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