Estimating urine albumin-creatinine ratio from protein-creatinine ratio: development of equations using same-day measurements

Supplementary material

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Table S1. Equations to estimate the median, 25th and 75th percentiles of ACR from a PCR measurement, by sex, based on quantile regression models for log(ACR) containing the linear spline terms for log(PCR), sex, and interactions between sex and the spline terms.

Range of PCR (mg/g)	Equation to estimate median of log(ACR)	Equation to estimate 25th percentile of log(ACR)	Equation to estimate 75th percentile of log(ACR)
Females:			
<40	1.7060 – 0.0572*log(PCR)	1.2796 – 0.0386*log(PCR)	1.6731 + 0.0642*log(PCR)
40 to <60	0.2183 + 0.3460*log(PCR)	0.7094 + 0.1159*log(PCR)	-1.4845 + 0.9202*log(PCR)
60 to <250	-6.2539 +1.9269*log(PCR)	-5.0158 + 1.5144*log(PCR)	-5.3268 + 1.8587*log(PCR)
250 to <1000	-4.4287 + 1.5963*log(PCR)	-9.0693 + 2.2486*log(PCR)	-1.9764 + 1.2519*log(PCR)
≥1000	0.0445 + 0.9488*log(PCR)	-0.0479 + 0.9426*log(PCR)	-0.1429 + 0.9864*log(PCR)
Males:			
<40	0.7373 + 0.1697*log(PCR)	0.5589 + 0.1083*log(PCR)	1.2593 + 0.1460*log(PCR)
40 to <60	-2.7625 + 1.1184*log(PCR)	-0.7944 + 0.4751*log(PCR)	-5.9091 + 2.0891*log(PCR)
60 to <250	-6.9212 + 2.1342*log(PCR)	-7.6388 + 2.1469*log(PCR)	-4.4236 + 1.7263*log(PCR)
250 to <1000	-1.9690 + 1.2372*log(PCR)	-4.8345 + 1.6390*log(PCR)	-1.1395 + 1.1315*log(PCR)
≥1000	-0.1522 + 0.9742*log(PCR)	0.0862 + 0.9267*log(PCR)	-0.2425 + 1.0016*log(PCR)

Log refers to the natural logarithm, so ACR = exp(log(ACR)) = $2.71828^{\log(ACR)}$. Median predicted ACR = exp(median of predicted log(ACR)). ACR and PCR are in mg/g.

Table S2. Regression coefficients for 4 models for median log(ACR), with log(PCR) represented by a 4-knot linear spline[a]

Coefficient	Model L1: spline of log(PCR) only	Model L2: spline of log(PCR), sex, and spline interactions	Model L3: spline of log(PCR), sex, age, diabetes, hypertension, eGFR category and spline interactions	Model L4: Spline of log(PCR), sex, age, diabetes, hypertension, eGFR category, lab location and spline interactions
Constant	0.9518	1.7060	1.3364	1.3150
S1	0.1264	-0.0572	0.0000	0.0065
S2	0.7251	0.3460	0.4057	0.6304
S3	2.0751	1.9269	2.0689	2.0960
S4	1.3834	1.5963	1.6078	1.4437
S5	0.9577	0.9488	0.8924	0.9078
Male		-0.9687	-0.4602	-0.3977
S1*male		0.2269	0.0769	0.0592
S2*male		0.7724	0.8306	0.8919
S3*male		0.2073	0.2046	0.1567
S4*male		-0.3591	-0.3364	-0.2948
S5*male		0.0255	0.0253	0.0188
Age2 (50-69)‡			-0.3893	-0.2468
Age3 (70+)			-0.8035	-0.8066
S1*age2			0.1315	0.0890
S2*age2			-0.5499	-0.5153
S3*age2			-0.0916	-0.0812
S4*age2			0.1495	0.1504
S5*age2			0.0443	0.0308
S1*age3			0.2864	0.2902
S2*age3			-0.7594	-0.8201
S3*age3			-0.2584	-0.2447
S4*age3			0.2392	0.2450
S5*age3			0.0734	0.0600
Diabetes			0.7794	0.7336
S1*Diabetes			-0.1576	-0.1446
S2*Diabetes			0.0269	-0.0305
S3*Diabetes			-0.0954	-0.0806
S4*Diabetes			-0.0842	-0.0614
S5*Diabetes			0.0318	0.0104
Hypertension			0.4015	0.4172
S1*Hypertension			-0.0750	-0.0806
S2*Hypertension			0.2104	0.2475
S3*Hypertension			0.0059	-0.0040
S4*Hypertension			-0.1450	-0.1496
S5*Hypertension			-0.0069	0.0110
eGFR2 (G4)[b]			0.9382	2.4382

Coefficient	Model L1: spline of log(PCR) only	Model L2: spline of log(PCR), sex, and spline interactions	Model L3: spline of log(PCR), sex, age, diabetes, hypertension, eGFR category and spline interactions	Model L4: Spline of log(PCR), sex, age, diabetes, hypertension, eGFR category, lab location and spline interactions
eGFR3 (G5)			0.0246	0.1705
S1*eGFR2			-0.2607	-0.6650
S2*eGFR2			0.5950	0.5470
S3*eGFR2			-0.2955	-0.2693
S4*eGFR2			0.0847	0.0718
S5*eGFR2			0.0343	0.0209
S1*eGFR3			0.0000	0.0000
S2*eGFR3			1.2408	1.1727
S3*eGFR3			-0.8760	-0.9144
S4*eGFR3			0.3702	0.3366
S5*eGFR3			0.0549	0.0600
Calgary lab[b]				-0.1802
Other lab				-0.0483
S1*Calgary lab				0.0073
S2*Calgary lab				-0.1450
S3*Calgary lab				0.1180
S4*Calgary lab				0.1904
S5*Calgary lab				-0.0079
S1*Other lab				0.0330
S2*Other lab				-0.8841
S3*Other lab				-0.1720
S4*Other lab				0.4166
S5*Other lab				0.0318

[a]The knots for the linear spline were at log(PCR) = 3.689, 4.094, 5.521 and 6.908, corresponding to PCR values of 40, 60, 250, 1000 mg/g. S1 to S5 represent the variables for the 5 linear spline segments.
[b]The reference age category was 18 to 59, the reference eGFR category was G1 to G3, and the reference lab location was Edmonton.

Table S3. Estimated median and interquartile range for ACR, at the KDIGO PCR category thresholds of 150 and 500 mg/g, for the overall cohort and for groups specified by covariates, and estimated PCR giving predicted median ACR at KDIGO ACR category thresholds.

Covariate	PCR = 150 mg/g		PCR = 500 mg/g		PCR (mg/g) giving predicted median ACR of 30 mg/g	PCR (mg/g) giving predicted median ACR of 300 mg/g
	Estimated median ACR	Estimated IQR for ACR	Estimated median ACR	Estimated IQR for ACR		
None (Overall estimates)	35.5	16.0, 65.8	301	213, 357	139	498
Sex						
Female	28.0	13.1, 54.5	277	176, 346	155	528
Male	45.5	21.2, 75.9	315	243, 362	123	481
Age, years						
18-49	41.0	15.9, 76.6	336	248, 381	130	460
50-69	35.6	15.7, 66.4	308	220, 359	139	491
≥70	32.2	16.5, 56.4	271	182, 331	145	538
No diabetes	31.4	13.8, 63.4	307	195, 368	147	492
Diabetes	39.2	18.4, 66.6	300	222, 348	132	500
No hypertension	31.0	12.6, 64.5	306	171, 366	148	493
Hypertension	36.9	17.8, 66.0	301	221, 354	136	499
eGFR category						
≥30 ml/min/1.73m^2	35.9	16.2, 66.6	310	227, 361	138	488
15-29 ml/min/1.73m^2	31.6	15.1, 53.7	257	175, 321	146	559
<15 ml/min/1.73m^2	19.3	7.9, 41.6	205	121, 282	184	647
Laboratory location						
Edmonton	42.3	17.3, 75.2	302	221, 348	127	497
Calgary	34.5	18.0, 58.7	341	258, 390	142	460
Other	22.8	11.9, 45.9	251	153, 316	169	564

The overall estimates are from quantile regression models containing only the cubic spline terms, while estimates for the effect of each covariate are from quantile regression models containing the cubic spline terms, the covariate(s), and interactions between the covariate(s) and the spline terms. Estimates of the median ACR are transformed from quantile regression models for the 50th percentile of log(ACR); estimates of the IQR of ACR are transformed from quantile regression models for the 25th and 75th percentiles of log(ACR). Estimates of PCR that give predicted median ACR at the KDIGO ACR category thresholds are from the 50th percentile models. IQR = interquartile range.

Figure S1. Median, 25th and 75th percentiles of predicted albumin:protein percent, by value of PCR, from quantile regression cubic spline models for log(ACR) including only the spline terms for log(PCR)

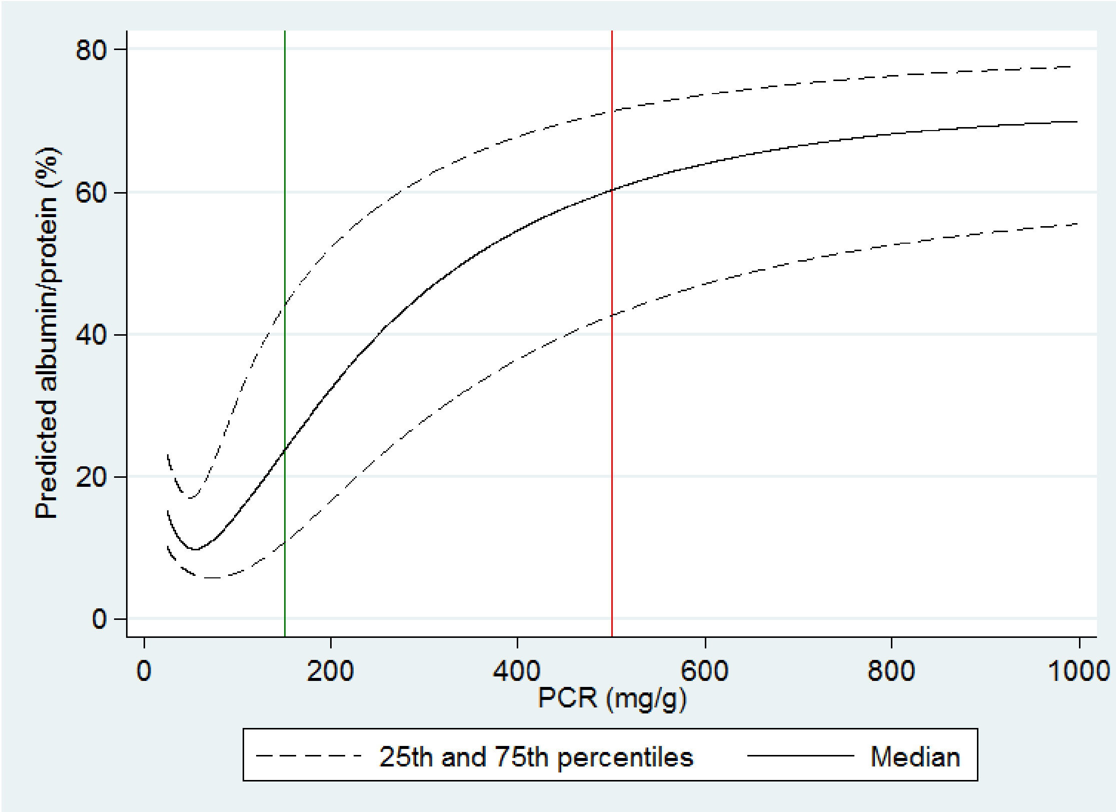


Figure S2. Median, 25th and 75th percentiles of predicted ACR by PCR value, log scale, from quantile regression cubic spline models of log(ACR) containing only the spline terms of log(PCR)

