

Supplementary Table 1. Information of gene location used from Vertebrates genomes as in Table 1.

Common Name	Scientific Name	Code	TLR Gene Family	ENSEMBL/ GENE BANK/ GENOMIC LOCATION
Human	Homo sapiens	HSA	TLR1	ENSG00000174125
			TLR2	ENSG00000137462
			TLR3	ENSG00000164342
			TLR4	ENSG00000136869
			TLR5	ENSG00000187554
			TLR6	ENSG00000174130
			TLR7	ENSG00000196664
			TLR8	ENSG00000101916
			TLR9	ENSG00000173366
			TLR10	ENSG00000174123
			TLR12P	Chromosome 1: 33,466,249-33,468,954
Cod	Gadus morhua	GMO	TLR3	ENSGMOG00000000786
			TLR7	ENSGMOG00000001675
			TLR8A-L	Sunderam et al 2012, Solbakken et al 2016
			TLR9A-E	Sunderam et al 2012, Solbakken et al 2016
			TLR18	ENSGMOG00000003793
			TLR21	ENSGMOG000000018200
			TLR22A-L	Sunderam et al 2012, Solbakken et al 2016
			TLR23	Sunderam et al 2012, Solbakken et al 2016
Fugu	Takifugu rubripes	TRU	TLR25A-G	Sunderam et al 2012, Solbakken et al 2016
			TLR1	XM_003970363.2
			TLR2	XM_011617903.1
			TLR3	XM_003972308.2
			TLR5b	XM_011611736.1_mem
			TLRs5a	XM_003971921.2_soluble
			TLR7	XM_011609151.1
			TLR8	XM_011609158.1
			TLR9	XM_003963302.2
			TLR18	XM_011605231.1
			TLR21	NM_001032579.1
			TLR22	XM_011608077.1
			TLR23	XM_003969133
Tetraodon	Tetraodon nigroviridis	TNI	TLR1	ENSTNIG00000014211
			TLR2	ENSTNIG00000003109
			TLR3	ENSTNIG00000007123
			TLR5b	ENSTNIG00000005998
			TLRs5a	ENSTNIG00000019132
			TLR7	ENSTNIG00000013960
			TLR8	Chromosome 2: 12,678,508-12,681,830:1
			TLR9	ENSTNIG00000015008
			TLR18	ENSTNIG00000006178
			TLR21	ENSTNIG00000008206
			TLR22	ENSTNIG00000013627
			TLR23	ENSTNIG00000005385

Zebrafish	Danio rerio	DAR	TLR1	ENSDARG00000043032
			TLR2	ENSDARG00000037758
			TLR3	ENSDARG00000016065
			TLR4aI	ENSDARG00000075671
			TLR4a	ENSDARG00000019742
			TLR4b	ENSDARG00000022048
			TLR5b	ENSDARG00000044415
			TLR5b2	ENSDARG00000052322
			TLR7	ENSDARG00000068812
			TLR7_PSEUDO	Chromosome 9: 30,399,886-30,403,138:1
			TLR7_PSEUDO	Chromosome 9: 54,582,021-54,582,864
			TLR8C	ENSDARG00000090119
			TLR8a	ENSDARG00000089151
			TLR8b	ENSDARG00000073675
			TLR9	ENSDARG00000044490
			TLR18	ENSDARG00000040249
			TLR19A	ENSDARG00000026663
			TLR19B	ENSDARG00000070392
			TLR20A	ENSDARG00000092668
			TLR20D	ENSDARG00000088701
			TLR20B	ENSDARG00000094411
			TLR20F	ENSDARG00000092355
			TLR20C	ENSDARG00000041164
			TLR20E	ENSDARG00000069593
			TLR21	ENSDARG00000058045
			TLR22	ENSDARG000000104045
Stickleback	Gasterosteus aculeatus	GAC	TLR1	ENSGACG00000017958
			TLR2	ENSGACG00000018669
			TLR3	ENSGACG00000016874
			TLR5Sb	ENSGACG00000007147
			TLR5M	ENSGACG00000004381
			TLR5Sa	ENSGACG00000007154
			TLR7	ENSGACG00000003996
			TLR8	ENSGACG00000003992
			TLR9	ENSGACG00000010164
			TLR18	ENSGACG00000001745
			TLR21a	ENSGACG00000009364
			TLR21b	ENSGACG00000008397
			TLR22	ENSGACG00000005449
Medaka	Oryzias latipes	ORL	TLR1	ENSORL.G00000004420
			TLR2	ENSORL.G00000002540
			TLR3	ENSORL.G00000008184
