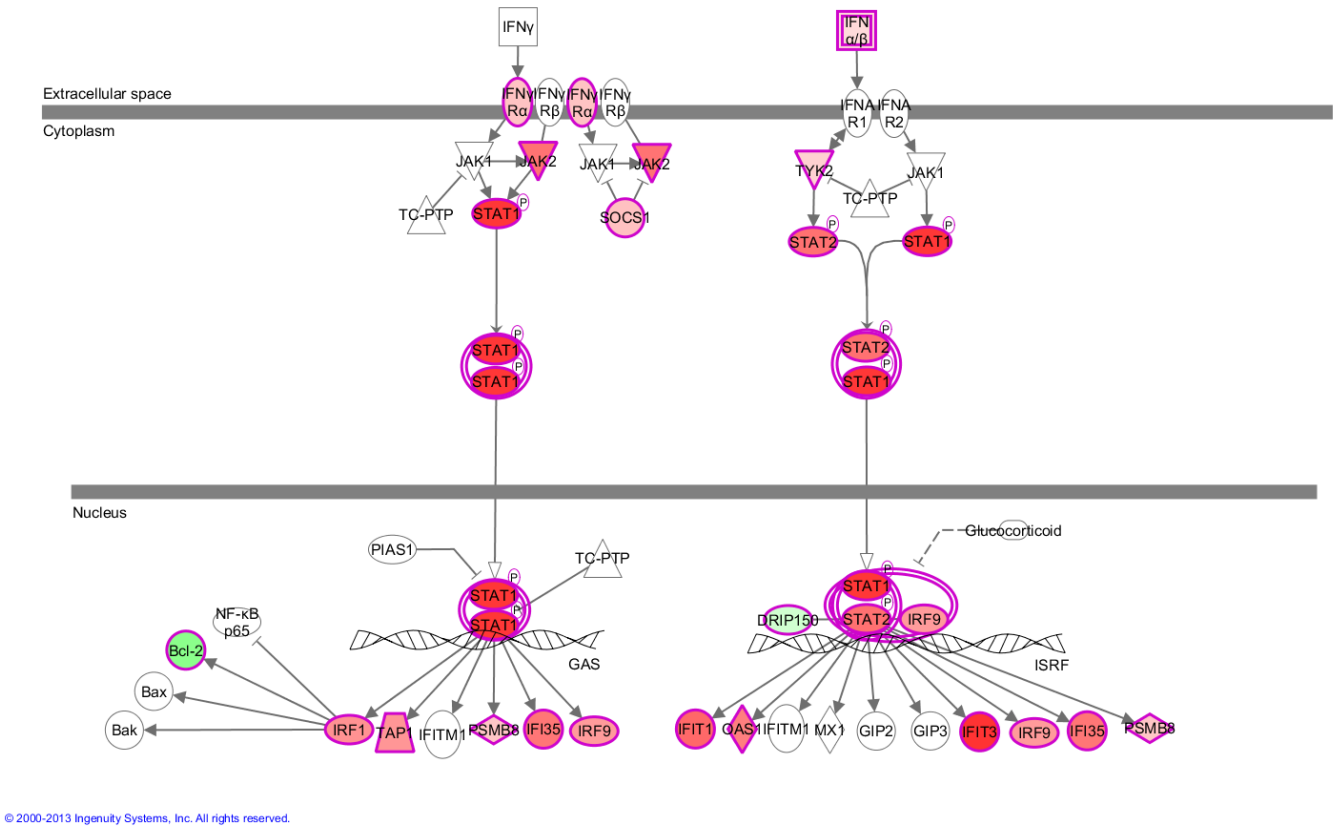
Supplementary Figure E1.



