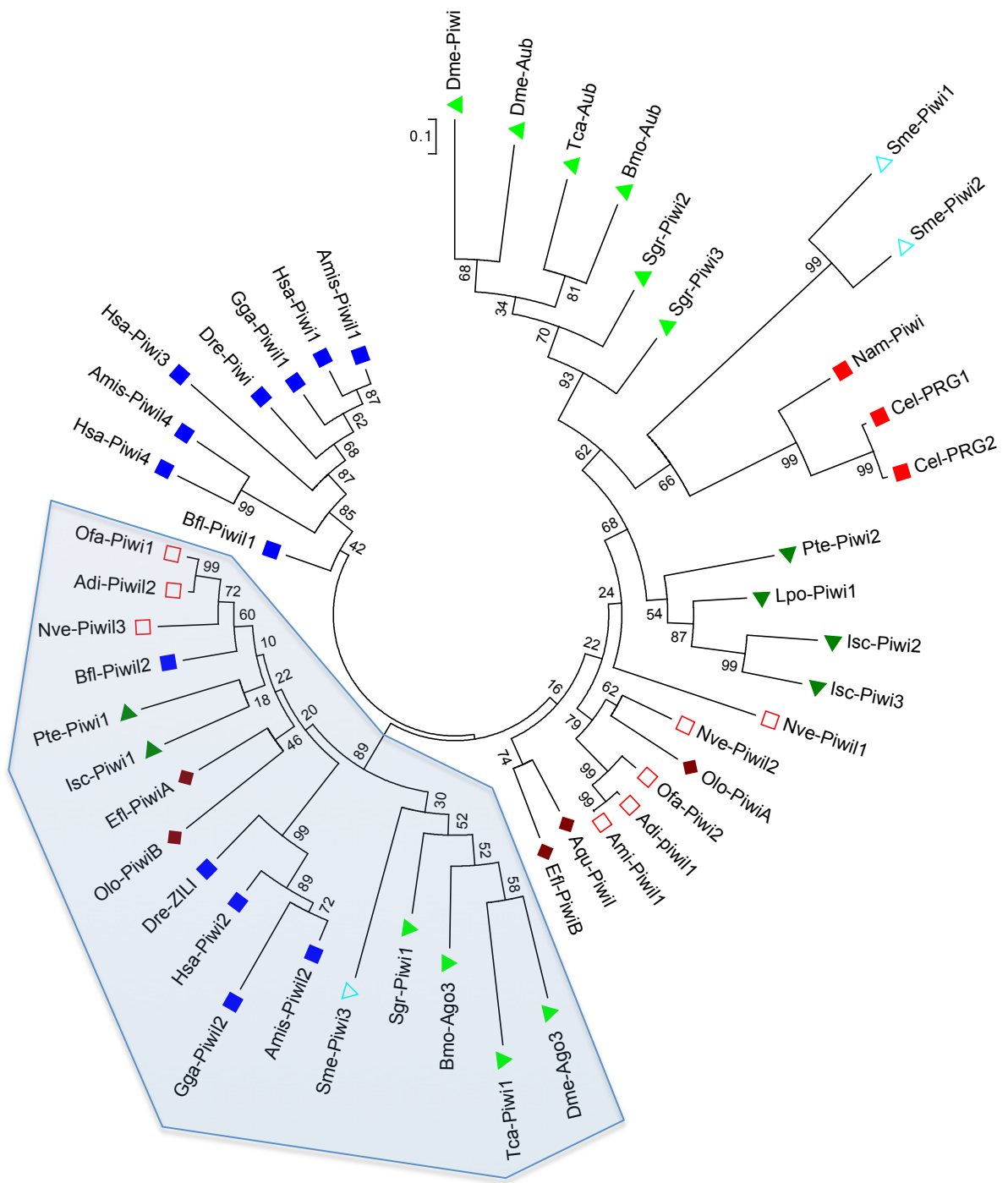


**The evolution of animal Argonautes: evidence for the absence of antiviral
AGO Argonautes in vertebrates**

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Supplementary Figure S1, related to Figure 1

