Supplementary table 8. Pathway analysis of top differentially methylated positions (KEGG pathways) among migrants compared to non-migrants.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Description | N | DE | P.DE | FDR |
| path:hsa00603 | Glycosphingolipid biosynthesis - globo and isoglobo series | 13 | 1 | 0.0059 | 1 |
| path:hsa00601 | Glycosphingolipid biosynthesis - lacto and neolacto series | 27 | 1 | 0.0107 | 1 |
| path:hsa00604 | Glycosphingolipid biosynthesis - ganglio series | 15 | 1 | 0.0125 | 1 |
| path:hsa04721 | Synaptic vesicle cycle | 78 | 1 | 0.0545 | 1 |
| path:hsa04928 | Parathyroid hormone synthesis, secretion, and action | 105 | 1 | 0.0885 | 1 |
| path:hsa04371 | Apelin signaling pathway | 135 | 1 | 0.0905 | 1 |
| path:hsa04022 | cGMP-PKG signaling pathway | 161 | 1 | 0.1092 | 1 |
| path:hsa04310 | Wnt signaling pathway | 159 | 1 | 0.1295 | 1 |
| path:hsa01100 | Metabolic pathways | 1403 | 1 | 0.5028 | 1 |
| path:hsa00010 | Glycolysis / Gluconeogenesis | 63 | 0 | 1 | 1 |
| path:hsa00020 | Citrate cycle (TCA cycle) | 28 | 0 | 1 | 1 |
| path:hsa00030 | Pentose phosphate pathway | 24 | 0 | 1 | 1 |
| path:hsa00040 | Pentose and glucuronate interconversions | 30 | 0 | 1 | 1 |
| path:hsa00051 | Fructose and mannose metabolism | 32 | 0 | 1 | 1 |
| path:hsa00052 | Galactose metabolism | 28 | 0 | 1 | 1 |
| path:hsa00053 | Ascorbate and aldarate metabolism | 26 | 0 | 1 | 1 |
| path:hsa00061 | Fatty acid biosynthesis | 16 | 0 | 1 | 1 |
| path:hsa00062 | Fatty acid elongation | 27 | 0 | 1 | 1 |
| path:hsa00071 | Fatty acid degradation | 42 | 0 | 1 | 1 |
| path:hsa00072 | Synthesis and degradation of ketone bodies | 10 | 0 | 1 | 1 |

N= number of genes in the KEGG term

DE= number of genes that are differentially methylated

P.DE=p-value for over-representation of the GO or KEGG term

FDR=False discovery rate