Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 19:39:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089665.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_SRR089665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089665.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 19:39:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,116,406
Mapped reads	16,307,676 / 77.23%
Unmapped reads	4,808,730 / 22.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	668 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,255,869 / 5.95%
Duplication rate	6.03%
Clipped reads	3,175,591 / 15.04%

2.2. ACGT Content

Number/percentage of A's	243,046,570 / 32.32%
Number/percentage of C's	152,778,755 / 20.32%
Number/percentage of T's	192,286,371 / 25.57%
Number/percentage of G's	163,605,992 / 21.76%
Number/percentage of N's	183,312 / 0.02%
GC Percentage	42.08%

2.3. Coverage

Mean	0.2429

Standard Deviation	1.2441

2.4. Mapping Quality

Mean Mapping Quality	42.32

2.5. Mismatches and indels

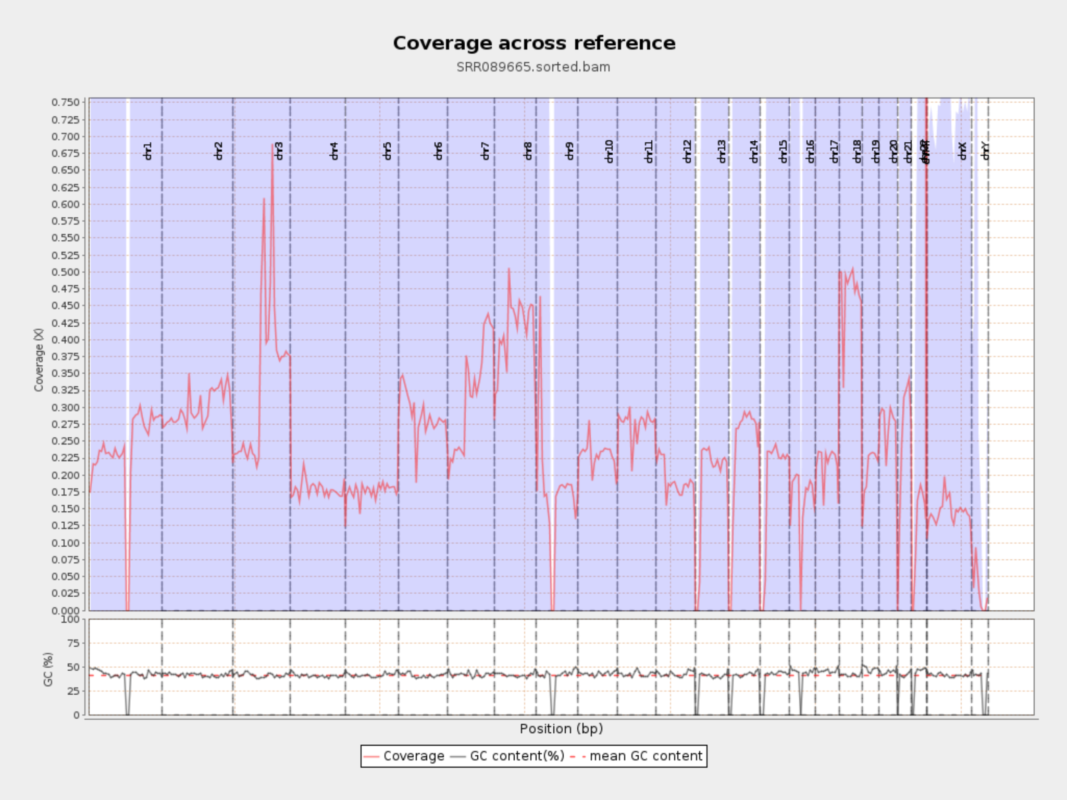
General error rate	0.5%
Mismatches	3,731,172
Insertions	35,836
Mapped reads with at least one insertion	0.22%
Deletions	105,580
Mapped reads with at least one deletion	0.65%
Homopolymer indels	42.39%

