

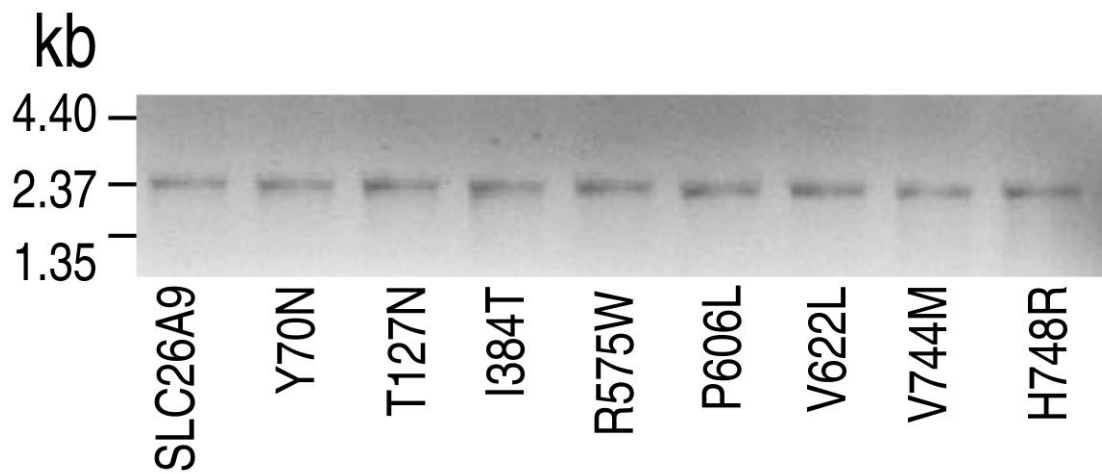
**Supp. Figure S1 (next page).** SLC26A9 aligned to BicA, SHST1 and SLC26A2. Predicted transmembrane helices of SLC26A9 were shaded in grey based on the membrane topology analysis of BicA (Shelden, et al., 2010). The locations of eight cSNPs of SLC26A9 were highlighted in blue. The STAS domain was indicated in green. The NCBI / GenBank accession numbers for these sequences are BicA (*Synechococcus* sp.PCC7002; ABG46427), SHST1 (*Stylosanthes hamata* high-affinity sulfate transporter; P53391), human SLC26A2 (*Homo sapiens* solute carrier family 26 member 9 isoform a; AAH59390), human SLC26A9 (*Homo sapiens* solute carrier family 26 member 9 isoform a; NP\_443166).