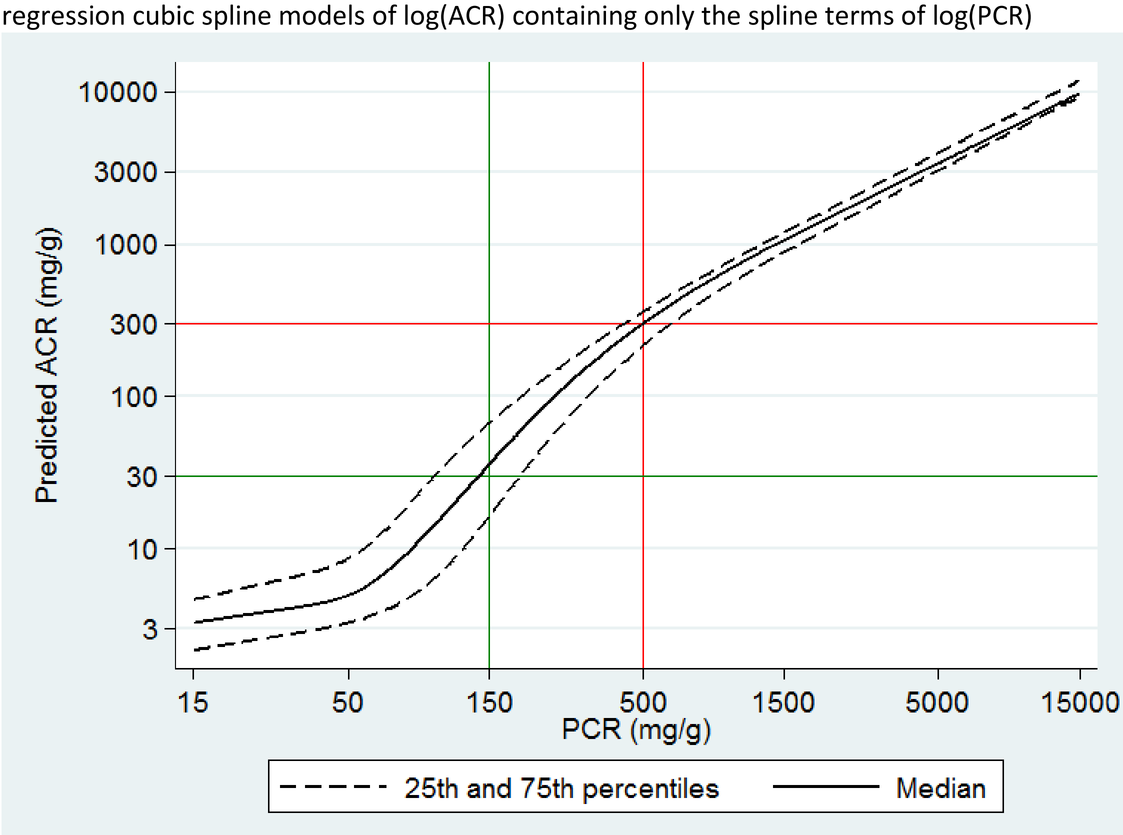


Figure S3. Effect of sex on predicted median ACR, log scale (from a model containing the cubic spline, sex, and spline interactions).

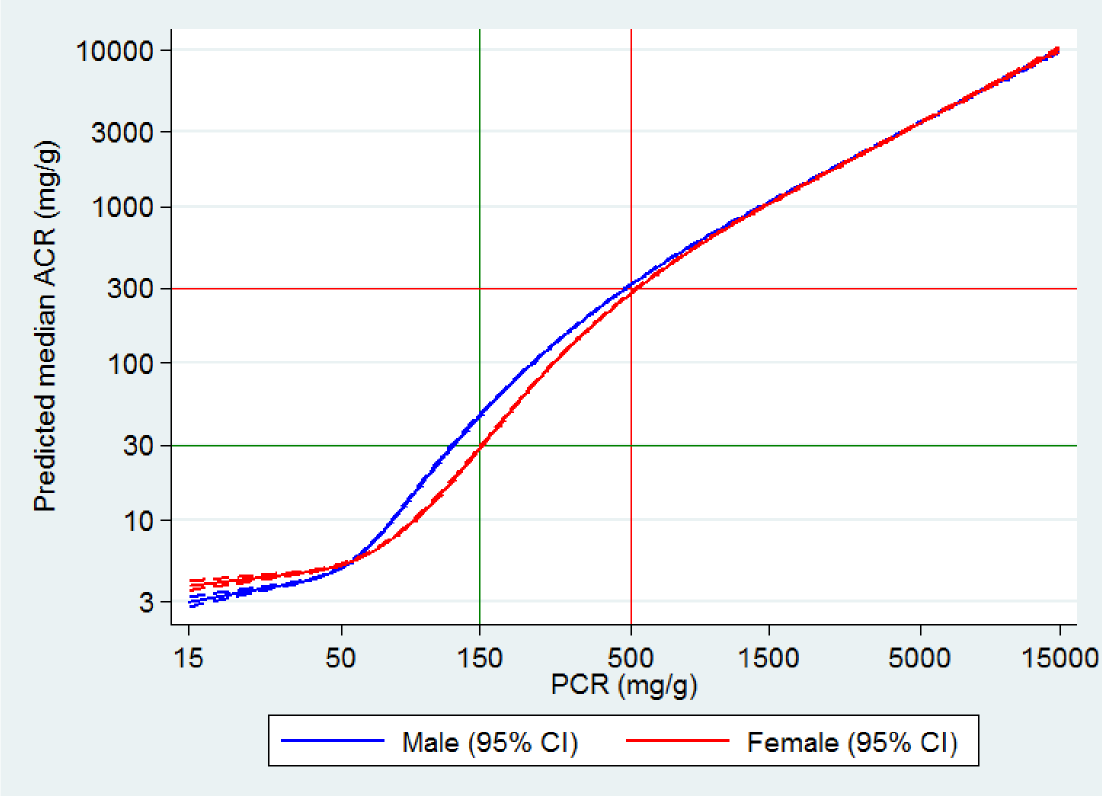


Figure S4. Predicted median, 25th and 75th percentiles of ACR for males and females, log scale (from quantile regression models containing the cubic spline, sex and spline interactions).

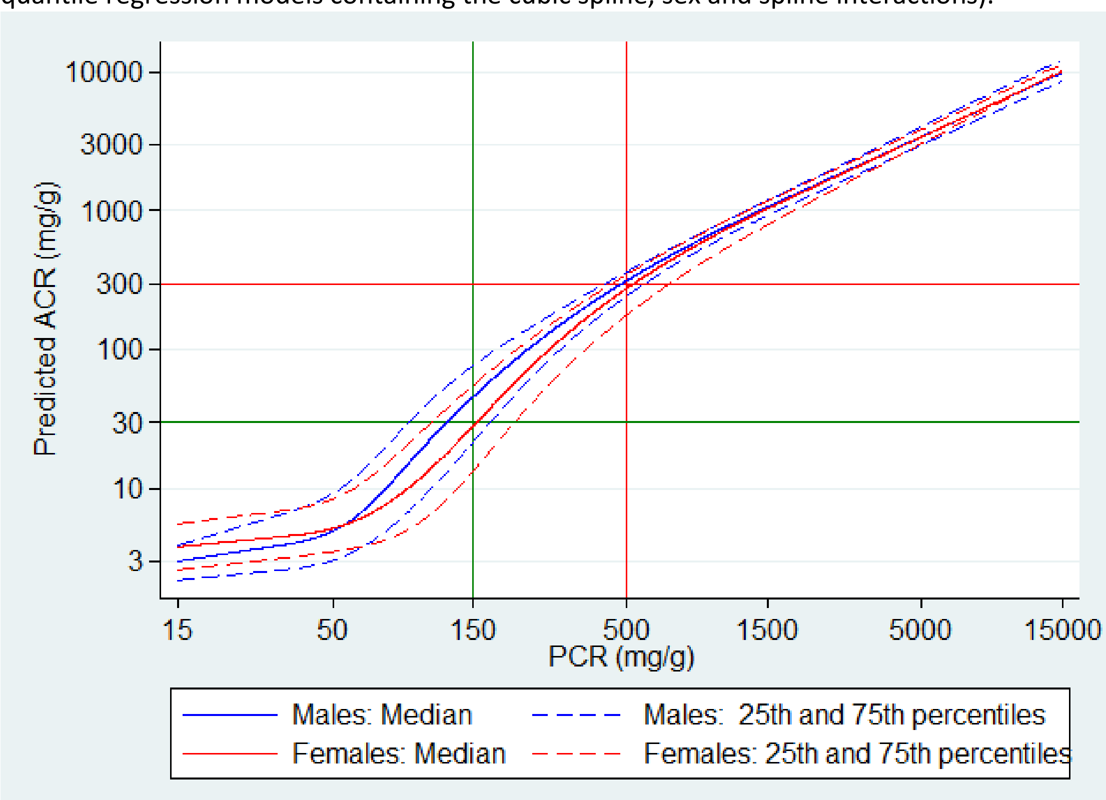


Figure S5. Effect of sex on predicted median ACR, linear scale, PCR < 600 mg/g (from a model containing the cubic spline, sex, and spline interactions).

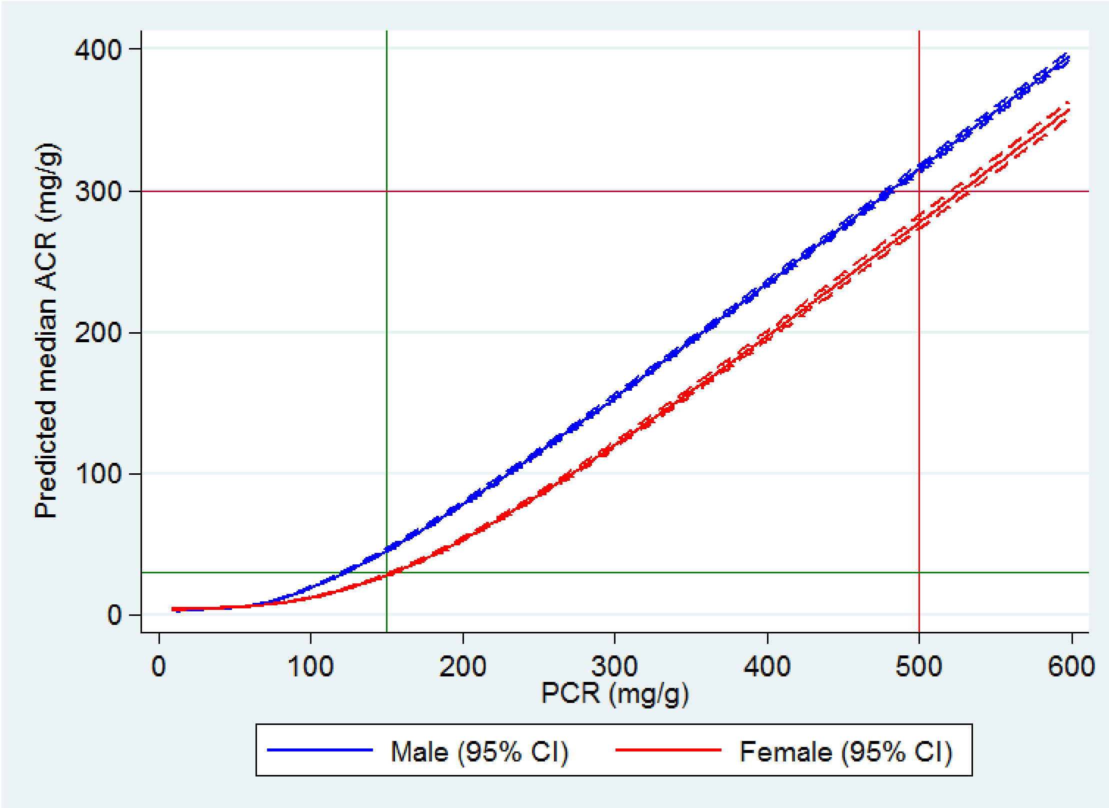


Figure S6. Effect of sex on predicted median albumin:protein percent (from a model containing the cubic spline, sex, and spline interactions).

