Supplementary File S1. List of 95 analyzed deuterostome genomes.

Echinoderms
Strongylocentrotus purpuratus

Hemichordates
Saccoglossus kowalevskii

Cephalochordates
Branchiostoma floridae

Urochordates
Ciona intestinalis
Ciona savignyi
Oikopleura dioica

Cyclostomes
Petromyzon marinus

Cartilaginous fishes
Callorhinchus milii
Leucoraja erinacea

Actinopterygii
Lepisosteus oculatus
Danio rerio
Dicentrarchus labrax
Gadus morhua
Gasterosteus aculeatus
Haplochromis burtoni
Labeotropheus fuelleborni
Maylandia zebra
Mchenga conophoros
Melanochromis auratus
Neolamprologus brichardi
Nothobranchius furzeri
Nothobranchius kuhntae
Oreochromis niloticus
Oryzias latipes
Pundamilia nyererei
Rhamphochromis esox
Salmo salar
Takifugu rubripes
Tetraodon nigroviridis
Xiphophorus maculatu

Coelacanths
Latimeria chalumnae

Amphibians

Xenopus (Silurana) tropicalis

Sauropsids
lepidosaurs
Anolis carolinensis
Python molurus

turtles
Chrysemys picta bellii
Pelodiscus sinensis

archosaurs
Alligator mississippiensis
Anas platyrhynchos
Gallus gallus
Geospiza fortis
Meleagris gallopavo
Melopsittacus undulatus
Taeniopygia guttata

Mammals
monotremes
Ornithorhynchus anatinus

marsupials
Macropus eugenii
Monodelphis domestica
Sarcophilus harrisii

Afrotheria
Echinops telfairi
Loxodonta africana
Procavia capensis
Trichechus manatus latirostris

Xenarthra
Choloepus hoffmanni
Dasypus novemcinctus

Boreoeutheria
-Laurasiatheria
Ailuropoda melanoleuca
Bos indicus
Bos taurus
Bubalus bubalis
Canis lupus
Canis lupus familiaris
Equus caballus
Erinaceus europaeus
Felis catus

Mustela putorius
Myotis lucifugus
Odocoileus virginianus
Ovis aries
Pteropus vampyrus
Sorex araneus
Sus scrofa
Tursiops truncatus
Vicugna pacos

-Euarchontoglires
Callithrix jacchus
Cavia porcellus
Cricetulus griseus
Daubentonia madagascariensis
Dipodomys ordii
Gorilla gorilla
Heterocephalus glaber
Homo sapiens
Ictidomys tridecemlineatus
Macaca fascicularis
Macaca mulatta
Microcebus murinus
Mus musculus
Nomascus leucogenys
Ochotona princeps
Oryctolagus cuniculus
Otolemur garnettii
Pan paniscus
Pan troglodytes
Pongo abelii
Rattus norvegicus
Saimiri boliviensis boliviensis
Tarsius syrichta
Tupaia belangeri

Supplementary file S2. Full length representatives of Metaviridae clades in Sauropsida

Chromovirus clade (in lepidosaurs)

>Sphenodon chromovirus-1 (AC154075)
orf1
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EPGPPPPPAQGAGPGPVRRSQRLEARRQGGACPTKAGAACWAVPVI*DWPLVRTLWKCSL
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Orf2
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HFIACKGLPSAYRTALLFIRHVVKLHGWPLEIISDRGSQFTSRFWKALFTTLRIQIKLTT
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GFHPQIAIPDLPATHVPAAGALIQHIHEAQSIARETLQKSRQSYKRQADKRRRAVKPLKP
GDYVWISRQHYPSQRPSRKLSDRYFGPYPVEKQVNEVTYRVTLPPKLKIHPTFHVSLLKR
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VSAPRLVRLFHTRHPEKPGPWRGFRRGACRGGTVNIRRLRRNHRQGGRPAGPPSPPREAR
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Size of LTRs: 897 bp, 99% ID

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 M S T A Q E L A E L V L A V R S L A M E
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 M R D V K T K Q A E L E N A L V A Q T T

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 V  V  A  Y  L  D  D  I  L  I  F  S  E  T  W  E  L  H  V  D
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V T L P P K L K I H P T F H V S L L K R
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A V P P E L T E Q P C E L L P D D S P E
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S Q A Y E V Q A I L D S K R R Y G K L H
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>Anolis Chromovirus (AAWZ01021304)
Orf1
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Orf2
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Gmr1 clade (in all reptiles)

>Anolis carolinensis Gmr1 (AAWZ02022550)
MATR
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Size of LTRs: 888 bp, 99% ID

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Size of LTRs: 422 bp, 99% ID

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>Sphenodon Gmr1 (AC154989)
orf1
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HLAEQVTALMTPALAAVTTSSHGGGEARGPQVRLTKMAPSDDPKAFLDIFERVTTASKWP
ED*WAVFLAPCLSGPA*AVYDWMEPRDVANFRKVKETILRGLDISEETYRKRFRGERYPP
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AVHLMENYEAFEGTASYELREGPRNYSREEKGPRGGEPRETRPVGPGRGHSREEGIPSGN
VRKEGDPRGPPGGSPRLLMPNPVPYPGPGGAREGTGAPATRVCYQCGRPGHFKRDCPLMD
CTFADGWLGEESGGRINL*

