

Fig. S1 Titers of phage P_{1Z} SAE-01E2 under different MOIs. The phage titers reached the highest peak at MOI of 0.00001.

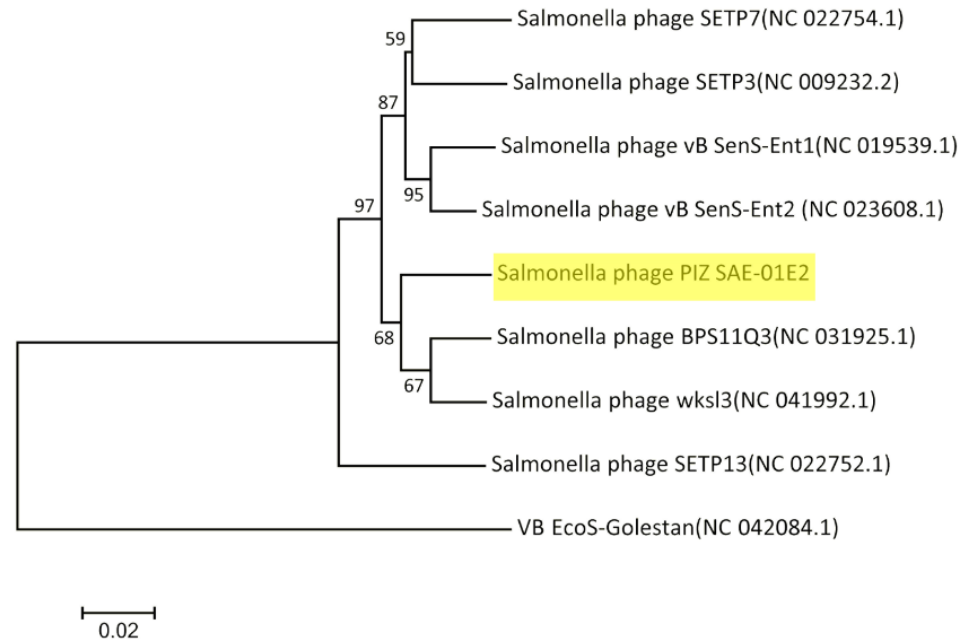


Fig. S2 Phylogenetic tree based on the terminase large subunits. Eight nucleotide sequences that shared a high similarity to the terminase large subunit of P_{IZ} SAE-01E2 were selected by BLAST. A neighbor-joining phylogenetic tree was constructed with a bootstrap of 1000 using MEGA 7.0.26 after sequence alignment by ClustalW.

