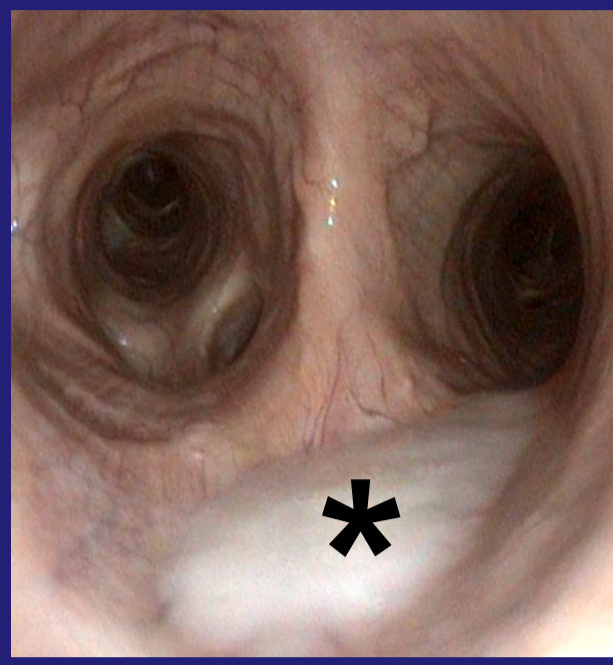


# VANIN-1 IS EXPRESSED IN THE AIRWAY EPITHELIUM OF HORSES AND HAS A HIGHER ABUNDANCE IN THE MUCUS OF HORSES WITH SEVERE EQUINE ASTHMA COMPARED TO HEALTHY HORSES

