

Supplementary Material

Prevalence of Worldwide Neonatal Calf Diarrhoea Caused by Bovine Rotavirus in Combination with Bovine Coronavirus, *Escherichia Coli* K99 and *Cryptosporidium spp.*: A Meta-Analysis

Michael Brunauer ^a, Franz-Ferdinand Roch ^a, Beate Conrady ^{a,b,c*}

^a *Institute of Food Safety, Food Technology and Veterinary Public Health, University of Veterinary Medicine, 1210 Vienna, Austria*

^b *Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, 1870 Frederiksberg C, Denmark*

^c *Complexity Science Hub Vienna, Josefstädter Straße 39, A-1080, Austria*

* Corresponding author.

E-mail address: bcon@sund.ku.dk (B. Conrady)

Supplementary Material I

Detail description of the methodology

The mean prevalences were weighted (w_i) based on the inverse of within-study variance (v_i) and the variability across the studies (τ^2) [1], according to the Paule and Mandel method based on the formula [2,3]:

$$w_i = 1/(v_i + \tau^2) \quad (1)$$

For variance-stabilization of the prevalence data distribution, Freeman-Tukey double arcsine transformation (P_i^{FT}) [4] was used, while e_i is the number of events in each study i and n_i shows the number of observations:

$$P_i^{FT} = 0.5 \left(\arcsin \sqrt{\frac{e_i}{n_i+1}} + \arcsin \sqrt{\frac{e_i+1}{n_i+1}} \right) \quad (2)$$

The corresponding back-transformation was conducted according to the approach by Miller [5,6]:

$$P_i^{FT} = 0.5 \left(1 - \sin(\cos(0_i^{FT})) \sqrt{1 - (\sin(20_i^{FT}) + [\sin(20_i^{FT}) - 1/\sin(20_i^{FT})]/\tilde{n})^2} \right) \quad (3)$$

hereby $\tilde{n}$ represented the harmonic mean of the sample size of studies I and its defined as follows:

$$\tilde{n} = I / \sum_{i=1}^I \frac{1}{n_i} \quad (4)$$

The Loess algorithm was applied with the locally weighted regression smoothing function and robust weightings implemented in R with the function `geom_smooth` and the corresponding method “loess” [7].

Reference of the Supplementary Material

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Supplementary data

Fig. S1: Funnel plot and influential case diagnostic for studies covering a) BRV-BCoV mixed infections, b) BRV-ETEC mixed infections and c) BRV-Crypto mixed infections. N.B. no outliers were identified for all mixed infections.

Fig. S2: Forest plot of studies with BRV-BCoV prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of the Supplementary Material.

Fig. S3: Forest plot of studies with BRV-ETEC prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of the Supplementary Material.

Fig. S4: Forest plot of studies with BRV-Crypto prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of the Supplementary Material.

Fig. S1: Funnel plot (left side) and influential case diagnostic (right side) for studies covering a) BRV-BCoV mixed infections, b) BRV-ETEC mixed infections and c) BRV-Crypto mixed infections. N.B. no outliers were identified for all mixed infections.

