|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| seq\_id | Cluster n° | Num. seqs | Prop.seqs | Species name | accession n° |
|  |  |  |  |  |  |
| 1109\_DAIUW | 53 | 648 | 2.3773% | *Mycobacterium chlorophenolicum* | X79292 |
| 1110\_HDX2W | 112 | 310 | 1.1373% | *Mycobacterium coloregonium* | AY624367 |
| 1108\_DIFS0 | 3 | 395 | 1.4491% | *Mycobacterium conceptionense* | GQ342298 |
| Cryfield\_EQKEM | 83 | 874 | 3.2064% | *Mycobacterium holsaticum* | AJ310467 |
| Cryfield\_ESRZU | 233 | 323 | 1.1850% | *Mycobacterium holsaticum* | AJ310467 |
| 1110\_HJ0NZ | 161 | 403 | 1.4785% | *Mycobacterium houstonense* | EU977810 |
| 1108\_C1LLA | 7 | 607 | 2.2269% | *Mycobacterium moriokaense* | AY859686 |
| Cryfield\_DZP48 | 189 | 348 | 1.2767% | *Mycobacterium moriokaense* | AY859686 |
| 1110\_HA1XO | 114 | 955 | 3.5036% | *Mycobacterium neglectum* | AJ580802 |
| 1108\_DOE1P | 0 | 641 | 2.3516% | *Mycobacterium neglectum* | AJ580802 |
| 1109\_EF3BL | 49 | 411 | 1.5078% | *Mycobacterium neglectum* | AJ580802 |
| 1109\_EPMC9 | 69 | 373 | 1.3684% | *Mycobacterium neglectum* | AJ580802 |
| 1108\_EFF8I | 10 | 462 | 1.6949% | *Mycobacterium pyrenivorans* | AJ431371 |
| 1108\_C22R2 | 14 | 528 | 1.9370% | *Mycobacterium sp. CNJ881 PL04* | DQ448781 |
| 1109\_EU91M | 62 | 574 | 2.1058% | *Mycobacterium sp. DCY42* | FJ605266 |
| Cryfield\_EQKTD | 104 | 377 | 1.3831% | *Mycobacterium sp. DSM 3803* | AY147261 |
| 1108\_ENQ3T | 16 | 350 | 1.2840% | *Mycobacterium sp. Ellin113* | AF408955 |
| 1109\_CZR5J | 54 | 512 | 1.8783% | *Mycobacterium sp. Ellin182* | AF409024 |
| Cryfield\_DKK1N | 149 | 1150 | 4.2189% | *Mycobacterium sp. GR-2009-164* | FJ555540 |
| Cryfield\_EW4KS | 103 | 488 | 1.7903% | *Mycobacterium sp. JS623* | AY162028 |
| 1109\_EW6MW | 47 | 477 | 1.7499% | *Mycobacterium sp. JS624* | AY162029 |
| 1110\_GUB6L | 116 | 293 | 1.0749% | *Mycobacterium sp. JS624* | AY162029 |
| Cryfield\_D27MP | 98 | 340 | 1.2473% | *Mycobacterium sp. KAR6* | EF451636 |
| 1108\_EGAQT | 45 | 606 | 2.2232% | *Mycobacterium sp. T126* | FJ719354 |
| 1109\_DZIGM | 78 | 371 | 1.3611% | *Mycobacterium tusciae* | AF058299 |
| 1108\_C942V | 4 | 896 | 3.2871% | *Mycobacterium vaccae* | AF544638 |
| 1108\_D3QDW | 6 | 333 | 1.2217% | *uncultured Mycobacteriaceae* | EF019277 |
| 1108\_EKDHQ | 24 | 1449 | 5.3159% | *uncultured Mycobacterium sp.* | FJ542897 |
| 1108\_DIHVQ | 34 | 277 | 1.0162% | *uncultured Mycobacterium sp* | FJ542897 |

