

Supplementary File S1: The sequences employed for molecular phylogenetic analysis (Figure S5)

Escherichia	1	-----MMSKINQTDIDRLIELVGGKRNIAIVSHCITRLRFV-----
GLUT12_Homo	1	-----MVFVENTEGPSLLNQ-----
GLUT10_Homo	1	-----
GLUT11_Homo	1	-----
GLUT2_Mus	1	-----MSEDKIT-----
GLUT3_Homo	1	-----
GLUT4_Homo	1	-----
GLUT1_Mus	1	-----
GLUT9_Homo	1	-----
GLUT5_Homo	1	-----
GLUT7_Homo	1	-----
Halyomorpha	1	-----MKDFGMWNGKELPRVYTSLPTGEGE-----
Bemisia	1	MESNDIYRMASRMLNNSVDRRTHRRLKPSGSIESLSEEELTAVYGA-----
Cimex	1	-----
Rhodnius	1	-----MSQKERNMLLV-----
Cinara	1	-----MDILRTLRLPSPSRLLHIRTRFYSTALSSHGQTKPRGDRRREYDSTGRENGLDPTGRPESSVQNGIPGRHA
Sipha	1	-----MPISEDQVAELFGE-----
Melanaphis	1	-----MAWIKRDRGDKAMQQTFTIDMPISEDQVAELYGE-----
Acyrtosiphon	1	-----MAWIRRGDKAMQQTFTIDMPISEDQVAELYGE-----
Diuraphis	1	-----MAWIRRGDKATQQTFTIDMPISEDQVAELYGE-----
Myzus	1	-----MAWIRRGDKATQQTFTIDMPISEDQVAELYGE-----
Rhopalosiphum	1	-----MPISEDQVAELYGE-----
Aphis	1	-----MPISEDQVAELYGE-----
Athalia	1	-----MSSSQKWPVCLMFSKSKERGILPRQ-----
Cephus	1	-----MSSQRRQMMQPWPLCLMFPFSKSKERTILPKY-----
Megachile	1	-----MERNILPRY-----
Bombus	1	-----MLRQPRVSTPLEHNVLPKY-----
Blattella	1	-----MRIPQTEDSFSS-----
Cryptotermes	1	-----VLWSVLLIVVRVYINKIGPSEWLVS-----
Nilaparvata	1	-----MWYESEELKCNKCLSSSQESLLEEQLLEASGG-----
Drosophila	1	-----
Culex	1	-----MWIEIPECYEVLRNVFSK-----
Anopheles	1	-----MEMGTKEENMRTA-----
Ceratitidis	1	-----
Lucilia	1	-----MSGRDNRGSGHHQPLSNAMGKIKDRLSRDQPYQRVDLDEAATLNSNTATSLDTILPEDPFLFSS
Musca	1	-----MSGRDNRGSGHQPLGNAMGKIKDRLSREEQPYQRVDLDEGTLSTNTATSLDTILPE-DPFLFSP
Stomoxys	1	-----MSGRDNRGSGHQPLGNAMGKIKDRLSREEQPYQRVDLDEGTLSTNTATSLDTILPE-DPFLFPA
GLUT	1	-----
GLUT8_Mus	1	-----

Escherichia	37	-----LNQPANARPKKEI-----EQLP ^M VKGC ^F INAGQFQV ^L GTNVGDYYQALIASTGQAQ
GLUT12_Homo	16	-----KGTAVETEG ^S GSRRHPPWARG-----
GLUT10_Homo	1	-----MG-----
GLUT11_Homo	1	-----MEDELEPSLRPRTQIQGR ^I -----
GLUT2_Mus	8	-----GTLAFTVFTAVL-----SSFQFGYD ^I GVINAPQEV ^I ISH
GLUT3_Homo	1	-----MGTQKVTPA-----
GLUT4_Homo	1	-----M-----PSGFQQIGSE ^D GEPPQQRVTGT
GLUT1_Mus	1	-----MDPSSKVTGR-----
GLUT9_Homo	1	-----MARKQNRNS-----KELG ^L VPLTDDTSHAGPPGPR
GLUT5_Homo	1	-----MEQQDQSMKEGR-----
GLUT7_Homo	1	-----MENKEAGTPPPIPSREGR-----
Halyomorpha	26	-----ESILIGVKS ^R DP-----P--S ^I ISSAT ^S SNASVAT ^T AST
Bemisia	47	-----GARIHSSH ^R PP-----P--S ^A LSS ^T C ^S SS ^S TSVAT ^N GST-----VAL
Cimex	1	-----
Rhodnius	12	-----GGDLEPVK ^S KS-----LNDFGLE ^T TV ^T SNRQ
Cinara	72	HHRP ^S GR ^T VRV ^H HR ^R PR-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Sipha	15	-----GARIH ^S VH ^H RSR-----PEQ ^S VFAST ^M SS ^S ASVDT ^T VGS-----TAAL
Melanaphis	36	-----GARIH ^S VH ^H RSR-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Acyrtosiphon	36	-----GARIH ^S VH ^H RSK-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Diuraphis	36	-----GARIH ^S VH ^H RSR-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Myzus	36	-----GARIH ^S VH ^H RSR-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Rhopalosiphum	15	-----GARIH ^S VH ^H RSR-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Aphis	15	-----GARIH ^S VH ^H RSK-----PEQ ^S VFAST ^M SS ^N ASVDT ^T VGS-----TAAL
Athalia	27	-----YTRVPTISR ^S ET-----ANS ^N IVAD ^C AS ^N T ^T LAT ^I PS ^P F-----TSQL
Cephus	32	-----YTRVPSIAR ^S AT-----TSS ^L IVSD ^C AS ^N AT ^L V ^T NAS ^P F-----
Megachile	10	-----YTKVPSVAR ^S T-----TNS ^S INLDC ^S SNAT ^L AT ^N VSP ^F -----
Bombus	20	-----YTRVPPVTR ^S VT-----NDS ^G INLDC ^S SN ^T IAT ^N AS ^P F-----
Blattella	13	-----EDSLLGR ^R SR ^N R-----GTISAS ^P ST ^T TF ^T ESTD ^S T ^I -----
Cryptotermes	26	-----QDSSVSGG ^A SEA-----SEVGT ^Y QND ^S FT ^S SESD ^L LGR-----H
Nilaparvata	34	-----VAKICYA ^H HR ^L P-----P--S ^A LSS ^V T ^S SAASVAT ^L T ^L -----R
Drosophila	1	-----MKILMRAD ^T HVS ^F SV ^P A-----
Culex	19	-----FRRHS-----LTAA ^M VKLLMRAD ^T HVS ^F TV ^P A-----
Anopheles	14	-----VPFVRQITEEGK-----PKLEVYR ^P T ^T NI-----
Ceratitidis	1	-----M-----KLLARAD ^T FM ^S FTVPEDEPK ^P T-----
Lucilia	67	HNRPTASQQ ^P IQQQ ^Q KQRRFETE ^I PLQFG ^P IIDADDINEP ^L PLVSAKATKI ^Q EPA ^L PL ^P PP-----PPSSQHS ^R RDH
Musca	65	HNRPTA--PSTQQ ^Q RQ ^R F ^E A ^E F ^L QFG ^P ----IIEADDINEP ^L PL ^P INPKV ^K NTQ ^E PL ^L PL ^P PP-----PPSSH ^R RDQ ^H
Stomoxys	65	QNRPPT ^T QLSP ^Q RQ ^R F ^E A ^E Y ^L QFG ^P ----IIEADDINEP ^L PL ^P VSQAK ^N TQ ^E PL ^L PL ^P PP-----PPA ^H HS ^R RDQ ^H
GLUT	1	-----MQEPLLGAEG-----PDYDTFPEK ^P PPSPGDRAR ^V GT-----
GLUT8_Mus	1	-----MS-----PEDQ ^E TQ ^L LR ^P PEART ^P GR-----

