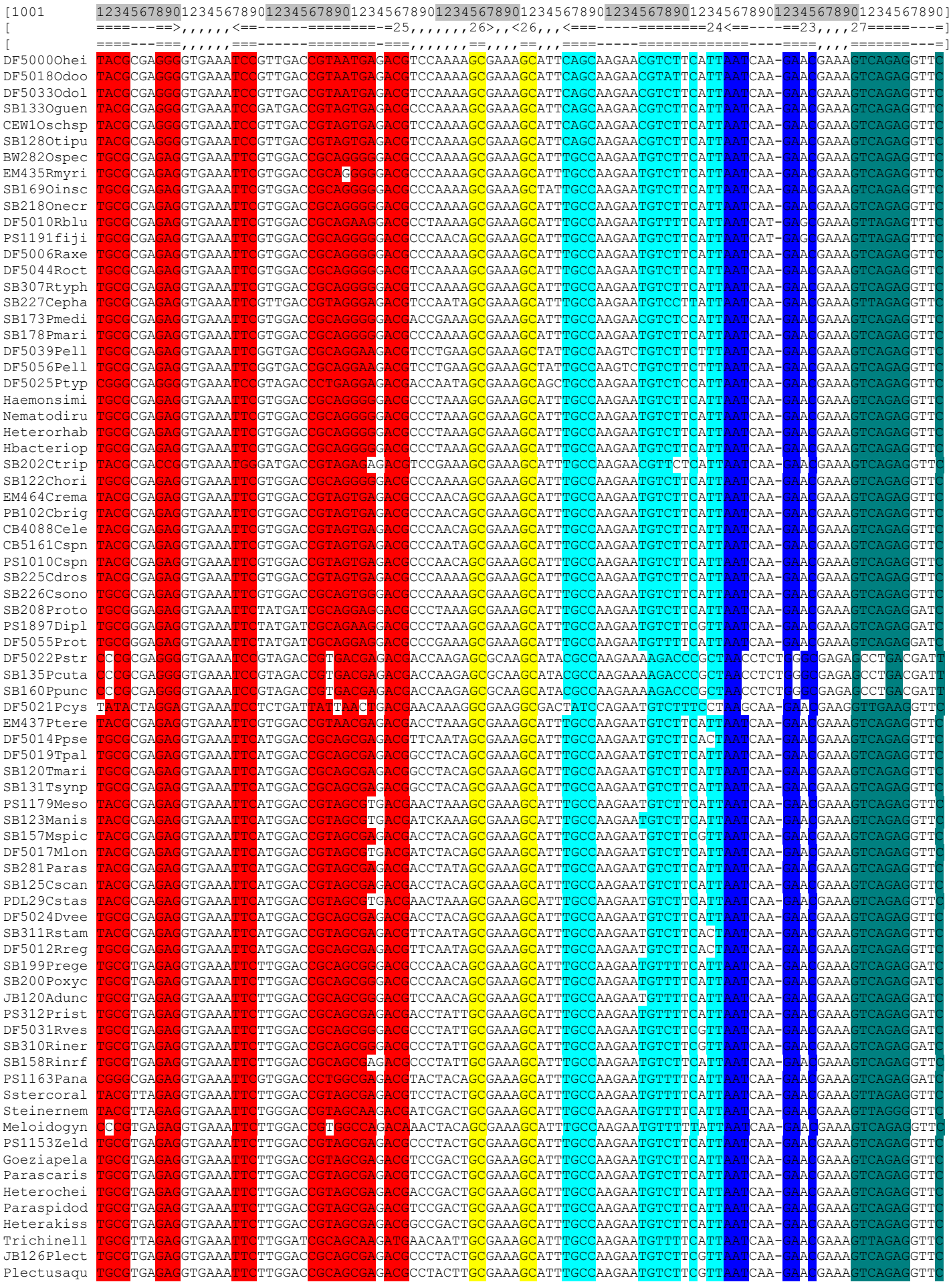
PARTIAL 18S ribosomal RNA gene alignment

Taxa:
DF5000Ohei = DF5000 Oscheius sp. (NCBI accession no. AF082995) (1)
DF5018Odoo = DF5018 Oscheius dolichuroides (NCBI accession no. AF082998) (1)
DF5033Odol = DF5033 Oscheius dolichura (NCBI accession no. _____) (1) *new*
SB133Oguen = SB133 Oscheius guentheri (NCBI accession no. _____) (1) *new*
CEW1Oschsp = CEW1 Oscheius sp. (NCBI accession no. _____) (1) *new* (same sp. as acc. U81587 PS1131 (syn. of BW29
SB128Otipu = SB128 Oscheius tipulae (NCBI accession no. _____) (1) *new*
BW282Ospec = BW282 Oscheius sp. (myriophila?) (NCBI accession no. AF082994) (1)
EM435Rmyri = EM435 Oscheius myriophila (NCBI accession no. U13936) (2)
SB169Oinsc = SB169 Oscheius insectivora (NCBI accession no. AF083019) (1)
SB218Onecr = SB218 Oscheius necromena (NCBI accession no. _____) (1) *new*
DF5031Rves = DF5031 Rhabditis vespillonis (NCBI accession no. _____) (1) *new*
DF5010Rblu = DF5010 Rhabditis blumi (NCBI accession no. U13935) (2)
PS1191fiji = PS1191 Rhabditis sp. (NCBI accession no. AF083008) (1)
DF5006Raxe = DF5006 Rhabditella axei (NCBI accession no. U13934) (2)
DF5044Roct = DF5044 Rhabditella sp. (cf. octopleura) (NCBI accession no. AF083000) (1)
SB307Rtyph = SB307 Rhabditella typhae (NCBI accession no. _____) (1) *new*
SB227Cepha = SB227 Cephaloboides sp. (NCBI accession no. AF083027) (1)
SB173Pmedi = SB173 Pellioditis mediterranea (NCBI accession no. AF083020) (1)
SB178Pmari = SB178 Pellioditis marina (NCBI accession no. AF083021) (1)
DF5039Pell = DF5039 Pellioditis sp. (cf. neopapillosa) (NCBI accession no. _____) (1) *new*
DF5056Pell = DF5056 Pellioditis sp. (cf. neopapillosa) (NCBI accession no. _____) (1) *new* (same sp. as DF5039
DF5025Ptyp = DF5025 Pellioditis typica (NCBI accession no. U13933) (2, CORRECTED)
Haemonsimi = Haemonchus similis (NCBI accession no. L04152) (?)
