

1 **Supplemental Material**

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3 Supplemental Results

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5 *Removal of Proteobacteria blooms*

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7 One Proteobacteria sequence tagged as a potential bloom due to storage conditions was  
8 filtered from the data. When the Proteobacteria bloom sequence was included in the analyses of  
9 GI-healthy and GI-unhealthy doucs, we still detected no effect of douc health status on alpha  
10 diversity ( $F_{1,31} = 0.32$ ,  $p = 0.57$ ), and gut microbial composition differed significantly in response  
11 to douc health status (weighted:  $F_{1,33} = 2.6$ ,  $r^2=0.07$ ,  $p < 0.01$ ; unweighted:  $F_{1,33} = 2.4$ ,  $r^2=0.07$ ,  $p <$   
12  $0.01$ ).

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14 *Utilization of one sample per body site per individual*

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16 Multiple samples were collected for each individual at each body site. Samples collected  
17 from the same body site within an individual clustered strongly as compared to samples  
18 from other body sites within the same individual or samples from the same body site  
19 within other individuals. For example, body site explained a large amount of variation in  
20 microbial community composition across samples for one douc (#45560; weighted:  $F_{5,21}$   
21  $= 3.1$ ,  $r^2=0.49$ ,  $p = 0.02$ ; unweighted:  $F_{5,21} = 2.0$ ,  $r^2=0.38$ ,  $p < 0.01$ ), one colobus (#45796;  
22 weighted:  $F_{5,17} = 3.3$ ,  $r^2=0.58$ ,  $p < 0.01$ ; unweighted:  $F_{5,17} = 3.6$ ,  $r^2=0.60$ ,  $p < 0.01$ ), and  
23 one langur (#54374; weighted:  $F_{4,13} = 2.4$ ,  $r^2=0.51$ ,  $p = 0.08$ ; unweighted:  $F_{4,13} = 2.8$ ,  
24  $r^2=0.55$ ,  $p < 0.01$ ) selected at random. Therefore, only one swab from each body site on  
25 each individual was included in statistical analyses.

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