Table S1. Description of the collection of oropharyngeal swabs. * indicates RferPV1 infection. ** indicates EserPV1 infection. *** indicates EserPV2 infection. **** indicates EserPV3 infection.

Sample ID	Bat species	Year	Colony location
Tte6Granada	*Tadarida teniotis*	2002	Granada
Tte8Granada	*Tadarida teniotis*	2002	Granada
080514Rfe2*	*Rhinolophus ferrumequinum*	2008	País Vasco
080514Rfe5	*Rhinolophus ferrumequinum*	2008	País Vasco
080514Reu5	*Rhinolophus euryale*	2008	País Vasco
080514Reu6	*Rhinolophus euryale*	2008	País Vasco
070704Pas3	*Plecotus austriacus*	2007	Montagut, Girona
070704Pas4	*Plecotus austriacus*	2007	Montagut, Girona
071018Par1	*Plecotus auritus*	2007	País Vasco
080605Par1	*Plecotus auritus*	2008	País Vasco
080527Ppy11	*Pipistrellus pygmaeus*	2008	Sevilla
080527Ppy7	*Pipistrellus pygmaeus*	2008	Sevilla
070925Ppi6	*Pipistrellus pipistrellus*	2007	Cortes, Málaga
070925Ppi2	*Pipistrellus pipistrellus*	2007	Cortes, Málaga
070925Pku6	*Pipistrellus khulii*	2007	Cortes, Málaga
070925Pku7	*Pipistrellus khulii*	2007	Cortes, Málaga
3x13454	*Nyctalus noctula*	2007	Pamplona, Navarra
3x13463	*Nyctalus noctula*	2007	Pamplona, Navarra
5x01011	*Nyctalus leisleri*	2007	Cortes, Málaga
5x01008	*Nyctalus leisleri*	2007	Cortes, Málaga
080801Mna1	*Myotis cf. nattereri*	2008	País Vasco
080801Mna2	*Myotis cf. nattereri*	2008	País Vasco
070724Mmy1	*Myotis myotis*	2007	El Coronil, Sevilla
070724Mmy2	*Myotis myotis*	2007	El Coronil, Sevilla
070625Mes1	*Myotis escalerai*	2007	Zalamea, Huelva
070625Mes5	*Myotis escalerai*	2007	Zalamea, Huelva
080529Mem1	*Myotis emarginatus*	2008	País Vasco
080529Mem2	*Myotis emarginatus*	2008	País Vasco
2x19048	*Myotis daubentonii*	2007	Benaoján, Málaga
2x19044	*Myotis daubentonii*	2007	Benaoján, Málaga
080721Mbl1	*Myotis blythii*	2008	El Coronil, Sevilla
080721Mbl2	*Myotis blythii*	2008	El Coronil, Sevilla
070925Mbe1	*Myotis bechsteinii*	2007	Cortes, Málaga
070925Mbe2	*Myotis bechsteinii*	2007	Cortes, Málaga
080514Msc2	*Miniopterus schreibersii*	2008	País Vasco
080514Msc3	*Miniopterus schreibersii*	2008	País Vasco
070925Hsa	*Hypsugo savii*	2007	Cortes, Málaga
080709Hsa9	*Hypsugo savii*	2008	La Morera de Montsant, Tarragona
030626Ese10**	*Eptesicus serotinus*	2003	País Vasco
030626Ese32***/****	*Eptesicus serotinus*	2003	País Vasco

Sample ID	Bat species	Year	Colony location
3x31179	*Eptesicus isabellinus*	2007	El Coronil, Sevilla
3x31192	*Eptesicus isabellinus*	2007	El Coronil, Sevilla
070703Bba2	*Barbastella barbastellus*	2007	Albanyà, Girona
070703Bba1	*Barbastella barbastellus*	2007	Albanyà, Girona

Table S2. List of PVs used for phylogenetic inference. Four-color code background represents the four PV crown groups: Red, Alpha+Omikron; green, Beta+Xi; blue, Delta+Zeta; ochre, Lambda+Mu. Grey background highlights unclassified PVs.

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
ALPHA + OMIKRON	**Alpha**	Alpha-1	X74475	HPV32	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-2	X74465	HPV10	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-3	U31793	HPV61	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-4	X55964	HPV2	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-5	X74472	HPV26	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-6	X74482	HPV53	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-7	X05015	HPV18	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-8	U21941	HPV7	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-9	K02718	HPV16	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-10	X00203	HPV6	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
			X62844	PpPV1	Pygmy chimpanzee	*Pan paniscus*	Hominidae	Primates	Mammalia
			AF020905	PtPV1	Common chimpanzee	*Pan troglodytes*	Hominidae	Primates	Mammalia
		Alpha-11	X74476	HPV34	Human	*Homo sapiens*	Hominidae	Primates	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
ALPHA + OMIKRON	**Alpha**	Alpha-12	M60184	MmPV1	Rhesus macaque	*Macaca mulata*	Cercopithecidae	Primates	Mammalia
			JF304764	PhPV1	Hamadryas Baboon	*Papio hamadryas*	Cercopithecidae	Primates	Mammalia
		Alpha-13	U37488	HPV54	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Alpha-14	U31779	HPV90	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
			GU014532	CgPV1	Colobus monkey	*Colobus guereza*	Cercopithecidae	Primates	Mammalia
	Omega	Omega-1	EF536349	UmPV1[2]	Polar bear	*Ursus maritimus*	Ursidae	Carnivora	Mammalia
		Unclassified	JQ814847	MrPV1[2]	Rickett's big-footed bat	*Myotis ricketti*	Vespertilionidae	Chiroptera	Mammalia
	Omikron	Omikron-1	JN709470	TtPV5[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia
			JN709471	TtPV6[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia
			AJ238373	PsPV1[2]	Burmeister's porpoise	*Phocoena spinipinnis*	Phocoenidae	Cetacea	Mammalia
			GU117621.1	PphPV1[2]	Harbor porpoise	*Phocoena phocoena*	Phocoenidae	Cetacea	Mammalia
	Upsilon	Upsilon-1	EU240894	TtPV1[2]	Bottlenosed dolphin	*Tursiops truncatus*	Phocoenidae	Cetacea	Mammalia
			EU240895	TtPV3[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
ALPHA + OMIKRON	**Upsilon**	Upsilon-1	JN709469	TtPV4[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia
			JN709472	TtPV7[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia
			GU117620	DdPV1[2]	Dolphin	*Delphinus delphis*	Delphinidae	Cetacea	Mammalia
		Upsilon-2	AY956402	TtPV2[2]	Bottlenosed dolphin	*Tursiops truncatus*	Delphinidae	Cetacea	Mammalia
		Upsilon-3	GU117622	PphPV2[2]	Harbor porpoise	*Phocoena phocoena*	Phocoenidae	Cetacea	Mammalia
	Dyodelta	Dyodelta-1	EF395818	SsPV1[2]	Domestic pig	*Sus scrofa*	Suidae	Artiodactyla	Mammalia
	Dyopi	Dyopi-1	GU117623	PphPV4[2]	Harbor porpoise	*Phocoena phocoena*	Phocoenidae	Cetacea	Mammalia
BETA + XI	**Beta**	Beta-1	M17463	HPV5	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
			EF028290	MfPV1	Rhesus macaque	*Macaca mulata*	Cercopithecidae	Primates	Mammalia
			GU014533	CgPV2	Colobus monkey	*Colobus guereza*	Cercopithecidae	Primates	Mammalia
		Beta-2	X74464	HPV9	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Beta-3	X74480	HPV49	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Beta-4	AF531420	HPV92	Human	*Homo sapiens*	Hominidae	Primates	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
BETA + XI	**Beta**	Beta-5	AY382779	HPV96	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Beta-6	GU014531	MfPV2	Rhesus macaque	*Macaca mulata*	Cercopithecidae	Primates	Mammalia
	Gamma	Gamma-1	X70827	HPV4	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-2	HPU31789	HPV48	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-3	U31790	HPV50	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-4	U31792	HPV60	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-5	EF467176	HPV88	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-6	DQ080081	HPV101[1]	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-7	EU541441	HPV109	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-8	EU541442	HPV112	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-9	FJ804072	HPV116	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-10	GQ845443	HPV121	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-11	AB646346	HPV126	Human	*Homo sapiens*	Hominidae	Primates	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
BETA + XI	**Gamma**	Gamma-12	HM011570	HPV127	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-13	GU225708	HPV128	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-14	GU117631	HPV131	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-15	HM999987	HPV135	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-16	HM999989	HPV137	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Gamma-17	HM999996	HPV144	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
	Pi	Pi-1	HQ625440	AsPv1	Long-tailed Field Mouse	*Apodemus sylvaticus*	Muridae	Rodentia	Mammalia
			E15111	MaPV1	Golden hamster	*Mesocricetus auratus*	Cricetidae	Rodentia	Mammalia
		Pi-2	DQ664501	McPV2	Multimammate mouse	*Mastomys coucha*	Muridae	Rodentia	Mammalia
			DQ269468	MmiPV1	Harvest mouse	*Micromys minutus*	Muridae	Rodentia	Mammalia
			GU808564	MmuPV1	House mouse	*Mus musculus*	Muridae	Rodentia	Mammalia
			HQ625439	MmuPV1-var	House mouse	*Mus musculus*	Muridae	Rodentia	Mammalia
			GQ180114	RnPV1	Norway rat	*Rattus norvegicus*	Muridae	Rodentia	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
BETA + XI	**Phi**	Phi-1	DQ091200	ChPV1	Domestic goat	*Capra hircus*	Bovidae	Artiodactyla	Mammalia
	Tau	Tau-1	AY722648	CPV2	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			FJ492742	CPV7	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
		Tau-2	JX141478	CPV13	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
	Xi	Xi-1	AF486184	BPV3[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			X05817	BPV4[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			AJ620208	BPV6[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			AB331650	BPV9[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			AB331651	BPV10[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			AB543507	BPV11[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
		Xi-2	JF834523	BPV12[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
	Dyoxi	Dyoxi-1	DQ217793	BPV7[1]	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
	Dyoeta	Dyoeta-1	FJ379293	EePV1	European hedgehog	*Erinaceus europaeus*	Erinaceidae	Erinaceomorpha	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
BETA + XI	**Dyokappa**	Dyokappa-1	GU220391	BpPV1	Brush-tailed Bettong	*Bettongia penicillata*	Potoroidae	Diprotodontia	Mammalia
DELTA + ZETA	**Delta**	Delta-1	M15953	AaPV1	European elk	*Alces Alces*	Cervidae	Artiodactyla	Mammalia
			AF443292	RtPV1	Reindeer	*Rangifer tarandus*	Cervidae	Artiodactyla	Mammalia
		Delta-2	M11910	OvPV1	American White-tailed deer	*Odocoileus virginianus*	Cervidae	Artiodactyla	Mammalia
		Delta-3	U83594	OaPV1	Domestic sheep	*Ovis aries*	Bovidae	Artiodactyla	Mammalia
			U83595	OaPV2	Domestic sheep	*Ovis aries*	Bovidae	Artiodactyla	Mammalia
		Unclassified	JX174437	BgruPV1	Domestic yak	*Bos grunniens*	Bovidae	Artiodactyla	Mammalia
		Delta-4	X02346	BPV1	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			M20219	BPV2	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
		Unclassified	JQ798171	BPV13	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
		Delta-5	EF680235	CcaPV1	Western roe deer	*Capreolus capreolus*	Cervidae	Artiodactyla	Mammalia
		Unclassified	JQ744282	CelaPV1	Red deer	*Cervus elaphus*	Cervidae	Artiodactyla	Mammalia
		Delta-6	HQ912790	CdPV1	Arabian camel	*Camelus dromedarius*	Camelidae	Artiodactyla	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
DELTA + ZETA	**Delta**	Delta-6	HQ912791	CdPV2	Arabian camel	*Camelus dromedarius*	Camelidae	Artiodactyla	Mammalia
	Epsilon	Epsilon- 1	AF457465	BPV5	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
			DQ098913	BPV8	Domestic cow	*Bos taurus*	Bovidae	Artiodactyla	Mammalia
	Zeta	Zeta-1	AF498323	EcPV1	Domestic horse	*Equus ferus caballus*	Equidae	Perissodactyla	Mammalia
	Dyoiota	Dyoiota-1	EU503122	EcPV2	Domestic horse	*Equus ferus caballus*	Equidae	Perissodactyla	Mammalia
	Dyorho	Dyorho-1	GU384895	EcPV3	Domestic horse	*Equus ferus caballus*	Equidae	Perissodactyla	Mammalia
LAMBDA+MU	**Lambda**	Lambda-1	AF480454	FcaPV1	Domestic cat	*Felis domesticus*	Felidae	Carnivora	Mammalia
			AY904722	LrPV1	Bobcat	*Lynx rufus*	Felidae	Carnivora	Mammalia
			AY904723	PcPV1	Puma	*Puma concolor*	Felidae	Carnivora	Mammalia
			AY904724	PlpPV1	Asiatic lion	*Panthera leo persica*	Felidae	Carnivora	Mammalia
			DQ180494	UuPV1	Snow leopard	*Uncia uncia*	Felidae	Carnivora	Mammalia
		Lambda-2	D55633	CPV1	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
		Lambda-3	FJ492744	CPV6	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
LAMBDA+MU	**Lambda**	Lambda-4	AY763115	PlPV1	Raccoon	*Procyon lotor*	Procyonidae	Carnivora	Mammalia
		Unclassified	HQ585856	CcroPV1	Spotted hyena	*Crocuta crocuta*	Hyaenidae	Carnivora	Mammalia
	Kappa	Kappa-1	AF227240	OcPV1	European rabbit	*Oryctolagus cuniculus*	Leporidae	Lagomorpha	Mammalia
		Kappa-2	K02708	SfPV1	Cottontail rabbit	*Sylvilagus floridanus*	Leporidae	Lagomorpha	Mammalia
	Mu	Mu-1	V01116	HPV1	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
		Mu-2	X70828	HPV63	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
	Nu	Nu-1	X56147	HPV41	Human	*Homo sapiens*	Hominidae	Primates	Mammalia
	Sigma	Sigma-1	AY684126	EdPV1	North American porcupine	*Erethizon dorsatum*	Erethizontidae	Rodentia	Mammalia
	Unclassified		JX123128	EhelPV1	Straw-coloured fruit bat	*Eidolon helvum*	Pteropodidae	Chiroptera	Mammalia
	Unclassified		JQ692938	MschPV2	Schreiber's long-fingered bat	*Miniopterus schreibersii*	Vespertilionidae	Chiroptera	Mammalia
	Unclassified	**Unclassified**	KC858266	RferPV1	Greater Horseshoe Bat	*Rhinolophus ferrumequinum*	Rhinolophidae	Chiroptera	Mammalia
		Unclassified	KC858263	EserPV1	Serotine bat	*Eptesicus serotinus*	Vespertilionidae	Chiroptera	Mammalia
			KC858265	EserPV3	Serotine bat	*Eptesicus serotinus*	Vespertilionidae	Chiroptera	Mammalia