2.6. Chromosome stats

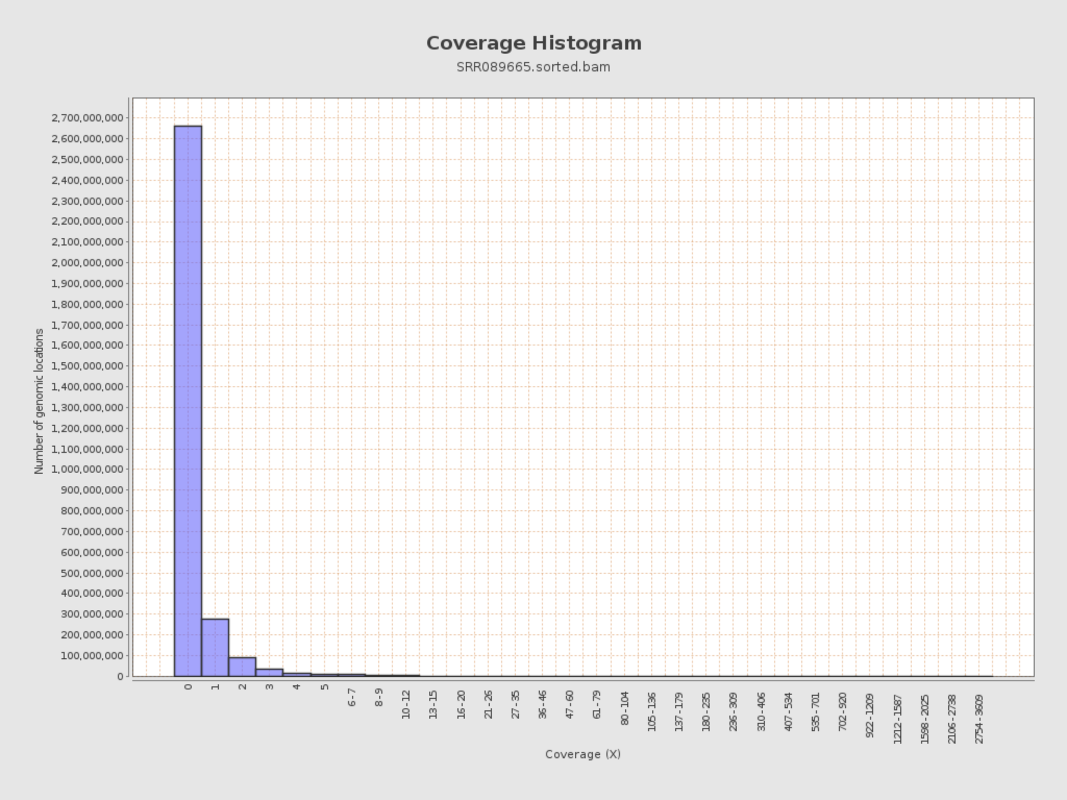
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58733771	0.2356	1.3038
chr2	243199373	72967475	0.3	1.8532
chr3	198022430	67330223	0.34	1.0102
chr4	191154276	34188523	0.1789	0.7149
chr5	180915260	31994137	0.1768	0.6672
chr6	171115067	49248729	0.2878	1.0816
chr7	159138663	51024495	0.3206	2.037

chr8	146364022	60629834	0.4142	2.3827
chr9	141213431	25171818	0.1783	1.0345
chr10	135534747	31304373	0.231	1.124
chr11	135006516	37047549	0.2744	1.1517
chr12	133851895	25655889	0.1917	0.7386
chr13	115169878	21516447	0.1868	0.6936
chr14	107349540	24890798	0.2319	0.8601
chr15	102531392	18960865	0.1849	0.6883
chr16	90354753	14746994	0.1632	0.7239
chr17	81195210	17544492	0.2161	0.8566
chr18	78077248	36699616	0.47	1.6719
chr19	59128983	12528458	0.2119	1.3177
chr20	63025520	17179043	0.2726	0.8934
chr21	48129895	11961796	0.2485	0.9566
chr22	51304566	6097338	0.1188	0.5554
chrMT	16571	223319	13.4765	13.015
chrX	155270560	22686773	0.1461	0.8865
chrY	59373566	1727553	0.0291	0.5117

