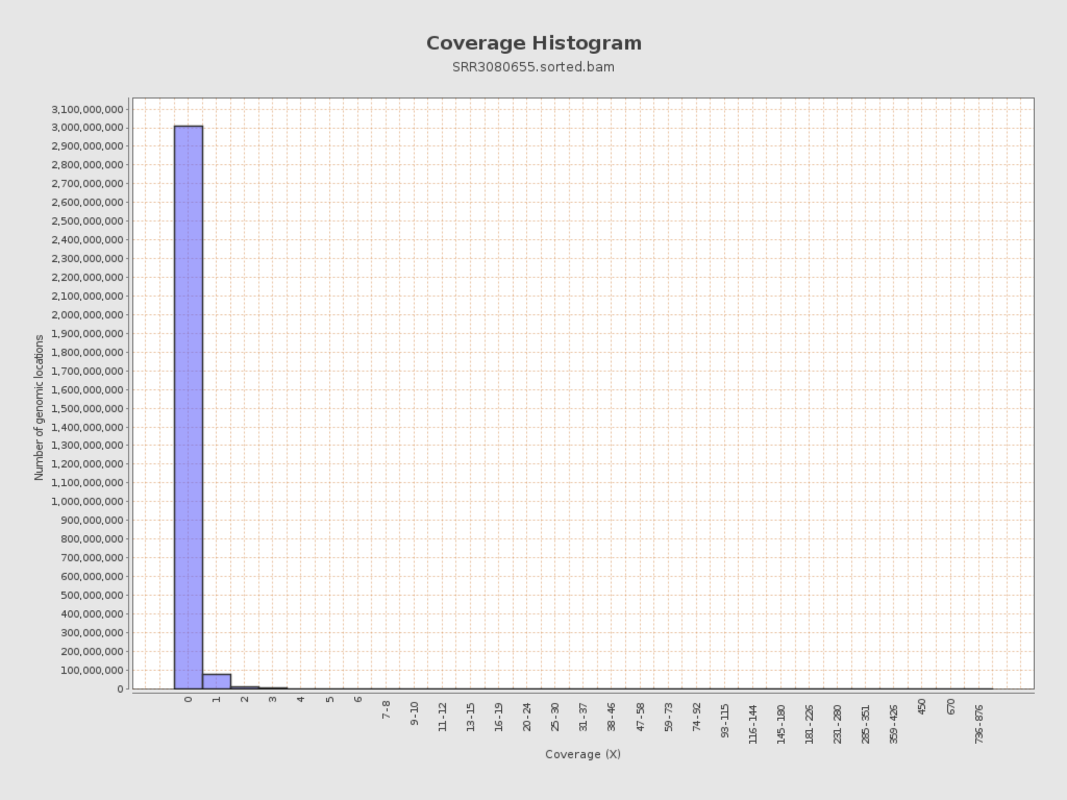
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12707406	0.051	0.3071
chr2	243199373	6931791	0.0285	0.4281
chr3	198022430	6440313	0.0325	0.2047
chr4	191154276	4469248	0.0234	0.1779