VIRUS					HOST				
CROWN GROUP	**GENERA**	**SPECIES**	**GENBANK ID**	**PV**	**COMMON NAME**	**SCIENTIFIC NAME**	**FAMILY**	**ORDER**	**CLASS**
	Chi	Chi-1	DQ295066	CPV3	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			FJ492743	CPV5	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			JF800656	CPV9	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			JF800658	CPV11	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
		Chi-2	EF584537	CPV4	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
		Chi-3	HQ262536	CPV8	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			JF800657	CPV10	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
			JQ754321	CPV12	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
		Unclassified	JQ701802	CPV14	Domestic dog	*Canis familiaris*	Canidae	Carnivora	Mammalia
	Eta	Eta-1	AY057109	FcPV1[1]	Common Chaffinch	*Fringilla coelebs*	Fringillidae	Passeriformes	Aves
	Iota	Iota-1	U01834	MnPV1	Multimammate mouse	*Mastomys natalensis*	Muridae	Rodentia	Mammalia
		Iota-2	HQ625441	RnPV2	Norway rat	*Rattus norvegicus*	Muridae	Rodentia	Mammalia

VIRUS	HOST

CROWN GROUP	GENERA	SPECIES	GENBANK ID	PV	COMMON NAME	SCIENTIFIC NAME	FAMILY	ORDER	CLASS
	Iota	**Unclassified**	JF755418	PmPV1	Deer mouse	*Peromyscus maniculatus*	Cricetidae	Rodentia	Mammalia
	Psi	Psi-1	DQ366842	RaPV1	Egyptian rousette fruitbat	*Rousettus aegyptiacus*	Pteropodidae	Chiroptera	Mammalia
	Rho	Rho-1	AY609301	TmPV1	Florida manatee	*Trichechus manatus latirostris*	Trichechidae	Sirenia	Mammalia
			JN709473	TmPV2	Florida manatee	*Trichechus manatus latirostris*	Trichechidae	Sirenia	Mammalia
	Theta	Theta-1	AF420235	PePV1[1]	Gray parrot	*Psittacus erithacus*	Psittacidae	Psittaciformes	Aves
	Dyoepsilon	Dyoepsilon-1	EU188799	FlPV1	Yellow necked Francolin	*Francolinus leucoscepus*	Phasianidae	Galliformes	Aves
	Dyolambda	Dyolambda-1	FJ796965	OaPV3	Domestic sheep	*Ovis aries*	Bovidae	Artiodactyla	Mammalia
	Dyomu	Dyomu-1	HQ262535	MsPV1	Diamond Python	*Morelia spilota spilota*	Pythonidae	Squamata	Reptilia
	Dyonu	Dyonu-1	HQ293213	ZcPV1	California sea lion	*Zalophus californianus*	Otariidae	Carnivora	Mammalia
	Dyotheta	Dyotheta-1	EU796884	FcaPV2	Domestic cat	*Felis domesticus*	Felidae	Carnivora	Mammalia
	Dyozeta	Dyozeta-1	EU493092	CcPV1	Loggerhead turtle	*Caretta caretta*	Cheloniidae	Testudines	Reptilia
			EU493091	CmPV1	Green seaturtle	*Chelonia mydas*	Cheloniidae	Testudines	Reptilia
VIRUS					**HOST**				

CROWN GROUP	GENERA	SPECIES	GENBANK ID	PV	COMMON NAME	SCIENTIFIC NAME	FAMILY	ORDER	CLASS
	Unclassified		JQ814848	MschPV2	Schreiber's long-fingered bat	*Miniopterus schreibersii*	Vespertilionidae	Chiroptera	Mammalia
			KC858264	EserPV2	Serotine bat	*Eptesicus serotinus*	Vespertilionidae	Chiroptera	Mammalia

[1]PVs lacking the E6 ORF [2]PVs lacking the E7 ORF

Table S3. Manually curated PV-like amino acid sequences.

>AAG37280_E1

PVEMKFPPMLITTNVDIMNEDQYKYLQSRVTCFKFDN---

>AAL06737_E1

FVNSASHFWLSPLVHAKFGLVDDATDQFWIY---

>AAM92153_E1

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>AAX86621_E1

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>AAX86621_E1(2)

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>AAX86628_E1

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>AAX86628_E1(2)

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>AAX86628_E1(3)

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>AAX86628_E1(4)

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>AAZ03735_E1

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>AB211993_E1

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>AB646346_E1

PLSECKVGFIDDATHPAWDYIDICRAP----------

>ABS12699_E1

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>ABX56058_E1

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>ABX56103_E1

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>ABX56103_E1(2)

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>ACC99401_E1

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>ACC99401_E1(2)

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>ACI46050_E1

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>ACO58658_E1

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>ACT32130_E1

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>ACV30150_E1

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>ACV30150_E1(2)

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>ACX32353_E1

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>ACZ58405_E1

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>ADH29821_E1

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>ADH29821_E1(2)

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>ADH29821_E1(3)

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>ADJ96360_E1

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>AEI61088_E1

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>AEI61392_E1

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>AEM05818_E1

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>AEP82743_E1

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>AEP82743_E1(2)

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>AEP82743_E1(3)

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>AET11874_E1

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>AET11874_E1(2)

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>AET11874_E1(3)

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>AF020905_E1

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>AF227240_E1

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>AF322245_E1

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>AF498323_E1

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>AF531420_E1

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>AF531420_E1(2)

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>AJ243287_E1

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>BAL14429_E1

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>BAL14429_E1(2)

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>BAL14429_E1(3)

TPKQHCMLIYGPPDSGKSYFCNSLLQFLQGKVISFL---

>BAL14429_E1(4)

VEPTWLPIGNLLKYQGVNVVSFLTVLRAMFNRTPKQHCMLIYGPS---

>BAL14429_E1(5)

IGNLLKYQGVNIVSFLTVLRAMFNRTPKQHCMLIYGPS----------

>BAL14429_E1(6)

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>CAF05704_E1

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MVSDLVDDSEVQQGDSLALFNEQVANETERSLMVLKRKFLKSPGSPDSPDQAVDISPRLASMTISPSKKVVKKR----------
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>CAW42216_E1

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>CAW42216_E1(2)

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>CAW42263_E1

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>DQ366842_E1

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>DQ366842_E1(2)

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>DQ366842_E1(3)

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>DQ366842_E1(4)

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>DQ366842_E1(5)

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>DQ366842_E1(6)

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>DQ366842_E1(7)

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>DQ664501_E1

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>EF558841_E1

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>GQ161313_E1

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>GU014531_E1

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>GU117620_E1

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>GU117622_E1

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>GU129016_E1

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>HQ537712_E1

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>NP_040891_E1

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>NP_040898_E1

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>NP_041784_E1

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>NP_042016_E1

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>NP_043439_E1

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>NP_043439_E1(2)

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>NP_057843_E1

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GVHPILYESAKHQLAEFCKYYFVTREVSGNKSIVLMLLNLKHQKSRECLTKSLVALLRVDAK----------
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>NP_597847_E1

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>NP_775307_E1

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>P36719_E1

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>Q05134_E1

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>Q07848_E1

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NRTPKQHCMLIYGPSNSGKSYFIFSLIHFLQGKVVSFLNRGSQFWLQPLSECKVGFIDDATHPAWDYIDVNMRTALDGNP
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>Q07848_E1(2)

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>Q07848_E1(3)

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>Q07848_E1(4)

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>U06714_E1

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>U31792_E1

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>U31792_E1(2)

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>U85660_E1

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>X74467_E1

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>X74480_E1

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>YP_001648802_E1

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>YP_002117841_E1

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>YP_002117841_E1(2)

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>YP_002427692_E1

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>YP_002427692_E1(2)

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>YP_003104799_E1

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>YP_003204677_E1

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>YP_003204677_E1(2)

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>YP_003668027_E1

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>YP_003668027_E1(2)

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>YP_003668027_E1(3)

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>YP_004111311_E1

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>YP_004169265_E1

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>YP_004346964_E1

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>YP_004646333_E1

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DLLRQHCSFIHMTHRPANTGSGALFLLRFNSQKSRDTLQKLFKQLMGMEDYQLLTEPPKNRGVAAALYWYKQSLGNAA
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>YP_004646333_E1(2)

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>YP_004857837_E1

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>YP_224223_E1

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>YP_249600_E1

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>YP_249600_E1(2)

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>YP_249600_E1(3)

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>YP_249600_E1(4)

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>YP_249600_E1(5)

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>YP_249600_E1(6)

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>YP_717909_E1

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>YP_717909_E1(10)

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>YP_717909_E1(11)

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>YP_717909_E1(12)

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>YP_717909_E1(13)

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>YP_717909_E1(14)

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>YP_717909_E1(15)

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>YP_717909_E1(16)

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>YP_717909_E1(17)

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>YP_717909_E1(18)

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>YP_717909_E1(19)

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>YP_717909_E1(2)

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CICGPPNTGKSMFGMSLMRFMHGAVISYCNSRSQFWLQPIVRAKIAMLDDATGAAWSYLDVYLRNMLDGNPISVDVK
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GSQRAFRCTARENTEAL----------

>YP_717909_E1(20)

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>YP_717909_E1(21)

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>YP_717909_E1(22)

APFDFSRMVQWAYDQGYQDEATIAYQYAQHAEEDRNAMAWLKT----------

>YP_717909_E1(23)

FLKRKHLCTPESKGMQALSPRLDAMRISPPRTGLVKKRLFNKGEDSGVELSMNVLHEAEDSAEQGLQTQVSEEPENRTPG
EGAEEGERS----------

>YP_717909_E1(24)

PAALYWVQKGTTKVADTTGNYPDWIAKQTLISHIMAEDATFNFGSMVQW----------

>YP_717909_E1(25)

TVYKVSFHDLIRQYKSDKTCNKAWVIAAFCLHEAYYDIFKTVLPQQCTFTHMQYRTEKQGCIAL----------
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>YP_717909_E1(26)

DWKPIIRFLRHQGVEIIPWLRTTRDWLAGIPKK----------

>YP_717909_E1(27)

ICRSSADIGEESGDDDDGSDASSVSDLFDETDQAQGNTLQLYQQQLAEEDERIIQALKRKHACTPESKALQA----------
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>YP_717909_E1(28)

RQYKSDKTCSKSWVLAVFGLCEAYYEVLKTLLVPQCSFSHMQYRTGKRG----------

>YP_717909_E1(29)

SSADIRGGLSLTDITRQFKSDKTTSYQWVAACFRVREELQEAAKLQLQEFCTYIYA----------
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>YP_717909_E1(3)

SSTQAKHVRECAQMVRYYMHAQMAEMTMAEWLAHRAEQVPDGQGDWKVIVSFLRMHGVEIIPFFRTFRDWLKGLP
KKNTLCLYGPPDTGKSMFGMSLMRYMKGTVISYVNSKSHFWLMPLTQ?AKVAMLDDATEPCWIYIDQNLRNLLDGNPL
SFDVKHRTPVQTTSPPLLITSNIDITQDDRHRYLRSRIKFIPFTCTLPL----------

>YP_717909_E1(30)

LSHFNAKSQFWLQPMVNSKVAMLDDATHQCWTYIDGNL----------

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>YP_717909_E1(31)

KSDKTCSKSWVLAVFGLCEAYYEVLKTLLVPQCSFSHMQYRTGKRG----------

>YP_717909_E1(32)

RSSSDIEELGETPTDISSEEVAGSQPDPVPGGEVLDFATAILRSSNRRACMYAQFKELYGIGFNDLVRKFKSN----------
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>YP_717909_E1(33)

FLRLQGVEVIPWLRTTRDWLKSIPKKNT----------

>YP_717909_E1(34)

WLRTWREWLKGTPKKNTICLYGPPDT----------

>YP_717909_E1(35)

DGNPLSFDLKHRAPVQATCPPLIITSN----------

>YP_717909_E1(4)

QTMLSMQQEEVQYDFSTMVQWAYDHHYMDEASIAYYYAQAAETDPNAMAWLKTTNQAKHVRDCAVMVRHYYTA
QMREMTMPQWIAYRCEQVTEEGDANDWKLVIKYLRHQGVEVIPWLRRLKDWLKGIPKKNCLCYWGPPNSGKSMFC
MGMVRFLGGAVLSYVNARSQFWLMPLASAKVALLDDATGPAWSYID----------

>YP_717909_E1(5)

MFGMSFINFMKGAVLSFVNSRSQFWLQPMLNNKVAMLDDATVPCWTYIDTNLRNMVDGNPISFDVKFRAPVQATCP
PLLITSNIDITTEDRFKYLRSRIKCIPFNCPLPMGDDGKPTVLLTNGSWKSFFSKFKQHLDLEVPEEESEDGCSQRSFRCTSRT
DSGTL----------

>YP_717909_E1(6)

YRTGKRGYIGLFLLEFNVAKNRDTVKKMLKTYINAPEDLSLIQPPNIRSSVAAMYWVQRGYSNMTDKEGQYPDWIKKQT
MLSHVMNEDVAFDFSKMVQWAYDCGLQDEAMIAYQYAQHAEEDSNAMAWLRTSSQAKHVKDCALMVRYYRNAQ
MKEMSMAQWIDYRCRETEGEGDWKLVIKFLRH----------

>YP_717909_E1(7)

ASNSQAKHVKDCAKMVGYYKAAEMAEMSMAQWILHRSEMVTEEGDWKTVIGFLRMQGVEIVPWLRTVRDWLKGIP
KKNTICYYGPPDTGKSMFGMSLIRFLKGAVLSHFNAKSQFWLQPMVNSKVAMLDDA----------
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>YP_717909_E1(8)

ACEGLCTDGKILQSCRNGRNDHGPVDMAQGRGGDRRGGLETGNRLSTTAG??????????????????????CYFGPPDT
GKSMFGMSLIKYLKGAVLSFVNSKSQFWLQPMVYSKVAMLDDATAPCWT----------

>YP_717909_E1(9)

PDTGKSMFGMSLIKFLKGAILSFVNSRSQFWLMPMVNSKVAMLDDATYPCWTYIDNNLRNMVDGNPLSFDLKHRAPV
QATCPPLII----------

>AAX86615_E2

YVDFKELLRKYGSKDTTLFKVKYGDMVLNVAIASSHRRPAAVLSEPEDTDAAEETTRATPSPPKAKRAARRDDTSPPRPKP
PEQPRAQPPRVSARLRRGGRSPAAGRRGKQRKRPTPVEKPGGSKSQPAPHAPTAAEVGRVTHRVAPRVAGRLGHLLAE
ARDPPVVVVKGSQNPLKCFRHRCEAKYKKLFYKVSTAWSWTKERGGGKSHIIFSFLGENQRKVFLSTITLPKSLKAFKGNFE
VDG----------

>AAX86629_E2

QNQSTPLPPSAGEVGRVHHTVQAAGSGRLRQLILEARDPPVLVVKGASNAIKCFRFRCKESHSKLFSAVSSTWSWTEERG
KHGHIILKFTSVTQRQQFMNIVKIPKSFVVFKGNFELDG----------