			TLR5b	ENSORL.G00000016221
			TLR5a	ENSORL.G00000017639
			TLR7	Chromosome 21: 26,169,747-26,173,142:1
			TLR8	Chromosome:21:26174579:26177859:1
			TLR9	ENSORL.G00000008852
			TLR18	ENSORL.G00000015704
			TLR21	ENSORL.G00000013437
			TLR22	ENSORL.G00000020413
			TLR25	ENSORL.G00000012771

Platyfish	Xiphophorus maculatus	XMA	TLR1	ENSXMAG00000008414
			TLR2a	ENSXMAG00000008258TLR2 (1 of 2)
			TLR2b	ENSXMAG00000008259TLR2 (2 of 2)
			TLR3	ENSXMAG00000018871TLR3
			TLR5A	ENSXMAG00000006310TLR5 (1 of 2)
			TLR5B	ENSXMAG00000001788TLR5 (2 of 2)
			TLR7	ENSXMAG00000004434TLR7
			TLR8	ENSXMAG00000004433TLR8
			TLR9	ENSXMAG00000007629TLR9
			TLR18	ENSXMAG00000013367
			TLR21	ENSXMAG00000010772
			TLR22A	ENSXMAG00000020395
			TLR22B	ENSXMAG00000003638
			TLR22C	ENSXMAG00000017252
			TLR23A	Scaffold JH556800.1: 602,908-605,667
			TLR23B	Scaffold JH556800.1: 614,188-616,918
			TLR23C	Scaffold JH556800.1: 625,221-625,610
			TLR23D	Scaffold JH556800.1: 629,640-632,373
			TLR23E	Scaffold JH556800.1: 646,924-647,791
			TLR23F	Scaffold JH556800.1: 655,116-655,930
Tilapia	Oreochromis niloticus	ONI	TLR1	XM_013271073.1
			TLR2A	XM_013264298.1
			TLR2B	XM_005460756.2
			TLR2	XM_005460757.1
			TLR2_PAR	XM_005466799.2
			TLR2_PAR	XM_005466800.2
			TLR3	XM_003449728.3
			TLR5_SOLU_a	XM_013271973.1
			TLR5_MEM_b	XM_005449891.2
			TLR7	XM_013264229.1
			TLR8a	XM_003460594.3
			TLR8b	XM_013264230.1
			TLR9	XM_005477981.2
			TLR18	XM_003450307.3
			TLR21a	XM_005463956.2
			TLR21b	XM_003458802.2
			TLR21c	NM_001311317.1
			TLR22a	XM_003460394.3
			TLR22b	XM_013264208.1
			TLR22c	XM_005449134.2
			TLR23a	XM_013264888.1
			TLR23b	XM_013264886.1
			TLR23c	XM_013264887.1
			TLR25	XM_005460356.2
Coelacanth	Latimeria chalumnae	LAC	TLR1	ENSLACG00000010038
			TLR2	ENSLACG00000012590
			TLR2L	ENSLACG00000004773
			TLR3	ENSLACG00000011410
			TLR5pseudo	AFYH01284233.1:49-1002

Xenopus	Xenopus tropicalis	XET	TLR5b_mem	ENSLACG00000015379
			TLR7a	ENSLACG00000004229
			TLR7b	ENSLACG00000001037
			TLR8	ENSLACG000000016637
			TLR9	ENSLACG000000018420
			TLR13	ENSLACG000000012864
			TLR18	ENSLACG000000017699
			TLR21a	ENSLACG000000001078
			TLR21b	ENSLACG000000006376
			TLR21c	ENSLACG000000002657
			TLR27	ENSLACG000000015138
			TLR1 1	GL173030.1:983000-985412
			TLR1 2	ENSXETG000000018477
			TLR1 3	ENSXETG000000018489
Mouse	Mus musculus	MUS	TLR3	ENSXETG000000005873
			TLR5	ENSXETG000000030446
			TLR2a	ENSXETG000000033109
			TLR2b	ENSXETG000000001817
			TLR5b	ENSXETG000000015027
			TLR7	ENSXETG000000027076
			TLR8a	ENSXETG000000030579
			TLR8b	GL172707.1:833802-836931
			TLR9	ENSXETG000000005958
			TLR13	ENSXETG000000004577
			TLR14A	ENSXETG000000031826
			TLR14b	ENSXETG000000021898
			TLR14c	ENSXETG000000021933
			TLR14d	ENSXETG000000017689
			TLR16	ENSXETG000000032510
			TLR21	ENSXETG000000032848
			TLR22	ENSXETG000000018306
			TLR1	ENSMUSG0000000044827
