CORRECTION

Correction: A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples

Kiran K. Mangalaparthi[1†], Sandip Chavan[1†], Anil K. Madugundu[1,2,3,4], Santosh Renuse[1,5], Patrick M. Vanderboom[1], Anthony D. Maus[1], Jennifer Kemp[1], Benjamin R. Kipp[6], Stefan K. Grebe[1,7], Ravinder J. Singh[1] and Akhilesh Pandey[1,4,5*]

Correction to: Clin Proteom (2021) 18:25
https://doi.org/10.1186/s12014-021-09331-z

The original version [1] of this article contains errors in Tables 2 and 3 as follows:

In Table 2: Because of a formatting error, the mean values of three peptides in Set 2 were listed under Set 1 and the mean values for Set 3 were listed under Set 2.

In Table 3: The values under "Positive" and "Negative" columns for the row describing "SARS-CoV-2 negative nasopharyngeal swab samples (n = 30)" were switched and the "Specificity" was incorrectly represented as "~ 100%" instead of "100%."

The authors regret these errors, which have now been corrected. The corrected Tables 2 and 3 are given.

Mangalaparthi *et al. Clinical Proteomics*   (2022) 19:11

Page 2 of 2

Table 2 Variability (reported as CV) for SISCAPA assay performed on 3 separate sets of pooled RT-PCR positive nasopharyngeal swab samples (Ct value < 24)

	DGIIWVATEGALNTPK	ITFGGPSDSTGSNQNGER	NPANNAAIVLQLPQGTTLPK
Set 1			
Mean	1.64E+08	4.90E+07	6.04E+06
SD	2.63E+07	3.37E+06	6.28E+05
CV	16.04	6.88	10.38
Set 2			
Mean	1.62E+08	5.15E+07	5.69E+06
SD	2.13E+07	4.30E+06	5.50E+05
CV	13.14	8.34	9.66
Set 3			
Mean	1.87E+08	4.28E+07	6.27E+06
SD	1.06E+07	3.60E+06	3.90E+05
CV	5.64	8.41	6.21

The total area was considered for calculating the mean and standard deviation

Table 3 Summary of MS-based detection of SARS-CoV-2 viral peptides from clinical nasopharyngeal swab samples using the SISCAPA workflow

	Detection of SARS-CoV-2 viral peptides by SISCAPA approach		
	Positive	Negative	
SARS-CoV-2 positive nasopharyngeal swab samples (n = 41)	38	3	Sensitivity—92.68%
SARS-CoV-2 negative nasopharyngeal swab samples (n = 30)	0	30	Specificity—100%

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Author details
[1] Department of Laboratory Medicine and Pathology, Division of Clinical Biochemistry and Immunology, Mayo Clinic, Rochester, MN 55905, USA. [2] Manipal Academy of Higher Education, Manipal, Karnataka 576104, India. [3] Institute of Bioinformatics, International Technology Park, Bangalore, Karnataka 560066, India. [4] Center for Molecular Medicine, National Institute of Mental Health and Neurosciences, Hosur Road, Bangalore, Karnataka 560029, India. [5] Center for Individualized Medicine, Mayo Clinic, Rochester, MN 55905, USA. [6] Department of Laboratory Medicine and Pathology, Division of Laboratory Genetics and Genomics, Mayo Clinic, Rochester, MN 55905, USA. [7] Department of Medicine, Division of Endocrinology, Mayo Clinic, Rochester, MN 55902, USA.

Reference
1. Mangalaparthi KK, Chavan S, Madugundu AK, Renuse S, Vanderboom PM, Maus AD, Kemp J, Kipp BR, Grebe SK, Singh RJ, Pandey A. A SISCAPA-based approach for detection of SARS-CoV-2 viral antigens from clinical samples. Clin Proteom. 2021;18:25.