>ABP99779_E2

SKELYQTEPAHTFKKGGIQVDVWFDGSEENSMRYVKWSRIYYQTEAN----------

>ABP99779_E2(2)

TLQDCSKELYQTEPAHTFKKGGIQVDVWFDGSEENSMRYVKW----------

>ABP99835_E2

QVVPPTRTSRSKAEQAIEMEITLRSLSQSQYANEDWTLQ----------

>ACI46051_E2

TWRFQSQKEAMEKLHDRLHVVQEKLLTLYEKDSTLLQDQILHYKLLRQENVLLHYVRGLGVNRIGMTSVP----------
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>ACZ58406_E2

STGEVDIAGLYFLRGEDKEYYVRFEHDAARYSKTGQYKVRC----------

>ADH29822_E2

GMQIVPPQQTSKTKAKQAIMMELVLKSLQQSAYGTEPWTLQETSLEHYHSQPH----------
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>ADH29829_E2

GLQTVERRAQGRLERLIAEARDPPIVVLQGAPNALKCYRNRVKNTHGSAFEYISTTLKYL----------
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>ADH29829_E2(2)

GLQTVERRAQGRLERLIAEARDPPIVVLQGAPNALKCYRNRVKNTHGS?LLSNIYQLNTHLYLIVE----------
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>CAA63876_E2

VIKRMASERLRERLDSLQETILSLYEKLSTKLEDHIKLWHAQRLEHALFYAARQQGVMRIGMQVVPPTRTSKYKAEQAIEM
ELH----------

>CAW42273_E2

PELCRYRCWQVIYYQDDEDNWQKTGAYYYEGTPYRVYYIDFYKEALRFSKQQYWEVLYKNQVFSPATSSATGSQPAILSA
PGRPGTVASASARSAQKRPLQEQKQRQQRSREEGGGQEEEEGEGEGEGEGQGGRRRKIQKVAQEGRKQREGEEGEGG
EEEEEEEGTRGGGRGGRGGTGGRLHAADTTYNTRSRSSPSGEEGSPRSSPVTYRPRLRP?KSPARTRTTCTKATRKTTRYL
QSSGRS----------

>DQ269468_E2

GARARRGRGTPSGRTGGLCTAPSPSEVGQRRTTTPPQGLGRYCRLLAEARDPPILVLR----------

>EF591300_E2

VQSLARSKYKDEKWTLQDLSLEVYHSSPRLCF----------

>EU918767_E2

LRDRLDALQDRILAHYDNQSEDINAHIDYWTLV----------

>HQ912791_E2

LRHVGGMPLPPTAVAQQRAREAITMQLVTASLAESRFANE----------

>NP_597740_E2

RHLFDTCSTTWNWTGSHTGPYAESRIIFLFTDPSQRKKFLDTVRFPTSVSYFSGLFNGI----------

>NP_848022_E2

LKSLQQSPYGAEEWTLQETSLEHYYSQPHSTLKKGPHFVDIEYNDSKENKTRETAWRYVYYQDEEGTWHKVKGDYVDGE
GVYYLEETGVRVYYVDFKE?LKRYGNVNT??FT??HDGKTINVAVASAHQRRTPTPIDSSDTEEGPRRPAENTRQETRASA
ASPRPSPKKRKPAQSRSPQPRPVPGRLRRRPSPGRRRQGKRATPDKSPIVPPEASAVGRVTSTVSPRLTGRLRRLVAEARD
PPVEVFKGPANALKCFRFRCTKHYRKYFSLVSTTWAWTSQRGKNHSHVIFSFENETQRCTFLNTVKIPHSFIHFSGSFDAQ
G?QRCTFLNTVKIPHSFIHFSGSFDAQG----------

>NP_848022_E2(2)

SQVSKRKAENAIEMHILLMSLNESPYRHEQWGLTDTSYEMWSQTPPKFTFKKKGEQVDVRYDNDANNQSREVFWRYIY
YQGDDGMWHKTESHFDERGVYYEDEGTRVYYVDFPDLAMRYSLTGTYSARHGNDIVRFSGSDGDLSPTPRRPARTPPH
TTPPATPERRRRESPVPRTSTPAPSTSKESPPPRPRRYIRGGGGRRSRRSTASRSPRSPKQREPGPIRPGEVGSVRRSVQKK
GQTRLARLLDEARDPAVLIFQGPPNNLKCFRYRAQQKHSQYYQLISTCFKWVSKQITQSRMLMSFNSPDQREAFIKK------
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>NP_848022_E2(3)

RVYYVDFKELLKRYGNVNTTLFTVRHDGKTINVAVASAH?RRT???IDSSD?EE??RR??ENTRQETRASAASPRPSPKKRKP
AQSRSPQPRPVPGRLRRRPSPGRRRQGKRATPDKSPIVPPEASAVGRVTSTVSPRLTGRLRRLVAEARDPPVEVFKGPAN
ALKCFRFRCTKHYRKYFSLVSTTWAWTSQRGKNHSHVIFSFENETQRCTFLNTVKIPHSFIHFSGSFDAQG?QRCTFLNTV
KIPHSFIHFSGSFDAQG----------

>NP_848022_E2(4)

VASAHHRRTPITIDSSDSEEGSRRSAENTRQETRASAASPRPSPKKRKPAQSRSPQPRPVPGRLRRRPSPGRRRQGKRATP
DKSPIVPPEASAVGRVTSTVSPRLTGRLRRLVAEARDPPVEVFKGPANALKCFRFRCTKHYRKYFSLVSTTWAWTSQRGKN
HSHVIFSFENETQRCTFLNTVKIPHSFIHFSGSFDAQG?QRCTFLNTVKIPHSFIHFSGSFDAQG----------

>NP_848022_E2(5)

ETRASSASPGPSPKKRKSPQPRPPPRSPRTVSGRLRGRPSPGRRKQGKRSPPDKSPIVPPEASAVGRVTSTVSPRLTGRLRR
LVAEARDPPVEVFKGPANALKCFRFRCTKHYRKYFSLVSTTWAWTSQRGKNHSHVIFSFENETQRCTFLNTVKIPHSFIHFS
GSFDAQG----------

>YP_002004570_E2

DALQETELRLIEKDSQDLADHIKYWSTIRAQNVLLHYARRRGLTMLGQHRVPSLATSGAAA----------

>YP_002756548_E2

AWHRVTSNVNARGIYYDEIDGTRHYYTLFADLANKYGTTGAYTVKVG----------

>YP_003858577_E2

TELTLIEKDSRDIEDHIKYWGTIRAQNVLLHYARTKNITTIGSFRVPSLATSEAAA----------

>YP_717910_E2

SAYGREPWTLHDMSLETFKCAPTGCFKKDPYTVEVIYDGDENNAMIYTVWSKVYVQEDTSWHRRESQVDVYGIFYHWL
GEKKYYVRFEEDANRFSARGAYSVRCKDGELTCFNPVSSSTPESSGPARHPGQDLSPPVKRRRLDPPSPQQARQAGLPGQ

GQGAG?GARQDREDRSPDPGGGHQREPRSPQGGAEAGPGRQRPPGRAAGPGRRAAPGGRHIRAYDPSDQTIPVVIVK
GSPNCVKCQRYRLHHNFQRLFHKVSTTHQYLDAGHSERNNEGHMIIQFLTVTQRTEF

>YP_717910_E2(10)

TPYPSPIIIITGSANNVKCLRYRLQKQHSGLFDKVTTTFRWLNAGHIDKDNDAQMLLSFVNSGQRERFLVSGALSEKVDYV
LGEMPI----------

>YP_717910_E2(11)

IKIQLLLRSLAGSKYADETWTLQDLSLETINSLPKGVVKKNGYPVEVIYDGDKDNSMVYQVWDDLYIQEDESTWYHRKS---
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>YP_717910_E2(12)

GDTDLNFFNPVSSSTPASSSRRDRGEVEEDPGEVQGREKKRRRRGLLVQEARRSQSPDRSRGPRGFAEEGEEEDTGRELA
GRSAGALPRPHPGSDRGSEGRPGESPGEEGSQCTFAPVLVVCGPPNALKCSRYRWHHTQRHNFAAVTTNYRWVASGG
TERGGLAQLIVRFDSDSQRDAFLKSGAISATLKAVPGNMPVFL----------

>YP_717910_E2(13)

PPRPTPYPSPIIIITGSANNVKCLRYRLQKQHSGLFDKVTTTFRWLNAGHIDKDNDAQMLLSFVNSGQRERFLVSGALSEK
VDYVL----------

>YP_717910_E2(14)

GARQDREDRSPDPGGGHQREPRSPQGGAEAGPGRQRPPGRAAGPGRRAAPGGRHIRAYDPSDQTIPVVIVKGSPNCV
KCQRYRLHHNFQRLFHKVSTTHQYLDAGHSERNNEGHMIIQFLTVTQRTEFLAAGALS----------
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>YP_717910_E2(15)

EKKYYVRFEEDANRFSARGIYTVRTKDGELTCFNPVSS----------

>YP_717910_E2(2)

PELCRYRFDVLQEQILSHYEQDSYE??????????????????YHYARGKGVRHLGYMPVPAQCVSQERARQAINMQLVA
ESLLKSPYAKEQWTLQDLSRETYMAAPQHTLKKGGHTVVVVYDGTEENSMEYVAWDFIYVPEEDDVWIKVPGEIDLKGL
FYTTDDIKTYYVTFEEDAEKYSKSGLYTVKSKYNELTNFVPVSSSTPGTGRAAEVGERRPGPILRRSASPEAASPAKRRRGVP
EGSPARPDPDPDPAYQQGGVREGEGAGQREGEGQGHPERREGGETPQEAAVGSGGRCPRRGARAARRGQGGSRRG
VGSLAAQSALAPVLILRGNGNSLKCLR----------

>YP_717910_E2(3)

ALVRQENVLYHYARGKGVRHLGYMPVPAQCVSQERARQAINMQLVAESLLKSPYAKEQWTLQDLSRETYMAAPQHTL
KKGGHTVVVVYDGTEENSMEYVAWDFIYVPEEDDVWIKVPGEIDLKGLFYTTDDIKTYYVTFEEDAEKYSKSGLYTVKSKY
NELTNFVPVSSSTPGTGRAAEVGERRPGPILRRSASPEAASPAKRRRGVPEGSPARPDPDPDPAYQQGGVREGEGAGQR
EGEGQGHPERREGGETPQEAAVGSGGRCPRRGARAARRGQGGSRRGVGSLAAQSALAPVLILQIGRASCR----------
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>YP_717910_E2(4)

AISHERAQQAIGIQLAIKTLANSAFATEPWTLQDLSLENYNCAPPGCFKKDPYQIEVVYDGDENNIMVYTVWSRVYLQED
DVWHLRESQVDVQGIYVHWLGQKKYYVEFEEDATRFSARGVYTVRSKDGDLTSFNPVSSSTPESCPRPARSPPEGAGRP
PKRRRLDREASPEAGLPEGGHGRSEGSPEPGGGGEE----------

>YP_717910_E2(5)

QLAIKTLANSAFATEPWTLQDLSLENYNCAPPGCFKKDPYQIEVVYDGDENNIMVYTVWSRVYLQEDDVWHLRESQVD
VQGIYVHWLGQKKYYVEFEEDATRFSARGVYTVRSKDGDLTSFNPVSSSTPESCPRPARSPPEGAGRPPKRRRLDREASPE
AGLPEGGHGRSEGSPEPGGGGEEEGQRQPHSPGRLEAAQGSGGRSPQERGGSAG----------
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>YP_717910_E2(6)

SEDIKSHVTYWSLVRKECVLMYYARTKGIKHLGYMPVPLAAVSQQRAKEAINMQLAVKSLSESRYKDEPWTLQELSLETF
QSAPQGTYKKGPYQVEVMYDGDPSNCMLYTAWTARYLQSSG----------

>YP_717910_E2(7)

DAIEIQLAIKSLAKSAYGREPWTLHDMSLETFKCAPTGCFKKDPYTVEVIYDGDENNAMIYTVWSKVYVQEDTSWHRRES
QVDVYGIFYHWLGEKKYYVRFEEDANRFSARGAYSVRCKDGELTCFNPVSS----------
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>YP_717910_E2(8)

SLAGSKYADETWTLQDLSLETINSLPKGVVKKNGYPVEVIYDGDKDNSMVYQVWDDLYIQEDESTWYHRKSYVDVTGIFY
YWLGEKCYY----------

>YP_717910_E2(9)

VRKECALLYYCRQKGYKTLGYVPVPVAAISHERAQQAIGIQLAIKTLANSAFATEPWTLQDLSLENYNCAPPGCFKKDPYQI
EVVY----------

>AAX86617_L2

LTDFTDIPIDVPGQPPETIAINTNTSEFGHDVATIEVSTHEPRLFSRSQYNNPAFDINIESSATAGETSDRDNIYVGGIGGEGE
TVGSWIKLTEFQSYPEVRGRFAPPRAP----------

>AAX86631_L2

DWARAQREAQGIAEEIPLMEFTPSAEIDVTLEPTFDEDIVEETSFRASTPEPRGPRPGRQPAQRLTQQVPLRSLTTLTRTQT
FPNLAFEGEGELADLFLSDLRELAEEVPEFGDIRGLDSPTFRRTAQGHVRVSRLGRRAQIQTRSGTYVGPMTQFYVDISPIQ
QPIVIDPADAVSLSPFAPRDAVESFEMSIFGEMSNEAVIIHGVQETPVDVHADSTPFDVISLSTTTTEYSETDLLDVSERVGE
NLHLIFQTRKGLQEVPIPNVSFDPAD----------

>ABA61876_L2

LTDFGGRRTPPQIEEETTFLTSTPTRVPTRRPTRLYGRRVSQVEVPDSDFLTQPRRLVTFGFDNPAFEDDLTLTFEQDVQAI
EEAAAAPHADFRDVVRLSRPEFGRGPSGR----------

>ACO58660_L2

GAGLAGCSCEMAPRRRTKRDSVDNLYRQCIIRGNCPPDVKNKVEGTTIADYILKYGAGAVYFGSLGIGTG----------
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>ACO58660_L2(2)

YPVCKVFGNCPSDVINKVEGKTIADQILKIGSGLTYFGGLGIGTAAS----------

>ACO58660_L2(3)

CKVFGNCPSDVINKVEGKTIADQILKIGSGLTYFGGLGIGTAASGGGRVIGSGLNIPPTRDGYIPVGPWPRVPSAVK---------
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>ACO58660_L2(4)

AFNTCPIDIVNKVEGKTVADNILKWGSGLTFF----------

>ADD14050_L2

PKPLRSFTLQIQLCCCESCVFIMIRRRVKRASVQELYPHCKQWNTCPADVVPKVEGDTIADRILKWISGFLYFGGLGIGTGR
GGGGVTLGTPIGTGTTGRTPVVTLHPDLPLDTITPELSIPVNVDAIPGIVPTDSSVIDLYD----------
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>ADQ85946_L2

