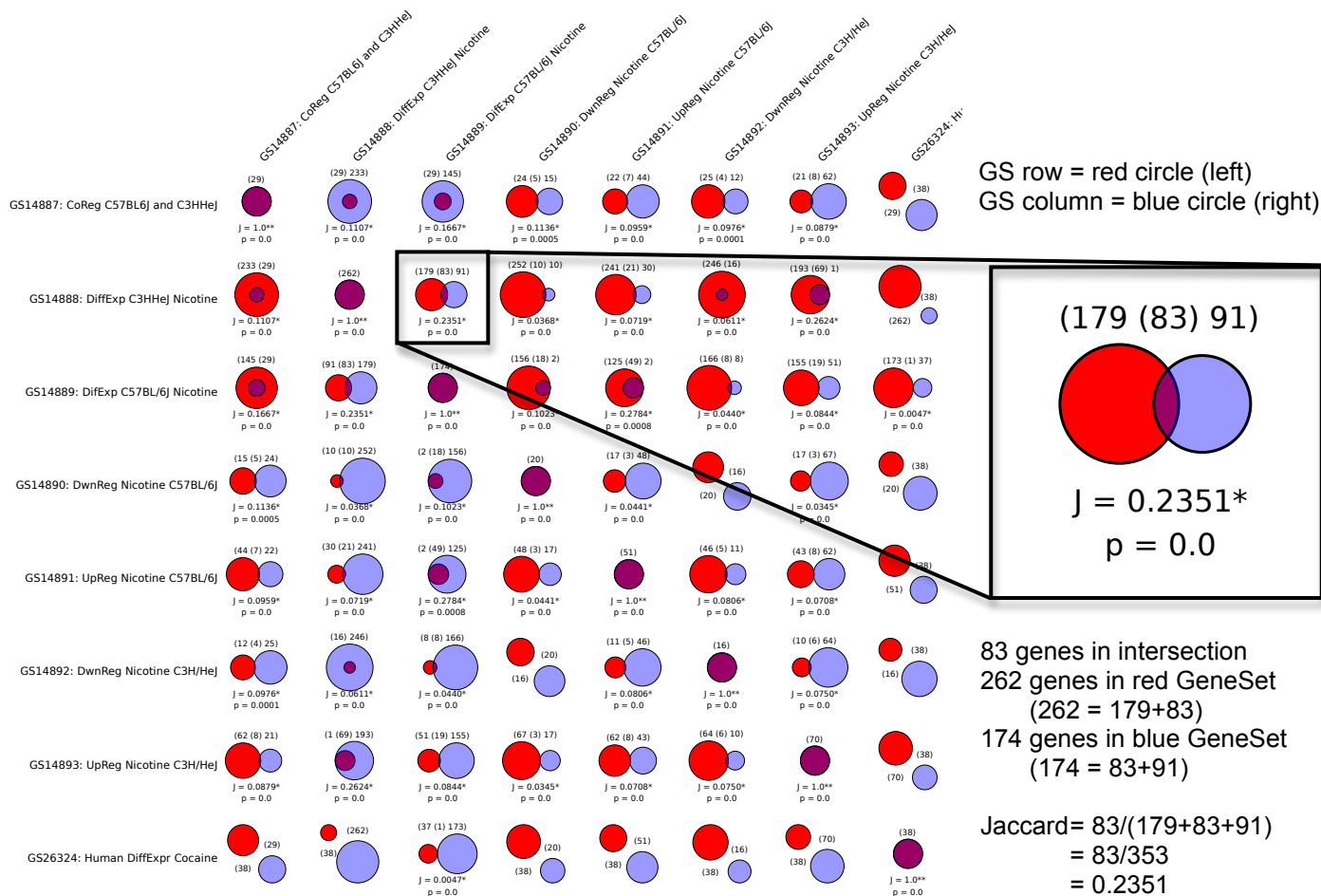


The Jaccard Similarity Tool

at ontologicaldiscovery.org

The Jaccard Similarity tool displays a matrix of venn diagrams, which can be very useful for quickly ascertaining gene sets which can be removed or kept for more complex analysis (such as the Phenome Map). Each venn diagram represents the pairwise gene overlap between the two gene sets depicted for each row and column. Text overlays show the exact gene counts, Jaccard Similarity coefficient and p-value for every pair.



$$Jaccard = \frac{TP}{TP + FP + FN} = \frac{|intersection|}{|union|}$$

The Jaccard Similarity matrix can be scrolled and browsed with the mouse, and more details of each intersection can be viewed by clicking on the venn diagrams in the display. In addition to these interactive features, there is a single option available to modify the resulting display:

Homology

Include homology in order to integrate multi-species data. If excluded, homologous genes from different species will not be counted as intersecting. Data from separate species will never show an overlap without homology.