

## Supplementary Table 2

### Domain characterization of TLR1A

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue.

TLR1A - Gallus gallus - NP_001007489.4			
Domain	Start	Stop	Sequence
Signal	1	24	MGSLTSIYVFACVFLSILWNNIQP
LRR-NT	25	52	TVENKITANYSGHLLTEVPKNIPVHTHI
LRR1	53	73	THILDLSHNSISEITNFRFTSLSD
LRR2	74	97	LQVLNLSHNLITELDFSAFMFNQD
LRR3	98	118	LEYLDLSHNNIWTAYCQLLAR
LRR4	119	143	LRHLDLSFNKFTVLPICQEFQIMFH
LRR5	144	166	LEYGLSAMMIRRSDFRYVAHLQ
LRR6	167	189	LDTVFLTLEDFSLYEPLSLTALN
LRR7	190	217	TRSLHIVFATNQNFNFSLLYDGMSTSEK
LRR8	218	244	LKIVNLRYTLSHKDFSPSLELQKKIK
LRR9	245	271	TTDLTLDTVDLWTVILQIFLLVWDSS
LRR10	272	310	VEHLTVRNLI <del>FR</del> GPVVELTEYKHVPLLRSLQQLSLGSS
LRR11	311	339	MKALT <del>LER</del> VNRNKLYYFNQEILYRQFSEMN
LRR12	340	361	ISLTIHDACMPHMLCPKKRSS
LRR13	362	385	FQYINFSRNALDEL <del>FQ</del> NCDTLAN
LRR14	386	411	LKIL <del>LHR</del> NKFESLSKVSFMTSRMKS
LRR15	412	436	LRYLDMSSNLLRNSRAEGRCQWADS
LRR16	437	458	LAELDLSSNQLTEAVFECLPAN
LRR17	459	481	IN <del>KVD</del> LQNNQIANVPKGITELHS
LRR18	482	503	LQELNLAS <del>NRL</del> ADLPGCRAFTG
LRR19	504	527	LEILNIERNLILTPSADFFETCPS
LRR20	532	554	VKE <del>LQAGQN</del> PFKCSCELOD <del>FL</del> RL
LRR-CT	555	591	ERQSGGKLSGWPEAYVCKYPEDLSGTQLED <del>FHL</del> TELACNTT
Transmembrane	592	614	LLLVTALLTLVLVAVVAF <del>PC</del> IIY
TIR	615	818	LDVPWYVRMLWQWTQTKRRAWHDCPEERETALQFHAFISYSERDSLWVKNELIP NLEKGEGCICLCQHERNFIPGKSIVENIINCIEKSYKSIFVLSPNFVQSEWCHYELYFA HHRLFSENSNLILILEPIPSYVIPARYHKLKALMAKRTYLEWPKERSKHALFWANL RAVVNIKLPSTFETDEEQSDVTSTSSITQCLIK

### Supplementary Table 3

#### Domain characterization of TLR1B

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue and *type 1 residue* in dark blue.

TLR1B - Gallus gallus - NP_001075178.3			
Domain	Start	Stop	Sequence
Signal	1	31	MTKNMRYLRNCFIYNCLFVFTFWDNIGLA
LRR-NT	32	76	NELFAS <b>V</b> P <b>N</b> NFLEDGLDKKNMSFPHSY <b>ANNQ</b> HYKADYGWVVIENT
LRR1	77	105	TES <b>L</b> <u>SLSEI</u> ADDNVRKLITLLSKFRKGSR
LRR2	106	132	<u>LRNLT</u> <b>L</b> <u>T</u> <b>N</b> MSVDW <b>KD</b> <b>I</b> KVLQV <sup>1</sup> VWHSS
LRR3	133	158	<u>IEYFN</u> <b>I</b> <u>N</u> <b>L</b> TQLGNV <b>V</b> STRFDYS <b>K</b> TS
LRR4	159	187	<u>MKAF</u> <b>A</b> V <b>N</b> K <b>V</b> LITDLYF <b>S</b> QDDIYNIFANMN
LRR5	188	209	<u>IAALT</u> <b>I</b> <u>A</u> <b>E</b> SELIHMLCPSSDSP
LRR6	210	233	<u>LR</u> <b>Y</b> <b>I</b> <u>N</u> <b>F</b> <b>S</b> K <b>N</b> DLTDLFQNCDKLIQ
LRR7	234	259	<u>LET</u> <b>F</b> <u>L</u> <b>H</b> <b>R</b> <b>N</b> K <b>F</b> ESL <b>S</b> KVSFMTSRMKS
LRR8	260	284	<u>LR</u> <b>Y</b> <b>L</b> <b>D</b> <b>M</b> <b>S</b> <b>S</b> <b>N</b> LLRNSRAE <b>G</b> RQCWADS
LRR9	285	306	<u>LA</u> <b>E</b> <u>L</u> <b>D</b> <b>L</b> <b>S</b> <b>S</b> <b>N</b> QLTE <b>A</b> VFECLPAN
LRR10	307	329	<u>I</u> <b>N</b> <b>K</b> <b>V</b> <b>D</b> <u>L</u> <b>Q</b> <b>N</b> <b>N</b> QIASVPKGITELHS
LRR11	330	351	<u>LQ</u> <b>E</b> <u>L</u> <b>N</b> <b>L</b> <b>A</b> <b>S</b> <b>N</b> RLADLPGCRAFTG
LRR12	352	375	<u>LE</u> <b>I</b> <b>L</b> <b>N</b> <b>I</b> <b>E</b> <b>R</b> <b>N</b> LILTPSADFF <b>E</b> TCPS
LRR13	376	398	<u>V</u> <b>K</b> <b>E</b> <b>L</b> <b>Q</b> <b>A</b> <b>G</b> <b>Q</b> <b>N</b> PFKCSELQDFL <b>R</b> <b>L</b>
LRR-CT	399	440	ERQSGGKL <b>S</b> GWPEA <b>Y</b> VCKYPEDLSGTQLKDFHLTELACNTTL
Transmembrane	441	463	LLVTALLTLVLVAVVAFLCIYL
TIR	495	652	DVPWYVRMLWQWTQTKRRAWHDCPEERETALQFHAFISYSERDSLWVKNELIP NLEKGEGCIQLCQHERNFIPGKSIVENIINCIEKSYKSIFVLSPNFVQSEWCHYELYFA HHKLFSSENSNLILLEPIPPYVIPARYHKLKALMAKRTYLEWPKERSKHALFWANLR AAISINLSVADEQNRTEV

