Supplementary Material

Screening of bacterial isolates for oil degradation capability.

Pure cultures from five of the 14 genera isolated (SSU rRNA gene sequences most similar to those from *Alcanivorax dieselolei, Acinetobacter sp., Pseudidiomarina maritima, Marinobacter hydrocarbonoclasticus,* and *Vibrio hepatarius*) were tested for oil consumption under aerobic conditions (Table 4). Oil degradation capability was confirmed from the quantification of residual oil and concomitant growth as optical density and/or cell protein. Strains were inoculated in triplicate into the artificial seawater medium buffered with 10 mM HEPES (pH 7.0) and supplemented with 0.5 to 1% of autoclaved crude oil as the sole carbon source. Cultures were incubated at room temperature along with an uninoculated control. Flasks were shaken intermittently by hand for aeration. For gravimetric testing, the entire volume of each culture was extracted in an equal volume of chloroform after 5 days of incubation (Nakamura et al., 2007; Okafor et al., 2009). After extraction, the organic phase was decanted into a round bottom flask and evaporated in a fume hood. Residual oil was transferred in chloroform to pre-weighed glass vials, evaporated again, and weight was determined with an electronic balance (OHaus, NJ, US).

To determine the growth kinetics of isolates during oil degradation, residual oil was quantified in chloroform extracts by spectrophotometry (Shimadzu) at 520 nm (Eze and Onwurah 2004, Rengathavasi *et al.*, 2010). Replicate cultures were sacrificed at regular intervals and residual oil was extracted as described above. Residual oil concentrations were determined by comparison to a standard calibration curve generated from standard additions of DH source oil in chloroform. Bacterial growth was monitored

during screening by optical density at 600 nm as well as by quantification of total cellular protein content using the Coomassie protein assay kit (Thermo Scientific; Bradford, 1976).

Results of gravimetric analysis indicated that the *Alcanivorax* strain followed by the *Acinetobacter* strain showed the highest oil degradation potential; these strains degraded 93 and 90% of extracted crude oil, respectively, in comparison to autoclaved and un-inoculated control cultures (Fig. S1). Strains of *Marinobacter* and *Pseudidiomarina* showed moderate (36%) and small (12%) amounts of oil degradation, respectively, while the *Vibrio* strain did not show any sign of oil degradation in pure culture (Fig. S1).

Growth of the isolates as measured by optical density (OD@600 nm) and by total cellular protein content was concomitant with the depletion of oil in culture. Un-inoculated control cultures showed no sign of weathering or depletion of oil (Fig. S2). The *Acinetobacter* strain grew most rapidly with a generation time of 30 h followed by the *Alcanivorax* strain (53 h), while the *Marinobacter* strain showed a longer generation time of 82 h among the selected isolates. The *Acinetobacter* strain produced the highest amount of cell biomass followed by *Marinobacter* and *Alcanivorax* strains with Macondo oil as the sole carbon source, while the other two strains produced a negligible amount of cell biomass under similar culture conditions. Similar results were obtained from these cultures when quantifying residual oil by either gravimetric or spectrophotometric assays.

Preliminary physiological testing of representative oil-degrading bacterial isolates.

Initial physiological characterization of representative oil-degrading isolates was conducted using Phenotypic MicroArray^{TM} (PM) analysis. PM tests were performed by

47 Biolog, Inc. (Hayward, CA) according to methods described previously (2, 7). PM
48 testing included salt tolerance, a wide variety of carbon sources (alcohols, amines, amino
49 acids, carbohydrates, carboxylic acids, esters, fatty acids, and polymers) as well as
50 inorganic and organic forms of major nutrients (N, P, and S). All strains metabolized in
51 the presence of NaCl concentrations up to 10 %. *Vibrio*, *Acinetobacter*, and
52 *Marinobacter* strains all utilized a fairly broad range of carbon substrates, with the *Vibrio*
53 strain using by far the largest number of different carbon sources. In contrast, the
54 *Alcanivorax* strain utilized relatively few carbon sources among those tested. The
55 *Alcanivorax* strain metabolized few amino acids, carboxylic acids, and polymers relative
56 to the other strains and no carbohydrates were utilized. Tween compounds, which
57 contain long-chain alkyl moieties, were metabolized by all strains tested.
58 Contrasts were observed between oil-degrading strains in their phenotypes of
59 major nutrient metabolism. The *Acinetobacter* strain showed by far the broadest range
60 for the utilization of all inorganic and organic nutrient forms. In contrast, the *Vibrio*
61 strain utilized the narrowest range of major nutrients. *Vibrio* and *Alcanivorax* tests
62 indicated a preference for organic N sources (other than amino acids) such as urea, while
63 neither strain metabolized inorganic N forms. *Vibrio* showed a relatively limited range
64 with regard to P utilization; a small number of organic P sources and no inorganic P
65 sources were utilized. The remaining strains utilized a wide variety of inorganic and
66 organic P and S forms.
67 **Quantitative molecular analyses for tracking *Alcanivorax* spp.**
68 This section provides further details on the design of PCR primers targeted to
69 *Alcanivorax* spp. Within the Greengenes database formatted for ARB (5), 88 sequences

