SUPPLEMENTARY MATERIAL FOR THE ARTICLE:

Homophily around specialized foraging underlies dolphin social preferences

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SUPPLEMENTARY MATERIAL S1: BIOPSY SAMPLING AND MOLECULAR ANALYSES

While following groups of dolphins to collect behavioural data and individual identification, we also attempted to collect skin samples using a remote biopsy system, consisting of custom-built darts with stainless-steel tips fired from a 120lb crossbow (research permit SISBIO#47876–1). We also opportunistically sampled skin from stranded carcasses. We collected a total of 25 biopsies from alive dolphins and ended up using skin samples from 13 highly resighted individuals; we collected samples from 12 stranded animals and included in the genetic analyses the three samples that came from well-known photo-identified individuals. We used skin samples to carry out genetic analyses to determine sex and genetic relatedness among individual bottlenose dolphins.

Genomic DNA was extracted from 25 mg of each skin sample using a salting-out protocol [1]. Samples were incubated overnight in a buffer containing 0.2 mg/mL Proteinase K (New England Biolabs, US; Tris 50 mM, NaCl 0.4 M, EDTA 20 mM, SDS 0.5%, pH 7.5). Remaining tissue fragments were digested through sonication (3 pulses of 5 seconds each at 30% of potency). Samples were centrifuged. Remaining supernatant was vortexed with NaCl 5M. Genomic DNA was precipitated with isopropanol, washed with 80% ethanol to remove

salt residues, and resuspended in TE buffer 1x. The DNA concentration was evaluated spectrophotometrically in a NanoDrop ND-1000 (Thermo Scientific, UK) at 260 nm. 230/260 and 280/260 ratios were used to assessed contamination by salt and proteins, respectively.

a) Genotypes

We genotyped 13 individuals using 15 microsatellite loci: Ttr36, Ttr54, Ttr55, Ttr61, Ttr90, Ttr98 [2]; Ttr04, Ttr11, Ttr19, Ttr58, Ttr63, TtrFF6 [3]; TexVet5 [4]; EV37Mn [5]; PPHO130 [6]. Similar numbers of variable loci have been used to provide information about dolphins' inter-individual kinship [e.g. 7–9]. The 15 loci were amplified in multiplexes using a Qiagen Type-it Microsatellite PCR kit and following the polymerase chain reaction (PCR) conditions described in Rosel *et al.* [2]. Genotyping was conducted on an ABI 3130 with the Genescan LIZ-600 size standard (conducted at Centro de Pesquisa sobre o Genoma Humano e Células-Tronco, Universidade de São Paulo, Brazil), and viewed with GeneMapper v5 (Applied Biosystems). Quality control was applied to all microsatellite genotyping to ensure consistency across PCR amplification and genotyping runs by adding one no-DNA and two positive controls in all PCRs.

Using MSTools [10], we found no pairs of duplicates based on the 15 microsatellite loci, sex, and photo-identification data. We also used the Microchecker v2.2.3 [11] with 10,000 iterations to check for the presence of genotyping errors due to null alleles, allelic dropout, and incorrect scoring of stutter peaks. Each locus was tested for departure from Hardy-Weinberg Equilibrium (HWE) [12] and linkage disequilibrium using the Fisher's exact tests with the software GENEPOP v4.6 [13] with 10,000 dememorizations, 1,000 batches, and 10,000 interactions per batch. The sequential Bonferroni technique was applied for the significance correction for multiple tests [14]. All loci passed in the quality control described

above. Finally, we used COANCESTRY v1.0.1.8 [15] to estimate mean pairwise relatedness values (*r*) for the 13 genotyped individuals using Queller and Goodnight's [16].

b) Sex

Molecular sexing was also conducted for the 16 skin samples. ZFX and SRY genes were amplified from genomic DNA extracted as described above, through a multiplex polymerase chain reaction (PCR). Primers were designed specifically for *Tursiops truncatus*, based on sequences publicly available on NCBI. For ZFX, five transcript variants were aligned, and primers were designed for the homologous region (accession numbers for ZFX: XM_019927721.1, XM_019927720.1, XM_019927719.1, XM_019927718.1 and XM_019927717.1; accession number for SRY: AB108521.2). The sequences of used primers were: ZFX Forward (TGCGACGAATGTGGGAAGCATTTC), ZFX Reverse (AGTACTGGCATTGGTACGGCTTCT); SRY Forward (ACATTCCCTACTGTGGACGGACAA), SRY reverse (GTGGCAGGAGTGAGCTGCTTATG). Amplified samples were visualized in a 2% agarose gel. The presence of two fragments, one of approximately 247bp (ZFX) and another of approximately 432bp (SRY) was considered diagnostic of male, while the presence of only one fragment around 247bp was diagnostic of a female. We conducted the DNA extraction procedures, the amplification of microsatellite loci and molecular sexing at the Laboratório de Biomarcadores de Contaminação Aquática e Imunoquímica, Universidade Federal de Santa Catarina, Brazil.

SUPPLEMENTARY MATERIAL S2: POTENTIAL STRUCTURAL FACTORS OF SOCIAL ASSOCIATIONS

We quantified five structural factors that could affect dolphin association patterns: frequency of participation in the foraging tactics, home range overlap, genetic relatedness, assortativity by sex and age classes.

a) Foraging tactics

We estimated the use of foraging tactics as the proportion of times individuals were observed engaged in the "cooperative foraging" tactic (specialized foraging interaction with artisanal fishermen) relative to the "non-cooperative" tactic (usual dolphin foraging, in the absence of fishermen). For each individual dolphin, we calculated the relative frequency of participation in the cooperative foraging as the proportion $fp_i = Cr_i/Tr_i$, where Cr_i is the number of cooperative foraging records of dolphin *i*, and *Tr* is the total number of foraging records of *i* [17]. To minimize pseudoreplication, whenever an individual was repeatedly observed across groups in the same sampling day, we randomly selected only one sighting per group and maximum two per day, collected at least two hours apart [17]. We represented the pairwise relationship between individuals *i* and *j* in a distance matrix **FP** where each element is the Euclidean distance d(i, j) between the fp_i and fp_j, which ranges from d(i, j) = 0 (when $fp_i = fp_j$) to d(i, j) = +∞.

