Pseudogenes are ideal markers of genome remodeling. In turn, the mouse is an ideal platform for studying them, particularly with the availability of transcriptional time course during development and the sequencing of 18 strains (just completed, respectively in phase 3 of ENCODE and by the Mouse Genome Project). Here we present a comprehensive genome-wide annotation of the pseudogenes in the mouse reference genome and associated strains. We compiled this by combining manual curation of >10,000 pseudogenes with results from automatic annotation pipelines. Also, by comparing human and mouse, we annotated 217 new unitary pseudogenes in human and 237, in mouse. We make all our annotations available through an online resource mouse.pseudogene.org. The overall mouse pseudogene repertoire (in the reference and strains) is similar to human with respect to overall size, biotype distribution (~80% processed, ~20% duplicated) and top family composition (many GAPDH, ribosomal and chemoreceptor pseudogenes). However, notable differences arise in the age distribution of pseudogenes with multiple retro-transpositional bursts in mouse evolutionary history compared to only a single one in human. Furthermore, in each strain ~20% of the pseudogenes are unique, reflecting strain-specific functions and evolution. To pick one example: the pseudogenization of taste receptors in the NZO[[?]] strain can be linked to a change in its diet. Additionally, we show that processed pseudogenes commonly arise from highly transcribed genes. Finally, we find that ~15% of the pseudogenes are transcribed, a fraction similar to that found for human, and that transcribed pseudogenes exhibit greater tissue and strain specificity compared to their protein coding parents.