Chun-Huo Chiu, Lou Jost, and Anne Chao. 2013. Phylogenetic beta diversity, similarity, and differentiation measures based on Hill numbers. *Ecological Monographs*.

APPENDIX G. Additional analysis of Examples 2 and 3

### Example 2. Two types of profiles of differentiation measures

In the main text, we suggest using two types of profiles to characterize the proposed differentiation measures $1-\overline{C}_{qN}(T)$ and $1-\overline{U}_{qN}(T)$. Here we illustrate these two types of profiles based on the hypothetical time-calibrated tree in Fig. 3 of the main text.

(1) The first type of profile shows how our differentiation measures vary with the time perspective T by evaluating the proposed differentiation measures as a function of the temporal perspective T over the interval $[-T, 0]$, for a fixed order q (including at least $q = 0$, 1 and 2). Here the time perspective can vary from $T = 0$ (the current time) to $T =$ infinity. For the tree in Fig. 3 of the main text, the splitting time between assemblages correspond to a specific value of $T = 200$, and the root of the pooled tree corresponds to a specific value of $T = 240$. In Fig. G1(a), we show profiles which plot the measures $1-\overline{C}_{qN}(T)$, $1-\overline{U}_{qN}(T)$ as a function of time perspective T, $0 < T < 250$, for $q = 0$, 1 and 2 separately. For comparison, we also include the profile for the traditional differentiation measure $J_{qN}(T)$ based on the phylogenetic generalized entropies.

(2) For any fixed time perspective T (including at least $T = 0$ and $T =$ the age of the root of the pooled tree), the other type of profile is obtained by plotting our differentiation measures with respect to the order q. In Fig. G1(b), for $T = 0$ (i.e., phylogeny is ignored), we plot the profiles for three non-phylogenetic measures ($1-C_{qN}$, $1-U_{qN}$ and J_{qN}^{*}) as a function of order q, $0 \leq q \leq 5$. Then for $T = 240$ My (the age of the root of the pooled phylogenetic tree), we also plot the corresponding profiles for three phylogenetic differentiation measures, $1-\overline{C}_{qN}(T)$, $1-\overline{U}_{qN}(T)$ and $J_{qN}(T)$.

The profile for each fixed value of q in Fig. G1(a) reveals that the additive differentiation measure $J_{qN}(T)$ based on the phylogenetic generalized entropies is hardly sensitive to the tree structure, as it remains at a almost constant level for any T, $0 < T < 250$. This is also clearly seen from comparing the two panels ($T = 0$ and $T = 240$ My) in Fig. G1(b); all values of the phylogenetic differentiation measures $J_{qN}(T)$ at $T = 240$ My are close to the values of their non-phylogenetic counterparts (i.e., the measure J_{qN}^{*}). In Fig. G1(b), for each fixed temporal perspective T, although J_{qN}^{*} and $J_{qN}(T)$ decrease gradually with the order of q as shown in each figure of G1(b), their values are very low (for $q \geq 1$), as predicted by our theory for the case of high alpha (and thus high gamma) phylogenetic entropies. This can also be seen by examining the level of $J_{qN}(T)$ for $q = 1$ and 2 in Fig. G1(a). Thus, the two types of profiles in Fig. G1 confirm by example our theoretical proof that the measure $J_{qN}(T)$ often will not reflect either tree structure or differences in species abundances.

The two proposed measures for $q = 1$ and 2 in Fig. G1(a) show high differentiation between the two assemblages when the perspective time T is less than 200 (the splitting time of the continents). After that, both measures start to decrease, and the decrease is sharper for $q = 2$. For $q \geq 1$, as T becomes larger so that more dominant shared lineages are added to the two assemblages, our two abundance-sensitive differentiation measures show the expected decreasing trend, especially for $q = 2$. Also, comparing the two panels ($T = 0$ and $T = 240$ My) in Fig. G1(b), we see that all values of the phylogenetic differentiation measure $1 - \overline{C}_{qN}(T)$ at $T = 240$ My are much lower than the corresponding non-phylogenetic measure at $T = 0$. Similar behavior is also observed for the measure $1 - \overline{U}_{qN}(T)$. These two types of profiles are very useful to characterize the behavior of the proposed differentiation measures as a function of the time perspective T and the order q.

