

Figure S2. Alignment of the amino acid sequences included in clade AQP9-like. The amino acids conserved in all the sequences are labelled with asterisks (*); the conservative and semi-conservative substitutions are labelled with colons (:) and periods (.), respectively. The NPA motifs are highlighted in yellow, the residues within the ar/R constriction are highlighted in green, and the aspartic acid downstream the second NPA motif is highlighted in gray. The O-glycosylation sites are marked in blue. The predicted immunogenic peptides from OmAQP90, Om20812 and Om22982 are highlighted in underlined red letters, and their homologous regions in the remaining clade members are highlighted in plain red letters.

OmAQP90	MKVYIRSLLLRELINEFIGTMLLILIGDSIMAIIT	<u>AGRQEENGH</u>	VIGPLG	GTAFCAVF	60
Om20812	--MKIQSTFVRELINEFLGTFTLIVFGDSVMAIIT	<u>AGRQEHNAG</u>	IIGPVG	GTAFCAVT	58
Om22982	--MKIQSTFVRELINEFLGTFTLIVFGDSVMAIIT	<u>AGRQEHNAG</u>	IIGPVG	GTAFCAVT	58
A0A293N7C6_ORNER	--MQIRNVLARELINEFLGTMLILIGDSIVAVII	<u>AGGQGHNAH</u>	VIGPIG	GTAFCAVF	58
XP_037563606.1	--MKIENLLVRQLINEFLGTMLVLLGDSVLAIIT	<u>AADNESIAA</u>	VVGPLG	GTAIYVAVQ	58
XP_037563608.1	--MKIENLLVRQLINEFLGTMLVLLGDSVLAIIT	<u>AADNESIAA</u>	VVGPLG	GTAIYVAVQ	58
XP_037563607.1	--MKIENLLVRQLINEFLGTMLVLLGDSVLAIIT	<u>AADNESIAA</u>	VVGPLG	GTAIYVAVQ	58
XP_037563609.1	--MKIENLLVRQLINEFLGTMLVLLGDSVLAIIT	<u>AADNESIAA</u>	VVGPLG	GTAIYVAVQ	58
XP_037510823.1	--MKIESLLVRQLISEFLGTMLITIGDAIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
XP_037510822.1	--MKIESLLVRQLISEFLGTMLITIGDAIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
XP_037292105.1	--MKIENLLIRQLINEFLGTMLITIGDSIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
XP_037292106.1	--MKIENLLIRQLINEFLGTMLITIGDSIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
AIT69684.1	--MKIENLLIRQLINEFLGTMLITIGDSIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
XP_037292107.1	--MKIENLLIRQLINEFLGTMLITIGDSIMAIIT	<u>AGDNESLAA</u>	CVGPLG	GVAIYVAVQ	58
XP_029845132.1	--MKIESRLIRELINEFIGTMLVLIGDSILAIIT	<u>AGDNEPLAP</u>	IVGPVG	GTAFVAVT	58
EEC20079.1	-----MLARDELIYTLKGLIGDSILAIIT	<u>AGDNEPLAP</u>	IVGPVG	GTAFVAVT	49
	* : : :*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*				
OmAQP90	VAGGVSAHINPA	VTLAFASVKEFPLKKVPLFWLAQYLGA	FVGA	VLVYVIY	120
Om20812	VSGGVSAHLNPA	VTLALASVKKFPIKKVPLFFVAQYTG	AFFAA	VVFAIY	118
Om22982	VSGGVSAHLNPA	VTLALASVKKFPIKKVPLFFVAQYTG	AFFAA	VVFAIY	118
A0A293N7C6_ORNER	VAGGVSAHINPA	VTLALASAKEFPLKKVPLFWLAQYLGA	FVGA	VLVYVMIY	118
XP_037563606.1	IAGGVTAHLNPA	VTLALASVRKFP	IAKVPLFFAAQYLGA	FVGAALVFVITY	118
