Genome of the Komodo dragon reveals adaptations in the cardiovascular and chemosensory systems of monitor lizards

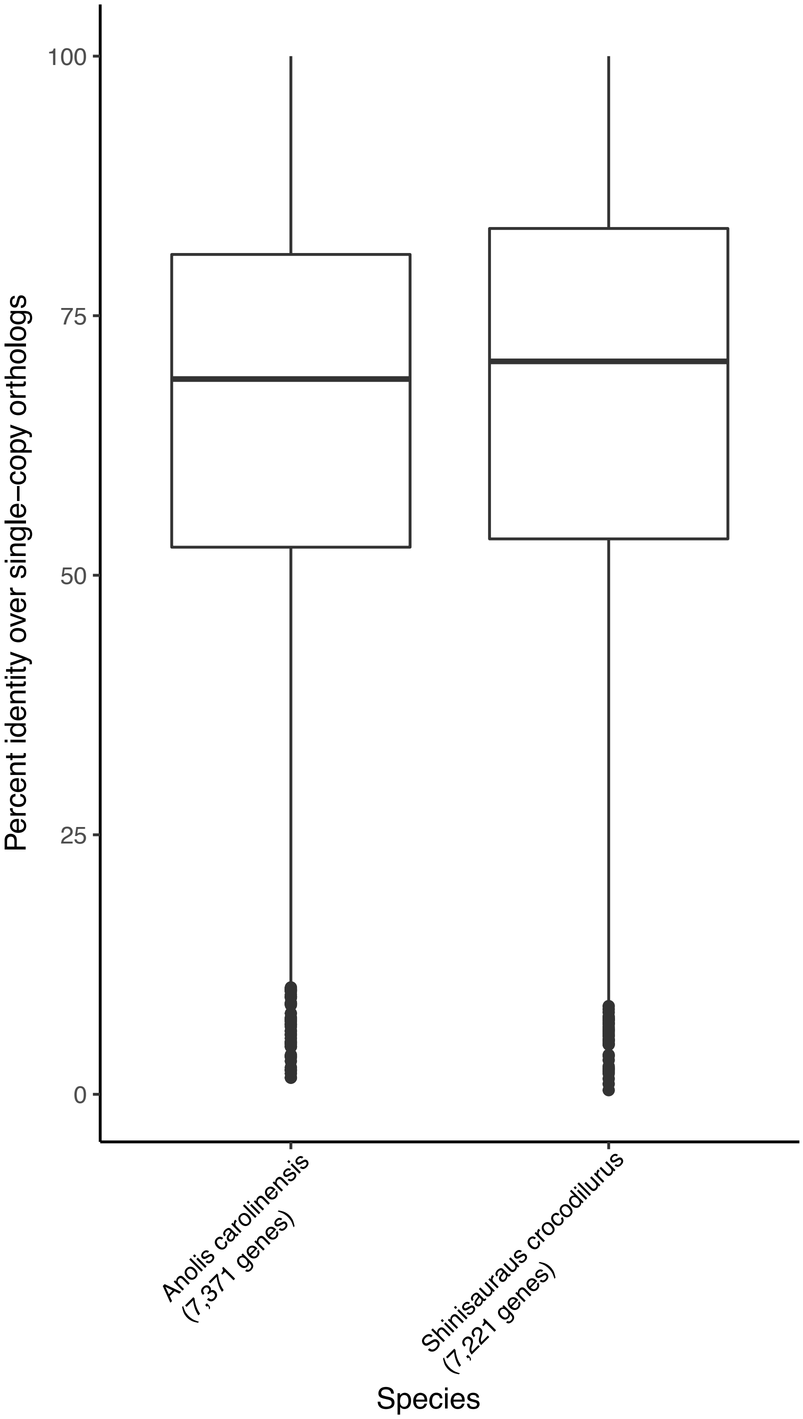

Figure S1. Percent identities of single-copy orthologs between the Komodo dragon and the green anole and the Komodo dragon and the Chinese crocodile lizard.

