**Supplemental Table 2**: OrthoMCL results: List of genes encoded in the genomes of *B. cereus* group isolates that can grow at 6°C

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster | Number of Genes | Number of Taxa | Presence Cold Growers | Absence Cold Growers | Presence Non-Cold Growers | Absence Non-Cold Growers | P-value *a* | FDR  *b* | Odds Ratio *c* | Products |
| Cluster\_5932 | 6 | 6 | 6 | 3 | 0 | 14 | 0.0008 | 0.0267 | Inf | 2'-5' RNA ligase |
| Cluster\_5930 | 6 | 6 | 6 | 3 | 0 | 14 | 0.0008 | 0.0267 | Inf | hypothetical protein |
| Cluster\_5931 | 6 | 6 | 6 | 3 | 0 | 14 | 0.0008 | 0.0267 | Inf | hypothetical protein |
| Cluster\_5933 | 6 | 6 | 6 | 3 | 0 | 14 | 0.0008 | 0.0267 | Inf | saccharopine dehydrogenase |
| Cluster\_5934 | 6 | 6 | 6 | 3 | 0 | 14 | 0.0008 | 0.0267 | Inf | transcriptional regulator |
| Cluster\_5661 | 7 | 7 | 7 | 2 | 0 | 14 | 0.0001 | 0.0113 | Inf | carboxymuconolactone decarboxylase family |
| Cluster\_5663 | 7 | 7 | 7 | 2 | 0 | 14 | 0.0001 | 0.0113 | Inf | hypothetical protein |
| Cluster\_5279 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | cold-shock protein |
| Cluster\_5269 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5277 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5301 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5374 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5375 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5376 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5377 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5378 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5380 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5381 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5384 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5388 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5391 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | hypothetical protein |
| Cluster\_5389 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | NUDIX hydrolase |
| Cluster\_5390 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | polysaccharide deacetylase |
| Cluster\_5382 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | RNA polymerase subunit sigma-24 |
| Cluster\_5379 | 8 | 8 | 7 | 2 | 1 | 13 | 0.0010 | 0.0316 | 34.39 | transcriptional regulator |
| Cluster\_4940 | 10 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | alpha/beta hydrolase |
| Cluster\_5086 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | cyclic pyranopterin monophosphate synthase |
| Cluster\_5189 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | hypothetical protein |
| Cluster\_5190 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | hypothetical protein |
| Cluster\_5194 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | hypothetical protein |
| Cluster\_5195 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | hypothetical protein |
| Cluster\_5193 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | phosphatase |
| Cluster\_5187 | 9 | 9 | 8 | 1 | 1 | 13 | 0.0002 | 0.0113 | 65.56 | recombinase RecQ |
| Cluster\_4939 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | acetyltransferase |
| Cluster\_4945 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | acetyltransferase |
| Cluster\_4972 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | acetyltransferase |
| Cluster\_4979 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | cold-shock protein |
| Cluster\_4978 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | copper oxidase |
| Cluster\_4967 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | cupin |
| Cluster\_4953 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | damage-inducible protein DinB |
| Cluster\_4968 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | dihydrolipoamide dehydrogenase |
| Cluster\_4925 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | DNA mismatch repair protein MutT |
| Cluster\_4922 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | flavoprotein |
| Cluster\_4937 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | glyoxalase |
| Cluster\_4966 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | GNAT family acetyltransferases |
| Cluster\_4934 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | group-specific protein |
| Cluster\_4955 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | group-specific protein |
| Cluster\_4938 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4942 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4950 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4951 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4962 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4970 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4971 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4974 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4975 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4976 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | hypothetical protein |
| Cluster\_4949 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | methyltransferase |
| Cluster\_4944 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | molybdopterin synthase sulfur carrier subunit |
| Cluster\_4936 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | N-acetylmuramoyl-L-alanine amidase |
| Cluster\_4918 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | PbsX family transcriptional regulator |
| Cluster\_4946 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | S-layer protein |
| Cluster\_4969 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | TetR family transcriptional regulator |
| Cluster\_4965 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | thiamine pyrophosphate-binding protein |
| Cluster\_4866 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | transcriptional regulator |
| Cluster\_4919 | 10 | 10 | 8 | 1 | 2 | 12 | 0.0007 | 0.0238 | 36.21 | Virginiamycin B lyase |
| Cluster\_4754 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | 6-phosphogluconolactonase |
| Cluster\_4736 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | ABC transporter permease |