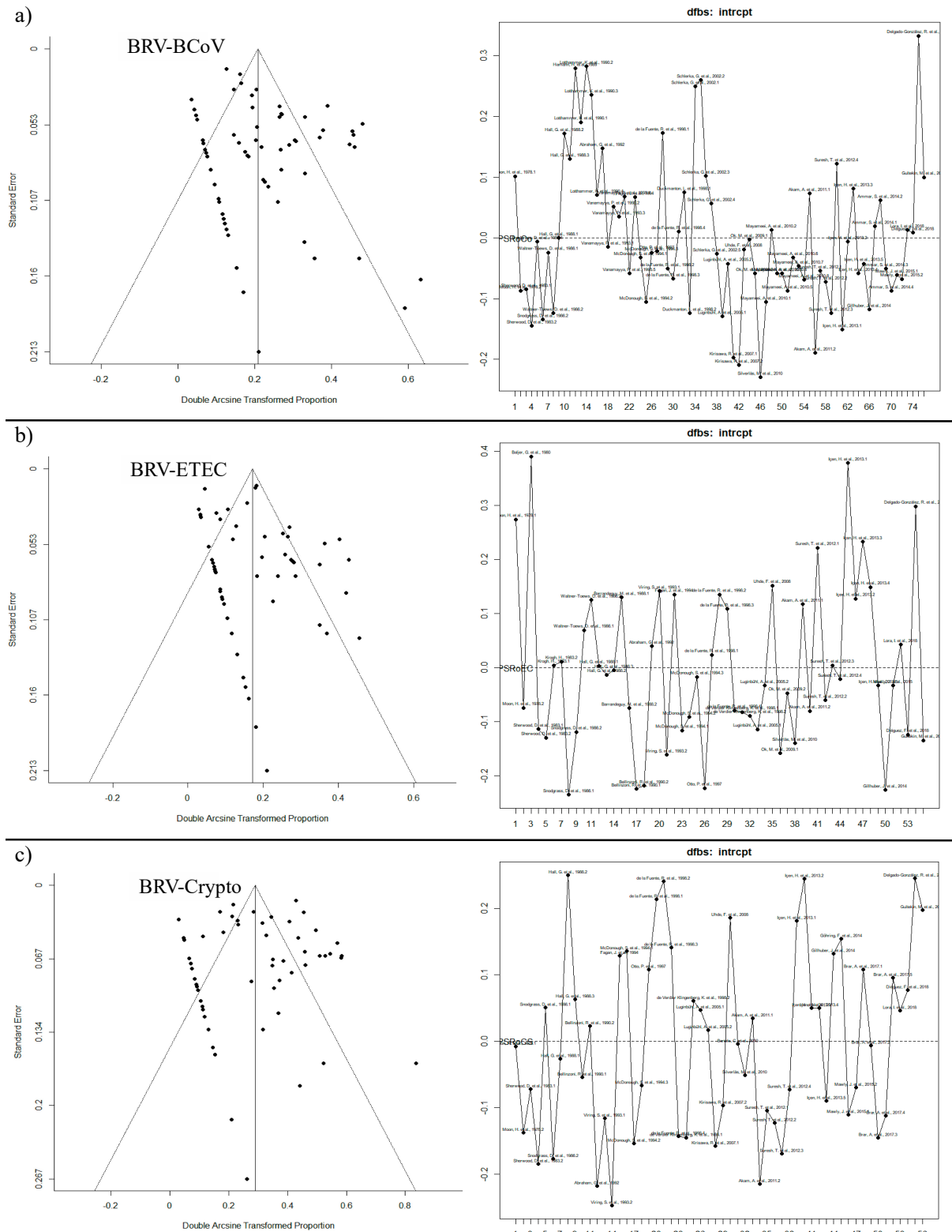


Fig. S2. Forest plot of studies with BRV-BCoV prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of the

