190220 Sequencing of HAP1 WT and HAP1 ΔDSG2 clone F9.

Used forward primer for exon 2, exon 5 and exon 8. Primer for exon 3 did not work (see previous results).

Amplify the different exons from the 2 cell lines.

Do a PCR clean (qiagen kit) to purify amplification from PCR products (DNTPs, polymeraze…)

After cleaning, measure the DNA concentration.

To send for sequencing:

Add 50-100ng of PCR product (amplification) total volyme is 5ul.

Also add primer (ONLY one), 5uM and 5ul.

Attach barcode and send. Remember to do this before 14.30.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3210298/>

Results:

Only exon 5 seems to have a frameshift in the HAP1 DSG2 deleted clone F9 cell.

Pairwise sequence alignment.

Exon 2

########################################

# Program: needle

# Rundate: Wed 20 Feb 2019 07:57:24

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190220-075722-0580-19974638-p1m.asequence

# -bsequence emboss\_needle-I20190220-075722-0580-19974638-p1m.bsequence

# -datafile EDNAFULL

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AH00\_90287084\_90287084\_ex2\_dsg2\_F9

# 2: 65AH01\_90287091\_90287091\_ex2\_wt

# Matrix: EDNAFULL

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 595

# Identity: 592/595 (99.5%)

# Similarity: 592/595 (99.5%)

# Gaps: 3/595 ( 0.5%)

# Score: 2960.0

#

#

#=======================================

65AH00\_902870 1 -AAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCAC 49

|||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 1 AAAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCAC 50

65AH00\_902870 50 AAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTC 99

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 51 AAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTC 100

65AH00\_902870 100 AGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGG 149

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 101 AGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGG 150

65AH00\_902870 150 GAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTG 199

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 151 GAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTG 200

65AH00\_902870 200 GTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGA 249

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 201 GTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGA 250

65AH00\_902870 250 ACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAA 299

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 251 ACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAA 300

65AH00\_902870 300 TTTTATTTTACAGATCTGCTTTAACGTTGGAAGTGGACTTCACTTACAGG 349

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 301 TTTTATTTTACAGATCTGCTTTAACGTTGGAAGTGGACTTCACTTACAGG 350

65AH00\_902870 350 TGAGGAAACAAAGGGATTATTTCTGCCTTCTGACTCAGGAGGGTTAATTC 399

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 351 TGAGGAAACAAAGGGATTATTTCTGCCTTCTGACTCAGGAGGGTTAATTC 400

65AH00\_902870 400 CATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTA 449

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 401 CATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTA 450

65AH00\_902870 450 TTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGG 499

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 451 TTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGG 500

65AH00\_902870 500 GTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAA 549

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 501 GTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAA 550

65AH00\_902870 550 TGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGAGAAG-- 592

|||||||||||||||||||||||||||||||||||||||||||

65AH01\_902870 551 TGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGAGAAGGT 595

#---------------------------------------

#---------------------------------------

**EXON 3**

########################################

# Program: needle

# Rundate: Tue 23 Apr 2019 14:49:25

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190423-144923-0392-66881369-p1m.asequence

# -bsequence emboss\_needle-I20190423-144923-0392-66881369-p1m.bsequence

# -datafile EDNAFULL

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 00AE14\_77061928\_77061928\_Ex3\_WT

# 2: 00AE13\_77061911\_77061911\_Ex3-F9

# Matrix: EDNAFULL

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 934

# Identity: 775/934 (83.0%)

# Similarity: 775/934 (83.0%)

# Gaps: 157/934 (16.8%)

# Score: 3856.5

#

#

#=======================================

00AE14\_770619 1 ----AAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTTCT 46

||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 1 ATACAAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTTCT 50

00AE14\_770619 47 TAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTACA 96

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 51 TAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTACA 100

00AE14\_770619 97 GTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAGAC 146

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 101 GTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAGAC 150

00AE14\_770619 147 CCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACTAG 196

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 151 CCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACTAG 200

00AE14\_770619 197 CTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATATAT 246

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 201 CTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATATAT 250

00AE14\_770619 247 TCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAAAA 296

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 251 TCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAAAA 300

00AE14\_770619 297 TTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGTTC 346

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 301 TTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGTTC 350

00AE14\_770619 347 TATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGGTC 396

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 351 TATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGGTC 400

00AE14\_770619 397 TTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTAGT 446

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 401 TTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTAGT 450

00AE14\_770619 447 GCGGCAAAAGCGCGCCTGGATCACCGCCCCCGTGGCTCTTCGGGAGGGAG 496

|||||||||||||||||||||||||| ||||||||||||||||||||||

00AE13\_770619 451 GCGGCAAAAGCGCGCCTGGATCACCG--CCCGTGGCTCTTCGGGAGGGAG 498

00AE14\_770619 497 AGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGGAA 546

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 499 AGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGGAA 548

00AE14\_770619 547 CATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTATGT 596

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 549 CATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTATGT 598

00AE14\_770619 597 CTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTAAA 646

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 599 CTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTAAA 648

00AE14\_770619 647 TATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTTTTAGCATAAAGT 696

|||||||||||||||||||||||||||||||||||||.||||||||||||

00AE13\_770619 649 TATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTCTTAGCATAAAGT 698

00AE14\_770619 697 ATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTGGC 746

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE13\_770619 699 ATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTGGC 748

00AE14\_770619 747 AATAATATAGATAACTTTGAGTTTTGATTTAACTAAGAGTAAAGGGATTT 796

|||||||||||||||||||||||||||.|||||

00AE13\_770619 749 AATAATATAGATAACTTTGAGTTTTGAGTTAAC----------------- 781

00AE14\_770619 797 GGCACTGGTAACACAAAATGTTCAGTGCTCAGAAGAGGATGTCATAAAAT 846

00AE13\_770619 782 -------------------------------------------------- 781

00AE14\_770619 847 GTCATTTTCAAGATGAACTGGTGTCTATTACTAGGTAGGGGGACCATCTT 896

00AE13\_770619 782 -------------------------------------------------- 781

00AE14\_770619 897 CATCTGCCTGAGACAGTCGTGGTTTATGCTGCTC 930

00AE13\_770619 782 ---------------------------------- 781

#---------------------------------------

#---------------------------------------

Exon 5

########################################

# Program: needle

# Rundate: Wed 20 Feb 2019 08:00:40

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190220-080037-0559-23994035-p2m.asequence

# -bsequence emboss\_needle-I20190220-080037-0559-23994035-p2m.bsequence

# -datafile EDNAFULL

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AH06\_90287145\_90287145\_ex5\_dsg2\_F9

# 2: 65AH02\_90287107\_90287107\_ex5\_wt

# Matrix: EDNAFULL

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 886

# Identity: 783/886 (88.4%)

# Similarity: 783/886 (88.4%)

# Gaps: 103/886 (11.6%)

# Score: 3895.0

#

#

#=======================================

65AH06\_902871 1 -TTACCAAAG-ACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTA 48

||||||||| |||||||||||||||||||||||||||||||||||||||

65AH02\_902871 1 ATTACCAAAGAACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTA 50

65AH06\_902871 49 AATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAA 98

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 51 AATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAA 100

65AH06\_902871 99 ATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATAC 148

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 101 ATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATAC 150

65AH06\_902871 149 ATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACT 198

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 151 ATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACT 200

65AH06\_902871 199 GGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGA 248

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 201 GGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGA 250

65AH06\_902871 249 TACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCAT 298

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 251 TACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCAT 300

65AH06\_902871 299 TTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCT 348

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 301 TTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCT 350

65AH06\_902871 349 GTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGT 398

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 351 GTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGT 400

65AH06\_902871 399 TTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGG 448

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 401 TTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGG 450

65AH06\_902871 449 TTACGCTTTGGATGCCAAGAGGAAACAATGTAGAGAAACCCTTAGAGCTA 498

|||||||||||||| |||||||||||||||||||||||||||||||||||

65AH02\_902871 451 TTACGCTTTGGATG-CAAGAGGAAACAATGTAGAGAAACCCTTAGAGCTA 499

65AH06\_902871 499 CGCATTAAGGTTCTTGATATCAATGACAACGAACCAGTGTTCACACAGGA 548

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 500 CGCATTAAGGTTCTTGATATCAATGACAACGAACCAGTGTTCACACAGGA 549

65AH06\_902871 549 TGTCTTTGTTGGGTCTGTTGAAGAGTTGAGTGCAGCACGTAAGAGTCTTT 598

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 550 TGTCTTTGTTGGGTCTGTTGAAGAGTTGAGTGCAGCACGTAAGAGTCTTT 599

65AH06\_902871 599 TTTTTTTTTTTTAAAAAATAAATACCTAAAATTACTTTATCCCCACTGTA 648

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 600 TTTTTTTTTTTTAAAAAATAAATACCTAAAATTACTTTATCCCCACTGTA 649

65AH06\_902871 649 AATAAACACTAAATTTCATATCTTAATGAAAGTTGAGTATTACCTACAGA 698

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 650 AATAAACACTAAATTTCATATCTTAATGAAAGTTGAGTATTACCTACAGA 699

65AH06\_902871 699 ACAAATGATAAGAAAGCAGTTCAGAACTGCTTTCCTTATAGGTTTAAAGG 748

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH02\_902871 700 ACAAATGATAAGAAAGCAGTTCAGAACTGCTTTCCTTATAGGTTTAAAGG 749

65AH06\_902871 749 ACTTTACATGCCATTGCTTTTACCCTCAGAACAGAT-------------- 784

||||||||||||||||||||||||||||||||||||

65AH02\_902871 750 ACTTTACATGCCATTGCTTTTACCCTCAGAACAGATAGGGTAGATTAATG 799

65AH06\_902871 785 -------------------------------------------------- 784

65AH02\_902871 800 TGATGGATAAGGTCTCTGTAGCAACTACTCAACTCTGCTATCTGCAGGAA 849

65AH06\_902871 785 ------------------------------------ 784

65AH02\_902871 850 AGCACCATAGACAATATGTAAACAATGAGCAGACTG 885

#---------------------------------------

#---------------------------------------

**Exon 8**

########################################

# Program: needle

# Rundate: Wed 20 Feb 2019 08:04:14

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190220-080412-0040-60773265-p2m.asequence

# -bsequence emboss\_needle-I20190220-080412-0040-60773265-p2m.bsequence

# -datafile EDNAFULL

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AG95\_90287039\_90287039\_ex8\_dsg\_F9

# 2: 65AH04\_90287121\_90287121\_ex8\_wt

# Matrix: EDNAFULL

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 892

# Identity: 886/892 (99.3%)

# Similarity: 886/892 (99.3%)

# Gaps: 5/892 ( 0.6%)

# Score: 4426.0

#

#

#=======================================

65AG95\_902870 1 -----AGTAAATAGTATCTTCACACAAATAATAGCAGATCATAAAACAGA 45

|||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 1 ACTGCAGTAAATAGTATCTTCACACAAATAATAGCAGATCATAAAACAGA 50

65AG95\_902870 46 TTTGTAAATAAAATATACTGTGGTACGTGATAAACTGGACTAAAACCAGA 95

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 51 TTTGTAAATAAAATATACTGTGGTACGTGATAAACTGGACTAAAACCAGA 100

65AG95\_902870 96 AAGCCAGATGTAAGAGTGACTCTTTTCACCCAGCTGGACATTTTTCATTG 145

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 101 AAGCCAGATGTAAGAGTGACTCTTTTCACCCAGCTGGACATTTTTCATTG 150

65AG95\_902870 146 CTCTGCAGGAACACAGCAGCTACACTTTGACAGTAGAAGCAAGAGATGGC 195

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 151 CTCTGCAGGAACACAGCAGCTACACTTTGACAGTAGAAGCAAGAGATGGC 200

65AG95\_902870 196 AATGGAGAAGTTACAGACAAACCTGTAAAACAAGCTCAAGTTCAGATTCG 245

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 201 AATGGAGAAGTTACAGACAAACCTGTAAAACAAGCTCAAGTTCAGATTCG 250

65AG95\_902870 246 TATTTTGGATGTCAATGACAATATACCTGTAGTAGAAAATAAAGTGGTAA 295

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 251 TATTTTGGATGTCAATGACAATATACCTGTAGTAGAAAATAAAGTGGTAA 300

65AG95\_902870 296 CTATTATTCTTCTAATAACTGTACCTATTTATTTATATTTCAGTCCTAAT 345

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 301 CTATTATTCTTCTAATAACTGTACCTATTTATTTATATTTCAGTCCTAAT 350

65AG95\_902870 346 TAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGT 395

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 351 TAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGT 400

65AG95\_902870 396 TCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAG 445

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 401 TCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAG 450

65AG95\_902870 446 AAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAAT 495

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 451 AAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAAT 500

65AG95\_902870 496 TGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCA 545

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 501 TGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCA 550

65AG95\_902870 546 CATAGAAACAGATGCTCAAACTAACGAAGGAATTGTGACCCTTATTAAGG 595

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 551 CATAGAAACAGATGCTCAAACTAACGAAGGAATTGTGACCCTTATTAAGG 600

65AG95\_902870 596 TAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGG 645

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 601 TAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGG 650

65AG95\_902870 646 AATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCA 695

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 651 AATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCA 700

65AG95\_902870 696 ATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCA 745

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 701 ATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCA 750

65AG95\_902870 746 AGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGG 795

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 751 AGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGG 800

65AG95\_902870 796 GACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGC 845

||||||||||||||||||||||||||||||||||||||||||||||||||

65AH04\_902871 801 GACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGC 850

65AG95\_902870 846 TCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGAGACAAT 887

||||||||||||||||||||||||||||||||||||.|||||

65AH04\_902871 851 TCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGATACAAT 892

#---------------------------------------

#---------------------------------------

RAW data of sequencing.

>65AG95\_90287039\_90287039\_ex8\_dsg\_F9

AGTAAATAGTATCTTCACACAAATAATAGCAGATCATAAAACAGATTTGTAAATAAAATATACTGTGGTACGTGATAAACTGGACTAAAACCAGAAAGCCAGATGTAAGAGTGACTCTTTTCACCCAGCTGGACATTTTTCATTGCTCTGCAGGAACACAGCAGCTACACTTTGACAGTAGAAGCAAGAGATGGCAATGGAGAAGTTACAGACAAACCTGTAAAACAAGCTCAAGTTCAGATTCGTATTTTGGATGTCAATGACAATATACCTGTAGTAGAAAATAAAGTGGTAACTATTATTCTTCTAATAACTGTACCTATTTATTTATATTTCAGTCCTAATTAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGTTCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAGAAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAATTGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCACATAGAAACAGATGCTCAAACTAACGAAGGAATTGTGACCCTTATTAAGGTAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGGAATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCAATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCAAGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGGGACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGCTCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGAGACAAT

>65AH00\_90287084\_90287084\_ex2\_dsg2\_F9

AAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCACAAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTCAGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGGGAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTGGTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGAACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAATTTTATTTTACAGATCTGCTTTAACGTTGGAAGTGGACTTCACTTACAGGTGAGGAAACAAAGGGATTATTTCTGCCTTCTGACTCAGGAGGGTTAATTCCATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTATTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGGGTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAATGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGAGAAG

>65AH01\_90287091\_90287091\_ex2\_wt

AAAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCACAAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTCAGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGGGAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTGGTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGAACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAATTTTATTTTACAGATCTGCTTTAACGTTGGAAGTGGACTTCACTTACAGGTGAGGAAACAAAGGGATTATTTCTGCCTTCTGACTCAGGAGGGTTAATTCCATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTATTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGGGTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAATGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGAGAAGGT

**WT Exon 3**

>00AE14\_77061928\_77061928

AAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTTCTTAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTACAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAGACCCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACTAGCTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATATATTCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAAAATTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGTTCTATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGGTCTTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTAGTGCGGCAAAAGCGCGCCTGGATCACCGCCCCCGTGGCTCTTCGGGAGGGAGAGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGGAACATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTATGTCTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTAAATATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTTTTAGCATAAAGTATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTGGCAATAATATAGATAACTTTGAGTTTTGATTTAACTAAGAGTAAAGGGATTTGGCACTGGTAACACAAAATGTTCAGTGCTCAGAAGAGGATGTCATAAAATGTCATTTTCAAGATGAACTGGTGTCTATTACTAGGTAGGGGGACCATCTTCATCTGCCTGAGACAGTCGTGGTTTATGCTGCTC

**F9 Exon 3**

>00AE13\_77061911\_77061911

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>65AH02\_90287107\_90287107\_ex5\_wt

ATTACCAAAGAACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTAAATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAAATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATACATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACTGGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGATACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCATTTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCTGTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGTTTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGGTTACGCTTTGGATGCAAGAGGAAACAATGTAGAGAAACCCTTAGAGCTACGCATTAAGGTTCTTGATATCAATGACAACGAACCAGTGTTCACACAGGATGTCTTTGTTGGGTCTGTTGAAGAGTTGAGTGCAGCACGTAAGAGTCTTTTTTTTTTTTTTTAAAAAATAAATACCTAAAATTACTTTATCCCCACTGTAAATAAACACTAAATTTCATATCTTAATGAAAGTTGAGTATTACCTACAGAACAAATGATAAGAAAGCAGTTCAGAACTGCTTTCCTTATAGGTTTAAAGGACTTTACATGCCATTGCTTTTACCCTCAGAACAGATAGGGTAGATTAATGTGATGGATAAGGTCTCTGTAGCAACTACTCAACTCTGCTATCTGCAGGAAAGCACCATAGACAATATGTAAACAATGAGCAGACTG

>65AH04\_90287121\_90287121\_ex8\_wt

ACTGCAGTAAATAGTATCTTCACACAAATAATAGCAGATCATAAAACAGATTTGTAAATAAAATATACTGTGGTACGTGATAAACTGGACTAAAACCAGAAAGCCAGATGTAAGAGTGACTCTTTTCACCCAGCTGGACATTTTTCATTGCTCTGCAGGAACACAGCAGCTACACTTTGACAGTAGAAGCAAGAGATGGCAATGGAGAAGTTACAGACAAACCTGTAAAACAAGCTCAAGTTCAGATTCGTATTTTGGATGTCAATGACAATATACCTGTAGTAGAAAATAAAGTGGTAACTATTATTCTTCTAATAACTGTACCTATTTATTTATATTTCAGTCCTAATTAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGTTCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAGAAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAATTGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCACATAGAAACAGATGCTCAAACTAACGAAGGAATTGTGACCCTTATTAAGGTAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGGAATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCAATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCAAGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGGGACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGCTCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGATACAAT

>65AH06\_90287145\_90287145\_ex5\_dsg2\_F9

TTACCAAAGACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTAAATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAAATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATACATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACTGGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGATACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCATTTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCTGTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGTTTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGGTTACGCTTTGGATGCCAAGAGGAAACAATGTAGAGAAACCCTTAGAGCTACGCATTAAGGTTCTTGATATCAATGACAACGAACCAGTGTTCACACAGGATGTCTTTGTTGGGTCTGTTGAAGAGTTGAGTGCAGCACGTAAGAGTCTTTTTTTTTTTTTTTAAAAAATAAATACCTAAAATTACTTTATCCCCACTGTAAATAAACACTAAATTTCATATCTTAATGAAAGTTGAGTATTACCTACAGAACAAATGATAAGAAAGCAGTTCAGAACTGCTTTCCTTATAGGTTTAAAGGACTTTACATGCCATTGCTTTTACCCTCAGAACAGAT

**H11 Exon 2**

>00AE12\_77061904\_77061904

AAAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCACAAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTCAGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGGGAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTGGTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGAACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAATTTTATTTTACAGATCTGCTTTAACGTTGGACTTTCTGCCTTCTGACTCAGGAGGGTTAATTCCATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTATTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGGGTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAATGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGACAG

**H11 Exon 8**

>00AE15\_77061935\_77061935

GCAGTCCTAATTAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGTTCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAGAAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAATTGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCACATAGAAACAGATGCTCAAACGAAGGAATTGTGACCCTTATTAAGGTAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGGAATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCAATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCAAGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGGGACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGCTCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGATCACATTCC

**H11 Exon 5**

>00AE16\_77061942\_77061942

CAAAGAACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTAAATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAAATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATACATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACTGGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGATACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCATTTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCTGTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGTTTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGGTTACGCTTTAGAAGA

**H11 Exon 3**

>00AE17\_77061959\_77061959

GAATACAAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTTCTTAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTACAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAGACCCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACTAGCTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATATATTCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAAAATTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGTTCTATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGGTCTTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTAGTGCGGCAAAAGCGCGCCTGGATCACCGCCCGTGGCTCTTCGGGAGGGAGAGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGGAACATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTATGTCTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTAAATATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTTTTAGCATAAAGTATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTGGCAAAAATATAGATAACTTTGAGTTTTGATTTAACTAAGAGTAAAGGGATTTGGCACTGGTAACACAAAATGTTCAGTGCTCAAAAGAGGATGTCATAAAATGTCATTTTCAAGATGAACTGGTGTCTATTACTAGGTAGGGGGACCATCTTCATCTGCCTGAGACAGTCGTGGTTTATGCTGTCCT

**EXON 2**

########################################

# Program: needle

# Rundate: Tue 23 Apr 2019 14:55:15

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190423-145513-0185-45468476-p2m.asequence

# -bsequence emboss\_needle-I20190423-145513-0185-45468476-p2m.bsequence

# -datafile EBLOSUM62

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -sprotein1

# -sprotein2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AH01\_90287091\_90287091\_ex2\_wt

# 2: 00AE12\_77061904\_77061904\_Ex2\_H11

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 595

# Identity: 552/595 (92.8%)

# Similarity: 552/595 (92.8%)

# Gaps: 40/595 ( 6.7%)

# Score: 3007.0

#

#

#=======================================

65AH01\_902870 1 AAAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCAC 50

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 1 AAAAACCATAGGATGCGGAGTAAAGGATGAGAGAATGTCTAAGATTTCAC 50

65AH01\_902870 51 AAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTC 100

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 51 AAGGCAGATTATTTTGTTTGTTTTTTAAGATACTGTTTTCTGGAGGAGTC 100

65AH01\_902870 101 AGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGG 150

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 101 AGTATGGATCCAGGAGAATATAGATTTCTCCTCGGGCACTTCCCATTAGG 150

65AH01\_902870 151 GAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTG 200

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 151 GAAGGCAATGGGAAAAATTAGTTTCCTCTTGACAAAGAATAGTAGTAGTG 200

65AH01\_902870 201 GTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGA 250

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 201 GTTAAACTTTTTTTATGTCTATAATATTCAATGCAGTAGGTTATTCATGA 250

65AH01\_902870 251 ACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAA 300

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 251 ACAATGTTTTCACACTGAATTGAGCAGTAAATTGGCTAAATATCAAATAA 300

65AH01\_902870 301 TTTTATTTTACAGATCTGCTTTAACGTTGGAAGTGGACTTCACTTACAGG 350

|||||||||||||||||||||||||||||||

00AE12\_770619 301 TTTTATTTTACAGATCTGCTTTAACGTTGGA------------------- 331

65AH01\_902870 351 TGAGGAAACAAAGGGATTATTTCTGCCTTCTGACTCAGGAGGGTTAATTC 400

.|||||||||||||||||||||||||||||||

00AE12\_770619 332 ------------------CTTTCTGCCTTCTGACTCAGGAGGGTTAATTC 363

65AH01\_902870 401 CATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTA 450

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 364 CATGGCAAACAGGTTGACTGGGCTTTACTAGATTGAAGACACATGTTGTA 413

65AH01\_902870 451 TTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGG 500

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 414 TTAGACCCAGCCATTCCCATTCAAACAAGTGCAGAGGAGCTTATCCAGGG 463

65AH01\_902870 501 GTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAA 550

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE12\_770619 464 GTATTCAGTGCAGCAGTTTTTGACAATGTAAATATCCACCAATAGGTGAA 513

65AH01\_902870 551 TGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGAGAAGGT 595

|||||||||||||||||||||||||||||||||||||||.|.

00AE12\_770619 514 TGTTAAAACCATTTATGGTACATGAAAGAATGTCCATGACAG--- 555

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#---------------------------------------

EXON 3

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# Program: needle

# Rundate: Tue 23 Apr 2019 14:52:27

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190423-145222-0933-33387554-p2m.asequence

# -bsequence emboss\_needle-I20190423-145222-0933-33387554-p2m.bsequence

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -sprotein1

# -sprotein2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 00AE14\_77061928\_77061928\_Ex3\_WT

# 2: 00AE17\_77061959\_77061959\_Ex3\_H11

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 937

# Identity: 924/937 (98.6%)

# Similarity: 924/937 (98.6%)

# Gaps: 9/937 ( 1.0%)

# Score: 5159.5

#

#

#=======================================

00AE14\_770619 1 ------AAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTT 44

||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 1 GAATACAAAAATTAGCCAGATGTGGTGGTGCATGCCTGTAATCCCAGCTT 50

00AE14\_770619 45 CTTAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTA 94

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 51 CTTAGGAGGCTGAGGCAGGAAGATGGCTTGATCCGGGGAAGTCAAGGCTA 100

00AE14\_770619 95 CAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAG 144

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 101 CAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAG 150

00AE14\_770619 145 ACCCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACT 194

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 151 ACCCTGTCTCAAAAGAAAAAATAAACCAGAAAAAACCCTACACTTTTACT 200

00AE14\_770619 195 AGCTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATAT 244

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 201 AGCTTGGAGACAATCTCTTGAGGCCCTATGCAGTTTGCTAGAATATATAT 250

00AE14\_770619 245 ATTCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAA 294

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 251 ATTCCCTTTTAGACAATGAAGCCTCATAGGAAATACGAAGCATACCTTAA 300

00AE14\_770619 295 AATTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGT 344

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 301 AATTTGCACTATTTAAAAGTTTATTATGTTATAGGACAGCATACTAATGT 350

00AE14\_770619 345 TCTATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGG 394

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 351 TCTATATTTATGACACATAATAAATTTTGGCAATATTCTATTGTTATAGG 400

00AE14\_770619 395 TCTTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTA 444

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 401 TCTTAAGCACAAGAAATGAAAATAAGCTGCTTCCTAAACATCCTCATTTA 450

00AE14\_770619 445 GTGCGGCAAAAGCGCGCCTGGATCACCGCCCCCGTGGCTCTTCGGGAGGG 494

|||||||||||||||||||||||||||| ||||||||||||||||||||

00AE17\_770619 451 GTGCGGCAAAAGCGCGCCTGGATCACCG--CCCGTGGCTCTTCGGGAGGG 498

00AE14\_770619 495 AGAGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGG 544

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 499 AGAGGATCTGTCCAAGAAGAATCCAATTGCCAAGGTACCTCCTAAAGAGG 548

00AE14\_770619 545 AACATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTAT 594

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 549 AACATGAAATACATGCATATGACTAAAATGTGGTGTGAGAGGACTTTTAT 598

00AE14\_770619 595 GTCTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTA 644

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 599 GTCTACTTTAAGATTTAAGGAAAATGTATGATGTGCTTACAGAATTTTTA 648

00AE14\_770619 645 AATATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTTTTAGCATAAA 694

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 649 AATATTCAAGATATATCTGAAAATTAGCAGAGCTTACTTTTTAGCATAAA 698

00AE14\_770619 695 GTATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTG 744

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 699 GTATCAACTTTAAGATTCTCTTTCCCATTCCGGAAGATGCAGCATCATTG 748

00AE14\_770619 745 GCAATAATATAGATAACTTTGAGTTTTGATTTAACTAAGAGTAAAGGGAT 794

||||.|||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 749 GCAAAAATATAGATAACTTTGAGTTTTGATTTAACTAAGAGTAAAGGGAT 798

00AE14\_770619 795 TTGGCACTGGTAACACAAAATGTTCAGTGCTCAGAAGAGGATGTCATAAA 844

|||||||||||||||||||||||||||||||||.||||||||||||||||

00AE17\_770619 799 TTGGCACTGGTAACACAAAATGTTCAGTGCTCAAAAGAGGATGTCATAAA 848

00AE14\_770619 845 ATGTCATTTTCAAGATGAACTGGTGTCTATTACTAGGTAGGGGGACCATC 894

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE17\_770619 849 ATGTCATTTTCAAGATGAACTGGTGTCTATTACTAGGTAGGGGGACCATC 898

00AE14\_770619 895 TTCATCTGCCTGAGACAGTCGTGGTTTATGCTGCTC- 930

|||||||||||||||||||||||||||||||||..|

00AE17\_770619 899 TTCATCTGCCTGAGACAGTCGTGGTTTATGCTGTCCT 935

**EXON 5**

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# Program: needle

# Rundate: Tue 23 Apr 2019 15:00:43

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190423-150041-0057-75980166-p2m.asequence

# -bsequence emboss\_needle-I20190423-150041-0057-75980166-p2m.bsequence

# -datafile EBLOSUM62

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -sprotein1

# -sprotein2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AH02\_90287107\_90287107\_ex5\_wt

# 2: 00AE16\_77061942\_77061942\_Ex5\_H11

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 885

# Identity: 457/885 (51.6%)

# Similarity: 457/885 (51.6%)

# Gaps: 425/885 (48.0%)

# Score: 2459.0

#

#

#=======================================

65AH02\_902871 1 ATTACCAAAGAACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTA 50

|||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 1 -----CAAAGAACTTCAGAAGGAAATTGTCCATAAAAATATTTACCTGTA 45

65AH02\_902871 51 AATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAA 100

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 46 AATTATAGAGAATCACTTCTTAGGCTTTTGGCTAAGATCAAATCTAGTAA 95

65AH02\_902871 101 ATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATAC 150

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 96 ATTACAGAGAGTTCAACCTGAAACATTCCTGTTATTTTTATGTTAGATAC 145

65AH02\_902871 151 ATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACT 200

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 146 ATTCTGATCTTGCAGAAGAAAGAGGACTCAAAATTACTTACAAATACACT 195

65AH02\_902871 201 GGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGA 250

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 196 GGAAAAGGGATTACAGAGCCACCTTTTGGTATATTTGTCTTTAACAAAGA 245

65AH02\_902871 251 TACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCAT 300

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 246 TACTGGAGAACTGAATGTTACCAGCATTCTTGATCGAGAAGAAACACCAT 295

65AH02\_902871 301 TTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCT 350

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 296 TTTTTCTGGTAAGAAGAATAATTTTAGATTTATTAGTTTGTAGTTTTTCT 345

65AH02\_902871 351 GTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGT 400

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 346 GTCATAATAAGTGTCATTTGTTTTATTTTTTCATAGTATGGTAATTTAGT 395

65AH02\_902871 401 TTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGG 450

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE16\_770619 396 TTTCTTAGCTTAAATCTAATCTTATTTATGTCATGATTTCAGCTAACAGG 445

65AH02\_902871 451 TTACGCTTTGGATGCAAGAGGAAACAATGTAGAGAAACCCTTAGAGCTAC 500

|||||||||.||.|.

00AE16\_770619 446 TTACGCTTTAGAAGA----------------------------------- 460

65AH02\_902871 501 GCATTAAGGTTCTTGATATCAATGACAACGAACCAGTGTTCACACAGGAT 550

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 551 GTCTTTGTTGGGTCTGTTGAAGAGTTGAGTGCAGCACGTAAGAGTCTTTT 600

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 601 TTTTTTTTTTTAAAAAATAAATACCTAAAATTACTTTATCCCCACTGTAA 650

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 651 ATAAACACTAAATTTCATATCTTAATGAAAGTTGAGTATTACCTACAGAA 700

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 701 CAAATGATAAGAAAGCAGTTCAGAACTGCTTTCCTTATAGGTTTAAAGGA 750

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 751 CTTTACATGCCATTGCTTTTACCCTCAGAACAGATAGGGTAGATTAATGT 800

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 801 GATGGATAAGGTCTCTGTAGCAACTACTCAACTCTGCTATCTGCAGGAAA 850

00AE16\_770619 461 -------------------------------------------------- 460

65AH02\_902871 851 GCACCATAGACAATATGTAAACAATGAGCAGACTG 885

00AE16\_770619 461 ----------------------------------- 460

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#---------------------------------------

**Exom 8**

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# Program: needle

# Rundate: Tue 23 Apr 2019 15:08:17

# Commandline: needle

# -auto

# -stdout

# -asequence emboss\_needle-I20190423-150816-0238-6251982-p1m.asequence

# -bsequence emboss\_needle-I20190423-150816-0238-6251982-p1m.bsequence

# -datafile EBLOSUM62

# -gapopen 10.0

# -gapextend 0.5

# -endopen 10.0

# -endextend 0.5

# -aformat3 pair

# -sprotein1

# -sprotein2

# Align\_format: pair

# Report\_file: stdout

########################################

#=======================================

#

# Aligned\_sequences: 2

# 1: 65AH04\_90287121\_90287121\_ex8\_wt

# 2: 00AE15\_77061935\_77061935\_Ex8\_H11

# Matrix: EBLOSUM62

# Gap\_penalty: 10.0

# Extend\_penalty: 0.5

#

# Length: 895

# Identity: 547/895 (61.1%)

# Similarity: 547/895 (61.1%)

# Gaps: 346/895 (38.7%)

# Score: 3037.5

#

#

#=======================================

65AH04\_902871 1 ACTGCAGTAAATAGTATCTTCACACAAATAATAGCAGATCATAAAACAGA 50

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 51 TTTGTAAATAAAATATACTGTGGTACGTGATAAACTGGACTAAAACCAGA 100

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 101 AAGCCAGATGTAAGAGTGACTCTTTTCACCCAGCTGGACATTTTTCATTG 150

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 151 CTCTGCAGGAACACAGCAGCTACACTTTGACAGTAGAAGCAAGAGATGGC 200

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 201 AATGGAGAAGTTACAGACAAACCTGTAAAACAAGCTCAAGTTCAGATTCG 250

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 251 TATTTTGGATGTCAATGACAATATACCTGTAGTAGAAAATAAAGTGGTAA 300

00AE15\_770619 1 -------------------------------------------------- 0

65AH04\_902871 301 CTATTATTCTTCTAATAACTGTACCTATTTATTTATATTTCAGTCCTAAT 350

.||||||||||

00AE15\_770619 1 ---------------------------------------GCAGTCCTAAT 11

65AH04\_902871 351 TAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGT 400

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 12 TAAAAATATATCACTTATATTTGTATTTCATTGAAATAAAAATCATGTGT 61

65AH04\_902871 401 TCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAG 450

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 62 TCATGTTTTGCAGCTTGAAGGGATGGTTGAAGAAAATCAAGTCAACGTAG 111

65AH04\_902871 451 AAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAAT 500

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 112 AAGTTACGCGCATAAAAGTGTTCGATGCAGATGAAATAGGTTCTGATAAT 161

65AH04\_902871 501 TGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCA 550

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 162 TGGCTGGCAAATTTTACATTTGCATCAGGAAATGAAGGAGGTTATTTCCA 211

65AH04\_902871 551 CATAGAAACAGATGCTCAAACTAACGAAGGAATTGTGACCCTTATTAAGG 600

|||||||||||||||||| ||||||||||||||||||||||||||||

00AE15\_770619 212 CATAGAAACAGATGCTCA----AACGAAGGAATTGTGACCCTTATTAAGG 257

65AH04\_902871 601 TAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGG 650

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 258 TAAGTACTAAGTATTCAAAACTGGCGTGGGCCAAGTTGGTGCTGGAAAGG 307

65AH04\_902871 651 AATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCA 700

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 308 AATCTAATATATTTTGAGCCCTGAACACTTAAAAGTGCTTTACATATTCA 357

65AH04\_902871 701 ATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCA 750

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 358 ATTAACTAGCACTACAGTTGTTTGAGAAAGGAGCCATCCCTATTTGCCCA 407

65AH04\_902871 751 AGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGG 800

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 408 AGTTCTGTGGTTAGGAAGTGGTCACACTATGGTTCAAATTCATATCAGGG 457

65AH04\_902871 801 GACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGC 850

||||||||||||||||||||||||||||||||||||||||||||||||||

00AE15\_770619 458 GACTCTAATCCTAGCCAGACAGCATGGTACCACCATCATTACTGCTTAGC 507

65AH04\_902871 851 TCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGAT-ACAAT-- 892

||||||||||||||||||||||||||||||||||||| |||.|

00AE15\_770619 508 TCATTTCCAGGCTTTCTTGCAGCTCATACCTGGCGATCACATTCC 552

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