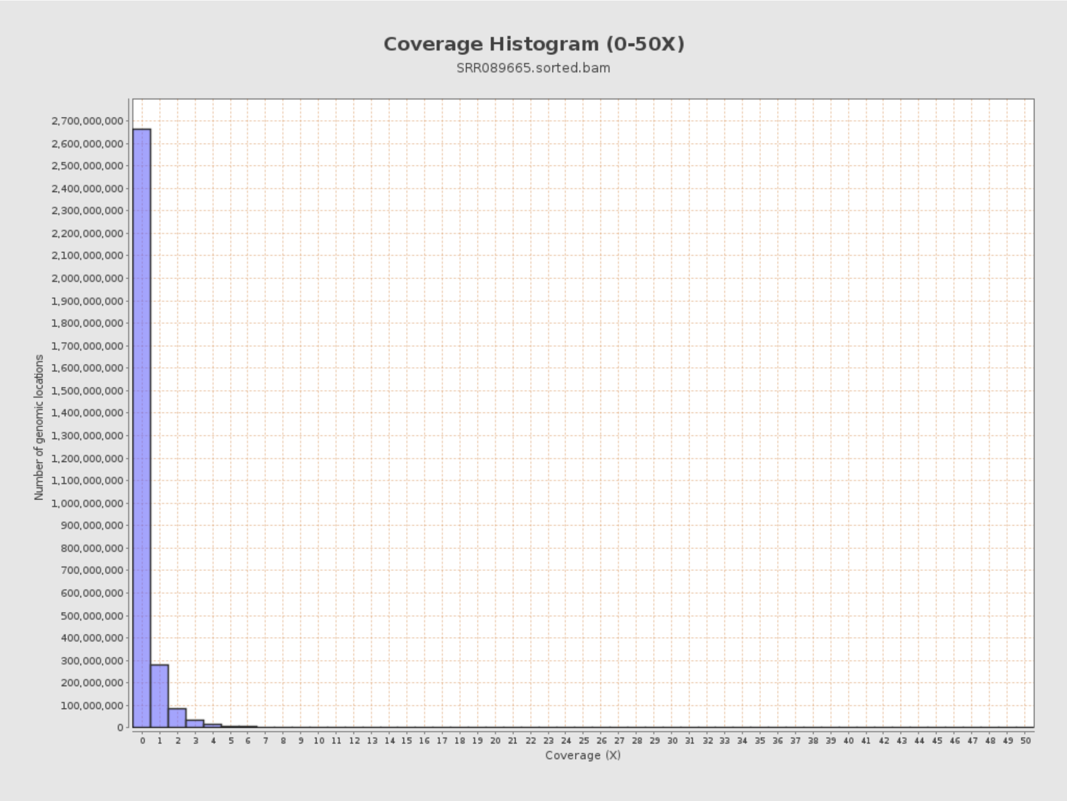
3. Results : Coverage across reference



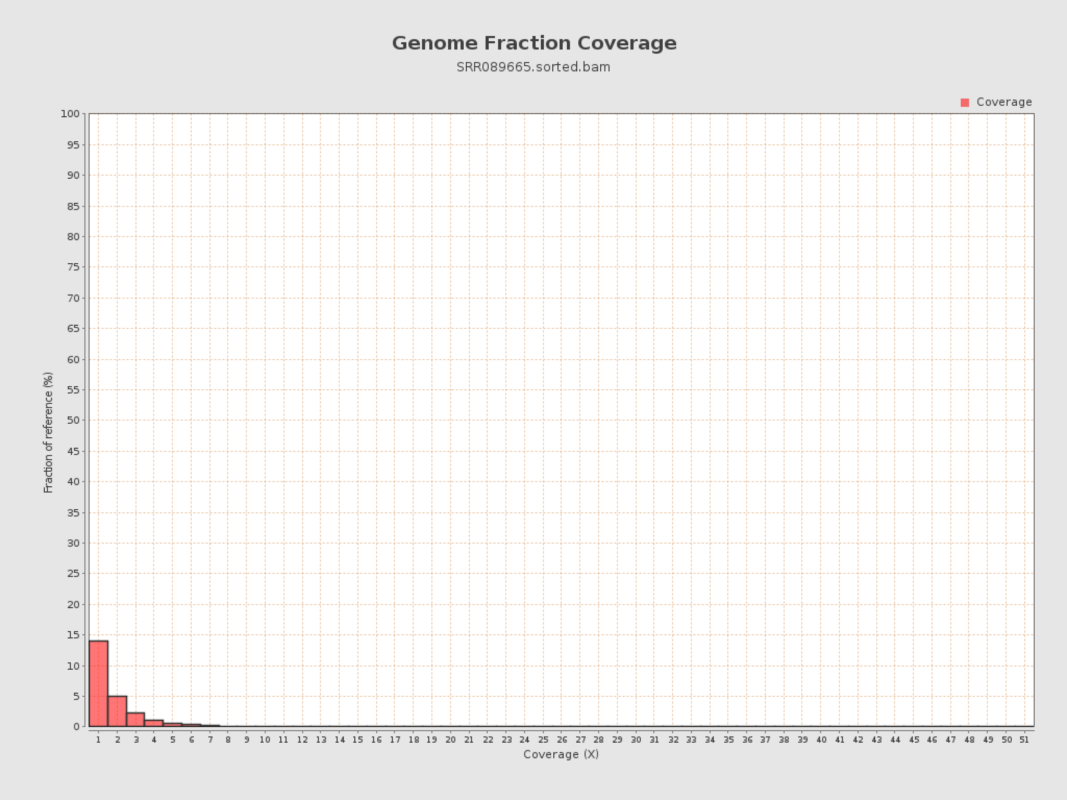