## Supplementary Table 4

### Domain characterization of TLR2A

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue and *type 1 residue* in dark blue.

TLR2A - Gallus gallus - NP_989609.1			
Domain	Start	Stop	Sequence
Signal	1	25	MFNQSQ <b>Q</b> KPTMKLMW <b>Q</b> AWLIYTALA
LRR-NT	26	63	AH <b>L</b> PEEQALRQACLSCDA <b>T</b> QSCNCSFMGLDFIP <b>P</b> G <b>L</b> T <b>G</b>
LRR1	65	88	<b>I</b> <b>T</b> <u><b>V</b>L<b>N</b>L<b>A</b>H<b>N</b>R<b>I</b>K<b>L</b></u> <b>I</b> R <b>T</b> H <b>D</b> L <b>Q</b> K <b>A</b> V <b>N</b>
LRR2	89	112	<b>L</b> <b>R</b> <u><b>T</b><b>L</b><b>L</b><b>L</b><b>Q</b><b>S</b><b>N</b><b>Q</b></u> <b>I</b> <b>S</b> <b>S</b> <b>I</b> <b>D</b> <b>E</b> <b>D</b> <b>S</b> <b>F</b> <b>G</b> <b>S</b> <b>Q</b> <b>G</b> <b>K</b>
LRR3	113	136	<b>L</b> <b>E</b> <b>L</b> <b>L</b> <b>D</b> <b>L</b> <b>S</b> <b>N</b> <b>N</b> <b>S</b> <b>L</b> <b>A</b> <b>H</b> <b>L</b> <b>S</b> <b>P</b> <b>V</b> <b>W</b> <b>F</b> <b>G</b> <b>P</b> <b>L</b> <b>F</b> <b>S</b>
LRR4	137	161	<b>L</b> <b>Q</b> <b>H</b> <b>L</b> <b>R</b> <b>I</b> <b>Q</b> <b>G</b> <b>N</b> <b>S</b> <b>Y</b> <b>S</b> <b>D</b> <b>L</b> <b>G</b> <b>E</b> <b>S</b> <b>S</b> <b>P</b> <b>F</b> <b>S</b> <b>S</b> <b>L</b> <b>R</b> <b>N</b>
LRR5	162	185	<b>L</b> <b>S</b> <b>S</b> <b>L</b> <b>H</b> <b>L</b> <b>G</b> <b>N</b> <b>P</b> <b>Q</b> <b>F</b> <b>S</b> <b>I</b> <b>R</b> <b>Q</b> <b>G</b> <b>N</b> <b>F</b> <b>E</b> <b>G</b> <b>I</b> <b>V</b> <b>F</b>
LRR6	186	209	<b>L</b> <b>N</b> <b>T</b> <b>L</b> <b>R</b> <b>I</b> <b>D</b> <b>G</b> <b>D</b> <b>N</b> <b>L</b> <b>S</b> <b>Q</b> <b>Y</b> <b>E</b> <b>P</b> <b>G</b> <b>S</b> <b>L</b> <b>K</b> <b>S</b> <b>I</b> <b>R</b> <b>K</b>
LRR7	210	233	<b>I</b> <b>N</b> <b>H</b> <b>M</b> <b>I</b> <b>S</b> <b>I</b> <b>R</b> <b>R</b> <b>I</b> <b>D</b> <b>V</b> <b>F</b> <b>S</b> <b>A</b> <b>V</b> <b>I</b> <b>R</b> <b>D</b> <b>L</b> <b>L</b> <b>H</b> <b>S</b>
LRR8	234	260	<b>A</b> <b>I</b> <b>W</b> <b>L</b> <b>E</b> <b>V</b> <b>R</b> <b>E</b> <b>I</b> <b>K</b> <b>L</b> <b>D</b> <b>I</b> <b>E</b> <b>N</b> <b>E</b> <b>K</b> <b>L</b> <b>V</b> <b>Q</b> <b>N</b> <b>S</b> <b>T</b> <b>L</b> <b>P</b> <b>L</b> <b>T</b>
LRR9	261	288	<b>I</b> <b>Q</b> <b>K</b> <b>L</b> <b>T</b> <b>F</b> <b>T</b> <b>G</b> <b>A</b> <b>S</b> <b>F</b> <b>T</b> <b>D</b> <b>K</b> <b>Y</b> <b>I</b> <b>S</b> <b>Q</b> <b>I</b> <b>A</b> <b>V</b> <b>L</b> <b>L</b> <b>K</b> <b>E</b> <b>I</b> <b>R</b> <b>S</b>
LRR10	289	317	<b>L</b> <b>R</b> <b>E</b> <b>L</b> <b>E</b> <b>A</b> <b>I</b> <b>D</b> <b>C</b> <b>V</b> <b>L</b> <b>E</b> <b>G</b> <b>K</b> <b>G</b> <b>A</b> <b>W</b> <b>D</b> <b>M</b> <b>T</b> <b>E</b> <b>I</b> <b>A</b> <b>R</b> <b>S</b> <b>K</b> <b>Q</b> <b>S</b>