Nematodiru = Nematodirus battus (NCBI accession no. U01230) (?)
Heterorhab = Heterorhabditis hepialus (NCBI accession no. AF083004) (1)
Hbacteriop = Heterorhabditis bacteriophora (NCBI accession no. AF036593) (?)
SB202Ctrip = SB202 Cruznema tripartitum (NCBI accession no. _____) (1) *new*
SB122Chori = SB122 Choriorhabditis dudichii (NCBI accession no. AF083012) (1)
EM464Crema = EM464 Caenorhabditis remanei vulgaris (NCBI accession no. U13931) (2)
PB102Cbrig = PB102 Caenorhabditis briggsae (NCBI accession no. U13929) (2)
CB4088Cele = N2 Caenorhabditis elegans (NCBI accession no. X03680) (?)
CB5161Cspn = CB5161 Caenorhabditis sp. (NCBI accession no. U13930) (2)
PS1010Cspn = PS1010 Caenorhabditis sp. (NCBI accession no. AF083006) (1)
SB225Cdros = SB225 Caenorhabditis drosophilae (NCBI accession no. AF083025) (1)
SB226Csono = SB226 Caenorhabditis sonorae (NCBI accession no. AF083026) (1)
SB208Proto = SB208 Protorhabditis sp. (NCBI accession no. AF083024) (1)
PS1897Dipl = PS1897 Diploscapter sp. (NCBI accession no. AF083009) (1)
DF5055Prot = DF5055 Protorhabditis sp. (NCBI accession no. AF083001) (1)
DF5022Pstr = DF5022 Pelodera strongyloides dermatitica (NCBI accession no. U13932) (2, CORRECTED)
SB135Pcuta = SB135 Pelodera cutanea (NCBI accession no. _____) (1) *new*
SB160Ppunc = SB160 Pelodera punctata (NCBI accession no. AF083018) (1)
DF5021Pcys = DF5021 Pelodera cystilarva (NCBI accession no. _____) (1) *new*
EM437Ptere = EM437 Pelodera teres (NCBI accession no. AF083002) (1)
DF5014Ppse = DF5014 Pelodera pseudoteres (NCBI accession no. _____) (1) *new*
DF5019Tpal = DF5019 Teratorhabditis palmarum (NCBI accession no. U13937) (2, CORRECTED)
SB120Tmari = SB120 Teratorhabditis mariannae (NCBI accession no. _____) (1) *new*
SB131Tsynp = SB131 Teratorhabditis synpapillata (NCBI accession no. AF083015) (1)
PS1179Meso = PS1179 Mesorhabditis sp. (NCBI accession no. U73452) (?)
