



University of Colorado  
Anschutz Medical Campus

# Nanostring Prognosis Panel for Progression of Persistent Bronchial Dysplasia to Squamous Cell Lung Cancer

Alyse Staley, Julia Nyiro, Dan Merrick, Meredith Tennis, Elizabeth Donald

## BACKGROUND

- To provide prognostic information for patients with premalignant airway disease in a clinical setting, it is important to classify whether patients will experience persistent or regressive behavior relative to baseline

## AIM

- Identify a prognostic panel of baseline gene ratios to predict whether patients will experience persistent or regressive bronchial dysplasia (BD).

## METHODS

- 63 baseline biopsies from patients with BD were collected between 1997 and 2017 and followed over time to determine whether their BD persisted or regressed
- Univariate associations between each baseline independent variable (age, sex, smoking status, etc.) and the outcome (persistent or regressive BD) were assessed with a logistic regression model.
- A multivariate model was selected to assess the association between the Nanostring gene ratios and persistence
- The best-fitting model according to the Bayesian Information Criterion (BIC) was chosen as the final multivariate model

RESULTS									
Parameter	BMP7_PRKCE	CALML3_PARVG	ESRP2_SCCPDH	PTK6_IQGAP2	SPRR1A_ARRB1	P2RY2_RGL1	CYP3A5_PLCB2	EPS8L1_ST3GAL6	ESPL1_RHOH
OR	1.64	1.04	1.26	1.56	1.03	1.15	1.23	1.07	0.87
95% CI	1.00, 2.92	1.00, 1.11	1.03, 1.62	1.12, 2.60	1.00, 1.08	1.02, 1.36	0.83, 1.98	1.01, 1.16	0.51, 1.39
p-value	0.066	0.11	0.043	0.034	0.096	0.05	0.323	0.036	0.559
PLK1_ELMO1	TMPRSS11E_DRD2	AKR1B10_C4A	ALDH4A1_UACA	CYP4F3_PRKCE	GALNT5_HLA.DRB4	GNAI3_HLA.DMA	S100A9_SLC5A8	SERPINB5_HLA.DPB1	YWHAZ_HLA.DPA1
2.52	1.06	1.08	1.88	4.36	1	1.11	1	1.1	0.73
1.19, 7.12	1.00, 1.21	0.99, 1.24	1.00, 4.17	1.20, 20.5	0.98, 1.03	0.94, 1.36	1.00, 1.00	0.89, 1.42	0.20, 1.91
0.036	0.246	0.154	0.075	0.039	0.732	0.242	0.136	0.393	0.552

Table: The univariate associations between each independent variable and persistence using a logistic regression model.

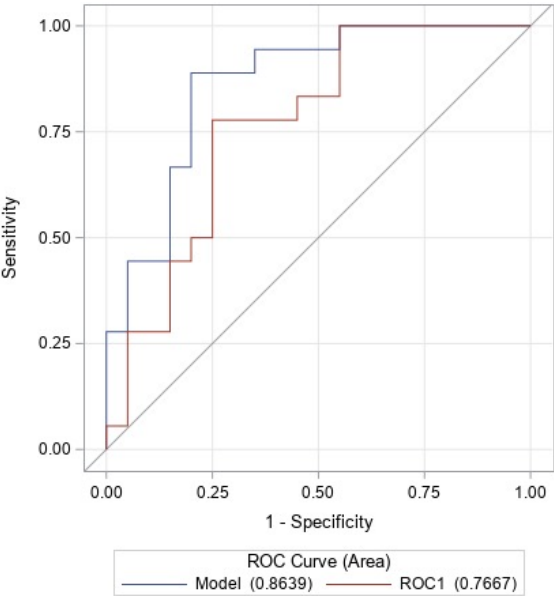


Figure: The Model ROC curve is plotted in blue with an Area under the ROC Curve (AUC) of 0.86 (95% CI: 0.75 to 0.98). The leave-one-out cross-validated ROC curve is presented in red and has an AUC of 0.77 (95% CI: 0.61 to 0.92). The sensitivity is 83.3% and the specificity is 80%.

- The following six gene ratios had significant ( $p < 0.05$ ) associations with persistence: CYP4F3\_PRKCE, EPS8L1\_ST3GAL6, ESRP2\_SCCPDH, P2RY2\_RGL1, PLK1\_ELMO1, and PTK6\_IQGAP2
- The model AUC suggests that there is an 86 percent chance that the model will correctly distinguish between persistent and regressive patients. The sensitivity for this model is 83.3% and the specificity is 80%

## CONCLUSIONS

- The baseline gene ratios of patients with BD had an excellent ability to discriminate between persistent and regressive BD
- These results are promising for the future prognostic ability of the Nanostring gene ratio panel