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1 **Figure legend**

2 **Supplementary Fig. 1** Bacteria community structure of the inoculated phytoplankton (coccolithophore:  
3 *E. huxleyi*; diatom: *P. tricornutum* and *T. weissflogii*) culture at phylum (a), class (b), order(c), family  
4 (d), genus (d), species (d) level.

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6 **Supplementary Fig. 2** The phylogenetic tree of OTUs from all samples.

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8 **Supplementary Fig. 3** Composition of the top 10 taxa at the (a) class, (b) order, (c) family or (d) genus  
9 level for all samples.

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11 **Supplementary Fig. 4** Rarefaction curves of samples from HC-2, HC-4, HC-7, LC-1, LC-6 and LC-8  
12 collected at various time points using different estimator methods including Observed species (a),  
13 Shannon index (b), Chao index (c), Simpson index (d).

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15 **Supplementary Fig. 5** Bacterioplankton community diversity variation of HC-2, HC-4, HC-7, LC-1,  
16 LC-6 and LC-8 over time using different estimator methods including Observed species (a), Shannon  
17 index (b), Chao index (c), Simpson index (d).

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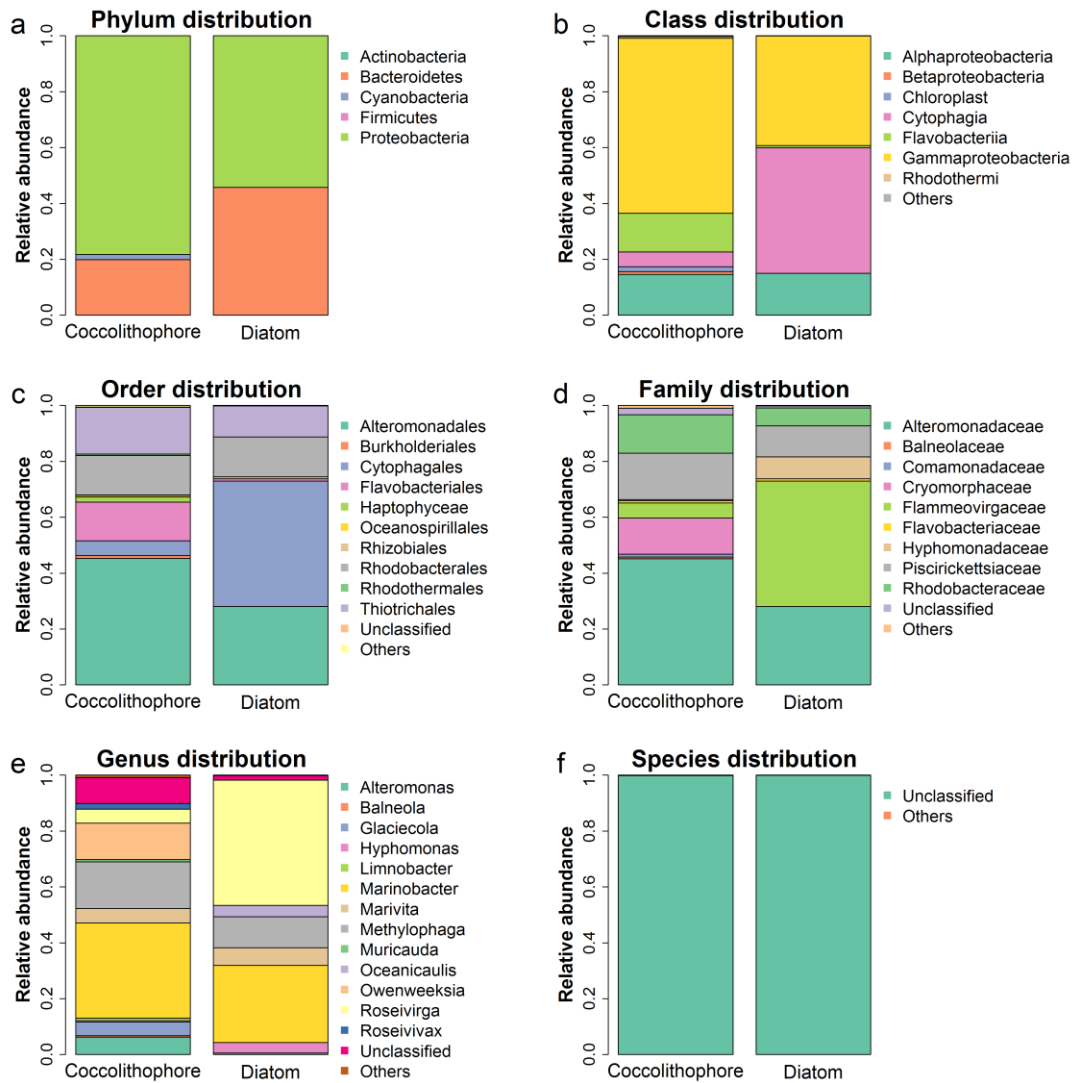
19 **Supplementary Fig. 6** Principle component analysis (PCA) of bacterioplankton community of all  
20 samples collected at different time points.

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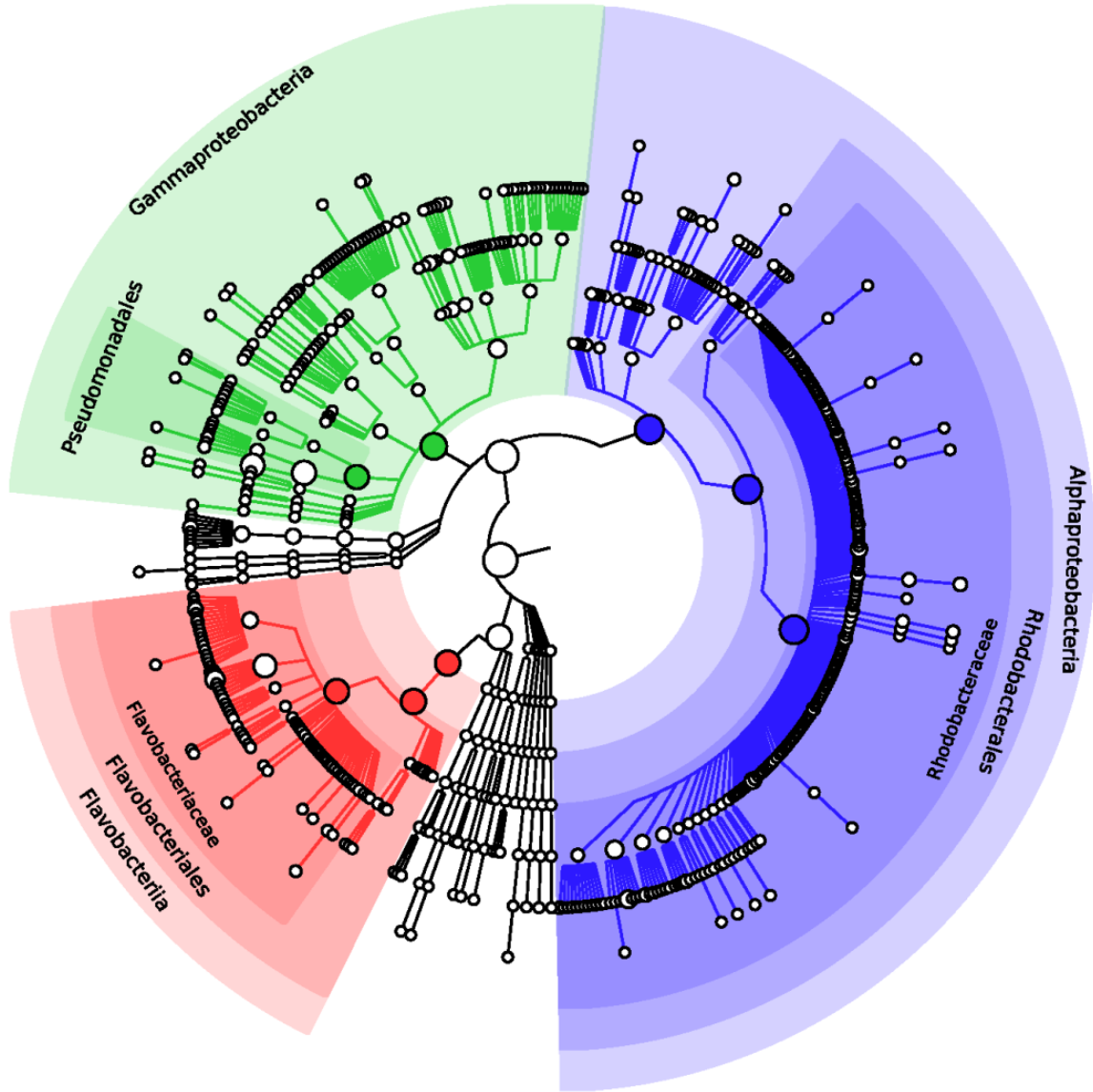


