Figure S1. Sequence alignments of *Plasmodium falciparum* retromer cargo-selective subunits and Rab7 with human and *Saccharomyces cerevisiae* homologs.

A. Vps29

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PfVps29        1 MSGKLEDIGELVLLIGDFHSPIRNLGLPDCFKELL-KTDKIKHVLCTGN-VG 50
HsVps29-1      1 ---------MLVLVLGDLHIPHRCNSLPAKFKKLL-VPGKIQHILCTGN-LC 41
ScVps29        1 ---------MLLLALSDAHIPDRATDLPVKFKKLLSVPDKISQVALLGNSTK 43

PfVps29       51 CNENLELLKNIADSVHITKGDMDDN-----------------FDFPEDITLC 85
HsVps29-1     42 TKESYDYLKTLAGDVHIVRGDFDEN-----------------LNYPEQKVVT 76
ScVps29       44 SYDFLKFVNQISNNITIVRGEFDNGHLPSTKKDKASDNSRPMEEIPMNSIIR 95
                               ■■■■         ■
PfVps29       86 IGDFKISLIHGHQIIPWGDMNALLQWQKKYDSDIIISGHTHKNSIVQYEGKY 137
HsVps29-1     77 VGQFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAFEHENKF 128
ScVps29       96 QGALKIGCCSGYTVVPKNDPLSLLALARQLDVDILLWGGTHNVEAYTLEGKF 147
                           ■
PfVps29      138 FINPGSVTGAFQ---------------------------------------- 149
HsVps29-1    129 YINPGSATGAYN---------------------------------------- 140
ScVps29      148 FVNPGSCTGAFNTDWPIVFDVEDSDEAVTSEVDKPTKENQSEDDDAKGGSTG 199
                                                          ■■
PfVps29      150 -----------------------------------------PWLSEPTPTFI 160
HsVps29-1    141 -----------------------------------------ALETNIIPSFV 151
ScVps29      200 KEQPGSYTPKEGTAGERENENESNVKPENQFKEDEVDMSDSDINGSNSPSFC 251
                 ★
PfVps29      161 LMAVAKSNIVLYVYEEKNGKTNVEMSELHKSTVI                   194
HsVps29-1    152 LMDIQASTVVTYVYQLIGDDVKVERIEYKKP                      182
ScVps29      252 LLDIQGNTCTLYIYLYVNGEVKVDKVVYEKE                      282
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B. Vps26

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PfVps26        1 --MLSTIFGSVCSIDLKIDADDNKKFAFLRK-------DKKGEKCPIFSDGE 43
HsVps26a       1 MSFLGGFFGPICEIDIVLNDGETRKMAEMKTE------DGKVEKHYLFYDGE 46
ScVps26        1 ---MSIFFKPPIDIEILFDNEESRKHVDIATRSSNSSYKSMKESLPVYEDGE 49

PfVps26       44 DINGTATISLK-PGKKFEHYGIKLELIGQINILNDKAN-------------- 80
HsVps26a      47 SVSGKVNLAFKQPGKRLEHQGIRIEFVGQIELFNDKSN-------------- 84
ScVps26       50 SLGGIVTLRVR-DSKKVDHLGIKVSVIGSIDMLKSHGSGNSSSKKVTSSTSS 100

PfVps26       81 -------------SYDFFSISKDLEPPGFLVESKQFKWKFSAVDKQHESYFG 119
HsVps26a      85 -------------THEFVNLVKELALPGELTQSRSYDFEFMQVEKPYESYIG 123
ScVps26      101 SSSNGSVDVRKNSVDQFLCQSYDLCPAGELQHSQSFPFLFRDLSKRYESYKG 152

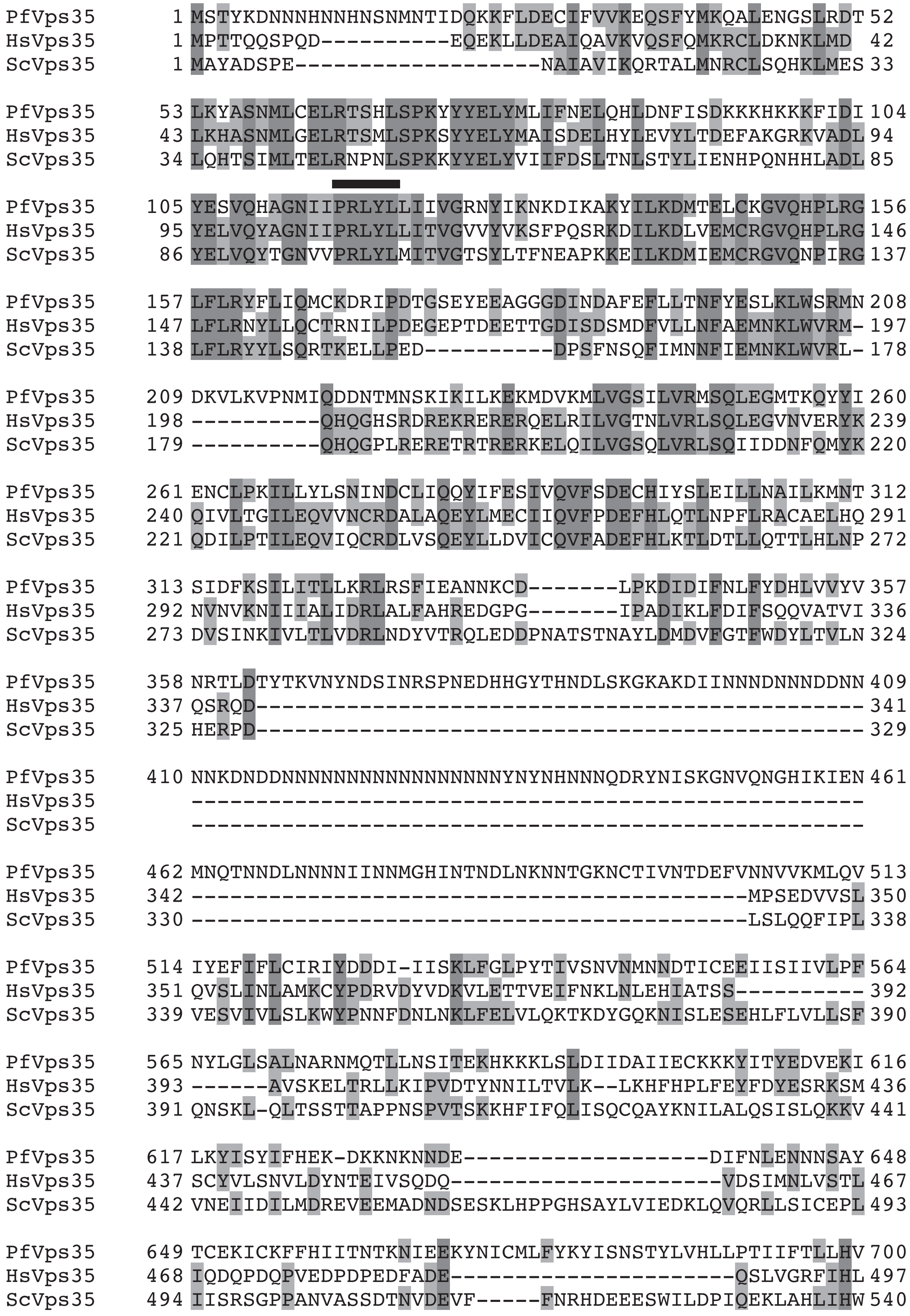
PfVps26      120 TNVQLRYFVRLNIIKGYSGNIQKEID-------------------------- 145
HsVps26a     124 ANVRLRYFLKVTIVRRLT-DLVKEYD-------------------------- 148
ScVps26      153 KNVDVAYYVKVTVMRKST-DISKIKRFWVYLYNSVTTAPNTLSANETKATTN 203
                                         ▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬▬
PfVps26      146 ------------------------FI-VQNLCIPPEINN---TIKMEVGIED 169
HsVps26a     149 ------------------------LI-VHQLATYPDVNN---SIKMEVGIED 172
ScVps26      204 DIAGGNYAADNASDNTQTKSTQGEAADVNQVLPISHSNNEPKPVRLDIGIEN 255

PfVps26      170 CLHIEFEYDKSKYHLKDVVVGKVYFLLVRIKIKHMELDIIKMETSGVGKNYT 221
HsVps26a     173 CLHIEFEYNKSKYHLKDVIVGKIYFLLVRIKIQHMELQLIKKEITGIGPSTT 224
ScVps26      256 CLHIEFEYAKSQYSLKEVIVGRIYFLLTRLRIKHMELSLITRESSGLQTSNV 307
                           ══ ══════════
PfVps26      222 TETVTLSKFEIMDGSPIKSECIPVRLYLSGFDLTPTYKNIQNKFSVKYYINL 273
HsVps26a     225 TETETIAKYEIMDGAPVKGESIPIRLFLAGYDPTPTMRDVNKKFSVRYFLNL 276
ScVps26      308 MTDSTAIRYEIMDGSSVKGETIPIRLFLSGYDLTPNMS--CNYFNVKNYLSL 357

PfVps26      274 IIVDEEERRYFKKQEIFLWRKKMG                             297
HsVps26a     277 VLVDEEDRRYFKQQEIILWRKAPEKLRKQRTNFHQRFESPESQASAEQPEM  327
ScVps26      358 VIIDEDGRRYFKQSEITLYRTR                               379
```

Figure S1. Sequence alignments

C. Vps35



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PfVps35     1 MSTYKDNNNHNNHNSNMNTIDQKKFLDECIFVVKEQSFYMKQALENGSLRDT 52
HsVps35     1 MPTTQQSPQD----------EQEKLLDEAIQAVKVQSFQMKRCLDKNKLMD  42
ScVps35     1 MAYADSPE-------------------NAIAVIKQRTALMNRCLSQHKLMES 33

PfVps35    53 LKYASNMLCELRTSHLSPKYYYELYMLIFNELQHLDNFISDKKKHKKKFIDI 104
HsVps35    43 LKHASNMLGELRTSMLSPKSYYELYMAISDELHYLEVYLTDEFAKGRKVADL 94
ScVps35    34 LQHTSIMLTELRNPNLSPKKYYELYVIIFDSLTNLSTYLIENHPQNHHLADL 85

PfVps35   105 YESVQHAGNIIPRLYLLIIVGRNYIKNKDIKAKYILKDMTELCKGVQHPLRG 156
HsVps35    95 YELVQYAGNIIPRLYLLITVGVVYVKSFPQSRKDILKDLVEMCRGVQHPLRG 146
ScVps35    86 YELVQYTGNVVPRLYLMITVGTSYLTFNEAPKKEILKDMIEMCRGVQNPIRG 137

PfVps35   157 LFLRYFLIQMCKDRIPDTGSEYEEAGGGDINDAFEFLLTNFYESLKLWSRMN 208
HsVps35   147 LFLRNYLLQCTRNILPDEGEPTDEETTGDISDSMDFVLLNFAEMNKLWVRM- 197
ScVps35   138 LFLRYYLSQRTKELLPED----------DPSFNSQFIMNNFIEMNKLWVRL- 178

PfVps35   209 DKVLKVPNMIQDDNTMNSKIKILKEKMDVKMLVGSILVRMSQLEGMTKQYYI 260
HsVps35   198 ----------QHQGHSRDREKRERERQELRILVGTNLVRLSQLEGVNVERYK 239
ScVps35   179 ----------QHQGPLRERETRTRERKELQILVGSQLVRLSQIIDDNFQMYK 220

PfVps35   261 ENCLPKILLYLSNINDCLIQQYIFESIVQVFSDECHIYSLEILLNAILKMNT 312
HsVps35   240 QIVLTGILEQVVNCRDALAQEYLMECIIQVFPDEFHLQTLNPFLRACAELHQ 291
ScVps35   221 QDILPTILEQVIQCRDLVSQEYLLDVICQVFADEFHLKTLDTLLQTTLHLNP 272

PfVps35   313 SIDFKSILITLLKRLRSFIEANNKCD-------LPKDIDIFNLFYDHLVVYV 357
HsVps35   292 NVNVKNIIIALIDRLALFAHREDGPG-------IPADIKLFDIFSQQVATVI 336
ScVps35   273 DVSINKIVLTLVDRLNDYVTRQLEDDPNATSTNAYLDMDVFGTFWDYLTVLN 324

PfVps35   358 NRTLDTYTKVNYNDSINRSPNEDHHGYTHNDLSKGKAKDIINNNDNNNDDNN 409
HsVps35   337 QSRQD----------------------------------------------- 341
ScVps35   325 HERPD----------------------------------------------- 329

PfVps35   410 NNKDNDDNNNNNNNNNNNNNNNNNYNYNHNNNQDRYNISKGNVQNGHIKIEN 461
HsVps35       ----------------------------------------------------
ScVps35       ----------------------------------------------------

PfVps35   462 MNQTNNDLNNNNIINNMGHINTNDLNKNNTGKNCTIVNTDEFVNNVVKMLQV 513
HsVps35   342 -------------------------------------------MPSEDVVSL 350
ScVps35   330 -------------------------------------------LSLQQFIPL 338

PfVps35   514 IYEFIFLCIRIYDDDI-IISKLFGLPYTIVSNVNMNNDTICEEIISIIVLPF 564
HsVps35   351 QVSLINLAMKCYPDRVDYVDKVLETTVEIFNKLNLEHIATSS---------- 392
ScVps35   339 VESVIVLSLKWYPNNFDNLNKLFELVLQKTKDYGQKNISLESEHLFLVLLSF 390

PfVps35   565 NYLGLSALNARNMQTLLNSITEKHKKKLSLDIIDAIIECKKKYITYEDVEKI 616
HsVps35   393 ------AVSKELTRLLKIPVDTYNNILTVLK--LKHFHPLFEYFDYESRKSM 436
ScVps35   391 QNSKL-QLTSSTTAPPNSPVTSKKHFIFQLISQCQAYKNILALQSISLQKKV 441

PfVps35   617 LKYISYIFHEK-DKKNKNNDE-------------------DIFNLENNNSAY 648
HsVps35   437 SCYVLSNVLDYNTEIVSQDQ---------------------VDSIMNLVSTL 467
ScVps35   442 VNEIIDILMDREVEEMADNDSESKLHPPGHSAYLVIEDKLQVQRLLSICEPL 493

PfVps35   649 TCEKICKFFHIITNTKNIEEKYNICMLFYKYISNSTYLVHLLPTIIFTLLHV 700
HsVps35   468 IQDQPDQPVEDPDPEDFADE----------------------QSLVGRFIHL 497
ScVps35   494 IISRSGPPANVASSDTNVDEVF-----FNRHDEEESWILDPIQEKLAHLIHW 540
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Figure S1. Sequence alignments

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PfVps35     701 VTQITKLGQEDHFNQNDDKNNNMNTIDTIDSNNNNNDNNSNCNNDNSNIDSN 752
HsVps35     498 LRSEDP-------------DQQYLILNTARKHFGAGGN-------------- 522
ScVps35     541 IMNTTSRKQTMKNKIQFSLEAQLEILLLIKSSFIKGG--------------- 577

PfVps35     753 HTMDNEKKEDFINSSDSYNIYPNDNDKQNLNNYLHNNQNNFILDEKKINQYN 804
HsVps35     523 ------QRIRFTLPPLVFAAYQLAFRYK--------------ENSKVDDKWE 554
ScVps35     578 ------INVKYTFPAIITNFWKLMRKCRMIQEYLLKKRP---DNKTLLSHYS 620

PfVps35     805 IYVKNIFKFIHTNLLTVAS----QMPILTFKLFLYSAIVVNNYNSFVQTHEF 852
HsVps35     555 KKCQKIFSFAHQTISALIK---AELAELPLRLFLQGALAAG----------E 593
ScVps35     621 NLLKQMFKFVSRCINDIFNSCNNSCTDLILKLNLQCAILAD----------Q 662

PfVps35     853 LTFDNLEAICYEFITQPLIIYEEDINISAQQFDCIVWIVGILCTHINLLDNE 904
HsVps35     594 IGFENHETVAYEFMSQAFSLYEDEISDSKAQLAAITLIIGTFERMK-CFSEE 644
