Supplementary Table 1. Full sequences of each of the five miRNA sponges used

hsa-mir-126-3p sponge: 10 MBS 287BP CTCGAGCCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGCGCATTATTAAGTCGGTACGACCGGGTTTAAACCTAGAGCGGCCGCGAATTC
hsa-mir-141-3p sponge: 10 MBS 287BP CTCGAGCCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGCCATCTTTACTCTCAGTGTTACCGGGTTTAAACCTAGAGCGGCCGCGAATTC
hsa-mir-155-5p sponge: 10 MBS 297BP CTCGAGCCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGACCCCTATCACTAAAGCATTAACCGGGTTTAAACCTAGAGCGGCCGCGAATTC
hsa-mir-210-3p sponge: 10 MBS 287BP CTCGAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGTCAGCCGCTGGTGACGCACAGCCGGGTTTAAACCTAGAGCGGCCGCGAATTC
hsa-mir-1246 sponge: 10 MBS 257BP EcoRICTCGAGCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGCCTGCTCTTTAATCCATTCCGGGTTTAAACCTAGAGCGGCCGCGAATTC

Supplementary Table 2. The miRNA binding site of each of the five miRNA sponges used

5′-CGCATTATTA-AGTCGGTACGA-3′	sponge-126-3p
3′-GCGTAATAATGAGTGCCATGCT-5′	miR-126-3p
5′-CCATCTTTAC-TCTCAGTGTTA-3′	sponge-141-3p
3′-GGTAGAAATGGTCTGTCACAAT-5′	miR-141-3p
5′-ACCCCTATCAC-TAAAGCATTAA-3′	sponge-155-5p
3′-TGGGGATAGTGCTAATCGTAATT-5′	miR-155-5p
5′-TCAGCCGCTGT-GTGACGCACAG-3′	sponge-210-3p
3′-AGTCGGCGACAAGTGTGCGTGTC-5′	miR-210-3p
5′-CCTGCTC-TTTAATCCATT-3′	sponge-1246
3′-GGACGAGGTTTTTAGGTAA-5′	miR-1246

Supplementary Table 3. List of qPCR primers used

GAPDH Forward ACCCACTCCACCTTTGAC GAPDH Reverse TGTTGCAGCCAAATTCGTT
IL-8 Forward CTGGCCGTGGCTCTCTTG IL-8 Reverse TTAGCACTCCTTGGCAAAACTG
CXCL1 Forward AACCGAAGTCATAGCCACAC CXCL1 Reverse GTTGGATTTGTCACTGTTCAGC
NFKB1 Forward AACAGAGAGGATTTCGTTTCCG NFKB1 Reverse TTTGACCTGAGGGTAAGACTTCT
IKKε Forward TGCCTGAGGATGAGTTCCTG IKKε Reverse CGATGCACAATGCCGTTCT

Supplementary Table 4. Differentially expressed genes between WT and miR-126 KD

Symbol	Name	FC	P value
	Overexpressed in miR-126 KD vs WT		
IFITM1	interferon induced transmembrane protein 1	53.15	1.74E-18
IFI44L	interferon-induced protein 44-like	41.11	2.04E-17
MX2	myxovirus (influenza virus) resistance 2 (mouse)	26.34	3.90E-18
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	25.39	1.85E-17
IFI44	interferon-induced protein 44	16.88	3.06E-16
IFI6	interferon, alpha-inducible protein 6	16.83	1.32E-14
MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	15.62	5.15E-16
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	12.74	1.29E-15
OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	12.28	1.37E-13
OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	11.56	3.53E-14
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	11.03	3.95E-14
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	10.84	1.41E-15
OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	10.64	4.30E-14
STAT1	signal transducer and activator of transcription 1, 91kDa	10.62	6.11E-14
IFI27	interferon, alpha-inducible protein 27	10.10	5.28E-15
STAT1	signal transducer and activator of transcription 1, 91kDa	9.05	3.51E-14
TRIM22	tripartite motif containing 22	8.58	2.69E-15
LAMP3	lysosomal-associated membrane protein 3	8.44	2.87E-13
ISG15	ISG15 ubiquitin-like modifier	8.18	1.59E-14
PRIC285	helicase with zinc finger 2, transcriptional coactivator	8.02	4.71E-14
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	7.89	6.28E-14
IFIT2	interferon-induced protein with tetratricopeptide repeats 2	7.83	2.39E-14
IRF7	interferon regulatory factor 7	7.72	1.93E-13
CX3CL1	chemokine (C-X3-C motif) ligand 1	7.33	1.63E-13
IFIT3	interferon-induced protein with tetratricopeptide repeats 3	7.19	5.89E-14
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	7.16	1.65E-13
FAM50B	family with sequence similarity 50, member B	7.00	2.07E-14
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	6.90	2.94E-12
IRF7	interferon regulatory factor 7	6.66	8.58E-14
PARP14	poly (ADP-ribose) polymerase family, member 14	6.63	2.59E-14
PARP9	poly (ADP-ribose) polymerase family, member 9	6.49	4.82E-12
IFI6	interferon, alpha-inducible protein 6	5.87	6.72E-13
PLSCR1	phospholipid scramblase 1	5.82	4.66E-14
OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	5.73	3.87E-13
STAT1	signal transducer and activator of transcription 1, 91kDa	5.73	1.12E-12
HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	5.68	1.47E-13
CLDN11	claudin 11	5.68	1.24E-11
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	5.67	4.60E-13
HLA-B	major histocompatibility complex, class I, B	5.55	7.80E-14

OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	5.29	2.95E-13
IFITM2	interferon induced transmembrane protein 2	5.26	3.47E-13
THBS1	thrombospondin 1	5.20	1.05E-10
IFITM3	interferon induced transmembrane protein 3	5.11	3.23E-13
OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	5.02	7.69E-13
COL4A1	collagen, type IV, alpha 1	5.02	3.16E-13
SP110	SP110 nuclear body protein	4.96	1.17E-13
EPSTI1	epithelial stromal interaction 1 (breast)	4.94	1.63E-13
IFI35	interferon-induced protein 35	4.88	5.62E-13
CLDN1	claudin 1	4.72	2.16E-11
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	4.38	1.34E-11
Overexpressed in WT vs miR-126 KD			
SPRR1B	small proline-rich protein 1B	16.41	1.18E-15
KRTDAP	keratinocyte differentiation-associated protein	15.73	4.77E-16
FABP4	fatty acid binding protein 4, adipocyte	13.32	1.22E-14
KRT1	keratin 1	11.34	6.84E-14
SPRR2D	small proline-rich protein 2D	8.56	3.55E-14
LOC729252	Similar to keratin, type I cytoskeletal 14 (predicted)	8.40	3.10E-11
SPRR1A	small proline-rich protein 1A	8.34	5.64E-15
CXCL14	chemokine (C-X-C motif) ligand 14	7.68	2.52E-13
SBSN	suprabasin	7.43	1.03E-13
KRT4	keratin 4	7.10	3.73E-14
LOC400578	Similar to keratin, type I cytoskeletal 14 (predicted)	6.71	4.71E-10
S100A8	S100 calcium binding protein A8	6.21	1.25E-13
KRT16	keratin 16	5.89	1.82E-13
SYNM	synemin, intermediate filament protein	5.64	2.90E-13
MGC102966	keratin 16 pseudogene 3	5.44	1.40E-12
AKR1B10	aldo-keto reductase family 1, member B10 (aldose reductase)	5.39	2.82E-11
GJB6	gap junction protein, beta 6, 30kDa	5.28	1.11E-13
LCE3D	late cornified envelope 3D	5.24	1.82E-11
LOC400578	keratin 16 pseudogene 3	5.12	7.57E-13
GJB2	gap junction protein, beta 2, 26kDa	4.97	7.47E-12
HOPX	HOP homeobox	4.81	4.13E-12
PI3	peptidase inhibitor 3, skin-derived	4.38	3.46E-13
CRYAB	crystallin, alpha B	4.26	9.94E-11
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	4.17	2.28E-11
KRT10	keratin 10	4.05	1.63E-11
KRT16	keratin 16	3.98	3.85E-11
S100A7	S100 calcium binding protein A7	3.87	6.34E-09
MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	3.65	5.22E-10
PCSK5	proprotein convertase subtilisin/kexin type 5	3.58	2.05E-10
CDH16	cadherin 16, KSP-cadherin	3.54	3.83E-11

GJB6	gap junction protein, beta 6, 30kDa	3.54	1.00E-07
KIAA0114	differentiation antagonizing non-protein coding RNA	3.51	1.42E-11
SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	3.50	5.95E-07
CYP4F3	Cytochrome P450, Family 4, Subfamily F, Polypeptide 3	3.48	2.02E-08
SPRR2E	small proline-rich protein 2E	3.42	4.00E-09
HSPB3	heat shock 27kDa protein 3	3.41	2.14E-09
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3.39	9.53E-10
PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	3.38	8.20E-11
S100A9	S100 calcium binding protein A9	3.31	4.08E-11
S100P	S100 calcium binding protein P	3.28	4.20E-09
CNTNAP2	contactin associated protein-like 2	3.23	6.44E-11
TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	3.20	2.11E-09
PRKCB1	protein kinase C, beta	3.19	5.73E-11
FABP5	fatty acid binding protein 5 (psoriasis-associated)	3.19	6.71E-07
STXBP6	syntaxin binding protein 6 (amisyn)	2.99	9.07E-09
KRT6B	keratin 6B	2.98	1.98E-10
CNFN	cornifelin	2.94	5.83E-09
PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	2.92	6.53E-10
FABP5L2	Fatty Acid Binding Protein 5 Pseudogene 2	2.92	4.66E-08
DLX1	distal-less homeobox 1	2.86	1.80E-10

Supplementary Table 5. Top 25 differentially enriched gene sets in TIGK Wild type stimulated by heat-killed *P. gingivalis.*

	Name	NES	FDR
1	Regulation of defense response	1.749	0.062
2	Interleukin receptor activity	1.71	0.062
3	Detection of abiotic stimulus	1.662	0.093
4	Response to other organism	1.661	0.085
5	Positive regulation of translation	1.659	0.08
6	Developmental maturation	1.655	0.077
7	Immune response	1.652	0.075
8	Cell maturation	1.651	0.074
9	Behavior	1.638	0.072
10	Cellular defense response	1.63	0.071
11	Extracellular structure organization and biogenesis	1.629	0.07
12	Receptor signaling protein activity	1.627	0.07
13	Apical junction complex	1.627	0.074
14	Apicolateral plasma membrane	1.627	0.069
15	Tight junction	1.617	0.072
16	Immune system process	1.614	0.077
17	Regulation of response to external stimulus	1.607	0.079
18	Locomotory behavior	1.606	0.078
19	Leukocyte differentiation	1.602	0.077
20	Positive regulation of cytokine biosynthetic process	1.596	0.082
21	Regulation of cytokine biosynthetic process	1.596	0.081
22	Defense response	1.582	0.114
23	Pattern binding	1.566	0.122
24	Interleukin binding	1.562	0.126
25	Transmembrane receptor activity	1.558	0.141

NES: *normalized enrichment score, FDR: false discovery rate*