

## PRRSV2 1H.18

### Situation Report of PRRSV Variant 1H.18, August 10, 2026

#### VUM: Category 1

PRRSV variant 1H.18, typically linked to RFLP pattern 1-12-2, has been demoted to a variant under monitoring (VUM) Category 1 on August 2026. VUM Category 1 are those with predicted growth in the next 12 months and with <31 new sites affected in the past 6 months. PRRSV 1H.18 was first detected in 2018, based on the MSHMP sequence dataset. It likely originated from a recombination event, combining genetic material from variants 1H.31 and 1C.3 (Herrera da Silva et al., 2025).

[Click here](#) to access monthly epidemiological updates on PRRSV variants under monitoring.

| Indicator                  | Evidence                                                                                                                                                                                                                                                                                                                                                                                                                             |
|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Populational growth        | This variant has been consistently circulating across multiple production systems since 2024, with a slight increase in the number of affected sites observed in spring 2025. As of August 2026, over 480 sequences have been identified, linked to over 120 unique sites across 18 production systems in 7 states. This variant continues to be detected both in breeding and in growing pig herds in primarily Iowa and Minnesota. |
| Production impact/severity | There are no reported or published studies on the impact of 1H.18 on clinical and production outcomes to date.                                                                                                                                                                                                                                                                                                                       |

#### Nucleotide similarity to vaccines

The following summarizes median nucleotide percent identity between all non-identical 1H.18 sequences captured through MSHMP up to date and commercially available PRRSV2 vaccines.

|                     |                     |                 |
|---------------------|---------------------|-----------------|
| <u>Ingelvac ATP</u> | <u>Ingelvac MLV</u> | <u>Fostera</u>  |
| 84.1%               | 84.1%               | 84.2%           |
| <u>Prime Pac</u>    | <u>Prevacent</u>    | <u>PRRSgard</u> |
| 84.7%               | 86.1%               | 89.1%           |

#### Disclaimer

Diagnostic data should be interpreted with caution because surveillance efforts vary between production systems and phase of production. Variant classifications, based on predefined criteria, are meant to inform industry-wide discussions, not to replace specific on-farm risk assessments or expert advice. This information is compiled from publicly available publications that either use recent variant nomenclature or can be verified as referencing this specific variant. Consequently, the data may not be entirely comprehensive. It is important to note that confirmatory studies and their findings often take time to be published, and some variants may not yet have generated sufficient reporting on their impact.

#### References

Herrera da Silva JP, Rossow S, Paploski IAD, Kikuti M, Corzo CA, VanderWaal K. Complete Genome and Recombination Analysis of a Novel Porcine Reproductive and Respiratory Syndrome Virus 2 (Variant 1H.18) Identified in the Midwestern USA. *Viruses* 2025, 17, 863. <https://doi.org/10.3390/v17060863>

Kikuti M, Paploski I, Pamornchainavakul N, Melini M, Yue X, Vadnais S, Baker J, Herrera da Silva JP, Wagner M, Kurt J, Schwartz M, Rossow S, Corzo C, VanderWaal K. Monitoring the detection of PRRSV variant 1H.18 [Internet]. 2024. Available from: <https://mshmp.umn.edu/sites/mnshmp.umn.edu/files/2024-05/SHMP%202023I24.43%20%5BMonitoring%20PRRS%20Variant%5D2.pdf>

### **Suggested citation**

National Surveillance Report. PRRSV Variants Under Monitoring Situation Report of PRRSV Variant 1H.18, August 2026 [Internet]. Available from: <https://mshmp.umn.edu/PRRS-variant-monitoring>