were identified as belonging to the family *Alcanivoraceaceae*. The forward primer (Alcvx-464F) was highly specific to this family and targeted 63 of the 88 sequences perfectly, and 87 of the 88 with a single mismatch. Even allowing for two mismatches, no non-*Alcanivoraceaceae* sequences matched this primer site. The reverse primer (Alcvx-675R) targeted all *Alcanivoraceaceae* sequences with no mismatches, and targeted, non-systematically, seven other Proteobacterial sequences. Allowing for 1 mismatch, the reverse primer targets a larger number of Proteobacterial and non-Proteobacterial sequences (452 out of a dataset of 137,853 sequences). In combination, the two primers provide conditions for highly-specific amplification of *Alcanivoraceaceae* sequences, though some members, such as *A. venustensis* (e.g. AF328762), may not be reliably amplified due to a single mismatch with the primer set. We attempted to employ a degenerate primer set to amplify these organisms as well, but were unable to generate high efficiency qPCR reactions (data not shown).

Community fingerprinting analysis: bacterial community shifts in response to oil contamination.

Bacterial community structure was initially assessed using automated ribosomal intergenetic spacer region analysis (ARISA), a community fingerprinting method based on length heterogeneity in the intergenic spacer region of the bacterial rRNA operon (11, 12). This technique allowed for the rapid comparison of a large number of samples and aided in identifying critical samples for pyrotag sequencing. The intergenic spacer region between the 16S SSU and 23S and large subunit (LSU) rRNA genes was amplified using previously published primers, S-D-Bact-1522-b-S-20 and L-D-Bact-132-a-A-18 (11). PCR reactions were conducted in 50 ul reactions containing 5 ul of 10X DreamTaq Green

93 Buffer (Fermentas, Glen Burnie, MD), 0.5 µM of each primer, 0.2 mM of each dNTP
94 (New England BioLabs, Ipswich, MA), and 1.25 U of DreamTaq Green DNA
95 polymerase. Reactions were subject to an initial denaturation at 95° C for 5 min, followed
96 by 28 cycles consisting of 30 seconds at 94° C, 1 min at 50° C, and 1 min at 72° C,
97 ending with a final elongation step at 72° C for 10 min.
98 PCR products were cleaned using a MoBio UltraClean PCR Clean-up Kit (Mo
99 Bio Laboratories, Carlsbad, CA) following manufacturer's protocol. However, PCR
100 products were eluted in 15 µl. DNA concentration was assessed using a NanoDrop
101 spectrophotometer and normalized to 100 ng/µl in each sample. PCR products were
102 separated on an Agilent 2100 Bioanalyzer using the Agilent DNA 7500 kit (Agilent
103 Technologies, Santa Clara, CA, USA).
104 Fragment peaks were assigned a size and DNA molarity value using algorithms
105 implemented in the Agilent 2100 Expert Software. Due to a ± 5% error associated with
106 fragment length, all peaks were binned within the percent error and the molarity values
107 were summed. Sample profiles were normalized and log(X+1) transformed in the
108 software package Primer6 to down weight dominant peaks (4). A non-parametric
109 multidimensional scaling (NMDS) plot was generated from a Bray-Curtis similarity
110 matrix to compare samples. Qualitative oil assessment was used to group samples and an
111 analysis of similarity (ANOSIM) test was used to determine the validity of using oil
112 contamination as a grouping factor (Figure S1B).
113 Over 150 samples, spanning three sampling trips, which were collected from
114 clean and oiled sands from Pensacola Beach, were analyzed using ARISA based
115 community fingerprinting. Results indicate a consistent microbial response pattern to the

response pattern seen in the pyrosequencing data (Figure S1). An analysis of similarity (ANOSIM) test was performed rejecting the null hypothesis with a global R value of 0.21 corresponding to a P value of 0.001. Furthermore, pairwise tests (Figure S1-B) were performed, revealing all but the low and moderate oil groupings are significant groupings. A similarity of percentages (SIMPER) test was used to determine key fragments that lead to significant oil level groupings (Figure S1-C).

Due to the high stress value in Figure S1-A, we are unable to look at variation on a smaller scale. Figures S1 D-J represent similar sample types and are subsets of Figure S1-A. Clustering of sectioned core samples (Figures S1 D,E,F) by oil level and grouping by depth or location on the beach face was not significant by an ANOSIM test (data not shown). In the case of the July 30th sampling trip, two clusters of clean sand samples were evident corresponding to surface layers of all four cores. There was a robust algal bloom during this sampling trip that could explain the separate surface group. Figures S1 G-H represent samples taken along a vertical transect beginning at the surface and spanning the oil layer to visibly clean sands below. In both cases, the deep clean sands were more similar than the sands sampled in the oil layer. Trajectories are overlaid on both plots starting at the surface and proceeding to the deepest samples. In overlying the trajectories, not all points were included. Samples were also collected along a horizontal transect following the oil layer from the high beach to the low beach (Figure S1-I,J).

