**Figure S1. Alignment of nucleotide sequences corresponding to *adssl1a* and *adssl1b*.**

 1 50

adssl1a\_NM\_001139706 (1) -----------------------------------------------GGA

adssl1b\_XM\_014210487 (1) CTGATATGGCAATGCTACTGTTAGAAACATTCTAGTCTGTTTCAGACAGA

 adssl1b\_DN163954 (1) --------------------------------------------------

 adssl1b\_GE623728 (1) --------------------------------------------------

 51 100

adssl1a\_NM\_001139706 (4) CAGCATAAGCAACATCATGTCGTTTAGCTGGTCAGCAAAAGACCACAAGA

adssl1b\_XM\_014210487 (51) CAGCCTAAGCAACATCATGTCGTTGAGCTGGTCAGCAAAAGACCACAAGA

 adssl1b\_DN163954 (1) ---------CAACATCATGTCGTTGAGCTGGTCAGCAAAAGACCACAAGA

 adssl1b\_GE623728 (1) --------------------------------------------------

 101 150

adssl1a\_NM\_001139706 (54) GTTATACAAATCCACCCTCCAACCCAACCCAAGGGCTGAAGCGGCCACGG

adssl1b\_XM\_014210487 (101) GTTATACAAATTCACCCTCCAACCCTACCCAAGGGCTGAAGCGGCCACGG

 adssl1b\_DN163954 (42) GTTATACAAATTCACCCTCCAACCCTACCCAAGGGCTGAAGCGGCCACGG

 adssl1b\_GE623728 (1) --------------------------------------------------

 151 200

adssl1a\_NM\_001139706 (104) AACGACACAGGGAACAAAGTGACAGTAGTGCTCGGTGCGCAATGGGGAGA

adssl1b\_XM\_014210487 (151) AATGACGCAGGGAACAAAGTGACAGTGGTGCTCGGTGCGCAATGGGGAGA

 adssl1b\_DN163954 (92) AATGACGCAGGGAACAAAGTGACAGTGGTGCTCGGTGCGCAATGGGGAGA

 adssl1b\_GE623728 (1) --------------------------------------------------

 201 250

adssl1a\_NM\_001139706 (154) TGAAGGCAAAGGAAAAGTCGTCGATTTATTGGCGACTGAGTCTGACCTTG

adssl1b\_XM\_014210487 (201) TGAAGGCAAAGGAAAAGTCGTCGATTTACTGGCGACTGAGTCTGACCTTG

 adssl1b\_DN163954 (142) TGAAGGCAAAGGAAAAGTCGTCGATTTACTGGCGACTGAGTCTGACCTTG

 adssl1b\_GE623728 (1) --------------------------------------------------

 251 300

adssl1a\_NM\_001139706 (204) TTTGCAGATGTCAGGGCGGTAACAATGCAGGCCACACAGTGGTTGTGGAA

adssl1b\_XM\_014210487 (251) TTTGCAGATGTCAGGGTGGTAACAATGCAGGCCACACAGTGGTAGTAGAA

 adssl1b\_DN163954 (192) TTTGCAGATGTCAGGGTGGTAACAATGCAGGCCACACAGTGGTAGTAGAA

 adssl1b\_GE623728 (1) --------------------------------------------------

 301 350

adssl1a\_NM\_001139706 (254) GGCAAAGAGTATGACTTCCACCTTCTCCCCAGTGGAATTATCAACCCCAA

adssl1b\_XM\_014210487 (301) GGCACAGAGTATGACTTCCACCTTCTCCCCAGTGGCATTATCAACCCCAA

 adssl1b\_DN163954 (242) GGCACAGAGTATGACTTCCACCTTCTCCCCAGTGGCATTATCAACCCCAA

 adssl1b\_GE623728 (1) --------------------------------------------------

 351 400

adssl1a\_NM\_001139706 (304) AAGTATATGTGTCATTGGTAATGGCGTAGTCATACACCTACCAGGTTTGT

adssl1b\_XM\_014210487 (351) AAGCATATGTGTCATTGGTAATGGCGTAGTCATACACCTACCGGGCTTGT

 adssl1b\_DN163954 (292) AAGCATATGTGTCATTGGTAATGGCGTAGTCATACACCTACCGGGCTTGT

