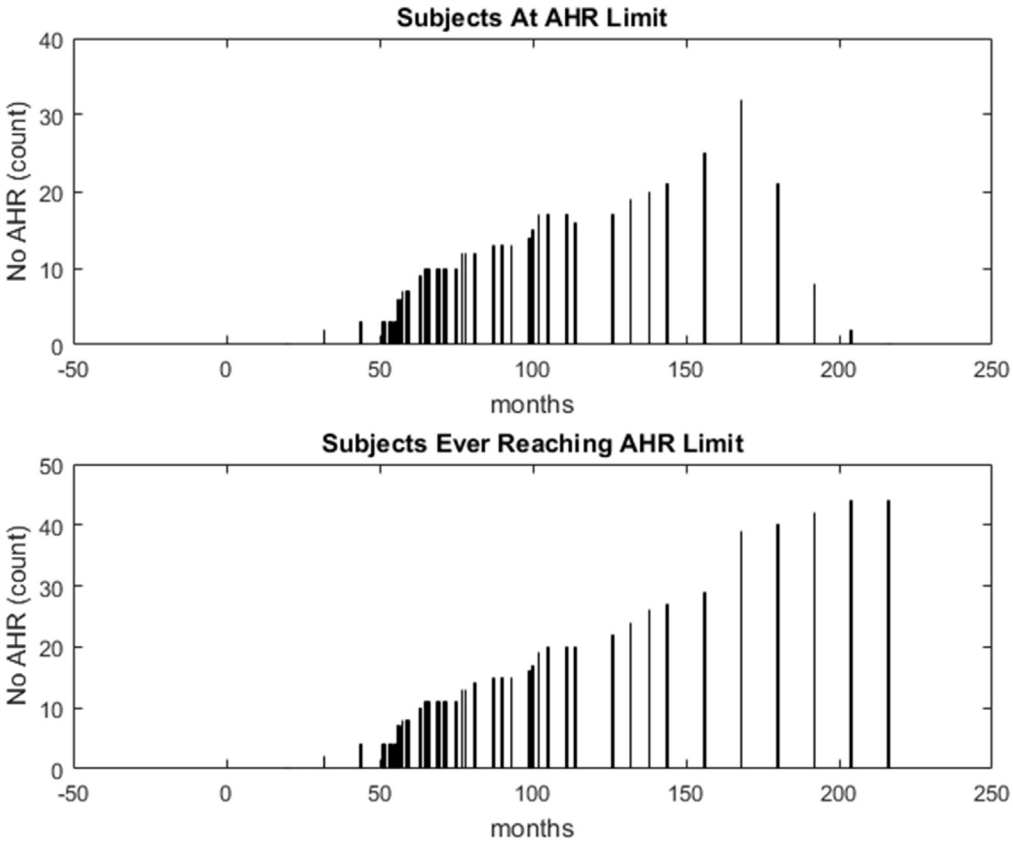

FIG E1. Number of subjects from the CAMP study who had microRNA data available and had AHR remission, as quantified by a PC_{20} value above the limit of 37.5 mg/mL in a methacholine challenge. The x-axis is displayed in months since randomization in the CAMP trial. Top panel: There was a noticeable peak at 168 months (14 years) from baseline of subjects in AHR remission.