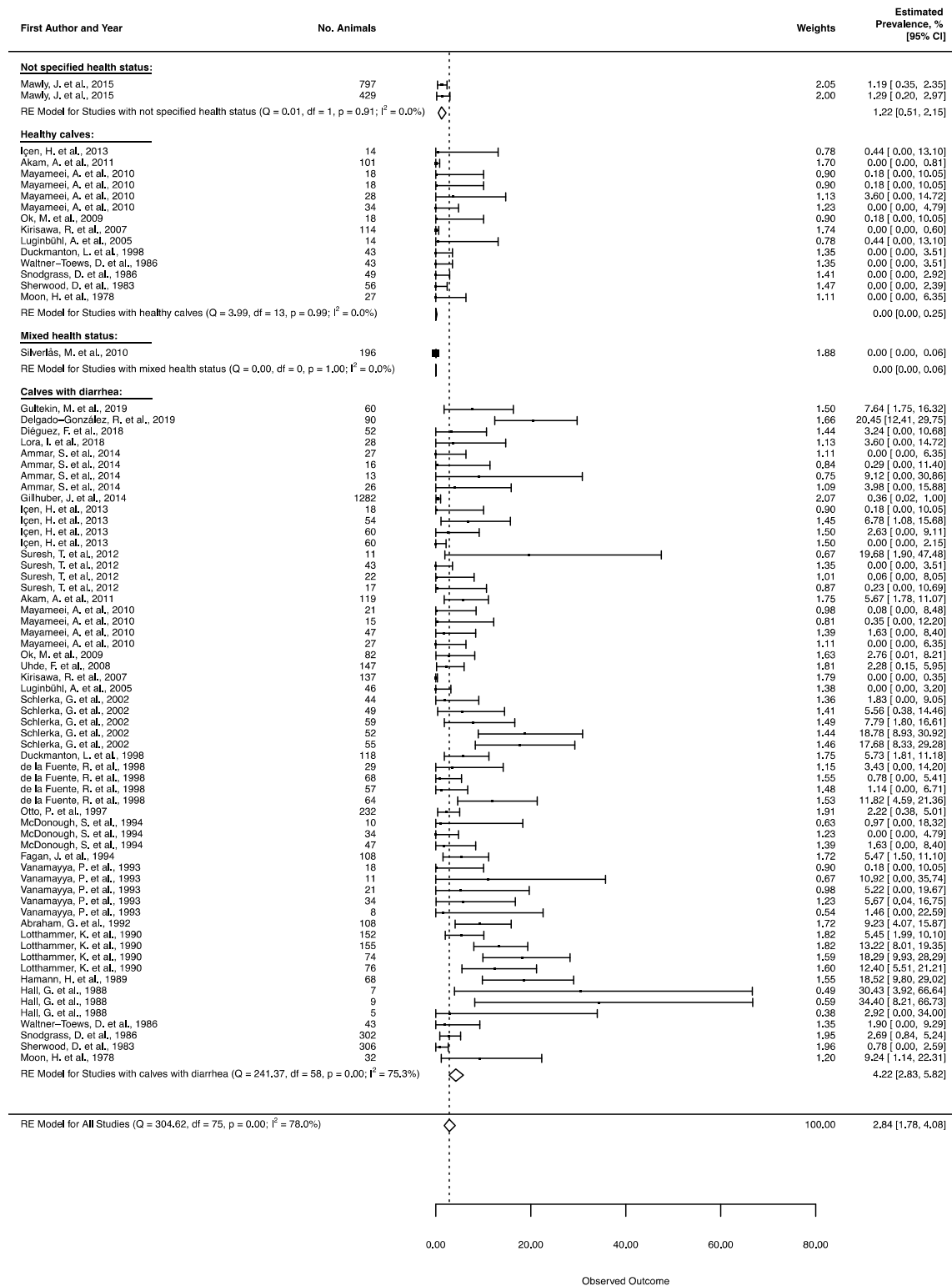


Fig. S3. Forest plot of studies with BRV-ETEC prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of the