			TLR2	ENSMUSG0000000027995
			TLR3	ENSMUSG0000000031639
			TLR4	ENSMUSG0000000039005
			TLR5	ENSMUSG0000000079164
			TLR6	ENSMUSG0000000051498
			TLR7	ENSMUSG0000000044583
			TLR8	ENSMUSG0000000040522
			TLR9	ENSMUSG0000000045322
			TLR10	Chromosome 5:64896921-64898474:MINUS
			TLR11	ENSMUSG0000000051969
			TLR12	ENSMUSG0000000062545
			TLR13	ENSMUSG0000000033777
Opossum	Monodelphis domestica	MOD	TLR2	XM_001375753.3
			TLR3	XM_007496034.2
			TLR4	XM_001368732.3
			TLR5	XM_007481456.1
			TLR6	XM_007496564.2
			TLR7	XM_007500926.2
			TLR8	XM_007500927.2
			TLR9	XM_007500513.1
			TLR10	XM_007496591.1
			TLR12	XM_001516788.1

Platypus	Ornithorhynchus anatinus	OAN	TLR13	XM_001372402.2
			TLR2	ENSOANG00000005291
			TLR3	ENSOANG00000004937
			TLR4	ENSOANG00000013202
			TLR5	ENSOANG00000001445
			TLR6	Ultra544:4634632-4637016 plus
			TLR7	ENSOANG00000002612
			TLR8	ENSOANG00000015882
			TLR9	ENSOANG00000014852
			TLR10	ENSOANG00000010318
			TLR12	ENSOANG00000001379
			TLR13Partial	Contig49661: 1-1,689
Anole lizard	Anolis carolinensis	ACA	TLR1a	ENSACAG00000024414
			TLR1b	ENSACAG00000007342
			TLR2a	ENSACAG00000023058
			TLR2b	ENSACAG00000021135
			TLR3	ENSACAG00000001732
			TLR4	ENSACAG00000013911
			TLR5b_Mem	ENSACAG00000002483
			TLR5a_solu	ENSACAG00000023912
			TLR7	ENSACAG00000001655
			TLR13	ENSACAG00000016646
			TLR18	ENSACAG00000024450
			TLR15	ENSACAG00000025732
			TLR21	ENSACAG00000015069
			TLR22	ENSACAG00000028117
Chinese softshell turtle	Pelodiscus sinensis	PSI	TLR1A	Scaffold JH210475.1: 1,926,342-1,926,908
			TLR1B	Scaffold JH210475.1: 1,908,091-1,910,123
			TLR2a	ENSPSIG00000000537
			TLR2b	ENSPSIG00000000529
			TLR3	ENSPSIG00000010900
			TLR4	ENSPSIG00000003827
			TLR5a	JH212639:593558-595522
			TLR5b	ENSPSIG00000000533
			TLR7	ENSPSIG00000000409
			TLR8a	ENSPSIG00000010094
			TLR8b	ENSPSIG00000000439
			TLR8c	ENSPSIG00000000427
			TLR9	ENSPSIG00000012812
			TLR18	Scaffold JH207675.1: 111,570-113,183
			TLR21	ENSPSIG00000014031
			TLR22a	ENSPSIG00000000250
			TLR22b	JH224649:4898350-4901214
			TLR2 pseudo	Scaffold JH210535:81435-82781
Chicken	Gallus gallus	GAL	TLR1A	ENSGALG00000017485
			TLR1B	ENSGALG00000027093
			TLR2A	ENSGALG00000009237
			TLR2B	ENSGALG00000009239
			TLR3	ENSGALG00000013468
			TLR4	ENSGALG00000007001
			TLR5	ENSGALG00000009392

Zebra Finch	Taeniopygia guttata	TGU	TLR7	ENSGALG00000016590
			TLR15	ENSGALG00000008166
			TLR21	ENSGALG00000000774
			TLR1A	ENSTGUG000000009041
			TLR1B	ENSTGUG000000009043
			TLR2A	ENSTGUG000000005179
			TLR2B	ENSTGUG000000005181
			TLR3	ENSTGUG000000006891
			TLR4	ENSTGUG000000003342
			TLR5	ENSTGUG000000002653
Turkey	Meleagris gallopavo	MGA	TLR7	ENSTGUG000000008250
			TLR15	ENSTGUG000000007261
			TLR21	ENSTGUG000000014873
			TLR1A	Chromosome 4:52459418-52460914
			TLR1B	ENSMGAG000000015741
			TLR2A	ENSMGAG000000001271
			TLR2B	Chromosome 4: 299,887-302,519
			TLR3	ENSMGAG000000011425
