

**Supporting information for:**

**Spatial but not Temporal Co-divergence of a Virus and its Mammalian**

**Host**

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Table S1. Sampling localities, numbers in Figure 1, number of sequences (N), and  
coordinates (in decimal degrees) for Andes virus (ANDV) and *O. longicaudatus* (OL)

Locality	ANDV Map number	ANDV (N)	OL Map number	OL (N)	Latitude	Longitude
Fray Jorge	1	2	1	10	-30.64	-71.68
Los Vilos	2	1	2	10	-31.83	-71.52
El Mauro			3	10	-31.98	-71
San Carlos de Apoquindo	3	3	4	11	-33.46	-70.48
Peñaflor	3	1			-33.57	-70.82
Lo Herrera	3	1			-33.57	-70.67
Quebrada de la Plata	4	1			-33.49	-70.89
Melipilla	5	1			-33.73	-71.21
Quilamuta			5	8	-34.06	-71.29
Picarquín	6	1			-33.96	-70.63
Nancahua	7	1			-34.6	-71.2

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Curicó	8	1	21	1	-34.59	-71.19
San Fernando	9	1			-34.76	-70.77
Duao	10	2	6	10	-34.88	-72.15
Los Ruiles	11	1	7	10	-35.83	-72.5
Chillán	12	2			-36.65	-71.99
Tomé	13	1	8	10	-36.64	-72.79
Concepción	14	1			-36.78	-73.01
Tucapel	15	1	9	9	-37.24	-71.79
Quilleco	16	2			-37.45	-71.97
Los Angeles	17	1			-37.56	-72.54
P.N. Nahuelbuta			10	7	-37.79	-73
Carahue	18	1	11	6	-38.52	-73.11
Temuco	19	1			-38.69	-72.61
P.N. Huerquehue	20	1	22	1	-39.17	-71.73
P.N. Villarrica	21	1	12	12	-39.45	-71.81
Neltume	22	1			-39.57	-71.77
Panguipulli	23	2	13	11	-39.73	-72.22
Puyehue			14	10	-40.72	-72.43
Chiloé	24	1	15	11	-41.88	-73.67
Aysén	25	2			-45.4	-72.7
R.N. Río	26	2	16	9	-45.46	-72.32
Simpson						
Lago Atravesado			17	9	-45.67	-72.32

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Coyhique	27	3			-45.57	-72.06
RN. Río Ibañez			18	10	-46.18	-72.77
Chile Chico	28	2	19	10	-46.78	-72.6
Torres de Paine			20	12	-51.28	-73.09

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Table S2: Selection analyses of ANDV S segment performed in Datamonkey and Selecton servers using 20 sequences and 921 nucleotides.

DataMonkey						SELECTON						
SLAC		FEL		REL		PARRIS	GA-Branch	M8a	M7	M5	M8	MEC
Selected sites	dN/dS	Selected sites	dN/dS	Selected sites	dN/dS	dN/dS		Ka/Ks	Ka/Ks	Ka/Ks	Ka/Ks	Ka/Ks
63	0.004 05	134	0	196	0	0.004 ± 0.00	0.0027 ± 0.0056	0.0233 [1.7e-11,0.21]	0.0219 [1.7e-11,0.21]	0.0229	0.025	0.04

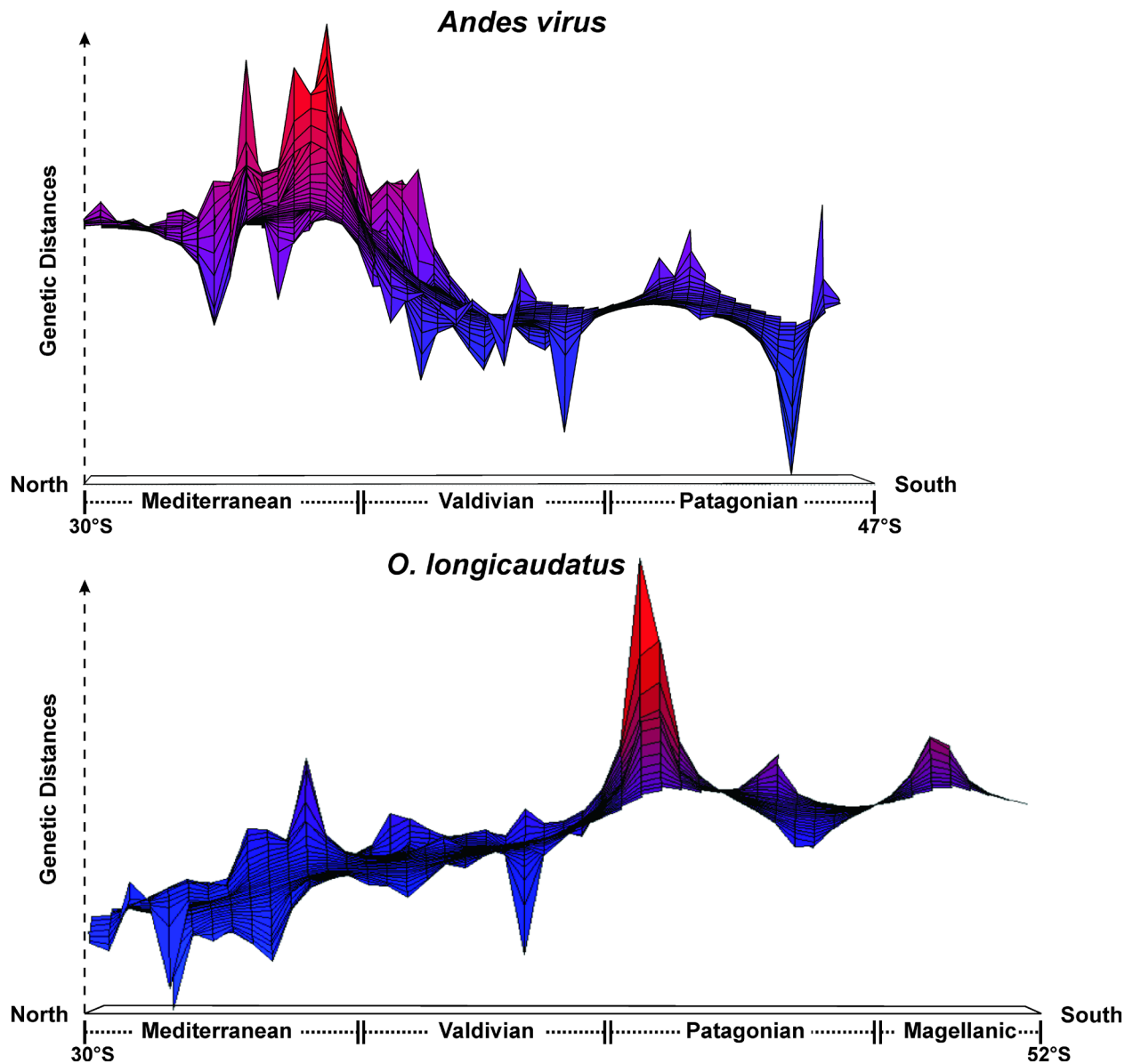


Figure S1. A graphical interpolation-based representation of the genetic structure made using a 50 x 50 grid and a distance weighting parameter of 0.5 for ANDV and 1.0 for *O. longicaudatus*. X- and y- axes represent geographic coordinates. Surface heights along the Z-axis indicate genetic distances. Colors are indicative of areas with high (red) or low (blue) pairwise genetic distance between individuals. All samples (197 sequences) were included for *O. longicaudatus*. Scale at the bottom represents latitude in degrees.