

**Supplementary materials for Journal of Wildlife Diseases DOI: 10.7589/JWD-D-21-00164:**

**Thierry M. Work, Renee Breeden, Julie Dagenais, Robert A. Rameyer, Holly Sellers, Hon S. Ip, and James W. Casey: MORBIDITY AND MORTALITY OF HAWAIIAN GEESE (*BRANTA SANDVICENSIS*) AND LAYSAN ALBATROSS (*PHOEBASTRIA IMMUTABILIS*) ASSOCIATED WITH RETICULOENDOTHELIOSIS VIRUS.**

Figure S1. Maximum likelihood tree from amino acid sequences of REV Gag gene. Tree was built based on the Jones-Taylor-Thornton model with 1000 bootstrap values and rooted with walleye dermal sarcoma virus (WDSV). Labels are Genbank accession, three letter ISO3166 country code (except for Hawaii-HI) and animal group. Hawaii labels end in V (virus variant) and i (gene isoform). Countries are AUS-Australia, BRA-Brazil, CHN-China, ITA-Italy, MDG-Madagascar, TWN-Taiwan, USA-United States of America. Animal groups are ANS-Anseriform, GAL-Galliformes, MAM-Mammalia. PRO-Procelariiformes, VAC-Vaccine origin. Circles represent Hawaiian goose (*Branta sandvicensis*) with neoplasia (open) or toxoplasmosis (filled) and triangles represent Laysan albatross (*Phoebastria immutabilis*). Scale is nucleotide substitutions per site, numbers at nodes are bootstrap values.