			TLR4	ENSMGAG000000005422
			TLR5	ENSMGAG000000015929
Lamprey	Petromyzon marinus	PMA	TLR7	ENSMGAG000000014706
			TLR15	ENSMGAG000000015891
			TLR21	ENSMGAG000000015581
			TLR3	ENSPMAG000000001609
			TLR7_8A	ENSPMAG000000002336
			TLR7_8B	ENSPMAG000000006251
			TLR14D	ENSPMAG000000001845
			TLR14B	scaffold:Pmarinus_7.0:GL482135:8342:10651:plus
			TLR14C	ENSPMAG000000010085
			TLR14A	ENSPMAG000000010230
			TLR24A	ENSPMAG000000010419
			TLR24B	ENSPMAG000000010418
			TLR21A	ENSPMAG000000010099
			TLR21B	ENSPMAG000000005013
			TLR21C	ENSPMAG000000010181
			TLR22	ENSPMAG000000009344
Cat Fish	Ictalurus punctatus			Zhang J et al. 2013. Dev. Comp. Immunol.
American alligator	Alligator mississippiensis	AMI	TLR1A_PARTIAL	XM_006258501.2
			TLR1B_PARTIAL	XM_006258498.2
			TLR2A	XM_006264461.2
			TLR2B_PARTIAL	XM_014611524.1
			TLR3	XM_014594861.1
			TLR4	XM_014608218.1
			TLR5MEM	XM_014598157.1
			TLR5SOL	XM_014596433.1
			TLR7	XM_006258898.1
			TLR8a	XM_006258899.1
			TLR8b	XM_014607765.1
			TLR13	XM_006277653.2
			TLR13 partial	XM_006277720.2

			TLR18	XM_006266453.2
			TLR15	XM_006274445.1
			TLR21	XM_014604107.1
			TLR22	XM_006278050.2
Green sea turtle	Chelonia mydas	CMY	TLR1	XM_007059713.1
			TLR2a	LOC102930340
			TLR2b	LOC102943966
			TLR2 Pseudo	LOC102944187
			TLR2 Pseudo	LOC102948090
			TLR3	XM_007063639.1
			TLR4	XM_007057276.1
			TLR5-b	XM_007070449.1
			TLR5-a	LOC102935193
			TLR7	XM_007060255.1
			TLR8a	LOC102936357
			TLR8b	LOC102929320
			TLR8c Pseudo	LOC102929541
			TLR9	XM_007072645.1
			TLR18	LOC102934124
			TLR21	LOC102932182
			TLR22	LOC102933568
Painted Turtle	TLR1b	NW_007281374.1	1073972-1075936	minus
Chrysemys picta bellii	TLR1a	NW_007281374.1	1052625-1082355	minus
CPI	TLR2a	NW_007281363.1	6915182-6922124	minus
	TLR2b	NW_007281363.1	6930769-6934678	minus
	TLR2 Pseudo	NW_007281478.1	2029068-2031867	minus
	TLR3	NW_007281348.1	3232636-3258099	plus
	TLR4	NW_007281396.1	2815764-2823017	minus
	TLR5b	NC_024220.1	29396277-29464002	plus
	TLR5a	NW_007359864.1	6454634-6456598	minus
	TLR7	NW_007281929.1	16159-158348	minus
	TLR8C	NW_007281432.1	486376-514205	minus
	TLR8A	NW_007281432.1	425823-433047	minus
	TLR8B	NW_007281432.1	448377-469596	minus
	TLR9	NW_007281433.1	3140067-3140628	plus
	TLR13	NW_007281758.1	356935-361762	plus
	TLR18	NW_007281382.1	239091-246077	minus
	TLR21	NW_007282527.1	35847-40133	minus
	TLR22	NW_007359863.1	3714789-3718615	minus
Saltwater crocodile	TLR1A	scaffold-2618	14028-26421	minus
Crocodylus porosus	TLR1B	scaffold-16355	54510-66333	minus
CPO	TLR2A	scaffold-5033	166862-178589	plus
	TLR2B	scaffold-7567	6888-18654	plus
	TLR3	scaffold-13333	34392-46380	minus
	TLR4	scaffold-5054	390416-402680	plus
	TLR5	scaffold-7445	166148-178679	minus
	TLR7	scaffold-7909	22433-35525	plus
	TLR8A	scaffold-7909	53369-66461	plus
	TLR8B	scaffold-10130	11455-24610	plus
	TLR13	scaffold-98	21348-33975	plus
	TLR15	scaffold-2513	298977-311601	minus