SB123Manis = SB123 Mesorhabditis anisomorpha (NCBI accession no. AF083013) (1)
SB157Mspic = SB157 Mesorhabditis spiculigera (NCBI accession no. AF083016) (1)
DF5017Mlon = DF5017 Mesorhabditis longespiculosa (NCBI accession no. _____) (1) *new*
SB281Paras = SB281 Parasitorhabditis sp. (NCBI accession no. AF083028) (1)
SB125Cscan = SB125 Crustorhabditis scanica (NCBI accession no. AF083014) (1)
PDL29Cstas = PDL29 Crustorhabditis sp. (cf. stasileonovi) (NCBI accession no. _____?_____) (1) *new*
DF5024Dvee = DF5024 Distolabrellus veechi (NCBI accession no. AF082999) (1)
SB311Rstam = SB311 Rhabditoides stammeri (NCBI accession no. _____) (1) *new*
DF5012Rreg = DF5012 Rhabditoides regina (NCBI accession no. AF082997) (1)
SB199Prege = SB199 Poikilolaimus regenfussi (NCBI accession no. AF083022) (1)
SB200Poxyc = SB200 Poikilolaimus oxycerca (NCBI accession no. AF083023) (1)
JB120Adunc = JB120 Aduncospiculum halicti (NCBI accession no. U61759) (?)
PS312Prist = PS312 Pristionchus pacificus (NCBI accession no. AF083010) (1)
SB310Riner = SB310 Rhabditoides inermis (NCBI accession no. AF082996) (1)
SB158Rinrf = SB158 Rhabditoides inermiformis (NCBI accession no. AF083017) (1)
PS1163Pana = PS1163 Panagrellus redivivus (NCBI accession no. AF083007) (1)
Sstercoral = Strongyloides stercoralis (NCBI accession no. M84229) (?)
Steinernem = Steinernema carpocapsae (NCBI accession no.AF036604) (?)
Meloidogyn = Meloidogyne arenaria (NCBI accession no. U42342) (?)
PS1153Zeld = PS1153 Zeldia punctata (NCBI accession no. U61760) (?)
Goeziapela = Goezia pelagia (NCBI accession no. U94372) (?)
Parascaris = Parascaris equorum (NCBI accession no. U94378) (?)
Heterochei = Heterocheilus tunicatus (NCBI accession no. U94373) (?)
Paraspidod = Paraspidodera sp. (sample 21303) (NCBI accession no. AF083005) (1)
Heterakiss = Heterakis sp. (sample 14690) (NCBI accession no. AF083003) (1)
Trichinell = Trichinella spiralis (NCBI accession no. U60231) (?)
JB126Plect = JB126 Plectus acuminatus (NCBI accession no. U61761) (?)
Plectusaqu = Plectus aquatilis (NCBI accession no. AF036602) (?)

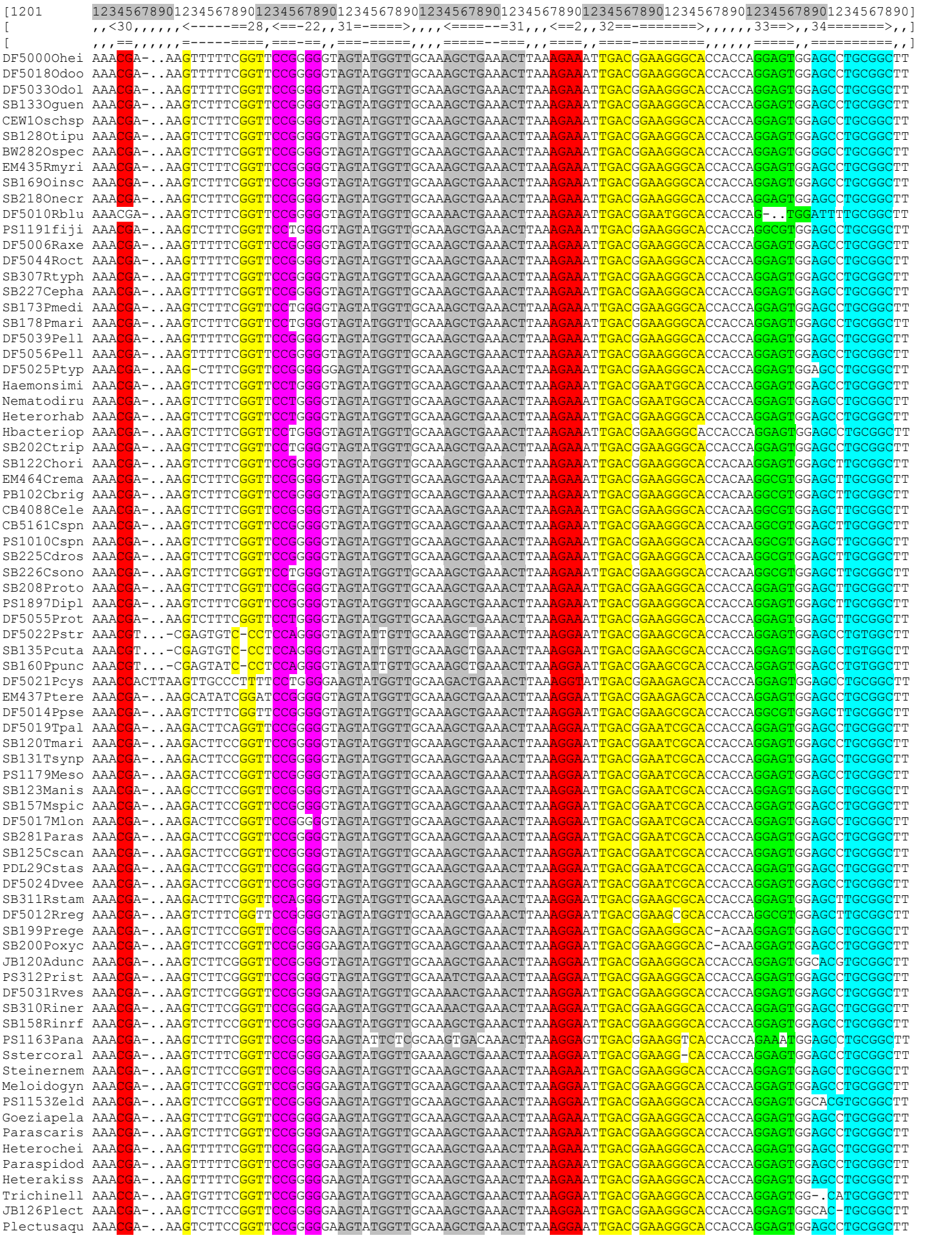
