Supplementary Information

Functional expression of TLR5 from different vertebrate species and diversification towards intestinal pathogen recognition

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Faber et al., Figure S1

Fig. S1: determination of protein amount and purity of highly purified recombinant *S*. Typhimurium FliC. Different amounts of recombinantly expressed and highly purified *S*. Typhimurium FliC (used as reference protein for TLR5 activation) were loaded on an SDS gel and stained with Simply Blue Safestain (Novex): M: protein molecular mass standard (Bench Mark Prestained, Novex), lane 1 from left: 20 ng FliC; lane 2: 100 ng FliC, lane 3: 200 ng FliC, lane 4: 100 ng BSA, lane 5: 200 ng BSA, lane 6: 300 ng BSA, lane 7: 500 ng BSA, lane 8: 1 μ g BSA.



Faber et al., Figure S2

Fig. S2: comparative expression of TLR signaling pathway components in HEK293-T and HeLa cells. A) Semiquantitative PCRs for MyD88 transcript were performed using cDNA of HEK293-T or HeLa cells as template and the following primers: hMyD88_F1 and hMyD88_R1. 5 µl of the amplified PCR product (after 20, 25 or 30 amplification cycles) was loaded on a 1% agarose gel. B) Western blot analysis using cleared lysates of empty vector (200 ng) or TLR5-V5 construct-transfected HEK293-T (h: 75 ng, ch: 200 ng, ch/h: 200 ng and 250 ng) or HeLa cells (h: 50 ng, ch: 500 ng, ch/h: 50 ng and 100 ng) using anti-MyD88, anti-IRAK-1, anti-IRAK-M and anti-GAPDH antibodies (see Table S6).



Faber et al., Figure S3

Fig. S3: C-terminal V5-tag or an alternative 3' upstream sequence have minor influence on the activation efficiency of expression constructs for chicken TLR5 by Salmonella FIIC. HEK293-T (A, C) or HeLa cells (B, D) were transiently transfected with empty vector pEF6-V5: 200 ng; human TLR5-V5: 100 ng; chicken TLR5-V5 or same construct without V5 tag: 200 ng. For comparison, expression constructs for chicken TLR5-V5 with alternative upstream (AL) sequences were analyzed. 48 h post transfection, cells were coincubated with purified recombinant Salmonella FliC (50 ng/well), followed by a measurement of secreted IL-8 in cell supernatants. C and D: IL-8 secretion of hTLR5-transfected and FliC-activated cells was set to 100 % (reference); relative IL-8 secretion of other constructs with regard to the reference is depicted in [%]. Mean and standard deviation from technical triplicates of biological duplicates of a representative experiment are shown. Significant differences between FliCstimulated hTLR5 and activated chicken TLR5 variants as well as between activated chTLR5 and activated mutated chTLR5 variants are indicated by asterisks (Student's *t*-test, unpaired, two-tailed) as follows: *, 0.01<p<0.05; **, 0.001<p<0.01; and ***, p<0.001, n.s. non-significant.

zfTLR5	lslmnndfrcdcdlkdfqtwlnqtnvtfvhsiedvtcaspedqymvpvvrssiqcede <mark>ee</mark>	644
chTLR5	ldithnkyvcdcalksllvwlnetnvtlagsesdrycvyppalagvpvsfltyddcde	633
mTLR5	ldithnefvcncelstfiswlnqtnvtlfgspadvycmypnsllggslynistedc <mark>de</mark>	646
hTLR5	ldithnkficecelstfinwlnhtnvtiagppadiycvypdsfsgvslfslstegc <mark>de</mark>	631
boTLR5	idithnnficecelsafihwlnqtnitiagspadmycmypnslagvsiyslstescee	631
piTLR5	vdlshnkfvcdcelstfinwlnqtnvtifgsrddiycmypsslagsplntvsmagcse	630
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	transmembrane domain	
zfTLR5	errteklrlvlfisctvliilftastivyisrrgvifkmykkligelvdekreepdpdrf	704
chTLR5	delqqtlrfsvfvflsvtllmflmstiiftrcrgicfvwyktitktligshppaadtsey	693
mTLR5	<pre>eeamrslkfslfilctvtltlflvitlvvikfrgicflcyktiqklvfkdkvwslepgay</pre>	706
hTLR5	eevlkslkfslfivctvtltlflmtiltvtkfrqfcficyktaqrlvfkdhpqqtepdmy	691
boTLR5	eevles1kfslfilvtvtltlflvitlavtkfrqfcficykkaqsllfkdpikgresdty	691
piTLR5	eevleslkfslfilftvtltllfvailvvmkfrqfcficykkvqrlvfkdpslqresdty	690
-		
	start TIR βA A αA A A A B βB αB αB	
zfTLR5	lydvylcfsskdmkwverallkrldsqfsehntlrccfeerdfipgedhltnmrsaiqns	764
chTLR5	mydaylcyskndfewvqnsllkhldsqyfdknrftlcfeerdflpgeehinnirdaiwks	753
mTLR5	rydayfcfsskdfewaqnallkhldahyssrnrlrlcfeerdfipgenhisniqaavwgs	766
hTLR5	kydaylcfsskdftwvqnallkhldtqysdqnrfnlcfeerdfvpgenrianiqdaiwns	751
boTLR5	kydaylcfsskdfewvqnallkhldvqyhsqnrfnlcfeerdfmpgenhianiqdavwss	751
piTLR5	kydaylcfsgkdfewvqeallknldaqysdqnrlnlcfeerdfvpgedrisniqdavwss	750
	** * * * * * * * * * * * * * * * * * * *	
	$BC \stackrel{\beta C}{\longrightarrow} \stackrel{\alpha C}{\longrightarrow} \stackrel{\alpha C'}{\longrightarrow} CD \qquad \underline{\beta}D \qquad DD \qquad \underline{\alpha}D$	
zfTLR5	rkticvvsehflkdgwcletftlaqkrmqaeledilvvlvvgnipqyrllkykqvrsfie	824
chTLR5	${\tt rkticvvtrqflkdgwcveafnfaqsryfsdlkevlimvvvgslsqyqlmkhkpiriflq}$	TIR 813
mTLR5	${\tt rktvclvsrhflkdgwcleafryaqsrslsdlksilivvvvgslsqyqlmrhetirgflq}$	826
hTLR5	${\tt rkivclvsrhflrdgwcleafsyaqgrclsdlnsalimvvvgslsqyqlmkhqsirgfvq}$	811
boTLR5	${\tt rkivclvsrhflrdgwcleafsyaqsrcladlngalimvvvgslsqfhlmrhqsirgfvq}$	811
piTLR5	${\tt rkvvclvsrhflrdgwcleafsyaqsrcladlngtlimvvvgslpqyqlmkhqsirgfvr}$	810
	** :*::*::**:**:* ** * ::*: *::*:*:*:*:	
	DΕβΕ ΕΕαΕ	
zfTLR5	nrsylvwpddgqdlewfydqllhkirkdikinqttketkreeanfntntav	875
chTLR5	rsrylrwpedyqdigwfldnlssqilkekkvqrnvsgielqtiatvsh	861
mTLR5	kqqylrwpedlqdvgwfldklsgcilkeekgkkrsssiqlrtiatis-	873
hTLR5	kqqylrwpedlqdvgwflhklsqqilkkekekkkdnniplqtvatis-	858
boTLR5	krqylrwpedlqdvdwflnklsqwlpkkkkerkkdmwiplqnvptis-	858
piTLR5	kqqylrwpedlqdvswflnklsqyilkkvkekkkdsdiqlqsvtis	856

Faber et al., Figure S4

Fig. S4: alignment of partial TLR5 amino acid sequences (focus and transmembrane and intracellular domains) from different vertebrate species. Amino acid sequences of TLR5 receptors from different vertebrate species (*z*f: zebrafish, ch: chicken, m: murine, h: human, bo: bovine, pi: porcine) were aligned using ClustalW2 (Larkin *et al.*, 2007). Structural components of intracellular TIR domains were assigned according to (Xu *et al.* 2000) and are depicted as abbreviations above the alignment. These components include the BB loop (BB in red) which is involved in TIR-TIR interactions. The start residue of the C-terminal human segment after the non-human N-terminal ECD domain within the chimeric receptor constructs is marked in red. Amino acid exchanges in chimeric mouse/human and bovine/human TLR5 generated in this study by the cloning strategy are marked in green and are as follows: m/h: RSL to TGT and bo/h: ESL to SGT. Acidic residues in the linker domain upstream of the transmembrane domain, which are most likely important for the interaction of TLR5 with UNC93B1 (as shown for mouse UNC93B1 and murine nucleotide-sensing TLRs (Kim *et al.*, 2013) and for proper TLR5 functionality (Huh *et al.*, 2013)), are not affected by the cloning strategy of the chimeric proteins and are shaded in blue.



Faber et al., Figure S5

Fig. S5: mutation of amino acid 744 in the chicken TIR domain to human counterpart results in abolished expression of receptor. HeLa cells were transiently transfected with human (h) TLR5-V5: 100 ng; chicken/human chimeric (ch/h) TLR5-V5: 100 ng or mutated chicken (ch*) TLR5-V5 (amino acid 744 N to A): 200 ng. 48 h post transfection, cells were coincubated with purified recombinant *Salmonella* FliC (50 ng/well), followed by a measurement of secreted IL-8 in cell supernatants. Mean and standard deviation from technical triplicates of biological duplicates of one representative experiment are shown. (**A**). Western Blot analysis of cleared lysates of transfected HeLa cells detected using anti-V5 antibody, anti-P-p38 antibody and anti-p38 antibody (**B**) (see Table S6).



Faber et al., Figure S6

Fig. S6: controls for experimental setup of ECD-dependent TLR5 signaling screening system. A) Non-linear regression curves of dose responses of chimeric TLR5 receptors for determination of optimal activation doses for the system (measured original values shown in Fig. 3 B). Values are depicted relative to a reference (corresponding TLR5 construct activated by maximal dosage of FliC), set as 100%. Regression was performed using GraphPad Prism 6 using the variable slope model (four parameter dose-response curve). B) NF-KB activation of human TLR5 by increasing amounts of C. jejuni and S. Typhimurium lysates (dose dependency determination). HEK-Blue Null1 NF-kB reporter cells were transiently transfected with 100 ng DNA of human TLR5-V5. After 24 hours, transfected cells were coincubated with 200 ng to 3 µg protein content of C. jejuni (isolate Cj 73 or Cj 75) or S. Typhimurium whole bacterial lysates per well for 11 h; NF-kB-dependent SEAP production was determined by colorimetric measurements at 620 nm (see Methods). Absolute values of the colorimetric tests are shown. Background activation was determined by activation of empty vector-transfected cells by the corresponding lysate and subtracted from each test value to quantify specifically the TLR5dependent activation. Mean and standard deviation from technical triplicates of a representative experiment are shown.





Fig. S7: comparison of flagellin expression by selected Salmonella enterica serovars (A) and *C. jejuni* (B) isolates in whole bacterial lysates. Western Blot analysis of selected Salmonella or *C. jejuni* lysates (5 µg total protein/lane) using anti-*E. coli* flagellin antibody, which specifically recognizes flagellin proteins in Salmonella and Campylobacter. S. Enteritidis B554 only expresses FliC, while S. Choleraesuis B815 expresses only FljB.



Faber et al., Figure S8

Fig. S8: pairwise amino acid sequence comparison of TLR5 from various vertebrate species. A to **F:** matrix depiction of pairwise amino acid sequence comparison of TLR5 from different vertebrate species regarding amino acid sequence identity (in [%], **A** to **C**) or amino acid sequence similarity (in [%], **D** to **F**) using pairwise alignment and final analysis with Needle (http://www.ebi.ac.uk/Tools/psa/emboss_needle/). ECD: ectodomain, TM: transmembrane domain, TIR: Toll/interleukin-1 receptor homology domain. ECD (**A**, **D**), TM plus TIR (**B**, **E**) and complete sequences (**C**, **F**) were analyzed separately. **G** and **H**) Maximum Likelihood Trees of ECD (**G**) and TM plus TIR (**H**) of TLR5 from different species (human (h), chicken (ch), mouse (m), pig (p) and bovine (b) TLR5) generated with MEGA5.2 (Tamura *et al.*, 2011) including 500 bootstrap repetitions.

