

Table S15 Description of targeted gene sets significantly enriched by genes called differentially expressed between FIR and nonFIR affected infants. The “Size” column specifies the number of genes in the gene set that map to the microarray expression data set analyzed in this article.

Gene Set	Size	Source
Inflammation (innate response)	800	Table S1 from Loza et al. Assembly of inflammation-related genes for pathway-focused genetic analysis. <i>PLOS One</i> , 2(10):e1035, 2007 [PMID:17940599]
Inflammation (Th17 - adaptive response)	72	Table S1 from ciofani et al. A validated regulatory network for Th17 cell specification. <i>Cell</i> , 151(2):289-303, 2012 [PMID:23021777]
Senescence	194	Belinky et al. PathCards: multi-source consolidation of human biological pathways. <i>Database</i> , 2015:bav006, 2015 [PMID:25725062]
Apoptosis	68	Table S1 from Loza et al. Assembly of inflammation-related genes for pathway-focused genetic analysis. <i>PLOS One</i> , 2(10):e1035, 2007 [PMID:17940599]
FMRP targets	823	Table S2 from Darnell et al. FMRP stalls ribosomal translocation on mRNAs linked to synaptic function and autism. <i>Cell</i> , 146(2):247-261, 2011 [PMID:21784246]
APC targets	243	Table S1 from Preitner et al. APC is an RNA-binding protein, and its interactome provides a link to neural development and microtubule assembly. <i>Cell</i> , 158(2):368-382, 2014 [PMID:25036633]
UC mesenchymal stem cells	19	Edgar et al. LifeMap discovery: the embryonic development, stem cells, and regenerative medicine research portal. <i>PLOS One</i> , 8(7):e66629, 2013 [PMID:23874394]