SAMPLE COLLECTION

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RNA PURIFICATION

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cDNA SYNTHESIS

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LOAD TLDA PLATES & RT-PCR

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CONVERT C_T TO LINEAR EXPRESSION VALUES, $=2^{(40-CT)}$

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IDENTIFY DISCRIMINATORY SINGLE EXPRESSION RATIOS; eg. GENE A/GENE B, WHERE THE GREATEST NUMBER OF SUBJECT RATIO SCORES ARE HIGHER THAN THE HIGHEST OR SECOND HIGHEST RATIO SCOREIN THE COMPARATOR SUBJECT GROUP

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ESTABLISH A POINT SYSTEM: ONE POINT IS AWARDED TO A SUBJECT FOR EACH EXPRESSION RATIO WHERE IT ACHIEVES A HIGHER SCORE THAN THE HIGHEST OR SECOND HIGHEST RATIO SCORE IN THE COMPARATOR SUBJECT GROUP

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PERMUTATION TESTING TO IDENTIFY COMBINATION OF RATIOS, RATIOSCORE, THAT BEST DISCRIMINATES ALL SUBJECTS IN THE TEST GROUP FROM ALL SUBJECTS IN THE COMPARATOR GROUP

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TRAIN AND VALIDATE SVM.

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EVALUATE PREDICTIVE ACCURACY WITH INDEPENDENT CASE COHORT

Supplementary Figure 1. Flow chart describing sample collection and processing, data generation, and methods of data analysis.