**Figure S5. Alignment of nucleotide sequences corresponding to *htra1a* and *htra1b*.**

 1 50

htra1a\_NM\_001141717 (1) ----------------------------------------------CAAC

 htra1b\_assembly (1) CCTTCAAAGGGAGTTACAGCAGCTTTGTTGTCTGACAGCAGTAGACCAAC

 htra1b\_EG831192 (1) --------------------------------------------------

 51 100

htra1a\_NM\_001141717 (5) AAAGCTCATTTTAGTGAAAAGCGTCTGACATTTATTTGCAAATGTATGTA

 htra1b\_assembly (51) GAAGCACAGCTTAGTGAAAAGCGACTCACATTTA--TGCAACG---TTTA

 htra1b\_EG831192 (1) --------------------------------------------------

 101 150

htra1a\_NM\_001141717 (55) ACGTTTATTTATGCAGATCAAACATATTTTTGTAGCAAGTCGTAAAGTTT

 htra1b\_assembly (96) ----TTATTTATGCAGATAAAACAT--TTTTGTAGAAAC-------GTTT

 htra1b\_EG831192 (1) --------------------------------------------------

 151 200

htra1a\_NM\_001141717 (105) TAAGAGTCGTTTTTTTTGGCAACTTTGTACCTTTTTAGATACTTTAATAT

 htra1b\_assembly (133) GAAAATTCGTTTTT--TGACAACATTGCATAGTTTTTCA--ATTGAATAT

 htra1b\_EG831192 (1) --------------------------------------------------

 201 250

htra1a\_NM\_001141717 (155) TTAACAATGTTTTGGTGCGTCTTCTGCGCAACTTTTATTCTTGCTCCTTT

 htra1b\_assembly (179) TTAACAATGTTTTGGTCGGTCATCTGCGCAACTTTTCTCCTTGCTCCTTT

 htra1b\_EG831192 (1) --------------------------------------------------

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 251 300

htra1a\_NM\_001141717 (205) AGTTTGCGAGTCAAGAGCCAAGCGATATGTCATCGGCTGTCCAGATAAAT

 htra1b\_assembly (229) AGTTTGCGAGGCAAGAACCAAGCGATATGTCATCGGCTGTCCAGATAAAT

 htra1b\_EG831192 (1) --------------------------------------------------

 301 350

htra1a\_NM\_001141717 (255) GTGACAAATTTCTATGTCCCCCGATCCCTGCGGACTGTTTGGCCGGCGAC

 htra1b\_assembly (279) GTGACAAATCTCTATGTCCCCCGATCCCTGCGGACTGCATGGCCGGCGAC

 htra1b\_EG831192 (1) --------------------------------------------------

 351 400

htra1a\_NM\_001141717 (305) ATCCTTGACCAATGCGACTGCTGTCCGGTCTGTGCGCACGGAGAAGGTGA

 htra1b\_assembly (329) ATACTTGACCAATGCGACTGTTGTCCGGTCTGTGCGTCCGAAGAGGGTGA

 htra1b\_EG831192 (1) --------------------------------------------------

 401 450

htra1a\_NM\_001141717 (355) GGTGTGCGGCGGCACGGGGAGACTAGGGGACCCGGAGTGCGGAGAGGGCA

 htra1b\_assembly (379) GGCATGCGGCGGCACAGGGAGATTAGGGGACCCGGAGTGCGGAGAGGGCA

 htra1b\_EG831192 (1) --------------------------------------------------

 451 500

htra1a\_NM\_001141717 (405) TGGACTGCTCGATATCGGACGGAATTGGGGTGTCCGCCACAGTAAGGCGT

 htra1b\_assembly (429) TGGAATGCTCGATAACGGACGGCATTGGGGTGTCCGCCACTGTGAGGCGT

 htra1b\_EG831192 (1) --------------------------------------------------

 501 550

htra1a\_NM\_001141717 (455) CGGGGCAAAAACGGTGTGTGCGTCTGCAAAGTTGCGGACCCGGTGTGCGG

 htra1b\_assembly (479) CGGGGCAAAAGCGGTGTGTGCGTCTGCAAAGGTTCGGACCCGGTGTGCGG