4. Results : Coverage Histogram



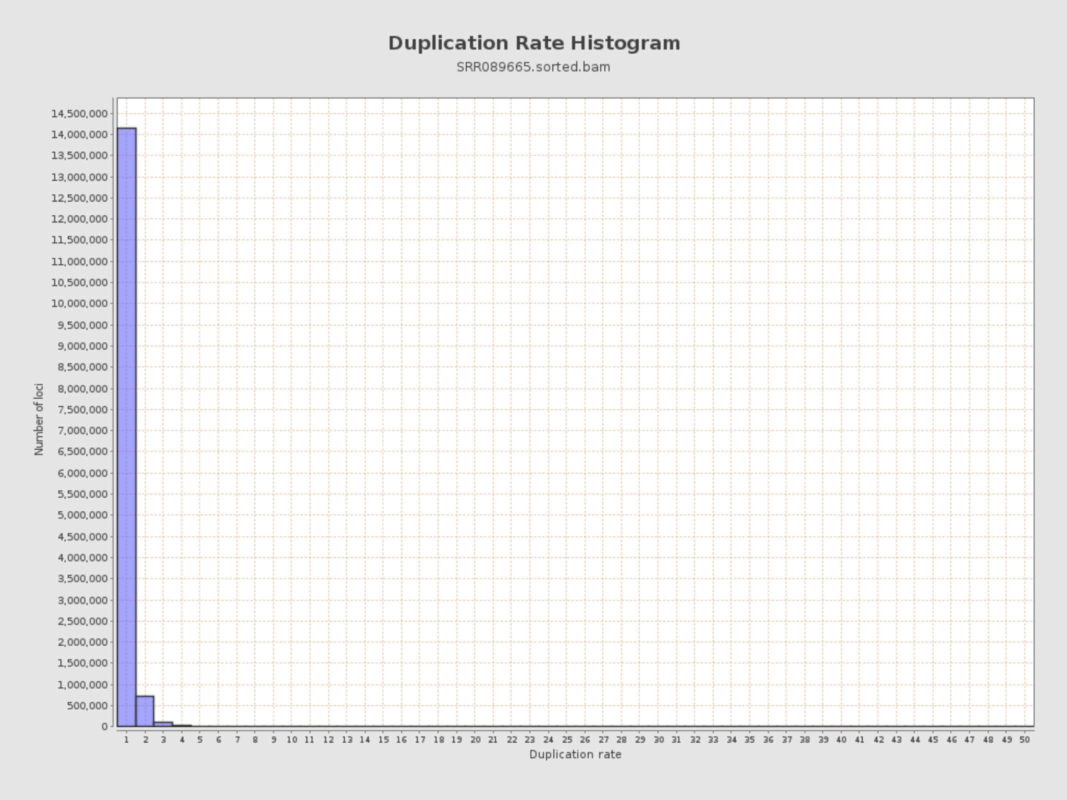
5. Results : Coverage Histogram (0-50X)