chr5	180915260	5088925	0.0281	0.1914
chr6	171115067	6274694	0.0367	0.2572
chr7	159138663	6669038	0.0419	0.4931

chr8	146364022	12394148	0.0847	0.3645
chr9	141213431	3296036	0.0233	0.2083
chr10	135534747	5128491	0.0378	0.2354
chr11	135006516	4351464	0.0322	0.2132
chr12	133851895	3449548	0.0258	0.1838
chr13	115169878	2033559	0.0177	0.1517
chr14	107349540	2032512	0.0189	0.1589
chr15	102531392	1952695	0.019	0.1664
chr16	90354753	2644225	0.0293	0.1999
chr17	81195210	1800081	0.0222	0.1706
chr18	78077248	3349708	0.0429	0.2751
chr19	59128983	1650039	0.0279	0.225
chr20	63025520	2775372	0.044	0.2431
chr21	48129895	1470720	0.0306	0.2018
chr22	51304566	1116453	0.0218	0.1674
chrMT	16571	17589	1.0614	1.2472
chrX	155270560	6793902	0.0438	0.2447
chrY	59373566	206958	0.0035	0.0706

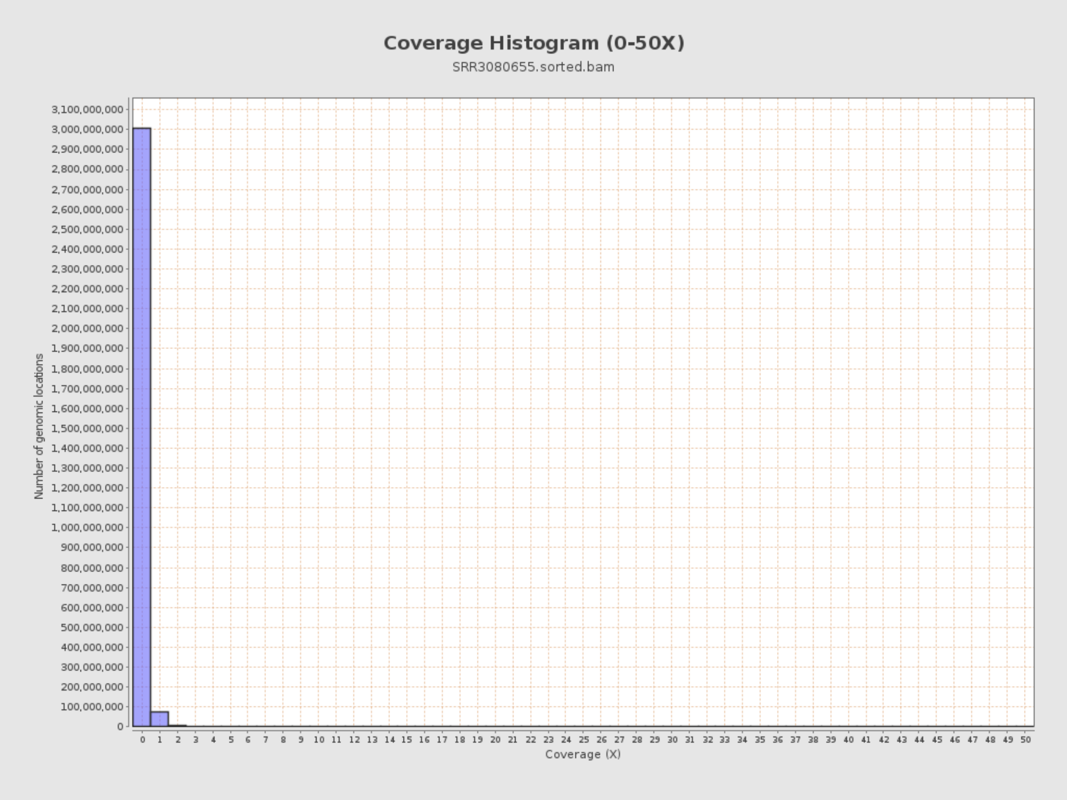
3. Results : Coverage across reference



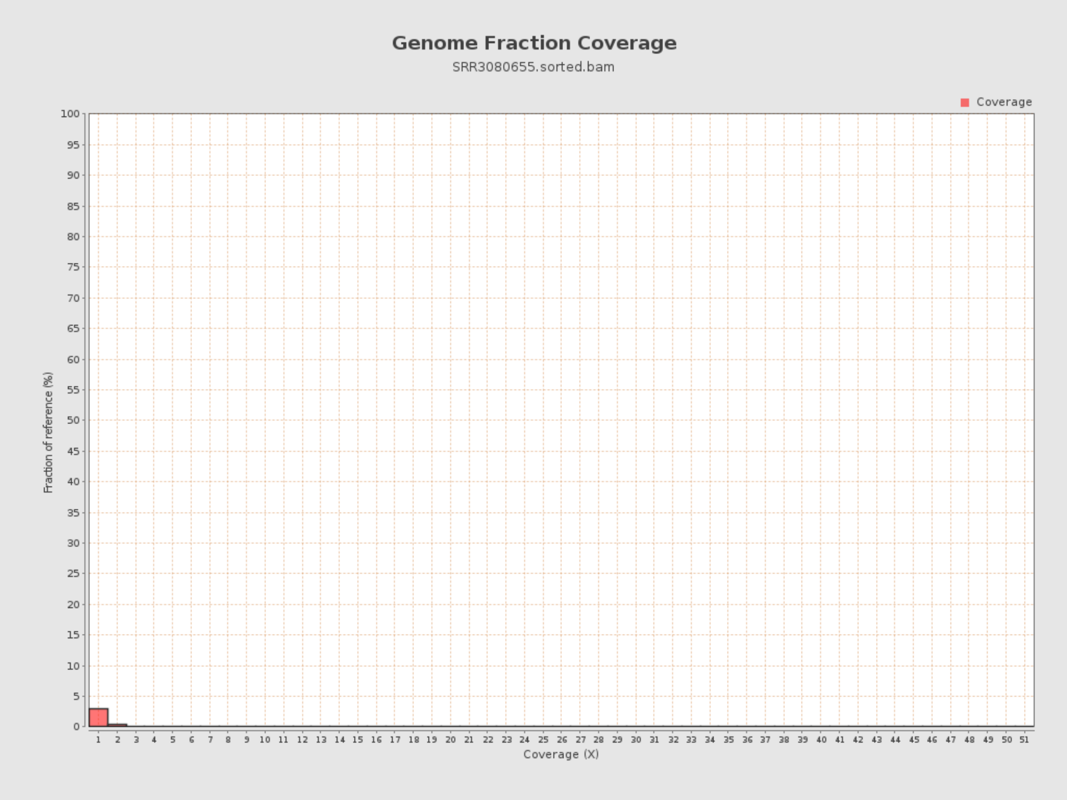
4. Results : Coverage Histogram



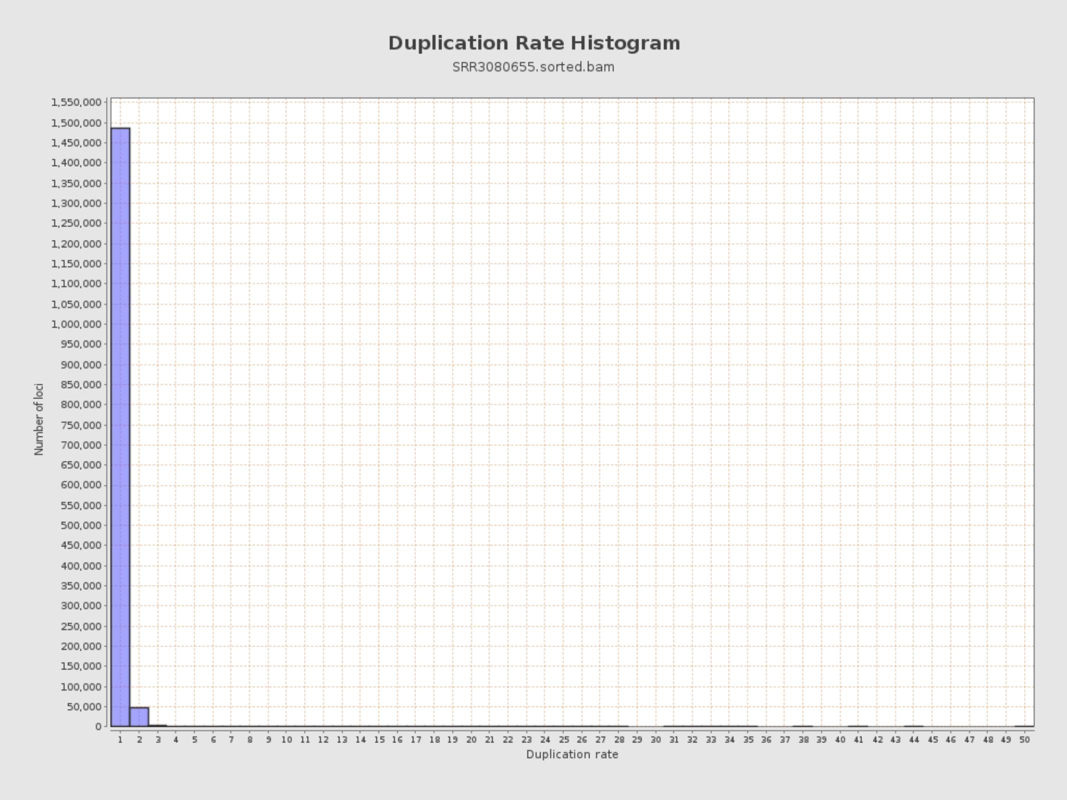
