**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) ---------------------------