	TLR18	scaffold-19646	79941-92256	plus
	TLR21	scaffold-12709	10-8641	plus
	TLR22	scaffold-16286	312758-325541	minus

Gharial	TLR1A	scaffold39093	2414-14813	minus
Gavialis gangeticus	TLR1B	scaffold37111	13777-25744	minus
GGA	TLR2A	scaffold25747	35451-47628	plus
	TLR2B	scaffold7208	5283-17625	plus
	TLR3	scaffold40862	2099-13919	minus
	TLR4	scaffold4129	233709-245964	plus
	TLR5	scaffold880	33731-46271	minus
	TLR7	scaffold26318	40719-53808	minus
	TLR8A	scaffold26318	2766-15885	minus
	TLR8B	scaffold6915	7137-20292	plus
	TLR13	scaffold11898	215983-228610	minus
	TLR15	scaffold3177	66099-78723	minus
	TLR18	scaffold13001	27411-39738	minus
	TLR21	scaffold10392	101071-113830	minus
	TLR22	scaffold166	501410-514196	plus
Python	TLR1	XM_007437894.2		
Python molurus	TLR2a	XM_015889785.1		
PMO	TLR2b	XM_007425609.2		
	TLR3	XM_007439002.2		
	TLR4	XM_007433542.2		
	TLR5a	XM_007439931.1		
	TLR5b	XM_015889124.1		
	TLR7	XM_007435644.1		
	TLR18	XM_007436577.2		
	TLR15	XM_007444506.1		
	TLR21	XM_015888483.1		
	TLR22	NW_006532080.1:41595-44441		
Spotted gar	TLR1	XM_015345878.1		
Lepisosteus oculatus	TLR1 partial	XM_015355233.1		
LEO	TLR2	XM_015344719.1		
	TLR3	XM_006630108.2		
	TLR4	XM_015366876.1		
	TLR5m	XM_006625986.2		
	TLR7	XM_015361454.1		
	TLR8a	XM_015361455.1		
	TLR8b	XM_015361493.1		
	TLR9a	XM_015348292.1		
	TLR9b	XM_015348046.1		
	TLR18	XM_015336729.1		
	TLR22	XM_015349956.1		
	TLR23	XM_006625652.2		
	TLR25	XM_015353150.1		
	TLR25	XM_015352785.1		
Equus_caballus	TLR1	ENSECAG00000038588		
Equus_caballus	TLR10	ENSECAG00000020892		
Equus_caballus	TLR11	ENSECAG00000006701		
Equus_caballus	TLR12	ENSECAG00000005400		
Equus_caballus	TLR13	X:61051093-61053730		
Equus_caballus	TLR2	ENSECAG00000018028		
Equus_caballus	TLR3	ENSECAG00000000197		
Equus_caballus	TLR4	ENSECAG000000033740		
Equus_caballus	TLR5	ENSECAG000000036553		
Equus_caballus	TLR6	ENSECAG000000001958		
Equus_caballus	TLR7	ENSECAG000000007883		
Equus_caballus	TLR8	ENSECAG000000009180		

Equus_caballus	TLR9	ENSECAG00000014294
Canis_familiaris	TLR1	ENSCAFG000000024010
Canis_familiaris	TLR10	ENSCAFG000000016175
Canis_familiaris	TLR2	ENSCAFG000000008351
Canis_familiaris	TLR3	ENSCAFG000000007406
Canis_familiaris	TLR4	ENSCAFG000000003518
Canis_familiaris	TLR5	ENSCAFG000000011368
Canis_familiaris	TLR6	ENSCAFG000000016172
Canis_familiaris	TLR7	ENSCAFG000000011698
Canis_familiaris	TLR8	ENSCAFG000000023498
Canis_familiaris	TLR9	ENSCAFG000000023201
Bos_taurus	TLR1	6:58051169-58053505
Bos_taurus	TLR10	6:58034660-58037079
Bos_taurus	TLR2	ENSBTAG000000008008
Bos_taurus	TLR3	ENSBTAG000000008682
Bos_taurus	TLR4	ENSBTAG000000006240
Bos_taurus	TLR5	ENSBTAG000000000477
Bos_taurus	TLR6	6:58068196-58070516
Bos_taurus	TLR7	ENSBTAG000000022161
Bos_taurus	TLR8	PENSBTAG000000031020
Bos_taurus	TLR9	ENSBTAG000000018198
Myotis_lucifugus	TLR1	ENSMUG000000008417
Myotis_lucifugus	TLR11	ENSMUG0000000026159
Myotis_lucifugus	TLR12	ENSMUG0000000028208
