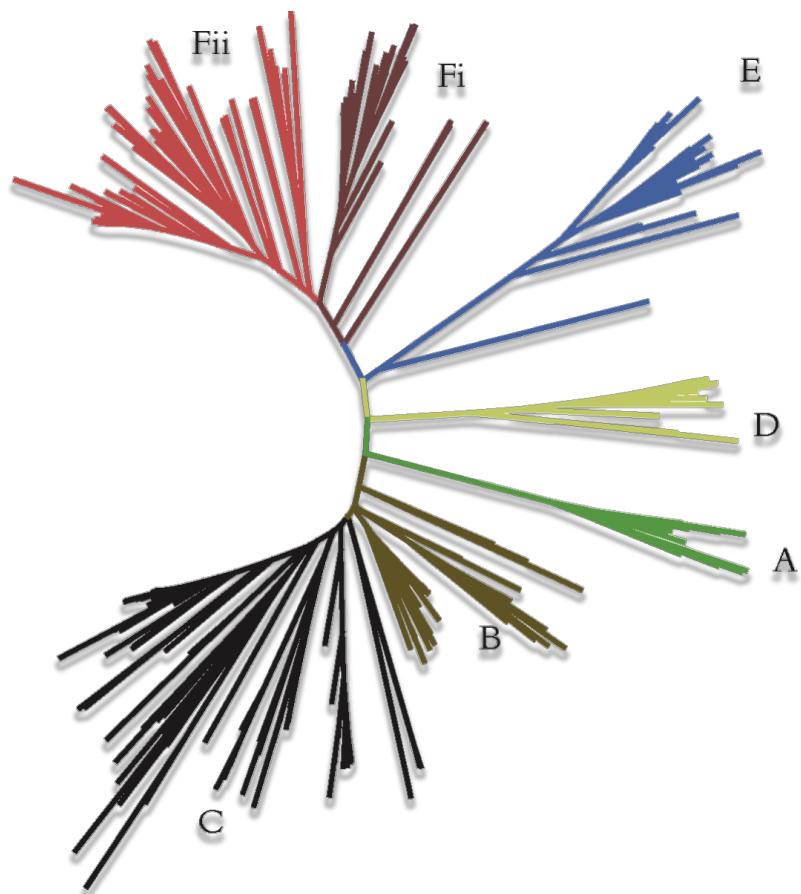


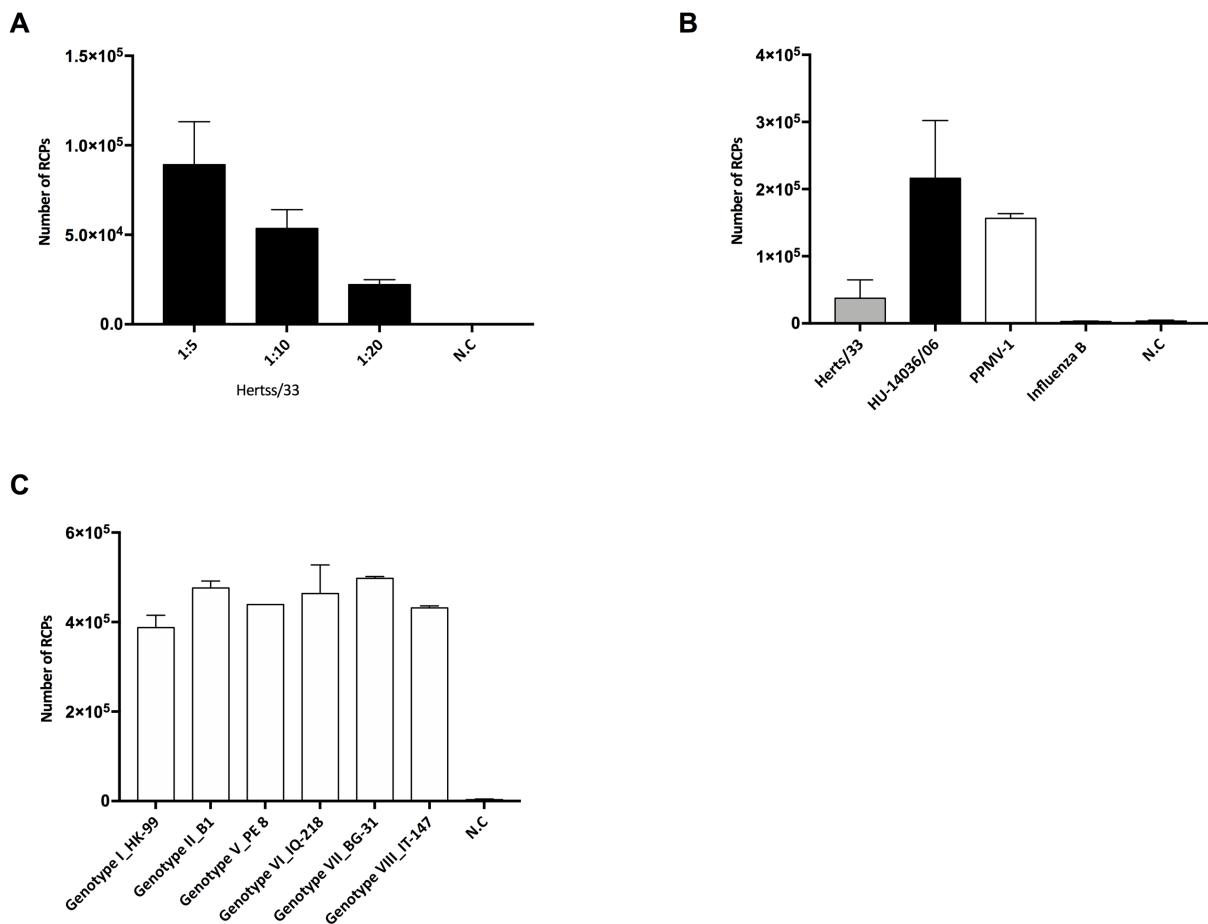
# A novel mutation tolerant padlock probe design for multiplexed detection of hypervariable RNA viruses

Sibel Ciftci<sup>1</sup>, Felix Neumann<sup>1</sup>, Iván Hernández-Neuta<sup>1</sup>, Mikhayil Hakhverdyan<sup>2</sup>, Ádám