GFENPAYIEDEVSLTFEQDLEDLEQAVAAPHPDFRDIVRLSKPEYRVGPTGRVRVSRVGTKGSIKLS----------
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>AEM05820_L2

GPPNALKCCRYRLTKQHSHTFVYASSTFKWLSSTAPALAQSRMLLTFKTKEQRAYFLTHVQIPKVFKCHLGNLSGL---------
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>CAW42231_L2

RVSRLGTKANIKLRSGIRIGGQAHYYQDLSSIIGPDDGIELSLLGEQSGESTILQPLAESGFESIDINDTADICRAPADRKSGSA
GM----------

>DQ366842_L2

GPVKAIKALYHRFVGQVPIEDPLFLQAPG----------

>FM212639_L2

SEGPTGHVRVSRIGDLLTLRTRSGARVGPKAHLF----------

>HM011570_L2

SRQLYGRRVSQVEIPDETFLTRPARLVTFGVDNPAFEDCC----------

>NP_040293_L2

SVIITQEDPEGLPDVIFIEGQTTSRTQYDNPTFEIDVTTNNTAGETSATDRIVVVGEGGGRRVGSDEELVPLLDLFGSG------
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>NP_040308_L2

HKMYRSRKRRAAVEDIYRHCKAFGTCPTDVLNKVERTTPADKILQYGSLGVFFGGLGIGTGAAEAGAAGAGRIGLTPLGE
GPGIRIGTTPSARPSAPFGHGFGRPIDPLSVGPKPFRPVNVVDPAGPAIIELQELPSIDLPGGDVQVIAELHPIPGEPTFISTN
GSRVPLLEVPGDVTVSSTKYDNPAFESSYTTNLLAESSSGENVFQTGGGGLFVGDDPPLPPVITEEIPLIEFSRTTVEEEDLPF
DTSIVEETEFRASTPDPGARRRRPVFAQRLMQQVPLRDLPTLRRAVTFPNLAFEGEGSLAEAFLSDVQQLAEEYPEFQDIR
ALESPTFRRTAEGTVRVSRVGKRAQIQTRSGAHIGPITNFYVDISPIQEVITIDPSEAITLSPMPELEVSESIEMSVIGEQSNTA
VIVHGVHETPAEIDVDTADFDIITLSRTSLHDSISETELLDLPEPVAERLQLLIRGYNGATKDIPIPNSRARPIPEDFFPNLRPDV
IGVNVSYPVVPESEPDITPTVIPEDIPYIVITYFPDTSGDFDLHPSLFRWKRKVCNHN----------
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>NP_040308_L2(2)

LHLSQQLDEELVPLLDLSGSARDPTRSFETTIEEETEFGTSTPVTRQVTRPRTGLYSRRYGQVRISEPAAILQPRSVYFENPAF
EEIEGIDPDVSIIFERDLQQVARELPEEMRSLTALSRPTYSREPTGRLRVSRIGRAKSIRTRSGLEIGPQTHFYVDLSPITYAEDI
ELATIVETSHDTNIIQPLAESAFERVDLNEITEPVPDDQLIDEDEMEISGTLELLGVEDVLIHEV----------
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>NP_040308_L2(3)

RRKRAAPKDIYPACLKFGTCPTDIKQKAEGTTIADQILKWGSVGVFLGGLGIGT----------
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>NP_040901_L2

DNPAFEDEVTLTFEQDVGDIEQAAAGPHEAFRDVVQLSRPIFGRAPTTGRVRVSRLGTKANIGLRSGLRIGGKTHYYQDLS
SIIPPDEGFEMYLLGEQSGQGTIVQPLAETGFESIPLEDIYSDPPLPDDMLLDEYEPVASSLSLQFEDFFGESEVSTIIPDLQYI
RRPPIAVTDIRLPGVIIDYPSSYFPQDIIPTDIPAILIDNFSLDYDIHPSLLRKRKKRRFF----------
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>NP_040901_L2(2)

DLPELCRYQQVPVSAPEIVTRTQETLFPNPVFEEVGEVDPDVSLIFERDQLELAQNVPPELTDVTELSRVTYSRSAAGHVRV
SRIGRTYSIRTRSGVQIGAQRHLYTDISPIPVWEQIELPTIAETSFEASIVQPLAETNLDIIDLEEITEPVSDEQLLDEDTYDIGG
TLELYGVEPIVVDEQPIRTTFVIDTVLKPPVFIGSTSEEFLLPSASEEEMALIPILEPRDIPMVLINVDSFDYYLHPSLRRKKRKR
KCFFYWFPDGGVAPGCQ----------

>NP_040901_L2(3)

GVDNPAFEDEVTLTFEQDVGDIEQAAAGPHEAFRDVVQLSRPIFGRAPTTGRVRVSRLGTKANIGLRSGLRIGGKTHYYQ
DLSSIIPPDEGFEMYLLGEQSGQGTIVQPLAETGFESIPLEDIYSDPPLPDDMLLDEYEPVASSLSLQFEDFFGESEVSTIIPDL
QYIRRPPIAITDVRLPGVIIDYPSSYFPQDI----------

>NP_040901_L2(4)

VGTKGSIKLRSGLTIGGQAHYFRDLSSVIAPEDGIELELLGEQSGQSTILQPLAEHGFESVAINDVSGPVPDEELLDVFEPVGT
TLTLEFTDPFHNFE----------

>NP_040901_L2(5)

GQTHFYQDFSSIVAPDDGLELALLGEISGESTIAEPLAESGFESVPINDVSGPVADEDLLDIFEPVAS----------
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>NP_041865_L2

RQLYGRRVSQVEIPDETFLSRPARLVTFGVDNPAFEDEV----------

>NP_043449_L2

CRYQELYPHCKQWNTCPADVVPKVEGDTIADRILKWVS----------

>NP_056818_L2

RTATGHVRVSRLGRRAQIQTRSGTYVGPMTQFYVDISPVQQPILIDPAEAVSLSPFAPP----------
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>NP_057847_L2

AEEIPEMEDIQALESPDYRRTAANLLRVSRIGRRAMIRTRAGTYIGPMHTFYFDVSPI----------
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>P50801_L2

VGYKMLHSRRKRAAAGDIYKHCKAFGTCSQFPDVVNKVEGTT----------

>X70827_L2

TALPISAPDADFADIVTIGRPRRSEERRV----------

>YP_001955935_L2

RSSADIYRHCKVVGNCPQDVVDKIEGTTPADKILQYGSLGVFLGGLGIGTGS----------
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>YP_002235541_L2

GTCPPDVVNKIEGTTVADKILQYGSVG----------

>YP_002635573_L2

RLKSLYNRFVKQVPVEDPLFYDEPGRLVEFGYSNPAYNAEDTIEFSFEGDEPRAAPDSRFQDIRTL----------
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>YP_002756550_L2

PARLVTFGVDNPAFEDEVTLTFEQDVGDIEQAAAGPHEAFRDVVQLSRPI----------

>YP_003204680_L2

VKGIMLKRKRRAAPQDIYPQCKIWNTCPPDIVNKAEGTTIADEILKWGSSIIFTGGLGIGTARGGGGTLLGGQIPLAKDYIPL
GNWPRPGNVRPGVPIKPRIPISSAGPPDIVPIDVLVPTGPPVDPGAPAVIIPEDVPITIEPYIPTDPSVRVPELPVGGAGAAD
TELIELTEIPTDIPREPSQTVTTTAIADFYHEHNNFATIEVTTHTPRLYSRSQYENPAFEVTIHSSAPAGETSAPDNVFVGGRG
DTGEVVGEWIPLRDFTTRPTPRPAIRPPPRAPQVRFIDETIVEEEFPMVELGDRRTPPLIEEETTFLTSTPI----------
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>YP_003204680_L2(2)

SSTPAGETSAPDNIYVGGLGDTGEVVGDWIRLTEFTTRPPQRPAIRPPPRAPQVRFIDETIIEEEFPMVDLGGRRTPPLIEEE
TSFLTSTPARRPINRPRQLYGRRISQVEIPDEDFLTRPARLVTFGVDNPAFED----------
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>YP_003204680_L2(3)

IQTRSGTHVGPISDFYVDISPISRPLVIDPAEAATLSPVLSADPIENIELSNLGEMSNDAVIIHSVQETPVEVHGDSSQFDVISL
TTTVSEYSETDLLDTSENVGENLLLIIPDRRGLTEIPIPNLITRPLPDIFYPDINPFNTGVTVDTHEIPDSDICRAPA----------
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>YP_003858578_L2

VEIPDSDFLIRPQRLVMFGVDNPAFEDEITLTFEDDVAALEGAAAPP----------

>YP_249603_L2

PDNIYVGGLGDTGEVVGDWIRLTEFTTRPPQRPAIRPPPRAPQVRFIDETIIEEEFPMVDLGGRRTPPLIEEETSFLTSTPAR
RPINRPRQLYGRRISQVEIPDEDFLTRPARLVTFGVDNPAFEDEVTLTFEQDLDDIEQAAAGPSEAFRDVVELSRPIFGRAPE
TGRVRVSRVGTKANIGLRSGLRIGGKTHYYQDLSSIVPPDEGLEMYLLGEQSGQGTIVQPLAESAFESIPLEEIHTDPPLPDD
MLLDEYEPVGSSLSLQFESLFGEPEAFTLLPDLQLIRRPPIAVTDVKLPGTIIDYPSSYF----------
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>YP_656497_L2

EEGTTFLTSTPTRRPTPRPTRLYGRRVAQVPVADTEFLTEPRRLVTFGFENPAYIEDEVSLTFEQDLEDLEQAVAAPHPDFR
DIVRLSKPEYRVGPTGRVRVSR----------

>YP_717912_L2

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NKIENKTPADKILQIGSSIVNFGGLGIGTGSGTGGRGGYIPLGAGRGIEVGSWPRPAYNLPRPTAPVIESIGPTINPTVPDIAI
PIIPENVTPELIELEPVIPLDHPSITGGIDAIDPEAPSVIQDLGDFPSRPAIIDESQPTFGGNRIEVIAEVHHPADIFPVHPISTG
GDVDPAIISVSEEIPLLPRSGVAHPQDPAVLQTTTSFGLNADLPGNRATFIDYDLSGGAVGDDIPLTDLSSRTYDPNSELEFR
TSTPTSGPRRNPLKAVKALYHRFVQQVPIEDPLFLEAPGGFVEFDNPAYDPDASIEFPSMGENPLASPDTRFQGITRLDRPI
LSEAPGTRTVRLSRLGKVGAMKTRSGARVGPRQHLYHDLSSIHEHIELTPLGVDLPAQSLEPAVEDTAVDVLTEVDDFEDP
ETGFEDVPLLDNHSGQNITLTTGRGRRTQVTTLEIPTSNRADGFGVDIGRNRDIYVHHPDGEDRPGVPPSLAPGIPLAPTT
PTYVVEDEYTPYDYWLDPYLHLPRRKRKRYSFSSFADVYLDT----------

>YP_717912_L2(10)

AMRTRSGATVGPRVHLYKDISSIEEPIELQPLDYPHASDSHTLSALPAETTFGGEVEVGAPAEVATEVSS----------
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>YP_717912_L2(11)

TPLSIPRPGALAESAIADTAVDVLPDSTVDVLTESSALEDGFEEVPLLDHRSGEVQRVSVGRGGSQNRSPVSLEL----------
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>YP_717912_L2(12)

RTSTPTNRRGPIERVRDLYHRLVKQVPVEDPLFYTAPGDLVEFAFN----------

>YP_717912_L2(13)

FRSPVQRLRDLYNRYVQQVPVEDPLFLTAPGELVWQIRPMPPDGVWTKE----------

>YP_717912_L2(14)

AGEGIGVGAWPRPGVANVPVLPPIEVVGPELPPTVFTDPTVINPVDVNPVEIELEPILPPQRPSVVDELEPIAPD----------
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>YP_717912_L2(15)

PAVIQATTSFGSAADVGGRYALVDYSLTDPTVSETSDIPLQVYDPEADIQFRTSTPT----------
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>YP_717912_L2(16)

HIFVEPCLCLHDGCTLCTSCLLCFAMPVPHKRGRRVIRDSAGNIYRNPGCRVFGNCPPDVVNKIENKTPADRILQIGSAITN
FGNLGI----------

>YP_717912_L2(2)

PGPAVRVPTVPAIETLVPDITVPVLPEAPGADLIELEPILPPSEPTDIIDSVAPIDPEDPVVVQDFGHFPARPAIIDESAPTAGG
NRIEVVAEVHHPADLFPVHTLSSGGDSSILQEAGEEIPLLPRSNAPHAHDPAVLHTTTTFGTRADVTGSKATIINYEASGSAI
GDDIPLMDMTYDPEADIEFRTSTPQSRPRQGPVKRLKALYNRYVKQVPVEDPLFMSAPGDMVVFGNPAFNPDETLEFPY
PGENPLASPDPRFRDITTLHRPTVAEVPGGRTLRLSRLGKIGAMQTRSGATIGPRAHLYYDLSSIHEAIELEPLGVEPVSVTG
EHAVEDTSVDVLTEYDEAEHGFEEVPLLGNRHGESVTLTSTGGGRRFRTPVTLELPSAPRAEGFGLNIGHDKEVYVHYPDE
KGWEPPSL----------

>YP_717912_L2(3)

GGRYALVDYSLTDPTVSETSDIPLQVYDPEADIQFRTSTPTARRGPVQRLRDLYNRYVQQVPVEDPLFLTAPGELVEFGFQ
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DLTPLGVPSVNDATPVGVDTAETSFGGAAVEDGIIPDVATEETSLEAGFEEVPLLEDHSGQQLTVGISRGGSGNRQWISFE
VPTPRKGLSALASDSDIFVYYPDDGQSSVHDTEDRDFVPARPVHPSVPDICRAPAD----------
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>YP_717912_L2(4)

EADLEFRTSTPTTRRGPLQRARDLYHRLVKQVPVEDPLFYTAPGELVEFGFTNPAYEGEETLEFDVDVSQPRAAPDERFRD
VQTLHRPRLSAAPGGRVRLSRLADLVTMRTRSGAKVGPKAHLYMDISSIWEPLELQPVLRPAPNDPSPVGVVSAETSFGG
AEVVPDTTPSIGTDLDTLEEGFEEVPLLDPHQTQQQTVGIGRGGSGNRQWISLEIPEPRQGFSSLASDADIFVYYPNEEG---
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>YP_717912_L2(5)

QIPVEDPLFMSAPGDMVVFGNPAYNPDETLEFPYPGENPLASPDPRFRDITTLHRPTVAEVPGGRTLRLSRLG----------
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>YP_717912_L2(6)

RLGKIGAMQTRSGATIGPRAHLYYDLSSIHEAIELEPLGIEPVSVTGEHAVEDTSV----------
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>YP_717912_L2(7)