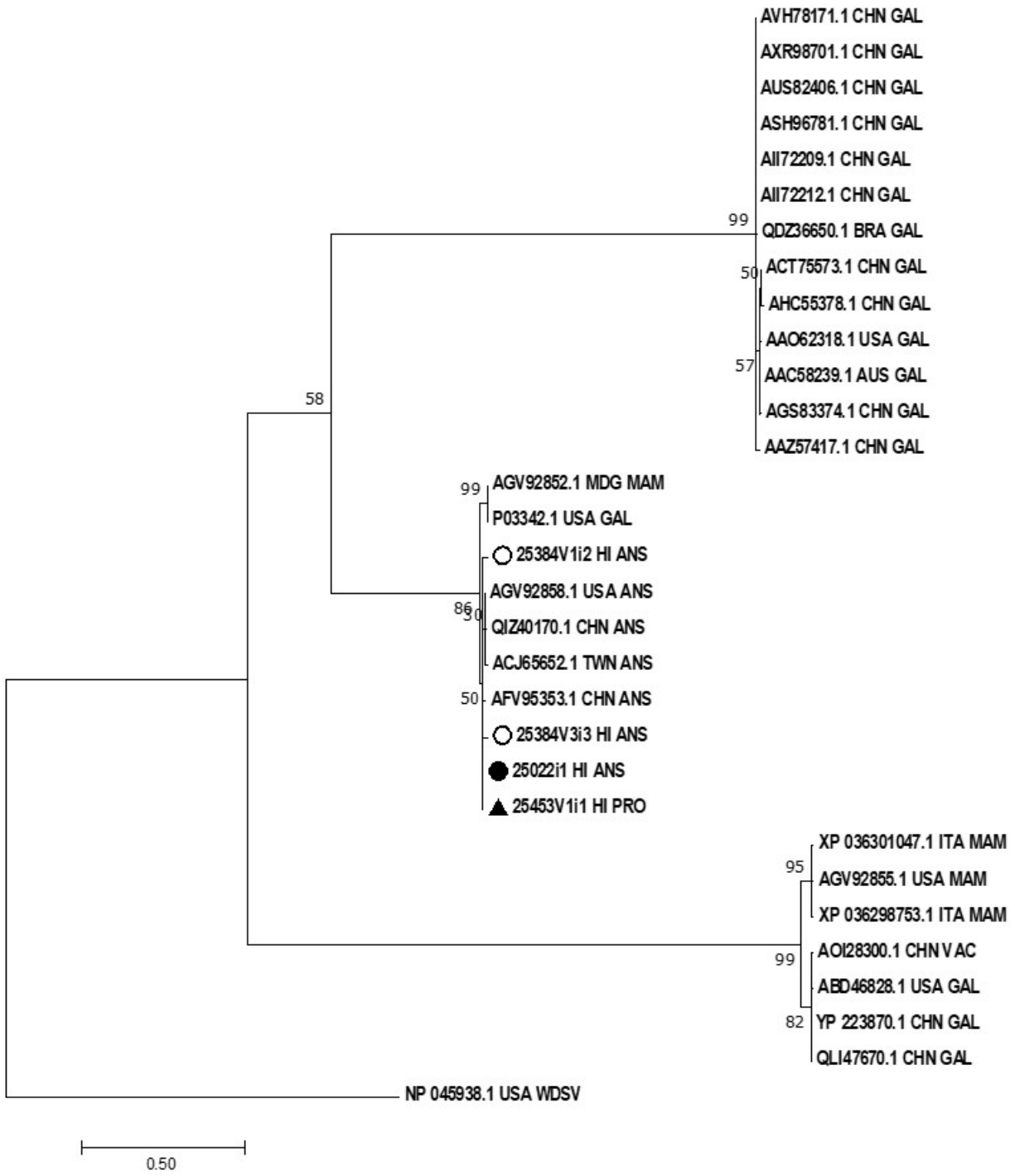


Figure S2. Maximum likelihood tree from amino acid sequences of REV Pol gene. Tree was built based on the Whelan and Goldman model with 1000 bootstrap and rooted with walleye dermal sarcoma virus (WDSV). Labels are Genbank accession, three letter ISO3166 country code (except for Hawaii-HI), and animal group. Hawaii labels end in V (virus variant) and i (gene isoform). Countries are CHN-China, TWN-Taiwan, USA-United States of America. Animal groups are ANS-Anseriform, CO-Columbiformes, GAL-Galliformes, PRO-Procelariiformes, VAC-Vaccine origin, MAM-Mammalia. Circles represent Hawaiian goose (*Branta sandvicensis*) with neoplasia (open) or toxoplasmosis (filled) and triangles represent Laysan albatross (*Phoebastria immutabilis*). Scale is nucleotide substitutions per site, numbers at nodes are bootstrap values.

