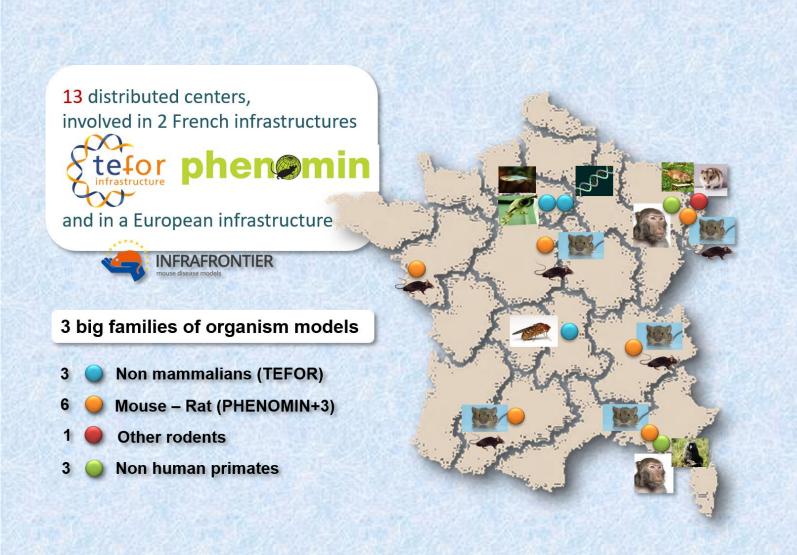


## Zebrafish genome-editing services TEFOR Paris-Saclay



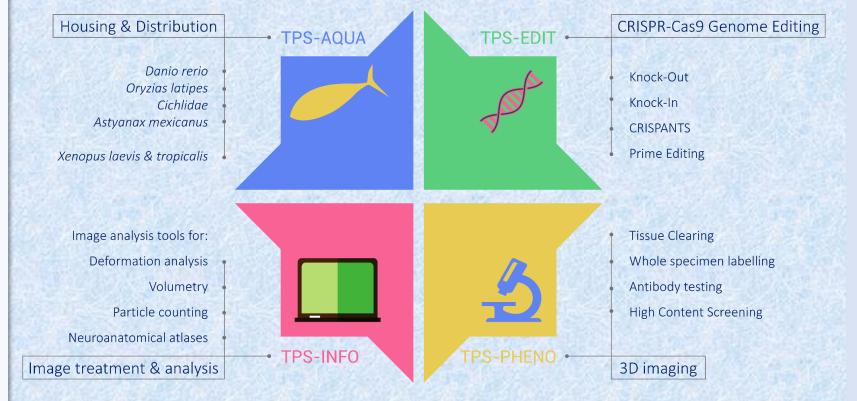


TEFOR Paris-Saclay (TPS) aims to promote the use of aquatic model organisms in fundamental and applied research, and is divided in 4 service units:

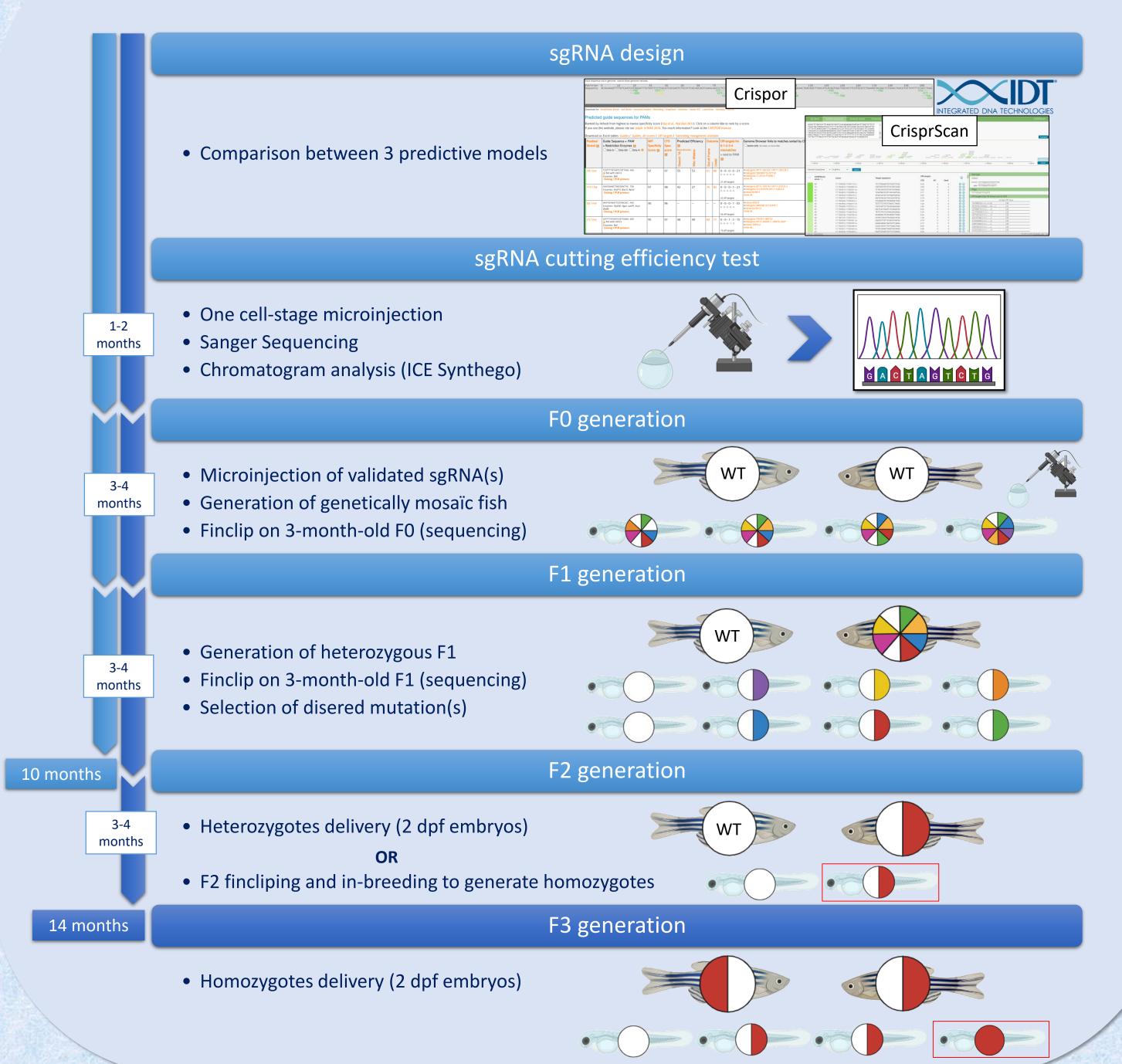
- TPS-AQUA specializes in breeding and housing aquatic models (*Danio Rerio, Xenopus* and other species) for user projects, as well as for animal or eggs distribution.
- TPS-EDIT generates new CRISPR-Cas9 genome-edited fish models on demand, selecting the most up-tothe-minute techniques.
- TPS-**PHENO** masters the techniques of tissue clearing, with immunofluorescence for 3D characterization of fluorescent or mutant fish lines at high throughput.
- TPS-INFO develops computer processing for 3D image analysis, such as cell counting, volumetric studies and volume rendering.



TPS is a center of Celphedia, a Research Infrastructure (RI) gathering 13 centers throughout France, and bringing together a remarkable range of expertise in the creation, functional exploration, archiving and distribution of organisms used as models for basic research and preclinical approaches.