EAPSGHVRLSRLGNFATMRLRSGAIAGPRAHIYTDLSSIQESFELTPLGFANATMETGPIVLDTPVDVLADAAV----------
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>YP_717912_L2(8)

PRPTAPVIESIGPRLPTVPEVSVSNVTPEVLELEPIIPVDHPSIIDATAPIDPEDPAVV??????????????????MFPVHPIST
GGTSDPAIIDIC----------

>YP_717912_L2(9)

IRELYNKYIRQVPVEDPLFLEAPGELVEFGF----------

>3696278_L1

VPKVSGSQYRVFRIRLPDPNKFAVPTPDL----------

>3696278_L1(2)

PDYLKMAKDSFGNSCFFSVRKEQTYT----------

>AAA47016_L1

DKFGDQLFFFARREQLYGRHFFTRAGRVAEEPVPPTFYVPAAKQLATYIYGVSPSGSLVSTESQLFNRPYWLQRA----------
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>AAB91540_L1

FILQMAVYLPSQNKFYLPPQPITKIQNTDDFVTRTSVFFHAASERLLTVGHPYFEFKEGKKVTVPKVSPNQYRVFRVKFADP
NNFHFENKNIFDPERERLVWAVRGIDIGRGQPLGPAISGHCLFNKLADVENALAYENNQAGDSDDRRNTAFDPKQNQC
FIIGSKPAMGEYWTVAEPCKKDAPVTDTCPPIELVNSIIEDGDMADVGFGALDFKELQPNKSDATLDVVNTVSKYPDYLQ
MAEDTYGDSLFFYARREQLYARHIFARGGMDSKEEPDETMFYKPGGAIVNRATTNYGILPSGSLLSSEGNLFNRPYWLQR
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>AAB91540_L1(2)

FILQMAVYLPSQNKFYLPPQPITKVQSTDDYVQRTGVFFHAASERLLTVGHPYYEIKDNGTVQVPKVNPNQYRVFRVKLP
DPNQFYFENKNIFDPEMERLVWAVRGVEISRGQPLGTGISGNPLFNKHEDVENPY?LMTKHIRQMVQTAERM----------
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>AAB91540_L1(3)

FILQMAVYLPSQNKFYLPPQPITKVQSTDDYVTRTSVFFHAASERLLTVGHPYYEIKDNAG?----------
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>AAF25684_L1

ICRKISQIPLWILAILSANTQTMWAWQRINLG?MFFYVRREQMYARHMMSRGGVAEEPIPQELFIKRKNDMAIATSNYA
ISPSGSLVSSEGQLFNKPYWLQRAAGQNNGILWANELFCTIGDNTRGTSFNLNVSVNGRKLENYSNKDYNAYLRHTEE---
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>AAG27046_L1

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>AAO48993_L1

YANSFKDGKDHRQNVAFDPKQLQLIIVGNTPATGEYWTLGQ----------

>AAQ72425_L1

PYTTLFRSTVVDTTRGLNFAINAASEEAVAGEWDAAKYNNYLRHVEEYEISMILQLCVVPLTPETLSLINTMDPSIL----------
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>AAX86625_L1

LAFIHTMNPRIIEQWHLAVASPPGNALEDIYRYITSKATKCPSEVPPAEPEDPYKKYKFWTVDLSD----------
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>AAX86625_L1(2)

GEAVYKSEYYNQYLRHVEEVQISLIVQLCRVQLTPENMAYIHTMNPRIIEKWHLAVDKP----------
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>ABA61877_L1

QDDSFNEYLRHVEEYQISVIVQLCKIDLTPES----------

>ABE73478_L1

RVFRIQLPDPNRFAFPDPD----------

>ACA61505_L1

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>ACC78262_L1

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>ACI46053_L1

EQVDEQQMVTVPKVSAHQYRAFRIRLADPNSFAFNDPAIYNPERERLVWAIRGIEVDRGQPLGIGISGNPLFNRFSDTEN
PGAIYPNNQHIAQDLRVNMSFDNKQSQIFLVGATPATGQHWENAKWCAEVEEANKYKCPPLQMVHSVLQD----------
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>ACI46053_L1(2)

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>ACO58660_L1

NITCPCPFPPPLSCVQDLRYLQSSGRS----------

>ACX32356_L1

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>ACX32368_L1

TGGDHDPPAPFAYYVSPSGSLVSSESQLFNRPYWLQRAQGQNNGIIWLNELFLTVMD----------
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>AEE80936_L1

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>AEP82740_L1

GALQISDAPLDLVNTRSVYP??????????????????????????RHFFARDGKVGTEPTPDALIAKSDPDQQQDQKTIGTDR
YFVQPSGSMVTSDSQLFNKPYWLQRAQGKNNGILWRNEMFVTVGDNTRGTIMSISLK----------
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>AEP82747_L1

WEIGVNPSVAGNLTDEYRYITSLATRCPDKDKKEKEDPYAKYQFWELDFTERLSADLSQFPLGRRFQAQTAR----------
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>AF227240_L1

NGHNLDADERKNQAFDPKQTQLFIIGCKP----------

>AF227240_L1(2)

AFKDTDIYDPEKERLVWLIRGLEVGR----------

>AF364505_L1

CSPNQYRVFRCKLPDPNKFAFKDTDIYDP----------

>AY904724_L1

EENIFFNLLQMAVYLPSQNKFYLPPQPITKVQ----------

>CAB96121_L1

VFFHAASERLLTVGHPYYEIKEGDTVQVPKVNPNQYRVFRVKLPDPNQFYFENKNIFDPEIERLVWAVRGVEISRGQPLGA
GISGNPLFNKHEDVENPYAYDQSYKTADTDTRKNVAFDPKQNQLFILGCKPATGEHWGAAKWCADKPPADPNKVCPPI
ELVNTIIEDGDMTDIGLGALDFKTLQPNKSDAPIDVSQSISKYPDYLKMAEDPFGDSMFFFARREQMYARHIFARAGDDA
KEMLDPSFYVAPGGDKNNKYSSPQYGILPSGSLVSSDSNLFNRPFWLQRASGMNNGIIWRNEMFLTVADNTRGTFFSIN

TDNKAGATWSNDRFYEYTRHVEEYQLAFIIQLCKIKLTPENLAYVHTMDPEIIEDWHLAVNPPPSSLLEDHYRYIQSRATKC
PTDVPATPKED?YKNKKFWEVDLRERLTEQLDQTPLGRRFIFQSGYRGPSTSRKRSRTVVASKTVVKKKRRA----------
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>CAB96121_L1(2)

DKFGDPMFFYVRREQMYARHMMSRGGVAEEPIPQELFIKRKNDMAIATSNYAISPRGA----------
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>CAF05790_L1

SIYPDYLKMSKEQFGNSLFF----------

>CCC55756_L1

QTPALEDTYRYITSAATPCPAKVDPKPKKDPYEKLKFWEVNLTDKLSDELDQFSLGRKFLFQSGYGSARGT?QIIHVCPCCS
VLFALCVLMYPMF----------

>DQ366842_L1

SIILQLCKVKLSAETIAVINTMDPEILEDWEIGVTPPAASQLNDKYRYITSMATRCPDKDKKQEREDPYAKLNFWVLDFTEK
LSSDLSQYPLGRRF----------

>DQ366842_L1(2)

SSKYYNNYLRHTEEYEVSIILQLCKVKLSAETIAVINTMDPEILEDWEIGVTPPAASQLNDKYRYITSMATRCPDKDKKQERE
DPYAKLNFWVLDFTEKLSSDLSQY?GSSHSLAEL----------

>DQ366842_L1(3)

DPNNFAFPDTSVFNPETERLVWGIR----------

>DQ366842_L1(4)

EQIFYDLQLPCTSCNQYMRIVISCSE----------

>DQ418472_L1

AYCPKENGANMLPSVLLQMAVWIPSAQKIYVAPTPVSTVPSTDEYIKRTSYFYHANSERLLTVGHPFYSIIDSATNKVTVPK
VSGSQYRVFRIRLPDPNKFALPEPSLYDPESARLVWCLRGLEVGRGGPLGMGVTGNPYFSRNTDAENPNQYDPVTWGN
RIRYNVAIEPKQTQMLIVGCTPADGEFWDKAIPCAQEPAPVPKKGDCPALELKTAPIQDGNMIDIGFGHMNFRALQEDR
SSAPIDINAN----------

>EU277647_L1

VFFHAASERLLTVGHPYYEIKDNAGNVKV----------

>FJ379293_L1

YFYHAHSDRLLTVGHPFFSISDASGKVTVPK----------

>FJ492744_L1

LQMAVWLPAQNQFYLPPAP----------

>FJ492744_L1(2)

RLLLVGHPYYNIEKKDNEDTILVPKCSPNQ----------

>FJ598133_L1

MAEDLYGDSLFFYARREQMYVRHMFA----------

>JF755418_L1

RGAEISRGQPLGVSVTGHPLFNRGND---

>JN171845_L1

GNRLFFFSRREQVYARHFFVRDGDLGTE---

>NP_040294_L1

RSAGALQISISKYPDYLKMAEDPFGDSMFFFARREQMYARHIYARAGDDAKEPLDASFYVAPGGDKNNTFSSPQYGILPS
GSLVSSDSNLFNRPFWLQRASGMNNGIIWRNEMFLTVADNTRGTFFSINTDNKAGASWSNDRFYEYTRHVEEYQLAFII
QLCKIKLTPENLAYVHTMDPEIIEDWHLAVNPPPSSLLEDHYRYIQSRATKCPTDVPATPKED?YKNKKFWEVDLRERLTEQ
LDQTPLGRRFIFQSGYRGPSTSRKRSRTVVASKTVVKKKRRA---

>NP_040294_L1(2)

NDELVPPSMYIKSSIQDQTIASSNYSVTPSGSLITTEAQLFNRPYWLQNAAGPNNGILWGNELYVTVGDNTRGLSFGISVP
YGNQDVTQWESKSFTEYLRHVEEYQIAVILQLCKVDLTPENLAFIHTMDPSIIERWHLSVNQPANEFLEQYRFITSVATKC--
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>NP_040294_L1(3)

TMNPRIIDQWHLAVTAPPDHAIEDIYRYIRSQATKCPKDVPATEPEDPYKDYKFWTVDLSERMTEQLDQTPLGRKFLFQT
GLSFNGSVASRSIKRLAATRRRSSQAKRRKTSS----------

>NP_040294_L1(4)

TMNPRIIDQWHLAVTAPPDHAIEDIYRYIRSQATKCPKDVPATEPEDPYKDYKFWTVDLSERMTEQLDQTPLGRKFLFQT
GLSFNGSVASRSIKRLAATRRRSSQAKRRKTSS----------

>NP_040294_L1(5)

FFSINKKKQDDTDSYSADKFYEFTRHVEEYQLSFIIQLCKVSLTPENLAYIHTMDPTIIDDWHLA----------
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>NP_040294_L1(6)

RHVEEYQLAFIVQLCKVSLTPENLAYIHTMDPKIMDICRAP----------

>NP_040294_L1(7)

NYKFWEVDLREHMTEQLDQTPLGRKFLFQTGVRTATSVRP----------

>NP_040294_L1(8)

WGIRGIEVSRGGPLGMGVTGNPLFDRN----------

>NP_040294_L1(9)

LSFIIQLCKVHLSPENLAYIHTMDPSIIE?----------

>NP_040308_L1

LLQMSAGGAVWLPSQNKFYIPPHPFTKIPSTDEYIIRTNLFFHAGSERLLIVGHPYYNIQTEDDDTVLVPKCSPN----------
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>NP_040309_L1

RNDLENQNPTKYKNSDFVEVLRHCEEFELELILQLGKVKLTPENIAFIHQMDPDILEDWNLTVAPG----------
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>NP_040309_L1(2)

EETYFLIVFQMAVWVPSQNKFYIPPTPYPKIPSTDEYVVRTSRFFHAGSERLLI----------
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>NP_040309_L1(3)

QMPIQTIICILALERNVENVKNILFGFQMAVRLPSANKFYLPPTPVTKVLSTDEYVERTSLFYHAT----------
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>NP_040309_L1(4)

ERLVWGIKGIEVGRGQPLGLAVTGHPFTNKLTDVENPTVLYEN----------

>NP_040309_L1(5)

VDNTRGTSLNISRDTSETPSTSYQPKNFKIYLRHCEEYQLSFIVQLCKVKLT----------
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>NP_040309_L1(6)

SFSHLDMTMICIQAYLNAKEKDISFNFLQMAVYVPSQNKFYLPPSPITKIQSTDEYVERTSVF----------
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>NP_040309_L1(7)

QMPIQTIICILALERNVENVKNILFGFQMAVRLPSANKFYLPPTPVTKVLSTDGYLQSS?----------
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>NP_040901_L1

DVKNAKENVFFIGFQMAVWLPAANKFYLPPKPITRVLSTDEYVQRTNIFYHAGTERLLTVGHPYFDVYDNGDK????????
????????????KFADPNNFAFPDTSVFNPDICRAPA----------

>NP_040902_L1

YRVFRVKLPDPNQFYFENKNIFDPELERLVWAVRGVEISRGQPLGTGISGNPLFNKHEDVENPFAYDQSYKSADADSRRN
VAFDPKQNQLFILGCKPATGEHWTAAKWCVGKEPVDPTKVCPPIELVNSIIEDGDMTDIGLGALDFKALQPNKSDAPLDV
NSTTSKYPDYLKMAEDPFGDSMFFFARREQMYARHLFARAGDDAKEMLDPSFYIAPGGDKNDTYSSPQYGILPSGSLVSS
DSNLFNRPFWLQRASGMNNGIIWRNEMFLTVADNTRGTFFSINTKSTDDNKWTNKKFFEYTRHVEEYQLAFIIQLCKIKL
TPENLAYVHTMDPEIIEDWHLAVNPPPSSLLEDHYRFIQSRATKCPTDVPATPKEDPYKNKKFWEVDLRERLTEQLDQTPL
GRRFIFQSGYRGASTSSRKRSRTVVASKTVVKKKRRT----------

>NP_040902_L1(2)

FAPQFD??????????????????MAVYLPQQNKFYLPPQPITKIQNTDDFVTRTSVFFHAASERLLTVGHPYFEFKEGKKVTV
PKVSPNQYRVFRVKFADPNNFHFENKNIFDPERERLVWAVRGIDIGRGQPLGPAISGHCLFNKLADVENALAYENNQAG
DSDDRRNTAFDPKQNQCFIIGSKPAMGEYWTVAEPCKKDAPVTDTCPPIELVNSIIEDGDMADVGFGALDFKELQPNKS
DATLDVVNTVSKYPDYLQMAEDTYGDSLFFYARREQLYARHIFARGGMDSKEEPDETMFYKPGGAIVNRATTNYGILPSG
SLLSSEGNLFNRPYWLQRAAGMNNGIMWKNELFVTVLDNTRGTTFFINRIPDKPETYSNKKVFEFSRHVEEYQLAFIVQL
CKVSLTPENLAYIHTMDPK----------

