

Supplemental Table 1. LOINC codes used to identify UACR, UPCR, DSP, and specific gravity

LOINC Code	Description
UACR	
14959-1	Microalbumin/Creatinine [Mass Ratio] in Urine
UPCR	
2890-2	Protein/Creatinine [Mass Ratio] in Urine
2161-8	Creatinine [Mass/volume] in Urine
2888-6	Protein [Mass/volume] in Urine
DSP	
50561-0	Protein [Mass/volume] in Urine by Automated test strip
Specific Gravity	
50562-8	Specific gravity of Urine by Refractometry automated
Creatinine	
2160-0	Creatinine [Mass/volume] in Serum or Plasma
38483-4	Creatinine [Mass/volume] in Blood

Abbreviations: DSP, dipstick urinalysis proteinuria; LOINC, Logical Observation Identifier Names and Codes; UACR, urine albumin to creatinine ratio; UPCR, urine protein to creatinine ratio.

Supplemental Table 2a. Model performance for detecting proteinuria from DSP alone

Metric (95% CI)	Overall N= 11,229	eGFR ≥90 N= 3,161	eGFR 60-89 N= 2,961	eGFR 45-59 N= 1,389	eGFR 30-44 N= 1,131	eGFR 15-29 N= 746	eGFR <15 N= 334
Sensitivity	0.61 (0.59, 0.62)	0.47 ^{a,b,c,d} (0.43, 0.51)	0.50 ^{f,g,h} (0.46, 0.53)	0.56 ^{i,j,k} (0.52, 0.60)	0.68 ^m (0.64, 0.72)	0.75 ⁿ (0.71, 0.78)	0.91 (0.87, 0.94)
Specificity	0.89 (0.88, 0.90)	0.88 (0.87, 0.89)	0.90 (0.89, 0.92)	0.90 (0.88, 0.92)	0.89 (0.86, 0.91)	0.85 (0.80, 0.90)	0.74 (0.56, 0.92)
Positive Predictive value	0.76 (0.74, 0.77)	0.55 ^{a,b,c,d} (0.52, 0.59)	0.63 ^{e,f,g,h} (0.59, 0.67)	0.80 ^{i,j,k} (0.76, 0.84)	0.88 ^m (0.86, 0.91)	0.94 ⁿ (0.92, 0.96)	0.98 (0.96, 1.00)
Negative Predictive Value	0.80 (0.79, 0.81)	0.84 ^{a,b,c,d} (0.83, 0.86)	0.84 ^{e,f,g,h} (0.83, 0.86)	0.75 ^{i,j,k} (0.72, 0.77)	0.68 ^{l,m} (0.65, 0.72)	0.53 (0.47, 0.58)	0.37 (0.23, 0.51)
Positive Likelihood Ratio	5.48 (5.09, 5.86)	3.93 (3.41, 4.45)	5.11 (4.36, 5.86)	5.66 (4.42, 6.90)	5.88 (4.41, 7.35)	4.94 (3.23, 6.64)	3.48 (1.08, 5.87)
Negative Likelihood Ratio	0.44 (0.42, 0.46)	0.60 ^{a,b,c,d} (0.56, 0.64)	0.56 ^{f,g,h} (0.52, 0.60)	0.49 ^{i,j,k} (0.44, 0.53)	0.36 ^m (0.32, 0.41)	0.30 ⁿ (0.25, 0.34)	0.13 (0.07, 0.18)

Abbreviations: DSP, dipstick proteinuria; eGFR, estimated glomerular function rate, ml/min/1.73 m².

^a*P* <0.05 for comparison of eGFR ≥90 and eGFR 45-59.

^b*P* <0.05 for comparison of eGFR ≥90 and eGFR 30-44.

^c*P* <0.05 for comparison of eGFR ≥90 and eGFR 15-29.

^d*P* <0.05 for comparison of eGFR ≥90 and eGFR <15.

^e*P* <0.05 for comparison of eGFR 60-89 and eGFR 45-59.

