

Supplementary file 5. RIPK3 and MLKL protein alignment from species from rodent and afrotheria lineages.

Supplementary file 5.1. Rodent RIPK3 protein alignment. RIPK3 protein alignment from human and 5 rodent genomes. Stop codons are indicated by an asterisk (*) and grey boxes.

	10	20	30	40	50	60	70	80	90	100
H. sapiens	MSCVKLWPSGAP-PLVSI	EELENQELVGKGG	FTVFR	QHRK	WGYDVAVKIVNSKAISREVKAMASLDNEFVLRLEGVIEKVNWDQPKPALVTKFMEN					
M. musculus	.S.....T.S.V....R..	KKL.F.....V...H..T.NH.....K..W.....VN.R..N..L.L..T.DLQ..FVSGQ...R...								
R. norvegicus	..S....LN..SSIS..GS...	LGF.....A...R.TA.NL.....K.....VN.RH.N..L.L..T.NLE..YVYG...Q...								
O. degus	.NRR-.ISVS..-SLVSS	ENLKNPDEVSE.GF.TVLR	QYRKWDCAA	AKIMHSDAISKEVKTITSLNN--QY...	L.ETKSLQ.XGMSR.....QL...					
F. damarensis	-----	-----	-----	-----	-----	-----	N.PHRQY....L..A.NLQ.EGVSG....P.L..			
H. glaber	-----	-----	-----	-----	-----	-----	N.R.LY....L..T.NLQ.NGVSG....Q...			
	110	120	130	140	150	160	170	180	190	200
H. sapiens	GSLSGLLQSQCPRPWPLLCRL	LKEVVLGMFYLHQB	NVLLRDLKPSNVLLDPELHV	KLADFG	LSTFGGSGSGTG---SGEPGGT	LGYLAP	ELFVN			
M. musculus	..A...PE.....Q.....C..SLD.P.....I.....A.....S.SGSG.RDS...A..D...LFK..									
R. norvegicus	PS.....E.....C..SL.S.....L..A.....S.SG--RDS...A...LD.DG									
O. degus	..CRDW.G.LF..C..Q.....N..SL.S.*.....S...TN..A.V.....P.....CE--TQQ.RD..A...LADI									
F. damarensis	S.....RD..X...V...L.M...S...IL.S..R.....TK..A.....K.....CR--FQ.....A...LADIF									
H. glaber	RD.....V...Q.....S..NL.....TN..A.....M...L..A.YG--QG.S.A...LADIF									
	210	220	230	240	250	260	270	280	290	300
H. sapiens	RKASTASDVYS--FGILM	AVLAGREVELPTEPS	LVYEAVCN	RQNRPSLAELPQAGPETPGL	EGLKELMQLCWSSEPKDRPSF-QECLPKTDEVFQMVEN					
M. musculus	L...K.....V.....A..VDKT..IR.T..D..S..P.T..PGS.....K.....IH..G.QSEN.....D.E...N..YNL.KD									
R. norvegicus	---K.....V.V.T.....A.VVDKT..IRG.....R..P.T..PDS.....TH.....D.ES..NN.YIL.QD									
O. degus	K...K.....KI...I..L*	P.V-----TKK.IQALMT..LSS.....E..K...RS..H..G..APL-PRMPGNNQKGLLGAHG								
F. damarensis	K..TK.....L*.X...P.VVPQI..IR.T.AEKRIQ.P.T..PSS.....E.EN...RF..H..S..LP.FFK.QET.KKA.*R.HD									
H. glaber	K..TK.....Q.....T.VVPQT..IH.T.VEK.I..P.T..PCR.....K.EK.I.C..H..N...R.FPGE.SFHWQLE*---									
	310	320	330	340	350	360	370	380	390	400
H. sapiens	NMNAAVSTVKDFLSQLRSSNR	RFSIPESGQGGTEMDGFRRTIENQHS	RNDVMVSEWLNKLNLEEPPSSVPPK	CPSLTKRSRAQEEQV	PQAWTAGTSSDSM					
M. musculus	KVD...E..HY...H...G.NL.AR.PS.R...CP.E-----T...KM.DR.H...SGP..G.---PERQ..DTS.GP.TP.R...PV									
R. norvegicus	KVD...K..HY...Y...DTKL.AR..S.K...V.CP.E-----TI.Y.M.DR.H...SG...ERLT...E.RGK--ASFHGH.TP...TL									
O. degus	..VD...ILEHRICEP-.STVA	AAMAKIV.QHKTPDISCYFS*								
F. damarensis	K.SD.I.K.TK...EH.....L.A..PS.R.....GTT--GS.CTKIGS.L..S..C.R.KQF.T...ET.TGF.EER...K...QH.R...Y..									
H. glaber	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	410	420	430	440	450	460	470	480	490	500
H. sapiens	AQPPQTPTSTFRNQMPSTT	GTGTPSPGPRNQGAERQGMNWS	CRTPEPNVPTGRPLVNI	NCSGVQVGDNNYLTMQTT-ALP--TWGLAPSGKGRGLQ						
M. musculus	.GT..I..H.LP..GTT.G.VF.E..G.H.QR...DG.H.TP.YPW...M..P.ALVFN...E..I.NY.S.VAPFR.T.SSSAKYDQ.QF.R...W.									
R. norvegicus	.GT..I..H.LPS.GTT.R.AF.E..G.D.QR...DG.NSNP.YTWNA--M..LQSIVLN...E..I.QH.CMSV.FR..F--KKEP.QF.R...W-									
O. degus	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
F. damarensis	..TL....LP.Q..TGR.IV.....AQ...VRNWRNCSLTRKNLGLR	HAHTLTQPVAGEFFLVFP	PGEGEAPLSSSVGLQTSSFRL*							
H. glaber	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	510	520								
H. sapiens	HPPPVGSQEGPKDPEAWSRPQGWYNHSGK									
M. musculus	PFHK-----									
R. norvegicus	-----									
O. degus	-----									
F. damarensis	-----									
H. glaber	-----									