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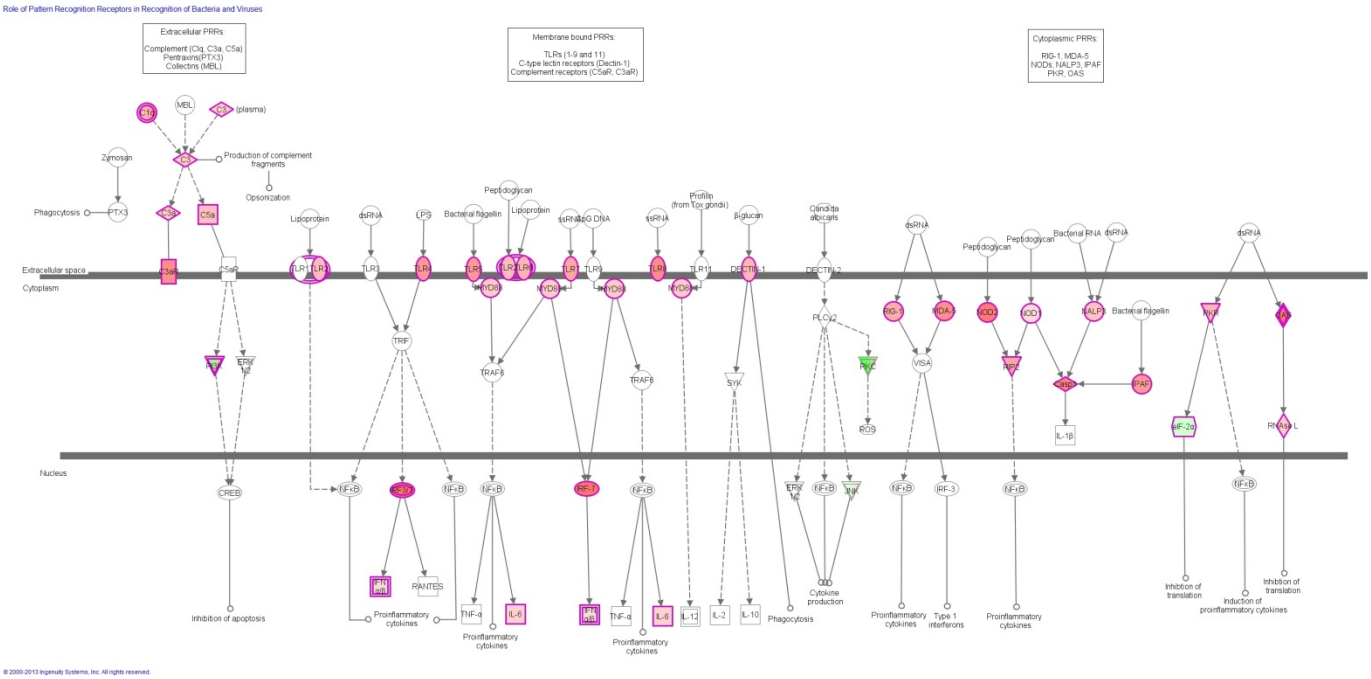
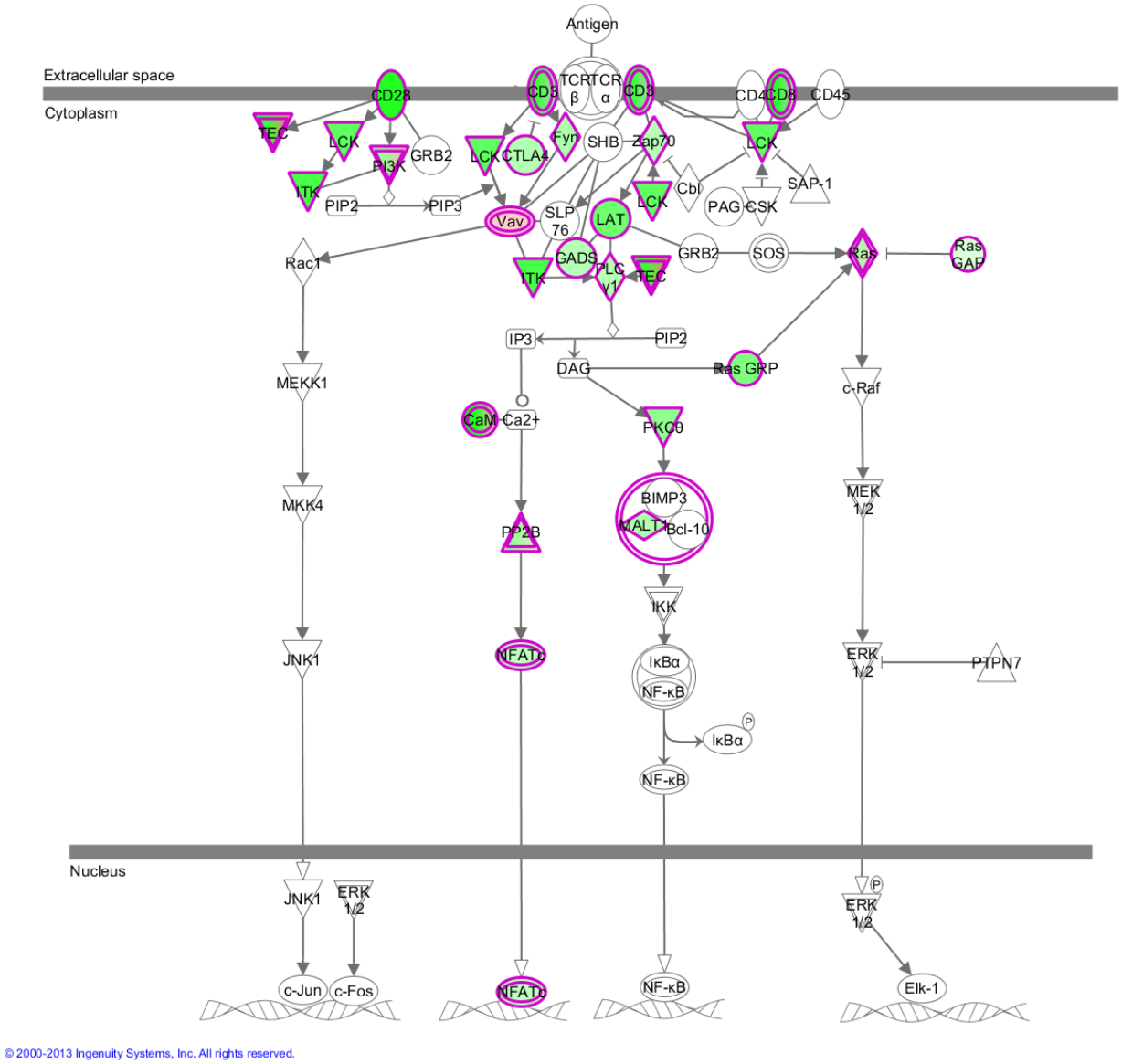
Ingenuity Pathway Analysis of the derivation sarcoidosis cohort blood microarray gene expression dataset (Gene Expression Omnibus, GSE19314) demonstrates an upregulation of the Interferon Signaling canonical pathway. Red color denotes increased expression, and green color denotes decreased expression relative to healthy controls. p = 0.0024