(a) Profiles of differentiation measures as a function of temporal perspective T
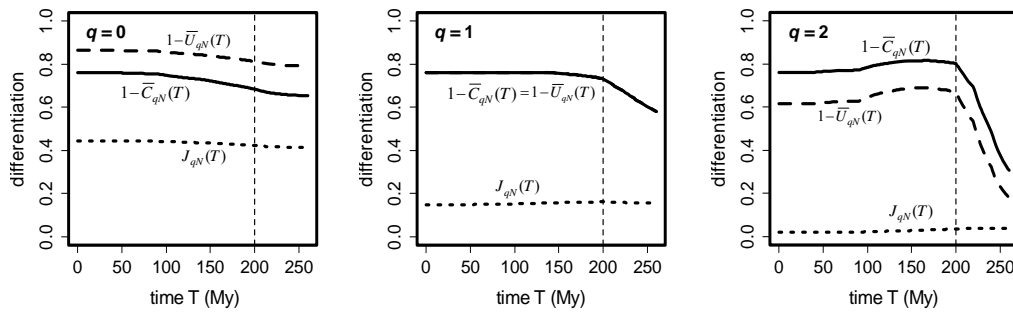
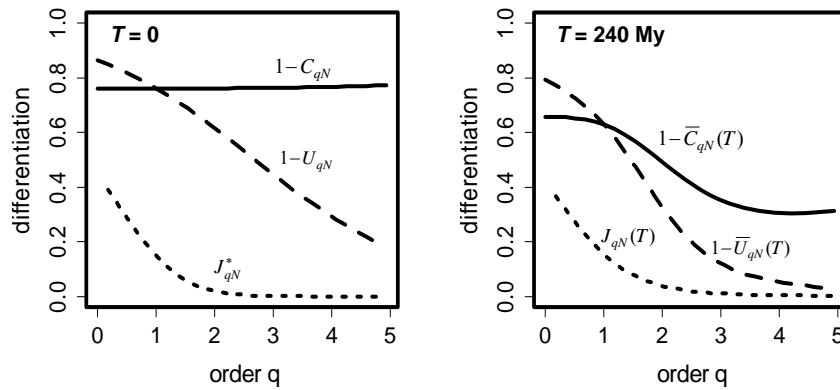(b) Profiles of differentiation measures as a function of order q

Fig. G1. Profiles of differentiation measures. (a) Profiles of three phylogenetic differentiation measures, $1 - \overline{C}_{qN}(T)$, $1 - \overline{U}_{qN}(T)$ and the traditional differentiation measure $J_{qN}(T)$, as a function of the time perspective T, $0 \leq T \leq 250$, for $q = 0$ (left panel), $q = 1$ (middle panel), and $q = 2$ (right panel). All measures are computed for the interval for the interval $[-T, 0]$, and T varies from 0 to 250. The vertical dotted line in all figures refers to the split time ($T = 200$ My, see Fig. 3 in the

main text). (b) (Left panel) Profiles of three non-phylogenetic differentiation measures (i.e., $T = 0$), $1 - C_{qN}$, $1 - U_{qN}$ and J^*_{qN}, as a function of order q, $0 \leq q \leq 5$. (Right panel) Profiles of three phylogenetic differentiation measures, $1 - \overline{C}_{qN}(T)$, $1 - \overline{U}_{qN}(T)$ and the traditional differentiation measure $J_{qN}(T)$, for the specific time perspective $T = 240$ My, the age of the root of the pooled phylogenetic tree.

Example 3. More analysis for two rockfish assemblages

As discussed in the main text, the full data set in Pavoine et al. (2009) contains a total of 52 rockfish species of the genus *Sebastes* collected over 20 years (1980-1986, 1993-1994, 1996, 1998-2007) from the Southern California Bight. It is helpful to first examine the time series of the whole 20 years data. For each of the 20 years, we computed three types of diversity measures: (1) the non-phylogenetic diversity (Hill numbers ^qD). (2) The phylogenetic mean diversity $^q\overline{D}(T)$ of Chao et al. (2010); see Eqs. 4a and 4b of the main text. (3) The phylogenetic generalized entropy $^qI(T)$ of Pavoine et al. (2009); see Eqs. 2c and 2d of the main text.