		*		20		*		40			*			
B554 FliC :	-TNK	SOSSISS	ATERLSS	GLR	TNSA		GOATA	NRETSN	TKCL	TOAS	RNAND	GTS	:	56
B2359 Flic .		SOSTAS	ATERLSS	GIR				NRETSN	TKCL	TOAS	NAND	GTS		56
D2000_File .									TROL				•	50
B2486_F11C :		5 0 55 1 551	ALERLSS	GLK	INSA	NDDAA	GQALA	N K F ISN	TKGT	IQAS	RNAND	GIS	:	56
B2334_FliC :	-L <mark>N</mark> K	S <mark>QSSLS</mark> SI	AIERLSS	GLR	I <mark>NSA</mark>	KDDAA	G <mark>Q</mark> AIA	N <mark>R</mark> F TSN	IKGL	TQAS	RNAND	GI <mark>S</mark>	:	56
R160_FliC :	-L <mark>N</mark> K	S <mark>Q</mark> SALGTI	AI <mark>ER</mark> LSS	GLR	I <mark>NSA</mark>	K DDAA	G <mark>Q</mark> AIAI	N <mark>R</mark> F TAN	I <mark>K</mark> GL	TQAS	R <mark>NAND</mark>	GIS	:	56
B1533 FliC :	-LNK	SOSALGT	AIERLSS	GLR	INSA	KDDAA	GOATA	N <mark>R</mark> FTAN	IKGL	TOAS	RNAND	GIS	:	56
B1830 Flic .		SOSAXCT	ATERXSX	GLR	TNSA				TKCT.	TOAS		GTS		56
D1000_F11C .	T	COCAT CT	ATERICS		TNCA				TVCT	TOAC			:	56
BI040_FIIC :		SUSALGI	ALCELSS	GLIN		DDAA	GUALA		TUGT	TQAS	NAND	GID	•	50
BI082_FIIC :	-T <mark>N</mark> K	SQSALGT	ATERLSS	GLR	INSA	KDDAA	G <mark>Q</mark> ATA.	N <mark>R</mark> ETAN	TKGT	TQAS	RNAND	GIS	:	56
B2075_FliC :	-L <mark>N</mark> K	S <mark>Q</mark> SALGTI	AIERLSS	GLR	I <mark>NSA</mark>	KDDAA	G <mark>Q</mark> AIA	N <mark>R</mark> F TAN	IKGL	TQAS	R <mark>NAND</mark>	GI <mark>S</mark>	:	56
B2078_FliC :	-L <mark>N</mark> K	SQSALGT	AIERLSS	GLR	INSA	K DDAA	G <mark>Q</mark> AIA	N <mark>R</mark> F TAN	IKGL	TQAS	RNAND	GIS	:	56
B2183 FliC :	-LNK	SOSALGT	ATERLSS	GLR	T <mark>NSA</mark>	K DDAA	G <mark>OATA</mark> I	N <mark>R</mark> FTAN	IKGL	TOAS	RNAND	GIS	:	56
B2257 Flic .		SOSALCT	ATEPT SS	CTP	TNICA				TKCT	TOAS		CTS		56
D2207_FILC .		COCALCE											•	50
B2396_F11C :		SUSALGI	AICRESS	GLK		DDAA	GQALA	N R F IAN	TRGT	IQAS	NAND	GIS	:	20
xy82_FliC :	-L <mark>N</mark> K	S <mark>Q</mark> SALGTI	AIERLSS	GLR	I <mark>NSA</mark>	KDDAA	G <mark>Q</mark> AIA	N <mark>R</mark> F TAN	IKGL	TQAS	RNAND	GI <mark>S</mark>	:	56
R269_FliC :	-L <mark>N</mark> K	S <mark>Q</mark> SALGT	AIERLSS	GLR	I <mark>NSA</mark>	KDDAA	G <mark>Q</mark> AIA	N <mark>R</mark> F TAN	I <mark>K</mark> GL	TQAS	RNAND	GIS	:	56
xv810 FliC :	-L <mark>N</mark> K	SOSALGT	AIERLSS	GLR	I <mark>NSA</mark>	K DDAA	G <mark>OAIA</mark>	N <mark>R</mark> FTAN	IKGL	TOAS	RNAND	GIS	:	56
B571 Flic .		POSALGT	ATERLSS	GLR	TNSA				TKGL	TOAS		GTS		53
DIGEL FLIC .	TNT								TTOT				:	50
BI951_FIIC :		SUSALGI	AICRESS	GLK		DDAA	GUALA		TNGL	IQAS	NAND	GID	•	50
B200_F11C :	-T <mark>N</mark> K	S <mark>Q</mark> SALGTI	AIERLSS	GLR	INSA	KDDAA	G <mark>QATA</mark>	N <mark>R</mark> FTAN	TKGL	TQAS	RNAND	GIS	:	57
B558_FliC :	-L <mark>N</mark> K	SQSALGT	AI <mark>ER</mark> LSS	GLR	I <mark>NSA</mark>	KDDAA	G <mark>Q</mark> AIAI	N <mark>R</mark> F TAN	IKGL	TQAS	RNAND	GI <mark>S</mark>	:	56
		QS 3	AIER S	GLR	INSA	KDDAA	GQAIA	NR T N	IKGL	TQASI	RNAND	GIS		
	6.0							-	~ ~					
	60	_	*	2	30		*	T	00		~	_		
B554_FliC :	IAQT	TEGALNEI	[NNNLQR	V REI	L <mark>SVQ</mark> Z	ATNGTI	NSDSD.	LK <mark>SIQ</mark> D	EIQQ	RLE <mark>E</mark> I	IDRVS	NQT	:	113
B2359_FliC :	IAQT	T <mark>EG</mark> ALNEI	[NNNL <mark>QR</mark>]	V <mark>RE</mark> I	L <mark>SVQ</mark> Z	ATNGTI	NS <mark>D</mark> SD	L <mark>K</mark> SIQD	EIQQ	RLE <mark>E</mark> :	IDRVS	Ν <mark>Q</mark> T	:	113
B2486_FliC :	IAOT	TEGALNE I		V <mark>RE</mark> I	LSVQ	ATNGTI	NSDSD	LKSIQD	EIQO	RLE <mark>E</mark> :	ID <mark>R</mark> VS	NOT	:	113
B2334 Flic .	TAOT				.svo	ATNGTI			ETOO	RLEE	TDRVS	NOT		113
D160 Elic .													:	112
RIGO_FIIC :						SANSII	NSUSDI		TIV			GQI	•	113
B1533_F11C :		IEGALNE -	LNNNLQR	V REI	LAVQ	SANGII		LDSIQA	ETIQ	KLNE.		GQI	:	113
B1830_FliC :	X <mark>AQ</mark> T	TEGALNEI	[NNNLQR	V REI	L <mark>AVQ</mark> S	SANGTI	NSQSD.	LD <mark>SIQ</mark> A	EITQ	RLN <mark>E</mark> :	IDRVS	G <mark>Q</mark> T	:	113
B1040_FliC :	IAQT	T <mark>EG</mark> ALNEI	INNNL <mark>QR</mark> Y	V <mark>RE</mark> I	L <mark>avq</mark> s	SANSTI	NSQSD	L <mark>D</mark> SIQA	EITQ	RLN <mark>E</mark> :	IDRVS	GQT	:	113
B1085 FliC :	IAOT	TEGALNEI		V <mark>RE</mark> I	LAV <mark>O</mark> S	SANSTI	NSOSD	LD <mark>SIO</mark> A	EITO	RLNE:	ID <mark>R</mark> VS	GOT	:	113
B2075 FliC .	TAOT					SANSTI	ISOSD		ETTO	RLNE		GOT		113
B2078 Elic .	TAOT					CANCTI						COT	:	113
B2070_FIIC .						DANO II							•	110
B2183_F11C :	T <mark>AQ</mark> T	TEGALNE.	LNNNL <mark>Q</mark> R	VRE	L <mark>AVQ</mark> S	SANSTI	NSQSD.	LD <mark>S IQ</mark> A	ETTQ	RLNE.	LDRVS	GQT	:	113
B2257_FliC :	IAQT	T <mark>EG</mark> ALN <mark>E</mark> I	[NNNLQ <mark>P</mark>]	V REI	L <mark>AVQ</mark> S	SANSTI	NSQSDI	L <mark>DSIQ</mark> A	EITQ	RLN <mark>E</mark> :	ID <mark>R</mark> VS	GQT	:	113
B2396_FliC :	IAQT	T <mark>EG</mark> ALNEI		V <mark>RE</mark> I	L <mark>AVQ</mark> S	SANSTI	NSQSD	L <mark>DSIQ</mark> A	EITQ	RLN <mark>E</mark> :	ID <mark>R</mark> VS	GQT	:	113
xv82 FliC :	TAOT	TEGALNEI		V REJ	LAVO	SANSTI		L <mark>DS TO</mark> A	EITO	RLNE	ID <mark>R</mark> VS	GOT	:	113
R269 Flic .	таот	TECALNET				SANSTI			F T TO			COT		113
N200_1110 .													:	110
XY810_F11C :		I E GALINE I		V KE		SANSII				KLINĽ.		GQI	:	113
B571_F1iC :	I <mark>AQ</mark> T	TEGALNE I	[NNNLQR	V REI	L <mark>AVQ</mark> S	SANSTI	NSQSD.	LD <mark>SIQ</mark> A	EITQ	RLNE :	IDRVS	GQT	:	110
B1951_FliC :	IAQT	T <mark>EG</mark> ALNE]	INNNL <mark>QR</mark>	V <mark>RE</mark> I	L <mark>AVQ</mark> S	SANSTI	NSQSD	L <mark>D</mark> S I <mark>Q</mark> A	EITQ	RLN <mark>E</mark> :	IDRVS	GQT	:	113
B560_FliC :	XAQT	T <mark>EGALNE</mark> I		V <mark>RE</mark> I	LAV <mark>O</mark> S	SANSTI		L <mark>DSIQ</mark> A	EITQ	RLN <mark>E</mark> :	ID <mark>R</mark> VS	GQT	:	114
B558 Flic :	TAOT					SANSTI	NSOSD		ETTO	RT.NE		GOT		113
	AOT	TECAINE				N TI					TDDUC	OT	•	110
	AQI	LEGATIVE	LININILQK	VREI	L VQ	IN II	N2 2D1	L SIQ	ст Q.	KL L.	IDRVS	QΙ		
	1	20	*		140	0		*	16	0		*		
B554 Flic .	OFNC								GENV			DT.K		170
D004_1110 .													:	170
BZ339_FIIC :			QMICT QV							GPN			•	170
B2486_FliC :	QFNG	V K V LSQDI	VQMKIQV	GANI	JGET.	I I I D L	QKIDVI	^{SLGLD}	GE'N V	NGP KI	SATVG		:	T/0
B2334_FliC :	QF NG	V <mark>K</mark> VLSQDI	<mark>VQM</mark> KIQV	G <mark>ANI</mark>	GET	ITIDL	QKIDVI	K <mark>SL</mark> GLD	GF <mark>NV</mark>	NGPKI	E <mark>AT</mark> VG	DLK	:	170
R160_FliC :	QF NG	V <mark>K</mark> VLAQDI	TLTIQ V	G <mark>ANI</mark>	GET	IDIDL	KQI <mark>NS</mark> (OTL <mark>G</mark> LD	TL <mark>SV</mark>	ODA <mark>Y</mark>	<mark>fpk</mark> gt	AVT.	:	170
B1533 FliC :	OFNG		UTLTTOV	G <mark>ANI</mark>			KET <mark>SS</mark> I	TLGLD	kp <mark>nv</mark>	DAY	г <mark>рк</mark> ет	AVT	:	170
B1830 Flic .	OXNC				CET		KETSSI		KT NV		тр <mark>и</mark> гт	AVT		170
D1000_F11C .													•	170
B1040_F11C :	Qr NG			GANI	GET.		KQINS		I L <mark>IN V</mark>	QQKII		AAI	:	170
B1085_FliC :	QFNG	V <mark>K</mark> VLAQDI	TLTIQV	G <mark>ANI</mark>	OGET.	IDIDL	KQI <mark>NS</mark> (2TLGLD	TL <mark>NV</mark>	QQK Y I	KVSDT	<mark>a</mark> at	:	170
B2075_FliC :	QFNG	V <mark>K</mark> VLAQDI	VTLTIQV	G <mark>ANI</mark>	GET	IDIDL	KQINS	<mark>DTLG</mark> L <mark>D</mark>	TL <mark>NV</mark>	QQKYI	K <mark>VS</mark> DT	<mark>A</mark> AT	:	170
B2078_FliC :	QFNG	V <mark>K</mark> VLAODI	TLTIOV	G <mark>ANI</mark>	GET	IDIDL	KQINS	<mark>DTLG</mark> LD	TL <mark>NV</mark>	QQKY	K <mark>VS</mark> DT	<mark>А</mark> АТ	:	170
B2183 FliC .	OFNG		TLTIOV	GAN	GET		KOTNS		TLNV	OOKY	T C <mark>ZV</mark> S	ААТ	:	170
B2257 Flic .	OFNC		TTTOW	GAN	CET		KOTNE		TT NTZ	OKV		АДТ		170
B3306 E1:0 .							KOTNE		T T	OVV			:	170
B2390_F11C :				GAN						QAI		TAD	•	170
xy82_FliC :	QFNG	V K V LAQDI	ATTTTO A	G <mark>ANI</mark>	GET.	IDIDL	KQINS(2 I LGLD	T L <mark>NV</mark>	QKYI	K V S D T	AAT	:	T/0
R269_FliC :	QF <mark>N</mark> G	V <mark>K</mark> VLAQDI	VILTIQV	G <mark>ANI</mark>) G <mark>E</mark> T	IDIDL	KQINS	2TL <mark>G</mark> L <mark>D</mark>	TL <mark>NV</mark>	QQK <mark>YI</mark>	K <mark>VS</mark> DT	<mark>a</mark> at	:	170
xy810_FliC :	QFNG	V <mark>K</mark> VLAQDI	VTLTIQV	G <mark>ANI</mark>) G <mark>E</mark> T	IDIDL	KQINS	<mark>QTLG</mark> L <mark>D</mark>	TL <mark>NV</mark>	QKK <mark>Y</mark> I	DV <mark>S</mark> DT	AVA	:	170
B571 FliC :	Q ENG	VKVLAODI	TLTIOV	G <mark>ANI</mark>	O <mark>GE</mark> T	IDIDL	KQINS	TLGLD	tl <mark>nv</mark>	OKAYI	σνοάτ	VEN	:	167
B1951 Flic .	OFNC		UT LT TOW	GAN	GET		KOTNS		TL <mark>NV</mark>	OKKY		AVT		170
B560 E140 .					C		KOTNO		TTNI				:	171
DOOD_LITC :							KOTNO		TT NT				:	170
вээх <u>г</u> 11С :	Qr NG			GANI		TOTOT.	NQINS(T T <mark>U N N</mark>		ST UST	GV1	:	T/0
	Q NG	VKVL QDÌ	N 6 IQVO	GANI	JGET :	I IDL	I	3LGLD	V					

