**Supplemental Figure 1.** Alignment of all bovine DH regions in clusters 2-4 was performed using Clustal Omega. (A) Percent identity matrix. (B) Sequence alignment. (C) Phylogenetic tree.

**A.**

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# Percent Identity Matrix - created by Clustal2.1

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 **2-2 2-3 2-4 1-3 1-2 1-4 5-2 5-3 5-4 3-3 3-4 7-3 7-4 8-2 6-2 6-3 6-4**

 1: IGHD2\_2 100.00 100.00 100.00 36.11 37.04 40.74 52.78 52.78 52.78 48.61 48.61 50.70 50.70 52.78 50.70 49.30 49.30

 2: IGHD2\_3 100.00 100.00 100.00 36.11 37.04 40.74 52.78 52.78 52.78 48.61 48.61 50.70 50.70 52.78 50.70 49.30 49.30

 3: IGHD2\_4 100.00 100.00 100.00 36.11 37.04 40.74 52.78 52.78 52.78 48.61 48.61 50.70 50.70 52.78 50.70 49.30 49.30

 4: IGHD1\_3 36.11 36.11 36.11 100.00 97.70 98.85 39.80 40.82 40.82 43.48 43.48 37.07 36.07 41.62 47.87 46.81 46.81

 5: IGHD1\_2 37.04 37.04 37.04 97.70 100.00 98.85 55.17 55.17 55.17 60.00 60.00 55.88 55.88 49.41 60.00 58.00 58.00

 6: IGHD1\_4 40.74 40.74 40.74 98.85 98.85 100.00 58.62 58.62 58.62 63.33 63.33 58.82 58.82 50.59 62.00 60.00 60.00

 7: IGHD5\_2 52.78 52.78 52.78 39.80 55.17 58.62 100.00 97.96 97.96 71.43 71.43 74.16 73.68 72.45 78.08 76.71 76.71

 8: IGHD5\_3 52.78 52.78 52.78 40.82 55.17 58.62 97.96 100.00 100.00 72.53 72.53 73.03 72.63 71.43 79.45 78.08 78.08

 9: IGHD5\_4 52.78 52.78 52.78 40.82 55.17 58.62 97.96 100.00 100.00 72.53 72.53 73.03 72.63 71.43 79.45 78.08 78.08

 10: IGHD3\_3 48.61 48.61 48.61 43.48 60.00 63.33 71.43 72.53 72.53 100.00 100.00 78.05 78.41 79.35 87.84 85.14 85.14

 11: IGHD3\_4 48.61 48.61 48.61 43.48 60.00 63.33 71.43 72.53 72.53 100.00 100.00 78.05 78.41 79.35 87.84 85.14 85.14

 12: IGHD7\_3 50.70 50.70 50.70 37.07 55.88 58.82 74.16 73.03 73.03 78.05 78.05 100.00 100.00 84.55 95.71 95.71 95.71

 13: IGHD7\_4 50.70 50.70 50.70 36.07 55.88 58.82 73.68 72.63 72.63 78.41 78.41 100.00 100.00 84.50 95.71 95.71 95.71

 14: IGHD8\_2 52.78 52.78 52.78 41.62 49.41 50.59 72.45 71.43 71.43 79.35 79.35 84.55 84.50 100.00 89.47 89.47 89.47

 15: IGHD6\_2 50.70 50.70 50.70 47.87 60.00 62.00 78.08 79.45 79.45 87.84 87.84 95.71 95.71 89.47 100.00 96.49 96.49

 16: IGHD6\_3 49.30 49.30 49.30 46.81 58.00 60.00 76.71 78.08 78.08 85.14 85.14 95.71 95.71 89.47 96.49 100.00 100.00

 17: IGHD6\_4 49.30 49.30 49.30 46.81 58.00 60.00 76.71 78.08 78.08 85.14 85.14 95.71 95.71 89.47 96.49 100.00 100.00

**B.**

IGHD2\_2 GCTTTTTGCCAAGGGCTCTACTGCGGT--------------------------------- 27

IGHD2\_3 GCTTTTTGCCAAGGGCTCTACTGCGGT--------------------------------- 27

IGHD2\_4 GCTTTTTGCCAAGGGCTCTACTGCGGT--------------------------------- 27

IGHD1\_3 GGATTTTGAGGGTGTGCGTGTCACCGTGAGACTATCGTGATGATGGTTACTG-------- 52

IGHD1\_2 GGATTTTGAGGGTGTGCGTGTCACCCTGAGAATATCGTGATGATGGTTACTG-------- 52

IGHD1\_4 GGATTTTGAGGGTGTGCGTGTCACCGTGAGAATATCGTGATGATGGTTACTG-------- 52

IGHD5\_2 GGTTTCTGATGCCGGCTGTGTTGTGGTGA------------------------------- 29

IGHD5\_3 GGTTTCTGATGCCGGCTGTGTTGTGGTGA------------------------------- 29

IGHD5\_4 GGTTTCTGATGCCGGCTGTGTTGTGGTGA------------------------------- 29

IGHD3\_3 GGTTTCTGATGCCGGCTGTGTCACGGTGGT------------------------------ 30

IGHD3\_4 GGTTTCTGATGCCGGCTGTGTCACGGTGGT------------------------------ 30

IGHD7\_3 GGTTTTTGATGCCGGCTGTGTCACGG---------------------------------- 26

IGHD7\_4 GGTTTTTGATGCCGGCTGTGTCACGG---------------------------------- 26

IGHD8\_2 GGTTTCTGATGCCGGCTGTGTCACGGTGGT--AGTTGTCCTGATGGTTATAGTTATGGTT 58

IGHD6\_2 GGTTTCTGATGCCGGCTGTGTCACGGTGGT--AGTTGTTATAGTGGTTATGGTTATGGTT 58

IGHD6\_3 GGTTTCTGATGCCAGCTGTGTCACGGTGGT--AGTTGTTATAGTGGTTATGGTTATGGTT 58

IGHD6\_4 GGTTTCTGATGCCAGCTGTGTCACGGTGGT--AGTTGTTATAGTGGTTATGGTTATGGTT 58

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IGHD2\_2 ------------------------------------------------------------ 27