Myotis_lucifugus	TLR13	ENSMUG0000000026413
Myotis_lucifugus	TLR2	ENSMUG000000012813
Myotis_lucifugus	TLR3	ENSMUG000000012567
Myotis_lucifugus	TLR4	ENSMUG000000007417
Myotis_lucifugus	TLR5	ENSMUG0000000030769
Myotis_lucifugus	TLR6	ENSMUG000000008430
Myotis_lucifugus	TLR7	ENSMUG0000000003912
Myotis_lucifugus	TLR8	ENSMUG000000012745
Myotis_lucifugus	TLR9	ENSMUG000000015097
Gekko_japonicus	TLR1A	LOC107116375
Gekko_japonicus	TLR1B	LOC107116262
Gekko_japonicus	TLR13	LOC107113131
Gekko_japonicus	TLR15	LOC107118830
Gekko_japonicus	TLR18	LOC107107978
Gekko_japonicus	TLR21	LOC107115007
Gekko_japonicus	TLR22	LOC107119739
Gekko_japonicus	TLR2a	Gene ID:107108593
Gekko_japonicus	TLR3	GenelD:107121983
Gekko_japonicus	TLR4	GenelD:107106055
Gekko_japonicus	TLR5	GenelD:107121624
Gekko_japonicus	TLR5	GenelD:107110111
Gekko_japonicus	TLR7	GenelD:107124266
Pogona_vitticeps	TLR1a	LOC110075223
Pogona_vitticeps	TLR1b	LOC110075222
Pogona_vitticeps	TLR13	LOC110078546
Pogona_vitticeps	TLR21	LOC110086777
Pogona_vitticeps	TLR22	LOC110072303
Pogona_vitticeps	TLR2	LOC110082123
Pogona_vitticeps	TLR2	GenelD:110072767
Pogona_vitticeps	TLR18	LOC110069865
Pogona_vitticeps	TLR3	GenelD:110083608
Pogona_vitticeps	TLR4	GenelD:110088887
Pogona_vitticeps	TLR5	GenelD:110069864
Pogona_vitticeps	TLR5	GenelD:110071659

<i>Pogona_vitticeps</i>	TLR5	GenelD:110071691
<i>Pogona_vitticeps</i>	TLR5	GenelD:110075393
<i>Pogona_vitticeps</i>	TLR7	LOC110075448
<i>Protobothrops_mucrosquamatus</i>	TLR1	LOC107293704
<i>Protobothrops_mucrosquamatus</i>	TLR13	GenelD:107282446
<i>Protobothrops_mucrosquamatus</i>	TLR2	LOC107288063
<i>Protobothrops_mucrosquamatus</i>	TLR2a	GenelD:107289574
<i>Protobothrops_mucrosquamatus</i>	TLR15	LOC107285496
<i>Protobothrops_mucrosquamatus</i>	TLR21	LOC107289709
<i>Protobothrops_mucrosquamatus</i>	TLR2	LOC107290599
<i>Protobothrops_mucrosquamatus</i>	TLR3	GenelD:107302660
<i>Protobothrops_mucrosquamatus</i>	TLR4	GenelD:107285740
<i>Protobothrops_mucrosquamatus</i>	TLR5	LOC107295996
<i>Protobothrops_mucrosquamatus</i>	TLR5	GenelD:107302774
<i>Protobothrops_mucrosquamatus</i>	TLR7	GenelD:107302471

Supplementary Table 2 Avian TLR genes used in this study for Positive selection analysis

SPECIES_NAME	1A	1B	2A	2B	3	4	5	7	15
<i>Calypte_anna</i>	Geno_scaff_region	XM_008491888.1	XM_008493863.1	XM_008493793.1	XM_008491852.1	XM_008499333.1	NA	XM_008494759.1	XM_008493258.1
<i>Caprimulgus_caroline</i> <i>nsis</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010170240.1	XM_010165071.1	XM_010164361.1	XM_010175260.1	XM_010174731.1
<i>Cariama_cristata</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009700362.1	XM_009702452.1	NA	XM_009696068.1	XM_009706095.1
<i>Colius_striatus</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010203505.1	XM_010195927.1	XM_010204457.1	XM_010209014.1	XM_010206127.1
<i>Columba_livia</i>	XM_005501264.1	XM_005501263.2	XM_021285390.1	XM_013372151.2	XM_005500210.1	XM_005498384.1	XM_021299623.1	XM_005512700.2	XM_021280471.1
<i>Corvus_brachyrhynch</i> <i>os</i>	XM_017744288.1	XM_008641370.2	XM_008635647.2	XM_017736870.1	XM_008641455.2	XM_008638328.2	XM_017730068.1	NU	XM_008642044.2
<i>Cuculus_canorus</i>	XM_009566580.1	Geno_scaff_region	Geno_scaff_region	XM_009567139.1	XM_009565656.1	XM_009569425.1	XM_009569717.1	NU	XM_009560965.1
<i>Acanthisitta_chloris</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009072290.1	XM_009073130.1	NA	NU	XM_009081785.1
<i>Egretta_garzetta</i>	XM_009641277.1	XM_009641275.1	XM_009639343.1	Geno_scaff_region	XM_009642418.1	XM_009634876.1	XM_009637106.1	XM_009646337.1	XM_009640695.1
<i>Eurypyga_helias</i>	Geno_scaff_region	Geno_scaff_region	NA	XM_010160072.1	XM_010156014.1	XM_010156250.1	NA	XM_010146638.1	XM_010151478.1
<i>Falco_peregrinus</i>	XM_005243208.1	XM_005243247.1	XM_005232499.2	XM_005232498.2	XM_005243141.1	XM_005231393.1	XM_005241848.1	XM_005239443.1	XM_005235036.1
<i>Fulmarus_glacialis</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009585392.1	XM_009586474.1	XM_009572390.1	XM_009572361.1	XM_009586905.1
<i>Gallus_gallus</i>	AB109401.1	DQ518918.1	FJ915432.1	AB046533.2	EF137861.1	AY064697.1	FJ915551.1	FJ915600.1	NM_001037835.1
<i>Anas_platyrhynchos</i>	JN572685.1	JN572686.1	HQ166194.1	JN572687.1	XM_005008981.1	JN048668.1	KF255555.1	DQ888644.1	JN618074.1
<i>Gavia_stellata</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009811989.1	XM_009809127.1	XM_009821515.1	XM_009813692.1	XM_009821678.1
<i>Geospiza_fortis</i>	XM_005431639.1	XM_005415453.1	XM_005415589.1	Geno_scaff_region	XM_005415516.1	XM_005423810.1	NA	NU	XM_005422604.2
<i>Haliaeetus_albicilla</i>	XM_010574438.1	XM_010574439.1	Geno_scaff_region	Geno_scaff_region	XM_009915940.1	XM_009915776.1	XM_009928565.1	XM_009913820.1	XM_009927303.1
<i>Chaetura_pelagica</i>	XM_010006120.1	XM_010006119.1	XM_009995900.1	XM_009995901.1	XM_010002467.1	XM_010007952.1	NA	XM_010008803.1	XM_010004652.1
<i>Charadrius_vociferus</i>	XM_009884994.1	XM_009884995.1	XM_009893695.1	XM_009893696.1	XM_009883901.1	XM_009888044.1	XM_009894296.1	NU	XM_009886001.1
<i>Leptosomus_discolor</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009953213.1	XM_009947763.1	XM_009950947.1	XM_009960331.1	XM_009953779.1
<i>Manacus_vitellinus</i>	XM_008927407.1	XM_008927408.1	XM_018071536.1	XM_018071543.1	XM_018069963.1	XM_018074164.1	XM_018085042.1	NU	XM_008924845.2
<i>Meleagris_gallopavo</i>	FJ477857.1	FJ477858.1	FJ477860.1	FJ477861.1	XM_003205774.1	XM_003211211.1	HQ436463.1	XM_003203086.1	HQ456924.1
<i>Melospittacus_undula</i> <i>tus</i>	XM_005149134.1	XM_005149188.1	NA	Geno_scaff_region	XM_005149053.1	XM_005145616.1	XM_005151875.1	XM_005151439.1	XM_005144697.1
<i>Merops_nubicus</i>	NA	NA	NA	NA	XM_008943939.1	NA	XM_008950209.1	XM_008935272.1	
<i>Mesitomis_unicolor</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010181262.1	XM_010193770.1	XM_010194240.1	NU	XM_010182944.1
<i>Nestor_notabilis</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010013832.1	XM_010014853.1	NA	XM_010019975.1	XM_010013070.1
<i>Nipponia_nippon</i>	XM_009461836.1	XM_009461835.1	Geno_scaff_region	XM_009474742.1	XM_009474837.1	XM_009475802.1	XM_009472928.1	XM_009476283.1	XM_009476126.1
<i>Opisthocomus_hoazin</i>	XM_009935562.1	XM_009935561.1	Geno_scaff_region	Geno_scaff_region	XM_009940192.1	XM_009935409.1	XM_009937341.1	XM_009943495.1	XM_009931299.1
<i>Pelecanus_crispus</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009486220.1	XM_009481688.1	XM_009485400.1	XM_009489888.1	XM_009492835.1
<i>Phaethon_lepturus</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010281742.1	XM_010293516.1	NA	XM_010290259.1	XM_010282406.1
<i>Phalacrocorax_carbo</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009505917.1	XM_009514274.1	XM_009513901.1	XM_009501983.1	XM_009507639.1
<i>Picoides_pubescens</i>	XM_009896574.1	XM_009896575.1	XM_009898369.1	XM_009898379.1	XM_009902217.1	XM_009907081.1	XM_009901238.1	XM_009896972.1	XM_009902092.1
<i>Pterocles_gutturalis</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010074246.1	XM_010073689.1	XM_010074631.1	XM_010076693.1	XM_010085978.1
<i>Pygoscelis_adeliae</i>	Geno_scaff_region	XM_009332470.1	XM_009329794.1	XM_009329795.1	XM_009330657.1	XM_009319316.1	XM_009333665.1	XM_009318873.1	XM_009319611.1
<i>Struthio_camelus</i>	XM_009673363.1	XM_009673448.1	XM_009677116.1	XM_009677114.1	XM_009676700.1	XM_009668178.1	XM_009686697.1	XM_009683661.1	XM_009669051.1
<i>Apaloderma_vittatum</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009871058.1	XM_009867818.1	NA	NU	XM_009870709.1
<i>Taeniopygia_guttata</i>	XM_012573617.1	XM_004176603.1	XM_002198470.2	XM_002196366.1	XM_002190852.2	FJ695612.1	XM_002188726.1	NU	XM_002197069.2
<i>Tauraco_erythrolophu</i> <i>s</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_009986371.1	XM_009978945.1	XM_009978079.1	XM_009991025.1	XM_009979140.1
<i>Tinamus_guttatus</i>	XM_010219197.1	XM_010219196.1	XM_010212759.1	XM_010212759.1	XM_010219604.1	XM_010219200.1	XM_010217273.1	XM_010228317.1	XM_010218127.1
<i>Tyto_alba</i>	Geno_scaff_region	NA	Geno_scaff_region	Geno_scaff_region	XM_009970053.1	XM_009970420.1	XM_009968647.1	XM_009975060.1	XM_009975442.1
<i>Aptenodytes_forsteri</i>	XM_009280175.1	XM_009280152.2	XM_009283352.2	XM_009283317.1	XM_009277378.2	XM_009282256.2	XM_009275754.1	XM_009278529.2	XM_009288440.1
<i>Balearica regulorum</i>	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010310965.1	XM_010304091.1	XM_010301313.1	XM_010309901.1	XM_010298512.1

Buceros_rhinoceros	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	Geno_scaff_region	XM_010135016.1	XM_010137451.1	XM_010140290.1	XM_010140535.1	XM_010142512.1
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