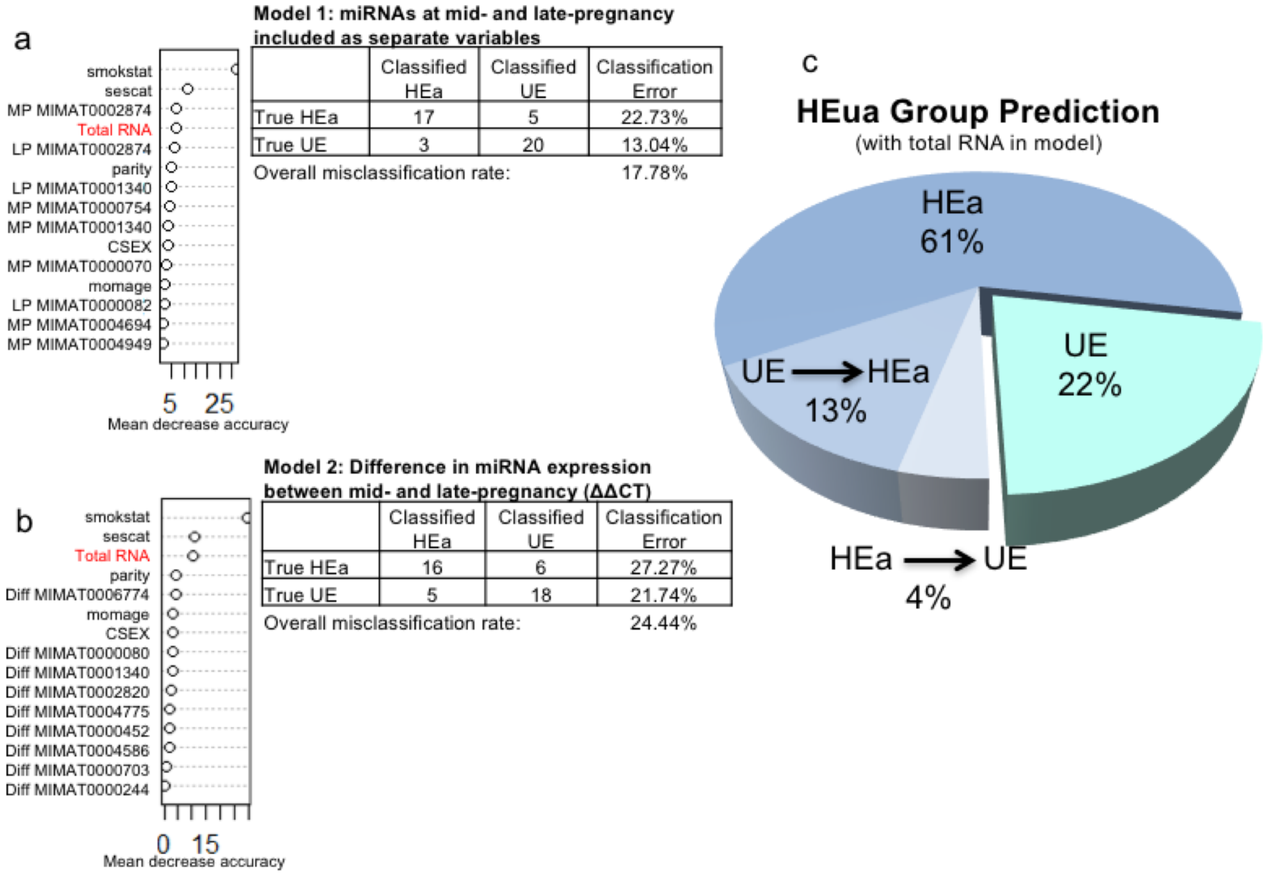
Models 1 & 2, including Total RNA in the Random Forest Classification Models



Model 1: miRNAs at mid- and late-pregnancy included as separate variables

	Classified HEa	Classified UE	Classification Error
True HEa	17	5	22.73%
True UE	3	20	13.04%

Overall misclassification rate: 17.78%

Model 2: Difference in miRNA expression between mid- and late-pregnancy (ΔΔCT)

	Classified HEa	Classified UE	Classification Error
True HEa	16	6	27.27%
True UE	5	18	21.74%

Overall misclassification rate: 24.44%

S5 Fig.

S5 Fig. Prediction model with the variable 'total recovered RNA' (total RNA) included. (a) Model 1 which includes miRNAs (classified by MIMAT#######) from mid-(MP) and late-(LP) pregnancy as separate variables. Overall misclassification rate was 17.78%. (b) Model 2 includes the difference in miRNA expression between mid- and late-pregnancy. Overall misclassification rate was 24.44%. (c) Using classification model #1 to classify the HEua group, results in a majority of the HEua group predicted to be HEa-like throughout pregnancy.