

Resulted (VADDs): n/c
Verified (VADDs): n/a

Molecular Diagnostics Sequence Identification Summary

Case# 2011-0855

Date Nov 23/11

Test ISAV (ILA Primers)

Pathologist GM

PCR Test# ISA #481

Tested by JS

Species Chinook Salmon

Specimens Organs #1-5

Target Region M1 gene

Percentage Match n/a (36/43) 84% (total sequence is 117bp)
(primers removed)

Result no significant match

Comments Good Sequence Data

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
JN951061.1	Mus musculus targeted deletion, lacZ-tagged mutant allele March11:tm1(KOMP)Wtsi; transgenic	46.4	46.4	36%	0.036	83%	
AC102845.9	Mus musculus chromosome 15, clone RP24-38907, complete sequence	46.4	46.4	36%	0.036	83%	
FJ426239.1	Contracaecum rudolphii A Bullini et al., 1986 isolate CrAA8 small subunit ribosomal RNA gene, partial sequence; mitochondrial	44.6	44.6	29%	0.12	91%	
FJ426238.1	Contracaecum rudolphii A Bullini et al., 1986 isolate CrAA5 small subunit ribosomal RNA gene, partial sequence; mitochondrial	44.6	44.6	29%	0.12	91%	
FJ426237.1	Contracaecum rudolphii A Bullini et al., 1986 isolate CrAA1 small subunit ribosomal RNA gene, partial sequence; mitochondrial	44.6	44.6	29%	0.12	91%	
AC101810.5	Mus musculus chromosome 15, clone RP24-278M16, complete sequence	44.6	44.6	31%	0.12	86%	
XM_003288191.1	Dictyostelium purpureum expressed protein, mRNA	42.8	42.8	41%	0.43	79%	G
CR854927.24	Zebrafish DNA sequence from clone DKEY-40M6 in linkage group 16, complete sequence	42.8	42.8	38%	0.43	82%	
CT485798.2	Medicago truncatula chromosome 5 clone mth2-24d7, COMPLETE SEQUENCE	42.8	42.8	41%	0.43	82%	
XM_709324.1	Candida albicans SC5314 hypothetical protein (CaO19.1772) mRNA, complete cds	42.8	42.8	23%	0.43	92%	G
XM_709284.1	Candida albicans SC5314 hypothetical protein (CaO19.9341) mRNA, complete cds	42.8	42.8	23%	0.43	92%	G
CR352242.13	Zebrafish DNA sequence from clone CH211-218G4 in linkage group 23, complete sequence	42.8	42.8	26%	0.43	90%	
AL935152.9	Mouse DNA sequence from clone RP24-387M5 on chromosome 2, complete sequence	42.8	42.8	35%	0.43	85%	
AL928660.4	Zebrafish DNA sequence from clone CH211-257L15, complete sequence	42.8	42.8	38%	0.43	82%	
AF187320.1	Homo sapiens transferrin receptor (TFRC) gene, complete cds	42.8	42.8	23%	0.43	92%	E
XM_003592845.1	Medicago truncatula Zinc finger CCCH domain-containing protein (MTR_2g005450) mRNA, complete cds	41.0	41.0	25%	1.5	90%	
JN963524.1	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sin3a:tm1e(EUCOMM)Hmgu; transgenic	41.0	41.0	35%	1.5	83%	
JN958148.1	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele 2810008M24Rik:tm1a(EUCOMM)Wtsi; transgenic	41.0	41.0	48%	1.5	79%	
JN956859.1	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Rps6ka1:tm1a(KOMP)Wtsi; transgenic	41.0	41.0	23%	1.5	92%	
JN952973.1	Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sin3a:tm1a(EUCOMM)Hmgu; transgenic	41.0	41.0	35%	1.5	83%	
JN952896.1	Mus musculus targeted non-conditional, lacZ-tagged mutant allele Rps6ka1:tm1e(KOMP)Wtsi; transgenic	41.0	41.0	23%	1.5	92%	
JN950171.1	Mus musculus targeted non-conditional, lacZ-tagged mutant allele 2810008M24Rik:tm1e(EUCOMM)Wtsi; transgenic	41.0	41.0	48%	1.5	79%	
CU467797.7	Pig DNA sequence from clone CH242-69D5 on chromosome X, complete sequence	41.0	41.0	27%	1.5	87%	
HQ406778.1	Enterobacteria phage SPC35, complete genome	41.0	81.9	40%	1.5	78%	
FP102222.4	Medicago truncatula chromosome 5 clone mth4-60h23, COMPLETE SEQUENCE	41.0	41.0	23%	1.5	92%	

