

Supplemental Table S1. Nucleotide sequences of the primers used for the cDNA cloning from *P. fulvidraco*.

Primers	Sequences (5'-3')
Primers for partial fragment	
<i>vps11</i> -F	CAACTBGACCGCCTNAAGARAAC
<i>vps11</i> -R	TGRTGAGBATGAACSTTAGTGCTT
<i>vps16</i> -F	TTKCTCADACCTCCAHAATGTCGC
<i>vps16</i> -R	GCCYTCTTGCYCCTCGTGKTCTAC
<i>vps18</i> -F	GCTHTGAGCGTCCSTCGGAGTA
<i>vps18</i> -R	GGGTBTTGTGGTGCYTGGGGTTA
<i>vps33b</i> -F	GCCATGBCCMCGTTTGAGTTCCC
<i>vps33b</i> -R	CTTGHTGGTGDAGGCRGGTTGTG
<i>vps41</i> -F	AGGATGRTGGAGADMAGGATGG
<i>vps41</i> -R	TGGGTGGTSTTCAVTGGTGAMTGT
<i>lamp1</i> -F	CTTHCTCBGCGCTCCACAAACG
<i>lamp1</i> -R	GCTCGRBGCHGTGAATCACCCT
<i>mcoln1</i> -F	ACTGGTSCGTTCYCTGCTVTCTG
<i>mcoln1</i> -R	GCTGACGCHCTGGGTGTGAATA
<i>ctsd1</i> -F	CTGTCATCCGTBTCCGTTTHCC
<i>ctsd1</i> -R	CTGACGCACYCTCGTBCHCTCCC
<i>tfeb</i> -F	TCGCCTGTATGADGTTTCCGAGT
<i>tfeb</i> -R	TAAAMGGGGTGATGASGGGACTG
Primers for 3'-RACE PCR	
3' GS- <i>vps11</i> -O	GGAGATCACCGAAGCACGACGCC
3' GS- <i>vps11</i> -I	AGGAGTACCCTAAAGTGGTCG
3' GS- <i>vps16</i> -O	TGATAAAGCAGACTGGGACGA
3' GS- <i>vps16</i> -I	CTGGCAGTAGGCGATTTGGAA
3' GS- <i>vps18</i> -O	GGACGAGTACCACCATCACAT
3' GS- <i>vps18</i> -I	CACCTGTGACTTTCCCTTACTC
3' GS- <i>vps33b</i> -O	AAGCACGAATCAAAACAGACC
3' GS- <i>vps33b</i> -I	GAGAAAGGCTATAAGTTTATCGTGG
3' GS- <i>vps41</i> -O	GCTGGGAAATGTCGATAAGGC
3' GS- <i>vps41</i> -I	AAAGATGCACAGAACCCAGAT
3' GS- <i>lamp1</i> -O	CGGCACGACCTGTCTTCTT
3' GS- <i>lamp1</i> -I	TGAATCCACGACCGCTACT
3' GS- <i>mcoln1</i> -O	GCGTATGAGACCATCAAGCA
3' GS- <i>mcoln1</i> -I	TGACAGAACCACCACTTATGAA
3' GS- <i>ctsd1</i> -O	GCCTTCCCTTCTACTATTTC
3' GS- <i>ctsd1</i> -I	CACCTGTGACTTTCCCTTACTC
3' GS- <i>tfeb</i> -O	ATGGAGGAAGTTATTGAGGACA
3' GS- <i>tfeb</i> -I	ACTCCTGCCCTGCCAACCTACA
3' RACE Outer	TACCGTCGTTCCACTAGTGATTT
3' RACE Inner	CGCGGATCCTCCACTAGTGATTTCACTATAGG

Primers for 5'-RACE PCR

5' GS- <i>vps11</i> -O	GAAGGCGATGAACTTATTGTCTAG
5' GS- <i>vps11</i> -I	CAAAAGCAAAACAAGGACCTCT
5' GS- <i>vps16</i> -O	GCTCATCGTCAGAAGAAAAGGCAATC
5' GS- <i>vps16</i> -I	TCAATGTTTGTGCCAGGGTA
5' GS- <i>vps18</i> -O	GGCGTGGTCTTTGGGTTTCAGTG
5' GS- <i>vps18</i> -I	TCCAGCCTCACGTTACAAAAT
5' GS- <i>vps33b</i> -O	TCACATCACCGTAAACACCCT
5' GS- <i>vps33b</i> -I	GCCTATGAGGTCCTTCCTGCTGA
5' GS- <i>vps41</i> -O	GGTGTTTGTTCGTTGCCTAA
5' GS- <i>vps41</i> -I	GTCTTCTTCCTCCGAGTCATC
5' GS- <i>lamp1</i> -O	GGGAAACTCCTGCTTCACC
5' GS <i>lamp1</i> -I	CTCGTGCCATTGATGATAGG
5' GS- <i>mcoln1</i> -O	GCTTTCTTCCCTTGGCATAGTA
5' GS- <i>mcoln1</i> -I	TTTGCCGTCATGCGAACCATA
5' GS- <i>ctsd1</i> -O	GCCCCATTATACTTGTGATGAAGC
5' GS- <i>ctsd1</i> -I	TCTCACCATAGTATTGGGCATC
5' GS- <i>tfeb</i> -O	TTCTGAGACTGGCGGATGTGG
5' GS- <i>tfeb</i> -I	TGTTTGTACCTTCAGCACCTC
5' RACE Outer	TAGGGCCTAATACGACTCACTA
5' RACE Inner	CTAATACGACTCACTATAGGGCA
	AGCAGTGGTATCAACGCAGAGT

Notes: K-G/T; M-A/C; R-A/G; S-G/T; Y-C/T; B-G/T/C; D-G/A/T; H-A/T/C; V-G/A/C; N-A/T/G/C. **Abbreviations:** *ctsd1*; Cathepsin D; *lamp*; lysosome-associated membrane glycoprotein1; *mcoln1*; mucolin-1; *tfeb*; transcription factor EB; *vps*, vacuolar protein sorting-associated protein.

Supplemental Table S2. Primers used for real-time quantitative PCR analysis.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')	Size	Accession no.
<i>vps11</i>	GCAGAGAGTGAGGCTGAGTG	AATCTGCCACCACCGAGAAG	150	MH301091
<i>vps16</i>	TGTCTGTCTCACTGTTTCGC	CCTGCAGGTTCCGTCTCATT	184	MH301092
<i>vps18</i>	CCGGAGAGAAGACGCAGATC	GGTGCTCCGGTTGTTGTAGA	182	MH301093
<i>vps33b</i>	TTGGGCCTGAGGTCCTTC	AGACGGTGCTCCTGTTTCAG	230	MH301094
<i>vps41</i>	TCTCACTGTCCGCAACTTCC	TTGTCAAGCAGCCAGTCGAT	153	MH301095
<i>lamp1</i>	CAGCAACAGCAGTAGTGGGA	AGCTCAGTGTAAGGTTGGCC	150	MH301096
<i>mcoln1</i>	ATCGTGACCCAAACTCGCTT	GGTCGGCGGGTATATCTTGG	184	MH301097
<i>ctsd1</i>	TTTGTAAGGGAGGCTGCGAG	TGTCCGCCCAAATTGAAGGA	150	MH301098
<i>tfeb</i>	ACCAGCGACCTCCTCCTAAT	AGCTCAAATCTCCCAGGCAC	240	MH459004
β -actin	GGACTCTGGTGATGGTGTGA	CTGTAGCCTCTCTCGGTCAG	138	EU161066
<i>rpl7</i>	GGCAAATGTACAGGAGCGAG	GCCTTGTTGAGCTTGACGAA	199	KP938522
<i>hprt</i>	ATGCTTCTGACCTGGAACGT	TTGCGGTTCACTGCTTTGAT	181	KP938523
<i>tuba</i>	TCAAAGCTGGAGTTCTCGGT	AATGGCCTCGTTATCCACCA	135	KP938526
<i>b2m</i>	GCTGATCTGCCATGTGAGTG	TGTCTGACACTGCAGCTGTA	186	KP938520
<i>ubce</i>	TCAAGAAGAGCCAGTGGAGG	TAGGGGTAGTCGATGGGGAA	150	KP938524
<i>tbp</i>	AGCAAAGAGTGAGGAGCAGT	ACTGCTGATGGGTGAGAACA	170	KP938525
<i>gapdh</i>	TTTCAGCGAGAGAGACCCAG	ATGACTCTCTTGGCACCTCC	132	KP938521
18s rRNA	AGCTCGTAGTTGGATCTCGG	CGGGTATTCAGGCGAGTTTG	196	KP938527
<i>elfa</i>	GTCTGGAGATGCTGCCATTG	AGCCTTCTTCTCAACGCTCT	151	KU886307
<i>fatp4</i>	TCGTGGTGGTGAGGACTTTG	CATTGAGCAAGACGGAAAC	164	MG637279
<i>fabp</i>	TGCCCCCTCACATAGT TGCTG	CACTTCCTCGAACA TCCCTCAT	148	MG882758

Abbreviations: *b2m*, beta-2-microglobulin; *ctsd1*; Cathepsin D1; *elfa*, translation elongation factor; *gapdh*, Glyceraldehyde-3-phosphate dehydrogenase; *hprt*, hypoxanthine-guanine phosphoribosyl transferase; *lamp1*; lysosome-associated membrane glycoprotein1; *mcoln1*: mucopolipin-1; *rpl7*, ribosomal protein L7; *tuba*, tubulin alpha chain; *tfeb*: transcription factor EB; *ubce*, ubiquitin-conjugating enzyme; *vps*, vacuolar protein sorting-associated protein; *fabp*, fatty acid binding protein;

<i>fatv</i>	fatty	acid	transport	protein
PF_VPS11	MAAFLQWRRFVFFDKETVKCPSENGKSFALPMGISACISGRGHVVLGDMGCIWFISRSLSCLTTSFQAYKIRVTHLYQLKQ			80
IP_VPS11	MAAFLQWRRFVFFDKETVKCPSENGANFALPVGISACIAGRHHVVLGDMGCIWFISRSLSCLTTSFQAYKIRVTHLYQLKQ			80
DR_VPS11	MAAFSQWRRFVFFDKETVKCPSENGKSNFLPMGISACISGRGHVVLGDMGCIWFISRSLSCLTTSFQAYKIRVTHLYQLKQ			80
RN_VPS11	ASKFLCLPPGIIIVCSGRGSLVFGDMEGCIWFIPRSLCLTGTGQAYKIRVTHLYQLKQ			57
HR_VPS11	MPWIWTAHQ.....KESQFADEYLREICELGQITCAVO			34
PF_VPS11	HSILVSVGQLEHGINPLVKVWNTTKRDSGSPLCRTRIFFAIPGNKEAEVSCLSVHENLNMAIGFTDGSVVLTKGLITRIR			160
IP_VPS11	HSILVSVGQLEHGINPLVKVWNTTKRDSGSPLCRTRIFFAIPGNKEAEVSCLSVHENLNMAIGFTDGSVVLTKGLITRIR			160
DR_VPS11	HNILVSVGQLEPGINPLVKVWNLTKRDSGSPLCRTRIFFAIPGNKEAEVSCLSVHENLNMAIGFTDGSVVLTKGLITRIR			160
RN_VPS11	HNIIASVGELEEGINPLVKIWNLEKRDGNNPLCTRILFAIPGTEPTVVSCLTVHENLNMAIGFTDGSVVLTKGLITRIR			137
HR_VPS11	QCIEAAGHEHQDPMCKSLIRVLGLGR.AGEGGAGRGWIGQQGSS.....ILSPSGSSQAFASFGKCFILR			97
PF_VPS11	HSKTLTLHEGSCFVIGIAFRQAGKVTFLVATIEKVQCYTLTVKVEYERVELITHGCALRCSALTIPSQDSQFIVAGDDCV			240
IP_VPS11	HSKTLTLHEGSCFVIGIAFRQAGKVTFLVATIEKVQCYTLTVKVEYERVELITHGCALRCSALTIPSQDSQFIVAGDDCV			240
DR_VPS11	HSKTLTLHEGSCFVIGIAFRQAGKVTFLVATIEKVQCYTLTVKVEYERVELITHGCALRCSALTIPSQDSQFIVAGDDCV			240
RN_VPS11	HSKTQILHGSYEVIGIAFRQAGKVTFLVATIEKVQCYTLTVKVEYERVELITHGCALRCSALTIPSQDSQFIVAGDDCV			217
HR_VPS11	FFPD.....SEVHMCQDLRVINAVRDHYHIGIPLTYSYKQITLIVL.....LDRLVLRRLVPLAIQIG			156
PF_VPS11	YLYQPIERGECEFAFLGHKLIIAHWHRGYLLISRDIKSNKPFPGPCLSPTEKQVITIYDIDNKIAFSAFEDDIIIDIA			320
IP_VPS11	YLYQPIERGECEFAFLGHKLIIAHWHRGYLLISRDIKSNKPFPGPCLSPTEKQVITIYDIDNKIAFSAFEDDIIIDIA			320
DR_VPS11	YLYQPIERGECEFAFLGHKLIITHWHRGYLLISRDIKSNKPFPGPCLSPTEKQVITIYDIDNKIAFSAFEDDIIIDIA			320
RN_VPS11	YLYQPIERGECEFAFLGHKLIIAHWHRGYLLIVSRDRKVSPPKSEFTSRCSNSKQIINIYDIDNKIAFSAFEDDIIIDIA			297
HR_VPS11	YLRLEPVQ.....VSRILA			171
PF_VPS11	EWGSFVYLTRDGMFMLEKQKDTQTKLEMLFKKNLFVMAINIAKSHQIDNDGISEIERQYGEHLVYKGDHIGAIQCYIRTI			400
IP_VPS11	EWGSFVYLTRDGMFMLEKQKDTQTKLEMLFKKNLFVMAINIAKSHQIDNDGISEIERQYGEHLVYKGDHIGAIQCYIRTI			400
DR_VPS11	EWGSFVYLTRDGMFMLEKQKDTQTKLEMLFKKNLFVMAINIAKSHQIDNDGISEIERQYGEHLVYKGDHIGAIQCYIRTI			400
RN_VPS11	EWGSLVYLTRDGRVFALEKQKDTQTKLEMLFKKNLFVMAINIAKSHQIDNDGISEIERQYGEHLVYKGNHIGAVQCYIRTI			377
HR_VPS11	HWACYKQKQD.....VSEEDVAFAINKQLG.....DTGVSYSIDAAAYCGGRTEIAIKLEYEP			228
PF_VPS11	GKLEPSYVIRKFLLAQRIHNLITAYLQALHRQSIANADHTLLNLCYTKLKDSKLEEFIKS.SESEVHFVIEIAIKVLRQ			479
IP_VPS11	GKLEPSYVIRKFLLAQRIHNLITAYLQALHRQSIANADHTLLNLCYTKLKDSKLEEFIKS.SESEVHFVIEIAIKVLRQ			479
DR_VPS11	GKLEPSYVIRKFLLAQRIHNLITAYLQALHRQSIANADHTLLNLCYTKLKDSKLEEFIKS.NESEVHFVIEIAIKVLRQ			479
RN_VPS11	GKLEPSYVIRKFLLAQRIHNLITAYLQALHRQSIANADHTLLNLCYTKLKDSKLEEFIKTKSESEVHFVIEIAIKVLRQ			457
HR_VPS11	RSGEQVPLLIKMKRSK.....IALSKAISGTDLVFTVLLHLKNELNRGDEFT.....LRNQFMAISLYRO			291
Clathrin repeat domain				
PF_VPS11	AGYHSEAVFIAEKSHHEWYLKICLEDLKN.YCEALRYIGRIPEFCABTNMRHYGKTLMHVPESTTVLIKRLCTINYQEI			558
IP_VPS11	AGYHSEAVFIAEKSHHEWYLKICLEDLKN.YCEALRYIGRIPEFCABTNMRHYGKTLMHVPESTTVLIKRLCTINYQEI			558
DR_VPS11	AGYHSEAVFIAERHMHHEWYLKICLEDLKN.YCEALRYIGRIPEFCABTNMRHYGKTLMHVPESTTVLIKRLCTINYQEI			558
RN_VPS11	AGYHSEAVFIAENHMHHEWYLKICLEDLKN.YCEALRYIGRIPEFCABTNMRHYGKTLMHVPESTTVLIKRLCTINYQEI			536
HR_VPS11	CKHQLETLTKDLYNQDDNHQELGSFHIAASYAEERIEGRVAALQTAALAFYKAKNEFAAKATEDQMRLRLQRRELE			371
Clathrin repeat domain				
PF_VPS11	QDS.TDRSDVLDKLVDAKSEEEFPIFANNPRELRAFLIEHMINVEFSECGGYDITILELRIDWAHEQDEEKKKHLQGS			637
IP_VPS11	QDS.TDRSDVLDKLVDAKSEEEFPIFANNPRELRAFLIEHMINVEFSECGGYDITILELRIDWAHEQDEEKKKHLQGS			637
DR_VPS11	KDS.TDRSDVLDKLVDAKSEEEFPIFANNPRELRLFLIEHMINVEFSECGGYDITILELRIDWAHEQDEEKKKHLQGS			637
RN_VPS11	IEGRGIRE....FPSCRANSEEEFPIFANNPRELRAFLIEHMINVEFSECGGYDITILELRIDWAHEQDEEKKKHLQGS			612
HR_VPS11	IGG.....QFLDLSEHDTVTTLIIGGHNKRAEQL			400
PF_VPS11	ILLLTTE..NTVFDALVLCQMHNEKEGVLYLYEKGKLYQQIMHYHMQNEEYKPVVEACKRYGDCBVCVLEWQALCYFAK			715
IP_VPS11	ILLLTRE..NTVFDALVLCQMHNEKEGVLYLYEKGKLYQQIMHYHMQNEEYKPVVEACKRYGDCBVCVLEWQALCYFAK			715
DR_VPS11	ISLLRSD..NTVFDALVLCQMHNEKEGVLYLYEKGKLYQQIMHYHMQNEEYKPVVEACKRYGDCBVCVLEWQALCYFAK			715
RN_VPS11	ISLLKSGRCFVDFDALVLCQMHNEQDGVLYLYEKGKLYQQIMHYHMQNEEYKPVVEACKRYGDCBVCVLEWQALCYFAK			692
HR_VPS11	ARDERIP.....DKRLWIKLTAAD.....LEDEWLEKESKSKSPIGLPPVEICMKQHN.....			453
PF_VPS11	EEDCKAYISEVLHHIDQNNIMPILVQVIAHNSSTATISVIKDYLINKIKRESKQIEEDERKIQCYREETAHRSBIQEL			795
IP_VPS11	EEDCKAYISEVLHHIDQNNIMPILVQVIAHNSSTATISVIKDYLINKIKRESKQIEEDERKIQCYREETAHRSBIQEL			795
DR_VPS11	EENCKYISEVLHHIDQNNIMPILVQVIAHNSSTATISVIKDYLINKIKRESKQIEEDERKIQCYREETAHRSBIQEL			795
RN_VPS11	EEDCKEYVAARHIEKNSIMPILVQVIAHNSSTATISVIKDYLINKIKRESKQIEEDERKIQCYREETAHRSBIQEL			772
HR_VPS11	KYEAQKVASRVGPECK....VKALLVGVACADVAIEHRNEAELSLSVLSHCTGATDG.....			508
RING-H2 finger motif				
PF_VPS11	STSAKIFQKTKCSNNSPLELPSVHELGGHSEHQHGFESYAESEAECPCTCTEENRKVMDMIRACQCKRDIHDHFNRLRS			875
IP_VPS11	STSAKIFQKTKCSNNSPLELPSVHELGGHSEHQHGFESYAESEAECPCTCTEENRKVMDMIRACQCKRDIHDHFNRLRS			875
DR_VPS11	KTCAKIFQKTKCSNNSPLELPSVHELGGHSEHQHGFESYAESEAECPCTCTEENRKVMDMIRACQCKRDIHDHFNRLRS			875
RN_VPS11	KASPKIFQKTKCSNNSALELPSVHELGGHSEHQHGFESYSESLADCPCTCLEENRKVMDMIRACQCKRDIHDHFNRLRS			852
HR_VPS11	ATAKIQFARACQCKK.....			524
Zn binding site				
PF_VPS11	SNDDGSVVALYFGRGVFNKTLITDPPGGKAGSGSLEADLQRLDILLHTKKNA			928
IP_VPS11	SNDDGSVVALYFGRGVFNKTLITDPPGGKAGSGSLEADLQRLDILLHTKKNA			927
DR_VPS11	SNDDGSVVALYFGRGVFNKTLITDPPGGKAGSGSLEADLQRLDILLHTKKNA			910
RN_VPS11	SNDDGSVVALYFGRGVFNKTLITDPPGGKAGSGSLEADLQRLDILLHTKKNA			903
HR_VPS11				524

Supplemental Figure 1. Multiple amino acid sequence alignment of VPS11 from *P. fulvidraco* and other species. Accession numbers as followed: *Pelteobagrus fulvidraco* (Pf), MH301091; *Ictalurus punctatus* (Ip), AAI66363.1; *Danio rerio* (Dr), NP_001032797.1; *Rattus norvegicus* (Rn), 1AAI68871.1; *Homo sapiens* (Hs) AAH12051.2). Arrows below the sequences represented Clathrin repeat domain and RING-H2 domain. RING-H2 finger motif were boxed. Zn binding site were marked with the symbol (▲).

PF_VPS16	NAFVTANWNPLG.ENFYRKIELYEMGNLKDGLRDCLIAAPYGGFIALLR..EPQRRSPNARFOLEIYSSASGGTIGSFP	77
IP_VPS16	NAFVTANWNPLG.ENFYRKIELYEMGNLKDGLRDCLIAAPYGGFIALLR..EPQRRSPNARFOLEIYSSASGGTIGSFP	77
DR_VPS16	NAFVTANWNPLG.EAFYRKIELYEMGNLKDGLRDCLIAAPYGGFIALLR..WNNRRSPNARFOLEIYSSSGLPIASFP	77
RN_VPS16	MDCYTANWNPLGDSAFYRKIELYEMGNLKDGLRDCLIAAPYGGFIALLRNCRWRKEFAASVREVEIYSSASGMPIASLL	80
HS_VPS16	MDCYTANWNPLGDSAFYRKIELYEMGNLKDGLRDCLIAAPYGGFIALLRNCRWRKEFAASVREVEIYSSASGMPIASLL	80
N-terminal region		
PF_VPS16	WKSQVVKQLGWTVCDLLCQVEDGTVLVVDLFGSEKRRHFSMGNEVGQSQVVEAKIFHSPYGTGVAIVTGASRFTLATNID	157
IP_VPS16	WKSQVVKQLGWTVCDLLCQVEDGTVLVVDLFGSEKRRHFSMGNEVGQSQVVEAKIFHSPYGTGVAIVTGASRFTLATNID	157
DR_VPS16	WKSQVVKQLGWTVCDLLCQVEDGTVLVVDLFGSEKRRHFSMGNEVGQSQVLETKIEHSPYGTGVAIVTGASRFTLATNID	157
RN_VPS16	WKSQPVVALGWSAEEELLGVQEDGAVLVVGLHGDERRHFSMGNEVLQNRVLDARIEHTEFGSGVAITLGAYRFTLSANVG	160
HS_VPS16	WKSQPVVSLGWSAEEELLGVQEDGAVLVVGLHGDERRHFSMGNEVLQNRVLDARIEHTEFGSGVAITLGAYRFTLSANVG	160
N-terminal region		
PF_VPS16	DLKLRRLFEVFGIGAPSCWAVLTQDRQCKVLVANGAEIFILEYGTCTIAVSFGLSPCATSIVHMCVSESYKYLAIFTDTS	237
IP_VPS16	DLKLRRLFEVFGIGAPSCWAVLTQDRQCKVLVANGAEIFILEYGTCTIAVSFGLSPCATSIVHMCVSESYKYLAIFTDTS	237
DR_VPS16	DLKLRRLFEVFGIGAPSCWAVLTQDRQCKVLVANGAEIFILEYGTCTIAVSFGLSPCATSIVHMCVSESYKYLAIFTDTS	237
RN_VPS16	DLKLRRLFEVFGIGAPSCWAVLTQDRQCKVLVANGAEIFILEYGTCTIAVSFGLSPCATSIVHMCVSESYKYLAIFTDTS	240
HS_VPS16	DLKLRRLFEVFGIGAPSCWAVLTQDRQCKVLVANGAEIFILEYGTCTIAVSFGLSPCATSIVHMCVSESYKYLAIFTDTS	240
N-terminal region		
PF_VPS16	GHVWMSGNLRKELSEVETKVRNPPKQNAWCRPPKQQPSVVMWDRYLLVVGVCKDTIPYHLEDDSVLPFELDGVRIIN	317
IP_VPS16	GHVWMSGNLRKELSEVETKVRNPPKQNAWCRPPKQQPSVVMWDRYLLVVGVCKDTIPYHLEDDSVLPFELDGVRIIN	317
DR_VPS16	GHVWMSGNLRKELSEVETKVRNPPKQNAWCRPPKQQPSVVMWDRYLLVVGVCKDTIPYHLEDDSVLPFELDGVRIIS	317
RN_VPS16	GIWMTASLKEKLCFENCNIRAPFKQMVWCSRRPSRERKAVVAVWERRLMVVGNAPESTQFVLDEDSYLPFELDGVRIIS	320
HS_VPS16	GIWMTASLKEKLCFENCNIRAPFKQMVWCSRRPSRERKAVVAVWERRLMVVGNAPESTQFVLDEDSYLPFELDGVRIIS	320
N-terminal region		
PF_VPS16	GTNHLLCEVEFAACEEIKFIASMAPGALLLEAHKEYEKESQKADXYLREIKEQDLLEAVRQCVEAAGHEHEPETQKTLT	397
IP_VPS16	GTNHLLCEVEFAACEEIKFIASMAPGALLLEAHKEYEKESQKADXYLREIKEQDLLEAVRQCVEAAGHEHEPETQKTLT	397
DR_VPS16	GTNHLLCEVEFAACEEIKFIASMAPGALLLEAHKEYEKESQKADXYLREIKEQDLLEAVRQCVEAAGHEHEPETQKTLT	397
RN_VPS16	RSTHFLHEVEFAACEEIKFIASMAPGALLLEAHKEYEKESQKADXYLREIKEQDLLEAVRQCVEAAGHEHEPETQKTLT	400
HS_VPS16	RSTHFLHEVEFAACEEIKFIASMAPGALLLEAHKEYEKESQKADXYLREIKEQDLLEAVRQCVEAAGHEHEPETQKTLT	400
N-terminal region		
PF_VPS16	FAASFGKCFLSNFFPEFVSMCRDLRVINAVRDYTVGIPLTHTQFKQMTVQVITDRLVYRKLYPLAIEICRYLKTPEYQG	477
IP_VPS16	FAASFGKCFLSNFFPEFVSMCRDLRVINAVRDYTVGIPLTHTQFKQMTVQVITDRLVYRKLYPLAIEICRYLKTPEYQG	477
DR_VPS16	FAASFGKCFLSNFFPEFVSMCRDLRVINAVRDYTVGIPLTHTQFKQMTVQVITDRLVYRKLYPLAIEICRYLKTPEYQG	477
RN_VPS16	FAASFGKCFLDREFFDSVHMGQDLRVINAVRDYTVGIPLTHTQFKQMTVQVITDRLVYRKLYPLAIEICRYLKTPEYQG	480
HS_VPS16	FAASFGKCFLDREFFDSVHMGQDLRVINAVRDYTVGIPLTHTQFKQMTVQVITDRLVYRKLYPLAIEICRYLKTPEYQG	480
N-terminal region		
PF_VPS16	VSRVLKHWACCKVQOQEEFADEVIAITVSLKLGIAAGISYSEIANKAYECGRTELAIKLLEFEPRSGEQVLLRMKRSQ	557
IP_VPS16	VSRVLKHWACCKVQOQEEFADEVIAITVSLKLGIAAGISYSEIANKAYECGRTELAIKLLEFEPRSGEQVLLRMKRSQ	557
DR_VPS16	VSRVLKHWACCKVQOQEEFADEVIAITVSLKLGIAAGISYSEIANKAYECGRTELAIKLLEFEPRSGEQVLLRMKRSQ	557
RN_VPS16	VSRILAHWACYKVOQQDVSDEDVARAINQKIGETPGVSXSDIARAYGCGRTTELAIKLLEFEPRSGEQVLLRMKRSQ	560
HS_VPS16	VSRILAHWACYKVOQQDVSDEDVARAINQKIGETPGVSXSDIARAYGCGRTTELAIKLLEFEPRSGEQVLLRMKRSQ	560
C-terminal region		
PF_VPS16	ALSKAIESGDTDLVYTVVTVYLNEMNNGDFFMTLRNQFVALSYLRGFCCKHCEQETLKDLFNQDDDHQELGNFVVKASYK.	636
IP_VPS16	ALSKAIESGDTDLVYTVVTVYLNEMNNGDFFMTLRNQFVALSYLRGFCCKHCEQETLKDLFNQDDDHQELGNFVVKASYK.	636
DR_VPS16	ALSKAIESGDTDLVYTVVTVYLNEMNNGDFFMTLRNQFVALSYLRGFCCKHCEQETLKDLFNQDDDHQELGNFVVKASYK.	636
RN_VPS16	ALSKAIESGDTDLVYTVVTVYLNEMNNGDFFMTLRNQFVALSYLRGFCCKHCEQETLKDLFNQDDDHQELGNFVVKASYK.	640
HS_VPS16	ALSKAIESGDTDLVYTVVTVYLNEMNNGDFFMTLRNQFVALSYLRGFCCKHCEQETLKDLFNQDDDHQELGNFVVKASYK.	640
C-terminal region		
PF_VPS16	EKRLEAARMSLLQSAVDEYNKAKNEFAAATATEEMRLLRFORKLEEKEGECVTFGLSHDTSLLSLGLHKKHABOLYKDFP	716
IP_VPS16	EKRLEAARMSLLQSAVDEYNKAKNEFAAATATEEMRLLRFORKLEEKEGECVTFGLSHDTSLLSLGLHKKHABOLYKDFP	716
DR_VPS16	EKRLEAARMSLLQSAVDEYNKAKNEFAAATATEEMRLLRFORKLEEKEGECVTFGLSHDTSLLSLGLHKKHABOLYKDFP	716
RN_VPS16	EERIEGRVAALQTAATAFYKAKNEFAAATATEEDCMRLLRLQRRLEDELGGFLLDLSLHDTVTTLILGGHNKFAEQLARDFP	720
HS_VPS16	EERIEGRVAALQTAATAFYKAKNEFAAATATEEDCMRLLRLQRRLEDELGGFLLDLSLHDTVTTLILGGHNKFAEQLARDFP	720
Coiled-coil region		
PF_VPS16	VDPKRYWWLKITALADKADWDELEKEAKSKKSPIGYMPFVEECVRRNNKFEAKKYVLKVTPECKVFAHLAGVELECAADA	796
IP_VPS16	VDPKRYWWLKITALADKADWDELEKEAKSKKSPIGYMPFVEECVRRNNKFEAKKYVLKVTPECKVFAHLAGVELECAADA	796
DR_VPS16	VDPKRYWWLKITALADKADWDELEKEAKSKKSPIGYLPFVDVCIKHHNKYEAKKYVSKVTPECKVFAHLAGVEMEGAAEA	796
RN_VPS16	IPDKRLWLWLKITALADLEWDELEKEAKSKKSPIGYLPFVEICMKCHNKHEAKKYASRVGFECKVFAHLLVGEVACAADV	800
HS_VPS16	IPDKRLWLWLKITALADLEWDELEKEAKSKKSPIGYLPFVEICMKCHNKHEAKKYASRVGFECKVFAHLLVGEVACAADV	800
Coiled-coil region		
PF_VPS16	AIERRNEGEISTVLSHCSFATDRTLVERLNFAFATATKK	835
IP_VPS16	AIERRNEGEISTVLSHCSFATDRTLVERLNFAFATATKK	835
DR_VPS16	AIERRNDEISTVLSHCSSTTDHALVERLNFAFATATKK	835
RN_VPS16	AIERRNETELSLVLSHCTGTTDGAIDAKIQAFACQKK	839
HS_VPS16	AIERRNEAELSLVLSHCTGATDGAIDAKIQAFACQKK	839
C-terminal region		

Supplemental Figure 2. Multiple amino acid sequence alignment of VPS16 from *P. fulvidraco* and other species. Accession numbers as followed: *Pelteobagrus fulvidraco* (Pf), MH301092; *Ictalurus punctatus* (Ip), XP_017336907.1; *Danio rerio* (Dr), NP_001091659.1; *Rattus norvegicus* (Rn), NP_001005541.1; *Homo sapiens* (Hs), AAH73959.1). Arrows below the sequences represented conserved domains: N-terminal region and C-terminal region. Coiled coil domain was boxed.

IP_VPS18	MATILDDYEDSCMIRHFVCSGRIPAA NMIGITHSGFVNIRLEEKPIFNKQRIDEFPFEKINHFVCVNQCIMSLGKRTLL	80
PF_VPS18	MATILDDYEDSCLIRHFVCFGRIPAA NMIGITHSGFVNIRLEEKPIFNKQRIDEFPFEKINHFVCVNQCIMSLGKRTLL	80
DR_Vps18	MASILLQYEDSCNIR...CHSRMSTAN.IGITHSGFVNIRLEEKPIFNKQRIDEFPFEKINCFVCVNQCIMSLGKRTLL	76
HS_VPS18	MASILLQYEDSILSRSAVLCTG...CFSVGIPIHSGYVNAQLEKEVPFIETKQRIDEFPSEKITSILVSSNQCIMSLGKRTLL	76
RN_VPS18	MASILLQYEDSILSRSAVLCTG...CFSVGIPIHSGYVNAHLEKEVPFIETKQRIDEFPSEKITSILVSSNQCIMSLGKRTLL	76
IP_VPS18	IRIDLKGFQIQNQEIEGRKDDGKVHKLFLDPTGSHIVISLSTSECYVILNRRNTCKVRGLSRWRGHLIESVGVNKLILGNETN	160
PF_VPS18	IRIDLKGFQIQNQEIEGRKDDGKVHKLFLDPTGSHIVISLSTSECYVILNRRNTCKVRGLSRWRGHLIESVGVNKLILGNETN	160
DR_Vps18	IRIDLKGFQIQNQEIEGRKDDSKVHRLFLDPTGSHIVISLSTSECYVILNRRNTCKVRGLSRWRGHLIESVGVNKLILGNETN	156
HS_VPS18	IRIDLKANEFNHVELGRKDDAKVHKMFLCHTGSHILIALSSTEVLYVNRNCKVRPLARWKGLVESVGVNKLALGTESS	156
RN_VPS18	IRIDLKASEFNHVELGRKDDAKVHKMFLCHTGSHILIALSSTEVLYVNRNCKVRPLARWKGLVESVGVNKLALGTESS	156
IP_VPS18	TGFILVGTGQGIIFEAELISASEGSLFNTNFOYERCVHSLEEDGKPAPVCCILVERGIESKYFIIATTRKRLFCFVGKLA	240
PF_VPS18	TGFILVGTGQGIIFEAELISASEGSLFNTNFOYERCVHSLEEDGKPAPVCCILVERGIESKYFIIATTRKRLFCFVGKLA	240
DR_Vps18	TGFILVGTGQGIIFEAELISASEGSLFNTNFOYERCVHSLEEDGKPAPVCCILVERGLETKYFIIATTRKRLFCFVGKLA	236
HS_VPS18	TGFILVGTGQAQGHIFEAELISASEGSLFAPFLYERFLVYLNEEGGAPVCSLEAERGFDRGSEVIATTRQRLFCFVIGRAA	236
RN_VPS18	TGFILVGTGQAQGHIFEAELISASEGSLFAPFLYERFLVYLNEEGGAPVCSLEAERGFDRGSEVIATTRQRLFCFVIGRAA	236
IP_VPS18	EGSECCGESSIFACNCLPSPSFCFEEFVNMGYSEIGFYTSKLRSSNSFAWMMGNVGFYGRIDYSREDSILLSVCVWEYTP	320
PF_VPS18	EGSECCGESSIFACNCLPSPSFCFEEFVNMGYSEIGFYTSKLRSSNSFAWMMGNVGFYGRIDYSREDSILLSVCVWEYTP	320
DR_Vps18	EGSECCGESSIFACNCLPSPSFCFEEFVNMGYSEITFYTSKLRSEKTFAWMMGNVGFYGRIDYSREDSILLSVCVWEYTP	316
HS_VPS18	EGAEACGSGFLFAAYTHFFPEREFPSNLGYSELAIFYTKLRSAERAFAWMMGDCVLYGALDCGRFDSILLSSEKRVWEYTP	316
RN_VPS18	EDAEACGSGFLFAAYTHFFPEREFPSNLGYSELAIFYTKLRSAERAFAWMMGDCVLYGALDCGRFDSILLSSEKRVWEYTP	316
IP_VPS18	LIDFLYNKFIISIVITCFHFLLILLPERVKAICTINGCVVYEEVFFDKFGFLKMKIKLPVGGILVWIYTEKAVFRYHIQRESR	400
PF_VPS18	LIDFLYNKFIISIVITCFHFLLILLPERVKAICTINGCVVYEEVFFDKYGFELKKIKLPVGGILVWIYTEKAVFRYHIQRESR	400
DR_Vps18	LIDFLNFKFIISIVITCFHFLLILLPERVGICTINGCVVYEEVFFDKFGFLKMKIKLPITGLVWIYTEKAVFRYHIQREAR	396
HS_VPS18	GVGPASPEFLAIVITCFHFLLILLARVEAVCTITGCVVIRHFFLEKFGFLKHMVKLSSTGCLWAYTERAVFRYHIQREAR	396
RN_VPS18	GIGPGANPEFLAIVITCFHFLLILLARVEAVCTITGCVVIRHFFLEKFGFLKHMVKLSSTGCLWAYTERAVFRYHIQREAR	396
IP_VPS18	LVMRMYSMKKEDLAKEYCKDRPECKIMVLAKAEHWEFCNKHYLESACRYALTONYFEEIALKFEIAKCEALKEFLIRK	480
PF_VPS18	LVMCMYMMKKEDLAKEYCKDRPECKITVLAKAEHWEFCNKHYLESACRYALTONYFEEIALKFEIAKCEALKEFLIRK	480
DR_Vps18	LVMCMYMMKKEDLAKEYCKDRPECKIMVLAKAEHWEFCNKHYLESACRYALTONYFEEIALKFEIAKCEALKEFLIKK	476
HS_VPS18	LVMRTYLLMNFEDLAKEYCREFERDCLITVLAREADFCEFRQRYLESACRYALTONYFEEIALKFELEAKCEALAEFLCRK	476
RN_VPS18	LVMRTYLLMNFEDLAKEYCREFERDCLITVLAREADFCEFRQRYLESACRYALTONYFEEIALKFELEAKCEALAEFLCRK	476
IP_VPS18	LIDNLKAKEKTGITLLVTWITELYLNRIQLEAEVVRKRAEFCTREEFRRFLCTNKHKECFYNNRSTIYLLASHGNVDCIM	560
PF_VPS18	LIDNLKAKEKTGITLLVTWITELYLNRIQLEAEENGARFKEMREEFRFLCTNKHKECFYNNRSTIYLLASHGNVDCIM	560
DR_Vps18	LIDNLKAKEKTGITLLVTWITELYLNRIQLEAEENGARFKEMREEFRFLCTNKHKECFYNNRSTIYLLASHGNVDCIM	556
HS_VPS18	LASLKEAERTGATLLTWTWITELYLSRIGALCGTEALTYLRETEKCFRTFLSSPRHKEWLFASRASIHELLASHGDTHEM	556
RN_VPS18	LASLKEAERTGATLLTWTWITELYLSRIGALCGTEALTYLRETEKCFRTFLSSPRHKEWLFASRASIHELLASHGDTHEM	556
IP_VPS18	YVESVIMCDYERVISHHCCHDYAAAILVLISKHDEKLFYKESFVIMOHIPKKVVDANICMGNRLFPKGLIFALVNYSGI	640
PF_VPS18	YVESVIMCDYERVISHHCCHDYAAAILVLISKHDEKLFYKESFVIMOHIPKKVVDANICMGNRLFPKGLIFALVNYSGI	640
DR_Vps18	YVESVIMCDYERVISHHCCHDYAAAILVLISKHDEKLFYKESFVIMOHIPKKVVDANICMGNRLFPKGLIFALVNYSCM	636
HS_VPS18	YVFAVIMCDYERVVAYHCCHAEYAEALAVIARHRDFOLFYKESFVILIRHIFRCLVDANICMGNRLFPKGLIFALVNYSGI	636
RN_VPS18	YVFAVIMCDYERVVAYHCCHAEYAEALAVIARHRDFOLFYKESFVILIRHIFRCLVDANICMGNRLFPKGLIFALVNYSGI	636
IP_VPS18	GSTQCIDETIRYMEFCVHEISVKEEAHNNYLLSIYAKYKPSLLIWLCEAGTHASEIHYDLKALRICAEGHYHCACVLV	720
PF_VPS18	GSTQCIDETIRYMEFCVHEISVKEEAHNNYLLSIYAKYKPSLLIWLCEAGTHASEIHYDLKALRICAEGHYHCACVLV	720
DR_Vps18	GSTQCIDETIRYMEFCVYELDVKEEAHNNYLLSIYAKHKEPALLIWLCEAGTHVSTIHYDLKALRICAEGHYHCACVLV	716
HS_VPS18	GEVQCVSCAIRYMEFCVNVIGETECIAHNNYLLSIYARGRPESLLIYLCEAGASPHRVHYDLKALRICAEGHHRACVHV	716
RN_VPS18	GDAQCVSCAIRYMEFCVNVIGETECIAHNNYLLSIYARGRPESLLIYLCEAGASPHRVHYDLKALRICAEGHHRACVHV	716
Clathrin repeat domain		
IP_VPS18	YRIMELYEEAVDLALQVDVLAKSCADILPEDEELRKKLWLKIARHVVCCEKDKVKAMNCLSSCNLLKIEILPFFFPFV	800
PF_VPS18	YRIMELYEEAVDLALQVDVLAKSCADILPEDEELRKKLWLKIARHVVCCEKDKVKAMNCLSSCNLLKIEILPFFFPFV	800
DR_Vps18	YRIMELYEEAVDLALQVDVLAKSCADILPEDEELRKKLWLKIARHVVCCEKDKVKAMNCLSSCNLLKIEILPFFFPFV	796
HS_VPS18	YKVLIELYEEAVDLALQVDVLAKQCADILPEDEELRKKLWLKIARHVVCCEEDVCTAMACIASCPLIKIEILPFFFPFV	796
RN_VPS18	YKVLIELYEEAVDLALQVDVLAKQCADILPEDEELRKKLWLKIARHVVCCEEDVCTAMACIASCPLIKIEILPFFFPFV	796
Clathrin repeat domain		
IP_VPS18	TIDHFKEAICVSLLEYNHIEELKCEMEEATESARRIRCDICEMRNKYGVVESQEKQATCCFFLLNRPFFYELGGMFHY	880
PF_VPS18	TIDHFKEAICVSLLEYNHIEELKCEMEEATESARRIRCDICEMRNKYGVVESQEKQATCCFFLLNRPFFYELGGMFHY	880
DR_Vps18	TIDHFKEAICVSLLEYNHIEELKCEMEEATESARRIRCDICEMRNKYGVVESQEKQATCCFFLLNRPFFYELGGMFHY	876
HS_VPS18	TIDHFKEAICVSLLEYNHIEELKCEMEEATESARRIRCDICEMRNKYGVVESQEKQATCCFFLLNRPFFYELGGMFHY	876
RN_VPS18	TIDHFKEAICVSLLEYNHIEELKCEMEEATESARRIRCDICEMRNKYGVVESQEKQATCCFFLLNRPFFYELGGMFHY	876
RING-H2 finger motif		
IP_VPS18	DLICFQVTHIHSAYHCSKLEELCKKLAATCTTKSRHREKEEDAVSLGKGQCSRECIKSTIDDIIVASECAYCGEIMIRSI	960
PF_VPS18	DLICFQVTHIHSAYHCSKLEELCKKLAATCTTKSRHREKEEDAVSLGKGQCSRECMKSTIDDIIVASECAYCGEIMIRSI	960
DR_Vps18	DLICFQVTHIHSAYHCSKLEELCKKLAATCTTKSRHREKEEDAVSLGKGQCSRECIKSTIDDIIVASECAYCGEIMIRSI	956
HS_VPS18	DLICFQVTHIHSAYHCSKLEELCKKLAATCTTKSRHREKEEDAVSLGKGQCSRECIKSTIDDIIVASECAYCGEIMIRSI	955
RN_VPS18	DLICFQVTHIHSAYHCSKLEELCKKLAATCTTKSRHREKEEDAVSLGKGQCSRECIKSTIDDIIVASECAYCGEIMIRSI	955
Zn binding sites		
IP_VPS18	DKFFIDPHSFEEMSSWL.....	978
PF_VPS18	DKFFIDPHNIFTKKCNMRYNCQPLSVNSRP	992
DR_Vps18	DKFFIDPKCFKQEMSSWL.....	974
HS_VPS18	DRFFIDPCRYEEELSWL.....	973
RN_VPS18	DRFFIDPCRYEEELSWL.....	973

Supplemental Figure 3. Multiple amino acid sequence alignment of VPS18 from *P. fulvidraco* and other species. Accession numbers (*Pelteobagrus fulvidraco* (Pf) VPS18, MH301093; *Ictalurus punctatus* (Ip) VPS18, AHH37325.1; *Danio rerio* (Dr) VPS18, 1, AAI54757.1; *Rattus norvegicus* (Rn) VPS18, 1AAI69083.1; *Homo sapiens* (Hs) VPS18, AAH01513.1). Arrows below the sequences represented conserved Domain: Clathrin repeat domain. The RING-H2 domains were boxed, and the six Zn binding site were marked with the symbol (▲).

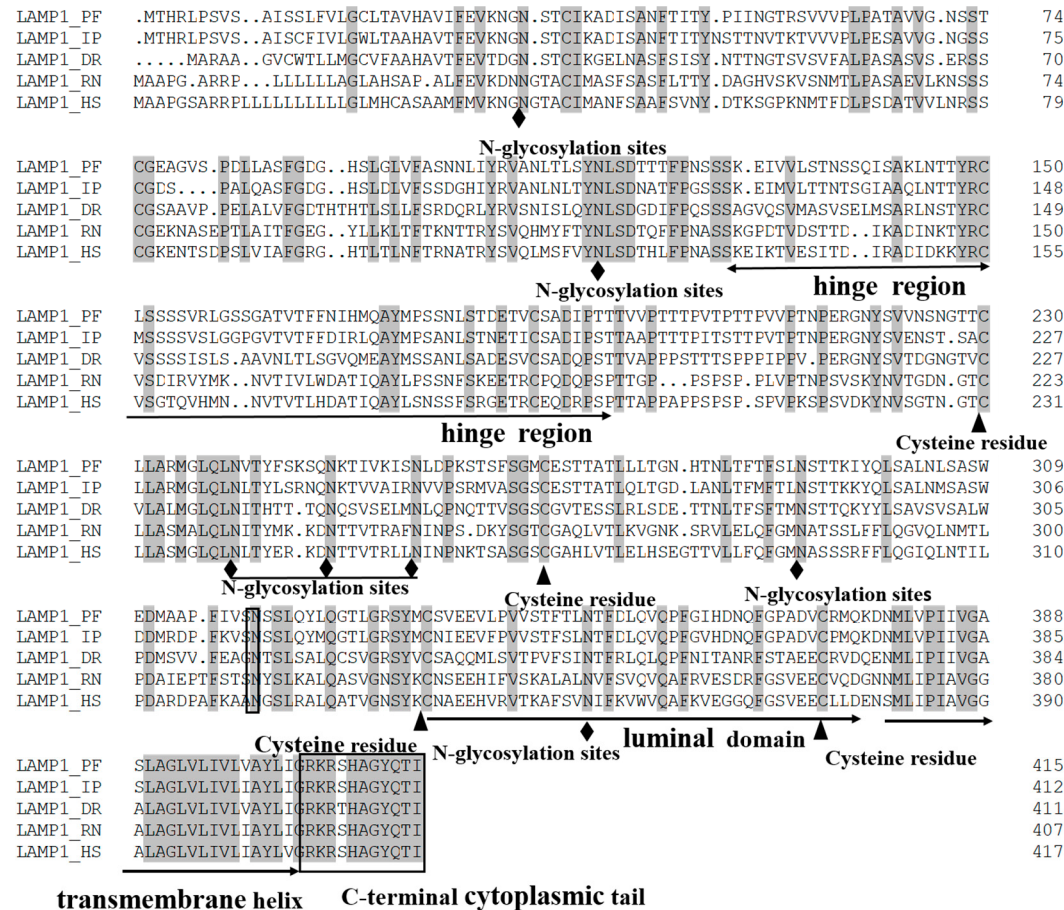
PF_VPS33B	MAQTERRDAPELPDFSLKRLARDQLIFLLEQLPGKKDLFIADLMSPLDRIANVTILKQHEVDKLYKVELKPIVSSSDQ	80
IP_VPS33B	MAHTGRKDAPELPDFALKRLAKDQLIYLLEQLPGKKDLFIADLMSPLDRIANVTILKQHEVDKLYKVELKPIVSVSDQ	80
DR_VPS33B	MAQTERRDAPELPDFSLKRLARDQLIFLLEQLPGKKDLFIADLMSPLDRIANVTILKQHEVDKLYKVELKPIVSSSDQ	80
HS_VPS33B	MAFFHRPDAPELPDFSLKRLARDQLIYLLEQLPGKKDLFIADLMSPLDRIANVTILKQHEVDKLYKVENKFALESNEQ	80
RN_VPS33B	MAFFHRLDAPELPDFSLKRLARDQLIYLLEQLPGKKDLFIADLMSPLDRIANVTILKQHEVDKLYKVENKLTLSNEQ	80
PF_VPS33B	LCFLIRPRIQTVKWIADIVNSDFASGRFRFYKIIFTPOKFYACEMVLEEQGVYGDVTSDEWAFYLLFLDDEIIISLELPEF	160
IP_VPS33B	LCFLIRPRIQTVKWIADIVNSDFASGRFRFYKIIFTPOKFYACDVLVEEQGVYGDVTSDEWSFYLLFLDDEIIISLELPEF	160
DR_VPS33B	LCFLIRPRIQTVKWIADIVNSDFASGRFRFYKIIFTPOKFYACETVLEEQGVYGDVTTDEWNFYLLFLDDEIIISLELPEF	160
HS_VPS33B	LCFLVRPRIKRMRYIASLVNADKLGRTRKVKVIFSPQKFYACEMVLEEEGIYGDVSCDEWAFSLFLDVLDSMELPEF	160
RN_VPS33B	LCFLVRPRIKTMRYIANLVNADKLGRTRKVKVIFSPQKFYACEMVLEEEGIYGDVSCDEWAFSLFLDVLDSMELPEF	160
Sec1 domain		
PF_VPS33B	FRDYFLEGDQRWVTAGSALHLLHSLYGFESKVGIGRCAKMYESWR...EQVEEGEQKARQPEIGNIFIIDRDVDFVTP	238
IP_VPS33B	FRDYFLEGDQRWVTAGSALHLLHSLYGFESKVGIGRCAKMYESWR...EQVEDGEQKARQPEIGNVFLIDRDVDFVTP	238
DR_VPS33B	FRDNFLEGDQRWVTGGGALHLLQSVYGSFESKVGIGRCAKMYESWR...ELMEEGEQRTRQPEFAKVFLIDRDVDFVTP	238
HS_VPS33B	FRDYFLEGDQRWINTVACALHLLSTLYGFENCYGIGRCAKMYELWRNLEEEEDGETKGRRPEIGHIFLLDRDVFVIA	240
RN_VPS33B	FRDYFLEGDQRWINTVACALHLLSTLYGFENCYGIGRCKMSYDLWRKLEEEEDSETKGRRPEIGHIFLLDRDVFVIA	240
Sec1 domain		
PF_VPS33B	LCSQVVYEGLVDDIFRIKCGCVFEGPEVTTSSDKSVKMLNSQDKVNEIRNEHFSNVFSLSQKARNLQIAYDKRRGMDI	318
IP_VPS33B	LCSQVVYEGLVDDIFRIKCGSVFEGPEVTTSSDKSIKVMMLNSQDKVNEIRNEHFSNVFGLSQKARSLQIAYDKRRGMDI	318
DR_VPS33B	LCSQVVYEGLVDDIFRIKCGSVFEGPDVTTSSDKSIKVMMLNSQDKVNEIRNEHFSNVFGLSQKAKNLQIAYDKRRGMDI	318
HS_VPS33B	LCSQVVYEGLVDDIFRIKCGSVDFGPEVTTSSDKSLKVLNLAEDKVEIRNEHFSNVFGLSQKARNLQIAYDRRRGMDI	320
RN_VPS33B	LCSQVVYEGLVDDIFRIKCGSVDFGPEVTTSSDKSLKVLNLAEDKVFSEIRNEHFSNVFGLSQKARNLQIAYDRRRGMDI	320
Sec1 domain		
PF_VPS33B	KQMKTFFVEELKGLKQEHRLLSLHIGASESIMKKKTQDQFQELKTEHSLLEDVEVRQCIGFIEEHINRQVSMIESLRLL	398
IP_VPS33B	KQMKTFFVEELKGLKQEHRLLSLHIGASESIMKKKTQDQFQELKTEHSLLEDVEVRQCISFIEEHINRQVSMIESLRLL	398
DR_VPS33B	QQMFAFVADELKGLKQEHRLLSLHIGASESIMKKKTQDQFQELKTEHSLLEGFEIRECIAYIEEHINRQVSMIDSLRLL	398
HS_VPS33B	KQMKNFVSQELKGLKQEHRLLSLHIGACESIMKKKTQDQFQELIKTEHALLEGFNIRESTSYIEEHIDRQVSPIESLRIM	400
RN_VPS33B	KQMKNFVSQELKGLKQEHRLLSLHIGACESIMKKKTQDQFQELIKTEHALLEGFNIRESTSYIEEHIDRQVSPIESLRIM	400
Sec1 domain		
PF_VPS33B	CLLSITENGLLPKDYRSKLAQYQLQSYGIEHLLTFANIKQIGLLVEQPGGEALTAVESKVGKLVNDKTAGHLLDAFSSSLAK	478
IP_VPS33B	CLLSITENGLLPKDYRSKLAQYQLQSYGIEHLLTFANIRQMGLLVEQPGGEALTAVVESKVGKLVNDKTVGKLLDAFSSSLAK	478
DR_VPS33B	CLLSITENGLLSKDYRSKLAQYQLQSYGIEHLLTFANIRQLGLLEEQQTGETLTVMESKVGKLVNDKTAGHLLDAFSSSLAK	478
HS_VPS33B	CLLSITENGLIPKDYRSKLTQYQLQSYGPEHLLTFESNIRFAGLLTECAPGDTLAVESKVSCLVTDKPAAGHITDAFSSSLAK	480
RN_VPS33B	CLLSITENGLIPKDYRSKLTQYQLQSYGPEHLLTFESNIRFAGLLTECAPGDTLAVENKVSCLVTDKPAAGHITDAFSSSLAK	480
Sec1 domain		
PF_VPS33B	KSNFRALSKKMLIIPKTGEYDLRVPRDMAYIFSGAYIPLSCKLIEQVLERDGTGLEEVTRLNGHEFAVTGGTSVSEA	558
IP_VPS33B	KSNFRALSKKMLIIPKTGEYDLRVPRDMAYIFSGAYVPLSCKLIEQVLERDGTGLEEVTRLNGHEFAVTGGTSGTEA	558
DR_VPS33B	KSNFRALSKRIALVPKSGEYDLRVPRDMAYIFSGAYIPLSCKLIEQVLERDGTGLEEVTRMLNGQDFAVTGGSSSEA	558
HS_VPS33B	RSNFRALSKKMLIIPRVDEYDLKVPDMAYVFGGAYVPLSRIIEQVLERRSWQGLDEVVRLNCSDFAFDTMTK...ED	558
RN_VPS33B	RSNFRALSKKMLIIPRVDEYDLKVPDMAYVFGGAYVPLSRIIEQVLDERSWQGLDEVVRLNCSDFAFDTMAK...ED	558
Sec1 domain		
PF_VPS33B	RIKTDQRIILVFLGGCTFSEISALRFIGREKGYRFIVTTAITNSGRLLLEAMLEYCA	617
IP_VPS33B	RIKTDQRIILVFLGGCTYSEMSALRFIGREKGYRFIVTTAITNSGRLLLEAMLEYCA	617
DR_VPS33B	RNKSNGQRIILVFLGGCTYSEISALRFLGKERGCRFIVTTAITNSGRLLLEALLDKHV	617
HS_VPS33B	FASSESRLILVFLGGCTFSEISALRFLGREGYRFIFLTIAVTNSARLMEAMSEVFA	617
RN_VPS33B	FASSESRLILVFLGGCTFSEISALRFLGREGYRFIFLTIAVTNSARLMEAMSEVKS	617

Supplemental Figure 4. Multiple amino acid sequence alignment of VPS33B from *P. fulvidraco* and other species. Accession numbers as follows: *P. fulvidraco* (Pf), MH301094; *Ictalurus punctatus* (Ip), XP_017314277.1; *Danio rerio* (Dr), NP_001014370.1; *Rattus norvegicus* (Rn) NP_071622.1; *Homo sapiens*

(Hs), CAB93109. Arrows below the sequences represented conserved Sec1 domain.

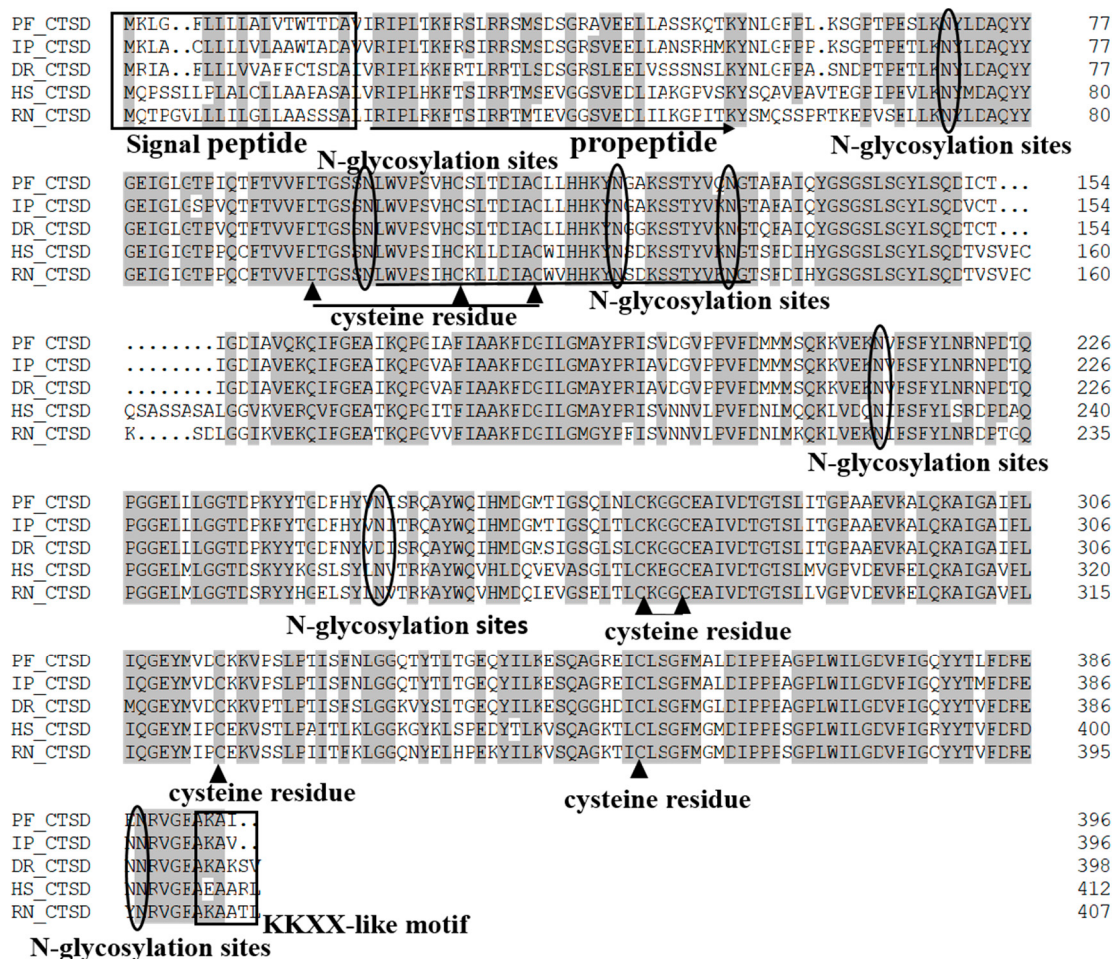
IP_VPS41	MSEVEEQQKKPSEESTDDSEEDSEEEFKLKYERLANGVTEILQTDAAASCLTVHDKFLALGTHFGKVFLLDIQGNITQHY	80
PF_VPS41	MSEVEEQQKKPSEESTDDSEEDSEEEFKLKYERLANGVTEILQTDAAASCLTVHDKFLALGTHFGKVFLLDIQGNITQHY	80
DR_VPS41	MAEVEEQGRKLSEESTDESEEDSEEEFKLKYERLANGVTEILQTDAAASCLTVHDKFLALGTHFGKVFLLDIQGNITQHY	80
HS_VPS41	...AEEQETGSLEESTDESEEDSEEEFKLKYERLANGVTEILQTDAAASCLTVHDKFLALGTHFGKVFLLDIQGNITQHY	77
RN_VPS41	MAEAEQETGSLEESTDESEEDSEEEFKLKYERLANGVTEILQTDAAASCLTVHDKFLALGTHFGKVFLLDIQGNITQHY	79
IP_VPS41	EISSVKINQISLDESGEFVGICSEDGKVCVFGLYTREGFHENFDCPIHVVVALHFCQFSKSNKQFVTGGNKLLIYERNWLN	160
PF_VPS41	EISSVKINQISLDESGEHMGICSEDGKVCVFGLYTREGFHENFDCPIHVVVALHFCQFSKSNKQFVTGGNKLLIYERNWLN	160
DR_VPS41	EISSVKINQISLDESDEGVGICSEDGKVCVFGLYTREGFHENFDCPIHVVVALHFCQFSKSNKQFVTGGNKLLIYERNWLN	160
HS_VPS41	IVSEVKINQISLDESGEHMGICSEDGKVCVFGLYSGEEFHETFDPCPIHIVVHEHVRSSCKQFVTGGNKLLIFERSWMN	157
RN_VPS41	IVSEVKINQISLDESGEHMGICSEDGKLCVFGLYSGEEFHETFDPCPIHIVVHEHVRSSCKQFVTGGNKLLIFERTWMN	159
IP_VPS41	RWKMVLHEGEGTITNKKWRANLIAWANNVGVKIIDISSKQRIINVLRDNSLRPDMYPCSLCWDKNTLLIIGWGTSVHI	240
PF_VPS41	NWMTVLHEGEGTITNKKWRANLIAWANNVGVKIIDISSKQRIINVLRDNSLRPDMYPCSLCWDKNTLLIIGWGTSVHI	240
DR_VPS41	RWMTVLHEGEGTITNKKWRANLIAWANNVGVKIIDISSKQRIINVLRDNTSLRPDMYPCSLCWDKNTLLIIGWGTSVHI	240
HS_VPS41	RWKSFLHEGEGTITNKKWRANLIAWANNVGVKIIDISSKQRIINVLRDNTSLRPDMYPCSLCWDKNTLLIIGWGTSVHI	237
RN_VPS41	RWKSFLHEGEGTITNKKWRANLIAWANNVGVKIIDISSKQRIINVLRDNTSLRPDMYPCSLCWDKNTLLIIGWGTSVHI	239
IP_VPS41	CVVKERDPEMRDLPSRIVEIVSAFETEFFISGLAPLADQLVTLIVVKNSEHMEEFRRSRPLDIICPLPESCEEISSD	320
PF_VPS41	CVVKERDPEMRDLPSRIVEIVSAFETEFFISGLAPLADQLVTLIVVKNSEHMEEFRRSRPLDIICPLPESCEEISSD	320
DR_VPS41	CAVVKERDPEMRDLPSRIVEIVSAFETEFFISGLAPLADQLVTLIVVKNSEHMEEFRRSRPLDIICPLPESCEEISSD	320
HS_VPS41	CSVKERHASEMRDLPSRIVEIVSAFETEFFISGLAPLADQLVTLIVVKNSEHMEEFRRSRPLDIICPLPESCEEISSD	317
RN_VPS41	CSVKERHASEMRDLPSRIVEIVSAFETEFFISGLAPLADQLVTLIVVKNSEHMEEFRRSRPLDIICPLPESCEEISSD	319
IP_VPS41	ALIVRHFGQENECRDYRLHSEGESLFYIISPKDIIIVAKERQDDHIDWLLDKKKYEEALMAAEISFKNIKRHHIVCKIGMA	400
PF_VPS41	ALIVRHFGQENECRDYRLHSEGESLFYIISPKDIIIVAKERQDDHIDWLLDKKKYEEALMAAEISFKNIKRHHIVCKIGMA	400
DR_VPS41	ALIVRHFGQENECRDYRLHSEGESLFYIISPKDIIIVAKERQDDHIDWLLDKKKYEEALMAAEISFKNIKRHHIVCKIGMA	400
HS_VPS41	ALIVRHFGQENECRDYRLHSEGESLFYIISPKDIIIVAKERQDDHIDWLLDKKKYEEALMAAEISFKNIKRHHIVCKIGMA	397
RN_VPS41	ALIVRHFGQENECRDYRLHSEGESLFYIISPKDIIIVAKERQDDHIDWLLDKKKYEEALMAAEISFKNIKRHHIVCKIGMA	399
IP_VPS41	YINHIVERGDIYAAARKCQKVLGNMMDLWNEVYRFTIGQLKAIISCYLPRGLRLRPAIYEMILHEFIKTDYDGFATLI	480
PF_VPS41	YINHIVERGDIYAAARKCQKVLGNMMDLWNEVYRFTIGQLKAIISCYLPRGLRLRPAIYEMILHEFIKTDYDGFATLI	480
DR_VPS41	YINHIVERGDIYAAARKCQKVLGNMMDLWNEVYRFTIGQLKAIISCYLPRGLRLRPAIYEMILHEFIKTDYDGFATLI	480
HS_VPS41	YINHIVERGDIYAAARKCQKVLGNMMDLWNEVYRFTIGQLKAIISCYLPRGLRLRPAIYEMILHEFIKTDYDGFATLI	477
RN_VPS41	YINHIVERGDIYAAARKCQKVLGNMMDLWNEVYRFTIGQLKAIISCYLPRGLRLRPAIYEMILHEFIKTDYDGFATLI	479
IP_VPS41	REWPGELYNNMTIVQAVDHIKKESTNSILLTTLAELYTYDQRYDRALEYLRLRHKIVYQLIHKHNLFSSIEDKIVLLM	560
PF_VPS41	REWPGELYNNMTIVQAVDHIKKESTNSILLTTLAELYTYDQRYDRALEYLRLRHKIVYQLIHKHNLFSSIEDKIVLLM	560
DR_VPS41	REWPGELYNNMTIVQAVDHIKKESTNSILLTTLAELYTYDQRYDRALEYLRLRHKIVYQLIHKHNLFSSIEDKIVLLM	560
HS_VPS41	REWPGELYNNMTIVQAVDHIKKESTNSILLTTLAELYTYDQRYDRALEYLRLRHKIVYQLIHKHNLFSSIEDKIVLLM	557
RN_VPS41	REWPGELYNNMTIVQAVDHIKKESTNSILLTTLAELYTYDQRYDRALEYLRLRHKIVYQLIHKHNLFSSIEDKIVLLM	559
IP_VPS41	DFEKEQAVDMLLDNEDKISVDFVVEELKDRPELLEFVYLHKLFRPDHKGQRYHEKQISLYAEYDRPNLLPFLRDSTHCP	640
PF_VPS41	DFEKEQAVDMLLDNEDKISVDFVVEELKDRPELLEFVYLHKLFRPDHKGQRYHEKQISLYAEYDRPNLLPFLRDSTHCP	640
DR_VPS41	DFEKEQAVDMLLDNEDKISVDFVVEELKDRPELLEFVYLHKLFRPDHKGQRYHEKQISLYAEYDRPNLLPFLRDSTHCP	640
HS_VPS41	DFEKEQAVDMLLDNEDKISVDFVVEELKDRPELLEFVYLHKLFRPDHKGQRYHEKQISLYAEYDRPNLLPFLRDSTHCP	637
RN_VPS41	DFEKEQAVDMLLDNEDKISVDFVVEELKDRPELLEFVYLHKLFRPDHKGQRYHEKQISLYAEYDRPNLLPFLRDSTHCP	639
Clathrin repeat domain		
IP_VPS41	EKALEICQQRHEVEETVFLSRMGNCRRAIQMIMEEIGVDRKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTH	720
PF_VPS41	EKALEICQQRHEVEETVFLSRMGNCRRAIQMIMEEIGVDRKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTH	720
DR_VPS41	EKALEICQQRHEVEETVFLSRMGNCRRAIQMIMEEIGVDRKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTH	720
HS_VPS41	EKALEICQQRHEVEETVFLSRMGNCRRAIQMIMEEIGVDRKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTH	717
RN_VPS41	EKALEICQQRHEVEETVFLSRMGNCRRAIQMIMEEIGVDRKAIEFAKEQDDAELWEDLISYSIDKPPFITGLLNNIGTH	719
Clathrin repeat domain		
IP_VPS41	VDFILLIHRKEGMEIPNLRSLVKILHDYNIQLILREGCKKIIIVADSLSLLQKMHRTQMRGVFVDEENICEACEVITLP	800
PF_VPS41	VDFILLIHRKEGMEIPNLRSLVKILHDYNIQLILREGCKKIIIVADSLSLLQKMHRTQMRGVFVDEENICEACEVITLP	800
DR_VPS41	VDFILLIHRKEGMEIPNLRSLVKILHDYNIQLILREGCKKIIIVADSLSLLQKMHRTQMRGVFVDEENICEACEVITLP	800
HS_VPS41	VDFILLIHRKEGMEIPNLRSLVKILHDYNIQLILREGCKKIIIVADSLSLLQKMHRTQMRGVFVDEENICEACEVITLP	797
RN_VPS41	MQ.....	721
RING-H2 finger motif		
IP_VPS41	SDTAQPFVSVVVEFCRHMEKHKCLFSESIIFGGQYCNICSAARRGPGSGIEMKK	854
PF_VPS41	ADTAQAFVSVVVEFCRHMEKHKCLFSESIIFGGQYCNICSAARRGPGSGIEMKK	854
DR_VPS41	SDTAQAFVSVVVEFCRHMEKHKCLFSESIIFGGQYCNICSAARRGPGSGIEMKK	854
HS_VPS41	SDAAKPFVSVVVEFCRHMEKHKCLFSESIIFGGQYCNICSAARRGPGSGIEMKK	851
RN_VPS41	RSFSAWSSIVGIG.....STRSAYICQA.....	745
RING-H2 domain		
Zn binding site		

Supplemental Figure 5. Multiple amino acid sequence alignment of VPS41 from *P. fulvidraco* and other species. Accession numbers as followed: *P. fulvidraco* (Pf), MH301095; *Ictalurus punctatus* (Ip), AHH39036.1; *Danio rerio* (Dr), XP_691671.2; *Rattus norvegicus* (Rn), NP_001100825; *Homo sapiens* (Hs), NP_055211.2. Arrows below the sequences represented the conserved domains: Clathrin repeat domain and RING-H2 domain. The RING-H2 domain were boxed; The Zn binding site was marked with the symbol (▲).



Supplemental Figure 6. Multiple amino acid sequence alignment of LAMP1 from *P. fulvidraco* and other species. Accession numbers as followed: *P. fulvidraco* (Pf), MH301096; *Ictalurus punctatus* (Ip), XP_017312814.1; *Danio rerio* (Dr), NP_001313461.1; *Rattus norvegicus* (Rn), NP_003556.1; *Homo sapiens* (Hs), NP003556.1. Arrows below the sequences represented conserved domains: luminal domain, one transmembrane helix domain and hinge region. The C-terminal cytoplasmic tail were boxed, and the cysteine residue was marked with the symbol (▲), and N-glycosylation was marked with the symbol (◆).

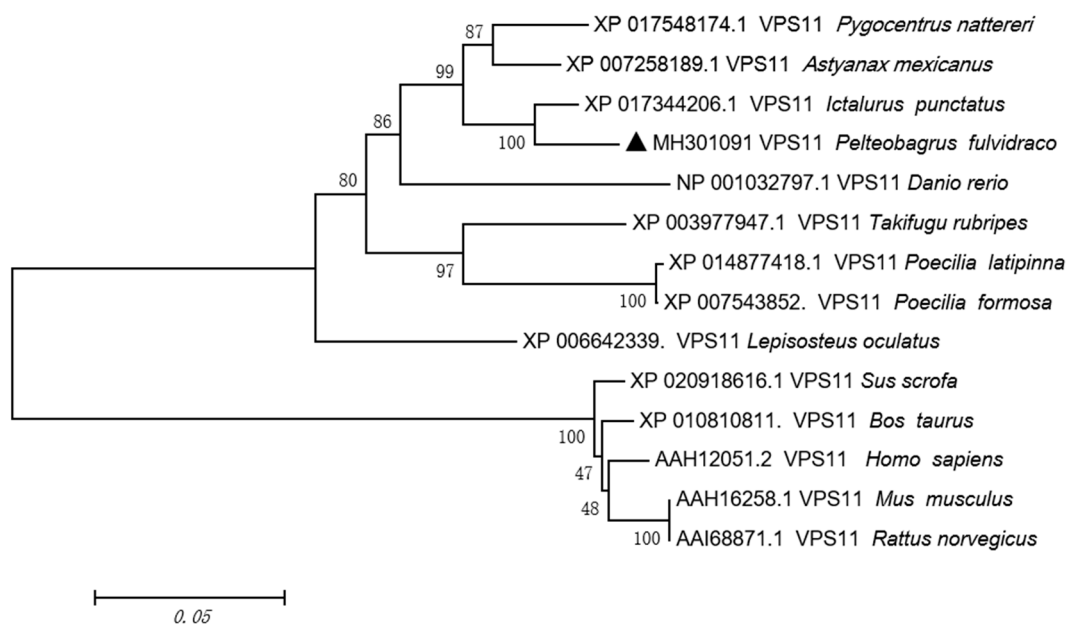
Supplemental Figure 7. Multiple amino acid sequence alignment of MCOLN1 from *P. fulvidraco* and other species. Accession numbers as follows: *P. fulvidraco* (Pf), MH301097; *Ictalurus punctatus* (Ip), XP017329106.1; *Danio rerio* (Dr), NP001299842.1; *Rattus norvegicus* (Rn), AAH61575.1; *Homo sapiens* (Hs), NP003891.1. Arrows below the sequences represented conserved domain: C-terminal cytoplasmic tails and channel pore. Six transmembrane domains were boxed, and lysosomal targeting signal was marked with circles.



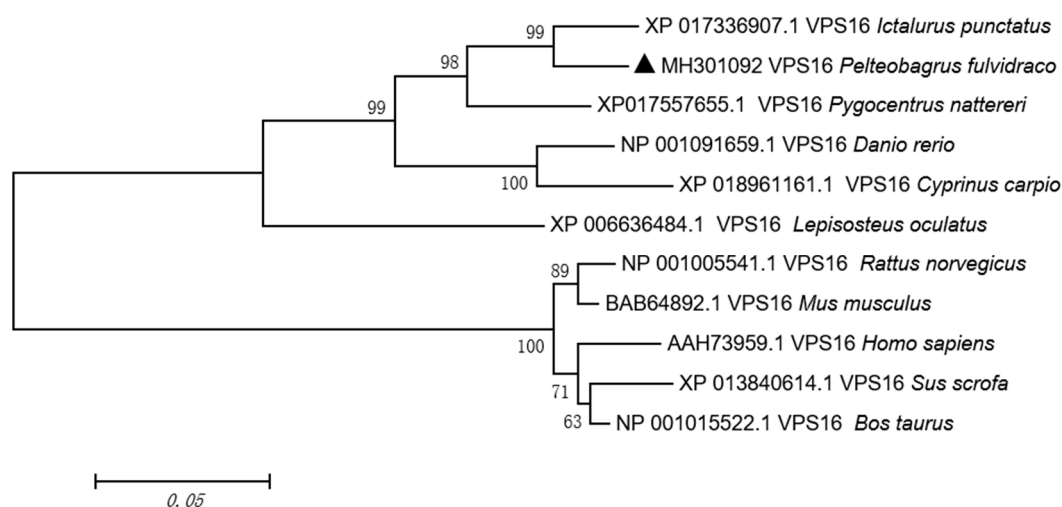
Supplemental Figure 8. Multiple amino acid sequence alignment of *cts1* from *P. fulvidraco* and other species. Accession numbers as follows: *P. fulvidraco* (Pf), MH301098; *Ictalurus punctatus* (Ip), NP_001244039.1; *Danio rerio* (Dr), AAI64814.1; *Rattus norvegicus* (Rn), NP_599161.2; *Homo sapiens* (Hs), CAG33228.1. Arrows below the sequences represented the conserved domain of the propeptide. Signal peptide and kxxx-like motif was boxed; N-glycosylation was circled, and cysteine residue site was marked with the symbol (▲).

PF_TFEB	NVSRVGMRCILIMFEGICCEEQ	21
IP_TFEB	NVSRVGMRCILIMFEGICCEEQ	21
DR_TFEB	NSTRIGIRICIMFICMCCEEQ	21
HS_TFEB	MTFSSGWEEFAAATNASRIGIRICIMFEGACCEEQ	35
RN_TFEB	MAQLACREWANFECFISVSEYACWCEFYIGCTIKSELIEYFMILSELICFEFESTANASRIGIRICIMFEGACCEEQ	80
CH		
PF_TFEB	FERCF....HLECMCCCVSG.....SPTEFZAINAEVHEIAEMCVFEVIVKCTHIENTDYHIRCSKCCVKEYIHSIF	91
IP_TFEB	FERCF....HLEHIGCFEEGF.....EPSSEZAINAEVHEIAEMCVFEVIVKCTHIENTDYHIRCSKCCVKEYISSTF	92
DR_TFEB	FERCCCCPVSMEYMGEMEGF.....FEETFAISAETHCEGEMCVFEVIVKCTHIENTDYHIRCSKCCVKEYISTTY	96
HS_TFEB	FERMCCC.AVMEYMCCECCCCCCCCCGGFEETFAINTFVHECSEFFVEGEVIVKCSYIENTTSYHICCSCHCKVREYISSTY	114
RN_TFEB	FERMCCC.AVMEYMCCECCCCCCCCCGGFEETFAINTFVHECSEFFVEGEVIVKCSYIENTTSYHICCSCHCKVREYISSTY	159
CH		
PF_TFEB	AFKCAVHPAAGIVHESSESMVCCCSAGAVCFIEFSECA...CLVTFETGNSAENSEMAMINISCSHEKEMEVEVIELIISMQ	168
IP_TFEB	AFKCAVSPAAGVHESSESMVCCCSAGAVCFIEFSECA...CLVTFETGNSAENSEMAMINISCSHEKEMEVEVIELIISMQ	169
DR_TFEB	AFKCAVHPVTSIVCESEFFEMVCACTGSPFENNHSFCMRT.ECINNSAGNSAENSEMAMINISSHENEMILLIINIISIQ	175
HS_TFEB	GKNEFAHISEFACGSEFF.....EPASGVRAGHVISSSAGNSAENSEMAMINISGNSFEERELICVINDIRID	182
RN_TFEB	GKNEFAHVSFACGSEFF.....EPASGVRAGHVISTAGNSAENSEMAMINISGNSFEERELICVINDIRID	227
MAPK		
PF_TFEB	SSYL.....FVVCMENTIEFISSSHILVYTG.FGMAGFAIGMTISNSCEANIHKKFEISIAEAFAMAFERCPFNENLIE	240
IP_TFEB	SSYLIIHNXGDMVCMENIEFI.FSHILVYTG.FGMAGHTIATISNSCEANIHKKFEISIAEAFAMAFERCPFNENLIE	247
DR_TFEB	SSYLIIQAYNDFVVCMENTIEFISSSHILVYTG.FGMSGFAIAMSNSCEANIAIKFEISIAEAFAMAFERCPFNENLIE	254
HS_TFEB	IVIG....YINEMCMENIEFISSSHINVSSEFCVTASIVGVTSSSCEADITCKFEITIAESFALAFERCPFNENLIE	258
RN_TFEB	SVIG....YINEMCMENIEFISSSHINVSSEFCVTASIVGVTSSSCEADITCKFEITIAESFALAFERCPFNENLIE	303
DNA binding region		
PF_TFEB	FRRRNINIRIPEIGTMIETNCLIVRWKKTIIIRASVYIKRMCKIMGRTEFEVESNFKFMEVVNKCIWIRICELEMCAQ	320
IP_TFEB	FRRRNINIRIPEIGTMIETNCLIVRWKKTIIIRASVYIKRMCKIMGRTEFEVESNFKFMEVVNKCIWIRICELEMCAQ	327
DR_TFEB	FRRRNINIRIPEIGTMIETNCLIVRWKKTIIIRASVYIKRMCKIMGRTEFEVENNFRFEMPNKCIWIRICELEMCAQ	334
HS_TFEB	FRRRNINIRIPEIGMIEFANCLIVRWKKTIIIRASVYIKRMCKIMGRTEFELENHRSFLEMNKNKIWIRICELEMCAQ	338
RN_TFEB	FRRRNINIRIPEIGMIEFANCLIVRWKKTIIIRASVYIKRMCKIMGRTEFELENHRSFLEMNKNKIWIRICELEMCAQ	383
basic helix-helix domain		
PF_TFEB	MHGLISNSESNGMNIETMNCVVKCENSELIEHCHREFEFCFIHSCGCCLEFCCIHECCIHFCVSCIEHCEFCIYSAVG	400
IP_TFEB	MHGLISTSFSGINNIEFCNCFVKCENSELIEHCHREFEFCFPHIHSCEFCFIHSCGCCLEFCCIHECCIHFCVSCIEHCEFCIYSAVG	407
DR_TFEB	IHGLISNSESNGITNHLHCNEFIKCESSEFENLCHCS.HIFERYECGFCEFFELFCHCHLH.....FCFELCYFAVG	406
HS_TFEB	VHGLITTSFSGNMMAELACCVVKCELFSEE.....GFGAEMIGAEVDFEELFELF.....FCFELFIFTCP	401
RN_TFEB	VHGLITTSFSGVNMMAELACCVVKCELFSEE.....NFGETIMIGSEVDFEELFELF.....FCFELFSAACP	446
leucine zipper domain		
PF_TFEB	ET..CHFIFSHLILICIGSIFGYPDGMCCIGLISSIGTAGSTMVHACK.NEMSW..MEEGISFEGTIFLISAMSEFASV	475
IP_TFEB	ET..CFNFSHLILICIGMAGYPDGMCCIGLISSIGTAGSTMVHACKKSIMAW..MEEAISFEGTIFLISAMSEFASV	483
DR_TFEB	SS..CHEFLACSLICIGGIFGYCDGLIGLIG..GG.....IACMCKKSELSFIIMEEALSEIIGGELISAMSEFASV	477
HS_TFEB	ESFFFHILFSHLSIFCGREIEGFF...GYFEELAFCHG...SFFFSLSK.KLIDIMILISILFIASLFIISTMSEFASK	474
RN_TFEB	CSFFFHILFSHLSIFGGGGIEGFA...GYFELIGTEHG...SFFFNLSK.KLIDIMILISILFIASLFIISTMSEFASK	519
basic helix-helix domain		
PF_TFEB	ISSRFSSESIIISLIL	491
IP_TFEB	ISSRFSSESIIISLIL	499
DR_TFEB	ISSRFSSESIIISLIL	493
HS_TFEB	ASSRFSSESMEEGIVL	490
RN_TFEB	ASSRFSSESMEEGIVL	535

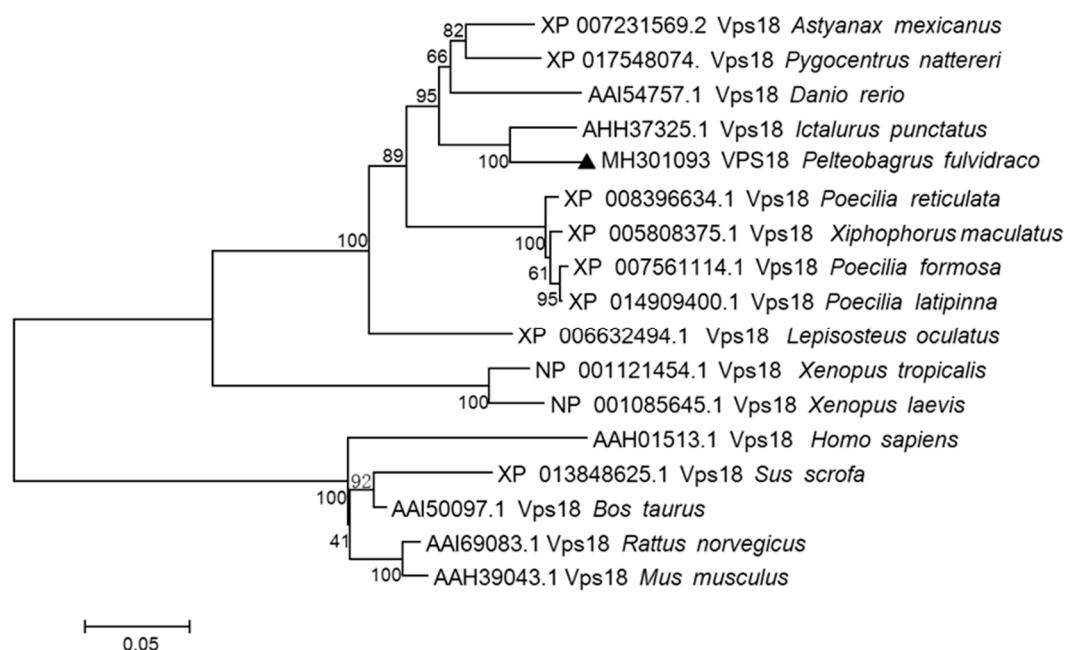
Supplemental Figure 9. Multiple amino acid sequence alignment of TFEB from *P. fulvidraco* and other species. Accession numbers as follows: *Pelteobagrus fulvidraco* (Pf), MH459004; *Ictalurus punctatus* (Ip), XP_017306305.1; *Danio rerio* (Dr), NP_001244121.1; *Rattus norvegicus* (Rn), NP_001020878.1; *Homo sapiens* (Hs), NP_001161299.2. Arrows below the sequences represented conserved domains: basic region helix-loop helix domain and the leucine zipper. DNA bind site was circled. Abbreviations: CH, charged helical domain; QB, glutamine-rich, basic domain; MAPK, consensus MAP kinase phosphorylation site.