>NP_040902_L1(3)

ERDGGNVFFNVFQMSGGGAVWLPSQNRFYLPPTPFTKIPSTDEFVTRTSLFFHAGSERLLLVGHPLYNIEKTDADNNVTV
LVPKCSPNSYRVFRVSLPDPNKFAFKDTTIYNPEDERLVWSVRGVQVSRGQPLGVPITGTPYYNRAGDAENPGNYNNSFE
DGKDHRRNVAFDPKQVQMFLIGNTPAIGEYWTIAAKCNGIGYAVGEGPPIELKHTPIQDGDMLEIGLGAIDFSNLQDNK
AEAPLDVVNTKSIYPDFIGMANEQFGHSLFFFARKEQVYARHYFLREGKLGSEKTPTSMYLPSDETIA???????????GSDR
YFVQPSGSMVTSDNQIF----------

>NP_040902_L1(4)

EGVPPFYFLATQGEQKQKTLGTSNYVSIPSGSLVTSDAQLLNRPYWIQRAQGKNNGVLWHNELFLTVGDNTRGVIMSIN
KPKANGAPKDYLNNIFEEYVRHVEEFELEFILQLCKVSLTPENVAFLHQMDPSILEEWNLTVTAQQGPSFEDSYRYITSAAT
PCPPQPAPKPAGDPYKDYKFWEVDLKEKLSDELDQFALGRKFLFQSGQTQRALASSLSSRTLVSRNLNRKRSSGVTKRTVK
RRKVVRV----------

>NP_040902_L1(5)

FIGMNNDTFGHSLFFFARKEQVYARHYFIREGLLGAEKTPESLYLPTDENIAKPNDQSKIGSDRYFVQPSGSMVTSDNQIF
NRPYWIQRAQGKNNGVLWNNELFITVGDNTRGTTLNINKK----------

>NP_040902_L1(6)

VPKVNPNQYRVFRVKFPDPNQFAFENRSIFNPETERLVWAI??SD
VYFRC----------

>NP_040902_L1(7)

GNVKVPKVNPNQYRVFRVKFPDPNQFAFENRSIFNPETERLVWAI----------

>NP_040902_L1(8)

DAVPTPEEKKDPYADYRFWDVDLSDKMSEQLDQTSLGRKFLYQSGLYTRA----------

>NP_040902_L1(9)

VPKVNPNQYRVFRVKFPDPNQFAFENRSIFNPETERLVWAIRGAEIGRGQ----------

>NP_042019_L1

YWLQRAQGQNNGIIWLNELFLTVMDNT----------

>NP_056819_L1

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>NP_057848_L1

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YPDFIKMSKDKLGDSMFFFARREQVYSRHFFVRDGQLGKETIPETFYVKSKAGQAQENIASSNYFATPSGSLVSSDAQLFN
RPYWIQRAQGKNNGVLWHNELFLTVGDNTRGVIMSINKPKANGAPKDYLNNIFEEYVRHVEEFELEFILQLCKVSLTPEN
VAFLHQMDPSILEEWNLTVTAQQGPSFEDSYRYITSAATPCPPQPAPKPAGDPYKDYKFWEVDLKEKLSDELDQFAL?----
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>NP_057848_L1(2)

ILIPLISICILLCKDGNVKGNVFFIGFQMAVWLPATNKFYLPPQPITRVLSTDEYVKRTDIFYHAATERLLTVGHPYFEIKEEDR
LLVPKVSPNQYRVFRLKLADPNTFAFGDSSIFDPEKERLVWAIKGAEIGRGQPLGIGVTGHPFYNKFNDVENPTLQYDNG
HDLDADDRRNQAFDSKQTQMFILGARPAVGEHWKRAKACMADQDRLQNKCPPIELENSTIQDGDMMDIGLGNLDFV
DLQENKADAPLDIIGTISKYPDYLKMTEDKYGDSMFF----------

>NP_057848_L1(3)

TLPDPNTFAFGDKSIFNPERERCVWALRGLEINRGGPLGCSITGSPLLNKRADVENPYAYENGQSNDSDKRNNIAFDAKQ
TQLFMVGCKPQVGEYWDT----------

>NP_057848_L1(4)

FFHAASERLLTVGHPYYEIKTDETVQVPKVNPNQFRVFRVLLPDPNQFAFENKSLFNPEIGRLVWAIRGIEVG----------
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>NP_057848_L1(5)

QIRVFRVKLPDPNKFAFPDRDVFDQEKERLVWAIRGLEVSRGQPLGNPVTGNVLFNRGIDVENGGKYELATQFADGNDH
RQNIAFD----------

>NP_057848_L1(6)

VNPNQYRVFRVKFPDPNKFAFENKSLYDPERERLVWAIRGLEIGRGQPLGLAAS----------

>NP_057848_L1(7)

LFLTIADNTRGTFFSINRPDNDEIATWANNSFHEYTRHVEEFQLAFIIQLCKVRLSP----------

>NP_057848_L1(8)

CPPIELVNTIIEDGDMTDIGLGALD----------

>NP_057848_L1(9)

NVAFDPKQLQLIIVGNTPATGEYWTLGQRC----------

>NP_848025_L1

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>NP_848025_L1(2)

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>P08341_L1

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>P50813_L1

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>Q05137_L1

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>X56147_L1

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>X56147_L1(2)

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>X70828_L1

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>YP_001595472_L1

YDQTYKTNGTDSRKNVAFDPKQNQLFILGCKPATGEHWGAAKWCADKEPQDPTKICPPIELVNTIIEDGDMTDIGLGAL
DFKALQPNKSD----------

>YP_001595472_L1(2)

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>YP_001931973_L1

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>YP_001931973_L1(2)

TPCPAKVDPRPKKDPYEKLKFWEVNLTDKLSDELDQFSLGRKFLFQSGYGSARGTTLTRSITAK----------
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>YP_002117846_L1

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>YP_002427696_L1

LTVGHPFWQILDNEGKVLVPKVSGNQFRV?----------

>YP_003169705_L1

PYTYGYSPSGSLVTSDGQVFNRPYWVQRAAGRNNGILWGNDLFVTMVDN----------

>YP_003204674_L1

SVRGLEVGRGQPLGVPVTGHPLYNRGADVENPGKYANSFADG----------

>YP_003204681_L1

YKDYKFWVVDLKERLTEQLDQTALGRRF----------

>YP_003622569_L1

IDINQDIVKYPDFLKMLEEPYGDSLFFFVRREQVYARH?----------

>YP_003778198_L1

ARREQVYARHFFARDGKVGTEPTPDALIAKSDPDQQQDQKTIGTDRYFVQPSGSMVTSDSQLFNKPYWLQRAQGKNN
GILWRNEMFVTVGDNTRGTIMSISLK----------

>YP_003778198_L1(2)

EYWDAAKPCGELPKGDCPPIQLESSIIQDGDMSDVGIGNMNFLQLSENKSA----------
---

>YP_004346968_L1

QIPAGFYLPSDDTIQGGAQEQATMGSDRYVAVPSGSMVSSDLQLFNRPYWLQRAQG----------
---

>YP_004857848_L1

FLAQSGRASSRRVVSRTTSRTVAVKRKSSAKYNTFLRHVEEYELAMILQLCIVPLDP??????????????????????????????
????????????EREDPYKGMQFWDVDFTERIS----------

>YP_224227

RANKFNVFVRHCEEYQLSFILQLCKVSLTPEHLAFI---

>YP_224227_L1

CEEYQLSFILQLCKVSLTPEHLAFIHTMNPR---

>YP_249604_L1

EENVFSIDFLQMAVWLPSQNKFYIPPTPYPRIPSTDEYVVRTSRFFHAGSDRLLLVGHPFYNIPSADDATVLVPKVSPNAYR
VFRVKLPDPNKFAFPDKDIYDVENERLVWACRGVEISRGLPLGIPVTGHPLFNRGNDVENRGAYDGQSFKDEADHRQNI
AFDPKQTQMFIIGSAPAIGEYWTSTAKCNGNNLKRDYGWPIELKHVTIQDGDMMDLGFGAMDFGALQDNKSDVPLDL
VNTFSVYPDFIKMSKDKLGDSMFFFARREQVYSRHFFVRDGQLGKETIPETFYVKSKAGQAQENIASSNYFATPSGSLVSS
DAQLFNRPYWIQRAQGKNNGVLWTNEIFVTVADNTRGTIMNLNQKHEDNQPAAQYTSQTFDEFLRHAEEFEIEFILQLC
KVRLTPENIAYIHQMNPDILEDWNLTVASQQTPAL---

>YP_249604_L1(10)

DLREHMTEQLDQTPLGRKFLFQTGVRTATSVRPGTRIVTNRKRVVRRVSTTPAKRRRV---
---

>YP_249604_L1(2)

QRAQGQNNGVLWENEMFLTVVDNTRGTSLNISRDTSETPSTSYQPKNFKIYLRHCEEYQLSFIV???LLYIP----------
---

>YP_249604_L1(3)

TPENLAFIHTMDPEIVDRWHLSVNQPANEFLEQYRYIKSVATKCPDTIVPADKADPYANYKFWEVDLREHMTEQLDQTP
LGRKFLFQSGLRRTGRVSPGTRVVTKRRTVKRVSTTVPAKRRRV----------

>YP_249604_L1(4)

IELKHTPIQDGDMLEIGLGAIDFSNLQDNKAEAPLDVVNTKSIYPDFIGMANEQFGHSLFFFARKEQVYARHYFLREGKLG
SEKTPTSMYLPSDETIAGNNDQQNV----------

>YP_249604_L1(5)

QDIVKYPDFLKMLEEPYGDSLFFFVRREQVYARHMFTKQG----------

>YP_249604_L1(6)

LDADERKNQAFDPKQTQLFIIGCKPALGEHWQKA----------

>YP_249604_L1(7)

DLREHMTEQLDQTPLGRKFLFQTGVRTASRVRPGTRIVTKRRAVRRVGSTSSAKRRRV----------
----

>YP_249604_L1(8)

DLREHMTEQLDQTPLGRKFLFQTGVRTATSVRPGTRIVTNRDRKSVV----------

>YP_249604_L1(9)

PQPITKVQSTDDFVTRTSVFFHAASERLLTVG----------

>YP_717906_L1

LEVGRGQPLGVPVTGHPLYNRGADVENPGKYANSFADGKDHRQNVAFDPKQVQLLMVGNTPAAGEYWTKAAVCTG--
----

>YP_717912_L1

WKMNTPHMIIGLIHICICLDENANGIPSLLLQMSIWIPSTQTVYVAPPAVTKVPSTEELITRTPYFYHGGSERLLTVGNPFYP
IKHADKIVVPKVSGNQYRVFRISLPDPNKFALPDPDVYDPNEERLVWSLRGLEVGRGGPIGMEVAGNPLLARNADVENP
NAPEPASGDANRKRFNVGMEPKQTQLLIVGCAPAWGEYWDKTIPCAEENLPRQQGDCPALELKSTRLQDGNMVDIGY
GHMNFGSLQEDRSGVPLEITNSICIYPDFYKMSKDAYGNSCFFSVRKEQMYSRHYFARTSKYADPIPTDLYIKDAGATVPK
GPVYFSTPSASIVNTESQVLNRPYWLLKAQGRNNG----------

>YP_717913_L1

TEGQVHGRPYWLLKAQGRNNGVLWLNQLFLTVVDNTRSFNFVLNVKNESGANQDKWQADRFTNYLRHTEEFEI--------
---

>YP_717913_L1(10)

RLPDPNKLALPDPNFYDVDNEKLVWGIRGIEVSRGGPLGMGGTG----------

>YP_717913_L1(11)

TVVDNTRSMNFVLNVRNAEAEVTEWSADKFNSFLRHVEEYEISLILQICRVRLTAENL----------
---

>YP_717913_L1(12)

VDPYAEMVFWNLDFTEQLSPDLDRFPLGRRFLTQSGRRSTSSASSRRPRTGTKRTLTATTVAVKSGPVGAK----------
---

>YP_717913_L1(13)

VQLTAENLSYLNTMNPDILEEWQIGVNPPVSSVVADRYLQSS----------

>YP_717913_L1(14)

ILQLCVVPLNPEILSLLNTMDPNILEDWEIGVNPSVASNLT----------

>YP_717913_L1(15)

QLCAVPLNPATLSLIKGMDPNILDDWEIGINPAVSGDLSDHYR----------

>YP_717913_L1(16)

LKGLLMISFLILPCLKGNVANTNTFFLLQMTMWIANPQKIYVPANPVTTIPSTDEYVTR?----------
----

>YP_717913_L1(17)

SLQISNVGSIVYYGTPSGSIVTTEGQVLSRPYWLLR----------

>YP_717913_L1(2)

WQIGVNPPVSSVVNDKYRFIDSWATRCKDKEPAKEREDPYKDMTFWKLDFTEKMSPDLDQFPLGRRFLT----------
----

>YP_717913_L1(3)

IVTTEGQVHNRPYWLLRGQGLNNGVLWNNQCFLTVVDTTRGLNFTINAANDQAVAGEWDATHYNNYLRHVEEFEVSL
IVQLC----------

>YP_717913_L1(4)

DISGTKSIYPDYLKMAKDIY??IVTTEGQVHNRP
YWLLRGQGLNNGVLWNNQCFLTVVDTTRGLNFTINAANDQAVAGEWDATHYNNYLRHVEEFEV----------
----

>YP_717913_L1(5)

LTAENLSAIHTMDPNILEDWQIGVNPPVSSVVTDHYRFVNSWATHCADKEADKKEREDPYKGMVFWNLDICRAPA------
----

>YP_717913_L1(6)

DIGFGHMNFKTLQVDKSGVPIEIADSICMYPDFYKMARDPHGNSCFFSVR----------

>YP_717913_L1(7)

PNILEDWQIGVNPPVSSVVTDHYRFVNSWATHCADKEADKKEREDPYKGMVFWNLDICRAPADRKSGSAGM----------
----

>YP_717913_L1(8)

LMHIYICLERNANAIPSLFLQMSMWNPSSQTIFVAPAAVTKVPSTEEIITRTQYFYHGGSERLLTV----------
----

>YP_717913_L1(9)

PDPNKLALPDPNFYDVDNEKLVWGIRGIEVSRGGPLGMGVTGNPLFD----------

Table S4. Description of samples included in the screening for EserPV1, EserPV2 and EserPV3. Asterisks (*) indicate available samples. Dashes (-) indicate non-available samples. For the infected samples, the name of the corresponding viral sequence in indicated. ‡ identifies the samples from which both partial E1 and L1 sequences were obtained. These sequences may or may not belong to the same virus. Cloning and whole-genome sequencing would be required to resolve this issue.