Escherichia 88 VDKEQVKKAAARQNMKWHEQLISHFAEIFFPLLPALISGGLILGFRNVIGDLPMSNG-----QTLAQMPYPSLQTIY----

GLUT12_Homo 36 -----

GLUT10_Homo 3 -----

GLUT11_Homo 20 -----

GLUT2_Mus 42 -----

GLUT3_Homo 10 -----

GLUT4_Homo 24 -----

GLUT1_Mus 12 -----

GLUT9_Homo 32 -----

GLUT5_Homo 13 -----

GLUT7_Homo 19 -----

Halyomorpha 58 -----SALLGVKVKKYLKSSKQDKLSQ-----KELNILLASQ-----

Bemisia 82 LHSSQRKKSNNKYNVHKYN-----LYNKGIKMTSGAQ-----KELNLLLAPTVP-----

Cimex 1 -----

Rhodnius 39 -----

Cinara 115 IHSAAKIKKKKYAFLRQGNQQT-----A---CSNGYTTGRHI---GSMIHSQ-----KEKNLLLATPNVP-----

Sipha 53 IHSAAKVKKKKYAFLRQGNNGH-----QQ---VASNGYITGRHCRGDSGVLFQ-----KERNIRLSAPTVP-----

Melanaphis 74 IHSAAKVKKKKYAFLRQGHSGGTAQOSASA---AANNGYVTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Acyrtosiphon 74 IHSAAKVKKKKYAFLRQGNSSG-AQOSASA---SGNNGYLTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Diuraphis 74 IHSAAKVKKKKYAFLRQGHSGG-AQOSASA---SSNNGFLTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Myzus 74 IHSAAKVKKKKYAFLRQGNSSG-TQLSASA---SSNNGFLTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Rhopalosiphum 53 IHSAAKVKKKKYAFLRQGHSGS-AQHSASA---AANNGYVTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Aphis 53 IHSAAKVKKKKYAFLRQGHGG-AQOSASA---ASNNGYLTGRHC--RDAAIHSQ-----KELNIRLATPTVP-----