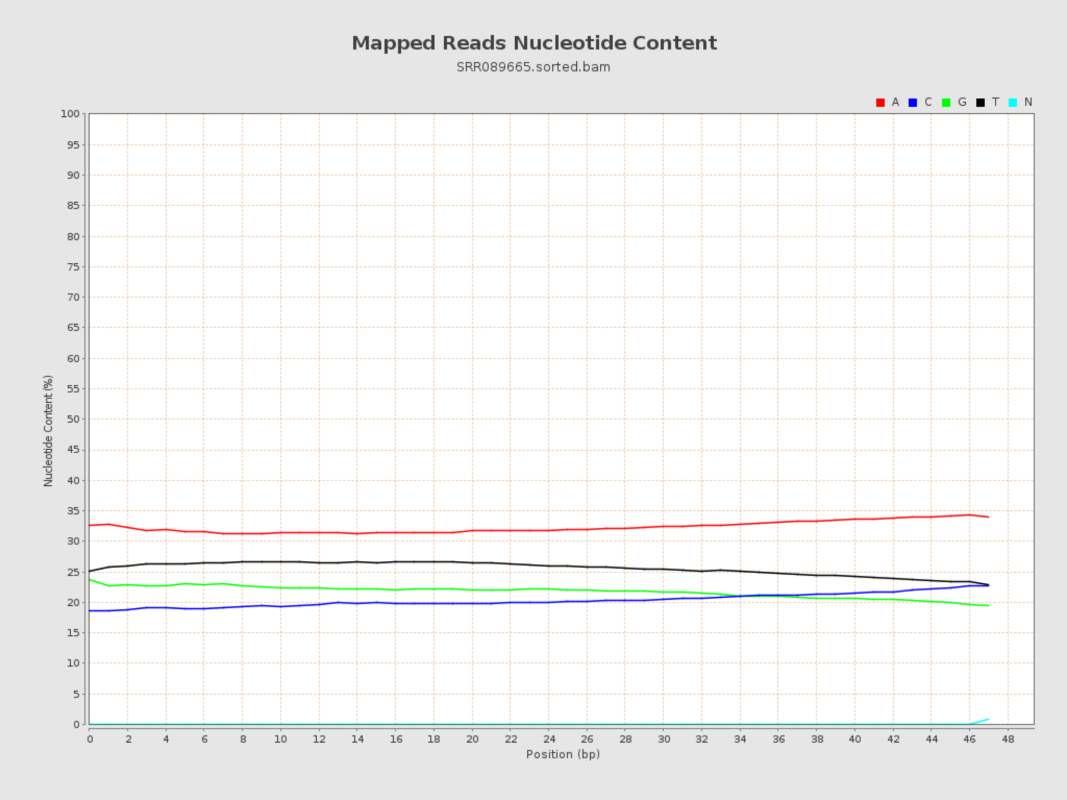
6. Results : Genome Fraction Coverage



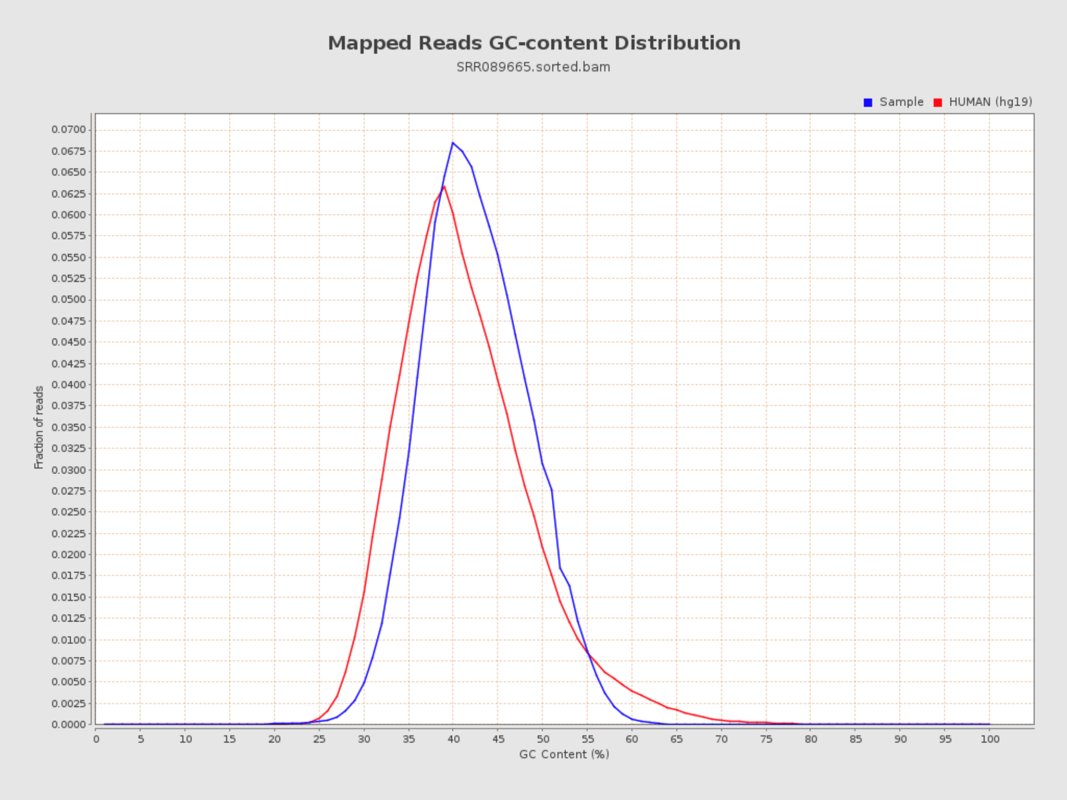
