|  |  |  |  |
| --- | --- | --- | --- |
| ID | Groups (%) | VIP | P value |
| TWAs | NPDDs |
|  Citrate cycle (TCA cycle) | 0.496  | 0.457  | 1.999  | 0.000  |
|  Pentose and glucuronate interconversions | 0.854  | 0.884  | 1.431  | 0.028  |
|  Fructose and mannose metabolism | 1.760  | 1.795  | 1.720  | 0.016  |
|  Photosynthesis | 0.260  | 0.281  | 1.146  | 0.025  |
|  Glycine, serine and threonine metabolism | 1.286  | 1.223  | 2.208  | 0.000  |
|  Cysteine and methionine metabolism | 1.444  | 1.399  | 2.268  | 0.000  |
|  Valine, leucine and isoleucine degradation | 0.395  | 0.350  | 1.938  | 0.000  |
|  Geraniol degradation | 0.121  | 0.112  | 1.056  | 0.001  |
|  Valine, leucine and isoleucine biosynthesis | 0.573  | 0.549  | 1.296  | 0.001  |
|  Lysine biosynthesis | 1.138  | 1.086  | 2.453  | 0.000  |
|  Arginine and proline metabolism | 1.856  | 1.803  | 2.587  | 0.031  |
|  Histidine metabolism | 1.035  | 0.992  | 2.302  | 0.000  |
|  Tyrosine metabolism | 0.495  | 0.481  | 1.113  | 0.004  |
|  Phenylalanine metabolism | 0.446  | 0.418  | 1.818  | 0.002  |
|  Benzoate degradation | 0.465  | 0.441  | 1.585  | 0.000  |
|  Phenylalanine, tyrosine and tryptophan biosynthesis | 1.260  | 1.221  | 1.705  | 0.001  |
|  Starch and sucrose metabolism | 2.856  | 2.973  | 2.683  | 0.008  |
|  Amino sugar and nucleotide sugar metabolism | 2.525  | 2.571  | 1.547  | 0.020  |
|  Lipopolysaccharide biosynthesis | 0.577  | 0.479  | 2.977  | 0.000  |
|  Inositol phosphate metabolism | 0.186  | 0.199  | 1.181  | 0.000  |
|  Pyruvate metabolism | 1.155  | 1.111  | 1.861  | 0.000  |
|  Glyoxylate and dicarboxylate metabolism | 0.767  | 0.735  | 1.726  | 0.000  |
|  Nitrotoluene degradation | 0.145  | 0.128  | 1.235  | 0.042  |
|  Propanoate metabolism | 0.394  | 0.374  | 1.365  | 0.000  |
|  Butanoate metabolism | 0.665  | 0.639  | 1.812  | 0.000  |
|  One carbon pool by folate | 0.571  | 0.553  | 1.377  | 0.000  |
|  Carbon fixation pathways in prokaryotes | 1.052  | 0.985  | 2.691  | 0.000  |
|  Riboflavin metabolism | 0.366  | 0.351  | 1.284  | 0.000  |
|  Pantothenate and CoA biosynthesis | 0.800  | 0.779  | 1.355  | 0.000  |
|  Folate biosynthesis | 0.514  | 0.496  | 1.146  | 0.001  |
|  Atrazine degradation | 0.100  | 0.087  | 1.072  | 0.000  |
|  Porphyrin and chlorophyll metabolism | 1.543  | 1.648  | 3.065  | 0.000  |
|  Nitrogen metabolism | 1.601  | 1.560  | 1.947  | 0.002  |
|  ABC transporters | 8.544  | 9.068  | 6.682  | 0.000  |
|  Bacterial chemotaxis | 1.254  | 1.385  | 3.322  | 0.000  |
|  Flagellar assembly | 1.042  | 1.153  | 2.972  | 0.000  |
|  Phosphotransferase system (PTS) | 0.347  | 0.373  | 1.164  | 0.024  |
|  Bacterial secretion system | 1.169  | 1.131  | 1.687  | 0.031  |
|  Base excision repair | 0.617  | 0.597  | 1.487  | 0.000  |
|  Meiosis - yeast | 0.117  | 0.136  | 1.101  | 0.005  |