b) Home range

For all sampled individuals, we estimated home range size based on location data from boat surveys as the area routinely used to meet daily needs [18]. We used fixed kernel methods with a 95% probability contour [19], always discarding land areas. A smoothing parameter was selected by least square cross-validation [20]. To minimize potential spatial

autocorrelation bias, we randomly selected a single record per individual per sampling day [21]. We represented the pairwise relationship between individuals *i* and *j* in a matrix **H** in which each element is the home range overlap calculated as $HRO_{ij} = \left(\frac{R_{ij}}{R_i}\right) \cdot \left(\frac{R_{ij}}{R_j}\right)$, where R_i and R_j are the total home range size for dolphins *i* and *j*, respectively, and $R_{i,j}$ is the overlap between their areas [22].

c) Genetic relatedness

We estimated genetic relatedness by carrying out microsatellite genotyping using 15 microsatellite loci amplified from DNA extracted from skin samples (electronic supplementary material S1). We then created a matrix **G** in which each element is the mean pairwise relatedness value [16] for genotyped individuals *i* and *j* given by the Queller and Goodnight [16] index that ranges from $r_{ij} = -1$ to $r_{ij} = 1$. A total of 12 out of the 13 genotyped and photo-identified dolphins were used after filtering the social data. Individuals *i* and *j* were considered highly related when $r_{ij} \geq 0.5$ (e.g. parent-offspring), moderate when $0.25 \leq r_{ij} < 0.5$ (e.g. half-siblings; grandparents) and considered unlikely related when $r_{ij} < 0.25$.

d) Sex

We determined sex using two complementary approaches. We first conducted molecular sexing for 16 skin samples of photo-identified individuals using polymerase chain reaction (PCR) to amplify fragments of ZFX and SRY genes with primers designed for *T. truncatus* (electronic supplementary material S1). We then relied on long-term field observations to infer the sex of the remaining individuals. We assumed as females the individuals sighted in close association with a dependent calf on more than three independent sampling days during the study period [*cf.* 23], and as males otherwise. We represented the pairwise relationships

with the binary matrix **S** in which elements s_{ij}=1 when individuals *i* and *j* were of the same sex and s_{ij}=0 otherwise.

e) Age classes

Finally, we classified individuals into age classes by combining field observations on body size, reproductive state, and knowledge of long-term life history [*cf.* 23,24]. Since we disregarded all calves and juveniles, we used two age classes: "senior" for all individuals observed in the area for more than 30 years based on previous field data [25–27], and "adult" for the remaining. We represented the pairwise relationships with a binary matrix **A** in which elements a_{ij}=1 when individuals *i* and *j* were of the same class and a_{ij} = 0 otherwise.

SUPPLEMENTARY MATERIAL S3: INFLUENCE OF STRUCTURAL FACTORS ON SOCIAL ASSOCIATIONS

We estimated pairwise associations among photo-identified individual dolphins seen in groups using the simple-ratio association index (SRI) [28]. The SRI_{ab} quantifies the association between two individuals, *a* and *b*, as the proportion of times they were observed in the same group in relation to the total number of times they were seen, in the same group or not, as: $SRI_{ab} = \frac{x}{x+ya+yb+yab}$, where *x* is the number of times *a* and *b* were seen in the same group; *ya* and *yb* are the number of times in which only *a* or only *b* were identified, respectively; and *yab* is the number of times in which *a* and *b* were identified but not in the same group. Imperfect detections of group membership (i.e. not identifying all group members) is typical in cetacean studies, and the half-weight association indices is commonly used to try and correct this bias [28]. Given that in our case the percentage of identified individuals in the group was high (74-83%) [26], we chose the SRI to avoid over-correction

[29]. Moreover, association indices are sensitive to sampling effort, thus we filtered the identification data to remove poorly re-sighted individuals to avoid spurious associations [28]. To remove eventual transient individuals passing through the area [26], we used a very restrictive observation threshold to include only individuals seen in more than the 5% of the sampling records (number of groups, n=503). That is, all individuals seen less than 25 times were removed from the analyses to ensure high that associations were estimated with high accuracy and precision. We then calculated the association for all individuals in each of the four behavioural contexts (cooperative foraging n=120; non-cooperative foraging n=219; non-foraging n=158; all behaviour n=497 groups).

Next, we quantified the contribution of all five structural factors in driving social patterns with multiple regression quadratic assignment procedure (MRQAP) and double-semi-partialling method [30]. In each of the four behavioural contexts (cooperative and non-cooperative foraging, non-foraging, all behaviour), we investigated possible linear relationships between the social associations and the structural factors using the context-dependent SRI association matrix as the dependent variable and the matrices representing the pairwise relationships among structural factors (foraging tactics, home range overlap, genetic relatedness, sex and age) as independent variables.

To evaluate the significance of the regression coefficients of the MRQAP models, we used permutation methods. We estimated the regression coefficients of the MRQAP models and used 20,000 permutations to build randomised distributions to compare the empirical coefficients with. The *P*–values were the proportion of the estimated coefficient regression being smaller or greater than expected by chance. We expected all empirical regression coefficients to be higher than the null expectancy, except for the frequency of participation in the cooperative foraging (*FP*) that was represented by a distance metric, so we expected its

regression coefficient to be smaller than the null expectancy. We used the *mrqap.dsp* function from the *asnipe* R package [31] to run the MRQAP tests.

a) Subsets of the dataset and MRQAP models

Since genetic relatedness and sex were not available for all individuals, we analysed three subsets of our dataset separately. First, we performed an MRQAP for individuals in which all structural variables were known (n =12; Figure S1). The results of the first MRQAP are in Table S1.

