SUPPLEMENT MATERIAL

CART ANALYSIS

CART analysis is a decision tree analysis for population-based statistical models that uses deterministic rules for non-parametric outcomes. It utilizes binary splits for both ordinal and continuous variables in order to predict outcome (17. 18). For CART analysis, we used age, Type I DM and Trisomy 21 analyzed with TTG-IgA as dependent variables. The outcome remained CD. The predictive variables for the first model include TTG-IgA, sex, and age.

SUPPLEMENTAL FIGURES

Figure 1 – ROC curve of TTG-IgA single serology; AUROC = 0.9466

AUROC, area under receiver operating characteristic curve; IgA, immunoglobulin A; TTG, tissue transglutaminase

Figure 2 – ROC curve of TTG-IgA + DGP-IgA serology; AUROC = 0.9464

AUROC, area under receiver operating characteristic curve; DGP, deamidated gliadin peptide; TTG, tissue transglutaminase; IgA, immunoglobulin A

Figure 3 – ROC curve of DGP-IgA single serology; AUROC = 0.6657

AUROC, area under receiver operating characteristic curve; DGP, deamidated gliadin peptide; IgA, immunoglobulin A

Figure 4 – ROC curve of TTG-IgG + DGP-IgG serology; AUROC = 0.5629

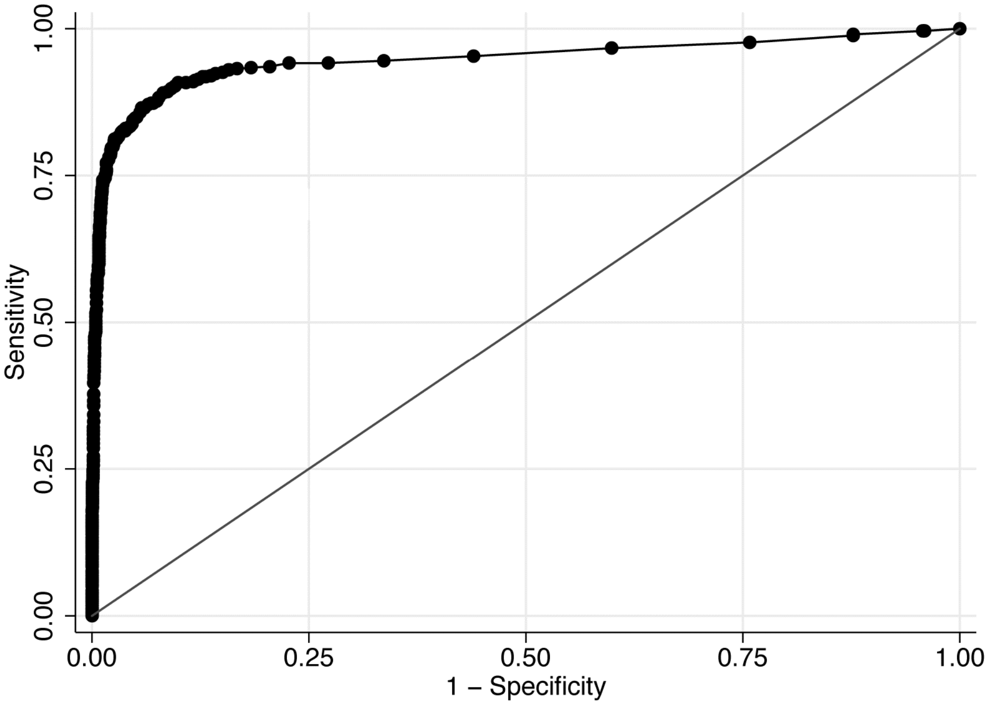
AUROC, area under receiver operating characteristic curve; IgG immunoglobulin G; TTG, tissue transglutaminase;

Figure 5 – CART analysis of CD with TTG-IgA & Type I DM

CD, Celiac disease; DM, diabetes mellitus; IgA, immunoglobulin A, PPV, positive predictive value; TTG, tissue transglutaminase