Comparison of Multivariate Ordination Methods.

Pyrosequencing data was analyzed using redundant methods in order to assure that ordination patterns effectively represented variations in bacterial community structure. In addition to Bray-Curtis distance, sample similarity was assessed with the

weighted UniFrac distance metric (3, 8). Unlike Bray-Curtis distance, weighted UniFrac is a phylogenetic metric that includes relative OTU abundances to calculate pairwise similarity. A high degree of similarity between Bray Curtis and weighted UniFrac distance matrices was observed as assessed statistically ($rho = 0.72$, $p < 0.0001$) by the RELATE test in Primer6. In order to visually compare these metrics, the resulting distance matrices were ordinated using NMDS plots. Both distance metrics produce similar large scale grouping patterns, although the weighted UniFrac method emphasized an outlier (Supplemental Figure 2). After further investigation, the outlier sample was dominated by OTU within the phylum *Spirochaeta*. Plots generated from weighted UniFrac distance did not distinguish between St. George Island and clean Pensacola Beach sands. In addition, the weighted UniFrac metric yielded larger distances between corresponding RNA-based and DNA-based sequence libraries. This pattern is likely due to increases in Alphaproteobacterial OTU in RNA based libraries.

Abundance data transformations were also employed to weigh the contributions of abundant and rare OTU (4). Surprisingly, Bray Curtis distance matrices after square root (includes common and intermediately abundant OTU) and forth root (include rare OTU) transformations were almost identical (rho values ranging for 0.98 to 0.99, $p < 0.001$).

Supplementary Information References

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210 FIGURE LEGENDS

211 Figure S1: Degradation of crude oil by representative pure cultures isolated from oiled
212 beach sands in this study. The proportion of residual oil is plotted along with the
213 concomitant increase in cell biomass. Residual oil was extracted with chloroform and
214 measured gravimetrically in pre-weighted glass vials. Values are the average of triplicates
215 and error bars represent one standard deviation.

216

217 Figure S2: Growth response (∇) as total cellular protein, of *Marinobacter* (A),
218 *Acinetobacter* (B) and *Alcanivorax* (C) strains with concomitant crude oil degradation
219 (●) in comparison to uninoculated control cultures (○). The concentration of residual oil
220 was determined spectrophotometrically in chloroform extracts (λ=520) and total cellular
221 protein was quantified using the Bradford method. Values represent the average of
222 triplicates and error bars represent one standard deviation.

223

224 Figure S3. Community fingerprinting data generated through ARISA based analysis.
225 These data represent 150 samples, spanning three sampling trips, that were collected from
226 clean and oiled sands from Pensacola Beach. All NMDS plots were generated from a
227 Bray-Curtis resemblance matrix calculated using log(X+1) transformed, normalized peak
228 data. Shading corresponds to qualitative assessment of oil contamination (white = clean,
229 light gray = low, gray = moderate, black = heavy). When present, clustering represents
230 Bray-Curtis similarity between samples. (A) All samples collected from the study area to
231 date. Clustering pattern indicates pronounced, if scattered, effect of oil contamination.
232 (B) Analysis of similarity (ANOSIM) test performed on all samples to determine

significance of grouping samples by qualitative oil contamination. The global R value was 0.21 corresponding to a global P value of 0.001. Pairwise p-values are indicated in the table and black cells are significant. (C) A similarity percentages (SIMPER) test was used to determine key fragments that lead to the significant grouping patterns. Note all 4 top peaks for the low and moderate groups are the same. (D-E) Sectioned core samples taken from all 3 sampling trips. † These samples were from the surface layer of the cores during an algal bloom are likely contaminated by chloroplast DNA (F,G) Vertical transect samples taken from beach surface, through the oil layer to clean underlying sediments. Trajectories are overlaid on both plots starting at the surface and preceding to the deepest samples. Note not all points were included in the trajectories. (H,I) Samples collected along a horizontal transect along the oil layer. Over laid trajectories began furthest from the beach and proceed to the water.

Figure S4. Bacterial community response to oil contamination in beach sands assessed using the weighted UniFrac metric and visualized with NMDS plots. Pensacola oiled samples are colored black, clean Pensacola and St. George Island samples are colored grey. Lowercase letters indicate samples derived from the same sand sample, asterisks (*) indicate RNA based sequence libraries. Subplot (A) includes all samples, while the outlier (dominated by Spirochaetes) is removed in subplot (B). Microbial communities reveal a strong response to oil contamination by grouping together on the left side of the plot. Notably, St. George Island samples (e,f) and clean Pensacola samples are not resolved using weighted UniFrac.