Sample ID	Bat species	Sample Collection	Colony location	Oropharyngeal swab	Anogenital swab	Hair follicles
3x31611	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31669	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31670	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31671	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31672	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31673	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	EisaPV_FAP1	*	*
3X31674	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31741	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	EisaPV_CP3	*	*
3X31742	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31743	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	EserPV3	*
3X31744	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	EserPV3	*
3X31745	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31746	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31747	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31748	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31749	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X31750	*E. isabellinus*	3-Jul-12	Serradilla, Cáceres	*	*	*
3X32318	*E. isabellinus*	3-Jul-12	Los Navalucillos, Toledo	*	*	*
3X32319	*E. isabellinus*	3-Jul-12	Los Navalucillos, Toledo	*	*	*
3X32320	*E. isabellinus*	3-Jul-12	Los Navalucillos, Toledo	*	*	-
3x31678	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	-	*
3x31679	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31680	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31681	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31682	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31683	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31684	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3X31685	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	EserPV2|EisaPV_FAP2	*	*
3x31686	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31687	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31688	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31689	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31690	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31691	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3x31803	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*
3X31804	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	*	*	*
3X31805	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	*	*	*

3x31806	*E. isabellinus*	10-Jul-12	Corrinches, Romangordo, Cáceres	-	*	*

Sample ID	Bat species	Sample Collection	Colony location	Oropharyngeal swab	Anogenital swab	Hair follicles
3X32325	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32326	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32327	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32328	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	EisaPV_CP4	*	*
3X32329	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32330	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32331	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32332	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32333	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3X32334	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3X32335	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3X32336	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3X32337	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3X32338	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	-	*
3x32339	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	-	-	*
3x32340	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	-	-	*
3x32341	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	-	-	*
3x32342	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	-	-	*
3X31660	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2|EserPV_FAP4	*	*
3X31661	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	‡ EserPV_FAP5|EserPV_CP6	EserPV2	*
3X31692	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2	*	*
3X31693	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X31694	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV_FAP7	*	*
3X31695	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV3	*	*
3X31696	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X31697	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2|EserPV_FAP4	*	*
3X31698	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X31699	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X31700	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV_FAP9	*	*
3X34377	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34378	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	EserPV2	*
3X34379	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	‡ EserPV_FAP10|EserPV_CP6	*	*
3X34380	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34381	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34382	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV_FAP12	*	*
3X34383	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34384	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X32321	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32322	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32323	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X32324	*E. isabellinus*	10-Jul-12	Navas de Estena, Ciudad Real	*	*	*
3X34385	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2	*	*

Sample ID	Bat species	Sample Collection	Colony location	Oropharyngeal swab	Anogenital swab	Hair follicles
3X34388	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	‡EserPV_FAP13|EserPV_CP14	*	*
3X34390	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34389	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34391	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34396	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34397	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2|EserPV_CP15	*	*
3X34399	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34401	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34402	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34404	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	*	*	*
3X34405	*E. serotinus*	16-Jul-12	Casatejada, Cáceres	EserPV2	*	*
3x34406	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34407	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34408	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34409	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34410	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34411	*E. isabellinus*	23-Jul-12	Charcas 1 y 2	-	-	*
3x34412	*E. isabellinus*	24-Jul-12	La Sartenilla, Romangordo, Cáceres	*	*	*
3x34413	*E. isabellinus*	24-Jul-12	La Sartenilla, Romangordo, Cáceres	*	*	*
3x34414	*E. isabellinus*	24-Jul-12	La Sartenilla, Romangordo, Cáceres	*	-	*
3X34415	*E. isabellinus*	24-Jul-12	La Sartenilla, Romangordo, Cáceres	*	-	*
3X34416	*E. isabellinus*	24-Jul-12	La Sartenilla, Romangordo, Cáceres	*	-	*
3x34421	*E. isabellinus*	25-Jul-12	Casa de Miravete, Cáceres	-	*	-
3X34422	*E. isabellinus*	25-Jul-12	Casa de Miravete, Cáceres	*	-	*

Table S5. Description of the primer sequences, targeted regions, amplicon sizes, and optimized PCR conditions and program applied for the screening of bat oropharyngeal, anogenital and hair bulb samples.

BAT PV	PRIMERS	PRIMER SEQUENCE	TARGET	TARGET SIZE
EserPV1	EserPV1_F	AAAGACTTCTCACTGTCGGTCA	**L1**	173bp
	EserPV1_R	CCAACCTCTCCTTTTCAGGGTC		
EserPV2	EserPV2_F	CTAGATATGCCAGACACGCAGA	**E1**	434bp
	EserPV2_R	TGGTTTCCAATCTCCAGAATCC		
EserPV3	EserPV3_F	TCAGGGTCAGATTTCCAGATCC	**L1**	192bp
	EserPV3_R	TTGTCATACACAAAGCTATTCTC		

PCR REACTION MIXTURE		
COMPONENTS	10 µL µL Reaction	Final Concentration
H_2O	5.1 µL	-
10X Buffer Reaction	1 µL	1X
5 mM dNTPs	0.4 µL	200 µM
2.5 µM Forward Primer	0.8 µL	0.2 µM
2.5 µM Reverse Primer	0.8 µL	0.2 µM
25 mM $MgCl_2$	0.8 µL	2 mM
DNA polymerase	0.1 µL	-
1:100 RCA product dilution	1 µL	-

PCR PROGRAM			
Cycle Step	Nº cycles	Temp.	Time
Initial denaturation	1	95ºC	5 min
Denaturation	35	95ºC	15 sec
Annealing		50ºC	60 sec
Extension		72ºC	30 sec
Final Extension	1	72ºC	60 sec

Table S6. Genome sequence analysis of EserPV1, EserPV2, EserPV3 and RferPV1.ntd: nucleotide; aa: amino acid; KDa: KiloDalton

EserPV1	Position (ntd)	Length (ntd)	Length (aa)	Molecular Mass(Kda)	pI	Position (ntd)					Position (aa)					
						TATA box	AATAAA	E1BS	E2BS	E2BS*	$CX_2X_{29}CX_2C$	$CX_2X_{30}CX_2C$	LXCXE	GX_4GKS	$LX_6LX_6LX_6L$	NLS
E6	1-468	468	155	17.7	7.46	-		-	-	-	42-78 115-151	-	-	-	-	
E7	465-782	318	105	11.6	8.40	-	-	-	-	-	-	51-88	-	-	-	-
E1	766-2694	1929	642	72.6	5.44	-	-	-	-	-	-	-	-	475-482	-	-
E2	2645-3940	1296	431	48.8	10.05	-	-	-	-	-	-	-	-	-	353-374	-
E4	3153-3701	549	183	20.1	6.49	-	-	-	-	-	-	-	-	-	-	-
L2	3984-5576	1593	530	57.9	4.73	-	4077-4082	-	-	5055-5066	-	-	-	-	-	517-525
L1	5583-7106	1524	507	58.1	6.13	-	-	-	-	-	-	-	-	-	-	498-501
NCR1	7107-7668	562	-	-	-	7624-7628	7283-7288	7592-7613	-	7424-7435	-	-	-	-	-	-
EserPV2	**Position (ntd)**	**Length (ntd)**	**Length (aa)**	**Molecular Mass(Kda)**	**pI**	**Position (ntd)**					**Position (aa)**					
						TATA box	**AATAAA**	**E1BS**	**E2BS**	**E2BS***	**$CX_2X_{29}CX_2C$**	**$CX_2X_{30}CX_2C$**	**LXCXE**	**GX_4GKS**	**$LX_6LX_6LX_6L$**	**NLS**
E6	1-495	495	164	18.3	5.20	-	-	-	-	-	53-89 126-162	-	-	-	-	-
E7	497-790	294	97	10.8	4.42	-	-	-	-	-	57-93	-	22-26	-	-	-
E1	791-2653	1863	620	70.6	5.23	-	-	-	-	-	-	-	-	448-455	-	-
E2	2577-3917	1341	446	49.9	10.34	-	-	-	-	-	-	-	-	-	-	-
E4	3127-3648	552	174	19.1	5.13	-	-	-	-	-	-	-	-	-	-	-
L2	4085-5638	1554	517	55.5	5.16	-	4097-4102	-	-	-	-	-	-	-	-	508-515
L1	5651-7150	1500	499	56.5	6.48	-	-	-	-	-	-	-	-	-	-	495-499
NCR1	7151-7574	424	-	-	-	7403-7408	7272-7277 7343-7348	7552-7568	7373-7384 7482-7493 7516-7527	-	-	-	-	-	-	-

EserPV3	Position (ntd)	Length (ntd)	Length (aa)	Molecular Mass(Kda)	pI	Position (ntd)					Position (aa)					
						TATA box	AATAAA	E1BS	E2BS	E2BS*	$CX_2X_{29}CX_2C$	$CX_2X_{30}CX_2C$	LXCXE	GX_4GKS	$LX_6LX_6LX_6L$	NLS
E6	1-420	420	139	15.8	7.46	-	-	-	-	-	26-62 99-135	-	-	-	-	-
E7	420-734	315	104	11.5	6.88	-	-	-	-	-	-	51-88	-	-	-	-
E1	721-2649	1929	642	72.9	5.57	-	-	-	-	-	-	-	-	476-483	-	-
E2	2600-3931	1332	443	50.2	10.80	-	-	-	-	-	-	-	-	-	365-386	-
E4	3108-3692	585	195	21.4	5.72	-	-	-	-	-	-	-	-	-	-	-
L2	3975-5570	1596	531	58.1	4.65	-	4068-4073	-	-	4763-4774	-	-	-	-	-	519-526
L1	5577-7097	1521	506	57.9	6.49	-	-	-	-	-	-	-	-	-	-	497-500
NCR1	7098-7711	614	-	-	-	7678-7683	7266-7271	7590-7606	-	7417-7428 7438-7449 7536-7547	-	-	-	-	-	-
RferPV1	**Position (ntd)**	**Length (ntd)**	**Length (aa)**	**Molecular Mass(Kda)**	**pI**	**Position (ntd)**					**Position (aa)**					
						TATA box	**AATAAA**	**E1BS**	**E2BS**	**E2BS***	**$CX_2X_{29}CX_2C$**	**$CX_2X_{30}CX_2C$**	**LXCXE**	**GX_4GKS**	**$LX_6LX_6LX_6L$**	**NLS**
E6	1-420	420	139	15.9	6.69	-	-	-	-	-	25-61 98-134	-	-	-	-	-
E7	417-713	297	98	11.3	4.92	-	-	-	-	-	52-88	-	22-26	-	-	-
E1	703-2535	1833	610	69.1	5.43	-	-	-	-	-	-	-	-	441-448	-	-
E2	2477-3667	1191	396	44.6	9.95	-	-	-	-	-	-	-	-	-	-	-
E4	2991-3428	438	146	17.2	5.21	-	-	-	-	-	-	-	-	-	-	-
NCR2	3668-4392	725	-	-	-	-	-	-	-	4223-4234	-	-	-	-	-	-
L2	4393-5985	1593	530	57.8	4.90	-	4480-4485	-	5145-5156	4588-4599	-	-	-	-	-	518-523
L1	5994-7523	1530	509	57.7	6.14	-	-	-	-	-	-	-	-	-	-	504-508
NCR1	7524-8249	726	-	-	-	7652-7657	7747-7752	8131-8147	7969-7980 8001-8012 8172-8183	-	-	-	-	-	-	-

Table S7. Pairwise nucleotide identities (above the diagonal) and amino acid similarities (below the diagonal) among the different ORFs of bat PVs.

HOST	*Eptesicus serotinus*	*Eptesicus serotinus*	*Rhinolophus ferrumequinum*	*Eidolon helvum*	*Miniopterus schreibersii*	*Eptesicus serotinus*	*Miniopterus schreibersii*	*Myotis ricketti*	*Rousettus aegyptiacus*
E6	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrV1**	**RaPV1**
EserPV1	-	69.3	44.6	45.6	40.8	47.3	43.7	43.7	40.9
EserPV3	82.7	-	50.8	50.8	45.9	43.0	45.6	37.4	39.9
RferPV1	49.0	53.9	-	47.7	44.5	45.5	48.3	42.3	40.0
EhelPV1	50.6	53.1	52.1	-	46.7	41.6	47.5	32.7	41.9
MschPV2	45.3	51.0	46.3	46.5	-	41.5	40.0	33.2	47.5
EserPV2	41.8	39.1	33.7	36.3	34.7	-	49.5	44.5	35.8
MschPV1	33.9	37.9	37.4	38.7	40.1	46.7	-	34.9	40.6
MrPV1	36.1	35.8	30.8	38.7	28.6	33.3	31.4	-	34.6
RaPV1	40.5	41.6	34.5	44.1	44.5	31.6	39.2	33.8	-
E7	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrPV1**	**RaPV1**
EserPV1	-	74.5	44.7	46.5	44.5	39.4	42.0	*	35.1
EserPV3	85.0	-	43.6	42.7	44.3	46.5	42.2	*	45.1
RferPV1	47.2	35.2	-	48.9	44.2	41.5	44.1	*	42.6
EhelPV1	40.7	34.2	52.0	-	40.4	56.2	40.1	*	47.9
MschPV2	30.6	34.2	27.5	33.3	-	43.4	40.7	*	40.4
EserPV2	33.6	36.0	42.5	47.6	26.7	-	55.8	*	46.4
MschPV1	33.6	35.1	45.9	43.7	27.3	59.6	-	*	43.7
MrPV1	*	*	*	*	*	*	*	-	*
RaPV1	31.6	31.9	43.0	46.8	24.1	43.0	44.0		-
E1	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrPV1**	**RaPV1**
EserPV1	-	81.2	57.8	55.3	52.7	54.4	54.3	52.5	47.9
EserPV3	90.5	-	59.4	53.9	54.7	53.0	54.2	51.9	49.5
RferPV1	65.6	64.6	-	52.7	52.6	54.9	55.0	50.7	50.1
EhelPV1	57.5	56.9	58.2	-	52.9	53.8	53.2	52.3	50.4
MschPV2	57.9	57.4	55.0	55.8	-	51.2	53.0	53.8	50.6
EserPV2	59.8	59.0	60.2	55.1	54.3	-	65.5	50.2	52.6
MschPV1	60.5	58.9	59.7	53.3	53.9	78.7	-	52.1	52.5
MrPV1	54.0	52.1	50.6	49.4	53.2	52.2	54.9	-	49.8
RaPV1	55.4	54.6	57.4	52.6	54.0	58.3	57.4	53.1	-
E2	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrPV1**	**RaPV1**
EserPV1	-	72.6	50.8	47.3	49.2	50.4	50.9	45.0	49.3
EserPV3	80.5	-	50.3	46.7	48.9	52.4	50.3	47.0	47.6
RferPV1	53.2	53.7	-	52.6	53.0	47.6	48.9	49.6	49.1
EhelPV1	52.5	51.6	54.4	-	49.2	48.8	46.2	48.3	46.5
MschPV2	54.6	52.1	56.0	56.0	-	48.7	44.1	48.6	49.3
EserPV2	51.2	50.5	50.7	51.2	50.3	-	52.2	43.9	48.0
MschPV1	47.2	52.0	49.4	45.3	46.7	57.3	-	44.6	48.2
MrPV1	40.9	42.8	46.3	47.5	47.5	44.3	41.0	-	47.3
RaPV1	48.3	47.6	47.9	47.5	50.5	47.1	46.6	47.6	-
L2	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrPV1**	**RaPV1**
EserPV1	-	75.2	50.9	47.6	46.0	46.9	44.4	45.7	43.3
EserPV3	92.7	-	53.7	49.0	48.1	46.5	44.7	43.1	44.8

