

Seroprevalence of *Toxoplasma gondii* in domestic pigs, sheep, cattle, wild boars, and moose in the Nordic-Baltic region: systematic review and meta-analysis

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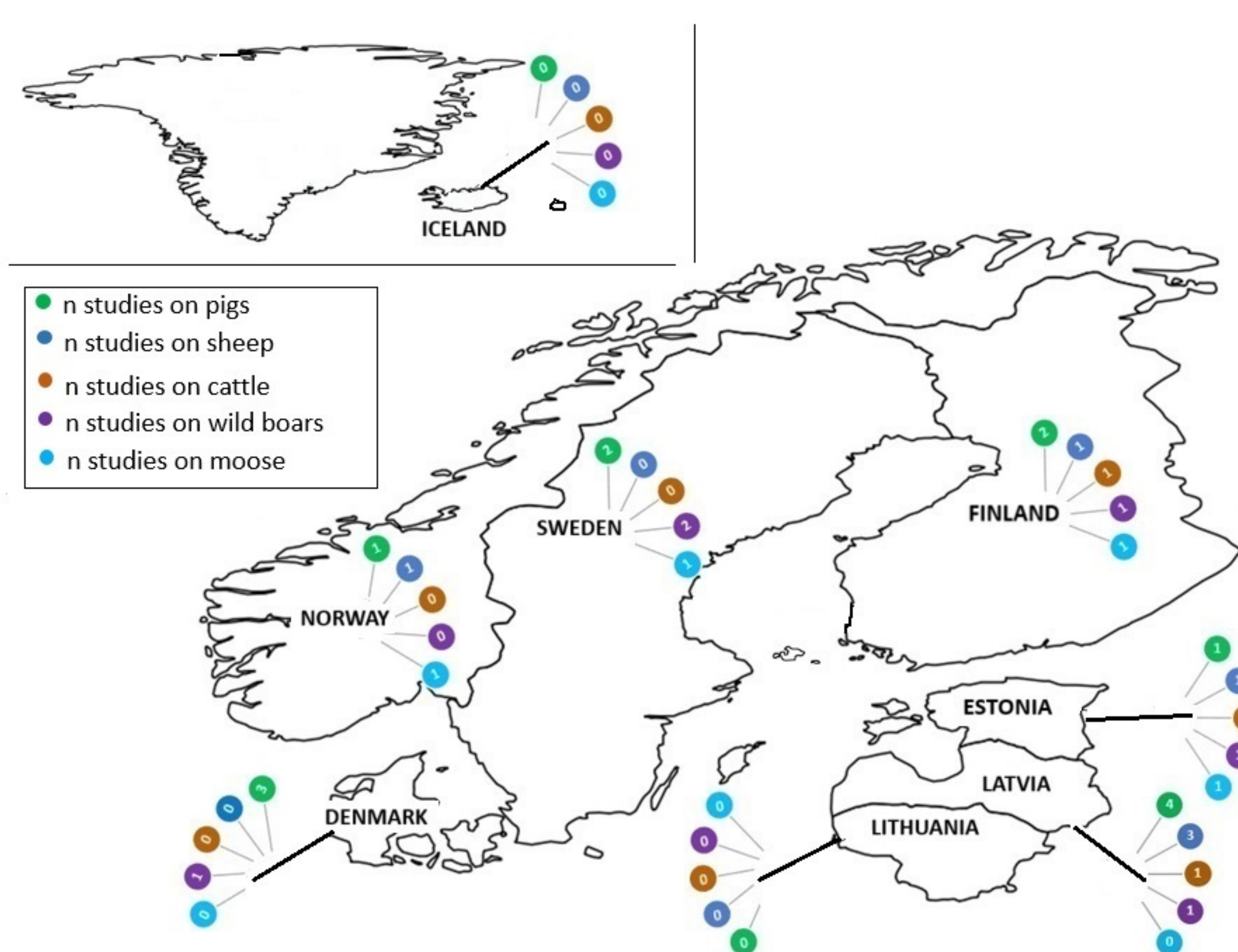
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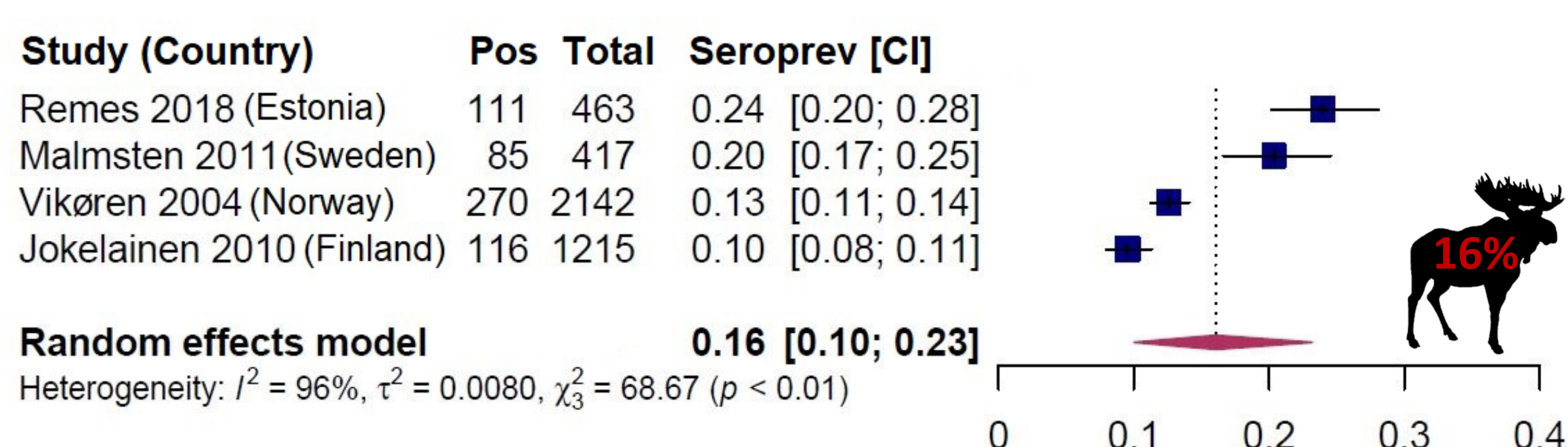
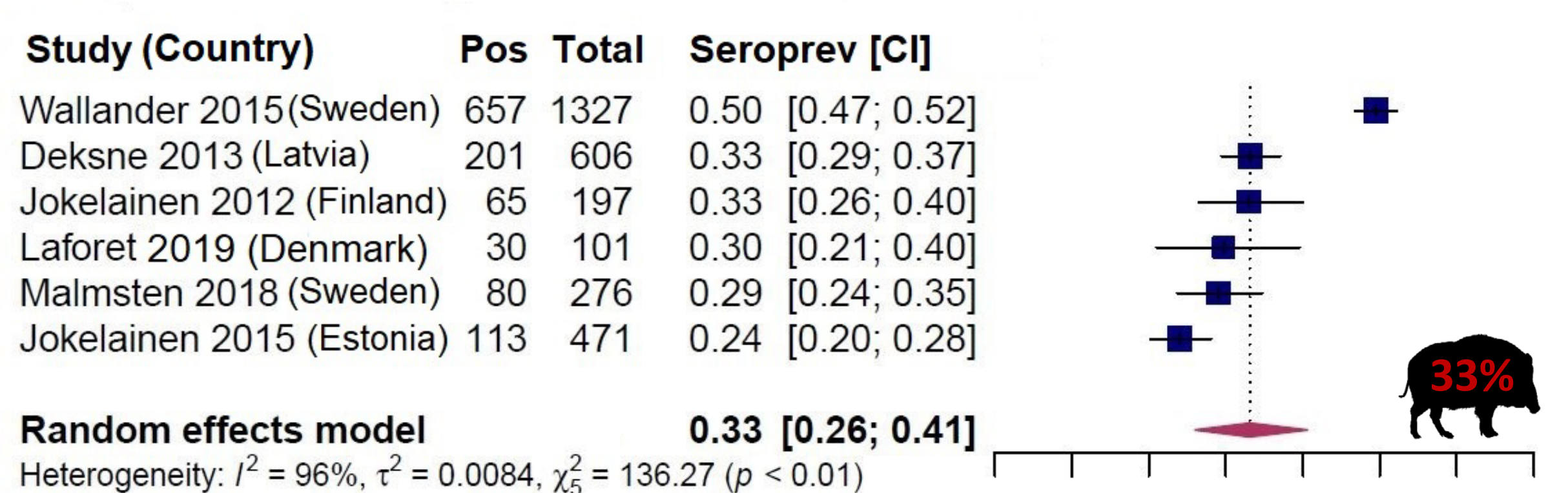
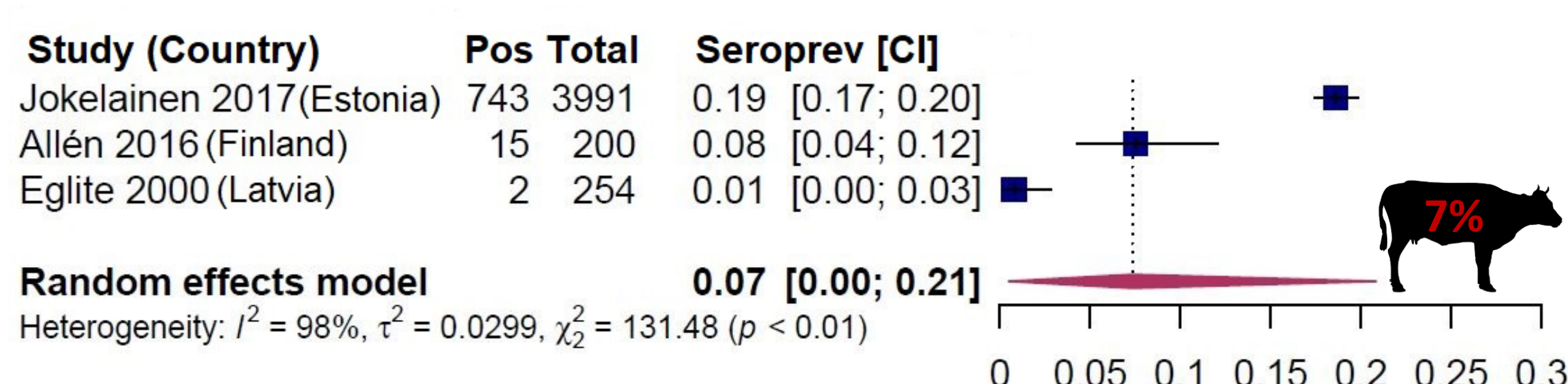
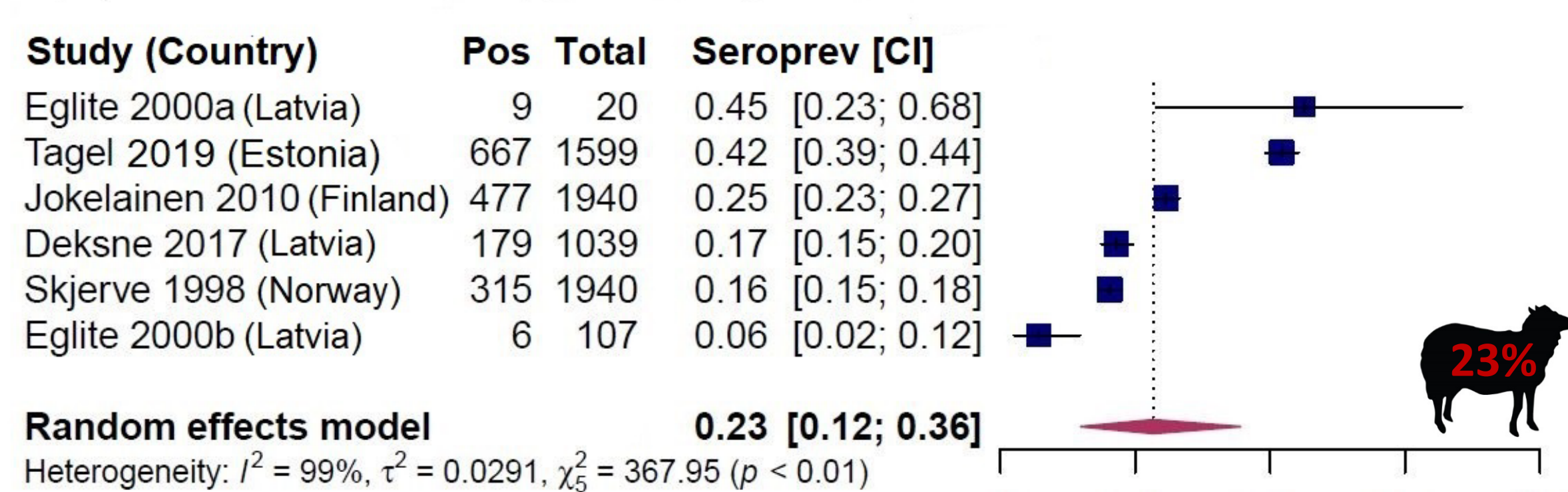