LRR11	318	346	<b>I</b> <b>E</b> <b>T</b> <b>L</b> <b>S</b> <b>I</b> <b>T</b> <b>N</b> <b>M</b> <b>T</b> <b>I</b> <b>L</b> <b>D</b> <b>F</b> <b>Y</b> <b>L</b> <b>F</b> <b>D</b> <b>L</b> <b>E</b> <b>G</b> <b>I</b> <b>E</b> <b>T</b> <b>Q</b> <b>V</b> <b>G</b> <b>K</b>
LRR12	347	370	<b>L</b> <b>K</b> <b>R</b> <b>L</b> <b>S</b> <b>I</b> <b>A</b> <b>S</b> <b>S</b> <b>K</b> <b>V</b> <b>F</b> <b>M</b> <b>V</b> <b>P</b> <b>C</b> <b>R</b> <b>L</b> <b>A</b> <b>R</b> <b>Y</b> <b>F</b> <b>S</b>
LRR13	371	397	<b>L</b> <b>L</b> <b>Y</b> <b>L</b> <b>D</b> <b>F</b> <b>H</b> <b>D</b> <b>N</b> <b>L</b> <b>L</b> <b>V</b> <b>N</b> <b>N</b> <b>R</b> <b>L</b> <b>G</b> <b>E</b> <b>T</b> <b>I</b> <b>C</b> <b>E</b> <b>D</b> <b>A</b> <b>W</b> <b>P</b> <b>S</b>
LRR14	398	423	<b>L</b> <b>Q</b> <b>T</b> <b>L</b> <b>N</b> <b>L</b> <b>S</b> <b>K</b> <b>N</b> <b>S</b> <b>L</b> <b>K</b> <b>S</b> <b>L</b> <b>K</b> <b>Q</b> <b>A</b> <b>A</b> <b>R</b> <b>Y</b> <b>I</b> <b>S</b> <b>N</b> <b>L</b> <b>H</b> <b>K</b>
LRR15	424	446	<b>L</b> <b>I</b> <b>N</b> <b>L</b> <b>D</b> <b>I</b> <b>S</b> <b>E</b> <b>N</b> <b>N</b> <b>F</b> <b>G</b> <b>E</b> <b>I</b> <b>P</b> <b>D</b> <b>M</b> <b>C</b> <b>E</b> <b>W</b> <b>P</b> <b>E</b> <b>N</b>
LRR16	447	467	<b>L</b> <b>K</b> <b>Y</b> <b>L</b> <b>N</b> <b>L</b> <b>S</b> <b>S</b> <b>T</b> <b>Q</b> <b>I</b> <b>P</b> <b>K</b> <b>L</b> <b>T</b> <b>T</b> <b>C</b> <b>I</b> <b>P</b> <b>S</b> <b>T</b>
LRR17	468	487	<b>L</b> <b>E</b> <b>V</b> <b>L</b> <b>D</b> <b>V</b> <b>S</b> <b>A</b> <b>N</b> <b>N</b> <b>L</b> <b>Q</b> <b>D</b> <b>F</b> <b>G</b> <b>L</b> <b>Q</b> <b>L</b> <b>P</b> <b>F</b>
LRR18	488	509	<b>L</b> <b>K</b> <b>E</b> <b>L</b> <b>Y</b> <b>L</b> <b>T</b> <b>K</b> <b>N</b> <b>H</b> <b>L</b> <b>K</b> <b>T</b> <b>L</b> <b>P</b> <b>E</b> <b>A</b> <b>T</b> <b>D</b> <b>I</b> <b>P</b> <b>N</b>
LRR19	510	533	<b>L</b> <b>V</b> <b>A</b> <b>M</b> <b>S</b> <b>I</b> <b>S</b> <b>R</b> <b>N</b> <b>K</b> <b>L</b> <b>N</b> <b>S</b> <b>F</b> <b>S</b> <b>K</b> <b>E</b> <b>E</b> <b>F</b> <b>E</b> <b>S</b> <b>F</b> <b>K</b> <b>Q</b>
LRR20	534	357	<b>M</b> <b>E</b> <b>L</b> <b>L</b> <b>D</b> <b>A</b> <b>S</b> <b>A</b> <b>N</b> <b>N</b> <b>F</b> <b>I</b> <b>C</b> <b>S</b> <b>C</b> <b>E</b> <b>F</b> <b>L</b> <b>S</b> <b>F</b> <b>I</b> <b>H</b> <b>H</b> <b>E</b>
LRR-CT	358	598	AGIAQVLVGWPESYICDSPLTVRGAQVGSVQLSLMECHR
Transmembrane	597	619	SLLVSLICTLVFLFILVVG
TIR	620	793	KYHAVWYMRMTWAWLQAKRKPKRAPTKDICYDAFVSYSENDSNWVENIMVQ QLEQACPPFRLCLHKRDFVPGKWIVDNIIDSIEKSHKTLFVLSEHFVQSEWCKYELD FSHFRLFDENNDVAILILLEPIQSQAIPKRFCCKLRKIMNTKTYLEWPPDEEQQMMF WENLKAALKS