^f*P* <0.05 for comparison of eGFR 60-89 and eGFR 30-44.

^g*P* <0.05 for comparison of eGFR 60-89 and eGFR 15-29.

^h*P* <0.05 for comparison of eGFR 60-89 and eGFR <15.

ⁱ*P* <0.05 for comparison of eGFR 45-59 and eGFR 30-44.

^j*P* <0.05 for comparison of eGFR 45-59 and eGFR 15-29.

^k*P* <0.05 for comparison of eGFR 45-59 and eGFR <15.

^l*P* <0.05 for comparison of eGFR 30-44 and eGFR 15-29.

^m*P* <0.05 for comparison of eGFR 30-44 and GFR <15.

ⁿ*P* <0.05 for comparison of eGFR 15-29 and GFR <15.

There were no *P*<0.05 in comparisons between eGFR ≥90 vs eGFR 60-89

Bootstrap percentile-based confidence interval was obtained from 2000 bootstrap samples for all CI. *P* value was adjusted with Holm's method.

Supplemental Table 2b. Model performance for detecting proteinuria from DSP and specific gravity by eGFR categories.

Metric (95% CI)	Overall N= 11,229	eGFR ≥90 N= 3,161	eGFR 60-89 N= 2,961	eGFR 45-59 N= 1,389	eGFR 30-44 N= 1,131	eGFR 15-29 N= 746	eGFR <15 N= 334
Sensitivity	0.57 (0.56, 0.60)	0.47 ^d (0.42, 0.67)	0.66 (0.59, 0.70)	0.56 (0.50, 0.65)	0.65 (0.60, 0.67)	0.72 (0.66, 0.77)	0.89 (0.72, 0.98)
Specificity	0.94 (0.92, 0.95)	0.90 (0.69, 0.95)	0.78 ^{f,g} (0.77, 0.85)	0.92 (0.85, 0.97)	0.93 (0.91, 0.97)	0.91 (0.87, 0.97)	0.78 (0.65, 0.96)
Positive Predictive value	0.85 (0.81, 0.87)	0.59 ^{a,b,c,d} (0.41, 0.72)	0.50 ^{e,f,g,h} (0.49, 0.57)	0.83 ^{j,k} (0.74, 0.92)	0.93 ^m (0.90, 0.96)	0.96 (0.95, 0.98)	0.98 (0.97, 1.00)
Negative Predictive Value	0.80 (0.79, 0.80)	0.84 ^{a,b,c,d} (0.84, 0.87)	0.878 ^{e,f,g,h} (0.86, 0.89)	0.748 ^{i,j} (0.73, 0.77)	0.68 ^l (0.65, 0.70)	0.52 (0.48, 0.57)	0.34 (0.19, 0.77)
Positive Likelihood Ratio	10.10 (7.39, 12.11)	4.60 (2.18, 8.15)	3.031 ^{f,g} (2.82, 3.95)	7.121 (4.04, 16.05)	9.75 (7.12, 20.94)	8.35 (5.72, 20.78)	4.08 (2.60, 12.60)
Negative Likelihood Ratio	0.45 (0.43, 0.47)	0.59 ^{b,c,d} (0.47, 0.63)	0.430 ^{g,h} (0.39, 0.49)	0.48 ^{i,k} (0.42, 0.53)	0.37 (0.33, 0.42)	0.30 (0.25, 0.36)	0.14 (0.02, 0.31)

Abbreviations: DSP, dipstick proteinuria; eGFR, estimated glomerular function rate, ml/min/1.73 m².

^aP <0.05 for comparison of eGFR ≥90 and eGFR 45-59.

^bP <0.05 for comparison of eGFR ≥90 and eGFR 30-44.

^cP <0.05 for comparison of eGFR ≥90 and eGFR 15-29.

^dP <0.05 for comparison of eGFR ≥90 and eGFR <15.

^eP <0.05 for comparison of eGFR 60-89 and eGFR 45-59.

