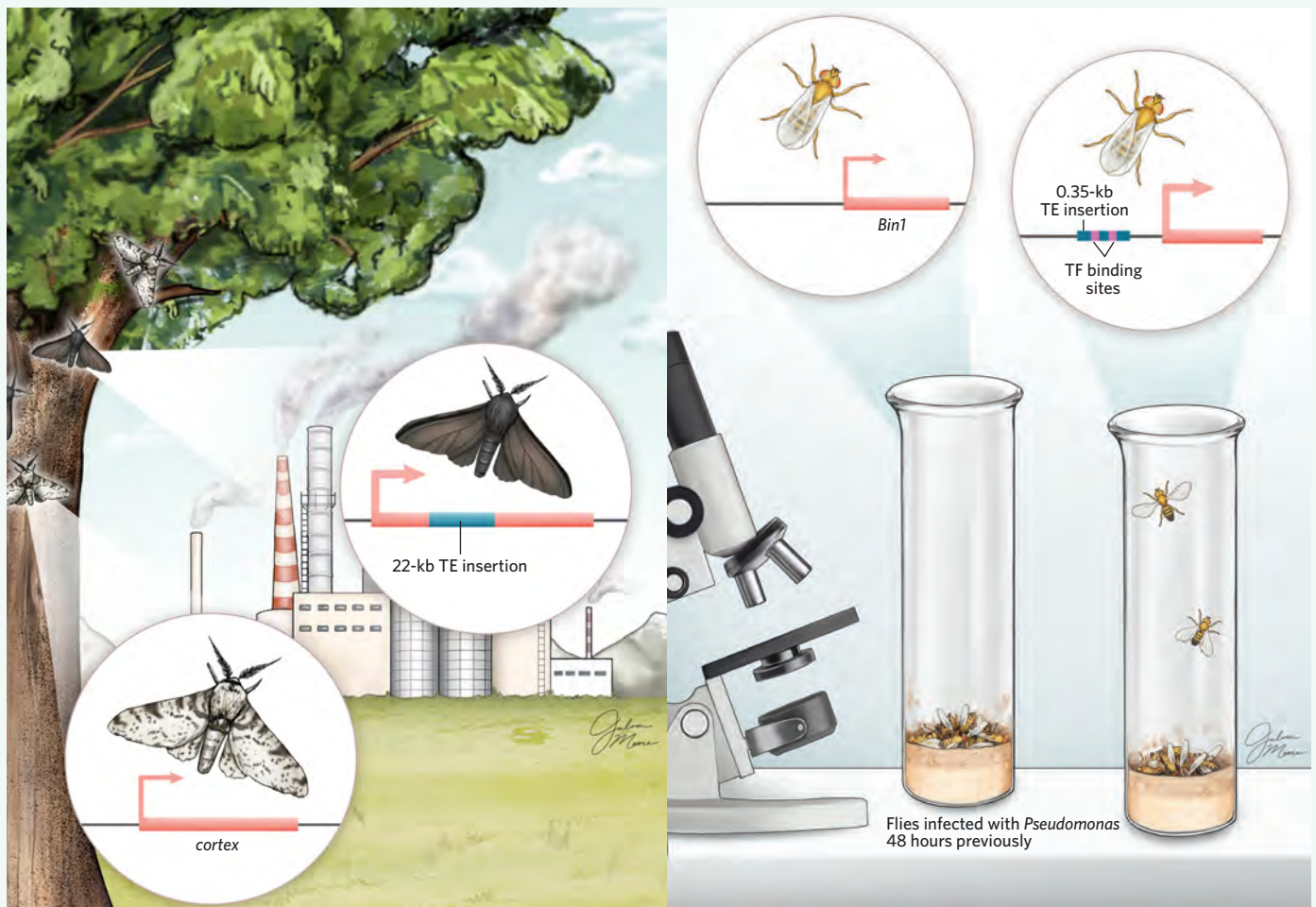


# EVOLUTIONARY LEAPS

There are numerous ways that mobile genetic elements can affect evolution. For example, many transposable elements (TEs), often called transposons, contain genes that code for their jumping or copying machinery, and over time these may be “domesticated” through mutation and selection, becoming integral parts of the organisms’ genome. The RAG1 and RAG2 enzymes that mix up DNA segments in immune proteins (antibodies and T cell receptors) are a notable example. “Wild” TEs can also have adaptive potential, creating genetic diversity as they leap. If TEs land inside a gene, they can directly alter coding regions, mRNA splice sites, or expression-related motifs (left). And because transposons often contain transcription factor binding sites and other regulatory sequences, they can alter a gene’s expression even if they land nearby (right). The transposable elements can also alter the genome in other ways—such as by picking up huge chunks of DNA as they jump (not pictured)—that scientists suspect are similarly altering the course of evolution.



## INSERTING INTO GENES

Arguably the most immediate and dramatic impacts TEs have on genomes occur when they insert into active genes. They can jump into coding regions, altering protein sequences, or they can insert into noncoding regions and alter gene splicing or expression. This is what happened in peppered moths, when a 22-kb TE inserted into the *cortex* gene and led to overproduction of melanin, turning dark the normally lightly bespeckled moths and improving their survival in polluted environments (*Nature*, 534:102-105, 2016).

## INSERTING NEAR GENES

Unlike point mutations, some TEs come preloaded with genetic motifs that may affect the expression of nearby genes. Certain populations of *Drosophila* carry the TE insertion *FBti0019386*, for example, which contains transcription factor binding sites that are activated during a bacterial infection and that increase expression of the immune-related gene *Bin1*. Flies carrying *FBti0019386* are more likely to survive inoculation with a pathogenic strain of *Pseudomonas* (*Genome Biol*, 22:265, 2021).