Orf2
ELIEDRLYRVTKEPERGEEVYQLLAPKEVQQELLRMAHEIPCVGHLGRERLVTRFYWPGI
RAAVQHYCASCPECQLTTKRKVAPAPLVPLPLVGVPFERMGIDIIGPIEQSSEGYRYILV
TVDYATRYPDAVALKSIKAPIIARELLKIFSRMGFPHTLLTDQGSNFMGRLMRQLCQLLR
IRQIRTSVYHPKTDGMVERFNQTLKAMLWKFVREEPKA*PSLLPALLFAY*EVPQASLGF
SPFELLYGHRPRGILDLVREGWEASAFSQHNVVLYVMRLRERLRQMWEWAERNGLEAQTK
QTAWFDKKA*PCQLQPGQRVLVLLPSTESKLLATWQGPYEVVKQVGDMDYTVWQPGRRPE
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FPHVFTSQPGCTPLTQHNIVKEPRKVAREAPWRHPRHLLQVMQDEVRAMLELGVIVESNS
PWRSQPVLVGKPDGSTRFCIDFRKVNAISRFDAYPMPRINLLLEHLGEAKYLPTMDLTKG
YWQIPLTPAAQEKTAFATPMALYQFVRMPFGLHGAPATFAPLMDKLLNHHGAYAAA**YIDD**
IIIFSNTWSEHLEHLTRIARALEETGLTANPKKCHLGVCPLGHLPGLPGGERADPPAVGQ
GQGGKGLDPPPATKKQVQQFFGLAGYYRQHVPHFATIAAPFSDTTKKGQPARVAWTPAVA
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QPYHFKIGHRAGKLHHNADFFSRQGDSAPQPIRPRRTLLNGGVCDEVRSGGPWSPGRSPD
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>Chrysemys Gmr1 (AC239223)
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ASVERNWLEWEKELKLRELEDRERQRQHEREEKERQHQREERQRQENERQRQHDLELARL
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PLLDPKAVALYRQLGEAEKGDYELFKKALLREFGLT**PEMYRERFRSQDKTPEISYLQLAV**
RMERYASKWAGGAQTKEDLIKLLVLEQLYERCPSDLRLWLVDRKPENPRHAGQLADEFVK
SRSGGGREEPQRNRPAAMQRESHPGTSQTGNMGNPLPRGMPSIRDNRPARGDPRDLS**C**YY
CGRRG**H**VRAQ**C**PKLKDRLSRPNPYRVNLVEASHTRGAGSLSTAQEREGPPASFSGGPDAP
DSKFSVYRVGAGLSLRSECLVP**LEVDGKKVYGYWDTGAEVTLARPEVVAPDRVVPNTFLT**
LTGVGGTPFKVPVARVHLKWGAKEGPKDVGVHHHLPTEVLMGGDLEDWPSSPQTALVVTR
SQSRRGALRPDLGKDVPPEAPNPSRVGREHPRTGRGVAGASDPADEREQVPIPSPAAEFQ
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PQKFRHKLLYLAHDIPLAGHQGIRRTRQRLLQNFYWPGVFTNVRQYCRSCDPCQRVGKAR
DKGKAALRPLPIIEEPFQKVAMDIVGPLSKTTRSGKKYILVVVDFATRYPEAVPLSSIEA
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FNGTLKMMLKTFMNQHPQDWDKYLPHLLFAYREVPQESTGFSPFELLYGRRVRGPLDLMR
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QVMVLIPVRKNKLQAAWE**GPF**KVVKQLNEVNYVVELSNRAHHHRVYHVNMMKPYYDRGNM
VLAVCGQWEGQGDDPLVDLFPGTRVGFPLEAIPLSDRLTPAQRAEIGGVLHLYQQLFSNQ
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VPKKDGSIRFCVDYRKLNAITVADAYPMPRPDELLDKLGGARYLTTMDLTKGYWQVPLDA
DARLKSAFVTPGLYEFLTLPFGLKGAPATFQHLVDQLLRGMESFAVA**YIDD**ICVFSQTWE
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QTKKQVQAFIGMAGYYRRFVPHFSAIAAPITELCKKGKPDKVVWTEECQEALRALKEALV
SGPVLANPDFDKPFMVFTDASDTGLGAVLMQEDEKGERHPIVYLSKKLLPREQNYAAIEK
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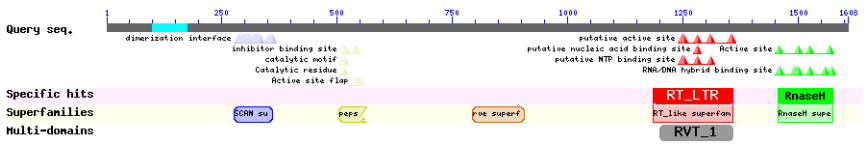

>Alligator Gmr1 (AKHW01010148)
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PKMVEEVLHLPEDYTTAEGEGETPKXERSGGPTFTHRPNTLAPHRRVETAQKEGHAGSYQ
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IIPAII**DTGC**SHLMVHSDLVPPHLGNFGTPVSMVCMHGAVYTYPRRKLKLSVLGWTEEIL
VGLTKPLPCLILLGLDWPHLGEVICQRMTDGHRAEEVRTHTLCFGDEEEGLNIDQIAEGG
NFCQGQRQEPLFHNIWKTQIERPEETTGTAPKPPWTLRCEVRTGLLYWVEDLEEGGERAQ