Table S1. Sample IDs from Pensacola Beach are described in the materials and methods section. The last 8 sample IDs refer to samples collected at the pristine beach of St. George Island. The first letter designates the site sampled (B, Bay side; G, Gulf side), and the second letter refers to the type of sample (S, sediment; W, water column), while the third letter designates whether the pyrosequence library was DNA (D) or RNA (R) based.

Sample ID	Qualitative Oil Assessment	Sequences	OTU	Percent Coverage	Shannon	%*Alcanivorax*
OS-55	0	4927	1116	77%	6.1	0.0%
OS-56	0	5094	698	88%	5.6	0.0%
OS-57	0	7061	1168	79%	5.9	0.0%
OS-58	0	9296	1274	79%	6.0	0.0%
OS-71	3	7091	942	84%	4.7	33.0%
OS-72	1	6859	1340	76%	5.0	30.0%
OS-73	0	3872	920	78%	5.2	11.0%
OS-74	0	6604	1296	76%	5.1	3.0%
OS.71R	3	2874	663	82%	4.9	12.0%
OS.72R	1	2623	1210	60%	6.0	6.0%
OS.73R	0	1673	981	56%	6.4	2.0%
OS.74R	0	2122	1058	60%	6.0	3.0%
OS-230	3	7122	1053	84%	4.9	9.0%
OS-231	3	5013	971	81%	4.9	15.0%
OS-233	3	5614	1065	80%	5.0	10.0%
OS-234	3	6181	1155	79%	5.1	10.0%
OS-236	3	6722	622	90%	3.6	1.0%
OS-237	3	7397	893	87%	4.8	5.0%
OS-239	3	8002	1127	83%	5.0	11.0%
OS-240	3	7396	1051	84%	5.0	9.0%
OS-242	0	7502	2139	64%	6.1	2.0%
OS-243	0	6793	2023	64%	6.2	2.0%
BSD	0	9837	3063	58%	6.3	0.0%
BSR	0	5078	1007	81%	5.8	0.0%
GSD	0	11015	3680	52%	6.6	0.0%
GSR	0	15244	5366	44%	6.8	0.0%
BWD	0	7609	1096	83%	4.9	0.0%
BWR	0	12673	1402	85%	4.6	0.0%
GWD	0	11986	1002	89%	4.0	0.0%
GWR	0	11238	1239	85%	4.6	0.0%

Table S2. Physiological characterization of representative oil-degrading isolates from this study conducted using Phenotypic MicroArray™ (PM) analysis. PM tests were performed by Biolog, Inc. (Hayward, CA) (see above for further details). Values represent the average height recorded from the OmniLog™ instrument as a proxy of metabolism for each strain and test conducted on the microarray. The microarray plate used is identified in column 1 and the location of the test on the array is given in column 2. Further information on PM Technology testing and reporting procedures can be found at: http://www.biolog.com/phenoMicro.html.

Plate	Well	Chemical	**Marinobacter sp. strain EN3**	**Alcanivorax sp. strain PN3**	**Vibrio sp. strain PN4**	**Acineotbacter sp. strain COS2**
			Average Height (2 replicates)			
PM1	A01	Negative Control	41.00	29.50	41.00	35.00
PM1	A02	L-Arabinose	70.00	20.50	20.00	26.50
PM1	A03	N-Acetyl-D-Glucosamine	32.00	15.00	189.00	22.00
PM1	A04	D-Saccharic acid	36.00	9.50	37.00	20.00
PM1	A05	Succinic acid	128.00	29.00	184.50	127.00
PM1	A06	D-Galactose	26.50	3.50	17.50	11.50
PM1	A07	L-Aspartic acid	38.00	18.50	209.50	27.00
PM1	A08	L-Proline	140.00	14.50	165.00	228.50
PM1	A09	D-Alanine	78.00	13.50	180.50	202.50
PM1	A10	D-Trehalose	32.50	15.00	177.50	25.50
PM1	A11	D-Mannose	44.50	20.50	200.50	31.50
PM1	A12	Dulcitol	45.50	31.00	67.50	41.00
PM1	B01	D-Serine	43.00	27.00	29.50	33.50
PM1	B02	D-Sorbitol	26.50	12.00	56.50	18.00
PM1	B03	Glycerol	24.50	10.00	156.00	16.00
PM1	B04	L-Fucose	36.50	8.00	163.50	18.00
PM1	B05	D-Glucuronic acid	43.00	14.00	30.00	20.50
PM1	B06	D-Gluconic acid	38.00	7.50	203.50	24.00
PM1	B07	D,L-a-Glycerol Phosphate	33.50	10.00	136.00	20.50
PM1	B08	D-Xylose	70.00	8.50	20.50	19.50
PM1	B09	L-Lactic acid	133.50	58.50	188.00	19.50
PM1	B10	Formic acid	28.50	11.50	32.00	21.00
PM1	B11	D-Mannitol	31.50	14.00	195.00	25.00
PM1	B12	L-Glutamic acid	95.50	33.50	222.50	232.00
PM1	C01	D-Glucose-6-Phosphate	49.50	27.00	63.50	32.00
PM1	C02	D-Galactonic acid-g-Lactone	28.00	13.50	27.00	16.50
PM1	C03	D,L-Malic acid	143.00	12.50	29.00	160.50
PM1	C04	D-Ribose	105.00	29.00	26.50	29.50
PM1	C05	Tween 20	85.00	87.00	139.50	109.00
PM1	C06	L-Rhamnose	39.50	15.50	21.00	21.00
PM1	C07	D-Fructose	34.50	6.00	178.50	24.50