		180		*		200			*		220			
B554_FliC	:	S <mark>S</mark> FKNV <mark>T</mark> GYI	DTYA <mark>A</mark>	GADK <mark>yr</mark> v	DINS <mark>G</mark>	AVV	T <mark>D</mark> AA <mark>A</mark>	PDK	V <mark>Y</mark> VN	AANGQ	LTTDDA	ENNT <mark>A</mark>	:	227
B2359_FliC	:	S <mark>S</mark> FKNV <mark>T</mark> GYI	dtya <mark>a</mark>	GADK <mark>YR</mark> V	DI <mark>NS</mark> G	AVV	T <mark>D</mark> AA <mark>A</mark>	PDK	V <mark>Y</mark> VN	AANGQ	LTTDDA	ennt <mark>a</mark>	:	227
B2486_FliC	:	S <mark>S</mark> FKNV <mark>T</mark> GYI) TYA <mark>A</mark>	GADKYRV	DI <mark>NS</mark> G	AVV <mark>A</mark> V	T <mark>D</mark> AA <mark>A</mark>	PDK	V <mark>Y</mark> VN	AANGQ	LTTDDA	ENNT <mark>A</mark>	:	227
B2334_FliC	:	S <mark>S</mark> FKNV <mark>T</mark> GYI) TYA <mark>A</mark>	GADKYRV	DINS <mark>G</mark>	AVV <mark>A</mark> V	T <mark>D</mark> AV <mark>A</mark>	PDK	V <mark>Y</mark> VN	AANGQ	LTTDDA	ENNT <mark>A</mark>	:	227
R160_FliC	:	R <mark>D</mark> VTTY <mark>K</mark> NGC	GTTL <mark>T</mark>	APNA	A	AID	T <mark>A</mark> LG <mark>T</mark>	TGA	AG	TAAVK	FKDGNY		:	213
B1533_FliC	:	V <mark>D</mark> KTTY <mark>K</mark> NGI	[DPI <mark>T</mark>	AQSN	I	' <mark>D</mark> IQ	T <mark>A</mark> IG <mark>G</mark>	GAT	GV	TGADI	KFKDGQ	YYLD-	:	217
B1830_FliC	:	V <mark>D</mark> KTTY <mark>K</mark> NGI	[DPI <mark>T</mark>	AQSN	I	DIQ	T <mark>A</mark> IG <mark>G</mark>	GAT	<mark>G</mark> V	TGADI	KFKDGQ	YYLD-	:	217
B1040_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	<mark>А</mark> ТТ	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B1085_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	а <mark>т</mark> т	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B2075_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	а <mark>т</mark> т	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B2078_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	з <mark>а</mark> тт	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B2183_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	З <mark>А</mark> ТТ	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B2257_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	З <mark>А</mark> ТТ	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
B2396_FliC	:	VTGYTDSATA	AIDK <mark>S</mark>	TFAA	s	а <mark>т</mark> т	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
xy82_FliC	:	VTGYTD <mark>S</mark> ATA	AIDK <mark>S</mark>	TFAA	S	З <mark>А</mark> ТТ	L <mark>G</mark> GT <mark>P</mark>	AIT	GD	LK-FD	DTTGKY	Y	:	213
R269_FliC	:	V <mark>T</mark> GYAD <mark>T</mark> TIA	ALDN <mark>S</mark>	TFKA	S	3 <mark>a</mark> tg	L <mark>G</mark> GT <mark>D</mark>	QKI	DG	DL-KF	DDTTGK	Y	:	213
xy810_FliC	:	A <mark>s</mark> ysds <mark>k</mark> qni	[A	-VPD	K	TAI	T <mark>A</mark> KI <mark>G</mark>	AAT	sG	GAGIK	ADISFK	DGKY-	:	213
B571_FliC	:	S <mark>V</mark> KLD- <mark>T</mark> SAI	LTAD <mark>A</mark>	IKGG	V	7 <mark>T</mark> GA	T <mark>T</mark> AG <mark>A</mark>	LK-	DG	KVYSN	GTDYYV	EV	:	210
B1951_FliC	:	P <mark>S</mark> ATLS <mark>T</mark> TAI	LDGA <mark>G</mark>	LKT	0	TGS	T <mark>T</mark> DT <mark>G</mark>	SIK	DG	KVYYN	STSKNY	YVEV-	:	216
B560_FliC	:	Q <mark>S</mark> LDLK <mark>T</mark> AGI	I TGA <mark>T</mark>	LKAG	I	ТGТ	T <mark>T</mark> ET <mark>G</mark>	SVK	DG	KVYYD.	ADSKNY	YVEV-	:	218
B558_FliC	:	QSLDLK T AGI	TGAT	LKAG	I	ТGТ	T <mark>T</mark> ET <mark>G</mark>	SVK	DG	KVYYD.	ADSKNY	YVEV-	:	217
_		-		-			_							
		*	240		*		260			*	2.80)		
B554 FliC	:	VDLEKTTKS	TAGTA	EAKATAC	AIKG	G <mark>K</mark> EC	DTFD	YKG <mark>V</mark>	TFT	-D1	KTGDD	NGKVS	:	281
B2359 FliC	:	VDLFKTTKS	LAGTA	EAKAIA	AIKG	GKEG	DTFDY	YKG <mark>V</mark>	TFT	I-D1	KTGDD	NGKVS	:	281
B2486 FliC	:	VDLEKTTKS		EAKATA	AIKG	GKEG	DTFDY	YKG <mark>V</mark>	TFT	I -D1	KTGDD	NGKVS	:	281
B2334 FliC	:	VDLFKTTKS		EAKAIA	AIKG	GKEG	DTFDY	YKGV	TFT	-D1	KTGDD	NGKVS	:	281
R160 FliC		FVE			-KDG	YEA		AGAV	тмт	ANKAT	TGAST	TENOT		256
B1533 FliC	:	VKGGA	SAGVY	KATYDET	-TKK			TPT.A	TAE	ATAT-F	GTATT	HNOTA	:	268
B1830 FliC		VKGGA	SAGVY	KATYDET	-TKK			TPT.A	TAE	ATAT-F	GTATT	HNOTA		268
B1040 FliC		ADVS-		AKDG		ZYEV		DGK-		TGTP-1	GPTTA	FPSTA		254
B1085 FliC	:	ADVS		AKDG		ZYEV		DGK-		TGTP-1	GPTTA	FPSTA	:	254
B2075 FliC	:	ADVS-		AKDC				DCK-		TGTP-1	COTTA	FDSTA	:	254
B2078 FliC	:	ADVS-		AKDG				DGK-		TGTP-1	CPTTA	FDSTA	:	254
B2183 FliC	:	ADVS		AKDG				DGK-		TGTP-1	CPTTA	FPSTA	:	254
B2257 Flic	:	ADVS						DGK-		TGTP-1	CDTTA	FDGTA	:	254
B2396 FliC	:	ADVS-						DGK-		TGTP-1	CDTTA	FDSTA	:	254
NUR2 FliC	:	ADVS						DGK-		TCTD-1	CDTTA	FDGTA	:	254
RY62_FIIC	:	XVKV-		CCTCK	DCV		UDKTN	JGR-				TDATA	:	258
XV810 Flic	:	VATUS			-NGT							TLAIN	:	250
P571 Flic	:	SEADA			NCE			TCAU				ANAVS	:	251
BJ/I_FIIC B1951 Elic	:	FFTDA		GR	KCC		VIN 1 1 1				VEATT	AGVSE	:	259
BIJJI_FIIC	:	DFTDA									EAVDTA	AVEVE	:	259
B560_F11C	:	DFIDI									EAREI		:	262
B330_F11C	•			AA	IIAG		1 <mark>0 v</mark> dai	JGIN		IGAI -I			•	201
		*	30	0	*		32	0		*		340		
B554_FliC	:	TTINGEKVTI	J <mark>TVA</mark> D	IATGATD	VN <mark>AA</mark> I	LQ <mark>S</mark>	SKNVY	TSV	VN <mark>G</mark> Ç	0FTFDD	KTK-NE	S <mark>A</mark> KLS	:	337
BZ359_FliC	:	TTINGEKVTI	J VAD	LAIGATD	VNAAI	LQS	SKNVY	ISV	V N <mark>G</mark> Ç	2F. I.F. DD	TK-NE	SAKLS	:	331
B2486_FliC	:	TTINGEKVTI	J <mark>TVA</mark> D	IATGATD	VN <mark>AA</mark> I	LQS	SKNVY		VNGÇ	je. <u>Te.</u> DD	KTK-NE	SAKLS	:	337
B2334_FliC	:	TTINGEKVTI	J <mark>TVA</mark> D	IAIGAAD	VNAAI	LQS	SKNVY	TSV	VN <mark>G</mark> Ç	0FTFDD	KTK-NE	SAKLS	:	337
R160_F11C	:	VDAVTPTPVL)T	VAAATAL	TNAGV	ТG <mark>А</mark>	-TGNT	SL <mark>V</mark>	KMSF	'EDKNG	KVTDAG	Y <mark>a</mark> lkv	:	309
B1533_FliC	:	EVTKEGVDTI	TVAA	QLAAAGV	TG <mark>AD</mark> -		-KDNT	SLV	KL <mark>S</mark> F	'EDKNG	KVIDGG	Y <mark>A</mark> VKM	:	320
B1830_FliC	:	EVTKEGVDTI	TVAA	QLAAAGV	TGAD-		-KDNT	SLV	KL <mark>S</mark> F	'EDKNG	KVIDGG	YAVKM	:	320
B1040_F11C	:	TKDVKQTQQE	SNAD L	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SVV.	KMSY	TDNNG	KTIDGG	L <mark>AV-</mark> K	:	308
B1085_FliC	:	TKDVKQTQQE	ENADL	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SVV	KM <mark>S</mark> Y	T <mark>DNNG</mark>	KTIDGG	L <mark>A</mark> V-K	:	308
B2075_FliC	:	TKDVKQTQQE	ENADL	TEAKAAL	T'A <mark>AG</mark> V	AA-	-AGTA	SVV	KM <mark>S</mark> Y	TDNNG	K TIDGG	L <mark>AV-</mark> K	:	308
B2078_FliC	:	TKDVKQTQQE	E <mark>NAD</mark> L	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SVV.	KM <mark>S</mark> Y	T <mark>DNNG</mark>	KTIDGG	L <mark>A</mark> V-K	:	308
B2183_FliC	:	TKDVKQTQQE	ENADL	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SV <mark>V</mark> I	KM <mark>S</mark> Y	TDNNG	K TIDGG	L <mark>A</mark> V-K	:	308
B2257_FliC	:	TKDVKQTQQE	ENADL	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SVV	KM <mark>S</mark> Y	TDNNG	K TIDGG	L <mark>A</mark> V-K	:	308
B2396_FliC	:	TKDVKQTQQE	E <mark>NAD</mark> L	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SV <mark>V</mark> I	KM <mark>S</mark> Y	T <mark>DN</mark> NG	K TIDGG	L <mark>A</mark> V-K	:	308
xy82_FliC	:	TKDVKQTQQE	E <mark>NAD</mark> L	TEAKAAL	TA <mark>AG</mark> V	AA-	-AGTA	SV <mark>V</mark> I	KM <mark>S</mark> Y	TDNNG	K TIDGG	L <mark>A</mark> V-K	:	308
R269_FliC	:	TEDVKNVQVA	A <mark>NAD</mark> L	TEAKAAL	TAA	GV-	-TGTA	SV <mark>V</mark> I	KM <mark>S</mark> Y	T <mark>D</mark> N <mark>NG</mark>	K <mark>TIDG</mark> G	L <mark>A</mark> V-K	:	310
xy810_FliC	:	KVQQNDTEIA	AA	TNAKAAL	KA <mark>AG</mark> V	AD <mark>A</mark>	EADTA	TL <mark>V</mark> I	KM <mark>S</mark> Y	T <mark>D</mark> N <mark>NG</mark>	K <mark>V</mark> IDGG	F <mark>A</mark> FKT	:	316
B571_FliC	:	VTEVQGLNTE	S	SAVQDQL	TA <mark>AG</mark> V	SA <mark>A</mark>	DAAKS	EV <mark>V</mark> I	KM <mark>S</mark> Y	T <mark>D</mark> K <mark>NG</mark>	K <mark>TIDG</mark> G	F <mark>G</mark> VKV	:	308
B1951_FliC	:	VTQVQKPVAA	AP	AAIQA	QL <mark>TA</mark> A	HVT	GADTA	EMV	KM <mark>S</mark> Y	T <mark>D</mark> K <mark>NG</mark>	K <mark>T</mark> I <mark>DG</mark> G	F <mark>G</mark> VKV	:	311
B560_FliC	:	KTIDEKPLKA	AS	SSVQDAL	KA <mark>SG</mark> I	AD <mark>A</mark>	VAEAA	TVV	KM <mark>S</mark> Y	T <mark>D</mark> K <mark>NG</mark>	K <mark>TIDG</mark> G	Y <mark>G</mark> IKV	:	316
B558_FliC	:	KTIDEKPLKA	4S	SS <mark>V</mark> QDAL	KA <mark>SG</mark> I	AD <mark>A</mark>	VAEAA	TVV	KM <mark>S</mark> Y	T <mark>D</mark> K <mark>NG</mark>	K <mark>T</mark> I <mark>DG</mark> G	Y <mark>G</mark> IKV	:	315
ied on nevt ner	٦e							V		1	K			

