S5 Table. Detection of proteins in the 00-1597 HS:9 CPB cluster using comparative 4-plex iTRAQ proteomic analysis.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Protein Identity** | **Non-exclusive peptides** | **Gene identity (LS-BSR)** | | | | **Protein average log2 fold change** | | | |
| **00-0949** | **01-1512** | **00-6200** | **00-1597** | **00-0949** | **01-1512** | **00-6200** | **00-1597** |
| *kpsS* capsule biosynthesis protein PJ17\_07435 | - | 1 | 1 | 0.99 | 0.88 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| *kpsC* capsule biosynthesis protein PJ17\_07440 | - | 1 | 1 | 0.95 | 0.85 | 0.05 | -1.55 | -1.55 | **1.52** |
|  | + |  |  |  |  | -0.066 | -0.16 | 0.12 | **0.90**‡ |
| inositol monophosphatase PJ17\_07445 | - | 0.15 | 0.15 | 0.15 | 1 | 0.01 | 0.37 | 0.54 | **3.99\*** |
|  | + |  |  |  |  | 0.01 | -0.40 | 0.47 | **3.98\*** |
| hypothetical protein PJ17\_07450 | - | 0 | 0 | 0 | 1 | -0.14 | -1.01 | 1.27 | **5.08\*** |
|  | + |  |  |  |  | -0.21 | -1.13 | 1.22 | **5.10\*** |
| 2-hydroxyacid dehydrogenase PJ17\_07455 | - | 0.21 | 0.21 | 0.21 | 1 | -0.04 | -0.69 | 0.87 | **4.77\*** |
|  | + |  |  |  |  | -0.06 | -0.75 | 0.81 | **4.81\*** |
| acetylneuraminate cytidylyltransferase PJ17\_07460 | - | 0.16 | 0.16 | 0.17 | 1 | -0.03 | -0.32 | 0.48 | **4.68\*** |
|  | + |  |  |  |  | -0.03 | -0.37 | 0.41 | **4.72\*** |
| oxidoreductase PJ17\_07465 | - | 0.12 | 0.12 | 0.12 | 1 | -0.03 | -0.77 | 0.51 | **4.40\*** |
|  | + |  |  |  |  | -0.01 | -0.78 | 0.45 | **4.44\*** |
| sugar isomerase PJ17\_07470 | - | 0.24 | 0.24 | 0.25 | 1 | 0.01 | -0.18 | 1.10 | **6.24\*** |
|  | + |  |  |  |  | 0.00 | -1.09 | 1.01 | **6.37\*** |
| cyclase PJ17\_07475 | - | 0.07 | 0.07 | 0 | 1 | 0.57 | 0.93 | 0.92 | **4.10\*** |
|  | + |  |  |  |  | 0.78 | 1.35 | 1.07 | **4.21**‡ |
| hypothetical protein PJ17\_07480 | - | 0.12 | 0.12 | 0.17 | 1 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| hypothetical protein PJ17\_07490 | - | 0.12 | 0.12 | 0.17 | 1 | 0.00 | -0.74 | 0.54 | **4.30\*** |
|  | + |  |  |  |  | -0.02 | -0.85 | -0.54 | **4.35\*** |
| hypothetical protein PJ17\_07495 | - | 0.06 | 0.06 | 0 | 1 | -0.02 | -0.47 | 0.07 | **2.71\*** |
|  | + |  |  |  |  | -0.03 | -0.52 | -0.02 | **2.68\*** |
| hypothetical protein /dehydratase PJ17\_07500 | - | 0.12 | 0.12 | 0.12 | 1 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| hypothetical protein PJ17\_07505 | - | 0.11 | 0.11 | 0.11 | 1 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| hypothetical protein PJ17\_07510 | - | 0.1 | 0.1 | 0.1 | 1 | 0.00 | -0.82 | 0.60 | **4.28\*** |
|  | + |  |  |  |  | 0.00 | -0.87 | 0.53 | **4.29\*** |
| hypothetical protein PJ17\_07515 | - | 0 | 0 | 0 | 1 | 0.02 | -0.54 | 0.31 | **4.83\*** |
|  | + |  |  |  |  | 0.03 | -0.73 | 0.32 | **4.92\*** |
