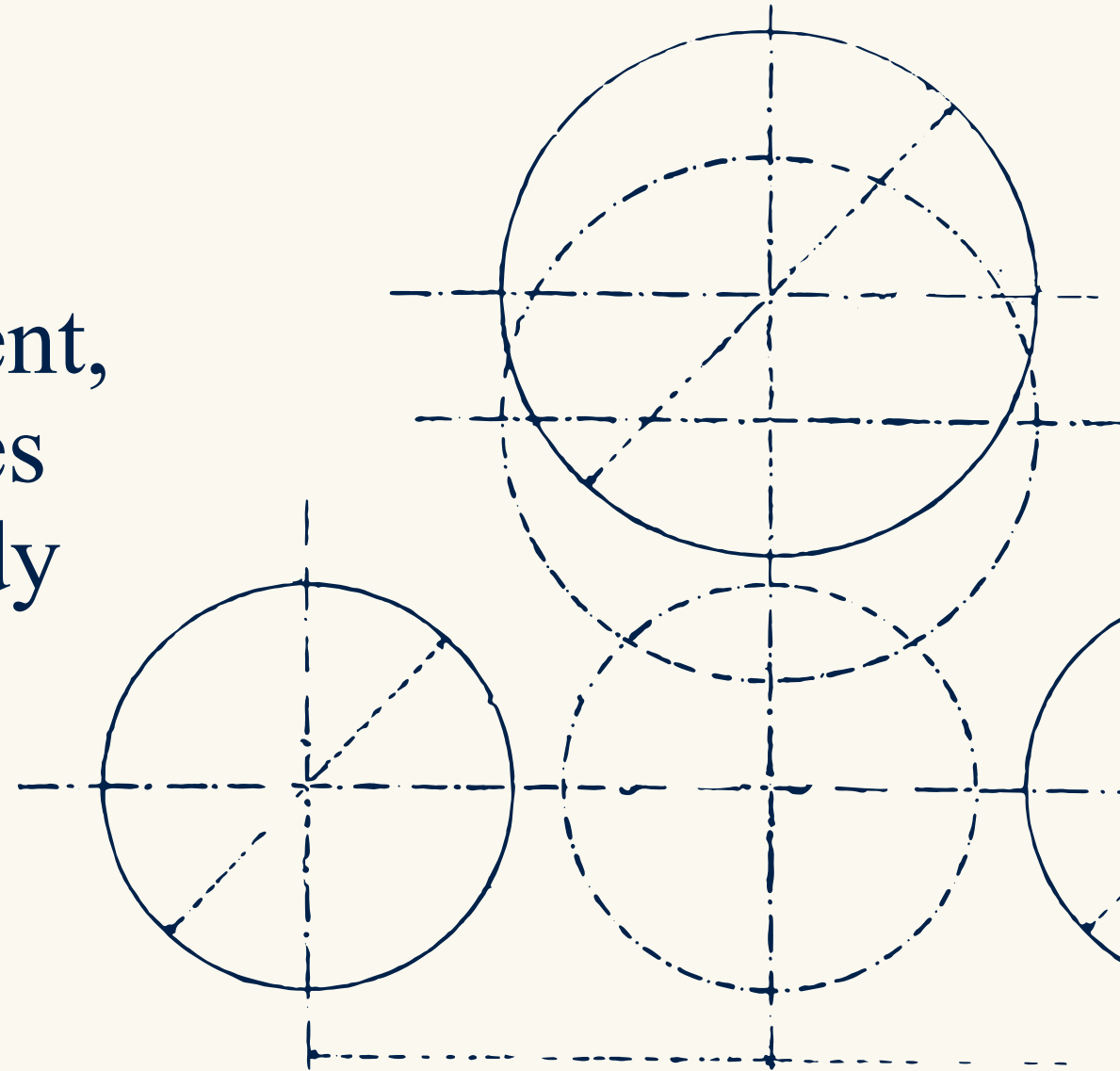


**INVIVYD INC.**

# VMS063: a novel, highly potent, half-life extended, pan-measles variant investigational antibody

TAVI 2026

Robert Allen, Ph.D.



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This presentation contains hyperlinks to information that is not deemed to be incorporated by reference in this presentation.

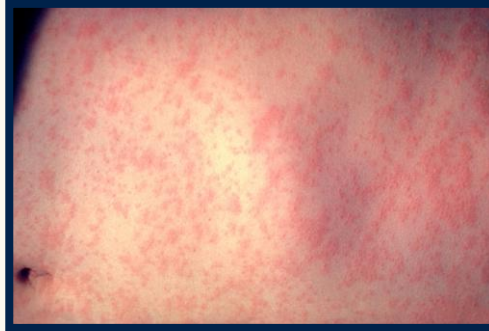
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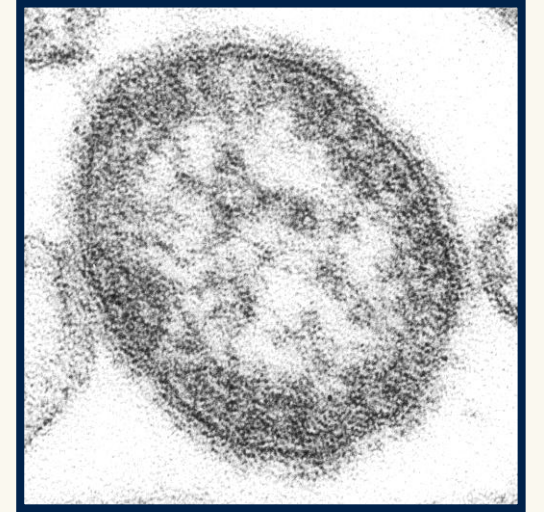
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# Measles Virus Background