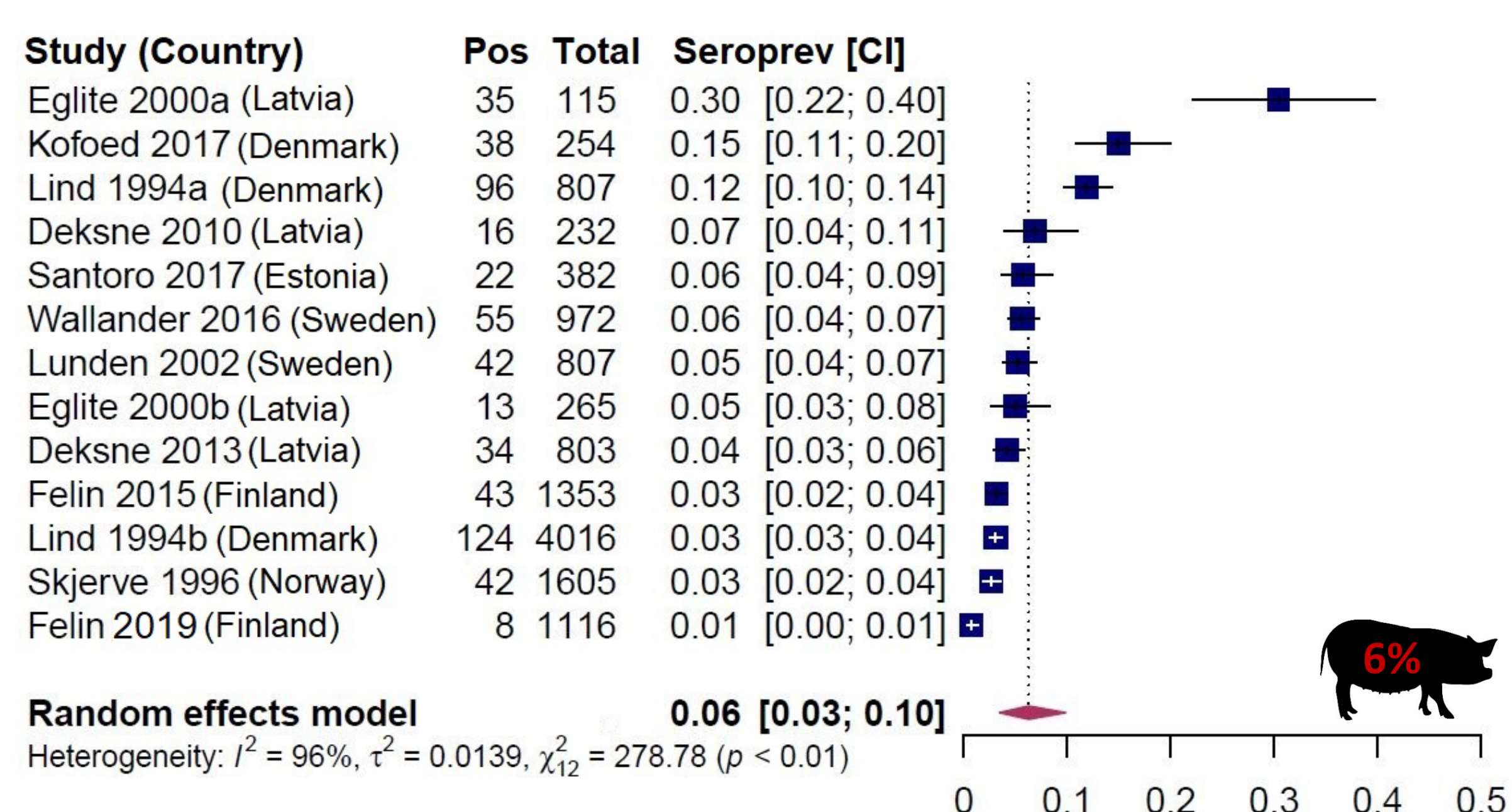
One of the ways humans may become infected with *Toxoplasma gondii* is if they consume undercooked meat of infected animals.

We conducted a systematic review and meta-analysis of *T. gondii* seroprevalence in pigs, sheep, cattle, wild boars and moose in the Nordic-Baltic region, including studies from January 1990 to June 2018. Thirty-two studies qualified for meta-analysis: 13 on domestic pigs, 6 on sheep, 3 on cattle, 6 on wild boars, and 4 on moose. For each host species, we estimated the pooled apparent seroprevalence using a random effects model, and subgroup analyses were performed using mixed-effects models.

The estimated pooled seroprevalence was 6% in pigs (CI95%: 3–10%), 23% in sheep (CI95%: 12–36%), 7% in cattle (CI95%: 1–21%), 33% in wild boars (CI95%: 26–41%), and 16% in moose (CI95%: 10–23%). In all host species except wild boars, the pooled seroprevalence estimate was higher in >1-year-old than in younger animals. The results indicate **widespread exposure to *T. gondii* among animals raised or hunted for human consumption in the region.**



Number of *T. gondii* seroprevalence studies that qualified for the meta-analysis, by host species and by country. Adapted from Olsen et al. 2019.



Estimated pooled seroprevalence of *T. gondii* in domestic pigs, sheep, cattle, wild boars and moose respectively, in the Nordic-Baltic region using a random effects model. Adapted from Olsen et al. 2019.