| Cluster\_4779 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | ABC transporter permease |
| Cluster\_4701 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | acetyltransferase |
| Cluster\_4717 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | acetyltransferase |
| Cluster\_4730 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | acetyltransferase |
| Cluster\_4768 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | acetyltransferase |
| Cluster\_4790 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | acetyltransferase |
| Cluster\_4711 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | alkyl hydroperoxide reductase |
| Cluster\_4703 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | alpha/beta hydrolase |
| Cluster\_4745 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | aminoglycoside phosphotransferase |
| Cluster\_4794 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | aminoglycoside phosphotransferase |
| Cluster\_4741 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | antibiotic biosynthesis monooxygenase |
| Cluster\_4739 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | AraC family transcriptional regulator |
| Cluster\_4793 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | AraC family transcriptional regulator |
| Cluster\_4803 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | capsular biosynthesis protein |
| Cluster\_4749 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | cell surface protein |
| Cluster\_4764 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | cell wall anchor protein |
| Cluster\_4778 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | chromosome segregation protein |
| Cluster\_4759 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein ComF |
| Cluster\_4731 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein ComG |
| Cluster\_4732 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein ComG |
| Cluster\_4733 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein ComG |
| Cluster\_4734 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein ComG |
| Cluster\_4719 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | competence protein |
| Cluster\_4756 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | cytochrome C oxidase subunit II |
| Cluster\_4781 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | DNA mismatch repair protein MutT |
| Cluster\_4735 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | DNA recombination protein RecO |
| Cluster\_4769 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | glutamine amidotransferase |
| Cluster\_4726 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | glycosyl transferase |
| Cluster\_4727 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | glycosyl transferase |
| Cluster\_4700 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | glyoxalase |
| Cluster\_4699 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | GNAT family acetyltransferase |
| Cluster\_4725 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | histidine kinase |
| Cluster\_4805 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | histidine kinase |
| Cluster\_4806 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | histidine kinase |
| Cluster\_4729 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | histidine phosphatase family protein |
| Cluster\_4358 | 13 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4697 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4698 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4704 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4705 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4707 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4709 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4721 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4728 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4737 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4740 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4742 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4743 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4744 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4746 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4748 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4750 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4767 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4782 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4787 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4791 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4792 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4797 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4800 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4801 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4802 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4804 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4808 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4973 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_5006 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_5007 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_5010 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | hypothetical protein |
| Cluster\_4691 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | invasion protein |
| Cluster\_4799 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | invasion protein |
| Cluster\_4718 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | LacI family transcriptional regulator |
| Cluster\_4770 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | LysR family transcriptional regulator |
| Cluster\_4738 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | MepB |
| Cluster\_4788 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | methyltransferase |
| Cluster\_4796 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | PadR family transcriptional regulator |
| Cluster\_4761 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | peptidase G2 |
| Cluster\_4708 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | peptide transporter |
| Cluster\_4798 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | peptide-binding protein |