PM1	C08	Acetic acid	122.50	20.00	17.50	111.00
PM1	C09	a-D-Glucose	28.50	4.50	175.00	16.00
PM1	C10	Maltose	31.50	12.00	209.00	19.50
PM1	C11	D-Melibiose	35.00	11.50	49.00	22.00
PM1	C12	Thymidine	43.00	28.00	134.50	37.00
PM1	D01	L-Asparagine	52.50	29.50	221.50	135.00
PM1	D02	D-Aspartic acid	47.00	20.50	36.00	30.50
PM1	D03	D-Glucosaminic acid	45.00	31.00	38.00	32.00
PM1	D04	1,2-Propanediol	38.00	21.00	38.00	26.50
PM1	D05	Tween 40	109.50	104.00	70.00	129.00
PM1	D06	a-Ketoglutaric acid	33.50	26.50	140.00	27.00
PM1	D07	a-Ketobutyric acid	24.50	3.00	41.00	30.00
PM1	D08	a-Methyl-D-Galactoside	24.00	5.00	37.00	14.50
PM1	D09	a-D-Lactose	28.50	6.50	53.00	16.50
PM1	D10	Lactulose	32.50	8.50	51.00	19.50
PM1	D11	Sucrose	32.00	19.00	181.00	23.00
PM1	D12	Uridine	40.50	22.50	131.50	36.00
PM1	E01	L-Glutamine	76.00	45.00	230.50	49.00
PM1	E02	m-Tartaric acid	46.50	23.50	31.50	31.00
PM1	E03	D-Glucose-1-Phosphate	40.00	19.50	52.00	28.50
PM1	E04	D-Fructose-6-Phosphate	40.50	18.50	18.50	24.00
PM1	E05	Tween 80	109.00	115.50	68.50	200.00
PM1	E06	a-Hydroxyglutaric acid-g-Lactone	35.00	11.00	14.00	22.50
PM1	E07	a-Hydroxybutyric acid	42.00	4.50	57.50	19.50
PM1	E08	b-Methyl-D-Glucoside	22.00	5.00	38.00	12.50
PM1	E09	Adonitol	25.50	9.00	59.00	15.50
PM1	E10	Maltotriose	34.50	12.00	187.00	21.00
PM1	E11	2`-Deoxyadenosine	30.00	11.00	94.50	20.00
PM1	E12	Adenosine	47.00	39.50	218.50	44.50
PM1	F01	Gly-Asp	66.50	51.50	199.50	52.00
PM1	F02	Citric acid	84.50	109.50	65.50	136.50
PM1	F03	m-Inositol	32.50	15.50	37.00	20.00
PM1	F04	D-Threonine	40.00	16.00	35.00	28.50
PM1	F05	Fumaric acid	131.00	42.00	198.00	116.50
PM1	F06	Bromosuccinic acid	42.00	18.50	93.50	72.00
PM1	F07	Propionic acid	131.00	50.50	22.00	126.50
PM1	F08	Mucic acid	24.50	7.00	20.50	15.50
PM1	F09	Glycolic acid	26.50	9.00	31.00	19.00
PM1	F10	Glyoxylic acid	37.50	21.00	43.50	31.50
PM1	F11	D-Cellobiose	44.00	23.00	74.50	33.50
PM1	F12	Inosine	51.00	35.00	234.50	46.50
PM1	G01	Gly-Glu	60.50	44.50	147.50	46.00

PM1	G02	Tricarballylic acid	43.50	26.50	38.00	31.50
PM1	G03	L-Serine	34.00	16.50	209.00	26.50
PM1	G04	L-Threonine	36.00	18.50	197.00	26.50
PM1	G05	L-Alanine	84.50	14.00	178.00	200.50
PM1	G06	Ala-Gly	29.50	13.50	183.50	21.00
PM1	G07	Acetoacetic acid	43.00	13.50	19.00	23.00
PM1	G08	N-Acetyl-D-Mannosamine	27.50	7.50	221.50	19.50
PM1	G09	Mono-Methylsuccinate	67.00	61.50	43.00	61.50
PM1	G10	Methylpyruvate	59.50	91.50	164.00	160.00
PM1	G11	D-Malic acid	46.00	31.00	42.50	77.50
PM1	G12	L-Malic acid	163.00	41.50	205.50	181.50
PM1	H01	Gly-Pro	61.00	48.00	126.50	49.00
PM1	H02	p-Hydroxyphenyl Acetic acid	52.00	100.00	87.00	38.00
PM1	H03	m-Hydroxyphenyl Acetic acid	47.50	71.50	30.50	35.50
PM1	H04	Tyramine	43.50	142.00	26.50	34.00
PM1	H05	D-Psicose	52.50	21.50	25.50	31.50
PM1	H06	L-Lyxose	108.50	27.50	31.50	31.50
PM1	H07	Glucuronamide	54.50	26.50	42.50	33.50
PM1	H08	Pyruvic acid	126.00	82.00	186.00	185.00
PM1	H09	L-Galactonic acid-g-Lactone	46.50	25.00	46.00	31.50
PM1	H10	D-Galacturonic acid	52.00	30.50	56.50	36.00
PM1	H11	Phenylethylamine	50.00	71.50	81.50	39.50
PM1	H12	2-Aminoethanol	58.00	39.00	78.50	50.50
PM2A	A01	Negative Control	45.00	37.00	51.50	44.00
PM2A	A02	Chondroitin Sulfate C	34.00	28.00	63.50	34.00
PM2A	A03	a-Cyclodextrin	32.50	19.00	32.50	29.50
PM2A	A04	b-Cyclodextrin	36.00	23.00	105.50	32.00
PM2A	A05	g-Cyclodextrin	33.00	18.00	191.00	27.00
PM2A	A06	Dextrin	38.50	25.00	29.50	44.50
PM2A	A07	Gelatin	28.50	17.00	57.00	29.00
PM2A	A08	Glycogen	33.00	21.00	192.00	32.00
PM2A	A09	Inulin	33.50	22.50	51.50	30.50
PM2A	A10	Laminarin	36.00	23.00	57.50	32.50
PM2A	A11	Mannan	40.00	26.00	111.00	38.00
PM2A	A12	Pectin	70.50	74.00	87.00	71.50
PM2A	B01	N-Acetyl-D-Galactosamine	39.00	28.50	191.50	38.00
PM2A	B02	N-Acetyl-Neuraminic acid	22.00	10.50	24.50	21.50
PM2A	B03	b-D-Allose	26.50	8.50	18.00	16.50
PM2A	B04	Amygdalin	24.50	9.50	43.00	18.00

PM2A	B05	D-Arabinose	70.00	21.50	24.50	27.50
PM2A	B06	D-Arabitol	22.00	11.00	19.00	18.50
PM2A	B07	L-Arabitol	21.50	7.50	29.00	16.50
PM2A	B08	Arbutin	24.50	11.00	39.00	19.50
PM2A	B09	2-Deoxy-D-Ribose	67.50	23.00	25.00	23.50
PM2A	B10	i-Erythritol	28.00	18.50	34.50	24.00
PM2A	B11	D-Fucose	34.00	18.50	39.00	27.00
PM2A	B12	3-O-b-D-Galactopyranosyl-D-Arabinose	43.50	31.00	30.50	38.50
PM2A	C01	Gentiobiose	40.00	28.50	45.50	35.50
PM2A	C02	L-Glucose	24.50	12.00	26.00	20.50
PM2A	C03	D-Lactitol	23.50	6.00	27.50	15.00
PM2A	C04	D-Melezitose	20.50	5.50	29.50	19.50
PM2A	C05	Maltitol	27.50	6.50	37.00	17.00
PM2A	C06	a-Methyl-D-Glucoside	21.50	6.50	27.00	16.50
PM2A	C07	b-Methyl-D-Galactoside	22.00	13.00	29.00	15.00
PM2A	C08	3-Methylglucose	19.00	5.50	18.50	14.50
PM2A	C09	b-Methyl-D-Glucuronic acid	25.00	9.00	34.50	26.00
PM2A	C10	a-Methyl-D-Mannoside	28.00	16.00	35.50	24.50
PM2A	C11	b-Methyl-D-Xyloside	28.00	21.00	38.00	25.50
PM2A	C12	Palatinose	39.50	26.50	30.50	38.00
PM2A	D01	D-Raffinose	39.00	27.00	71.00	35.00
PM2A	D02	Salicin	22.00	9.50	29.50	19.00
PM2A	D03	Sedoheptulosan	24.50	6.00	29.00	15.50
PM2A	D04	L-Sorbose	28.00	6.50	9.50	16.50
PM2A	D05	Stachyose	22.00	4.00	31.00	16.00
PM2A	D06	D-Tagatose	36.50	7.00	8.50	21.50
PM2A	D07	Turanose	22.50	3.00	28.00	16.00
PM2A	D08	Xylitol	17.00	2.50	22.50	13.00
PM2A	D09	N-Acetyl-D-Glucosaminitol	23.50	8.50	21.00	18.50
PM2A	D10	g-Amino-N-Butyric acid	26.50	11.00	40.00	188.00
PM2A	D11	d-Amino Valeric acid	22.00	10.00	28.00	19.00
PM2A	D12	Butyric acid	128.50	59.00	70.00	110.00
PM2A	E01	Capric acid	21.00	27.00	23.00	42.00
PM2A	E02	Caproic acid	114.00	36.00	11.00	139.00
PM2A	E03	Citraconic acid	19.50	10.00	23.50	17.50
PM2A	E04	Citramalic acid	21.50	6.50	23.00	17.50
PM2A	E05	D-Glucosamine	114.50	15.50	11.00	22.00
PM2A	E06	2-Hydroxybenzoic acid	14.50	9.00	8.50	6.00
PM2A	E07	4-Hydroxybenzoic acid	13.50	5.50	9.50	13.50
PM2A	E08	b-Hydroxybutyric acid	101.50	45.50	176.50	103.50