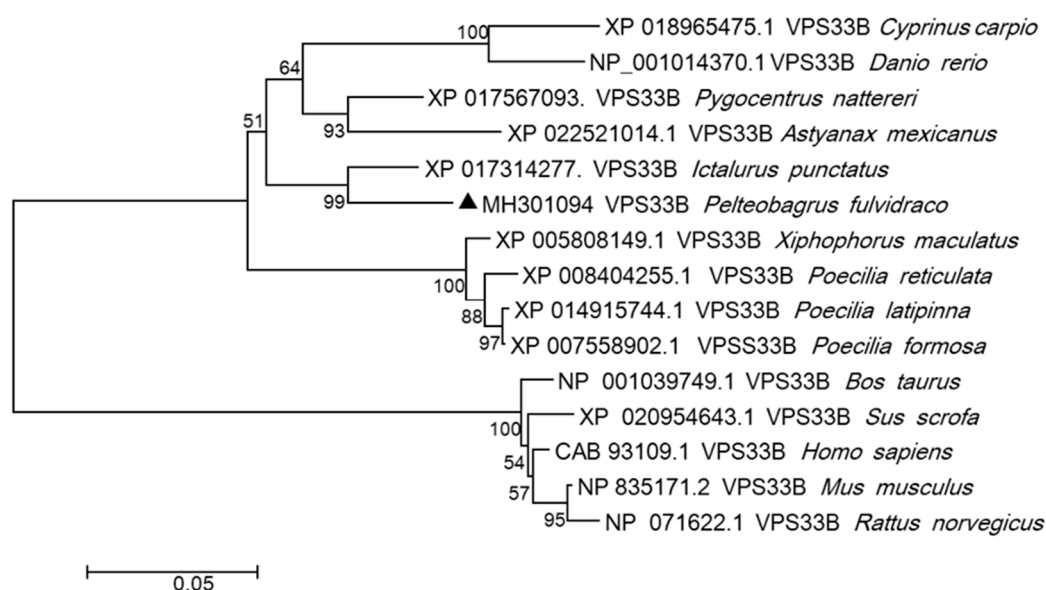
Supplemental Figure 10. Phylogenetic tree based on the protein sequences of VPS11 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0⁽³³⁾ based on the JTT+G model⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



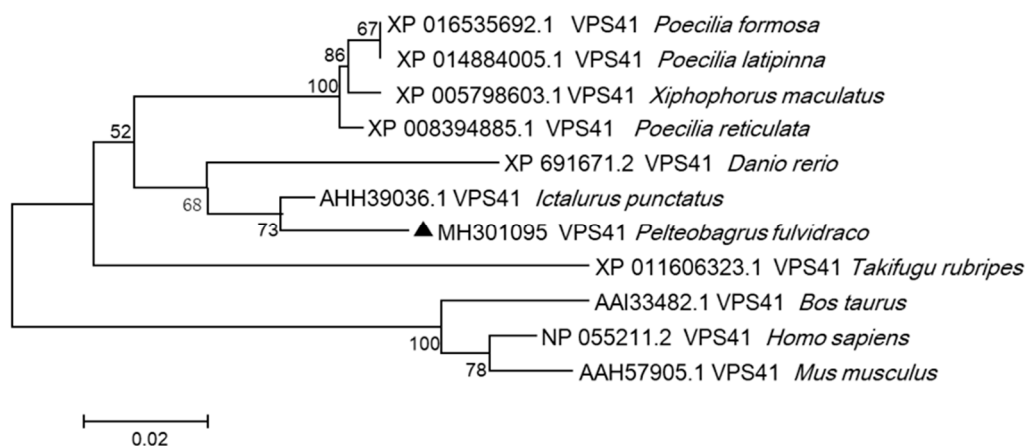
Supplemental Figure 11. Phylogenetic tree based on the protein sequences of VPS16 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0⁽³³⁾ based on the JTT+G model⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



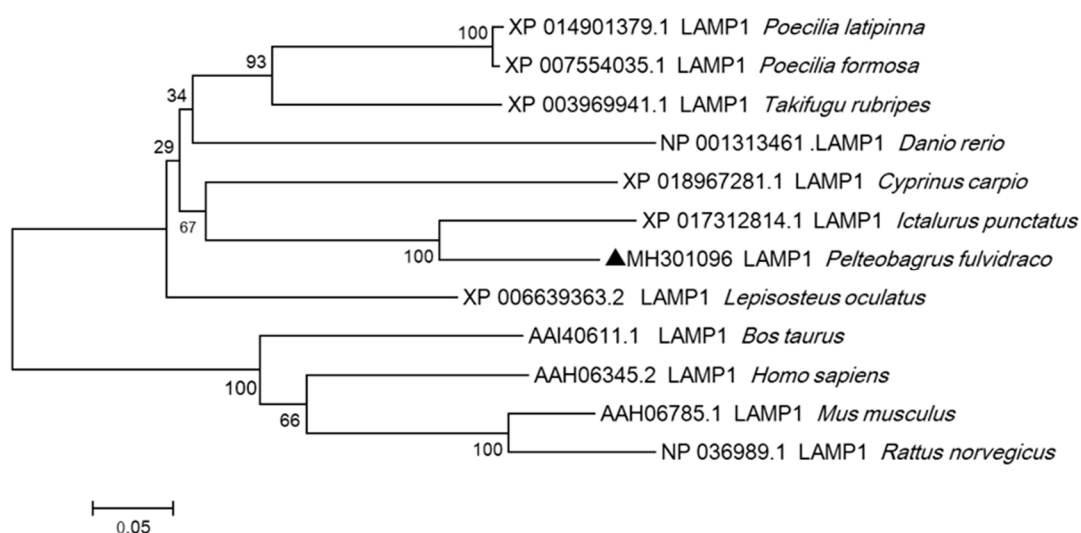
Supplemental Figure 12. Phylogenetic tree based on the protein sequences of VPS18 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0 ⁽³³⁾ based on the JTT+G model ⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



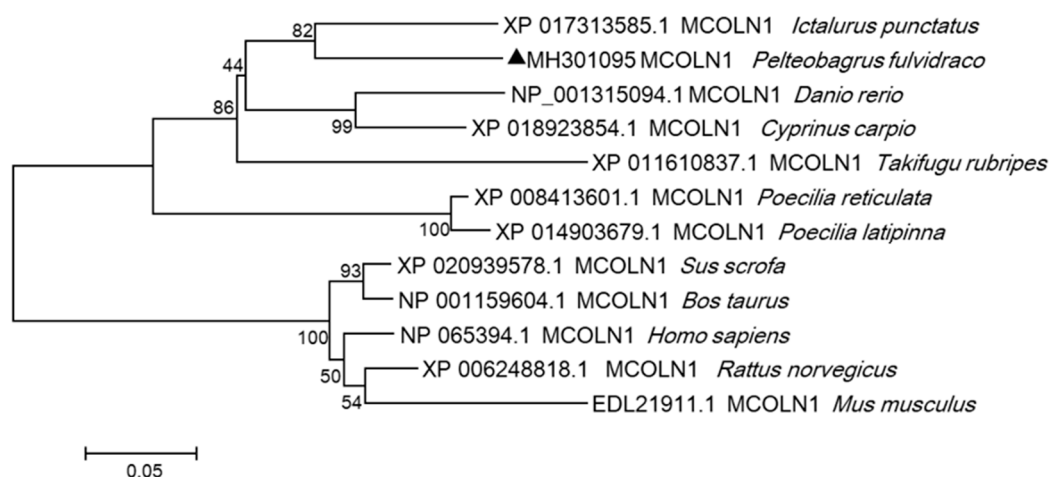
Supplemental Figure 13. Phylogenetic tree based on the protein sequences of VPS33B from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0 ⁽³³⁾ based on the JTT+G model ⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



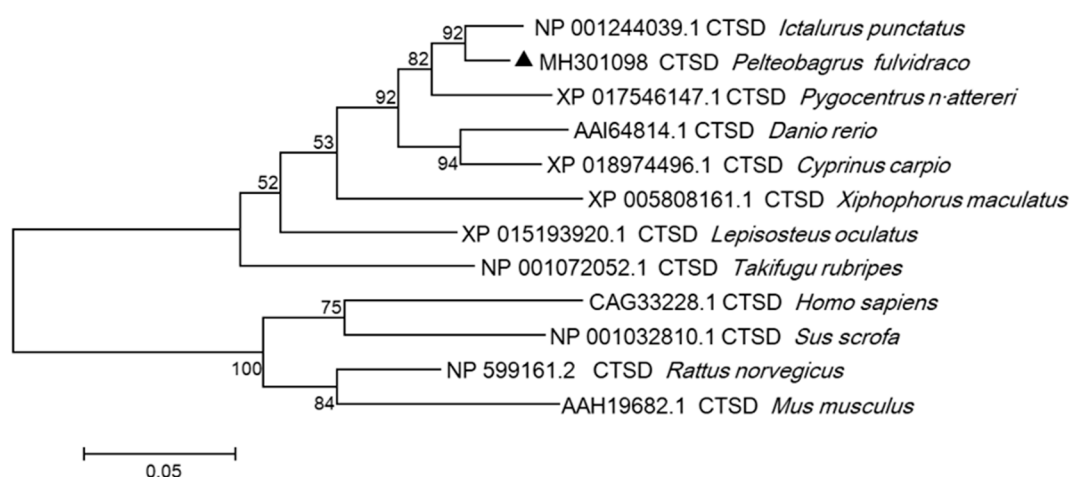
Supplemental Figure 14. Phylogenetic tree based on the protein sequences of VPS41 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0 ⁽³³⁾ based on the JTT+G model ⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



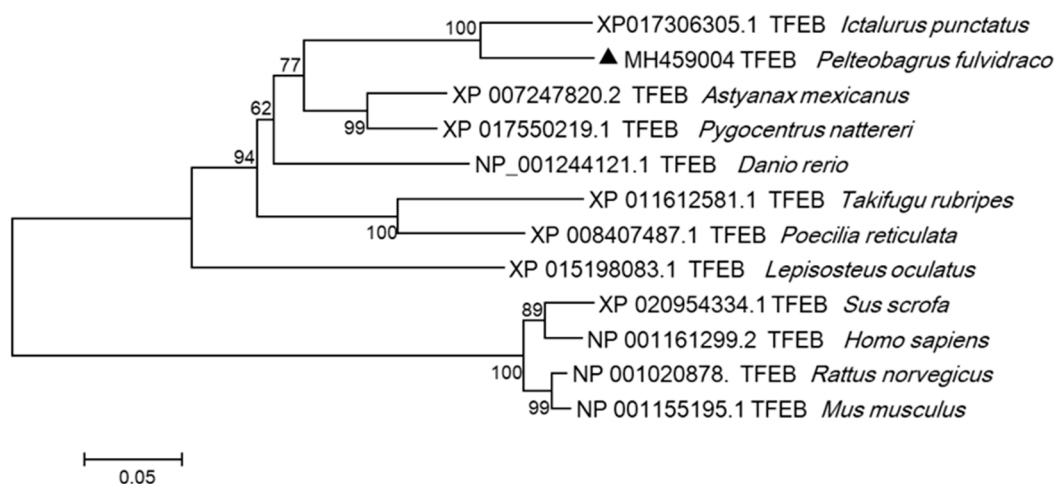
Supplemental Figure 15. Phylogenetic tree based on the protein sequences of LAMP1 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0 ⁽³³⁾ based on the JTT+G model ⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



Supplemental Figure 16. Phylogenetic tree based on the protein sequences of MCOLN1 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0⁽³³⁾ based on the JTT+G model⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



Supplemental Figure 17. Phylogenetic tree based on the protein sequences of CTSD1 from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0⁽³³⁾ based on the JTT+G model⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



Supplemental Figure 18. Phylogenetic tree based on the protein sequences of TFEB from *P. fulvidraco* and other vertebrate species using the neighbor-joining (NJ) method in MEGA 5.0⁽³³⁾ based on the JTT+G model⁽³⁴⁾. Branch support values represented a percentage of 1000 bootstrap replicates.



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