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## Introduction

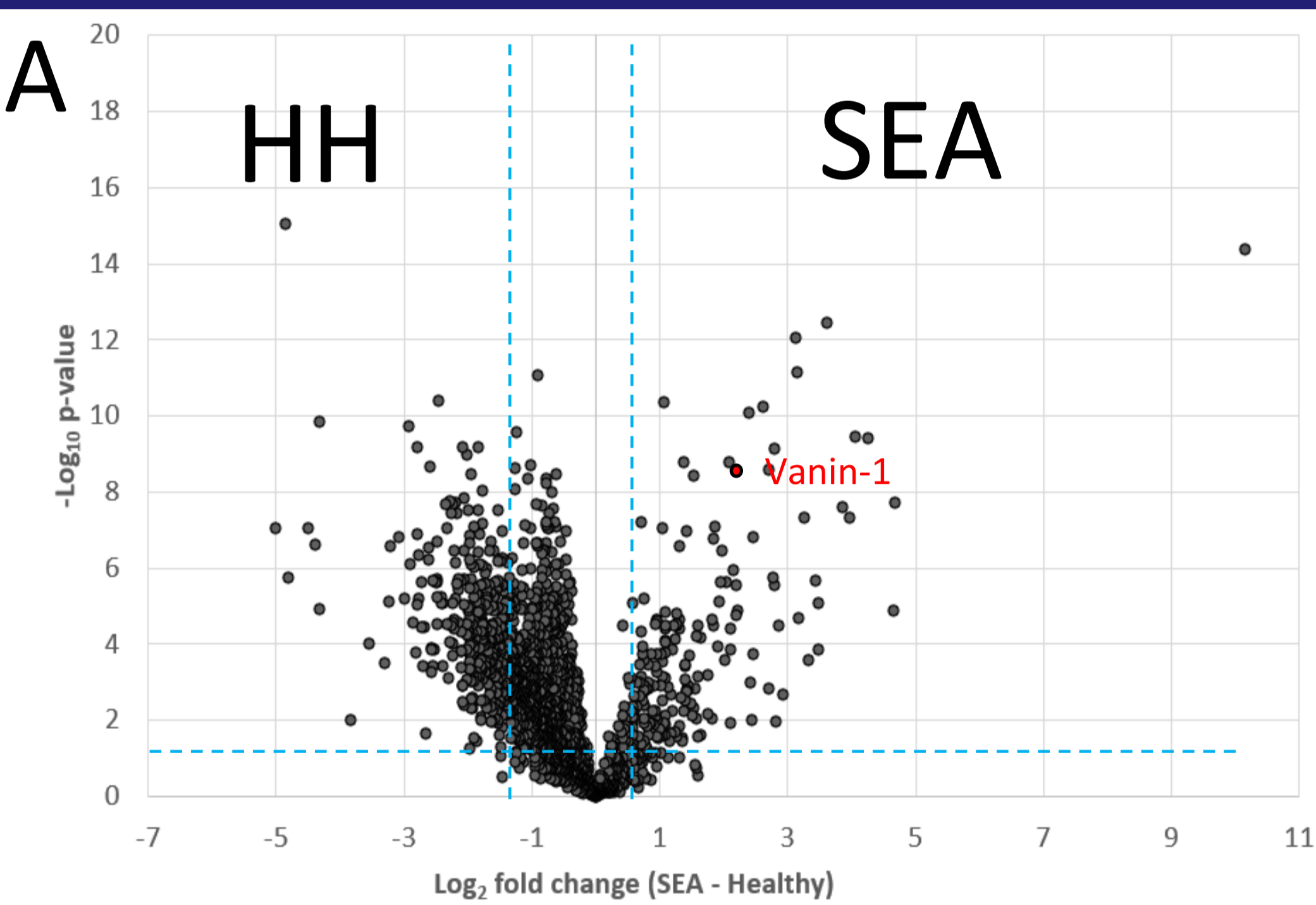


Hypersecretion (\*) and mucus plugging (#) are hallmarks of equine asthma (EA), one of the most important respiratory diseases of horses. However, the proteins in the mucus, their compositional changes in EA and their characteristics are widely unknown. The genomic characteristics, tissue and cellular expression pattern of Vanin-1, a protein which was abundantly detected in the mucus of horses with severe EA (SEA) were further investigated in healthy horses (HH).

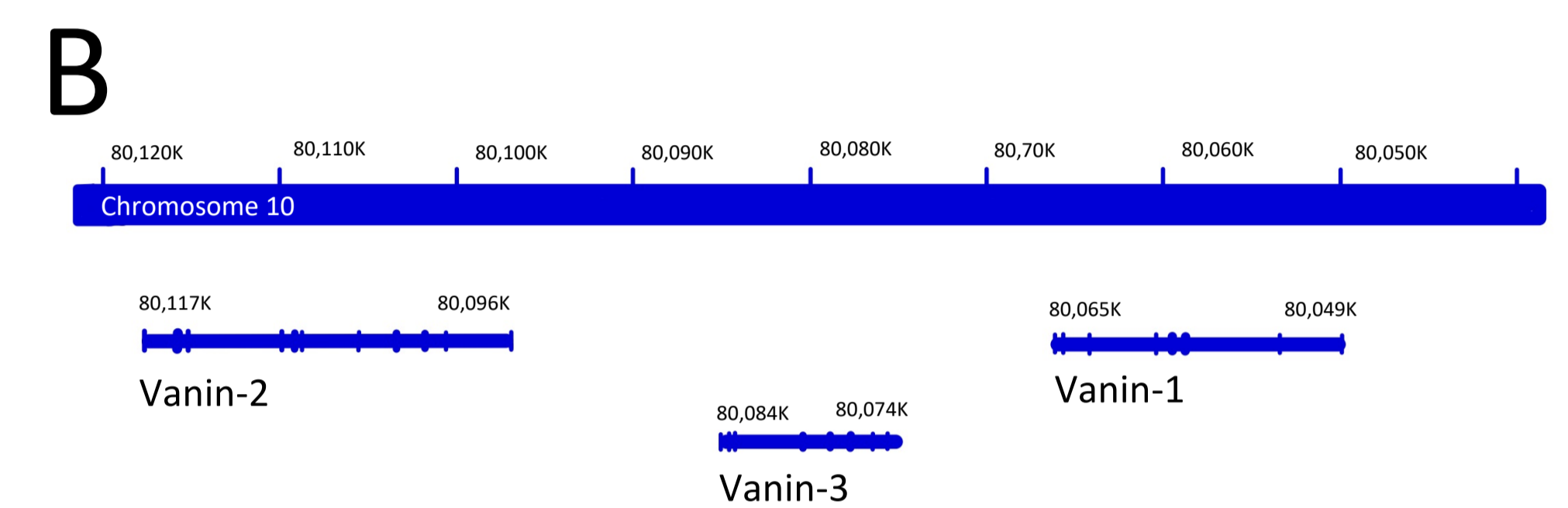
## Materials and Methods

In a landscaping approach, the proteome of the airway mucus of HH (n=9) and horses with SEA (n=10) was analysed using liquid chromatography tandem mass spectrometry. Protein identification and quantification was performed using the MaxQuant software. The experimental data was searched against the reference proteome of *Equus caballus*. Further statistical analysis was done using the Perseus software. Vanin-1, which was massively found in the mucus of horses with SEA was further genomically characterised *in silico* using the NCBI Nucleotide-BLAST (basic local alignment search tool). The tissue and cellular expression pattern was subsequently analysed via RT-qPCR (n=5) and *in situ hybridisation* (n=3) in the airways of HH.