ScVps35     663 LQLN---EISYDFFSQAFTIFEESLSDSKTQLQALIYIAQSLQKTRSLYKE  711

PfVps35     905 NYNNIALKLTQHANKLLKKKDQCIGVLKCSHLYW-------------ENKKY 943
HsVps35     645 NHEPLRTQCALAASKLLKKPDQGRAVSTCAHLFW------SGRNTDKNGEEL 690
ScVps35     712 YYDSLIVRCTLHGSKLLKKQDQCRAVYLCSHLWWATEISNIGEEEGITDNFY 763

PfVps35     944 RNSNKVIECLQKSIKNAEIAIQSNNDNIILFTYMLDKYLYYYEAQN---IDV 992
HsVps35     691 HGGKRVMECLKKALKIANQ-CMDPSLQVQLFIEILNRYIYFYEKEN---DAV 738
ScVps35     764 RDGKRVLECLQRSLRVADS-IMDNEQSCELMVEILNRCLYYFIHGDESETHI 814

PfVps35     993 SEETLHYLIDICQDYYNKT--NDDTN-------------------------- 1016
HsVps35     739 TIQVLNQLIQKIREDLPNLESSEETEQ------------------------- 765
ScVps35     815 SIKYINGLIELIKTNLKSLKLEDNSASMITNSISDLHITGENNVKASSNADD 866

PfVps35    1017 -------------------------------------------------FKQ 1019
HsVps35         ---------------------------------------------------I 766
ScVps35     867 GSVITDKESNVAIGSDGTYIQLNTLNGSSTLIRGVVATASGSKLLHQLKYIP 918

PfVps35    1020 EYKKVIKYVHDKQKNSNVFQKINIDTSILRS                      1050
HsVps35     767 NKHFHNTLEHLRLRRESPESEGPIYEGLIL                       796
ScVps35     919 IHHFRRTCEYIESQREVDDRFKVIYV                           944
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D. Rab7

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                                     ■
PfRab7        1 MSNKKRTILKVIILGDSGVGKTSLMNQYVNKKFTNQYKATIGADFLTKETIVD-N  54
HsRab7a       1 MTSRKKVLLKVIILGDSGVGKTSLMNQYVNKKFSNQYKATIGADFLTKEVMVD-D  54
Ypt7p         1 MSSRKKNILKVIILGDSGVGKTSLMHRYVNDKYSQQYKATIGADFLTKEVTVDGD  55

                            ●
PfRab7       55 EQITMQIWDTAGQERFQSLGVAFYRGADCCVLVFDLTNYKTYESLESWKDEFLIQ  109
HsRab7a      55 RLVTMQIWDTAGQERFQSLGVAFYRGADCCVLVFDVTAPNTFKTLDSWRDEFLIQ  109
Ypt7p        56 KVATMQVWDTAGQERFQSLGVAFYRGADCCVLVYDVTNASSFENIKSWRDEFLVH  110

                               ★
PfRab7      110 ASPKDPENFPFVIIGNKVDET-NKRKVQSLKVLQWCKSNNNIPYFETSAKNAINV  163
HsRab7a     110 ASPRDPENFPFVVLGNKIDLE-N-RQVATKRAQAWCYSKNNIPYFETSAKEAINV  162
Ypt7p       111 ANVNSPETFPFVILGNKIDAEESKKIVSEKSAQELAKSLGDIPLFLTSAKNAINV  165

PfRab7      164 DQAFDEIARKAMKQEHQEEQIY--LPETFALNNQSEQKMYKSRCC           206
HsRab7a     163 EQAFQTIARNALKQE-TEVELYNEFPEPIKLDKNDRAKASAESCSC          207
Ypt7p       166 DTAFEEIARSALQQNQADTEAF---EDDYNDAINIRLDGENNSCSC          208
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