

CLUSTAL O(1.2.4) multiple sequence alignment

```

AY724739.1 ----- 0
AY959097.1 TTCGCCCTTAGAGTTTGGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGC 60
OTU5 ----- 0

AY724739.1 ----- 0
AY959097.1 AAGTCGAACGAAGTGCTACGACGGAAGTTTTTCGGACGGAAGATGTAGTTACTTAGTGGCG 120
OTU5 ----- 0

AY724739.1 ----- 0
AY959097.1 GACGGGTGAGTAACGCGTGGGGAACCTGCCCTGTACCGGGGGATAGCAGCCGGAACGGC 180
OTU5 ----- 0

AY724739.1 ----- 0
AY959097.1 TGATAATACCGCATAAGCGCACGAATGTCGCATGACATGGTGTGAAAACTCCGGTGGTA 240
OTU5 ----- 0

AY724739.1 ----- 0
AY959097.1 TAGGATGGACCCGCGTCTGATTAGCCGGTTGGTGGGGTAAAAGCCTACCAAAGCGAAGAT 300
OTU5 ----- 0

AY724739.1 ----- 0
AY959097.1 CAGTAGCCGAGTTGAGAGACTGACCGGCCACATTGGGACTGAGACACGGCCCAGACTCCT 360
OTU5 ----- 0

AY724739.1 -----TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC 46
AY959097.1 ACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC 420
OTU5 -----TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGC 46
*****

AY724739.1 GTGAGCGAAGAAGTATTTTCGGTATGTAAAGCTCTATCAGAAGGGAAGAAAATGACGGTAC 106
AY959097.1 GTGAGCGAAGAAGTATTTTCGGTATGTAAAGCTCTATCAGAAGGGAAGAAAATGACGGTAC 480
OTU5 GTGAGCGAAGAAGTATTTTCGGTATGTAAAGCTCTATCAGAAGGGAAGAAAATGACGGTAC- 105
*****

AY724739.1 CTTACTAAGAAGCTCCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGAGCAAG 166
AY959097.1 CTTACTAAGAAGCTCCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGAGCAAG 540
OTU5 ----- 105

AY724739.1 CGTTATCCGGATTTACTGGGTGTAAAGGGAGTGTAGGCGGCACTATAAGTCTGATGTGAA 226
AY959097.1 CGTTATCCGGATTTACTGGGTGTAAAGGGAGTGTAGGCGGCACTATAAGTCTGATGTGAA 600
OTU5 ----- 105

AY724739.1 AACCTAAGGCTTAACCATAGGATTGCATTGGAAACTGTAGAGCTGGAGTATCGGAGAGGC 286
AY959097.1 AACCTAAGGCTTAACCATAGGATTGCATTGGAAACTGTAGAGCTGGAGTATCGGAGAGGT 660
OTU5 ----- 105

AY724739.1 AAGCGGAATTCCTGGTGTAGTGGTGAATACGTAGATATCAGGAAGAACATCGGTGGCGA 346
AY959097.1 AAGCGGAATTCCTGGTGTAGTGGTGAATACGTAGATATCAGGAAGAACATCGGTGGCGA 720
OTU5 ----- 105

```

AY724739.1	AGGCGGCTTGCTGGACGATAACTGACGCTAAGGCTCGAAAGCGTGGGAAGCGAACAGGAT	406
AY959097.1	AGGCGGCTTGCTGGACGATAACTGACGCTAAGGCTCGAAAGCGTGGGAAGCGAACAGGAT	780
OTU5	-----	105
AY724739.1	TAGATACCCTGGTAGTCCACGCTGTAAACGATGAACACTAGGTGTTGGGAGGCTAAGCCT	466
AY959097.1	TAGATACCCTGGTAGTCCACGCTGTAAACGATGAACACTAGGTGTTGGGAGGCTAAGCCT	840
OTU5	-----	105
AY724739.1	TTCAGTGCCGCAGCAAACGCAATAAGTGTTCACCTGGGGAGTACGTTGCAAGAATGAA	526
AY959097.1	TTCAGTGCCGCAGCAAACGCAATAAGTGTTCACCTGGGGAGTACGTTGCAAGAATGAA	900
OTU5	-----	105
AY724739.1	ACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCA	586
AY959097.1	ACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCA	960
OTU5	-----	105
AY724739.1	ACGCGAAGAACCTTACCAAGTCTTGACATCCCTGTGACAGTATATGTAATGTATATTTTC	646
AY959097.1	ACGCGAAGAACCTTACCAAGTCTTGACATCCCTGTGACAGTATATGTAATGTATATTTTC	1020
OTU5	-----	105
AY724739.1	TACGGAACACAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTGTCGTGAGATGTTGG	706
AY959097.1	TACGGAACACAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTGTCGTGAGATGTTGG	1080
OTU5	-----	105
AY724739.1	GTTAAGTCCCGCAACGAGCGCAACCCTTGTACTTAGTAGCCAGCATTAAAGGTGGGCACTC	766
AY959097.1	GTTAAGTCCCGCAACGAGCGCAACCCTTGTACTTAGTAGCCAGCATTAAAGGTGGGCACTC	1140
OTU5	-----	105
AY724739.1	TAAGTAGACTGCCGGGGTGAACCCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCC	826
AY959097.1	TAAGTAGACTGCCGGGGTGAACCCGGAGGAAGGTGGGGACGACGTCAAATCATCATGCCC	1200
OTU5	-----	105
AY724739.1	CTTATGACTTGGGCTACACACGTGCTACAATGGCGTGAACAGAGGGAAGCGAAGGAGCGA	886
AY959097.1	CTTATGGCTTGGGCTACACACGTGCTACAATGGCGTGAACAGAGGGAAGCGAAGGAGCGA	1260
OTU5	-----	105
AY724739.1	TCCGGAGCAAATCTCATAAAGCACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACTGCA	946
AY959097.1	TCCGGAGCAAATCTCATAAAGCACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACTGCA	1320
OTU5	-----	105
AY724739.1	CGAAGCTGGAATCGCTAGTAATCGCAGATCATCATGCTGCGGTGAATACGTTCCCGGGTC	1006
AY959097.1	CGAAGCTGGAATCGCTAGTAATCGCAGATCATCATGCTGCGGTGAATACGTTCCCGGGTC	1380
OTU5	-----	105
AY724739.1	T-----	1007
AY959097.1	TTGTACACACCCCGTCCACACCATGGGAGTCTGGAATGCCCGAAGTCAGTGGCCAAACC	1440
OTU5	-----	105
AY724739.1	-----	1007

AY959097.1
OTU5

GAAAGGATGGAGCTGCCGAAGGCAGGCCCGGTAAGTGGGTGAA 1483
----- 105