

**Figure S1.** Nucleotide (a) and amino acid (b) sequences of the seven *Ornithodoros moubata* AQP<sub>s</sub> amplified by PCR. (c) Nucleotide sequence alignments of the amplified *O. moubata* AQP<sub>s</sub> with each corresponding transcript as obtained by RNA-seq.

**a**

>OmAQP90

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>Om20812

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**b**

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**C**

[illegible]

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651 660 670 680 690 700 710 720 730 740 750 760 770 780  
0hAQP97 ACGTGTCTTGGCTTCCATTTGGGATATGAGACCGAGGTGTCAGCATGACACCTTCTGGTGGATTCGATGTTTCATTCCTCATGTTGGGGGACTCATCGGCACATGGCTAGCTGCTAGCTATTGAG  
ci1000113997 ACGTGTCTTGGCTTCCATTTGGGATATGAGACCGAGGTGTCAGCATGACACCTTCTGGTGGATTCGATGTTTCATTCCTCATGTTGGGGGACTCATCGGCACATGGCTAGCTGCTAGCTATTGAG  
Consensus  
781 790 800 810 820 830 840 850 860 870 879  
0hAQP97 ATGCACATAGTCCAGAAAGGGTACGGGACGATAGGACTGAGCGGAGATGACCACTATTACCGCTTCCACCGAGGACAGAAAGACCGGTGTCTAA  
ci1000113997 ATGCACATAGTCCAGAAAGGGTACGGGACGATAGGACTGAGCGGAGATGACCACTATTACCGCTTCCACCGAGGACAGAAAGACCGGTGTCTAA  
Consensus  
ATGCACATAGTCCAGAAAGGGTACGGGACGATAGGACTGAGCGGAGATGACCACTATTACCGCTTCCACCGAGGACAGAAAGACCGGTGTCTAA

1 10 20 30 40 50 60 70 80 90 100 110 120 130  
0hAQP23 ATGATTCTGGATTAAGTGAAGATTARGAGCTTGGCTCTGCGGGAGAGCTTCGCCGACCTTCTGGGACCTTTCTGCTTTGTGCTGTTTCGGTACCGAGATCTGGCAGCCCTGAAGTTCGACAGAGCTGGAA  
ci1000114723 ATGATTCTGGATTAAGTGAAGATTARGAGCTTGGCTCTGCGGGAGAGCTTCGCCGACCTTCTGGGACCTTTCTGCTTTGTGCTGTTTCGGTACCGAGATCTGGCAGCCCTGAAGTTCGACAGAGCTGGAA  
Consensus  
131 140 150 160 170 180 190 200 210 220 230 240 250 260  
0hAQP23 ACATTGGCTACGCCCGGTTTCTGGGGTTGGGTTTGGCTCTTGGATGGAGTGTCTGCTCTTGGTGGAGCTCAGGTGCCACCTGARCCCGCTATTACCGTGGCTTGGCAACCATCGGAARATG  
ci1000114723 ACATTGGCTACGCCCGGTTTCTGGGGTTGGGTTTGGCTCTTGGATGGAGTGTCTGCTCTTGGTGGAGCTCAGGTGCCACCTGARCCCGCTATTACCGTGGCTTGGCAACCATCGGAARATG  
Consensus  
261 270 280 290 300 310 320 330 340 350 360 370 380 390  
0hAQP23 CCAATGGAGAAAGTGCACATATACCTGGTAGCCAGTACTTAGGTGCTTCTTGGAGCTGCCGTGCTTCTTGACATACAGGGTGCCTTCGACACATATGACGGTGGTTTTCGTGCGACTACCCGT  
ci1000114723 CCAATGGAGAAAGTGCACATATACCTGGTAGCCAGTACTTAGGTGCTTCTTGGAGCTGCCGTGCTTCTTGACATACAGGGTGCCTTCGACACATATGACGGTGGTTTTCGTGCGACTACCCGT  
Consensus  
391 400 410 420 430 440 450 460 470 480 490 500 510 520  
0hAQP23 GTGACCGAGACGGCGGATGTGTTGCTTCATATCCAGAGACTTCGTTGGCACTGGAGACTGCTTTTGGACAGGCTGCTGGGACTGGCTCTTTGTGATGTGATCTGGCTATCACAGACACCA  
ci1000114723 GTGACCGAGACGGCGGATGTGTTGCTTCATATCCAGAGACTTCGTTGGCACTGGAGACTGCTTTTGGACAGGCTGCTGGGACTGGCTCTTTGTGATGTGATCTGGCTATCACAGACACCA  
Consensus  
521 530 540 550 560 570 580 590 600 610 620 630 640 650  
0hAQP23 ACATGGCAGTGCCTCAGGCTTCGACCTCTGTTGATCGGCTTTCTTGGACACGACTGCTCTGCTTCGGTACACATGTTGGTTCCTCCCTCAGCCAGCCGAGATTGGGACACATCTTTCAC  
ci1000114723 ACATGGCAGTGCCTCAGGCTTCGACCTCTGTTGATCGGCTTTCTTGGACACGACTGCTCTGCTTCGGTACACATGTTGGTTCCTCCCTCAGCCAGCCGAGATTGGGACACATCTTTCAC  
Consensus  
651 660 670 680 690 700 710 720 730 740 750 760 770 780  
0hAQP23 TGGCATGGCTGGGTGGGACAGAGGCTTTCAGCTTCCGAGACTACACTGGTTCTGGGTGCCGGTAGTGGCGCCCACTCGAGCCATCGTTGGAGCATGGCTGTACAGACTCTGGTTGGCTTCCAC  
ci1000114723 TGGCATGGCTGGGTGGGACAGAGGCTTTCAGCTTCCGAGACTACACTGGTTCTGGGTGCCGGTAGTGGCGCCCACTCGAGCCATCGTTGGAGCATGGCTGTACAGACTCTGGTTGGCTTCCAC  
Consensus  
781 790 800 810 820 830 840 849  
0hAQP23 TGGCTCAGAGACTCGTACGACATGGACAGAGAGACAGGGCCAGGATGGTGGGATTTCCTCGATGA  
ci1000114723 TGGCTCAGAGACTCGTACGACATGGACAGAGAGACAGGGCCAGGATGGTGGGATTTCCTCGATGA  
Consensus  
TGGCTCAGAGACTCGTACGACATGGACAGAGAGACAGGGCCAGGATGGTGGGATTTCCTCGATGA