Bálint<sup>3</sup>, David Herthnek<sup>1</sup>, Narayanan Madaboosi<sup>1\*</sup>, Mats Nilsson<sup>1\*</sup>

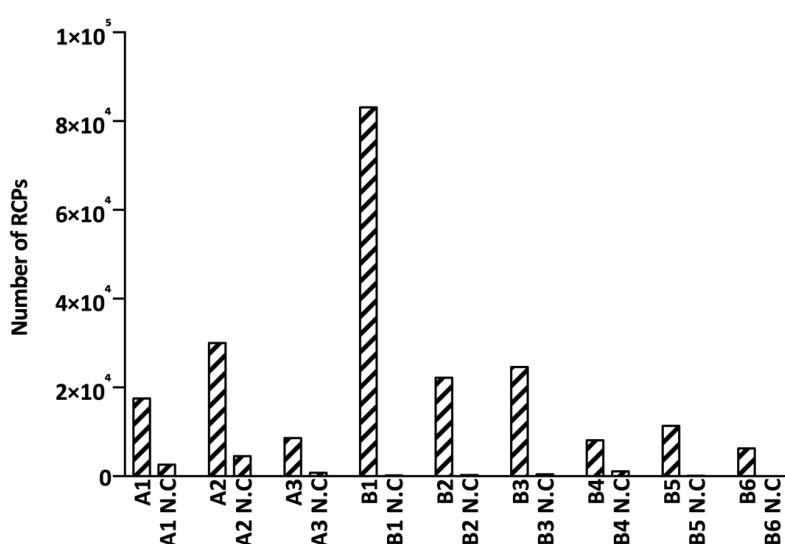


**SI, Fig. S1:** Phylogenetic tree construction over N-gene of IBV, and its groups (A, B, C, D, E, F<sub>i</sub>, F<sub>ii</sub>).