 adssl1b\_GE623728 (1) --------------------------------------------------

 401 450

adssl1a\_NM\_001139706 (354) TTGAGGAGGCAGAGAACAATGAGAAGAAAGGTCTCAAAGGCTGGGAGAAG

adssl1b\_XM\_014210487 (401) TTGAGGAGGCGGAGAAGAATGAGAAGAAAGGTCTCAAAGGCTGGGAGAAG

 adssl1b\_DN163954 (342) TTGAGGAGGCGGAGAAGAATGAGAAGAAAGGTCTCAAAGGCTGGGAGAAG

 adssl1b\_GE623728 (1) --------------------------------------------------

 451 500

adssl1a\_NM\_001139706 (404) AGACTAATAGTCTCTGACAGAGCTCACCTTGTGTTTGATTTCCATCAGGT

adssl1b\_XM\_014210487 (451) AGACTAATAGTCTCTGACAGAGCTCACCTCGTGTTTGATTTCCACCAGGT

 adssl1b\_DN163954 (392) AGACTAATAGTCTCTGACAGAGCTCACCTCGTGTTTGATTTCCACCAGGT

 adssl1b\_GE623728 (1) --------------------------------------------------

 501 550

adssl1a\_NM\_001139706 (454) TGTGGA**TGGAATTCAGGAGACCCAGA**GACAAGCAACAGAGGGAAAGATAA

adssl1b\_XM\_014210487 (501) TGTGGATGGAATTCAGGAGAGCCAGCGACAAGCAACAGAGGGAAAGATTA

 adssl1b\_DN163954 (442) TGTGGATGGAATTCAGGAGAGCCAGCGACAAGCAACAGAGGGAAAGATTA

 adssl1b\_GE623728 (1) --------------------------------------------------

 551 600

adssl1a\_NM\_001139706 (504) TTGGAACAACCAAGAAAGGCATTGGACCCACCTATGCCAG**CAAGGCATCT**

adssl1b\_XM\_014210487 (551) TTGGAACGACCAAGAAAGGCATTGGACCCACCTATACCAGCAAAGCATCT

 adssl1b\_DN163954 (492) TTGGAACGACCAAGAAAGGCATTGGACCCACCTATACCAGCAAAGCATCT

 adssl1b\_GE623728 (1) --------------------------------------------------

 601 650

adssl1a\_NM\_001139706 (554) **CGCATAGGAC**TGCGTGTCTGTGACCTGCTGGGAGACTTCAAGGAGTTCTC

adssl1b\_XM\_014210487 (601) CGCATTGGACTGCGTGTCTGTGACCTGCTGGGAGACTTTAAAGAGTTCTC

 adssl1b\_DN163954 (542) CGCATTGGACTGCGTGTCTGTGACCTGCTGGGAGACTTTAAAGAGTTCTC

 adssl1b\_GE623728 (1) --------------------------------------------------

 651 700

adssl1a\_NM\_001139706 (604) TACCAAATTCAAGAACCTTGTCGAACAGTACCAGTCCATGTACTCATCCC

adssl1b\_XM\_014210487 (651) TACCAAATTCAAGAACCTTGTCGCGCAGTACCAGTCCATGTACTCATCCC

 adssl1b\_DN163954 (592) TACCAA--------------------------------------------

 adssl1b\_GE623728 (1) -----------------------------------------ACTCATCCC

 701 750

adssl1a\_NM\_001139706 (654) TGACAGTTGATACTGAAAGTCAGCTGAAAAAACTGAAGGAGTATGGAGAG

adssl1b\_XM\_014210487 (701) TGACAGTTGATACTGATACTCAGCTGAAAAAACTGAAGGAGTATGGAGAG

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (10) TGACAGTTGATACTGATACTCAGCTGAAAAAACTGAAGGAGTATGGAGAG

 751 800

adssl1a\_NM\_001139706 (704) AGGTTGCGGCCGATGGTTCGGGATGGAGTCTACTACATGTACGAGGCTCT

adssl1b\_XM\_014210487 (751) AGGTTGCGGCCGATGGTGCGGGATGGAGTCTACTACATGTATGAGGCTCT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (60) AGGTTGCGGCCGATGGTGCGGGATGGAGTCTACTACATGTATGAGGCTCT

