Supplemental Materials

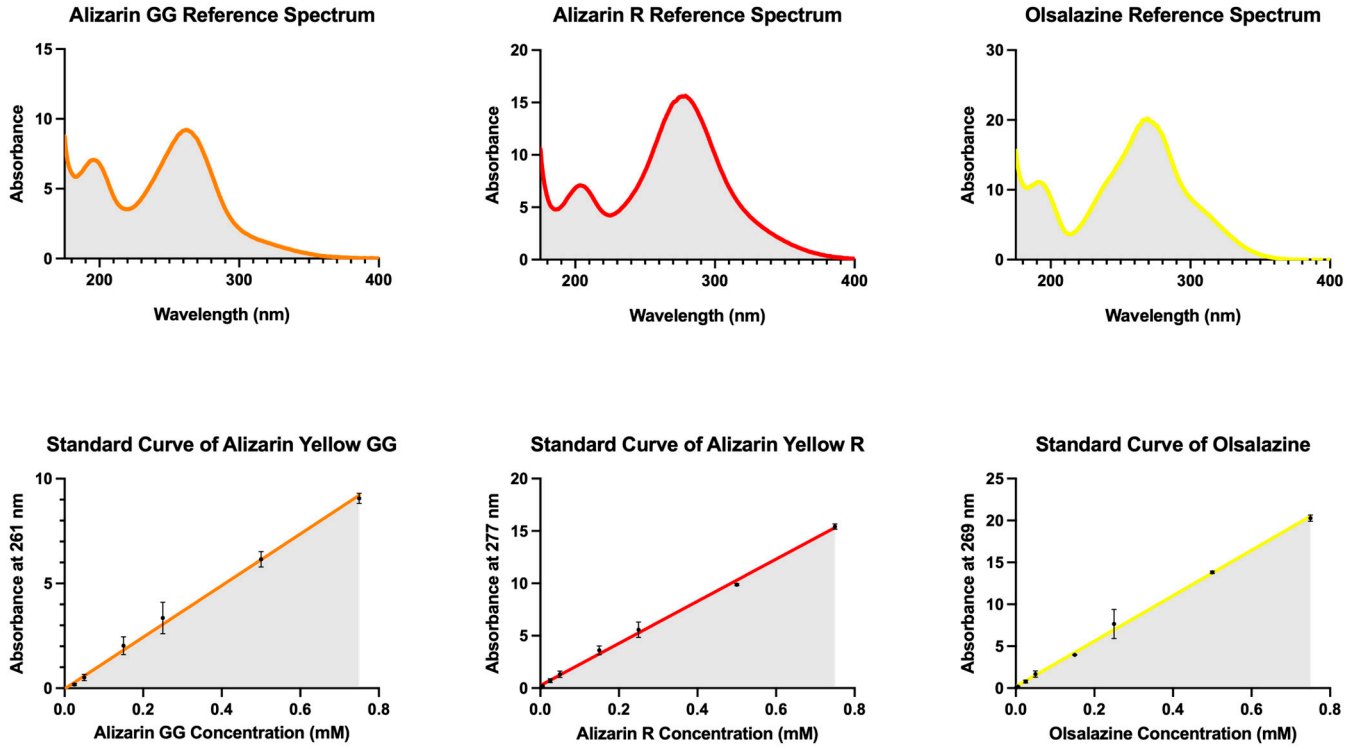


Figure S1. Absorbance spectra and standard curves of Alizarin Yellow GG, Alizarin Yellow R, and Olsalazine in PBS. Standard curves were generated by serial dilutions of each dye in PBS. Dilutions were performed in triplicate and absorbance was measured using a NanoDrop One Spectrophotometer.

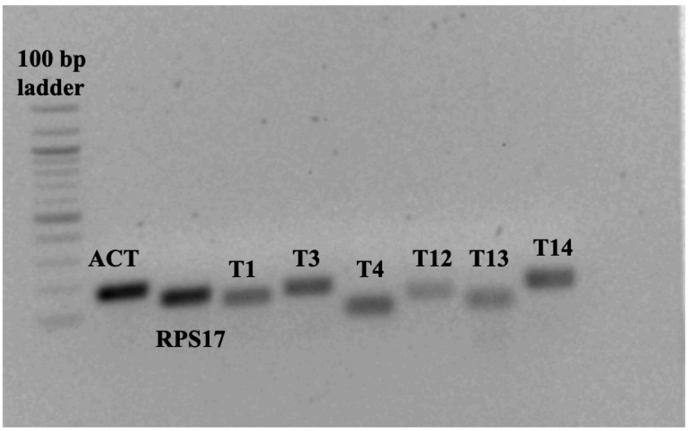


Figure S2. Gel electrophoresis of amplicons for qPCR. PCR products were separated on a 1% agarose gel. Ladder was Quick-Load® Purple 100 bp DNA Ladder (New England Biolabs, Ipswich, MA, USA). Each primer pair produced a single amplicon. ACT (*AAEL011197*), RPS17 (*AAEL004175*), T1 (*AAEL004451*), T3 (*AAEL012443*), T4 (*AAEL000902*), T12 (*AAEL024953*), T13 (*AAEL026837*), and T14 (*AAEL004479*).

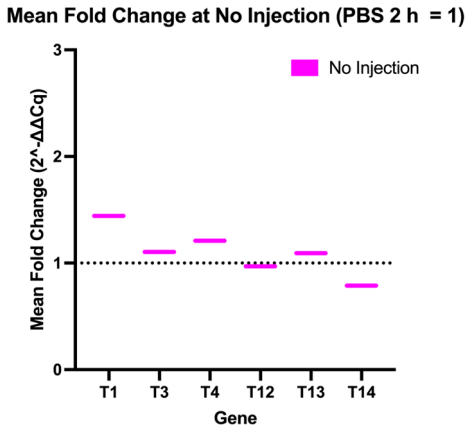


Figure S3. Preliminary qPCR of putative transporters: expression 2 hours after anesthetizing and wounding by a needle. Data is from one biological replicate, the genes were abbreviated as: T1 (*AAEL004451*), T3 (*AAEL012443*), T4 (*AAEL000902*), T12 (*AAEL024953*), T13 (*AAEL026837*), and T14 (*AAEL004479*).



Figure S4. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A. Human SLC22A proteins are in Bold. Similarity and identity threshold was set at 70% using the Color Align Conservation feature of the Sequence Manipulation Suite (Stothard, P. The Sequence Manipulation Suite: JavaScript Programs for Analyzing and Formatting Protein and DNA Sequences. *Biotechniques* **2000**, 28, 1102–1104). The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

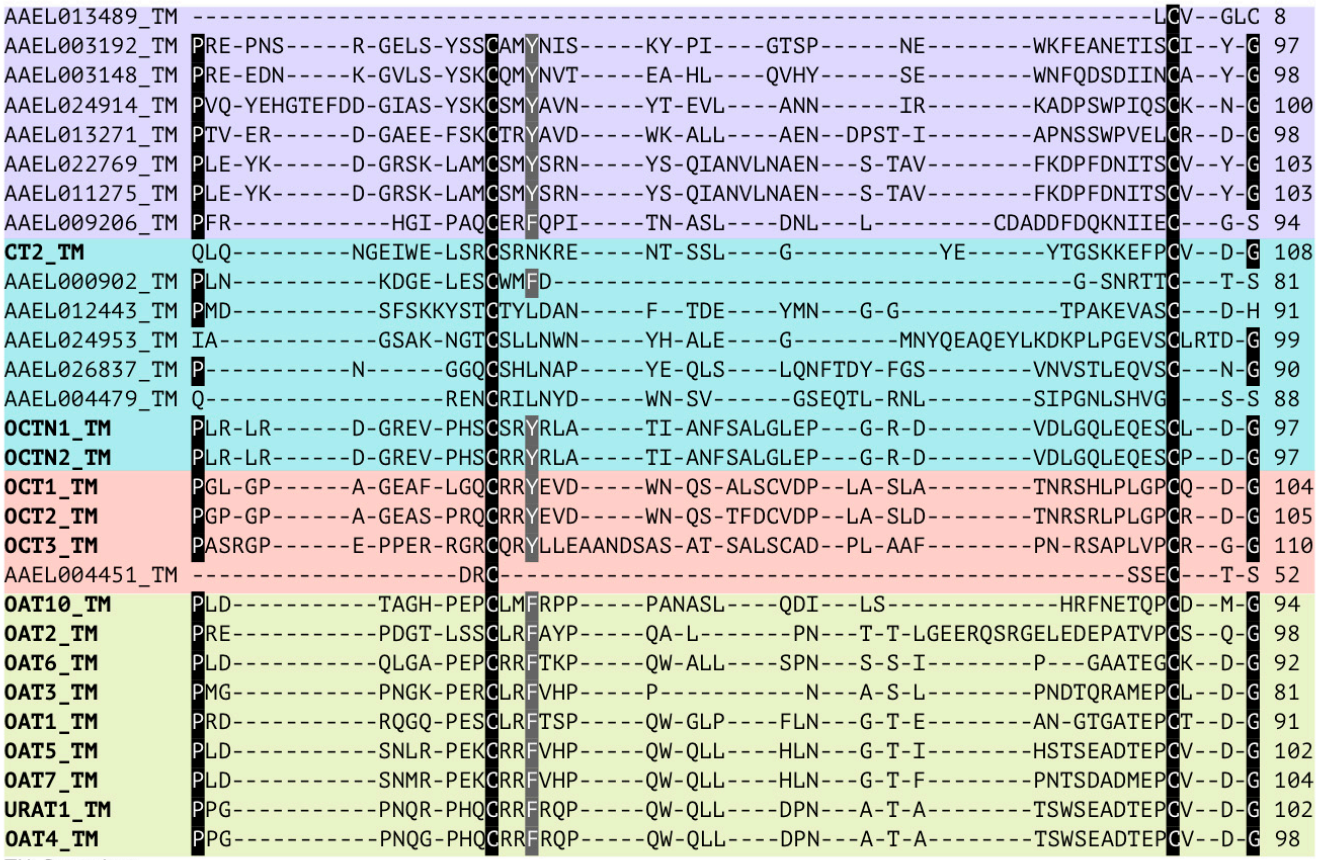


Figure S4 continued. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A in Bold. Similarity and identity threshold was set at 70%. The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

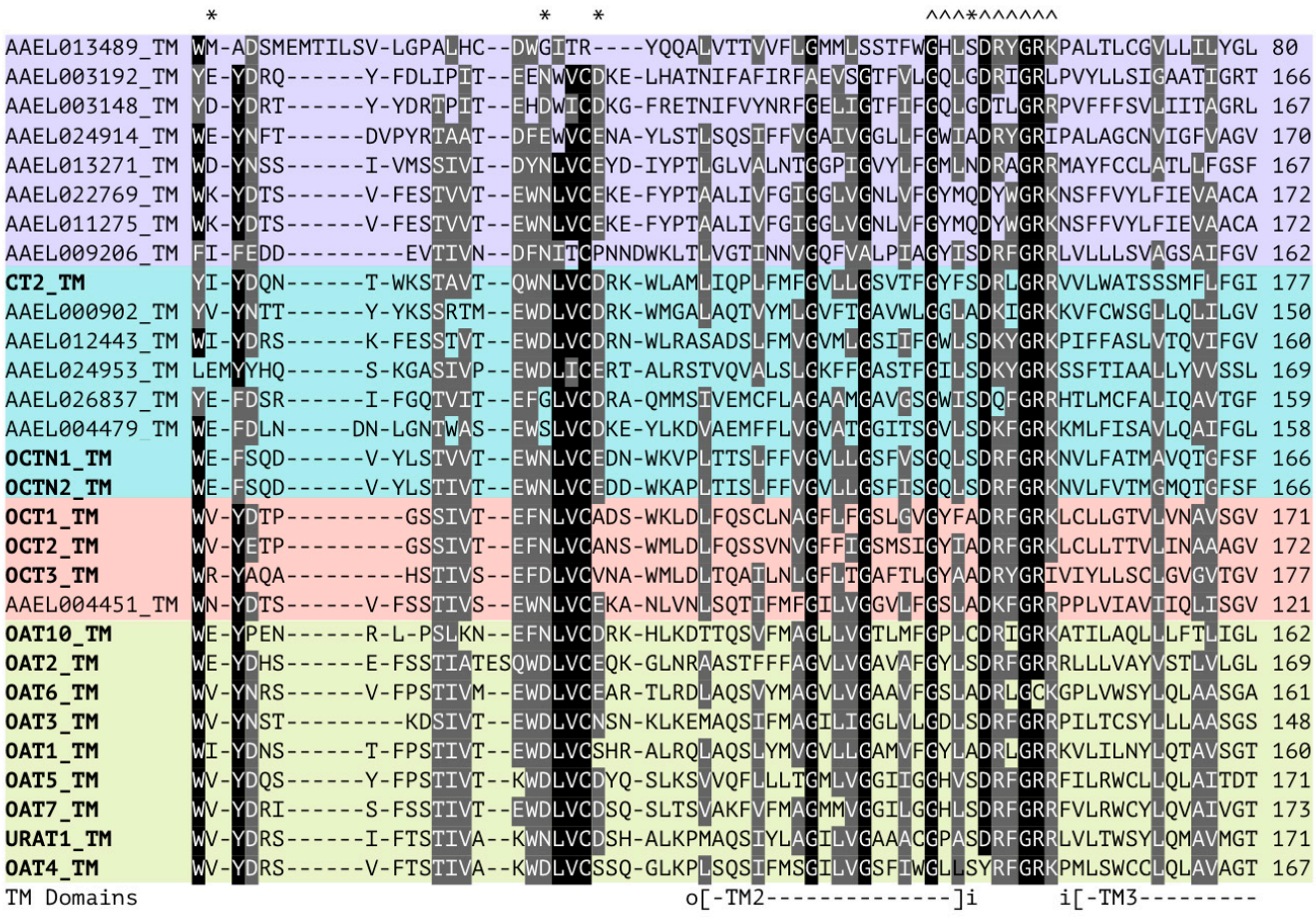


Figure S4 continued. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A in Bold. Similarity and identity threshold was set at 70%. The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

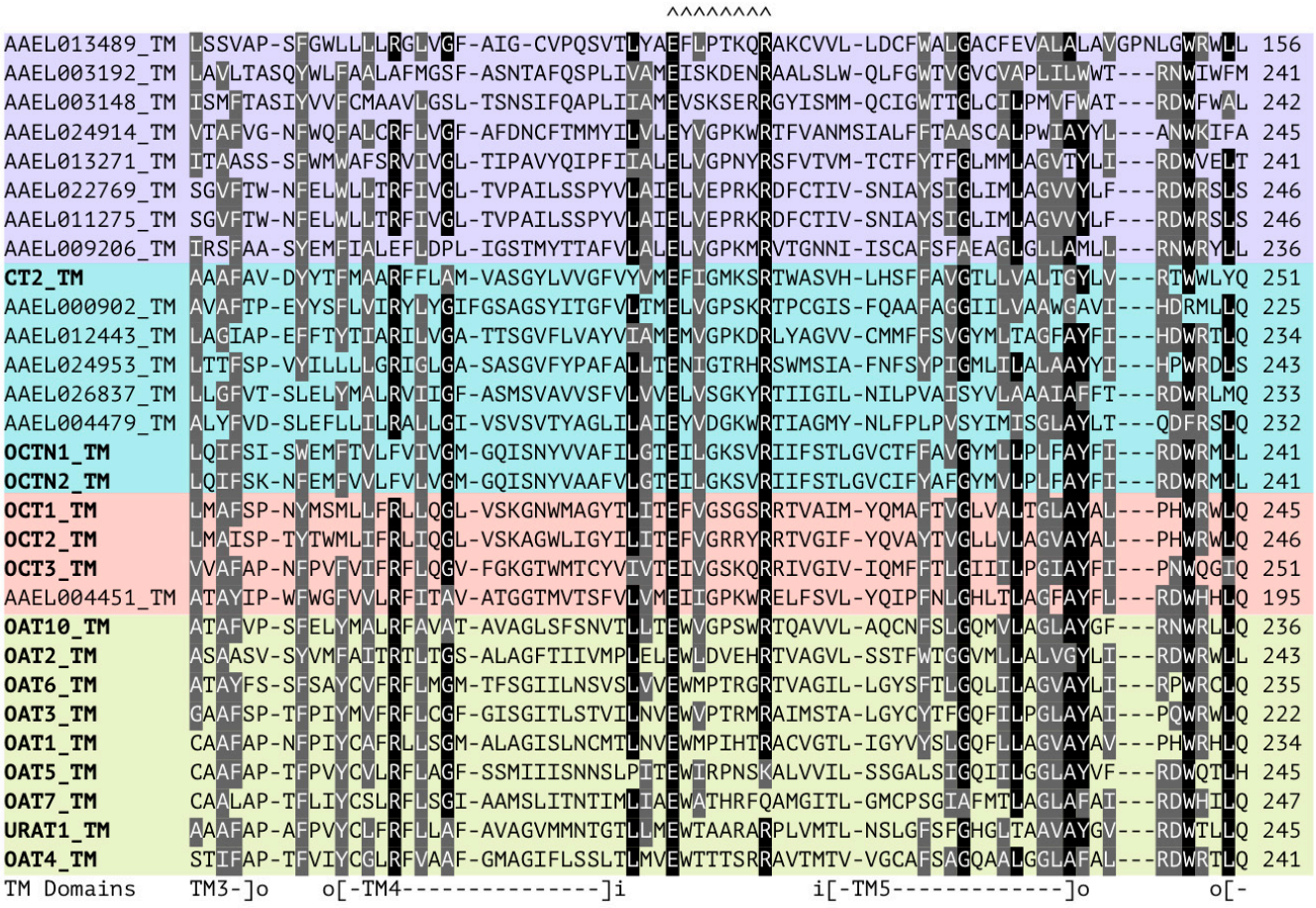


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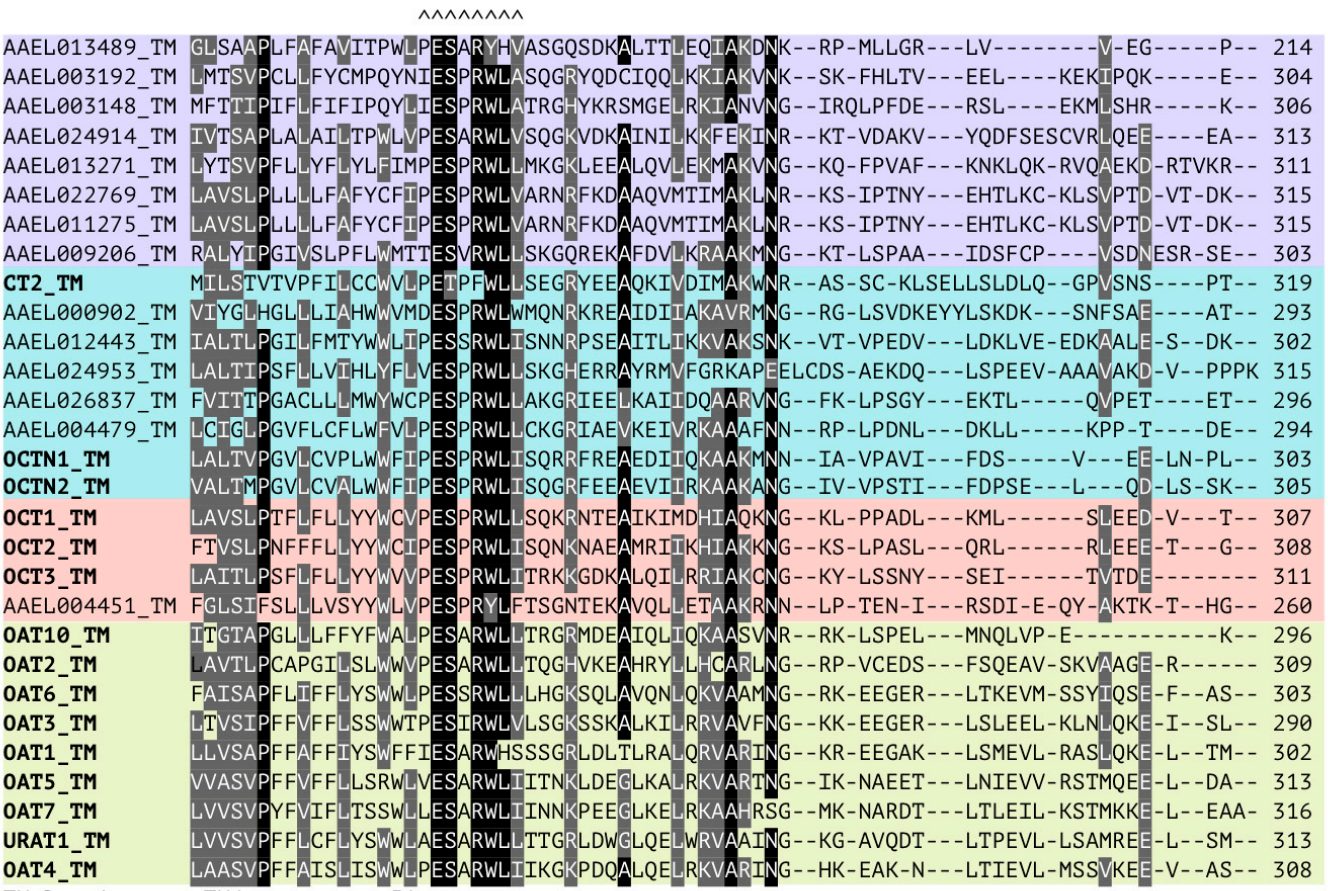


Figure S4 continued. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A in Bold. Similarity and identity threshold was set at 70%. The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

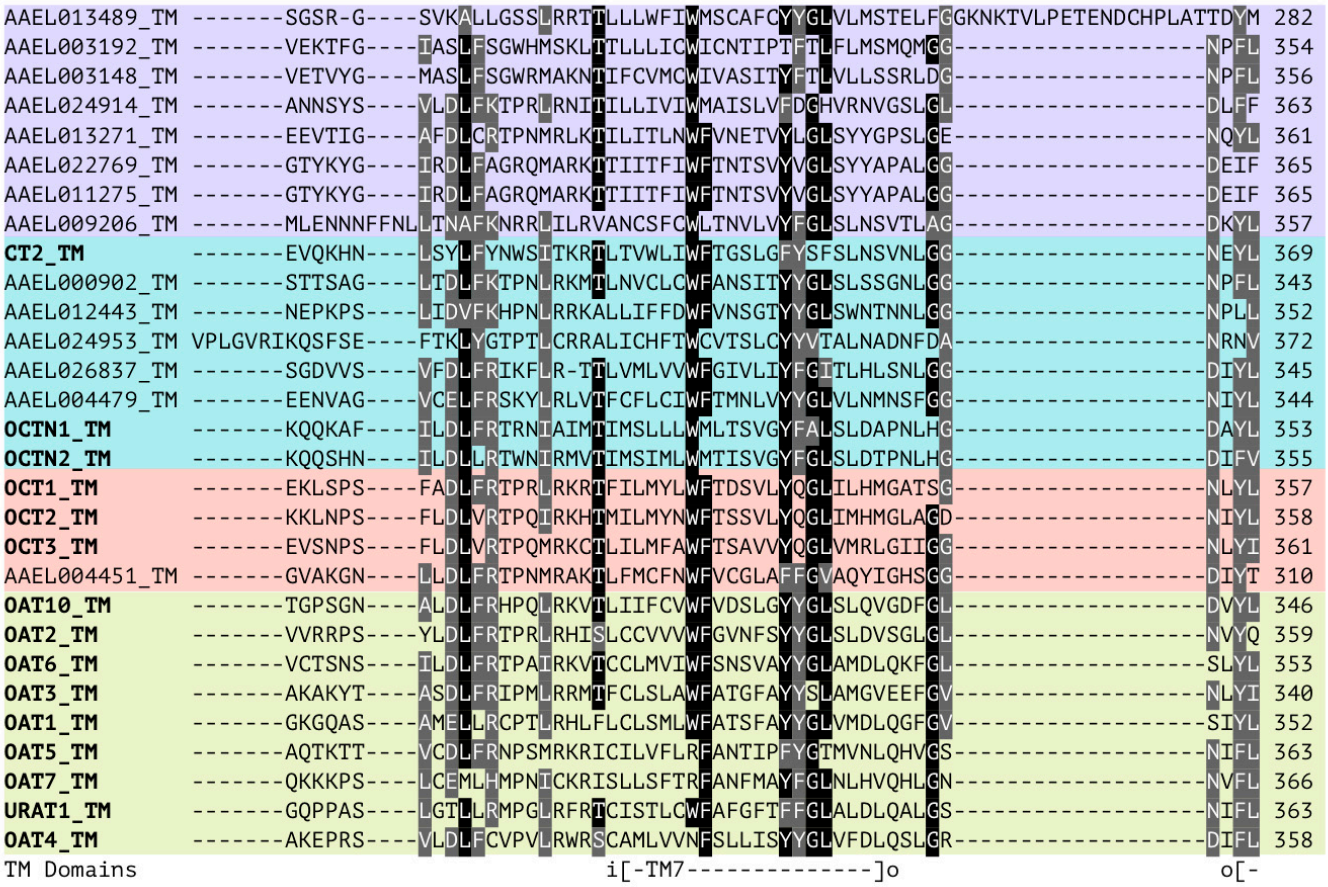


Figure S4 continued. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A in Bold. Similarity and identity threshold was set at 70%. The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

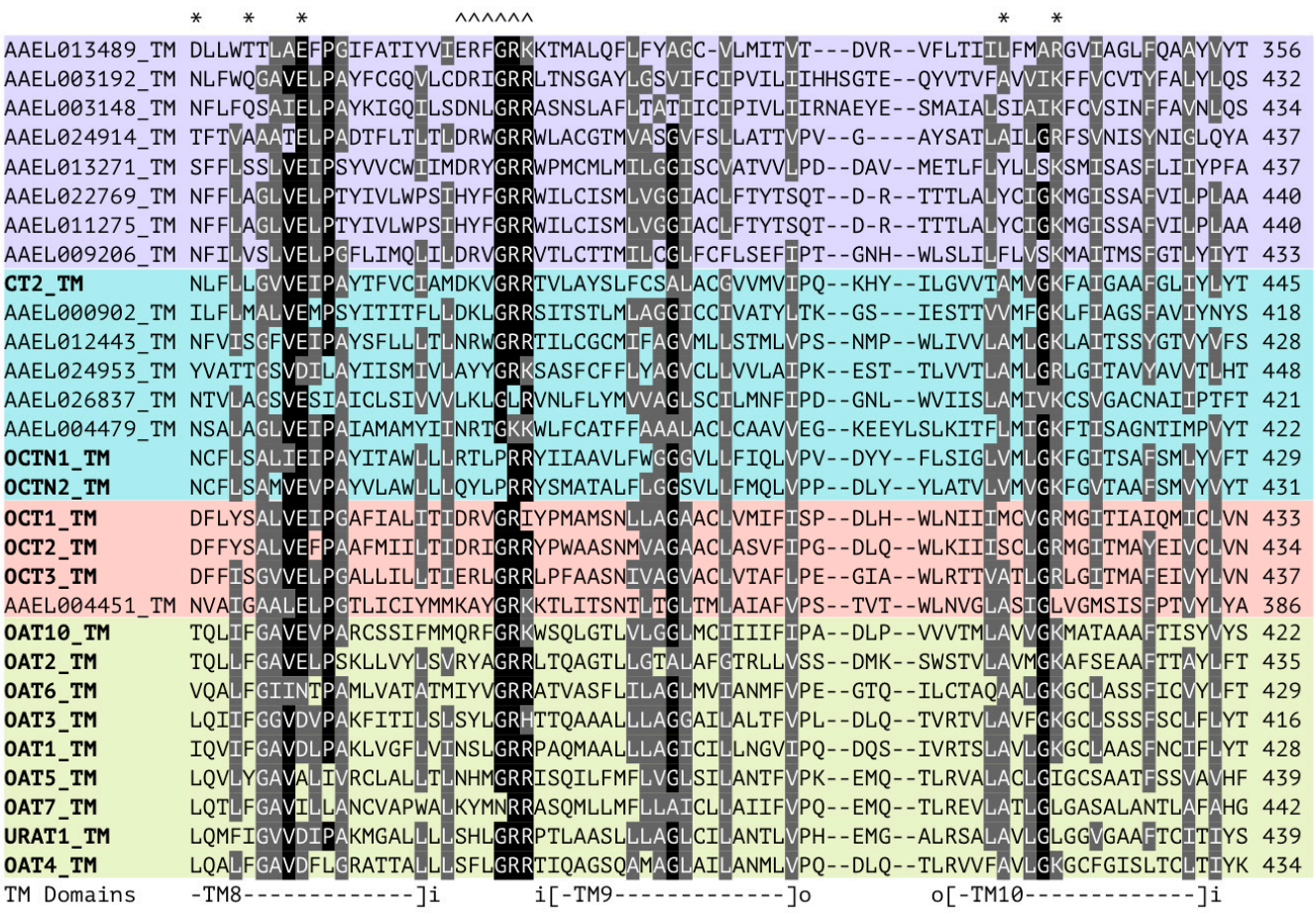


Figure S4 continued. Amino acid sequence alignment of the putative organic cation transporters and putative organic cation transporter novel from *Aedes aegypti* with human SLC22A in Bold. Similarity and identity threshold was set at 70%. The top line indicates the strongly conserved regions among SLC22A peptides "^" and positions of class specific amino acids "*". The bottom line indicated the predicted transmembrane domains by CCTOP where "i" signals intracellular loops and "o" signals extracellular loops.

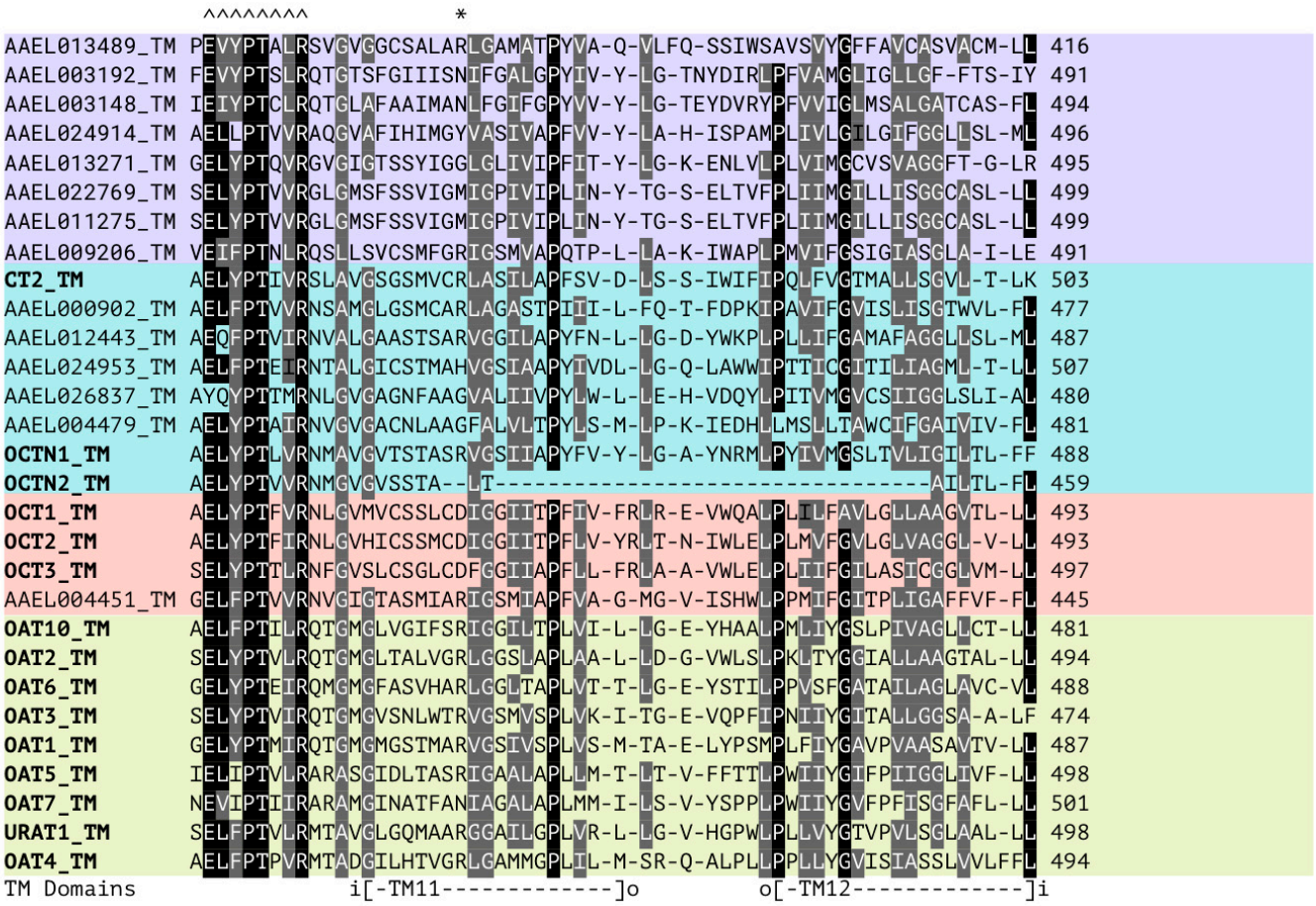


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Table S1. Primer sequences for qPCR. (Note "¦" indicates the exon-exon junction in amplicon.)

Gene	Sense Primer Antisense Primer	Amplicon
AAEL004451	TGGTTAGTTTCGTTAGGCTGG GTCGCTCTTTTTCGCAGTTG	TGGTTAGTTTCGTTAGGCTGGTTGTGGATACCGTTGAGAAGTGGGTGGCGAAAGATGGGCGAATCTA ACATTGAAATGCGCGGTCGAACGGAAGACGGAG¦TGACCGCAACTGCGAAAAAGAGCGAC
AAEL012443	GTCTCCTGTCGTTGATGCTG ATCTCTTCGGCAGTCTTGTTC	GTCTCCTGTCGTTGATGCTGCCGGAAACGCACAACCAGAAGCTACCGGAAACGATTGCCGATGGGGA AAACTTTGGCAAGGTGAAAGTCATGCCCGGCGAAGAGGGTCGCCGGGGGGACGTGGAGAACAAGACT GCCGAAGAGAT
AAEL000902	GCGGTTGATCATACACTGGAG GAATTGGAATGCCTGGTAACG	GCGGTTGATCATACACTGGAGGAGCTGATGGGAATGTTGG¦ GCGACTTCGGTCGTTACCAGGCATTCCAATTC
AAEL024953	TGTTGCTTGGACGGATCG AAGGCAATACTCATCCACGAC	TGTTGCTTGGACGGATCGGGCTGGGTGCTTCCGCTTCCGGAGTTTTCTACCCGGCGTTTGCGTTGT¦ TGACTGAAAACATCGGAACCCGTCATCGGTCGTGGATGAGTATTGCCTT
AAEL026837	TGGGTGATTATCTCGTTGGC TTGGTAGGCTGTAAACGTCG	TGGGTGATTATCTCGTTGGCTATGATAG¦ TCAAGTGTTCCGTAGGGGCGTGCAATGCTATCATTCCGACGTTTACAGCCTACCAA
AAEL004479	AACTGTACCCAACTGCCATC ATATACACCAAGCCGTGAGC	AACTGTACCCAACTGCCATCAGGAACGTTGGCGTGGGGGCTTGTAATCTCGCGGCTGGATTCGCTTT AGTGCTTACCCCTTATCTTTCCATGTTG¦ CCAAAGATCGAGGATCATCTTCTTATGTCCCTGCTCACGGCTTGGTGTATAT
RPS17 *(AAEL004175)*	GATTTCCACACGAACAAGCG TGCAGCTTGATGGAGATACC	GATTTCCACACGAACAAGCGGATCGTCGAAGAAGTGGCCATCATTCCAACGAAGCCCCTGCGCAACA AGATCGCTGGG¦ TTTCGTGACACATCTGATGAAGCGCCTGCGCCACTCCCAGGTCCGTGGTATCTCCATCAAGCTGCA
ACT *(AAEL011197)*	CGTTCGTGACATCAAGGAAA GAACGATGGCTGGAAGAGAG	CGTTCGTGACATCAAGGAAAAACTGTGCTACGTTGCACTGGACTTTGAACAGGAAATGGCCACCGCT GCCTCGTCCTCCTCCCTGGAGAAATCGTACGAACTTCCCGATGGACAAGTCATCACCATCGGCAATG AACGTTTCCGTTGCCCAGAGGCTCTCTTCCAGCCATCGTTC

Table S2. Thermocycle utilize for qPCR.

Step	1	2	3	4	5	Repeat 40X Steps 3-5	6	7	8
Phase	Activation		Amplification				Melt Analysis		
Temp (°C)	50	50	95	95	95	95	95	95	95
Time (sec)	95	95	53	53	53	53	60	60	60
Trans. Rate (°C/s)	120	120	60	60	60	60	95	95	95