- The Measles Virus (MeV) is an RNA *Morbillivirus*
  - There are 24 strains of MeV divided into 8 clades: A-H
- Transmission occurs through respiratory droplets and is highly infectious
  - Symptoms include fever, coughing, malaise, and a rash
  - Complications occur in ~30% of cases requiring hospitalization
  - ~2/1000 children infected results in death



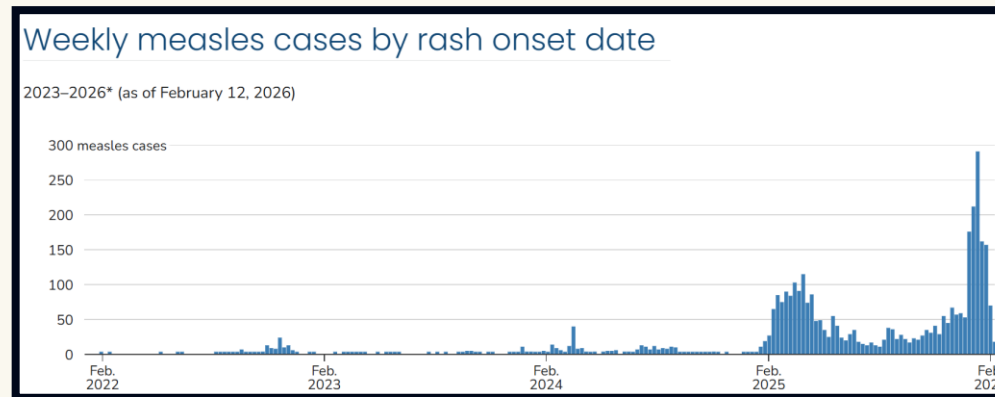
Measles



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# Measles Virus Background

- Vaccination is the primary form of preventing Measles
  - The first Measles vaccine was introduced in 1963
  - Introduction of the MMR vaccine in 1971 reduced Measles cases by >99%
  - MMR-II was approved in 1978 for children 12 months and older
- There are few treatments for Measles
  - IVIg/IMlg is an expensive option reserved for the most at risk patients
- Less than 220 cases per year were reported in the USA between 1997 and 2013
  - In 2025 there were 2285 confirmed cases of Measles in the USA
  - As of March 16 2026, there have been 1487 confirmed cases of Measles reported in the USA in 24 states



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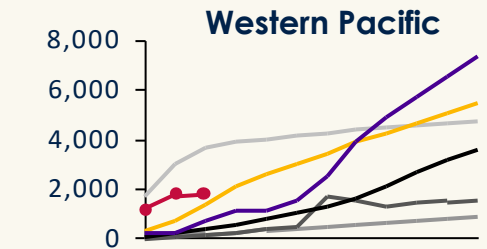
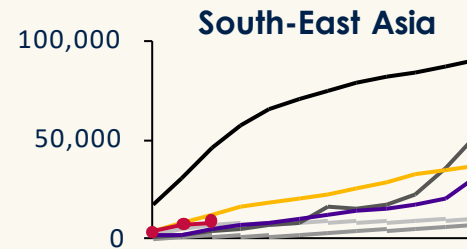
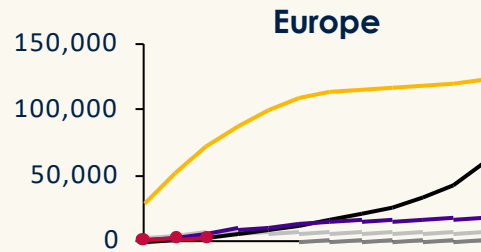
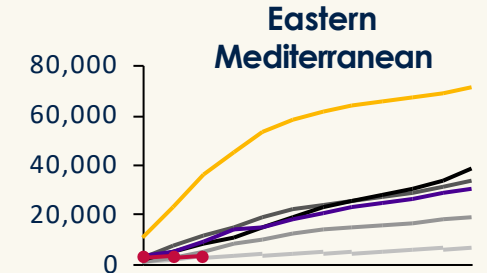
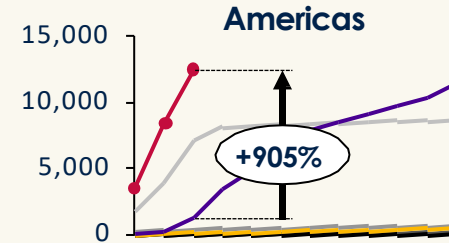
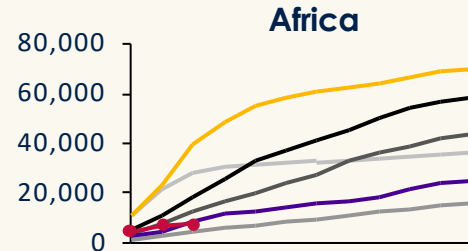
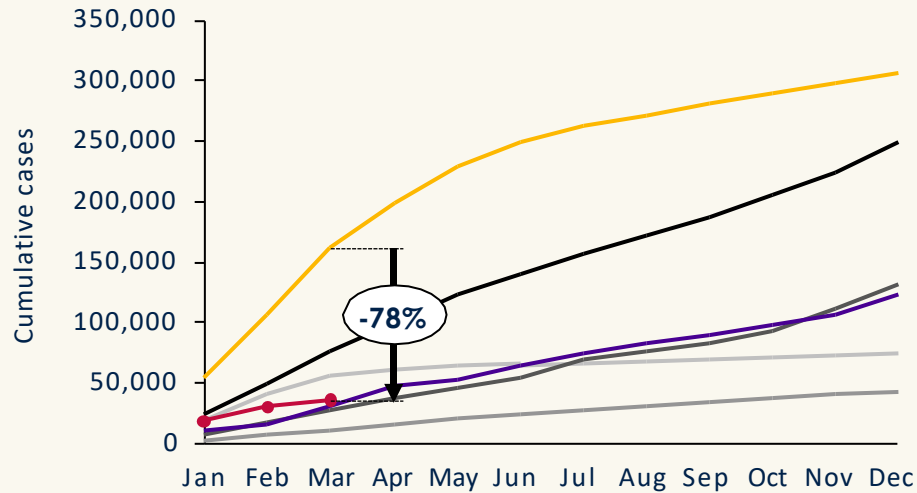
# CURRENT measles virus disease burden

