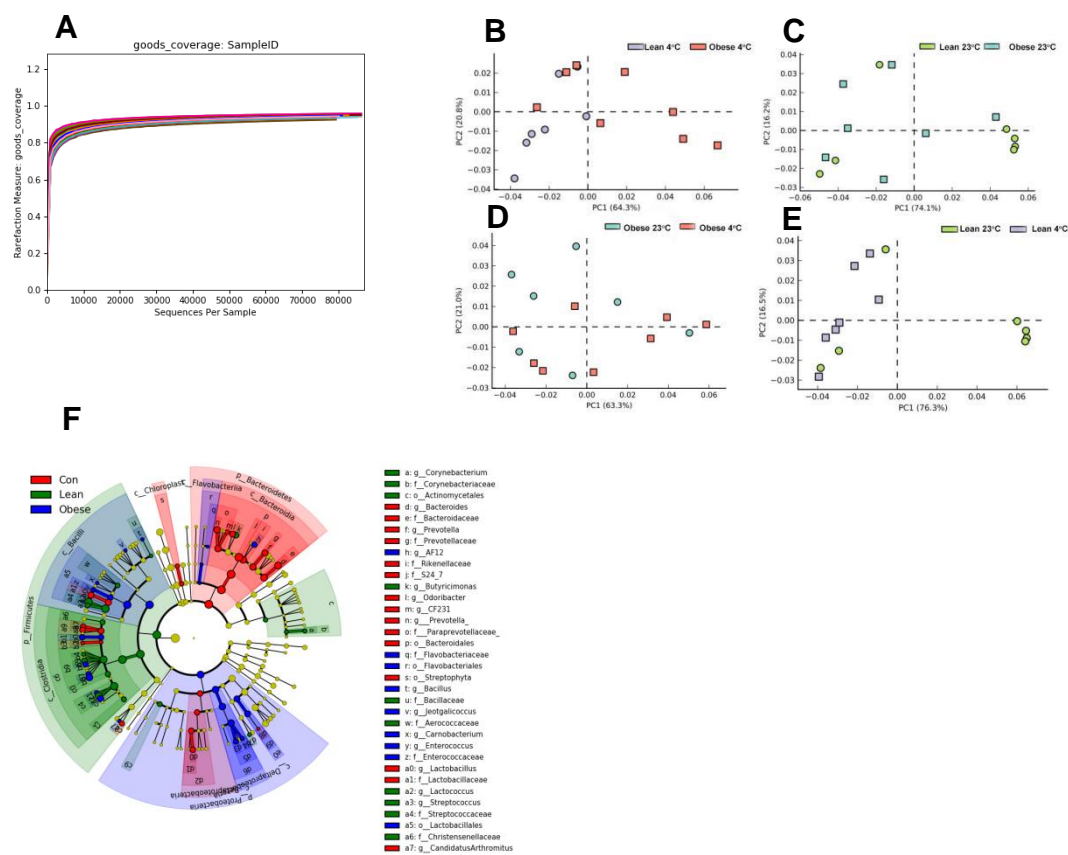


Table S1 Prediction of the function of the gut microbiota associated with lipid metabolism

	Fat			<i>P</i> fat	Ambient temperature (Ta)		<i>P</i> Ta
	Con	Obesity	Lean		23°C	4°C	
<b>Adipocytokine signaling pathway</b>	35193.800±2059. 739 <sup>a</sup>	28156.571±168 5.519 <sup>b</sup>	27483.000±174 0.797 <sup>b</sup>	*	30142.610±151 3.148	30412.971±148 5.072	<i>ns</i>
<b>Fatty acid biosynthesis</b>	153708.900±910 5.456 <sup>b</sup>	254233.982±74 51.151 <sup>a</sup>	245999.143±76 95.515 <sup>a</sup>	**	216635.914±66 89.149	219325.436±65 65.036	<i>ns</i>
<b>Lipid biosynthesis proteins</b>	226159.100±109 39.766 <sup>b</sup>	307230.089±89 52.197 <sup>a</sup>	297295.714±92 45.790 <sup>a</sup>	**	274898.848±80 36.690	278891.088±78 87.573	<i>ns</i>
<b>Lipid metabolism</b>	35798.600±2962. 246 <sup>b</sup>	64158.991±242 4.057 <sup>a</sup>	61717.571±250 3.555 <sup>a</sup>	**	53089.067±217 6.158	54694.375±213 5.780	<i>ns</i>
<b>Glycerolipid metabolism</b>	149049.800±102 42.972 <sup>b</sup>	224724.429±83 81.999 <sup>a</sup>	214273.500±86 56.892 <sup>a</sup>	**	192695.076±75 24.804	199336.743±73 85.185	<i>ns</i>
<b>Glycerophospholipid metabolism</b>	204349.400±985 1.181 <sup>b</sup>	281218.071±80 61.390 <sup>a</sup>	274066.429±83 25.768 <sup>a</sup>	**	249782.657±72 36.982	256639.943±71 02.704	<i>ns</i>
<b>Fatty acid metabolism</b>	74009.100±5996. 628 <sup>b</sup>	130701.429±49 07.143 <sup>a</sup>	120999.143±50 68.076 <sup>a</sup>	**	109195.371±44 05.308	107944.410±43 23.570	<i>ns</i>

Data are means ± SEM.  $P_{\text{fat}}$ , effect of DIO,  $P_{\text{Ta}}$ , effect of ambient temperature, \*\*,  $P < 0.01$ ; *ns*, non-significant ( $P > 0.05$ ).

Different letters indicate significant between-group differences determined by Tukey post-hoc test ( $P < 0.05$ ).



**Fig. S1. DIO and cold exposure alter the diversity and composition of fecal microbiota.** The OTU-level rarefaction curve of Goods coverage across all samples has reached stable values(A). Principal coordinates analysis (PCoA) plots based on unweighted UniFrac distance (B-E). Cladogram representing taxa enriched in fecal microbiota community of the six groups detected by the LEfSe tool. Differences were represented by the color of the most abundant class (F).