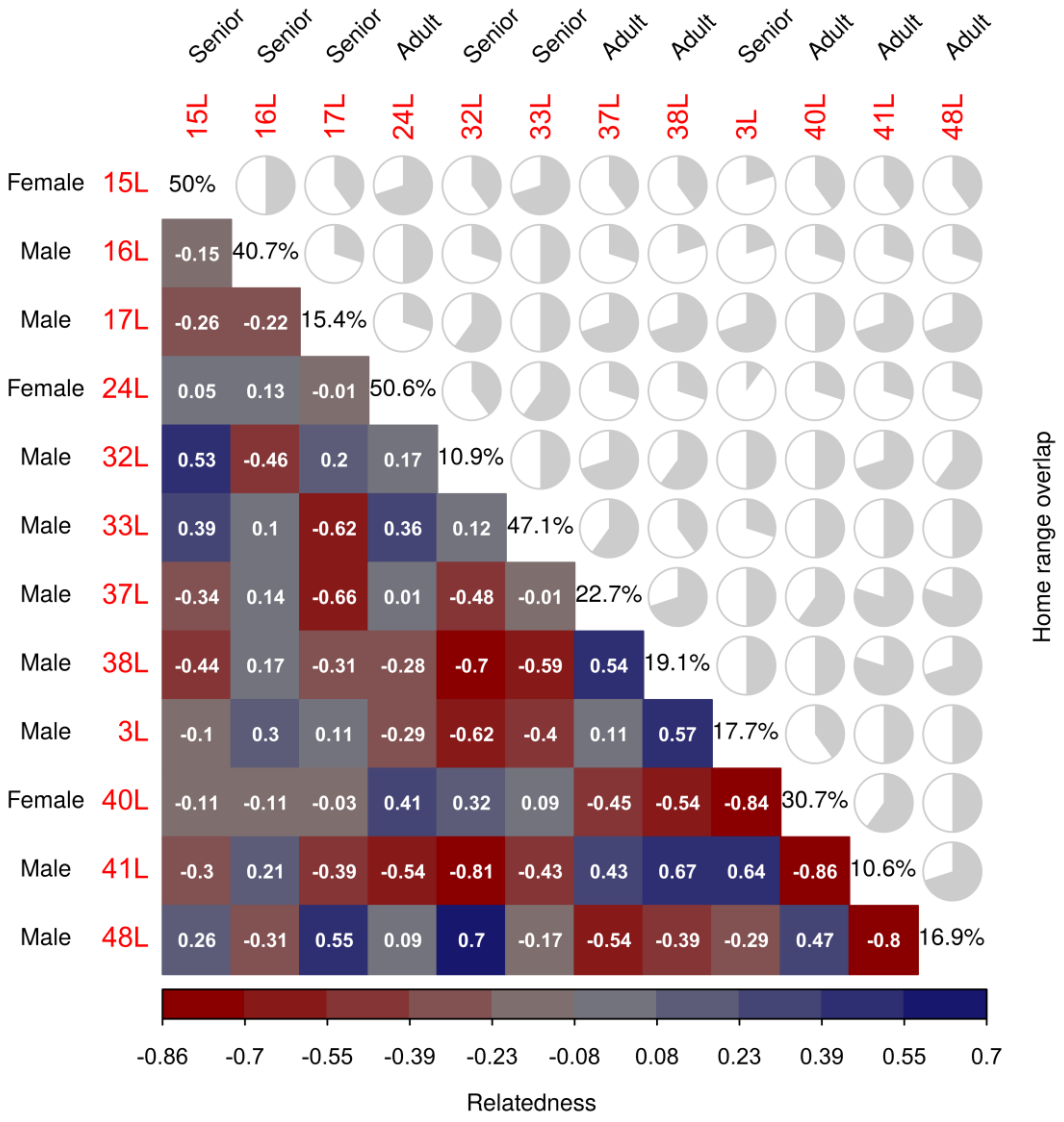

Figure S1: The subset of 12 individual bottlenose dolphins for which all individual traits were available: age and sex classes, home range overlap, the relative frequency of participation with fishermen, and genetic relatedness. Alphanumeric codes indicate individual photo-identification labels, along with genetically-determined sex, and field-based age classes. In the upper triangle, the grey portion of the pie charts indicates home range overlap (*HRO*) between pairs of individuals. Numbers in the diagonal indicate the relative frequency of participation in the cooperative foraging tactic with fishermen (*FP*). In the lower triangle, the colour code indicates genetic relatedness between individuals (*r*), where values greater than 0.5 are deemed highly-related pairs (i.e. parent-offspring), and values lower than 0.25 indicate unlikely-related pairs.

Table S1: Multiple Regression Quadratic Assignment Procedure and the influence of all structural variables on dolphin social associations. Matrices representing structural variables (predictors) were regressed against the association matrix (SRI) in each behavioural context (all behaviour, cooperative foraging, non-cooperative foraging, non-foraging) using a subset of the individuals in the population ($n = 12$) to which data on all predictors were available. FP: Euclidean distance of relative frequency of participation in the cooperative foraging tactic; HRO: home range overlap; Age and Sex: binary matrices where individuals of the same age/sex classes are represented by 1, and different classes by 0. Relatedness: genetic relatedness. Adjusted R^2 indicates how much of the variation on association indices was explained by the predictors. Bold font indicates significant predictors in which *P*-values are given by the proportion of times the empirical regression coefficient was smaller or greater than the null expectancy from 20,000 randomisations (*P*–values are complementary, totalling 1). We considered *FP* significant when $\beta \geq r$ thus $P < 0.05$ (*); all the other predictors were significant when $\beta \leq r$, thus $P > 0.95$ (**).

Context (SRI)	Predictors	Regression Coefficient (β)	*P* (β≥r)	*P* (β≤r)	Adjusted R^2
All Behaviour	FP	-0.0001	0.263	0.736	58%
	HRO	0.0683	1.000**	<0.001*	
	Age	0.0113	0.922	0.077	
	Sex	-0.0152	0.048	0.981	
	Relatedness	0.0068	0.753	0.246	
Cooperative foraging	FP	0.0004	0.781	0.219	27%
	HRO	0.0694	0.990**	0.009*	
	Age	-0.0042	0.373	0.626	
	Sex	-0.0245	0.048*	0.951**	
	Relatedness	0.0135	0.789	0.210	
Non-Cooperative foraging	FP	$-1.15 \cdot 10^{-5}$	0.450	0.549	36%
	HRO	$5.17 \cdot 10^{-2}$	0.982**	0.018*	
	Age	$1.64 \cdot 10^{-2}$	0.940	0.059	
	Sex	$-1.64 \cdot 10^{-2}$	0.078	0.921	
	Relatedness	$3.61 \cdot 10^{-3}$	0.590	0.409	
Non-Foraging	**FP**	-0.0006	0.062	0.937	44%
	HRO	0.061	0.990**	0.009*	
	Age	0.012	0.880	0.119	
	Sex	0.0010	0.533	0.466	
	Relatedness	0.002	0.567	0.432	

To test for correlation between association indices and genetic relatedness matrices, we used a Mantel test with 9999 permutations. We found no correlation between association indices and genetic relatedness matrices ($r = 0.134$, $P = 0.138$, Figure S2), in agreement with the results of the MRQAP. Given the lack of correlation between association and relatedness, we omitted relatedness and created another four MRQAP models, one for each behavioural state. But now, we used a subset of 30 individuals with all structural variables available, except for the genetic relatedness (Table S2).

