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Supplemental Figure 3. Ingenuity pathway analysis shows that the majority of candidate causal genes for seropositive RA have evidence for biological interactions. (A) The network illustrates that the proteins coded by 18 of the 25 candidate causal genes (described in Figure 2b, here marked in red) have experimental evidence for direct interaction (whole lines) or indirect interaction (dotted lines, e.g. one affecting the level of another), supporting biological connection and a central role of interferon alpha/beta and IL-12/23 pathway (blue). (B) The remaining seven candidate causal genes for seropositive RA (red) are linked in network related to TGFB1 signaling (blue). The network analysis was performed with the IPA software (QUIAGEN Inc., <https://www.qiagenbioinformatics.com/products/ingenuitypathway-analysis>).