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TQMDSPQPRLVGEFCK*LQKAQEIAQRHLNQSQERQRQQYDVWAV*RELQVGDWVVVLLP
DSTHKLTAQW*GPFQVIQRTGPVNYEVLRTEPTRRRQIYHINLLRKWRQGEGWLVQQKEE
AEEGDMTTVRDLTGAPETPRVDDQLDQNRQTEVKALIAEFQDVFNEMPGEAKGVCHRITT
PAGRIIRDHWRRLPCHSWPVVWQEIDQMKEQGIIEES*SPWRSPIVVVPKPDGSIWVXVD
YRKLNEIARFDAFPMPQIDDMLKKIGQTRFISTLDLIKGYWKIPMAEEDKEKMAFRTPWG
LFQFKRMPFGLHGAAASFQWLMEHLLGPHQEYAAA**YIND**IIIFSPSWETHCEHLWKVLGS
FWRAGLMANPRKCALGK*ETQYLGFTVGQGTIKPITDKVAAIKQQSLPQTLKQLQSFLGF
ANYYRRFILNYSAKATLLTEELTRGCCNPISWNPEVLQAFD*LKETLSQHPVLYMPDFRT
TFFLQTDASAVALRVILFXKDQGAERPAAFASRKLKPAETPYSTIERECLAVRWGIELFQ
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>Alligator Gmr1 (AKHW01070087), 1438 aa
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LVQATLDSACAQLLVRSDLVGAQGQRGACPVRVACLHGETKLVECLRVRLRVMEHQGELL
VGVMLQLSCELLLGRDWVPVYDVLDRVRDTEVARRRIQDCEGWLGKTQENEESTDETNEL
DLNNFTSCLQFREAQAEDHEIRELQEHA*GPQDIPVPLPEGPPCFEVRNRLLYRVQGDRR
GETLGSQLVVPARFHQTIWRLAHASPTGGHLARDKTLARISQWFFWPGMGEEVARQCAAC
PECQKTRAERPAQAPLQPMPIIDTPFSRIALDVIGPLPRSSSGNQYILVIVDYATRYTET
IPLRAVTAPRIAEELIKWIARMGILQEILMDQGRNFMFGVLRVVCRTLQIKQLCTSVYHP
QTNGLVECLNGTIKQVL*CCIQGDPRKWDLLLPLVLFTLRDAPQDMMKFSPFELVLGHQP
RGLLQVLREGWEQETGPSQEPKTYQRELQQRIKVAQDLAHENTREAQACQKEKYDRHAXE
REFEPGQRVLVLLPTSTSKLLTQWQGPFEILR*VGPVDYEVHKPSHLREKQIYHINLLRE
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FREEPGWIQDSFHAINPPGAIVRERWRPIPHHLLEAIRREVDSMLKLGVIQLSRSPWRSP
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QTWAQHKRALRAILMELRRAGLMANPRKCALAQKETKYLGFLFGRGMIKPFADKVEIIRN
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QALCEEVVIHTPDFRKPFILQTDASETAVGAILTQEDRGSERPVVYASRKLLPVERRYST
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>Alligator Gmr1 (AKHW01055145)
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TKFSPFELVLGHRP*SLLQVLREEWEQGEGPSQEPKTYQ*AFQRRIRLAQDLAQENLREA
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LREKQVYHVNLLWEWREPEGWAAFSETDNKNLGPQGLGGEFEPPPGGTPVTIGEELSSAQ
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RLRVIRPSRSPWRSPLVPVRKPDGSLRLRVDYRRLNAMAVFDAFPMPHVAELIERIGDSR
YISTLDLAKGYWQIPVAKTDWLKTAFGTPWGLYEFIRMPFGLHGAAAMFQCLMDQILAPH
AEYTAA**YIDD**IIIYTRTWEQHKSTLRAILTELRRAGLTANPQKCALAQKETKYLGFLVGR
GMIKPLTDKXETIXNFXAPQGCRQLRSFLGLTNYYRRFVPHFAELAAPLSEALKGWKTGA
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ITRWALALQPYKFRVIHRSGKANKV**ADFLSR**CGDGDQIEDLGSRGKGQPKPAGTTRMGNK
EAPQGILRGGVMSQGRQG*

Barthez clade (in turtles and crocodiles)

>Chrysemys Barthez gag/pol (AHGY01367317)
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KDCLDALNHTFGSVEGPEDSYCKFLNSQQQIGEKISAYIQRLERLLQRAVMRGAVTAEQV
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PAGTTPLQTASVLMVSTTEKLAQQVQVLTERIAKLQSTIDRAKTSGNKEPLTVAIKKSAF
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SQWFSVLDLRSEYYQIPLGEKNKKKTAFICPLGFYQFKRMPQEISGAPATFQRLMKKVVE
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FRNYLYGAQFQV*TDNNPLTYVLTSAKLNATGQKWVAALASYNFSIQYQSGKSNVN**ADAL**
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>Chrysemys Barthez (AHGY01045193)
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AKLGATGQRWVAALASYDFIIQYRSGRSNVD**ADALSR**RPQAPGVAVIPTDGVRAI
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>Alligator Barthez (AKHW01075081),(stop codons repaired)
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pol
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PG*

>Alligator Barthez (AKHW01033193)
Gag
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ERVLQQLVAQGGLTQEMASKAHLQQPRVGMLYDEQLVGELNLTGRRENPPTFGQLLREIR
EAESLQAVKASIKAVTPAPARGLAVAPCPP*ALVVEMLKVPDFDNDAPQPLVVLHQQAQV
TRGNQPRASQVPPAIR*QWPHQPEEREKFCYRCGEDGHFKRQCTSQGNPPLVWQRLQATR

KQW*

pol
MPHSH*LCCTSKPR
*HGEINPGPPKSHRLSGNNGLTSLRKERNFVTGAGKTDISSASVQVRETRPWYGSDCRQQ
GNSGETRVKSRPKSQLPPGSDSSGIPAWFPPGLVGPRAEVPVVIEGWKCIAVL**DSGS**QVT
IIFQSFFDKFLKQLPLQSLTGLGLCGLSQAVYPYSGYVTAQLEFPKEVAGVCKSVAVTVL
VCPDPKWMRGANIIVRTNSSLF*VLTRHCQQKAGKQFLTALPMHALCAGAYQQIETSASP
ETDVRLGALYYAGKTPEKVPAQGRQFLFTAPKRIARTHHKKLAVVEPPKNSGPLRQMLVP
SGVVDIGWQASSSVTVLVVNPTGKDITVKPGQCVAELVEAEVAVSPTQSSQTQVVDPAKF
NFGSSPVPAAWKTRLQEKLSARGNVFSVHEWDVGLAKGVEHSIRLQDTRPFWEHSR*IAL
SEMEDVRQHLQELLDHGIISETRSLYASPTVVMRKKSGKIRMCIDYQTLNSRTTVDQYTV
CQEQDALDCLLGSQWFSVLDLRSSYYQILLAQEDKEKTAFICPLGFYQFEWMPQGISSAP
ATFQRLMEKVVGDMNMTQVLV**YLDD**LIFRKTLEEHEERLLKVLDRLQAAGLKLALDKWQF
CQMSVKYVGHIVSQEGVRTDPDKINAMATWPRPRNFQELKRFFGFAGYYRRFVQNYAKLA
KPLNDLTRGYQVRRSQIRSKGALSKATVGRPLGLQDPLESFGL*WDENCEQAFRALIWSL
TCAPVLVCADPQQPFVLHTDATLEGLGAVLYQEHRGKLKPVAFVSGGLVDSETQYPVHKL
EFLVLKWAVTDKFKDYLYGTQFEVWTDNNPLTYVLTSAKLDATGHRWVAALADYRFSLRY
RAGKKNIE**ADALSQ**QPYKQEREIVTVDEVQSICGLKERKTSEAESLPDCAAEVLGLPPDS
VPQATVGYVTLDQSPLPRLNAMGWRQAQEADPDIKEILEKKKKGDLSKEFKPKTLGGQHL
LCEWPRLRVVEGVLY*MVTAPDVGTHKQLVLPQEYQTLAMRALHDDLGHLGVKRMLSLVR
D*FYWPGMARDVQKKCETCARCVQRKTLPTRTAYLNTISSSKPLDPVCIDFLTIETDHKN
ISNVLIVTDHFTRYAQAYPTRDQRAITVAKVLWEKHFVVYGFPEWIHSDQERDFESHLLR
KIFQMAGIWKSQTTPYHPQGDPQLERFNRTLLNMLGTLRNEQKDRWSQHLAFLVHVYNAT
RNDATGASPYSLMFGWEPRLPIDLPGESGKGVKGRGRLSCRNCRGAAACCPETLGAQRQT
PVPGSIHRPRAGTQTVPLPEIPHQGQCTRDPQNTVCK*

Cigr2 clade (only in crocodiles)

>Alligator Cigr2 (AKHW01064915) (stop codons repaired)
PFLEGLSREKVVSQAGKLRQEVEKGPSTADTTRDPQEDLVVIKSAG
LGYYLEGKLGRVPCQFLL**DSGA**QVSLVHHQVWAQATTRIQSGLRPCSLVVKAANGKTLPI
LGEWGTSIYFQDLWLPCTFLVLEGARQDAFLGIDLVEQFQVTINFADCSFSLLGQCFPLY
ITDSQNEVCEVAVEESWIVPPRSEMMIMGRLKGWCHKDEEGLFEPKPNKELGLLVGTAMV
KSHWGEIPVCIANMSAEPQVAYQGTVIGTFETGIAVLQGDPVTQWSAAIRALSVDKNYHR
GEPDENLQWTAGKLTCEFKLNHHGLEPEQEEAVQEVLPEYASIFSLRDHDLGRTGLTKRW
IDMGSARPIKQGPRRVPIYFQQEFDQQLQEMKERGYQALCQPMSCPRGACKEERWRHAGL
CGLPETERCYC*GCLPQIDDTLNLLARARWFSTFDLASWYWQVKVHLEDRAKTAFYTKKG
LFEFNIMPFGLCNAPGTFQTLMDIILADLQGTSCLV**YLDD**IIIIGQTFQKHLQKLKAVLE
RLREANLKIKPTKYQLFCREVNFMGHAISTEGVGPDPGKAETIKTWPVPQNVKELCSFLG
QASYYRRFVAGFATIASPLHKLSDKAKFIWTRECQDAFQELKQRLMSSPVLAYPGPQLPF
VMDAHASDAGIGAVSSQVEEGEERVIAYASQTLNKAECQYVSTRKELLSIVALTKHFRHF
LLGRHFTLRTDHSSLQYLHNFQQPEGQLARWLEWLVEFNYHILHCPGQQHQN**ADALSR**RP
HLVDSRLEGEAVGIQTLSIAEVAKSEAQEQPEVSNYQVGHHPKGQPWNANVLFCGPITME
GDPGAATVALQPLPTTGTAKSEPAPDVREDWWEKQQKDADIKQLTGWKEHESKEFPEEGQ
YHPYLKQYQAVWPELSIRQGVRVRKLPRSAQGPECTQLVVPEQEILTILQDLHDSNTRGH
LGIEKVSCKVQVWYFWLGWRQSVVDWCRSCEMCGMCKGARSNTRVPVVSTQARRPLEKIA
MDILGPLPTIPCGNKYVLVVADYFSKRVEAYPLSDQEAQTVAKIFIEKFVRYHDTPQSLH
ANQGRNFESQLFNHICDLLEINNNCTTPYHPQRAIWHTN*

Mag clade

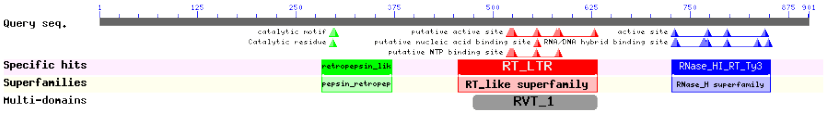
a) Mag/Jule subclade (in tuatara, turtles and crocodiles)

>Chrysemy mag (AC239519)
MATLTGTLEPFDENIGQWHVYTERFEL
FVIANDITEAKKVPVFLSVVGAKTYSLLRSLLHPVKPETKSYSDIVEILGSHFSPKPLVI
AERYRVHKRDQKEDETLVQFVATLRKLAEHCEFKEMLNDALRDRLVCDLYSEAIWKRLLT
KAQLTLQKAVDIAVSMELATKKAQYIGASPRVHKVSQEPTHKTVGSQE**C**YR**C**GKPG**H**QAS
E**C**WCKDLVCRHCGKKGHIECACKQKKKRSVVWPTKRGILHTLEQTQDDQGDTSSQEEVPL
HILSLAVGSHEYWVTPLLDGKPIRMEL**DTGA**AVSLVSETVYKEKLQHLPLKATKTVLKTY
KGEAVPMLGTIDVKVELNGQAAKLPLFVVRGNCPALMGRSWLGKIQLNWAEVHRMTKEET
GLTTILRKHAAVFGEDLGSMKGITVTLNIKPNSPPKYLKARTVPYAIRPKVEADLERLVT

NGVLIPVTHSPWATPIVPIVKKEGSLRICGDFKVTVNPVLCAEQYPFPCIDDLFAGLAGG
QKFCKLDLSQAYLQMHVYEKSQELLTIVTRKGLYQYCRLPFGITSAPALFQRAMDQILCG
LSGVQC**YLDD**ILVTERNEEDHLKNLEATLQRLEEYGLRVLKDKCEFFQPSVEYLGNIIDA
TGLHKAPAKVKAIVEAPPSRNVSQLRSFLGLLNYYGKFISQLATLLKPLHKLLGQNKAWK
CTEACDVAFNKAKDALLNSEVLTHFDPSLPLQLACDASPYGVGAVMSHIMPSGEERPIAF
ASRPLSKAETNYAQIEREALGIIFGIRKFHQYLFGWKFTLLTDHRPLTSIFGPYTGIPPL
TASRMQCWALLLSAHTYEIKYRKSTLHGN**ADDLSR**LPLPVKHQDSAQKEIFYFEQVENTP
IAATQIKKATRVDPVLSQVMDLVMHGKSRHTSPVSPDLVTYMSRRTELSIQSGCLLWGRR
VIIPPPLRSQMLEQLHSSHSGIVRMKEIARSYFWWPRLDSAIEEKAKACMSCQGVRNASQ
WAPLHPWDWPENPWKRIHIDFAGPLEGSMFLVVVDAHSKWPEVSIMQSTTAESTIQKLRR
LFSRFGLPEQLLSDNGPQFVSQGFQNFMKANGIHHITSAPYHPSTNGLAERFVQTMKQAL
KSARGQHSHSKLDTFLLSYRKTPHAMTKASPAFLMMGRQLDTCFDLLKPSEPRQIVQRQQ
QYQVIRRAPRAKDRTFSLGQPVLAQNYTSGAKWVPAMIITQTGPVSYTVRTAENLTWWQH
VDQLLPGQDTSSVELSDFTSSGETPNQESPVPDCSPLLLPAVEIPLCLARADTTSSPVRA
ANPEPIVRPAPMVLLGATPPEFRCNPPRDRRPPQWLNL*

>Alligator mag (AKHW01014103)
MGHIEEFDVSQLASWDSYAEKVFYYLGANKVENPAQKHVILLTVCGAKTLAIVCSLPAPA
LPNTKSYAELIALLKAHFCPRPSVTLQRFNFFKQTQKANEGIADYLTDFHRLAEFCEFGD
LLDGLLHNCLICGVQDKAIQHCLLSEPNLTLATTQEKAFAAEAASHNVREIHQAFSSNVH
LLQKDQEPDHHQQIQQIIPSPTSPHKPINPQTCLSCGGQHRQRECRFRKAECHACKKKGH
INRVCHLKASSRRQKDCSKCIHSQSTHRLESSPKREVQKLYLIQNVGVVETQGSEMIATV
VINGKKCKLEE**DSGL**EVSLIDENTFCQLLWHPLSKLLKPECRLSDYNGQSMETLGSCSVD
VQYGSVRQRLPLIVIKGSRKSLLGRNWFSPLGISIQGVHSLCTESLERLAREFPQVFSNV
LGTYSGPPVMFQMDPAIAPIFMKSRNIPLALRPKIDAELGLLITQGVVEPIIHTSWATPI
VPVLKPKGSICICGDYKYTVNKALKQDPHPVPTIKQLLSVLVGGKVFAKLDLAQAYQRLI
VDDKAAEAQTIITHQGAFGVRCLQFGISVAPGIFQWFMEKMLAGIPRVVP**YFDD**VLIMGP
SREKLTERLREVLQRFDKAGVRVKREKCQLGVSSINLLGYQIDDSGIHPFEDKVKAIHDV
PIPKCNQDLQEFLGRLNFYHIFLKDKATIAEPLHHLLDKGAQWKWTCQHNEAFQGFKKLP
TSDSVLVHYGKQKPLSITCNASPFGVGTVLSHTLLDGTDTPVAFYSRTMTSTERNYAQID
KEALAIIAGVKKIHNYVYGHKFEIRIDHKPLLRIFTTDKPTPILSPCMQHWSIMLNAYDY
ILMYKPGKTIAN**ADALSR**LPLQIPDCTTPLPAEVLMLESMPEAPLQDDQIARITEKDSIL
ARVLNWVWRGSPADKLAEEFRPFSSCQHELSAHKGCFLWGNRAIIPEAGHQIILTTLHAA
HPGIVRMKSLVRSYVWWPGMDSDIERVVRERSTCQATHHNPTTAPVFPWEMQRNPLSRIY
IDFAGPFQGKNFLIVVDSYSKWLEVITVSTLTSTATITALCQLFATHGMPDTIVSDNGSA
FTSLEFQDFASCNLIQTVTIAPRRPQTNEGQVERMVQTMKGALKRIVVGDWATRLARFLF
AQHVIPCPTTGSSPSELLMGCHLKTCLDLVNPDLVRDMQFRKEKELDSALESGPLCLFIP
QETVFAQNYGTAPQWTKSKIVSATGPVSYTDNGQVWRRHMDQPCGRSPTDNPTPEQASST
YPPPTDMDSLEKYLPVSTNANPLLSPSEGSVAVESSDRLIGPSFAELITEPGSMGRPQWK
WSPPKWLAN*

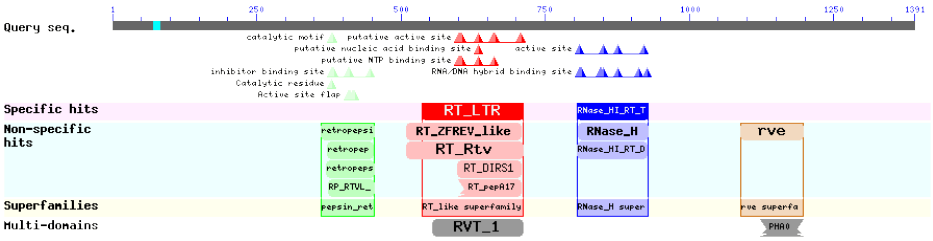
>Sphenodon mag (AC154075) (just a fragment of the full length element)
MSQREFMDSFDNTVEDWSTYIERLEQYFALHDTPDDKKVPALLNYMGGKTYRLLRSLTYP
NKPCTKTFAEIVTLLQEHSSPKPLETAE*FRFHKRNQQEGETVMAYGVALQRLAEHCNFG
NTLQMDLRDQLVCGIRDETIQKSLLTSETLSFKKAMEIATSMEAATRESQEFQAVSRSEN
ATHKXXXXEKCSYCGKGGHKSMFCRFQNVVCWHCGKKGHIQAACRSTTPNKIKSEKKKTP
EGHHRVHAIETETDSSEEDLAELSIAYVRVSCVEDGDKEPI*VTPIVEGKVLKMEL**DTGS**
AVSVIPHKEFTKQFSNVQLRKTRTILKTYTEERIXXLGVCTVEVKYNGQSNKLDLYVVPT
RGPALFGRSWLKKIRLDWQSIKALQVHQKSTSHQQLEELFAKAAPVFQKGIGHLRDIKAS
ITLIEGAQPKFLKARQVPLGIREAVAKELEWLEGMGILTKVDWSEWTTPIVPVIKKNGTL
RTCGDFKVTINPVLRTEHYALPCIEDIFLSLARGKKFSKLDLAQAYLQMEVEAESRKFLT
ISTEKGLFQYN*LVFGVASAPALWQRAMDQVLQGIPSCRC**YLDD**IIVTGSNDEDHLKNLA
QILKRLEEYGLRVNRDKCEFFKEAVTYCGHIIDSERLHKSPEKTHAVLRAPHPENISQVR
SIIGFVNYFHKFLPNIATVLHPLNQMLWKGKHWD*TELCERAFQEAKKLVTSEQVLTHYN
PELEILLACDASAYGLGAVISHAMPDGQECPIAFASRSLSAAECNYAQIDREALSLVWGV
KKFRHYLYGRKFTLVTDHKPLLSIFNPSKGIPEMAAAQIQRWALFLGAHKYDVKFKGTSQ
HSN**ADGLSH**LPYERQVMPQRNKMHSRLGSCSRCSACHPQLQPALYKFSEAFLLEQGCLYKL



b) New Mag subclade (in turtles only)

>Chrysemys new Mag gag/pol (AHGY01516055)

MLHVIIRTGSTGCWESERTGNRKEEGGVKEAGRVTECAATAWKRDFHCK*SSVEV
VNTLLGGCNILATRIALLPLNPPAPFLQSPGEPPIAFTVWIHMFETYLLAISATDISEVR
KHALLIHCLGAEGQHIFYTFPLADDKYETALTALKNFFVPKMNVVANFYRFRQREQKPGE
TIMQYIASLRRLIATCDFGNMADEMIRDQLIEKTIMLRVRQRLLLEPQLTLKAITIATQ
IESATAEAKIMSKDTGGPVQTVTPLQKSSLSLQTNNCKRKTNEKPLNQMQNTVKAFRC
GSPQHLANYTECPAKVAQCNHCKKIGHFAKVCCSSQFNQQVHAVTIPDVTVLSVDKITTA
HIPEQIKYTVNVSAIPSGKSHSIQLML**DTGS**AVSILPDSIYLHYFKDVPLTEPKLHLVCY
LKNHIPVHGCLPAIVTFGDRCITAEFYIVHKGTPILGRDLLAALNLRVVNGRIDLPQQST
LAVHTPASAGTQLQVEEKLSCAYGFLHKVKMRNNLLPVRQKLWCLPFSVREAVSEELRKL
VQKDIIEEINSSEWVSPIVVTHKKGGDIRLCVDLREPNKAIVIDSHPLPHIEEVFAELRG
AKMFSTLDLQSAYHQVMLHEDSRDLTAFITQEGLFRFKRVPYGLASAPSAFQKMMSLILK
NQHGVQC**YLDD**IIVFGNTTEEHENNLQSVLNCISKAGLKLNRSRCKFRQTELSFLGHTIS
QAGLKPDPDHILAISNAPPPTDLQTLRSFLGLTSWYAKFIPNYASFIEPLRELLWRSSTL
VWTTDAQVSFERVKDLIVHSPVLALFSPALPTIVTTDASDYGLGAVLTQLHEDNTERIVA
FASRTLSNAERKYSTVEKEALACVWATEKWRTYLWGRTFKFRTNHSPLMTLLTMKGLGRA
GYRIARWSARLLSFNYELEYKPGNQNVV**ADCLSR**LPLPSPDGPPEDEDVVVALITSTLTA
VTIEQFQAACSACPIQQKLREFLTKRWSSNPKNLDPVLLPYFRVRDELSLLDGCVLRGTH
RLLVPEELQSKLIHLAHNTHQGIVRTKQGLRDLYWWPGMDSQTEALIKSCITCQMHDKTA
VTCIPPLQPVPLPESAWEKVAIDIVGPFDTAPIDCHYAITLIAYFSKWLEVAFTLQICSA
IVIKFLSSFFSREGNPKKLVSDNGSQFTSLEFETFLAERNILHRRSSLYYPQASGEIERF
NRSLKESLQTAKLEGRLWISFTTDFLQASCHAVMQRSPAELLHGKQMTTKLNIAGLLKA*
PDAPNKDDVRKTVEQNQAKSKAFTDKQRGAKEPKFECGSFVRIRKPGILRKGDHKFTAPL
KIIEKK**GPY**TYRLSDGRVWNASYLPPAYAPRGDYANTQSALDDSTVEPTQQNIALELGLE
RWPVRFRRPPAWTKDYVM*



c) SURL subclade (in all reptiles)

>Anolis SURL (AAWZ02012013)

MESFRPPPPLAMQGNLAENWRRWEQAFQLYLAAAGLENVSKKRQIAILLHCVGE
EGVSLYNTFDFAEENPKDIAEVLEQFRTYFLPRKNIVFERFCFWNHMQSPGVTNVQFIAE
LKLKAASCEFGMAVNEMIRDKVVFSLQQEKLKQKLLQEADLTLEKAVEICRVDETTRAQL
RTMAITSEEGVFELQDSHGENREIITQALGTRESRHRDNWKNQNKCGYCGTAHEPRRCPA
FGKTCNKCGKKNHYARLCRSRVTNPVNIQARQHIHELNVSNLMIGKLDEEMKDTQITNKA
GWYADISIRDCIIKFKL**DTGA**EANVLPFSIFSRIPGAKQMSKSKVVLVAYGGTKIQPMGA
VEFDCITAKGVYNLLFYVTDCSTTPLLGRPACENLGLIYRVDLIQAEGLLTQEKLLSLYP
EVFQGLGEFQGHHHIHTDPTMVPVIQGCRRVPFAIHDRLKDTLDQMENMGVITKVVGPTD
WVSSLVITEKKNGSLRICLDPRDLNKAVRRQHYTIPTVEEVLSHLAGKKIFTIIDEKDSY
WQVKLDKASSRLCTFNTPWGRYCFNRLPFGLKSSSEVFQQKNQETFGHIKGVYM**IADD**MI
IAAETSKQHDEILHQVMETARVKNIKFNKEKIQFRVNSVRYMGHIVTAEGVRPDTEKVKA
IQEMKPPNDRQGVLRFLGSVQYLAKYIPKEAELTAPLRSLLKKNMSFQWMPEHQKAFEAI
KQKLCDAPVLQYFDVTKPVVIQADASKDGLGACLLQDNKPVSYASRALSSAEKNYAQIEK
ELLAVVYAVQKFHQYVFGKMVLVQTDHKPLESIYKKPIGSAPARLQRMLLQLQKYQLNFV
YTPGKLMYL**ADTLSR**ATVDHPGSQENPIGDEKVIYEVNTLAMHPDKMGLIQEATKRDPQL
RMIQTYLNQGWPKYMRKVAPIAKSFWPVKDHLRYRDGALFMGERIIIPASQRQNVLAQLH
ESHQGIQRTKERARQLMYWPGMSKDIESAVGSCFVCACFAPNNQKEPLKPHEIPEGPWQK
VGVDIFEQDNRSFLLVIDYFSKYPEVVSLHDKTARTVIVKMKSVFARHGTPLIVVSDNMP

FASQEFKVFAKEWGFEQCFSSPGYPQSNGMVERAIQSIKQLTHKVGKARGDLYAALLEYR
NTPVTGLSYSPAQILMGRMLRSKLPITTDLLCPRIPINVHQDLQRAQERQKHFYDRTARP
LKPLREGDLVWMQSNNCKERWLPAVVIEKCKQPRSYLIKNQDGRVYRRNRRQLKQRNQTP
ETTIQGNTTYNGSKGMFVNKSDAHVIADRKPTYVTSHGRPVFEPVRYIP*

>Alligator SURL (AKHW01056905)
MEGLKPSGQLHFNTKSLAQAWKQWKQEFSLYTELTMADKEEKMKVMLFYYLVVEKGCEVS
VTLMESNPDTLKQLIEAFDACCDPRKNETVERYQFFTQNQEEEEGIETCITALKTLASSC
NFGNIKDSLIRDRIVCGTWDSALRERLLKEVDLTMEKCHQIARAAELSKQRIKMISTATC
TEQVHRLNLKDSGKEEPDRPTANTYSMIECIYCGKLHERRKDKCPAYGKECKKYGKKNHF
RGLCRSHRNRKKTVHAVMRDQETTDEEEAFSVNLTDSQTH*RKGF*TRKLA**LFSNHLGW*
*SNKRYQIHPRNLVCQIH*RIHTLQKNVGNNSAIFAT**M**MLEQRPIRFQVDCVATCNVLPVNL
LSSSIRMEKCHYVLLKYNKITVRPLGKCQLTIINPRNKKQYQLKFIVIDRAGTHPLLDSW
TAQAMDLITVQHHNILQVTEEQEWSLGSLPNILLRYGDIFQGTGLFKGKLKLEIDPQVQP
VQLPKHRVLLALLESLKKELTNLQKKGIITPVEKSTDWISSLVVVRIPSGKLRICIDPKP
LNRALKKSHYPLPAIEAVLPDLSRAKVCTVCDVKNGFWHVELDKSSHLTTFSMPFGRYRW
LRMPMGISPALKVFQQKLNQELEGIKI**VADD**ILVIGDGDDKDHDTKLQQLLNRCRERNIK
LNANKIQLRRTEVPYIGHLLTSEGLRPDPEKVRAIMEMPRPQDVKGVQRLIGRVNYLSKF
CAYLSNACEPLRLLTHNDAAWEWAQTQEEAFKRIKKLISEAPILKYYNTAKQLVLQCDVS
EGGLGAVLMQKQQLVAFASRAMTETERRYAQIEKELLEVLFGLEWFHQFTFGQRVDVQSD
HKPLEIIMKKPLLSAPKRLQCMLLRLQAYDMNIKYYPGKSLQV**ADTLSR**AYLPECSTDGS
VEQEIESINMVQDLPIFKSSLKAIQQSMEQDGVLQAVKRTILEGWPQHKAQVPPEVAAYY
QWRDEQCTQDGILFKGDRVVIPAALQRDIMNRLHASHMGIESCLRRAWECIYWPGMNAHL
RTYMEQCEVCKEYSDKQQKETLNPHDIPSWPWEKVGTNLFNVNDRNYTVTVDSYSNFWEV
DYLEDTQARTVIRKLKAHFAWHGILDTVLSDNGLQYTSREFKQFCTKWEFQHKTSSPGYP
QSNGKAEPAVKTAKRLLVKAKKTAGDPYLALLDHRNTPSQGMDSSSPAQSLMGWRIKTLL
PVRDCLLQPQRGRGNSSWKQLKKQQSQQVSQYNKEARDLRPLRRGEKVWVQPVSPHVKEW
QKATVEGAVGDRSYEVVIDSGQCLRRNQKQLRSAGRVEIQVSKRFQDQDQDNFDNWSVIS
EPQIGEKDAMDSTKERGTQAESSLQNKDMDRTEAGVAPRKIN*

Supplementary File S3. Transcription factor binding sites in promoters of human and mouse RDDGs.

Chromovirus-related RDDGs

LDOC1:
Homo: AP-1, ATF-2, AP-2gamma, FOXL1, Egr-4, COMP1, AP-2beta, c-Jun, AP-2alpha, AP-2alphaA
Mus: Elk-1, Meis-1, Meis-1b, HOXA9, HOXA9B, Nkx5-1, SEF-1(1), p300, POU3F2, Nkx6-1

LDOC1L:
Homo: NF-1, Tal-1, CUTL1, Tal-1beta, E47, NRF-2, COMP1, STAT3, ITF-2
Mus: RFX1, PPAR-gamma1, PPAR-gamma2, HOXA9, HOXA9B, Meis-1, Meis-1a, c-Myb, Meis-1b, POU3F2

RGAG4:
Homo: E2F-4, E2F-3a, E2F-5, E2F-2, Egr-4, MZF-1, E2F, E2F-1, COMP1, Pax-4a
Mus: XBP-1, Cdc5, IRF-1, PPAR-gamma1, PPAR-gamma2, HTF, CUTL1, NCX/Ncx, HEN1, GR

FAM127A:
Homo: Elk-1, Nkx5-1, c-Ets-1
Mus: -

FAM127C:
Homo: Elk-1, Nkx5-1, c-Ets-1
Mus: -

PEG10:
Homo: C/EBPbeta
Mus: -

ZCCHC5:
Homo: Sox5, PPAR-gamma1, Olf-1, FOXO1a, PPAR-gamma2, HNF-3beta, Arnt, FOXO1
Mus: POU3F2, POU3F2 (N-Oct-5a), POU3F2 (N-Oct-5b), POU2F1, POU2F1a, Bach1, Pax-6, Brachyury, Evi-1, Roaz

ZCCHC16:
Homo: Sp1, RREB-1, NF-YA, HNF-3beta, NF-YB, CBF-A, CBF-B, CP1A, NF-Y, CBF(2)
Mus: PPAR-gamma1, PPAR-gamma2, C/EBPalpha, LCR-F1, RREB-1, HNF-4alpha1, HNF-4alpha2, FOXD1, NF-E2, NF-E2 p45

RTL1:
Homo: AML1a, Pax-5, Olf-1, MyoD, E4BP4, C/EBPalpha, FOXJ2 (long isoform), FOXJ2
Mus: FOXC1, ARP-1, HFH-1, RP58, STAT1, STAT1alpha, STAT1beta, STAT2, STAT3, STAT4

RGAG1:

Homo: STAT5B, AP-4, CUTL1, Evi-1, MEF-2A, SRY, POU2F1, POU2F1a, aMEF-2, RSRFC4
Mus: LCR-F1, GCNF-2, GCNF, GCNF-1, POU3F2, aMEF-2, MEF-2A, MZF-1, PPARalpha, Roaz

C22orf29:
Homo: E2F-4, E2F-3a, E2F-5, E2F-2, LCR-F1, C/EBPalpha, CHOP-10, E2F, E2F-1, Pax-4a
Mus: -

PNMA family

PNMA1:
Homo: E2F-3a, E2F-4, E2F-5, Brachyury, HSF1 (long), E2F-2, E2F-1, E2F, HSF1short, ATF
Mus: ZIC2/Zic2, Roaz, Nkx3-1v1, Nkx3-1v2, Nkx3-1v3, Nkx3-1v4, Nkx3-1, Msx-1, Zic1, RFX1

PNMA2:
Homo: AML1a, Pax-5, MyoD, Lmo2, AP-4, GATA-1, Egr-4, FOXL1, HEN1
Mus: NRSF form1, NRSF form2, GATA-1, ITF-2, Tal-1beta, HSF1 (long), HSF1 (short), YY1, MyoD, C/EBPalpha

PNMA3:
Homo: E2F-3a, E2F-4, E2F-5, SREBP-1c, E2F-2, SREBP-1b, E2F-1, E2F, SREBP-1a, HOXA5
Mus: ATF2, CRE-BP1, ATF, Ik-3, c-Jun, RP58, NF-kappaB1, Roaz, ISGF-3, p53

MOAP1:
Homo: AML1a, ATF-2, NF-kappaB, FOXL1, AREB6, IRF-2, NF-kappaB2, Meis-1a, NF-kappaB1, RSRFC4
Mus: Evi-1, ZID, c-Myb, STAT3, POU3F1, FOXJ2, FOXJ2 (long isoform), Nkx3-1, Nkx3-1 v1, Nkx3-1 v2

PNMA5:
Homo: COUP-TF1, LHX3b/Lhx3b, C/EBPbeta, AML1a, HNF-4alpha2, HNF-4alpha1, GATA-2, COUP-TF, CP2, LHX3a/Lhx3a
Mus: Nkx6-1, Evi-1, HSF1 short, HSF1 (long), Nkx2-5, NF-kappaB1, Pax-2, Pax-2a, SREBP-1a, SREBP-1b

PNMA6A:
Homo: CREB, SREBP-1a, deltaCREB, SREBP-1c, MyoD, NRSF form 2, SREBP-1b
Mus: -

PNMAL1:
Homo: ER-alpha, USF1, USF2, USF-1:USF-2, GATA-1, POU2F1, POU2F1b, POU2F1a, USF-1, POU2F1c
Mus: -

PNMAL2:
Homo: AhR, NF-1, Pax-5, Lmo2, Arnt, E47, AREB6, STAT3, Hand1, MRF-2

Mus: -

ZCCHC12:
Homo: GR, GR-beta, Nkx2-2, Meis-1b, POU2F1, POU2F1a, c-Myb, GR-alpha, Meis-1a, Meis-1
Mus: POU2F1, POU2F1a, POU2F2, POU2F2 (Oct-2.1), POU2F2B, POU2F2C, Oct-B1, oct-B2, oct-B3, Pax-3

ZCCHC18:
Homo: STAT5B, AP-1, XBP-1, STAT5A, NF-E2 p45, POU2F1, GATA-6, POU2F1a, Zic3, NF-E2
Mus: Pax-3, GATA-1, Olf-1, GR, GR-alpha, CBF(2), CBF-A, CBF-B, CBF-C, CP1A

CCDC8:
Homo: NRSF form 1, Nkx2-5, NRSF form 2, AP-2gamma, Ik-2, HSF2, AP-2beta, AP-2alpha, Hlf, AP-2alphaA
Mus: -

ARC:
Homo: Sp1, NRSF form 1, STAT5A, NRSF form 2, NF-kappaB, NF-kappaB1
Mus: SRF, SRF (504 AA), HOXA9B, Meis-1, Meis-1b, HOXA9, SREBP-1a, SREBP-1b, SREBP-1c, E47

Retroviral protease-derived RDDG

ASPRV1:
Homo: Max1, AML1a, MAZR, NCX/Ncx, Pax-2, Pax-2a, LCR-F1, ATF6, c-Myc
Mus: ARP-1, FOXD1, HNF-1, HNF-1A, SEF-1 (1), ROR-alpha2, NF-kappaB, NF-kappaB1, RelA, Lmo2

Integrase-derived RDDGs

GIN1:
Homo: AML1a, POU3F2 (N-Oct-5a), POU3F2 (N-Oct-5b), CUTL1, POU3F2, CREB, deltaCREB, Meis-1a, Meis-1
Mus: -

NYNRIN (KIAA1305):
Homo: ISGF-3, Ik-3, HEN1, Evi-1, GATA-1, GATA-2, GATA-3, LyF-1, HNF-4alpha1, CREB
Mus: -

KRBA2:
Homo: HOXA3, AML1a, GCNF, GATA-1, C/EBPalpha, AREB6, Nkx6-1, GCNF-1, COMP1, IRF-7A
Mus: -

SCAND3:
Homo: RFX1, NRSF form 1, Olf-1, NRSF form 2, TGIF, MRF-2, Roaz
Mus: -