**Table S3:**

**Predicted abundance of KEGG ortholog groups (Level 2 KOs) from skin bacterial communities of *Duttaphrynus melanostictus* and *Ptychadena mascareniensis*.**

Groups that present significant difference (Kruskal-Wallis test) in the abundance levels between host species are colored. In yellow are the groups that were more abundant in *D. melanostictus* and in blue the groups more abundant in *P. mascareniensis****.***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **KEGG pathways** **(Level 2)** | ***Duttaphrynusmelanostictus*** | ***Ptychadenamascareniensis*** | **% Difference(*D.melanostictus*/*P.mascareniensis*)** | **Kruskal-Wallis** | **p-value** |
| Amino Acid Metabolism | 122,871 ± 7,309 | 118,494 ± 5,958 | 3.694 | 3.714 | 0.054 |
| Biosynthesis of Other Secondary Metabolites | 10,345 ± 781 | 9,210 ± 1,406 | 12.323 | 5.106 | **0.024** |
| Cancers | 1,987 ± 319 | 1,843 ± 224 | 7.816 | 1.637 | 0.201 |
| Carbohydrate Metabolism | 120,127 ± 3,883 | 115,492 ± 7,917 | 4.013 | 2.439 | 0.118 |
| Cardiovascular Diseases | 197 ± 141 | 166 ± 78 | 19.012 | 0.000 | 1.000 |
| Cell Growth and Death | 6,713 ± 1,186 | 5,285 ± 791 | 27.013 | 13.851 | **0.000** |
| Cell Motility | 41,219 ± 10,280 | 41,297 ± 6,407 | -0.190 | 0.134 | 0.715 |
| Cellular Processes and Signaling | 49,935 ± 5,082 | 57,201 ± 7,529 | -12.703 | 7.067 | **0.008** |
| Circulatory System | 531 ± 154 | 451 ± 209 | 17.697 | 1.202 | 0.273 |
| Digestive System | 563 ± 181 | 500 ± 113 | 12.518 | 0.159 | 0.690 |
| Endocrine System | 4,305 ± 728 | 3,157 ± 819 | 36.352 | 12.175 | **0.000** |
| Energy Metabolism | 62,872 ± 2,430 | 59,216 ± 2,696 | 6.173 | 11.488 | **0.001** |
| Environmental Adaptation | 1,857 ± 402 | 1,512 ± 256 | 22.788 | 6.046 | **0.014** |
| Enzyme Families | 21,559 ± 1,071 | 23,234 ± 1,004 | -7.210 | 14.478 | **0.000** |
| Excretory System | 373 ± 123 | 339 ± 81 | 10.079 | 0.961 | 0.327 |
| Folding, Sorting and Degradation | 28,094 ± 3,007 | 27,190 ± 1,120 | 3.326 | 0.283 | 0.595 |
| Genetic Information Processing | 28,305 ± 2,338 | 27,950 ± 1,783 | 1.271 | 0.159 | 0.690 |
| Glycan Biosynthesis and Metabolism | 24,857 ± 3,384 | 24,675 ± 2,783 | 0.738 | 0.054 | 0.816 |
| Immune System | 683 ± 116 | 694 ± 106 | -1.642 | 0.216 | 0.642 |
| Immune System Diseases | 624 ± 106 | 603 ± 66 | 3.381 | 1.637 | 0.201 |
| Infectious Diseases | 5,400 ± 692 | 6,299 ± 1,031 | -14.276 | 7.067 | **0.008** |
| Lipid Metabolism | 44,600 ± 4,336 | 40,721 ± 2,386 | 9.524 | 8.746 | **0.003** |
| Membrane Transport | 150,688 ± 19,303 | 175,935 ± 16,617 | -14.351 | 10.389 | **0.001** |
| Metabolic Diseases | 844 ± 91 | 851 ± 69 | -0.793 | 0.033 | 0.855 |
| Metabolism | 33,727 ± 2,544 | 33,087 ± 3,337 | 1.934 | 0.134 | 0.715 |
| Metabolism of Cofactors and Vitamins | 49,309 ± 2,384 | 46,805 ± 1,219 | 5.350 | 8.551 | **0.003** |
| Metabolism of Other Amino Acids | 23,486 ± 1,814 | 22,916 ± 1,172 | 2.491 | 1.276 | 0.259 |
| Metabolism of Terpenoids and Polyketides | 24,216 ± 2,527 | 21,535 ± 1,374 | 12.449 | 10.389 | **0.001** |
| Nervous System | 884 ± 185 | 1,159 ± 411 | -23.727 | 5.106 | **0.024** |
| Neurodegenerative Diseases | 4,001 ± 719 | 3,812 ± 770 | 4.942 | 0.040 | 0.842 |
| Nucleotide Metabolism | 37,513 ± 1,925 | 36,121 ± 2,759 | 3.855 | 1.594 | 0.207 |
| Poorly Characterized | 65,318 ± 3,873 | 67,917 ± 3,919 | -3.827 | 3.102 | 0.078 |
| Replication and Repair | 80,284 ± 4,807 | 79,728 ± 5,180 | 0.697 | 0.110 | 0.740 |
| Signal Transduction | 28,736 ± 2,430 | 31,462 ± 4,108 | -8.666 | 4.665 | **0.031** |
| Signaling Molecules and Interaction | 2,084 ± 304 | 2,259 ± 521 | -7.735 | 0.487 | 0.485 |
| Transcription | 29,913 ± 1,699 | 31,744 ± 1,774 | -5.767 | 6.718 | **0.010** |
| Translation | 49,828 ± 5,245 | 45,541 ± 3,983 | 9.413 | 4.109 | **0.043** |
| Transport and Catabolism | 4,053 ± 532 | 3,408 ± 639 | 18.900 | 5.884 | **0.015** |
| Xenobiotics Biodegradation and Metabolism | 43,846 ± 9,770 | 36,934 ± 3,530 | 18.712 | 4.244 | **0.039** |