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AUTHOR CORRECTION

Correction for Chen et al., Divergent MicroRNA Targetomes of Closely Related Circulating Strains of a Polyomavirus

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Authors C. J. Chen, R. P. Kincaid, A. Martinez, and C. S. Sullivan would like to note the following. We have deemed some work from a previous lab member to be unreliable. Therefore, we have initiated a systematic review of all published work performed by this person. The sole contribution of this person to the present manuscript involves the microarray data presented in Fig. 4 and the associated portions of Tables S3 and S4 in the supplemental material. These microarray data comprised one of two criteria used to identify candidate transcripts that are regulated by 776 or RI257 microRNAs (miRNAs). The original basis for identifying candidate transcripts involved criteria including (i) reduced expression in the microarray analysis and (ii) bioinformatic analysis demonstrating that the 3′ untranslated region (UTR) of the transcript contains a heptameric seed match to at least one miRNA derivative from the 776 or RI257 pre-miRNA. We are unable to find a proper record of the microarray studies being completed and no longer have confidence in these data. However, we remain confident in the bioinformatic analysis that identified candidate transcripts with heptameric seed matches for subsequent wet-bench validation. The reporter-based assays show that the RI257 and 776 miRNAs have the ability to differentially regulate some target transcripts, consistent with their having different targetomes (as would be predicted from their different seed sequences). Importantly, all major conclusions from the original manuscript remain valid, including: (i) RI257, a strain of SV40, was discovered to express a pre-miRNA that gives rise to derivative miRNAs with different seeds than the prototypic 776 strain miRNAs. (ii) miRNA derivatives from the 776 and RI257 pre-miRNAs differentially regulate at least some transcripts, consistent with what would be predicted from their different seeds. (iii) Both 776 and RI257 miRNAs can autoregulate early viral gene expression via cleavage of early mRNAs. (iv) The overall model presented in Fig. 8 remains valid and is unaffected by these errors.

To accurately reflect how we chose candidate transcripts for validation studies, we are replacing the original microarray shown in Fig. 4 with a modified schematic-only version, which shows that a subset of transcripts with seed complements were selected for further analysis by 3′ UTR luciferase reporter assays.

Page 11141: Figure 4 and its legend should appear as shown below.

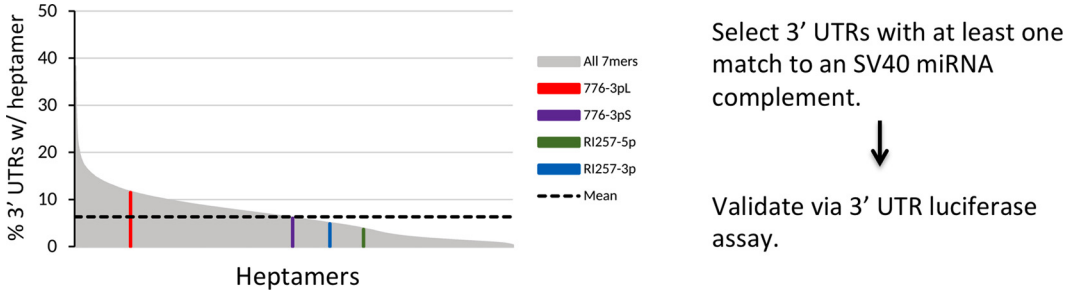

FIG 4 Target transcript identification. Candidate target 3′ UTRs were selected from the pool of 3′ UTRs that contain at least one seed component to an SV40 mimRNA. Ten 3′ UTRs were selected for subsequent reporter analysis. The dashed line indicates that average number of 3′ UTRs that contain a complement to any individual heptamer. The vertical axis indicates the percentage of 3′ UTR containing a particular heptameric complement sequence.

We are also replacing Tables S3 and S4 with a modified Table S3 that lists the results of the 3′ UTR luciferase reporter assay in a single-table format.

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J. E. Cox could not be reached when asked to agree to the correction.

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Revised supplemental data are available at http://jvi.asm.org/content/87/20/11135/suppl/DCSupplemental.

In summary, although the candidate transcripts tested were in fact derived from a bioinformatics-only approach, the major conclusions of this paper were vetted by wet-bench experiments and remain valid.

We apologize for and deeply regret the errors in this publication. C. S. Sullivan, the principal investigator of the lab and senior author, accepts full responsibility for allowing these errors to be included in the original paper.