## Supplementary Table 5

### Supplementary Domain characterization of TLR2B

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue and *type 1 residue* in dark blue.

TLR2B - Zebrafinch - XP_002196402.1			
Domain	Start	Stop	Sequence
Signal	1	20	MTAHIWRVLAIVILAASLS
LRR-NT	25	54	LKQACPSCDGSQLCNCSSMGLDFIPPGVTA
LRR1	56	79	<u>ITVLNLAHNR</u> IKRIQSQDLQQAVN
LRR2	80	103	<u>LRALLQSN</u> KISSIDEDSF <i>W</i> SLEK
LRR3	104	127	<u>LELLDLSNNS</u> LAHLSPVWFGHLFS
LRR4	128	152	<u>LQHLHLEGNS</u> YRDLGQSSPFSCLKN
LRR5	153	176	<u>LSSLHLGNPQ</u> FSVIRHGNFEGIEL
LRR6	177	200	<u>LHKLWIDGSNLS</u> QYEQGSLKSIKQ
LRR7	201	224	<u>INHMILNLRNG</u> YIFSEIVRDLHS
LRR8	225	251	<u>VTWLEVRRIA</u> FSIAAEMQVLRVMSSSF
LRR9	252	279	<u>AKKISFRQTL</u> LDATVPEIVSILEDMPQ
LRR10	280	307	<u>LVELELVDCR</u> LLGTGQWKMEIQAKKSQT
LRR11	308	336	<u>LRILTIKKLS</u> IEEFYLFIDLHSVEGLLSL
LRR12	337	360	<u>LTRVTVQNT</u> KVFLVPCRISQNLLS
LRR13	361	387	<u>LVYLDLSANLL</u> GDLSLEHSACQGGWPS
LRR14	388	413	<u>LQALNLSQNS</u> LSDLERTSKSLSHLGN
LRR15	414	436	<u>LIVLDISQNN</u> FGIPEIDVCDWPKS
LRR16	437	457	<u>LKYLNLSTQ</u> IPKVTTICIPQT
LRR17	458	477	<u>LEVLDVSGNN</u> LKEFGLRLPL
LRR18	478	499	<u>LKELYLTRNQ</u> LKTLPGAAPIPN
LRR19	500	523	<u>LVSLSVSRN</u> KLNSFSKEEFESFRR
LRR20	524	547	<u>MKLLDASGN</u> NFICSCEFLSFIHHE
LRR-CT	548	586	AGISQVLVGWPDKYVCDSP LAVRGAQVGAVHLSLMECHR
Transmembrane	587	609	SLVVSLLICVLVFLVILLVAVGY
TIR	610	783	KYHMMVWYLRMTAWWLQAKRKPKRAPPKDV CYDAFVSYSENDSWVENTMVREL EQACPPFRLCLHKRDFVPGKWIVDNIIDSIEKSRKTLFVLSEHFVQSEWCKYELDFSHF RLFDENNDAAAILVLEPIQSKAIPKRFCCLKRIMNTKTYLEWPLEEEQQQMFWFNLKI ALRS

Supplementary Table 6

## Domain characterization of TLR3

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue.

