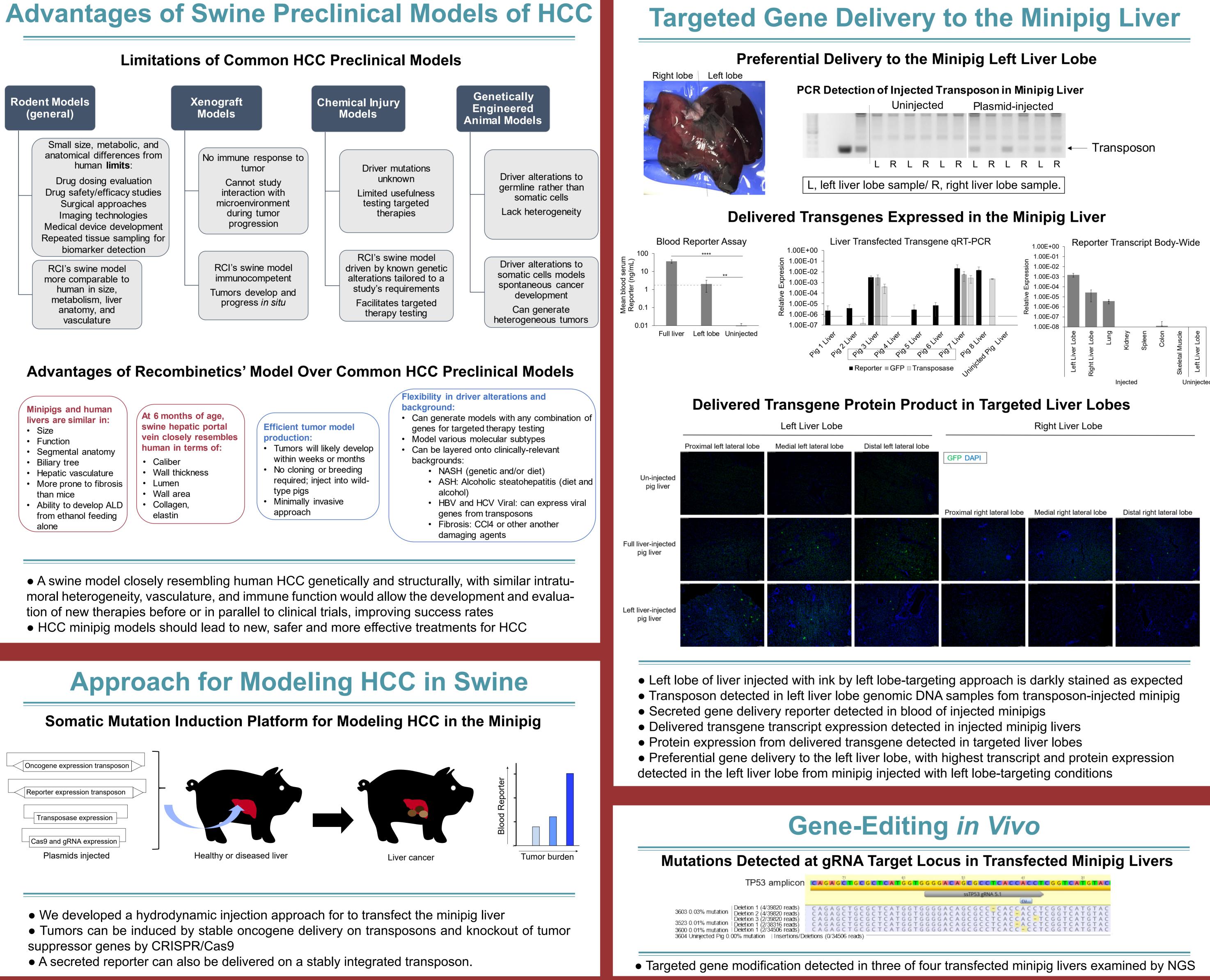