Athalia 65 TLSNDKKSPEVTEYPEPAH-----YYADNLLNNQNL--KKAKIYNE-----

Cephus 66 -NSQITLITDRKGSYPNGSNAASH-----YYAENLRNNHQSGLKGSIYNM-----

Megachile 44 -NSQALIAEKKALPPGNVADASTNH-----YYAQNLRNNHQKALNGSRVYDP-----LDKGIDHDYKQLDP----

Bombus 54 -NSQALIAEKKVILSGSVTASSNH-----YYAQNLRNNHQKTLGSHMYDP-----LDKGIDHDYKQLDP----

Blattella 45 -----VNIHKYHQYNQCRHNMSVSAQ-----KELNILIATPQVP-----

Cryptotermes 61 RNRTTISASSSTSTFITGSGSSI-----VNIHKHHDYKCHDRRMSVTQ-----KELNLLITAPQVPELSTG

Nilaparvata 67 TDKHTAAATLLTNKLL-----VNVHKHKLYNKATAKPNM-----KELNLLIASPTV-----

Drosophila 18 -----DGLKAN-----

Culex 46 -----

Anopheles 39 -----

Ceratitidis 24 -----

Lucilia 141 HTRSVVSI PSEDLQRSKQSLKGSRVSEFKRRANDSDEDSFEEKRSQFQQKAVSVDHKGILKDLRTILANDNRRQFQAK

Musca 134 TRSVVSTEDLQRSKSSLKGSRVSEFKRGG--DESEDDSFEEERTGFQQKAVSSVDHRGILKDLKTLANDNRRQFQSK

Stomoxys 135 TRSVVSTEDLQRSRQSLKGSRVSEFKRAGANNESDEDNFEERTGFQKQKALSSADHKGILKDLKTLANDNRRQFQSK

GLUT 33 -----

GLUT8_Mus 25 -----

Escherichia 158 --DFLWLIGEAIFFYLPVIGICWSAVKKMGGTPILGIVLGV--TLVSPQLMNAAYLLGQQLPEVWDFGMFSIAKVGYQAQVI

GLUT12_Homo 36 -----

GLUT10_Homo 3 -----

GLUT11_Homo 20 -----

GLUT2_Mus 42 -----YRHVLGVPLDDRKAAINYDVN-----

GLUT3_Homo 10 -----

GLUT4_Homo 24 -----

GLUT1_Mus 12 -----

GLUT9_Homo 32 -----ALLECDHLRSGVPGRRRKD-----

GLUT5_Homo 13 -----

GLUT7_Homo 19 -----

Halyomorpha 90 -----PDMEAGKMEMEDPSVDKAPVYSYRG-----

Bemisia 127 -----EIKSESEKDPKDEANDGRLQNSHEATFETLN-----

Cimex 1 -----

Rhodnius 39 -----

Cinara 171 --NFID-----HILKKKQAIVVAQSSPKRLSSDDEDDDDDDDD-DDD-----VVPIK

Sipha 113 --NLFD-----QMIKKKQAL--DQVSAKRLSSDDDDDDDDDD-DDDEHEDDD--PRRK

Melanaphis 138 --NFID-----QILKKKQAT--EQVSAKRLSSDDDDDDDDDD-DDRDEDDVFLQDLK

Acyrtosiphon 137 --NFID-----QILKKKQAT--EQVSAKRLSSDDDDDDDDDD-DDRDEDDVFLQDLK

Diuraphis 137 --NFID-----QILKKKQAT--EQVAAKRLSS-----DDDDC-DDRDEDDVFLQDLK

Myzus 137 --NFID-----QILKKKQAT--EQVSAKRLSS-----DDDDC-DDRDEDDVFLQDLK

Rhopalosiphum 116 --NFID-----QILKKKQAT--EQVSAKRLSS-DDDDDDDDC-DDRDEDDVFLQDLK

Aphis 116 --NFID-----QILKKKQAT--EQVSAKRLSS-----DDDDC-DDRDEDDVFLQDLK

Athalia 105 -----HIQREDPNADHKQLDPLLDHGIQPD TAKMFHSQEFQVKMTSGPPFKSY

Cephus 111 -----EKATDADYKQLNPLCNKEHTES PDSKDPMDQDVKQKTADSVPLTSYQ

Megachile 92 -----LDKDHDRDYKQLDPLL---NDESPFVGVANERKMSSQDIKMKESA

Bombus 115 -----LLVGEPPYAGIELTKPMSQQNVKPTKDSVTVMQFQKEPKPSIM----

Blattella 80 -----ELSTGDEDL--KKVTAEQPSIQDVDFPATEIVTSDKVAKLNNEEPTKSQV

Cryptotermes 125 DDSLKN-----KVTVEEPSIQDNHVCEIKPQPQPQPEHRCSSKNNLGGSAAPQVQI--

Nilaparvata 113 -----GLDECRDKVPGQLTTTIVV I PYSEMERDDKHNIYEKQPQPQHPKQPPTAL

Drosophila 24 -----

Culex 46 -----EPPVAK-----

Anopheles 39 -----

Ceratitidis 24 -----

Lucilia 221 KHVSLDLKGTRYLKDLLKESSEEEFRKNRREFQGRKHQSLDPRVSFKLEKVLQGSSEDSDEENDVEQKRLIHRPKDIT

Musca 212 KHVSLDLKGTRYLKDLLKESSEEEFRKNRREFQGRKHQSLDPRVSFKLEKVLQGSSTDSDEENDVEHKRLIYRPKDIT

Stomoxys 215 KHVSLDLKGTRHLKDLLKDSSEEEFRKNRREFQGRKHQSLDPRVSFKLEKVLQGSSTDTDEENDVEQKHLIYRPKDIT

GLUT 33 -----

GLUT8_Mus 25 -----

Escherichia	234	PALLA-----	-----GLALGVIETRLK
GLUT12_Homo	36	-----	-----
GLUT10_Homo	3	-----	-----
GLUT11_Homo	20	-----	-----
GLUT2_Mus	63	-----	-----
GLUT3_Homo	10	-----	-----
GLUT4_Homo	24	-----	-----
GLUT1_Mus	12	-----	-----
GLUT9_Homo	52	-----	-----
GLUT5_Homo	13	-----	-----
GLUT7_Homo	19	-----	-----
Halyomorpha	116	-----	-----
Bemisia	160	SSGII-----	-----IKEKQDSSQSA-
Cimex	1	-----	-----
Rhodnius	39	-----	-----
Cinara	214	NTTKI-----	-----RTPQN-----
Sipha	160	TAVKI-----	-----RTPQN-----
Melanaphis	189	SAAKI-----	-----RTSQN-----
Acyrtosiphon	187	SAAKI-----	-----RTPQN-----
Diuraphis	182	SAAKI-----	-----RTPQN-----
Myzus	183	SAAKI-----	-----RTPQN-----
Rhopalosiphum	165	SAAKI-----	-----RTSQN-----
Aphis	163	SAAKI-----	-----RTPQN-----
Athalia	154	FQAEV-----	-----APRRRC-----
Cephus	160	FQRET-----	-----KPEKA-----
Megachile	135	STGKI-----	-----RGTMKPLPDPKP
Bombus	159	-----	-----
Blattella	127	-----	-----
Cryptotermes	178	-----	-----
Nilaparvata	162	SLA-----	-----
Drosophila	24	-----	-----
Culex	52	-----	-----
Anopheles	39	-----	-----
Ceratitidis	24	-----	-----
Lucilia	301	KPVIIDLKDLSESEEDYVSSRQHFFQQRSISTDSRKSIRFFEMDEMGSKKGENLRSAVFFVRQITEDGKPKLEVYRPTT	
Musca	292	KPVVIDLKDLSESEEDYVSSRQHFFQQRSISTDSRKSIRFFEMDEMGRKKGENLRQAVFFVRQITEDGKPKLEVYRPTT	
Stomoxys	295	KPLVIDLKDLSESEEDYDLRQHFFQQRSISTDSRKSIRFFEMDEIGRKKGDNLRQSVFFIRQITEDGKPKLEVYRPTT	
GLUT	33	-----	-----L-----
GLUT8_Mus	25	-----	-----

Escherichia	251	---RIVPDYLYLVVVPVCSLILAVFLAHLALIGPFGRMI-GDG-VAF-----	---AVRHLMTGCSFAPIGGAL
GLUT12_Homo	36	---CGMFTFLSSVTAAMVSG-LIVGYELCIISGALLQIK-----TLI-----	---ALSCH---EQEM---VSSVIVIGALL
GLUT10_Homo	3	---HSPPVLPPLCASVSLGGLTFGYELAVISSALLPLQLDFGLSCL	---EQEF---IVGSLILGALL
GLUT11_Homo	20	-----LLLTICAAGIGGTFQFGYNLSIINAPTLHIQ-EFTNETWQARTG---	---EPLPDHLVLLMWSLIVSLYPLGGIF
GLUT2_Mus	63	-----GIDTPITVTPAYTTPAPWDEEETEGSAHI	-----VTMLWSLSVSSFAVGGMI
GLUT3_Homo	10	-----LIFAITVATIIGS-FQFGYNTGVINAPKVIIE-EFINKITLTDKGN---	---APPSEVLLTSLWSLSVAIFSVGGMI
GLUT4_Homo	24	-----LVLAVFSAVLGS-LQFGYNTGVINAPQKVIIE-QSYNETLWLRQGGPEGPSSIPPGLTTLTWSLSVAIFSVGGMI	
GLUT1_Mus	12	-----LMLAVGGAVLGS-LQFGYNTGVINAPQKVIIE-EFYNETWLNHRYG---	---EPIPTSTLTLTWSLSVAIFSVGGMI
GLUT9_Homo	52	---WCSCLLVASLAGAFSSFLVGYNLSVVNAPTPYIK-AFYNESWERRHG---	---RPIDPDTLTLTWSVTVSIFAIIGGLV
GLUT5_Homo	13	---LTLVLALATLIAAFSSFQYGYNVAAVNSPALLMQ-QFYNETYYGRGT---	---EFMEDFPLTLTWSVTVSMFPIGGFI
GLUT7_Homo	19	---LQPTLLLATLSAAFSSAFQYGYNLSVVNTPHKVFK-SFYNETYFERHA---	---TFMDGKMLMLLWSCTVSMFPIGGFL
Halyomorpha	116	---SLVKQVLAALAVSLGS-MVVGFSASATAPALESMN-DED-SRI-----	---HITDA---EASW---IGSLMPLSALF
Bemisia	176	---SIIPQVLAALSLSVSLGS-LAVGFSSAYTSPALPSMT-DAT-SILYG---	---KVSAAE---EMSW---IGSIMPLAALF
Cimex	1	-----	---SW---IGSLMPLCALL
Rhodnius	39	---AYIRQGLAAFSVSLGS-MVVGFSASAYTSPALPSMK-QPG-STL-----	---HITDQ---QTSW---IASIMPLSALL
Cinara	224	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-SPG-STL-----	---SVSEE---EGSW---IGSLMPLAALI
Sipha	170	---TYVPOVLAASLTVSLGS-MVVGFSASAYTSPALPSMN-SPG-SPL-----	---SVSEE---EGSW---IGSLMPLAALI
Melanaphis	199	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---TVSEE---EGSW---IGSLMPLAALI
Acyrtosiphon	197	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---TVTEE---EGSW---IGSLMPLAALI
Diuraphis	192	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---TVTEE---EGSW---IGSLMPLAALI
Myzus	193	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---TVTEE---EGSW---IGSLMPLAALI
Rhopalosiphum	175	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---TVTEE---EGSW---IGSLMPLAALI
Aphis	173	---TYVPOILASLTVSLGS-MVVGFSASAYTSPALPSMN-RPG-SPL-----	---SVTEE---EGSW---IGSLMPLAALI
Athalia	165	---HYIPQVLAALSLSVSLGS-MVVGFSASAYTSPALPSMK--NETSL-----	---AMSAQ---AASW---VGGIMPLSALV
Cephus	170	---GYGAQVLAALSLSVSLGS-MVVGFSASAYTSPALPSMY-NDTNTPL-----	---HINAQ---IBSW---IGSIMPLSALF
Megachile	152	SIMHYASQVLAALSLSVSLGS-MVVGYSSTYTSPLVSMQ-NNATSF-----	---EVTKE---IGMW---IGSIMPLSALF
Bombus	159	---RYANQVLAALSLSVSLGS-MVVGYSSTYTSPLVSMR-DNATATF-----	---EVTKE---TCMW---IGSIMPLSALF
Blattella	127	---SWGPOVMAAASVSLGS-MVVGFTSAYTSPALVSMK-KAN-STV-----	---QPDTQ---EASW---IGSLMPLSALI
Cryptotermes	178	---HWGPOVMAAALSLSVSLGS-MVVGFSASAYTSPALVSMK-EPN-STV-----	---QPDLQ---QKSW---IGSLMPLSALI
Nilaparvata	165	---AIMPQVLAALSLSVSLGS-MVVGFSASAYTSPALPSMN--SNASSI-----	---HVTPO---EBSW---IGSLMPLCALF
Drosophila	24	---TTFQVLAALSLSVSLGS-LVVGFVSAAYTSPALVSMR-DRNITSF-----	---EVTKD---AGSW---VGGIMPLAALA
Culex	52	---CTFSQVLAALSLSVSLGS-MVVGFSASAYTSPALVSMK-DRNITSF-----	---EVTDQ---SGSW---VGGIMPLAGLV
Anopheles	39	---YIWTQVLAALSLSVSLGS-MVVGFSASAYTSPALVSMK-DRNITSF-----	---EVTDQ---SGSW---VGGIMPLAGLA
Ceratitidis	24	---GVRROVLAALSLSVSLGS-LVVGFSSAYTSPALVSMR-DRNITSF-----	---EVTPO---EASW---VGGIMPLAGLA
Lucilia	381	NPIYIWTQVLAALSLSVSLGS-LVVGFSSAYTSPALVSMR-DRNITSF-----	---EVTPO---DASW---VGGIMPLAGLA
Musca	372	NPIFIWTQVLAALSLSVSLGS-LVVGFSSAYTSPALVSMR-DRNITSF-----	---EVTPO---TASW---VGGIMPLAGLA
Stomoxys	375	NPIFIWTQVLAALSLSVSLGS-LVVGFSSAYTSPALVSMR-DRNITSF-----	---EVTPO---TASW---VGGIMPLAGLA
GLUT	34	---QNKRVFLATFAAVLGN-FSFGYALVYTSFVHPALE-RSLDPDL-----	---HLTKS---QASW---FGSVFTLGAAA
GLUT8_Mus	25	-----RVFLASFAAALGP-LISGFALGYSSPALPSLR-RTAPPAL-----	---RLGDN---AASW---FGAVVTLGAAA

Escherichia 463 RKYRLGLTDDFDLVTQAKSRGRIITIDMVFNH---TSQHAWFREALNKESPYRQFYIWRDGEPEPTPPNNWRSKFGGS
 GLUT12_Homo 187 YAFANV-HHGKYMFGVLIPIGLVQAIAIMYFLP---PSPR--E-LVMKGOEGAKSKVIGRLRL-SDTTEELTVIKSSL
 GLUT10_Homo 160 T-----PWGWRHMFVGWITAPAWLQSLSLFLPAGTDEIAT--H-----KDLIPLQGEAP
 GLUT11_Homo 185 LRELLGGFQAMPILLASCLVPGALQLASLPLIP---ESPR--YLLIDCGDTEACLAALRRLRG-SCDLAGELFELEER
 GLUT2_Mus 207 LSFILGNQDHWIILGLSAPVAILQCILLLFPCP---ESPR--YLYIKLEEEVRAKKSILKRLRGTE-DVTKDINEMKKEK
 GLUT3_Homo 174 LEFILGSEELWPIILGFTILPAILQSAAPFCP---ESPR--ELLINRKEENAKOILQRLRGTDQ-DVSDIQEMKDES
 GLUT4_Homo 192 LESLLGTASLWPIILGLITVLPAILQSLPLPFCP---ESPR--YLYITQNLLEGPAKSKLKRITGW-ADVSGVLAELKDEK
 GLUT1_Mus 176 LDSIMGNADLWPIILSVIFIPAILQCILLLPFCP---ESPR--ELLINRNEENRAKSVLKKLRG-TADVTRDLOEMKEEG
 GLUT9_Homo 221 LPELLGKESTWPIYLVGVIVVPAVQLLSLPPFP---DSPR--YLLIEKHNEARAVKAFQTFGLK-ADVSQVEVEVLAES
 GLUT5_Homo 182 LRNLLANVDGWPIILGLITGVPAALQLLPLPFP---ESPR--YLLIQKDEAAAKALQTLRGWDS-VDREVAEIRQED
 GLUT7_Homo 188 LQAILGNPAGWPIILALTCVPAILQLLTLPPFP---ESPR--YSLIQKGDPAARQALRRLRG-HTDMEAELEDMRAEA
 Halyomorpha 270 T-----YLDWTHLAILGACIPPLPFFICTILIP---ETPT--W-EINKGKKEQAEASLOWLRGKANKVSEMSNIVKAH
 Bemisia 332 A-----YLDWSMLAFAGALIPVPFLICMFFIP---ETPR--W-YIGRNKHKARKALQWLGRQONADISAEFDEIEKTN
 Cimex 108 K-----YLDWSELALFALLPVPFFIIMFFIP---ETPS--W-YISKEKETRAKMLQWRGASATDIKKEYAELIKIR
 Rhodnius 193 K-----YLDWSKLALFACILPVPFFIIMFFIP---ETPR--W-FIGKMEHAKKSLKWLRTGENADLNKEMSELQKST
 Cinara 378 K-----YLNWQMLAILGACIPPLPFLICMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADITQEFSETEKAN
 Siphia 324 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Melanaphis 353 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Acyrthosiphon 351 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Diuraphis 346 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Myzus 347 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Rhopalosiphum 329 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Aphis 327 K-----YLNWQMLAILGACIPPLPFLVCMFLIP---ETPQ--W-YISRNKSKKAKKALQWLGRKNADVTQEFSETEKAN
 Athalia 318 M-----YLNWSNLAILGAILPVPFFIIMFLIP---ETPR--W-YIANGNREARAKSLQWLGRKNTDVEETAATEKAH
 Cephus 325 M-----YLNWSHLAILGATLPVPFFIIMFLIP---ETPR--W-FISKGTKKARQSLQWLGRKNSDISEELTAVEKSH
 Megachile 310 M-----YLDWRNLAILGAILPVPFFIIMFLIP---ETPR--W-YISKGTKKARKALQWLGRKGTDTIDELTAVEKHL
 Bombus 314 M-----YLDWRNLAILGAILPVPFFIIMFLIP---ETPR--W-YISKGTKKARKALQWLGRKGTDTIDELTAVEKHL
 Blattella 281 K-----YLDWSMLAILGACIPVPFLICMFLIP---ETPR--W-FFSKNKDEAKKALQWLGRKNDISHELKEDENNN
 Cryptotermes 332 K-----YLNWSMLAILGACIPVPFLVCMFLIP---ETPR--W-YFSKAKGKCAKSLQWLGRKNDADISQELKEDENIN
 Nilaparvata 319 K-----YLDWSLAILGAILPVPFLICMFLIP---ETPR--W-FVEKNGKQARAKALQWLGRKNNTDVSYEFSETEKSN
 Drosophila 179 S-----EMNWSMLAFLGAILPVPFLIIMFLIP---ETPR--W-FVNRGQERARAKALVWLRGKEADVPELKGIMRSQ
 Culex 207 N-----YMDWSELALFATLPVPFLIIMFLIP---ETPR--W-YVSRGRDDRARKALQWLGRKADVPDELKGIKSH
 Anopheles 194 K-----YLDWSGLAFLGAILPVPFLIIMFLIP---ETPR--W-YVSRNREDRARKALQWLGRKADVPDELKGIKSH
 Ceratitis 179 T-----YMDWSLAILGAILPVPFLIIMFLIP---ETPR--W-FVSRGREDRARRALQWLGRQADVPDELKGLMRTQ
 Lucilia 539 T-----YMDWSLAILGAILPVPFLIIMFLIP---ETPR--W-YVSRNREERARKALVWLRGKEADVPELKGIMRSQ
 Musca 530 T-----YMDWSLAILGAILPVPFLIIMFLIP---ETPR--W-YVSRNREERARKALVWLRGKEADVPELKGIMRSQ
 Stomoxys 533 T-----YMDWSLAILGAILPVPFLIIMFLIP---ETPR--W-YVSRNREERARKALVWLRGQADVPDELKGLMRSQ
 GLUT 189 L-----LLPWRWLAAGEAPVIMITLISFMP---NSPR--E-LLSRGRDEBALRALAWLRGTDVVDVHWEFEQIQD--
 GLUT8_Mus 177 W-----VLEWRWLAFLGCVPEFLMLIMCYMP---ETPR--E-LLTQHQQBAMAALREFLWG-----SREGWEE