## Global measles resurgence continues into 2026, with the Americas emerging as the new crisis frontline

Global and regional cumulative measles cases, 2020-2026\*

Confidence: ● Moderate (3.5)

Global 2026 cases are ahead of 2025, with the Americas accelerating the fastest



— 2020 — 2021 — 2022 — 2023 — 2024 — 2025 — 2026\*

Data: [WHO](#), [Bangladesh](#), [Latvia](#), [Bulgaria](#), [Indonesia](#), [Guatemala](#), [UK](#), [US](#), [Africa](#)  
 Visualisation: Airfinity

\* 2026 data are incomplete, with latest data for Mar 2026, though not for all countries due to reporting delays.

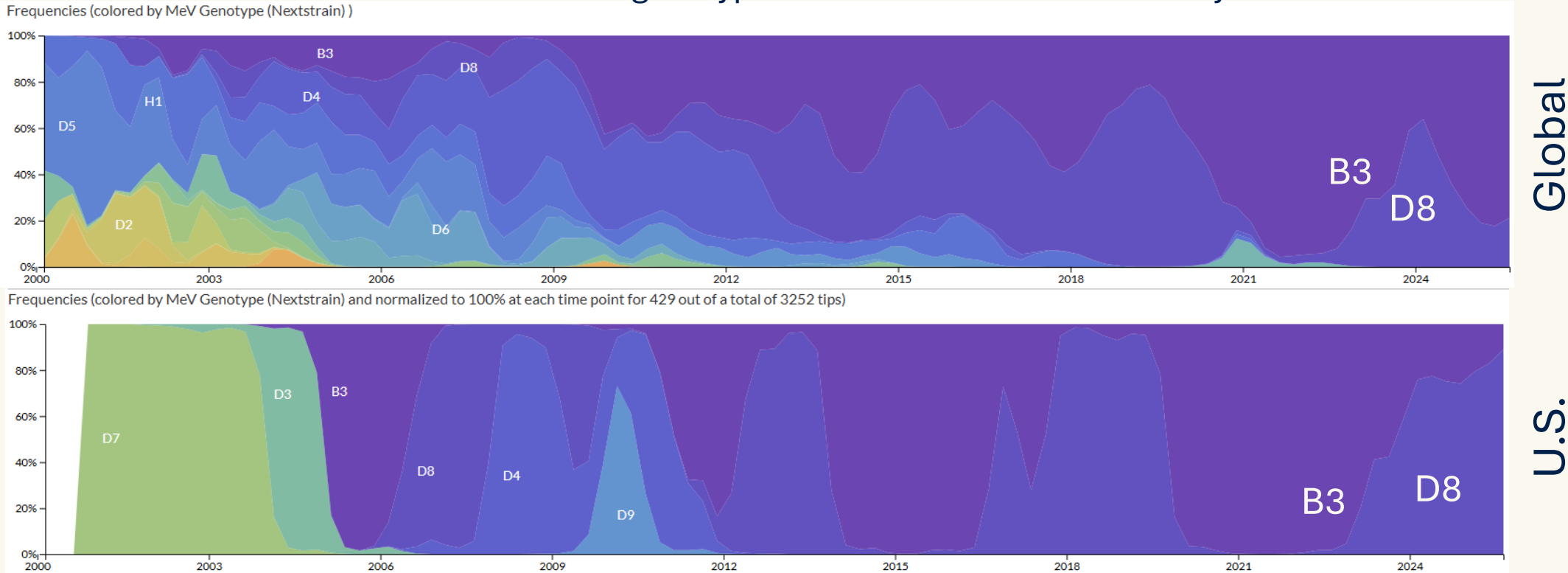
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# CURRENT measles virus variants

