

Supplementary Table 6B. Statistics for logistic regression in NoDR versus MO NPDR using 4-marker panel

Dependent Y	NoDR vs MO NPDR
Method	Enter
Sample size	30
Cases with Y=0	15 (50.00%)
Cases with Y=1	15 (50.00%)

A. Overall Model Fit

Null model -2 Log Likelihood	41.589
Full model -2 Log Likelihood	0.000000304
Chi-square	41.589
DF	4
Significance level	P < 0.0001

B. Coefficients and Standard Errors

Variable	Coefficient	Std. Error	P
Afamin_DADPDTFFAK_y7 (563.8/825.4)	-0.8769	305.2902	0.9977
Kallistatin_FFSAQTNR_a1 (485.7/120.1)	5.7316	888.5799	0.9949
Complement factor B_EELLPAQDIK_b2 (578.3/259.1)	1.6446	1052.1482	0.9988
Apolipoprotein C III_GWVTDGFSSLK_y9 (598.8/854.4)	-0.5907	121.0903	0.9961
Constant	7.2822		

C. Odds Ratios and 95% Confidence Intervals

Variable	Odds Ratio	95% CI
Afamin_DADPDTFFAK_y7 (563.8/825.4)	0.4161	0.0000 to 30.7E+258
Kallistatin_FFSAQTNR_a1 (485.7/120.1)	308.4713	0.0000 to 0.0000
Complement factor B_EELLPAQDIK_b2 (578.3/259.1)	5.179	0.0000 to 0.0000
Apolipoprotein C III_GWVTDGFSSLK_y9 (598.8/854.4)	0.5539	0.0000 to 6.57E+102

D. Classification table (Original Model)

Actual group	Predicted group		Percent correct
	No DR	MO NPDR	
NoDR	15	0	100.00%
MO NPDR	0	15	100.00%
Accuracy			100.00%

E. Classification table (Cross validated, Leave-one out)

Actual group	Predicted group		Percent correct
	No DR	MO NPDR	
NoDR	13	2	86.67%
MO NPDR	1	14	93.30%
Accuracy			90.00%

E. ROC curve analysis

Area under the ROC curve (AUC)	1
Standard Error	0
95% Confidence Interval	0.884 to 1.000

F. Collinearity analysis

Variable	Collinearity Statistics	
	Tolerance	VIF
Afamin_DADPDTFFAK_y7 (563.8/825.4)	0.343	2.916
Kallistatin_FFSAQTNR_a1 (485.7/120.1)	0.281	3.558
Complement factor B_EELLPAQDIK_b2 (578.3/259.1)	0.304	3.294
Apolipoprotein C III_GWVTDGFSSLK_y9 (598.8/854.4)	0.757	1.322

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Result of logistic regression for NoDR versus moderate NPDR group is tabulated as five contents. In this case, sample number of each group is 15, respectively, and 4 marker proteins (afamin, kallistatin, complement factor B and apolipoprotein C III) are selected from the result of expression pattern (Linear increase or linear decrease). In Table A, overall model fit the results such as null model -2 log likelihood, full model -2 log likelihood, chi-square, degree of freedom (DF) and significance level are shown. Table B shows coefficients and standard errors of 4 variables. In Table C, odds ratios and 95% confidence intervals of 4 marker protein are shown. In Table D, classification table is shown when the cut-off value is set as 0.5. The result of ROC curve analysis, which contains AUC, standard error and confidence interval are shown in Table E.