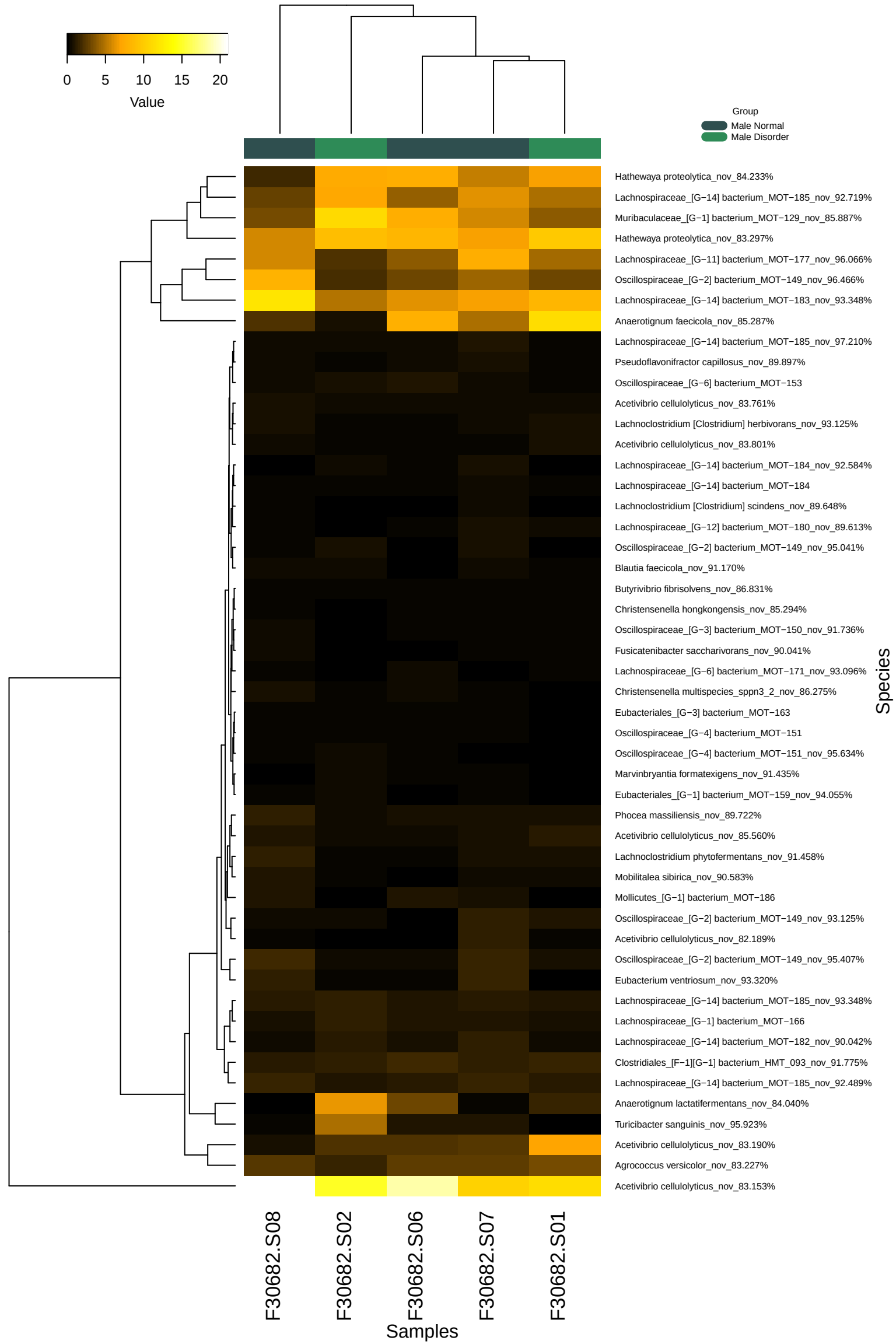
0
5
10
15
20
Value
Group
Male Normal
Male Disorder
Hathewaya proteolytica_nov_84.233%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_92.719%
Muribaculaceae_[G−1] bacterium_MOT−129_nov_85.887%
Hathewaya proteolytica_nov_83.297%
Lachnospiraceae_[G−11] bacterium_MOT−177_nov_96.066%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_96.466%
Lachnospiraceae_[G−14] bacterium_MOT−183_nov_93.348%
Anaerotignum faecicola_nov_85.287%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_97.210%
Pseudoflavonifractor capillosus_nov_89.897%
Oscillospiraceae_[G−6] bacterium_MOT−153
Acetivibrio cellulolyticus_nov_83.761%
Lachnoclostridium [Clostridium] herbivorans_nov_93.125%
Acetivibrio cellulolyticus_nov_83.801%
Lachnospiraceae_[G−14] bacterium_MOT−184_nov_92.584%
Lachnospiraceae_[G−14] bacterium_MOT−184
Lachnoclostridium [Clostridium] scindens_nov_89.648%
Lachnospiraceae_[G−12] bacterium_MOT−180_nov_89.613%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_95.041%
Blautia faecicola_nov_91.170%
Butyrivibrio fibrisolvens_nov_86.831%
Christensenella hongkongensis_nov_85.294%
Oscillospiraceae_[G−3] bacterium_MOT−150_nov_91.736%
Fusicatenibacter saccharivorans_nov_90.041%
Lachnospiraceae_[G−6] bacterium_MOT−171_nov_93.096%
Christensenella multispecies_sppn3_2_nov_86.275%
Eubacteriales_[G−3] bacterium_MOT−163
Oscillospiraceae_[G−4] bacterium_MOT−151
Oscillospiraceae_[G−4] bacterium_MOT−151_nov_95.634%
Marvinbryantia formatexigens_nov_91.435%
Eubacteriales_[G−1] bacterium_MOT−159_nov_94.055%
Phocea massiliensis_nov_89.722%
Acetivibrio cellulolyticus_nov_85.560%
Lachnoclostridium phytofermentans_nov_91.458%
Mobilitalea sibirica_nov_90.583%
Mollicutes_[G−1] bacterium_MOT−186
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_93.125%
Acetivibrio cellulolyticus_nov_82.189%
Oscillospiraceae_[G−2] bacterium_MOT−149_nov_95.407%
Eubacterium ventriosum_nov_93.320%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_93.348%
Lachnospiraceae_[G−1] bacterium_MOT−166
Lachnospiraceae_[G−14] bacterium_MOT−182_nov_90.042%
Clostridiales_[F−1][G−1] bacterium_HMT_093_nov_91.775%
Lachnospiraceae_[G−14] bacterium_MOT−185_nov_92.489%
Anaerotignum lactatifermentans_nov_84.040%
Turicibacter sanguinis_nov_95.923%
Acetivibrio cellulolyticus_nov_83.190%
Agrococcus versicolor_nov_83.227%
Acetivibrio cellulolyticus_nov_83.153%
Species
F30682.S08
F30682.S02
F30682.S06
F30682.S07
F30682.S01
Samples