Table S5. Assessment of the predictive value of proteinuria in the risk of ESRD. The best model (model 1) excludes proteinuria, has lowest AIC and BIC, and explains 22% of variance in the outcome. Proteinuria is not significant in the full model (model 2), although the effect estimate is suggestive of increased risk with higher urine protein excretion (HR 1.21, p=0.32). Exclusion of albumin in model 3 unmasks highly significant association of proteinuria with the risk of progression (HR 1.56, p=9.7 x 10-3). Additional exclusion of hemoglobin has little effect on the strength of this association (model 4).

	Selection Criteria			Significance of Individual Predictors in the Model (Wald test)					
	R2	AIC	BIC	eGFR P-value	SBP P-value	Hemoglobin P-value	Albumin P-value	Proteinuria # P-value	Proteinuria # HR (95%CI)
Model 1	0.22	523.8	541.5	1.3 x 10-14 ***	5.4 x 10-3 **	1.2 x 10-5 ***	7.4 x 10-5 ***		
Model 2	0.22	524.8	547.0	1.4 x 10-13 ***	0.012 *	1.1 x 10-5 ***	3.1 x 10-3 **	0.32 (NS)	1.21 (0.83-1.75)
Model 3	0.21	531.1	548.8	5.6 x 10-12 ***	0.081	7.6 x 10-7 ***		9.7 x 10-3 **	1.56 (1.11-2.19)
Model 4	0.18	552.4	565.7	2.9 x 10-13 ***	0.037 *			8.1 x 10-3 **	1.55 (1.12-2.15)

^{*} Two-sided P<0.05

Model 1: predictors include baseline eGFR, systolic blood pressure (SBP), hemoglobin, albumin (the best model used for risk score derivation).

Model 2: predictors include baseline eGFR, SBP, hemoglobin, albumin, and proteinuria (proteinuria is not significant in this model).

Model 3: predictors include baseline eGFR, SBP, hemoglobin, and proteinuria (proteinuria becomes highly significant after exclusion of albumin).

Model 4: predictors include baseline eGFR, SBP, and proteinuria (proteinuria slightly more significant after exclusion of albumin and hemoglobin).

^{**} Two-sided P<0.01

^{***} Two-sided P<0.001

[#] Log-transformed