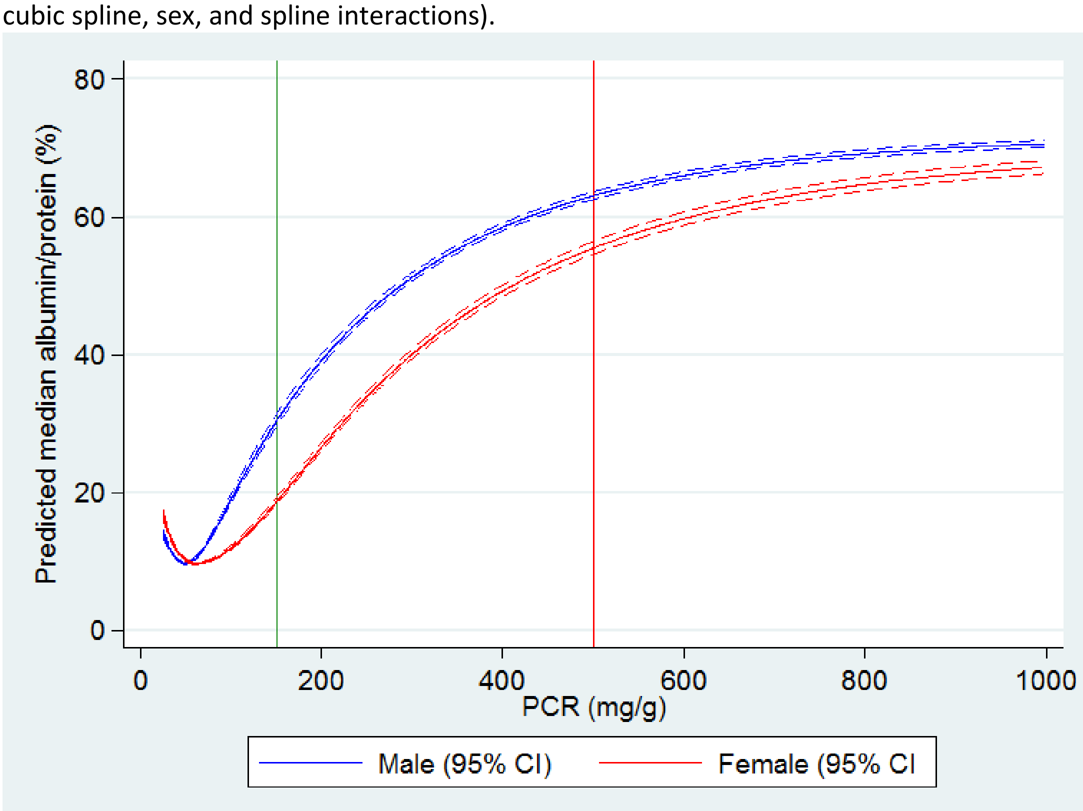


Figure S7. Effect of age on predicted median ACR, log scale (from a model containing the cubic spline, age, and spline interactions).

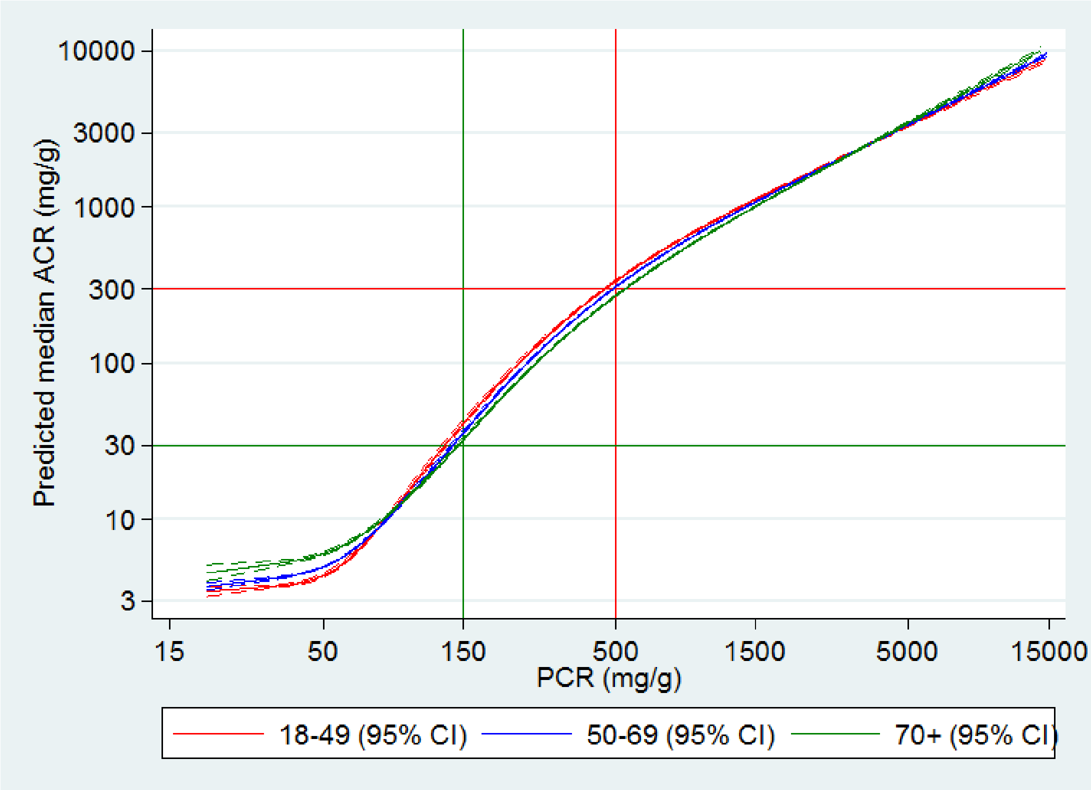


Figure S8. Effect of age on predicted median ACR, linear scale (from a model containing the cubic spline, age, and spline interactions).

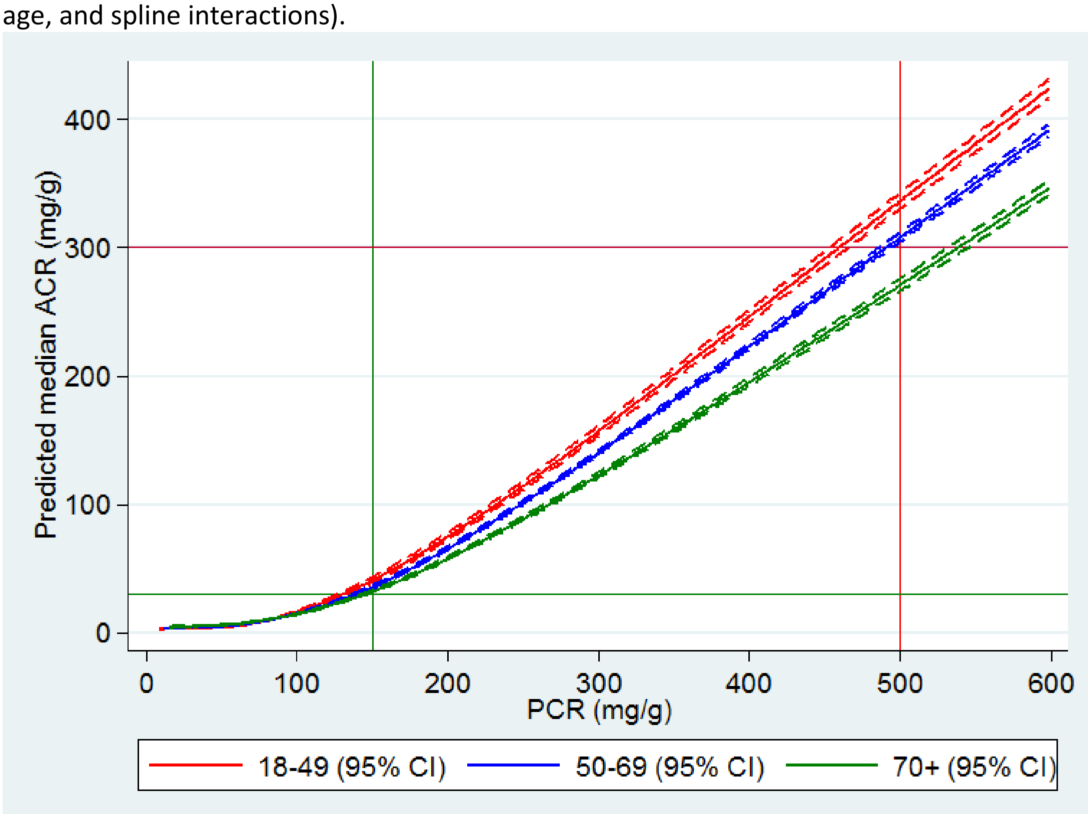


Figure S9. Effect of age on predicted median albumin:protein percent (from a model containing the cubic spline, age, and spline interactions).