5. Results : Coverage Histogram (0-50X)



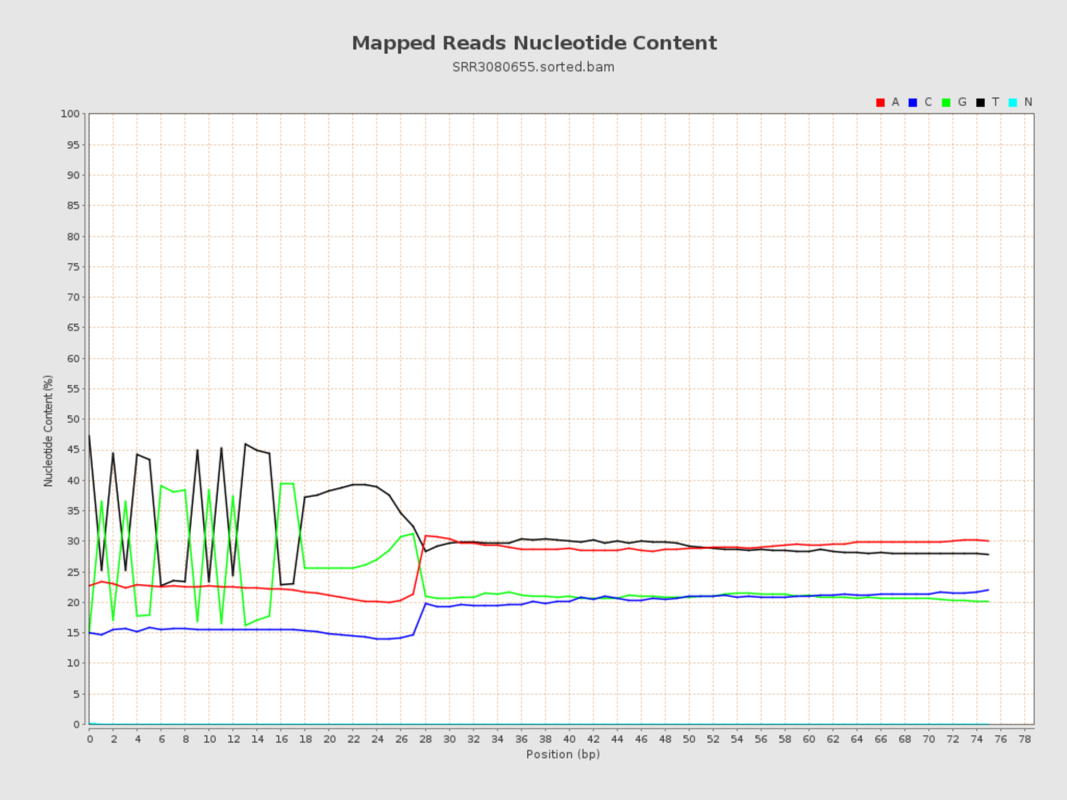
6. Results : Genome Fraction Coverage



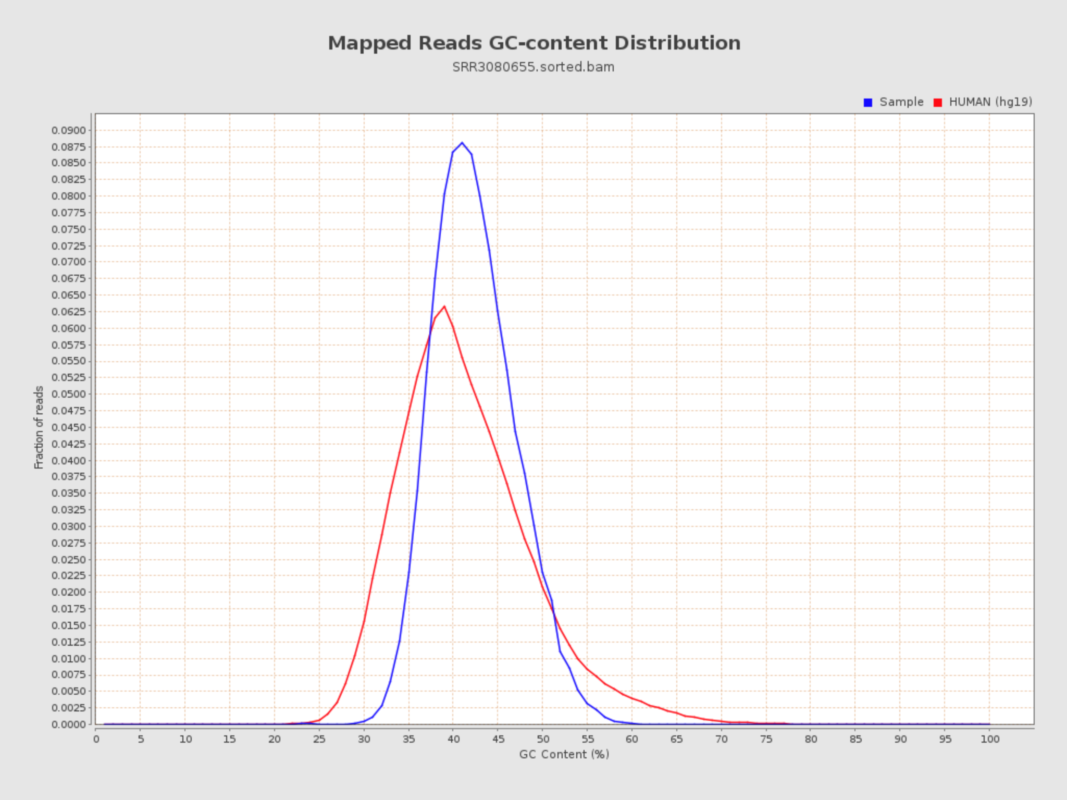
7. Results : Duplication Rate Histogram



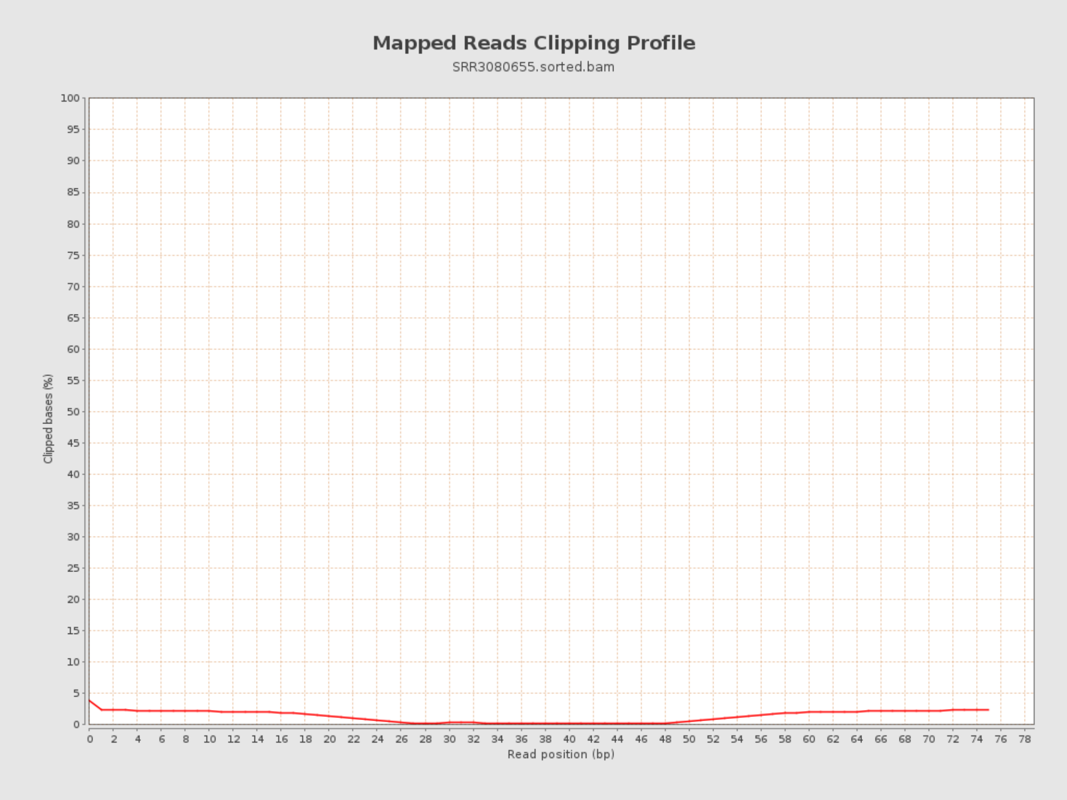