Supplementary Figure. 1

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# Phylogenetic Tree

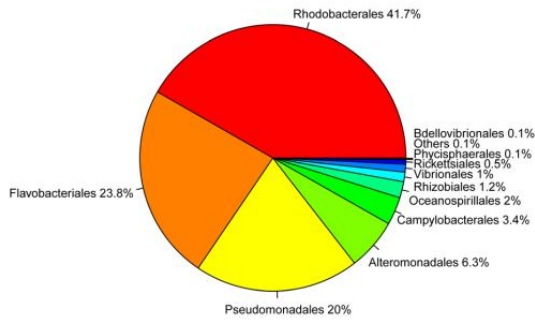
- ALPHAPROTEOBACTERIA
- FLAVOBACTERIIA
- GAMMAPROTEOBACTERIA



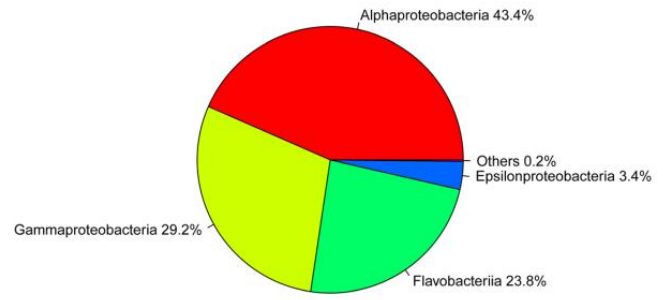
Supplementary Figure. 2

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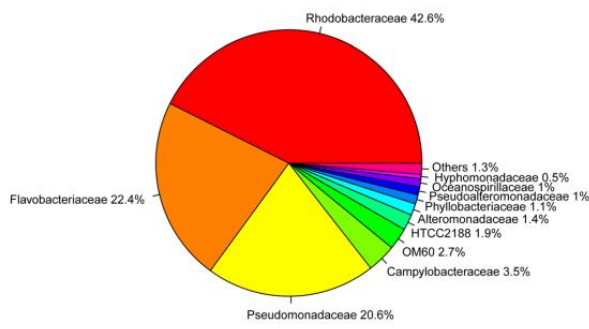
**a** Composition of the top 10 taxa at the order



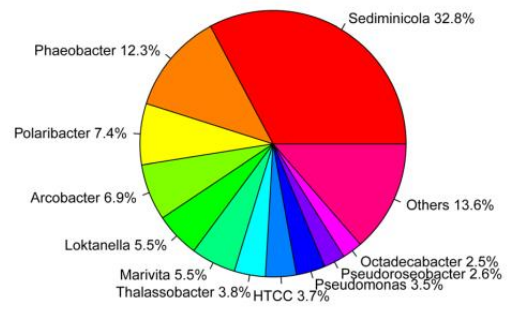
**b** Composition of the top 10 taxa at the class



**c** Composition of the top 10 taxa at the family

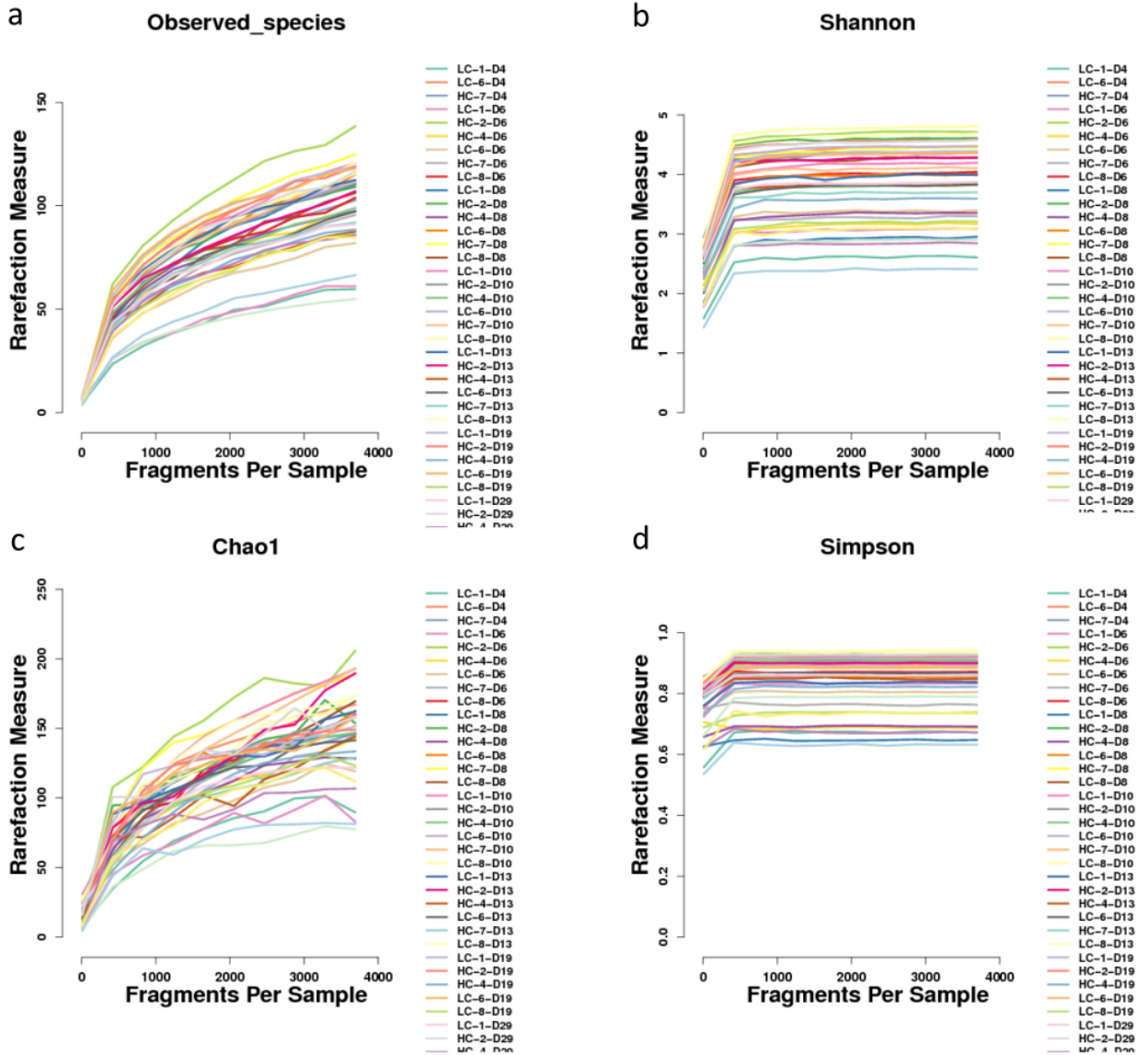


**d** Composition of the top 10 taxa at the genus



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