	1	10	20	30	40	50	60	70	80	90	100	110	120	130
0nAQP15	-----													
ci1000148315	ATGATTCTGGATAAGTGAAGATTAGAGCCTGGCTCTGCGGGAGACGTTCCGCCGACCTTCGCGGACCTTACGCTGCTTGTGCTGTTCCGTACCGGAGTCTGGCAGCCTGAGGTCGACAGAGCTGGAA													
Consensus	ATGATTCTGGATAAGTGAAGATTAGAGCCTGGCTCTGCGGGAGACGTTCCGCCGACCTTCGCGGACCTTACGCTGCTTGTGCTGTTCCGTACCGGAGTCTGGCAGCCTGAGGTCGACAGAGCTGGAA													
	131	140	150	160	170	180	190	200	210	220	230	240	250	260
0nAQP15	-----													
ci1000148315	ACATTGGCTACGCCGCCGCTTCTGGGGTTGGGTTTGGCTCTTGGATTGGAGTGCTCTCTTGGTGGAGCGTCAGGTGCCACCTGARCCCGCTATTACCGTGCTTGGCACCATCGGAAATG													
Consensus	ACATTGGCTACGCCGCCGCTTCTGGGGTTGGGTTTGGCTCTTGGATTGGAGTGCTCTCTTGGTGGAGCGTCAGGTGCCACCTGARCCCGCTATTACCGTGCTTGGCACCATCGGAAATG													
	261	270	280	290	300	310	320	330	340	350	360	370	380	390
0nAQP15	-----													
ci1000148315	CCAGTGGAGAAAGTGCCACATTACCTGGTAGCCCACTACTAGGTGCTTCTTGGAGCTGCCGCTCTCTTGGACATACAGGGTGGCTTCGACACATATGACGGTGGTTTGGTGGACTACCGGT													
Consensus	CCAGTGGAGAAAGTGCCACATTACCTGGTAGCCCACTACTAGGTGCTTCTTGGAGCTGCCGCTCTCTTGGACATACAGGGTGGCTTCGACACATATGACGGTGGTTTGGTGGACTACCGGT													
	391	400	410	420	430	440	450	460	470	480	490	500	510	520
0nAQP15	-----													
ci1000148315	GTGACGGAGACGGCGGATGTGTTTCGCTTCATATCCAGAGACTTCGTTGGCACTGGGAACTGCTTTTGGACAGGTGCTCGGACTGGTCTCTTTGTGATGTGATCGTGGCTATCAGACACACCA													
Consensus	GTGACGGAGACGGCGGATGTGTTTCGCTTCATATCCAGAGACTTCGTTGGCACTGGGAACTGCTTTTGGACAGGTGCTCGGACTGGTCTCTTTGTGATGTGATCGTGGCTATCAGACACACCA													
	521	530	540	550	560	570	580	590	600	610	620	630	640	650
0nAQP15	-----													
ci1000148315	ACATGGCAGTGCTCAGGCTCGCACCTCTGTGATCGGCTTCTTTGGCAACGACTGCTCTGCTCGGCTACACTGTGGTGTCCCTTCACCCAGCCGAGATTTGGGACCACTATCTTCAC													
Consensus	ACATGGCAGTGCTCAGGCTCGCACCTCTGTGATCGGCTTCTTTGGCAACGACTGCTCTGCTCGGCTACACTGTGGTGTCCCTTCACCCAGCCGAGATTTGGGACCACTATCTTCAC													
	651	660	670	680	690	700	710	720	730	740	750	760	770	780
0nAQP15	-----													
ci1000148315	TGGCATGGCTGGGTGGGAAACAGAGGCTTTCAGCTTCCGAGACTACACTGGTTCTGGGTGCCGGTAGTGGCGCCCACTCGAGCCATCGTTGGAACTGGCTGTACAGACTCTGGTTGGCTCCAC													
Consensus	TGGCATGGCTGGGTGGGAAACAGAGGCTTTCAGCTTCCGAGACTACACTGGTTCTGGGTGCCGGTAGTGGCGCCCACTCGAGCCATCGTTGGAACTGGCTGTACAGACTCTGGTTGGCTCCAC													
	781	790	800	810	820	830	840	850	860	870	880	890	900	910
0nAQP15	-----													
ci1000148315	TGGCTTCAGACTCGTACGACATGGACAGAGAGACAGGGCCAGGATGATACATGCCATCGGAGTTACGATGCTGCGCCAAAGGACACACATCAGCCTCATCTCCGACGAAACAGTCTGAGGG													
Consensus	TGGCTTCAGACTCGTACGACATGGACAGAGAGACAGGGCCAGGATGATACATGCCATCGGAGTTACGATGCTGCGCCAAAGGACACACATCAGCCTCATCTCCGACGAAACAGTCTGAGGG													
	911	915	---											
0nAQP15	TCTAG													
ci1000148315	TCTAG													
Consensus	TCTAG													