Supplementary Material for "The RIG-I like Receptor LGP2 recognizes the Termini of Double-

stranded RNA"

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		551	561	571	581	591	L 601
LGP2	542	NQRQQFPVEHV	QL <mark>LCINCMV</mark> A	AVGHGS <mark>D</mark> LRKV	/ <mark>E</mark> GT <mark>H</mark> HVNVN	PNFSNYYNVS	SRDPVVIN <mark>K</mark> VF
RIG-I	796	KPKPVPDKENK	KLLCRKCKAI	L <mark>A</mark> CYTA <mark>D</mark> VRV	[<mark>E</mark> EC <mark>H</mark> YTVLG	DA <mark>FKECF</mark> V	/SRPHPKP <mark>K</mark> QF
MDA5	893	AKHYKNNP <mark>S</mark> LI	TFLCKNCSVI	LACSGEDIHVI	E <mark>EKM</mark> HVNMT	PE <mark>FK</mark> ELY-IV	/RENKALQ <mark>K</mark> KC
					* ***		*** * *
		611	619	629	637	647	7 657
LGP2	602	KDWKPGGVISC	RNCGEVW	LQMIYKSVKI		MLLETPQGRI	QAK <mark>KW</mark> SRVPF
RIG-I	854	SSFEKRAKIFC	CARQNC <mark>SH</mark> DW	<mark>G</mark> IHVKYKTFEI	[PVI <mark>K</mark> IESFV	VEDIATGVQT	LY <mark>SKW</mark> KDFHF
MDA5	952	ADYQINGEIIC	KC <mark>GQ</mark> AW	GTMMVHKGLDI	LPCL <mark>KIR</mark> NFV	VVFKNNSTKF	KQYK <mark>KW</mark> VELPI
		* *	k.	* *	* * * * *		* * * *
		667	677	7			
LGP2	658	SVPDFDFLQH	AENLSDLSLI	, C			
RIG-I	914	EKIPFDPAEMS	К	-			
MDA5	L009	TFPNLDYSEC	LFSDED	-			

Supplementary Figure 1 Sequence alignment of human LGP2, RIG-I, and MDA5 Cterminal domains. Residues of LGP2 involved in binding with the 5' end of the dsRNA are labeled with red asterisks; residues involved in binding with the 3' end of the dsRNA are labeled with black asterisks. His576, which is involved in binding of both strands, is labeled with brown asterisk. Residues conserved in all three proteins are in red. Conserved residues involved in dsRNA binding highlighted in yellow. Conservatively replaced residues are in green and blue.



Supplementary Figure 2 Molecular models of LGP2 CTD bound to a 12 bp and a 26 bp dsRNA. A, Stereo view of the structure of LGP2 CTD bound to the 8 bp dsRNA. Residues Arg636, Lys650, Lys651, and Arg654 are shown as stick models. B, Stereo view of the molecular model of LGP2 CTD bound to a 12 bp dsRNA. C, Stereo view of the molecular model of LGP2 CTD bound to the middle of a 26 bp dsRNA.

Supplementary Table 1 Sequences of dsRNA used in binding studies, analytical ultracentrifugation, and cell-based assays.

8 bp dsRNA	5' GCGCGCGC 3'					
1	CGCGCGCG					
	ААА					
24 nucleotides small	5' CCGCAUUG A					
hairpin RNA (shRNA)	3' GGCGUAAC G					
	GUU					
24 hn dsRNA (dsR24)	5' GCGCGCAUGCGCGCGCGCGCGCGC 3'					
$24 \text{ bn } 5^{\circ} \text{ nnn } \text{dsRNA}$	CGCGCGUACGCGCGCGUACGCGCG					
27 bp 68 P bp 43 H M	5' AAGCGCGCUGCGCGCAGCGCGC 3'					
5' overbangs						
22 bp. dsPNA with	5' CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC					
22 OP USKNA with						
3 overnangs						
19 bp dsRNA (dsR19)	5 UGGUUUACAUGUUCCAAUA 3					
	ACCAAAUGUACAAGGUUAU					
27 bp dsRNA (dsR27)	5' AAGCUGACCCUGAAGUUCAUCUGCACC 3'					
	UUCGACUGGGACUUCAAGUAGACGUGG					
27 bp dsRNA with	5' AAGCUGACCCUGAAGUUCAUCUGCACCUU 3'					
3' overhangs (27UU2)	UUUUCGACUGGGACUUCAAGUAGACGUGG					
27 bp dsRNA with	5' AAGCUGACCCUGAAGUUCAUCUGCACCUU 3'					
only one 3' overhang	UUCGACUGGGACUUCAAGUAGACGUGG					
(27UU)						



Supplementary Figure 3 Binding studies of RIG-I CTD with different dsRNAs by gel filtration chromatography. A, RIG-I CTD binding with a 24 bp dsRNA containing two blunt ends. B, RIG-I CTD binding with a 22 bp dsRNA containing two overhanging nucleotides at the 3' ends. C, RIG-I CTD binding with a 22 bp dsRNA with two overhanging nucleotides at the 5' ends.



Supplementary Figure 4 Double-stranded RNAs with blunt end can activate RIG-I signaling. Different forms of dsRNA were transfected into HEK 293T cells with RIG-I-expressing vector (grey bars) or an empty vector control (white bars) and luciferase driven from an NF- κ B (A) or IFN- β (B) promoter. All signals shown are the ratios of the NF- κ B or IFN- β luciferase versus *Renilla* luciferase driven from a constitutive herpesvirus thymidine kinase promoter. dsRNA with blunt ends (dsR24, dsR27, and 27UU) stimulated the activation of RIG-I more efficiently than dsRNA with either 5' or 3' overhangs (dsR22 5' over, dsR22 3' over, and 27UU2).



Supplementary Figure 5 Analysis of LGP2 CTD mutant proteins binding to dsRNA using gel filtration chromatography. Each panel contains the elution profile of the 8 bp dsRNA (green chromatogram), LGP2 CTD mutant protein (black chromatogram), and a 2:1 mixture of the protein and the RNA (red chromatogram). A, Analysis of LGP2 CTD mutant E573A. B, Analysis of mutant I597S. C, Analysis of mutant K634E. D, Analysis of mutant K651E. E, Analysis of a double mutant K634E/R636E.