**Supplemental Figure 7.** Alignment of IGHD3 and IGHD6 family members with IGHD8-2.

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

# Program: matcher

# Rundate: Sat 5 Oct 2019 00:41:09

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191005-004107-0321-40057744-p1m.asequence

# -bsequence emboss\_matcher-I20191005-004107-0321-40057744-p1m.bsequence

# -datafile EDNAFULL

# -gapopen 16

# -gapextend 4

# -alternatives 1

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

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

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

#

# Aligned\_sequences: 2

# 1: IGHD8\_2

# 2: IGHD3\_4

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 65

# Identity: 52/65 (80.0%)

# Similarity: 52/65 (80.0%)

# Gaps: 5/65 ( 7.7%)

# Score: 184

#

#

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

IGHD8\_2 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTA--GTTGTCCTGATGGTTAT 48

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

IGHD3\_4 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTATTGTGGTAGCTATTGTGGT 50

IGHD8\_2 49 AGTTATGGTTATGGT 63

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

IGHD3\_4 51 AGTTAT---TATGGT 62

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

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

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

# Program: matcher

# Rundate: Sat 5 Oct 2019 00:42:25

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191005-004222-0822-86095519-p2m.asequence

# -bsequence emboss\_matcher-I20191005-004222-0822-86095519-p2m.bsequence

# -datafile EDNAFULL

# -gapopen 16

# -gapextend 4

# -alternatives 1

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

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

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

#

# Aligned\_sequences: 2

# 1: IGHD8\_2

# 2: IGHD3\_3

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 65

# Identity: 52/65 (80.0%)

# Similarity: 52/65 (80.0%)

# Gaps: 5/65 ( 7.7%)

# Score: 184

#

#

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

IGHD8\_2 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTA--GTTGTCCTGATGGTTAT 48

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

IGHD3\_3 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTATTGTGGTAGCTATTGTGGT 50

IGHD8\_2 49 AGTTATGGTTATGGT 63

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

IGHD3\_3 51 AGTTAT---TATGGT 62

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

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

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

# Program: matcher

# Rundate: Fri 4 Oct 2019 23:30:39

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191004-233038-0324-2606874-p2m.asequence

# -bsequence emboss\_matcher-I20191004-233038-0324-2606874-p2m.bsequence

# -datafile EDNAFULL

# -gapopen 16

# -gapextend 4

# -alternatives 1

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

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

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

#

# Aligned\_sequences: 2

# 1: IGHD8\_2

# 2: IGHD6\_2

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 85

# Identity: 76/85 (89.4%)

# Similarity: 76/85 (89.4%)

# Gaps: 0/85 ( 0.0%)

# Score: 344

#

#

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

IGHD8\_2 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTAGTTGTCCTGATGGTTATAG 50

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

IGHD6\_2 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTAGTTGTTATAGTGGTTATGG 50

IGHD8\_2 51 TTATGGTTATGGTTGTGGTTATGGTTATGGTTGTA 85

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

IGHD6\_2 51 TTATGGTTGTGGTTATGGTTATGGTTATGATTATA 85

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

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

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

# Program: matcher

# Rundate: Fri 4 Oct 2019 23:33:07

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191004-233305-0188-59118204-p1m.asequence

# -bsequence emboss\_matcher-I20191004-233305-0188-59118204-p1m.bsequence

# -datafile EDNAFULL

# -gapopen 16

# -gapextend 4

# -alternatives 1

# -aformat3 pair

# -snucleotide1

# -snucleotide2

# Align\_format: pair

# Report\_file: stdout

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

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

#

# Aligned\_sequences: 2

# 1: IGHD8\_2

# 2: IGHD6\_3

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 85

# Identity: 78/85 (91.8%)

# Similarity: 78/85 (91.8%)

# Gaps: 0/85 ( 0.0%)

# Score: 362

#

#

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

IGHD8\_2 1 GGTTTCTGATGCCGGCTGTGTCACGGTGGTAGTTGTCCTGATGGTTATAG 50

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

IGHD6\_3 1 GGTTTCTGATGCCAGCTGTGTCACGGTGGTAGTTGTTATAGTGGTTATGG 50

IGHD8\_2 51 TTATGGTTATGGTTGTGGTTATGGTTATGGTTGTA 85

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

IGHD6\_3 51 TTATGGTTATGGTTGTGGTTATGGTTATGGTTATA 85

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

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