

## Ingenuity<sup>®</sup> Science Spotlight:

Articles featured in the Ingenuity Science Spotlight represent some of the best and most diverse examples of how IPA<sup>®</sup> has contributed to research across multiple platforms, research areas, and research goals.



---

### Gene Expression Profiling of the Left Ventricles in a Rat Model of Intrinsic Aerobic Running Capacity.

Soon Jin Lee, Justin A. Ways, John C. Barbato, David Essig, Krista Pettee, Sarah J. DeRaedt, Siming Yang, David A. Weaver, Lauren G Koch, and George T Cicila. *Physiol Genomics* 2005 Jul 20.

<http://www.ncbi.nlm.nih.gov/pubmed/16033863>

In a study of cardiorespiratory function and aerobic running capacity (ARC), scientists used global genomic approaches to identify differentially expressed cardiac genes that may serve as cardiovascular risk factors. They employed a rat model comprising two strains: DA (a high ARC strain) and COP (a low ARC strain). Genetic linkage demonstrated that genes associated with aerobic capacity were heritable and the chromosomal locations were identified.

Inbred strains of DA and COP as well as bred F1(DAXCOP) were used in the experiment. RNA isolated from left ventricles after tests was applied to the Affymetrix 7 Rat Genome U34 array set. Quantitative PCR and identification of chromosomal locations were performed to validate and confirm the signature genes. IPA was used to generate gene networks and identify the functional relationships of the candidate genes.

By comparing the high ARC strain (DA) to the low ARC strain (COP), 199 differentially expressed probe sets were identified. Nine probe sets were matched to known chromosomal locations based on their sequences and validated by quantitative real time PCR. Using IPA, 50 differentially expressed genes were identified from 13 biological networks containing a total of 135 genes, as shown in supplemental Table 3 of the paper. Three large networks with 40 differentially expressed genes indicating potential functions are listed in Table 4 of the paper. Chromosomal locations of 85 genes from these networks were examined, but these genes were not among the 199 genes identified by the microarray analysis. Four genes recognized by IPA were mapped to known ARC regions. These genes may be considered potential risk factors for cardiorespiratory disease.