Escherichia 539 AWRWHAESQYYIHLFAPEQADLNWEN-PAVRAELKKVCFWADRQVGLRLDVTNLLISKDPRFPEDLGG-DGRFFYTDG
 GLUT12_Homo 258 ---KDEYQYSFWDLFRSK---DNMRTRI---MIGITLIVFVQITGQPNILFYAS-
 GLUT10_Homo 208 -KLGPRPRYSFLDLFRAR---DNMRGRT---TVGLGLVLFQQLGQPNVLCYAS-
 GLUT11_Homo 258 AACQGCRRRPW-ELFQHR---ALRR-QV---TSLVVLGS--AMELCNDSSVAYAS-
 GLUT2_Mus 280 -EEASTEQKVSIVLQFETDA---NYRQ-PI---LVAIDMLHMAQQFSGINGIFYYST-
 GLUT3_Homo 247 ARMSQ-EKQVTVELEFRVS---SYRQ-PI---IISIVLQLSQQLSGINAVFYST-
 GLUT4_Homo 265 RKLER-ERPLSLQLLGSR---THRQ-PL---IIAVVLQLSQQLSGINAVFYST-
 GLUT1_Mus 249 RQMMREKVT-IIELEFRSP---AYRQ-PI---LIAVVLQLSQQLSGINAVFYST-
 GLUT9_Homo 294 -RVQRSIRLVSVLELLR-A---PYVWQV---VTVIVTMACYQLCGINAVWFYTN-
 GLUT5_Homo 255 -EAEKAAGFISVVKLFRMR---SLRW-QL---LSIIVLMGGQQLSGINAVFYAD-
 GLUT7_Homo 261 -RAERAEGHLSVHLCAIR---SLRW-QL---LSIIVLMAGQQLSGINAVFYAD-
 Halyomorpha 337 KEAYHEQNQNVLKELFS-K---RYYL-PE---VISIGLMFFQQLSGINAVIFYTV-
 Bemisia 399 AESNKNEKTAGCSEIFA-K---MYRR-PL---LISIGLMFFQQLSGINAVIFYTV-
 Cimex 175 ---KMDNETVSFKELFS-R---KYIW-PL---CISIGLMFFQQLSGINAVIFYTV-
 Rhodnius 260 -ELFK-ENKSSIKELFN-K---KYLK-PE---AISMGLMFFQQLSGINAVIFYTV-
 Cinara 445 -HVGKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Siphia 391 -HVGKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Melanaphis 420 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Acyrthosiphon 418 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Diuraphis 413 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Myzus 414 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Rhopalosiphum 396 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Aphis 394 -HMGNKNEEMPGYLSLFS-K---MYSK-PL---LISMGLMFFQQLSGINAVIFYTV-
 Athalia 385 AESERNVSRGALKELLK-K---AYVK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Cephus 392 VDSERNASQSACVELFK-G---NNLK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Megachile 377 VESERNVSQGAFFELFK-R---NHK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Bombus 381 TDSERNVSQGAFFQLFK-K---NHK-PL---FISIGLMFFQQLSGINAVIFYTV-
 Blattella 348 KQMEKGSN--STFELFN-K---SNLR-PL---LISIGLMFFQQLSGINAVIFYTV-
 Cryptotermes 399 NESLKSPPSGSSF-ELFN-K---SNLK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Nilaparvata 386 KDAEKENESAFKELFS-A---KYSR-PL---IISIGLMFFQQLSGINAVIFYTV-
 Drosophila 246 ADADRQATQNTCELFLK-R---NNLK-PL---SISIGLMFFQQLSGINAVIFYTV-
 Culex 274 QDAERHASQSAMLDLLK-K---TNLK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Anopheles 261 QDAERHASSAMLDLLN-K---ANLK-PL---LISIGLMFFQQLSGINAVIFYTV-
 Ceratitis 246 AQADRHATGNQVLELLR-R---NNLK-PL---SISIGLMFFQQLSGINAVIFYTV-
 Lucilia 606 ADADRQATKNQFMELLK-R---NNLK-PL---SISIGLMFFQQLSGINAVIFYTV-
 Musca 597 ADDERQARQNQFMELLK-R---NNLK-PL---SISIGLMFFQQLSGINAVIFYTV-
 Stomoxys 600 ADDDRQAKNNQFMELLK-R---NNLK-PL---SISIGLMFFQQLSGINAVIFYTV-
 GLUT 254 -NVRQSSRSVWAEARA-P---HVCR-PI---TVALLMRLQLLGIPTIIVYVYVQ-
 GLUT8_Mus 235 PPGVAEHQGFQALRRR-P---GIYK-PL---ITIGSLMFFQQLSGINAVIFYAN-

Escherichia	712	-----CNHDQ-----	-----PRIVSRFGDEGEYRVPAKMLAM
GLUT12_Homo	429	RGETTSASLINA-----	-----GLSHTEYQIVTDPGDVPAFLK---
GLUT10_Homo	348	-----LQDSSLPPIPRTNEDQREPI	-----LSTAKKTKPHPRSGDPSAPPRLALSSALP
GLUT11_Homo	368	-----LQSS-----	-----PPPLPARCHALLR-----
GLUT2_Mus	388	-----LLDK-----	-----FP-----
GLUT3_Homo	355	-----LKDN-----	-----YNGMSLV-----
GLUT4_Homo	373	-----LLER-----	-----VPAMS-----
GLUT1_Mus	357	-----LLER-----	-----LP-----
GLUT9_Homo	404	-----LQDH-----	-----AP-----
GLUT5_Homo	365	-----LQDT-----	-----VS-----
GLUT7_Homo	371	-----FQNR-----	-----VPELS-----
Halyomorpha	446	-----GKTN-----	-----CYDLESYGC-----
Bemisia	508	-----AKER-----	-----NIDVTAAG-----
Cimex	281	-----LKDR-----	-----GTDLTEFG-----
Rhodnius	367	-----MKNS-----	-----GTDMTQYG-----
Cinara	553	-----YKKS-----	-----GYDVSNYG-----
Sipha	499	-----YKNS-----	-----GADVSOYG-----
Melanaphis	528	-----YKNS-----	-----GYDVSQYG-----
Acyrtosiphon	526	-----YKNS-----	-----GYDVSQYG-----
Diuraphis	521	-----YKNN-----	-----GYDVSQYG-----
Myzus	522	-----YKNN-----	-----GYDVSQYG-----
Rhopalosiphum	504	-----YKNN-----	-----GYDVSQYG-----
Aphis	502	-----YKNN-----	-----GYDVSQYG-----
Athalia	494	-----LKES-----	-----GTNVESYGC-----
Cephus	501	-----QKES-----	-----GAHVASYG-----
Megachile	486	-----VKEL-----	-----GSDVSAYG-----
Bombus	490	-----VKAT-----	-----GVDVTAAG-----
Blattella	455	-----LKDVT-----	-----KADTSTYGC-----
Cryptotermes	507	-----LKDHT-----	-----DTNVTPYGC-----
Nilaparvata	495	-----VKNV-----	-----QIDTTEYGC-----
Drosophila	355	-----CKAH-----	-----GPDVSHYG-----
Culex	383	-----VKNN-----	-----GGDVSHYG-----
Anopheles	370	-----MKNN-----	-----GPDVSEYG-----
Ceratitidis	355	-----CKAS-----	-----GMNTEVGC-----
Lucilia	715	-----CKSS-----	-----GIDVSNVGC-----
Musca	706	-----CKAS-----	-----EMDVSNVGC-----
Stomoxys	709	-----CKAS-----	-----DMDVSNVGC-----
GLUT	362	-----FGPRPLSPNSTA-----	-----GLESESYGDLAQPLAAPAG-----
GLUT8_Mus	343	-----LTQSL-----	-----PSNSSHVGLVPIAAEPVDVQVGL

Escherichia	740	VLHGMQGTPYLYQGEEIGMTNPHFTRITDYRDV	ESLNFMAELRNDGRDADELLAILASKSRDNSRTPMQWSNGDNA	GFIA
GLUT12_Homo	462	-----WL-----	-----SLASLLVYV-----	-----AAFSI-----
GLUT10_Homo	410	-----WT-----	-----ALLCLMVYV-----	-----SAFSF-----
GLUT11_Homo	374	-----WTLYL-----	-----AMACIFAFI-----	-----LSFGI-----
GLUT2_Mus	394	-----WMSYV-----	-----SMTAIFLFV-----	-----SFFEI-----
GLUT3_Homo	366	-----WL-----	-----CTGAILVYV-----	-----AFFEI-----
GLUT4_Homo	382	-----YV-----	-----SIVVAIFGV-----	-----AFFEI-----
GLUT1_Mus	363	-----WMSYL-----	-----SIVVAIFGV-----	-----AFFEV-----
GLUT9_Homo	410	-----WVPYL-----	-----SIVGILATL-----	-----ASFCS-----
GLUT5_Homo	371	-----WMPYI-----	-----SIVCVISYV-----	-----IGHAL-----
GLUT7_Homo	380	-----YL-----	-----GICVFAYI-----	-----AGHSI-----
Halyomorpha	458	-----WV-----	-----PLPAFVIEI-----	-----FGFAI-----
Bemisia	520	-----WI-----	-----PLASFVIYV-----	-----IGFSI-----
Cimex	293	-----WI-----	-----PLVSEVLFV-----	-----IGFSI-----
Rhodnius	379	-----WI-----	-----PLASSVIYV-----	-----IGFSI-----
Cinara	565	-----WL-----	-----PLASFVBEI-----	-----IGFAI-----
Sipha	511	-----WI-----	-----PLASFVBEI-----	-----IGFAI-----
Melanaphis	540	-----WL-----	-----PLVSFVBEI-----	-----IGFAI-----
Acyrtosiphon	538	-----WL-----	-----PLASFVBEI-----	-----IGFAI-----
Diuraphis	533	-----WL-----	-----PLVSFVBEI-----	-----IGFAI-----
Myzus	534	-----WL-----	-----PLASFVBEI-----	-----IGFAI-----
Rhopalosiphum	516	-----WL-----	-----PLVSFVBEI-----	-----IGFAI-----
Aphis	514	-----WL-----	-----PLVSFVBEI-----	-----IGFAI-----
Athalia	506	-----WL-----	-----PLASFVIYV-----	-----IGFSL-----
Cephus	513	-----WL-----	-----PLASLVYV-----	-----IGFSL-----
Megachile	498	-----WI-----	-----PLMSLIVYV-----	-----IGFSL-----
Bombus	502	-----WI-----	-----PLMSLIVYV-----	-----IGFSL-----
Blattella	468	-----WL-----	-----PLASFVIYV-----	-----IGFSF-----
Cryptotermes	520	-----WL-----	-----PLVSFVIYV-----	-----IGFSF-----
Nilaparvata	508	-----WV-----	-----PLGSFVYV-----	-----IGFSI-----
Drosophila	367	-----WL-----	-----PLTCFVIYI-----	-----IGFSL-----
Culex	395	-----WL-----	-----PLASFVIFV-----	-----IGFSL-----
Anopheles	382	-----WL-----	-----PLAFAVYV-----	-----VGFSL-----
Ceratitidis	367	-----WL-----	-----PLASFVIYV-----	-----VGFSL-----
Lucilia	727	-----WL-----	-----PLASFVYI-----	-----IGFSL-----
Musca	718	-----WL-----	-----PLASFVYV-----	-----IGFSL-----
Stomoxys	721	-----WL-----	-----PLASFVYV-----	-----IGFSL-----
GLUT	393	-----YLTLV-----	-----PLLATMLFI-----	-----MGYAV-----
GLUT8_Mus	371	A-----WL-----	-----AVGSMCLFI-----	-----AGFAV-----

Supplementary File S2: Columns are: VectorBase code—the official gene number in the RproC3 genome assembly; OV_FC, OV_UFC, FB_FC, FB_UFC show the readcount after normalization. Log2FoldChange: \log_2 (fed condition/unfed condition); p-adj: pvalue after normalization (the smaller the p-adj, the more significant the difference). Transcripts highlights in red: trehalose transporters. FB_FC, fat body in FC; FB_UFC, fat body in UFC; OV_FC, ovary in FC; OV_UFC, ovary in UFC.

Gene_id	Suggested identity (by BLASTp)	OV_F	OV_UF	log ₂ FoldChange	padj
RPRC002241	facilitated glucose transporter	1.484333	0.546686	1.441	0.86967
RPRC002688	facilitated trehalose transporter	146.231	174.1264	-0.25189	0.4134
RPRC002833	facilitated trehalose transporter	1020.189	581.5957	0.81075	4.84E-07
RPRC004616	facilitated glucose transporter	17.57322	11.17511	0.65309	0.52979
RPRC005613	facilitated trehalose transporter	2677.428	1658.913	0.69061	0.03631
RPRC010167	facilitated glucose transporter	0	0	NA	NA
RPRC010168	facilitated glucose transporter	0	0	NA	NA
RPRC011096	facilitated glucose transporter	0	0	NA	NA
RPRC011385	facilitated trehalose transporter	77.03544	71.30437	0.11153	0.87263
RPRC011469	ribonuclease P protein subunit	1499.828	1271.66	0.23808	0.1685
RPRC014535	facilitated glucose transporter	308.1095	339.9465	-0.14186	0.6825
RPRC015169	facilitated trehalose transporter	1.998917	12.06625	-2.5937	0.02998
RPRC007957	facilitated trehalose transporter	1730.754	22.9776	6.235	5.28E-43

Gene_id	Suggested identity (by BLASTp)	FB_FC	FB_UFC	log ₂ FoldChange	padj
RPRC002241	facilitated glucose transporter	0	0	NA	NA
RPRC002688	facilitated trehalose transporter	9.556347	10.04905	-0.072528	1
RPRC002833	facilitated trehalose transporter	6.674395	10.1139	-0.59963	0.77413
RPRC004616	facilitated glucose transporter	2.161835	3.248373	-0.58746	0.99291
RPRC005613	facilitated trehalose transporter	3160.701	2329.008	0.44053	0.84978
RPRC010167	facilitated glucose transporter	0	0	NA	NA
RPRC010168	facilitated glucose transporter	0	0	NA	NA
RPRC011096	facilitated glucose transporter	0	0	NA	NA
RPRC011385	facilitated trehalose transporter	2178.7	1839.659	0.24403	0.86874
RPRC011469	ribonuclease P protein subunit	95.04148	63.0561	0.59192	0.2874
RPRC014535	facilitated glucose transporter	429.4323	361.5216	0.24835	0.77178
RPRC015169	facilitated trehalose transporter	7.36546	0	Inf	0.02565
RPRC007957	facilitated trehalose transporter	1801.396	268.3714	2.7468	3.85E-05

Supplementary File S3: The sequences employed for phylogenetic analysis (Figure S4).

RPRC011385 1 GSGFSLAPIVLLWLTSEESEINMTLTQFSWLTSCPQIGFLLSVVPSGMLADRYGRKTVLI
RPRC002688 1 ----WMAPYSIWLKGNHELOMTTSEFAWLTSIIIEVGAIIGCIPSAIYIADRWGRKSLIL
RPRC015169 1 ----WLSPTYTIKLTGTENPI-LTTSMLATLLSITEIGEAGSIPSAIFSDFRGRKKSLL
RPRC002833 1 -----
Rhopr-TRET 1 -----
RPRC005613 1 -----

RPRC011385 61 SAAPLSLLAWILVATTRDITVLFIVRLIQGITIAIAFTVAPVYVAEVSSPKVVRGLLGGQF
RPRC002688 56 SSGPIYLAIWLLTAFTKNIIVFYIARILQGFLLAIADCVCSVYVAETSHPKRRGTLVGYF
RPRC015169 55 LAGPLIIFSFLISLLTKNIIALLVMRILQGYVAATVEVVAPVYLAEISGAKIRGTVCGYY
RPRC002833 1 -----
Rhopr-TRET 1 -----
RPRC005613 1 -----

RPRC011385 121 SLMLOVGTVVSIVAGLYLSYQTYIYVQMILSLMFLATFSFMPESPYYYFMVKRKEQAYSS
RPRC002688 116 TVFWNLGILYVYTLGNYLNFDHYILTLTALPLLFCVFSFALMPESPYYYFMINEPARAESS
RPRC015169 115 SVFWNLGIVVVFVSEYLSFDMYTLSTLVVPIIFCGTFFIFMPESPYYCLMKGETDGARSS
RPRC002833 1 -----
Rhopr-TRET 1 -----
RPRC005613 1 -----

RPRC011385 181 YYWLS-GKQATEELLKIEENVQEDMKNKTGWVDLIARKCDRRALWLVLVFSFMRAATGMP
RPRC002688 176 LKWL RHGKDIEVEYKQIEEAVRDDMKNSANWTELIATRSNRRALFIVQMCISRYMIGII
RPRC015169 175 LQWLRHGEDIKYELEIEFAVREDMKYAGSWIDLIAATKEDRRALWIVLIGCMARYLIGIS
RPRC002833 1 -----
Rhopr-TRET 1 -----
RPRC005613 1 -----

RPRC011385 240 SYAAYGTQIFAASS-KNIFPTDVLALIMVIVLLICTFLAALFSDTAGRRFLLILSSVGTI
RPRC002688 236 TFTVYAEELSKVG-NMFTPSELSIFMGIVFALTAFISSFFSDSVGRKAMLLFSLAGCA
RPRC015169 235 TFIAYAEDIFAKAGQNNLFTPNHLATFYALLFTVSSAVASFFSDTVGRRKLLIYSLIGTV
RPRC002833 1 -----
Rhopr-TRET 1 -----
RPRC005613 1 -----

RPRC011385 299 ISNLAAGVYFYLELETSVN--LTIWILYLAVLGF CMSANTGTGNLQTVVQAEFFPSHTRG
RPRC002688 295 VTNIIVAVYYLEHSRIDVLPYVWVLYLNLMGFCIFSNLTGLVQLMPTIKSEYFPTHIRS
RPRC015169 295 ISNVIIAVYFCLLELTSLOITSHIWIWYLGSTVCCIFTNTGIGQLVPTIKAEFLPSHTRN
RPRC002833 1 -----
Rhopr-TRET 1 -----MSQKE---RNMLLVGGDLEPVKSK-
RPRC005613 1 -----MRQT-

RPRC011385 357 KGGAITGITSALSTFLVVKLYQPLIDSVGIYMNFFFYAVSIA-VSLFLIHIYLPESAGKT
RPRC002688 355 KGSAITSLTSAICIFIQLRLYTSINESIGIYMNFIIFAVFAI-ISIFLVVYFYLTESAGYL
RPRC015169 355 RGSALTNAIASLAIFVQLFLFPMIAAYIGMYFNFITFAAAIKLVTAPPLLHLHPNKRCYL
RPRC002833 1 -----FTVNL
Rhopr-TRET 22 -----KSLNDFGLE---TTVTSN-----RQA-YIRQGLAAFSVSL
RPRC005613 5 -----VGISQA---TLVSDG-----TKAYKVPQYIAALIVTI

RPRC011385 416 LAEV--NSLVKVEKSTLWLTSDQSEIKMTDKDFSWITATIELGILAFVIPAGILADRYGR
RPRC002688 414 SVLMVGTCTFVWMAFYATSFTSSNGEIHMSHSLFAWLTSTVGI GEVISSLPSGILADMGR
RPRC015169 415 CVMTASFVFNWLSPTYTIKLTSGESPVL-TPTILATLISVIEIGEAVTCIPVAIFSDFRGR
RPRC002833 6 LYVGVGCVMAWTSPTVPKL----SKFITHEEASWIGSLYSLGATFGPIITYLGLDNIGR
Rhopr-TRET 53 GSMVVGFSAYTSPALES MKQPGSTLHITEQQTSWIASLMPLSALLGGIIGGALVETLGR
RPRC005613 34 GGLAMGTILGWTSPTELPLKAGQYGFVNNSEFPWIGSLMSIGAIFGAAFTGTITDKIGR

RPRC011385 474 KRVLLSAAPLCFLSWILATLTRDIVLVYVIRFIQGIFAAVAFTVAPMYVAEISDPKIRGF
RPRC002688 474 KTVLLSVGPMCAITWLTAFTRNIVVLFIVRLIQGIAQGLVFTVAPIYIAEISSPNRRGT

RPRC015169 474 KISLLWIGPLTASLWILSLFTKNTVVLYIIRLLQGVMMAAIEETVVPVYLAEISGAERRGA
RPRC002833 61 KGTLYLILAGCYIISWITLAVSTNIYVIYAGRIIGGIGVGGTFSCCPVFVAEITD DENRGM
Rhopr-TRET 113 KKTILLTAIPFGISFILIAFASNVSMMAGRSLAGFCVGIASLALPVYLGEAIQPDVVRGT
RPRC005613 94 RTTIIGIVIPSVVGMALMIWAVNPFMMVGRVILGLASGAYSVACPMYTNEISEVEIRGT

RPRC011385 534 LGGHFCVLLSSGTLFCHVIGSYLNYVTYLRILMVLVPGFFLLLLFMPETPYYYFMVVGKTA
RPRC002688 534 LGGYFTVFWNLGLLYAYCTSYFLSYEHYILSLTFLPLIYFVTYLFPESPYLLEMAKNKG
RPRC015169 534 LGGYYSVFWNLGLVGVYINSEYLSFDMYTLVSVIVVPIIFFTTFIFMPESPYFYLLMTNQLD
RPRC002833 121 LGSVTOATMAIGFLMEYCIGPYTTIYFVLTITISVIPITIVFIALFYLIPESPYYLLIKNRKA
Rhopr-TRET 173 LGLLPITAIAGNGGILICFLAGKYLDWSKLALFGACLPIPFILMFLIPETPRWFITGKKMEH
RPRC005613 154 LGTYFQLQITIGILLSYVIGAVVYVYVWLSVICAIIPILTSVLMAFMPETPYYLLMKNQDVQ

RPRC011385 594 EAVKSYNWLKNDN-----GDLSKIEQAVQDEMASRGGWKDLIATKSDRKALLIVQSTICI
RPRC002688 594 KAMASLAWLRHGE---DIEEECKKIEETVEEDMSNWGNWEDLVADKSDRRILLIVLIICV
RPRC015169 594 DAKLSLOWLRHGE---DIKEEYEQIEEAVREDMKNAGSWKDLVATKKDRRSLIVLVVCL
RPRC002833 181 EAIESLKWYRGADQLYSVQKELTSIEESVELR-KNKVGISGLWQR-GPKKALLISLYLLI
Rhopr-TRET 233 KAKKSLWLRGEN--ADINKEMSELQKSTELFKENKSSIKELFNK-KYLCPFATSMGLMF
RPRC005613 214 KAROSLQKLRGKK--YNIDGIEEQFQATIERVAAEKLSFRQAFITVAAKRGLAVGLGIMF

RPRC011385 648 AKCAIGLPTYISFGROMFQTLSSNQLLASDQLAIAMGVILTVSALISSLVSDMLGRRTL
RPRC002688 651 SRYLIGMDAFVAYSKDTFTR--GTQGLISPDQLSVMGVVFAVTAFLASSFSDTVGRKRL
RPRC015169 651 SRYLIGTAVFVIFAEDIFAK--AGOHMFTANQQAIGLALLFTISSAVASFFSDTVGRKRL
RPRC002833 239 IQQSGNNAIISFAEYIFEM---GHIAVTGSMCAIIGGFTNLVGGIMTPFVVRKFSMKTS
Rhopr-TRET 290 FQQLSGINAVIFYTVTIFKD---AGSTIDSNLSAIIIVGLVNLGATLVATALIDRVGRKVL
RPRC005613 272 FQQLSGINAVIFYTSQIFQS---AGSKLAPSVATIIIVGAVSVVATYVSTLMVDRLGRKPL

RPRC011385 708 LIWTSLGAAVANLTIIVAVFYLYKEVSLNLAGTEWIMYLAVAFCTAANMGLAQQLVMVVOA
RPRC002688 709 LLFSLSGTAISDLIIIVAVYFLDEKTSVSMKSDVWIMYIGVVALCIMS NVGLVQLMHTIKA
RPRC015169 709 LIYSLIGTAISNIIIIIVYFCILELTSLOVTPYVWVMYIGIVGFCIFTSIGLGLMPTIKA
RPRC002833 296 FLISAFGVAITLGLLALFYLQSSG-ADGAKVWFLPLAAYIILFNIFFCIGCGPLPWPMLIA
Rhopr-TRET 347 MYFSNCIMAATLAILGTFYFMKNSG-TDMTQYGWIPLASSVIYVIGFSIGAGPIPWLMMG
RPRC005613 329 LFIISDLVMAISSLVLGIFFWIQTHEPEKATSIGWLPICL SVFIIIVFSIGYGPWPMLIA

RPRC011385 768 EFFPSNTRGKGGAISGIVSAVVTFFIVLKLQVLTVAVGIYINYAIFSFALIT---AVVI
RPRC002688 769 EFFPSHTRGRGSAVTSLSLTAALCTFLQLRLYTTITDMYGVYLNLFVIFAFATIS---AMFV
RPRC015169 769 EFFPSHTRSKGGAITNLACSLAVFVQISMFPVISMVGMVFNFVIFSI VAVIG---CIFV
RPRC002833 355 EMYPPIEVKSMASFVCGMFSCLEGFIVIEVTAEFLNLAGPTTV---FASLCLFITLITFGA
Rhopr-TRET 406 EILPAKIRGSAGSMVTSFNWACTFLVTKTYVDLTLIGSHGAFWLFGGICLIS---LAFV
RPRC005613 389 EIFSPAIKGPASSIACLFNWVCAFLVTLFPIVKDAIGSATTFWIFTVISFIG---TAFV

RPRC011385 825 YVILPESAGKILAEVNAIK-----
RPRC002688 826 INYVTEPAGKSLAEI-----
RPRC015169 826 IIFLPESAGKILHEV-----
RPRC002833 412 VFLVPTTGLSLSEIHNYLATGKRPOKSE---
Rhopr-TRET 463 IIFVPKTTGKSLQKI-----
RPRC005613 446 YFEVPEKTKGKSLDEVVKIFGGSSSSSSDATIEASGEGLYFVEKSRLISYACIAVVYLYII

RPRC011385 -----
RPRC002688 -----
RPRC015169 -----
RPRC002833 -----
Rhopr-TRET -----
RPRC005613 506 CFAVGAGAI PWLIGPELFNTAARPMASIGVLVNWFFNFIVGLTFLPIQLLIGPATFLIF

RPRC011385 -----
RPRC002688 -----
RPRC015169 -----
RPRC002833 -----
Rhopr-TRET -----

RPRC005613 566 IICQILALIFILAKVPETKGRPIEEITALFE