Published online 14 April 2021

NAR Genomics and Bioinformatics, 2021, Vol. 3, No. 2 **1**
doi: 10.1093/nargab/lqab029

Corrigendum

Nanopore sequencing of native adeno-associated virus (AAV) single-stranded DNA using a transposase-based rapid protocol

Marco T. Radukic[1,†], David Brandt[2,†], Markus Haak[2], Kristian M. Müller[1,*] and Jörn Kalinowski[2,*]

[1]Faculty of Technology, Bielefeld University, D-33501 Bielefeld, Germany and [2]Center for Biotechnology (CeBiTec), Bielefeld University, D-33501 Bielefeld, Germany

NAR Genomics and Bioinformatics 2020;2(4). https://doi.org/10.1093/nargab/lqaa074

In the above article, Table 1 has been updated as follows online:

Previous version

Table 1. BLASTn read assignments and qPCR results for two independently produced and sequenced rAAV samples (sample 1 and 2).

A nanopore BLAST bins as percent of total hits				
	Run 1 (sample 1)		Run 2 (sample 2)	
Group/threshold	>500 nt	>1000 nt	>500 nt	>1000 nt
rAAV genome	97.00%	97.34%	97.91%	97.96%
pITR	1.11%	1.29%	0.97%	1.25%
pRepCap	0.47%	0.49%	0.23%	0.27%
pHelper	0.25%	0.24%	0.17%	0.17%
hg38	1.18%	0.65%	0.72%	0.35%
B qPCR (and *insilico* fragmentation) results as percent of total measurable with 95% confidence interval				
Primer	Sample 1	Sample 2	(*in silico*)	
Bla	2.0 ± 0.3%	2.9 ± 0.4%	(1.79%)	
Rep	0.22 ± 0.04%	0.24 ± 0.04%	(0.13%)	
E4	0.062 ± 0.009%	0.08 ± 0.01%	(0.10%)	

A: Total contamination levels in both samples are independent of the read-quality thresholds tested here, however the individual share of contaminations shifts towards higher amounts of human genomic sequences for the lower threshold. B: qPCR results lay in comparable ranges to the sequencing results, although a larger discrepancy is seen for the second sample in terms of *bla* and for *rep* gene sequences in general. The *in silico* read fragmentation and binning to qPCR targets was performed for reads from run 2.

*To whom correspondence should be addressed. Kristian M. Müller. Tel: +49 521 106 6323; Fax: +49 521 106 156318; Email: kristian@syntbio.net
Correspondence may also be addressed to Jörn Kalinowski. Tel: +49 521 106 8756; Fax: +49 521 106 89041; Email: joern@cebitec.uni-bielefeld.de
†The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors.

Corrected version

Table 1. BLASTn read assignments and qPCR results for two independently produced and sequenced rAAV samples (sample 1 and 2).

A: nanopore BLAST bins as percent of total hits

	Run 1 (sample 1)		Run 2 (sample 2)	
Group\threshold	>500 nt	>1000 nt	>500 nt	>1000 nt
rAAV genome	97.00%	97.34%	97.91%	97.96%
pITR	1.11%	1.29%	0.97%	1.25%
pRepCap	0.47%	0.49%	0.23%	0.27%
pHelper	0.25%	0.24%	0.17%	0.17%
hg38	1.18%	0.65%	0.72%	0.35%

B: qPCR (and *insilico* fragmentation) results as percent of total measurable with 95% confidence interval

Primer	Sample 1	Sample 2	(*in silico*)
bla	$2.0 \pm 0.3\%$	$2.9 \pm 0.4\%$	(1.79%)
Rep	$0.22 \pm 0.04\%$	$0.24 \pm 0.04\%$	(0.13%)
E4	$0.062 \pm 0.009\%$	$0.08 \pm 0.01\%$	(0.10%)

A: Total contamination levels in both samples are independent of the read-quality thresholds tested here, however the individual share of contaminations shifts towards higher amounts of human genomic sequences for the lower threshold. B: qPCR results lay in comparable ranges to the sequencing results, although a larger discrepancy is seen for the second sample in terms of *bla* and for *rep* gene sequences in general. The *in silico* read fragmentation and binning to qPCR targets was performed for reads from run 2.