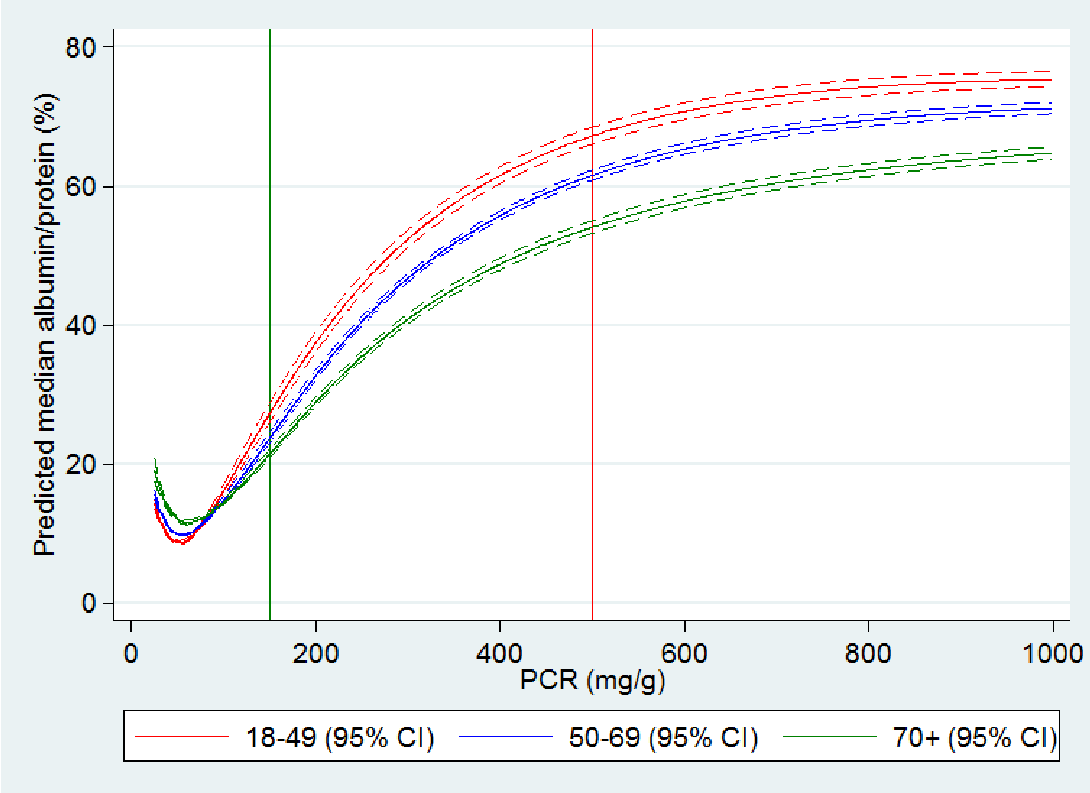


Figure S10. Effect of eGFR category on predicted median ACR, log scale (from a model containing the cubic spline, eGFR category, and spline interactions).

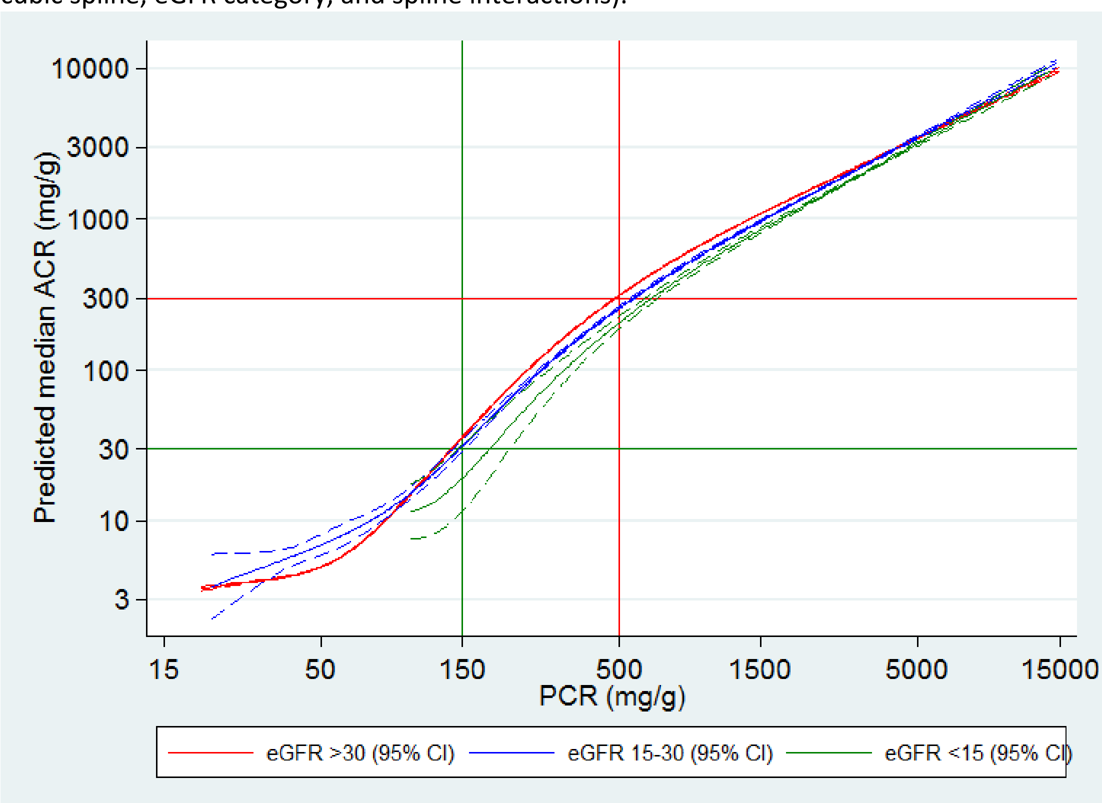


Figure S11. Effect of eGFR category on predicted median ACR, linear scale (from a model containing the cubic spline, eGFR category, and spline interactions).

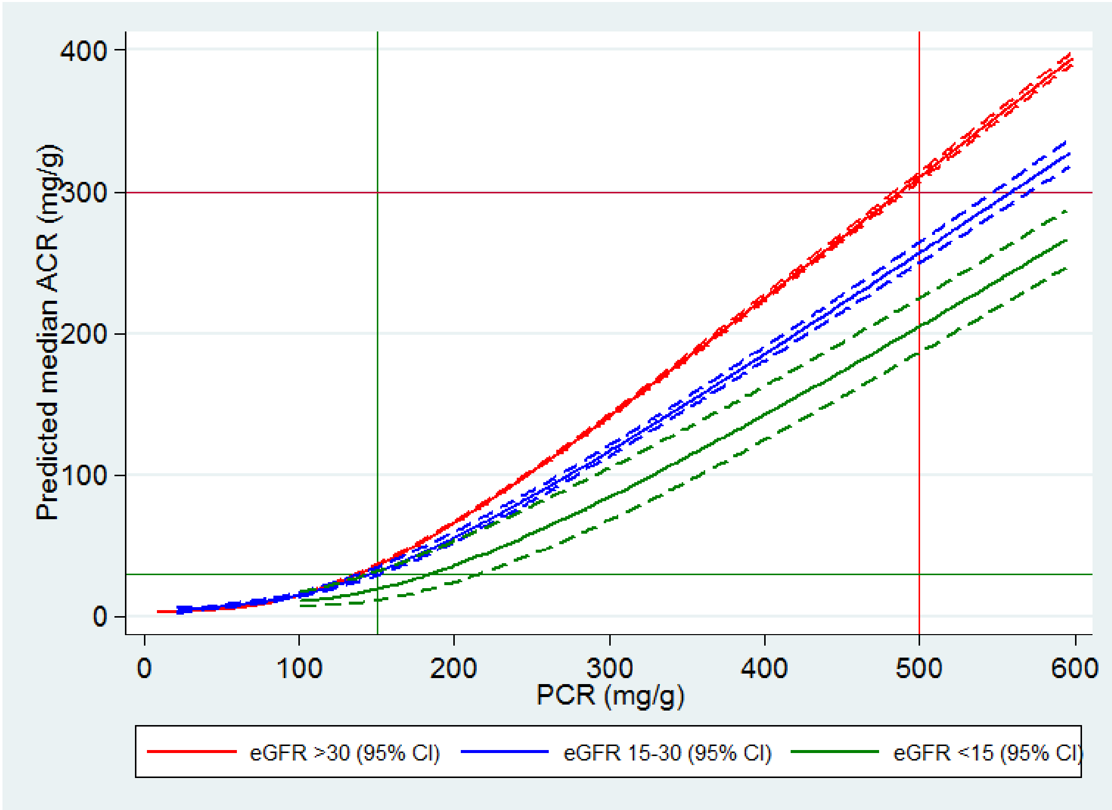


Figure S12. Effect of eGFR category on predicted median albumin to protein percent (from a model containing the cubic spline, eGFR category, and spline interactions).

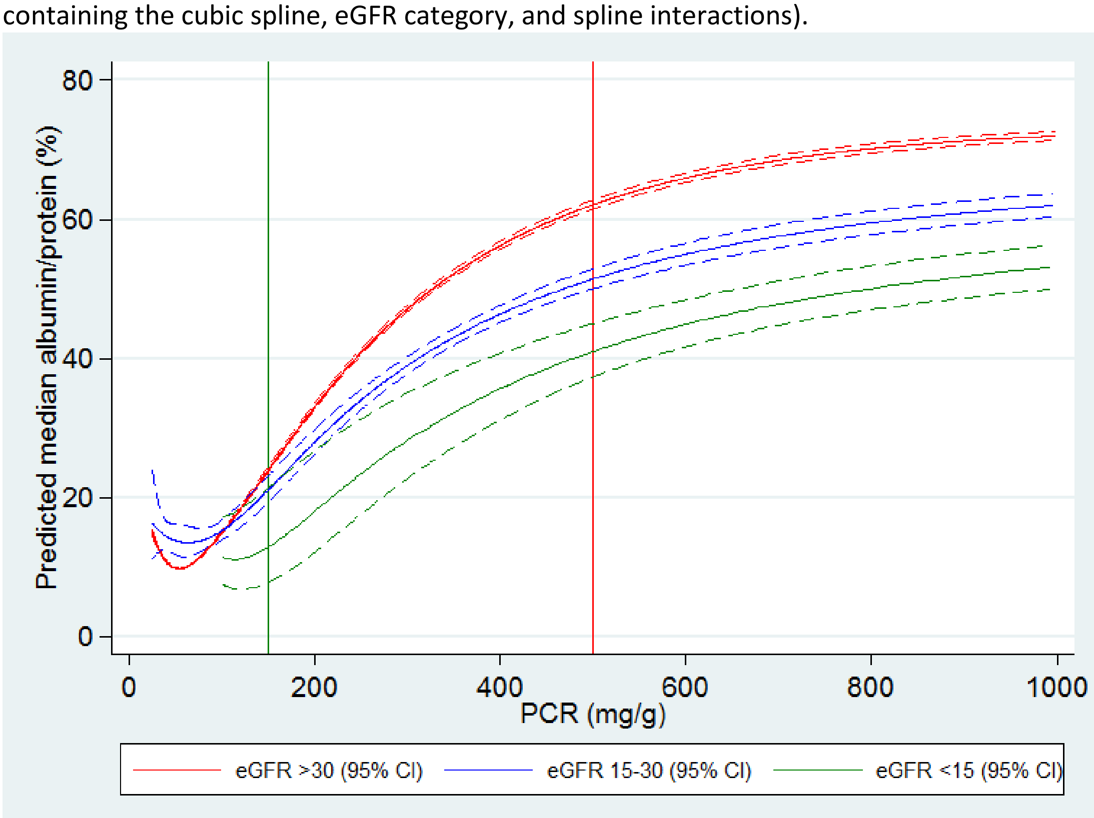


Figure S13. Effect of diabetes on median ACR, log scale (from a model containing the cubic spline, diabetes, and spline interactions).

