

**Table S1. The Wcs proteins used for phylogenetic analysis**

<b>Protein</b>	<b>Accession No.</b>	<b>Species Name</b>	<b>Order</b>
MmuWcs1	NP_080156.2	<i>Mus musculus</i>	Rodentia
MpuWcs1	XP_004767240.1	<i>Mustela putorius</i>	Carnivora
CbaWcs1	XP_010945334.1	<i>Camelus bactrianus</i>	Cetartiodactyla
PalWcs1	XP_006905058.1	<i>Pteropus alecto</i>	Chiroptera
EprWcs1	XP_008505767.1	<i>Equus przewalskii</i>	Perissodactyla
MdoWcs2	XP_007493718.1	<i>Monodelphis domestica</i>	Didelphimorphia
PciWcs2	XP_020862835.1	<i>Phascolarctos cinereus</i>	Diprotodontia

**Table S2. The representative retrovirus gag and Fv1 sequences used for phylogenetic reconstruction**

<b>Name</b>	<b>Abbreviation</b>	<b>Accession No./Source</b>
Meleagris endogenous retrovirus	Meleagris-ERV	ADDD01127175.1
Mus dunni endogenous virus	MDEV	AF053745
Walleye epidermal hyperplasia virus 1	WEHV-1	AF133051
Walleye epidermal hyperplasia virus 2	WEHV-2	AF133052
Koala retrovirus	KoRV	AF151794.2
Simian immunodeficiency virus	SIVcol	AF301156.1
Python molurus endogenous retrovirus	PyERV	AF500296.1
Danio rerio endogenous retrovirus	ZFERV	AF503912.1
Porcine endogenous retrovirus C	PERV-C	AJ293656.1
Xenopus laevis endogenous retrovirus 1	Xen-1	AJ506107.1
Porcine endogenous retrovirus B	PERV-B	AY099324
Baboon endogenous virus strain M7	BaEV	D10032.1
Human T-lymphotropic virus 3	HTLV-3	DQ093792.1
Atlantic salmon swim bladder sarcoma virus	SSSV	DQ174103.1
Human immunodeficiency virus 1	HIV-1	EF029066.1
Bos taurus endogenous virus beta3	BERV-beta3	EF030818.1
Human T-lymphotropic virus 4	HTLV-4	EF488483.1
Simian immunodeficiency virus	SIVcpz	EF535994.1
Spider monkey simian foamy virus	SFVspm	EU010385.1
Western lowland gorilla simian foamy virus	SFVgor	HM245790.1
Rhinolophus ferrumequinum retrovirus	RfRV	JQ303225.1
Simian retrovirus 1	SRV-1	M11841.1
Simian retrovirus 2	SRV-2	M16605.1
Squirrel monkey retrovirus-H	SMRV-H	M23385.1
Chimpanzee simian foamy virus	SFVcpz	NC_001364.1
Rous sarcoma virus	RSV	NC_001407.1
Bovine immunodeficiency virus	BIV	NC_001413.1
Bovine leukemia virus	BLV	NC_001414.1
Human T-cell leukemia virus type I	HTLV-1	NC_001436.1
Equine infectious anemia virus	EIAV	NC_001450.1
Caprine arthritis encephalitis virus	CAEV	NC_001463.1
Feline immunodeficiency virus	FIV	NC_001482.1
Human T-lymphotropic virus 2	HTLV-2	NC_001488.1
Jaagsiekte sheep retrovirus	JSRV	NC_001494.1
Moloney murine leukemia virus	Mo-MLV	NC_001501.1
Mouse mammary tumor virus	MMTV	NC_001503.1
Ovine lentivirus	SRLV	NC_001511.1
Human immunodeficiency virus 2	HIV-2	NC_001722.1
Snakehead retrovirus	SnRV	NC_001724.1
Bovine foamy virus	BFV	NC_001831.1
Walleye dermal sarcoma virus	WDSV	NC_001867.1
Gibbon ape leukemia virus	GaLV	NC_001885.3
Feline leukemia virus	FeLV	NC_001940.1
Equine foamy virus	EFV	NC_002201.1
Reticuloendotheliosis virus	REV	NC_006934
Woolly monkey sarcoma virus	WMSV	NC_009424
RD114 retrovirus	RD114	NC_009889.1

Macaque simian foamy virus	SFVmac	NC_010819.1
African green monkey simian foamy virus	SFVagm	NC_010820.1
Avian leukemia virus	ALV	NC_015116.1
Feline foamy virus	FFV	NC_001871.1
Lymphoproliferative disease virus	LDV	U09568.1
Jembrana disease virus	JDV	U21603.1
Mus musculus endogenous retrovirus	MuERV-L	Y12713.1
Friend virus susceptibility protein 1 of Mus musculus	MmuFv1	NP_034374.2
Friend virus susceptibility protein 1 of Mus caroli	McaFv1	XP_021019979.1
Coelacanth endogenous foamy-like virus	CoeEFV	Ref.1
Human endogenous retrovirus T	HERV-T	Ref.2
Human endogenous retrovirus 3	HERV-3	Ref.2
Human endogenous retrovirus 1	HERV-1	Ref.2
Human endogenous retrovirus I	HERV-I	Ref.2
Human endogenous retrovirus E	HERV-E	Ref.2
Human endogenous retrovirus HARLEQUIN	HARLEQUIN	Ref.2
Pseudoautosomal boundary-like sequence	PABL	Ref.2
Human endogenous retrovirus ADP	HERV-ADP	Ref.2
Human endogenous retrovirus IP	HERV-IP	Ref.2
Human endogenous retrovirus Fb	HERV-Fb	Ref.2
Human endogenous retrovirus H	HERV-H	Ref.2
Human endogenous retrovirus H48	HERV-H48	Ref.2
Human endogenous retrovirus LTR46	LTR46	Ref.2
Human endogenous retrovirus Fa	HERV-Fa	Ref.2
Human endogenous retrovirus Fc	HERV-Fc	Ref.2
Human endogenous retrovirus MER84	MER84	Ref.2
Human endogenous retrovirus PRIMA4	PRIMA4	Ref.2
Human endogenous retrovirus FRD	HERV-FRD	Ref.2
Human endogenous retrovirus 4	HERV-4	Ref.2
Human endogenous retrovirus-like sequences P2	HUERSP2	Ref.2
Human endogenous retrovirus MER52	MER52	Ref.2
Human endogenous retrovirus-like sequences P3	HUERSP3	Ref.2
Human endogenous retrovirus LTR25	LTR25	Ref.2
Human endogenous retrovirus 9	HERV-9	Ref.2
Human endogenous retrovirus W	HERV-W	Ref.2
Human endogenous retrovirus 30	HERV-30	Ref.2
Human endogenous retrovirus PRIMA41	PRIMA41	Ref.2
Human endogenous retrovirus HEPSI3	HEPSI3	Ref.2
Human endogenous retrovirus HEPSI1	HEPSI1	Ref.2
Human endogenous retrovirus HEPSI2	HEPSI2	Ref.2
Human endogenous retrovirus MER34	MER34	Ref.2
Human MMTV-like 1	HML-1	Ref.2
Human MMTV-like 3	HML-3	Ref.2
Human MMTV-like 9	HML-9	Ref.2
Human MMTV-like 2	HML-2	Ref.2
Human MMTV-like 4	HML-4	Ref.2
Human MMTV-like 7	HML-7	Ref.2
Human MMTV-like 8	HML-8	Ref.2
Human MMTV-like 5	HML-5	Ref.2
Human MMTV-like 6	HML-6	Ref.2
Human endogenous retrovirus L	HERV-L	Ref.2

Human endogenous retrovirus S	HERV-S	Ref.2
Gallus endogenous retrovirus R	Gallus-R	Ref.3
Melopsittacus endogenous retrovirus R	Melopsittacus-R	Ref.3
Taeniopygia endogenous retrovirus R	Taeniopygia-R	Ref.3
Anas endogenous retrovirus R	Anas-R	Ref.3
Falco endogenous retrovirus H	Falco-H	Ref.3
Melopsittacus endogenous retrovirus H	Melopsittacus-H	Ref.3
Taeniopygia endogenous retrovirus H	Taeniopygia-H	Ref.3
Columba endogenous retrovirus H	Columba-H	Ref.3
Pseudopodoces endogenous retrovirus H	Pseudopodoces-H	Ref.3
<i>Gallus gallus</i> endogenous retrovirus 10	GGERV-10	Ref.3
<i>Gallus gallus</i> endogenous retrovirus LA	GGERV-LA	Ref.3
<i>Zonotrichia albicollis</i> endogenous retrovirus type A	ZAERV-A	Ref.3

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1. Han GZ, Worobey M. 2012. An endogenous foamy-like viral element in the coelacanth genome. *PLoS Pathog.* 8:e1002790.
2. Vargiu L, Rodriguez-Tomé P, Sperber GO, Cadeddu M, Grandi N, Blikstad V, Tramontano E, Blomberg J. 2016. Classification and characterization of human endogenous retroviruses; mosaic forms are common. *Retrovirology.* 13:7.
3. Niewiadomska AM, Gifford RJ. 2013. The extraordinary evolutionary history of the reticuloendotheliosis viruses. *PLoS Biol.* 11:e1001642.

**Table S3. The SRA accession number used for expression pattern analyses**

	<i>Mus musculus</i>	<i>Mustela putorius</i>	<i>Bos taurus</i>	<i>Hipposideros armiger</i>	<i>Equus caballus</i>	<i>Monodelphis domestica</i>	<i>Phascolarctos cinereus</i>
Brain	SRX5397290	SRX3316193	SRX211674	SRX761339	SRX211684	SRX217694	SRX501343
Liver	SRX5391775	SRX3316207	SRX211579	SRX764325	SRX211589	SRX2704263	SRX501262
Kidney	SRX5184837	SRX3316202	SRX211629	SRX764324	SRX211641	SRX2704259	SRX501314
Lung	SRX5382226	SRX3316212	ERX480073	SRX764326	NA	SRX3316214	SRX501320
Heart	SRX5089077	SRX3316197	SRX1538121	SRX764323	NA	SRX2704257	SRX501342
Spleen	SRX4937288	SRX112776	SRX2506272	SRX764328	NA	SRX290646	SRX500280
Muscle	SRX5260775	SRX3316217	ERX480070	SRX764327	SRX147023	SRX3316219	NA
Testis	SRX5382129	SRX3316222	SRX3766817	NA	SRX3022257	SRX3316223	NA
Blood	SRX5282936	SRX4948654	SRX5062183	NA	SRX147033	SRX149629	NA
Lymph node	SRX4941344	SRX112780	SRX978280	NA	NA	NA	NA
Skin	SRX5305348	SRX112815	SRX5057749	NA	ERX117850	NA	NA
Placenta	SRX5330873	NA	SRX4551179	NA	SRX128106	SRX217696	NA
Pancreas	SRX4900154	SRX112782	NA	NA	NA	SRX290644	NA

**Table S4. The 261 vertebrate proteomes used for the similarity search**

<b>Species</b>	<b>Assembly No.</b>	<b>Assembly Level</b>	<b>Size(Mb)</b>	<b>Scaffolds</b>
Acanthisitta chloris	GCA_000695815.1	Scaffold	1035.88	53875
Acanthochromis polyacanthus	GCA_002109545.1	Scaffold	991.585	30414
Acinonyx jubatus	GCA_003709585.1	Scaffold	2384.85	3220
Ailuropoda melanoleuca	GCA_000004335.1	Scaffold	2299.51	81467
Amazona aestiva	GCA_001420675.1	Scaffold	1129.54	3232
Amphiprion ocellaris	GCA_002776465.1	Scaffold	880.721	6405
Anas platyrhynchos	GCA_003850225.1	Chromosome	1126.18	2150
Anser cygnoides domesticus	GCA_000971095.1	Scaffold	1119.15	7593
Antrostomus carolinensis	GCA_000700745.1	Scaffold	1119.68	70122
Aotus nancymae	GCA_000952055.2	Scaffold	2861.68	28922
Apaloderma vittatum	GCA_000703405.1	Scaffold	1070.84	54728
Aptenodytes forsteri	GCA_000699145.1	Scaffold	1254.35	10672
Apteryx australis mantelli	GCA_001039765.1	Scaffold	1523.97	24720
Aquila chrysaetos canadensis	GCA_000766835.1	Scaffold	1192.74	1142
Astyanax mexicanus	GCA_000372685.2	Chromosome	1335.24	2415
Austrofundulus limnaeus	GCA_001266775.1	Scaffold	866.963	29785
Balaenoptera acutorostrata scammoni	GCA_000493695.1	Scaffold	2431.69	10776
Balearica regulorum gibbericeps	GCA_000709895.1	Scaffold	1127.62	53491
Bambusicola thoracicus	GCA_002909625.1	Scaffold	1032.3	163748
Bison bison bison	GCA_000754665.1	Scaffold	2828.03	128431
Boleophthalmus pectinirostris	GCA_000788275.1	Scaffold	955.752	16620
Bos indicus	GCA_000247795.2	Chromosome	2673.97	32
Bos mutus	GCA_000298355.1	Scaffold	2645.16	41192
Bos taurus	GCA_002263795.2	Chromosome	2715.85	2211
Bubalus bubalis	GCA_003121395.1	Chromosome	2655.78	509
Buceros rhinoceros silvestris	GCA_000710305.1	Scaffold	1065.78	62257
Calidris pugnax	GCA_001431845.1	Scaffold	1229.09	3753
Callipepla squamata	GCA_002218305.1	Scaffold	1045.28	34302
Callithrix jacchus	GCA_000004665.1	Chromosome	2914.96	16399
Callorhinchus milii	GCA_000165045.2	Scaffold	974.499	21204
Calypte anna	GCA_000699085.1	Scaffold	1105.68	54736
Camelus bactrianus	GCA_000767855.1	Scaffold	1992.66	35455
Camelus dromedarius	GCA_000767585.1	Scaffold	2004.06	32573
Camelus ferus	GCA_000311805.2	Scaffold	2009.19	13334
Canis lupus dingo	GCA_003254725.1	Scaffold	2439.83	2444
Canis lupus familiaris	GCA_000002285.2	Chromosome	2410.98	3310
Capra hircus	GCA_001704415.1	Chromosome	2922.81	29907
Cariama cristata	GCA_000690535.1	Scaffold	1132.25	53474
Carlito syrichta	GCA_000164805.2	Scaffold	3453.86	337189
Castor canadensis	GCA_001984765.1	Scaffold	2518.31	21157
Cathartes aura	GCA_000699945.1	Scaffold	1152.57	104141
Cavia porcellus	GCA_000151735.1	Scaffold	2723.22	3144
Cebus capucinus imitator	GCA_001604975.1	Scaffold	2717.7	7156

<i>Ceratotherium simum simum</i>	GCA_000283155.1	Scaffold	2464.37	3087
<i>Cercocebus atys</i>	GCA_000955945.1	Scaffold	2848.25	11433
<i>Cervus elaphus hippelaphus</i>	GCA_002197005.1	Chromosome	3438.62	11479
<i>Chaetura pelagica</i>	GCA_000747805.1	Scaffold	1119.19	19072
<i>Charadrius vociferus</i>	GCA_000708025.2	Scaffold	1219.86	15167
<i>Chelonia mydas</i>	GCA_000344595.1	Scaffold	2208.41	140023
<i>Chinchilla lanigera</i>	GCA_000276665.1	Scaffold	2390.87	2839
<i>Chlamydotis macqueenii</i>	GCA_000695195.1	Scaffold	1086.57	59693
<i>Chlorocebus sabaeus</i>	GCA_000409795.2	Chromosome	2789.66	2022
<i>Chrysemys picta bellii</i>	GCA_000241765.2	Chromosome	2365.77	78631
<i>Chrysochloris asiatica</i>	GCF_000296735.1	Scaffold	4750.46	20500
<i>Clupea harengus</i>	GCA_000966335.1	Scaffold	807.712	6915
<i>Colinus virginianus</i>	GCA_000599465.2	Scaffold	1254.15	42369
<i>Colius striatus</i>	GCA_000690715.1	Scaffold	1075.93	70188
<i>Colobus angolensis palliatus</i>	GCA_000951035.1	Scaffold	2970.12	13124
<i>Columba livia</i>	GCA_000337935.1	Scaffold	1107.99	14923
<i>Condylura cristata</i>	GCA_000260355.1	Scaffold	1769.66	2040
<i>Corvus brachyrhynchos</i>	GCA_000691975.1	Scaffold	1091.31	10547
<i>Corvus cornix cornix</i>	GCA_000738735.2	Scaffold	1042.28	113
<i>Coturnix japonica</i>	GCA_001577835.1	Chromosome	927.657	2531
<i>Cricetulus griseus</i>	GCA_000223135.1	Scaffold	2399.79	109152
<i>Crocodylus porosus</i>	GCA_001723895.1	Scaffold	2049.54	70
<i>Cuculus canorus</i>	GCA_000709325.1	Scaffold	1153.89	14930
<i>Cyanistes caeruleus</i>	GCA_002901205.1	Scaffold	1186.98	29297
<i>Cynoglossus semilaevis</i>	GCA_000523025.1	Chromosome	470.199	31181
<i>Cyprinodon variegatus</i>	GCA_000732505.1	Scaffold	1035.18	9259
<i>Cyprinus carpio</i>	GCA_000951615.2	Chromosome	1713.66	9378
<i>Danio rerio</i>	GCA_000002035.4	Scaffold	1411.76	32031
<i>Dasypus novemcinctus</i>	GCA_000208655.2	Scaffold	1679.2	2848
<i>Delphinapterus leucas</i>	GCA_002288925.2	Scaffold	2358.52	6972
<i>Desmodus rotundus</i>	GCA_002940915.2	Scaffold	2063.81	29801
<i>Dipodomys ordii</i>	GCA_000151885.2	Scaffold	2236.37	65193
<i>Echinops telfairi</i>	GCA_000313985.1	Scaffold	2947.02	8402
<i>Egretta garzetta</i>	GCA_000687185.1	Scaffold	1206.5	11791
<i>Elephantulus edwardii</i>	GCA_000299155.1	Scaffold	3843.98	8768
<i>Enhydra lutris kenyonii</i>	GCA_002288905.2	Scaffold	2455.28	6771
<i>Eptesicus fuscus</i>	GCA_000308155.1	Scaffold	2026.63	6789
<i>Equus asinus</i>	GCA_001305755.1	Scaffold	2391.05	2167
<i>Equus caballus</i>	GCA_002863925.1	Chromosome	2506.97	4701
<i>Equus przewalskii</i>	GCA_000696695.1	Scaffold	2395.95	53097
<i>Erinaceus europaeus</i>	GCA_000296755.1	Scaffold	2715.72	5803
<i>Eschrichtius robustus</i>	GCA_002738545.1	Scaffold	2922.98	1213011
<i>Esox lucius</i>	GCA_000721915.3	Chromosome	904.497	1211
<i>Eurypyga helias</i>	GCA_000690775.1	Scaffold	1088.02	62699
<i>Falco cherrug</i>	GCA_000337975.1	Scaffold	1174.81	5863
<i>Felis catus</i>	GCA_000181335.4	Chromosome	2521.86	4525

<i>Ficedula albicollis</i>	GCA_000247815.2	Chromosome	1118.34	21836
<i>Fukomys damarensis</i>	GCA_000743615.1	Scaffold	2333.89	74730
<i>Fulmarus glacialis</i>	GCA_000690835.1	Scaffold	1141.4	57389
<i>Fundulus heteroclitus</i>	GCA_000826765.1	Scaffold	1021.9	10180
<i>Galeopterus variegatus</i>	GCA_000696425.1	Scaffold	3187.66	179514
<i>Gallus gallus</i>	GCA_000002315.5	Chromosome	1065.37	525
<i>Gambusia affinis</i>	GCA_003097735.1	Scaffold	598.663	2943
<i>Gavia stellata</i>	GCA_000690875.1	Scaffold	1129.69	61831
<i>Gekko japonicus</i>	GCA_001447785.1	Scaffold	2490.27	191500
<i>Geospiza fortis</i>	GCA_000277835.1	Scaffold	1065.29	27239
<i>Gorilla gorilla gorilla</i>	GCA_000151905.3	Chromosome	3063.36	40730
<i>Haliaeetus albicilla</i>	GCA_000691405.1	Scaffold	1133.55	50905
<i>Haliaeetus leucocephalus</i>	GCA_000737465.1	Scaffold	1178.41	1023
<i>Haplochromis burtoni</i>	GCA_000239415.1	Scaffold	831.412	8001
<i>Heterocephalus glaber</i>	GCA_000247695.1	Scaffold	2618.2	4229
<i>Hippocampus comes</i>	GCA_001891065.1	Scaffold	493.776	37377
<i>Hipposideros armiger</i>	GCA_001890085.1	Scaffold	2236.58	7571
<i>Homo sapiens</i>	GCA_000001405.27	Scaffold	2911.24	125643
<i>Ictalurus punctatus</i>	GCA_001660625.1	Chromosome	783.275	9975
<i>Ictidomys tridecemlineatus</i>	GCA_000236235.1	Scaffold	2478.39	12483
<i>Jaculus jaculus</i>	GCA_000280705.1	Scaffold	2835.25	10898
<i>Kryptolebias marmoratus</i>	GCA_001649575.1	Scaffold	680.367	3073
<i>Labrus bergylta</i>	GCA_900080235.1	Scaffold	805.481	13466
<i>Larimichthys crocea</i>	GCA_000972845.2	Chromosome	657.94	9998
<i>Lates calcarifer</i>	GCA_001640805.1	Scaffold	668.481	3808
<i>Latimeria chalumnae</i>	GCA_000225785.1	Scaffold	2860.59	22819
<i>Lepidothrix coronata</i>	GCA_001604755.1	Scaffold	1079.58	4612
<i>Lepisosteus oculatus</i>	GCA_000242695.1	Chromosome	945.878	2106
<i>Leptonychotes weddellii</i>	GCA_000349705.1	Scaffold	3156.9	16711
<i>Leptosomus discolor</i>	GCA_000691785.1	Scaffold	1136.24	57160
<i>Leucoraja erinacea</i>	GCA_000238235.1	Contig	1555.46	2962366
<i>Limosa lapponica baueri</i>	GCA_002844005.1	Scaffold	1034.77	32319
<i>Lipotes vexillifer</i>	GCA_000442215.1	Scaffold	2429.21	30713
<i>Lonchura striata domestica</i>	GCA_002197715.1	Scaffold	1060.17	3014
<i>Loxodonta africana</i>	GCA_000001905.1	Scaffold	3196.74	2352
<i>Macaca fascicularis</i>	GCA_000364345.1	Chromosome	2946.84	7625
<i>Macaca mulatta</i>	GCA_000772875.3	Chromosome	3236.22	286263
<i>Macaca nemestrina</i>	GCA_000956065.1	Scaffold	2948.7	9733
<i>Malaclemys terrapin terrapin</i>	GCA_001728815.2	Contig	2439.75	21684
<i>Manacus vitellinus</i>	GCA_001715985.2	Scaffold	1213.15	15315
<i>Mandrillus leucophaeus</i>	GCA_000951045.1	Scaffold	3061.99	12821
<i>Manis javanica</i>	GCA_001685135.1	Scaffold	2547.4	80670
<i>Marmota marmota marmota</i>	GCA_001458135.1	Scaffold	2510.59	14543
<i>Maylandia zebra</i>	GCA_000238955.5	Chromosome	957.485	1690
<i>Meleagris gallopavo</i>	GCA_000146605.3	Chromosome	1128.34	233806
<i>Melopsittacus undulatus</i>	GCA_000238935.1	Scaffold	1117.37	25212



<i>Meriones unguiculatus</i>	GCA_002204375.1	Scaffold	2523.12	68793
<i>Merops nubicus</i>	GCA_000691845.1	Scaffold	1062.96	53499
<i>Mesitornis unicolor</i>	GCA_000695765.1	Scaffold	1087.29	67520
<i>Mesocricetus auratus</i>	GCA_000349665.1	Scaffold	2504.93	21484
<i>Microcebus murinus</i>	GCA_000165445.3	Chromosome	2487.41	7678
<i>Microtus ochrogaster</i>	GCA_000317375.1	Chromosome	2287.34	6450
<i>Miniopterus natalensis</i>	GCA_001595765.1	Scaffold	1803.1	1269
<i>Monodelphis domestica</i>	GCF_000002295.2	Chromosome	3598.44	5223
<i>Monopterus albus</i>	GCA_001952655.1	Scaffold	684.144	20622
<i>Mus caroli</i>	GCA_900094665.2	Chromosome	2553.13	3163
<i>Mus musculus</i>	GCA_000001635.8	Scaffold	2505.02	2314
<i>Mus pahari</i>	GCA_900095145.2	Chromosome	2475.01	2581
<i>Mustela putorius furo</i>	GCA_000215625.1	Scaffold	2410.88	7783
<i>Myotis brandtii</i>	GCA_000412655.1	Scaffold	2107.24	169750
<i>Myotis davidii</i>	GCA_000327345.1	Scaffold	2059.8	101769
<i>Myotis lucifugus</i>	GCA_000147115.1	Scaffold	2034.58	11654
<i>Nannospalax galili</i>	GCA_000622305.1	Scaffold	3061.42	154976
<i>Nanorana parkeri</i>	GCA_000935625.1	Scaffold	2053.87	25188
<i>Neolamprologus brichardi</i>	GCA_000239395.1	Scaffold	847.91	9099
<i>Neomonachus schauinslandi</i>	GCA_002201575.1	Scaffold	2400.93	7873
<i>Neophocaena asiaeorientalis</i> <i>asiaeorientalis</i>	GCA_003031525.1	Scaffold	2284.63	13699
<i>Neotoma lepida</i>	GCA_001675575.1	Scaffold	2353.86	119373
<i>Nestor notabilis</i>	GCA_000696875.1	Scaffold	1053.56	42180
<i>Nipponia nippon</i>	GCA_000708225.1	Scaffold	1223.86	59555
<i>Nomascus leucogenys</i>	GCA_000146795.3	Chromosome	2962.06	17524
<i>Nothobranchius furzeri</i>	GCA_001465895.2	Chromosome	1242.52	6013
<i>Notothenia coriiceps</i>	GCA_000735185.1	Scaffold	636.614	38657
<i>Numida meleagris</i>	GCA_002078875.2	Chromosome	1043.26	2739
<i>Ochotona princeps</i>	GCA_000292845.1	Scaffold	2229.84	10421
<i>Octodon degus</i>	GCA_000260255.1	Scaffold	2995.89	7135
<i>Odobenus rosmarus divergens</i>	GCA_000321225.1	Scaffold	2400.15	3893
<i>Odocoileus virginianus texanus</i>	GCA_002102435.1	Scaffold	2380.51	17026
<i>Oncorhynchus kisutch</i>	GCA_002021735.1	Chromosome	2369.93	22813
<i>Oncorhynchus mykiss</i>	GCA_002163495.1	Chromosome	2179	139800
<i>Oncorhynchus tshawytscha</i>	GCA_002872995.1	Chromosome	2425.71	15946
<i>Ophiophagus hannah</i>	GCA_000516915.1	Scaffold	1594.07	296399
<i>Opisthocomus hoazin</i>	GCA_000692075.1	Scaffold	1203.71	10256
<i>Orcinus orca</i>	GCA_000331955.2	Scaffold	2372.92	1668
<i>Oreochromis niloticus</i>	GCA_001858045.3	Chromosome	1005.68	2460
<i>Ornithorhynchus anatinus</i>	GCF_000002275.2	Chromosome	1995.61	200283
<i>Orycteropus afer afer</i>	GCA_000298275.1	Scaffold	4444.08	22509
<i>Oryctolagus cuniculus</i>	GCA_000003625.1	Chromosome	2737.46	3318
<i>Oryzias latipes</i>	GCA_002234675.1	Chromosome	734.057	25
<i>Oryzias melastigma</i>	GCA_002922805.1	Scaffold	779.47	8603
<i>Otolemur garnettii</i>	GCA_000181295.3	Scaffold	2519.72	7793

<i>Ovis aries</i>	GCA_002742125.1	Chromosome	2869.91	2641
<i>Ovis aries musimon</i>	GCA_000765115.1	Scaffold	2589.83	6173
<i>Pan paniscus</i>	GCA_000258655.2	Chromosome	3286.64	10984
<i>Pan troglodytes</i>	GCA_002880755.3	Chromosome	3050.4	4432
<i>Pan troglodytes verus</i>	GCA_000002175.2	Chromosome	12.2633	2
<i>Panthera pardus</i>	GCA_001857705.1	Scaffold	2578.02	50377
<i>Panthera tigris altaica</i>	GCA_000464555.1	Scaffold	2391.08	1479
<i>Pantholops hodgsonii</i>	GCA_000400835.1	Scaffold	2696.89	15059
<i>Papio anubis</i>	GCA_000264685.2	Chromosome	2959.37	71135
<i>Paralichthys olivaceus</i>	GCA_001970005.2	Scaffold	643.911	9525
<i>Paramormyrops kingsleyae</i>	GCA_002872115.1	Scaffold	799.421	4667
<i>Parus major</i>	GCA_001522545.3	Chromosome	1020.31	1675
<i>Pelecanus crispus</i>	GCA_000687375.1	Scaffold	1160.92	63982
<i>Pelodiscus sinensis</i>	GCA_000230535.1	Scaffold	2202.48	19904
<i>Peromyscus maniculatus bairdii</i>	GCA_000500345.1	Scaffold	2630.54	30921
<i>Phaethon lepturus</i>	GCA_000687285.1	Scaffold	1152.96	66785
<i>Phalacrocorax carbo</i>	GCA_000708925.1	Scaffold	1138.97	64312
<i>Phascolarctos cinereus</i>	GCA_002099425.1	Contig	3192.58	1907
<i>Phoenicopterus ruber ruber</i>	GCA_000687265.1	Scaffold	1132.18	76189
<i>Physeter catodon</i>	GCA_002837175.2	Chromosome	2512.15	14677
<i>Picoides pubescens</i>	GCA_000699005.1	Scaffold	1167.32	31254
<i>Piliocolobus tephrosceles</i>	GCA_002776525.2	Scaffold	3038.01	47449
<i>Podiceps cristatus</i>	GCA_000699545.1	Scaffold	1134.92	82923
<i>Poecilia formosa</i>	GCA_000485575.1	Scaffold	748.923	3985
<i>Poecilia latipinna</i>	GCA_001443285.1	Scaffold	815.145	17988
<i>Poecilia mexicana</i>	GCA_001443325.1	Scaffold	801.711	18105
<i>Poecilia reticulata</i>	GCA_000633615.2	Chromosome	731.622	3029
<i>Pogona vitticeps</i>	GCA_900067755.1	Scaffold	1716.68	13749
<i>Pongo abelii</i>	GCA_002880775.3	Chromosome	3065.05	5300
<i>Propithecus coquereli</i>	GCA_000956105.1	Scaffold	2798.15	22539
<i>Protobothrops mucrosquamatus</i>	GCA_001527695.3	Scaffold	1673.88	52280
<i>Pseudopodoces humilis</i>	GCA_000331425.1	Scaffold	1043	5406
<i>Pterocles gutturalis</i>	GCA_000699245.1	Scaffold	1069.32	58607
<i>Pteropus alecto</i>	GCA_000325575.1	Scaffold	1985.98	65598
<i>Pteropus vampyrus</i>	GCA_000151845.2	Scaffold	2198.28	36094
<i>Pundamilia nyererei</i>	GCA_000239375.1	Scaffold	830.133	7236
<i>Pygocentrus nattereri</i>	GCA_001682695.1	Scaffold	1285.35	283518
<i>Pygoscelis adeliae</i>	GCA_000699105.1	Scaffold	1216.62	19265
<i>Python bivittatus</i>	GCA_000186305.2	Scaffold	1435.05	39113
<i>Rana catesbeiana</i>	GCA_002284835.2	Scaffold	6250.35	1544635
<i>Rattus norvegicus</i>	GCA_000001895.4	Chromosome	2870.18	1395
<i>Rhincodon typus</i>	GCA_001642345.2	Scaffold	2931.6	57334
<i>Rhinolophus sinicus</i>	GCA_001888835.1	Scaffold	2073.34	63439
<i>Rhinopithecus bieti</i>	GCA_001698545.1	Scaffold	2977.07	105032
<i>Rhinopithecus roxellana</i>	GCA_000769185.1	Scaffold	2899.55	135512
<i>Rousettus aegyptiacus</i>	GCA_001466805.2	Scaffold	1910.25	2490

<i>Saimiri boliviensis boliviensis</i>	GCA_000235385.1	Scaffold	2608.59	2686
<i>Salmo salar</i>	GCA_000233375.4	Chromosome	2966.89	241573
<i>Salvelinus alpinus</i>	GCA_002910315.2	Chromosome	2169.55	16702
<i>Sarcophilus harrisii</i>	GCA_000189315.1	Scaffold	3174.69	35974
<i>Scleropages formosus</i>	GCA_001624265.1	Scaffold	777.359	4819
<i>Scophthalmus maximus</i>	GCA_003186165.1	Chromosome	524.979	22
<i>Serinus canaria</i>	GCA_000534875.1	Scaffold	1152.1	304400
<i>Seriola dumerili</i>	GCA_002260705.1	Scaffold	677.686	34656
<i>Seriola lalandi dorsalis</i>	GCA_002814215.1	Scaffold	732.51	99598
<i>Sinocyclocheilus anshuiensis</i>	GCA_001515605.1	Scaffold	1632.72	85682
<i>Sinocyclocheilus grahami</i>	GCA_001515645.1	Scaffold	1750.29	31277
<i>Sinocyclocheilus rhinoceros</i>	GCA_001515625.1	Scaffold	1655.79	164173
<i>Sorex araneus</i>	GCA_000181275.2	Scaffold	2423.16	12845
<i>Stegastes partitus</i>	GCA_000690725.1	Scaffold	800.492	5818
<i>Struthio camelus australis</i>	GCA_000698965.1	Scaffold	1225.04	6915
<i>Sturnus vulgaris</i>	GCA_001447265.1	Scaffold	1036.76	2361
<i>Sus scrofa</i>	GCA_000003025.6	Chromosome	2501.91	706
<i>Taeniopygia guttata</i>	GCA_000151805.2	Chromosome	1232.14	37422
<i>Takifugu rubripes</i>	GCA_000180615.2	Chromosome	391.485	7091
<i>Tauraco erythrolophus</i>	GCA_000709365.1	Scaffold	1155.54	59587
<i>Terrapene mexicana triunguis</i>	GCA_002925995.2	Scaffold	2571.27	52260
<i>Tetraodon nigroviridis</i>	GCA_000180735.1	Scaffold	342.403	25773
<i>Thamnophis sirtalis</i>	GCA_001077635.2	Scaffold	1424.9	7930
<i>Theropithecus gelada</i>	GCA_003255815.1	Chromosome	2889.63	15308
<i>Tinamus guttatus</i>	GCA_000705375.2	Scaffold	1047.06	82514
<i>Trichechus manatus latirostris</i>	GCA_000243295.1	Scaffold	3103.81	6323
<i>Tupaia chinensis</i>	GCA_000334495.1	Scaffold	2846.58	50750
<i>Tursiops truncatus</i>	GCA_001922835.1	Scaffold	2132.52	2648
<i>Tyto alba</i>	GCA_000687205.1	Scaffold	1120.14	62122
<i>Ursus maritimus</i>	GCA_000687225.1	Scaffold	2301.38	23819
<i>Vicugna pacos</i>	GCA_000164845.3	Scaffold	2172.21	276725
<i>Xenopus laevis</i>	GCA_001663975.1	Chromosome	2718.43	108033
<i>Xenopus tropicalis</i>	GCA_000004195.3	Chromosome	1440.4	6822
<i>Xiphophorus maculatus</i>	GCA_002775205.2	Chromosome	704.321	102
<i>Zonotrichia albicollis</i>	GCA_000385455.1	Scaffold	1052.6	6018

**Table S5. The *wcs* genes in representative mammals**

<b>Order</b>	<b>Species Name</b>	<b>Assembly No.</b>	<b>Accession No. of annotated proteins</b>	<b>The <i>wcs1/wcs2</i> gene location</b>
Carnivora	<i>Mustela putorius</i>	GCF_000215625.1	XP_004767240.1	NW_004569271.1; 511191-517139
	<i>Gulo gulo</i>	GCA_900006375.1	-	CYRY01007490.1; 30570-31445
	<i>Neomonachus schauinslandi</i>	GCF_002201575.1	XP_021537091.1	NW_018734283.1; 5480286-5485923
	<i>Ursus maritimus</i>	GCF_000687225.1	XP_008682926.1	NW_007907049.1; 194187-199842
	<i>Canis lupus</i>	GCF_000002285.3	XP_013970526.1	NC_006583.3; 106044100-106050204
	<i>Lycaon pictus</i>	GCA_001887905.1	-	CM007565.1; 106017032-106017963
	<i>Felis catus</i>	GCF_000181335.3	XP_023100688.1	NC_018737.3; 7510146-7515634
Perissodactyla	<i>Panthera pardus</i>	GCF_001857705.1	XP_019281070.1	NW_017619948.1; 1531829-1537015
	<i>Equus asinus</i>	GCF_001305755.1	XP_014719200.1	NW_014638281.1; 7411040-7419383
	<i>Equus przewalskii</i>	GCF_000696695.1	XP_008505767.1	NW_007678110.1; 72459-75543
	<i>Tursiops aduncus</i>	GCA_003227395.1	-	NCQN01016172.1; 132659-133487
	<i>Lipotes vexillifer</i>	GCF_000442215.1	XP_007463474.1	NW_006790237.1; 1991729-1992565
Cetartiodactyla	<i>Balaenoptera acutorostrata</i>	GCF_000493695.1	XP_007179977.1	NW_006726699.1; 2079862-2086128
	<i>Ovis aries</i>	GCF_000765115.1	XP_014944740.1	NC_019471.2; 55792422-55797540
	<i>Capra hircus</i>	GCF_001704415.1	XP_017918366.1	NC_030825.1; 57960701-57967132
	<i>Bos taurus</i>	GCF_002263795.1	NP_001039692.2	NC_037345.1; 56859876-56866365
	<i>Bison bison</i>	GCF_000754665.1	XP_010847965.1	NW_011494857.1; 2180321-2187416

	<i>Elaphurus davidianus</i>	GCA_002443075.1	-	JRFZ01026799.1; 349692-350516
	<i>Camelus bactrianus</i>	GCF_000767855.1	XP_010945334.1	NW_011511555.1; 5218030-5224219
	<i>Vicugna pacos</i>	GCA_000767525.1	XP_015098307.1	NW_005882787.1; 1977864-1984143
	<i>Rhinolophus sinicus</i>	GCF_001888835.1	XP_019597236.1	NW_017739093.1; 110007-115759
Chiroptera	<i>Hipposideros armiger</i>	GCF_001890085.1	XP_019513661.1	NW_017731633.1; 2162321-2171724
	<i>Pteropus alecto</i>	GCF_000325575.1	XP_006905058.1	NW_006430464.1; 797058-801909
	<i>Mus musculus</i>	GCA_000001635.8	NP_080156.2	NC_000073.6; 44246720-44252319
	<i>Apodemus sylvaticus</i>	GCA_001305905.1	-	LIPJ01004130.1; 41554-42407
	<i>Microtus agrestis</i>	GCA_001305995.1	-	LIQJ01000765.1; 69196-70049
	<i>Cricetulus griseus</i>	GCF_000223135.1	XP_003510246.3	NW_003614844.1; 195628-202136
Rodentia	<i>Nannospalax galili</i>	GCA_000622305.1	XP_008843388.1	NW_008348313.1; 2489091-2494924
	<i>Jaculus jaculus</i>	GCA_000280705.1	XP_004672622.1	NW_004504511.1; 768201-769049
	<i>Marmota marmota</i>	GCA_001458135.1	XP_015351935.1	NW_015351255.1; 450486-454453
	<i>Cavia aperea</i>	GCA_000688575.1	-	No wcs1/wcs2
	<i>Cavia porcellus</i>	GCA_000151735.1	-	No wcs1/wcs2
	<i>Macaca mulatta</i>	GCF_000772875.2	-	NC_027911.1; 46166071-46166355 and 46166414-46166671
Primates	<i>Cercocebus atys</i>	GCF_000955945.1	-	NW_012001739.1; 6350532-6351125
	<i>Chlorocebus sabaues</i>	GCF_000409795.2	-	NC_023647.1; 43847003-43847299
	<i>Rhinopithecus roxellana</i>	GCF_000769185.1	-	NW_010809787.1; 1662238-1662426 and 1662510-1662580 and 1662530-1662828

	<i>Colobus angolensis</i>	GCF_000951035.1	-	NW_012115710.1; 3111987-3112148 and 3112204-3112488
	<i>Homo sapiens</i>	GCF_000001405.38	-	NC_000019.10; 50798339-50798451 and 50798544-50798837
	<i>Callithrix jacchus</i>	GCF_000004665.1	-	NC_013917.1; 42634234-42634377 and 42634383-42634724
	<i>Eulemur macaco</i>	GCA_001262655.1	-	LGHX01005996.1; 263684-263804 and 263948-264217
	<i>Prolemur simus</i>	GCA_003258685.1	-	MPIZ01000407.1; 672236-672607 and 672648-672827
Dermoptera	<i>Galeopterus variegatus</i>	GCF_000696425.1	-	NW_007734068.1; 62183-62605
Afrosoricida	<i>Echinops telfairi</i>	GCF_000313985.1	-	NW_004558746.1; 16030568-16031425
	<i>Chrysochloris asiatica</i>	GCF_000296735.1	-	No wcs1/wcs2
Macroscelidea	<i>Elephantulus edwardii</i>	GCF_000299155.1	-	No wcs1/wcs2
Sirenia	<i>Trichechus manatus</i>	GCF_000243295.1	-	NW_004444023.1; 5916284-5916649 and 5916658-5916744 and 5916737-5917069
Proboscidea	<i>Loxodonta africana</i>	GCF_000001905.1	-	NW_003573424.1; 10634710-10635076
Pilosa	<i>Choloepus hoffmanni</i>	GCA_000164785.2	-	KN189048.1; 212821-213123
Cingulata	<i>Dasybus novemcinctus</i>	GCF_000208655.1	-	NW_004499039.1; 142598-142954 and 142947-143447
	<i>Phascolarctos cinereus</i>	GCF_002099425.1	XP_020862835.1	NW_018344070.1; 2529148-2530875
Diprotodontia	<i>Vombatus ursinus</i>	GCA_900497805.1	-	UNPS01001419.1; 22363703-22365057 and 22365071-22365397
	<i>Notamacropus eugenii</i>	GCA_000004035.1	-	GL053672.1; 6548-8113 and 8124-8330
Dasyuromorphia	<i>Sarcophilus harrisii</i>	GCF_000189315.1	-	NW_003831580.1; 2019579-2021139
Didelphimorphia	<i>Monodelphis domestica</i>	GCF_000002295.2	XP_007493718.1	NC_008804.1; 73129202-73135896

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**Table S6. Sequences used for inferring the phylogenetic tree of ACP proteins**

<b>Order</b>	<b>Species Name</b>	<b>Accession No.</b>	<b>Annotation</b>
Carnivora	<i>Mustela putorius</i>	XP_012919578.1	ACPT
		XP_004763128.1	ACP2
		XP_004762560.1	ACPP
		XP_004779679.1	ACP6
Perissodactyla	<i>Equus asinus</i>	XP_014718797.1	ACPT
		XP_014716804.1	ACP2
		XP_014713490.1	ACPP
		XP_014722553.1	ACP6
Chiroptera	<i>Pteropus alecto</i>	XP_006905160.1	ACP4
		XP_024899878.1	ACP2
		XP_006907308.2	ACPP
		XP_006919758.1	ACP6
Cetartiodactyla	<i>Bos taurus</i>	NP_001193896.1	ACP4
		XP_005216540.1	ACP2
		NP_001092336.1	ACPP
		NP_001092843.1	ACP6
Rodentia	<i>Mus musculus</i>	NP_001181963.1	ACP4
		XP_011249074.2	ACPT
		NP_031413.1	ACP2
		NP_997551.1	ACPP
		NP_062774.2	ACP6
Primates	<i>Homo sapiens</i>	NP_149059.1	ACP4
		NP_001601.1	ACP2
		NP_001127666.1	ACPP
		NP_057445.4	ACP6
Dermoptera	<i>Galeopterus variegatus</i>	XP_008590706.1	ACPT
		XP_008572913.1	ACP2
		XP_008582843.1	ACPP
		XP_008584870.1	ACP6
Afrosoricida	<i>Echinops telfairi</i>	XP_004710509.1	ACPT
		XP_004708405.1	ACP2
		XP_004704234.1	ACPP
		XP_004717322.1	ACP6
Afrosoricida	<i>Chrysochloris asiatica</i>	XP_006868200.1	ACPT
		XP_006865134.1	ACP2
		XP_006846702.1	ACPP
		XP_006861753.1	ACP6
Macroscelidea	<i>Elephantulus edwardii</i>	XP_006897413.1	ACPT

		XP_006896764.1	ACP2
		XP_006902611.1	ACPP
		XP_006899586.1	ACP6
Sirenia	<i>Trichechus manatus</i>	XP_004381771.1	LOC101344314 (ACPT/ACP4)
		XP_004387749.1	LOC101351012 (ACP2)
		XP_012412448.1	LOC101348525 (ACPP)
		XP_004380386.1	LOC101355450 (ACP6)
Proboscidea	<i>Loxodonta africana</i>	XP_003406888.1	ACP4
		XP_003412297.2	ACP2
		XP_003420955.2	ACPP
		XP_010599619.1	ACP6
Cingulata	<i>Dasybus novemcinctus</i>	XP_004458002.1	ACP2
		XP_023444307.1	ACPP
		XP_023441314.1	ACP4
		XP_004469024.1	ACP6