References:
(1) Fitch et al., in prep.
(2) Fitch, D. H. A., Bugaj-Gaweda, B., and Emmons, S. W. 1995. 18S Ribosomal RNA gene phylogeny for some Rhabditid related to *Caenorhabditis*. Mol. Biol. Evol. 12(2):346-358.

Notes:
1. PRIMER sequences are shown in upper case if on the sense strand or in lower case if on the antisense strand.
2. Header for modeled SECONDARY STRUCTURES: pairs of stems are numbered with equal signs (=) designating columns in which one or more of the derived rRNA sequences may be involved in base-pairing and with hyphens (-) designating columns in which no sequence is involved in base-pairing (though the position is within a stem structure); numbers and carats (<, >) designate the termini of base pairing; commas (,) designate columns not contained in "stem" structures. The only exception is for stem E23-1; the structure of this stem is very different in *Pellioditis typica* from all the other species and is ignored in designating the columns involved in base-pairing. Because some columns may include bases that are involved in pairing in only one or a few taxa, we have been very conservative in our hypotheses about which positions are evolving independently.
3. Bases predicted to be involved in base-pairing in the rRNA of each species are HIGHLIGHTED.
4. MISSING DATA at the beginning and end of any sequence are designated with periods (.).
5. Single nucleotide INDELS (alignment gaps) are each designated with one hyphen (-); indels covering more than one alignment position (column) are each designated with one hyphen (-) at a particular position and with other positions filled with periods (.). Hyphens are only aligned if indels in different species are of the same length and cover the same positions (i.e., hyphens designate indels that are proposed to be "homologous"). This system of indel coding allows alignment gaps to be scored as a single change, regardless of length.

Note! This is only a partial alignment for demonstration purposes only. It is not intended yet to be used for distribution. These data are still unpublished. Please only use with permission of David Fitch.