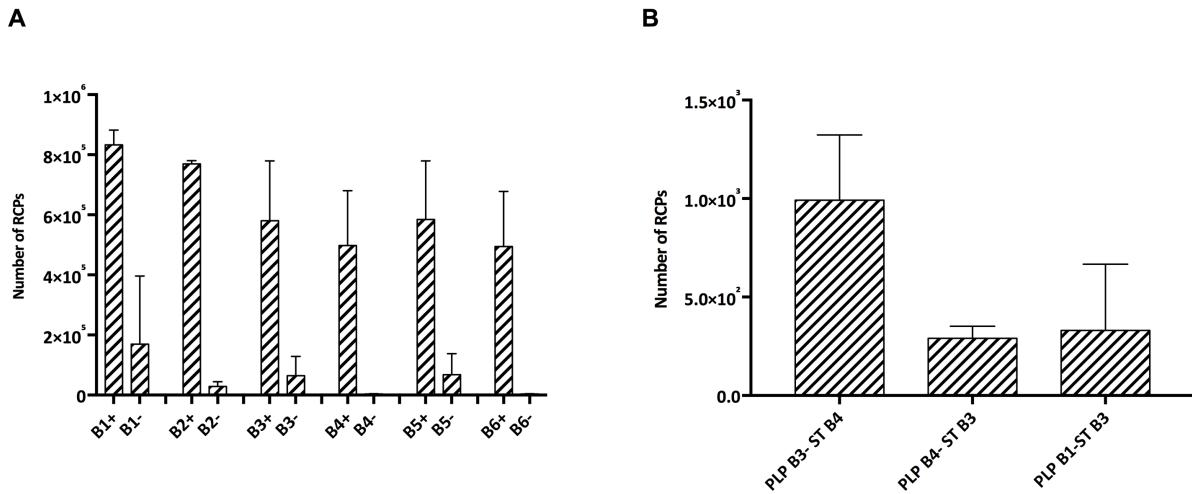
**SI, Fig. S2:** Output of extracted sequences obtained from Geneious ‘Alignment View’, showing the position of mismatches in individual sequences relative to the consensus. The position of yellow coloured bases in the consensus will be accommodated by Wobbles during PLP design. Mismatches to any of the consensus sequences is represented in red colour. ‘True’ or ‘False’ scoring is based on the positioning of mismatches (5 bp) in relation to the ligation site.



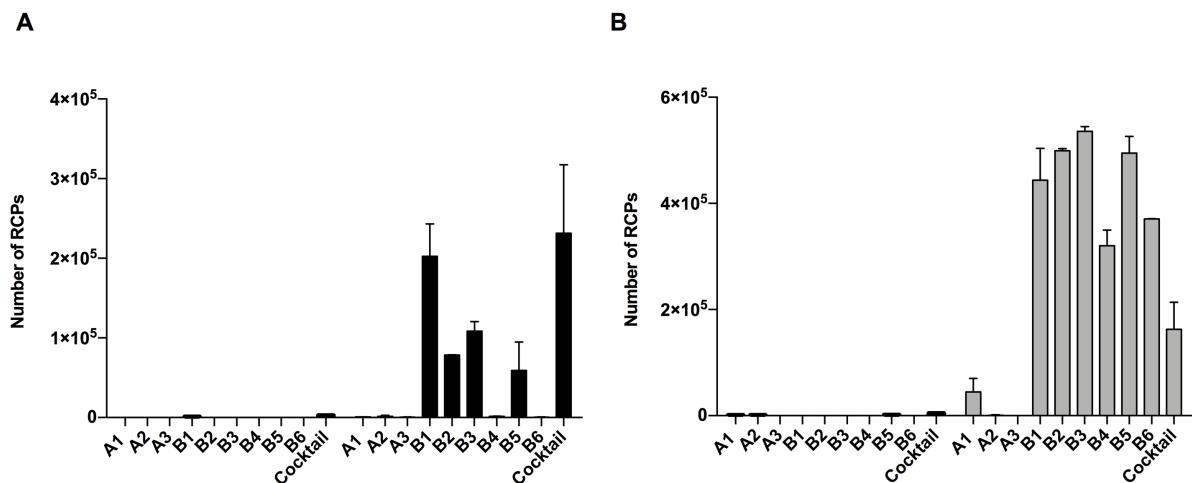
**SI, Fig. S3:** Optimization of RT-C2CA experiments. **A.** Different concentrations of cDNA from Herts/33 synthesized using SP (B1) and amplified using PLP (B1). **B.** 1:40 dilution of cDNA from different strains (along with Influenza B virus as specificity control), synthesized using RP and amplified using cocktail PLP. **C.** 1:10 dilution of cDNA from different strains, synthesized and amplified as in **B**.