8. Results : Mapped Reads Nucleotide Content



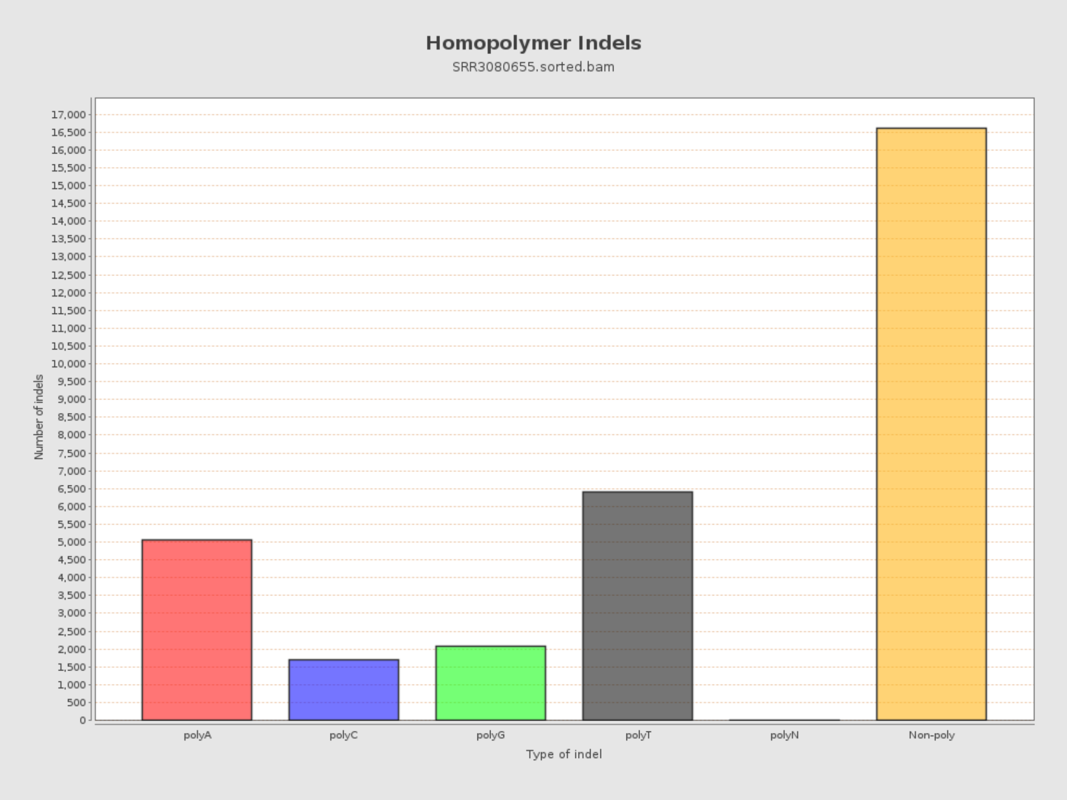
9. Results : Mapped Reads GC-content Distribution



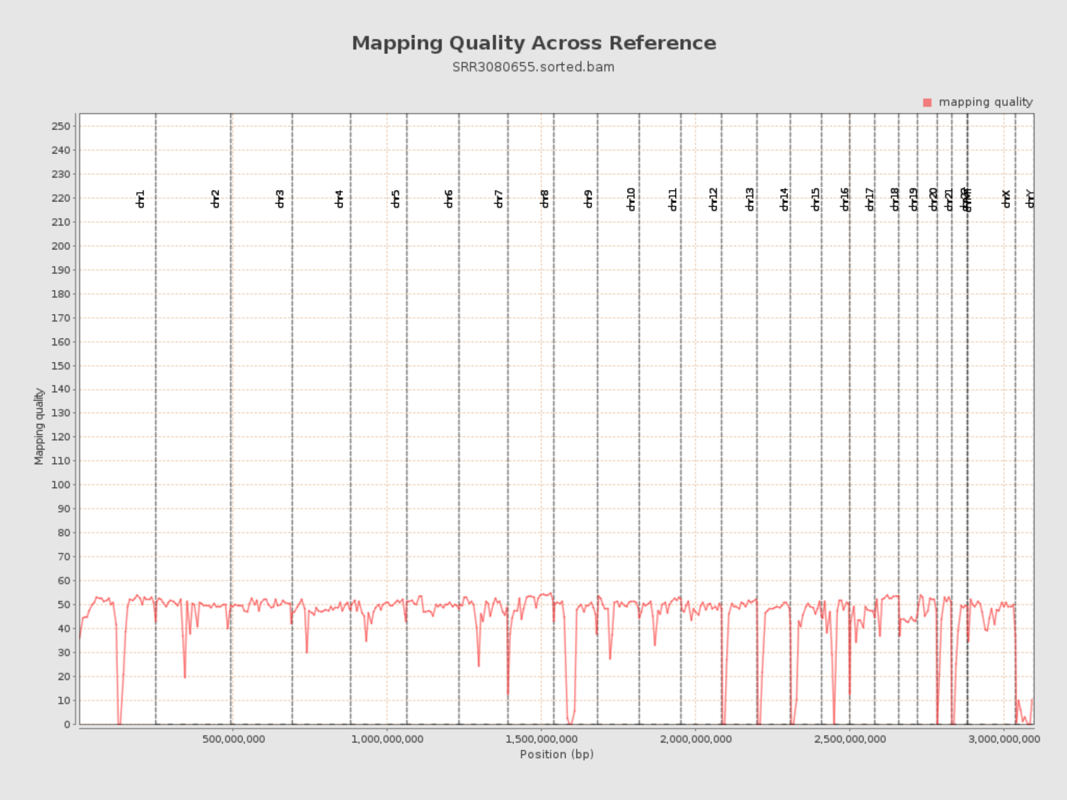
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram