

# Supplementary table

Table S1. The number of reads of potential human pathogens obtained by the sequencing at the species level

Species	R	S0	S5	S40	T15	TM	G10	G20	G30
<i>Salmonella sp. DAP8</i>	n/d	n/d	3	n/d	n/d	2	2	n/d	n/d
<i>Uncultured Salmonella sp</i>	n/d	n/d	n/d	n/d	n/d	n/d	50	n/d	2
<i>Salmonella enterica subsp. enterica serovar Typhi</i>	n/d	n/d	n/d	n/d	n/d	n/d	9	n/d	2
<i>Salmonella enterica subsp. enterica serovar Typhimurium</i>	n/d	n/d	n/d	n/d	n/d	n/d	n/d	n/d	n/d
<i>Salmonella enterica subsp. houtenae str. ATCC BAA-1581</i>	n/d	n/d	n/d	n/d	n/d	n/d	n/d	2	3
<i>Salmonella sp. Co9936</i>	n/d	n/d	n/d	2	n/d	n/d	n/d	2	n/d
<i>Salmonella enterica</i>	n/d	n/d	n/d	n/d	n/d	n/d	10	n/d	n/d
<i>Escherichia coli</i>	21	11	21	14	11	14	n/d	8	8
<i>Escherichia sp. 4B</i>	n/d	n/d	n/d	2	n/d	n/d	2	n/d	n/d
<i>Uncultured Escherichia sp</i>	n/d	n/d	n/d	n/d	n/d	n/d	n/d	n/d	2
<i>Uncultured Shigella sp</i>	n/d	n/d	n/d	n/d	n/d	n/d	2	n/d	2
<i>Staphylococcus aureus</i>	4	2	5	6	4	2	n/d	4	1
<i>Listeria monocytogenes</i>	2	n/d	n/d	2	n/d	2	n/d	n/d	n/d
<i>Bacillus cereus</i>	n/d	3	n/d	n/d	n/d	n/d	n/d	n/d	n/d