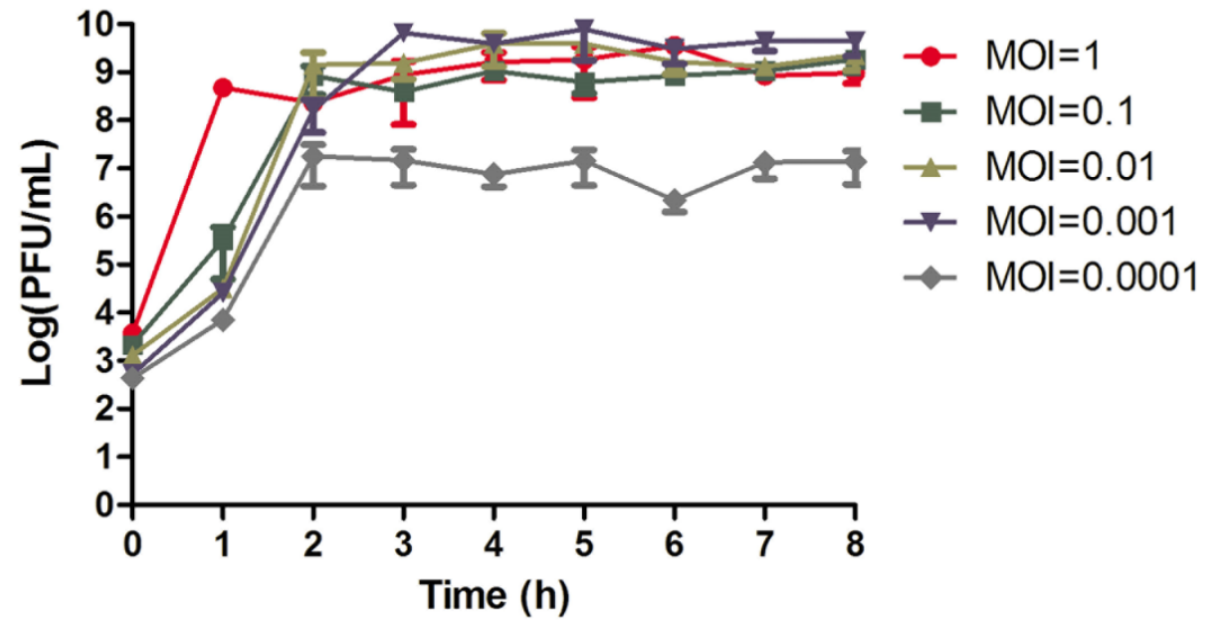


Fig. S3 The growth curve of phage P_{1Z} SAE-01E2 *in vitro*. *S. abortus equi* ATCC 9842 were cocultured with phage P_{1Z} SAE-01E2 in LB medium at different MOIs. The phage titers were counted at the indicated time points by the double-layer agar plate method. The values represent means and SD (n = 3).

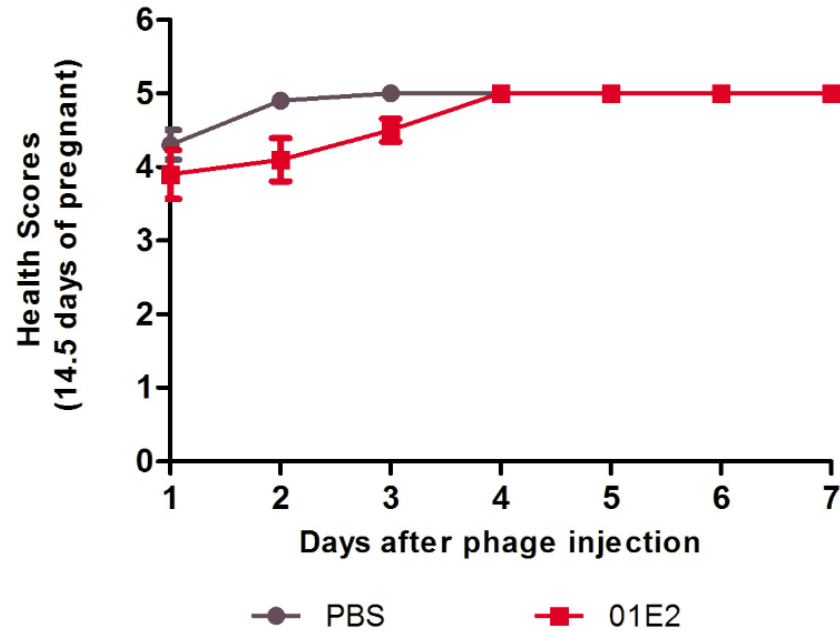


Fig. S4 Health status of pregnant mice after phage P_{Iz} SAE-01E2 (01E2) administration. Mice on gestational day 14.5 were injected with 10⁹ PFU/mouse of P_{Iz} SAE-01E2 or PBS. The health status of mice was monitored and scored for six days. 0: dead; 1: near death; 2: exudative accumulation around partially closed eyes; 3: lethargy and hunched back; 4: decreased physical activity and ruffled fur; 5: normal health, condition unremarkable. The values represent the means and SD (n = 10).

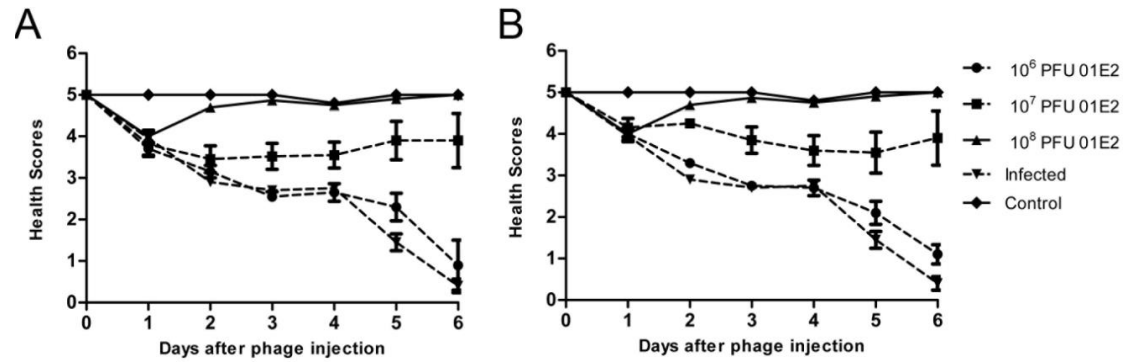


Fig. S5 Health score of bacterial infection mice and phage P_{IZ} SAE-01E2 (01E2) treated mice. (A) Treatment with phage P_{IZ} SAE-01E2 after 1 h of *S. abortus equi* ATCC 9842 infection. (B) Treatment with phage P_{IZ} SAE-01E2 before 1 h of *S. abortus equi* ATCC 9842 infection. Mice were monitored until two days after giving birth.

