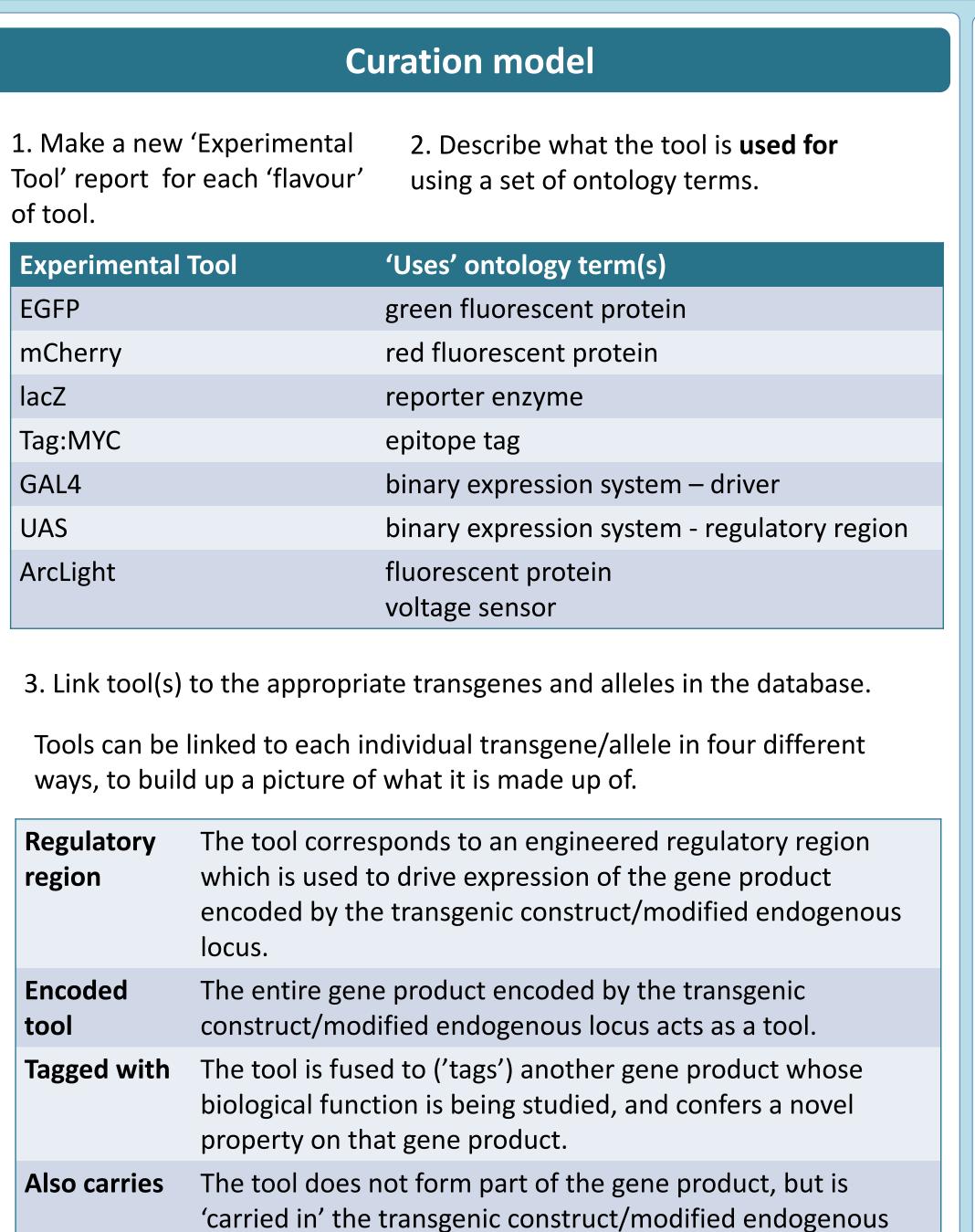


Experimental tools: a new way to categorise transgenic alleles in FlyBase

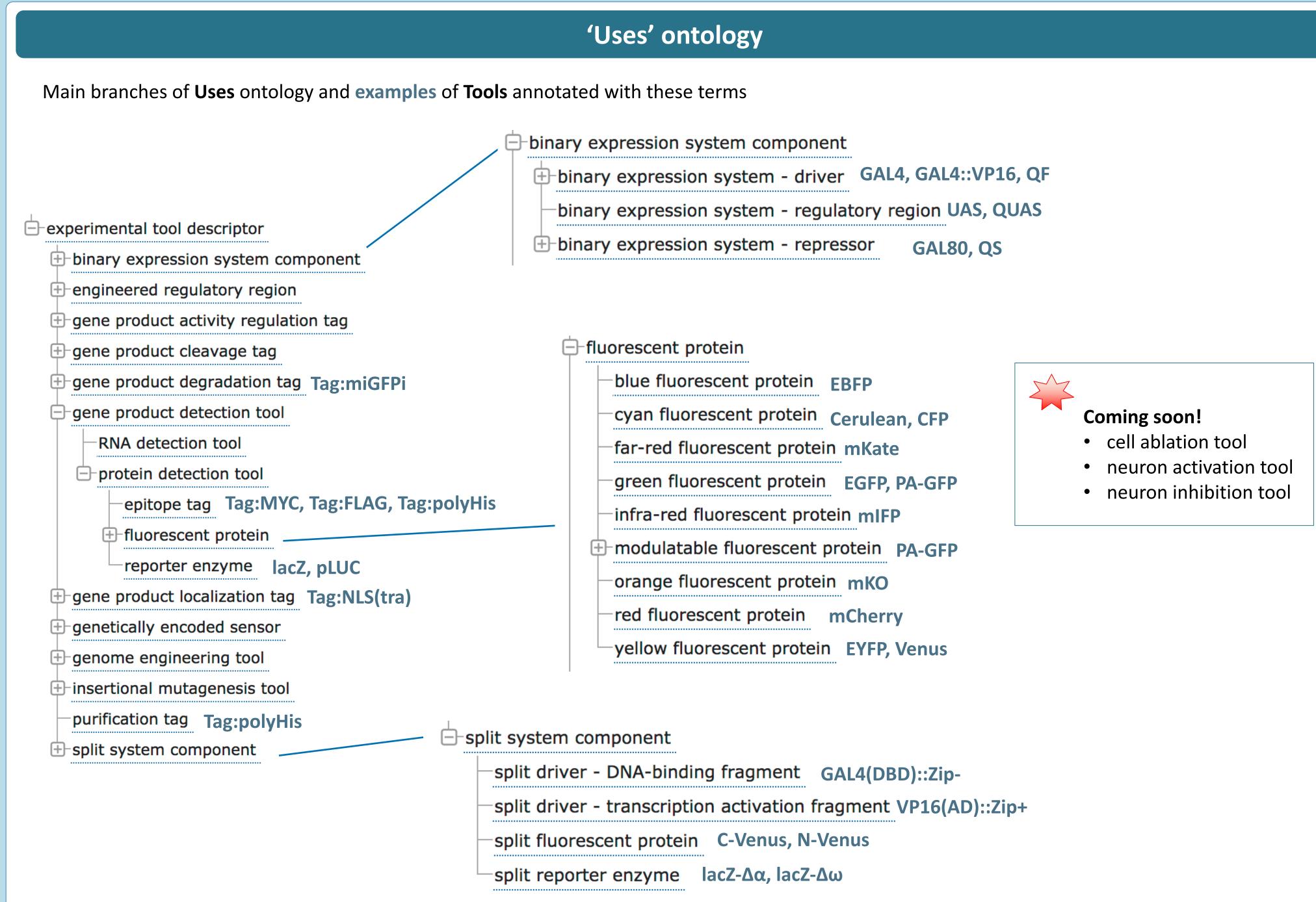
Gillian Millburn and the FlyBase Consortium

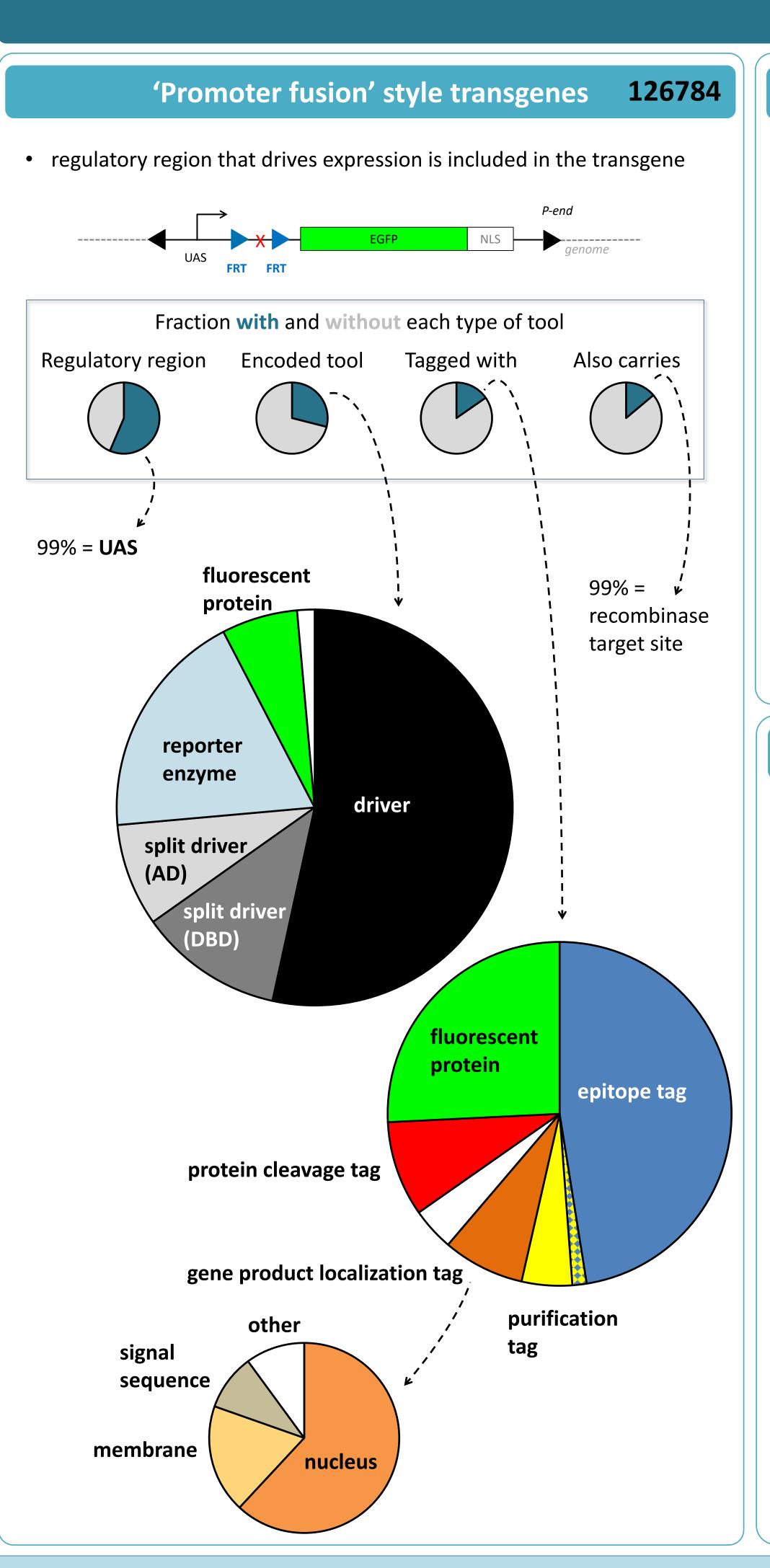
Abstract

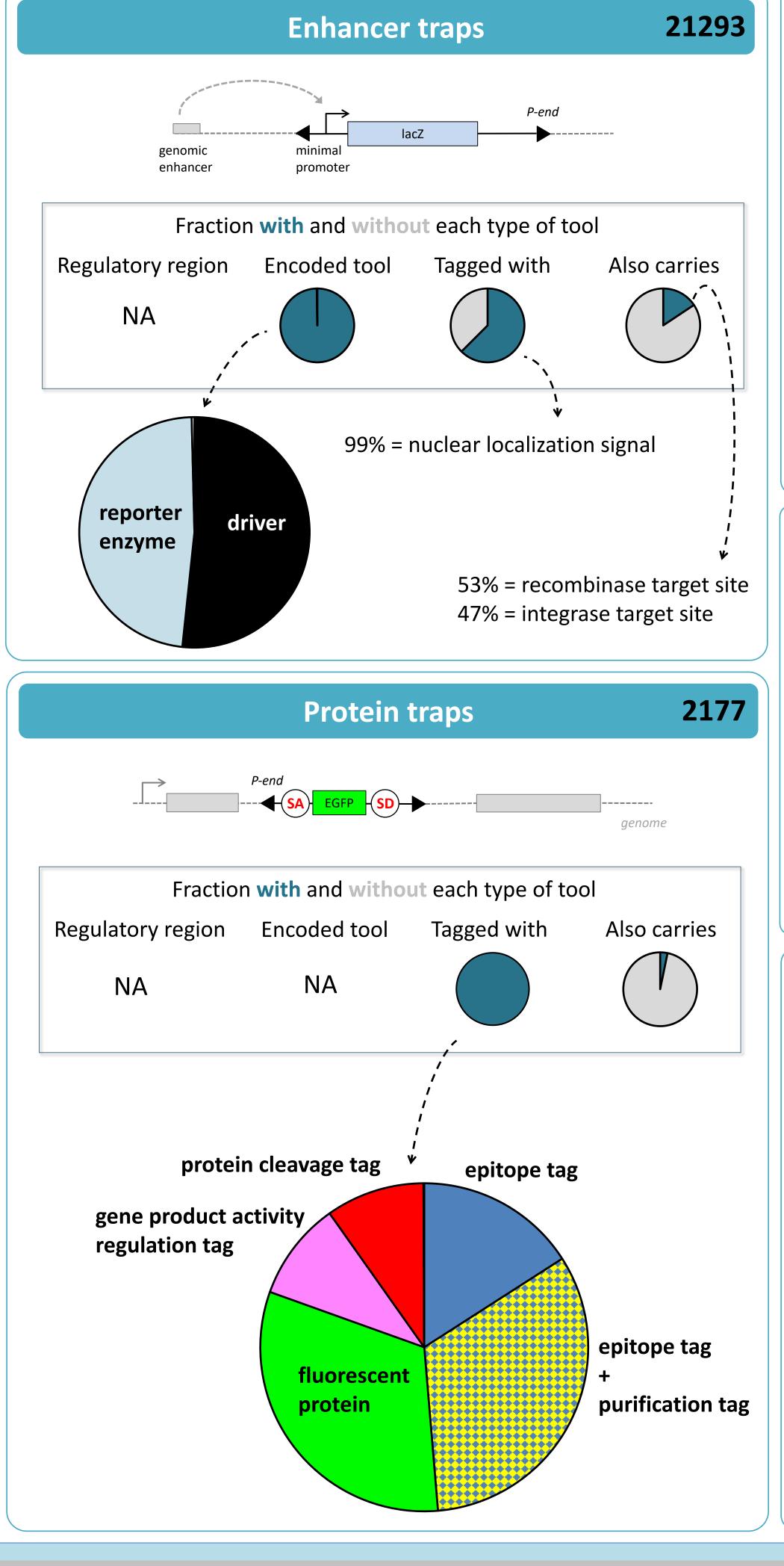
The long history of fly research plus the sophisticated range of applicable genetic engineering techniques mean that a large number of increasingly complex transgenic fly lines have been generated and described in the literature. While this rich genetic tool-kit helps to make *Drosophila melanogaster* an ideal model organism to answer a wide range of biological questions, it also creates a potential problem - how to find the most appropriate fly line for a particular experiment from the large set that are available. To help address this issue, FlyBase has recently introduced the 'experimental tool' data class. Reports have been generated for commonly used sequences with useful properties that are exploited to study the biological function of another gene product or a biological process. These include tools that enable a gene product to be detected (e.g. the **FLAG** tag, **EGFP**, **mCherry**), target a gene product somewhere specific within a cell (e.g. *nuclear localization signal, signal sequence*), drive expression in a binary system (e.g. **QAS, GAL4**) or enable clonal/conditional expression (e.g. **FLP, FRT**). Controlled vocabulary terms are used to describe the common uses for each tool (e.g. *epitope tag, green fluorescent protein, recombinase*). Linking the appropriate experimental tools to transgenic constructs and insertions allows researchers to more easily identify constructs and fly stocks that have the particular characteristics they are interested in. Experimental tools have been linked to all relevant transgenic constructs and this curation is now included as a standard part of the curation of new genetic reagents.