EhelPV1	50.4	49.6	51.0	-	46.3	46.7	43.5	46.2	42.3
MschPV2	45.7	48.6	47.1	42.6	-	47.8	40.8	44.1	43.5
EserPV2	51.5	52.5	52.1	50.5	48.4	-	50.4	45.2	45.9
MschPV1	44.7	46.2	43.5	37.7	40.2	55.8	-	38.6	41.6
MrPV1	41.3	42.3	43.9	41.4	39.8	43.6	33.9	-	42.7
RaPV1	41.4	40.8	42.1	40.8	40.3	44.6	36.7	40.1	-

L1	**EserPV1**	**EserPV3**	**RferPV1**	**EhelPV1**	**MschPV2**	**EserPV2**	**MschPV1**	**MrPV1**	**RaPV1**
EserPV1	-	77.8	64.3	61.6	59.4	58.3	57.0	54.9	51.8
EserPV3	94.1	-	64.6	60.4	57.2	56.2	57.3	55.7	52.9
RferPV1	79.1	78.7	-	61.0	59.1	56.1	57.9	55.5	53.6
EhelPV1	72.6	71.9	76.4	-	60.0	58.3	57.9	56.4	55.3
MschPV2	71.8	72.6	73.0	69.7	-	58.8	57.1	54.3	54.6
EserPV2	70.7	71.5	71.9	69.2	69.8	-	69.5	60.9	55.7
MschPV1	70.5	73.0	71.9	68.7	70.2	84.8	-	58.2	55.0
MrPV1	66.0	66.0	68.6	67.1	66.7	73.5	74.8	-	51.9
RaPV1	63.1	66.0	63.2	65.8	63.5	67.2	67.1	63.8	-

Table S8. L1 pairwise nucleotide identities (above the diagonal) and amino acid similarities (below the diagonal) among Lambda+Mu-PVs. *Unclassified

HOST ORDER	CHIROPTERA					RODENTIA	PRIMATES	CARNIVORA									PRIMATES		LAGOMORPHA	
PV GENUS	*			*	*	Sigma	Nu	Lambda									Mu		Kappa	
L1	EserPV1	EserPV3	RferPV1	EhelPV1	MschPV2	EdPV1	HPV41	PlPV1	CPV1	CPV6	CcroPV1	FcaPV1	LrPV1	PcPV1	PlpPV1	UuPV1	HPV63	HPV1	OcPV1	SfPV1
EserPV1	-	77.8	64.3	61.6	59.4	59.3	57.3	61.9	58.3	60.0	57.4	57.6	60.3	60.1	60.0	59.4	59.9	59.0	59.7	58.1
EserPV3	94.1	-	64.6	60.4	57.2	59.0	58.1	62.4	59.9	59.9	57.4	57.8	59.4	58.7	58.9	58.3	60.0	59.7	58.8	59.3
RferPV1	79.1	78.7	-	61.0	59.1	58.6	60.8	66.1	62.4	62.1	61.7	62.0	61.6	61.6	62.8	61.3	62.0	58.9	63.5	59.4
EhelPV1	72.6	71.9	76.4	-	60.0	60.2	58.3	58.8	61.0	58.9	60.9	60.5	61.1	60.2	61.2	59.2	59.6	61.2	60.3	57.9
MschPV2	71.8	72.6	73.0	69.7	-	59.9	58.9	60.1	60.0	61.4	58.4	58.2	60.0	59.1	59.6	60.0	58.4	59.2	58.2	57.9
EdPV1	71.1	71.6	71.1	70.8	69.5	-	59.6	57.9	60.0	58.6	57.4	58.6	58.6	58.3	57.0	56.7	58.8	57.5	57.2	59.2
HPV41	71.3	70.2	72.2	70.7	70.1	75.6	-	58.3	58.3	57.3	57.9	57.2	56.9	57.2	57.6	57.2	59.6	60.4	57.5	59.1
PlPV1	74.0	74.5	76.9	71.8	73.4	70.4	71.4	-	69.0	67.4	65.0	66.0	68.3	68.0	68.3	68.4	63.1	59.5	61.7	60.4
CPV1	71.0	71.2	72.9	69.9	71.8	69.2	70.2	83.2	-	68.5	65.5	68.6	68.0	68.4	67.0	65.6	61.2	61.7	61.7	62.3
CPV6	70.7	70.0	73.6	69.6	72.6	69.2	67.6	83.1	82.4	-	69.6	69.4	69.2	69.9	69.5	69.3	60.2	59.8	61.7	59.9
CcroPV1	70.1	69.1	73.4	71.0	70.7	68.2	69.6	79.4	78.4	81.1	-	68.7	67.8	69.0	68.2	67.6	62.0	62.0	60.7	58.6
FcaPV1	70.9	69.2	74.5	72.0	71.4	71.1	68.3	83.0	84.8	86.8	83.1	-	81.8	81.8	78.0	78.0	60.0	59.6	60.4	59.0
LrPV1	70.9	71.1	74.7	71.1	70.6	71.0	68.1	82.7	84.6	85.7	82.2	97.4	-	85.1	79.4	79.9	59.7	59.6	60.6	58.2
PcPV1	70.8	71.0	74.5	71.3	71.2	71.3	68.1	82.1	84.8	86.0	82.5	97.6	97.6	-	80.4	78.4	57.3	59.2	58.5	60.2
PlpPV1	71.4	71.5	74.4	72.4	71.4	70.4	70.0	83.6	84.4	85.4	82.9	94.9	94.3	94.7	-	84.9	58.1	61.7	61.3	60.4
UuPV1	72.4	71.3	74.5	71.2	71.4	72.4	68.6	83.1	84.4	86.4	81.9	95.0	94.4	94.4	96.2	-	59.6	61.1	59.9	59.4
HPV63	74.0	74.7	74.9	70.4	72.0	70.5	71.3	76.3	73.0	72.3	69.7	71.0	70.9	71.2	71.4	72.5	-	67.0	62.1	61.6
HPV1	72.2	72.4	73.8	72.0	71.4	70.0	70.4	75.8	72.7	71.0	72.3	69.8	71.5	71.7	69.8	71.5	83.1	-	61.0	60.7
OcPV1	71.6	74.2	76.5	72.1	69.4	70.1	70.7	76.1	74.4	72.8	71.4	73.9	74.1	74.9	74.6	75.0	77.1	75.6	-	66.3
SfPV1	72.7	74.2	76.8	71.0	71.5	69.4	69.8	74.3	71.9	72.1	70.1	71.7	71.9	71.5	71.0	71.2	76.3	73.9	83.5	-

Table S9. Alignments information and likelihood score values of the Maximun Likelihood trees constructed in this study (nt: nucleotide matrix; aa: amino acid matrix).

* Forced monophyly for Alpha-PVs, Delta-PVs, Lambda-PVs, EePV1 and RferPV1

Genes	Alignment length (nt|aa)	Filtered alignment length (GBlocks) (nt|aa)	Number of alignment patterns (nt|aa)	Optimized likelihood score
E1	2802|934	1713|571	1614|558	-
E2	2154|718	918|306	907|305	-
E1E2	-	2631|877	2521|863	-282225.929162|-153118.161527
L2	4518|1506	1038|346	1030|345	-
L1	2043|681	1428|476	1304|457	-
L2L1	-	2466|822	2334|802	-242172.992267|-112448.146981
E1E2L2L1	-	5097|1699	4855|1665	-525196.379356|-266303.515321
Constrained* E1E2L2L1	-	5097|1699	4855|1665	-578304.301503| -308257.041960

Table S10. EserPV1, EserPV2 and EserPV3 prevalence in seven different Iberian *E. serotinus* and *E. isabellinus* colonies. The FAP and CP primers investigated the prevalence of other unknown PV infections. O (oropharyngeal swab); A (anogenital swab)

			EserPV1		EserPV2		EserPV3		Other PVs	
									FAP	CP
Colony location	**Host**	**n**	**O**	**A**	**O**	**A**	**O**	**A**	**O**	
Serradilla, Cáceres	*E. isabellinus*	17	0	0	0	0	0	2	1	1
Casatejada, Cáceres	*E. serotinus*	33	0	0	6	2	1	1	8	4
Corrinches, Romangordo, Cáceres	*E. isabellinus*	17	0	0	1	0	0	0	1	0
Los Navalucillos, Toledo	*E. isabellinus*	3	0	0	0	0	0	0	0	0
Navas de Estena, Ciudad Real	*E. isabellinus*	18	0	0	0	0	0	0	0	1
La Sartenilla, Romangordo, Cáceres	*E. isabellinus*	5	0	0	0	0	0	0	0	0
Casas de Miravete, Cáceres	*E. isabellinus*	2	0	0	0	0	0	0	0	0
Total	*E. isabellinus*	62	0	0	1	0	0	2	2	2
	E. serotinus	33	0	0	6	2	1	1	8	4

Table S11. GenBank Accession numbers for the partial L1 and E1 gene sequences obtained in this study.

Sequence ID	GenBank Accesion Number
EserPV_FAP4	KF208363
EserPV_FAP5	KF208364
EserPV_CP6	KF208373
EserPV_FAP7	KF208367
EserPV_FAP9	KF208369
EserPV_FAP10	KF208370
EserPV_FAP12	KF208371
EserPV_FAP13	KF208372
EserPV_CP14	KF208377
EserPV_CP15	KF208378
EisaPV_FAP1	KF208365
EisaPV_FAP2	KF208366
EisaPV_CP3	KF208374
EisaPV_CP4	KF208375

Table S12. Pairwise nucleotide identity values among the novel bat PVs described and the closely related new partial L1 and E1 bat PV sequences.

	EserPV2	EserPV1	EserPV3	RferPV1
EisaPV_FAP1	80.8	-	-	-
EisaPV_CP3	70.1	-	-	-
EserPV_FAP4	-	75.2	73.7	69.6
EserPV_FAP5	-	70.2	72.0	60.0
EserPV_FAP7	-	72.7	71.8	65.3
EserPV_FAP9	-	71.0	71.0	65.6
EserPV_FAP10	-	74.1	72.7	60.6
EserPV_FAP12	-	74.3	72.0	64.2
EisaPV_CP4	-	69.8	71.4	54.8
EserPV_CP6	-	75.4	72.9	59.2

Table S13. Alignment of the novel sequences against the FAP and the CP primer sets.

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>FAP59
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TAACWGTIGGICAYCCWTATT-------------------------------------------------
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>EserPV1_L1
ATGGCTGTGTGGCTTCCAGCAGCAAATAGGTTTTACCTGCCTCCACAACCTATCACTAGAGTGAAGAACACTG
ATGAATTTGTCTCCAGAACAAGCATCTTCTACCATGCTGCAACAGAAAGACTTCTCACTGTCGGTCATCCTTA
TTATGAGATAAAGGGCGCTAATGG------
CAATGTGACAGTGCCAAAGGTTTCAGGGAACCAATTCAGGGTTTTTAGAGTTAAATTTCCAGATCCAAACAAC
TTTGCCTTTGGTGATAAGGACATTTTTGACCCTGAAAAGGAGAGGTTGGTATGGGCTCTCAGGGGATTAGAAA
TAGACAGGGGGCAACCTTTGGGCATTGCACTTTCAGGGAATCCATTCTTCAACAAATTCACAGATGCTGAGAA
CAGCTTTGTTTATGACAATTCACAAGGGACT---
GATCAGGACAAAAGGCAGAATATGGCCTTTGATGTGAAGCAGATACAGCTTTTCATGGTTGGCTGCAAACCCC
AAACAGGAGAATACTGGGATAAAGCCCCTTCATGTGACTCTGCCCCCCTGCAGGCTGGGGATTGCCCCCCTAT
ACAGCTTGTAAATAAGATTATTGAGGATGGAGACATGGCTGCTGTTGGGATGGGCAATCTGAACTTCTCTGCT
CTACAGGAAAGCAAAGCTGACGCCCCTTTAGACCTAGTTAACACTTTCAGTATATATCCTGATTTCTTGAGAA
TGGTTGAGGAACCTTTTGGTCACTCTCTGTTCTTTTTTTCCAGGAGAGAGCAGATGTATGCACGACACATGTT
CAATAGGGATGGCCT---
TGTAGGCGAGGCTATTCCTGAGGACATGTACCTCAAAAAGGATGACAGGAACCCT------------
ACCTCTGACAACTACAGTTTTAGTCCCTCTGGTTCCCTTGTGACTTCTGAAGCCCAGTTGTTCAATAGGCCAT
ACTGGCTTCAGAAAGCACAGGGGCAAAACAATGGGATTATTTGGCGCAATGATCTCTTCCTTACTGTGGCGGA
TAACACTCGAGGCACAATCTTCAGCATTTCACAGTCCACAGAGGCGCTGCAAACATGGGACCCCACTAAGA--
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TAAAATCATACATGAGGCATGTGGAGGAATATCAGCTTTCCTTTGTATTGCAACTTTGCAAGGTAAAGCTGAC
TCCTGAGAATTTGGCTTTCATTCACAGTATGGACCCTGATATAGTAGAGGACTGGCACCTTACAGTGAACAAC
CCCCCAAGCACAGTTATTGAGGACCATTATAGGTACATAAATTCTTTAGCTACCAAGTGCCCTGATAGTGTGG
TCCCCCAGGAAAAGCCA---
GACCCTTACAAGGACTACAAATTTTGGGAAATTGACATGTCAGATAGATTGACTGAGCAGCTTGATCAAACTC
CACTTGGGAGAAAATTTCTGTTTCAAACTGGTTACCAACAGGTGGACACTGGTAAGTCTATTGTCTCAAACCC
TAGA--ATAAGAAATGTGCGCACTTCCAGAAGGGCTCCTAAAAGAAAAAGAACAACTTCCAGGAGCACCTAA
>EserPV2_L1
ATGGCATTCTGGCTCCCAAGCAGTAACAAGCTGTACCTGCCGCCTACCCCAGTGGCCCGGGTCCTTAACACTG
AAGAGTACATACAGAGGACATCTGTTTTCTACCATGCTAGCAGTGACCGCCTACTGACAGTCGGACATCCTTA
CTTCAGCATCGTAGATTCAAATGATCCAACCAAGGTGTTGGTCCCTAAGGTCACGGGAAACCAGTATAGGGTT
TTTAGGGTAAAGCTACCTGACCCGAACCAGTTTGCTATTCCTGATGACAAGCTATATGACCCTACAAAGGAAA
GGCTTGTGTTTGGCCTGCGGGGTGTACAGGTGGACAGGGGCCTTCCCTTAGGAGTGGGTCTCTCTGGACATCC
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