

SUPPLEMENTARY TABLES

NB. We first calculated expression divergence between human-rat orthologous gene pairs and between human-rat random gene pairs using four distances; next we selected conserved orthologous gene pairs at the 1% significance level. For these gene pairs we implemented GO enrichment analysis in Gostat (Bioconductor). Genes identified using correlation-based distance, binary correlation distance, and GA distances shared 15 overrepresented GO categories (Table S1), whereas genes identified using the Euclidean distance were from completely different GO categories (Table S2). Conclusion: different distances select functionally different conserved orthologous gene pairs.

Table S1. The intersection of overrepresented GO categories for conserved orthologous gene pairs identified using correlation-base, GA and binary correlation distances.

| GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|------------|--------|-----------|----------|-------|------|--|
| GO:0006941 | 0.000 | 10.8 | 1.92 | 12 | 28 | striated muscle contraction |
| GO:0003012 | 0.000 | 4.5 | 6.79 | 23 | 99 | muscle system process |
| GO:0030048 | 0.000 | 21.0 | 0.69 | 6 | 10 | actin filament-based movement |
| GO:0055010 | 0.000 | 17.4 | 0.62 | 5 | 9 | ventricular cardiac muscle morphogenesis |
| GO:0060415 | 0.000 | 13.9 | 0.69 | 5 | 10 | muscle tissue morphogenesis |
| GO:0060047 | 0.000 | 4.3 | 2.95 | 10 | 43 | heart contraction |
| GO:0000272 | 0.002 | 11.1 | 0.62 | 4 | 9 | polysaccharide catabolic process |
| GO:0002026 | 0.002 | 11.1 | 0.62 | 4 | 9 | regulation of the force of heart contraction |
| GO:0007512 | 0.002 | 20.7 | 0.34 | 3 | 5 | adult heart development |
| GO:0003013 | 0.004 | 2.3 | 7.89 | 16 | 115 | circulatory system process |
| GO:0006091 | 0.004 | 2.4 | 7.20 | 15 | 105 | generation of precursor metabolites and energy |
| GO:0043462 | 0.005 | 13.9 | 0.41 | 3 | 6 | regulation of ATPase activity |
| GO:0007517 | 0.005 | 2.5 | 5.97 | 13 | 87 | muscle organ development |
| GO:0003007 | 0.005 | 4.4 | 1.71 | 6 | 25 | heart morphogenesis |
| GO:0009150 | 0.009 | 3.4 | 2.47 | 7 | 36 | purine ribonucleotide metabolic process |

Table S2. The overrepresented GO categories for conserved orthologous gene pairs identified using the Euclidean distance.

| GOBPID | Pvalue | OddsRatio | ExpCount | Count | Size | Term |
|---------------|---------------|------------------|-----------------|--------------|-------------|--|
| GO:0007268 | 0.000 | 4.8 | 3.73 | 14 | 168 | synaptic transmission |
| GO:0050877 | 0.000 | 3.5 | 6.68 | 18 | 301 | neurological system process |
| GO:0014059 | 0.000 | 34.6 | 0.16 | 3 | 7 | regulation of dopamine secretion |
| GO:0007154 | 0.001 | 5.1 | 2.06 | 8 | 124 | cell communication |
| GO:0050432 | 0.001 | 23.1 | 0.20 | 3 | 9 | catecholamine secretion |
| GO:0015872 | 0.003 | 13.8 | 0.29 | 3 | 13 | dopamine transport |
| GO:0045620 | 0.003 | 45.5 | 0.09 | 2 | 4 | negative regulation of lymphocyte differentiation |
| GO:0006811 | 0.003 | 2.6 | 6.36 | 14 | 287 | ion transport |
| GO:0007165 | 0.004 | 2.0 | 22.33 | 33 | 1007 | signal transduction |
| GO:0051952 | 0.005 | 10.6 | 0.35 | 3 | 16 | regulation of amine transport |
| GO:0007186 | 0.005 | 2.6 | 5.28 | 12 | 238 | G-protein coupled receptor protein signaling pathway |
| GO:0048609 | 0.006 | 6.2 | 0.75 | 4 | 34 | reproductive process in a multicellular organism |
| GO:0045577 | 0.007 | 22.7 | 0.13 | 2 | 6 | regulation of B cell differentiation |
| GO:0022602 | 0.009 | 8.1 | 0.44 | 3 | 20 | ovulation cycle process |
| GO:0020027 | 0.009 | 18.2 | 0.16 | 2 | 7 | hemoglobin metabolic process |