7. Results : Duplication Rate Histogram



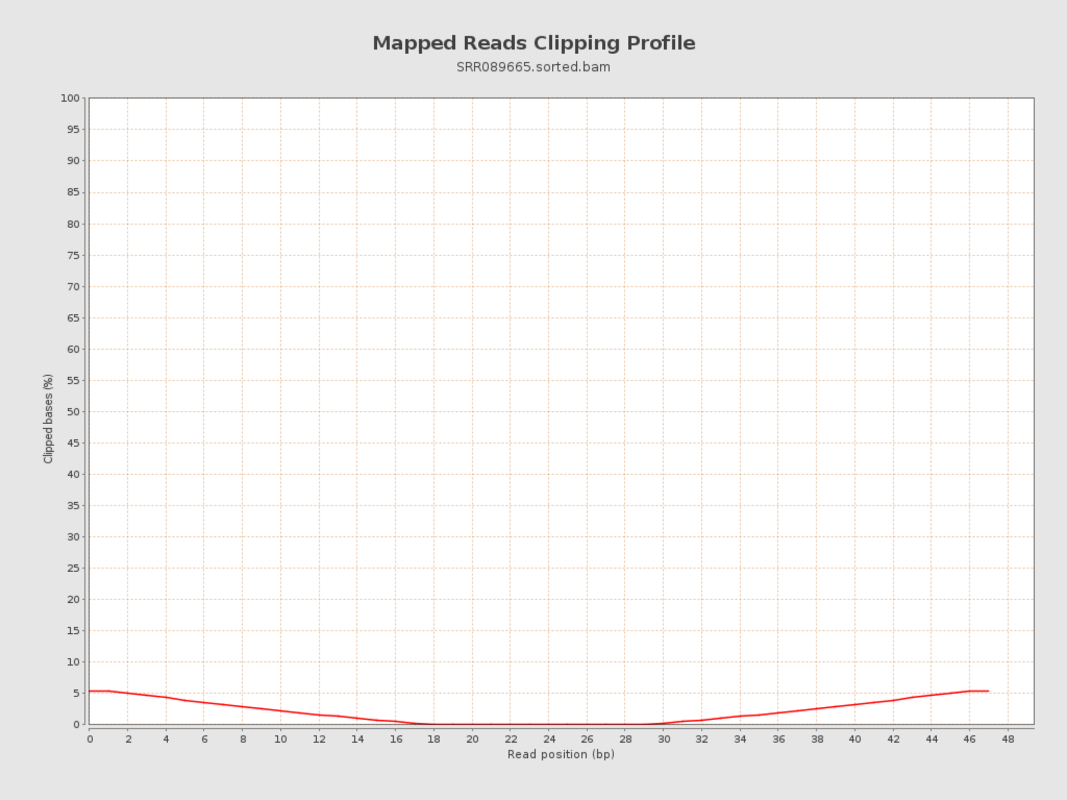
8. Results : Mapped Reads