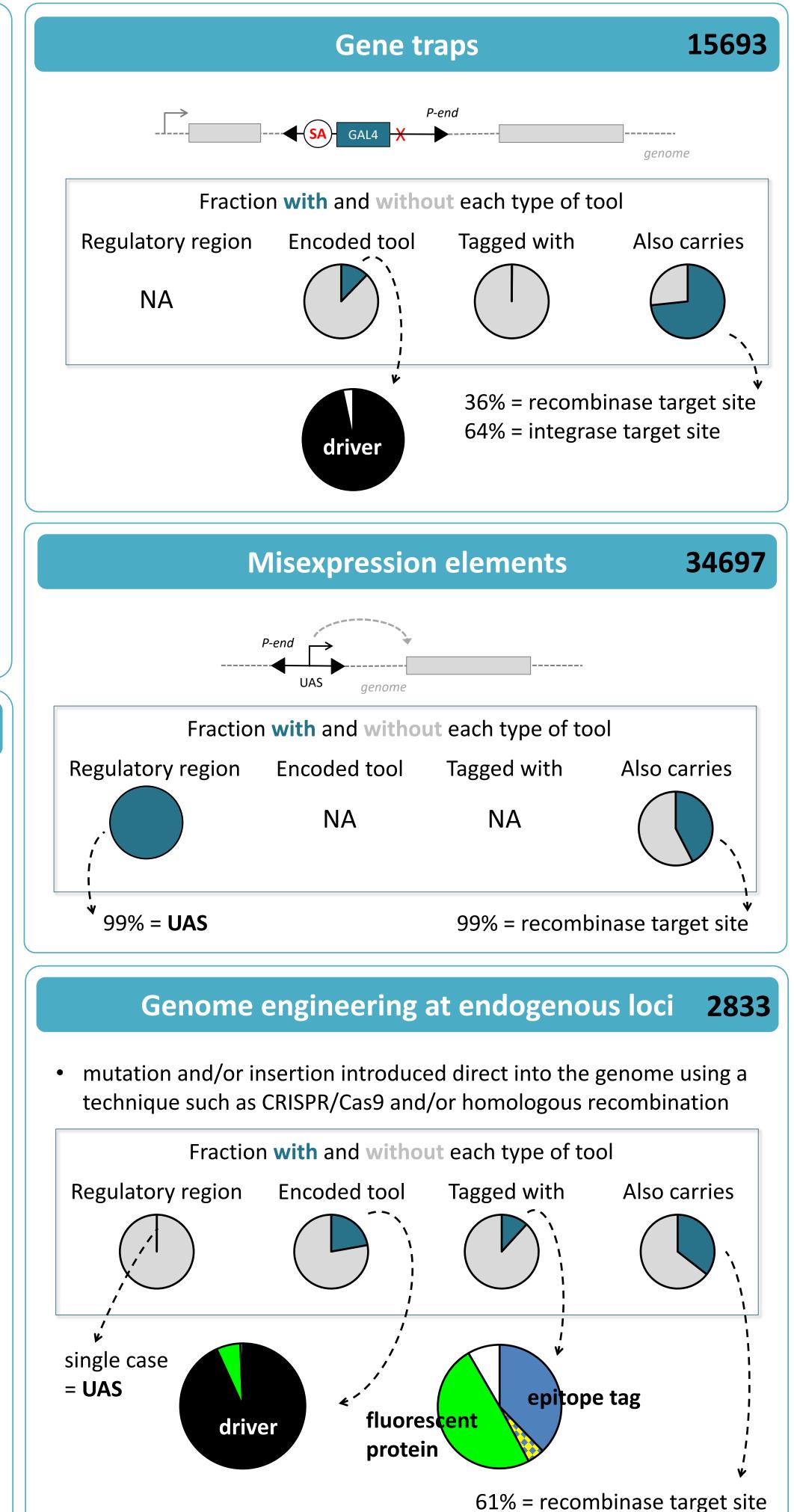
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The data



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