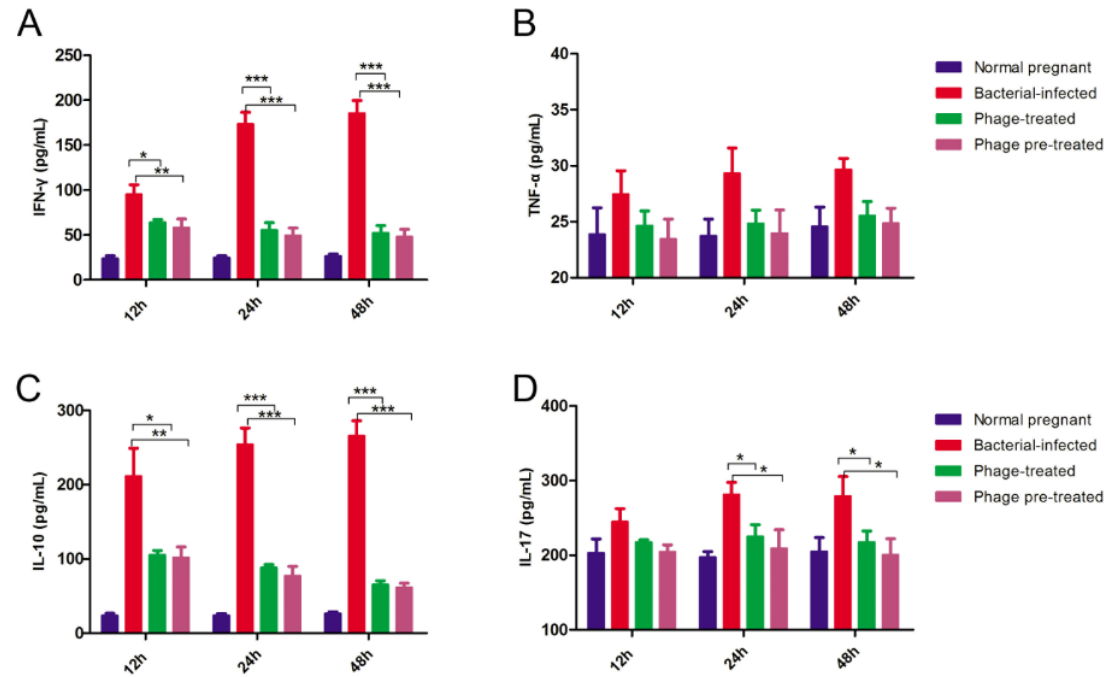


Fig. S6 Inflammatory cytokine expression in the serum of bacterial infection mice and phage P_{IZ} SAE-01E2 treated mice. The levels of inflammatory cytokines IFN- γ , TNF- α , IL-10, and anti-inflammatory cytokine IL-17 in the serum of the mice were determined at 12 h, 24 h and 48 h after *S. abortus equi* ATCC 9842 infection. The values represent the means and SD (n = 3). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Table S1. General features of the putative ORFs with the best matches in the database.

ORF ^a	Bp		Amio acid	Size (kDa)	pI	Annotated function	Representative similarity to proteins in database	E value	Identity (positives)	Query cover	Accession no.
	Start	Stop									
1§-	1537	1770	77	8.568	9.42	uvvX-like protein	[<i>Salmonella</i> phage Ent1]	3e-45	95%(97%)	100%	YP_007010497.1
2†-	1767	1937	56	6.637	9.18	DNA-binding protein	[<i>Gammaproteobacteria</i>]	3e-33	100%(100%)	100%	WP_016047069.1
3†+	2532	2726	64	7.389	10.03	hypothetical protein	[<i>Salmonella</i> phage S100]	6e-36	95%(95%)	96%	AXC39534.1
4†+	2930	3094	54	6.493	11.39	hypothetical protein BPS11Q3_28	[<i>Salmonella</i> phage BPS11Q3]	8e-31	96%(98%)	100%	YP_009322835.1
5†+	3158	3271	37	4.319	3.35	hypothetical protein BPS11Q3_27	[<i>Salmonella</i> phage BPS11Q3]	8e-19	100%(100%)	100%	YP_009322834.1
6†+	3264	3761	165	18.904	5.26	hypothetical protein BPS11Q3_26	[<i>Salmonella</i> phage BPS11Q3]	5e-103	89%(90%)	99%	YP_009322833.1
7†+	3758	3961	67	7.406	7.04	hypothetical protein	[<i>Salmonella</i> phage SE2]	1e-42	100%(100%)	100%	YP_005098114.1
8†+	3964	4335	123	14.130	10.46	hypothetical protein	[<i>Salmonella</i> phage SE2]	4e-85	100%(100%)	100%	YP_005098115.1
9†+	4341	4775	144	15.570	4.59	hypothetical protein LPSE_00022	[<i>Salmonella</i> phage LPSE1]	5e-100	99%(99%)	100%	APU02983.1
10§+	4854	5135	93	10.293	7.85	putative holin	[<i>Salmonella</i> phage Jersey]	1e-59	96%(100%)	95%	YP_008239771.1

11 [†] +	5137	5427	96	10.707	9.98	putative holin, class II	[<i>Salmonella</i> phage vB_SenS-Ent2]	4e-61	97%(98%)	98%	YP_009009974.1
12 [†] +	5405	5893	162	17.333	9.61	lysozyme	[<i>Salmonella</i> phage LPSE1]	1e-113	99%(98%)	100%	APU02985.1
13 [†] +	6078	6263	61	6.861	6.32	hypothetical protein STP03_039	[<i>Salmonella</i> phage STP03]	1e-34	92%(98%)	100%	APM00294.1
14 [†] +	6260	6415	51	5.761	10.39	hypothetical protein	[<i>Salmonella</i> phage SE2]	3e-29	100%(100%)	100%	YP_005098120.1
15 [†] +	6412	6594	59	6.961	5.68	hypothetical protein	[<i>Salmonella</i> phage SE2]	1e-33	95%(98%)	100%	YP_005098121.1
16 [†] +	6591	6740	49	5.898	8.16	hypothetical protein]	[<i>Salmonella</i> phage vB_SpuS_Sp4]	2e-23	96%(95%)	100%	AWY03000.1
17 [†] +	6737	6961	74	8.578	9.27	hypothetical protein	[<i>Salmonella</i> enterica]	3e-474	100%(100%)	100%	WP_015976715.1
18 [‡] +	7141	7263	40	5.016	7.16	putative membrane protein	[<i>Salmonella</i> phage vB_SenS_phi135]	4e-14	84%(89%)	92%	AST15499.1
19 [†] +	7260	7442	60	6.858	8.68	hypothetical protein	[<i>Salmonella</i> phage SE2]	2e-34	100%(100%)	100%	YP_005098124.1
20 [†] +	7503	7634	43	4.805	4.02	hypothetical protein	[<i>Salmonella</i> phage SE2]	4e-23	100%(100%)	100%	YP_005098125.1
21 [†] +	7663	8169	168	18.820	6.18	terminase small subunit	[<i>Salmonella</i> phage BPS11Q3]	3e-118	99%(98%)	100%	YP_009322818.1
22 [§] +	8159	9430	423	47.640	6.20	terminase large subunit	[<i>Salmonella</i> phage BPS11Q3]	0.0	99%(99%)	100%	YP_009322817.1
23 [†] +	9443	10918	491	53.972	4.68	DUF4055 domain-containing protein	[<i>Salmonella</i> virus VSe103]	0.0	99%(99%)	99%	AXQ70131.1

24 [†] -	10949	11599	216	24.966	5.75	amidase	[<i>Salmonella</i> phage SE2]	1e-153	95%(98%)	100%	YP_005098129.1
25 [†] +	11765	12808	347	38.687	7.35	head morphogenesis protein	[<i>Salmonella</i> phage FSL SP-101]	0.0	94%(96%)	100%	AGF87707.1
26 [†] +	12811	13269	152	16.399	4.39	putative head decoration protein	[<i>Salmonella</i> phage Ent1]	3e-101	99%(100%)	100%	YP_007010459.1
27 [§] +	13423	13542	39	4.653	10.98	hypothetical protein	[<i>Salmonella</i> phage ST3]	3e-20	100%(100%)	100%	ASZ77969.1
28 [†] +	13587	13973	128	14.228	9.74	o-spanin	[<i>Salmonella</i> phage vB_SenS_PVP-SE2]	3e-81	91%(96%)	100%	AST15489.1
29 [†] +	13957	14082	41	4.764	4.36	i-spanin	[<i>Salmonella</i> phage vB_SenS_PVP-SE2]	2e-20	98%(100%)	100%	AST15516.1
30 [†] +	14167	14868	233	25.710	5.88	putative scaffold protein	[<i>Salmonella</i> phage Ent1]	7e-163	98%(99%)	100%	YP_007010462.1
31 [†] +	14872	15921	349	37.887	4.55	capsid protein	[<i>Salmonella</i> phage MA12]	0.0	99%(98%)	100%	YP_009280185.1
32 [†] +	15982	16266	94	9.325	9.79	head protein	[<i>Salmonella</i> phage BPS11Q3]	4e-57	100%(100%)	100%	YP_009322872.1
33 [†] +	16278	16628	115	12.157	4.02	hoc protein	[<i>Salmonella</i> phage BPS11Q3]	2e-75	99%(99%)	100%	YP_009322871.1
34 [†] +	16665	16853	62	7.088	4.69	head-tail joining protein	[<i>Salmonella</i> phage STP03]	2e-35	98%(100%)	100%	APM00274.1
35 [†] +	16857	17366	169	17.806	4.60	head-tail joining protein	[<i>Salmonella</i> phage BPS11Q3]	2e-119	100%(100%)	100%	YP_009322869.1
36 [†] +	17369	17974	201	20.612	8.13	neck protein	[<i>Salmonella</i> phage BPS11Q3]	1e-139	99%(99%)	100%	YP_009322868.1

37 [†] +	17974	18333	119	13.085	9.23	tail protein	[<i>Salmonella</i> phage BPS11Q3]	4e-80	100%(100%)	100%	YP_009322867.1
38 [†] +	18330	18725	131	14.430	9.71	tail protein	[<i>Salmonella</i> phage BPS11Q3]	1e-90	98%(100%)	100%	YP_009322866.1
39 [†] +	18725	19144	139	15.058	4.42	phage tail protein	[<i>Salmonella</i> phage FSL SP-101]	3e-92	94%(95%)	100%	AGF87719.1
40 [†] +	19144	20313	389	41.161	4.40	putative tail protein	[<i>Salmonella</i> phage wksI3]	0.0	98%(99%)	100%	AFO12387.1
41 [†] -	20342	21013	223	25.665	7.30	tail protein	[<i>Salmonella</i> enterica]	9e-162	99%(99%)	100%	WP_016062375.1
42 [†] -	21126	21356	76	8.690	6.33	DNA-binding protein	[<i>Salmonella</i> enterica]	7e-49	100%(100%)	100%	WP_015984945.1
43 [†] -	21353	22483	376	42.485	8.82	oxidoreductase winged	[<i>Salmonella</i> enterica]	0.0	99%(99%)	100%	WP_064624764.1
44 [†] -	22546	22725	59	6.603	9.63	superinfection immunity protein	[<i>Salmonella</i> enterica]	2e-32	100%(100%)	100%	WP_015984947.1
45 [†] +	22783	22905	40	4.417	10.22	hypothetical protein phi135_35	[<i>Salmonella</i> phage vB_SenS_phi135]	4e-20	100%(100%)	100%	AYP69716.1
46 [†] +	22895	23311	138	15.877	5.24	tail assembly chaperone	[<i>Salmonella</i> phage vB_SenS_PVP-SE2]	5e-96	99%(99%)	100%	AST15484.1
47 [‡] +	23317	23676	119	13.552	4.88	hypothetical protein	[<i>Salmonella</i> enterica]	8e-84	100%(100%)	100%	WP_015976751.1
48 [†] +	23669	26002	777	83.004	4.66	putative tape measure protein	[<i>Salmonella</i> phage LPSE1]	0.0	99%(99%)	100%	APU03018.1
49 [†] +	26004	26504	166	18.638	4.72	hypothetical protein	[<i>Salmonella</i> phage SETP13]	1e-121	100%(100%)	100%	YP_008767027.1

50 [‡] +	26501	27016	171	19.225	4.29	DUF1833 domain-containing protein	[<i>Salmonella</i> enterica]	2e-122	99%(100%)	100%	WP_015976748.1
51 [†] +	27013	27378	121	13.911	6.60	hypothetical protein	[<i>Salmonella</i> phage vB_SpuS_Sp4]	5e-86	99%(100%)	100%	AWY03032.1
52 [‡] +	27369	29927	852	93.928	5.16	tail fiber protein	[<i>Salmonella</i> phage vB_SpuS_Sp4]	0.0	99%(99%)	100%	AWY03031.1
53 [†] +	29940	31994	684	73.052	5.14	tail spike protein	[<i>Salmonella</i> phage BPS11Q3]	0.0	99%(99%)	100%	YP_009322852.1
54 [†] -	32024	32116	30	3.069	9.00	hypothetical protein	[<i>Salmonella</i> phage SG2]	3e-23	100%(100%)	100%	ASZ76550.1
55 [†] -	32113	32334	73	8.722	4.75	hypothetical protein	[<i>Salmonella</i> phage SS3e]	6e-42	100%(100%)	100%	YP_224070.1
56 [†] -	32331	34796	821	92.394	8.38	putative intein containing helicase precursor	[<i>Salmonella</i> phage vB_SenS-Ent2]	0.0	97%(98%)	100%	YP_009009958.1
57 [†] -	34793	35290	165	18.769	9.79	HNH endonuclease	[<i>Salmonella</i> phage STP03]	4e-117	98%(99%)	100%	APM00325.1
58 [†] -	35292	35483	63	7.084	8.54	hypothetical protein	[<i>Salmonella</i> phage vB_SpuS_Sp4]	8e-37	100%(100%)	100%	AWY03027.1
59 [†] -	35515	35802	95	10.808	9.77	putative restriction endonuclease	[<i>Salmonella</i> phage LPSE1]	1e-60	96%(98%)	100%	APU03027.1
60 [†] -	35889	38987	1032	116.136	7.29	intein-containing DNA polymerase precursor	[<i>Salmonella</i> phage BPS11Q3]	0.0	99%(99%)	100%	YP_009322845.1

61 †-	39045	39671	208	23.471	4.94	DNA polymerase	[<i>Salmonella</i> phage BPS11Q3]	1e-151	99%(100%)	100%	YP_009322844.1
62 †-	39753	39929	58	6.937	10.32	hypothetical protein	[<i>Salmonella</i> phage MA12]	1e-33	100%(100%)	100%	YP_009280156.1
63 †-	39926	41353	475	53.348	6.77	DUF2800 domain-containing protein	[<i>Salmonella</i> enterica]	0.0	94%(97%)	99%	WP_109251281.1
64 †-	41395	41907	170	19.245	4.45	13.88 kDa late protein	[<i>Salmonella</i> phage SETP7]	2e-98	91%(94%)	100%	YP_008767212.1
65 †+	42041	42259	72	7.920	8.57	XRE family transcriptional regulator	[<i>Salmonella</i> enterica]	1e-45	100%(100%)	100%	WP_015984911.1

^a †, AUG start codons; ‡, UUG start codons; §, GUG start codons; *, CUU. +, right orientation; -, left orientation.

Table S2. Average fetal weight and FGR analysis of different dose of phage P_{IZ} SAE-01E2 treated mice.

Fetal growth	Control	Phage P _{IZ} SAE-01E2					
		10 ⁶ PFU/mouse	10 ⁷ PFU/mouse	10 ⁸ PFU/mouse	10 ⁶ PFU/mouse	10 ⁷ PFU/mouse	10 ⁸ PFU/mouse
		treated	treated	treated	pre-treated	pre-treated	pre-treated
FGR ^a	1.072±0.053 (8/107) ^c	-	1.054±0.044 (15/38) ^c	1.046±0.052 (15/110) ^c	-	1.061±0.025 (10/48) ^c	1.074±0.022 (10/115) ^c
NFW ^b	1.630±0.078 (99/107) ^c	-	1.602±0.087 (23/38) ^c	1.566±0.042 (95/110) ^c	-	1.572±0.092 (38/48) ^c	1.602±0.087 (105/115) ^c

Eighty mice on gestational days 14.5 received a 10⁶ PFU/mouse, 10⁷ PFU/mouse, or 10⁸ PFU/mouse of P_{IZ} SAE-01E2 or PBS. The fetuses were weighted and fetal growth restriction was evaluated as described in the materials and methods. “-” represents the mice miscarried. ^a FGR, fetal growth restriction; ^b NFW, normal fetal weight; ^c the proportion of FGR or NFW in all fetuses.