^fP <0.05 for comparison of eGFR 60-89 and eGFR 30-44.

^gP <0.05 for comparison of eGFR 60-89 and eGFR 15-29.

^hP <0.05 for comparison of eGFR 60-89 and eGFR <15.

ⁱP <0.05 for comparison of eGFR 45-59 and eGFR 30-44.

^jP <0.05 for comparison of eGFR 45-59 and eGFR 15-29.

^kP <0.05 for comparison of eGFR 45-59 and eGFR <15.

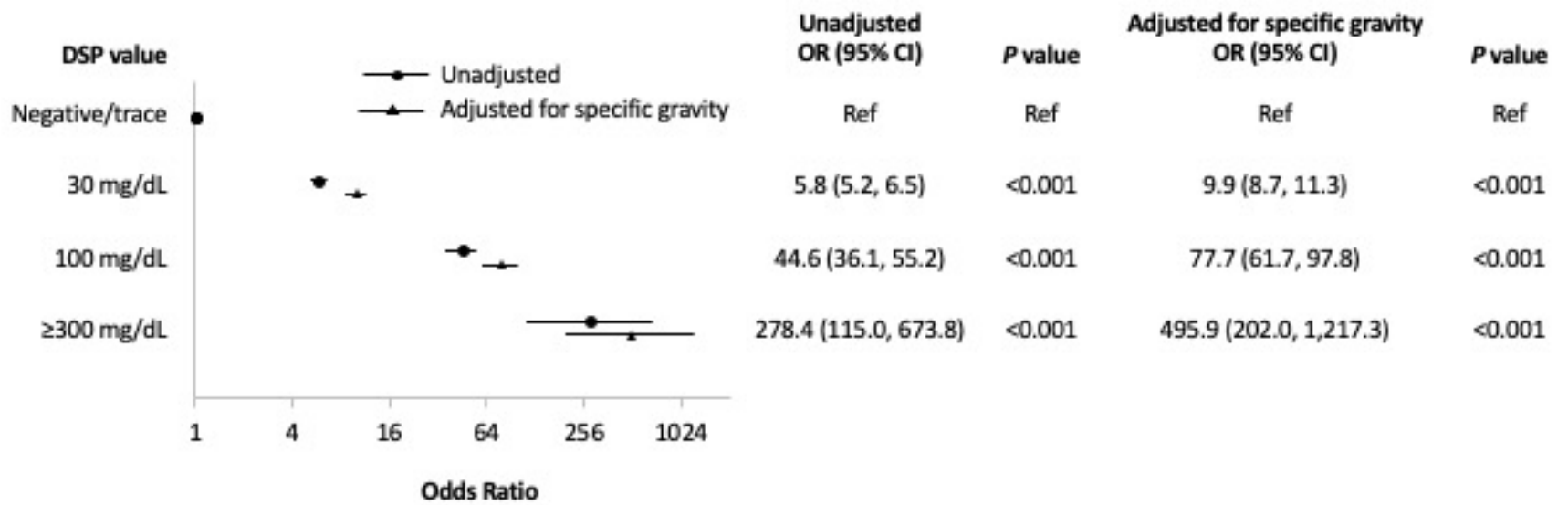
^lP <0.05 for comparison of eGFR 30-44 and eGFR 15-29.

^mP <0.05 for comparison of eGFR 30-44 and GFR <15.

There were no P<0.05 in comparisons between eGFR ≥90 vs eGFR 60-89 and eGFR 15-29 vs eGFR <15.

Bootstrap percentile-based confidence interval was obtained from 2000 bootstrap samples for all CI. *P* value was adjusted with Holm's method.

Supplemental Figure 1.



Supplemental Figure Legend

Supplemental Figure 1. Increasing levels of DSP in univariable models and when adjusting for specific gravity were associated with clinically significant proteinuria. Circles represent unadjusted models and triangles represent models adjusted for specific gravity. As compared with unadjusted models, adjustment for specific gravity increased the odds ratios for clinically significant proteinuria at each level of DSP.