PM2A	E09	g-Hydroxybutyric acid	20.00	26.50	24.00	23.00
PM2A	E10	a-Keto-Valeric acid	28.00	8.00	25.50	18.00
PM2A	E11	Itaconic acid	33.00	9.00	13.00	16.00
PM2A	E12	5-Keto-D-Gluconic acid	67.00	30.00	31.50	39.50
PM2A	F01	D-Lactic acid Methyl Ester	60.00	38.50	121.50	35.50
PM2A	F02	Malonic acid	24.50	8.00	44.50	157.50
PM2A	F03	Melibionic acid	26.00	8.00	56.50	20.50
PM2A	F04	Oxalic acid	21.50	7.50	21.00	19.50
PM2A	F05	Oxalomalic acid	74.00	3.00	6.00	15.00
PM2A	F06	Quinic acid	18.50	6.00	25.00	16.50
PM2A	F07	D-Ribono-1,4-Lactone	16.00	3.50	19.00	14.00
PM2A	F08	Sebacic acid	20.50	33.00	16.50	15.00
PM2A	F09	Sorbic acid	105.00	51.00	16.00	140.00
PM2A	F10	Succinamic acid	28.00	37.50	61.50	32.50
PM2A	F11	D-Tartaric acid	27.50	13.50	23.00	24.50
PM2A	F12	L-Tartaric acid	39.00	22.50	35.50	33.00
PM2A	G01	Acetamide	30.00	31.00	41.00	32.50
PM2A	G02	L-Alaninamide	17.00	8.50	37.00	17.50
PM2A	G03	N-Acetyl-L-Glutamic acid	19.00	6.50	82.50	14.50
PM2A	G04	L-Arginine	20.00	6.50	135.00	172.00
PM2A	G05	Glycine	14.00	1.00	35.50	9.00
PM2A	G06	L-Histidine	28.00	2.00	57.50	193.00
PM2A	G07	L-Homoserine	14.50	2.00	13.50	13.00
PM2A	G08	Hydroxy-L-Proline	27.50	6.00	27.50	19.50
PM2A	G09	L-Isoleucine	27.50	11.50	20.50	15.00
PM2A	G10	L-Leucine	45.50	12.50	45.00	16.50
PM2A	G11	L-Lysine	24.50	13.00	42.50	22.00
PM2A	G12	L-Methionine	38.00	26.00	36.00	31.50
PM2A	H01	L-Ornithine	33.50	21.50	60.50	31.00
PM2A	H02	L-Phenylalanine	22.00	9.50	36.00	19.50
PM2A	H03	L-Pyroglutamic acid	23.00	9.00	27.00	22.00
PM2A	H04	L-Valine	109.50	7.00	30.00	16.50
PM2A	H05	D,L-Carnitine	13.00	3.00	20.50	9.50
PM2A	H06	sec-Butylamine	13.50	2.50	5.50	14.00
PM2A	H07	D,L-Octopamine	21.50	9.50	17.00	17.50
PM2A	H08	Putrescine	25.00	11.50	31.50	20.00
PM2A	H09	Dihydroxyacetone	118.00	67.50	60.50	67.00
PM2A	H10	2,3-Butanediol	20.00	19.00	39.00	17.00
PM2A	H11	2,3-Butanedione	41.00	25.50	23.50	32.00
PM2A	H12	3-Hydroxy-2-butanone	40.00	26.50	53.00	35.00
PM3B	A01	Negative Control	43.00	31.50	64.00	47.50