XP_037563608.1	IAGGVTAHLNPA	VTLALASVRKFP	IAKVPLFFAAQYLGA	FVGAALVFVITY	118
XP_037563607.1	IAGGVTAHLNPA	VTLALASVRKFP	IAKVPLFFAAQYLGA	FVGAALVFVITY	118
XP_037563609.1	IAGGVTAHLNPA	VTLALASVRKFP	IAKVPLFFAAQYLGA	FVGAALVFVITY	118
XP_037510823.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
XP_037510822.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
XP_037292105.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
XP_037292106.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
AIT69684.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
XP_037292107.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
XP_029845132.1	IAGGVSSHLPNPA	VTLAQASVRKFP	IAKVPLYFAAQYLGGFVGA	ALVFVITY	118
EEC20079.1	IAGGVSSHLPNPA	VTLALASTKKFP	INKVPLYFAVQYLGA	FVGAALVYLLY	109
	: :*				
OmAQP90	<u>VRSVVGPTGTAS</u>	<u>IFSTY</u>	PREGV	STLT	179
Om20812	<u>VRSVLGPTGT</u>	<u>APIFATY</u>	PREGI	STLT	178
Om22982	<u>VRSVLGPTGT</u>	<u>APIFATY</u>	PREGI	STLT	178
A0A293N7C6_ORNER	<u>VRSVVGEGKTA</u>	<u>IFSTY</u>	PREEV	STLT	177
XP_037563606.1	<u>VRHVMGAKATAA</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037563608.1	<u>VRHVMGAKATAA</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037563607.1	<u>VRHVMGAKATAA</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037563609.1	<u>VRHVMGAKATAA</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037510823.1	<u>VRQVTGEKSTAG</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037510822.1	<u>VRQVTGEKSTAG</u>	<u>IFATY</u>	PKPHV	STLT	178
XP_037292105.1	<u>IRQVTGEKATAG</u>	<u>IFATY</u>	PRPHV	STLT	178
XP_037292106.1	<u>IRQVTGEKATAG</u>	<u>IFATY</u>	PRPHV	STLT	178
AIT69684.1	<u>IRQVTGEKATAG</u>	<u>IFATY</u>	PRPHV	STLT	178
XP_037292107.1	<u>IRQVTGEKATAG</u>	<u>IFATY</u>	PRPHV	STLT	178
XP_029845132.1	<u>VRQITGKHGTAP</u>	<u>IFATY</u>	PREQI	STLT	178
EEC20079.1	<u>VRQITGKHGTAP</u>	<u>IFATY</u>	PREQI	STLT	169
	: * : * .** ***:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*				
OmAQP90	LMLGMLIVAE	IFAF	<u>SYNCAALNPAD</u>	DIGPRVFTAVAGWGSEVFSFRNYQ	239
Om20812	LALGLMISAE	IFAF	<u>SYNCAALNPAD</u>	DIGPRVFTAIAGWGMEVFSVRDYY	238
Om22982	LALGLMISAE	IFAF	<u>SYNCAALNPAD</u>	DIGPRVFTAIAGWGMEVFSVRDYY	238
A0A293N7C6_ORNER	LMLGMLIVAE	IFAF	<u>SHNCAALNPAD</u>	DIGPRIFTAISGWSQVFTFRNYQ	237
XP_037563606.1	ICLALMIMSL	IFSF	<u>PYNCAALNPAD</u>	DISPRLFTLIAGWGPETFTLRGG	238
XP_037563608.1	ICLALMIMSL	IFSF	<u>PYNCAALNPAD</u>	DISPRLFTLIAGWGPETFTLRGG	238
XP_037563607.1	ICLALMIMSL	IFSF	<u>PYNCAALNPAD</u>	DISPRLFTLIAGWGPETFTLRGG	238
XP_037563609.1	ICLALMIMSL	IFSF	<u>PYNCAALNPAD</u>	DISPRLFTLIAGWGPETFTLRGG	238