| Cluster\_4809 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | permease |
| Cluster\_4771 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | phage tail protein |
| Cluster\_4807 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | phosphoglycerol transferase |
| Cluster\_4722 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | preprotein translocase |
| Cluster\_4710 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | ROK family transcriptional regulator |
| Cluster\_5008 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | serine hydrolase |
| Cluster\_4963 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | serine/threonine protein kinase |
| Cluster\_4702 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | siderophore biosynthesis protein |
| Cluster\_4389 | 13 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | sporulation protein |
| Cluster\_4789 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | sporulation protein |
| Cluster\_4832 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | sugar ABC transporter ATP-binding protein |
| Cluster\_4692 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | teicoplanin resistance protein VanZ |
| Cluster\_4943 | 10 | 10 | 9 | 0 | 1 | 13 | 1.22E-05 | 0.0053 | Inf | transglycosylase |
| Cluster\_4367 | 13 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | translation initiation inhibitor |
| Cluster\_4706 | 11 | 11 | 9 | 0 | 2 | 12 | 6.73E-05 | 0.0053 | Inf | uridine kinase |
| Cluster\_4510 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | 3-phosphoshikimate 1-carboxyvinyltransferase |
| Cluster\_4518 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | 4-hydroxy-2-ketovalerate aldolase |
| Cluster\_4533 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | ABC transporter |
| Cluster\_4541 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | ABC transporter |
| Cluster\_4523 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | alkaline phosphatase |
| Cluster\_4449 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | alpha/beta hydrolase |
| Cluster\_4507 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | betaine-aldehyde dehydrogenase |
| Cluster\_4457 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | damage-inducible protein DinB |
| Cluster\_4511 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | DNA helicase |
| Cluster\_4450 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | DNA-binding response regulator |
| Cluster\_4529 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | epimerase |
| Cluster\_4506 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | Fis family transcriptional regulator |
| Cluster\_4526 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | GntR family transcriptional regulator |
| Cluster\_4432 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | hypothetical protein |
| Cluster\_4505 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | hypothetical protein |
| Cluster\_4509 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | hypothetical protein |
| Cluster\_4522 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | hypothetical protein |
| Cluster\_4537 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | hypothetical protein |
| Cluster\_4530 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | MBL fold metallo-hydrolase |
| Cluster\_4527 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | MFS transporter |
| Cluster\_4536 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | MFS transporter |
| Cluster\_4539 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | MFS transporter |
| Cluster\_4532 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | multidrug ABC transporter ATP-binding protein |
| Cluster\_4508 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | putrescine aminotransferase |
| Cluster\_4504 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | Putrescine importer PuuP |
| Cluster\_4535 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | short-chain dehydrogenase |
| Cluster\_4500 | 12 | 12 | 9 | 0 | 3 | 11 | 0.0003 | 0.0126 | Inf | sporulation protein |
| Cluster\_4370 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | ABC transporter ATP-binding protein |
| Cluster\_4377 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | amino acid permease |
| Cluster\_4336 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | cyclic nucleotide-binding protein |
| Cluster\_4407 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | cysteine ABC transporter permease |
| Cluster\_4213 | 15 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0412 | Inf | DUF3948 domain-containing protein |
| Cluster\_4379 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | Fe-S oxidoreductase |
| Cluster\_4380 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | hydroxyglutarate oxidase |
| Cluster\_4345 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | hypothetical protein |
| Cluster\_4375 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | hypothetical protein |
| Cluster\_4376 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | hypothetical protein |
| Cluster\_4388 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | hypothetical protein |
| Cluster\_4378 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | lactate utilization protein C |
| Cluster\_4363 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | NADPH:quinone oxidoreductase |
| Cluster\_4382 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | ornithine cyclodeaminase |
| Cluster\_4381 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | protein CsiD |
| Cluster\_4409 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | ribonucleotide-diphosphate reductase subunit |
| Cluster\_4371 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | spore coat protein |
| Cluster\_4359 | 13 | 13 | 9 | 0 | 4 | 10 | 0.0016 | 0.0411 | Inf | stage II sporulation protein P |

*a* P-values from two-sided Fisher's Exact Tests

*b* P-values were corrected using the False Discovery Rate (FDR) approach

*c* Odds ratios marked as INF (Infinite) are a result of dividing by zero