[1001 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890]
DF5000Ohei
DF5018Odoo
DF5033Odol
SB133Oguen
CEW1Oschsp
SB128Otipu
BW282Ospec
EM435Rmyri
SB169Oinsc
SB218Onecr
DF5010Rblu
PS1191fiji
DF5006Raxe
DF5044Roct
SB307Rtyph
SB227Cepha
SB173Pmedi
SB178Pmari
DF5039Pell
DF5056Pell
DF5025Ptyp
Haemonsimi
Nematodiru
Heterorhab
Hbacteriop
SB202Ctrip
SB122Chori
EM464Crema
PB102Cbrig
CB4088Cele
CB5161Cspn
PS1010Cspn
SB225Cdros
SB226Csono
SB208Proto
PS1897Dipl
DF5055Prot
DF5022Pstr
SB135Pcuta
SB160Ppunc
DF5021Pcys
EM437Ptere
DF5014Ppse
DF5019Tpal
SB120Tmari
SB131Tsynp
PS1179Meso
SB123Manis
SB157Mspic
DF5017Mlon
SB281Paras
SB125Cscan
PDL29Cstas
DF5024Dvee
SB311Rstam
DF5012Rreg
SB199Prege
SB200Poxyc
JB120Adunc
PS312Prist
DF5031Rves
SB310Riner
SB158Rinrf
PS1163Pana
Sstercoral
Steinernem
Meloidogyn
PS1153Zeld
Goeziapela
Parascaris
Heterochei
Paraspidod
Heterakiss
Trichinell
JB126Plect
Plectusaqu


[1101 1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890]
[---===>,,,,,,,,,<======-======27,,,,,,,,,28=-->,29==-============>,,,,,,,<==========-===-=29,,,30>,]
[---====,,,,,,,,,===============,,,,,,,,,===--=,====-============,,,,,,,==========-===-===,,,===,]
DF5000Ohei GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATT-.....TTGCCTTGTCG-GGGAGCTCGTC-GG
DF5018Odoo GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATT-.....TTGCCTTGTCG-AGGAGCTTGTC-GG
DF5033Odol GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATT-.....TTGCCTTGTCG-GGGAGCTCGTC-GG
SB133Oguen GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCTGGTGG-GGTAAT-.....TTGCCTTGCCA-GGGAGCTTTCC-GG
CEW1Oschsp GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTAAT-.....TTGCCTTGTCG-GGGAGCTTACC-GG
SB128Otipu GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTAAT-.....TTGCCTTGTCG-GGGAGCTTACC-GG
BW282Ospec GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGGTGG-GGTTAT-.....TCGCCTCGCCG-GGGAGCTTCCC-GG
EM435Rmyri GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGGTGG-GGTTAT-.....TCGCCTCGCCG-GGGAGCTTCCC-GG
SB169Oinsc GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGGTGG-GCTTAT-.....TCGGCTCGCCG-GGGAGCTTCCC-GG
SB218Onecr GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGGTGG-GGTTAT-.....TCGCCTCGCCG-GGGAGCTTCCC-GG
DF5010Rblu GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCAATGG-GATGTT-.....AAGTCTCGTTG-GGGAGCT.-.....
PS1191fiji GAAGGCGATTAGATACCGCCCTAGTTCTAACCGTAAACTATGCCATCTAGCGATCCAACGG-GATATTT-....ATGTCTCGGAG-GGGAGCTTCCC-GG
DF5006Raxe GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATAG-GGTATTC-....ATGCCTTG----GGGAGCTTCCC-GG
DF5044Roct GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATAG-GGTATTC-....ATGCCTTGTCG-GGGAGCTTCCC-GG
SB307Rtyph GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTAGCGATCCGATAG-GGTTATTC-....AGCCTTGTCG-GGGAGCTTCCC-GG
SB227Cepha GAAGGCGATTAGATACCGCCCTAGTTCTAACCGTAAACTATGCCATCTAGCGATCCGAAGA-GGTATTT-.....ATGTCTCGTCG-GGGAGCTTCCC-GG
SB173Pmedi GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGCATTT-....CTGCCTCGTCG-GGGAGCTTCCC-GG
SB178Pmari GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGCATCT-....TTGCCTCGTCG-GGGAGCTTCCC-GG
DF5039Pell GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATTCGGAGA-GGTAATTTA-..TTGCTTTTCCG-AGGAGCTTCCC-GG
DF5056Pell GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATTCGGAGA-GGTAATTTA-..TTGCTTTTCCG-AGGAGCTTCCC-GG
DF5025Ptyp GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATACCAGCTCATGACTAGTTGG-GATGTAA-....TGTCCACAACG-GGTCGC-CCCC-GG
Haemonsimi GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATAG-....TTGCCTTGTCG-AGGAGCTTCCC-GG
Nematodiru GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATAT-....TTGCCTTGTCG-AGGAGCTTCCC-GG
Heterorhab GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCAATGG-GGTATTG-....TAGCCTTGTTG-GGGAGCTTCCC-GG
Hbacteriop GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCAATGG-GGTATTG-....TAGCCTTGTTG-GGGAGCTTCCC-GG
SB202Ctrip GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCTGATTG-GGTATTT-....TTGCCTGATCA-GGGAGCTTCCC-GG
