

# Does the Positive Affective Quality of Social Interactions Predict Leukocyte Gene Expression?

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## INTRO

- Social connection is important for health and longevity (Holt-Lunstad et al., 2010).
- Adults who experienced early-life stress and/or social disconnection, show higher levels of inflammatory markers and are more susceptible to chronic disease (Milaniak & Jaffee, 2019).
- The Conserved Transcriptional Response to Adversity (CTRA) is a genetic profile marked by increased expression of proinflammatory genes and decreased expression of antiviral and antibody-related genes (Cole, 2019).
- The CTRA has been associated with loneliness and social isolation, however, it has not been assessed in association to markers of relationship quality.
- The positive affective quality of social interactions, termed *positivity resonance*, emerges when two or more people share positive emotions and caring synchrony (Fredrickson, 2016).
- We hypothesize that people who have greater positive affective quality social interactions show downregulated CTRA expression profiles. We also explore the effect of interaction quantity.

## METHODS

- Positivity resonance measured using validated 7-item positivity resonance scale (PPRS).
  - “...did you feel energized and uplifted by the company of the other(s)?”
  - “...did you feel in “in sync” with the other(s)?”
- CTRA gene expression measured via genome-wide transcriptional profiling of PBMC.
- 53-gene CTRA indicator was aggregated into a composite score (Boyle et al., 2019).

In a sample of midlife adults selected for low early-life socioeconomic status,

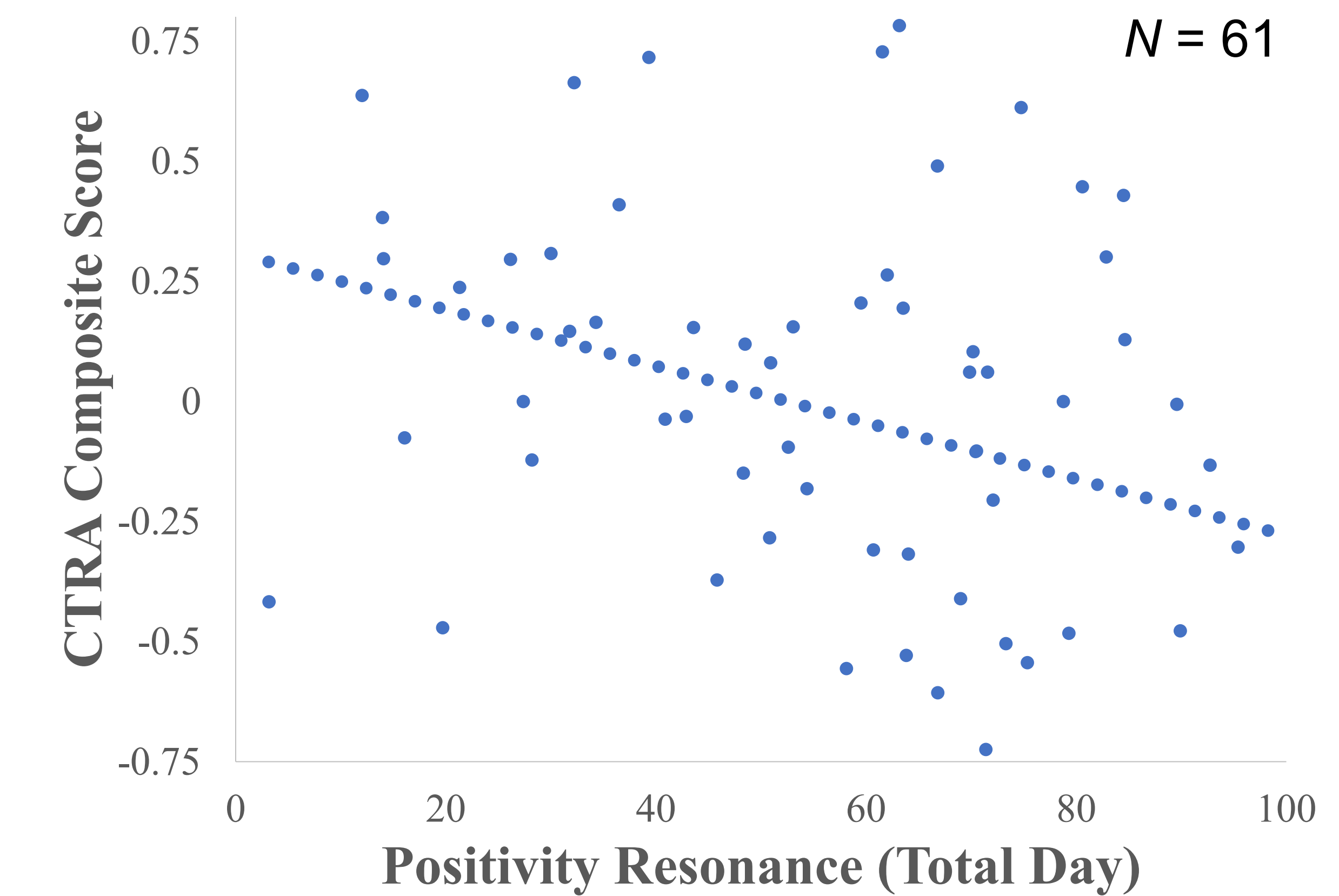
# Quantity of social interactions, and potentially their affective quality, predicts leukocyte gene expression profiles,

characterized by down-regulated expression of pro-inflammatory genes and up-regulated expression of genes involved in Type I interferon responses and antibody production.

