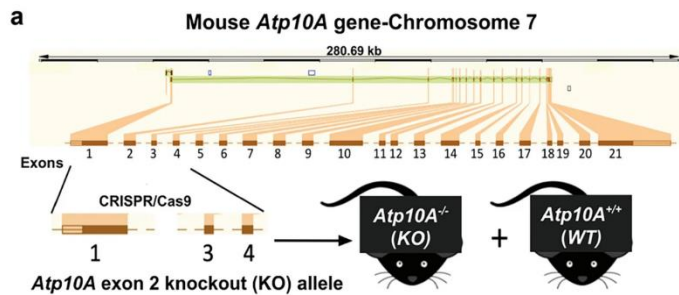


## WINTER 2024 NEWSLETTER

**Publication highlight.** VGER helped Todd Graham (A&S) make an *Atp10a* knockout mouse. In humans, ATP10A and other family members are genetically linked to insulin resistance and vascular complications. Studies of these mice revealed two sex-specific phenotypes; mutant females exhibited dyslipidemia whereas mutant males were infertile.

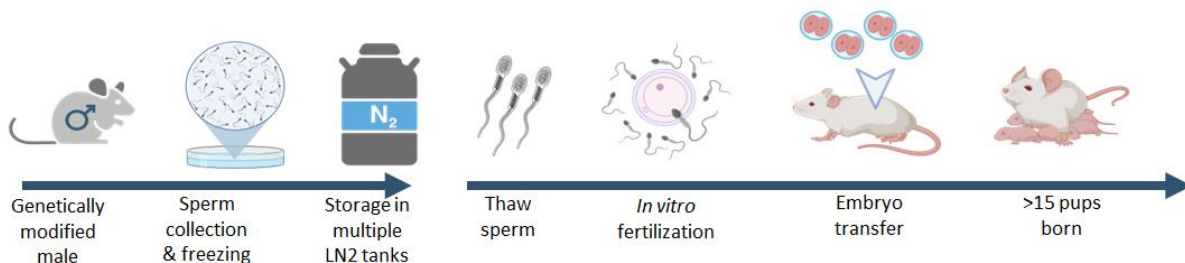


Norris, A.C., Yazlovitskaya, E.M., Zhu, L. *et al.* Deficiency of the lipid flippase ATP10A causes diet-induced dyslipidemia in female mice. *Sci Rep.* 2024 ([PMID:38172157](https://pubmed.ncbi.nlm.nih.gov/38172157/))

Norris AC, Yazlovitskaya EM, Yang TS, Mansueto A, Stafford JM, Graham TR. ATP10A deficiency results in male-specific infertility in mice. *Front Cell Dev Biol.* 2024 ([PMID:38415274](https://pubmed.ncbi.nlm.nih.gov/38415274/))

**Rederivation of mouse strains.** VGER often rederives live mice from imported or stored frozen gametes because cryopreservation is the best method for preserving and distributing genome modified mouse strains. This process involves the thawing and surgical transfer of embryos, or embryos produced by *in vitro* fertilization (IVF) of donor eggs with thawed sperm, into female recipient animals housed in the specific pathogen-free barrier facility. Rederivation from frozen sperm can produce hundreds of offspring, making it also a cost-effective, efficient, and reliable method for moving mice into cleaner housing levels or to rapidly expand a strain for study.

Since 2009, we have successfully completed over 120 IVF rederivations for 58 investigators. More than 55% of these rederivations have used imported cryopreserved sperm samples.



**Oxford Nanopore Long Read Sequencing.** Recently, we established protocols for long-read sequencing. These protocols use CRISPR/Cas9 ribonucleoproteins to enrich up to 20 kb regions of DNA at targeted genomic sites. Although Nanopore long-read sequencing is error-prone, it is easy to produce enough reads to ensure that your mouse strain or stem cell line does not contain large deletions or rearrangements that might go undetected with standard PCR approaches. A slightly modified approach can also be used to map the position of randomly inserted transgenes. If you are interested, please contact us for more information.

**Make a new mouse or human stem cell line!** Please see our [website](#) for an overview of the currently available technologies. We are always happy to discuss potential new projects.



# Vanderbilt Genome Editing Resource

**Contact VGER.** As always, please contact Leesa Sampson at [leesa.sampson@vanderbilt.edu](mailto:leesa.sampson@vanderbilt.edu) or Jennifer Skelton at [jennifer.skelton@vanderbilt.edu](mailto:jennifer.skelton@vanderbilt.edu) to discuss or initiate a project. Also, please email [Jennifer Skelton](mailto:jennifer.skelton@vanderbilt.edu) to let us know about your recent publications describing new VGER strains.

**Happy Holidays!** We look forward to working with you in 2025.

Leesa Sampson  
Jennifer Skelton  
Linda Gower  
Kasia Jopek  
Mark Magnuson

Years in existence	31
Investigators served	369
Unique lines produced since 1993	>3500
CRISPR-edited lines since 2013	186
Lines cryopreserved	>1000
Lines shared in VCMR	63