SB122Chori GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGATGG-GGTATRT-....ATACCTTGTCG-GGGAGTTTCCC-GG
EM464Crema GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTCGCGATTCGG-AG-GGTTT-.....TTGCCCTGCCG-AGGAGCTATCC-GG
PB102Cbrig GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTCGCGATTCGG-AG-GGTTT-.....TTGCCCTGCCG-AGGAGCTATCC-GG
CB4088Cele GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTCGCGATTCGG-AG-GGTTT-.....TTGCCCTGCCG-AGGAGCTATCC-GG
CB5161Cspn GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTCGCGATTCGG-AG-GGTTT-.....TTGCCCTGCCG-AGGAGCTATCC-GG
PS1010Cspn GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATGCCATCTCGCGATTCGG-AG-GGTTT-.....TTGCCTTGCCG-AGGAGCTATCC-GG
SB225Cdros GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCAGCTCGCGATTCGG-AA-GGTTT-.....TTGCCTTACCG-AGGAGCTATCC-GG
SB226Csono GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGATCCGGTAG-GGTATT-.....TCGCCTTGCCG-GGGAGCTTCCC-GG
SB208Proto GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATACCATCCAGCGATCCGATAG-GGTCATTC-...TAGCCTTGTCG-GGGAGCTTCCC-GG
PS1897Dipl GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGATAG-GGTCTATC-...TAGCCTTGTCG-GGGAGCTTCCC-GG
DF5055Prot GAAGGCGATTAGATACCGCCCTAGTTCTGACTGTAAACGATACCATCTAGCGATCCGATAG-GGTGTT-.....ATGCCTTGTCG-GGGAGCTTCCC-GG
DF5022Pstr AAAGACGATTAGATACCGTCGTAGTTTTATCTGTGAACGATGGGAACTGACTGAAGTTTTATGCGAAGTA-...CTACAAGAGTT-GTTTGAATTCCTGG
SB135Pcuta AAAGACGATTAGATACCGTCGTAGTTTTATCTGTGAACGATGGGAACTGACTGAAGTTTTATGCGAAGTA-...CTACAAGAGTT-GTTTGAATTCCTGG
SB160Ppunc AAAGACGATTAGATACCGTCGTAGTTTTATCTGTGAACGATGGGAACTGACTGAAGTTTTATGCGAAGTA-...CTACAAGAGTT-GTTTGAATTCCTGG
DF5021Pcys GAAGGTGATTAGATACCGCCGTAGTTTCAACGTTAAACGATGTTTCCTAATAGATCGTTCCTCGTGA-.....ATGTCTAACGA-AAGATGGTACAGGG
EM437Ptere GAAGGCGATTAGATACCGCCATAGTTCTGACCTTAAACAATACCTGCTGGCGAACCGATGGTGGCGAAAG-...CTGCCTTTTCG-GGGAGCACCCC-GG
DF5014Ppse GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATTCCATCTAGCGATCCGACGGCGGTTTTT-....CTGCCTTGTCG-GGGAGCTTCCC-GG
DF5019Tpal GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGCGGCGGTATTT-....TCGCCTCGCCG-GGGAGCTTTCC-GG
SB120Tmari GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGTGGTGGTATTT-....TTGCCTCGCCG-GGGAGCTTTCC-GG
SB131Tsynp GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGCGGCGGTATTT-....TTGCCTCGCCG-GGGAGCTTTCC-GG
PS1179Meso GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGTGGTGGTTTTA-....CCGCCTTGCCG-GGGAGCTTCCC-GG
SB123Manis GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGCGGCGGTWMTAA-...CCGCCTCGCCG-GGGAGCTTCCC-GG
SB157Mspic GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGCGGTGGTATTA-....TTGCCTCGCCG-GGGAGCTTCCC-GG
DF5017Mlon GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGTGGCGGTATTA-....CCGCCTCGCCG-GGGAGCTTCCC-GG
SB281Paras GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGTGGTGGTGATC-....TTGCCTCATCG-GGGAGCTTCCC-GG
SB125Cscan GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATTCGGTAGTGGTTTTA-....TATCCTTACCG-AGGAGCTTCCC-GG
PDL29Cstas GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGGTGGTGGTAATA-....CCGCCTCGCCG-GGGAGCTTCCC-GG
DF5024Dvee GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGATGGCGGTATTA-....CCGCCTCGTCG-GGGAGCTTCCC-GG
SB311Rstam GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATACCATCTAGCGATCCGACGGAGGTCTTG-....TTGCCTTGTCG-GGGAGCTTCCC-GG
DF5012Rreg GAAGGCGATTAGATACCGCCGTAGTTCTGACCGTAAACGATTCCATCTAGCGATCCGACGGCGGTTTTT-....CTGCCTTGTCG-GGGAGCTTCCC-GG
SB199Prege GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGATCCGCCGGTGGTAATT-....ACGCCCTGGCG-GGGAGCTTCCC-GG
SB200Poxyc GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGATCCGCCGGTGGTAATT-....ACGCCCTGGCG-GGGAGCTTCCC-GG
JB120Adunc GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAATGATGCCATCTAGCGATCAGGAGTTGGTTGTT-....TCACCATTCCTCGGGAGCTTCCC-GG
PS312Prist GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCAACTAGCGATCAGGTGGTGGTAGTT-....TAGCCCTGCCT-GGGAGCTTCTC-GG
DF5031Rves GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCAACTCGCGATCAGATGGTGCCATA-.....TCGGCCCGTCT-GGGAGCGTCCC-GG
