

## Supplementary materials

**Table S1** gBlock gene fragments used in this study

<b>gBlock No.</b>	<b>Gene of interest</b>	<b>sequence length</b>	<b>DNA content (in ng/ <math>\mu</math>l)</b>	<b>copy No. of stock solution</b>
I	PPV-1	499 bp	1,69	$3,3 \times 10^9$ copies/ $\mu$ l
	PCMV			
	PLHV-3			
	HEV			
	PCV3			
II	PLHV-1	653 bp	2,62	$3,9 \times 10^9$ copies/ $\mu$ l
	PLHV-2			
	PCV4			
	SARS-CoV-2			
	TTSuV-1			
TTSuV-2				
III	pGAPDH	690 bp	1,13	$1,6 \times 10^9$ copies/ $\mu$ l
	huGAPDH			
	PERVpol			
	PCV2			
V	PCV1	623 bp	4,72	$7,4 \times 10^9$ copies/ $\mu$ l
	PCV2			
	PCV3			
	PCV4			
	PLHV-3			

**Table S2:** Experimental details concerning quality control criteria when applying a log<sub>10</sub> dilutional series of the gBlock in the respective qPCR approaches

PCR assay	reference	internal control	PCR efficiency <sup>1</sup>
HEV	[4]	Flu (NA)	0.90
PCMV	[2]	pGAPDH	1.07
PLHV-1	[3]	pGAPDH	1.01
PLHV-2	[3]	pGAPDH	1.01
PLHV-3	[13]	pGAPDH	1.00
PCV1	[12]	pGAPDH	0.90
PCV2	[12]	pGAPDH	1.09
PCV3	[12]	pGAPDH	0.95
PCV4	[12]	pGAPDH	0.85
PPV-1	[1]	pGAPDH	0.94
PERV pol	[11]	pGAPDH	0.95

<sup>1</sup>PCR efficiency curve was calculated with the qPCRsoft software from Analytik Jena (Jena, Germany) and the PCR efficiency was determined as the slope R<sup>2</sup>

**Table S3** Virus-specific oligosequences integrated in gBlocks I, II, III and IV

GOI*	reference	Oligosequence of the amplicon (5' → 3')
<b>gBlock I</b>		
PPV-1	[1]	CAGAATCAGCAACCTCACCACCAACCAAAATATATAATAATGATCTAACT GCAAGCTTAATGGTCGCACTAGACACCAATAACACACTTCCATACACACC AGCAGC
PCMV	[2]	ACTTCGTGCGCAGCTCATCTGAGAGAGCTCGACCGCCGCCCTGGCAACCTC GGAATCCCAGAAC
PLHV-3	[3]	AAGGACCCCAAAGAGGAAAATCAATTTTATGGTTCACCTTCTACCTTCC TTACAGAGTATGCAGTGCCTCAG
HEV	[4]	GGTGGTTTCTGGGGTGACCGGGCTGATTCTCAGCCCTTCGCAATCCCCTA TATTCATCCAACCAACCCCT
PCV3	[5]	AGTGCTCCCCATTGAACGGTGGGGTCATATGTGTTGAGCCATGGGGTGG GTCTGGAGAAAAGAAGAGGCTTTGTCCTGGGTGAGCGCTGGTAGTTCCC GCCAGAAGTGGTTTGGGGGTGAAGTAACGGCTGTGT
<b>gBlock II</b>		
PLHV-1	[3]	CTCACCTCAAATACAGCGACCTGGTCTACTGAATCGCCGCTAACAGGTC ACTATGGAACACACGATTCAAGC
PLHV-2	[3]	GTCACCTGCAAATACACAGGCCTGGTCTACTGAAGCGCTGCCAATAGGTC AATATGGAACATACGATTCAAGCC
PCV4	[6]	CAGCGACCTTAAAGCGGCTGTGGCCGCCCTGAATGCCGGCAGCTCAATGA GTGAAGTGGCCCGTGAGTTCCCGTCTGTATTTATAAGGTATGGGCGTGGC CTCCGGGACTACGTCATTAAGTGC
SARS-CoV-2	[7]	ACAGGTACGTTAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCGTGGT ATTCTTGCTAGTTACTAGCCATCCTTACTGCGCTTCGATTGTGTGCGT ACTGCTGCAATAT