<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query cover</u>	<u>E value</u>	<u>Identity</u>	<u>Accession n°</u>	<u>Ago-type</u>
Bf-AGO2; Branchiostoma floridae hypothetical protein. mRNA	388	388	61%	1.00E-115	35%	XM_002589997.1	miRNA-class AGO

Supplementary Table S1, related to Figure 1

Phylum	class	order	species	gene name	Accession number	Argonaute-type*							
Chordata	Mammalia	Primates	<i>Homo sapiens</i>	Hsa-Ago1	NM_012199.4	miRNA-class AGO							
				Hsa-Ago2	XM_011516968.2	miRNA-class AGO							
				Hsa-Ago3	NM_177422.2	miRNA-class AGO							
				Hsa-Ago4	XM_011540884.2	miRNA-class AGO							
				Hsa-piwil1	XM_017020229.1	PIWI							
				Hsa-piwil2	NM_001135721.1	PIWI							
				Hsa-piwil3	NM_001008496.3	PIWI							
				Hsa-piwil4	NM_152431.2	PIWI							
	Reptila	Crocodilla	<i>Alligator mississippiensis</i>	Amis-Ago1	XM_006269876.3	miRNA-class AGO							
				Amis-Ago2	XM_006258700.3	miRNA-class AGO							
				Aism-Ago3	XR_002090536.1	miRNA-class AGO							
				Aism-Ago4	XM_006269875.3	miRNA-class AGO							
				Amis-Piwil1	XM_019486674.1	PIWI							
				Amis-Piwil2	XM_019491533.1	PIWI							
				Amis-Piwil4	XM_006018646.1	PIWI							
				Aves	Galliformes	<i>Gallus gallus</i>	Gga-Ago1	NM_001317212.1	miRNA-class AGO				
	Gga-Ago3	NM_001030900.1	miRNA-class AGO										
	Gga-Ago4	NM_001039276.1	miRNA-class AGO										
	Gag-Piwil1	XM_015275263.1	PIWI										
	Gga-Piwil2	XM_015273687.1	PIWI										
	Actinopterygii	Cypriniformes	<i>Danio rerio</i>				Dre-Ago1	XM_005158472.3	miRNA-class AGO				
				Dre-Ago2	XM_009294368.2	miRNA-class AGO							
				Dre-Ago3	XM_005159456.2	miRNA-class AGO							
				Dre-Ago4	NM_001252559.2	miRNA-class AGO							
				Dre-ZILI	FJ168029.1	PIWI							
				Dre-PIWIL1	NM_183338.1	PIWI							
				Leptocardii	Amphioxiformes	<i>Branchiostoma floridae</i>	Bfl-AGO1	XM_002589344.1	miRNA-class AGO				
							Bfl-AGO2	XM_002589997.1	miRNA-class AGO				
							Bfl-Piwil1	KC516709.1	PIWI				
							Bfl-Piwil2	KC516710.1	PIWI				
							Nematoda	Chromadorea	Rhabditidae	<i>Caenorhabditis elegans</i>	Cel-Alg1	NM_001270310.1	miRNA-class AGO
											Cel-Alg2	NM_061436.3	miRNA-class AGO
	Cel-Ergo1	NM_070961.7	siRNA-class AGO										
	Cel-Rde1	NM_171525.4	siRNA-class AGO										
	Cel-SAGO1	NM_072209.3	WAGO										
	Cel-SAGO2	NM_182059.3	WAGO										
	Cel-WAGO1	NM_059644.5	WAGO										
	Cel-WAGO2	F55A12.1	WAGO										
	Cel-PPW2	NM_059134.5	WAGO										
	Cel-CSR1	NM_001047473.3	WAGO										
Cel-Hpo24	NM_060242.4	Hpo24-like*											
Cel-Alg3/4	NM_066791.4	alg3/4-like*											
Cel-PRG1	NM_059720.5	PIWI											
Cel-PRG2	NM_068593.6	Piwi											
Ascaridia	<i>Ascaris suum</i>	Asu-Alg1	HQ611964.1	miRNA-class AGO									
		Asu-ALG7	HQ611968.1	siRNA-class AGO									
		Asu-ALG5	HQ611966.1	siRNA-class AGO									
		Asu-ALG6	HQ611967.1	Hpo-like*									
		Asu-ALG4	HQ611965.1	alg3-like*									
		Asu-WAGO	HQ611970.1	WAGO									
		Asu-WAGO2	HQ611971.1	WAGO									
		Asu-WAGO3	HQ611972.1	WAGO									
		Asu-CSR1	HQ611969.1	WAGO									
		Asu-NRDE3	HQ611973.1	WAGO									
		Secernentea	Spiurida	<i>Brugia malayi</i>	Bma-Alg1	XM_001894221.1		miRNA-class AGO					
					Bma-Alg2	XM_001894221.1		miRNA-class AGO					
Bma-Rde1	XM_001898588.1				siRNA-class AGO								
Bma-Alg3	XM_001891898.1				alg3/4-like*								
Bma-NRDE3	XM_001900278.1				WAGO								
Bma-WAGO2	XM_001895162.1				WAGO								
Bma-WAGO1	XM_001895162.1				WAGO								
Bma-CSR1	XM_001901544.1				WAGO								
Strongylida	<i>Necator americanus</i>		Nam-ALG1	XM_013443759.1	miRNA-class AGO								
			Nam-RDE1-like	XM_013450933.1	siRNA-class AGO								
			Nma-WAGO1	XM_013451313.1	WAGO								
			Nam-WAGO2	XM_013437700.1	WAGO								
			Nam-PIWI	XM_013437264.1	PIWI								