XP_037510823.1	ICLGLLIMAL	IFSF	<u>AYNCAALNPAD</u>	DIAPRLFTLMAGWGPETFTLRGG	238

XP_037510822.1	ICLGLLIMAIIFSFAYNCCPLNPADIDIPRLFTLMAGWGPETFTLRGGNYVWVPLLGPH	238
XP_037292105.1	ICLGLMIMAIIFSFAYNCCPLNPADIDISPRLFTLMAGWGPETFTLRGWNVWVPLLGPH	238
XP_037292106.1	ICLGLMIMAIIFSFAYNCCPLNPADIDISPRLFTLMAGWGPETFTLRGWNVWVPLLGPH	238
AIT69684.1	ICLGLMIMAIIFSFAYNCCPLNPADIDISPRLFTLMAGWGPETFTLRGWNVWVPLLGPH	238
XP_037292107.1	ICLGLMIMAIIFSFAYNCCPLNPADIDISPRLFTLMAGWGPETFTLRGWNVWVPLLGPH	238
XP_029845132.1	LALGFMIMALIFGFSYNCAPLNPADIDIGPRIFTAAGWGTEVFTYRNWNYIWVPIFGPH	238
EEC20079.1	LALGFMIMALIFGFSYNCAPLNPADIDIGPRIFTAAGWGTEVFTYRNWNYIWVPIFGPH	229
	:*.:*: **.* :***.*****.:**:* ::* :.* :.:**:.**	
OmAQP90	IGAIVGVWIYKLCIGDHWPIETTPALKQVLSSNDKSGPAAEPKETTNI-----	288
Om20812	VGGVLGAWTYKVCVEDNWPEEPTVILPVSTSKNSELGPTWL-----	280
Om22982	VGGVLGAWTYKVCVEDNWPEEPTVILPVSTSKNSELGTTASAEMNILFS----CDSCV-	293
A0A293N7C6_ORNER	IGAIIGLWIYKLCIRDHWPVQEMTSLKQVVSAAANGDNPGKTVESIVLR-----PAG	289
XP_037563606.1	IGAILGAWLYKVAIADHWDPKPKPTVSTNGESTT-----GRSRPMDCCPM-----RKVS	287
XP_037563608.1	IGAILGAWLYKVAIADHWDPKPKPTVST-----	266
XP_037563607.1	IGAILGAWLYKVAIADHWDPKPKPTVSKELPVPDVAVVDGKKPAAVAAPP-----PPAA	292
XP_037563609.1	IGAILGAWLYKVAIADHWDPKPKPTVSTEHLVASPSPG-----QL-----	278
XP_037510823.1	IGAILGVWLYKVAIGDHWDPDRPKPAST-N-----	266
XP_037510822.1	IGAILGVWLYKVAIGDHWDPDRPKPAST-NGESTTG----RPRPTDCWPMR-----KVS	286
XP_037292105.1	IGAILGVWLYKVAIGDHWPEKPKPAISTNGEPTTGR---PRPA--DCWP---MRK--VS	287
XP_037292106.1	IGAILGVWLYKVAIGDHWPEKPKPAIST-----	266
AIT69684.1	IGAILGVWLYKVAIGDHWPEKPKPAISMDHPVAVVV---AKKAPSRTPPALSPSAAPTTS	295
XP_037292107.1	IGAILGVWLYKVAIGDHWPEKPKPAISNEHVVASP---S---PGQ---LAKEA-----	283
XP_029845132.1	IGAIIGAWIYKVGIGDNFPDDEPKLNGDLERGVVLEQEAAAYRPIDDKLNLEAHTNEALK	298
EEC20079.1	IGAIIGAWIYKVGIGDNFPDDEPKLRAESGVQLVVYQPGAEQPVPEAPAPVP-----	282
	:*.:*: * **.: *:.*	
OmAQP90	-----	288
Om20812	-----	280
Om22982	-----	293
A0A293N7C6_ORNER	ENR----TEGDQTN TGKI-----	303
XP_037563606.1	TSRVVGS PDGREVKDDL VETLYKVDGERLVVELEPSQPQKL-	328
XP_037563608.1	-----DGREVKDDL VETLYKVDGERLVVELEPSQPQKL-	299
XP_037563607.1	AAQAQAS PQTA-----VRQTS D IEAGTPRKSP	319
XP_037563609.1	AKEA-----	282
XP_037510823.1	-----GKETKEDLVETLYKVDGDKMVLELEPAQQHQRL	299
XP_037510822.1	TSRVVGS PNGKETKEDLVETLYKVDGDKMVLELEPAQQHQRL	328
XP_037292105.1	TSRVVGS PDGKETKEDLVETLYKVDGDKMVLELEPTQHQR-	328
XP_037292106.1	-----DGKETKEDLVETLYKVDGDKMVLELEPTQHQR-	299
AIT69684.1	TSPQPAAPQATDVNAGS-----PAKA----	316
XP_037292107.1	-----	283
XP_029845132.1	L-----	299
EEC20079.1	-----	282