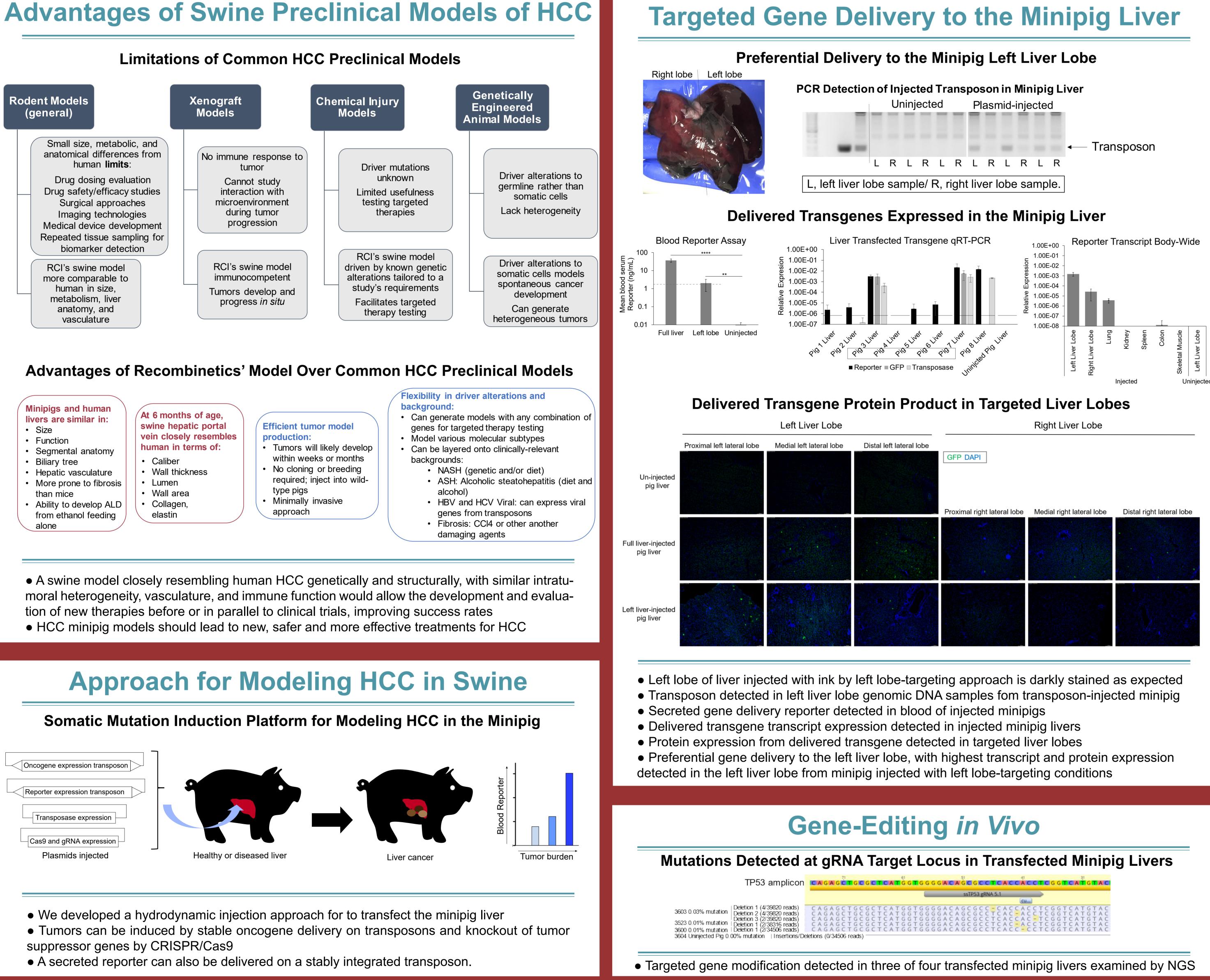