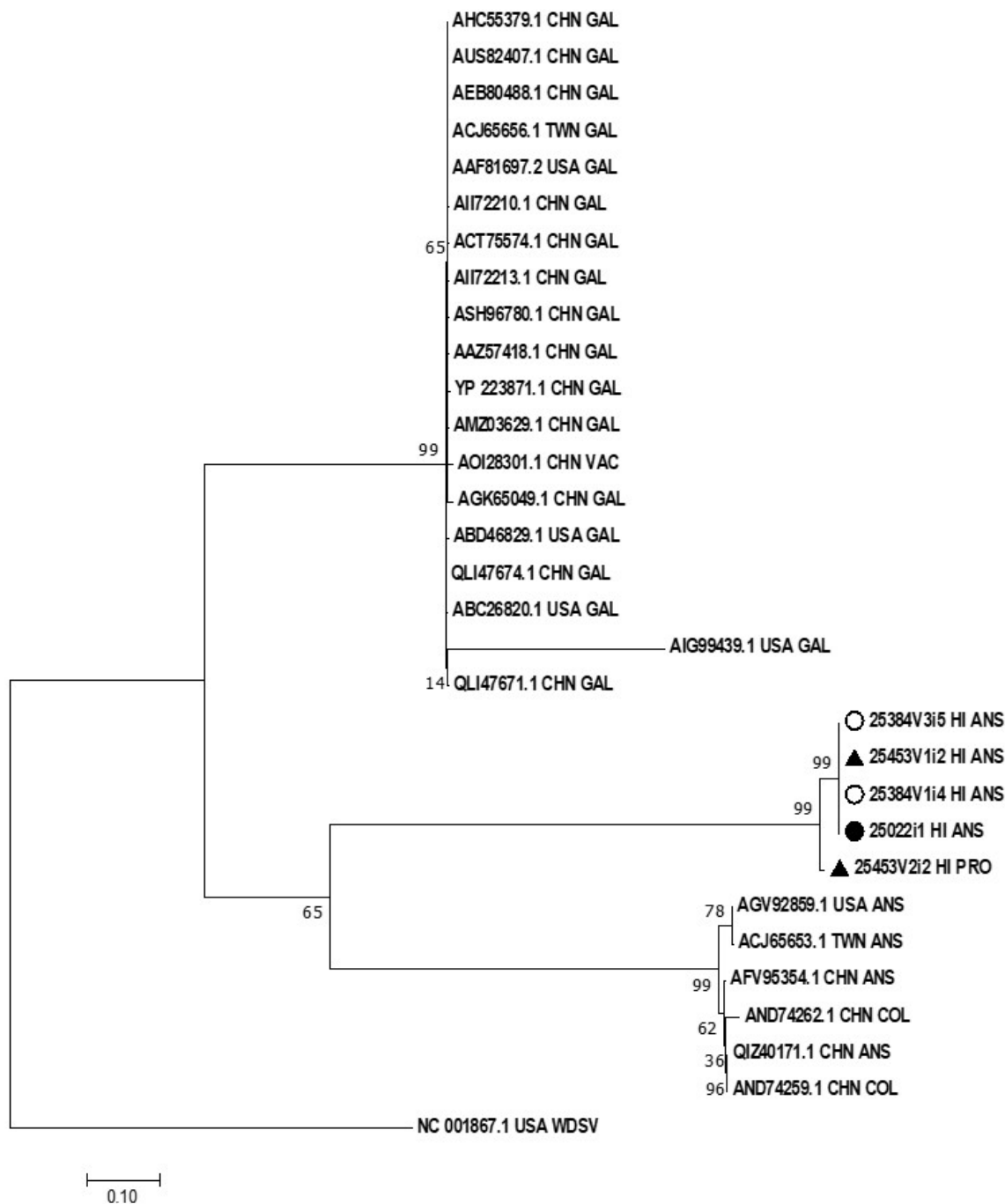


Figure S3. Maximum likelihood tree from amino acid sequences of REV Env gene. Tree was built based on the Whelan and Goldman model with 1000 bootstraps and rooted with walleye dermal sarcoma virus. Labels are Genbank accession, three letter ISO3166 country code (except for Hawaii-HI), and animal group. Hawaii labels end in V (virus variant) and i (gene isoform). Countries are CHN-China, TWN-Taiwan, USA-United States of America. Animal groups are ANS-Anseriform, COL-Columbiformes, GAL-Galliformes, MAM-Mammalia, PAS-Passeriformes, PEL-Pelecaniformes, PRO-Procelariiformes, UNK-Unknown, VAC-Vaccine origin Circles represent Hawaiian goose (*Branta sandvicensis*) with neoplasia (open) or toxoplasmosis (filled) and triangles represent Laysan albatross (*Phoebastria immutabilis*). Scale is nucleotide substitutions per site, numbers at nodes are bootstrap values.