 htra1b\_EG831192 (1) --------------------------------------------------

 551 600

htra1a\_NM\_001141717 (505) CAGTGACGGGGTGTCCTACCGAAACATCTGCGAACTGAAGAGATTGAGTA

 htra1b\_assembly (529) CAGTGACGGGGTGTCCTACCAAAACATCTGCGAACTGAAGAGAGTGAGTA

 htra1b\_EG831192 (1) --------------------------------------------------

 601 650

htra1a\_NM\_001141717 (555) ACCGGGCTCTGAAGCTTCAGCAGCCACCGGTCATCTTCATACAGAGAGGA

 htra1b\_assembly (579) ACCGGGCTCTGAAGCTGCAGCAGCCACCGGTCATCTTCATACAGAGAGGA

 htra1b\_EG831192 (1) --------------------------------------------------

 651 700

htra1a\_NM\_001141717 (605) ACCTGTAGCAAAGGCCAGGAGAATCCAGACAGTCTGCGCCACAGATATAA

 htra1b\_assembly (629) ACCTGTGGCAAAGGCCAGGAGAATCCAGACAGTCTGCGCCACAGATACAA

 htra1b\_EG831192 (1) --------------------------------------------------

 701 750

htra1a\_NM\_001141717 (655) CTTCATC**GCTGATGTGGTGGAGGAGAT**CGCTCCCGCTGTGGTTCATATTG

 htra1b\_assembly (679) CTTTATTGCTGACGTGGTTGAGAAGATTGCTCCTGCTGTGGTTCATATTG

 htra1b\_EG831192 (1) --------------------------------------------------

 751 800

htra1a\_NM\_001141717 (705) AACTTTACCGCAAGATGGTGTTCTCTAAGCGTGAGGTGGCGGTGGCCAGC

 htra1b\_assembly (729) AACTCTACCGCAAGATGGTATTCTCTAAGCGGGAGGTGGCGGTGGCCAGC

 htra1b\_EG831192 (1) --------------------------------------------------

 801 850

htra1a\_NM\_001141717 (755) GGGTCTGGCTTCGTG**GTGTCAGAGGACGGCTTGA**TTGTGACCAACGCCCA

 htra1b\_assembly (779) GGTTCTGGCTTTGTGGTGTCAGAGGACGGCCTGATCGTGACCAACGCCCA

 htra1b\_EG831192 (1) --------------------------------------------------

 851 900

htra1a\_NM\_001141717 (805) CGTGGTGGCCAATAAGCACCGGGTGAAGGTGGAGCTGAAGAGTGGCGCCA

 htra1b\_assembly (829) CGTGGTGGCCAATAAGCACCGGGTGAAGGTGGAGCTGAAGAGTGGCGCTA

 htra1b\_EG831192 (1) --------------------------------------------------

 901 950

htra1a\_NM\_001141717 (855) CCTTCGACGCCAAGATCACAGACGTGGACGAGAAGGCAGACATTGCCCTC

 htra1b\_assembly (879) CCTTCGACGCCAAGATCAAAGACGTGGACGAGAAGGCCGACATCGCCCTC

 htra1b\_EG831192 (1) --------------------------------------------------

 951 1000

htra1a\_NM\_001141717 (905) ATCAAGATCGACACCCCGATGAAACTGCCGGTGCTGCTGCTGGGTCGTTC

 htra1b\_assembly (929) ATCAAGATCGACGTCCCGATGAAGCTGCCGGTGCTGCTGCTGGGTCGTTC

 htra1b\_EG831192 (1) --------------------------------------------------

 1001 1050

htra1a\_NM\_001141717 (955) AGCTGACCTGAGGCCTGGTGAGTTTGTTGTGGCCATCGGCAGCCCCTTCT

 htra1b\_assembly (979) AGCTGACCTGAGGCCTGGTGAGTTTGTGGTGGCCATCGGCAGCCCCTTCT

 htra1b\_EG831192 (1) ---------------GGGGGAGTTTGTGGTGGCCATCGGCAGCCCCTTCT

 1051 1100

htra1a\_NM\_001141717 (1005) CCCTGCAGAACACGGTCACCACAGGTATCGTCAGCACCACCCAAAGAGGA

 htra1b\_assembly (1029) CCCTGCAGAACACGGTCACCACAGGTATCGTCAGCACCACCCAGAGAGGA

 htra1b\_EG831192 (36) CCCTGCAGAACACGGTCACCACAGGTATCGTCAGCACCACCCAGAGAGGA

