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# Corrigendum: The Vacc-SeqQC project: Benchmarking RNA-Seq for clinical vaccine studies

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## KEYWORDS

RNA-Seq, statistical power, ERCC, tularemia vaccine (DVC-LVS), gene filtering, sequencing depth, read length, reproducibility

## A corrigendum on

**The Vacc-SeqQC project: Benchmarking RNA-Seq for clinical vaccine studies**

by Goll JB, Bosinger SE, Jensen TL, Walum H, Grimes T, Tharp GK, Natrajan MS, Blazevic A, Head RD, Gelber CE, Steenbergen KJ, Patel NB, Sanz P, Rouphael NG, Anderson EJ, Mulligan MJ and Hoft DF (2023) *Front. Immunol.* 13:1093242. doi: 10.3389/fimmu.2022.1093242

In the published article, there was an error in the **Figure 7** legend as published. The figure legend effect size values were incorrectly displayed as “>1.25, 51.5, 51.75, 52” instead of “>1.25, ≥1.5, ≥1.75, ≥2”. The corrected **Figure 7** and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

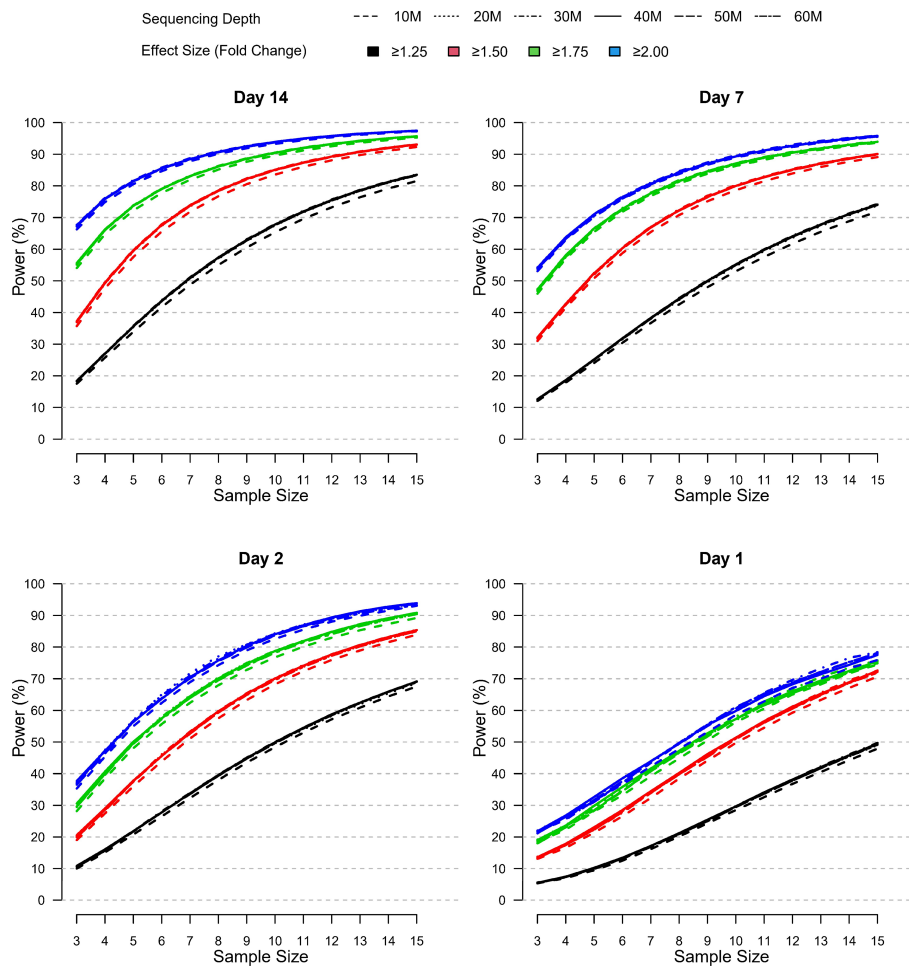


FIGURE 7

Relative power by sample size, effect size, and sequencing depth at each post-vaccination day as simulated using the modified PROPER R package. Days were sorted by decreasing vaccination effect based on overall fold changes and DEG responses observed for this study (see Figure 3A). Power was assessed for different fold-change cutoffs (indicated by color-coded lines), sequencing depth (as indicated by the line type), and sample size (x-axis).

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