Supplementary file 5.2. Afrotheria RIPK3 protein alignment. RIPK3 protein alignment from human and 2 afrotheria genomes. Stop codons are indicated by an asterisk (*) and grey boxes.

	10	20	30	40	50	60	70	80	90	100
H. sapiens	-----	-----	-----	-----	-----	-----	MSCVKLWPSGAPAPLVSI	EELENQELVGKGG		
L. africana	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
T. manatus	MQGGTVEAPVT	CRRRKLLSPSVLRSDPGSETV	PRLEIAPLQRLPPTPPRSHPIRVSHDFQKPLTPSSLT.SS...S..GS...PNK...LKF..Q..							
	110	120	130	140	150	160	170	180	190	200
H. sapiens	FGTVFRAQHRKGYDVAVKIVNSKAISREVKAMASLDNEFVLRLEGVIEKVNWDQPKPALVTKFMEN	GSLSGLLQSQCPRPWP	LLCRL	LKEVVLGMF						
L. africana	-----	MAGWWTWL.QAQQL	LRTPGAQRE.DSPSSA.TGVGECVGS...*	T...E...H.R.G..L*L.R.L.PR...X---						
T. manatus	..A...H..A.....LL.....N.R.QY..L.L..T..LE.ENVCG.T..R.....E..H.....Q*Q.G...H.....C									
	210	220	230	240	250	260	270	280	290	300
H. sapiens	YLHDQNVFVLLHRDLKPSNVLLDPELHV	KLADFG	LSTFGGSGSGTGSGGE--GGTLGYLAPELFVN	NRKASTASDVYSFGILM-----WAVLA---GRE						
L. africana	..NL.....*G.....L..RA.....S.....*FFFVR.RVR*V..A.S.....LAD..QR..MDTSRP.PSC.STQTILLPSH.PLDHTQL									
T. manatus	..SL.....Q.....L..A.....R..A.FS..-----S.....LAD..QR.TMD.....S.....									
	310	320	330	340	350	360	370	380	390	400
H. sapiens	-----	VELPTEPS	LVYEAVCN	RQNRPSLAELPQAGPETPGL	EGLKELMQLCWSSEPKDRPSFQEC	LPKTDEVFQMVENNMNAAV				
L. africana	PFSMMKKGAYPQCLLFSSTPH	PAVVIQTW.AQV.M.EK...L.S...EPR.N.L...K...H..HK.....D.*S..S...LLEQDKRD...								

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T. manatus -----A.MVVQT..AQV...EK.E..X.S...EL..N...X---.K...H...H..R....HD.*S..S.A.LL.QDK.D...
               410      420      430      440      450      460      470      480      490      500
H. sapiens  STVKDFLSQLRSSNRRFSIPESGQGGTEMDFRRTIENQHSRNDVMVSEWLNKLNLEPPSSVPPKKCPSLTKRSRAQEEQVPPQAWTAGTSSDSMAQPPQT
L. africana .M..K...EH..R...LFSL.P.R.E...DPGGIMGSLC.W..ST...S..S.H...C..T.L...T...E-I.T.R...QDTKI..A...TT*L...
T. manatus  .M..K...EQ.G...L.LL.P.P.ER...DPG.IMGS.C.W..SI...S..N.H...C.GT..E.ST...EKI.T.GG..QDTRI..A...T...