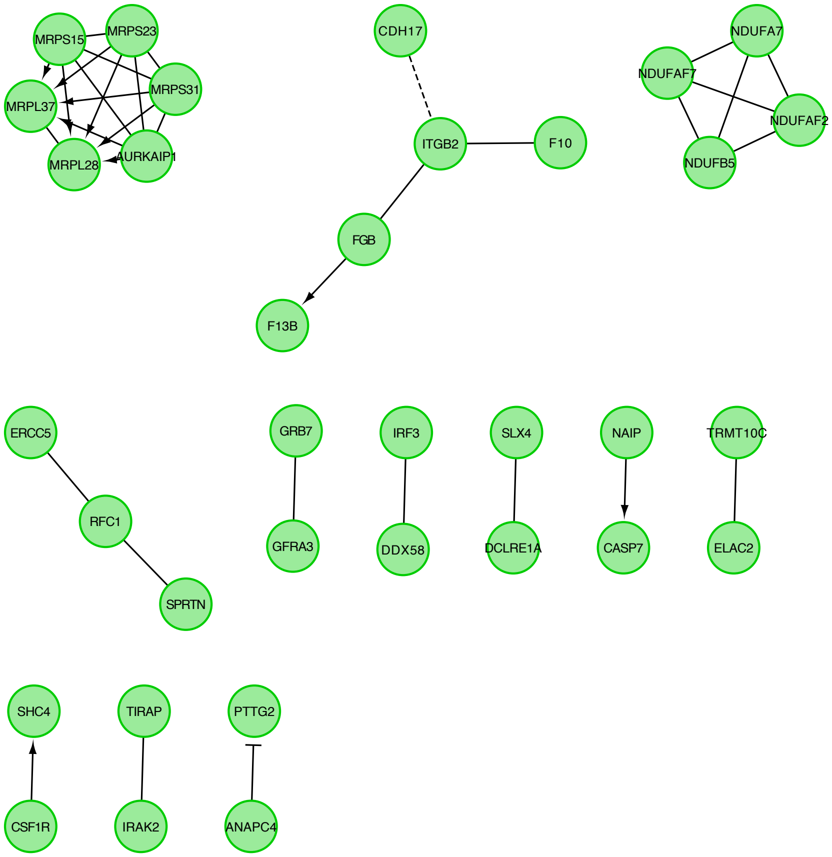

Figure S2. Network of positively selected genes with functional interactions as determined by Reactome FIViz.