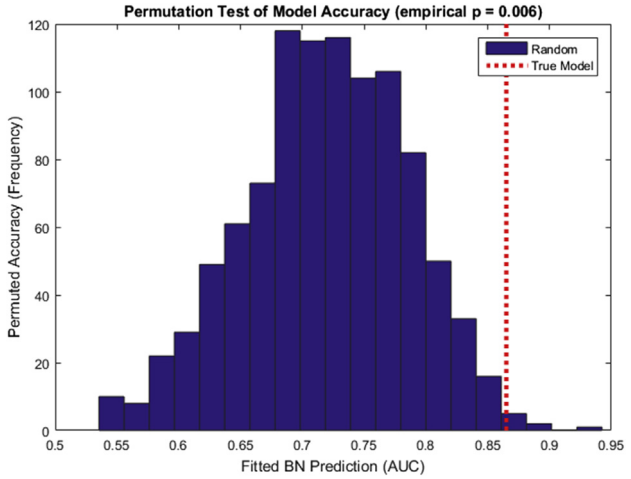

FIG E2. Empirical distribution of permutation test realizations for BN predicting 14-year AHR remission. For each of 1000 iterations, the phenotype labels were shuffled (AHR remission) and a new BN was learned from the miRs to predict the scrambled phenotype. For each iteration, the BN's prediction on the scrambled phenotype is reported (AUC), and shown in the histogram above. The BN model on the true data exhibits statistically significant prediction (86% AUC; $P = .006$).