## Fusion (F) conservation



- B3 and D8 genotypes have dominated for several years



### Current outbreak in South Carolina

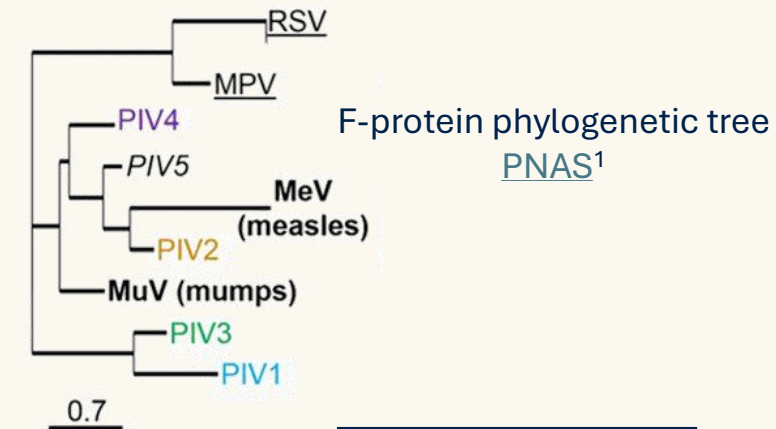
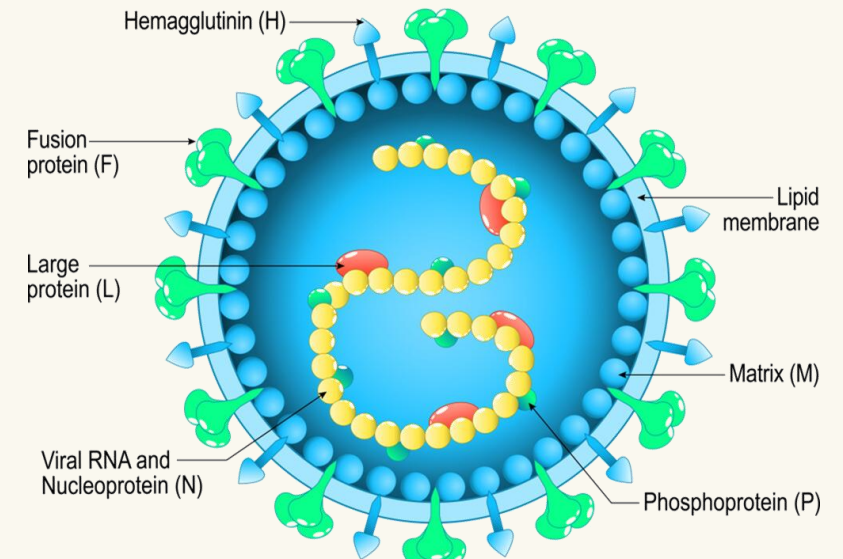
- 139 complete F sequences from the past 6 months, all of genotype D8
- 125 (90%) are identical
- 14 carry a single amino acid change
  - T95A (x3) L197S (x1) H297Y (x1) D472N (x1) G541R (x8)



\*based on N450 sequences (<https://nextstrain.org/measles/N450>)