| dTDP-4-deoxyrhamnose 3,5-epimerase PJ17\_07520 | - | 0.18 | 0.18 | 0 | 1 | -0.03 | -0.65 | 0.42 | **4.47\*** |
|  | + |  |  |  |  | -0.03 | -0.69 | 0.35 | **4.50\*** |
| UDP-glucose-6-dehydrogenase PJ17\_07525 | - | 0.14 | 0.14 | 0 | 1 | -0.06 | -0.63 | 0.75 | **4.97\*** |
|  | + |  |  |  |  | -0.05 | -0.67 | 0.69 | **5.03\*** |
| epimerase PJ17\_07530 | - | 0.12 | 0.12 | 0.11 | 1 | -0.07 | -0.81 | 0.90 | **5.62\*** |
|  | + |  |  |  |  | -0.07 | -1.04 | 0.84 | **5.69\*** |
| glucose-1-phosphate cytidylyltransferase PJ17\_07535 | - | 0.12 | 0.12 | 0.12 | 1 | -0.05 | -0.72 | 0.85 | **5.44\*** |
|  | + |  |  |  |  | -0.04 | -1.14 | 0.80 | **5.46\*** |
| hypothetical protein PJ17\_07540 | - | 0.09 | 0.09 | 0.15 | 1 | -0.09 | -0.72 | 0.77 | **4.70\*** |
|  | + |  |  |  |  | -0.11 | -0.86 | 0.72 | **4.71\*** |
| hypothetical protein PJ17\_07545 | - | 0.3 | 0.3 | 0.28 | 1 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| glycosyltransferase family 2 PJ17\_07550 | - | 0.49 | 0.49 | 0.09 | 1 | 0.00 | -0.38 | 0.65 | **4.37\*** |
|  | + |  |  |  |  | -0.02 | -0.51 | 0.56 | **4.42\*** |
| UDP-galactopyranose mutase PJ17\_07555 | - | 0.8 | 0.8 | 0.04 | 1 | -0.02 | -0.37 | 0.87 | **4.81\*** |
|  | + |  |  |  |  | -0.02 | -0.47 | 0.58 | **4.51\*** |
| capsular biosynthesis protein PJ17\_07560 | - | 0.05 | 0.05 | 0.57 | 1 | 0.01 | -0.35 | 0.12 | **4.01** |
|  | + |  |  |  |  | -0.04 | -0.12 | 0.92 | **3.28** |
| capsular biosynthesis protein PJ17\_07565 | - | 0.11 | 0.11 | 0.11 | 1 | 0.03 | -0.45 | 0.16 | **3.77**‡ |
|  | + |  |  |  |  | 0.01 | -0.54 | 0.05 | **3.24**‡ |
| *kpsF* arabinose-5-phosphate isomerase PJ17\_07570 | - | 1 | 1 | 1 | 0.97 | 0.02 | 0.01 | 0.15 | **4.55\*** |
|  | + |  |  |  |  | 0.01 | -0.05 | 0.06 | **1.58** |
| *kpsD* sugar ABC transporter substrate-binding protein PJ17\_07575 | - | 1 | 1 | 1 | 0.99 | -0.29 | -0.10 | 1.43 | **6.12**† |
|  | + |  |  |  |  | 0.02 | -0.02 | 0.07 | 0.23 |
| *kpsE* capsule biosynthesis protein PJ17\_07580 | - | 1 | 1 | 0.98 | 1 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| *kpsT* ABC transporter ATP-binding protein PJ17\_07585 | - | 1 | 1 | 1 | 0.98 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |
| *kpsM* capsule biosynthesis protein PJ17\_07590 | - | 1 | 1 | 0.97 | 0.97 | ND | ND | ND | ND |
|  | + |  |  |  |  | ND | ND | ND | ND |

Isolate 00-0949was used as the reference strain for iTRAQ analysis; NP – not present; ND – not detected/no data; hypothetical protein PJ17\_07480 and hypothetical protein PJ17\_07485 were actually a single protein with expression controlled by a homopolymeric tract, mis-annotated in the GenBank record used for proteomics analysis

Statistical analysis using Mann-Whitney test with Benjamini-Hochberg correction, 00-1597 vs the other three isolates: †*P* <0.05, §*P* <0.01, ‡*P* <0.001, \**P* <0.0001