The plots of the two diversities ^qD and $^q\overline{D}(T)$ for $q = 0$, 1 and 2 as a time series are shown in Fig. G2. A general decline trend is clearly seen for species richness ^0D and the mean lineage length $^0\overline{D}(T)$, but the long-term decreasing trend for each of $q = 1$ and 2 for both diversities is not significant over the 20 years. Since the units for the measure $^qI(T)$ for $q = 0$, 1 and 2 are different, it is meaningless to plot the three-order phylogenetic generalized entropies in a graph, thus the corresponding plots for the measure $^qI(T)$ are omitted. It is noteworthy that the phylogenetic diversity measures are much less "noisy" across years than the ordinary diversity measures; they may measure a more stable and characteristic property of assemblages.
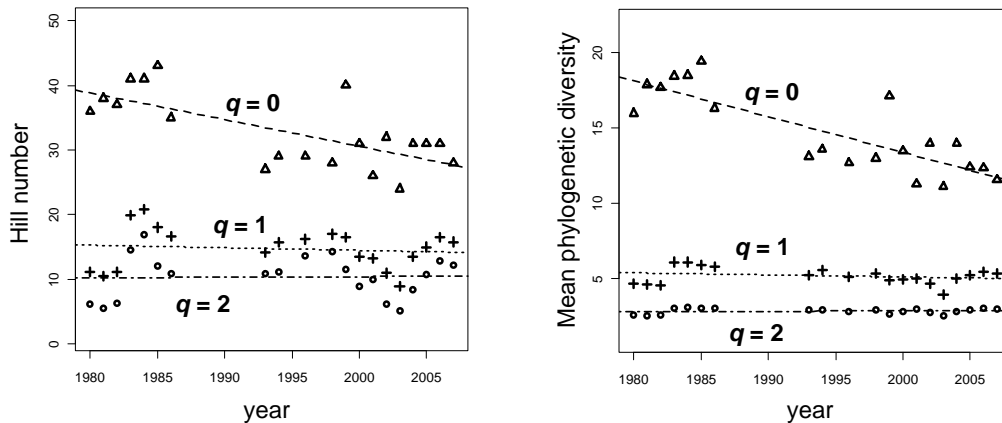

Fig. G2: Hill numbers and mean phylogenetic diversity for 1980-2007 rockfish data (Pavoine et al. 2009). (Left panel) Non-phylogenetic diversity (Hill numbers). (Right panel) Mean phylogenetic diversity. A regression line is fitted to each time series of diversities for each order of q.

As in the main text, we focus on comparing the 1981 assemblage and 2003 assemblage, and

these two assemblages are referred to as Assemblage 1 and 2 respectively. The species abundance and phylogenetic data are provided in Fig. 5a of the main text for the 1981 and 2003 assemblages. For these two contrasting assemblages, we show In Table G1 three types of diversity measures for each of the two assemblages. For each diversity measure, we calculated values for three orders $q = 0$, 1 and 2. The mean diversity $^{q}\overline{D}(T)$ and the measure $^{q}I(T)$ are calculated for $T = 7.9$ My, which is the age of the root in the pooled phylogenetic tree. In the following analysis, unless otherwise stated, T always refers to this age.

Table G1: Three types of diversity measures for two rockfish assemblages.
T = age of the root node.

Order	Assemblage 1 (1981)			Assemblage 2 (2003)		
q	^{q}D	$^{q}\overline{D}(T)$	$^{q}I(T)$	^{q}D	$^{q}\overline{D}(T)$	$^{q}I(T)$
$q = 0$	38	17.86	133.34	24	11.12	80.05
$q = 1$	10.47	4.62	12.10	8.93	3.95	10.85
$q = 2$	5.54	2.57	4.83	5.17	2.52	4.77

Table G1 shows that for each type of diversity measures and each order $q = 0$, 1 and 2, the non-phylogenetic diversity (Hill numbers), mean phylogenetic diversity, and phylogenetic generalized entropy of rockfish in Assemblage 2 is less than the corresponding value in Assemblage 1. For all measures based on Hill numbers, the values for $q = 0$, 1 and 2 are in the same units of "effective number of species", so they can be compared directly. The decline in species richness (^{0}D) is more pronounced than the decline in typical species (^{1}D) and abundant species (^{2}D). This implies the change in non-phylogenetic diversity is mainly due to fewer rare species in Assemblage 2. The units of our phylogenetic measure $^{q}\overline{D}(T)$ are also the same, "effective number of lineages", for all orders of q. Table G1 therefore also implies that the decline in phylogenetic diversity over the past 7.9 My is mainly due to fewer rare lineages in Assemblage 2. Since the effective total branch lengths is $T \times {}^{q}\overline{D}(T)$, we can also conclude that the total lineage length is significantly reduced due to fewer rare lineages in Assemblage 2. While the measure $^{q}I(T)$ also reveals a decline in phylogenetic generalized entropies, different orders of this measure have different units and thus are not comparable.

Table G2 presents the decomposition for the three types of diversity measures considered in Table G1. Since our target is to compare the relative abundances of the two assemblages, the weights for the two assemblages are equal in our following analysis. For both Hill numbers and the mean phylogenetic diversity, our beta is interpreted as "the effective number of completely distinct assemblages", which ranges between 1 and 2 for $N = 2$ assemblages. The gamma, alpha and diversity/lineage excess for these two measures decreases with the order q. For the three orders of $q=0$, 1, and 2, the phylogenetic beta diversities are very stable in a narrow range of 1.20 and 1.28, whereas non-phylogenetic beta diversity varies in a range of 1.26 and 1.67. Again, the excess based on phylogenetic generalized entropy have different units for the three orders, and thus are not comparable.

Table G2: Decomposition of Hill numbers, mean phylogenetic diversity, or generalized entropy for two rockfish assemblages, $T = 7.9$ My, the age of the root node

Order q	Diversity components	Measures		
		^qD	$^q\overline{D}(T)$	$^qI(T)$
$q = 0$	Gamma	39	18.38	137.39
	Alpha	31	14.49	106.69
	Excess	8	3.88	30.70
	Beta	1.26	1.27	--
$q = 1$	Gamma	13.82	5.47	13.43
	Alpha	9.67	4.27	11.48
	Excess	4.15	1.20	1.95
	Beta	1.43	1.28	--
$q = 2$	Gamma	8.95	3.05	5.31
	Alpha	5.35	2.55	4.80
	Excess	3.60	0.50	0.51
	Beta	1.67	1.20	--

For the two rockfish assemblages, we applied in the main text the traditional differentiation measure J_{qN} (based on phylogenetic generalized entropies), and the two proposed differentiation measures $1 - \overline{C}_{qN}$ and $1 - \overline{U}_{qN}$ (based on our mean phylogenetic diversity) as well as their corresponding non-phylogenetic measures; see Tables 1 and 2 of the main text and related discussion. There we evaluated these differentiation measures for the interval $[-T, -T+t]$, an interval of time t after the root of the phylogenetic tree (see Fig. 6 of the main text). Here we apply the three phylogenetic differentiation measures to compare the two assemblages in each evolutionary time period from the root to the tips. We follow Pavoine et al. (2009) in dividing the evolutionary tree by each speciation event, producing 50 periods indexed from root to tips by 1, 2, …, 50. The starting time of the first period represents the age of the root whereas the end of the last period represent the current time. This is the reverse ordering of Pavoine et al. (2009) as they indexed periods from tips to root. We chose an index from root to tips in order to be consistent with our other graphs in the main text.

(1) Within each evolutionary period, we calculated the proposed phylogenetic gamma diversity $^q\overline{D}_\gamma$, alpha diversity $^q\overline{D}_\alpha$, and lineage excess $^q\overline{D}_\gamma - {}^q\overline{D}_\alpha$. In the left panel of Fig. G3, we show the plots for the alpha, gamma and lineage excess in each time period for $q = 0$ (first row), 1 (second row) and 2 (third row). As we have shown in the main text, both the beta diversity and lineage excess lead to the same classes of normalized differentiation measures: $1 - \overline{C}_{qN}$ and $1 - \overline{U}_{qN}$. So in the right panels of the same figure, we show the corresponding

plots for the differentiation between the two assemblages based on the two convergent measures $1 - \overline{C}_{qN}$ and $1 - \overline{U}_{qN}$ for $q = 0$, 1 and 2. All measures are calculated within a time period.

(2) Within each evolutionary period, we also calculated alpha and gamma phylogenetic generalized entropies ($^{q}I_{\alpha}$ and $^{q}I_{\gamma}$) and phylogenetic generalized entropy excess $^{q}I_{\gamma} - {}^{q}I_{\alpha}$. These measures are plotted in the middle panels of Fig. G3 for $q = 0$ (first row), 1 (second row) and 2 (third row). The differentiation measure $J_{qN} = 1 - {}^{q}I_{\alpha}/{}^{q}I_{\gamma}$ based on the phylogenetic generalized entropies is shown in the right panels of the same figure for $q = 0$, 1 and 2. All measures are calculated within a time period.

From Appendix A our mean phylogenetic diversity measures, when applied to an evolutionary period without any internal nodes, reduce to Hill numbers of the importance values of lineages (the total abundance of the descendants of lineage in the present assemblage). The phylogenetic generalized entropies reduce to generalized entropies of the importance values of lineages; see Fig. A1 (Appendix A). So the diversities based on ordinary Hill numbers ^{q}D in Table G2 represent the phylogenetic diversity at the tips (i.e., the 50th period or the present time). Also, within each period, our comparison is simply based on the non-phylogenetic differentiation measures. That is, the two measures $1 - \overline{C}_{1N} \ (= 1 - \overline{U}_{1N})$ and $1 - \overline{C}_{2N}$ respectively reduce to the complement of classical Horn and Morisita-Horn similarity measures within each period (see Table 1 of the main text). The two differentiation measures J_{1N} and J_{2N} reduce respectively to additive "beta"/gamma based on Shannon entropy and Gini-Simpson indices. Therefore, the differentiation measure $1 - C_{qN}$ based on Hill numbers in Table 3 of the main text is identical to the phylogenetic measure at the tips or the present time.

For both traditional and proposed approaches, the left and middle panels of Fig. G3 show that the gamma value (black bar plus white bar in each interval) and alpha value (white bar) are increasing from root to tips for all values of q. For $q = 0$, the distributional patterns for the alpha, gamma and lineage excess are similar for the two approaches; and the three differentiation measures exhibits similar behaviors (see the first row, right panel). However, for $q = 1$ and 2, the patterns are drastically different. In our approach, the lineage excess (black bar in the left panels) in each interval tends to increase as time period moves from root to tips especially for $q = 2$. (For $N = 2$, the maximum possible percentage of lineage excess is 50% of gamma when the two assemblages are completely distinct). In the case of $q = 2$, the percentage tends to 40% (=excess/gamma = 3.6/8.95, see Table G2) at the tips. In the case of $q = 1$, the percentage tends to 30% (= 4.15/13.82, see Table G2) at the tips.

The two measures $1 - \overline{C}_{2N}$ and $1 - \overline{C}_{1N} \ (= 1 - \overline{U}_{1N})$ are very low in the first six periods. They then start to increase and reach a relatively high level, and increasing up to 80% for $q = 2$ and 52% for $q = 1$ in the present time. The measure $1 - \overline{U}_{2N}$ behaves similarly and increases to 67% in the present time. See Table 3 of the main text. In contrast, the generalized entropy excess becomes a strikingly small portion of gamma for all intervals when time period moves from root to tips. The two differentiation measures J_{1N} and J_{2N} are low in the first six periods and exhibit a slightly increasing trend from the seventh to the eighth (for $q = 2$) or ninth (for $q = 1$) period. But after that,

the two differentiation measures steadily decrease, as shown in the second and third rows, right panel of Fig. G3. (Theoretically, these differentiation measures will tend to zero whenever gamma is high for $q = 1$, and whenever alpha is high for $q = 2$.)

As explained, the two measures $1 - \overline{C}_{1N} (= 1 - \overline{U}_{1N})$ and $1 - \overline{C}_{2N}$, when applied to each interval, respectively reduce to the complement of classical Horn and Morisita-Horn similarity measures, we can use the properties of these two classical measures to explain our results. It is known that the Morisita-Horn measure ($q = 2$) is dominated by the very abundant species. Thus our measure $1 - \overline{C}_{2N}$ in each period is dominated by the "very important lineages" (those with high node abundances). As indicated in the main text, the most abundant species in Assemblage 1 are *S. paucispinis* (36.45%), *S. mystinus* (15.19%) and *S. goodei* (12.72%), and the total relative abundances for these three species is around 64%, but they became quite rare in Assemblage 2 (the relative abundance are respectively 0.13%, 8.19% and 0); see Fig. 5b of the main text. In Assemblage 2, the three most abundant species are *S. miniatus* (39.9%), *S. caurinus* (9.17 %) and *S. mystinus* (8.19 %), but the two most abundant species were quite rare in Assemblage 1 (3.82 % and 2.23 % respectively). As will be explained below, the split between these species is also evolutionarily deep; they have been in isolated lineages from the eleventh period to the present. Therefore, the measure for $q = 2$ from the eleventh period onward is mainly determined by those lineages.