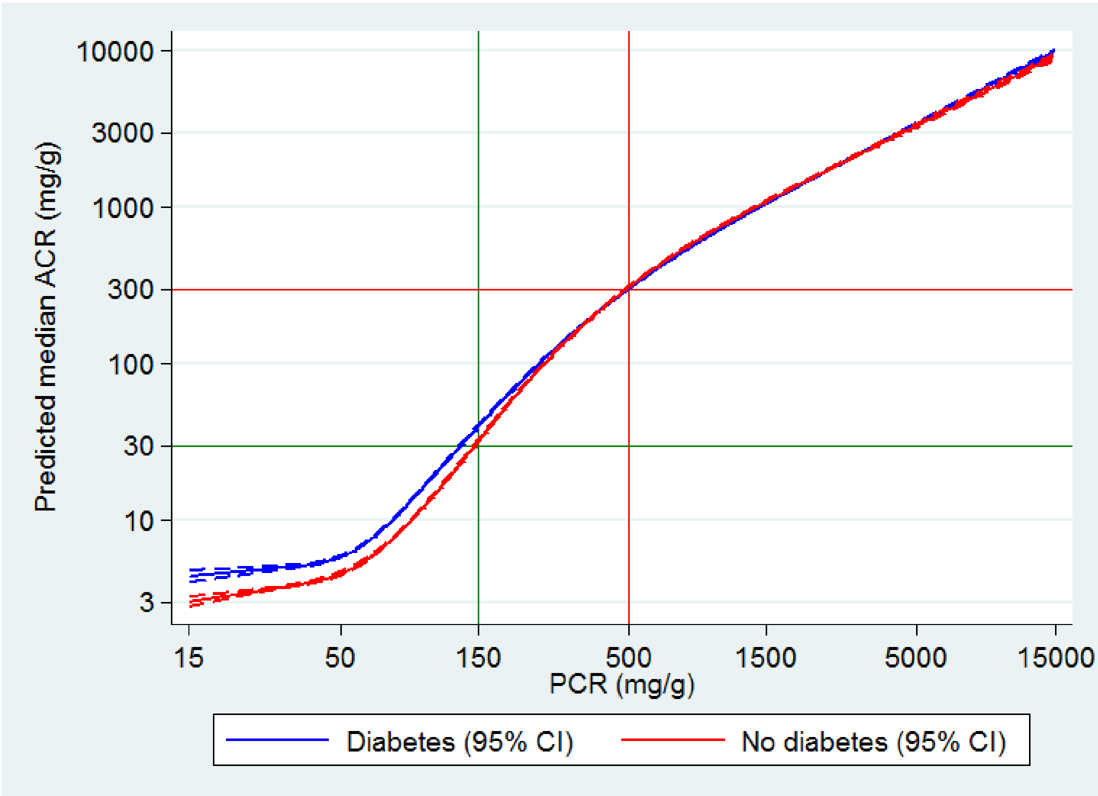


Figure S14. Effect of diabetes on median ACR, linear scale (from a model containing the cubic spline, diabetes, and spline interactions).

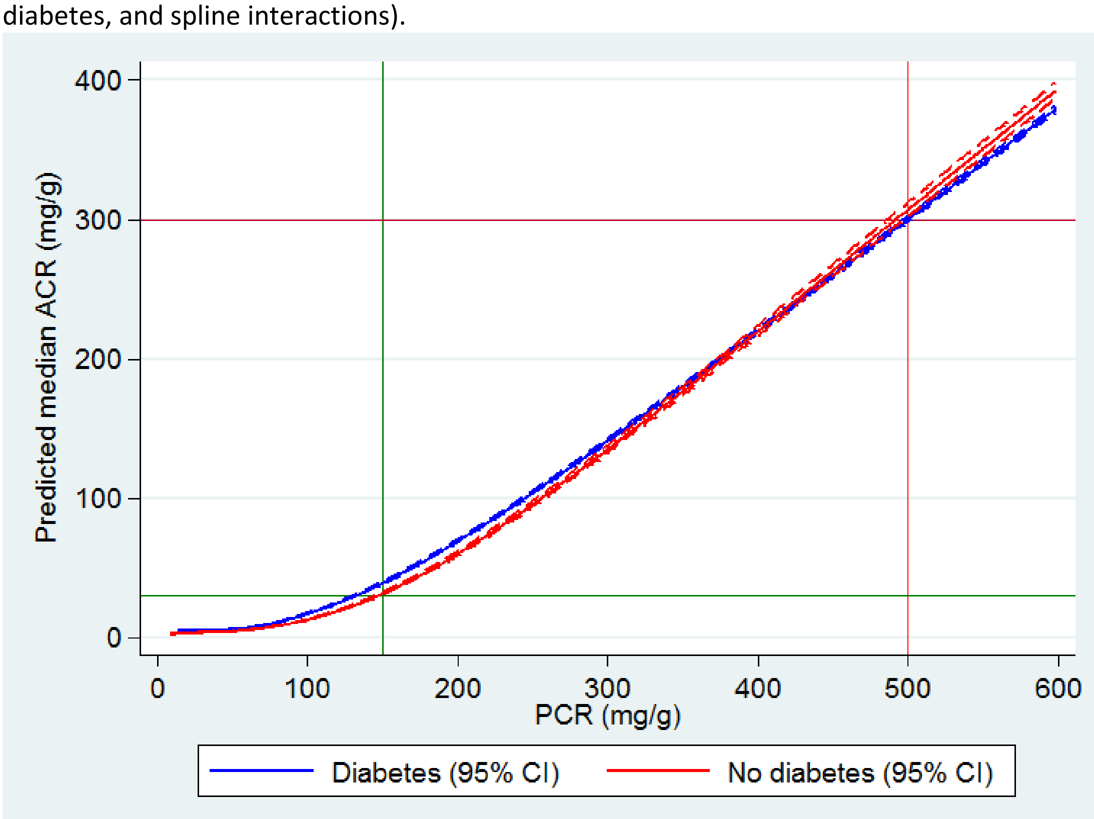


Figure S15. Effect of diabetes on percent albumin (from a model containing the cubic spline, diabetes, and spline interactions).

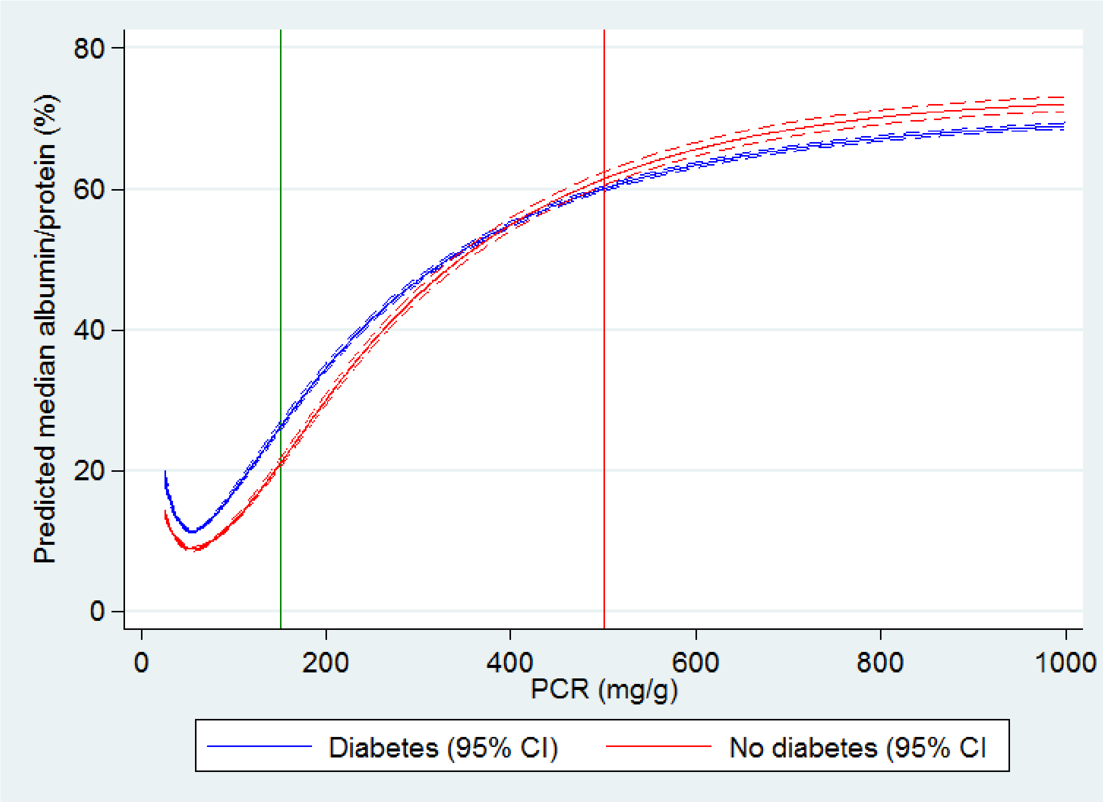


Figure S15. Effect of hypertension on median ACR, log scale (from a model containing the cubic spline, hypertension, and spline interactions).

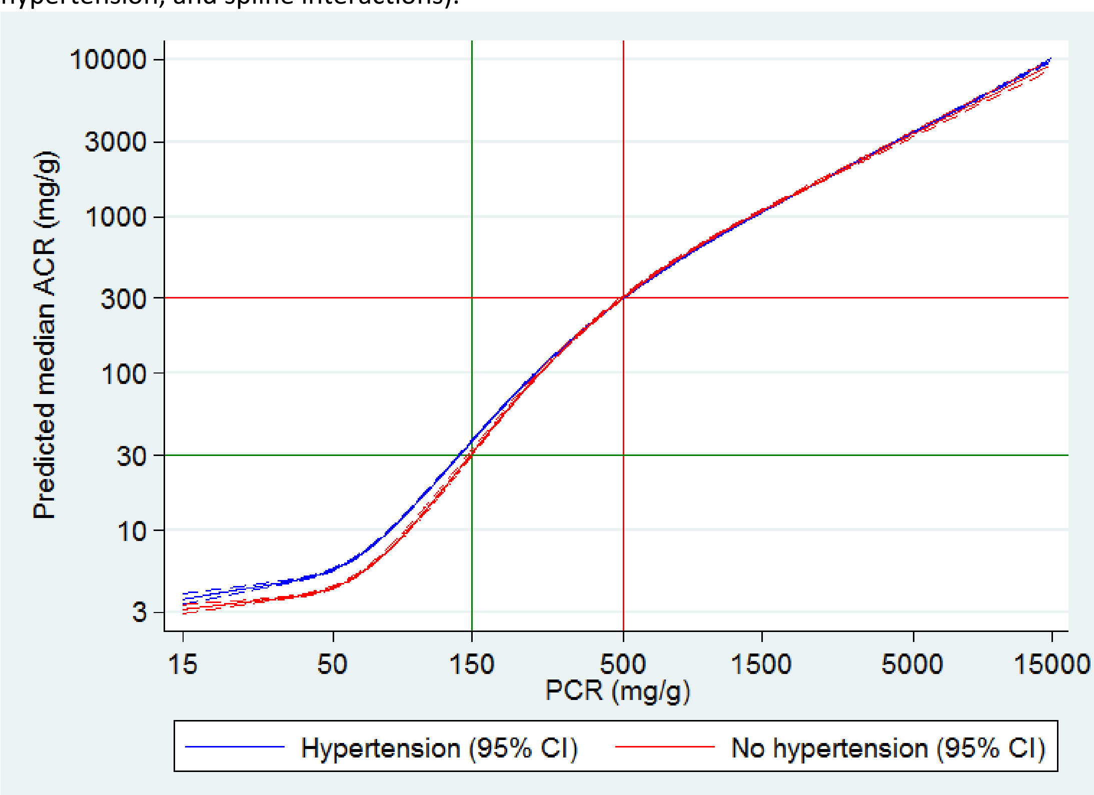


Figure S17. Effect of hypertension on median ACR, linear scale (from a model containing the cubic spline, hypertension, and spline interactions).