TLR3 – Gallus gallus- NP_001011691.3			
Domain	Start	Stop	Sequence
Signal	1	26	MGCSIPCW <b>N</b> SLSFRLVFCCLLCAS <b>V</b> G
LRR-NT	27	52	KQC <b>Q</b> IRNTMADCSHLKLTQIPSDLP <b>K</b>
LRR1	54	77	ITG <b>L</b> DISH <b>N</b> QLKKL <b>D</b> PENLT <b>E</b> YSN
LRR2	78	101	LIY <b>L</b> NAGY <b>N</b> IISKLPGLCKNLPL
LRR3	102	125	LQ <b>L</b> KLEH <b>N</b> QLHELPDGVFASCSN
LRR4	126	148	LT <b>E</b> L <b>N</b> LG <b>N</b> IIEVKNDPFKTLEN
LRR5	149	172	LN <b>I</b> LDLSH <b>N</b> HLKSANLG <b>L</b> QQQLKN
LRR6	173	198	LR <b>E</b> LVL <b>S</b> <b>N</b> QITELNKEDLKFLSNTS
LRR7	199	222	LN <b>S</b> LD <b>L</b> SS <b>N</b> PLKEFH <b>T</b> GCLHAIGN
LRR8	223	249	LFGL <b>L</b> LN <b>N</b> VELGEN <b>R</b> TKKLCTELSDTA
LRR9	250	275	IQN <b>L</b> SLSHVKLSHINRLTLQGLQGTN
LRR10	276	299	LT <b>V</b> L <b>N</b> LSK <b>N</b> SLSVIEDDSFQWLSK
LRR11	300	323	LE <b>Y</b> L <b>N</b> LE <b>D</b> NNIINVSSHLFYGLSS
LRR12	324	347	IT <b>H</b> L <b>N</b> L <b>I</b> NS <b>L</b> TGKIEDFSFQWL <b>H</b> H
LRR13	348	371	LE <b>Y</b> L <b>I</b> MD <b>N</b> NNFPRITTNMFTGLKN
LRR14	372	399	L <b>K</b> YLS <b>L</b> Y <b>N</b> CNTNLQRITNKT FVSLANSS
LRR15	400	423	LQ <b>V</b> L <b>N</b> LTK <b>T</b> RISTVESGAFSSLGQ
LRR16	424	448	L <b>K</b> ILD <b>L</b> GL <b>N</b> EINQELTGHEFGL <b>N</b> N
LRR17	449	472	IE <b>Y</b> I <b>L</b> SY <b>N</b> K <b>N</b> V <b>T</b> LRSESFIFVPS
LRR18	473	498	LR <b>K</b> LM <b>L</b> RKVGCNNLAISPSPFHPLRN
LRR19	499	522	LT <b>V</b> LD <b>I</b> SN <b>N</b> IANIKEDLFNGLHE
LRR20	523	554	LD <b>I</b> L <b>N</b> LQH <b>N</b> NLARLWKCANPGGPVFLKDVPN
LRR21	555	578	L <b>H</b> I <b>L</b> N <b>L</b> KS <b>N</b> GFDEIPVHVFKGLHQ
LRR22	579	602	L <b>K</b> D <b>L</b> DLGS <b>N</b> NLNPATLFDDQTS
LRR23	603	627	L <b>N</b> TL <b>N</b> LQ <b>K</b> N <b>L</b> ITSVEENVFGPAFKS
LRR24	628	651	L <b>R</b> T <b>L</b> EM <b>D</b> FN <b>P</b> FDCTCESIAWFASW
LRR-CT	652	696	LN <b>D</b> TQAYIPGLQSQYICNTPPKYHGTLVLHFDT <b>S</b> ACKDSAPFKLL
Transmembrane	697	719	F <b>L</b> ITTT <b>V</b> VVMQFMFIVLLIHFE <b>G</b> W
TIR	720	896	RIAFYWNISINRILGFKELDRLPG <b>V</b> <b>F</b> DYDAYVIHARKDTNWWLTNFTSLENEQFQ VKFCLEERDFEAGISEFEAIINCIRRSRKIIIFIVTEHLL <b>Q</b> DPWCRKFKVHHALQQAIEQ SRDSIILFLHNIQDYKLNHALCLRRGMFRSCCINWPVQKERINAFHQQLMMALK SNSKVR

## Supplementary Table 7

### Domain characterization of TLR4

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue and *type 1 residue* in dark blue.

TLR4 – Gallus Gallus- NP_001025864.1			
Domain	Start	Stop	Sequence
Signal	1	30	MPSRAAPTALTGLVLLQLLLVSLLAGCIP
LRR-NT	31	58	SPCLEVIPSTAFRCTGQNISGVPAEIPN
LRR1	60	83	<u>TLDLDSFN</u> SLKLLSSNYFSSVPE
LRR2	84	107	<u>LQFLDLSRCHI</u> HTIEDNSFVDLYN
LRR3	108	131	<u>LSTLILTANSL</u> QHLGLAAFHGLTS
LRR4	132	155	<u>LKKLVLVET</u> SISSLDLPIGHLNT
LRR5	156	180	<u>LQELNLGHN</u> NIASLKLPHYFANLTS
LRR6	181	208	<u>LRHLSFSN</u> NITYISKGDLDALRETNRL
LRR7	209	231	<u>NLTVLVLSL</u> NNIKYIQSGSFAKIH
LRR8	232	258	<u>LGEILRSF</u> ENLAMHSSLQGLAGLQ
LRR9	259	288	<u>VNRLIVGEFTN</u> LKITAFQNGLLSGLCQVQ
LRR10	289	313	<u>MQEFVLMCFR</u> EFENDTDTLFDCIGN
LRR11	314	335	<u>VTTIRLVDL</u> NLETLSEVPMFSQ
LRR12	336	359	<u>VKHLEWKR</u> CKEQELPAEKLSLFKE
LRR13	360	383	<u>LRVLRITK</u> SKDLNGFEQKF <sup>GS</sup> LT
LRR14	384	409	<u>LEVVDLSE</u> NRLSFLTCCSPK <sup>PR</sup> SPN
LRR15	410	432	<u>LKHLNLSFN</u> SDISLTGEFANLRN
LRR16	433	457	<u>LLYDLQHT</u> KLIHHGTYPVFLLLQK
LRR17	458	481	<u>LIYLDISY</u> TKTHVMShLIFHGLNS
LRR18	482	506	<u>LQVLKMAG</u> NSFENNTLTNNFENVRR
LRR19	507	530	<u>LRILDISS</u> CKLVWVDQSTFNALSE
LRR20	531	554	<u>LKELIISN</u> NKLLTFDPVYTKPLQA
LRR21	555	579	<u>LTALDFS</u> NNQMSFLSDSALEILPDS
LRR22	580	603	<u>LVLLDISH</u> NLFECSC <sup>HL</sup> NFLKW <sup>V</sup>
LRR-CT	604	639	KEKQDLLQNKHSMICHTPAYM <sup>K</sup> N <sup>M</sup> SLSNFDMSCHP
Transmembrane	640	662	<u>N</u> PTTVACSVTVLLAAGVFLFIY
TIR	663	843	KYYFQLYYSVLVLSGCKHSAERGDYDAFVIHSSKDQEWVMKELVEPLEEGKPPQLCLY FRDFLPGVPIVTNIIQEGFLSSRNVIAVISADFLESKWCSFEFDIARSWQLVEGKAGIIMII LGEVDKTLRLQRLGSLRYLRRNTYLEWKNKEISRHIFWRQLTSVLLEGKKWNHHEIKLM

Supplementary Table 8

## Domain characterization of TLR5

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue.

TLR5 – <i>Gallus Gallus</i> - NP_001019757.1			
Domain	Start	Stop	Sequence
Signal	1	22	MMLHQRLIIVFGIALAGDI <b>CAS</b>
LRR-NT	23	47	R <b>SCY</b> SEDQVSMY <b>N</b> SCNLTGVPPVPK
LRR1	49	72	TAK <b>LFLTY</b> <b>NY</b> IRQVTATSFILLED
LRR2	73	98	<b>LFLLE</b> IG <b>TQ</b> RVFPLYIGKEAFRNLPN
LRR3	99	122	<b>LRVLD</b> L <b>GF</b> <b>N</b> NILLDLDSFAGLQR
LRR4	123	148	<b>LTILRL</b> <b>FQ</b> <b>NN</b> LGD <b>SILEERY</b> FQDL <b>RS</b>
LRR5	149	173	<b>LEELD</b> L <b>SG</b> <b>NQ</b> ITKLHPHPLFYNTI
LRR6	174	199	<b>LKAVNL</b> K <b>F</b> <b>N</b> KISNLCESNLT <b>SFQ</b> GKH
LRR7	200	229	<b>FSF</b> SL <b>STN</b> <b>T</b> LYKTDKMIWAKCPN <b>PF</b> <b>R</b> NIT
LRR8	230	256	<b>FNS</b> L <b>DVSE</b> <b>NG</b> WSTETVQYFCTAIKGTQ
LRR9	257	291	<b>IN</b> <b>YLS</b> <b>FR</b> SHTMGSGFGFN <b>LN</b> KNP <b>D</b> TDTFTGLARSD
LRR10	292	315	<b>LHLLD</b> I <b>SN</b> GFIFSLNSLIFESLRN
LRR11	316	339	<b>LEFLNL</b> <b>FR</b> <b>N</b> KINQIQKQAF <b>G</b> LEN
LRR12	340	363	<b>LEILNL</b> <b>SS</b> <b>N</b> LLGELYDYTFEGLHS
LRR13	364	387	<b>IMYID</b> L <b>QQ</b> <b>N</b> HIGMIGEK <b>S</b> FSNLVN
LRR14	388	406	<b>LKIIDL</b> RD <b>NA</b> IKKLPSFPH
LRR15	407	426	<b>LSAFL</b> SD <b>N</b> K <b>M</b> MSVA <b>H</b> TAIV
LRR16	427	451	<b>ATHIEL</b> R <b>N</b> WLANLGDLVLFQVPG
LRR17	452	476	<b>VQYLL</b> L <b>KQ</b> <b>N</b> RFSY <b>C</b> V <b>K</b> HVD <b>AI</b> EN <b>N</b> Q
LRR18	477	505	<b>LIYMD</b> L <b>GEN</b> <b>N</b> MLQLVWERGLCLDV <b>F</b> RTL <b>S</b> K
LRR19	506	529	<b>LQVLHL</b> NN <b>NY</b> LSALPQE <b>I</b> F <b>N</b> GLTS
LRR20	530	551	<b>LKRLNL</b> AS <b>N</b> LLSHLSLRVFPQS
LRR21	552	572	<b>LTN</b> LN <b>LSG</b> <b>N</b> QLFSPKPEVFMT
LRR22	573	596	<b>LSILD</b> ITH <b>N</b> KYVCD <b>C</b> ALKSLLVWL
LRR-CT	597	645	NETNVTLAGESED <b>RY</b> CVYPALAGVPVSFLTYDDC <b>D</b> EDELQQTLRFSVF
Transmembrane	646	668	VFLSVTLLMF <b>LM</b> ST <b>I</b> IFTRCRGI
TIR	669	861	CFVWYKTITKTLIGSHPPAADTSEYMYDAYLCYSKNDFEWVQNSLLKHLDSQYFDK NRFTLCFEERDFLPGEHINNIRD <b>AI</b> WKS <b>R</b> KTICVVTRQFLKDGWCVEAF <b>N</b> FAQSR YFSDLKEVLIMVVVGSLSQYQLMKHKPIRIFLQ <b>RS</b> RYLRWPEDYQDIGWFLD <b>N</b> LSS QILKEKKVQR <b>N</b> VSGIELQTIATVSH

**Supplementary Table 9 Domain characterization of TLR7**

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue and *type 1 residue* in dark blue.

TLR7 – Gallus gallus - NP_001011688.1			
Domain	Start	Stop	Sequence
Signal	1	36	MTNLSEVAHRKMMVHHARTSNALLFVLLFLFPMLLS
LRR-NT	38	73	RWFPKTLPCDVEAFESTVRVDCSDRRRLKEVPRGIPG
LRR1	75	98	ATNLTLTINHIPRISPVSTQLEN
LRR2	99	136	LVEIDFRCNCVPPRLGPKDNVCITPPSIENGSAALSR
LRR3	137	157	LKSLYLDANQLSKIPRGLPAT
LRR4	158	181	LRLSLEANNIFSIKKNTFSELRN
LRR5	182	213	IELLYLGQNCYRNPNCNVSFEIETAFLNLKN
LRR6	214	234	LTVLSLKSNNLTFIPPNLSST
LRR7	235	258	LKELYIYNNRIQEVQEHDSLNLN
LRR8	259	298	LEILDLSGNCPRCYNAPYCTPCPN/IKIHSKAFYSLKK
LRR9	299	322	LRIRLHSNSLQSISSWFKNIKN
LRR10	323	348	LKNLDLSQNF/KEIGDAEFLKLIPS
LRR11	349	378	LVELDLSNFELQMYSPFLNLSKTFSCLSN
LRR12	379	405	LETLRIGYVEKELRENLDPLLNLRN
LRR13	406	429	LTVLDLGTNFIKIADLRVFKKFRS
LRR14	430	504	LKIIDLSMNKISPSSGESNFYGFCDHRITVEQYSRHVLQEMHYFRYDEYGRSCKSKDK EADSYQPLVNGDCMSY
LRR15	505	528	GETLDLSRNNIFFVNSIDFQDLSF
LRR16	529	553	LKCLNLSGNAISQTLNGSEFYLSG
LRR17	554	577	LKYLDFSNNRIDLLYSTAFKELKF
LRR18	578	607	LEILDLSNNKHFLAEGVSHVLSFMKNLAY
LRR19	608	630	LKKLMMNENEISTSISTGMESQS
LRR20	631	661	LQLEFRGNRLDIFWSDGKKEYLSFFKNLTN
LRR21	662	686	LEQLDISPNMLNFLPPDVFEAMPPE
LRR22	687	710	LKILNLTSNRLHTFNWGLHLLTK
LRR23	711	734	LITLDLSNLLTVP RKLSNCTST
LRR24	735	758	LQELILRNNRITRITKYFLRGAIQ
LRR25	759	784	LTYLDSLSSNKIQIKKSSFPENIINN
LRR26	785	807	LRMLLLHNNPFCNCDAVWFGW
LRR-CT	808	852	INQTQVAIPLLATDVTGAGPGAHKGRSLVFLDLNTCELDTSYFIM
Transmembrane	853	875	YALSTSAVLCLMMFAVMShlyFW
TIR	876	1059	DMWYSYHYCTAKLKGRRIPDPACYDAFIAYDNTDLAVNEWVMTLVEKLEDQK ARQFNLCLEERDWLPGQPVFDNLSQSIQLSKKTIFVLTNKKYIKSGTFKTTFYMAHQRL LDEKIDVILIFLEKVLQKSRYVQLRKRLCRSSVLEWPTNPRSQPYFWQRLKNAIAMN NTLSYNKLLQETV



Supplementary Table 10

## Domain characterization of TLR15

The conserved segment of each LRR is underlined. The conserved leucine or equivalent hydrophobic residues are in green and the conserved asparagine or equivalent hydrogen-donor residues are in red. The amino acids identified as under positive selection are in bold. In addition to that, *M8 sites under positive selection* are in italic, with *Type 2 residue* colored in light blue.

TLR15 – Gallus gallus- NP_001032924.1			
Domain	Start	Stop	Sequence
Signal	1	22	MRILIGSLYFYFISFLFS <b>K</b> VNG
LRR-NT	23	55	FLT <b>Q</b> RTSPV <b>S</b> FPFY <b>N</b> YSYLNLSVSQAQAPKT
LRR1	56	79	<u>ARALNFSYNAIEKITKRDFEGFHV</u>
LRR2	80	103	<u>LEVLDLSHNHIKDIEPGAFENLLS</u>
LRR3	104	202	<u>LVSVDLSFNDK</u> NLLVSGLAPHKLIPITSGASG <b>P</b> SQIYMYFQ <b>K</b> SAEAA <b>L</b> EPSAPAE <b>L</b> PHLEDPPN <b>P</b> GNVNPRFRQRRTEEN <b>K</b> TSPPA <b>A</b> TLRPDL <b>C</b> GAPI
LRR4	203	233	<u>NGLLDLSRTKLSNEELTAKLDADLCQAQLGT</u>
LRR5	234	260	<u>VLEFNISHSDLEMDLLSLFILFLPMKD</u>
LRR6	261	288	<u>IQSVDA<b>S</b>YNRITINNIDVEAICHFPFSN</u>
LRR7	289	310	<u>FSFLNISNNPINSLETVCPLAS</u>
LRR8	311	334	<u>ITVIDLSFTNISTIPANFAKKLSK</u>
LRR9	335	365	<u>LERMYVQGNQLIYTVRPENPSATPR<b>P</b>PGTVQ</u>
LRR10	366	387	<u>ISAISLVRNQAGTPIESLPES</u>
LRR11	388	411	<u>VKHLKVSNC<b>S</b>IVELPEWFANRMQE</u>
LRR12	412	431	<u>LLFLDLSSNRISMLPDLPI<b>S</b></u>
LRR13	432	454	<u>LQQLDISNSDIKIIPPRFKLSLN</u>
LRR14	455	476	<u>VTVFNIQNNKLTEMHPEYFPST</u>
LRR15	477	498	<u>LTTCDISK<b>N</b>KLKVLSTKALEN</u>
LRR16	499	520	<u>LESINVSGNLITRLEPACQLPS</u>
LRR17	521	544	<u>LTNLDSSHNLISELPDHLGQSLLM</u>
LRR18	545	566	<u>LKHFNLSGNKISFLQRGSLPAS</u>
LRR19	567	590	<u>LEELDISDN<b>A</b>ITTIVQDTFGQLTS</u>
LRR20	591	615	<u>LSVLT<b>V</b>QGHFFCNCPLYWVFN<b>I</b></u>
LRR-CT	616	653	RNPHL <b>Q</b> INGK <b>D</b> LRC <b>S</b> FPDRRGSLVKSSNLT <b>L</b> LHCSL
Transmembrane	654	676	GI <b>Q</b> MAIT <b>A</b> CMAILVVVLTLGLCW
TIR	677	868	RFDGLWYVRMGWYWCMARRQYKKRPENKPFDAFISYSEHDADWTKEH <b>L</b> LKKL ETDGFKICYHERDFKPGHPVLGNIFYCIENSHKVLFLVSPSFVNSWCWCQYELYFAEH RVLDENQDSLIMVVLEDLPD <b>S</b> VPQKFSKLRKLLKRKTYLKWSPEEHKQKIFWHQL AAVLKTTNEPLVRAENGP <b>N</b> EDV <b>I</b> EME

