

Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay

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In our original paper we described the validation of the variant rs9283753, a risk allele for ankylosing spondylitis, as a modulator of PTGER4 expression. Upon review we discovered that we had incorrectly reported that the risk allele causes decreased expression of PTGER4, when in fact it causes increased expression of the gene. This incorrect conclusion was due to two interrelated errors during the final manuscript preparation. First, we inadvertently used data for the variant rs922483, instead of rs9283753, to present MPRA and eQTL results in figures 6B and 6C. This variant has an opposite direction of allelic effect to that seen for rs9283753. Second, we also made a sign error during the final qPCR calculations for rs9283753. We overlooked this second mistake since the (incorrect) sign was consistent with the results presented for rs922483. The combination of these two errors resulted in a flipped direction of effect in figures 6B–6E. We have included the correct allele, rs9283753, in our updated Figures 6B and 6C (available online), which supports the conclusion that the risk allele for ankylosing spondylitis increases expression of PTGER4.

In addition, we specified an incorrect cell line in figure 6D, reporting results for NA11831 rather than for NA12812. NA11831 was edited in the same direction as NA12878, while NA12812 was edited in the opposite direction. Edits in all three cell lines affected expression in the expected directions, but it was NA12812 whose effect we intended to present in the figure. We have updated figure 6D online to include NA12812.

While these errors did not affect the broader conclusions of our study, they prompted us to perform a thorough review of all aspects of the manuscript and to seek further confirmation of our results. As we prepared this correction, we confirmed the directionality of our edited cell lines for PTGER4 by qPCR. In our larger review of all aspects of the paper, we also discovered a minor error in our discussion of PTGER4, where we stated that a strong CREB motif falls over rs9283753. While there is a predicted CREB motif over the variant, the strongest predicted binding motif is CEBP. We have updated the text online to reflect this.

We apologize for any inconvenience these errors may have caused and stand by the conclusions of our study.