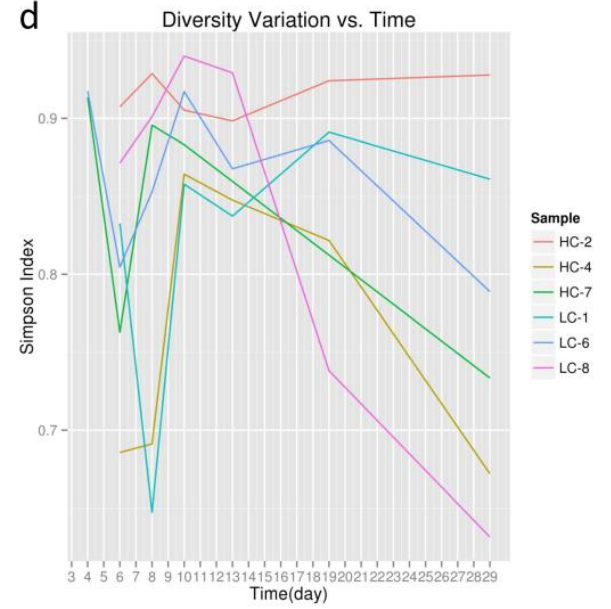
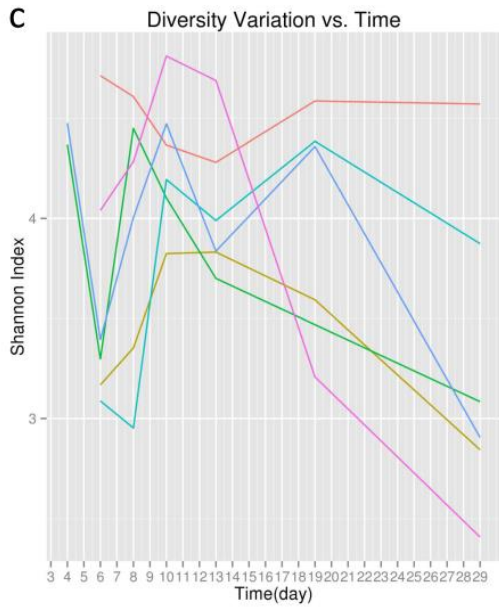
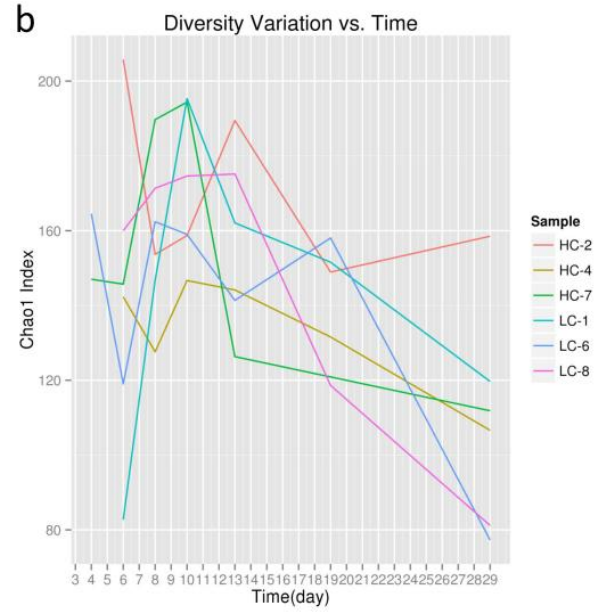
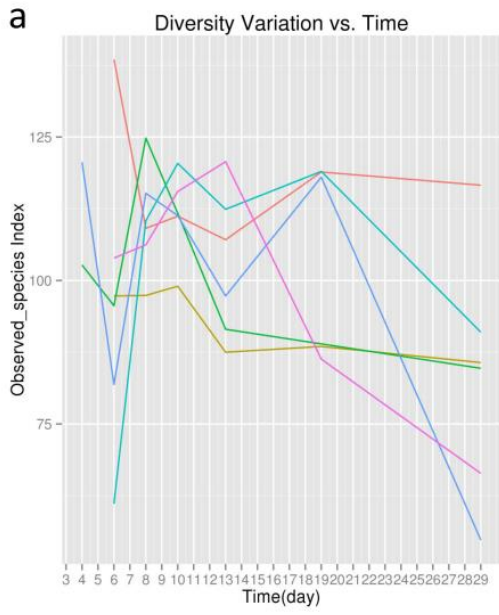
**Supplementary Figure. 3**



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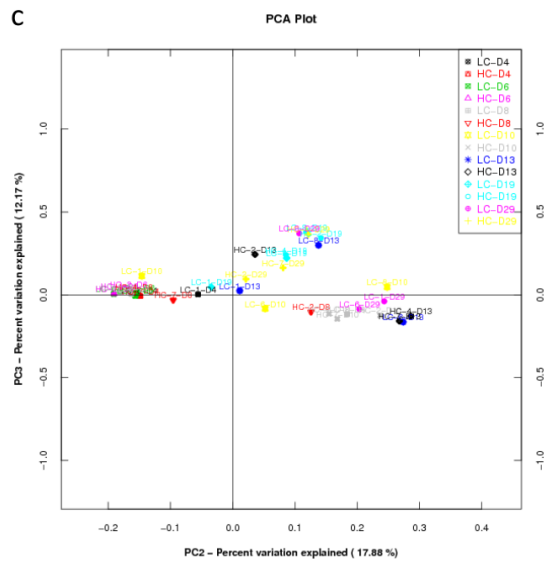
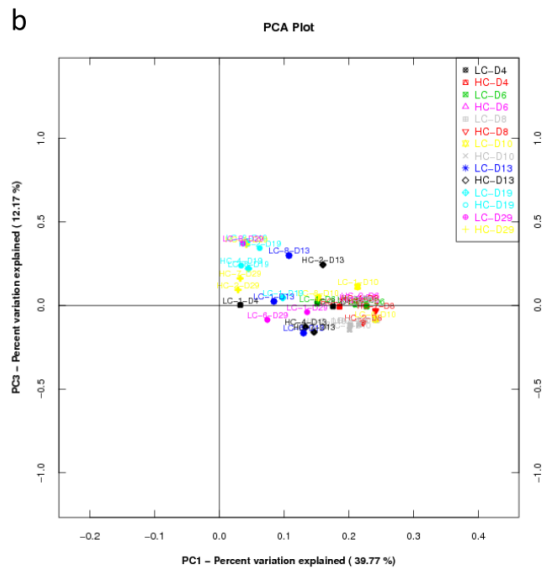
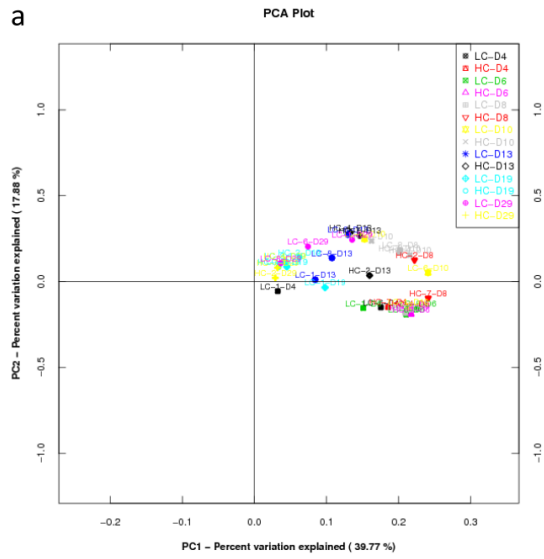
Supplementary Figure. 4



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**Supplementary Figure. 5**



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Supplementary Figure. 6