# Measles virus Surface proteins

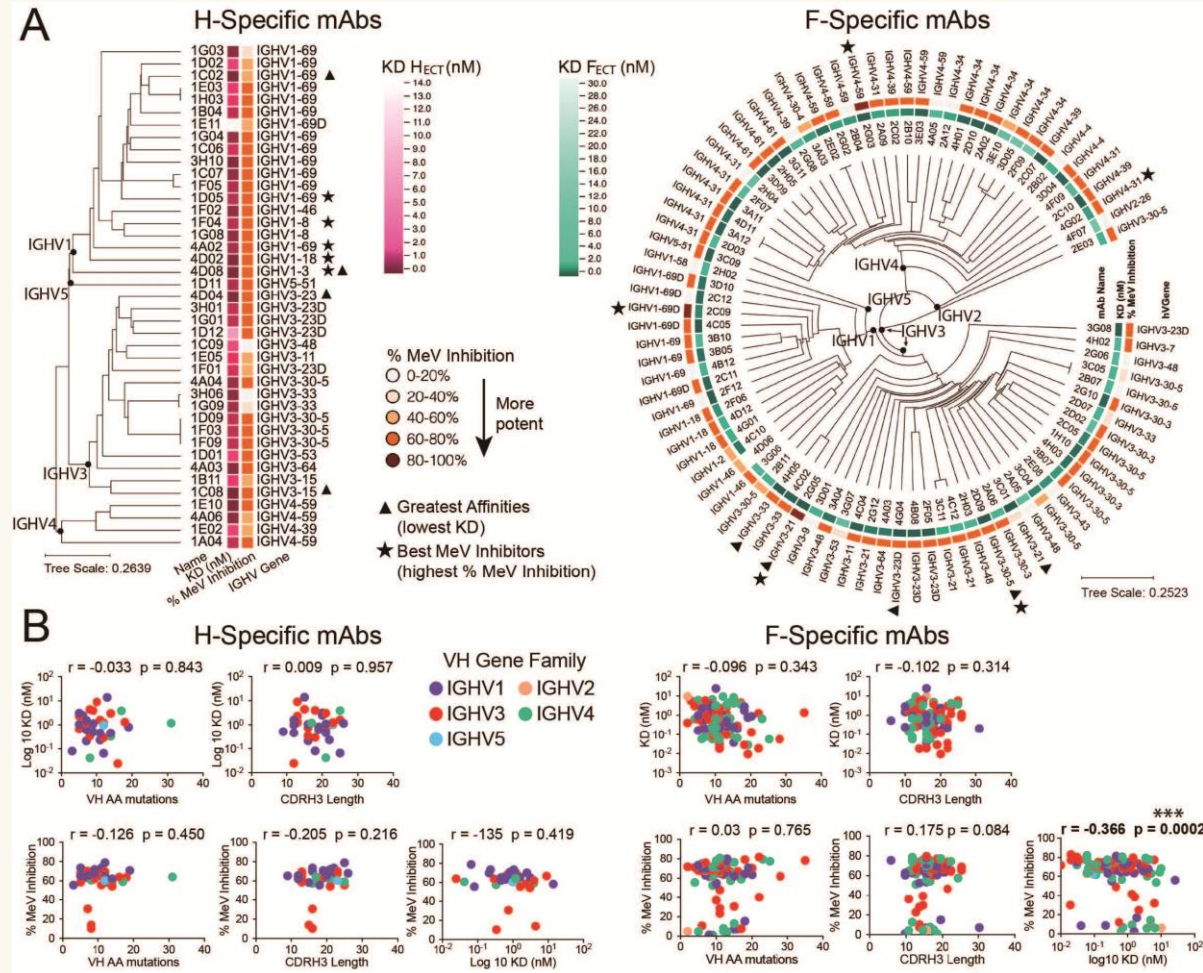
- Like PIV and MuV, the MeV genome encodes for two surface proteins: Fusion (F) and Hemagglutinin (H)
  - The F-protein is the trimeric fusion protein responsible for viral membrane fusion
  - The H-protein is responsible for cell adhesion
- Antibodies isolated from vaccinated individuals show anti F- and H-protein antibodies that are neutralizing
- Measles can utilize multiple receptors for cell entry including CD150 (SLAM), CD46, and Nectin-4
- The MeV-H protein is responsible for receptor binding. When it binds to a receptor MeV-H undergoes a conformational change that triggers the MeV-F protein that is responsible for viral fusion
- We produced several MeV-F variants internally at Invivyd in HEK293 cells
  - This preserves the native glycosylation structures
  - These include the Edmonston, B3, and D8 variants



1. Stewart-Jones GBE et al. Structure-based design of a quadrivalent fusion glycoprotein vaccine for human parainfluenza virus types 1–4, PNAS. 2018.

# V-Gene Representation in H- and F-Specific Measles Antibodies from Vaccinated Donor

Figure S1



- H-Specific antibody responses are predominated by IGHV1-69 and IGHV3 V-gene usage
- F-Specific antibodies following MMR immunization have a similar V-gene usage with an increased representation of IGHV4 clones
  - 4-31, 4-34, 4-59 predominate the IGHV4 response
- VMS063 is an IGHV1-46 F-Specific mAb
  - This V-gene usage is among the documented V genes utilized in post-vaccination immune responses
- Notably, IGHV1 gene family members represent some of the highest affinity and most potent inhibitors isolated from vaccinated donors

<https://doi.org/10.1101/2025.09.09.675230>

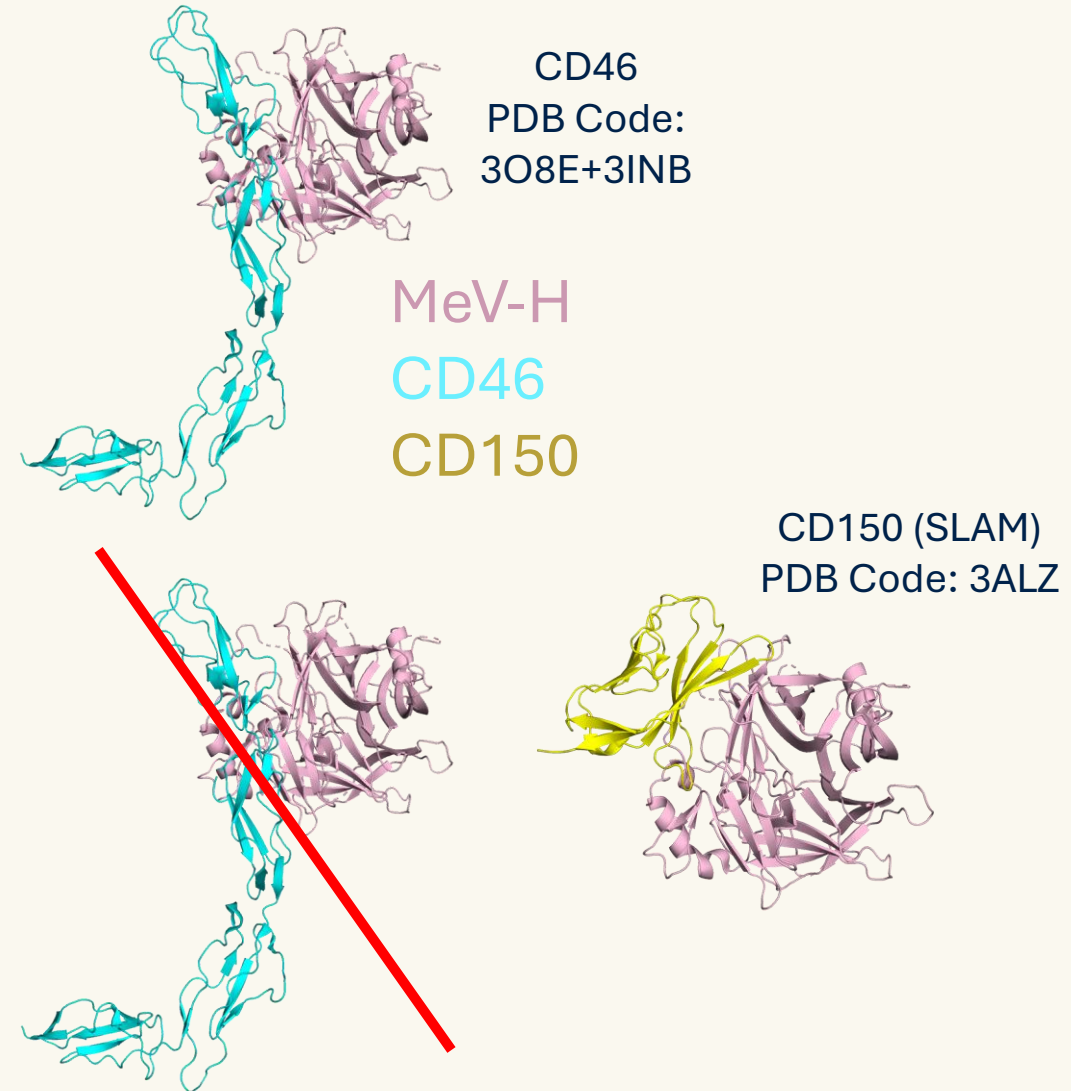
# Measles Pseudovirus screening of VMS063