SB310Riner GAAGGCGATTAGATACCGCCCTAGTTCTGACCGTAAACTATGCCAACTCGCGATCAGATGGTGCCATA-.....TCGGCCCGTCT-GGGAGCGTCCC-GG
SB158Rinrf GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATGCCAACTAGCGATCCGGCAGTGGTAATT-....ACGCCCTGTCG-GGGAGCTTCCC-GG
PS1163Pana GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACTATGCCATCTAGCGAGTCGCATGCGGATTTTCTTATTCGCCTCTGTG-ACGAGCTTTCC-GG
Sstercoral GAAGGCGATCAGATACCGCCCTAGTTCTAACCGTAAACTATGCCTACTAGATGTATGAATTATTAGTT-.....ATAATTATTTA-TGCATCTTCTC-GG
Steinernem GAAGGCGATCAGATACCGCCCTAGTTCTAACCCTAAACTCTGCCAACTAGCGATTCGTCGATGGTAATT-....TTGCCTTGATG-AGGAGCTAATC-GG
Meloidogyn GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATGCCAACTAGCGATCCGCCGATGGAAATTATA-.TTGCCTTGGTG-GGGAGCTTCCC-GG
PS1153Zeld GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATGCCAACTAGCGATCCGCCGGTGGATTTT-....TAGCCCTGGTG-GGTAGCT-CCC-GG
Goeziapela GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTCCGTCGGCGGTAAAT-....ACGCCTTGACG-GGCAGCTTCCC-GG
Parascaris GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTCCGTCGGCGGTAAAT-....ATGCCTTGACG-GGTAGCTTCCC-GG
Heterochei GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTCCGTCGGCGGTAAAT-....ACGCCTTGACG-GGCAGCTTCCC-GG
Paraspidod GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTCCGTCGGCGGTAAAT-....TTGCCTTGACG-GGCAGCTTCCC-GG
Heterakiss GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATACCAACTAGCGTTCCGTCGGCGGTAAAT-....ATGCCTTGGCG-GGCAGCTTCCC-GG
Trichinell GAAGGCGATCAGATACCGCCCTAGTTCTAACGGTAAACTATGCCAACCAGCGATTCGCCGAAGTTCATTT-....AAGACTCGGCG-AGCAGCTTCCC-GG
JB126Plect GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATGCCAACTAGCGATCCGCCGGTGGTAATT-....ACGCCC-GGCG-GG-AGCTTCCC-GG
Plectusaqu GAAGGCGATCAGATACCGCCCTAGTTCTGACCGTAAACGATGCCAACTAGCGATCCGCCGGTGGTAATT-....ACGCCCCGGCG-GGGAGCTTCCC-GG


[1201 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 1234567890]
DF5000Ohei AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5018Odoo AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5033Odol AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB133Oguen AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
CEW1Oschsp AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB128Otipu AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
BW282Ospec AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGGGCCTGCGGCTT
EM435Rmyri AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB169Oinsc AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB218Onecr AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5010Rblu AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAACTGAAACTTAAAGAAATTGACGGAATGGCACCACCAG-..TGGATTTTGCGGCTT
PS1191fiji AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGCGTGGAGCCTGCGGCTT
DF5006Raxe AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5044Roct AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB307Rtyph AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB227Cepha AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB173Pmedi AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB178Pmari AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5039Pell AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5056Pell AAACGA-..AAGTTTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5025Ptyp AAACGA-..AAG-CTTTCGGTTCCGGGGGGAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Haemonsimi AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAATGGCACCACCAGGAGTGGAGCCTGCGGCTT
Nematodiru AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAATGGCACCACCAGGAGTGGAGCCTGCGGCTT
Heterorhab AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Hbacteriop AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB202Ctrip AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB122Chori AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGAGTGGAGCTTGCGGCTT
EM464Crema AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
PB102Cbrig AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
CB4088Cele AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
CB5161Cspn AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
