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described in randomized controlled trials of CV endpoints in the context of OSA (3, 7). The second comment from Donovan and Patel concerns the healthy adherer effect and the interpretation of E-values in our study. The healthy adherer effect arises when patients who adhere to preventive therapy are more likely to engage in other healthy behaviors than their nonadherent counterparts. This phenomenon can result in biased estimates of the effect of adherence on clinical outcomes (8). We completely agree with Donovan and Patel that the healthy adherer effect is particularly relevant to comparisons between patients with OSA who are adherent and those who are nonadherent to PAP therapy. This is why we have made the effort to capture the healthy adherer effect by adjusting for chronic CV active drug adherence as assessed by the Medication Possession Ratio, which is considered a valuable proxy (9). Several measures that are particularly relevant to the assessment of CV outcomes in the context of PAP use, such as alcohol intake, tobacco consumption, and socioprofessional status, were also taken into account. Moreover, we applied the recently described E-value to quantify the potential for unmeasured confounding to negate observed treatment effects (10). However, there is no simple way to control for all biases using healthcare datasets (8). We agree with Donovan and Patel that adherence to chronic CV active drugs does not fully capture the healthy adherence effect and that concern for residual confounding remains. Further studies are needed to fully explore the healthy adherer effects in the context of PAP adherence and CV outcomes in patients with OSA.

<u>Author disclosures</u> are available with the text of this letter at www.atsjournals.org.

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Erratum: Transcriptomic Signatures in Sepsis and a Differential Response to Steroids. From the VANISH Randomized Trial

The authors have recently discovered errors in the article by Antcliffe and colleagues (1) published in the April 15, 2019 issue of the Journal. The authors informed the *Journal* that 39 of the 176 patients (22%) had been misclassified into the wrong transcriptomic sepsis response signature (SRS) group. This was discovered in subsequent work when later sample timepoints from the same patients were analyzed using different laboratory assays. To allow alignment of results from the different assays, some original samples were reanalyzed. It then became apparent that some original assays were incorrect. On further investigation, it was found that this error occurred when one box of samples was inadvertently rotated through 180 degrees. When the samples were then transferred into the assay plate, they were mislabelled; thus 39 samples were misclassified. This error has now been corrected and further checks between RNA results and newly obtained DNA genetic results have confirmed the revised assignments.

The original analyses reported in the article have all been rerun. Although the numbers differ, the authors maintain that the overall results and conclusions have not changed. There is still a significant interaction between assignment to hydrocortisone or placebo, and SRS phenotype (P = 0.02 – the same P value as before). The increased

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mortality associated with hydrocortisone treatment in the SRS2 phenotype is still seen, although the point estimate is smaller but with tighter confidence intervals and still well above 1: OR, 4.6; 95% CI, 1.5-14.4, compared with OR, 7.9; 95% CI, 1.6-39.9, previously. There are some other variations in the secondary outcomes. The tables have been extensively updated, revised figures included, and some minor text changes in the article and associated online supplement have been made. Therefore, the *Journal* is replacing the online version of the article with a corrected version. In addition, a document showing all the changes to the results will be posted as an online supplement to the original article.

The authors would like to apologize to the readership for any confusion caused by these errors. \blacksquare

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