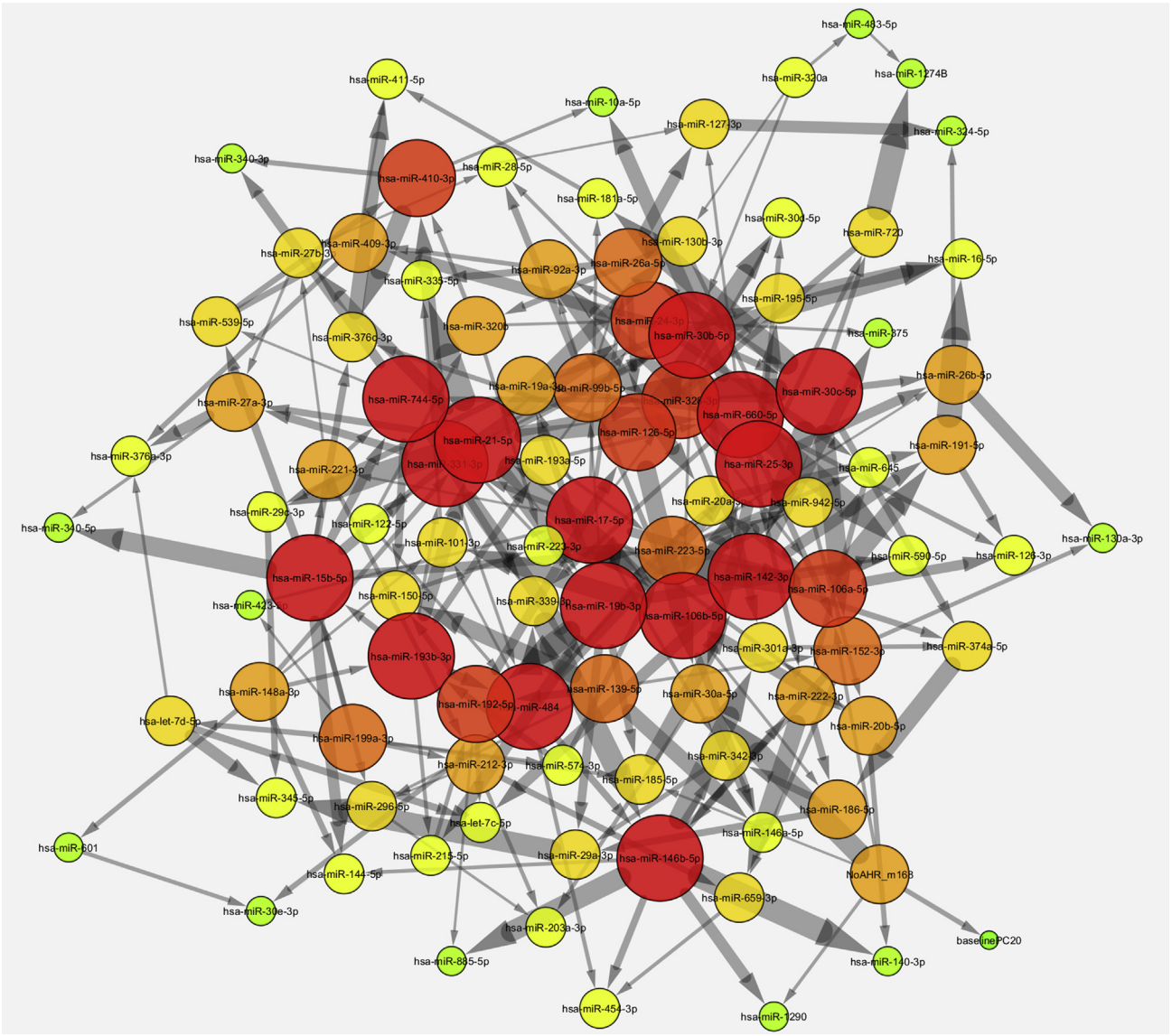

FIG E3. Conditional Gaussian BN predictive of AHR remission at 14 years. *Arrows* indicate statistical dependence of the target node on the source node. Arrow thickness indicates the strength of connection in log Bayes factor. Node color and size indicate the number of connections.

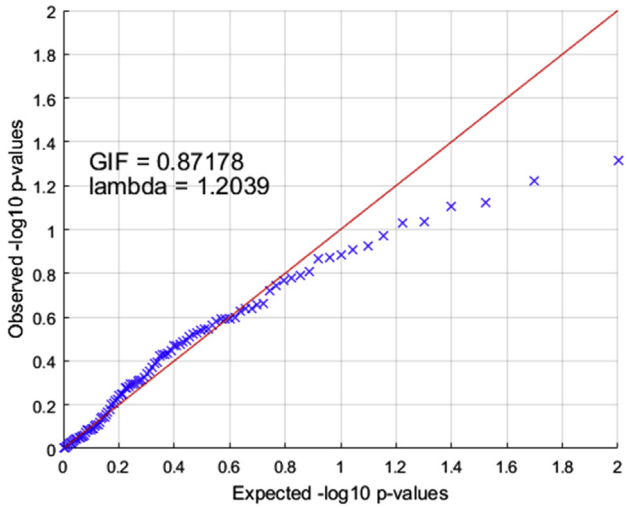

FIG E4. Quantile-Quantile plot of logistic regression tests for each miR's association with 14-year AHR remission. This indicates that no miRs are significantly associated with AHR remission after correction for multiple testing. *GIF*, Genomic inflation factor.

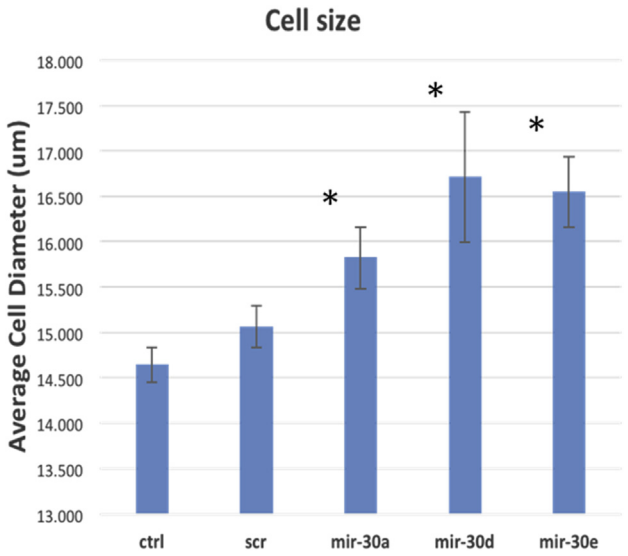

FIG E5. HASM cells were transfected with 10 nM of either scramble control or miR-30a/d/e mimics. Seventy-two hours after transfection, cells were trypsinized for 8 minutes and measured for cell size by the Moxi Z Cell Analyzer. Average cell diameter (μm) was compared in mimic-transfected versus scramble-transfected HASM cells. Data (mean ± SE) were obtained from 3 independent experiments. *ctrl*, Control samples; *scr*, scramble-transfected control samples. *Statistically significant increases in cell diameter (hypertrophy) over scramble cells at $P < .05$.