TTSuV-1	[8]	CGAATGGCTGAGTTTATGCCGCCAGCGGTAGACAGAACTGTCTAGCGAC TGGGCGGGTGCCGGAGGATCCCTGATCCGGAGTCAAGGGCCTATC
TTSuV-2	[8]	CGAATGGCTGAGTTTATGCCGCTGGTGGTAGACACGAACAGAGCTGAGT GTCTAACCGCCTGGGCGGGTGCCGGAGCTCCTGAGAGCGGAGTCAAGGG GCTTATC
<b>gBlock III</b>		
pGAPDH	[9]	ACATGGCCTCCAAGGAGTAAGAGCCCCTGGACCACCAACCCCAGCAAGAG CACGCGAGGAGGAGAGAGGCCCTCAGCTGCTGGGGAGTCACAGCCCCAAC TCGATC
huGAPDH	[10]	GGCGATGCTGGCGCTGAGTACGTCGTGGAGTCCACTGGCGTCTTACCAC CATGGAGAAGGCTGGGGCTCATTTGCAGGGGGGAGCCAAAAGGGTCATCA TCTCTGCCCCCTCTGCTGATGCCCCATGTTTCGTATGGGTGTGGACCA
PERV pol	[11]	CGACTGCCCAAGGGTTCAAGAACTCCCCGACCATCTTTGACGAAGCCCT ACACAGGGACCTGGCCAACCTCAGGATCCAACACCCTCAGGTGACCCTCC TCCAGTACGTGGATGACCTGCTTCTGGCGGGAGCCACCAAACAGGACTGC TTAGAAGGTACGAAGGCACTACTGCTGGAATTGTCTGACCTAGGCTACAG AGCCTCTGCTAAGAAGGCCAGATTTGCAGGAGAGA
PCV2	[12]	CGGATATTGTATTCTGGTCGTATATACTGTTTTCGAACGCAGTGCCTAG GCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCATAGCTGAT TTCTTTGTTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGG

**Table S2** (Continuation)

<b>GOI</b>	<b>reference</b>	<b>Oligosequence of the amplicon (5' → 3')</b>
<b>gBlock IV</b>		
PCV1	[12]	AACCCCATAGAGGTGGGTGTTACCCCTTAATAATCCTTCCGAGGAGGAG AAAAACAAAATACGGGAGCTTCCAATCTCCCTTTTGGATTATTTGTTTG CGGAGAGGAAGGTTTGAAGAGGGTAGAA
PCV2	[12]	CTGAGTCTTTTTATCACTTCGTAATGGTTTTTATTATCACTTAGGGTT AAGTGGGGGGTCTTTAAGATTAATTCTCTGAATTGTACATACATGGTTA TACGGATATTGTAATCCTGGTTCGTATATACTGTTTTCGAACGCAGT
PCV3	[12]	CATAAATGCTCCAAAGCAGTGCTCCCCATTGAACGGTGGGGTCATATGTG TTGAGCCATGGGGTGGGTCTGGAGAAAAGAAGAGGCTTTGTCCTGGGTGA
PCV4	[12]	ATTATTAACAGACTTTATTTGTGTCATCACTTCGGATACTACACTTGAT CTTAGCCAAAAGGCTCGTTGATTGAGTGATCACTACGCATTATCCCTGT
PLHV-3	[13]	AACAGCGCCAGAAAAAAGGACCCCAAAGAGGAAAATCAATTTTATGGTT CACCTTCTACCTTTCC

\*GOI = gene of interest

**Figure S1** Workflow of using gBlock gene fragments as standard for the determination of the copy number using gBlock I as example

**(1) Determination of the genes of interest**



**(2) Design of a gBlock**

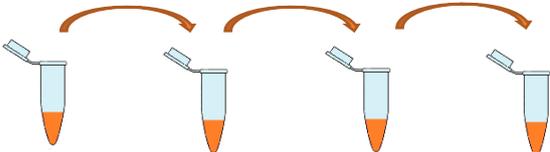


**(3) Calculation of the copy number**

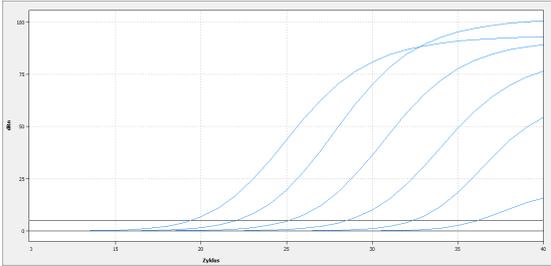
$$\text{copy number per } \mu\text{l} = c \times M \times 1 \times 10^{-15} \frac{\text{mol}}{\text{fmol}} \times \text{Avogadro's number}$$



**(4) Preparation of a log<sub>10</sub> dilutional series**



**(5) Comparative analysis of the qPCR assays using the log<sub>10</sub> dilutional series of the gBlock**



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