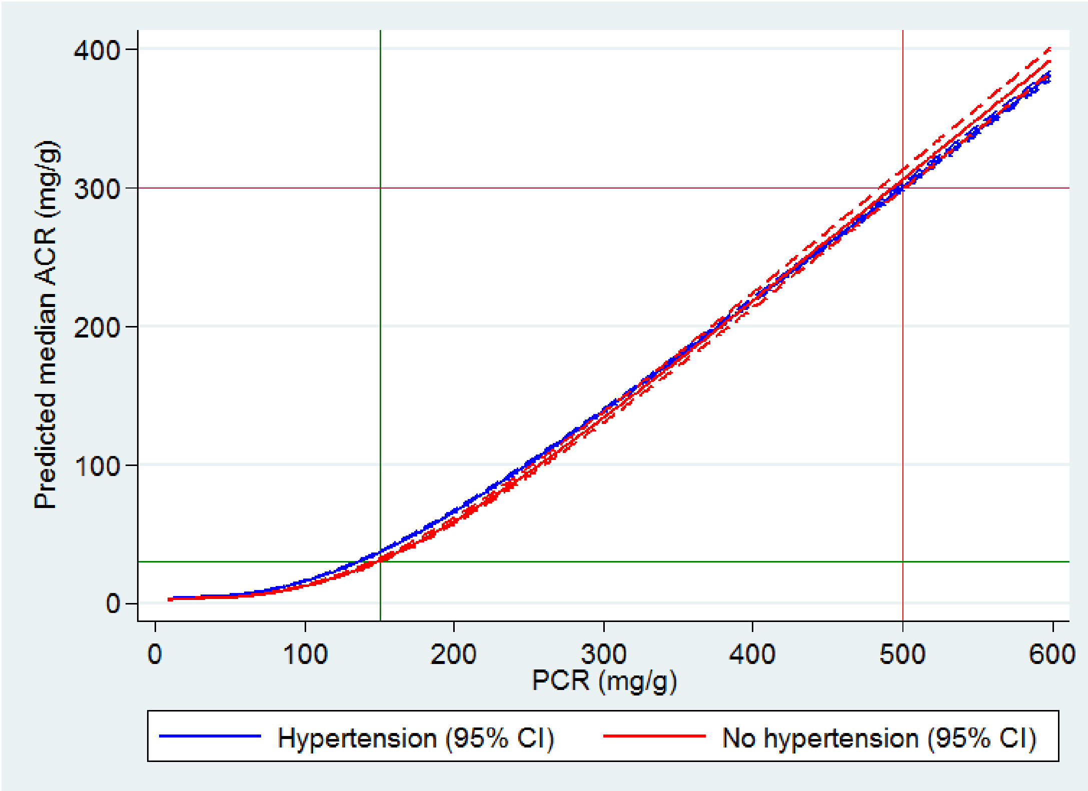


Figure S18. Effect of hypertension on percent albumin (from a model containing the cubic spline, hypertension, and spline interactions).

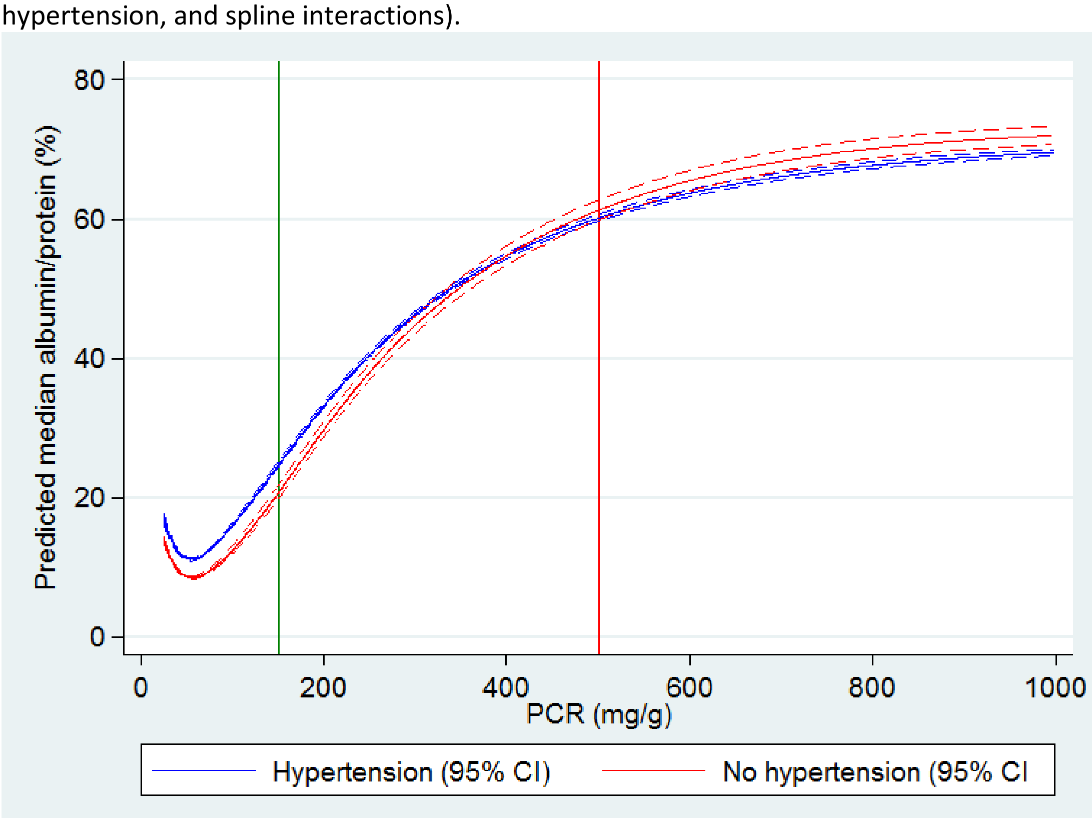


Figure S19. Effect of lab location (proxy for analyzer and method) on median ACR, log scale (from a model containing the cubic spline, lab location, and spline interactions).

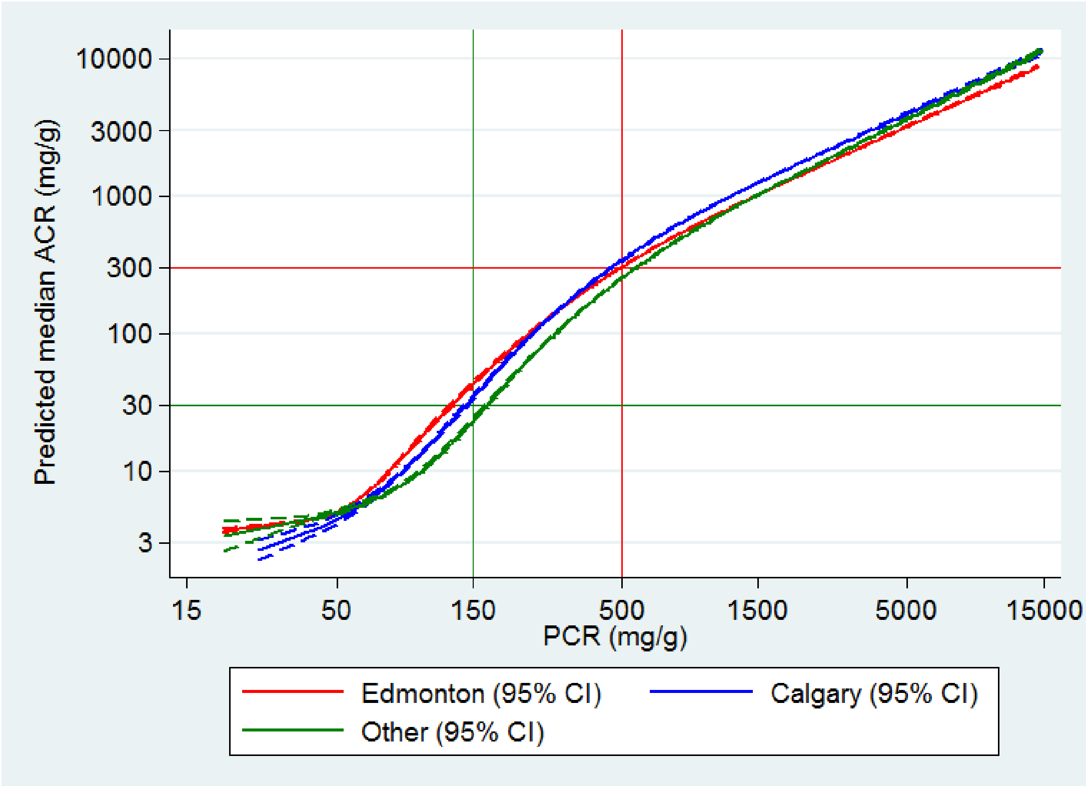


Figure S20. Effect of lab location (proxy for analyzer & method) on median ACR, linear scale (from a model containing the cubic spline, lab location, and spline interactions).

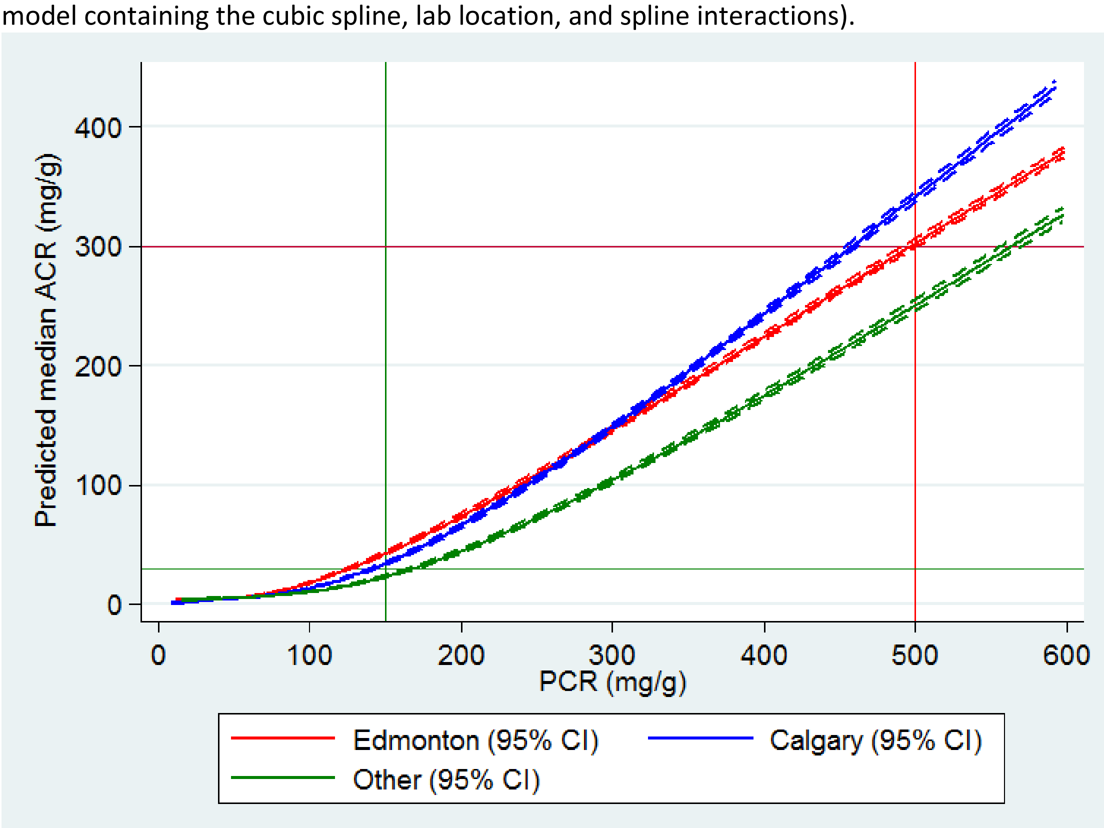


Figure S21. Effect of lab location (proxy for analyzer and method) on percent albumin (from a model containing the cubic spline, lab location, and spline interactions).

