HANPO 1 MSANDN--------------DTGRTSPTVIVAPTTSGRDKADRLGKKFADAKRNNRSRFA  
OGAPO 1 MSANDN--------------DTGRTSPTVIVAPTTSGRDKADRLGKKFADAKRNNRSRFA  
OGAPH 1 MFYSILPLKGSQENSPE-MENTTSTSPTARLSPSMSGRDKANLLDRKFADAKRNSRSKFA  
OGAKO 1 MFLNKEPSSIDR-RSPSQWTEEDKQIPTVILAPTLSGRDKADRLGKKFADAKKNSRNKFS  
OGAMI 1 MFLDKQPTSIDR-RSMS-PGDKDKPSPMVILAPTSSGRDKADRLGKKFADAKRNSRSRFA  
OGANOn 1 MFLDKQTTSIER-RSMS-PSDKDKPSPIVILAPTSSGRDKADRLGKKFADAKRNSRSRFS  
  
HANPO 47 PSRSAESPYNVLT-SPSKNDPVKLSRLYSIMNSKRST-NNKSKRQREEP-AL-QRSA---  
OGAPO 47 PSRSAESPYNVLT-SPSRNDPVKLSRLYSIMNSKRTS-NNKSRRQREEP-AL-QRAA---  
OGAPH 60 ATKHQESSPQPSTA-PSGNDPVKLQRIYSILNAKRST-PSKAPQPQEQRSSSGENGLAAK  
OGAKO 60 AARNGTSPDRALAATQSKNDPVKLNKLYSILNSKRTS-NSKKPTADVSD-GF-IRTRARR  
OGAMI 59 LSRSAESPNNVLNTSSSRSDPVKLNKLYSILNSKKRQTRSKKQ--KQSPSGS-RQSPSSE  
OGANOn 59 LSRSAESPYNVLNAPSSKSDPVKLNKLYSILNSKKRPAKSRKQ--KQTAATALQQVPPAE  
  
HANPO 100 --SDISQAQVSTDENA--SIPQDA-LVTRSQPA-----IATPNIVDDPSTTDPRAGEQ--  
OGAPO 100 --SDISQAKVSPDENV--GSPHNA-LVTRSQPA-----IATPIVLDDPSTTSLLADEQ--  
OGAPH 118 ---------STSSQETTLGLRSGVRDASSLGLASLNSAASYRDLMIAKRNAFKQRMIQNE  
OGAKO 117 ALSEVDQA--STDATS--AQPQ----------------TYQEIVR---------ARKR--  
OGAMI 116 SI-------QQTDPET--SIESDA-PISSLENTNLSPQALYKNVLIAKRNAFKEQLEKSE  
OGANOn 117 PV-------RETDPET--TIDSDV-PIPSLNNDNVSPQALYKNVLIAKRNAFKEQIEKSQ  
  
HANPO 148 --------------------------------------SGPSPNKSMESKSQSQSKALQT  
OGAPO 148 --------------------------------------SGSSPNKSVVSTPQSQSKAPQT  
OGAPH 169 AAMRSAAEDSAETTIEAQPPKPDSQPPVKSLLDHAPVQETPVPDTPRETRQARAAVEKQT  
OGAKO 146 --------------------------------------ARATRSLSVELTPAKPQPIPQT  
OGAMI 166 --------------------------------------RSASPK--ITERSSSSSAQPET  
OGANOn 167 --------------------------------------KEIPPDTNLKSHDEQISPIVEG  
  
HANPO 170 APNGNSQSTPTKGSQP-------SPSQFGSNN------T-HLAPGQRHLRISKQAFEKNI  
OGAPO 170 ARNGSS--------QP-------SPTQFASND------T-HLAPGQHHTCISKQAFEKNI  
OGAPH 229 VKSARKRSSPSKSPSPEKTPSKVTKTVPASEAHTPSNSRPSSAPSSGRTRRATRGPVPRA  
OGAKO 168 PA----------------------------------------------------------  
OGAMI 186 VSMSQQASAPSI-----------------------------IADPQRESQWSNNSPKERS  
OGANOn 189 SPSVVSQQEPSQEPED---SEAISVSQPTSVS------K-KVAAPARRSRSYNHSPNPKI  
  
HANPO 216 AQ----IS------DNISTFQAVVRNPARTSHTD--------------------------  
OGAPO 208 AQ----IS------DTISTFQAVVRNPARTSHAD--------------------------  
OGAPH 289 PFQGPAIPAAAATAIKSSSFANVTRASDRTSAA------VISED----------LSPAEK  
OGAKO 170 ------KG------VQVSPFQNIVRSPKQNNVSP------RPEE----------EKP---  
OGAMI 217 TTCNNTGQ------SLLAALKNVVRNTKLPS-PQCTPPPPEQITEPTDVIEVPVEGQ---  
OGANOn 239 PVSNPAGN------SLLAAFKNVVKNATLTRSSECEPATADTTS----------KKP---  
  
HANPO 240 -----------QQSSAEKTPKE------------P-AVPTPQTPTRQAGS---------R  
OGAPO 232 -----------QQPSAQNPPKE------------P-TAPTPQTPTRQAVF---------Q  
OGAPH 333 SRKTMSDSELHAKRIEEKTKPEFSAVEPQPTIIEKETLQVDSTPQKPASNGPGLFVEDTD  
OGAKO 199 --------EHHQESIAETQQQT------------SDLPDLPSTPQTSATR---------A  
OGAMI 267 --------EAQETTGIVTTKST----TDQSSESLSQTAVEPSTPLSRPVP---------A  
OGANOn 280 --------EVQQQSVVATTKSA----LEQPAQSQNETIIEPSTPQKRPIG---------A  
  
HANPO 267 DAAGNQTGSDKKVLFSGNVDKSPIASSPIKEPYEPRSILK  
OGAPO 259 DRNGNQTGSDKKVLFSSNVDKSPIASSPIKEPSEPRSILK  
OGAPH 393 -NDDDVPLSAKRVLFSSDIELSPPAQEPAKTIAEPKSILK  
OGAKO 230 -LQNPASTSAKRVLFSAEIDRSPVGSSPIKSPEEPRSILK  
OGAMI 306 -LQEDIQQSAKRVLFSSDVEDSPTASSPIREAMEPRSILK  
OGANOn 319 -LQEDVQQSVKRVLFSSDVEESPTASSPIREPLEPRSILK

**Supplementary File 2.** Multiple alignment of Rif1NTE regions from *H. polymoprha* DL-1 (HANPO) and five of its closest relatives. Sequences were aligned using T-Coffee and shaded with BoxShade. OGAPO – *Ogataea polymorpha*, OGAPH – *Ogataea philodendri*, OGAKO – *Ogataea kodamae*, OGAMI – *Ogataea minuta*, OGANOn – *Ogataea nonfermentans*.