Gene Editing Solutions for Human and Food Animal Health

Introduction: Hepatocellular carcinoma (HCC) is the fourth deadliest cancer in the world, with a 5-year survival rate of only 17.7%. Development of safe and effective therapies for HCC are limited and insufficient. Rodent models are valuable for identifying potential therapeutic targets and serving as preliminary preclinical and insufficient. models. Additional studies, however, in a disease model more similar to humans in size, anatomy, and metabolism would improve preclinical evaluation of drug delivery devices, imaging technologies, and surgical approaches for HCC. To address this need, we have developed a platform for modeling HCC by inducing genetics, anatomy, biliary tree, and biliary tree, and hepatic vasculature of the pig is particularly similar to human, making swine ideal for evaluating therapies, radiological, and surgical approaches for HCC treatment. **Methods:** We have delivered a combination of expression vectors for oncogenes and targeted nucleases to disrupt tumor suppressor genes commonly altered in human HCC to promote tumorigenesis in the minipig liver. These are being monitored for tumorigenesis in the minipig liver. These are being monitored for tumorigenesis using a secreted reporter, detectable through a simple, rapid, luminescence-based blood assay. Results: We have developed and optimized methods for efficiently, reproducibly, and stably inducing genetic alterations in the livers of minipigs. We have demonstrated efficient gene-delivery to the left liver lobe and the whole liver using a secreted gene-delivery to the left liver lobe and the whole liver using a secreted gene-delivery reporter. Conclusion: We have developed an adaptable and efficient hepatic gene-delivery system to model human HCC in the minipig. Since HCC research is progressing rapidly, the flexibility of our platform is critical. The ability to generate models with combinations of genetic alterations tailored to an individual study's needs allows control over the presence of molecular targets for therapeutic testing, the subclass of HCC being modeled, tumor penetrance, and tumor size. Tumorigenesis can be targeted to a single liver lobe or diffuse over the liver. Since the alterations are induced somatically, this can be performed in the context of clinically relevant backgrounds and liver damage. The FDA has emphasized the need for testing new therapies in large animal models, in addition to rodent models, prior to human studies. Our swine HCC models will provide a platform to 1) evaluate the safety and efficacy of molecularly targeted therapies, 2) test drug delivery devices, 3) apply in vivo imaging technology, 4) understand tumor natural history without intervention, and 5) support longitudinal blood and tissue sampling to detect biomarkers. This will lead to earlier HCC detection in patients and safer, more effective HCC treatments entering clinical trials, improving patient outcomes and clinical trial success rates.



