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648 **Supplementary Table S1. Bacterial and archaeal Shannon Diversity Index, dry matter intake, and methane emissions**
649 **from Hanwoo steers linear regression analyses**

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<i>Item</i> ¹	<i>Microbes</i>	<i>Group</i> ²	<u>Confidence Intervals</u>		<i>Goodness of Fit</i>	<i>P-value</i>	<i>r</i> ²	
			<i>Coefficient</i>	<i>Lower</i>				<i>Upper</i>
<i>DMI</i>	Bacteria	SF	0.38	4.24	6.58	5.41	0.07	0.448
		TMR	-0.012	4.72	5.17	4.95	0.71	0.025
	Archaea	SF	0.14	1.64	3.34	2.49	0.31	0.167
		TMR	0.1	1.79	3.09	2.44	0.30	0.176
<i>CH₄</i>	Bacteria	SF	0.013	0.67	4.30	2.48	0.035	0.552
		TMR	0.00043	4.35	5.48	4.91	0.78	0.014
	Archaea	SF	0.0078	-0.09	2.02	0.97	0.031	0.568
		TMR	0.0063	-0.31	2.67	1.18	0.15	0.314
<i>MEF</i>	Bacteria	SF	0.036	1.07	4.40	2.73	0.04	0.531
		TMR	0.0012	4.41	5.43	4.92	0.78	0.014
	Archaea	SF	0.02	0.14	2.25	1.20	0.064	0.460
		TMR	0.017	-0.04	2.63	1.29	0.15	0.314

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652 ¹DMI = dry matter intake (kg/d); CH₄ = methane (g/d); MEF = methane emission factor (kg CH₄/head/year).

653 ²SF = separate feeding concentrate and forage; TMR = total mixed ration.

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