 1101 1150

htra1a\_NM\_001141717 (1055) GGCAAGGAGCTTGGCCTGAGGAACTCTGATATGGAATACATCCAGACGGA

 htra1b\_assembly (1079) GGCAAGGAGCTGGGCCTGAGGAACTCTGATATGGACTACATCCAGACGGA

 htra1b\_EG831192 (86) GGCAAGGAGCTGGGCCTGAGGAACTCTGATATGGACTACATCCAGACGGA

 1151 1200

htra1a\_NM\_001141717 (1105) CGCTATCATCAACGAAGGAAGTGTAGATCTACCATCTGATCATCCCTTTA

 htra1b\_assembly (1129) CGCTATCATCAAC--------------------------T----------

 htra1b\_EG831192 (136) CGCTATCATCAAC--------------------------T----------

 1201 1250

htra1a\_NM\_001141717 (1155) ACCTGAATGCTGTTCCTTTTCAGTATGGGAACTCTGGCGGACCCCTGGTC

 htra1b\_assembly (1143) ------------------------ATGGGAACTCTGGCGGACCCCTGGTC

 htra1b\_EG831192 (150) ------------------------ATGGGAACTCTGGCGGACCCCTGGTC

 1251 1300

htra1a\_NM\_001141717 (1205) AATCTGGACGGAGAGGTGATTGGGATCAACACACTGAAGGTGACAGCAGG

 htra1b\_assembly (1169) AATCTGGATGGAGAGGTGATTGGGATCAACACACTGAAGGTGACAGCAGG

 htra1b\_EG831192 (176) AATCTGGATGGAGAGGTGATTGGGATCAACACACTGAAGGTGACAGCAGG

 1301 1350

htra1a\_NM\_001141717 (1255) AATCTCCTTCGCCATCCCCTCAGACAAGATCCGTCAGTTCTTGGCAGAGT

 htra1b\_assembly (1219) AATCTCCTTCGCCATCCCCTCAGACAAGATCCGTCAGTTCCTGGCAGAGT

 htra1b\_EG831192 (226) AATCTCCTTCGCCATCCCCTCAGACAAGATCCGTCAGTTCCTGGCAGAGT

 1351 1400

htra1a\_NM\_001141717 (1305) CCCACGGCAGACAATCTAAAGGTAGA---------------------TTA

 htra1b\_assembly (1269) CCCATGACAGGCAATCTAAAGGTACAGATTACCAATCTAAAGGGAAATTA

 htra1b\_EG831192 (276) CCCATGACAGGCAATCTAAAGGTACAGATTACCAATCTAAAGGGAAATTA

 1401 1450

htra1a\_NM\_001141717 (1334) TTACCAAAGAAGAAGTATATCGGTGTGAGGATGATGACTCTCACTACAAC

 htra1b\_assembly (1319) TCAACAAGTAAGAAATATATCGGTGTGAGGATGATGACTCTCACACCAAT

 htra1b\_EG831192 (326) TCAACAAGTAAGAAATATATCGGTGTGAGG**ATGATGACTCTCACACCAAT**

 1451 1500

htra1a\_NM\_001141717 (1384) GCTTGCAAAGGAGCTGAAGGAGAGAACATCAGACTTCCCTGATGTTACCT

 htra1b\_assembly (1369) GCTTGCAAAGGAGCTGAAGGAGAGACAATCAGACTTCCCCGATGTTACCT

 htra1b\_EG831192 (376) **GC**TTGCAAAGGAGCTGAAGGAGAGACAATCAGACTTCCCCGATGTTACCT

 1501 1550

htra1a\_NM\_001141717 (1434) CAGGGGCATATGTCATCGAGGTCATCCCAAAAACACCAGCTGAGACAGGT

 htra1b\_assembly (1419) CAGGGGCATATGTAATCGAGGTCATCCCAAAAACACCAGCTGAGACAGGT

 htra1b\_EG831192 (426) CAGGGGCATATGT**AATCGAGGTCATCCCAAAAAC**ACCAGCTGAGACAGGT

 1551 1600

htra1a\_NM\_001141717 (1484) GGCCTGCAGGAGAGTGACGTCATAATCACCATCAACAGCCAGCGAATCAC

 htra1b\_assembly (1469) GGCCTGCAGGAGAGTGATGTCATAATCACCATCAACAGCCAGCGAATCAC

 htra1b\_EG831192 (476) GGCCTGCAGGAGAGTGATGTCATAATCACCATCAACAGCCAGCGAATCAC

 1601 1650

htra1a\_NM\_001141717 (1534) CTCGGCCAGTGATGTCAGCAGCTCTATCAAGAGGGACGACACGCTGCGAA

 htra1b\_assembly (1519) CTCAGCCAGTGACGTCAGCAGCTCCATCAAGAGGGAAGACACGCTGCGCA

 htra1b\_EG831192 (526) CTCAGCCAGTGACGTCAGCAGCTCCATCAAGAGGGAAGACACGCTGCGCA