               510      520      530      540      550      560      570      580      590      600
H. sapiens  PETSTFRNQMPSTSTGTTPSPGPRGNQGAER-----QGMNWSCRTPEPNVPTGRPLVNIYNCSEGVQVGDNNYLTMQQTALPTWGLAPSGKGRGLQH
L. africana .K..P..S.I.N.PQV.SQVL..KEIRDPI--LAFPQGEREVPLRLILLILLISLK.QLSIVLDG.Q...I.N...NILGRPT...Q.P..PSV...W.N
T. manatus  .KI.P..S.T.NS..VWV.D..TQ.....-----RHDK..PHWDS.L..IPAVYSPTWVARGADWKQLHEH.RETHP.HGGPSTSRQ.-----

               610      620      630
H. sapiens  PPPVGSQEGPKDPEAWSRPQGWYNHSGK---*
L. africana L.G.S.E...EE.....S..E.KNVNCCTF*
T. manatus  -----*

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Supplementary file 5.3. Rodent MLKL protein alignment. RIPK3 protein alignment from human and 3 rodent genomes. Stop codons are indicated by an asterisk (*) and grey boxes.

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               10      20      30      40      50      60      70      80      90      100
H. sapiens  -----MENLKHIIITLGVVHKKRCEEMKYCKKQCRRLGHRVLGLIKPLEMLQDQKRSVPSEKLTMTAMNRFKAALAEANGIEKFSNRSN
H. glaber   MPEIVDFNKFHPLLPG.DK.GQ..S...Q.L.QW..F...QN.SQ..RDH.S..LQV.QW....T.NLSP.ITAVLD.FQN-...K.MEKM...NTQTI
O. degus    -----
F. damarensis -----

               110      120      130      140      150      160      170      180      190      200
H. sapiens  ICRFLTASQDKILFKDVRNKLSDVWVKELSLLLQVEQRMVSPISQGSWAQEDQDQDAEDRR--AFQM--LRDNEKIEASLRRLLEINMKEIKE-TLRQ
H. glaber   FRKV.MPGSN....E..QM.R...EVFM.Q..ID.HVCI..S..K.EF.P...S..EK...FLL...SLKEVKSCLPRAR.ACLHARFSAWTLAWRRCC
O. degus    -----
F. damarensis -----MIHAYNPRTFVAEDGGLPQHTNTDV.HFSTSDSEGNHYNK

               210      220      230      240      250      260      270      280      290      300
H. sapiens  YL-----PP-KC-MQEIQQEIKKEIKKEQLSGSPWILLRNEVSTLYKGEYHRAVPAIKVFKKLQAGSTAIIVRQTFNKEIKTMKKFESPNILRFIFGICI
H. glaber   RAAATVVLIA.LGFVRR.P.GARDAPAPPHGGRALRKLPHVRLVLTEDESLPDMTSLVVMAMAVDISYISVYDH.ARFTHQIVR.HFHKE.SHMRFKDS
O. degus    KEIMETMKQYSLRPAYQTA.AK...M.E.E.L.FS*T.I.QSKF.KP.....P.....NQ..KR.RTA.EH.H.-SSAV..SD..KN.H....T
F. damarensis NMEATLRWLEVDLK*IKETLSRTNK..E.E.L.F..T...QS.F.K...A..X---I.N..*TKC.GK.KEH.XT.TSAL..SH..N.H.CEV..

               310      320      330      340      350      360      370      380      390      400
H. sapiens  DETVTTPQFSIVMEYCELGTLRELLDREKDLTLGKRMVLVLGAARGLYRL-----HHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQT
H. glaber   PNILXTFGIC..ERGSSPQFCMVMEYC.CRSLRDVLDEDRNLQL--..ILLALGAAGFYWL...GG.H.QRN.S.S...KS.GSE--GFELREAQ
O. degus    VL.GSS...M.A.F.KHS...VWVK...S..LCFL..G-NXL*GL-----YC.R..S..RN.SC.S...R..K..-LIEFEL.QT*
F. damarensis V..GSL...M.T...CS..K.V..K.R..S..LCVL.L...K...*-----CK.LP..RNSS..S...A..E..-TGFEMRETQ

               410      420      430      440      450      460      470      480      490      500
H. sapiens  SMSLGTTRKTRDKVSTAYLSPOLELVFYQYDVKSEIYSFGIVLWEIATGDIPEQGCNSEKIRKLVAVKRQOEPLGEDCPSELREIIDECAHDPSPVRP
H. glaber   TSISQKIK.TK-----I..R.NNP.HK..I.A.....R...E...KE.CQ..CE.QL.QMRSK..SPL.Q.V...Q.YE..AW.
O. degus    TFSISQK.QONKTXQTTAYFSPQKLE-NLLRE*.TIA...R...*..T..K...ES.A.EF*..FENP..GSKTQTHRVKAATLQL-----
F. damarensis TSISQK.KGIEQSNPTFYFSPQNLK-NLLCEK.TIAK.....K...*GWAFFK.ICQLVFNKPQ.DLLREDYP.QL*EVTDEFRASEPSGQPS

               510      520      530
H. sapiens  SVDEILKKLSTFSK-----*
H. glaber   .M.SKALPTERGMSPVFLSQL-----*
O. degus    -----*
F. damarensis GDEILE.TVDFCCVACKNLQRVLVDKRLKETQTGHL*

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Supplementary file 5.4. Afrotheria MLKL protein alignment. MLKL protein alignment from human and 2 afrotheria genomes. Stop codons are indicated by an asterisk (*) and grey boxes.

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               10      20      30      40      50      60      70      80      90      100
H. sapiens  MENLKHIIITLGVVHKKRCEEMKYCKKQCRRLGHRVLGLIKPLEMLQDQKRSVPSEKLTMTAMNRFKAALAEANGIEKFSNRSNCRFLTASQDKILFKD
T. manatus  .DE..Q..S...LVYQQ...WN..Q..KHIH..LQ.....QKNL..TQ..A.LLS.QTV...KDQ.K..N.K..VOK...GT...SA
C. asiatica .DT..Q...LVYNQ...C.RH..Q..N.IQH.L..Q...EKNL..VQ..D.LHH.QTI...KMR...K...LK..K.RD...SA

               110      120      130      140      150      160      170      180      190      200
H. sapiens  VNRKLSDVWVKELSLLLQVEQRMVSPISQGSWAQEDQDQDAEDRRAFMLRRDNEKIEASLRRLLEINMKEIKEITLRQYLPKCMQEIPEQEIKEIKKEQ
T. manatus  .KR.R..SE...V..Q..T-----FHQP.QK..R..E..MIFALFPAEK.N.DLL..*..S...-I.....-K.PINKL.....E...
C. asiatica L.KR.E..SQ..L.V..AD..KLILNTLHRG..QE...K..MG..*RVE.QMGENIEF.L.QLEKN---I.....Q.P.KQL.....

               210      220      230      240      250      260      270      280      290      300

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H. sapiens      LSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVRQTFNKEIKTMKKFESPNILRIFGICIDEVTPPQFSIVMEYCELGTLRELLDREKD
T. manatus      I.....Q..K..D.....KC..T..A..SNP..T..GT.....N..R.....D..V.....KEN..A..C..I..H..F.....K..QN
C. asiatica      .L.A...E..K..Y.....SKC..T.....NNS..-S..GL..S..KN..R.....D.....EK..TK..C..I..H..D.....K..QN

                310        320        330        340        350        360        370        380        390        400
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
H. sapiens      LTLGKRMVLVLGAARGLYRLHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTTRKTDVVKSTAYLSPQLEDVFYQYDVKSEIYSFGI
T. manatus      .EF.VCIF.SX.....E.....RN..S..TS...AE..H.....S.....I..RKVKERRAEK..N...V...G..KN.YHK..I..A.....
C. asiatica      .EF.V..IF.A.....AE.....RN..S..T...G..H.....T.....I..GQVKEKRAE..N...F...V..KN..HK...A.....

                410        420        430        440        450        460        470        480
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
H. sapiens      VLWEIATGDIPFQGCNSEKIRKLVAVKRQQEPLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK-----*
T. manatus      .....K..L..K..D..RR..E..AESDGY.....P..Q....G...YE..E..L..VRAFSGRSIFQLQARATHVPSHL*
C. asiatica      .....N.....G..R..QE..KSGGCP.....D.....Q..V..G..Q..YE..AE.....GYPA-----*

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