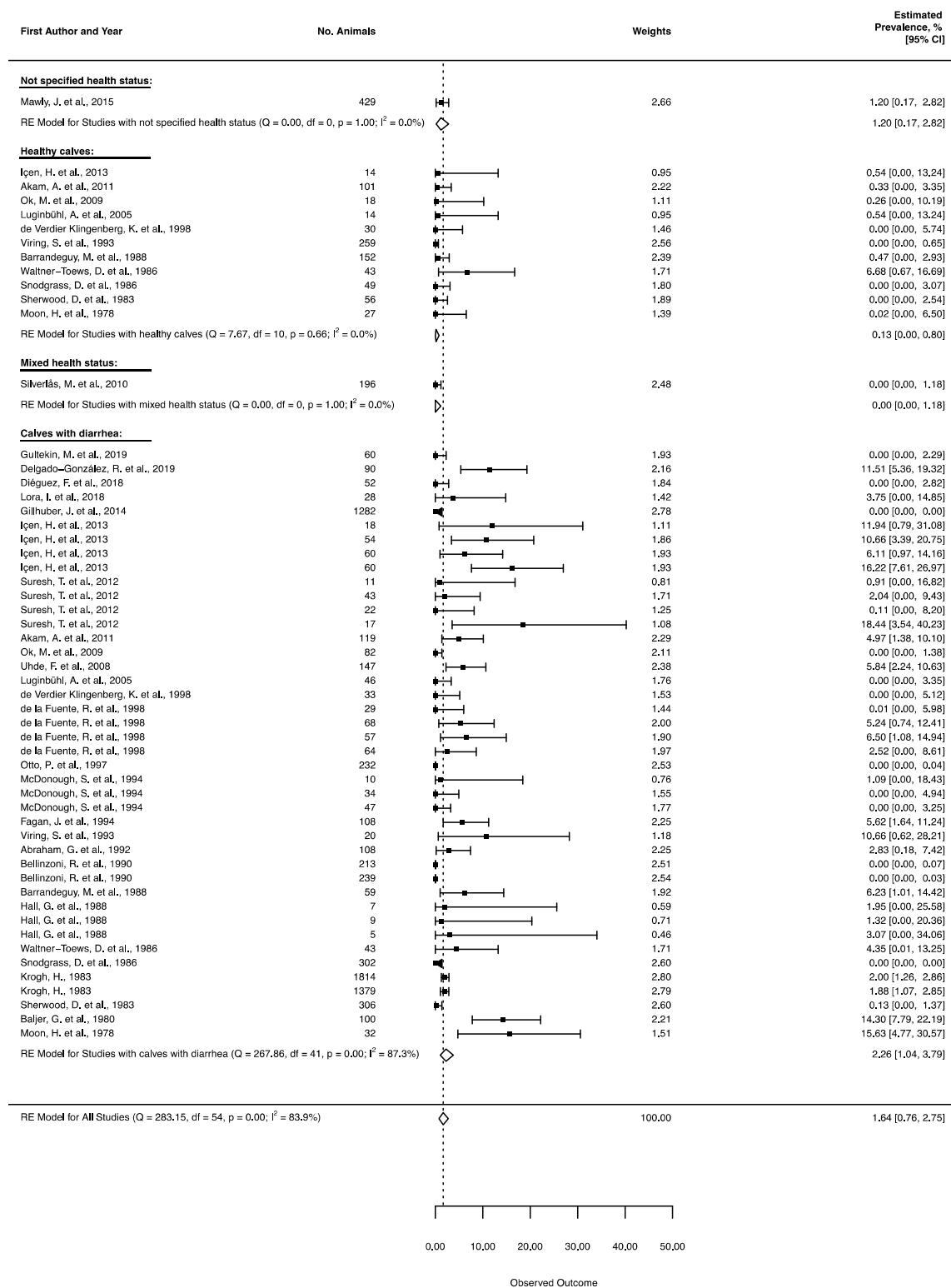
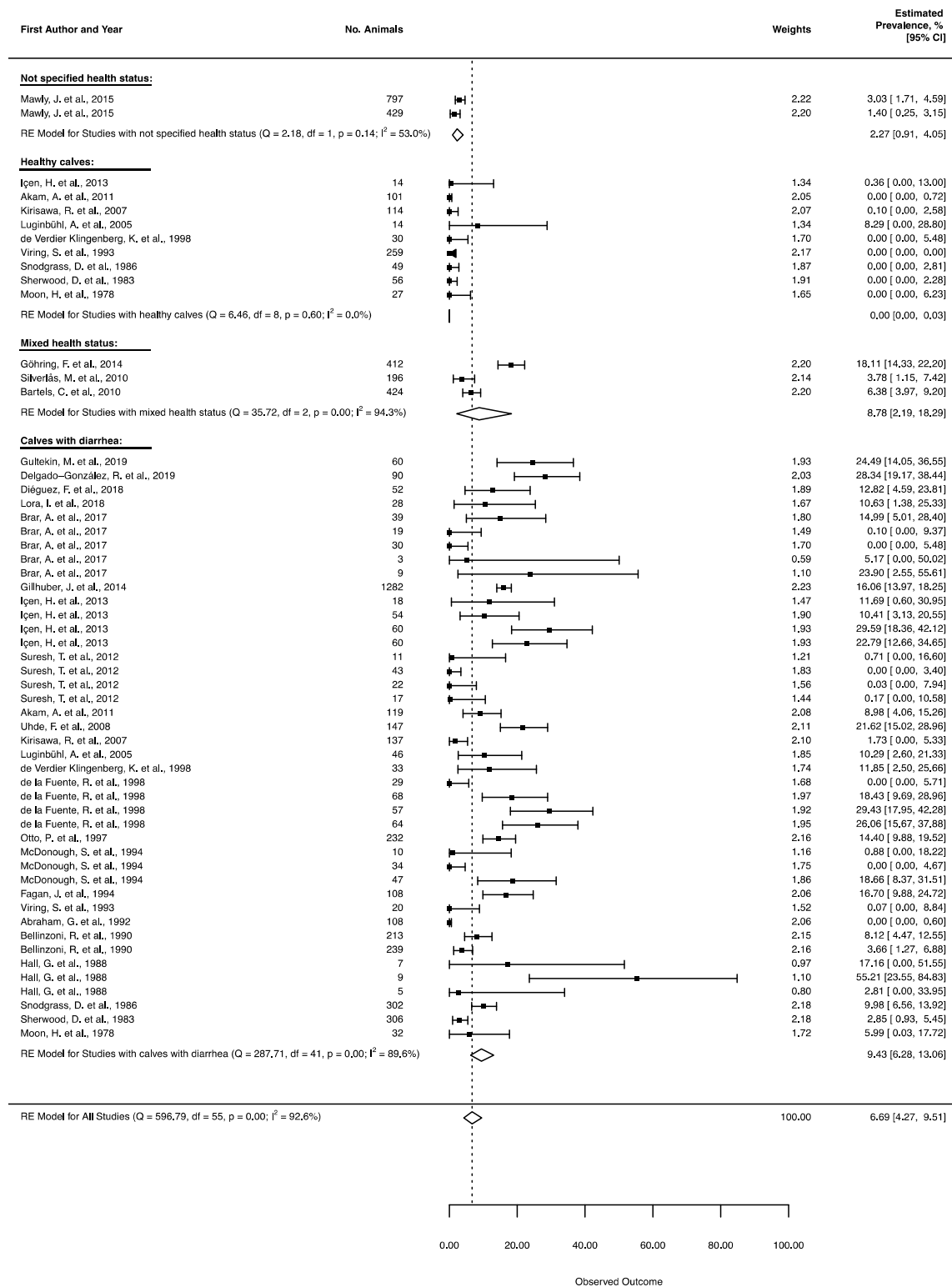


Fig. S4. Forest plot of studies with BRV-Crypto prevalences ordered by health status of the calves and publication year. N.B. The full references are provided at the end of



References of the 41 studies included in the Meta-analysis

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