IGHD2\_3 ------------------------------------------------------------ 27

IGHD2\_4 ------------------------------------------------------------ 27

IGHD1\_3 ----------------CTACACCCACAGTGACTCAGGCCCTGACATAAAGTCT------G 90

IGHD1\_2 ----------------CTACACCCACAGTGACTCAGGCCCTGACATAAAGT--------- 87

IGHD1\_4 ----------------CTACACCCACAGTGACTCAGGCCCTGACATAAAGT--------- 87

IGHD5\_2 ------------------------------------------------------------ 29

IGHD5\_3 ------------------------------------------------------------ 29

IGHD5\_4 ------------------------------------------------------------ 29

IGHD3\_3 ------------------------------------------------------------ 30

IGHD3\_4 ------------------------------------------------------------ 30

IGHD7\_3 -------------------------------------------TGGTAGTTATGGTGGTT 43

IGHD7\_4 -------------------------------------------TGGTAGTTATGGTGGTT 43

IGHD8\_2 ATGGTTGTGGTTATGGTTATGGTTGTAGTGGTTATGATTGTTATGGTTATGGTGGTTATG 118

IGHD6\_2 GTGGTTATGGTT------------------------------------------------ 70

IGHD6\_3 ATGGTTGTGGTT------------------------------------------------ 70

IGHD6\_4 ATGGTTGTGGTT------------------------------------------------ 70

IGHD2\_2 -----------------------------------------GTTACTATAGTGACCACCA 46

IGHD2\_3 -----------------------------------------GTTACTATAGTGACCACCA 46

IGHD2\_4 -----------------------------------------GTTACTATAGTGACCACCA 46

IGHD1\_3 ACCCGCACAC-AGGTGTGGAGCTGGCCAATGCATCCCCAGGGGCACTGGGCTCCCAAGCA 149

IGHD1\_2 ------------------------------------------------------------ 87

IGHD1\_4 ------------------------------------------------------------ 87

IGHD5\_2 -----------------TGATACGATAGGTGTGGTTGTAGTTATTGTAGTGTTGCTACCA 72

IGHD5\_3 -----------------TGATACGATAGGTGTGGTTTTAGTTATTGTAGTGTTGCTACCA 72

IGHD5\_4 -----------------TGATACGATAGGTGTGGTTTTAGTTATTGTAGTGTTGCTACCA 72

IGHD3\_3 ------------------------ATTGTGGTAGCTATTGTGGTAGTTATTATGGTACCA 66

IGHD3\_4 ------------------------ATTGTGGTAGCTATTGTGGTAGTTATTATGGTACCA 66

IGHD7\_3 ATGGTTATGGTGGTTATGGTTGTTATGGTTATGGT------TATGGTTATGGTTATACCA 97

IGHD7\_4 ATGGTTATGGTGGTTATGGTTGTTATGGTTATGGTTATGGTTATGGTTATGGTTATACCA 103

IGHD8\_2 GTGGTTATGGTGGTTATGGTTATAGTAGTTATAGTTATAGTTATACTTACGAATATACCA 178

IGHD6\_2 ------------------------------------------ATGGTTATGATTATACCA 88

IGHD6\_3 ------------------------------------------ATGGTTATGGTTATACCA 88

IGHD6\_4 ------------------------------------------ATGGTTATGGTTATACCA 88

IGHD2\_2 CAGTGAGACATGGGGCAGCAAACCCT 72

IGHD2\_3 CAGTGAGACATGGGGCAGCAAACCCT 72

IGHD2\_4 CAGTGAGACATGGGGCAGCAAACCCT 72

IGHD1\_3 AGGTGCCTATCCCCCCAACTCGGGAC 175

IGHD1\_2 -------------------------- 87

IGHD1\_4 -------------------------- 87

IGHD5\_2 CAGTGATGCTCTCAGTGTCAGAAACC 98

IGHD5\_3 CAGTGACGCTCTCAGTGTCAGAAACC 98

IGHD5\_4 CAGTGACGCTCTCAGTGTCAGAAACC 98

IGHD3\_3 CAGTGACACTGTCCAGGACAGAAACC 92

IGHD3\_4 CAGTGACACTGTCCAGGACAGAAACC 92

IGHD7\_3 CAGTGATACTCTCTGGGACAAAAACC 123

IGHD7\_4 CAGTGATACTCTCTGGGACAAAAACC 129

IGHD8\_2 CAGTGATACTCTCTGGGACAAAAACC 204

IGHD6\_2 CAGTGACACTCTCTGGGACAAAAACC 114

IGHD6\_3 CAGTGACACTCTCTGGGACAAAAACC 114

IGHD6\_4 CAGTGACACTCTCTGGGACAAAAACC 114

**C.**

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