**SI, Fig. S4:** PLP validation by RT-C2CA assay on their respected synthetic targets (100 fM) along with their negative controls (water instead of synthetic target).



**SI, Fig. S5:** RT-C2CA assay performed using synthetic targets (ST) at a concentration of 100 fM and cocktail PLP for the specific performance of the PLPs used. **A.** Use of specific PLPs, alongside showing the results after the elimination of the respective PLP from the cocktail (e.g., B1+ uses cocktail PLP for detecting B1 synthetic target; B1- has elimination of B1 PLP from the cocktail). **B.** Cross-reactivity of PLPs on synthetic targets.



**SI, Fig. S6** Performance of individual and cocktail PLPs for C2CA validation using **A.** Herts/33 and **B.** HU-14036/06, along with their respective negative controls (water instead of template). cDNA (dilution of 1:20) synthesized by SP (B1 for Herts/33 and B3 for HU-14036/06) + RP was used.

## SI, ST1. Synthetic targets used in this study

Name	5' modification	Sequence
NDV.A1	Biotin	TGCGAGAGGGGGWATTGAGGGGCTTGCCAGAA
NDV.A2	Biotin	AAGACAGAGAGACTATCAGRTCAGATACTTCTTCATCTA
NDV.A3	Biotin	TATATCGAGTGTCTCATATGTCCATATCAATGACT
NDV.B1	Biotin	CAGGGAAATGGGTCAATTGARGATAGCATATCCTT
NDV.B2	Biotin	TGCAAAAGTATTGCTTAAYTGAGATATCAGACAGTCAA
NDV.B3	Biotin	GTGAAAACACTGTAATGTCYGTGCCAACATTGCATC
NDV.B4	Biotin	AGATTATGCCGGAAYAGAAGCTGGTCACCTTGACAGG
NDV.B5	Biotin	CACCTTACATTACATATCYAATGATTYCAGGCTATT
NDV.B6	Biotin	TGACTCGTGCCTAACAAAATTSTAYATGAAACCATAGG