 1651 1700

htra1a\_NM\_001141717 (1584) TGGTGGTCCGGCGGGGGAACGAGGACATCATGCTCACCGTCGTCCCCGAG

 htra1b\_assembly (1569) TGGTGGTCCGGCGGGGGAACGAGGACGTCATGCTCACCGTCGTCCCAGAG

 htra1b\_EG831192 (576) TGGTGGTCCGGCGGGGGAACGAGGACGTCATGCTCACCGTCGTCCCAGAG

 1701 1750

htra1a\_NM\_001141717 (1634) GACATTGACCCTTGACCTCTCAGCAACCACGAGCTGGTTCTCAGTGTTTA

 htra1b\_assembly (1619) GAGATTGACCCTTGACCTCTCAGCAACCACGAGCTGGTTCTCAGTGTTGA

 htra1b\_EG831192 (626) GAGATTGACCCTTGACCTCTCAGCAACCACGAGCTGGTTCTCAGTGTTGA

 1751 1800

htra1a\_NM\_001141717 (1684) AAACCACGGAC-TTAAACCGGTTGTGTGTCTGGATCCACACCCTACCATA

 htra1b\_assembly (1669) AAATCACGGACCTTAAACCGG--GTGTGTCTGGAGCCACACCCTACCTTA

 htra1b\_EG831192 (676) AAATCACGGACCTTAAACCGG--GTGTGTCTGGAGCCACACCCTACCTTA

 1801 1850

htra1a\_NM\_001141717 (1733) GAACCTGTAACTACGGGTG----CTCTTCGCTCTCAGTGAA--ACTGATT

 htra1b\_assembly (1717) GAACCTGTAACTACTAGTGTCTCCCCCCCACTCCCCTCAAACTACAGAGG

 htra1b\_EG831192 (724) GAACCTGTAACTACTAGTGTCTCCCCCCCACTCCCCTCAAACTACAGAGG

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 1851 1900

htra1a\_NM\_001141717 (1777) ATTGTTTTATACTCTACTAACGTCCTTGCA-CAGAAAACCCACCTCAATC

 htra1b\_assembly (1767) TCTGTGAGGCCCACAACTAACCCTCTGGGAGCTCAAATGTGTCCAGGGTA

 htra1b\_EG831192 (774) TCTGTGAGGCCCACAACTAACCCTCTGGGAGCTCAAATGTGT--------

 1901 1950

htra1a\_NM\_001141717 (1826) AGATAGAAAAGTGGGTGTCACAGATTACCGTAGTTTTG---TAGTTGTTT

 htra1b\_assembly (1817) ATAAAGACATATTTTAG-CACCCCTGCTAGTTTTTTTGGATTATTTGTCC

 htra1b\_EG831192 (816) --------------------------------------------------

 1951 2000

htra1a\_NM\_001141717 (1873) T--TGTTGCTGTTGATATTATGTTTTTTTTTT-ATTG--------TATTT

 htra1b\_assembly (1866) TCATGTATGAGTCAAAAAGATACTTCTACACTCATTGAAACTGATTATTG

 htra1b\_EG831192 (816) --------------------------------------------------

 2001 2050

htra1a\_NM\_001141717 (1912) TAATTGCATTTCTCTTGATACGTTTTGACGACAATTTCACAGAGGGAATA

 htra1b\_assembly (1916) CCATCACGTTTGTTTTTATACTCTATTAACATCCTTGCACAGAGA-ACCC

 htra1b\_EG831192 (816) --------------------------------------------------

 2051 2100

htra1a\_NM\_001141717 (1962) AAAAGATTTTGAAAAAAAAAAAAAAAAAAAAAAAAAGA------------

 htra1b\_assembly (1965) TCCTCAGTCAGAGAGAAGAAGTGAAGGGTGTCCTTAATCTGGTTTGTTGT

 htra1b\_EG831192 (816) --------------------------------------------------

 2101 2150

htra1a\_NM\_001141717 (2000) --------------------------------------------------

 htra1b\_assembly (2015) TGATATTGTTGATGTTTTTAGTTGTATTTCTCTTGGTATGTTTTGACCAC

 htra1b\_EG831192 (816) --------------------------------------------------

 2151 2177

htra1a\_NM\_001141717 (2000) ---------------------------

 htra1b\_assembly (2065) AATTTCACAGAGGGAATAAAATGGTTT

 htra1b\_EG831192 (816) ---------------------------