Supplementary Figure E2.



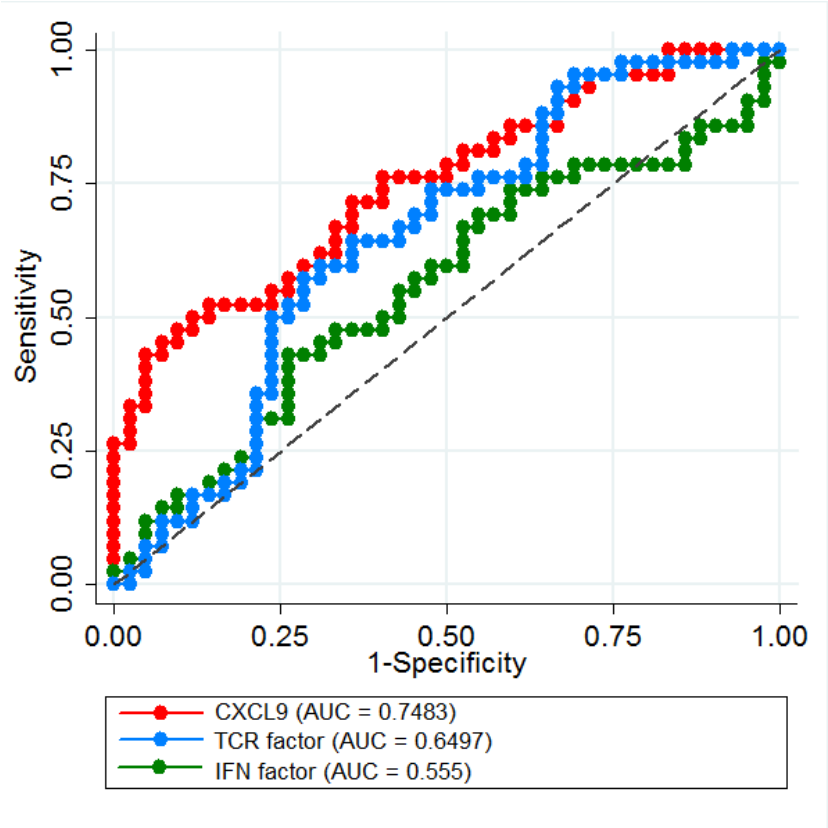
Ingenuity Pathway Analysis of the derivation sarcoidosis cohort blood microarray gene expression dataset (Gene Expression Omnibus, GSE19314) demonstrates an upregulation of the Role of Pattern Recognition Receptors in Recongition of Bacteria and Viruses canonical pathway. Red color denotes increased expression, and green color denotes decreased expression relative to healthy controls. p=0.0006

Supplementary Figure E3.



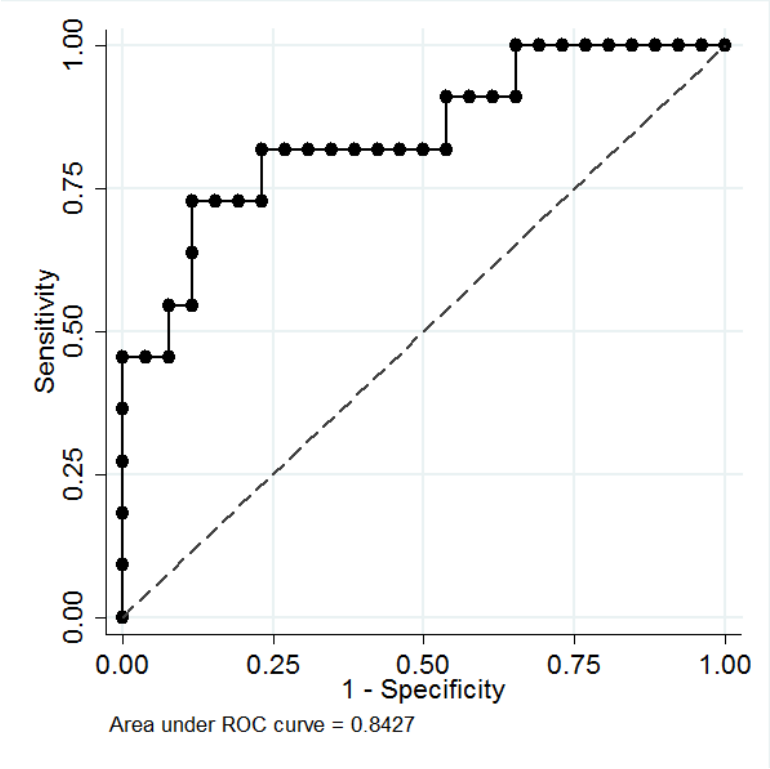
Ingenuity Pathway Analysis of the derivation sarcoidosis cohort blood microarray gene expression dataset (Gene Expression Omnibus, GSE19314) demonstrates a downregulation of the T Cell Receptor Signaling canonical pathway. Red color denotes increased expression, and green color denotes decreased expression relative to healthy controls. $p = 0.019$

Supplementary Figure E4.



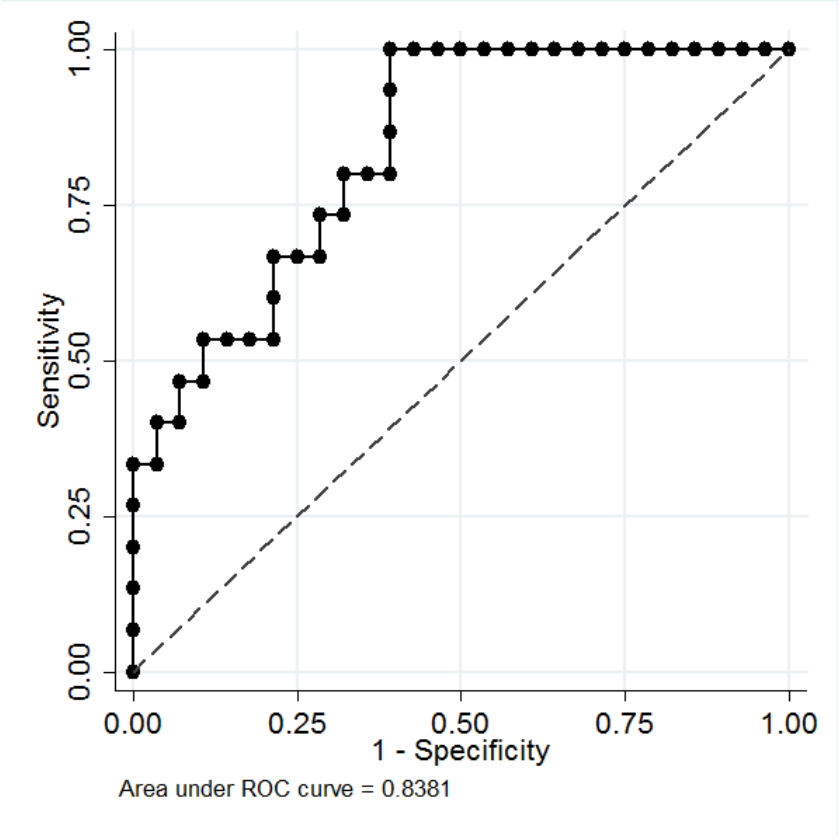
Shown are the receiving operator characteristic (ROC) curves of individual factors in discriminating between non-progressive and chronic sarcoidosis (n=91). IFN factor in itself has no predictive value in discriminating chronic versus non-progressive disease.

Supplementary Figure E5



Using logistic regression-based prediction probabilities, CXCL9 and TCR factors predict chronic versus non-progressive sarcoidosis disease among subjects who enrolled early in their disease course (ie. enrolled within 2 years of diagnosis). n=37

Supplementary Figure E6



In a sensitivity analysis of only sarcoidosis subjects who are not on any immunosuppression (n=43), CXCL9 and TCR factors-based prediction probabilities discriminates between chronic versus non-progressive disease at enrollment.