Table S2: Alignment between hglut2 and hglut3 sequences performed with ClustalOmega.

```
hglut2      MTEDKVTGTLVFTVITAVLGSFQFGYDIGVINAPQQVIISHYRHVLGVPLDDRKAINNYV    60
hglut3      MGTQKVTPALIFAITVATIGSFQFGYNTGVINAPEKIIKEFITKTLT----D--------    48
            *  :*** :*:*:: .*.:*******: ******:::* ..  :.*     *

hglut2      INSTDELPTISYSMNPKPTPWAEEETVAAAQLITMLWSLSVSSFAVGGMTASFFGGWLGD    120
hglut3      ----------------------KGNAPPSEVLLTSLWSLSVAIFSVGGMIGSFSVGLFVN    86
                                  : ::  :  *:* ******: *:**** .**  * : :

hglut2      TLGRIKAMLVANILSLVGALLMGFSKLGPSHILIIAGRSISGLYCGLISGLVPMYIGEIA    180
hglut3      RFGRRNSMLIVNLLAVTGGCFMGLCKVAKSVEMLILGRLVIGLFCGLCTGFVPMYIGEIS    146
             :** ::**:.*:*::.*. :**:.*:. *  ::* ** : **:*** :*:********:

hglut2      PTALRGALGTFHQLAIVTGILISQIIGLEFILGNYDLWHILLGLSGVRAILQSLLLFFCP    240
hglut3      PTALRGAFGTLNQLGIVVGILVAQIFGLEFILGSEELWPLLLGFTILPAILQSAALPFCP    206
            *******:**::**.**.***::**:*******. :** :***:: : *****  * ***

hglut2      ESPRYLYIKLDEEVKAKQSLKRLRGYDDVTKDINEMRKEREEASSEQKVSIIQLFTNSSY    300
hglut3      ESPRFLLINRKEEENAKQILQRLWGTQDVSQDIQEMKDESARMSQEKQVTVLELFRVSSY    266
            ****:* *: .** :*** *:** * :**::**:**:.*  . *.*::*:::**  ***

hglut2      RQPILVALMLHVAQQFSGINGIFYYSTSIFQTAGISKPVYATIGVGAVNMVFTAVSVFLV    360
hglut3      RQPIIISIVLQLSQQLSGINAVFYYSTGIFKDAGVQEPIYATIGAGVVNTIFTVVSLFLV    326
            ****:::::*:::**:****.:*****.**: **:.:*:*****.*.** :**.**:***

hglut2      EKAGRRSLFLIGMSGMFVCAIFMSVGLVLLNKFSWMSYVSMIAIFLFVSFFEIGPGPIPW    420
hglut3      ERAGRRTLHMIGLGGMAFCSTLMTVSLLLKDNYNGMSFVCIGAILVFVAFFEIGPGPIPW    386
            *:****:*.:**:.** .*: :*:*.*:* ::: **:*.: **::**:***********

hglut2      FMVAEFFSQGPRPAALAIAAFSNWTCNFIVALCFQYIADFCGPYVFFLFAGVLLAFTLFT    480
hglut3      FIVAELFSQGPRPAAMAVAGCSNWTSNFLVGLLFPSAAHYLGAYVFIIFTGFLITFLAFT    446
            *:***:*********:*:*. ****.**:*.* *   *.: * ***::*:*.*::*  **

hglut2      FFKVPETKGKSFEEIAAEFQKKSGSAHRPKAAVEM--KFLGATETV----  524
hglut3      FFKVPETRGRTFEDITRAFEGQAHGADRSGKDGVMEMNSIEPAKETTTNV  496
            *******:*::**:*:  *: :: .*.*      *  : :  :: .
```