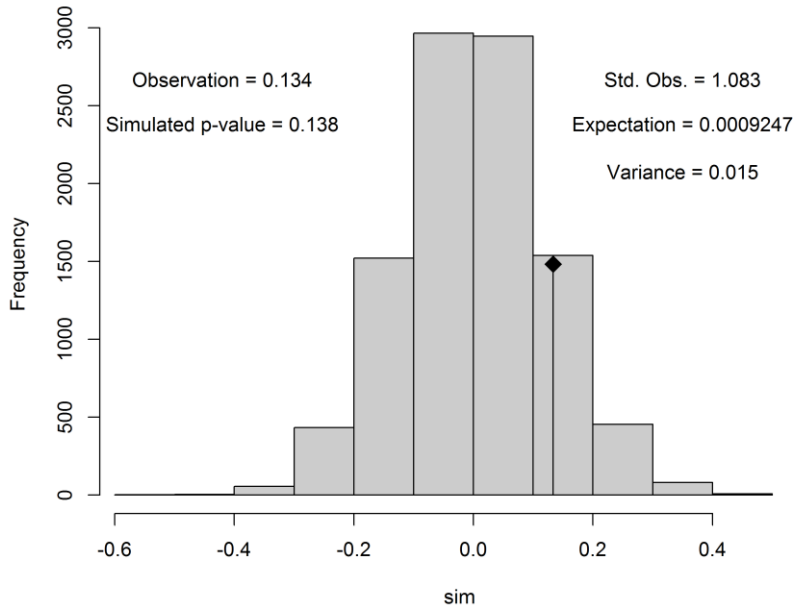

Figure S2: **No correlation between social association and genetic relatedness**. Mantel test for the correlation between the simple-ratio association matrix (SRI) considering all behavioural contexts and the pairwise genetic relatedness among individual dolphins. Histogram depicts the expected distribution of the correlation between the two variables and the diamond black symbol indicates the empirical correlation.

Table S2: Multiple Regression Quadratic Assignment Procedure and the influence of all structural variables but genetic relatedness on dolphin social associations. Matrices representing four structural variables (predictors) were regressed against the association matrix (SRI) in each behavioural context (all behaviour, cooperative foraging, non-cooperative foraging, non-foraging) using the subset of the population (n = 30) to which all structural variables, except the genetic relatedness, were available. *FP*: Euclidean distance of relative frequency of participation in the cooperative foraging tactic; *HRO*: home range overlap; Age and Sex: binary matrices where individuals of the same age/sex classes are

represented by 1, and different classes by 0. Adjusted R^2 indicates how much of the variation on association indices was explained by the predictors. Bold font indicates significant predictors in which *P*-values are given by the proportion of times the empirical regression coefficient was smaller or greater than the null expectancy from 20,000 randomisations (*P*–values are complementary, totalling 1). We considered FP significant when $\beta \geq r$ thus $P < 0.05$ (*); all the other predictors were significant when $\beta \leq r$, thus $P > 0.95$ (**).

Context (SRI)	Predictors	Regression Coefficient (β)	P (β≥r)	P (β≤r)	Adjusted R^2
All Behaviour	**FP**	-0.0003	<0.001*	0.999**	47%
	HRO	0.061	1.000**	<0.001*	
	Age	0.0024	0.736	0.263	
	Sex	0.001	0.609	0.390	
Cooperative foraging	FP	$-3.79 \cdot 10^{-5}$	0.367	0.623	16%
	HRO	$4.52 \cdot 10^{-2}$	0.999**	<0.001*	
	Age	$-1.74 \cdot 10^{-3}$	0.380	0.619	
	Sex	$7.57 \cdot 10^{-4}$	0.548	0.451	
Non-Cooperative foraging	FP	-0.0001	0.114	0.885	34%
	HRO	0.053	1.000**	<0.001*	
	Age	0.001	0.629	0.370	
	Sex	0.0005	0.537	0.462	
Non-Foraging	**FP**	-0.0006	<0.001*	1.000**	34%
	HRO	0.069	1.000**	<0.001*	
	Age	0.008	0.943	0.056	
	Sex	0.004	0.798	0.201	

Given that similarity in sex classes were not significant, we omitted this variable to perform a third MRQAP that included all the 34 individuals (Table S3).

Table S3: Multiple Regression Quadratic Assignment Procedure and the influence of cooperative foraging behaviour, home range and age on dolphin associations. Matrices representing structural variables (predictors) among all the individuals (*n* = 34) were regressed against the association matrix (SRI) in each behavioural context (all behaviour, cooperative foraging, non-cooperative foraging, non-foraging). FP: Euclidean distance of relative frequency of participation in the cooperative foraging tactic; HRO: home range

overlap; Age: binary matrix where individuals of the same age classes are represented by 1, and different classes by 0. Adjusted R^2 indicates how much of the variation on association indices was explained by the predictors. Bold font indicates significant predictors in which *P*-values are given by the proportion of times the empirical regression coefficient was smaller or greater than the null expectancy from 20,000 randomisations (*P*–values are complementary, totalling 1). We considered FP significant when $\beta \geq r$ thus $P < 0.05$ (*); all the other predictors were significant when $\beta \leq r$, thus $P > 0.95$ (**).

Context (SRI)	Predictors	Regression Coefficient (β)	P (β≥r)	P (β≤r)	Adjusted R^2
All Behaviour	**FP**	-0.063	<0.001*	1.000**	46%
	HRO	-0.0003	1.000**	<0.001*	
	Age	0.003	0.823	0.176	
Cooperative foraging	FP	-0.0001	0.542	0.457	18%
	HRO	0.048	1.000**	<0.001*	
	Age	0.0008	0.542	0.457	
Non-Cooperative foraging	**FP**	-0.0002	0.011*	0.988**	35%
	HRO	0.058	1.000**	<0.001*	
	Age	0.003	0.780	0.219	
Non-Foraging	**FP**	-0.0005	<0.001*	1.000**	31%
	HRO	0.066	1.000**	<0.001*	
	Age	0.004	0.850	0.149	

SUPPLEMENTARY MATERIAL S4: REMOVING THE EFFECT OF STRUCTURAL FACTORS FROM SOCIAL ASSOCIATIONS

a) Social affiliations

We developed general affiliation indices (GAI) [32] to remove the effect of the structural factors from the association indices and test the existence of true affiliations between dyads. Formally, GAI are the residuals of a generalized linear model between a social metric and multiple structural factors; biologically, GAI indicate the assortment of individuals that is not explained by the structural factors which are interpreted as social affiliations, i.e. active association preferences among individuals [32]. To create GAIs in each behavioural context

(cooperative and non-cooperative foraging, non-foraging, all behaviour), we fitted a binomial generalized linear model (GLM) with the corresponding unfolded simple-ratio association index matrices (SRI) as the dependent variables, and the significant structural factors selected from the MRQAP as independent variables [*cf.* 32]. Following the final MRQAP results (Table S3), the GAIs for each behavioural context were: $SRI_{(all\ behaviour)} \sim FP + HRO$; $SRI_{(cooperative\ foraging)} \sim HRO$; $SRI_{(non\text{-}cooperative\ foraging)} \sim FP + HRO$; $SRI_{(non\text{-}foraging)} \sim FP + HRO$, where SRI_x = the context-dependent simple-ratio association index matrix, FP = Euclidean distance of relative frequency of participation in the cooperative foraging tactic; HRO = home range overlap.

b) Social preferences

We tested the null hypothesis that individual dolphins associate at random using a null model approach (electronic supplementary material S6). In each behavioural context, we compared the Standard Deviation (SD) of the observed simple-ratio associations (SRI) and the SD of the observed generalized affiliation index (GAI) with their corresponding benchmark distributions of the SD resultant from the randomised SRI and GAI matrices generated by the null model. We considered preferred and avoided associations and social affiliations to exist between daily sampling periods whenever the observed SD was significantly higher than the null expectancy. When the observed social metrics (SRI and GAI) were more variable than expected by chance, there are evidence for unexpectedly high indices (which is suggestive of social preferences) and unexpectedly low indices (suggestive of social avoidances, [28,32]). The results of the permutation tests are presented in Figure 1 (main text).

SUPPLEMENTARY MATERIAL S5: SOCIAL NETWORKS

We built networks for each social metric, the simple-ratio association index, SRI, and the generalized affiliation index, GAI, in each behavioural context. In the association networks, nodes representing photo-identified individuals were connected by links whose thicknesses were proportional to their SRI. In the affiliation networks, individuals were linked by GAI given by the best-fitting model (following MRQAP results in Table S3).

We then calculated modularity and assortativity for the associations and affiliation networks to test for social division and assortment around the specialized foraging tactic in all behavioural contexts. We first evaluated whether networks were structured into strongly connected subgroups (i.e. modules) by calculating modularity using an algorithm that maximized the metric *Q* [see 33]. We highlight that the affiliation networks can contain negative links (since GAIs are the residuals of a generalized linear model [32]) and that only positive links (i.e. positive affiliations) were considered when calculating modularity [33]. We then tested whether the social preferences that underpin the formation of social modules were related to the specialized foraging tactic. Given that the specialized foraging tactic implies high frequency of participation in the foraging with fishermen (*fp*) and small home range size (*hr*) [17], we calculated assortativity indices to evaluate whether links in the networks typically occurred between similar nodes, that is individuals with high or low frequency of participation in the cooperative foraging (*fp*) and large or small home range size (*hr*). We used a weighted, continuous assortativity index for each trait—*fp* and *hr*—which ranges from r_c^w= -1 (a fully disassorted network) to r_c^w= 1 (a fully assorted network) [34].

We used a null model approach to test the significance of modularity and assortativity (electronic supplementary material 6). We calculated the modularity and assortativity of an ensemble of 20,000 randomised association and affiliation networks and considered the

empirical values to be statistically significant when they fell outside the 95% confidence interval of their corresponding benchmark distributions [28]. Further, we expected that the modularity and assortativity results would be coupled, thus the social modules would predominantly contain dolphins that use the same foraging tactic—that is, modules of individuals that frequently interact with fishermen (high *fp*) and so forage over small areas (low *hr*); and modules of individuals that rarely interact with fishermen (low *fp*) and so forage over large areas (high *hr*) [17]. To evaluate this, we compared the mean *fp* and *hr* values across modules of the same network, and used network node permutation methods [35,36] to calculate the 95% confidence interval of the expected distribution of *fp* and *hr* if the individuals were distributed randomly across the network. The results of the social network analyses are presented in Figure 1 (main text) and the Table S4 further details the modularity and assortativity results.

Table S4. Summary of the network metrics for the association (SRI) and affiliation (GAI) dolphin networks in the four behavioural contexts. Modularity values (Q), number of social modules, size of modules (number of individuals), within-module mean values of frequency of participation in the foraging with fishermen (*fp*) and within-module mean home range size (*hr*). SD: standard deviation; 95% CI: confidence intervals estimated with null models. The assigned predominant foraging tactic to each module relies on the fact that specialized foraging ("with fishermen") implies high frequency of interaction with artisanal fishermen and small home range sizes, and the opposite tactic ("without fishermen") implies low frequency of interaction and large home ranges [17]. The mixed modules include dolphins that use both tactics.