## PVNA using HEK293T-TIM1 (Natively CD46 expressing)

Antibody	B3	B3.1.1	D8.1.2	Average
	IC <sub>50</sub> (µg/mL)			
VMS063	0.0009	0.0008	0.0008	0.0009

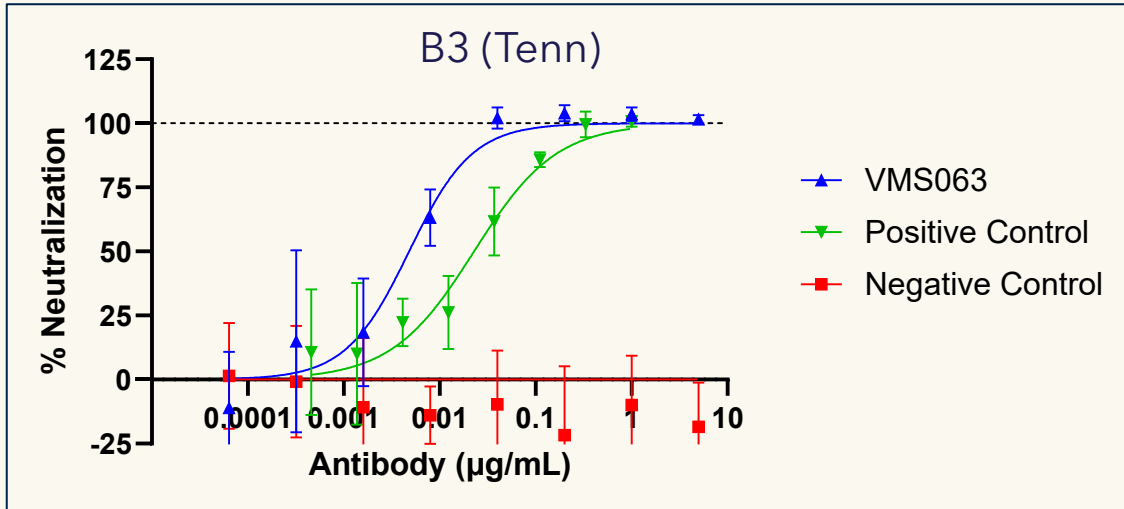
## PVNA using HEK293T-CD46KO-CD150

Antibody	B3	B3.1.1	D8.1.2	Average
	IC <sub>50</sub> (µg/mL)			
VMS063	0.0016	0.0021	0.0023	0.0019