 801 850

adssl1a\_NM\_001139706 (754) TCATGGACCCCCAAAGAAAATTCTGGTGGAAGGGGCCAACGCTGCCCTCC

adssl1b\_XM\_014210487 (801) TCATGGACCCCCAAAGAAAATTCTGGTGGAAGGGGCCAATGCTGCCCTCC

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (110) TCATGGACCCCCAAAGAAAATTCTGGTGGAAGGGGCCAATGCTGCCCTCC

 851 900

adssl1a\_NM\_001139706 (804) TCGACATTGACTTTGGCACATATCCTTTTGTGACCTCATCAAACTGCACC

adssl1b\_XM\_014210487 (851) TCGACATTGACTTTGGCACATATCCTTTTGTGACCTCATCAAACTGCACT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (160) TCGGCATTGACTTTGGCACATATCCTTTTGTGACCTCATCAAACTGCACT

 901 950

adssl1a\_NM\_001139706 (854) GTTGGTGGGGCATGCACTGGTCTTGGCATCCCTCCTCTGAATATTGGTGA

adssl1b\_XM\_014210487 (901) GTTGGTGGGGCATGCACTGGTCTTGGCATCCCTCCCCTGAATATTGGTGA

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (210) GTTGGTGGGGCATGCACTGGTCTTGGCATCCCTCCCCTGAATATTGGTGA

 951 1000

adssl1a\_NM\_001139706 (904) AGTGTATGGTGTATCAAAGGCCTACACCACCAGGGTGGGAATTGGTGCCT

adssl1b\_XM\_014210487 (951) AGTGTATGGTGTATCAAAGGCCTACACCACCAGGGTAGGAATTGGTGCCT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (260) AGTGTATGGTGTATCAAAGGCCTACACCACCAGGGTAGGAATTGGTGCCT

 1001 1050

adssl1a\_NM\_001139706 (954) TCCCAACAGAACAACTCAATGCAACAGGTGAGCTGCTGCAGACAAGGGGT

adssl1b\_XM\_014210487 (1001) TCCCCACAGAACAGCTCAATGCGACAGGTGAGCTGCTGCAGACGAGAGGT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (310) TCCCCACAGAACAGCTCAATGCGACAGGTGAGCTGCTGCAGACGAGAGGT

 1051 1100

adssl1a\_NM\_001139706 (1004) CATGAGGTGGGCGTGACCACAGGCAGGAAACGTCGCTGTGGCTGGCTGGA

adssl1b\_XM\_014210487 (1051) CATGAGGTGGGCGTGACAACGGGCAGGAAACGTCGCTGTGGCTGGCTGGA

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (360) CATGAGGTGGGCGTGACAACGGGCAGGAAACGTCGCTGTGGCTGGCTGGA

 1101 1150

adssl1a\_NM\_001139706 (1054) CCTGGTCATCCTGAGATACGCTCACATGATCAATGGCTTCACTGCAATTG

adssl1b\_XM\_014210487 (1101) CCTGGTCATCCTGAGATACGCCCACATGATCAATGGCTTCACTGCCATTG

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (410) CCTGGTCATCCTGAGATACGCCCACATGATCAATGGCTTCACTGCCATTG

 1151 1200

adssl1a\_NM\_001139706 (1104) CTTTGACAAAACTTGACATCCTTGATGTGCTGGATGAGATCAAAGTAGGA

adssl1b\_XM\_014210487 (1151) CTTTGACAAAACTTGACATCCTTGATGTGCTGGATGAGATCAAAGTAGGA

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (460) CTTTGACAAAACTTGACATCCTTGATGTGCTGGATGAGATCAAAGTAGGA

 1201 1250

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adssl1a\_NM\_001139706 (1154) ATGGCCTACAAAATCAATGGCAAAAGAATTCCCCATTTCCCAGCTGACAT

adssl1b\_XM\_014210487 (1201) GTGGCCTACAAAATCAGTGGCAAAAGAATTCCCCATTTCCCAGCTAACAT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (510) GTGGCCTACAAAATCAGTGGCAAAAGAATTCCCCATTTCCCAGCTAACAT