Phylum	class	order	species	gene name	Accession number	Argonaute-type*	
Arthropoda	Insecta	Diptera	<i>Drosophila melanogaster</i>	Dme-Ago1	NM_079010.4	miRNA-class AGO	
				Dme-Ago2	NM_140518.3	siRNA-class AGO	
				Dme-Ago3	NM_001043162.3	PIWI	
				Dem-Piwi	AF104354.1	PIWI	
				Dme-Aub	NM_057386.5	PIWI	
		Lepidoptera	<i>Bombyx mori</i>	Bmo-Ago1	NM_001102461.1	miRNA-class AGO	
				Bmo-Ago2	XM_012693089.1	siRNA-class AGO	
				Bmo-Ago3	XM_012695095.1	PIWI	
				Bmo-Aub	XM_012689822.1	PIWI	
				Tca-Ago1	XM_015982502.1	miRNA-class AGO	
		Coleoptera	<i>Tribolium castaneum</i>	Tca-Ago2a	M_008202051.2	siRNA-class AGO	
				Tca-Agob	XM_008194763.2	siRNA-class AGO	
				Tca-Piwi1	XM_008194203.2	PIWI	
				Tca-Aub	XM_008198081.2	PIWI	
				Sgr-Ago1	KY555621	miRNA-class AGO	
	Orthoptera	<i>Schistocerca gregaria</i>	Sgr-Ago2	JX516788.1	siRNA-class AGO		
			Sgr-Piwi1	KY555624	PIWI		
			Sgr-Piwi2	KY555622	PIWI		
			Sgr-piwi3	KY555623	PIWI		
			Isc-Ago1	XM_002413143.1	miRNA-class AGO		
	Arachnida	Ixodida	<i>Ixodes scapularis</i>	Isc-Ago2	XM_002412215.1	siRNA-class AGO	
				Isc-Ago3	XM_002412954.1	miRNA-class AGO	
				Isc-Ago4	XM_002405620.1	siRNA-class AGO	
				Isc-Ago5	XM_002399349.1	miRNA-class AGO	
				Isc-Ago5	XM_002401346.1	PIWI	
				Isc-Piwi1	XM_002413940.1	PIWI	
				Isc-Piwi2	XM_002411725.1	PIWI	
				Isc-Piwi3	XM_002399349.1	PIWI	
				Pte-Ago1	XM_016050247.1	miRNA-class AGO	
				Pte-Ago2	XM_016050249.1	siRNA-class AGO	
		Pte-Ago3	XM_016074512.1	miRNA-class AGO			
		Pte-Ago4	XM_016050252.1	siRNA-class AGO			
		Pte-Piwi1	XM_016048783.1	PIWI			
		Pte-Piwi2	XM_016075529.1	PIWI			
		Merostomata	Xiphosura	<i>Limulus polyphemus</i>	Lpo-Ago1	XM_013931086.1	miRNA-class AGO
					Lpo-Ago2	XM_013926285.1	siRNA-class AGO
					Lpo-Piwi1	XM_013918768.1	PIWI
	Platyhelminthes	Cestoda	Cyclophyllidea	<i>Echinococcus multilocularis</i>	Emu-Ago1	FN690741.1	miRNA-class AGO
					Emu-Ago2	KF768022.1	siRNA-class AGO
		Trematoda	Stringeidida	<i>Schistosoma japonicum</i>	Sja-Ago1	KC345759.1	miRNA-class AGO
					Sja-Ago2	KC345760.1	siRNA-class AGO
					Sja-Ago3	KC345761.1	siRNA-class AGO
		Rhabditophora	Tricladida	<i>Schmidtea mediterranea</i>	Sme-Ago1	JF263459	miRNA-class AGO