Simple-Ratio Association Index, SRI				Frequency of foraging with fishermen, *fp*		Home range size, *hr*		Predominant foraging tactic within modules
Behavioural context	***Q*** **(95%CI)**	**Number of modules**	**Module size**	**Mean ± SD**	**95% CI**	**Mean ± SD**	**95% CI**	
All behaviour	0.254 (0.056 - 0.095)	2	15	0.441 ± 0.084	0.204 - 0.337	14.247 ± 6.838	22.867 - 33.793	With fishermen
			19	0.135 ± 0.072	0.216 - 0.322	39.432 ± 8.344	23.989 - 32.616	Without fishermen
Cooperative foraging	0.273 (0.163 - 0.286)	1	34	-	-	-	-	Mixed
Non-cooperative foraging	0.220 (0.102 - 0.166)	3	15	0.431 ± 0.107	0.206 - 0.332	15.233 ± 9.827	22.6 - 33.54	With fishermen
			10	0.163 ± 0.095	0.187 - 0.357	36.75 ± 9.937	20.83 - 35.98	Without fishermen
			9	0.121 ± 0.064	0.178 - 0.363	40.767 ± 6.225	19.911 - 36.633	Without fishermen
Non-foraging	0.336 (0.131 - 0.213)	5	7	0.476 ± 0.073	0.161 - 0.387	10.943 ± 3.401	17.729 - 37.529	With fishermen
			7	0.402 ± 0.088	0.16 - 0.38	16.871 ± 8.544	18.943 - 38.157	With fishermen
			3	0.168 ± 0.065	0.088 - 0.459	30.333 ± 16.372	10.967 - 43.3	Without fishermen
			10	0.158 ± 0.072	0.182 - 0.355	40.09 ± 5.184	20.52 - 35.69	Without fishermen
			7	0.137 ± 0.154	0.161 - 0.38	39.471 ± 10.327	19.386 - 37.286	Without fishermen

Generalized Affiliation Index, GAI				Frequency of foraging with fishermen, *fp*		Home range size, *hr*		Predominant foraging tactic within modules
Behavioural context	***Q*** **(95%CI)**	**Number of modules**	**Module size**	**Mean ± SD**	**95% CI**	**Mean ± SD**	**95% CI**	
All behaviour	0.247 (0.144 - 0.228)	7	5	0.367 ± 0.184	0.139 - 0.413	19.52 ± 11.457	16.38 - 40.38	With fishermen
			4	0.367 ± 0.193	0.114 - 0.424	18.15 ± 14.316	14.725 - 42.05	With fishermen
			8	0.327 ± 0.136	0.168 - 0.379	25.488 ± 16.046	19.1 - 37.225	With fishermen
			5	0.281 ± 0.199	0.128 - 0.403	29.68 ± 12.852	16.3 - 39.28	Mixed
			7	0.188 ± 0.156	0.171 - 0.379	32.114 ± 15.489	18.6 - 37.914	Without fishermen
			1	0.125	0 - 0.571	38.4 ± -	7.3 - 51.4	Without fishermen
			4	0.105 ± 0.049	0.113 - 0.421	44.3 ± 5.293	15.5 - 42	Without fishermen
Cooperative foraging	0.246 (0.163 - 0.266)	1	34	-	-	-	-	Mixed
Non-cooperative foraging	0.192 (0.151 - 0.240)	1	34	-	-	-	-	Mixed
Non-foraging	0.268 (0.158 - 0.252)	6	4	0.417 ± 0.074	0.116 - 0.429	16.7 ± 9.622	14.825 - 41.95	With fishermen
			9	0.398 ± 0.143	0.155 - 0.378	17.3 ± 12.65	18.657 - 38.029	With fishermen
			8	0.281 ± 0.182	0.162 - 0.371	27.838 ± 15.2	19.438 - 36.875	Mixed
			7	0.18 ± 0.08	0.095 - 0.461	41 ± 2.081	10.767 - 43.9	Without fishermen
			3	0.166 ± 0.163	0.174 - 0.37	36.9 ± 11.558	20.289 - 35.811	Without fishermen
			3	0.147 ± 0.079	0.097 - 0.455	32.4 ± 18.777	11.933 - 43.1	Without fishermen

In brief, the association (SRI) networks were divided into more than one social module in all behavioural contexts but the cooperative context; the affiliation networks (GAI) were divided modules only outside of the foraging contexts (Figure 1b). In all behavioural contexts where there was social division, the social network structure was related to the specialized foraging tactic, as seen by the significant assortativity by both frequency of foraging with fishermen and home range size (Figure 1c,d) and by social modules that were distinguished by the predominant foraging tactic (Table S4).

SUPPLEMENTARY MATERIAL S6: NULL MODELS

We used a null model to test both for social preferences (electronic supplementary material S4) and the significance of the observed network modularity and assortativity (electronic supplementary material S5). For each behavioural context, we generated an ensemble of 20,000 randomised association and affiliation networks based on 25,000 data-stream permutations of the raw observation data with a swapping algorithm [37] but restricting permutations within sampling periods to control for demographic effects [28]. We permuted the empirical group-by-individual matrix constraining the number of groups, individuals and occurrences (matrix dimension and fill), group size (row totals) and individual frequency of observation (column totals). We discarded the first 5,000 randomised matrices to minimize the effect of initial values potentially correlated to the empirical data (inspired by the limitations of a similar randomization algorithm; [38]). From each randomised group-by-individual matrix, we calculated a simple-ratio index association matrix, with which we built a generalized affiliation index using the same predictors selected via MRQAP for the empirical data (see Table S3).

SUPPLEMENTARY MATERIAL S7: R SESSION INFORMATION

The R code is available at https://bitbucket.org/alexandremarcelsm/botonet/src/master/.