		*			360				*		380		*				
B554 FliC :	DLEANN	– <mark>A</mark> N	/KG	SK	ITVNG	Б <mark>А</mark> Е	ΥTΑ	NAT	GDKI	L				-AGKT	MFID	: 3	377
B2359 FliC :	DLEANN	– <mark>A</mark> T	7KG	SK	ITVNG	Б <mark>А</mark> Е	YTA	NAT	GDKI'	rL				- <mark>ag</mark> kt	MFID	: 3	377
B2486 Flic .	DIEANN	_ <mark>7</mark> 7		C V	TTUNG		VT7	NAT	CDKT	гт							77
D2400_FILC .	DIEANN				TTUNC				CDVT								,,, ,,,,
B2334_FIIC :	DLEANN		rG	Sh	TIVNG	-AL	ILE		GURI					AGRI		: 3	0//
R160_FliC :	GNDY YA	AD	YDE	KTG:	EIKAK	(TV	NYI	DAT	G <mark>a</mark> tki	[GA]	(KFGG	G <mark>AN</mark> G	KTEVVT	TVDG <mark>N</mark>	tyq <mark>a</mark>	: 3	366
B1533_FliC :	GDDF <mark>Y</mark> A	AT 1	Y <mark>de</mark> i	KTG.	AITAK	TT.	ΤYΙ	'DG <mark>T</mark>	G <mark>V</mark> AQ	[G <mark>A\</mark>	<mark>/K</mark> FGG	G <mark>AN</mark> G	K <mark>se</mark> vvt	A <mark>TD</mark> G <mark>K</mark>	TYL <mark>A</mark>	: 3	377
B1830_FliC :	GDDFYA	AT	Y D E I	KTG.	AITAK	ТT	ΤYΤ	DGT	G <mark>V</mark> AQ	[GAN	/ <mark>K</mark> FGG	<mark>AN</mark> G	K <mark>SE</mark> VVT	A <mark>TD</mark> G <mark>K</mark>	TYL <mark>A</mark>	: 3	377
B1040 FliC :		SA	FON		STSTN	и <mark>т</mark> т	K Y T	םם <mark>בי</mark>	GTSK				K TEVVS	TGGKT	YAAS		865
B1085 Flic .		CA			CTCTN				CTCK				TEMUS	TCCKT	VAAC		265
BIUOJ_FIIC :	VGDD I I	SA.		UG	SISIN	1 <u>1</u>			GISK		IN LOO			TGGKI		• •	005
B20/5_F11C :	VGDD Y Y	SA:	I QNI	G	SISIN	1 <u>.</u>	K Y I	ADD.	GISK		(KEGG	<mark>AD</mark> G	KTEVVS	T <mark>GG</mark> KT	YAA <mark>S</mark>	: 3	365
B2078_FliC :	VGDD <mark>Y</mark> Y	SAI	Γ <mark>Q</mark> N	<mark>C</mark> DG	SISIN	ΙTΤ	KY 1	'ADD	GTSK	[AL	IKLGO	6 <mark>AD</mark> G	K T E VVS	I <mark>GG</mark> K <mark>T</mark>	YAA <mark>S</mark>	: 3	865
B2183_FliC :	<mark>V</mark> GDD <mark>Y</mark> Y	SA	Γ <mark>Q</mark> N	<mark>K</mark> DG	SISIN	Ι <mark>Τ</mark> Τ	KY1	'AD <mark>D</mark>	GTSK	[ALN	IKLGO	G <mark>AD</mark> G	K T E VVS	I <mark>GG</mark> K <mark>T</mark>	YAA <mark>S</mark>	: 3	865
B2257 FliC :		SA	FON	CDG.	SISIN	IТТ	<mark>κ</mark> γτ		GTSK	LAT'N	IKLGO	ADG	KTEVVS	I <mark>GG</mark> KT	YAAS	: 3	365
B2396 Flic .		SA			STSTN	TTT			CTSK			ADC	KTEWUS	TCCKT	VAAS		865
D2000_1110 .		011			CTCTN				CTCZ								D C E
xy82_F11C :	VGDDIY	SA.		DG	SISIN	1 <u>1</u> 1	K I I	ADD	GISK		IN EGO	ADG	KIEVVS	IGGKI	IAAS	: 3	505
R269_FliC :	VGDD Y Y	SA	rQNI	<mark>C</mark> DG	SISIN	ITT	KY1	'ADD	GTSK	TAL	IKLGO	G <mark>AD</mark> G	KTEVVS	I <mark>GG</mark> K <mark>T</mark>	YAA <mark>S</mark>	: 3	367
xy810_FliC :	SGGY <mark>Y</mark> A	AS (/DK	<mark>G</mark> A.	ASLKV	7 <mark>T</mark> S	YVD	AT <mark>T</mark>	G <mark>T</mark> EK	[AA]	I <mark>K</mark> LGO	G <mark>AD</mark> G	K <mark>te</mark> vvt	I <mark>DG</mark> K <mark>T</mark>	YNA <mark>S</mark>	: 3	373
B571 FliC :	GDDIYA	- <mark>A</mark>	r <mark>k</mark> n <mark>i</mark>	CDG.	SISIN	I <mark>А</mark> Т	ΕYΊ	DKD	G <mark>N</mark> TK	[ALN	IOLGO	<mark>VD</mark> G	K <mark>TE</mark> VVT	IDGKT	YNA <mark>S</mark>	: 3	364
B1951 FliC :		<u>_</u> _	r K N		SESTN	л <mark>т</mark> т	EYT	סאסי	GNTK'				K TEVVS	TDGKT	YNAS		367
DIJOI_IIIC .					OVCIN				CNTR					TDCVT			272
BJOU_FIIC :	GDDITA	-		UG	SISIN									TDGKI		• •	71
B558_F11C :	<mark>g</mark> dd y <mark>y</mark> a	- <mark>A</mark>	I' <mark>k</mark> ei	<mark>(</mark> DG	SYSIN	I <mark>S</mark> T	SYI	DKD	G <mark>N</mark> TK		I <mark>Q</mark> LGG	5 <mark>AD</mark> G	KTEVVS	T <mark>DG</mark> K <mark>T</mark>	yna <mark>s</mark>	: :	3/1
									G	Г							
			*		4	20			*		4	40		*			
B554_FliC :	KTA-SG	VS	LI	ED.	AA <mark>AA</mark> K	KS	TAN	PLA	SIDS	ALSE	VDA	R <mark>SS</mark>	L <mark>GAIO</mark> N	RFDSA	I <mark>TN</mark> L	: 4	133
B2359 FliC .	KTA-SG	vs	Т. Т		AAAAK	KS	TAN		STDS	ALSE		7RSS		REDSA	TTNT.	• 4	133
B2486 Flic .			TT	FD	אַקּקּאַ	V C			STDS	TCE				PEDGA	TTNT		133
B2400_FIIC .	ATA-36	v 5							01001		VDA				T T T T	• •	100
B2334_F11C :	KIA-SG	vs.	цпт	ED	AA <mark>AA</mark> K	KS		P LA	SIDS	ALSE		RSS	L <mark>GALQ</mark> N	REDSA	T _{TN} P	: 4	133
R160_FliC :	<mark>SD</mark> V <mark>K</mark> GH	NF	SG	AL	SE <mark>AV</mark> T	Τ <mark>Κ</mark>	TEN	PLA	K I DAI	ALA <mark>Ç</mark>	VDA <mark>I</mark>	J <mark>R</mark> SD	l <mark>gavq</mark> n	r fnsa	I <mark>TN</mark> L	: 4	123
B1533_FliC :	<mark>S</mark> DL <mark>D</mark> KH	NF	TG	EL	KE <mark>VN</mark> T	D <mark>K</mark>	TEN	PLQ	KIDA/	ALA <mark>C</mark>	VDT	J <mark>R</mark> SD	l <mark>g</mark> avqn	RFNSA	I <mark>TN</mark> L	: 4	134
B1830 FliC :	SDL <mark>D</mark> KH	NF	TG	EL	ke <mark>vn</mark> t	D <mark>K</mark>	TEN	PLO	KIDA/	ALAC	VDTI	RSD	l <mark>gavo</mark> n	RENSA	ITNL	: 4	134
B1040 FliC .	KAE-GH	NF.	AO	DT.	AEAAA	тт	TEN	PLÕ	K T D A		VDTT	RSD	LGAVON	RENSA	TTNT.	• 4	121
DIONE FILC .														DENCA	TTNT		101
BIU85_FIIC :			AQ		ALAAA		1 E N	E LV	NIDA			RSD	LGAVQN		TINT	: 4	±ZI
B20/5_FliC :	KAE-GH	NF.	AQ	DL	AE <mark>AA</mark> A	TT	TEN	PLQ	K I DA	ALA <mark>C</mark>	2VDT	RSD	L <mark>GAVQ</mark> N	RENSA	T _{IN} T	: 4	121
B2078_FliC :	K <mark>A</mark> E−G <mark>H</mark>	NF	(AQ	DL	AE <mark>AA</mark> A	TT	TEN	PLQ	KIDA/	ALA <mark>Ç</mark>	VDT	J <mark>R</mark> SD	l <mark>gavq</mark> n	RFNSA	I <mark>TN</mark> L	: 4	121
B2183 FliC :	KAE-GH	NF	AO	DL	AE <mark>AA</mark> A	TT	TEN	PLO	KIDA/	ALAC	VDTI	RSD	l <mark>gavo</mark> n	RENSA	ITNL	: 4	121
B2257 FliC .	KAE-GH	NF	AO		AEAAA	тт	TEN	PLÕ	K T D A			RSD	LGAVON	RENSA	t <mark>tn</mark> t.	• 4	121
D2207_TITC .				DT											T TNTT		101
B2396_F11C :			AQ		ALAAA		1 E N	ΞŲ	L IDA			RSD	LGAVQN		TINT	: 4	±ZI
xy82_FliC :	KAE-GH	NF.	AQ	DL	AE <mark>AA</mark> A	V.L.T	TEN	ЪТŐ	K I DA	ALA <mark>C</mark>	2VDT1	RSD	L <mark>GAVQ</mark> N	RENSA	T _{TN} P	: 4	121
R269_FliC :	K <mark>a</mark> e-gh	NF	(AQ	DL	AE <mark>AA</mark> A	TT	TEN	PLQ	K I DAI	ALA <mark>C</mark>	VDT	J <mark>R</mark> SD	l <mark>gavq</mark> n	R FNSA	I <mark>TN</mark> L	: 4	123
xy810_FliC :	KAA−GH	NF	AQ	EL	AE <mark>AA</mark> A	TT	TEN	PLQ	KIDA/	ALAC	VDAI	RSD	L <mark>G</mark> AVQN	RFNSA	ITNL	: 4	129
B571 FliC :	KAA-GH	DF	AO	EL	ae <mark>aa</mark> a	TT	TEN	PLO	K I DAZ	ALAC		RSD	l <mark>gavo</mark> n	RENSA	ITNL	: 4	120
B1951 Flic .				FT		АТ	TEN					PSD		PENSA	TTNT	. /	123
DISSI_FIIC .			AQ						KIDA		VDAL						120
B560_F11C :	KAA-GH	NET	AQ	DL	AEAAA		TEN	FLQ	KIDA		VDAL	RSD	LGAVQN	RENSA	TINT	: 4	128
B558_F11C :	KAA-GH	NF.	AQ	DL	AE <mark>AA</mark> A	TT	TEN	PLQ	K I DAA	A LAÇ		RSD	L <mark>GAVQN</mark>	RENSA (T <mark>LN</mark> T	: 4	127
							TN	IPL	ID A	AL	VD 6	SRS	LGA6QN	RF1SA	ITNL		
	460			*		4	180			*		50	0	*	_		
B554_FliC :	G <mark>NTVTN</mark>		ARS	RI	DADY.	ATE	r <mark>vs</mark> i	NMS	AQIL.	QQA	G <mark>TSV</mark> I	L <mark>AQ</mark> A	NQVPQN	IVL <mark>S</mark> LL	R* :	488	3
B2359_FliC :	G <mark>NTVTN</mark>	LNS	ARS	RI	CDADY.	AT I	r <mark>vs</mark> i	NM <mark>S</mark>	AQIL.	QQA	G <mark>TSV</mark> I	L <mark>AQ</mark> A	NQVPQN.	IV <mark>LS</mark> LL	R* :	488	3
B2486_FliC :	G <mark>NTVTN</mark>	L <mark>N</mark> S	ARS	RI	DADY	AT <mark>P</mark>	VSI	NMS I	AQIL	QQA	G <mark>TSV</mark> I	L <mark>aq</mark> a	NQVPQN	IV <mark>LS</mark> LL	R* :	488	3
B2334 FliC :	G <mark>NTVTN</mark>		ARS	RI		АТ	vsi	NMS		OOA	GTSV		NOVPON	IVLSLL	R* :	488	3
P160 Elic .	CNTUNN			DT			VSI	MMS		002	CTSV		NOVPON	UT STT		478	2
DIE22 ELC .															• •	100	2
B1555_F11C :	GNIVNN		ARS	K1			V SI	NMS	AULL	QQA						405	2
B1830_F11C :	G <mark>NTVNN</mark>		ARS	RT	DSDY.	ATE	r <mark>v S</mark> l	NMS	AQ I L	QQA	GTSV.	LAQA	NQVPQN	IV LS L L	K * :	489	9
B1040_FliC :	G <mark>NTVNN</mark>	LTS	A <mark>R</mark> S	RI	DSDY.	AT <mark></mark>	2 <mark>VS</mark> I	NM <mark>S</mark>	AQIL	QQA	G <mark>TSV</mark> I	L <mark>aq</mark> a	N <mark>QVP</mark> QN.	IV <mark>LS</mark> LL	R* :	476	5
B1085_FliC :	G <mark>NTVNN</mark>	LTS	ARS	RI	DSDY	AT	VSI	NMS	AOIL	00A	G <mark>TSV</mark>	LAQA	N <mark>QVP</mark> QN	IV <mark>LS</mark> LL	R* :	476	5
B2075 FliC :	GNTVNN	LTS	ARS	RT		АT	vsi	NMS		AOO	GTSV		NOVPON	VI.SLL	R* •	476	5
B2078 Flic .	CNTVNN	Т	APS	RT			VSI	MMS			CTSV		NOVPON	VISLL		476	5
D2102 E1:C .				DT												170	5
DZIOJ_FIIC :			AND				v SI		AVI L	2QA		AVA				4/6	-
BZZ5/_FliC :	GNIVNN		ARS	RI	USDY.	AL	VS.	NMS	AQIL	QQA	GISV.	LAQA	NQVPQN		K* :	4/6	C
B2396_FliC :	G <mark>NTVNN</mark>		ARS	RI	DSDY.	AT	vs:	NMS	AQIL	QQA	G <mark>TSV</mark>	LAQA	NQVPQN	IVL <mark>S</mark> LL	R* :	476	C
xy82_FliC :	G <mark>NTVNN</mark>	LTS	ARS	RI	DSDY	AT	VSI	NMS	AQIL	QQA	G <mark>TSV</mark>	L <mark>AQ</mark> A	NQVPQN	IVL <mark>S</mark> LL	R* :	476	5
R269_FliC :	GNTVNN	LTS	ARS	RI	DSDY	AT	VS	NMS	AOIL	QOA	GTSV	LAOA	NOVPON	VLS LL	R* :	478	3
xv810 FliC .	GNTVNN		ARS	RT		AT	VS	NMS	AOTT	AOO	GTSV		NOVPON	VLSLL	R* •	484	1
B571 Flic .	GNTUNN		ADO	BT	DSDY	AT	VC	MMS	AOTT		TCV		NOVPON		P * .	475	5
DJ/I_FIIC :				DT												170	2
D1931_F11C :	GNT VNN		ARS		USUI.		v S.	MAN SI	AVIL	2QA		LAQA			1 :	4/8	
R200_L11C :	GNTVNN	L <mark>S</mark> S	ARS	K1	USDY.	AT	V SI	NMS	AQIL	QQA	GISV.	LAQA	NQVPQN		K* :	483	5
					the second se		and the second s	and the second se						TOTT			-
B228_F11C :	G <mark>NTVNN</mark> I	L <mark>S</mark> S	A <mark>R</mark> S	RI	DSDY.	AT I	r <mark>vs</mark> i	NMS	AQIL	QQA	G <mark>TSV</mark>	L <mark>AQ</mark> A		IV LS L L	R* :	482	2

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Fig. S9: amino acid alignment of FliC flagellin sequences of Salmonella isolates used in this study. *fliC* genes of Salmonella isolates were amplified using the primers FSa1 and rFSa1 (Dauga *et al.*, 1998) and Sanger-sequenced using the same primers and additionally primer rFSa1_2 (see Suppl. Tab. 7). Derived amino acid sequences (first 17 amino acids not sequenced) were aligned using ClustalOmega (Sievers *et al.*, 2011) and depicted according to their physico-chemical properties using GeneDoc (Nicholas *et al.*, 1997). Strain numbers of strains listed in Table 1 which are included in this alignment but not in Fig. S10 only possess the *fliC* gene (e.g. B571) and served as experimental controls for the strains' FliC flagellin-specific activation potential.

		*	20	*		40	*	60		*	
B558_FljB :	NLNKSQS	AL <mark>G</mark> TAI <mark>ER</mark> I	. <mark>SS</mark> GL <mark>R</mark> I	N SA<mark>K</mark>DDAAG	QAIAN <mark>R</mark> I	F <mark>TAN</mark> I <mark>K</mark>	GLT <mark>Q</mark> AS <mark>R</mark> NA	ND <mark>GISIAQ</mark>	TT <mark>EG</mark> ALNE	INNNLQRV	: 76
B560 FljB :	NLNKSOS	ALGTAIERI	SSGLRI	NSAKDDAAG	OAIAN <mark>R</mark> I	F <mark>TAN</mark> I <mark>K</mark>	GLTQASENA	NDGISIAO	TT <mark>E</mark> GALNE	INNNLQRV	: 76
xv82 FliB :	-LNKSOS	ALGTA TERT	SSGLET	NSAKDDAAG		F TANIK	GLTOASENA	NDGISIAO	TT <mark>E</mark> GALNE	INNNLORV	: 75
R269 FliB ·		ALGTA TERT	SSGLET	NSAKDDAAG			GLTOASENA	NDGTSTAO	TTEGATNE	TNNNT.OPV	• 75
R160 F1-5B ·				NSAKDDAAC					TTECALNE		. 76
NICO_FIJD .											. 76
NYOIU_FIJD :		ALGIAIDAI		NSANDDAAG							. 70
				NSANDDAAG				NDGISIAO			: 75
BI951_FIJB :		ALGIAIERI	155GLKI	NSANDDAAG			GLIQASENA		I I E GALNE		: /5
B1040_F1jB :		ALGIAIERI	SSGLKI	NSANDDAAG		TANIK	GLIQASENA	NDGISIAO	TTEGALNE	INNNLORV	: /5
BI085_FIJB :		ALGIAIERI	SSGLRI	NSARDDAAG		TANIK	GLIQASRNA	NDGISIAQ	TIEGALNE	INNNLQRV	: /5
B2078_F1jB :	-LN <mark>KSQS</mark>	ALGTAIERI	I <mark>SS</mark> GLRI	N SAKDDAAG	QALANRI	TANIK	GLT <mark>Q</mark> ASRNA	NDGISIAQ	TTEGALNE	T <u>NNNL<mark>O</mark>R</u> V	: 75
B2183_F1jB :	-LN <mark>KSQ</mark> S	ALGTAIERI	. <mark>SS</mark> GLRI	N SAK DDAAG	QAIANRI	FTANIK	GLT <mark>QAS</mark> RNA	NDGISIAQ	TTEGALNE	I NNNL <mark>Q</mark> RV	: 75
B2257_F1jB :	-LN <mark>KSQ</mark> S	ALGTAIERI	. <mark>SS</mark> GLRI	N SAK DDAAG	QAIANRI	F TAN I K	GLT <mark>Q</mark> ASRNA	ND <mark>GISIAQ</mark>	TT <mark>E</mark> GALNE	I NNNLQRV	: 75
B2396_FljB :	-LN <mark>KSQ</mark> S	AL <mark>G</mark> TAIERI	. <mark>SS</mark> GLRI	N SAK DDAA <mark>G</mark>	QAIAN <mark>R</mark> I	F <mark>TAN</mark> I <mark>K</mark>	GLT <mark>Q</mark> AS <mark>R</mark> NA	ND <mark>GISIAQ</mark>	TT <mark>E</mark> GALNE	I NNN L <mark>Q</mark> RV	: 75
B1050_FljB :	-LN <mark>KSQ</mark> S	AL <mark>G</mark> TAIERI	. <mark>SS</mark> GLRI	N SAK DDAA <mark>G</mark>	QAIANRI	F <mark>TAN</mark> I <mark>K</mark>	GLT <mark>Q</mark> AS <mark>R</mark> NA	ND <mark>GISIAQ</mark>	IT <mark>E</mark> GALNE	I NNNL <mark>Q</mark> RV	: 75
xy92_FljB :	-LN <mark>KSQ</mark> S	AL <mark>GTAIER</mark> I	J <mark>SS</mark> GLRI	N SAK DDAAG	QAIANRI	F <mark>TAN</mark> I <mark>K</mark>	GLT <mark>Q</mark> AS <mark>R</mark> NA	ND <mark>GISIAQ</mark>	TT <mark>E</mark> GALNE	INNNL <mark>Q</mark> RV	: 75
2075_FljB :	–LN <mark>KSQ</mark> S	AL <mark>G</mark> TAIERI	J <mark>SS</mark> GL <mark>R</mark> I	NSA <mark>K</mark> DDAA <mark>G</mark>	QAIANRI	F <mark>TAN</mark> I <mark>K</mark>	GLT <mark>Q</mark> AS <mark>R</mark> NA	ND <mark>GISIA</mark> Q	TT <mark>E</mark> GALNE	I NNN L <mark>O</mark> RV	: 75
	LNKSQS	ALGTAIERI	SSGLRI	NSAKDDAAG	QAIANRI	FTANIK	GLTQASRNA	NDGISIAQ	TTEGALNE	INNNLQRV	
	80	*	1	00	*	12	0	*	140	*	
B558_FljB :	RELAVQS	ANSTNSOSI	LDSIQA	EITQRLNEI	D <mark>RVS</mark> GQ	I <mark>Q</mark> FN <mark>G</mark> V	K <mark>VLAQ</mark> DNTL	T I <mark>Q</mark> V <mark>G</mark> AND (GETIDIDL	QINSQTL	: 152
B560_FljB :	RELAVQS	ANSTNSQSI	LDSI <mark>Q</mark> A	EITQRLNEI	D <mark>rvsg</mark> q:	I <mark>Q</mark> FN <mark>G</mark> V	K <mark>VLAQ</mark> DNTL	TI <mark>Q</mark> V <mark>G</mark> AND	GETIDIDL	<mark>QINSQ</mark> TL	: 152
xy82_FljB :	RELAVQS	ANSTNSQSI	LDSI <mark>Q</mark> A	EITQRLNEI	D <mark>RVS</mark> GQ:	I <mark>Q</mark> FN <mark>G</mark> V	K <mark>VLAQ</mark> DNTL	TIQV <mark>G</mark> AND(GETIDIDL	<mark>(</mark> QI <mark>NSQ</mark> TL	: 151
R269_FljB :	RELAVQS	ANSTNSQSI	LDSIQA	EITQRLNEI	DRVSGQ	I <mark>QFNG</mark> V	K <mark>vlaq</mark> dntl	T I <mark>Q</mark> V <mark>G</mark> AND (GETIDIDL	Q INSQTL	: 151
R160_FljB :	RE LAVQS	ANSTNSOSI		EITORLNEI	DRVS <mark>G</mark> Q	I <mark>QFNG</mark> V	K <mark>VLAQ</mark> DNTL	TIQV <mark>GAND</mark> (GETIDIDL	QINSQTL	: 152
xy810_FljB :	RELAVQS	ANSTNSOSI	LDSIQA	EITQRLNEI	D <mark>rvsg</mark> q:	I <mark>QFNG</mark> V	K <mark>VLAQ</mark> DNTL	TIQV <mark>G</mark> AND	GETIDIDL	QINSQTL	: 152
B815_FljB :	RELAVQS	ANSTNSQSI	LDSIQA	EITQRLNEI	D <mark>rvsg</mark> q:	I <mark>QFNG</mark> V	K <mark>VLAQ</mark> DNTL	TIQV <mark>G</mark> AND	GETIDIDL	QINSQTL	: 151
B1951 FljB :	RE LAVOS	ANSTNSOSI		EITORLNEI		I <mark>OFNGV</mark>	KVLAODNTL	TIQVGAND	GETIDIDL	QINSQTL	: 151
B1040 FljB :	RELAVOS	ANSTNSOS		EITORLNEI	DRVSG <mark>O</mark> I	I <mark>OFNG</mark> V	KVLAODNTL	TI <mark>OV</mark> GAND	GETIDIDL	OINSOTL	: 151
B1085_FljB :	RE LAVOS	ANSTNSOSI		EITORLNEI		I <mark>Q</mark> FNGV	KVLAQDNTL	TIQV <mark>GAND</mark> (GETIDIDL	QINSQTL	: 151
B2078 FljB :	RELAVOS	ANSTNSOS		EITORLNEI	DRVSG <mark>O</mark> I	I <mark>OFNG</mark> V	KVLAODNTL	TIOVGAND	GETIDIDL	OINSOTL	: 151
B2183 FliB :	RELAVOS	ANSTNSOS		EITORLNEI		I <mark>OFNG</mark> V	KVLAODNTL	TIOVGAND	GETIDIDL	OINSOTL	: 151
B2257 FliB :	RELAVOS	ANSTNSOS		EITÕRLNEI		I <mark>OFNGV</mark>	KVLAODNTL	TI <mark>OVG</mark> AND	GETIDIDL	OINSOTL	: 151
B2396 F1jB :	RELAVOS	ANSTNSOS		EITORLNEI		I OFNGV	KVLAODNTL	TIOVGAND	FTIDIDL	OINSOTL	: 151
B1050 FliB :	RELAVOS	ANSTNSOS		EITORLNEI		I OFNGV	VLAODNTL	TIOVGAND	FTIDIDL	OINSOT L	: 151
xv92 FliB :	RELAVOS	ANSTNSOS		EITORLNEI		IOFNGV	VLAODNTL	TTOVGAND	FTIDIDL	OINSOTL	: 151
2075 FljB :	RELAVOS	ANSTNSOS		EITORLNEI		I OFNGV	VLAODNTL	TIOVGAND	FTIDIDL	OINSOTL	: 151
20,0_11,0	RELAVOS	ANSTNSOSI	LDSIOA	EITORLNEI	DRVSGO	FOFNGV	KVLAODNTL	TIOVGAND	GETIDIDL	KOINSOTL	
	<u>F</u>	£				2				EE	
	16	0	*	180		*	200	*	220	_	
B558_F1jB :	GL <mark>DS</mark> LNV	QKAYDV <mark>S</mark> AI	IDVI S <mark>S</mark> T	Y <mark>S</mark> DGT <mark>Q</mark> ALT.	APTA	LDIKAY	L GNP TV T GD'	TLTAAVS	SFKDGKYY/	ATVSGYTD	: 224
B560_F1jB :	GLDSLNV	<mark>QKA</mark> YDV <mark>S</mark> AI	IDVIS <mark>S</mark> T	YSDGT <mark>Q</mark> ALT.	APTA	IDIKAA	L GNP TV T GD'	TLTAAVS	SFKDGKYY/	ATV <mark>S</mark> GYTD	: 224
xy82_FljB :	GL <mark>DS</mark> LNV	<mark>Qk</mark> aydv <mark>k</mark> di	IAVT <mark>T</mark> KA	Y <mark>A</mark> DNG <mark>T</mark> TLD.	ASG <mark>L</mark> DD	AAI <mark>K</mark> AA	I G <mark>GTTGTAA`</mark>	V <mark>T</mark> GGTV <mark>K</mark> FI	O <mark>AD</mark> NNKYFV	/TI <mark>G</mark> GFTG	: 227
R269_FljB :	GLDSLNV	<mark>QK</mark> AYDV <mark>K</mark> DI	IAV <mark>T</mark> T <mark>K</mark> A	Y <mark>ANNG</mark> TLD	VSG <mark>L</mark> DDA	AAI <mark>K</mark> AA	I <mark>GGTNGTA</mark> S	V <mark>T</mark> GGAV <mark>K</mark> FI	O <mark>ADNN</mark> KYFV	/TI <mark>G</mark> GFTG	: 227
R160_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	IAV <mark>T</mark> T <mark>K</mark> A	Y <mark>ANNG</mark> TLD	VSG <mark>L</mark> DD2	AAI <mark>K</mark> AA	I <mark>G</mark> GTNGTAS	V <mark>T</mark> GGAV <mark>K</mark> FI	O <mark>ADNNK</mark> YFV	/TI <mark>G</mark> GFTG	: 228
xy810_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	'AV <mark>T</mark> T <mark>K</mark> A	Y <mark>ANNG</mark> TLD	VSG <mark>L</mark> DD1	raikaa	I <mark>G</mark> GTTGT A A`	V <mark>T</mark> GSAV <mark>K</mark> FI	O <mark>ADNNK</mark> YFV	/TI <mark>G</mark> GFTG	: 228
B815_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	[AV <mark>T</mark> T <mark>K</mark> A	Y <mark>ANNG</mark> TLD	VSG <mark>L</mark> DD1	rai <mark>k</mark> aa	I G <mark>GTTGTAA`</mark>	V <mark>T</mark> GSAV <mark>K</mark> FI	O <mark>AD</mark> NN <mark>K</mark> YFV	/TI <mark>G</mark> FTG	: 227
B1951_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	IAV <mark>T</mark> T <mark>K</mark> A	Y <mark>ADNG</mark> TTLD	ASG <mark>L</mark> DD	AAI <mark>K</mark> AA	I G <mark>GTTGTAA`</mark>	V <mark>T</mark> SGTV <mark>K</mark> FI	O <mark>AD</mark> NN <mark>K</mark> YFV	/TI <mark>G</mark> FTG	: 227
B1040_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	Y <mark>A</mark> DNG <mark>T</mark> TLD	VSG <mark>L</mark> TD2	AAI <mark>K</mark> TA	I <mark>GGTTGTAS</mark>	V <mark>T</mark> GGAV <mark>K</mark> FI	O <mark>ADNNK</mark> YFV	/TI <mark>G</mark> FTG	: 227
B1085_FljB :	GLDSLNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	I <mark>GGTTGTA</mark> S	V <mark>T</mark> G G AV <mark>K</mark> FI	O <mark>AD</mark> NN <mark>K</mark> YF	/T <mark>IG</mark> GFTG	: 227
B2078_FljB :	GLD <mark>S</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	Y <mark>ADNG</mark> TTLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	I <mark>G</mark> GTTGTAS	V <mark>T</mark> G G AV <mark>K</mark> FI	O <mark>ADNNK</mark> YF	/T <mark>IG</mark> GFTG	: 227
B2183_FljB :	GLDSLNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	I <mark>GGTTGTAS</mark>	V <mark>T</mark> G G AV <mark>K</mark> FI	<mark>ADNN</mark> KYFV	/TI <mark>G</mark> GFTG	: 227
B2257_F1jB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AVTT <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD2	AAI <mark>K</mark> TA	I <mark>GGTTGTA</mark> S	V <mark>T</mark> GGAV <mark>K</mark> FI	<mark>ADNN</mark> KYFV	/TI <mark>G</mark> GFTG	: 227
B2396_F1jB :	GLDSLNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD2	AAI <mark>K</mark> TA	I <mark>GGTTGTAS</mark>	V <mark>T</mark> G G AV <mark>K</mark> FI	<mark>ADNN</mark> KYFV	/TI <mark>G</mark> GFTG	: 227
B1050_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	I <mark>GGTTGTA</mark> S	V <mark>T</mark> G G AV <mark>K</mark> FI	<mark>ADNN</mark> KYFV	/TI <mark>G</mark> GFTG	: 227
xy92_FljB :	GLDSLNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	IGGTTGTAS	V <mark>T</mark> GGAV <mark>K</mark> FI	D <mark>ADNNK</mark> YFV	/TI <mark>G</mark> GFTG	: 227
2075_FljB :	GL <mark>DS</mark> LNV	<mark>QK</mark> AYDV <mark>K</mark> DI	AV <mark>T</mark> T <mark>T</mark> A	YADNG <mark>T</mark> TLD	VSG <mark>L</mark> TD	AAI <mark>K</mark> TA	I <mark>GGTTGTAS</mark>	V <mark>T</mark> G G AV <mark>K</mark> FI	O <mark>AD</mark> NN <mark>K</mark> YF	/T <mark>IG</mark> GFTG	: 227
	GLDSLNV	QKAYDVkd1	TaVt3 a	YalngttLd	sgl d	aIK A	GgttgTa	vtg aVkfo	dad1nKY5	/T6gG5Tg	

	*	240	*	2	60	1	*	280	*	300		
B558_FljB :	A <mark>G</mark> DTAKN	G <mark>K</mark> Y <mark>E</mark> VTV	DSAT <mark>G</mark> AVSF(SATPT <mark>K</mark> S'	IVI- <mark>G</mark> I	<mark>) TA</mark> V <mark>T</mark> K-	VQV <mark>NA</mark>	P <mark>VAADAAT</mark>	K <mark>KA</mark> LQ <mark>D</mark> G	G <mark>VSSADASA</mark>	ATLV	: 297
B560 FljB :	AGDTAKN	G <mark>k</mark> yevtv	DSAT <mark>G</mark> AVSF	ATPTKS	TVT- <mark>G</mark> I	DTA <mark>VT</mark> K-	VQV <mark>NA</mark>	P <mark>VAADAAT</mark>	K <mark>KA</mark> LQ <mark>D</mark> G	G <mark>VSSADASA</mark>	ATLV	: 297
xv82 FliB :	A-DAAKN	GDY <mark>EVNV</mark>	ATD-GKVTL	TGAT <mark>K</mark> T	TMPAG	ATKTE	OELKDT	P <mark>avvsada</mark>	K <mark>NA</mark> LIAG	g <mark>vdtadana</mark>		: 301
R269 FliB :		GDYEVNV	ATD-GTVTL	AGAT		ATTKTE	OELKDT	P <mark>AVVSADA</mark>	KNALIAG	G <mark>VDATDANG</mark>	AELV	: 301
R160 FljB ·			ATD - GTVTI	ACATKT		TTKTE		PAVVSADA	KNALTAG	GVDATDANG	AFLV	: 302
VV810 F1-B .			ATD - CTVTT	ACATKT				PAVVSADA	KNALTAG	GVDATDANG	AFIN	· 302
DOID FIJD .			ATD = GTVTD	ACAT				PAWS A DA		CVDATDANC		. 301
DOID_FIJD :		GDIE VIV						PAVVSADA		GVDAIDANG		. 201
BI951_FIJB :	A-DAANN				IMPAG			PAVVSADA	NALIAG	GVDIADANA		: 301
BI040_FIJB :	A-DAAKN	GDYEVNV	ATD-GTVIL	AGAIKI	IMPAG		CELT II	PVVAS A DA	NALIAG	GVDIADANA		: 301
BI085_FIjB :	A-DAAKN	GDYE <mark>VNV</mark>	ATD-GTVTL	AGATKT	IMPAG	TTKIE		PVVASADA	K NALIAG	GVDTADANA		: 301
B2078_FljB :	a-daakn	GDY <mark>E</mark> VNV	ATD-GTVTL	AGAT <mark>K</mark> T	TMPAG	/TTKTE	QELTTT	P <mark>VVASADA</mark>	K <mark>N</mark> ALIAG	G <mark>VDTADANA</mark>		: 301
B2183_FljB :	a-daakn	GDY <mark>E</mark> VNV	ATD-GTVTL	AGAT <mark>K</mark> T'	TMPAG	/TTKTE	/QELTTT	P <mark>VVASADA</mark>	K <mark>N</mark> ALIAG	G <mark>VDTADANA</mark>	AT LV	: 301
B2257_FljB :	a-daakn	GDY <mark>E</mark> VNV	ATD-GTVTL	AGAT <mark>K</mark> T'	TMPAG	/TTKTE	/QELTTT	P <mark>VVASADA</mark>	K <mark>NA</mark> LI <mark>A</mark> G	G <mark>VDTADANA</mark>	ATLV.	: 301
B2396_FljB :	⊂ <mark>A−</mark> DAA <mark>K</mark> N	GDY <mark>E</mark> VNV	ATD- <mark>GTVTL</mark>	AGAT <mark>K</mark> T'	T <mark>MPA</mark> G	/TTKTEN	/QELT <mark>TT</mark>	P <mark>VVASADA</mark>	K <mark>NA</mark> LI <mark>A</mark> G	G <mark>VDTADANA</mark>	A <mark>T</mark> LV	: 301
B1050_FljB :	□ <mark>A</mark> −DAAKN	G <mark>D</mark> Y <mark>E</mark> VNV	ATD- <mark>GTVTL</mark> Z	AGAT <mark>K</mark> T'	T <mark>MPA</mark> G	/TTKTEN	/QELT <mark>TT</mark>	P <mark>VVASADA</mark>	K <mark>NA</mark> LI <mark>A</mark> G	G <mark>VDTADANA</mark>	A <mark>T</mark> LV	: 301
xy92_FljB :	∣ <mark>A</mark> − <mark>daak</mark> n	GDY <mark>EVNV</mark>	ATD- <mark>G</mark> TVTL	AGAT <mark>K</mark> T'	T <mark>MPA</mark> G	VTTKTEN	/QELT <mark>TT</mark>	P <mark>VVASADA</mark>	K <mark>NA</mark> LI <mark>A</mark> G	G <mark>VDTADANA</mark>	A <mark>T</mark> LV	: 301
2075_FljB :	∣ <mark>A</mark> − <mark>DAA</mark> KN	G <mark>D</mark> Y <mark>EVNV</mark>	ATD- <mark>G</mark> TVTL	AGAT <mark>K</mark> T'	T <mark>MPA</mark> G	/TTKTEN	/QELT <mark>TT</mark>	P <mark>VVASADA</mark>	K <mark>NA</mark> LI <mark>A</mark> G	G <mark>VDTADANA</mark>	A <mark>T</mark> LV	: 301
	A DaAKN	GdYEVnV	a3d G V31a	agaTK3	T6paG	ttkTev	vqel t	P v sAda	KnALiaG	GVd DAn	A LV	
	*	3	20	*	34	0	*	360)	*	380	
8558 F1-B .												• 373
B560 F14B .			CYALKACDK				ST TAADG	TTCTAN				. 373
500_FIJE .							CVTAADC					· 3/3
XYOZ_FIJD :			GIALNAGUN.				STTAADG			T T V V I I D G		: 311
R269_F1jB :			GYALRAGUN	CIAADID		INAKIII	SYTAADG					: 3//
RIGO_FIJB :	KMSYIDK		GYALKAGDK	CIAADID		IKAKIII	SYTAADG					: 3/8
XY810_FIJB :	KMS YTD K	NGKTIEG	GYALKAGDK:	(YAADYD	EATGA	T KAKTT	SYTAADG	TT KTAAN <mark>(</mark>	2LGGVDGK	TEVVTIDG		: 378
B815_F1jB :	KMSYTDK	NGKTIEG	GYALKAGDK:	(YAADYD	EATGA	l K <mark>a k</mark> tti	SY TAADG	TT <mark>K</mark> TAAN <mark>(</mark>	2LGG <mark>VD</mark> GK	TEVVTIDG	TYNA	: 377
B1951_F1jB :	KMS Y TD K	NGKTIEG	GYALKAGDK:	(Y <mark>AAD</mark> YD	EATGA	I KA KTT	SYTAAD <mark>G</mark>	TT <mark>K</mark> TAAN <mark>(</mark>	2LGG <mark>VD</mark> GK	TEVVTIDG	(TYNA	: 377
B1040_FljB :	K M S Y T D K	NGKTIEG	GYALKAGDK	(Y <mark>AAD</mark> YD	E <mark>AT</mark> GA	I <mark>K</mark> A <mark>K</mark> TT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN <mark>(</mark>	2LGG <mark>VD</mark> G <mark>K</mark>	T <mark>E</mark> VVTIDG	(TYNA	: 377
B1085_FljB :	KMSYTDK	NGKTIEG	GYALKAGDK	(Y <mark>AAD</mark> YD	E <mark>AT</mark> GA	I <mark>K</mark> A KTT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN <mark>(</mark>	2LGG <mark>VD</mark> G <mark>K</mark>	T <mark>E</mark> VVTIDG	TYNA (: 377
B2078_FljB :	K <mark>m</mark> sytd K	NGKTIEG	GYALKAGDK	(Y <mark>aadyd</mark>	E <mark>AT</mark> GA	I <mark>K</mark> A <mark>K</mark> TT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN <mark>(</mark>	LGG <mark>VD</mark> G	TEVVTIDG	TYNA	: 377
B2183_FljB :	KMSYTDK	N <mark>GK</mark> TIEG	GYALKAGDK	(Y <mark>aad</mark> yd	E <mark>AT</mark> GA	I <mark>K</mark> A <mark>K</mark> TT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN <mark>(</mark>	LGG <mark>VD</mark> G	TEVVTIDG	(TYNA	: 377
B2257_FljB :	K <mark>ms</mark> ytdk	NGKTIEG	GYALKAGDK Y	YY <mark>AADYD</mark>	E <mark>AT</mark> GA	I <mark>K</mark> A <mark>K</mark> TT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN	LGG <mark>VD</mark> G	TEVVTIDG	TYNA	: 377
B2396_FljB :	K <mark>m</mark> sytdk	NGKTIEG	GYALKAGDK	(Y <mark>AAD</mark> YD	E <mark>AT</mark> GA	I <mark>K</mark> A <mark>K</mark> TT:	SY <mark>TAAD</mark> G	TT <mark>K</mark> TAAN <mark>(</mark>	LGG <mark>VD</mark> G	TEVVTIDG	TYNA	: 377
B1050_FljB :	KMS YTDK	NGKTIEG	GYALKAGDK	(Y <mark>AAD</mark> YD	E <mark>AT</mark> GA	I <mark>K</mark> a ktt:	SY <mark>TAAD</mark> G	TT <mark>KTAAN</mark>	LGG <mark>VD</mark> G	TEVVTIDG	TYNA	: 377
xy92 FljB :	KMS Y TD K	NGKTIEG	GYALKAGDK	YY <mark>AAD</mark> YD	EATGA	I <mark>K</mark> A <mark>K</mark> TT	SYTAAD <mark>G</mark>	TTKTAAN		TEVVTIDG	TYNA	: 377
2075 FliB :	KMS YTDK	NGKTIEG	GYALKAGDK	(Y <mark>AAD</mark> YD	EATGA	I <mark>K</mark> A K TT	SYTAADG	TTKTAAN		TEVVTIDG	TYNA	: 377
	KMsYTDK	NGKTIEG	GYALKAGDK'	YAADYD	EATGA	ΤΚΑΚΤΤ	SYTAADG	TTKTAANC	LGGVDGK	TEVVTIDGE	TYNA	• • • •
	101011011		o mbranop na		2112 011		0		,2001201			
		*	400	*		420		*	440	*		
B558_FljB :	SKAAGE D	FK <mark>AQPE</mark> L	ALAAAKTTEN	IP LQ <mark>K I D</mark>	AALAQ	/DALRSI	DE <mark>GAVQ</mark> N	RE'NSAITN	L <mark>GNTVNN</mark> .	LSEARSRIE	DSDY	: 449
B560_F1jB :	SKAAGHD	FKAQPEL	AEAAAKTTE1	IPLQKID/	AALAQ	/DALRSI	DL <mark>GAVQ</mark> N	RFNSAITN	LG <mark>NTVNN</mark>	LSE <mark>ARSRIE</mark>	DSDY	: 449
xy82_FljB :	S <mark>KAAGH</mark> D	F <mark>KAQ</mark> P <mark>E</mark> L	AFAAAKTTE1	IPLQ <mark>K</mark> IDZ	AAL <mark>AQ</mark> V	/DALRSI	DL <mark>GAVQ</mark> N	RF'NSAITN	l G <mark>NTVNN</mark>	LS <mark>EARSRÍE</mark>	DSDY	: 453
R269_FljB :	S <mark>K</mark> AAGED	F <mark>KAQ</mark> PEL	A <mark>eaaak</mark> tt <mark>e</mark> i	IPL <mark>QK</mark> IDZ	AALA <mark>Q</mark> V	/DA <mark>LR</mark> SI) L <mark>GAVQ</mark> N	RFNSAITN	L <mark>G</mark> NTVNN	L <mark>SE</mark> ARS <mark>RIE</mark>	DSDY	: 453
R160_FljB :	S <mark>KAAGH</mark> D	F <mark>KAQ</mark> P <mark>E</mark> L	AEAAAKTTE1	IPLQ <mark>K</mark> ID2	AALAQ	/DAL <mark>R</mark> SI	DL <mark>GAVQ</mark> N	RFNSAITN	L <mark>GNTVNN</mark>	LS <mark>EARS</mark> RIE	DSDY	: 454
xy810_FljB :	S <mark>K</mark> AA <mark>GH</mark> D	F <mark>KAQ</mark> P <mark>E</mark> L	A <mark>E</mark> AAA <mark>K</mark> TT <mark>E</mark> N	IPLQKID/	AALAQ	/DAL <mark>R</mark> SI	DL <mark>GAVQ</mark> N	RF <mark>NSAI</mark> TN	L <mark>G</mark> NTVNN	LS <mark>EARSRIE</mark>	DSDY	: 454
B815_FljB :	S <mark>K</mark> AA <mark>GH</mark> D	F <mark>KAQ</mark> P <mark>E</mark> L	A <mark>E</mark> AAA <mark>K</mark> TT <mark>E</mark> N	IPLQ <mark>K</mark> IDZ	AALAQ	/DAL <mark>R</mark> SI	DL <mark>GAVQ</mark> N	RF <mark>NSA</mark> ITN	L <mark>G</mark> NTVNN	LS <mark>EARSRIE</mark>	DSDY	: 453
B1951_FljB :	S <mark>KAAGH</mark> D	F <mark>KAQ</mark> PEL	A <mark>F</mark> AAA <mark>K</mark> TT <mark>E</mark> N	IPLQ <mark>K</mark> ID2	AALAQ	/DAL <mark>R</mark> SI	DL <mark>GAVQ</mark> N	RENSAITN	L <mark>G</mark> NTVNN	LS <mark>EARSRIE</mark>	DSDY	: 453
B1040_FljB :	S <mark>K</mark> AA <mark>GH</mark> D	F <mark>KAQPE</mark> L	AEAAA <mark>K</mark> TTEN	I <mark>PLQK</mark> ID2	AALAO	/DAL <mark>R</mark> SI	L <mark>GAVO</mark> N	RFNSAITN	L <mark>GNTVNN</mark>	L <mark>SE</mark> ARSRIE	DSDY	: 453
B1085_FljB :	SKAAGHD	F <mark>KAOPE</mark> L	AEAAAKTTEN		AALAO	/DAL <mark>R</mark> SI	L <mark>GAVO</mark> N	RF <mark>NSA</mark> ITN	l <mark>gntvnn</mark>	LS <mark>EARS</mark> RIE	DSDY	: 453
B2078_F1jB :	SKAAGHD	FKAOPEL	A <mark>E</mark> AAA <mark>K</mark> TTEN	PLOKID/	AALAO	/DALRSI	L <mark>GAVO</mark> N	RENSAITN	L <mark>GNTVNN</mark>	L <mark>SEARSRIE</mark>	DSDY	: 453
B2183 FliB :	SKAAGHD	FKAOPEL	AEAAAKTTEN	PLOKID	AALAO	/DALRSI	LGAVON	RENSAITN	L <mark>GNTVNN</mark>	LS <mark>E</mark> ARSRIE	DSDY	: 453
B2257 FliB	SKAAGHD	FKAOPEL			AALAO		LGAVON	RENSATTN	L <mark>GNTVNN</mark>	LSEARSETE		: 453
B2396 FliB :	SKAAGHD	FKAOPEL			AALAO		LGAVON	RENSAITN	L <mark>GNTVNN</mark>	LSEARSRIE	DSDY	: 453
B1050 FliB .	SKAACHD	FKAOPFL	AFAAAKTTEN		AALAO		DI GAVON	RENSATTN	L <mark>GNTVNN</mark>		DSDY	: 453
xv92 FliB	SKAAGHD	FKAOPEL			AALAO			RENSATTN	I G <mark>NTVNN</mark>	LSEAPSPIE		: 453
2075 51-50							TCAVON	FNSATTN				• 453
	SKAAGE		ANAAAA									



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Fig. S10: amino acid alignment of FIJB flagellin sequences of *Salmonella* isolates used in this study. *fljB* genes of *Salmonella* isolates were amplified using the primers FSa2 and rFSa2 (Dauga *et al.*, 1998) and Sanger-sequenced using the same primers and additionally primer rFSa1_3 (see Suppl. Tab 7). Derived amino acid sequences (first 16 or 17 amino acids not sequenced) were aligned with ClustalOmega (Sievers *et al.*, 2011) and depicted according to their physico-chemical properties using GeneDoc (Nicholas *et al.*, 1997). Strain numbers of strains listed in Table 1 which are included in this alignment but not in Fig. S9 only possess the *flgJ* gene (e.g. B815) and served as controls for the strains' FlgJ flagellin-specific activation potential.

chTLR5	mmlhqrliivfg-ialagdicasrscysevqvsmynscnltgvppvpk	47
mTLR5	mdaefphaphfsrimacqldlligvifmaspvlvispcssdgriaffrgcnltqipwiln	60
hTLR5	mgdhldlllgvvlmagpvfgipscsfdgriafyrfcnltqvpqvln	46
bTLR5	fdgwraiylscnltqvpqvpn	46
pTLR5	fdqqraiyrgcnltqvpqvps	45
	· * · · · · · · · · · · · · · · · · · ·	
chTLR5	d-taklfltvnvirgytatsfplledlflleigtgryfplvigkeafrnlpplryldlgf	106
TIDE	tttarlllefnuismuratefnllarlellelefour-anltiongafunlmilvidige	110
hTIDE	- toull of an interest of a lala lala and in the fundamental distances and the second	104
hilks	t-terilisinyirtvtassipiledidileidsdy-tpitiakeairniphirildids	104
DILKS	t-tkslllsinyirtvttasipileqiqileigtqi-tpitiyreairnipnirildigg	104
pirk?	g-txsilisinyirtvtagspilegigileigtgi-tpisiarearrnipnirilaign	103
chTLR5	nnillldldsfaglgrltilrlfgnnlgdsileervfgdlrsleeldlsgngitklhphp	166
mTLP5	saievlnrdafaalphllelrlfscalssavlsdavfrnlvslarldlsanaihslrlhs	179
hTLD5	skivflbndafaalfblfalrlvfaaledavlkdavfrnlkaltrldleknairelvlbn	164
hTLD5	sainflbndafaalnbltklrlfscalsdaulkdaufrnlasltbldlsknkiaslulbn	164
TIDE	sqiniinpaalqqiphickiiiiseqisdavikaqyiiniasionidisknkiqsiyinp	162
PILKS	sqlalinpdalqelphisellisogisdalikdqylinlasicildisknqlqsininp	103
chTLR5	lfvnltilkavnlkfnkisnlcegnltsfogkhfsffslstntlvktdkmiwakconpfr	226
mTLP5	efreineledunfefnaiftigedelenlaaktieffalkitkiferueuauetornnfr	239
hTLD5	efaklnelkeidfeenaifluaahalanlaaktleffelsenelverveuduakamnnfr	224
hTIDE	siyainsiasidisingiiivcenelepiqqabisiisiaansiysivsvawqacampii sfyalaslasidisfakiniyosoofbolooktlsflsladaqlysyysydymkalaafy	224
DILKS	sireinsiksidisinkipivcederkpidgktisiisiadndiysrvsvdwnkcinpir	224
pTLR5	sigeinsikaldisingipivceqgikpiqgktisiisiadnniysrvsvdwgkcmnpir * :*. *. ::: *:* : :*** : :*** : *: . *:: * .* ****	223
		200
CHILKS	nitinslavsengwstetvqyictaikgtqinyisirsntmgsgiginniknpatatitg	286
mTLR5	gvrletldlsengwtvditrnfsniiggsgisslilkhhimgpgfgfgnirdpdgstfas	299
hTLR5	nmvleildvsgngwtvditgnfsnaisksgafslilahhimgagfgfhnikdpdgntfag	284
bTLR5	nmvletldvsgngwgvdimrnfsnaingsqifslvltrhimgssfgfsnlkdpdyhtfag	284
pTLR5	nmalemldvsgngwtadttrnfsqavngsqisslvlahhimgsgfgfhnikdpdhhtfas	283
chTLR5	larsdlhlldisngfifslnslifeslrnleflnlfrnkingigkgaffglenleilnls	346
mTLR5	larssvloldlshqfifslnprlfqtlkdlkmlnlafnkinkigenafygldslovlnls	359
hTLR5	larssyrhldlshofvfslnsryfetlkdlkvlnlavnkinkiadeafvoldnlovlnls	344
bTLR5	larssmigldishgvifslnfrifetlgelkvlnlavnkinsisrnafvgldnlgvlnis	344
DTLPS	larssligldlshafifslnfrlfatlkelkulnlefnkinkiedaefhaldnlailnms	343
212100	*.**.: **:*:*:**** :* :*::*:*** ****.* :***	010
chTLR5	snllgelvdvtfeglhsimvidlggnhigmigeksfsnlvnlkiidlrdnaikklosfoh	406
mTLP5	wnllgelwnsnfwglnrweywdlgrnhigiigdatfrllktlatldlrdnelkeigfins	419
hTLD5	unligely confuging wave dig whist is is dot fkflakigtidirdnaittib fine	404
hTIDE	ynigelyssniggipavayidigamiaiigdgolaileaigdidianaicoinips ymllgelyssnigdighavayidigamiaiigdietfkflgklatidigdaalktiyflaa	404
TIDE	yniigelynydiagipkvayidigknnigiigdktikiigkintidiidnaiktiyiips	404
PILKS	<pre>yniigelynsniegipklayldidknnigiidadtirikkintidiranalktidrips *******. * ** : *:***:***.:* *.*: :******:: :*</pre>	403
ChTLRS	ltsaflsdnklmsvahtaivathielernwlanlddlwulfonnowoulllkomrfsvou	466
mTLR5	igmvllggnklvhlphihftanflelsenrlenlsdlvfllrvpglaflilngnrlesck	479
bTLD5	indiflegnklutlnkinltanlihleanrlanldilufllrumhlgililngnrfesse	464
hTI DE	ipailisynalvoipainioaniiniseniieniailyiiiivphigiliingniissos	164
DILRS	iphilisgnkimciphipicaniigisenrienindiyiiigvphigiliindnrisich	404
p1LK5	: :****: : : :.*. *** **. **.**.**	403
chTLR5	khydaiennglivmdlgenmlglwergloldyfrtlsklgylhlnnnylselngeifng	526
mTLP5	ashtnsennsled fitenmid avetal cydufad sylai lylenny nfirmai fod	520
ATIDE	adata complexificential avetal avetal control and the structure and the second structure and the	524
hTLRS	gadupsenpsiediligenmidiaweteicwaviedishidvlyinnnyinsippgvish	524
DILKS	duu absenssiekiiigen midiawetgscwaiikgishidiiyin knyiniippgvinn	524
p1LK5	drnapsenpsiedirigenmidiaweadrcwdvrxdisnidviyinnnyinrippdvrn	523
chTLR5	lts]krlnlasnllshls]rufnælin]nlsanalfenknkufmtlsildithnkurd	586
mTLP5	lvalrmlslsankltulspaslpanlaildiernalfendnalfeelvuldithnafuan	500
hTLD5	ltslralelnenritulehndlmanlaildiernallammadufueleuldithebfiaa	504
hTI DE	lealealalkander: fordloanlaildi amallandrid faalaaidi taafi	504
DILK5	italigisikanfitviipgaipanieilaisgngiispapaifasisaidithnnfice	504
DITK2	*.:*: *.* * *: * :* * *::* ***::*.* :* :* :* :* :*:*	583
chTLR5	calksllvwlnetnytlagsesdrycympalagypysfltyddodedelggtlrfsyfy	646
mTLP5	celstfiswlngtnytlfgspadyygmunsllggslunistedodeeemrslkfslfi	650
hTLP5	celetfinwlnhtnutiagnnadi ugumdefeguelfeletegodaaaulkelkfelfi	644
bTLP5	calcafibulnatnitiagenadmucromonelagueiueletassaaaaulaslbfalfi	644
DTLDE	celsalimingunitiagspadnycmyphistagvitysistesteeeeviesikisiii	640
PILKS	<pre>cersorramingonvorrgsrddrycmypssrdysprnovsmagdseeeviesikisiii * * * *** ***** * * ***** * * *** </pre>	043

chTLR5 mTLR5 hTLR5 bTLR5 pTLR5	<pre>flsvtllmflmstiiftrcrgicfvwyktitktligshppaadtseymydaylcyskndf lctvtltlflvitlvvikfrgicflcyktiqklvfkdkvwslepgayrydayfcfsskdf vctvtltlflmtiltvtkfrgfcficyktaqrlvfkdhpqgtepdmykydaylcfsskdf lvtvtltlflvitlavtkfrgfcficykkaqsllfkdpikgresdtykydaylcfsskdf lftvtltllfvailvvmkfrgfcficykkvqrlvfkdpslgresdtykydaylcfsgkdf . :*** :::: : . : **:**: **. :: : * ****:*:*</pre>	706 719 704 704 703
chTLR5 mTLR5 hTLR5 bTLR5 pTLR5	<pre>ewvqnsllkhldsqyfdknrftlcfeerdflpgeehinnirdaiwksrkticvvtrqflk ewaqnallkhldahyssrnrlrlcfeerdfipgenhisniqaavwgsrktvclvsrhflr twvqnallkhldtqysdqnrfnlcfeerdfvpgenrianiqdaiwnsrkivclvsrhflr ewvqnall-hldvqyhsqnrfnlcfeerdfmpgenhianiqdavwssrkivclvsrhflr ewvqeallknldaqysdqnrlnlcfeerdfvpgedrisniqdavwssrkvvclvsrhflr *.*::** :** :* ::*:**:*****************</pre>	766 779 764 763 763
chTLR5 mTLR5 hTLR5 bTLR5 pTLR5	dgwcveafnfaqsryfsdlkevlimvvvgslsqyqlmkhkpiriflqrsrylrwpedyqd dgwcleafryaqsrslsdlksilivvvvgslsqyqlmrhetirgflqkqqylrwpedlqd dgwcleafsyaqgrclsdlnsalimvvvgslsqyqlmkhqsirgfvqkqqylrwpedfqd dgwcleafsyaqsrcladlngalimvvvgslsqfhlmrhqsirgfvqkrqylrwpedlqd dgwcleafsyaqsrcladlngtlimvvvgslpqyqlmkhqsirgfvrkqqylrwpedlqd ****:*** :**.* ::**: **:***** *::*:**	826 839 824 823 823
chTLR5 mTLR5 hTLR5 bTLR5 pTLR5	igwfldnlssqilkekkvqrnvsgielqtiatvsh 861 vgwfldklsgcilkeekakkrsssiqlrtiatis- 873 vgwflhklsqqilkkekekkdnniplqtvatis- 858 vdwflnklsqcilkkekerkkdsaiqlqnvttis- 857 vswflnklsqyilkkvkekkdsdiqlqsv-tis- 856 :.***.:** ***: * :: * *:.::	

Faber et al., Figure S11

Fig. S11: amino acid alignment of all full-length TLR5 proteins expressed from pEF6-V5 constructs and used for activation in this study. chTLR5 = *Gallus gallus* TLR5; m = *Mus musculus* TLR5; hTLR5 = *Homo sapiens* TLR5; bTLR5 = *Bos taurus* TLR5; pTLR5 = *Sus scrofa* TLR5. Symbols below the alignment designate the level of amino acid (aa) identity or conservation at each site: asterisk = identical aa; two dots = highly conserved aa; one dot = moderately conserved aa. Nucleotide sequences of each cloned insert were determined by Sanger sequencing and translated into amino acid sequences. The alignment was prepared using ClustalOmega (Sievers *et al.*, 2011).

Supplementary Tables

Bacterial isolate	lso desig	olate gnation	Isolated from	Host species
Campylobacter jejuni (ST-50)	68		Human feces	Humans, poultry, swine, cattle,
Campylobacter ieiuni (ST-45)	60		Human faces	sneep, cais, dogs
Campylobacter jejuni (ST-50)	09		Human leces	S. a.
Campylobacter jejuni (ST-21)	70		Human fees	S. a.
Campylobacter jejuni (ST-50)	71		Human leces	S. a.
Campylobacter jejuni (ST-30)	72		Human feces	s. a.
Campylobacter jejuni (ST-21)	73		Human feces	s. a.
Campylobacter jejuni (ST 21)	75		Human leces	s. a.
Campylobacter jejuni (ST-21)	87		Human feces	s. a.
Campylobacter jejuni (ST-21)	89		Human feces	s. a.
Campylobacter jejuni (31-21)	90 NoTo		Human feces	s. a.
Campylobacter jejuni ATCC 700019	NCIC	11168	Human feces	s. a.
Campylobacter jejuni (ST-21)	FBI 04	321 ^A	Aviary bird	s. a.
Campylobacter jejuni (ST-21)	FBI 04	371 ^A	Sheep	s. a.
Campylobacter jejuni (ST-21)	1		Broiler	s. a.
Campylobacter jejuni (ST-21)	FBI 04	197 ^A	Cattle feces	s. a.
Campylobacter jejuni (ST-21)	FBI 02	2626 ^A	Broiler	s. a.
Campylobacter jejuni (S1-21)	FBI 04	199 ^A	Cattle feces	s. a.
Salmonella enterica serovar Bovismorbificans	ху	82	n. s.	Cattle, horses
Salmonella enterica serovar Choleraesuis	В	815	Human blood	Swine
Salmonella enterica serovar Choleraesuis	xy	810	n. s.	s. a.
Salmonella enterica serovar Typhimurium	RV	269	n. s.	Humans, cattle, swine, sheep, horses, rodents, poultry
Salmonella enterica serovar Enteritidis	В	554	Human feces	Humans, rodents, poultry, horses
Salmonella enterica serovar Enteritidis	В	558	Human feces	s. a.
Salmonella enterica serovar Enteritidis	В	560	Human feces	s. a.
Salmonella enterica serovar Enteritidis	В	571	Human feces	s. a.
Salmonella enterica serovar Enteritidis	В	2334	Human blood	s. a.
Salmonella enterica serovar Enteritidis	В	2359	Human feces	s. a.
Salmonella enterica serovar Enteritidis	В	2486	Human feces	s. a.
Salmonella enterica serovar Infantis	В	1040	Human urine	Humans, poultry
Salmonella enterica serovar Infantis	В	1050	Human feces	s. a.
Salmonella enterica serovar Infantis	В	1085	Human feces	s. a.
Salmonella enterica serovar Infantis	В	2075	Human feces	s. a.
Salmonella enterica serovar Infantis	В	2078	Human feces	s. a.
Salmonella enterica serovar Infantis	В	2183	n. s.	s. a.
Salmonella enterica serovar Infantis	В	2257	n. s.	s. a.
Salmonella enterica serovar Infantis	В	2396	Human feces	s. a.
Salmonella enterica serovar Infantis	xy	92	n. s.	s. a.
Salmonella enterica serovar Paratyphi A	В́	1951	Human blood	Humans
Salmonella enterica serovar Paratyphi B	RV	160	n. s.	Humans

 Table S1: Campylobacter jejuni or Salmonella enterica isolates used in this study.

Salmonella enterica serovar Typhi	В	1533	Human feces	Humans
Salmonella enterica serovar Typhi	В	1830	Human blood	s. a.

ST: sequence type

n. s.: not specified

s. a.: see above

^A: *C. jejuni* isolates published in (Gripp *et al.*, 2011)

Plasmid	Vector	Description	Resistance	Reference or Source
	pEF6-V5	mammalian protein expression vector, originated from pEF6-TLR5-V5 by excision of the insert and removal of His-tag, EF-1α promoter, V5-tag	Amp ^R	(Lee <i>et al</i> ., 2003)
pEF6- hTLR5	pEF6-V5	protein expression plasmid for human TLR5; removal of His-tag	Amp ^R	(Smith, Jr. <i>et al.</i> , 2003; Lee <i>et al.</i> , 2003)
pCJ800	pEF6-V5	protein expression plasmid for mouse TLR5 (pEF6-mTLR5-V5)	Amp ^R	This study
pCJ801	pEF6-V5	protein expression plasmid for chicken TLR5 (pEF6-chTLR5-V5)	Amp ^R	This study
pCJ1413	pEF6	Protein expression plasmid for chTLR5 without V5	Amp ^R	This study
pCJ1414	pEF6-V5	protein expression plasmid for pig TLR5 (pEF6-piTLR5-V5)	Amp ^R	This study
pCJ1406	pEF6-V5	protein expression plasmid for bovine TLR5 (pEF6-boTLR5-V5)	Amp ^R	This study
pCJ1045	pEF6-V5	protein expression plasmid for chimeric mouse/human TLR5 (pEF6- m/hTLR5-V5)	Amp ^R	This study
pCJ1040	pEF6-V5	protein expression plasmid for chimeric chicken/human TLR5 (pEF6- ch/hTLR5-V5)	Amp ^R	This study
pCJ1044	pEF6-V5	protein expression plasmid for chimeric pig/human TLR5 (pEF6- pi/hTLR5-V5)	Amp ^R	This study
pCJ1407	pEF6-V5	protein expression plasmid for chimeric bovine/human TLR5 (pEF6- bo/hTLR5-V5)	Amp ^R	This study
	pET28a	Protein expression vector, T7 <i>lac</i> promoter, 6xHis tag, T7 tag	Km ^R	Novagen
pCJ375	pET28a	<i>S. enterica</i> serovar Typhimurium LT2 <i>fliC</i> cloned into pET28a via BamHI and Xhol	Km ^R	S. K. Lee and C. Josenhans, unpublished

 Table S2: Plasmids used in this study.

 Amp^R : ampicillin resistance, Km^R : kanamycin resistance

Gene	Primers	Sequence (5'-3') ^a	T _m (°C)	Reference
SalTy LT2 fliC	SalLT2FliCBamHI(F)	CG <u>GGATCC</u> ATGGCACAAGTCAT TAATAC	49	S. K. Lee and C. Josenhans, unpublished
	SalT2FliCEcoRI(R)	CG <u>GAATTC</u> CGCAGTAAAGAGAG GACG	51	S. K. Lee and C. Josenhans, unpublished
chTLR5	chTLR5_F1	AAA <u>GGTACC</u> GAGTCCGGATCCA TGATGTTACA ATCAACGGCTAATAATTG	65	This study
	chTLR5_R1	AAAA <u>GCGGCCGC</u> CGTGTGAGA CTGTCGCTATA GTTTG	69	This study
	chTLR5_R2	A <u>GAACTT</u> AAGTGTCTGCTGGAG	55	This study
mTLR5	mTLR5_F2	AAAA <u>GGTACC</u> GCCGCCACCATG GCATGTCAACTTGACTTG	65	This study
	mTLR5_R2	AAAA <u>GGTACC</u> GCCGCCACCATG GCATGTCAACTTGACTTG	51	This study
	mTLR5_R4	GGAAAAC <u>TTAAAGAGACC</u> CATG GCTTC	57	This study
piTLR5	piTLR5_F1	AAAA <u>GGTACC</u> GAGTCCGGATCC ATGGGAGACTGCCTGGTCCTG	59	This study
	piTLR5_F2	A <u>CCAAGTACATGGG</u> AGTCCGGA TCCATGGGAGACTGCCTGGTC	53	This study
	piTLR5_R1	AAAA <u>GCGGCCGC</u> CGGAGATGG TCACGCTTTGCAAC	67	This study
	piTLR5_R2	AAAA <u>CTTAAG</u> GGACTCTAAGAC	55	This study
boTLR5	boTLR5_BstXI_F	AAA <u>CCAAGTACATGG</u> GCCGCCA CCATGGGAGACTGCCTTGA	51	This study
	boTLR5_NotI_R2	AAA <u>GCGGCCGC</u> CGGAGATGGT GGTTACATTTT	51	This study
	boTLR5_Bsal_R	GGAAAAC <u>TTAAAGAGACC</u> TAAA ACTTC	51	This study
hMyD88	hMyD88_F1	TAAGAAGGACCAGCAGAGCC	59	S. K. Lee and C. Josenhans, unpublished
	hMyD88_R1	CATGTAGTCCAGCAACAGCC	59	S. K. Lee and C. Josenhans, unpublished

 Table S3: Oligonucleotides used for gene amplification and cloning.

arestriction sites in oligonucleotides are underlined; T_{m} : annealing temperature.

Gene	Primers	Sequence (5'-3') ^a	T _m (°C)	Reference
	pEF6_R2	ACAGATGGCTGGCAACTAGAAG	61	C. Josenhans, unpublished
hTLR5	hTLR5_2025_ R	CTGGGCTGTCTTATAACAG	56	This study
chTLR5	chTLR5_F1	AAAGGTACCGAGTCCGGATCCATG ATGTTACATCAACGGCTAATAATTG	65	This study
	chTLR5_R2	AGAACTTAAGTGTCTGCTGGAG	55	This study
piTLR5	piTLR5_F1	AAAAGGTACCGAGTCCGGATCCAT GGGAGACTGCCTGGTCCTG	59	This study
	piTLR5_R2	AAAACTTAAGGGACTCTAAGAC	55	This study
boTLR5	boTLR5_738_ F	AGCAATGCCATCAATGGGAG	55	This study
	boTLR5_1438 _F	TTGGAGAAAATATGTTGCAGC	53	This study
	pUNO1_hEF1 -HTLV_F	TCCCTTGGAGCCTACCTA	51	This study
	pUNO1_SV40 _R	ATTGCAGCTTATAATGGTTAC	51	This study
Sal_fliC	FSa1	CAAGTCATTAATACMAACAGCC	55	(Dauga <i>et al.</i> , 1998)
	rFSa1	TTAACGCAGTAAAGAGAGGAC	55	(Dauga <i>et al.</i> , 1998)
	rFSa1_2	CGTAGCCGTATCGAAGAT	49	This study
Sal_fljB	rFSa2	CAAGTAATCAACACTAACAGTC	58	(Dauga <i>et al.</i> , 1998)
	rFSa2	TTAACGTAACAGAGACAGCAC	58	(Dauga <i>et al.</i> , 1998)
	rFSa1_3	CAACCTGTCTGAAGCGCGTAG	61	This study

 Table S4: Oligonucleotides used for sequencing.

Gene	Primers	Sequence (5'-3') ^a	T _m (°C)	Reference
Insertion of stop codon upstream of V5 tag	pEF6_noV5_F	CCGCTCGAGTCTATAGGGCCCGC GGTTCG	>81	This study
U U	pEF6_noV5_R	CGAACCGCGGGCCCTATAGACTC GAGCGG	>81	This study
Change N to A in chTLR5 (aa 744)	chTLR5_Ala_F	GCCTGGGGAAGAACATATCGCCA ATATTCGTGATGCTATTTGG	>81	This study
	chTLR5_Ala_R	CCAAATAGCATCACGAATATTGGC GATATGTTCTTCCCCAGGC	>81	This study

 Table S5: Oligonucleotides used for site-directed mutagenesis.

aa: amino acid

Antibody ^a	Application	Description/Dilution	Source
α-V5	WB, IF	Mouse, monoclonal/	Invitrogen, R960-25
		1:5,000 (WB), 1:500 (IF)	
$lpha$ -actin a	WB	Mouse, monoclonal/1:30,000	Chemicon, MAB1501
α-GAPDH ª	WB	Rabbit, monoclonal/1:1,000	Cell Signaling, 14C10
a p20 a		Rabbit palvalanal/1:1.000	Coll Signaling 0212
a-p36 °	VVD		Cell Signaling, 9212
α-Ρ-p38 ª	WB	Rabbit, polyclonal/1:1,000	Cell Signaling, 9211
(Thr180/Tyr182)			
α-IRAK-I ª	WB	Rabbit, polyclonal/1:500	Cell Signaling, 4359
		Pabbit 1:1 000	Abcom $ab16534$
	VVD		Abcalli, ab 10554
α -MyD88 ^a	WB	Rabbit, polyclonal/1:1,000	Abcam, ab2068
a E co <i>li</i> flogollin		Mausa managlang//1:500	Hälzel Diegneetike, 15D9
a- <i>E. con</i> nagemin	VVD	Mouse, monocional/1.500	Holzel Diagnostika, 15Do
Goat α-rabbit IgG	WB	Peroxidase-conjugated,	Dianova/Jackson
(H+L)		AffiniPure/1:10,000	
Goat α-mouse IgG	WB	Peroxidase-conjugated,	Dianova/Jackson
(H+L)		AffiniPure F(ab')₂/1:10,000	
Goat α -mouse	IF	1:5,000	Molecular Probes/
Alexa Fluor [™] 488			ThermoScientific

Table S6: Antibodies used in this study.

^a detected species: human

WB: Western Blot

IF: Immunofluorescence

Gene	Primers	Sequence (5'-3') ^a	T _m (°C)	Reference ^a
chGAPDH	chGAPDH_F2	AGGGTGGTGCTAAGCGTGTT	59	(Faber <i>et al.</i> ,
				2016)
	chGAPDH_R2	AAGGGTGCCAGGCAGTTG	59	(Faber <i>et al.</i> ,
				2016)
chIL-CXCLi2	chIL-8_F1	CTGGCCCTCCTCCTGGTTTC	59	(Faber <i>et al</i> .,
(chIL-8)				2016)
	chIL-8_R1	TGGCGTCAGCTTCACATCTTG	59	(Faber <i>et al.</i> ,
				2016)
chIL-1β	chIL-1_F1	CTGAGTCATGCATCGTTTATGTTT	59	(Faber <i>et al</i> .,
		С		2016)
	chIL-1_R1	AAATACCTCCACCCCGACAAG	59	(Faber <i>et al.</i> ,
				2016)

 Table S7: Oligonucleotides used for RT-PCR of chicken (Gallus gallus) genes.

^a primers were designed and generously provided by Bernd Kaspers (LMU Munich)

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