**Table S2: 52 functions statistically up-represented on the skin metagenomic datasets**

Functions of MG-RAST level 3 subsystem differentially detected in skin datasets in comparison to other environments datasets (Whelch’s test, other environments are grouped as one unique environment for the statistical test).

|  |  |  |  |
| --- | --- | --- | --- |
| MG-RAST level 3 subsystem | P-value | Skin: mean relative frequency ± standard deviation (%) | Other environments: mean relative frequency ± standard deviation (%) |
| Alpha-acetolactate operon | 4,36E-30 | 0,08 ±0,03 | 00 |
| Cannabinoid biosynthesis | 3,77E-25 | 0,05 ±0,01 | 0,010 |
| Triacylglycerol metabolism | 1,70E-24 | 0,18 ±0,02 | 0,02 ±0,02 |
| Glutathione analogs: mycothiol | 2,80E-24 | 0,2 ±0,05 | 0,01 ±0,02 |
| Multi-subunit cation antiporter | 3,14E-24 | 0,42 ±0,15 | 0,02 ±0,03 |
| Biofilm formation in Staphylococcus | 1,46E-22 | 0,23 ±0,12 | 0 ±0,01 |
| Adhesins in Staphylococcus | 2,41E-22 | 0,3 ±0,13 | 0,01 ±0,02 |
| Petrobactin-mediated iron uptake system | 9,86E-22 | 0,05 ±0,03 | 00 |
| Methicillin resistance in Staphylococci | 2,19E-20 | 0,48 ±0,13 | 0,11 ±0,04 |
| D-Alanyl Lipoteichoic Acid Biosynthesis | 5,18E-18 | 0,04 ±0,02 | 00 |
| Lactate utilization | 2,57E-15 | 0,26 ±0,02 | 0,07 ±0,04 |
| Bacitracin Stress Response | 1,50E-14 | 0,05 ±0,03 | 0 ±0,01 |
| Cytolysin and Lipase operon in Vibrio | 1,52E-14 | 0,03 ±0,02 | 00 |
| Toxin-Antitoxin MT1 | 1,20E-13 | 0,01 ±0,01 | 00 |
| Anaerobic Oxidative Degradation of L-Ornithine | 2,17E-13 | 0,09 ±0,07 | 0 ±0,01 |
| SecY2-SecA2 Specialized Transport System | 3,15E-13 | 0,08 ±0,03 | 0 ±0,01 |
| Teicoplanin-resistance in Staphylococcus | 1,95E-12 | 0,02 ±0,02 | 00 |
| Siderophore Anthrachelin | 3,76E-12 | 0,03 ±0,02 | 00 |
| CoA disulfide thiol-disulfide redox system | 1,38E-11 | 0,02 ±0,01 | 00 |
| Mannitol Utilization | 3,32E-11 | 0,23 ±0,01 | 0,07 ±0,04 |
| Fructose utilization | 8,73E-11 | 0,33 ±0,05 | 0,07 ±0,07 |
| Prophage lysogenic conversion modules | 1,38E-10 | 0,03 ±0,01 | 0 ±0,01 |
| Acetoin, butanediol metabolism | 2,23E-10 | 0,32 ±0,07 | 0,14 ±0,04 |
| Teichoic and lipoteichoic acids biosynthesis | 2,94E-10 | 0,31 ±0,1 | 0,08 ±0,06 |
| Pyruvate Alanine Serine Interconversions | 1,03E-09 | 0,37 ±0,04 | 0,19 ±0,05 |
| Glycine and Serine Utilization | 2,20E-09 | 0,87 ±0,05 | 0,54 ±0,09 |
| CBSS-196164.1.peg.461 | 2,20E-09 | 0,19 ±0,02 | 0,06 ±0,04 |
| Menaquinone and Phylloquinone Biosynthesis | 3,08E-09 | 0,2 ±0,03 | 0,08 ±0,03 |
| Dihydroxyacetone kinases | 8,51E-09 | 0,08 ±0,04 | 0,02 ±0,02 |
| Staphylococcal pathogenicity islands SaPI | 1,10E-08 | 0,49 ±0,08 | 0,24 ±0,07 |
| Murein hydrolase regulation and cell death | 1,11E-08 | 0,11 ±0,06 | 0,03 ±0,02 |
| Purine conversions | 2,85E-08 | 1,02 ±0,06 | 0,67 ±0,11 |
| Glycerol and Glycerol-3-phosphate Uptake and Utilization | 3,12E-08 | 0,36 ±0,02 | 0,2 ±0,05 |
| Arginine Deiminase Pathway | 3,83E-08 | 0,21 ±0,01 | 0,07 ±0,04 |
| Sialic Acid Metabolism | 8,69E-08 | 0,86 ±0,08 | 0,41 ±0,15 |
| L-Cystine Uptake and Metabolism | 1,23E-07 | 0,08 ±0,03 | 0,03 ±0,02 |
| Galactose-inducible PTS | 1,48E-07 | 0,1 ±0,01 | 0,04 ±0,02 |
| TCA Cycle | 2,01E-07 | 1,47 ±0,16 | 0,73 ±0,25 |
| DNA repair, bacterial RecBCD pathway | 4,95E-07 | 0,2 ±0,07 | 0,07 ±0,04 |
| Cluster-based Subsystem Grouping Hypotheticals - perhaps Proteosome Related | 5,32E-07 | 0,21 ±0,07 | 0,06 ±0,05 |
| Alpha-Amylase locus in Streptocococcus | 1,45E-06 | 0,06 ±0,01 | 0,02 ±0,01 |
| D-gluconate and ketogluconates metabolism | 2,03E-06 | 0,27 ±0,07 | 0,11 ±0,06 |
| At5g63420 | 2,14E-06 | 0,59 ±0,09 | 0,36 ±0,09 |
| D-Sorbitol(D-Glucitol) and L-Sorbose Utilization | 2,27E-06 | 0,04 ±0,03 | 0,01 ±0,01 |
| Proton-dependent Peptide Transporters | 2,45E-06 | 0,07 ±0,02 | 0,03 ±0,02 |
| Acetone Butanol Ethanol Synthesis | 2,61E-06 | 0,17 ±0,01 | 0,4 ±0,09 |
| CBSS-262719.3.peg.410 | 3,10E-06 | 0,19 ±0,07 | 0,1 ±0,03 |
| Ubiquinone Menaquinone-cytochrome c reductase complexes | 3,56E-06 | 0,19 ±0,02 | 0,06 ±0,05 |
| KDO2-Lipid A biosynthesis | 5,39E-06 | 0,01 ±0,01 | 0,27 ±0,1 |
| CBSS-280355.3.peg.2835 | 6,09E-06 | 0,28 ±0,04 | 0,18 ±0,04 |
| tRNA aminoacylation, Lys | 7,10E-06 | 0,15 ±0,05 | 0,08 ±0,03 |
| Vibrio Core Oligosaccharide Biosynthesis | 7,71E-06 | 0,010 | 0,09 ±0,03 |