Sequence 1: ABHD16A predicted transcript sequence

ATGGCGAAGCTGCTGAGCTGCGTTCTGGGCCCGCGCCTCTACCGCGTCCACCGGCGGCGCGCCGAGGGG
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CGTCCTGGCTCTGGCCTCGGTGCTGTGGTCCATTTCATACTACGCTTCGCCTTTGGCCGTGTTTTATCTGTA
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GCTGGCGGGGGTGGCCTGTCTGAGAGGGCTAGGCCGCTGGAGCAACCCGCAGTACGTGGAGTTCATCAC
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ACTTCCGCAGCTGGCCCGTTGACTTCCGCTGGGACAGCGCCGGGCAGCCCTGGGGTGGGGCTAAAGCCG
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CAAAATCATGGCGGAGGAGGGGCTGCGCGTGGTGAAGGAGTGGTTGGGGGCCGCCACCCCCAGCGAGG
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GCGTTGTTTTTGGCTCAGAAGCACCTGCAGAACTTCGAGGCCTCGCACTGCACCCCTTTGCCCCCCCCCG
CCTTCCGCCTCCCATGGACTCTGTGA

Complete coding sequence of the chicken *ABHD16A* gene was deduced from Genbank available RNA-seq data in the SRA as described in the Material and Methods section.