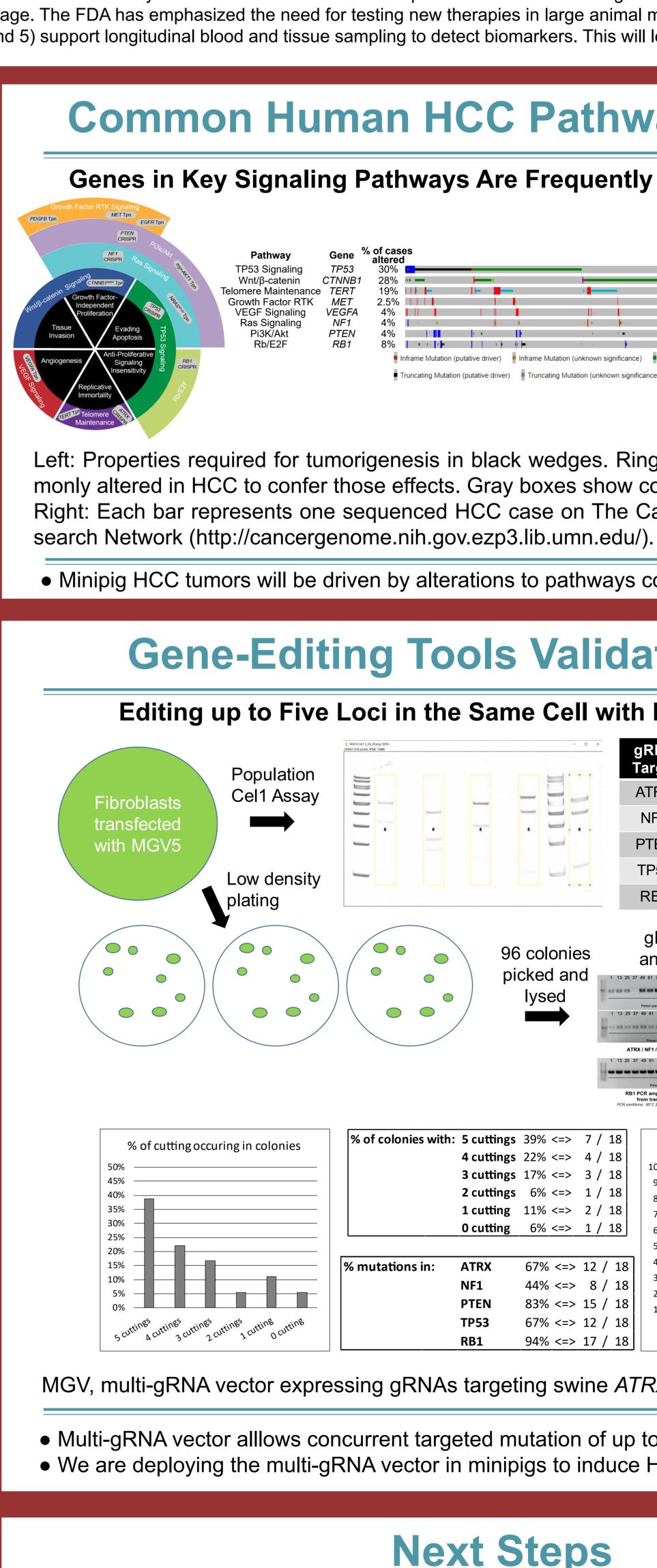


Modeling Hepatocellular Carcinoma in the Minipig

Recombinetics, Inc. Eagan, Minnesota, USA

Abstract

Barbara R. Tschida, PhD., Dylan J. Duerre, BS., Mandy E. Taisto, MS., Stanislas Corbiere, BS., and Adrienne L. Watson, PhD.





Delivering Better Models to Understand Human Disease

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ponsor by:

Common Human HCC Pathway Alterations

Genes in Key Signaling Pathways Are Frequently Altered in Human HCC

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			-	•									
9%		-	-						1	-			
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• 1	Truncating	g Mutation (p	utative	driver)	Truncating Muta	tion (unknow	n significar	nce) Fusion	Amplifica	tion	Deep Deletion No alterations - Not	profiled	

Left: Properties required for tumorigenesis in black wedges. Ring segments show pathways commonly altered in HCC to confer those effects. Gray boxes show constructs we propose to deliver. Right: Each bar represents one sequenced HCC case on The Cancer Genome Atlas (TCGA) Re-

• Minipig HCC tumors will be driven by alterations to pathways commonly altered in human HCC

Gene-Editing Tools Validated *in Vitro*

Editing up to Five Loci in the Same Cell with Multi-gRNA Vector gRNA % Target Editing ATRX 13% 26% NF1 15% TP53 25% RB1 35% gRNA target loci PCR amplified 96 colonies and sequenced from 18 colonies picked and 37 49 61 73 85 2 14 26 38 50 62 74 86 3 15 😤 📱 🔜 1 13 25 37 49 61 73 85 2 14 26 38 50 62 74 86 3 15 😤 🚆 lysed \bigcirc 37 49 61 73 85 2 14 26 38 50 62 74 86 3 15 😤 13 25 37 49 61 73 85 2 14 26 38 50 62 74 86 3 15 ATRX / NF1 / PTEN / TP53 HiFi PCR amplification for sequencing submission, from transfected Oss10 with MGV5 vector PCR conditions: 95°C 2min; 95°C 20sec, 60°C 30sec, 72°C 5min 3 25 37 49 61 73 85 2 14 26 38 50 62 74 86 3 15 🎐 💈 m transfected Oss10 with MGV5 vector 95°C 2min; 95°C 20sec, 58°C 30sec, 72°C 1min (x35); % of colonies with: 5 cuttings 39% <=> 7 / 18 % of mutation of each target 4 cuttings 22% <=> 4 / 18 **3 cuttings** 17% <=> 3 / 18 **2 cuttings** 6% <=> 1 / 13**1 cutting** 11% <=> 2 / 18 **0 cutting** 6% <=> 1 / 18 ATRX 67% <=> 12 / 1 NF1 44% <=> 8 / 1 83% <=> 15 / 18 67% <=> 12 / **TP53** ATRX NF1 PTEN RB1 94% <=> 17

MGV, multi-gRNA vector expressing gRNAs targeting swine ATRX, NF1, PTEN, TP53, and RB1

• Multi-gRNA vector allows concurrent targeted mutation of up to five tumor suppressor genes • We are deploying the multi-gRNA vector in minipigs to induce HCC tumors

Next Steps

• Monitor cohort of transfected minipigs for tumorigeneisis by monthly reporter assay • Apply this method to model various molecular subclasses of human HCC • Generate models in context of clinically relevant backgrounds such as cirrhosis, fatty liver disease, nonalcoholic steatohepatitis (NASH), and other types of liver damage

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