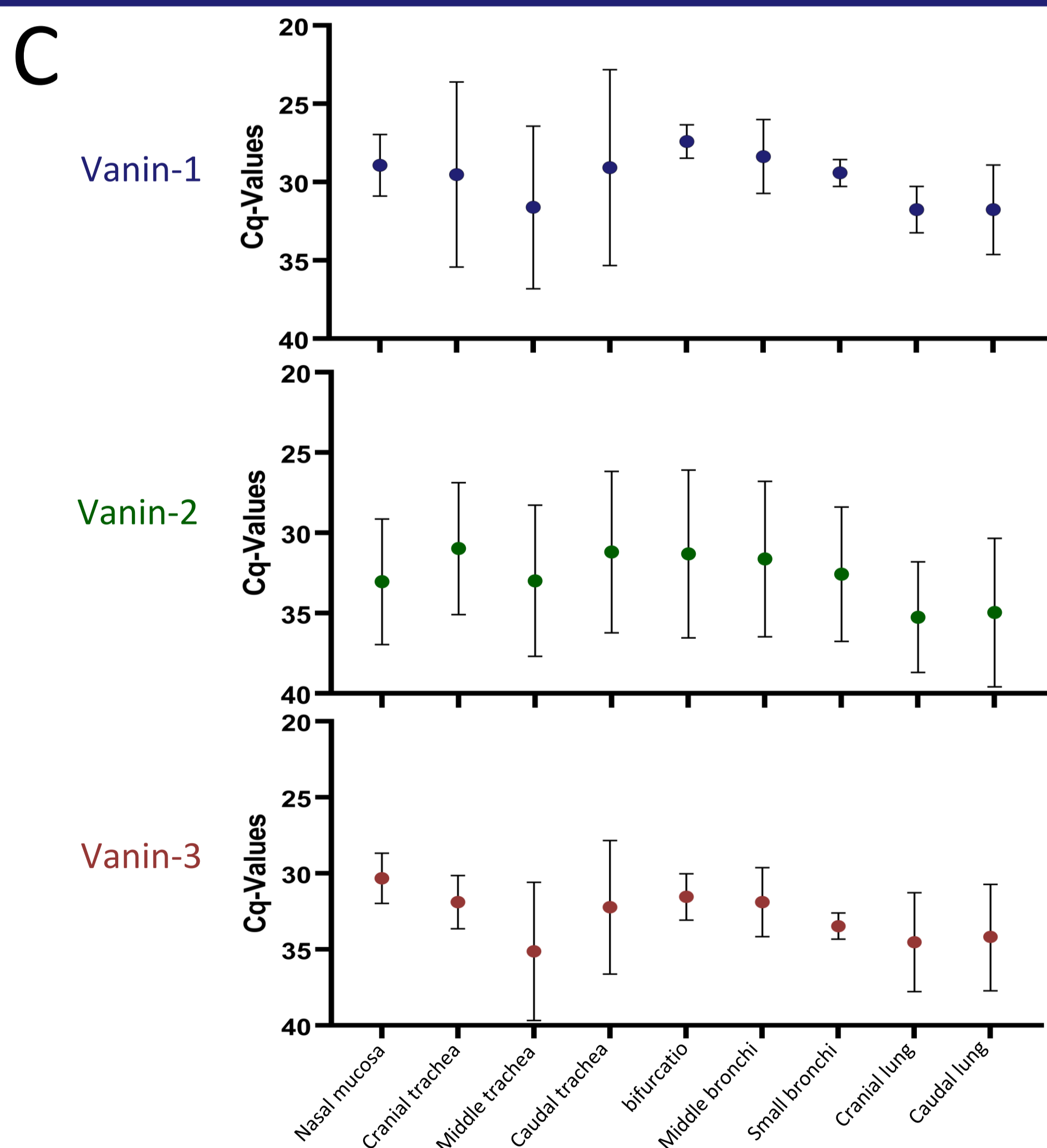
## Results



**A.** Compositional changes in the mucus proteome of HH and horses with SEA. In comparison to HH, 111 proteins were identified in higher abundance in the mucus of bronchioalveolar lavage fluid of horses affected by SEA. An enzyme with pantetheinase activity called vascular non-inflammatory molecule-1 (Vanin-1) was one of the proteins showing a very strong relative increase in its abundance in SEA compared to HH.

