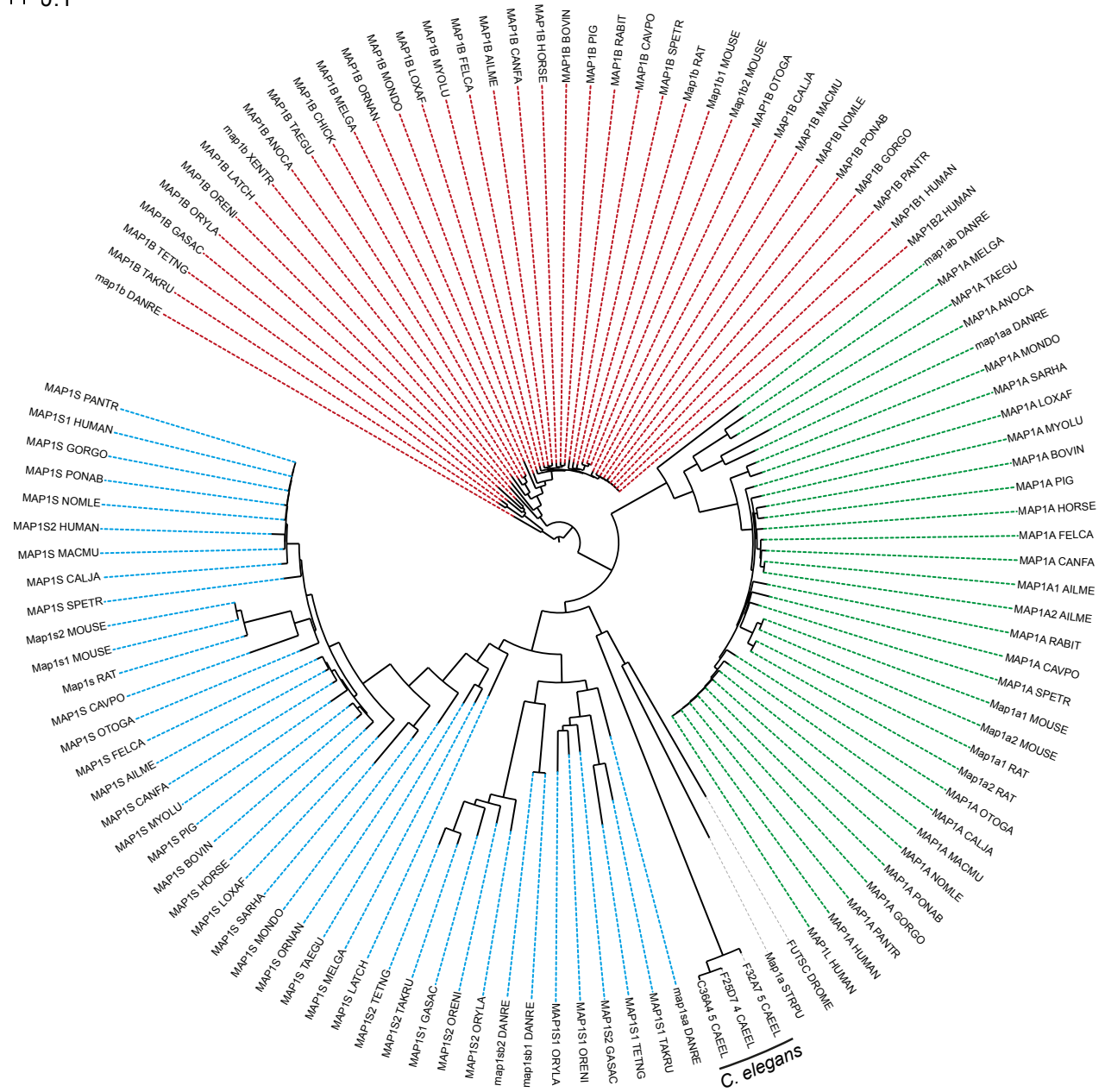


≈ 0.1 

MAPH-1.1 1 M.....
 MAP1A 1 METEAEPARPHGVAMETTPGLGLRSPGAPLAQNPAELLCEAGAAVAAARWDLQKHSLLIV

MAPH-1.1 2
 MAP1A 61 IGDIGTESQLRAVRAHLEQGILSWNIDLSSFDLNQQRLRFITRHLAHFSSEVKGQRTLCH

MAPH-1.1 2
 MAP1A 121 QSEILETIILVNPSADSISSSEVHLLSSSSAYKLLILSGQSLEPGGDLILQSGTYSYENF

MAPH-1.1 2PE.....
 MAP1A 181 AQVLHNPEISQLLSNRDPGIQAFITVSCLGEGDWSHLGLSSSQETHLRLNPEPTLPTMD

MAPH-1.1 4EYIMS.....SKACIYVLGGAANTAALFDFDGVYILD
 MAP1A 241 GVAEFSEYVSETVDVPSPFDLLEPPTSGGFLKLSKPCCYIFPGGRGDSALFAVNGFNILV

MAPH-1.1 36 GGFAEKNPGF...VAHV RDVSAVLLAAPTLGNLGTTSALLEQ.....
 MAP1A 301 DGGSDRKSCFWKLVRHLDRIDSVLLTHIGADNLPGINGLLQRKVAELEEEESQSGSSSYSD

MAPH-1.1 75GKPLPVFTNTKPFKTAKPGSSGEIAKAIQEANSKILSV.....APPLF....N
 MAP1A 361 WVKNLISPELGVVFFNVPEKLRLPDASRKAKRSIEEA CLTLQH LNR LGIQAEPLYRVVSN

MAPH-1.1 119 PKYPANIIYQSAAKGVLSLYIL..AGDVKDAEVITKALAG.....GNEAEVEK
 MAP1A 421 TIEPLTLFHKMGV.GRLDMYVLNPVKDSKEMQFLMQKWAGNSKAKTGIVLPNGKEAEISV

MAPH-1.1 165 AAAEHGTIGVLLWRPAMTDQS VVRVLISGTSSLSRIQQSLDKAAKSLPFLNVPTVKS KDA
 MAP1A 480 PYLTSIT.ALVVWL PANPTEKIVRVLFPGNAPQNKILEGLEK.LRHLDFLRYPVATQKDL