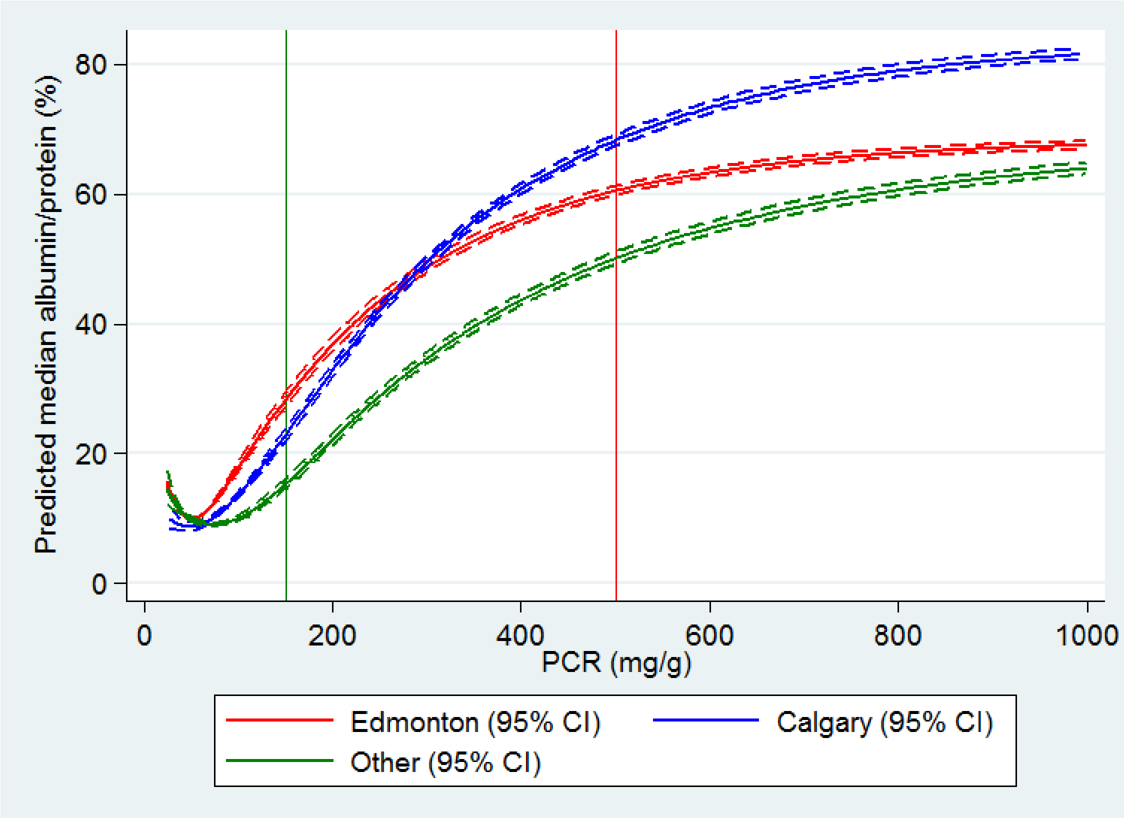


Figure S22. Comparison of predicted median ACR based on models with PCR transformed with a restricted cubic spline (C1), and with PCR transformed with a linear spline (L1). The knots for the restricted cubic spline were at percentiles 5, 27.5, 50, 72.5 and 95 of log(PCR) (3.4668, 4.0625, 4.5664, 5.3992 and 7.7333, corresponding to PCR values of 32.0, 58.1, 96.2, 221 and 2283 mg/g). Knots for the linear spline were at values of log(PCR) of 3.689, 4.094, 5.521 and 6.908, corresponding to PCR values of 40, 60, 250 and 1000 mg/g.

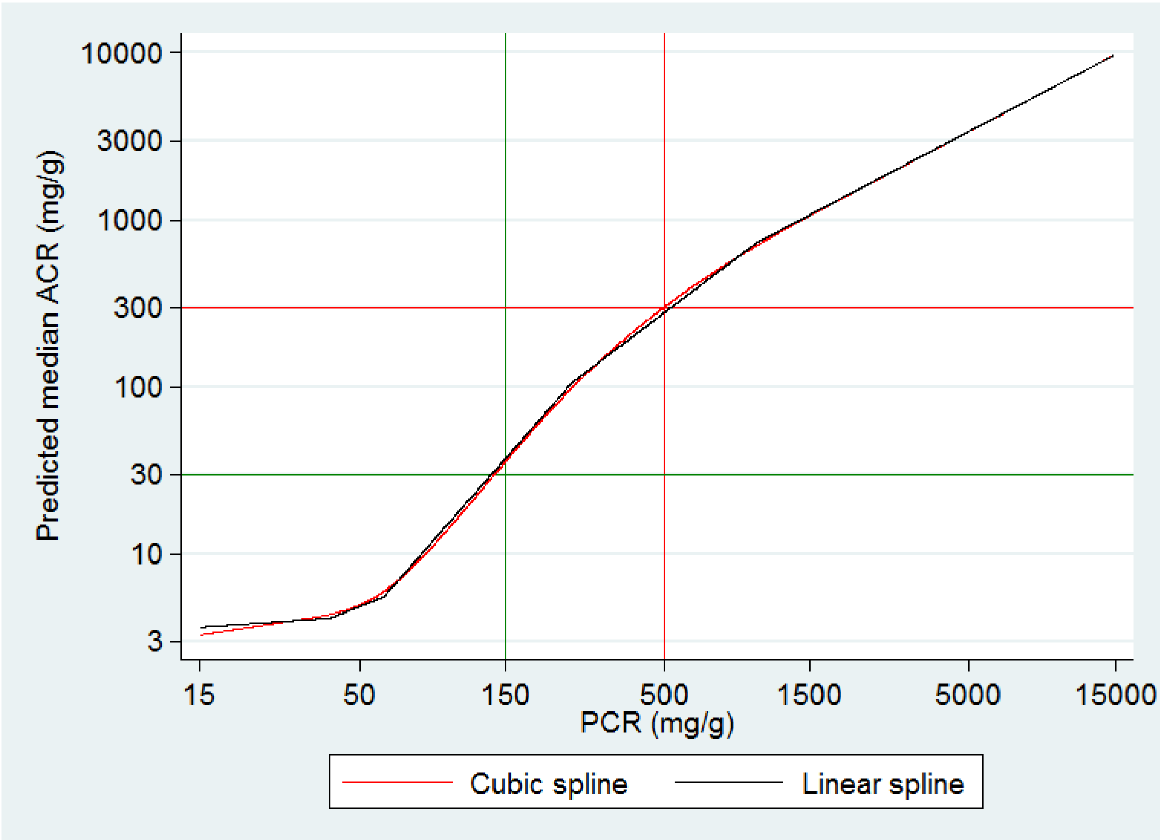


Figure S23. Scatterplot of measured ACR and median ACR predicted from the linear spline model (L2) for a 20% random sample. The blue dots represent males and the red dots females. To convert ACR or PCR from mg/g to mg/mmol, multiply by 0.113.

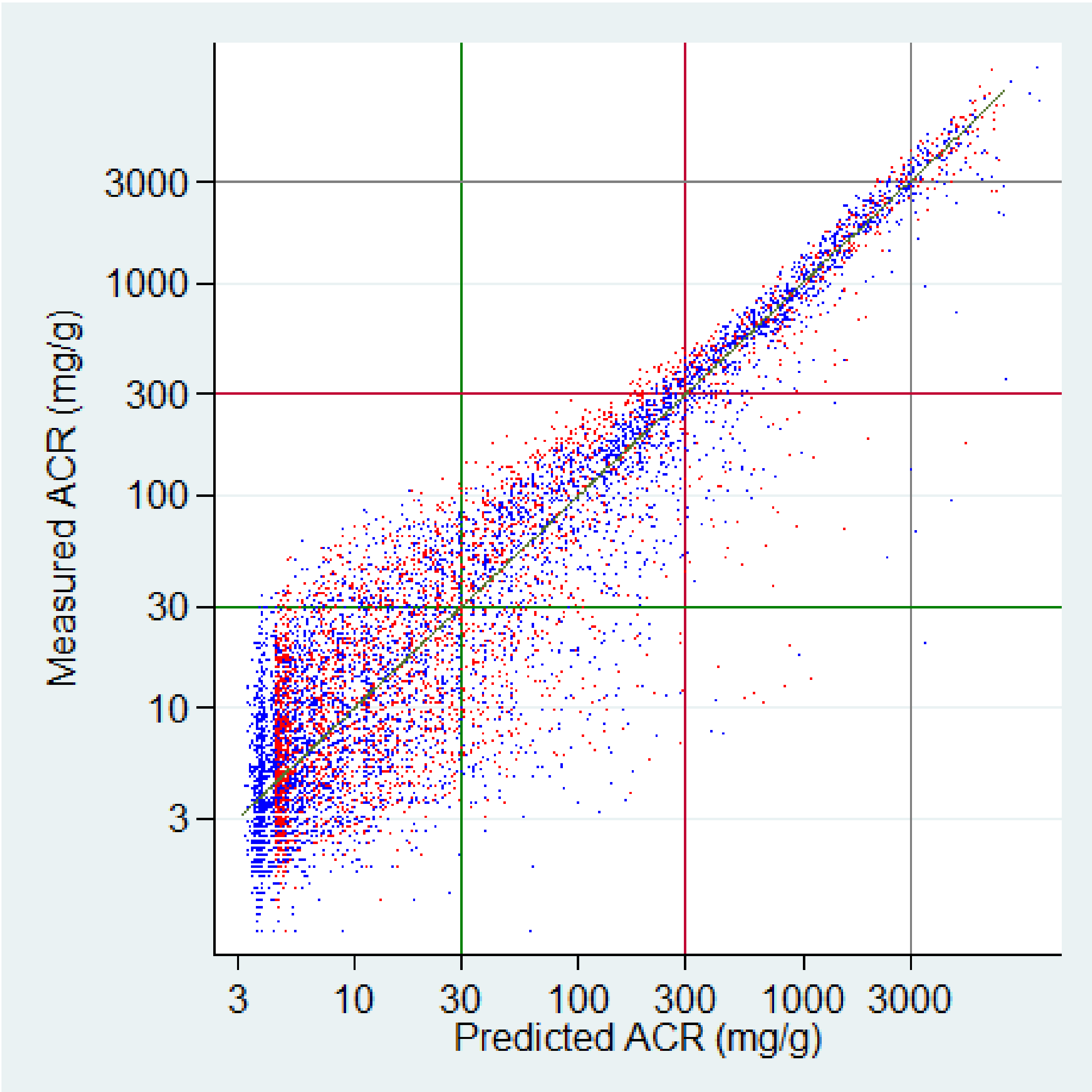


Figure S24. Scatterplot of measured ACR versus ACR estimated from PCR measurements for a 20% random sample, using the equations of Tangri et al.[1] The equations are: ACR = PCR/1.7566 if female; ACR = PCR/2.655 if male. Blue dots represent males, red dots females.