TABLE E1. List of 11 miRs used in BN and the genes they are confirmed to target using miRTarBase and restricting to strong functional evidence of a microRNA-mRNA interaction

miRs	Gene targets
hsa-miR-106a-5p	APP, ARID4B, ATM, BCL10, BMP2, CASP7, CCND1, CDKN1A, CYP19A1, E2F1, FAS, HIPK3, IL10, MAPK9, MYLIP, PTEN, RB1, RBL2, RUNX1, RUNX3, SIRPA, SLC2A3, STAT3, TGFBR2, TIMP2, VEGFA
hsa-miR-126-5p	ADAM9, CXCL12, MMP7, MYC, PTPN7, SLC45A3
hsa-miR-1290	—
hsa-miR-146b-5p	HNRNPD, IRAK1, KIT, MMP16, NFKB1, PDGFRA, TLR4, TRAF6, UHRF1
hsa-miR-17-5p	ADAR, APP, BCL2, BCL2L11, BMP2, BMPR2, CCL1, CCND1, CCND2, CDKN1A, CLU, DNAJC27, DNMT1, E2F1, EPAS1, ETV1, FBXO31, GPR137B, HBP1, HIF1A, HSPB2, ITGB8, JAK1, KAT2B, LDLR, MAP3K12, MAPK9, MDM2, MEF2D, MMP2, MYC, NABP1, NCOA3, NPAS3, NPAT, PDLIM7, PHLPP1, PKD2, PTEN, PTPRO, RB1, RBL1, RBL2, RND3, RUNX1, SIRPA, SMAD4, SMURF1, SOCS6, STAT3, TBC1D2, TCEAL1, TCF3, TGFBR2, TIMP3, TNFSF12, TP53INP1, UBE2C, VEGFA, WEE1, YES1, ZBTB4, ZNFX1
hsa-miR-185-5p	ALOX12, AQP3, AR, ARC, ATR, CAMK4, CASP14, CDC42, CDK6, DNMT1, DUSP4, EPAS1, EPHB2, EZH2, HMGA1, IGF1R, MCM10, MZB1, NFATC3, NTRK3, RHOA, SCARB1, SIX1, SREBF1, SREBF2, VEGFA
hsa-miR-199a-3p	APOE, CAV2, CD44, DNAJA4, FUT4, HGF, IGF1, MAPK1, MET, MTOR, PTGS2, SMARCA2, STK11, ZHX1
hsa-miR-19b-3p	ATXN1, BCL2L11, BMPR2, CUL5, CYP19A1, DNMT1, ESR1, GCM1, HIPK1, HIPK3, MXD1, MYCN, MYLIP, PPP2R5E, PRKAA1, PTEN, SMAD4, SOCS1, TLR2, TP53
hsa-miR-25-3p	ATP2A2, BCL2L11, CCL26, CDH1, CDKN1C, DSC2, ERBB2, EZH2, FBXW7, HAND2, KAT2B, KLF4, LATS2, MDM2, PRMT5, PTEN, RECK, REV3L, SMAD7, TCEAL1, TP53, WDR4
hsa-miR-30a-5p	ABL1, AVEN, BCL11A, BCL9, BDNF, BECN1, CD99, CDH1, DTL, ERG, ESR2, EYA2, FOXD1, HSPA5, MTDH, NEUROD1, NOTCH1, PIK3CD, PRDM1, RUNX2, SEPT7, SMAD1, SNAI1, SOX4, TNRC6A, TP53, TUBB4B, VIM
hsa-miR-328-3p	ABCG2, BACE1, CD44, H2AFX, MMP16, PTPRJ, SFRP1

TABLE E2. Relative expression levels of miR-30 family members in human ASM cells

	miR-30 family				
Member	a	b	c	d	e
% Total reads	2.5%	0.06%	0.06%	0.75%	0.45%

miR-30 family members are among the most abundant found in ASM cells, with mir-30a accounting for 2.5% of all reads in these cells.