					Sme-Piwi1	DQ186985.1	siRNA-class AGO
	Sme-Piwi2				DQ186986.1	PIWI	
	Cnidaria	Anthozoa	Scleractinia	<i>Acropora digitifera</i>	Adi-Ago1	XM_015896058.1	miRNA-class AGO
					Adi-Ago2	XM_015896084.1	siRNA-class AGO
Adi-Ago3					XM_015896077.1	siRNA-class AGO	
Adi-Ago4					XM_015896088.1	siRNA-class AGO	
Adi-Piwi1					XM_015921219.1	PIWI	
Adi-Piwi2					XM_015908676.1	PIWI	
<i>Acropora millipora</i>					Ami-Ago1	JR981312.1	miRNA-class AGO
					Ami-Ago2	JT022739.1	siRNA-class AGO
					Ami-Piwi1	EZ001072.1	PIWI
					Ami-Piwi2	EZ012267.1	PIWI
		<i>Orbicella faveolata</i>	Ofa-Ago1	XM_020761752.1	siRNA-class AGO		
Ofa-Ago2			XM_020761847.1	siRNA-class AGO			
Ofa-Ago3			XM_020761831.1	siRNA-class AGO			
Ofa-Piwi1			XM_020745504.1	PIWI			
Ofa-Piwi2			XM_020776165.1	PIWI			
Actiniaria		<i>Nemastella vectensis</i>	Nve-Ago1	KF192061.1	miRNA-class AGO		
			Nve-Ago2	KF192062.1	siRNA-class AGO		
			Nve-Piwi1	KU746924.1	PIWI		
			Nve-Piwi1	XM_001641944.1	PIWI		
			Nve-Piwi1	XM_001626077.1	PIWI		
Porifera	Demospongiae	Haplosclerida	<i>Amphimedon queenslandica</i>	Aqu-Ago1	XM_019995499.1	miRNA-class AGO	
				Aqu-Ago2	XM_020008918.1	siRNA-class AGO	
				Aqu-Piwi1	XM_020007102.1	PIWI	
				Efl-Ago	AB533507	miRNA-class AGO	
				Efl-PiwiA	XM_020761752	PIWI	
	<i>Ephydatia fluviatilis</i>	Efl-PiwiB	XM_020761753	PIWI			
		<i>Oscarella lobularis</i>	Olo-Ago	KX216818.1	/		
			Olo-PiwiA	KX216816.1	PIWI		
			Olo-PiwiB	KX216817.1	PIWI		
			Bacteroidetes	Bacteroidetes	Bacteroidales	<i>Bacteroides fragilis</i>	OUT-GROUP
Firmicutes	Bacilli						Bacillales

Supplementary Table S2, related to Figure 1.

Legends:








Figure S1: Unrooted maximum likelihood phylogenetic tree (100 bootstraps) using the AGO Argonaute members belonging to Porifera (sponges; ) , Cnidaria (jellyfish, coral animals and anemones, ) , Chordata () , Nematoda () , Arthropoda (Insecta:  and Chelicerata: ) and Platyhelminthes () .

Table S1: *Branchiostoma floridae* Bf-AGO2 is the chordate sequence with highest sequence similarity (depicted by lowest E-value) to *Drosophila melanogaster* Dm-AGO2.

Table S2: Detailed sequence information of the Argonaute sequences used for the construction of a Maximum Likelihood (ML-) phylogenetic tree.