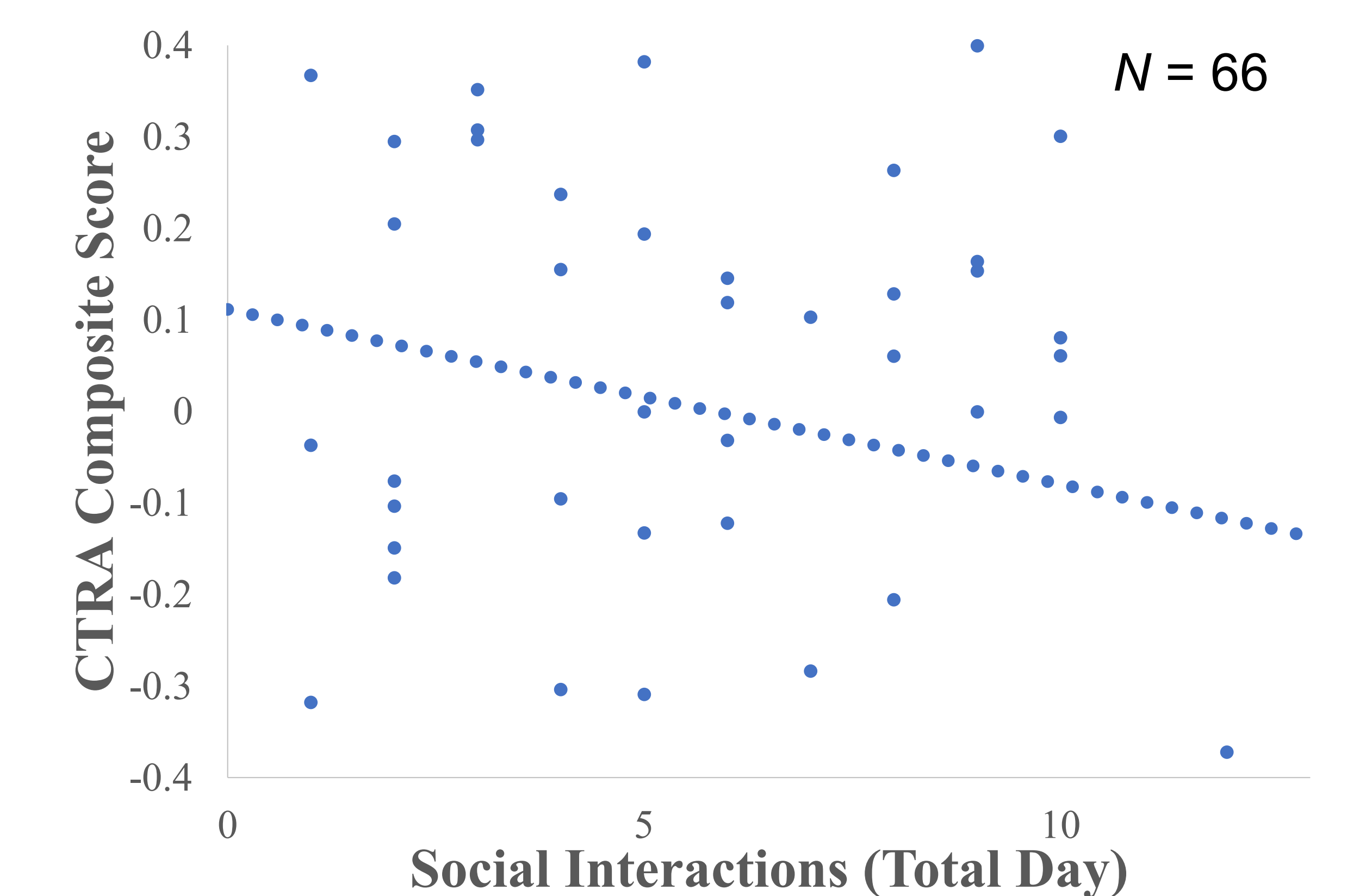


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## RESULTS



- Greater positivity resonance at baseline was associated with downregulated CTRA expression before ( $b = -0.06$ ,  $p = 0.007$ ) and after controlling for demographic covariates ( $b = -0.05$ ,  $p = 0.025$ ).
  - Became insignificant after controlling for genomic covariates.



- Greater quantity of social interactions at baseline (marginally) associated with downregulated CTRA expression ( $b = -0.02$ ,  $p = 0.071$ ) after controlling for demographic and genomic covariates.
  - Not significant ( $b = -0.02$ ,  $p = 0.140$ ) without controlling for demographic and genomic covariates.

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