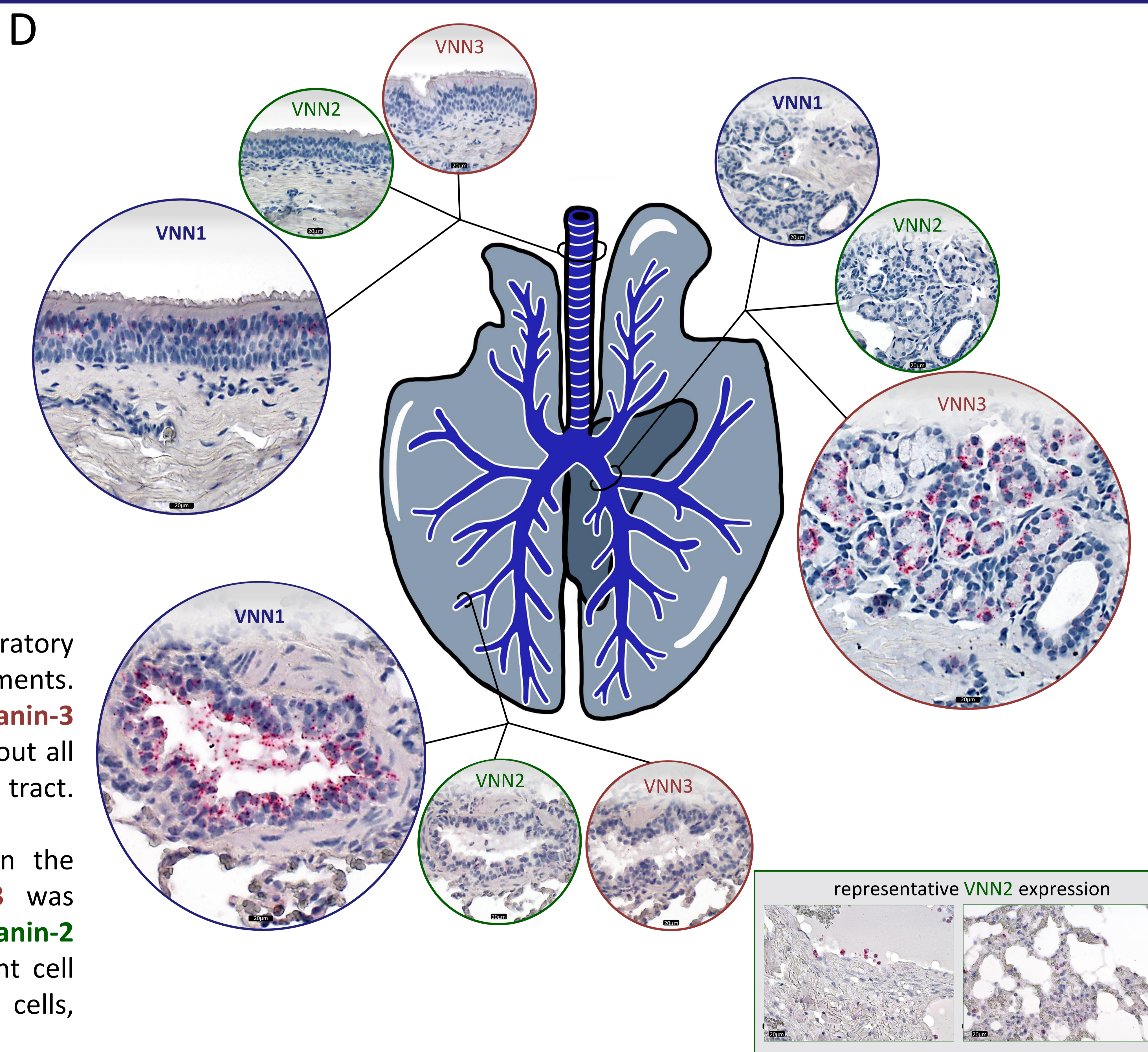


**B.** The equine Vanin gene family consists of three members. Three Vanin-genes were identified on chromosome 10 of the equine genome. All members are putatively functional genes.



All Vanin members are expressed in the respiratory tract, however in different cellular environments. **C.** **Vanin-1** (VNN1), **Vanin-2** (VNN2) and **Vanin-3** (VNN3) were found to be expressed throughout all analysed locations of the respiratory tract. (black circle = median; error bar = SD)

**D.** **Vanin-1** was predominantly expressed in the airway lining epithelium, whereas **Vanin-3** was predominantly found in submucosal glands. **Vanin-2** was observed in a wide spectrum of different cell types, such as bronchial epithelial cells, pneumocytes, and immune cells.



## Conclusion

Vanin-1 is one of three members of a gene family which are expressed in the equine respiratory tract. It is a highly abundant protein in the mucus of horses with SEA compared to HH. Its role in SEA will be further investigated.

## Funding

## Contact