Platform:

- **version**: R version 3.4.2 (2017-09-28)
- **system**: x86_64, mingw32
- **ui**: RTerm
- **language**: (EN)
- **collate**: Portuguese_Brazil.1252
- **tz**: America/Sao_Paulo
- **date**: 2018-08-29

Packages:

package	version	date	source
ade4	1.7-6	2017-03-23	CRAN (R 3.4.1)
asnipe	1.1.4	2017-07-24	CRAN (R 3.4.1)
assertthat	0.2.0	2017-04-11	CRAN (R 3.4.0)
assortnet	0.12	2016-01-18	CRAN (R 3.4.1)
backports	1.1.0	2017-05-22	CRAN (R 3.4.0)
base	3.4.2	2017-09-28	local
bindr	0.1	2016-11-13	CRAN (R 3.4.0)
bindrcpp	0.2	2017-06-17	CRAN (R 3.4.0)
broom	0.5.0	2018-07-17	CRAN (R 3.4.4)
cellranger	1.1.0	2016-07-27	CRAN (R 3.4.0)
cli	1.0.0	2017-11-05	CRAN (R 3.4.2)
cluster	2.0.6	2017-03-10	CRAN (R 3.4.2)
codetools	0.2-15	2016-10-05	CRAN (R 3.4.2)
colorspace	1.4-0	2018-06-08	R-Forge (R 3.4.4)
compiler	3.4.2	2017-09-28	local
corrplot	0.84	2017-10-16	CRAN (R 3.4.3)
crayon	1.3.4	2017-09-16	CRAN (R 3.4.2)
datasets	3.4.2	2017-09-28	local
devtools	1.13.4	2017-11-09	CRAN (R 3.4.3)
digest	0.6.15	2018-01-28	CRAN (R 3.4.3)
dplyr	0.7.4	2017-09-28	CRAN (R 3.4.3)
evaluate	0.10	2016-10-11	CRAN (R 3.4.0)
forcats	0.2.0	2017-01-23	CRAN (R 3.4.0)
ggplot2	3.0.0.9000	2018-08-08	Github (*tidyverse/ggplot2@4d2ca99*)
glue	1.2.0	2017-10-29	CRAN (R 3.4.4)
graphics	3.4.2	2017-09-28	local
grDevices	3.4.2	2017-09-28	local
grid	3.4.2	2017-09-28	local
gtable	0.2.0	2016-02-26	CRAN (R 3.4.0)
haven	1.1.2	2018-06-27	CRAN (R 3.4.4)
hms	0.3	2016-11-22	CRAN (R 3.4.0)
htmltools	0.3.6	2017-04-28	CRAN (R 3.4.0)
httr	1.3.1	2017-08-20	CRAN (R 3.4.4)
igraph	1.1.2	2017-07-21	CRAN (R 3.4.3)
jsonlite	1.5	2017-06-01	CRAN (R 3.4.0)
knitr	1.20	2018-02-20	CRAN (R 3.4.4)
lattice	0.20-35	2017-03-25	CRAN (R 3.4.2)
lazyeval	0.2.1	2017-10-29	CRAN (R 3.4.3)
lubridate	1.7.4	2018-04-11	CRAN (R 3.4.4)

magrittr	1.5	2014-11-22	CRAN (R 3.4.0)
MASS	7.3-49	2018-02-23	CRAN (R 3.4.3)
Matrix	1.2-11	2017-08-21	CRAN (R 3.4.2)
memoise	1.1.0	2017-04-21	CRAN (R 3.4.0)
methods	3.4.2	2017-09-28	local
mgcv	1.8-20	2017-09-14	CRAN (R 3.4.2)
modelr	0.1.2	2018-05-11	CRAN (R 3.4.4)
munsell	0.5.0	2018-06-12	CRAN (R 3.4.4)
nlme	3.1-131	2017-02-06	CRAN (R 3.4.2)
pander	0.6.0	2015-11-23	CRAN (R 3.4.0)
parallel	3.4.2	2017-09-28	local
patchwork	0.0.1	2018-04-25	Github (*thomasp85/patchwork@49e6ba4*)
permute	0.9-4	2016-09-09	CRAN (R 3.4.0)
pillar	1.1.0	2018-01-14	CRAN (R 3.4.3)
pkgconfig	2.0.1	2017-11-16	Github (*gaborcsardi/pkgconfig@96a1413*)
plyr	1.8.4	2016-06-08	CRAN (R 3.4.0)
purrr	0.2.5	2018-05-29	CRAN (R 3.4.4)
R6	2.2.2	2017-06-17	CRAN (R 3.4.0)
Rcpp	0.12.18	2018-07-23	CRAN (R 3.4.4)
readr	1.1.1	2017-05-16	CRAN (R 3.4.0)
readxl	1.0.0	2017-04-18	CRAN (R 3.4.0)
rlang	0.2.1	2018-05-30	CRAN (R 3.4.4)
rmarkdown	1.10	2018-06-11	CRAN (R 3.4.4)
rprojroot	1.2	2017-01-16	CRAN (R 3.4.0)
rstudioapi	0.7	2017-09-07	CRAN (R 3.4.1)
rvest	0.3.2	2016-06-17	CRAN (R 3.4.0)
scales	1.0.0	2018-08-08	Github (*hadley/scales@b614d9f*)
stats	3.4.2	2017-09-28	local
stringi	1.1.7	2018-03-12	CRAN (R 3.4.4)
stringr	1.3.1	2018-05-10	CRAN (R 3.4.4)
tibble	1.4.2	2018-01-22	CRAN (R 3.4.4)
tidyr	0.8.1	2018-05-18	CRAN (R 3.4.4)
tidyverse	1.2.1	2017-11-14	CRAN (R 3.4.4)
tools	3.4.2	2017-09-28	local
utils	3.4.2	2017-09-28	local
vegan	2.4-3	2017-04-07	CRAN (R 3.4.0)
withr	2.1.2	2018-08-08	Github (*jimhester/withr@fe56f20*)
xml2	1.1.1	2017-01-24	CRAN (R 3.4.0)
yaml	2.1.19	2018-05-01	CRAN (R 3.4.4)

SUPPLEMENTARY MATERIAL S8: BASIC DESCRIPTIVE RESULTS

We studied a total of 41 well-known mature individual dolphins (accounting for almost 70% of the population [39]) that were photo-identified multiple times (mean = 31.5 ± 9.11 SD, range = 9 - 48) in 503 independent small groups (mean = 2.57 ± 0.82 SD, range =1-6).

Group size was small, across all behavioural contexts (Table S5). Out of these individuals, we analysed the association patterns, foraging and ranging behaviour of the 34 individuals that were seen in more than 5% of the sampling recordings (mean = 34.6 ± 5.97 SD, range = 26–48 resightings).

The overall mean association index was SRI = 0.026 ± 0.033 SD. Their mean relative frequency of participation in the foraging with fishermen was *FP* = 0.27 ± 0.17 SD and the mean home range was HR = 28.32 km² ± 14.79 SD, and highly overlapped (*HRO* = 47% ± 17 SD; Figure S3). The average pairwise genetic relatedness among the individuals that were both genotyped and photo-identified (n=13) was *r* = -0.07 ± 0.39 SD. We classified 26 of the 34 individuals as adults and 8 as senior. Using molecular analyses, we classified 6 individuals as females and 10 as males; using observations we classified other 14 as possible females and 2 as possible males (the sex of 4 individuals could not be determined).

Table S5: Group characteristics of bottlenose dolphins (*Tursiops truncatus gephyreus*) sighted in boat surveys from September 2007 to September 2009 in Laguna, southern Brazil. Group sightings were assigned to four behavioural contexts.

Context	Number of groups	Mean group size (SD)	Group size range
All Behaviour	497	2.37 ± (0.86)	1-6
Cooperative	120	2.44 ± (0.83)	1-6
Non-Cooperative	219	2.34 ± (0.91)	1-6
Non-Foraging	158	2.35 ± (0.83)	1-6

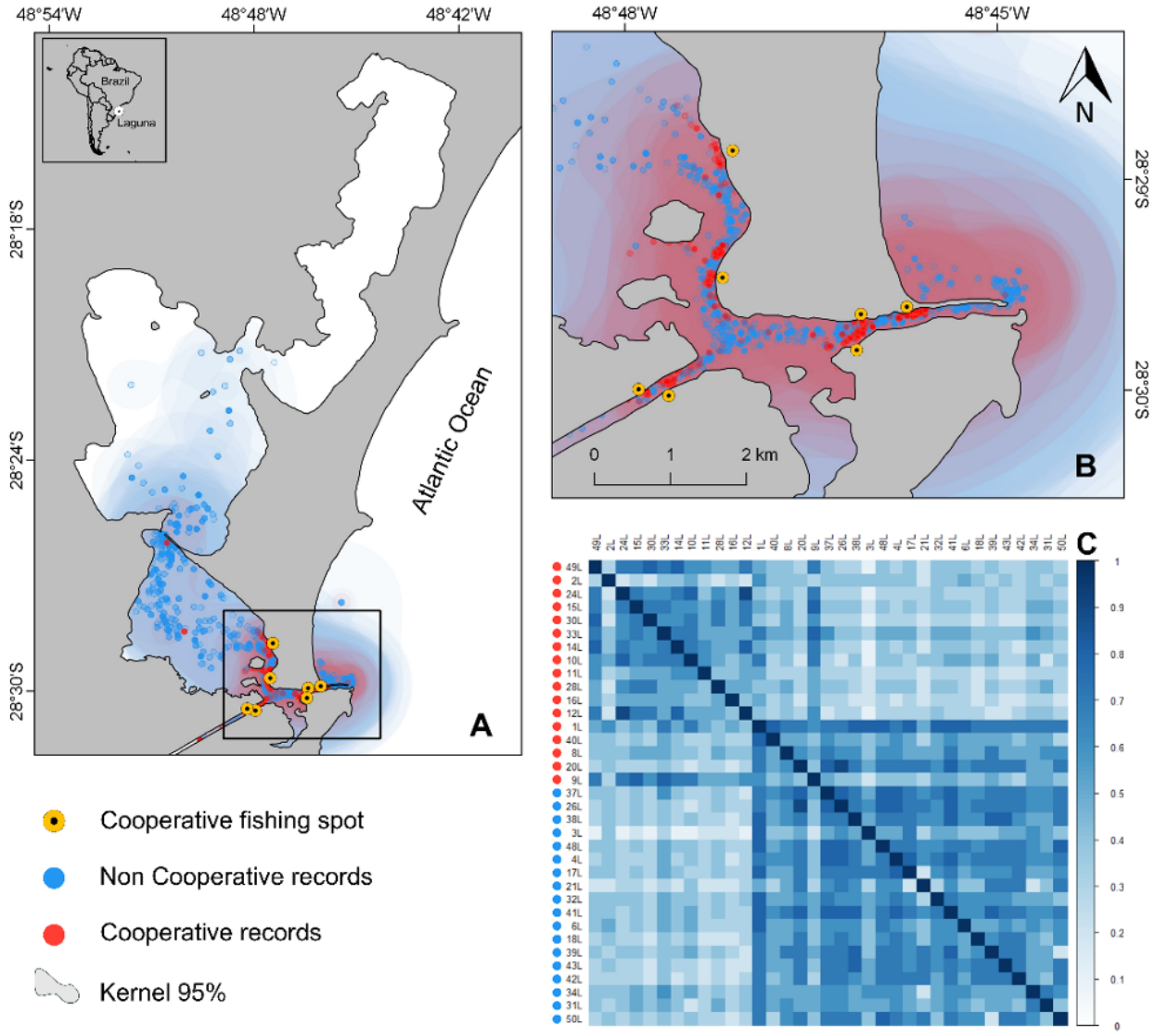

Figure S3: Home ranges of individual bottlenose dolphins in Laguna, southern Brazil. (A) The study area, Santo Antônio-Imaruí-Mirim lagoon system. Yellow circles indicate the sites where dolphins forage with artisanal fishermen. Blue circles indicate sightings of photo-identified individuals during the non-cooperative foraging behavioural context. Red circles indicate individuals recorded during the cooperative foraging context with fishermen. The overlapped shaded areas indicate the 95% kernel estimates of individual home ranges. Individuals that frequently interact with fishermen were considered 'more cooperative' dolphins (red), and the remaining were considered 'less-cooperatives' (blue) (*cf.* [40]). (B) Detail of the individual home range overlap and foraging behaviour around the cooperative fishing sites. (C) Home range overlap

between pairs of individuals, in which darker shades indicate greater overlap and lighter shades otherwise. Individuals are sorted by relative frequency of participation in cooperative foraging tactic (higher *FP* at the top-left; lower *FP* at the bottom-right).

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