>gb|JN951061.1| **D** Mus musculus targeted deletion, lacZ-tagged mutant allele March11:tml(KOMP)Wtsi;
transgenic
Length=37222

Score = 46.4 bits (50), Expect = 0.036
Identities = 36/43 (84%), Gaps = 0/43 (0%)
Strand=Plus/Plus

Query 55 TATTTAAACATGATAATCTTGAATTTCTTAGAGTGTGCTTGTG 97
|||||
Sbjct 26564 TATTTAAACATTTTAACCTTTATTTTCTTAGTGTGTGCATGTG 26606

>gb|AC102845.9| **D** Mus musculus chromosome 15, clone RP24-38907, complete sequence
Length=125424

Score = 46.4 bits (50), Expect = 0.036
Identities = 36/43 (84%), Gaps = 0/43 (0%)
Strand=Plus/Plus

Query 55 TATTTAAACATGATAATCTTGAATTTCTTAGAGTGTGCTTGTG 97
|||||
Sbjct 24131 TATTTAAACATTTTAACCTTTATTTTCTTAGTGTGTGCATGTG 24173

>gb|FJ426239.1| Contracaecum rudolphii A Bullini et al., 1986 isolate CrAA8 small
subunit ribosomal RNA gene, partial sequence; mitochondrial
Length=532

Score = 44.6 bits (48), Expect = 0.12
Identities = 31/34 (91%), Gaps = 1/34 (3%)
Strand=Plus/Plus

Query 65 TGATAATCTTGAATTTCTTAGAGTGTGCTTGTGA 98
||
Sbjct 48 TGTTAATCTTGAATTT-TTAGAGTGTGCTTTTGA 80

>gb|FJ426238.1| Contracaecum rudolphii A Bullini et al., 1986 isolate CrAA5 small
subunit ribosomal RNA gene, partial sequence; mitochondrial
Length=532

Score = 44.6 bits (48), Expect = 0.12
Identities = 31/34 (91%), Gaps = 1/34 (3%)
Strand=Plus/Plus

Query 65 TGATAATCTTGAATTTCTTAGAGTGTGCTTGTGA 98
||
Sbjct 48 TGTTAATCTTGAATTT-TTAGAGTGTGCTTTTGA 80

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ISA-11-0855-3R_2011-10-27.ab1 (19>105)

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ISA-11-0855-5R_2011-10-27.ab1 (15>104)

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ISA-11-0855-1R_2011-10-27.ab1 (63>108)

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ISA-11-0855-4F_2011-10-27.ab1 (3>104)

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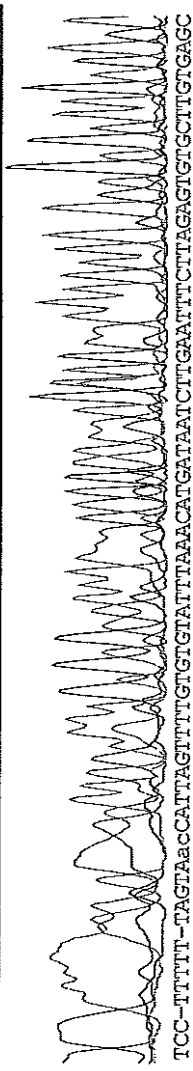
ISA-11-0855-5F_2011-10-27.ab1 (3>102)

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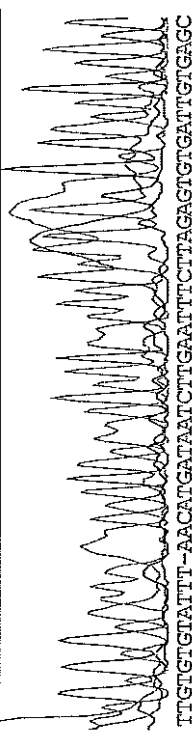
Project: 2011-0855 investigation of suspect ISA band (ILA).sqd Contig 1

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ISA-11-0855-3F_2011-10-27.ab1 (3>105) →

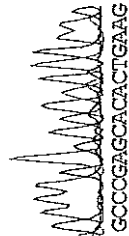


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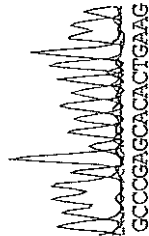


110
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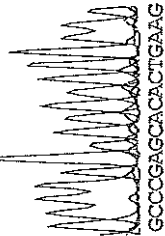
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ISA-11-0855-5F_2011-10-27.ab1 (3>102) →



ISA-11-0855-3F_2011-10-27.ab1 (3>105) →



ISA-11-0855-1F_2011-10-27.ab1 (85>103) →