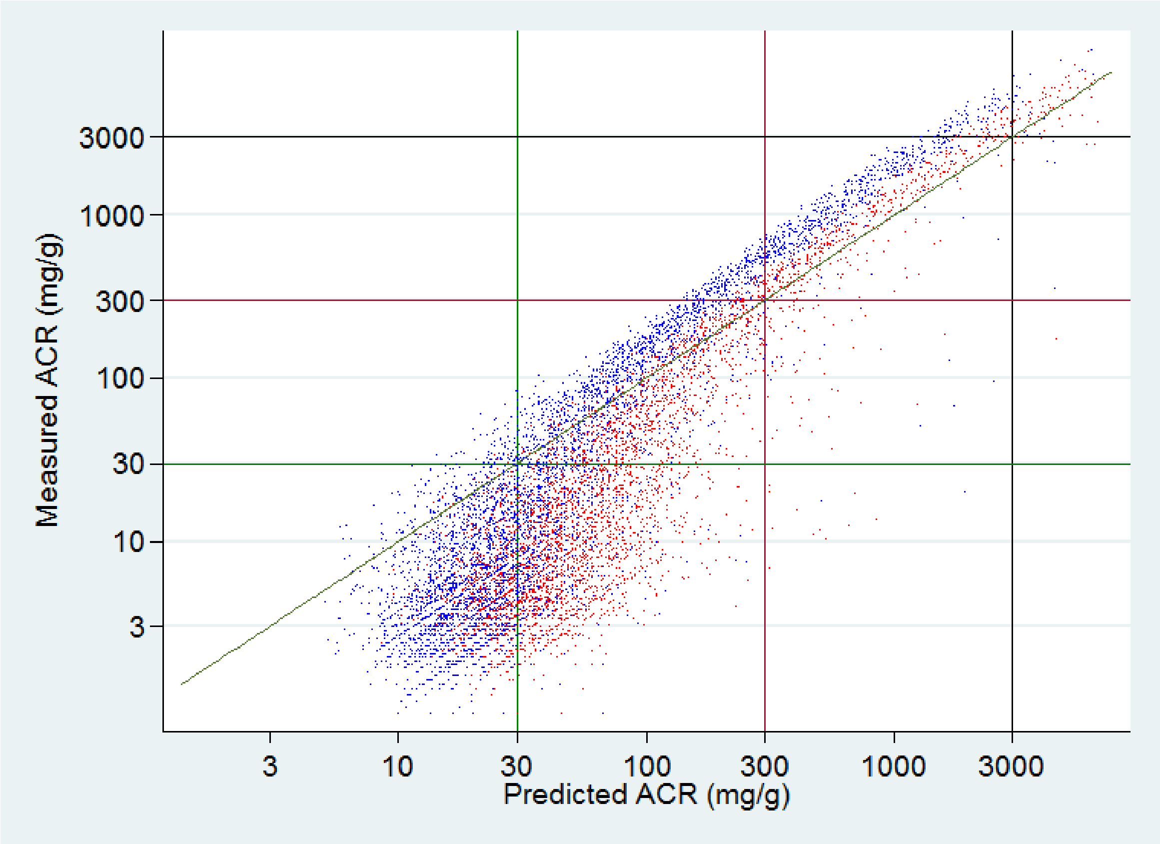


Figure S25. Scatterplot showing measured ACR versus ACR estimated from PCR measurements for a 20% random sample, using the equation of Collier et al.[2] Note that the lowest 22% of PCR values could not be shown as the predicted ACR was negative if the PCR was <52 mg/g. The equation is: ACR = (-4 + 0.68*PCR)/0.113. Blue dots represent males, red dots females.

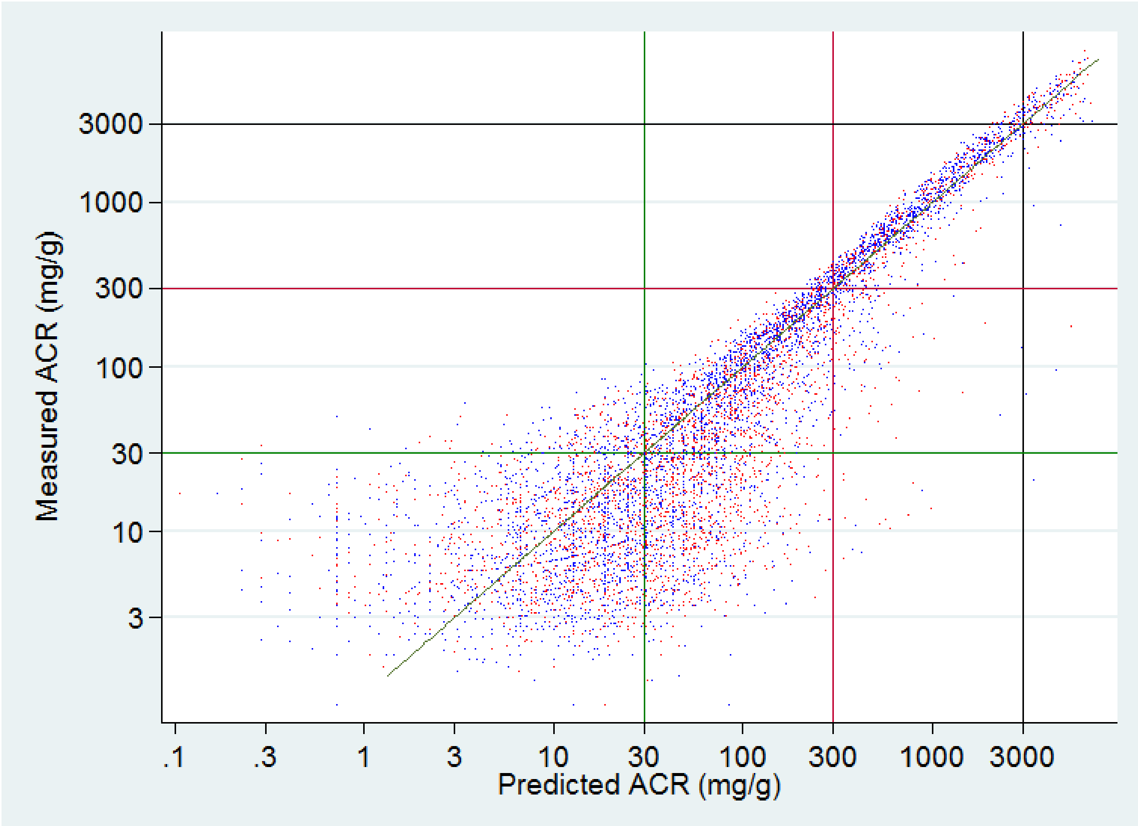
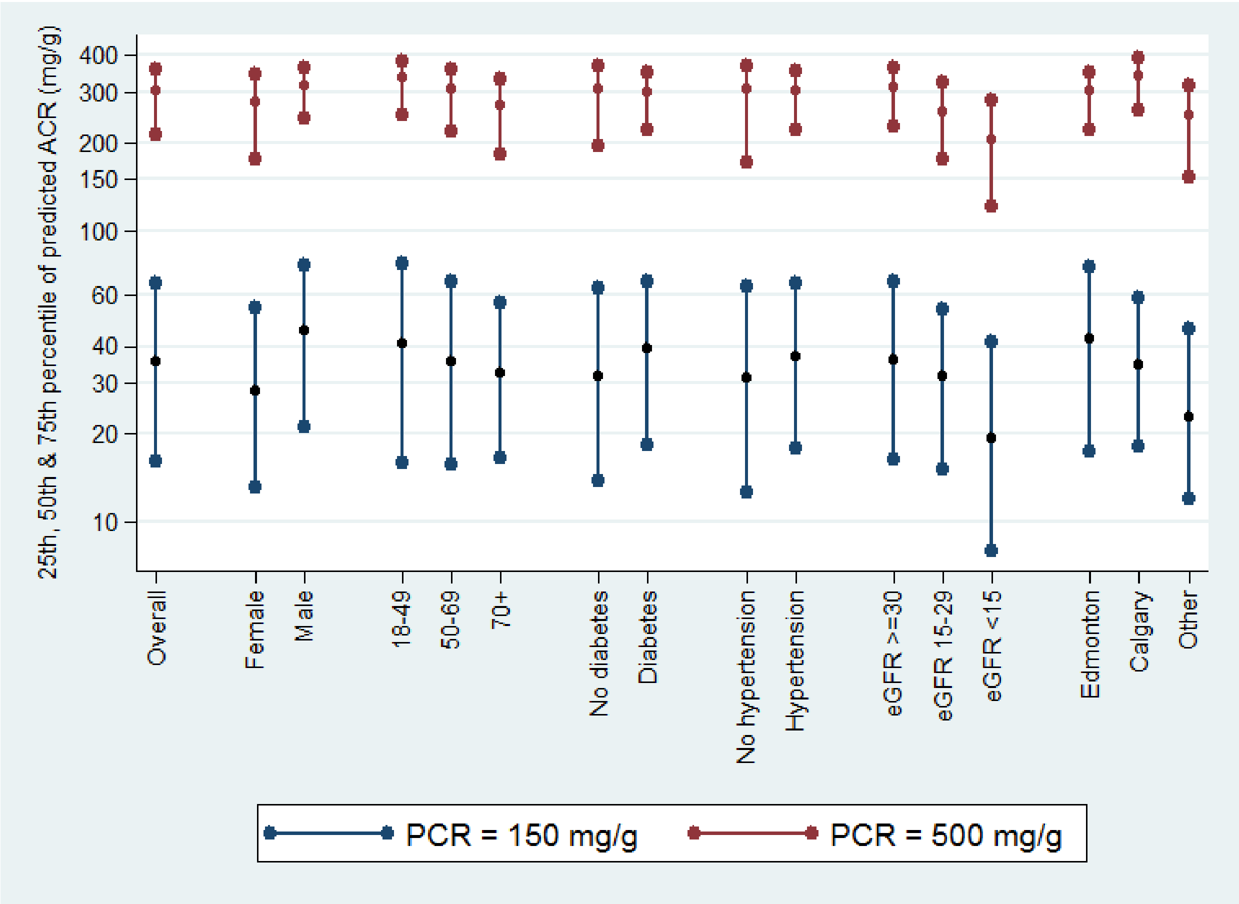


Figure S26. Estimated median, 25th and 75th percentiles of ACR at the KDIGO A1/A2 and A2/A3 PCR thresholds of 150 and 500 mg/g, overall and by specified covariate. To convert ACR or PCR from mg/g to mg/mmol, multiply by 0.113. The estimates are based on quantile regression models for the 25th, 50th and 75th percentiles of log(ACR), with log(PCR) transformed with a restricted cubic spline, and with each model containing only the specified covariate, the spline terms, and the interactions between the specified covariate and the spline terms.



References:

1. Tangri, N, Grams, ME, Levey, AS, Coresh, J, Appel, LJ, Astor, BC, et al., C. K. D. Prognosis Consortium: Multinational Assessment of Accuracy of Equations for Predicting Risk of Kidney Failure: A Meta-analysis. *JAMA,* 315**:** 164-174, 2016.
2. Collier, G, Greenan, MC, Brady, JJ, Murray, B, Cunningham, SK: A study of the relationship between albuminuria, proteinuria and urinary reagent strips. *Ann Clin Biochem,* 46**:** 247-249, 2009.