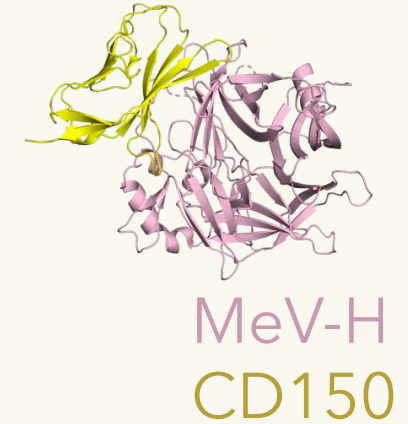
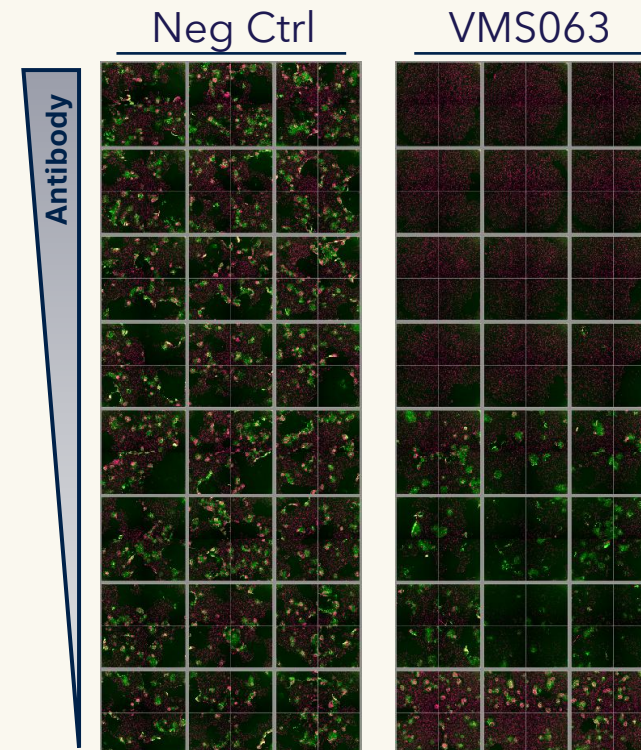
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# VRS - Authentic MV neutralization – Curves and IC50



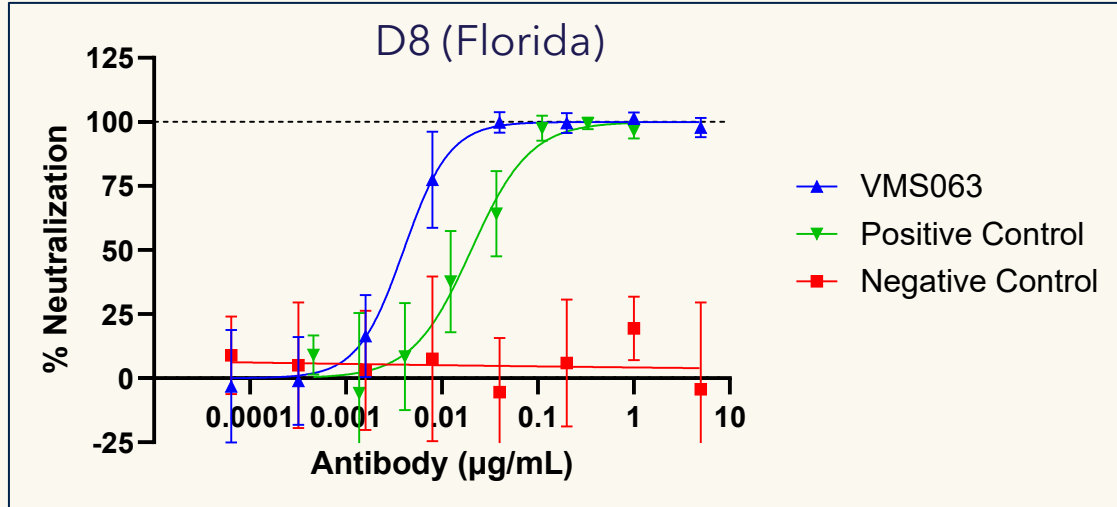
Antibody	B3 IC <sub>50</sub> (µg/mL)
VMS063	0.0042
Positive Control	0.0211
Negative Control	>5

## Representative Staining



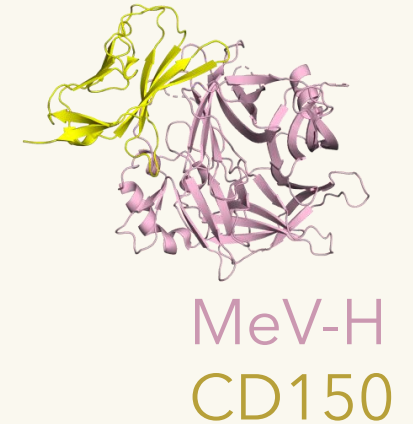
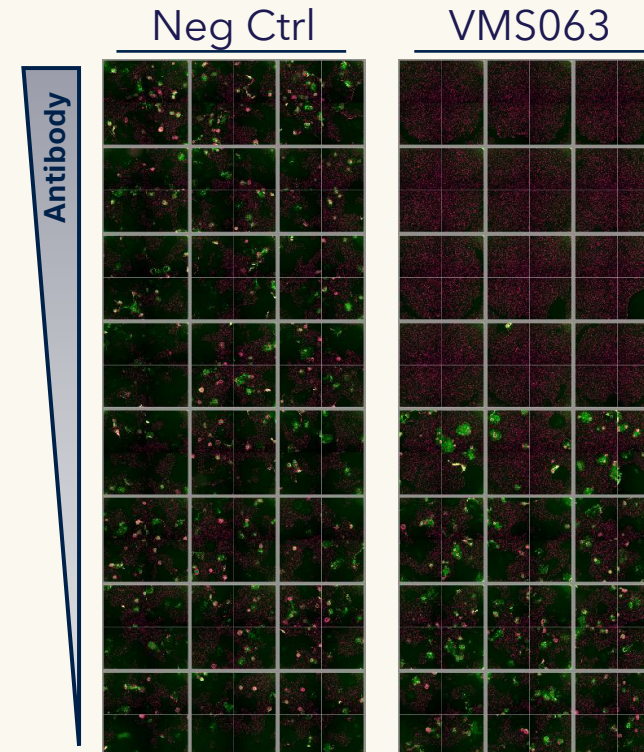
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# VRS - Authentic MV neutralization – Curves and IC50