Nucleotide Content



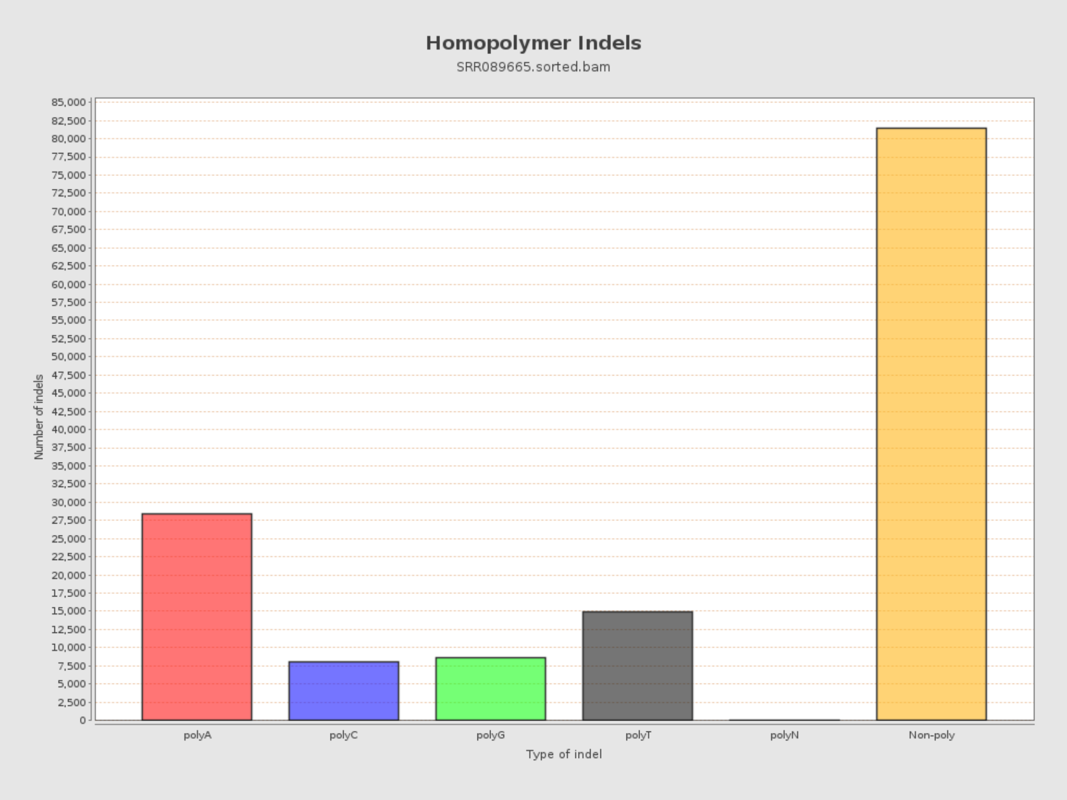
9. Results : Mapped Reads GC-content Distribution



