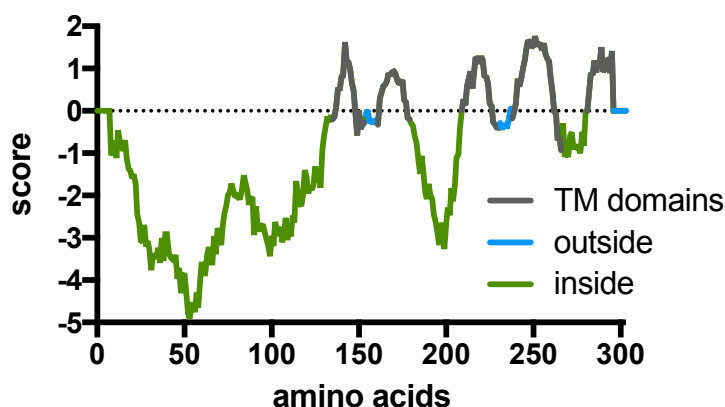


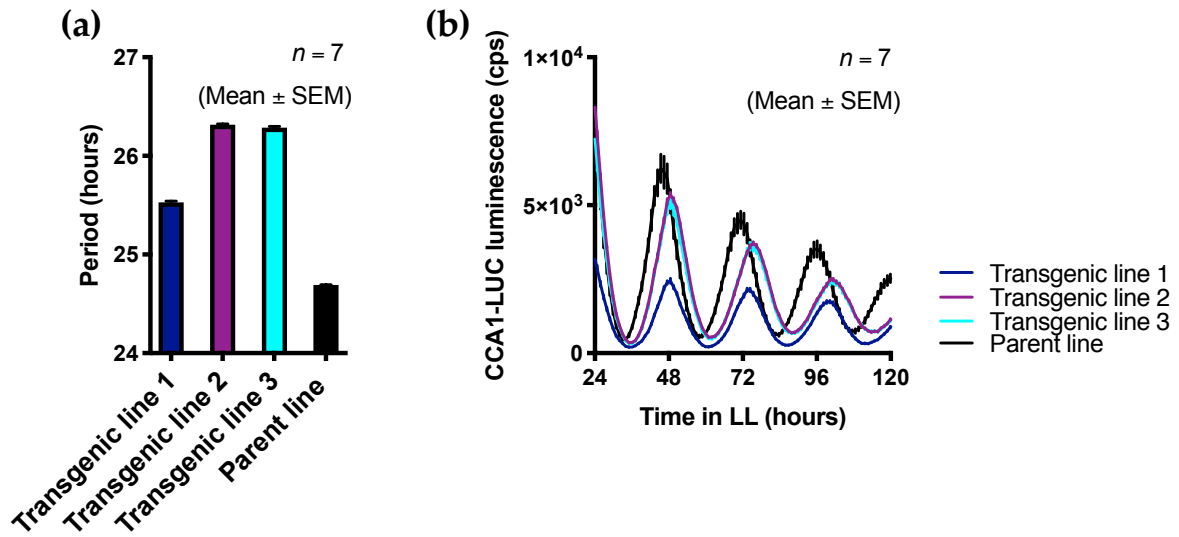
(a)

OtMgtE	-- <b>TMLVGAGGN</b> AGNQSAIHVIRGLATGEMENTNE-----CMRKTIVEQFQVGLM---LGVV	51
MgtE	<b>VPVLLGTGGNT</b> GNQSATLIIRALATRDLDLR-----dWRRVFLKEMGVGLL---LGLT	50
SLC41A3*1	<b>VPPLVGLKGNLE</b> MTLASRLSTAANTGQIDDPQE-----QHRVISSNLALIQQVQATVVGLL	55
SLC41A2*1	<b>VPALLGLKGNLE</b> MTLASRLSTAVNIGKMDSPIE-----KWNLIIGNLALKQVQATVVGF	55
SLC41A1*1	<b>VPALLGLKGNLE</b> MTLASRLSTAANIGHMDTPKE-----LWRMITGNMALIQVQATVVGF	55
SLC41A3*2	<b>TPVICG</b> VGGNLVAIQTSRISTYLHMWSAPGVLPQMKKFWPNPCSTFCTSEIN-----	53
SLC41A2*2	<b>TPVINGIG</b> GNLVAIQASRISTYLHLHSIPGELPD-EPKGCYYPFRFFGPGVN-----	52
SLC41A1*2	<b>TPVINGVGG</b> NLVAVQASRISTFLHMNGMPGENSEQAPRRCPSPCTFFSPDVN-----	53
	: * ** : :	:
OtMgtE	LSSAGFVRVLLTSPQGTDDLIG-----PFAIATALFAIVTT-----STCVGTALP	96
MgtE	LSFLLVGKVIYWD---GHPLLLP-----VVGVSIVLVVFFAN-----LV--GAMLP	90
SLC41A3*1	AAVAALLL-GVV-SREEVDVAKVELLCA--SSVLTAFLAALFALG-----VLMVCIV	102
SLC41A2*1	AAVAAILL-GWI-PEGKYLDHSILLCS--SSVATAFIASLLQG-----IMVGV	102
SLC41A1*1	ASIAAVVF-GWI-PDGHF SIPHAFLLCA--SSVATAFIASLVLG-----MIMIGVI	102
SLC41A3*2	SMSARVLLLLLV-PGHLIFFYIIYV-EGQSVINSQTFVVLYLLAGLIQVTILLYLAEVMV	111
SLC41A2*2	NKSAQVLLLLVI-PGHLIFLYTIHLMKSGHTSLTIIFIVVYLFQAVLQVFTLLWIADWMV	111
SLC41A1*2	SRSARVFLLVV-PGHLVFLYTISCMQGGHTTLTLIFIFVYMTAALLQVLILLYIADWMV	112
	. . : :	:
OtMgtE	FLLMRLNQD <b>PANAGTSVQVVM</b> -DVSGVIIT-----	125
MgtE	FLLRRRGVD <b>PALVSNPLVATLS</b> DVTGLLIYL-----	121
SLC41A3*1	IGARKLGVN <b>PDNIATPIAASL</b> GD LITLSILA-----	133
SLC41A2*1	VGSKKTGIN <b>PDNVATPIAASFG</b> D LITLAILA-----	133
SLC41A1*1	IGSRKIGIN <b>PDNVATPIAASL</b> GD LITLALL-----	132
SLC41A3*2	RLTWHQALD <b>PDNHCIPYLTGL</b> GD LLLGSS-----	139
SLC41A2*2	HHFWRKGGK <b>PD</b> SF <b>SIPYLTAL</b> GD LLLGTALLA-----	142
SLC41A1*2	HWMWGRGLD <b>PD</b> NF <b>SIPYLTAL</b> GD LLLGTGLLAXSLCA	148
	:* . : * :	

(b)



**Supplementary Figure 1:** (a) The *OtMgtE* MgtE domain shares homology with the bacterial MgtE domain (here from *Thermus thermophilus*) and all three human SLC41 proteins as shown with this multiple sequence alignment. The two conserved motifs outlined by Wabakken *et al.* (2003) are shown in green. \* denotes a fully conserved residue, : denotes conservation between groups of strongly similar properties and . denotes conservation between groups of weakly similar properties. (b) The hydrophobicity plot predicting transmembrane domains indicates that this protein is a transmembrane protein.



**Supplementary Figure 2:** Luminescent traces and period analysis of OtMgtE overexpression lines. (a) Period analysis of 3 transgenic lines and parent line. (b) Luminescent traces: OtMgtE overexpression induces a long period phenotype compared to the parent line in free running conditions (constant light). Figure shows CCA1 bioluminescent traces over 4 days.

**Supplementary Table 1:** Protein accession numbers for proteins used in figure 4

Species (NCBI taxonomic ID)	NCBI/Uniprot accession number, (homolog number where >1)
<i>Homo sapiens</i> (9606)	Q8IVJ1 (1) (SLC41A2) Q96JW4 (SLC41A3) Q96GZ6
<i>Drosophila melanogaster</i> (7227)	M9PHE6
<i>Crassostrea gigas</i> (29159)	K1QPN0
<i>Amphimedon queenslandica</i> (400682)	XP_019864491.1
<i>Monosiga brevicollis</i> MX1 (431895)	A9VBR3
<i>Salpingoeca rosetta</i> (946362)	F2UAH4
<i>Chlamydomonas reinhardtii</i> (3055)	A8J2E0
<i>Ostreococcus tauri</i> (70448)	A0A096P9B9
<i>Emiliana huxleyi</i> (2903)	(1) R1EK90 (2) R1DRZ5 (3) R1FDF9 (4) R1CTW0 (5) R1CBM8 (6) R1EBL0 (7) R1F8I7
<i>Thalassiosira pseudonana</i> (35128)	B8CF51
<i>Cyanidioschyzon merolae</i> (45157)	M1V9W9
<i>Naegleria gruberi</i> (5762)	D2VNX4
<i>Chlamydia trachomatis</i> (813)	A0A0E9C5A4
<i>Pseudomonas aeruginosa</i> (208964)	Q9I544
<i>Bacillus subtilis</i> (224308)	O34442
<i>Providencia stuartii</i> (471874)	B2PYL8
<i>Tolypothrix campylonemoides</i> (1136105)	WP_071838811.1
<i>Treponema azotonutricium</i> (545695)	F5YDZ2
<i>Pelolinea submarina</i> (913107)	WP_116224794.1
<i>Thermus thermophilus</i> ( 274)	Q5SMG8
<i>Acidobacteriaceae bacterium</i> KBS 96 (1267535)	WP_020720448.1
<i>Oceanotoga teriensis</i> (515440)	WP_109604606.1
<i>Natronomonas pharaonic</i> (348780)	A0A1U7EW96
<i>Pyrococcus abyssi</i> (272844)	Q9UZ17
<i>Hyperthermus butylicus</i> (54248)	WP_048061491
<i>Methanosarcina mazei</i> (2209)	A0A0F8MPI8
<i>Ulva mutabilis</i> proteome accessed from ORCAE, gene ID: UM021_0210.1	