Antibody	D8 IC <sub>50</sub> (µg/mL)
VMS063	0.0042
Positive Control	0.0198
Negative Control	>5

## Representative Staining



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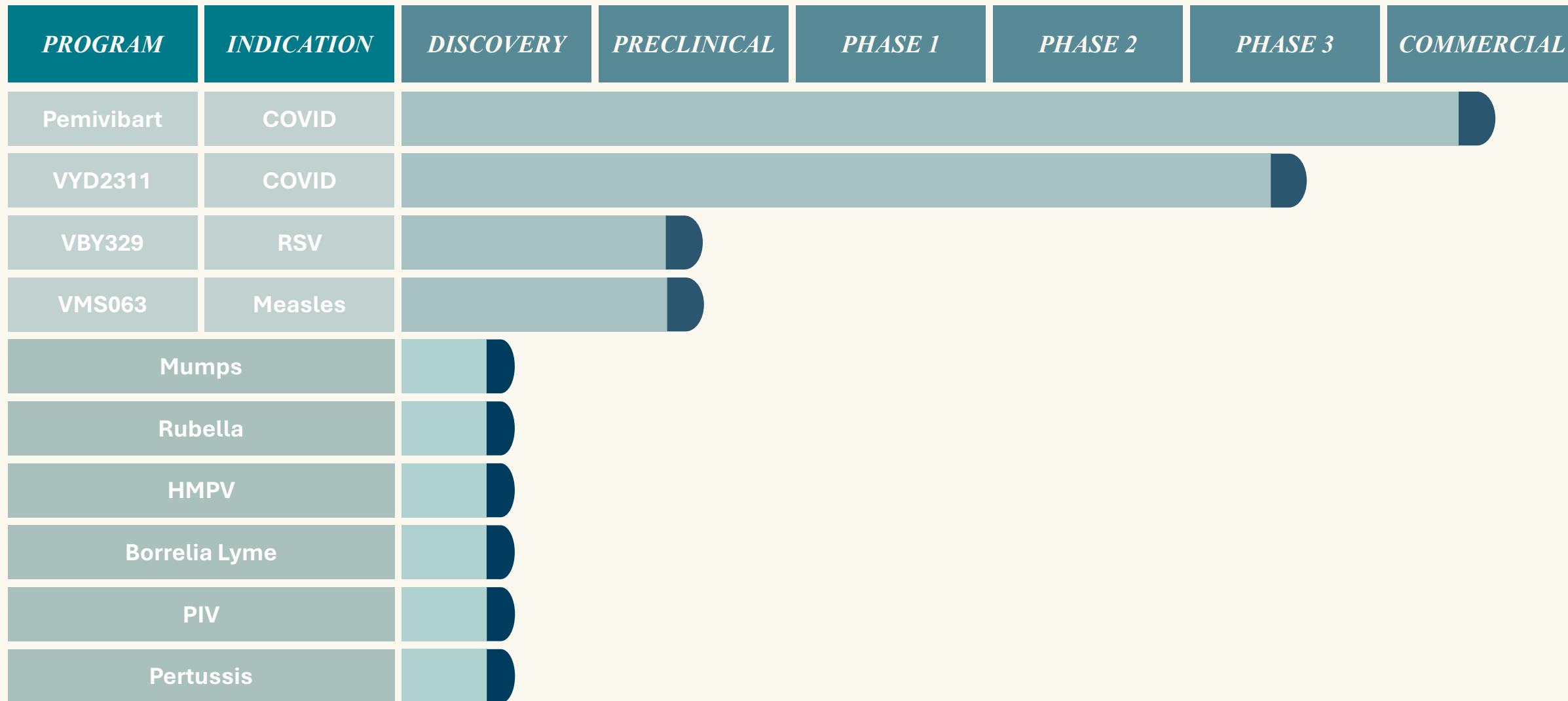
# VMS063

- VMS063 has an ideal profile for continued progression to IND readiness
  - VMS063 is highly potent in vitro:
    - Modern B3 and D8 Variants: avg **4.2** ng/mL (Authentic Virus Assays), avg **1.4** ng/mL (Pseudovirus Assays)
  - VMS063 has a desirable developability profile and is currently in preclinical development:
    - Based on  $T_M$ ,  $T_{agg}$ , HIC, and self-association profiles
  - The epitope for the VMS063 parental mAb has been determined and is well conserved among sequenced variants submitted to public databases, including those from the most recent US outbreaks.
- VMS063 is being considered for potential use in treatment, post-exposure prophylaxis, pre-exposure prophylaxis in adults and pediatric bridge to first vaccination\*.
- From a public health perspective, if approved, VMS063 could be deployed by public health authorities to attempt to respond to outbreaks and drive continued measles elimination in the U.S. and abroad\*.

\*Subject to clinical development and regulatory approval

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# PIPELINE



RSV: respiratory syncytial virus; HMPV: Human metapneumovirus; PIV: Human parainfluenza viruses