## SI, ST2. Table of oligonucleotides used for other avian viruses

Name	5' modification	Sequence
ILTV_PLP.1	Phosphate	GAAGGGATTGTTCTGGAACGTGTATGCAGCTCTCAGTAATAGTGTCTTACCGCCAACGTGAGCATCGTATAATGCGTCTGGTCGATT
ILTV_PLP.2	Phosphate	CGACGTAAGAAAGTACAACGCTGTATGCAGCTCTCAGTAATAGTGTCTTACCGCCAACGTGAGCATCGTATACTCGAATGGCCCGT
IBDV_PLP.1	Phosphate	GTCAATTGAGGTGAGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTCGCAGTGGTCAGGTACACTGACCCCTGTGCCCCACA
IBDV_PLP.2	Phosphate	CCACAGTCATTGAGGTGAGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTCGCAGTGGTCAGGTACACTGACCCCTGTGCTCC
IBDV_PLP.3	Phosphate	CACTCAGTATCAATTGAGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTCGCAGTGGTCAGGTACACTGACCCCTGTGCTCC
IBDV_PLP.4	Phosphate	TTCTGACGGGGCTGGGTATGCAGCTCTCAGTAATAGTGTCTTACCTCGCAGTGGTCAGGTACACTGAGGCAAGACGGTCCCT
IBDV_PLP.5	Phosphate	TCTCTGAGTACACTAGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTCGCAGTGGTCAGGTATATGATGCCAACCGCTCT
IBV_PLP.1	Phosphate	CACTTGGTAAAGAACCTGGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAGATTTGGGTGATTAG
IBV_PLP.2	Phosphate	AAAGCATTGACCTCAGATGAGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAGCAGGATGATGAAGTRGAT
IBV_PLP.3	Phosphate	GTTGCTGCAAAGGGTGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATACAGATGGTATAGTGTGG
IBV_PLP.4	Phosphate	AATGAGGARGGTATTAAGGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATATTGGTATGACAAGATG
IBV_PLP.5	Phosphate	AATGAGGARGGTATTAAGGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATG
IBV_PLP.6	Phosphate	GTTGGGTTCTGCAAAGGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATGGTATA
IBV_PLP.7	Phosphate	GTTGGGTTCTGCAAAGGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATGGTATA
IBV_PLP.8	Phosphate	TTTTGGAAGTAGAGTGACGGGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATGGTCT
IBV_PLP.9	Phosphate	CGTACTAAAGGTAAGGGGGGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATGGTCT
IBV_PLP.10	Phosphate	CCTGATAATGAAAATCTTAAAGGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAATTGGTATGACAAGATGGTCT
IBV_PLP.11	Phosphate	GACCTGAATTGGGGTGTGTATGCAGCTCTCAGTAATAGTGTCTTACCTGTCCCGTGTGCTGAGATAACAGGACCAGCCGCT
AIV_PLP.1	Phosphate	CRCTGGCACGGTAGTGTATGCAGCTCTCAGTAATAGTGTCTTACAAATCGTCATAGCAGGCGCCGTCAGTCYCGYT

## SI, ST3. Concentrations of cDNA samples used for assay optimization.

Primer and cDNA conditions	RP	SSP	SP mix	RP + SP mix
Genotype IV_Herts/33	3.8 ng/µL	0.800 ng/µL	3.16 ng/µL	4.64 ng/µL
Genotype VII_HU-14036/06	7.00 ng/µL	4.60 ng/µL	8.20 ng/µL	12.3 ng/µL

**SI, ST4.** List and details of viral strains used in the study.

	Strain Name	Genotype /virus	NCBI	Virulence*	cDNA (ng/ $\mu$ l)	Copy number/ $\mu$ l	Provider
BATCH-I	HK-99	I	EU604269	L	1.87		SVA (Sweden)
	B1	II	AF309418	L	4.40		
	Herts/33	IV	FJ687487	V	3.8		
	PE-8	V	EU604263	V	1.62		
	IQ-218	VI	EU604254	M	3.70		
	BG-31	VII	EU604250	V	5.16		
	IT-147	VIII	EU604262	V	3.18		
BATCH-II	Ulster 2C	I	AY562991	L		$10^4$	NEBIH (Hungary)
	La Sota	II	AJ629062	L		$10^5$	
	Ph/80	III	FJ687488	M		$10^4$	
	Herts/33	IV	FJ687487	V		$10^5$	
	HU-206/81	V	-	V		$10^5$	
	HU-202/16**	VI	-	M		$10^5$	
	HU-14036/06	VII	-	V		$10^4$	
Non-NDV strains	IT-147/94	VIII	EU604262	V		$10^4$	
	Cevac LT L	ILTV	-			$10^4$	NEBIH (Hungary)
	Hipragumboro-CH/80	IBDV	-			$10^6$	
	11518/10	IBV	-			$10^7$	
	A/duck/Hungary/5	AI	-			$10^6$	
	4494/16 (H5N8)						
	B/Stockholm/5/2014 (Victoria)	Influenza B	-			$2 \times 10^4$	Karolinska institute (Sweden)

\* L: Lentogenic M: Mesogenic V: Velogenic

\*\* PPMV-1: Pigeon paramyxovirus type 1  
(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2566108/>)