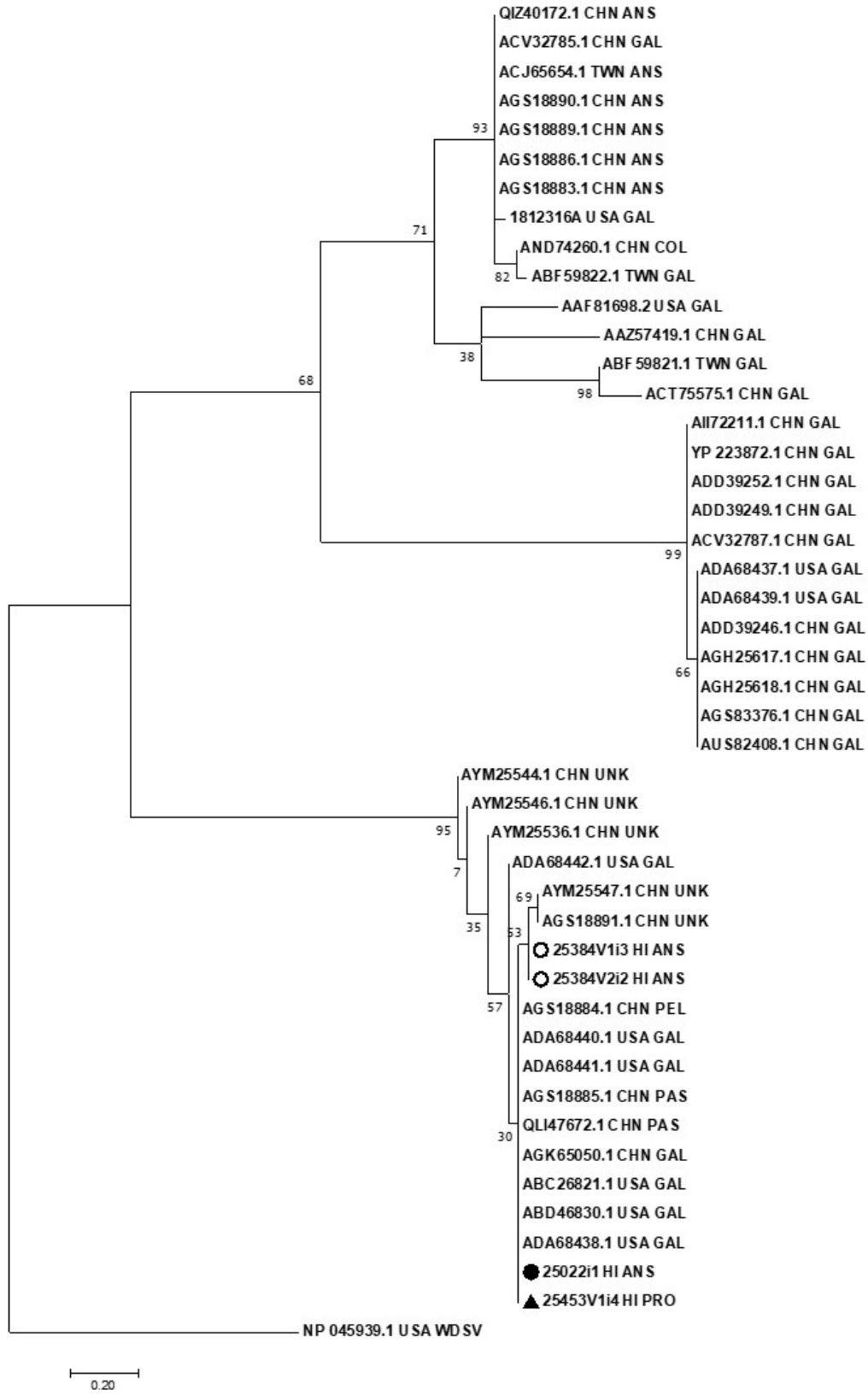


Table S1. Primers used to assemble Gag-Pol-Env cassette for REV for two Hawaiian Geese (*Branta sandvicensis*) and one Laysan albatross (*Phoebastria immutabilis*) partitioned by primer name, sequence, gene targeted, start (forward primer 5') and end (reverse primer 5') and expected base pairs.