MAPH-1.1 225 LSD.IPA.....
 MAP1A 538 ASGAVPTNLKPSKIKQRADSKESLKATTKTAVSKLAKREEVVVEGAKEARSELAKE LAKT

MAPH-1.1 231PAVPRPVA.....
 MAP1A 598 EKKAKESSEKPEKPAKPERVKTESSEFALKA EKRLIKDKVGKHLKEKISKLEEKDKE

MAPH-1.1 239GKPSARPATTT.....
 MAP1A 658 KKEIKKERKELKKDEGRKEEKKDAKKEEK RKDTKPELKKISKPD LKPF TP EVRK TLYKAK

MAPH-1.1 250
 MAP1A 718 VPGRVKIDRSRAIRGEKELSSEPQTTPAQKGTVPLPTISGHRELVLSSPEDLTQDFEEMK

MAPH-1.1 250GTATRPTRPAVPA.....
 MAP1A 778 REERALLAEQRDTGLGDKPFPLDTAEEGPPSTAIQGTTPPSVPG LGQEEHV MKEKELVPEV

MAPH-1.1 263ASAPRALTSRA.....
 MAP1A 838 PEEQGSKDRGLDSGAETEEEEKDTWEEKKQREAE RLPDRTEAREESEPEVKEDVIEKAELE

MAPH-1.1 274
 MAP1A 898 EMEEVHPSDEEEEDATKAEGFYQKHMQEPLKVTPRSREAFGGRELGLQGAPEKETSLFL

MAPH-1.1 274PAG.....PSRPTTTRNAAPAPR
 MAP1A 958 SSLTTPAGATEHVS YIQDETIPGYSETEQTISDEEIHDEPEERPAPPRFHTSTYDLPGE

MAPH-1.1 292 TAVP.....SRATVLTk.....
 MAP1A 1018 GAGPFEASQPADSAVPATSGKVYGT PETELTYPTNIVAAPLAEEHVSSATSITECDKLS

MAPH-1.1 304TAPASK.....APTR
 MAP1A 1078 SFATSVAEDQSVASLTAPQTEETGKSSLLLDVTSTIPSSRTEATQGLDYVPSAGTISPTS

MAPH-1.1 314 APVPARSAPAPP.....RGA.....
 MAP1A 1138 SLEEDKGFKSPPCEDFSVTGESEKRGEEIIGKGLSGERAVEEEEEETANVEMSEKLCSEQY

MAPH-1.1 329PAKPAANTAKAEPTAQKKTVGKVQGTAPSKPAPAAPASAATSPA....
 MAP1A 1198 TPVFSAPGHALHPGEPALGEAEERCLSPDDSTVKMASPPSPGPPSATHTPFHQSPVFEES

MAPH-1.1 373PAPPE.....APRRDP.....
 MAP1A 1258 EPQDFQEADSWGDTKRTPGVGKEDAAETVKPGPEEGTLEKEEKVPPPPRSPOAQEAPVNI

MAPH-1.1 383NNVTI
 MAP1A 1318 DEGLTGCTIQLLPAQDKAIVFEIMEAGEPTGPILGAEALPGGLRTPQEPGKPKQDEVLR

MAPH-1.1 388 VLDDSLSPEDFNQGSAPMDIVVIP.....PTPEPPRHEVAQATH...PEESIIDAE
 MAP1A 1378 YPDRSLSPED....AESLSVLSVSPSDTANQEPTPKSPCGLTEQYLHKDRWPEVSPEDTQ

MAPH-1.1 436 DLA.....KAPLEVDVANLADVED.....EI
 MAP1A 1434 SLSLSEESPSKETSLDVSSKQLSPESLGTLOFGELNLGKEEMGHLMQAEDTSHHTAPMSV

MAPH-1.1 458 P.....PPVDAF.....
 MAP1A 1494 PEPHAATASPPTDGTTRYSAQTDITDDSLDRKSPASSFSHSTPSGNGKYLPGAITSPEH

MAPH-1.1 465KKPEPHPEPNVSG.....GSEEDKIPEPV.....
 MAP1A 1554 ILTPDSSFSSPESLPGPALEDIAIKWEDKVPGLKDRTSEQKKEPEPKDEVLLQKDKTLE

MAPH-1.1 490AFKKPD.....
 MAP1A 1614 HKEVVEPKDTAIYQKDEALHVKNEAVKQQDKALEQKGRDLEQKDTALEQKDKALEPKDKD

MAPH-1.1 496
 MAP1A 1674 LEEKDKALEQKDKIPEEKDKALEQKDTALEQKDKALEPKDKDLEQKDRVLEQKEKIPEEK

MAPH-1.1 496
 MAP1A 1734 DKALDQKVRVSEHKAPEDTVAEMKDRDLEQTDKAPEQKHQAQEQKDKVSEKKDQALEQKY

MAPH-1.1 496
 MAP1A 1794 WALGQKDEALEQNIQALEENHQTQEQESLVQEDKTRKPKMLEEKSPEKVKAMEEKKLEALL

MAPH-1.1 496
 MAP1A 1854 EKTALGLEESLVQEGRAREQEEKYWRGQDVVQEWQETSPTREEPAGEQKELAPAWEDTS

MAPH-1.1 496PVELD.....
 MAP1A 1914 PEQDNRYWRGREDVALEQDTYWRELS CERKVVFPHELDGQGARGPHYTEERESTFLDEGPD

MAPH-1.1 501DFDPLKPSHPE.....
 MAP1A 1974 DEQEVPLREHATRSPWASDFKDFQESSPOKGLEVERWLAESPVGLPPEEEDKLTRSPFEI

MAPH-1.1 512PSA
 MAP1A 2034 ISPPASPPPEMVQQRVPSAPGQESPIPDPKLMPHMKNEPTTPSWLADIPPWVPKDRPLPPA

MAPH-1.1 515 PVVPSDHIIIIATPDPELP.....DIVAAV.....
 MAP1A 2094 PLSPPAGPPTPAPESHTPAPFSWGTAIFYDSVVAAVQEGAAEELEGGPYSPLGKDYRKAEGE