Figure 6 – CART analysis of CD with TTG-IgA & Trisomy 21

CD, Celiac disease; IgA, immunoglobulin A, PPV, positive predictive value; TTG, tissue transglutaminase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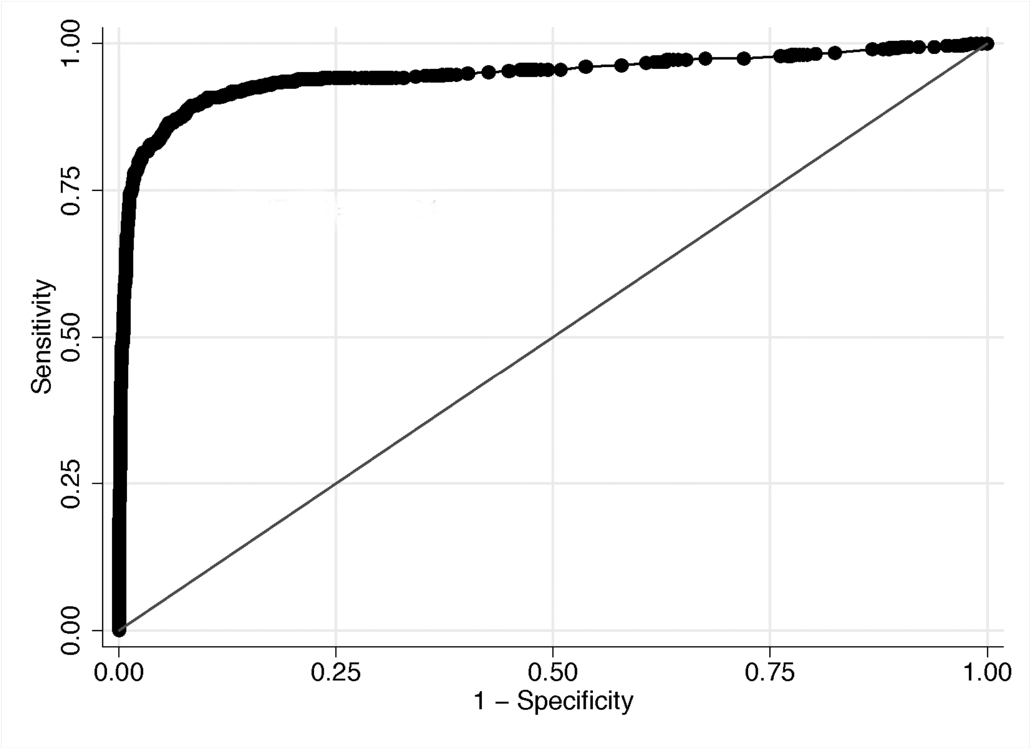
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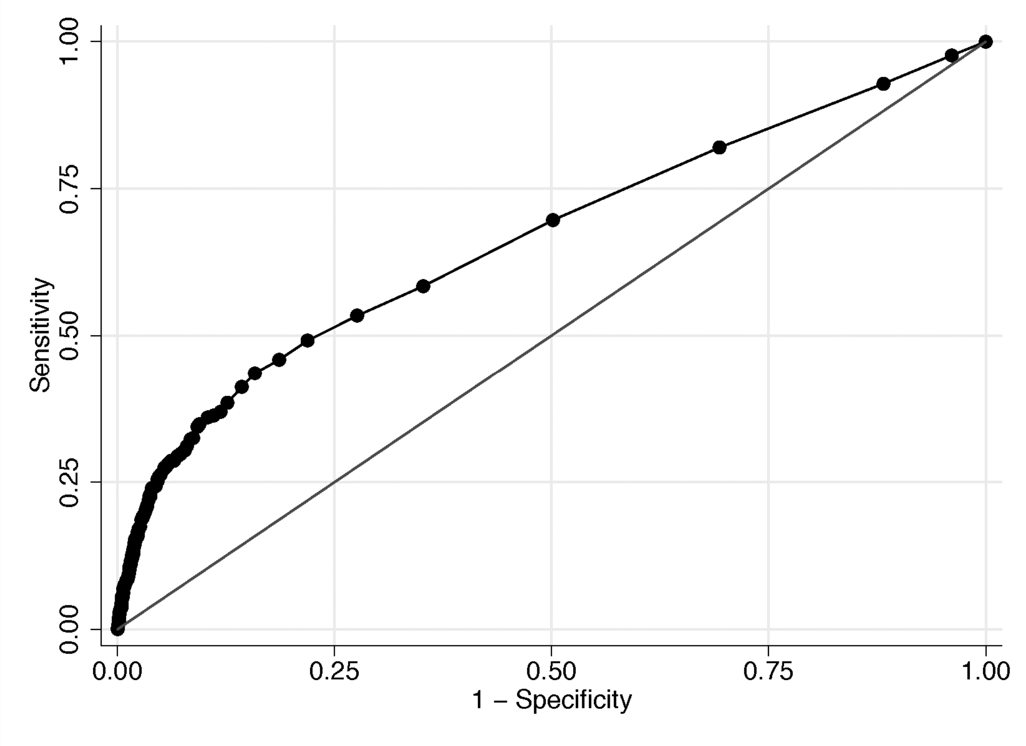
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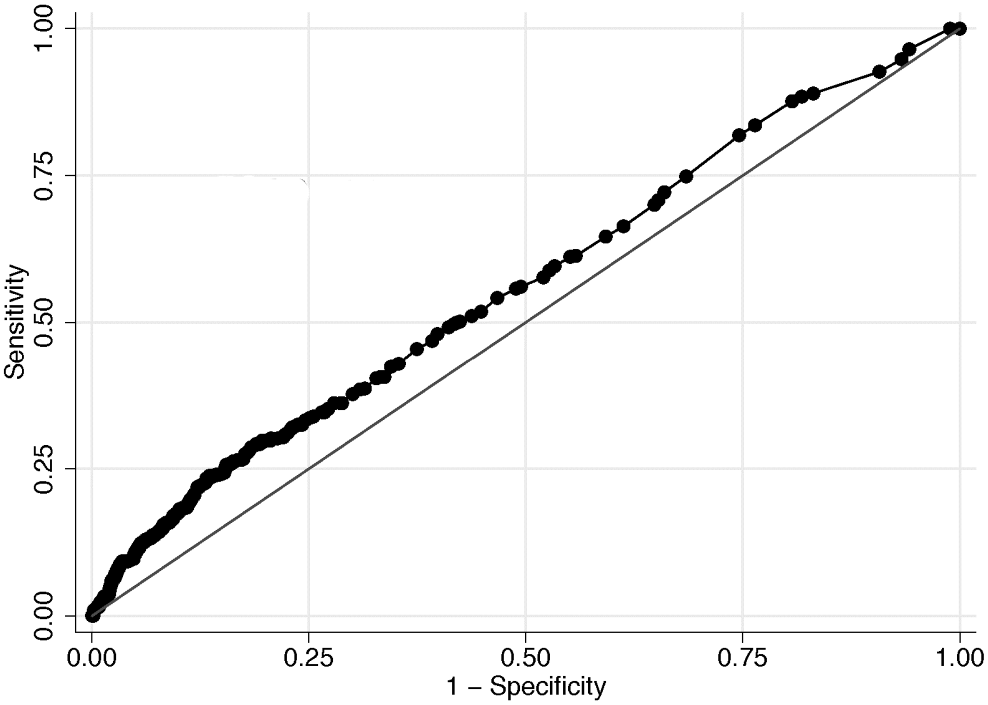