Forward	Forward sequence	Reverse	Reverse sequence	Gene	Start	End	BP
25453-1F_Pol	AGACGATGCACCCACATCAG	25453-1R_Pol	TTTCTCCACGGGAGTTGCTC	pol	3892	4300	408
25453-2F_Pol	ATTCTAGCCTTGCTGACCGC	25453-2R_Pol	CACACAGCGGGTGGTGATA	pol	3821	4258	437
25453-3F_Pol	GGGTAGAGGCATATCCAGCA	25453-3R4R_Pol	AACAGTGGGGTACGGTCTTG	pol	4425	4956	531
REVdistF2_Pol	AGGGAGGGATTGTCACCCTT	REVdistR2_Pol	GTAAGTCAGGTAGGCGGTGG	pol	4751	5355	604
REVproxF1_Gag	TAAGAAGACGCCTCCGGGTA	REVproxR1_Gag	CTGGACATGAATGGGGGCTT	gag	1468	2119	651
REVproxF2_Gag	CGCGCCCGATATTAGGAAGA	REVproxR2_Gag	CCCGGTGAACGAGATGGTAG	gag	1282	1924	642
REVdistF1_Pol	GAAGGGAAACCTCCCAGGTG	REVdistR1_Pol	GGGTGCTGAGGACTACAGTG	pol	4446	5048	602
REVdistF2_Pol	AGGGAGGGATTGTCACCCTT	REVdistR2_Pol	GTAAGTCAGGTAGGCGGTGG	pol	4751	5355	604
REVPolFa	GGCCGTCAGGGTTCTTCC	REVPolRa	ATTTGCGAATAGTTTCGCGCAG	pol	1610	2207	597
REVPolF02c	ACCTCCGGGCAGGACATAGA	REVPolR02c	ACGTTTAGGTAGCCAGACCG	pol	3248	3859	611
REVPolF02b	GCCGAACTCAGGCTATTCTTC	REVPolR02b	TAGCCGGATTGAGGGCCG	pol	2814	3413	599
REVEnvF05a	TATGTCCTCCACGGGTCAT	REVEnvR05a	GTCCCTGAAAGAGCCTGGAC	env	6143	6464	321
REVPolF05b	GCTCAATTCCCGCATCAGAG	REVPolR05b	GCTGCCCCGAGCCAGAG	pol	4303	4902	599
REVPolF05c	TAGTTCCCCGTGTAGGATGTGA	REVPolR05c	TGTCTAAATCCCCCTCCCCAG	pol	4800	5399	599
REVPolF03a	TGATCTACAGAGAAAGGGGACTG	REVPolR03a	TGAAATCCACCTCCCAGTGT	pol	3759	4358	599



REVPoIF02a	AGGAAGAAGCGTTCCAGAGC	REVPoIR02a	TCCAGAGTTACCACTGCTGC	pol	2988	3603	615
REVEnvF	TGGATCCACCACTCTCGACT	REVEnvR	AGACATACACAGGGGCTA	env	5081	5680	599
REVEnvF01	TTCAAGCCTCTTGACGGGA	REVEnvR01	TTTATTAGGGAGCGCCGTGT	env	5612	6210	598
REVEnvF02	GTGTGTGGGAACAACATGGC	REVEnvR02	GCCGAGGGTCAGGAACAATA	env	6169	6768	599
REVPoIF	CTACCATCTCGTTCACCGGG	REVPoIR	ATTCTCCTTCCTCCGCATCTG	pol	1905	2504	599
REVPoIF01	TTTCTGCATCCCTCTGGCCC	REVPoIR01	GGCTGTGTGAGGGCTAGTTT	pol	2431	3030	599
REVPoIF03	GATTCTCTGACCTCACCCG	REVPoIR03	TTTGGTCCCCCTTAGTCGATG	pol	3470	4069	599
REVPoIF04	ATTCGCATGTAGAGGAGGCT	REVPoIR04	ATTCGCATGTAGAGGAGGCT	pol	4023	4811	788
REVGagF01	ACCCACAGGACCCTCTAAAGT	REVGagR01	GTAGCTGGGAACTGGGCTTC	gag	424	1023	599
REVGagF03	GGAGAGTAGAGCGGAGAGAGG	REVGagR03	CCACTGCTCTAGCAGCGTAA	gag	1444	2041	597
REV-ENV-1F_NS	TGACCAGGCGGGCAAACC	REV-ENV-2R_NT	CGAAAGGGAGGCTAAGACT	env	5169	5990	821
REV-env_NU	CCACCGGGTCAATAGATGTCAACTG	REV-env_NV	AGTGGCTTGACTGCGGGACTAATG	env	5999	6857	858