 1251 1300

adssl1a\_NM\_001139706 (1204) GGAGCTGTTGCACAAAGTGGAGGTAGAGTATGAGACCTTCCCCGGCTGGA

adssl1b\_XM\_014210487 (1251) GGAGCTGTTGCACAAAGTGGAGGTTGAGTATGAGACCTTCCCAGGCTGGA

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (560) GGAGCTGTTGCACAAAGTGGAGGTTGAGTATGAGACCTTCCCAGGCTGGA

 1301 1350

adssl1a\_NM\_001139706 (1254) AGAGTGACACGTCTGCAGCCAGGAAGTGGAATAATCTCCCCCAGAAGGCT

adssl1b\_XM\_014210487 (1301) AGAGTGATACGTCTGCAGCCAGGAAGTGGAATGATCTCCCCCAGAAGGCT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (610) AGAGTGATACGTCTGCAGCCAGGAAGTGGAATGATCTCCCCCAGAAGGCT

 1351 1400

adssl1a\_NM\_001139706 (1304) CAGAACTACATCCGCTTTGTGGAGAGCCACATTGGAGTACCCATTAAGTG

adssl1b\_XM\_014210487 (1351) CAGAACTACATCCGCTTTGTGGAGAACCACATTGGAGTACCCATTAAGTG

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (660) CAGAACTACATCCGCTTTGTGGAGAACCACATTGGAGT------------

 1401 1450

adssl1a\_NM\_001139706 (1354) GGTCGGTGTAGGAAAGTCCAGAGAGTGCATGATCCAGATGTTCTAGAGAG

adssl1b\_XM\_014210487 (1401) GGTCGGCGTCGGAAAGTCCAGAGAGTGCATGATCCAGATGTTCTAGAGAC

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------

 1451 1500

adssl1a\_NM\_001139706 (1404) TTTACCTCCTCTCTCCCCAAGATGGATGCGCAA---------AGATGTGG

adssl1b\_XM\_014210487 (1451) TTTTCCTTTTCTCTCCCCAAGATGGATGCACATGGATGGACGAGATGTGG

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------

 1501 1550

adssl1a\_NM\_001139706 (1445) CATGATGTGACATATGTTTGCAACCCCCAAACTGTCTAATATTAGGTAAA

adssl1b\_XM\_014210487 (1501) CTTGATGTGACATAAGTTTACAATCCTCAAACTATCTAATATTCTGTAAA

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------

 1551 1600

adssl1a\_NM\_001139706 (1495) AAAAACTTATGCCAACAGATTTGTGTAGCTTTGAAACAATGTTGACTGCT

adssl1b\_XM\_014210487 (1551) AC---CTGTTAACAACAAATACGTGTAGCCTTGAAACAATGTTGAGTGGA

 adssl1b\_DN163954 (598) --------------------------------------------------

**C098R022**

 adssl1b\_GE623728 (698) --------------------------------------------------

 1601 1650

adssl1a\_NM\_001139706 (1545) AATGTTGGTAACTTTACATCTATCTATGCAGTGCTTCTCATCAGTAAGTT

adssl1b\_XM\_014210487 (1598) AACGTTGGTAACTTTACATCTATCTGTGTTG-------CATCAGTAAATT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------

 1651 1700

adssl1a\_NM\_001139706 (1595) GCCTTGTGATGATGTCGGCCAGAAAGTCCTA-----TTACTGACCCAGGA

adssl1b\_XM\_014210487 (1641) GCCTTGTAGTGATGTCTGCCAGAAAGTCCTACAGTATGACTGAGCCATGT

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------

 1701 1750

adssl1a\_NM\_001139706 (1640) GTAAATCTTACCTTGTGCCACACAACAAACATGAAAGATAAAAACACATC

adssl1b\_XM\_014210487 (1691) GTAAATCTTACCTTGTGCCACACAACAACCCAGAAAGAAAAAAACACATC

 adssl1b\_DN163954 (598) --------------------------------------------------

 adssl1b\_GE623728 (698) --------------------------------------------------