MAPH-1.1 539
 MAP1A 2154 REEEGRAEAPDKSSHSSKVPEASKSHATTEPEQTEPEQREPTYPDERSFOYADIYEQMM

MAPH-1.1 539
 MAP1A 2214 LTGLGPACPTREPPLGAAGDWPPCLSTKEAAAGRNTSAEKELSSPISPKSLQSDTPTFSY

MAPH-1.1 539KGPNDGL.....
 MAP1A 2274 AALAGPTVPPRPPEPGPSMEPSLTTPPAVPPRAPILSKGPSPLNGNILSCSPDRRSPSPKE

MAPH-1.1 553VKLDDDELEK.....IAPGFEEPLI
 MAP1A 2334 SGRSHWDDSTSDSELEKGAEREQPEKEAQSPSPHPPIPMGSPTLWPETEAHVSPPLDSHLG

MAPH-1.1 572 PQAPRDD.....GTLAECSEEVSKLVEISMDTDNSAEVAAD..LAKAVGEVTQLSAD
 MAP1A 2394 PARPSLDLFPASAFGFSSLLQPAPPQLPSPAEPFRSAPCGSLAFSGDRALALAPGPPTTR....

MAPH-1.1 622 LQNLGLDEKTDDEYVRKLSNQMIEDATLP.....FTSALA
 MAP1A 2450TRHDEYLEVTKAPSL.DSSLPQLPSPSSPGAPLLSNLPRPASFALSEGSSSEA

MAPH-1.1 656 SSIVTSNGSETNGHGEOAHAAQNGGIDHQKEIPKHDL.....
 MAP1A 2502 TTPVISVAERFSPSLEAAEQESGELDPGMEPAAHSLWDLTPLSPAPPASLDLALAPAPS

MAPH-1.1 693MQSRSSVIENGAAVQYEKTD.....
 MAP1A 2562 LPGDMGDGILPCHLECEAAATEKPSPFQVPSEDCAANGPTETSPNPPGPAPAKAENEEAA

MAPH-1.1 713
 MAP1A 2622 ACPAWERGAWPEGAERSSRPDTLLSPEQPVCFAGGSGGPPSSASPEVEAGPQGCATEPRP

MAPH-1.1 713PALDD.....
 MAP1A 2682 HRGELSPSFLNPPLPPSIIDDRDLSTEEVRLVGRGGRRRVGGPGTTGGPCPVTDETPTSA

MAPH-1.1 718VLNACAQSESEKID.....ASHPDNLHMPA..
 MAP1A 2742 SDSGSSQSDSDVPPETEECPISITAEAAALDSDEGDFLPVDKAGGVSGTHHPRPGHDPPL

MAPH-1.1 742APGSAAPAKPVKF..
 MAP1A 2802 PQPDPRPSPRPDVCMDPEGLSSESGRVERLREKEKVQGRVGRRAPGKAKPASPARRLD

MAPH-1.1 755ARPYFDVVTVPARNKLETSVAADGL.....
 MAP1A 2862 LRGKRSPTPGKGPADRASRAPPRPRSTTSQVTPAEKDGHSPMSKGLVNGLKAGPMALSS

MAPH-1.1 781QEFISKVRSRNVILASKDISGEQ.....LQAILCG
 MAP1A 2922 KGSSGAPVYVDLAYIPNHCSGKTADLDFFRRVRASYVVSNGNDPANGEPRAVLDALEGG

MAPH-1.1 811 KQTWCDSAHPCNVIPTHSSPMLLDLFRQKNEEQFAANNLQFSIPVEKQRTTV.....SSDA
 MAP1A 2982 KAQWGENLQ.VTLIPTHDTEVTREWYQQTHEQ....QQQLNVLVLASSSTVVMQDESFPA

MAPH-1.1 866 GAIEYEELARVDLL
 MAP1A 3037 CKIEF.....