PS1010Cspn AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
SB225Cdros AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
SB226Csono AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACAAGGCGTGGAGCTTGCGGCTT
SB208Proto AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTT
PS1897Dipl AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTT
DF5055Prot AAACGA-..AAGTCTTTCGGTTCCTGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCTTGCGGCTT
DF5022Pstr AAACGT...-CGAGTGTC-CCTCCAGGGGTAGTATTGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGAGTGGAGCCTGTGGCTT
SB135Pcuta AAACGT...-CGAGTGTC-CCTCCAGGGGTAGTATTGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGAGTGGAGCCTGTGGCTT
SB160Ppunc AAACGT...-CGAGTATC-CCTCCAGGGGTAGTATTGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGAGTGGAGCCTGTGGCTT
DF5021Pcys AAACCACTTAAGTTGCCCTTTTCCTGGGGAAGTATGGTTGCAAGACTGAAACTTAAAGGTATTGACGGAAGAGCACCACCAGGAGTGGAGCCTGCGGCTT
EM437Ptere AAACGA-..AAGCATATCGGATCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGAGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5014Ppse AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGCGTGGAGCTTGCGGCTT
DF5019Tpal AAACGA-..AAGACTTCAGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB120Tmari AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB131Tsynp AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
PS1179Meso AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB123Manis AAACGA-..AAGCCTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB157Mspic AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5017Mlon AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB281Paras AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB125Cscan AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
PDL29Cstas AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5024Dvee AAACGA-..AAGACTTCCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAATCGCACCACCAGGAGTGGAGCCTGCGGCTT
SB311Rstam AAACGA-..AAGACTTTCGGTTCCAGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGAGTGGAGCTTGCGGCTT
DF5012Rreg AAACGA-..AAGTCTTTCGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGCGCACCACCAGGCGTGGAGCTTGCGGCTT
SB199Prege AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCAC-ACAAGGAGTGGAGCCTGCGGCTT
SB200Poxyc AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCAC-ACAAGGAGTGGAGCCTGCGGCTT
JB120Adunc AAACGA-..AAGTCTTCGGGTTCCGGGGGTAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGCACGTGCGGCTT
PS312Prist AAACGA-..AAGTCTTCGGGTTCCGGGGGTAGTATGGTTGCAAATCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
DF5031Rves AAACGA-..AAGTCTTCGGGTTCCGGGGGAAGTATGGTTGCAAAACTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB310Riner AAACGA-..AAGTCTTCGGGTTCCGGGGGAAGTATGGTTGCAAAACTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
SB158Rinrf AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
PS1163Pana AAACGA-..AAGTCTTTCGGTTCCGGGGGAAGTATTCTCGCAAGTGACAAACTTAAAGGAGTTGACGGAAGGTCACCACCAGAAATGGAGCCTGCGGCTT
Sstercoral AAACGA-..AAGTCTTTCGGTTCCGGGGGAAGTATGGTTGAAAAGCTGAAACTTAAAGGAATTGACGGAAGG-CACCACCAGGAGTGGAGCCTGCGGCTT
Steinernem AAACGA-..AAGTCTTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Meloidogyn AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
PS1153Zeld AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGCACGTGCGGCTT
Goeziapela AAACGA-..AAGTCTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Parascaris AAACGA-..AAGTCTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Heterochei AAACGA-..AAGTTTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Paraspidod AAACGA-..AAGTTTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Heterakiss AAACGA-..AAGTTTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGAAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT
Trichinell AAACCA-..AAGTGTTTCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-.CATGCGGCTT
JB126Plect AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGCAC-TGCGGCTT
Plectusaqu AAACGA-..AAGTCTTCCGGTTCCGGGGGAAGTATGGTTGCAAAGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT