**Supplemental Figure 5.** Local alignment of IGHD7-3 and IGHD7-4 with IGHD8-2.

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

# Program: matcher

# Rundate: Sat 5 Oct 2019 00:28:58

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191005-002855-0888-87948780-p2m.asequence

# -bsequence emboss\_matcher-I20191005-002855-0888-87948780-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: IGHD7\_3

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 97

# Identity: 83/97 (85.6%)

# Similarity: 83/97 (85.6%)

# Gaps: 0/97 ( 0.0%)

# Score: 359

#

#

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

IGHD8\_2 108 TGGTGGTTATGGTGGTTATGGTGGTTATGGTTATAGTAGTTATAGTTATA 157

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

IGHD7\_3 27 TGGTAGTTATGGTGGTTATGGTTATGGTGGTTATGGTTGTTATGGTTATG 76

IGHD8\_2 158 GTTATACTTACGAATATACCACAGTGATACTCTCTGGGACAAAAACC 204

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

IGHD7\_3 77 GTTATGGTTATGGTTATACCACAGTGATACTCTCTGGGACAAAAACC 123

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

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

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

# Program: matcher

# Rundate: Sat 5 Oct 2019 00:30:17

# Commandline: matcher

# -auto

# -stdout

# -asequence emboss\_matcher-I20191005-003015-0194-38128626-p2m.asequence

# -bsequence emboss\_matcher-I20191005-003015-0194-38128626-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: IGHD7\_4

# Matrix: EDNAFULL

# Gap\_penalty: 16

# Extend\_penalty: 4

#

# Length: 132

# Identity: 102/132 (77.3%)

# Similarity: 102/132 (77.3%)

# Gaps: 3/132 ( 2.3%)

# Score: 378

#

#

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

IGHD8\_2 73 GGTTATGGTTGTAGTGGTTATGATTGTTATGGTTATGGTGGTTATGGTGG 122

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

IGHD7\_4 1 GGTTTTTGATGCCGGCTGTGTCACGGTGGTAGTTATGGTGGTTATG---G 47

IGHD8\_2 123 TTATGGTGGTTATGGTTATAGTAGTTATAGTTATAGTTATACTTACGAAT 172

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

IGHD7\_4 48 TTATGGTGGTTATGGTTGTTATGGTTATGGTTATGGTTATGGTTATGGTT 97

IGHD8\_2 173 ATACCACAGTGATACTCTCTGGGACAAAAACC 204

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

IGHD7\_4 98 ATACCACAGTGATACTCTCTGGGACAAAAACC 129

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

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