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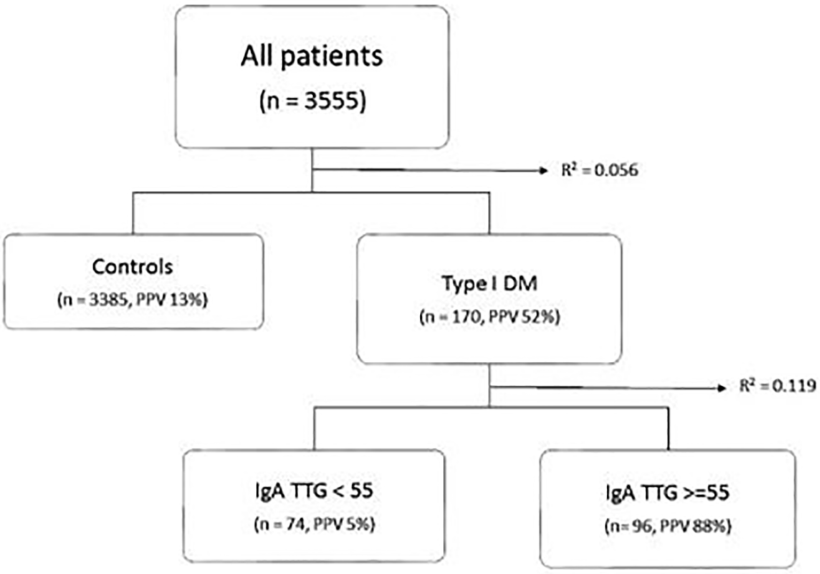
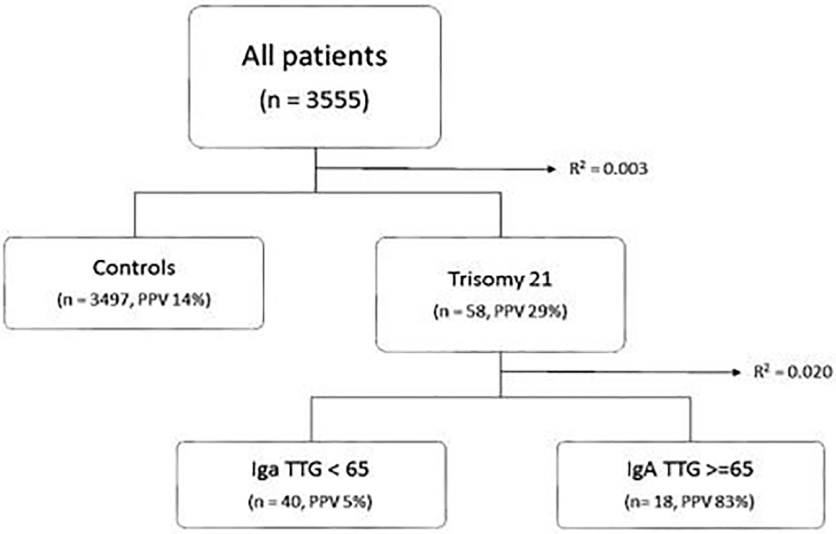

All patients
(n = 3555)
R² = 0.056
Controls
(n = 3385, PPV 13%)
Type I DM
(n = 170, PPV 52%)
R² = 0.119
IgA TTG < 55
(n = 74, PPV 5%)
IgA TTG >=55
(n= 96, PPV 88%)


All patients
(n = 3555)
R² = 0.003
Controls
(n = 3497, PPV 14%)
Trisomy 21
(n = 58, PPV 29%)
R² = 0.020
Iga TTG < 65
(n = 40, PPV 5%)
IgA TTG >=65
(n= 18, PPV 83%)