**Table S1**.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| seq\_id | Cluster n° | Num. seqs | Prop. seqs | Species name | accession n° |
|  |  |  |  |  |  |
| 1111\_G8OR5 | Cluster 3 | 1519 | 13.8469% | *Mycobacterium aemonae* | FJ794352 |
| 1108\_DPW29 | Cluster 6 | 6 | 0.0547% | *Mycobacterium angelicum* | AM884328 |
| Cryf\_EFNM8 | Cluster 13 | 142 | 1.2944% | *Mycobacterium angelicum* | GQ153277 |
| 1110\_GJTYR | Cluster 24 | 5 | 0.0456% | *Mycobacterium asiaticum* | EF428556 |
| 1110\_HERCL | Cluster 19 | 10 | 0.0912% | *Mycobacterium asiaticum* | EF428556 |
| 1111\_F9Q43 | Cluster 25 | 14 | 0.1276% | *Mycobacterium asiaticum* | GQ153275 |
| Cryf\_DFKV1 | Cluster 17 | 1011 | 9.2160% | *Mycobacterium asiaticum* | AF480595 |
| 1110\_GRVIL | Cluster 31 | 1 | 0.0091% | *M. avium subsp. paratuberculosis* | GQ153278 |
| 1109\_EY4NC | Cluster 32 | 1 | 0.0091% | *Mycobacterium colombiense* | AM884328 |
| 1109\_DIX0Z | Cluster 27 | 2 | 0.0182% | *Mycobacterium colombiense* | GQ153275 |
| 1109\_EM8U7 | Cluster 28 | 2 | 0.0182% | *Mycobacterium colombiense* | AM884330 |
| 1109\_C33JP | Cluster 29 | 3 | 0.0273% | *Mycobacterium colombiense* | AY604571 |
| 1109\_DD2ZK | Cluster 10 | 25 | 0.2279% | *Mycobacterium colombiense* | AF480595 |
| 1109\_D41P7 | Cluster 9 | 145 | 1.3218% | *Mycobacterium colombiense* | X58890 |
| 1111\_HFZ0R | Cluster 4 | 4183 | 38.1313% | *Mycobacterium colombiense* | AM935142 |
| 1110\_FZ7QO | Cluster 30 | 2 | 0.0182% | *Mycobacterium gordonae* | GQ153278 |
| 1109\_EAUYM | Cluster 8 | 24 | 0.2188% | *Mycobacterium gordonae* | EF428556 |
| Cryf\_DOS3I | Cluster 15 | 29 | 0.2644% | *Mycobacterium gordonae* | AF480595 |
| 1110\_GR3E9 | Cluster 18 | 90 | 0.8204% | *Mycobacterium gordonae* | GQ153275 |
| Cryf\_C0F9Y | Cluster 12 | 162 | 1.4768% | *Mycobacterium gordonae* | GQ153275 |
| 1110\_FWVYG | Cluster 2 | 268 | 2.4430% | *Mycobacterium gordonae* | AY652958 |
| 1108\_D7EMJ | Cluster 5 | 516 | 4.7037% | *Mycobacterium gordonae* | X52934 |
| Cryf\_EV5CX | Cluster 22 | 650 | 5.9253% | *Mycobacterium gordonae* | GQ153275 |
| 1109\_D2ZA0 | Cluster 21 | 1 | 0.0091% | *Mycobacterium intracellulare* | DQ536404 |
| 1110\_F0IRM | Cluster 1 | 285 | 2.5980% | *Mycobacterium malmoense* | GQ153275 |
| Cryf\_ELYED | Cluster 16 | 734 | 6.6910% | *Mycobacterium malmoense* | EF428556 |
| Cryf\_DQP67 | Cluster 11 | 46 | 0.4193% | *Mycobacterium nebraskense* | EF428556 |
| 1110\_GJKFJ | Cluster 0 | 760 | 6.9280% | *Mycobacterium riyadhense* | AF480595 |
| 1108\_DMODA | Cluster 20 | 5 | 0.0456% | *Mycobacterium salmoniphilum* | DQ866767 |
| 1108\_D7NVM | Cluster 23 | 15 | 0.1367% | *Mycobacterium sp. 31181* | EU274642 |
| 1108\_DFJIQ | Cluster 7 | 302 | 2.7530% | *Mycobacterium sp. NLA000202017* | EF428556 |
| Cryf\_D2JVM | Cluster 14 | 11 | 0.1003% | *Mycobacterium tuberculosis* | EF428556 |
| 1111\_FP5ZG | Cluster 26 | 1 | 0.0091% | *uncultured Mycobacterium sp.* | GQ153275 |

**Table S2**.



**Table S3.**

 **Table S4.**