For the initial six periods, all those abundant lineages in the assemblages had not diverged yet (see Fig. 5a in the main text), so that the two assemblages have the same dominant ancestral species. Thus the difference between the two assemblages in the first six periods is low for all mesaures, as shown by almost no differentiation for the time periods 1 to 6 in Fig. G3 for $q = 2$ case. At the beginning of the seventh period, S. *caurinus* diverged from the lineage of the other four dominant species (see Fig. 5b). Then at the beginning of the eighth period (about 1.6 My after the root), the most dominant species of Assemblage 2 (*S. miniatus*) diverged from the lineage of the three dominant species in Assemblage 1 (*S. paucispinis*, *S. mystinus*, and *S. goodei*). At the beginning of ninth period, *S. mystinus* diverged from the lineage of the two species (*S. paucispinis*, and *S. goodei*). Then the two species *S. paucispinis*, and *S. goodei* diverged at the beginning of the eleventh period (about 2.2 My after the root). All the five dominant species evolved independently after that time.

Since those dominant species started to diverge between the seventh and eleventh evolutionary periods, all our measures $1 - \overline{C}_{1N} (= 1 - \overline{U}_{1N})$, $1 - \overline{C}_{2N}$ and $1 - \overline{U}_{2N}$ sharply increases in these periods. From the eleventh period, the considerable discrepancy between our differentiation measure and the traditional one for $q = 1$ and 2 leads to totally opposite conclusions. Based on the phylogenetic entropy and especially quadratic entropy, the two assemblages have low differentiation in each time period after the eleventh period. However, our measure indicates high differentiation in each period after the eleventh. Note that the dominant species are in isolated lineages in time periods 11 to 50, implying that the sharp abundance difference for the dominant ancestral lineages remains unchanged in these periods. Thus the difference between the two assemblages from periods 11 to 50 should all be quite high (as shown in the third row, right panels of Fig. G3); the differentiation values of the measure $1 - \overline{C}_{2N}$ from periods 11 to 50 are between 60% and 80% (period 50) as shown in Fig. G3 for $q = 2$; the differentiation values of the measure

$1 - \overline{U}_{2N}$ from period 11 to 50 are between 50% and 67% (period 50). However, the differentiation based on quadratic entropy counter-intuitively shows very low differentiation value of around 8% throughout the time periods 11 to 50.

Similarly for $q = 1$, the differentiation measure $1 - \overline{C}_{1N}$ $(= 1 - \overline{U}_{1N})$ increases from zero to 52% from root to tips whereas the corresponding curve for phylogenetic entropy rises briefly and then counter-intuitively drops to a low value around 14% at the tips. As explained, we think an increasing trend and relatively high differentiation should be the more intuitive and sensible answer from periods 11 to 50 for this real tree. These observations also help explain the findings for our case study in the main text; see Fig. 6 of the main text and related discussion.
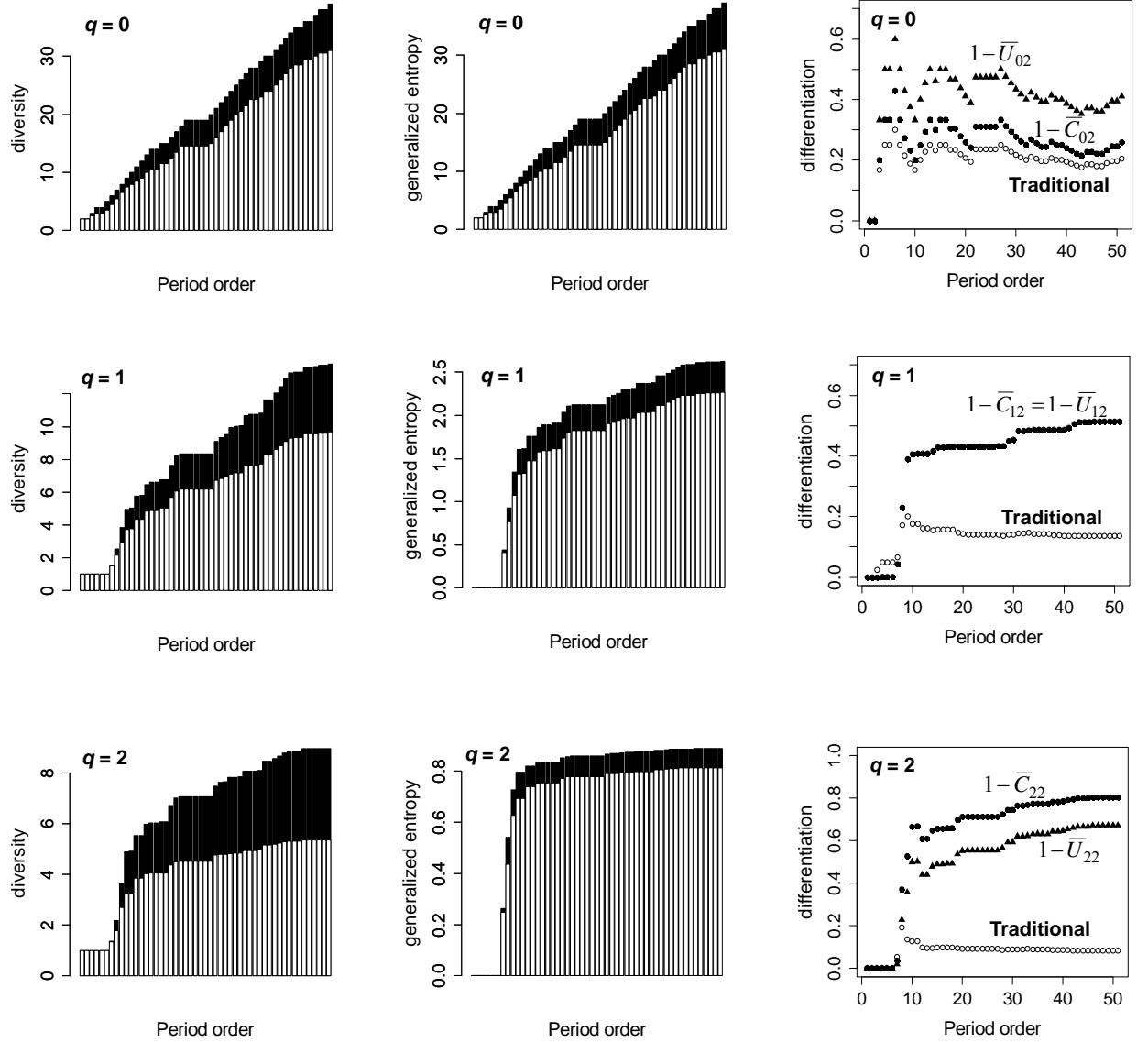
Fig. G3: Phylogenetic partitioning and differentiation within each evolutionary period (periods are ordered from the root to tips) for two rockfish assemblages (the 1981 assemblage and 2003 assemblage). $q = 0$ (the first row), $q = 1$ (the second row) and $q = 2$ (the third row).

(Left panels) Plots of our phylogenetic gamma diversity $^q\overline{D}_\gamma$ (white plus black bar) and alpha diversity $^q\overline{D}_\alpha$ (white bar), black bar denotes lineage excess $^q\overline{D}_\gamma - {}^q\overline{D}_\alpha$. All measures are calculated within each period; see Eqs. 7a, 7b, 8a and 8b of the main text. (The maximum possible percentage of beta is 50% of gamma.)

(Middle panels) Plots of the gamma phylogenetic generalized entropy $^qI_\gamma$ (white plus black bar)

and alpha $^{q}I_{\alpha}$ (white bar), black bar denotes phylogenetic generalized entropy excess $^{q}I_{\gamma} - {}^{q}I_{\alpha}$. All measures are calculated within each period; see Eqs. 2c and 2d of the main text.

(Right panels) Plots of the proposed differentiation measure $1 - \overline{C}_{qN}$ (solid circles) and $1 - \overline{U}_{qN}$ (solid triangles) based on our mean phylogenetic diversity, and the traditional differentiation measure $J_{qN} = 1 - {}^{q}I_{\alpha}/{}^{q}I_{\gamma}$ (open circles) based on the phylogenetic generalized entropy.

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