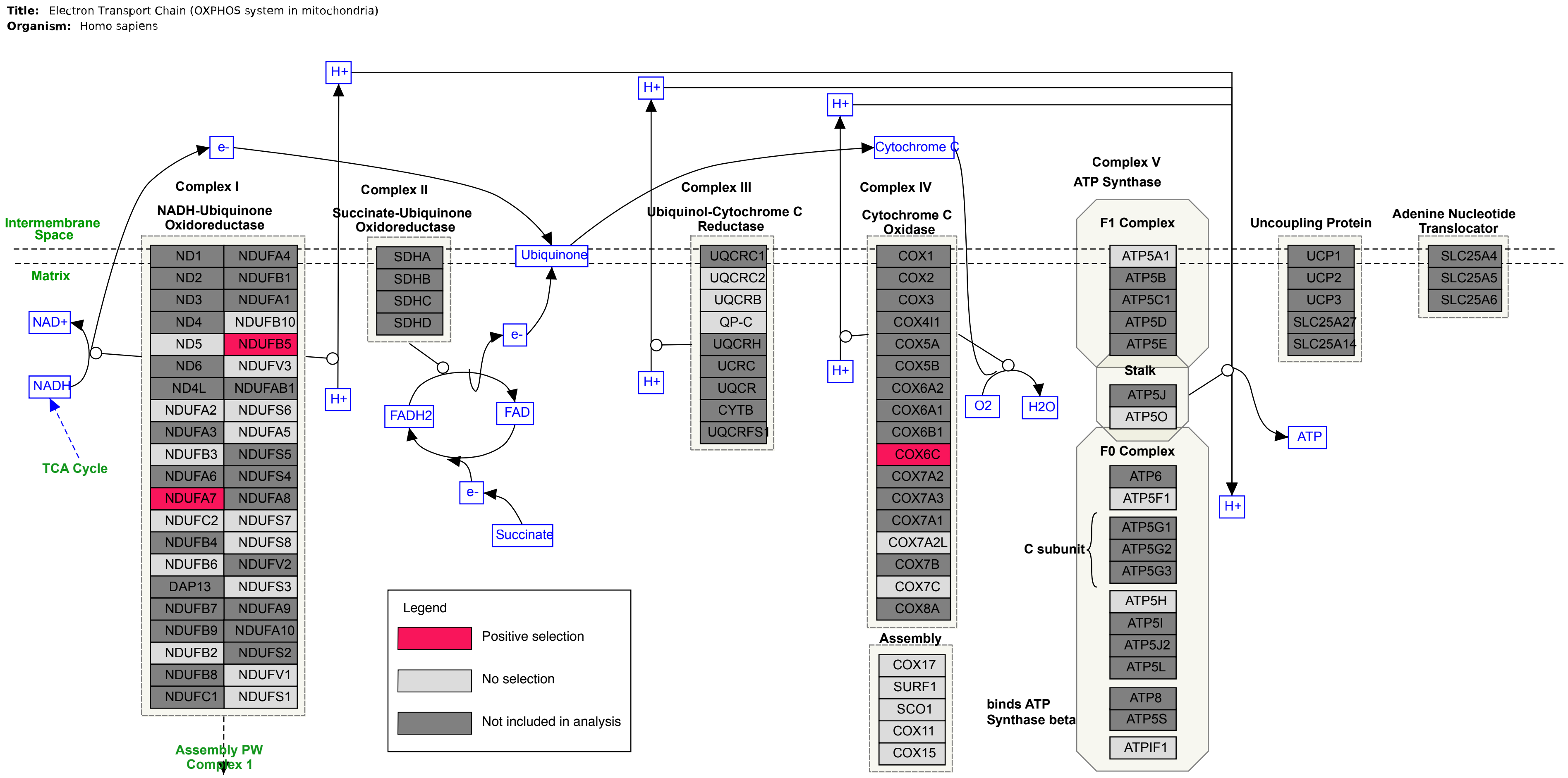

Figure S3. Positive selection on genes encoding structural proteins in the electron transport chain. Dark gray genes were not tested for positive selection due to either missing data in one or more species or difficulty resolving ortholog/paralog relationships. Pink genes have signatures of positive selection, and light gray genes did not have signatures of positive selection. Figure modified from WikiPathways.

Table S1. Genome statistics and sources for non-avian reptiles used in this study.

Species scientific name	**Species common name**	**Assembly size (Gb)**	**GC content (%)**	**Protein-c**	**Source**	**Accession**
Varanus komodoensis	Komodo dragon	1.51	44.04	18,462	This study	This study
Shinisaurus crocodilurus	Chinese crocodile lizard	2.24	44.46	20,150	GigaDB	DOI: 10.5524/100315
Ophisaurus gracilis	Burmese glass lizard	1.78	43.71	19,513	GigaDB	DOI: 10.5524/100119
Pogona vitticeps	Australian dragon lizard	1.82	41.81	21,994	NCBI	GCF_900067755.1
Anolis carolinensis	Green anole	1.78	40.32	22,293	NCBI	GCF_000090745.1
Python molurus bivitattus	Burmese python	1.44	39.61	20,240	NCBI	GCF_000186305.1
Eublepharis macularius	Leopard gecko	2.02	43.55	24,755	GigaDB	DOI: 10.5524/100246
Gekko japonicus	Japanese gecko	2.55	45.47	21,971	NCBI	GCF_001447785.1
Crocodylus prosus	Saltwater crocodile	2.12	43.90	19,551	NCBI	GCF_001723895.1
Pelodiscus sinensis	Chinese softshell turtle	2.21	44.41	21,900	NCBI	GCF_000230535.1
Chelonia mydas	Green sea turtle	2.24	43.48	19,575	NCBI	GCF_000344595.1
Alligator mississippiensis	American alligator	2.17	44.29	25,279	NCBI	GCF_000281125.3
Alligator sinensis	Chinese alligator	2.30	44.49	22,381	NCBI	GCF_000455745.1
Chrysemys picta bellii	Western painted turtle	2.59	44.19	24,740	NCBI	GCF_000241765.3
Gavialis gangeticus	Indian gharial	2.88	43.94	18,887	NCBI	GCF_001723915.1

Table S2. Repetitive elements in Komodo.

Repeat type	Number of elements	Length occupied	Percentage of sequence
SINEs:	228529	26019684 bp	1.72%
-ALUs	0	0 bp	0.00%
-MIRs	86618	9611722 bp	0.64%
LINEs:	724347	202613692 bp	13.43%
-LINE1	38583	14006748 bp	0.93%
-LINE2	294549	68579729 bp	4.55%
-L3/CR1	255901	72214163 bp	4.79%
LTR_elements:	42768	16998342 bp	1.13%
-ERVL	0	0 bp	0.00%
-ERVL-MaLRs	0	0 bp	0.00%
-ERV_classI	5934	2798550 bp	0.19%
-ERV_classII	362	300979 bp	0.02%
DNA_elements:	374603	53497854 bp	3.55%
-hAT-Charlie	60163	13443390 bp	0.89%
-TcMar-Tigger	28482	6519272 bp	0.43%
Unclassified:	883265	166908695 bp	11.07%
Total_interspersed_repeats:		466038267 bp	30.90%
Small_RNA:	11639	837637 bp	0.06%
Satellites:	8940	752582 bp	0.05%
Simple_repeats:	420254	15381445 bp	1.02%
Low_complexity:	50016	2338271 bp	0.16%
Total repeats		485348202 bp	32.18%

Table S3. Universal single copy genes in reptile genomes (BUSCO: vertebrata set)

Species	Single-copy BUSCO	Duplicated BUSCO	Fragmented BUSCO	Missing BUSCO	Total number BUSCOs
American alligator	96.10%	0.70%	2.20%	1.00%	2586
Australian dragon lizard	94.30%	0.60%	3.10%	2.00%	2586
Burmese glass lizard	94.70%	0.70%	2.80%	1.80%	2586
Burmese python	91.00%	0.70%	5.40%	2.90%	2586
Chinese alligator	94.40%	0.70%	3.20%	1.70%	2586
Chinese crocodile lizard	91.60%	0.90%	4.80%	2.70%	2586
Chinese softshell turtle	93.50%	0.50%	3.80%	2.20%	2586
Green anole	88.10%	0.80%	5.60%	5.50%	2586
Green sea turtle	93.90%	0.80%	3.80%	1.50%	2586
Indian gharial	91.70%	0.50%	3.50%	4.30%	2586
Japanese gecko	89.80%	1.10%	6.30%	2.80%	2586
Komodo dragon	95.70%	0.40%	2.00%	1.90%	2586
Leopard gecko	94.00%	1.20%	3.30%	1.50%	2586
Saltwater crocodile	94.10%	0.60%	2.10%	3.20%	2586
Western painted turtle	95.20%	0.70%	2.60%	1.50%	2586

Table S6. Number of reads, positions and scaffolds assigned to chromosomes

Chromosome	No. of total reads	No. of total positions	No. of total scaffold	Total length of assigned scaffolds (bp)
Chr1	2,325,629	502,804	94	245,019,529
Chr2	10,010,878	1,032,999	14	156,023,568
Chr3	3,921,580	458,921	11	115,571,927
Chr4	1,645,424	491,065	39	117,170,416
Chr5	1,130,763	121,596	6	75,951,376
Chr6, 7, 8	8,726,785	1,442,537	25	200,178,831
Chr9, 10	485,383	131,769	8	69,008,218
Chr11, 12	497,393	107,230	6	52,491,606
Chr13	231,907	48,372	9	19,625,567
Chr14	213,215	21,088	3	21,537,982
Chr15	215,482	58,565	4	14,821,201
Chr16	283,123	17,245	2	13,367,238
Chr17, 18	414,067	61,220	10	17,262,365
Chr19	168,685	36,954	6	11,765,548
ChrZ	414,067	61,220	6	10,642,498

No. of total positions: Total number of positions on scaffolds assigned to a given chromosome. A position being the sequence resulting by the merging of all reads that are consecutively aligned on a specific section of a scaffold

Table S7. V1R and V2R genes across reptiles.

Species	V1R genes	V2R genes
Komodo dragon	0	129
Chinese crocodile lizard	1	195
Burmese glass lizard	1	58
Australian dragon lizard	0	71
Green anole	0	53
Burmese python	0	114
Leopard gecko	1	254
Japanese gecko	0	150
Chinese softshell turtle	0	1
Western painted turtle	1	2
Green sea turtle	1	0
American alligator	1	0
Chinese alligator	1	0
Indian gharial	0	0
Saltwater crocodile	1	0