BicA	-----			-
SHST1	MSQRVSDQVMADVIAETRNSSSSHRHGGGGGGD---DTTSLPYMHKVGTPPKQTLFQEIKHSFN-----ET			63
SLC26A2	-----MSSESKEQHNVSPRDSAEGNDSYPSGIHLELQRESSTDFKQFETNDQCRPYHRILIERQEKSDTNFKE			68
<b>SLC26A9</b>	-----MSQPRPRYVVDVDR-----AAYSLTLFDD-----EFEKKDRTPYVG-----			34
		<b>TM1</b>	<b>TM2</b>	
BicA	-----MQITNKIHFNRN-IRGDI	IFGGLTAAVIALPMALAFGVASGAGAEAGLWGAVL		50
SHST1	FFPDKPFGKFKDQSGFRKLELGLQYIFPILEWGRHYDLKK-FRGDF	FIAGLTIASLCIPQDLAYAKLANLDPWYGLYSSFV		142
SLC26A2	FVIKKLQKNCQCSP--AKAKNMILGFLPVLQWLPKYDLKKNILGDVMSGLIVGILLVPQSIAYSLLAGQEPVYGLYTSFF			146
<b>SLC26A9</b>	---EKLRNAFRCSS--AKIKAVVFGLLPVLSWLPNYKIKD	YIIPDLLGGLSGGSIQVPQGMFAFALLANLPAVNGLYSSFF		109
	<b>TM2</b>	<b>TM3</b>	<b>TM4</b>	
BicA	VGFFAALFGGTPTLISEPTGPMTVVMTAVIAHFTASAATPEE--G-----		LAI AFTVV	101
SHST1	APLVYAFMGTSRDIAIGPVAVVSLLLGTLLSNEISNTKSHDY-----		LRLAFTAT	192
SLC26A2	ASIIYFLLGTSRHSISVGI FGVLC LMIGETVDRELQKAGYDNAHSAPSLGMVSNGSTLLNHTSDRICDKSCYA		IMVGSTVT	226
<b>SLC26A9</b>	PLLTYYFLLGGVHQMPVG	IFAVISILVGNICLQLAPESKFQVFNNATNESYVDTAAMEAER-----	LHVSATLA	177
	<b>TM4</b>	<b>TM5</b>	<b>TM6</b>	
BicA	MMAGVFQII FGS LKLGKYVTMMPYTVISGFM	SGIGIILVILQLAPFLGQASPG-GGVIGTLQNLPTLLSNIQP--	GETAL	178
SHST1	FFAGVTQMLLGVCR LGFLIDFLSHAAIVGFMAGAAITIGLQQLKGLLGISNNTFTKKTDIISVMRSVWTHVHHGWNWETI			272
SLC26A2	FIAGVYQVAMGFFQVGFVSVYLS DALLSGFVTGASFTILTSQAKYLLGLNLPRTNGVGLITTWIHFVFRNIHK-TNLCDL			305
<b>SLC26A9</b>	CLTAIIQMG LGFMQFGFVAIYLSSEFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPH-TNIASL			256
	<b>TM6</b>	<b>TM7</b>	<b>TM8</b>	
BicA	ALGTVAIIWFMP-----EKFKKVI	PPQLVALVLTGTVIAFFVFPPEVSDLRRIGEIRAGFPELVRPSFSPVEFQRM		249
SHST1	LIGLSFLIFLLITKYIAKKNKFLVWSAISPMISVIVSTFFVYITRADKR-GVSIVKHIKSGVNPSSANEIF--FHGKYL			349
SLC26A2	ITSLCLLVLLPTKELNEHFKSKLKAPIPIELVVVAATLASHFGKLNHENYNSSIAGHIPTGFMPPKVPENW--LIPSPA			383
<b>SLC26A9</b>	IFALISGAFVLVVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKHYHMQIVGEIQRGFPTVSPVVS--QWKDMI			334
	<b>TM8</b>	<b>TM9</b>		
BicA	LDAAVLGM LG----CIDALLTSVADSLTRTEHNSKELIGQGLGNLFSGLFGGIAGAGATMGTVVNIQSGGRTALSGLV			325
SHST1	GAGVRVGVVAGLVALTEAIAIGRTFAAMKDYALDGNKEMVAMGTMNIVGSLSSCYVTTGFSRSRAVNYMAGCKTAVSNIV			429
SLC26A2	VDAIAISIIIG----FAITVSLSEMF AKKHGYTVKANQEMYAIGFCNII PSFFHCFTTSAALAKTLVKESTGCHTQLSGVV			459
<b>SLC26A9</b>	GTAFSLAIVS----YVINLAMGRTLANKHGYDVDSNQEMIALGCSNFFGSGFFK	IHVICCALSVTLAVDGGGKSQVASLC		410
	<b>TM9</b>	<b>TM10</b>	<b>TM11</b>	<b>TM12</b>
BicA	RAFVLLVVILGAASLTATIPLAVLAGIAFKVGVD-IIDWSFLKRAHEISPKGALIMYGVILLTVLVDLIVAVGVGVFVAN			
SHST1	MSIVVLLTLLVITPLFKYTPNAVLASIIIAAVVN-LVNIEMVLLWKIDKDFVACMGAFFGVIFKSVEIGLLIAVAISF			508
SLC26A2	TALVLLVLLVIAPLFYSLQKSVLGVITIVNLRGALRKFRDLPKMWSISRMDTVIWFVMTLSSALLSTEIGLLVGVCFSI			539
<b>SLC26A9</b>	VSLVVMITMLVLGIYLYPLPKSVL GALIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPLPYGVAVGVAFSV			490
	<b>TM12</b>			
BicA	VLTIERMSNLQSEKVQTVSDADDNIRLTTTEKRWLDEGQGRVLLFQLSGPMIFGVAKAIAREHNAMG-----			471
SHST1	AKILLQVT	RPRTAVLGKLPGTSVYRNIQYYPK--AAQIPG-MLIIRVDSAIYFSNSNYIKERILRWL-----	IDE	575
SLC26A2	FCVILRTQKP	KSSLLGLVEESEVFESVSAYKN--LQTKPG-IKIFRFVAPLYYINKECFKSALYKQT-VNPILIKVAWKK		615
<b>SLC26A9</b>	LVVVFQTTQFR	NGYALAQVMDTDIYVNPKTYNR--AQDIQG-IKIITYCSPLYFANSEIFRQKVIAKTGMDPQKVLAKQK		567
	-----			-
BicA	-----			-
SHST1	GAQR-----		TESELP-----	585
SLC26A2	AAKR--K-----	IKEKVVTLGGIQDEMS-----	VQLSHDP-----	643
<b>SLC26A9</b>	YLKKQEK	RRMRPTQQRSLFMKTKTVSLQELQDFENA	PPTDPNNTQTPANGTSVSYITFSPDSSSPAQSEPPASAEAPG	647
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BicA	-----DCDALVFDIGEVPHMGV TASLALENAIEEALDKERQVYIVGAAGQTRRRLEKLFKRVV--PDKCL			536
SHST1	-----EIQHLITEMSPVPDIDTSGIHAFEELYKTLQKREVQLILANPGPVVIEKLGASKLTELIG--EDKIF			650
SLC26A2	-----LELHTIVIDCSAIQFLDTAGIHTLKEVRRDYEAIGIQVLLAQCNPTVRDSL TNGEYCKKE--EENLLF			709
<b>SLC26A9</b>	EPDMLASVPPFVTFHTLILDMSGVSFV DLMGICALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVF			727
	-----			-
BicA	MSREEAL	KNAVLGIY-----	PHLADGV TAP SSEMG-----	566
SHST1	LTVADAV	ATYGPKT-----	AA----F-----	667
SLC26A2	YSVYEAM	AFAEVSK-----	NQKGVCVPNGLSLSSD-----	739
<b>SLC26A9</b>	PSIHDAV	LFAQANARD	VTPGHNFGQAPGDAELSLYDSEEDIRSYWDLEQEMFGSMFHAETLTAL	791

- SLC26A9 cSNPs -

- TM# -

- STAS domain -



**Supp. Figure S2.** RNA quality for oocyte injections. RNA gel-electrophoresis of capped cRNA used for *Xenopus* oocytes injections. Approximately 100ng cRNA of SLC26A9 and eight cSNPs were loaded on 0.8% formaldehyde agarose gel. The cRNAs were then diluted 20 fold for injection (5ng). The 0.24 to 9.5kb RNA ladder is indicated on the left. The predicted cRNA sizes are 2.3kb.