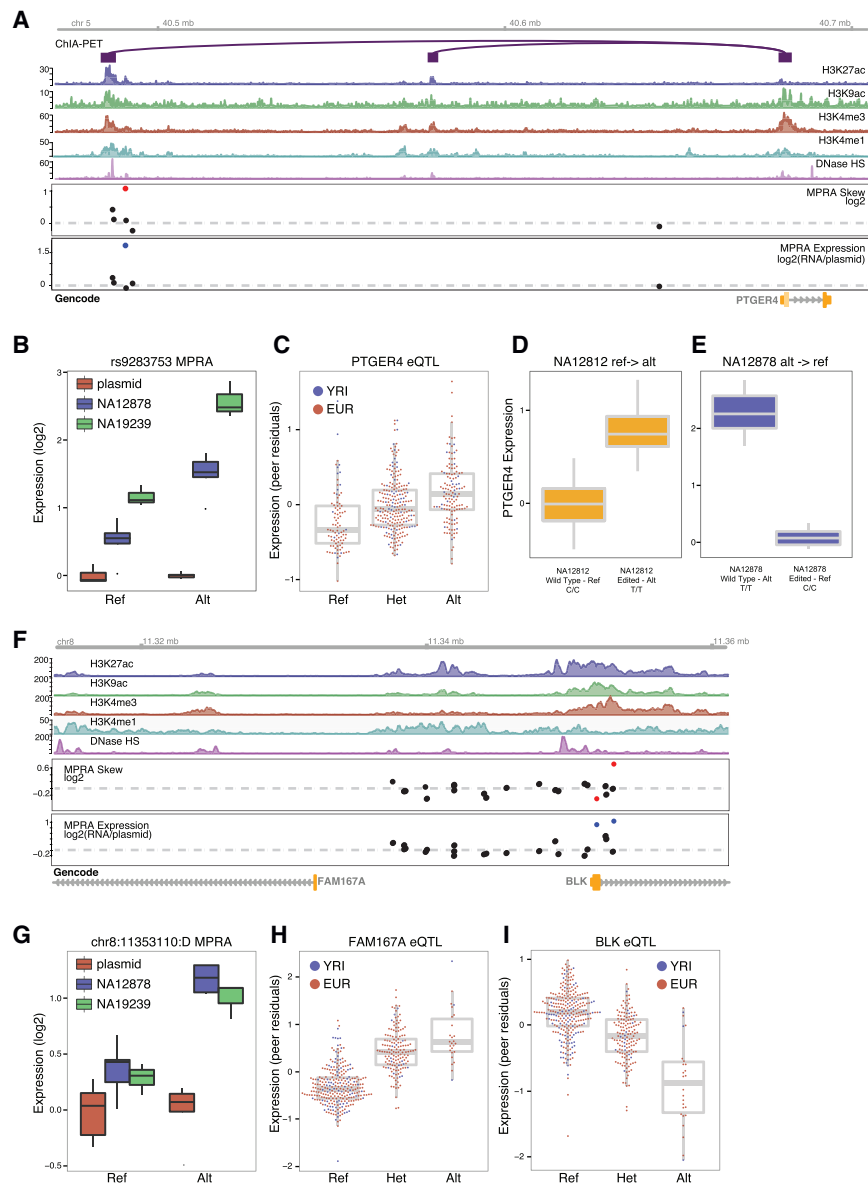


Figure 6. emVars Associated with Ankylosing Spondylitis and SLE (corrected)

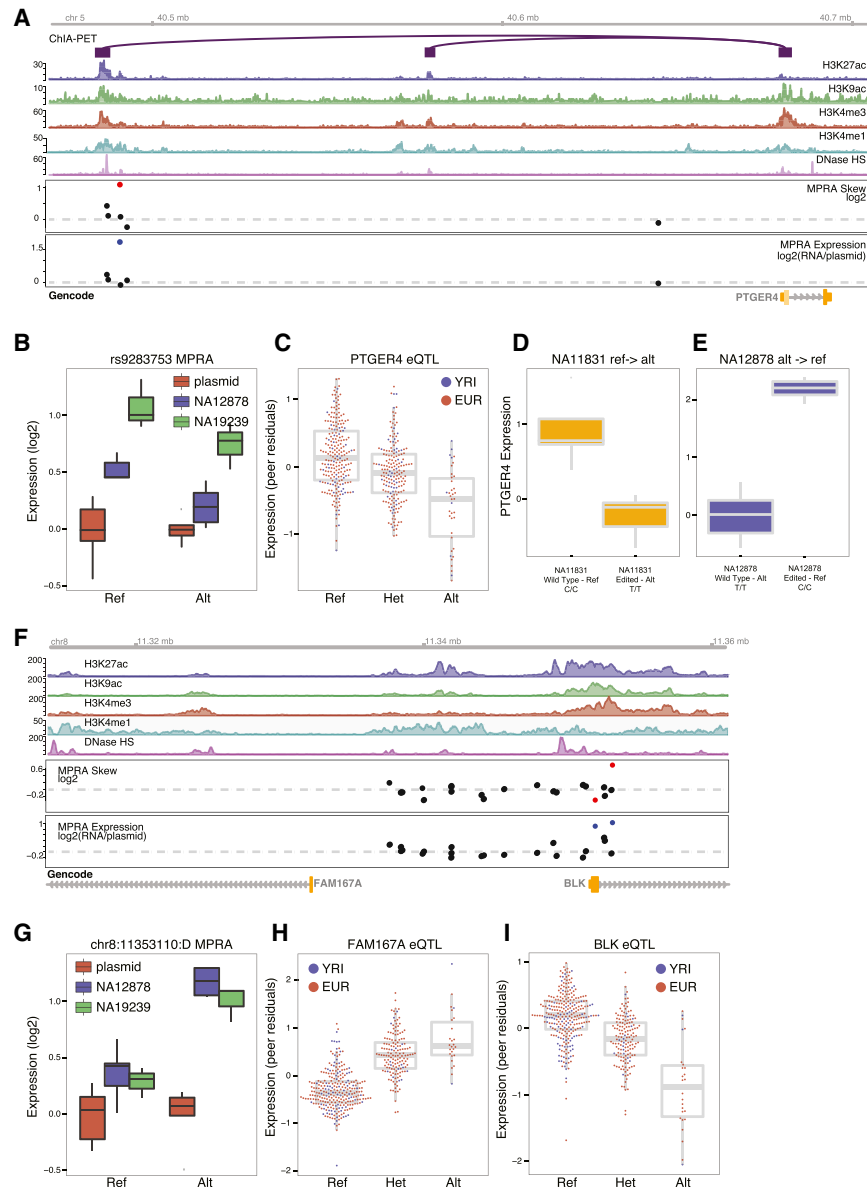


Figure 6. emVars Associated with Ankylosing Spondylitis and SLE (original)