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		<u> </u>
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	1 MP-TVDDVLEQVGEFGWFQKQAFLTLCLLSAAFAPIYVGIVFLGFTPDHR-C	SQ 61 SQ 60 SL 61 AE 61 SH 60 NAS 56
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8	61 RCGWSLAEELNYTVPGL-GAAGEAFPROCREYEVDWNQ SALSCVDPLASLAANRSHL 62 RCGWSLEEELNYTVPGV-GSSGEASPSOCREYEVDWNQ TGLSCTDPLASLAANRSHL 61 RCGWSPAEELNYTVPGU-GSSGEASPSOCREYEVDWNQ SALSCVDPLASLANRSHL 62 RCGWSPAEELNYTVPGU-GPAGEAFLGCCREYEVDWNQ SALSCVDPLASLANRSHL 62 RCGWSPAEELNYTVPGU-GPAGEAFLGCCREYEVDWNQ SALSCVDPLASLANRSHL 62 RCGWSPAEELNYTVPGP-GPAGEAFLGCCREYEVDWNQ SALSCVDPLASLANRSHL 62 RCGWSPAEELNYTVPGP-GPAGEASPROCREYEVDWNQ SALSCVDPLASLAFTNESSCA 62 RCGWSPAEELNYTVPGP-GPAGEASPROCREYEVDWNQ SALSCADPLASLAFTNESSCA 63 RCGWSPAEENSTAFASSCADPLASSCADPLASSCADPLASSCADPLASSSCADPLASTNESSCADPLASSCADPLASSCADPLASSSCADPLASSCADPLASSCADPLASSCAT	- 117 - 116 - 117 - 122 EP 108 - 90
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	117 PLGPCQHGWVYDTPG SSIVTE FNLVCADSWKVDLFQSCVNVGFFLGSLGVGYIADRFGRKLCLLAT 118 PLGPCQDGWVYDTPG SSIVTE FNLVCADSWKLDLFQSCVNVGFFVGSMSIGYIADRFGRKLCLLVT 117 PLGPCQDGWVYDTPG SSIVTE FNLVCADSWKLDLFQSCVNVGFFGSLGVGYFADRFGRKLCLLTT 118 PLGPCRGGWRYAQAH STIVSE FNLVCANSWKLDLFQSSVNVGFFIGSMSIGYIADRFGRKLCLLGT 129 PLVPCRGGWRYAQAH STIVSE FNLVCANSWMLDLFQSVVVGFFIGSMSIGYIADRFGRKLCLLTX 109 ATVPCSQGWEYDHSEFSSTIATESQWDLVCEQKGLNRAASTFFFACVLVGAVAFGYLSDRFGRRLLLVA 91 AMEPCLDGWVYNSTK DSIVTE WDLVCNSNKLKEMAGIFMAGILIGGLVLGDLSDRFGRRPLLTCS 112 DMEPCVDGWVYDRISFSSTIVTE WDLVCDSNKLKEMAGGILIGGLVGAUSDRFGRRPLTCS 112 DMEPCVDGWVYDRISFSSTIVTE WDLVCDSNKLKEMAG	F 184 F V 183 F V 184 SC 189 A Y 179 SY 157
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	184 LISAV SGVLMAVAPDYT SMLLFRLLQGLVSKG SWMSGYTLITEFVG SGYRRTVAILYOMAFTVGLVL- 185 LINAISGVLMAVAPNYTWMLIFRLIQGLVSKG SWMSGYTLITEFVG SGYRRTVAILYOMAFTVGLVL- 185 LINAAGVLMAISPNYMSMLLFRLIQGLVSKG SWMSGYTLITEFVG SGSRRTVAIMYOMAFTVGLV- 185 LINAAGVLMAISPTYTWMLIFRLIQGLVSKG SWMSGYTLITEFVG SGSRRTVAIMYOMAFTVGLV- 190 LGYGVT GVVA FAPNFPVFVIFRFLQGVFGKG TWMTCYVIVTEIVG SKORRIVGIVIOM FFTLGIII- 180 V STLVLGLA SAASV SYVMFAITRTLTG SALAGFTIIVMPLELEWLDVEHRTVAGVLSSTFWTGGVML- 184 LLAASG SGAAFSPTFPIYMVFRFLCGFGISGITLSTVILNVEWYPTRMRAIMSTALGYGYTFGQFI- 185 LLAASG SGAAFSPTFPIYMVFRFLCGFGISGITLSTVILNVEWYPTRMRAIMSTALGYGYTFGQFI- 181 LQVAIVGTCAALAPTFLIYCSLBFLSGIAAMSLLTNTIMLIAEWATHRFQA-MGITLGMCPSGIAFMT_A	A G 254 T G 253 A G 254 P G 259 A L 249 P G 227 A G 250
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	254 VAYA I PHWRWLQ LAV SLPT FLFLLYYWCYP ESPRWLLSQKRNTQA I KIMDHIAQKNGK LPPADL 255 VAYA I PHWRWLQ LAV TLPN FFFLLYYWCYP ESPRWL I SONKNAKAMK I I KHIAKKNGK KLPK SL 254 LAYA LPHWRWLQ LAV SLPT FLFLLYYWCYP ESPRWL I SONKNAKAMK I I KHIAKKNGK KLPPADL 255 VAYA LPHWRWLQ FTV SLPN FFFLLYYWCYP ESPRWL I SONKNA EAMR I I KHIAKKNGK SLPASL 260 I AY FI PHWRWL I AV SLPT FFFLLYYWCYP ESPRWL I SONKNA EAMR I I KHIAKKNGK SLPASL 250 VGYL I RDWRWL LAV TLPCAPGILSLWWYP ESPRWL I TRKKGKALQI LRRI AKOGKYLSSNY 250 VGYL I RDWRWL LAV TLPCAPGILSLWWYP ESARWL I TQGHVK EAHRYLLHCARLNGR VCED SFSQ EAA 228 LAYA I POWRWL LI TV SIPFFVFFLSSWYP ESIRWL VLSGKSSKALKI LRRVAV FNGKK EEGERLSLEEI 251 LAFAIRDWHILQLVVSVPY VI FLTSSWL ESARWL I INNKP EGLKELRKAAHRSMKNARD LTLEII 700 TM8	 317 318 317 318 317 318 318 323 V S 320 L K 298
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A3 hSLC22A4 hSLC22A8 hSLC22A8	318 KML SLKED ST EKL SP SFADL FRTPQL-RKHT FILMY LWFT SSVL YQGL IMHMGAT GGN LYLD FFY SAL Y 319 QEERK ET EVGEK LNP SFLDL VRTPQI-RKHT LILMY LWFT SSVL YQGL IMHMGI AGGN I YLD FFY SAL Y 318 KML SLEED VT EKL SP SFADL FRTPRI-RKRT FILMY LWFT SSVL YQGL I LHMGAT SGNLY LD FLY SAL Y 319 QR LRLEET GKKL NP SFLDL VRTPQI-RKHT MILMY NWFT SSVL YQGL I LHMGAT SGNLY LD FLY SAL Y 324 SEIT VT DE - EV SNP SFLDL VRTPQM-RKCT LILM FAWFT SAV YQGL VMRLG II GGNLY ID FFI SGV Y 321 KVAAGERV VRP SYL DL FRTPRL-RH I SLCCV V WFGVN FSYYGL SLDV SGLGL NV YQTQLL FGAY 322 STMKKELEAAQKKKP SLCEMLHMPN I CKR I SL-LSFT REAN FMAY FGLNLH YQHLGN VFLQTL FGAY TMS TM9 TM9 TM9 TM10	E F 388 E I 387 E F 388 E L 391 E L 387 D V 367
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	388 PAAFIILVTIDRVGRIYPLAVSNLVAGAACLIMIFISQDLHWLNITVACVGRMGITIVFDMVCLVNALL 389 PAAFIILTIDRIGRRYPWAAANMVAGAACLITAFIPDGLFWLKTTVACLGRMGITMAFEMVCFVNTEL 389 PAAFIILTIDRIGRRYPWAAANMVAGAACLITAFIPDGLFWLKTTVACLGRMGITMAFEMVCFVNTEL 389 PAAFAIILTIDRIGRRYPWAAANMVAGAACLITAFIPDGLFWLKTTVACLGRMGITMAFEMVCFVNTEL 389 PAAFMIILTIDRIGRRYPWAAANMVAGAACLASVFIPGDLGWLKTTVACLGRMGITMAFEMVCFVNTEL 389 PAAFMIILTIDRIGRRYPWAASNMVAGAACLASVFIPGDLGWLKTINSCLGRMGITMAFEWVCFVNTEL 392 PGALLILLTIERLGRRLPFAASNIVAGVACLASVFIPGDLGWLKTTVATLGRLGITMAFEIVYLVNSEL 398 PSKLLVYLSVRYAGRRLTOAGTLLGTALAFGTRLLVSSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSEL 388 PSKLLVYLSVRYAGRRLTOAGTLLGTALAFGTRLLVSSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSEL 388 PAKFITILSLSYLGRHTTOAAALLLAGGAILAFGTRLLVSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSEL 388 PAKFITILSLSYLGRHTTOAAALLLAGGAILAFGTRLLVSDMKSWSTVLAVMGKAFSEAAFTTAYLFTSEL 388 PAKFITILSLSYLGRHTTOAAALLLAGGAILAFGTRLLVSDMKSWSTVLAVMGKAFSEAAFTAYLFTSEL 392 LANCVAPWALKYMNRRASOMLLMFLLAICLAIFVPLDLOTVRTVLAVFGKGCLSSSFSCLFLYTSEL 392 LANCVAPWALKYMNRASOMLMFLLAICLAIFVPLDLOTVRTVLAVFGKGCLSSALANTLAFAHGNEV	Y P 459 Y P 458 Y P 459 Y P 462 Y P 458 Y P 438 I P 438
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8 hSLC22A9	459 TFIRNLGVMVCSSLCDLGGIITPFLVFRLMEVWQGLPLILFTVVGLVAGGMTLLLPETKGVALPETIED 460 TFIRNLGVLVCSSLCDIGGIITPFLVYRLASIWLELPLVVFAVLGLIAGGLVLLPETKGVALPETIED 459 TFVRNLGVMVCSSLCDIGGIITPFLVYRLASIWLELPLILFAVLGLIAAGVTLLLPETKGVALPETMKD 460 TFIRNLGVHICSSMCDIGGIITPFLVTRLNELELPLMVFGVLGLVAGGLVLLPETKGVALPETME 463 TTLRNFGVSLCSGLCDFGGIIAPFLLFRLAAVWLELPLIIFGILASICGGLVMLLPETKGKALPETVD 459 TVLFQTGMGLTALVGRLGGSLAP-LAALDGVWLSLPKLTYGGIALAAGTALLPETRQAQLPETICD 439 TVIFQTGMGVSNLWTRVGSMVSP-LVKITGEVQPFIPNIIYGITALLGGSAALFLPETLNQPLPETIED 463 TIIFARAMGINATFANIAGALAP-LMMISVYSPPLOWIIYGVFPFISGFAFLLPETRNKPLFDTICD	A E 530 A E 529 A E 530 V E 533 V E 528 L E 508
OCT1_consensus OCT2_consensus hSLC22A1 hSLC22A2 hSLC22A3 hSLC22A3 hSLC22A7 hSLC22A8 hSLC22A8	530 NLG- RKA KPKENTIYLQVQTSELPGT 531 NPH- RPR KNKEKMIYLQVLLSDIPDN 530 NLG- RKA KPKENTIYLKVQTSEP 531 NMQ- RPR KNKEKMIYLQVQKLDI	554 555 554 555 556 548 542 553

732 Supplemental Figure 1 | Multiple Sequence alignment.

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- 733 Multiple sequence alignment of OCT1_{CS}, human OCTs (SLC22A1-3), and representative human
- 734 OATs (SLC22A7-9). Sequences are aligned using MAFFT⁵⁶. E386 and D474 (numbering
- according to hOCT1) positions are highlighted in red and 217, 244, 354, and 446 (numbering
- according to hOCT1) in green.

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