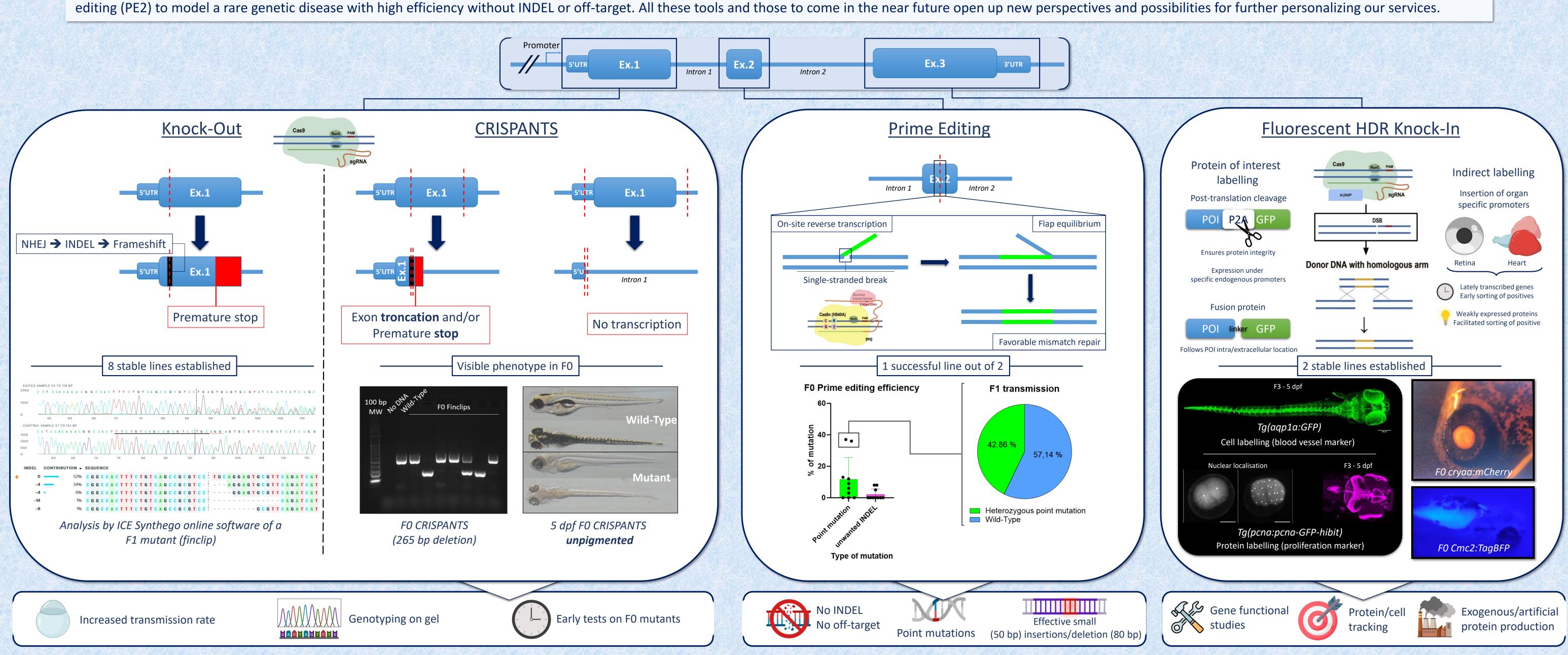
## **Genome Editing Pipeline**

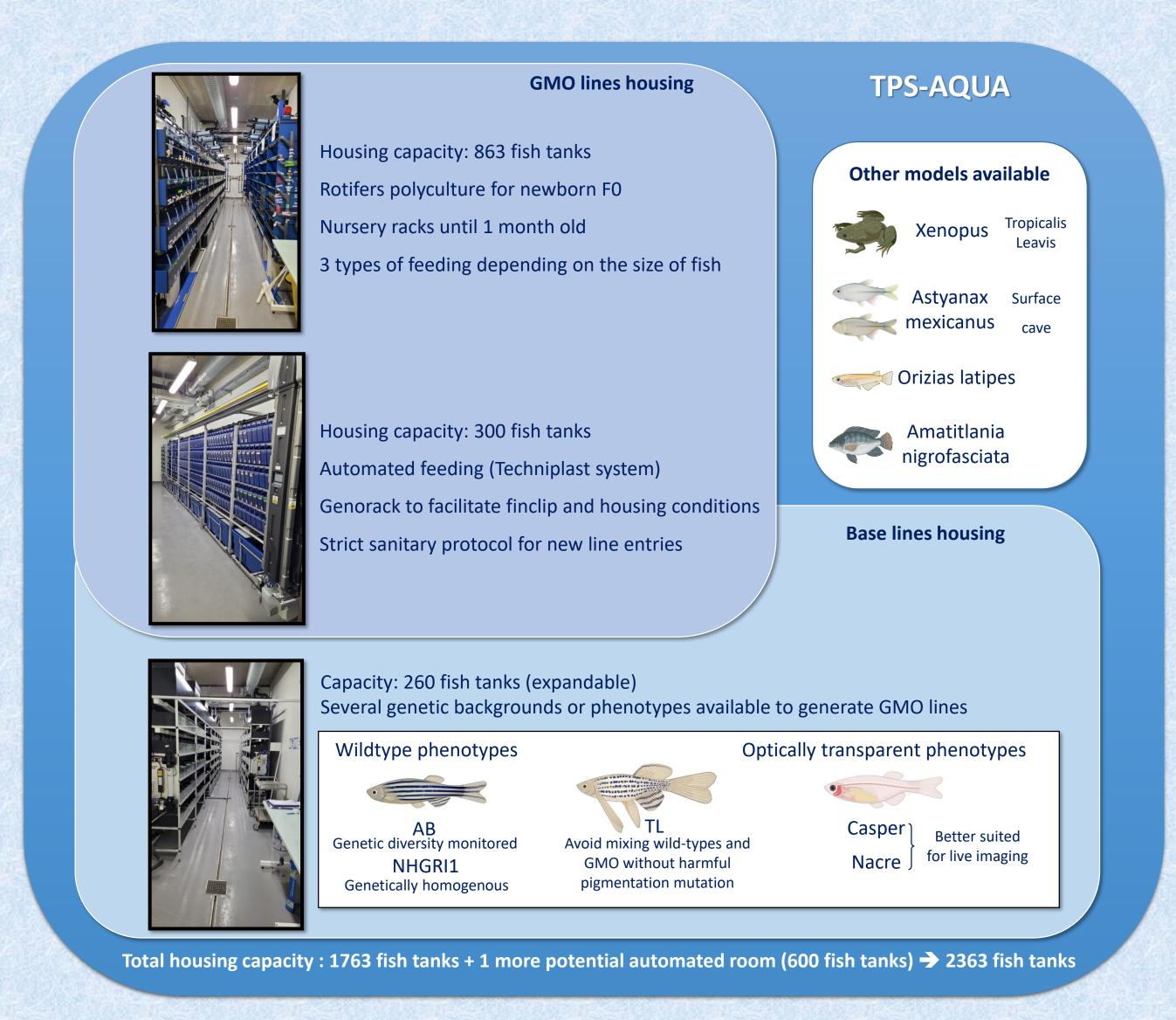


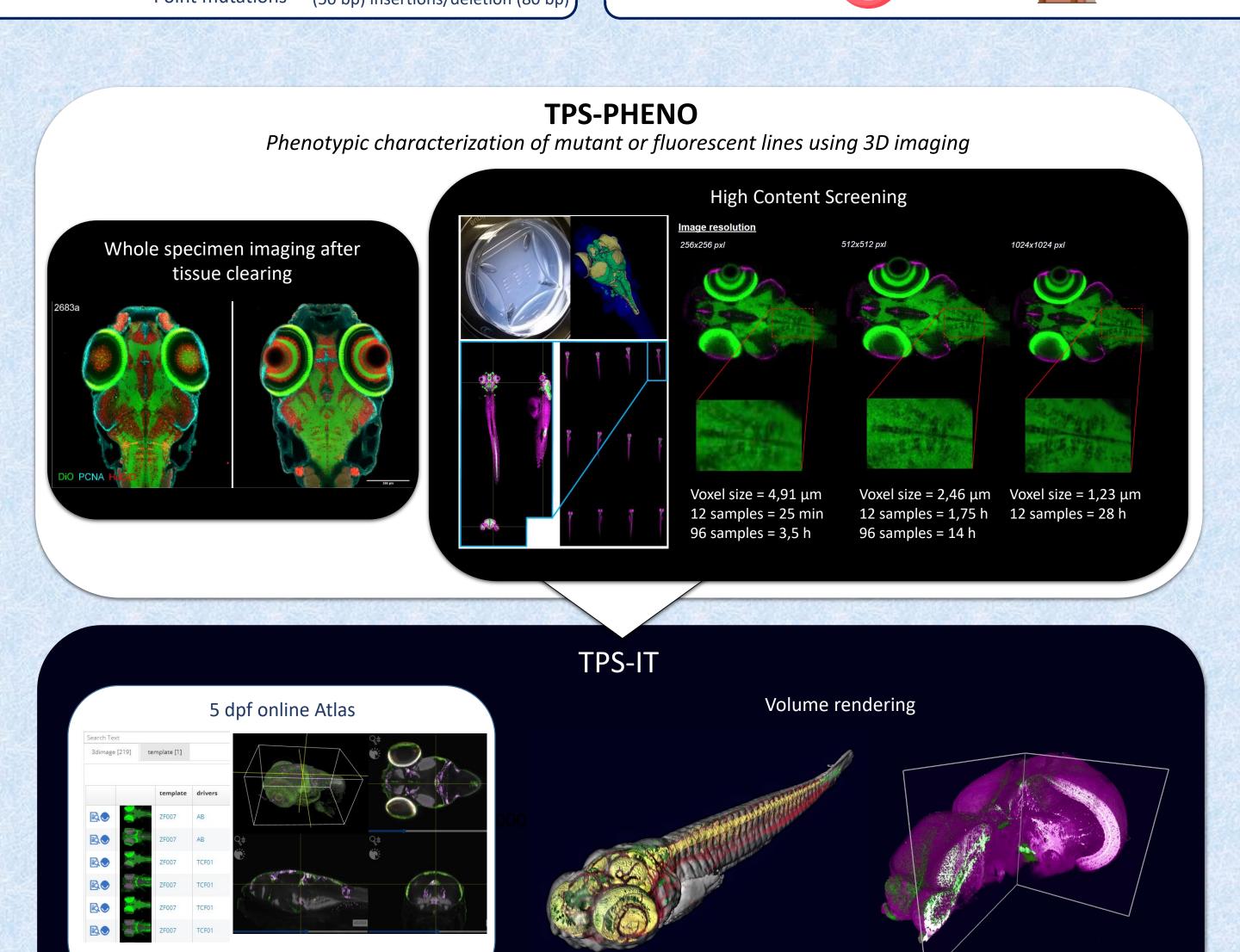
## Genome editing strategies

Generating mutant lines is a long and tedious process, requiring a great deal of expertise to complete. Since 2021 we have generated 12 stable lines and 17 others are in progress for a wide variety of partners.

If TPS has now mastered the Knock-Out strategy for invalidating genes of interest, it's thanks to the successful development of CRISPANTS. This technique makes it possible to generate bi-allelic modifications at F0 generation by cutting at several loci on one or more genes in the same injection, enabling preliminary testing after injection instead of 6 months (stable line). CRISPANTS can also be used to enhance Knock-In success by providing 100% cutting efficiency. To achieve this, we are relying primarily on the HDR pathway, the chances of which we can increase by using inhibitors of the NHEJ pathway as well as CRISPR target sites to actively transport the donor into the nucleus. This brand-new strategy makes it possible to increase the length of KI donors and thus the complexity of the constructs. However, for small insertions or deletions and even single nucleotide polymorphisms, we have recently succeeded in using prime editing (PE2) to model a rare genetic disease with high efficiency without INDEL or off-target. All these tools and those to come in the near future open up new perspectives and possibilities for further personalizing our services.







https://zebrafish.tefor.net