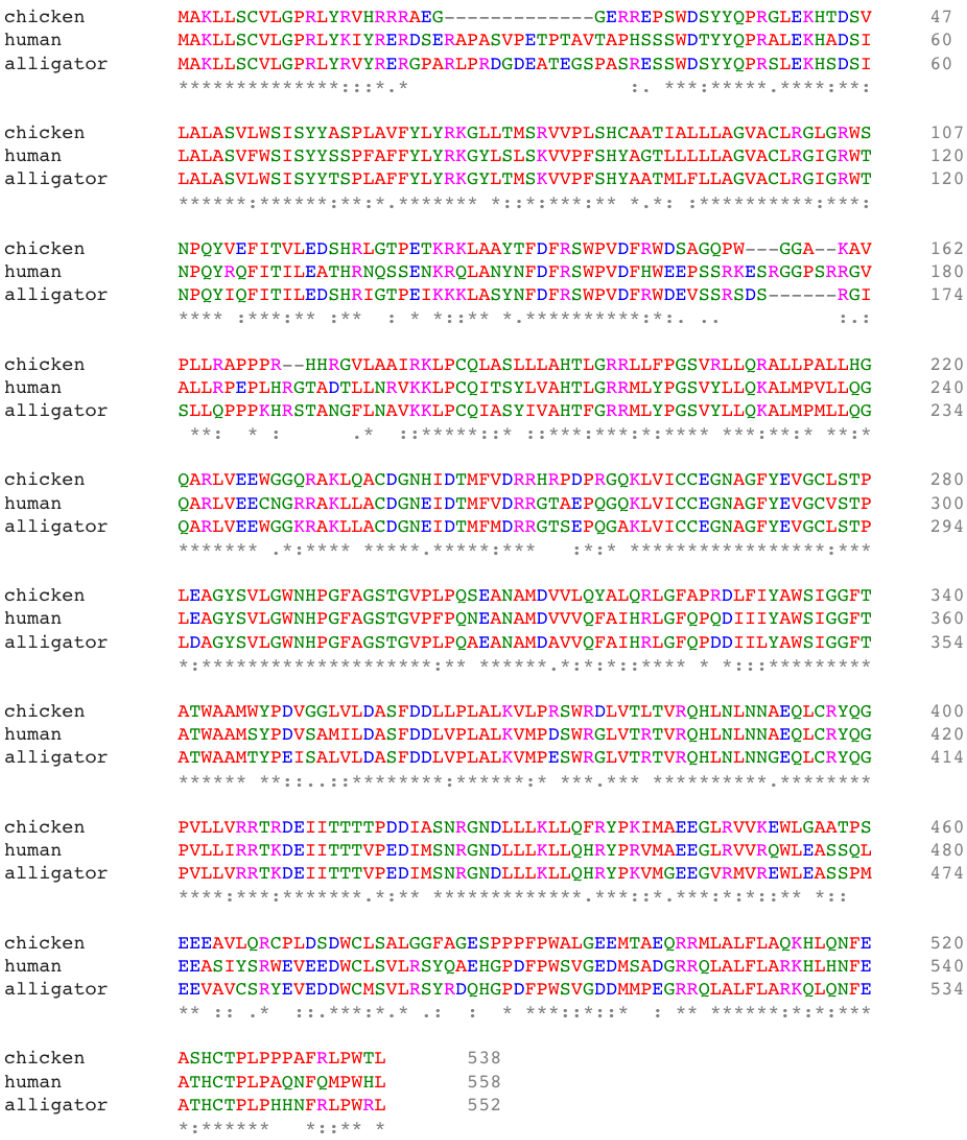

Figure S1.Alignment of the predicted protein sequence of chicken ABHD16A (Figure 1S) with those of human (GenBank accession AQY76647) and alligator (GenBank accession XP_006037708), using Clustal Omega software. Periods, colons and asterisks indicate weakly similar, strongly similar and identical amino acids, respectively.

Supplementary Table 1, Primers used for RH-mapping

Marker	Forward	Reverse	TM (°C)
SEQ0367	AGAGGGAAGGAGCGAGAG	GCGACCAAAGGAACCATAAC	55
SEQ0368	CCAGTGCGGTAACGCAAG	GCGAGATTTACACCCTCTC	55
GCT2046	GCAATTATTCCCCATGAACG	AGTTCGACCGTCTTCTCGAC	52
SEQ0464	GGTGCCGAAAGTCAGACAAC	AAAGCGACCCTCAGACAGG	58
SEQ0113	TCTCTGCACCCAACCTATCC	TCAGAAGTGAGAGCGAAAGC	55
523B09	ACGTTCCCTTCTCACTCTGC	CATCTGACACCCTGCCTTC	50
SEQ0111	TACTTCCTGACCGGGATGAC	CTTCTGTTGTAGCGCACCTG	55
TNF	TCGTGGCATCGTCCTCTCAG	ACCAATTTGTTCCTTCTCAGCAC	58
CSNK2B	GGGAGGCGATGGTGAAGCTG	GCACGAATTGGTTTGCGGGGC	60
GCT2022	CGGAACTTCGCCTTCATCTC	AGTCGTTGTCGTGGTGCTG	58
GCT1823	CTGGTGATCCCGGAGAAG	ATGGCGAAGGCGATCTTG	60
GCT2027	ATTACATCGCGGTGAAGGAG	TGAGCAGATGGATGATCTCG	58
ABHD16	CCTGTTGCTGGCGCACAC	CGCTATGGGTCCTGACCTCCTC	55
BRD2	GAGCTTCGATTTCCTGTGC	GTGTGGGCTCTTCCAGTTC	60
MCW370	AAAGAGGAGAGTAGTTCACG	CCCACCTCATCATGCATTCC	55
TAP2	TACGAGCACCGCTACCTG	AGAGATGAAGCCCAAAGCAC	55
TRIM7	GTCCCTGTGTGAGAGACCCCG	AGCGAGGAGCCCACGTAGAAG	58

Supplementary Table 2, Primers used for FISH analysis

Gene name	Accession numbe/other reference	Forward	Reverse	Probe length (bp's)
TNF	MF000729	GTGGGCGGTGCGGCCATA	TTAATCCACTCCCACCACCCCG	697
CSNK2B	NM_001257204	GCTCCGAGGAGGTGTCGTGGATCT	TTCACGGGGCTCTTGAAGTTGCTG	628
ABHD16A	Suplementary sequence	GGCCTCAGTGCTGTGGTCCATT	GAGAGGCACCAATCGGAGTCCA	1284
BRD2	NM_001030674	TCAAGTCGCTGCACTCCACTG	AGGACGAGGAGCTGGAACTGG	1560
TRIM7.2	NM_001099354	GTGCGTTGTGTGCCACCTCT	AGCGAGGAGCCCACGTAGAAG	1068