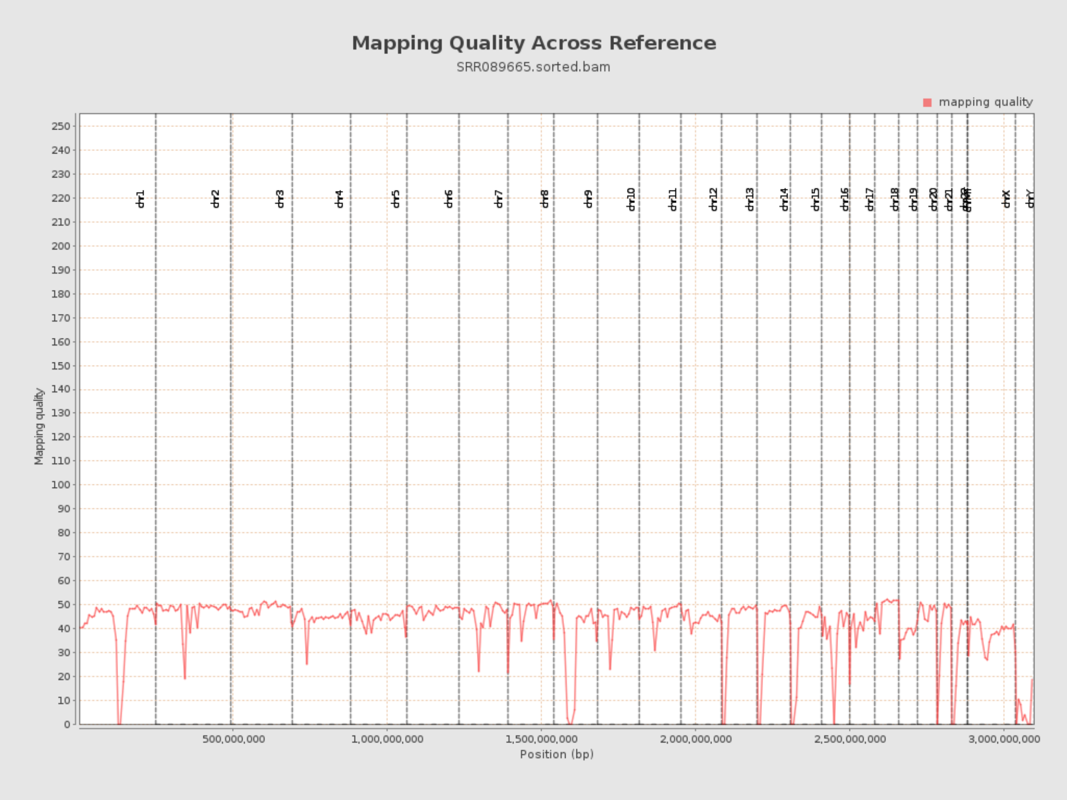
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram