

1 Frequent Cross-Species Transmission of Parvoviruses  
2 Among Diverse Carnivore Hosts

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37 **Although parvoviruses are commonly described in domestic carnivores, little is known**  
38 **about their biodiversity in non-domestic species. A phylogenetic analysis of VP2 gene**  
39 **sequences from puma, coyote, gray wolf, bobcat, raccoon, and striped skunk revealed**  
40 **two major groups related to either feline panleukopenia virus ('FPV-like') or canine**  
41 **parvovirus ('CPV-like'). Cross-species transmission was commonplace, with multiple**  
42 **introductions into each host species but, with the exception of raccoons, relatively little**  
43 **evidence for onward transmission in non-domestic species.**

44

45 Determining how viruses infect and spread in new host species is central to the study of disease  
46 emergence (10, 16). The spread of canine parvovirus (CPV) in dogs during the late 1970s is  
47 one of the best documented examples of viral emergence leading to a pandemic in a new host  
48 (17). It has been widely assumed that the new canine virus (initially known as CPV-2) emerged  
49 in dogs following the cross-species transfer of feline panleukopenia virus (FPV) from cats or a  
50 related carnivore host (16, 18, 22). Comparing isolates of FPV and CPV has provided important  
51 insights into the viral mutations controlling host range, and how different interactions with the  
52 host transferrin receptor type-1 (TfR) enabled both adaptation to dogs and the later evolution of  
53 the CPV-2a, CPV-2b and CPV-2c variants that exhibit characteristic differences in antigenic  
54 sites and in cell tropism (17, 21, 23).

55 A variety of host species other than domestic cats and dogs harbor closely related  
56 parvoviruses, and it has become increasingly apparent that non-domestic animals are  
57 commonly infected, even though little disease is observed in many cases (3, 7, 12, 19, 20).  
58 However, those parvoviruses previously detected in a variety of other species – including many  
59 different large cats, raccoons, raccoon dogs, arctic foxes, and mink – often represent  
60 opportunistic samples obtained from animals in artificial settings such as zoos or fur farms (6,  
61 13, 24), with the majority of these viruses falling into a single ‘FPV-like’ clade distinct from CPV  
62 in dogs (15, 18). More recently, raccoons from a variety of locations in the United States have  
63 been shown to commonly harbor parvoviruses, which they have likely been associated with for  
64 at least 20 years (1). Notably, most raccoon parvovirus sequences, as well as a single isolate  
65 from a bobcat, fell in ‘intermediate’ locations between the dog-associated CPV-2 and CPV-2a  
66 strains in a phylogenetic tree of the VP2 protein (1). Hence, raccoon parvoviruses may have  
67 played a central role in the transition between CPV-2 and the later CPV-2a, -2b and -2c variants  
68 that not only infected dogs, but regained the ability to infect cats (a property lost in CPV-2).  
69 Indeed, the CPV-like viruses from raccoons possess multiple amino acid changes on the

70 surface of their capsids that affect binding to the host-specific TfR, resulting in loss of the canine  
71 host range and altering neutralizing antibody epitopes (1, 4).

72 To further clarify virus-host relationships we characterized parvoviruses that circulate in  
73 several species of wild carnivore in the United States, determining those which represent viable  
74 hosts for parvoviruses by sustaining prolonged viral transmission, and those in which parvovirus  
75 infections are apparently transient spill-overs. Accordingly, we sampled 58 novel parvoviruses  
76 from either free-ranging (gray wolf, coyote, bobcat, puma, striped skunk, raccoon) or wild  
77 species that were brought into captive outdoor facilities for rehabilitation (raccoon) or  
78 containment (gray [Mexican] wolf) purposes (Table 1). All new FPV and CPV sequences were  
79 obtained from carnivores that were either showing typical clinical signs of parvovirus infection  
80 (e.g. hemorrhagic enteritis), or were asymptomatic, suggestive of either an active, but  
81 subclinical infection, or recovery from a previous infection in which persistent DNA could be  
82 detected in tissues. The detection of viral DNA in animals without active infection is likely due to  
83 residual DNA in tissues after virus was inactivated by the host immune response, and parallels  
84 the results reported for life-long residual DNA of human parvoviruses (14), as well as recent  
85 reports of persistent DNA in cats (9). In most cases, tissue samples (gastrointestinal tract,  
86 mesenteric lymph node, spleen, tongue, or feces) approximately 0.5mm<sup>3</sup> in size were placed in  
87 1.5 ml microcentrifuge tubes and stored at -20°C until further processing. DNA was extracted  
88 from tissues using a commercial kit (Qiagen, Valencia, CA) according to the manufacturer's  
89 instructions and the complete VP2 gene was amplified as described previously (1). Care was  
90 taken to avoid PCR contamination, and samples were handled in a series of separate work  
91 areas to avoid cross contamination.

92 Viral sequences from additional hosts, largely domesticated or farmed animals, were  
93 obtained from GenBank. CPV sequences were sub-sampled so that only representative strains  
94 with known year of isolation (which is not necessarily the date of infection) were included in the  
95 final analysis, resulting in a final data set of 234 sequences, 1755 nucleotides in length. These

96 sequences were found to be free of recombination using the RDP3 package (11). The numbers  
97 of sequences available for each group are given in the legend to Fig. 1. To estimate rates of  
98 evolutionary change, times to common ancestry, and the phylogenetic history of the carnivore  
99 parvoviruses we employed the Bayesian Markov chain Monte Carlo method available within the  
100 BEAST package (5). To account for statistical uncertainty all estimates are based on values of  
101 the 95% Highest Probability Density (HPD). We employed the GTR+ $\Gamma_4$  model of nucleotide  
102 substitution along with an uncorrelated lognormal relaxed molecular clock and a Bayesian  
103 skyline coalescent prior. Two BEAST runs were undertaken of 200 million steps each and  
104 combined for the final analysis, with a 10% burnin. We also estimated the Maximum Clade  
105 Credibility (MCC) tree for the data in hand, with support for individual groupings reflected in  
106 posterior probability values.

107 Our phylogenetic analysis of complete VP2 sequences from 234 carnivore parvoviruses  
108 reveals a major division between the 'FPV-like' and 'CPV-like' viruses (Fig. 1). However,  
109 determination of the exact evolutionary relationships, and hence the number and direction of  
110 cross-species transmission events, was often difficult because of a lack of resolution in some  
111 parts of the phylogeny. Despite this uncertainty, it was striking that viruses sampled from  
112 individual species usually fell in diverse locations across the phylogeny indicative of multiple  
113 introduction events. The most notable case in point are those viruses sampled from raccoons.  
114 A minority of raccoon sequences (6 of 40) fell into the FPV-like group, four of which were  
115 sampled more than 20 years ago (from 1979 to 1990). That two viruses sampled from 1990  
116 and 2010 cluster together (although with weak support) is compatible with the continuous  
117 circulation of this particular lineage of FPV-like parvoviruses in raccoons, albeit at low frequency.  
118 The majority of raccoon parvoviruses (34 of 40) cluster with the CPV-like viruses, and occupy  
119 diverse positions, both phylogenetically and geographically. In particular, there is a cluster of  
120 eight raccoon viruses, as well as two puma viruses and single bobcat sequence, that occupy a  
121 phylogenetic position intermediate between CPV-2 and CPV-2a, and which has strong statistical

122 support (Fig. 1). That this multi-host viral lineage diverged early in the evolutionary history of  
123 CPV, yet has persisted to the present day, indicates that it has circulated for an extended time  
124 period. In addition, there is a large (although poorly supported) clade of 20 CPV-like raccoon  
125 viruses, along with all three viruses from the striped skunk, and single viruses from a bobcat and  
126 a coyote. These evolutionary patterns add to the details revealed of our previous study of VP2  
127 evolution (1), where most of the raccoon viruses fell in intermediate positions between CPV-2  
128 and CPV-2a, and highlight the complexity of the virus-host relationships.

129 All the CPV-like raccoon viruses from this and our previous study (1) were sampled  
130 between 2007-2012, such that they represent the current genetic diversity of parvoviruses in  
131 raccoons, and from diverse locations throughout the United States (California, Colorado, Florida,  
132 Georgia, Illinois, Kentucky, Maine, Mississippi, New Jersey, New York, South Carolina,  
133 Tennessee, Wisconsin, Virginia). That there are well-supported sub-clusters that only contain  
134 raccoon viruses, and which cover multiple years and locations, strongly suggests that there is  
135 sustained onward transmission of parvoviruses in raccoons. The raccoon viruses are also often  
136 very closely related to those sampled from other carnivore species (see below), suggesting that  
137 raccoons may represent conduits for parvovirus transmission to other hosts.

138 The seven virus sequences from mink (MEV) also represent clear examples of sustained  
139 transmission in a single host species. These sequences fall into three distinct locations in the  
140 FPV-like cluster, indicative of three cross-species events from cats or a closely related host (Fig.  
141 1). However, as these MEV sequences are associated with outbreaks in farm situations, it is  
142 unclear whether sustained transmission also occurs in wild mink (2).

143 Of the 16 puma virus VP2 sequences analyzed, five are FPV-like and 11 are CPV-like.  
144 Along with raccoons, pumas are the only species whose viruses are detected on both the FPV-  
145 like and CPV-like parts of the phylogenetic tree. Three of the FPV-like sequences are identical,  
146 which is tentatively compatible with onward viral transmission in this species. The remaining  
147 two FPV-like puma sequences are singletons and indicative of separate viral introductions,

148 while the 11 CPV-like puma sequences fall in diverse locations across that part of the phylogeny.  
149 Hence, there have clearly been multiple independent cross-species transmissions into pumas  
150 and these occurred from both CPV and FPV ancestors.

151 A similar pattern of multiple introductions was apparent for those viruses sampled from  
152 coyotes, gray wolves, and bobcats, although these viruses were all CPV-like. Of the nine  
153 coyote sequences, one clustered with raccoon viruses, while the remainder were closely related  
154 to CPV-2b and -2c. Although only four bobcat sequences are available, three cluster within the  
155 main groups of raccoon-associated viruses, while the other groups with a number of CPV-2c  
156 isolates. The four gray wolf sequences also fall at multiple locations within the CPV-2b and -2c  
157 sequences, again indicative of independent cross-species transmission events. The only case  
158 in which multiple sequences sampled from a single host group together, which is tentatively  
159 compatible with a single cross-species transmission event, is that of the striped skunk; the three  
160 sequences from this species are identical and fall within the main cluster of raccoon viruses.

161 Finally, the CPV-like phylogeny also contained individual sequences from a virus  
162 sampled from a masked palm civet (GenBank accession EU441280, unpublished), which was  
163 linked by a long branch to the 'intermediate' raccoon group (although with weak support), and a  
164 virus associated with an outbreak in rhesus monkeys (GenBank accession FJ231389, ref. 26)  
165 that falls at the base of the CPV-like part of the tree, again with weak support. Because these  
166 are single viral sequences it is difficult to determine whether they simply represent transient  
167 spill-over infections.

168 A number of cross-species transmission events were also documented with the FPV-like  
169 viruses, in addition to the raccoon and puma parvoviruses described above. Two identical  
170 sequences from arctic ('blue') foxes sampled in 2007 and 2008 cluster with a single MEV  
171 sequence collected in 1978, a single puma sequence sampled in 2010, and the oldest FPV (cat)  
172 virus that was sampled in 1964. Furthermore, two sequences from lion and tiger clearly  
173 represent spill-over infections of FPV in a zoological setting (6). Overall, our phylogenetic



174 analysis reveals a significant biodiversity of parvoviruses in non-domestic animals, and which is  
175 clearly the result of multiple cross-species transmission events, but with relatively little evidence  
176 at present for onward transmission in the new host species.

177         One of the most striking features of this analysis was that the majority of the carnivore  
178 parvoviruses described here are CPV-like rather than FPV-like; for example, 85% of the  
179 raccoon parvoviruses are CPV-like, including all but two of the viruses sampled between 2007-  
180 2012. It is possible that this bias toward CPV-like viruses reflects the phylogenetic relationships  
181 of the host species in question, such that fewer adaptive mutations are required for viruses to  
182 infect phylogenetically similar hosts. Specifically, most of the carnivore parvoviruses – dog,  
183 raccoon, coyote, gray wolf, mink, striped skunk and fox – infect hosts within the suborder  
184 Caniformia. Of these, the viruses from coyote, gray wolf, and striped skunk are only CPV-like,  
185 as are most raccoon parvoviruses. However, any such phylogenetic ‘rule’ is clearly a weak one  
186 because viruses from bobcats and pumas (suborder Feliformia) are either exclusively or  
187 predominantly CPV-like, and FPV-like viruses were recently discovered in Eurasian badgers (3),  
188 a caniform species. Alternatively, some of the virus-host relationships depicted in our  
189 phylogenetic analysis may reflect the ecological relationships among the species in question,  
190 especially predator-prey relationships. In particular, it is well documented that large carnivores  
191 such as pumas, wolves, and coyotes feed on other smaller species, such as raccoons. It is  
192 therefore conceivable that parvoviruses are able to move between hosts during predation and/or  
193 scavenging of carcasses, although seemingly with little onward transmission.

194         Early studies suggested that CPV in dogs was directly derived from an FPV in a  
195 domestic cat (15, 18). However, the diverse range of parvoviruses in other carnivore species  
196 means that is no longer necessary to think that cats must be the source of the virus that  
197 emerged in dogs in the late 1970s. We therefore attempted to root the carnivore parvovirus tree  
198 using the closest exogenous parvovirus (porcine parvovirus 27a; GenBank accession  
199 AY684871) as an outgroup in a phylogenetic analysis of VP2 amino acid sequences. However,

200 the porcine virus is so divergent (mean pairwise amino acid identity to the carnivore  
201 parvoviruses of 58%) that it provided insufficient resolution. Consequently, we relied on our  
202 MCC tree, which is rooted under the assumption of a relaxed molecular clock (Fig. 1), and  
203 which placed the root between the FPV-like and CPV-like groups. If this rooting scheme is  
204 correct, then CPV was not directly derived from the known genetic diversity of FPV in domestic  
205 cats as previously supposed. Rather, this phylogenetic analysis suggests that CPV and FPV  
206 were separately derived from common ancestors the nature of which – i.e. which host(s) they  
207 infected – is unknown, and that their progenitor lineages evolved independently for a time period  
208 that extends beyond the first description of CPV in dogs.

209 This analysis also suggested a relatively recent evolutionary history for this diversity of  
210 carnivore parvoviruses. Our estimate of the rate of evolutionary change was between 1.09 and  
211  $1.79 \times 10^{-4}$  nucleotide substitutions per site, per year (95% HPD values). Under these rates, the  
212 Time to the Most Recent Common Ancestor (TMRCA) of the entire tree was between 60-118  
213 years before present, with the sampled diversity within the FPV-like and CPV-like clades having  
214 TMRCA of 57-89 (1923-1955) and 40-79 (1933-1972) years before present, respectively.  
215 Infections attributable to FPV have been reported in cats and raccoons from the 1920s and  
216 1940s (8, 25, 26), although any earlier history is not known. The approximate time-scale of the  
217 myriad of other cross-species transmission events can be inferred from the MCC tree (Fig. 1),  
218 and indicate that the frequent species jumping depicted in this phylogeny occurred within the  
219 last century. For example, the common ancestors of the ‘intermediate’ and main groups of  
220 raccoon viruses existed 1991-2009 and 1981-1995, respectively.

221 While epidemiological studies indicate that CPV spread worldwide among domestic dogs  
222 in a pandemic after 1977, our phylogenetic analysis shows that the FPV and CPV clades are  
223 separated by a relatively long branch, and that there is no virus that is obviously the ancestor of  
224 CPV. Our molecular dating analysis suggests that both clades have been evolving  
225 independently for part of the last century, although their ultimate origins, and particularly the

226 animal species from which they are derived, are unclear. In this context it is important to note  
227 that the new samples described here were all collected from wild hosts in North America, and  
228 CPV antibodies in dogs were present in dogs in Europe (but not in North America, Australia or  
229 Japan) up to four years before the virus spread worldwide (15). Evidently, future studies of  
230 parvovirus evolution should be based on a broader sampling of domestic and wild hosts in  
231 different parts of the world, and on an analysis of complete viral genomes.

232

233

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314 **FIGURE LEGENDS**

315 **Fig. 1.** Phylogenetic history (MCC tree) of carnivore parvoviruses inferred from 234 complete  
316 VP2 sequences. Clusters of viruses are labeled and colored according to host species (note  
317 that the division between CPV-2a, 2b and 2c sequences is not shown in this figure). Hosts in  
318 the 'other' group, which represent singleton viruses, are lion, palm civet, monkey and tiger.  
319 Because the tree was inferred using a relaxed molecular clock, all tip heights are scaled to the  
320 year of sampling. Posterior probability values > 0.9 at major nodes or which connect multiple  
321 species are marked by a \* symbol. A time-scale in years is given by the x-axis. The number of  
322 sequences from each species or antigenic group is as follows: FPV (cat, *Felis catus*), n = 52  
323 sequences; CPV-2 (dog, *Canis lupus familiaris*), n = 7; CPV-2a (dog), n = 48; CPV-2b (dog), n =  
324 28; CPV-2c (dog), n = 9; raccoon (*Procyon lotor*), n = 40; puma (*Puma concolor*), n = 16; coyote  
325 (*Canis latrans*), n = 9; mink (mink enteritis virus, MEV; *Neovison vison*), n = 7; bobcat (*Lynx*  
326 *rufus*), n = 4; gray wolf (*Canis lupus*), n = 4; arctic fox (*Vulpes lagopus*; arbitrarily designated as  
327 'blue fox' parvovirus (BFPV)), n = 3; striped skunk (*Mephitis mephitis*), n = 3; palm civet  
328 (*Paradoxurus hermaphroditus*), n = 1; tiger (*Panthera tigris*), n = 1; lion (*Panthera leo*), n = 1;  
329 and monkey (*Macaca fascicularis* or *Macaca mulatta*), n = 1.

330

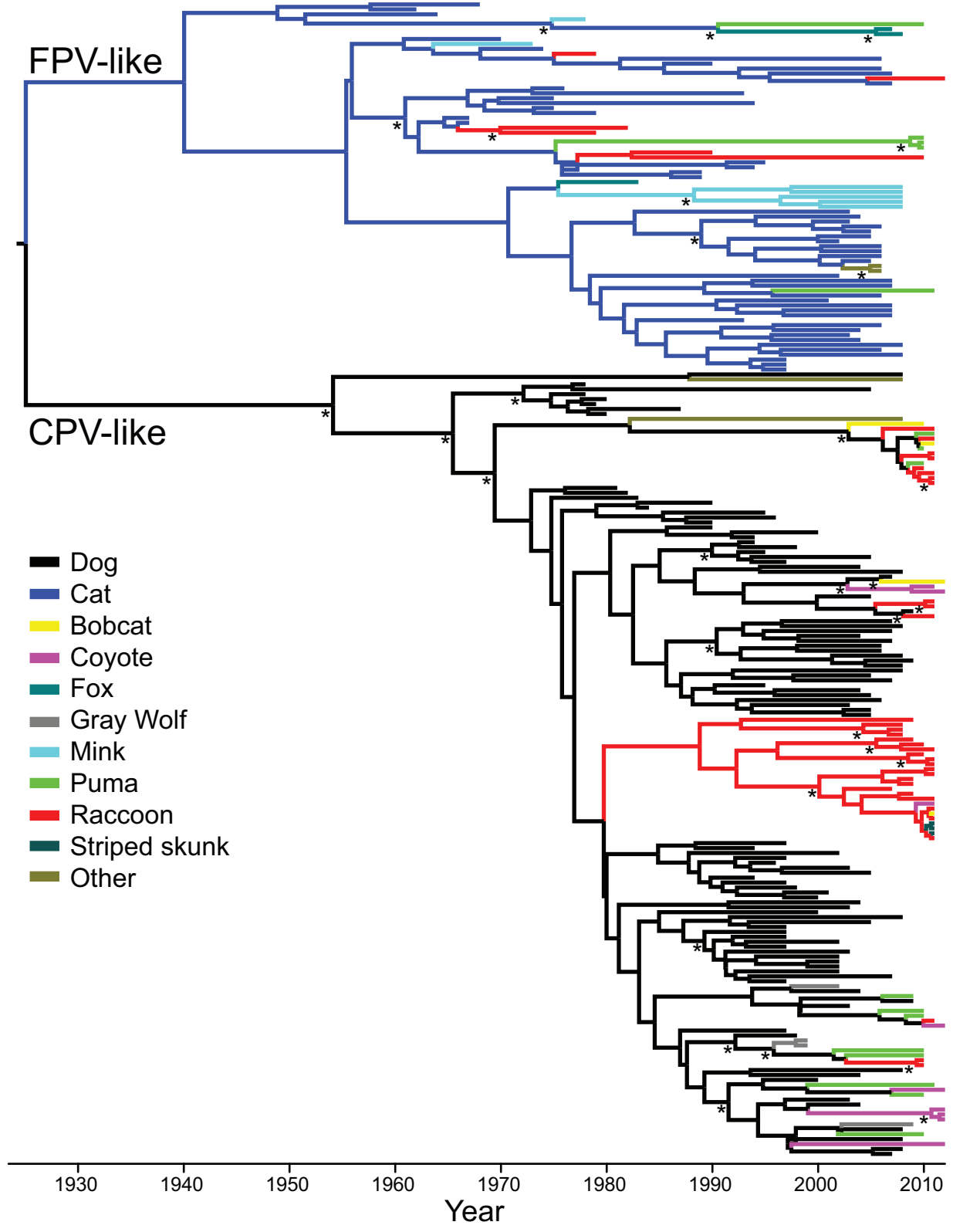




TABLE 1. Carnivore parvoviruses sequenced and analyzed here

Isolate	Virus	Host	County	State	Year	GenBank
CPV-2b/Gray wolf/AZ/16382-01/99	CPV-like	<i>Canis lupus baileyi</i>	Greenlee	Arizona	1999	JX475240
CPV-2b/Gray wolf/NM/16401-01/99	CPV-like	<i>Canis lupus baileyi</i>	Socorro	New Mexico	1999	JX475241
CPV-2b/Gray wolf/WI/18268/02	CPV-like	<i>Canis lupus nubilus</i>	Langlade	Wisconsin	2002	JX475242
CPV-2c/Gray wolf/ID/22772/09	CPV-like	<i>Canis lupus occidentalis</i>	Camas	Idaho	2009	JX475243
CPV-2b/Puma/CO/2235/09	CPV-like	<i>Puma concolor</i>	Douglas	Colorado	2009	JX475251
FPV/Puma/CO/952/10	FPV-like	<i>Puma concolor</i>	Yuma	Colorado	2010	JX475245
CPV/Puma/CO/2503/10	CPV-like	<i>Puma concolor</i>	Larimer	Colorado	2010	JX475246
CPV-2b/Puma/CO/1246/10	CPV-like	<i>Puma concolor</i>	Jefferson	Colorado	2010	JX475247
CPV-2b/Puma/CO/898/10	CPV-like	<i>Puma concolor</i>	Larimer	Colorado	2010	JX475249
CPV-2b/Puma/CO/728/10	CPV-like	<i>Puma concolor</i>	Larimer	Colorado	2010	JX475250
CPV-2c/Puma/CO/1316/10	CPV-like	<i>Puma concolor</i>	Boulder	Colorado	2010	JX475252
FPV/Puma/CO/546/10	FPV-like	<i>Puma concolor</i>	Jefferson	Colorado	2010	JX475253
FPV/Puma/CO/977/10	FPV-like	<i>Puma concolor</i>	Clear Creek	Colorado	2010	JX475254
CPV-2b/Puma/CO/1237/10	CPV-like	<i>Puma concolor</i>	Weld	Colorado	2010	JX475257
CPV/Puma/CO/1321/10	CPV-like	<i>Puma concolor</i>	Larimer	Colorado	2010	JX475258
FPV/Puma/CO/545/10	FPV-like	<i>Puma concolor</i>	Chaffee	Colorado	2010	JX475259
CPV-2c/Puma/CO/704/10	CPV-like	<i>Puma concolor</i>	Jefferson	Colorado	2010	JX475260
CPV/Raccoon/CA/334-A/10	CPV-like	<i>Procyon lotor</i>	Contra Costa	California	2010	JX475261

CPV/Raccoon/CA/334-B/10	CPV-like	<i>Procyon lotor</i>	Contra Costa	California	2010	JX475262
CPV/Raccoon/CO/280/11	CPV-like	<i>Procyon lotor</i>	Jefferson	Colorado	2011	JX475231
CPV/Raccoon/VA/243-A/11	CPV-like	<i>Procyon lotor</i>	Clarke	Virginia	2011	JX475232
CPV/Raccoon/SC/182-A/11	CPV-like	<i>Procyon lotor</i>	Greenville	South Carolina	2011	JX475233
CPV/Raccoon/ME/258/11	CPV-like	<i>Procyon lotor</i>	Cumberland	Maine	2011	JX475234
CPV/Raccoon/ME/259/11	CPV-like	<i>Procyon lotor</i>	Cumberland	Maine	2011	JX475235
CPV/Raccoon/NY/87648/11	CPV-like	<i>Procyon lotor</i>	Oswego	New York	2011	JX475236
CPV-2b/Raccoon/CT/372/11	CPV-like	<i>Procyon lotor</i>	New Haven	Connecticut	2011	JX475237
CPV-2c/Coyote/GA/11/11	CPV-like	<i>Canis latrans</i>	Putnam	Georgia	2011	JX475238
CPV/Coyote/GA/06/11	CPV-like	<i>Canis latrans</i>	Putnam	Georgia	2011	JX475239
CPV-2c/Puma/CO/1269/11	CPV-like	<i>Puma concolor</i>	Boulder	Colorado	2011	JX475244
CPV/Puma/CO/1102/11	CPV-like	<i>Puma concolor</i>	Jefferson	Colorado	2011	JX475248
CPV/Raccoon/MS/257/11	CPV-like	<i>Procyon lotor</i>	DeSoto	Mississippi	2011	JX475255
FPV/Puma/CO/1103/11	FPV-like	<i>Puma concolor</i>	Boulder	Colorado	2011	JX475256
CPV/Raccoon/VA/218-A/11	CPV-like	<i>Procyon lotor</i>	Fairfax	Virginia	2011	JX475263
CPV/Striped skunk/TN/29/11	CPV-like	<i>Mephitis mephitis</i>	Knox	Tennessee	2011	JX475286
CPV/Striped skunk/TN/30/11	CPV-like	<i>Mephitis mephitis</i>	Knox	Tennessee	2011	JX475287
CPV/Striped skunk/TN/31/11	CPV-like	<i>Mephitis mephitis</i>	Knox	Tennessee	2011	JX475288
CPV/Raccoon/TN/1/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475279
CPV/Raccoon/TN/4/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475280

CPV/Raccoon/TN/5/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475281
CPV/Raccoon/TN/6/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475282
CPV-2b/Raccoon/TN/18/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475283
CPV/Raccoon/TN/26/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475284
CPV/Raccoon/TN/27/11	CPV-like	<i>Procyon lotor</i>	Knox	Tennessee	2011	JX475285
CPV/Raccoon/CO/585/11	CPV-like	<i>Procyon lotor</i>	Boulder	Colorado	2011	JX475264
CPV/Raccoon/CO/983/11	CPV-like	<i>Procyon lotor</i>	Boulder	Colorado	2011	JX475265
CPV-2b/Raccoon/IL/357/11	CPV-like	<i>Procyon lotor</i>	Franklin	Illinois	2011	JX475266
CPV-2b/Raccoon/CT/2D/11	CPV-like	<i>Procyon lotor</i>	New Haven	Connecticut	2011	JX475267
CPV/Bobcat/KS/3/11	CPV-like	<i>Lynx rufus</i>	Sheridan	Kansas	2011	JX475268
CPV/Bobcat/TN/10/11	CPV-like	<i>Lynx rufus</i>	Knox	Tennessee	2011	JX475271
CPV-2c/Coyote/CO/422/12	CPV-like	<i>Canis latrans</i>	Denver	Colorado	2012	JX475269
FPV/Raccoon/GA/1/12	FPV-like	<i>Procyon lotor</i>	Gwinnett	Georgia	2012	JX475270
CPV-2c/Bobcat/AL/362/12	CPV-like	<i>Lynx rufus</i>	Pike	Alabama	2012	JX475272
CPV-2c/Coyote/MT/909/12	CPV-like	<i>Canis latrans</i>	Prairie	Montana	2012	JX475273
CPV-2c/Coyote/MT/911/12	CPV-like	<i>Canis latrans</i>	Prairie	Montana	2012	JX475274
CPV-2c/Coyote/MT/914/12	CPV-like	<i>Canis latrans</i>	Prairie	Montana	2012	JX475275
CPV-2c/Coyote/MT/915/12	CPV-like	<i>Canis latrans</i>	Prairie	Montana	2012	JX475276
CPV-2c/Coyote/AL/361/12	CPV-like	<i>Canis latrans</i>	Butler	Alabama	2012	JX475277
CPV-2b/Coyote/AR/1069/12	CPV-like	<i>Canis latrans</i>	Prairie	Arkansas	2012	JX475278

