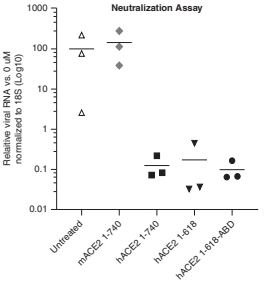
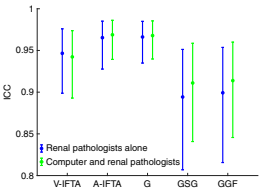
This Month's Highlights

Inhibiting SARS-CoV-2 with a Soluble ACE2 Variant



Use of a soluble angiotensin-converting enzyme 2 (ACE2) protein has been proposed as a way to inhibit binding of the S spike of SARS-CoV-2 to the full-length membrane-bound ACE2 receptor. Wysocki *et al.* developed a newly bioengineered soluble ACE2 protein of shorter molecular size and fused it with an albumin-binding domain tag to extend its duration of action. They then found that human kidney organoids can be infected by SARS-CoV-2, because they possess the human full-length ACE2 receptor and transmembrane serine protease 2 needed for infectivity. Using this model, they demonstrated that their novel soluble ACE2 variant can inhibit SARS-CoV-2 infection, suggesting it has potential preventive and therapeutic use. *See Wysocki et al., pages 795–803.*

Computational Assessment of Kidney Fibrosis

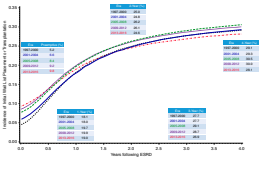


Reliable digital automated detection of interstitial fibrosis and tubular atrophy (IFTA) has not been available. Ginley *et al.* developed and tested machine learning algorithms for their ability to replicate the renal pathologist's visual assessment of IFTA and glomerulosclerosis. They found that well-trained machine learning methods showed agreement similar to that seen among renal pathologists, as well as equivalent statistical association with patient outcome. These methods can help expedite research on very large digital archives of renal biopsies, and may also benefit clinical practice by acting as a stand-in reading for pathology scenarios in which renal expertise is limited or unavailable. *See Ginley et al., pages 837–850. Also see related editorial by Hodgin and Mariani, pages 767–768.*

Single-Cell Data Resource

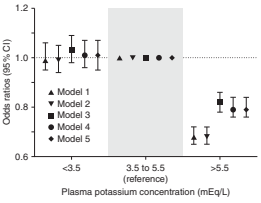
Each of the 14 or more different renal tubule segments has characteristic cell types with distinct functions. Although the advent of RNA sequencing (RNA-seq) has greatly improved understanding of gene expression in these renal epithelial cell types, detailed mapping of transcripts has been limited by methods that tend to be biased toward transcript ends. Coupling full-length RNA-seq analysis with renal tubule microdissection characterized gene expression along the mouse renal tubule, including mapping of transcript abundance and alternative exon usage. The data provide a comprehensive view of gene expression along the nephron and collecting duct, available to scientists *via* a user-friendly web resource. *See Chen et al., pages 897–912. Also see related editorial by Ellison, pages 768–771.*

Access to Kidney Transplantation



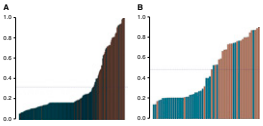
There have been numerous efforts over past decades to improve access to kidney transplantation among patients with ESKD. Schold *et al.* conducted a retrospective cohort study in this population to evaluate the longitudinal pattern of rates of transplant waiting list placement and transplantation. They found that rates of waitlist placement and transplantation following ESKD onset did not improve over two decades and were consistently reduced among vulnerable populations. These results indicate that more effective interventions are needed to improve access to transplantation in the United States. *See Schold et al., pages 913–926.*

Laxative Use and Abnormality of Serum Potassium



Although it is possible that increased excretion of intestinal potassium as a compensatory mechanism in patients with advanced CKD is enhanced by laxative use, little is known about the association of laxative use with risk of abnormality of serum potassium in such patients. In a large cohort of adults who transitioned to ESRD, time-varying laxative use was significantly associated with lower risk of hyperkalemia but not with risk of hypokalemia during the last year prior to ESRD. These findings suggest a putative role of constipation in potassium abnormality and also support—with careful consideration for risks and benefits—therapeutic potential of laxatives for hyperkalemia management in advanced CKD. *See Sumida et al., pages 950–959.*

Urinary Exosomal mRNA Signature of Rejection



Traditional biomarkers used to monitor for kidney allograft rejection are late markers of injury and lack sensitivity and specificity, and allograft biopsies are invasive and costly. El Fekih *et al.* describe the discovery and validation of two urinary exosomal mRNA multigene signatures for diagnosing acute T cell–mediated and antibody-mediated rejection and chronic active antibody-mediated rejection in kidney transplant recipients. They also demonstrated urinary exosomes' high stability and the approach's reliability in monitoring for rejection. Two gene signatures for all-cause rejection or for discriminating rejection mediated by T cells versus antibodies showed high predictive performances, offering clinicians the possibility of new tools for monitoring emergence of rejection in kidney allografts. *See El Fekih et al., pages 994–1004.*