

Fig. 1 Supplement 1

S1		
	1.51 1.58	
62	RYYFIFTRLDLIWLSLNYFALLFLNFFEQP-----LWCE	At TPC1 DI
430	PNFGYAISFILIINFIADVVEETLTDIE-----	At TPC1 DII
30	SFFTKFIIYLIVLNGITMGLTSTKTFM-----	Ab Nav
12	RIFQFTVVSIIILNAVLIG-ATTYELD-----	Rh Nav
189	KILAIISIMFIVLSTIALSLNTLPQL-----SLD	Hs Kv2.1
163	RIIAIVSVMVILISIVSFCLTLPPIFRDENEDMHGSGVTFHT	Hs Kv1.2
227	RVVAIISVVFVILLSTIVIFCLTLPPEFK----HYK----VFNT	Dm Shaker
	241 247	
116	LGMRVFGVFLIFLDIILMIIDLSLPGK-----	Ci VSP
147	KPIHVAIIVLVVLDSFLVVGELLIDLK-----VII	Ci Hv1
42	HRFQVIIICLVVLDALLVLAELLLDLK-----IIE	mHv1cc
95	HRFQVIIICLVVLDALLVLAELLLDLK-----IIE	Mm Hv1
99	HRFQVIIICLVVLDALLVLAELLLDLK-----IIQ	Hs Hv1
	112 119	
S2		
	2.43 2.50 2.57	
95	KNPKPSCKDRDYYYLGELPYLTNAESIIYEVIITLAILLVHTF	At TPC1 DI
457	-----ESSAQKPWQVAEFVFGWIYVLEMALKIYT--	At TPC1 DII
57	-----QSFGVYTTLFNQIVITIFTIETIILRIY--	Ab Nav
38	-----PLFLETIHLLDYGITIFFVIEILIRFIG--	Rh Nav
219	EFG-----QSTDNPQLAHVEAVCIAWFTMEYLLRFLS--	Hs Kv2.1
205	YSN-STIGYQQSTSFTDPFFIVETLCIIWFSFEFLVRFFA--	Hs Kv1.2
261	TTNGTKIEEDEVPDITDPFFLIETLCIIWFTFELTVRFLA--	Dm Shaker
	283 287 293	
143	-----SESSQSFYDGMALALSCYFMLDLGLRIFA--	Ci VSP
177	VPH-----GNPAPEILHGFSLSILSIFMVIALKIIA--	Ci Hv1
72	PDE-----QDYAVTAFHYMSFAILVFFMLDLGLRIFA--	mHv1cc
125	PDE-----QDYAVTAFHYMSFAILVFFMLEIFFKIFV--	Mm Hv1
129	PDK-----NNYAAMVFHYMSITILVFFMMEIIFKLFV--	Hs Hv1
	150	
S3		
	3.50 3.61	
137	FPISYEGSRIFWTSRLNLVKVACVVILFVDVLVDFLYLS---	At TPC1 DI
486	----YG-FENYWREGANRFDFLVTWVIVIGETATFITP----	At TPC1 DII
84	----VHRISFFKDPWSLFDFFVVA---ISLVPTS-----	Ab Nav
66	----EKQKADFFKSGWNIFDTVIVA---ISLIPIPNN-----	Rh Nav
251	----SPKKWKFFKGPLNAIDLLAILPYYVTIFLTESNK----	Hs Kv2.1
244	----CPSKAGFFTNIIMNIDIVAIIPYFITLGTLEAEK----	Hs Kv1.2
301	----CPNKLNFCRDVMNVIDIIAIIPYFITLATVVAEEEDTL	Dm Shaker
	316	
172	----YGP-KNFFTNPWEVADGLIIVVTFVVTIFYTVLDEY--	Ci VSP
209	----DH--RHFIHHKVEVLDAVVVVISFGVDIALIFVG----	Ci Hv1
104	----YGP-KNFFTNPWEVADGLIVVVSFVLDLVLLFK-----	mHv1cc
157	----FR--LEFFHHKFEILDADFVVVSFVLDLVLLFK-----	Mm Hv1
161	----FR--LEFFHHKFEILDADFVVVSFILDIVLLFQ-----	Hs Hv1
	174 185	
S4		
	4.43 4.47 4.50 4.53 4.56	
176	-----PLAFDFLP--FRIAPYRVVIIIFILSIRELRDTLV	At TPC1 DI
519	-----DENTFFSNGEWIRYLLLARMLRLILLMNVRQYRA	At TPC1 DII
111	-----SGFEILRVLRVLRRLFRIVTAVPQ	Ab Nav
96	-----SSFLVRLRLRIFRVLRRLISVIPE	Rh Nav
285	-----SVLQFQ-----NVRRVQIFRIMRILILKLARH	Hs Kv2.1
278	-----PEDAQQ--GQQAMSLAILRVIRLVRFVIFKLSRH	Hs Kv1.2
339	NLPKAPVSPQDKSSNQAMSLAILRVIRLVRFVIFKLSRH	Dm Shaker
	362 371	
207	----VQETGADGL--GRLVVLARLLRVVRLARIFYSHQQ	Ci VSP
241	-----ESEALAAI----GLLVILRLWRVFRINGIIVTVK	Ci Hv1
136	-----SHHFEAL----GLLILLRLWRVARIINGIISRM	mHv1cc
188	-----SHHFEAL----GLLILLRLWRVARIINGIISVK	Mm Hv1
192	-----EHQFEAL----GLLILLRLWRVARIINGIISVK	Hs Hv1
	205 214	