PM3B	A02	Ammonia	132.50	36.00	11.50	106.50
PM3B	A03	Nitrite	47.00	21.50	9.50	99.00
PM3B	A04	Nitrate	116.00	20.00	5.00	107.00
PM3B	A05	Urea	179.00	68.00	1.50	140.00
PM3B	A06	Biuret	29.50	58.00	0.50	31.00
PM3B	A07	L-Alanine	137.50	15.00	8.00	203.00
PM3B	A08	L-Arginine	126.00	15.00	9.50	233.00
PM3B	A09	L-Asparagine	116.50	13.50	7.50	200.00
PM3B	A10	L-Aspartic acid	32.00	15.50	8.00	47.50
PM3B	A11	L-Cysteine	173.50	26.50	31.00	58.00
PM3B	A12	L-Glutamic acid	153.00	34.50	25.50	248.50
PM3B	B01	L-Glutamine	166.50	104.50	102.50	222.50
PM3B	B02	Glycine	43.50	17.00	20.50	185.00
PM3B	B03	L-Histidine	31.50	8.00	42.50	212.50
PM3B	B04	L-Isoleucine	60.00	8.00	3.00	105.50
PM3B	B05	L-Leucine	52.00	6.50	2.00	119.50
PM3B	B06	L-Lysine	39.00	8.50	48.00	33.00
PM3B	B07	L-Methionine	41.50	7.50	53.00	89.00
PM3B	B08	L-Phenylalanine	30.00	6.50	2.50	143.50
PM3B	B09	L-Proline	158.50	7.50	4.50	229.00
PM3B	B10	L-Serine	71.00	10.00	8.00	184.00
PM3B	B11	L-Threonine	45.50	14.50	10.50	57.50
PM3B	B12	L-Tryptophan	65.50	34.50	24.00	60.50
PM3B	C01	L-Tyrosine	66.50	77.00	71.50	219.50
PM3B	C02	L-Valine	65.00	13.00	6.00	129.00
PM3B	C03	D-Alanine	109.50	10.00	3.50	190.50
PM3B	C04	D-Asparagine	28.50	13.00	4.50	91.00
PM3B	C05	D-Aspartic acid	27.00	5.00	3.00	27.50
PM3B	C06	D-Glutamic acid	81.50	6.50	2.00	27.50
PM3B	C07	D-Lysine	22.00	5.00	1.50	26.00
PM3B	C08	D-Serine	40.50	7.00	2.50	94.50
PM3B	C09	D-Valine	21.00	7.00	4.00	32.00
PM3B	C10	L-Citrulline	33.00	9.00	20.50	35.00
PM3B	C11	L-Homoserine	43.00	12.50	10.00	49.00
PM3B	C12	L-Ornithine	115.00	27.50	94.50	54.50
PM3B	D01	N-Acetyl-L-Glutamic acid	41.00	31.00	24.00	42.00
PM3B	D02	N-Phthaloyl-L-Glutamic acid	33.00	20.00	24.50	37.00
PM3B	D03	L-Pyroglutamic acid	33.00	16.50	10.00	36.00
PM3B	D04	Hydroxylamine	24.50	16.00	9.00	31.00
PM3B	D05	Methylamine	37.00	10.50	1.00	23.50
PM3B	D06	N-Amylamine	29.00	12.00	5.00	25.00
PM3B	D07	N-Butylamine	22.50	11.00	3.00	22.00
PM3B	D08	Ethylamine	23.00	7.50	1.00	24.00

PM3B	D09	Ethanolamine	26.00	47.00	6.50	29.00
PM3B	D10	Ethylenediamine	28.50	10.50	11.50	29.50
PM3B	D11	Putrescine	26.00	10.50	7.50	31.00
PM3B	D12	Agmatine	41.00	26.00	20.00	48.00
PM3B	E01	Histamine	51.50	45.00	34.00	54.50
PM3B	E02	b-Phenylethylamine	34.00	107.00	17.50	34.50
PM3B	E03	Tyramine	36.00	153.50	7.50	32.00
PM3B	E04	Acetamide	126.00	85.50	5.50	31.00
PM3B	E05	Formamide	100.00	65.00	3.50	27.00
PM3B	E06	Glucuronamide	45.50	20.50	4.00	93.00
PM3B	E07	D,L-Lactamide	53.00	192.00	1.00	21.50
PM3B	E08	D-Glucosamine	45.00	10.50	128.50	24.00
PM3B	E09	D-Galactosamine	36.00	12.50	7.50	30.00
PM3B	E10	D-Mannosamine	87.00	19.50	65.50	46.50
PM3B	E11	N-Acetyl-D-Glucosamine	28.00	13.50	186.50	31.00
PM3B	E12	N-Acetyl-D-Galactosamine	51.50	35.00	202.50	62.00
PM3B	F01	N-Acetyl-D-Mannosamine	54.50	46.00	126.50	56.50
PM3B	F02	Adenine	43.00	26.50	16.50	64.50
PM3B	F03	Adenosine	22.50	19.50	188.00	28.50
PM3B	F04	Cytidine	29.50	19.50	7.00	26.50
PM3B	F05	Cytosine	34.50	48.50	10.00	28.50
PM3B	F06	Guanine	36.50	61.00	22.50	167.50
PM3B	F07	Guanosine	28.50	24.50	6.00	121.00
PM3B	F08	Thymine	25.00	14.50	14.00	26.50
PM3B	F09	Thymidine	30.50	11.50	12.50	27.50
PM3B	F10	Uracil	38.50	24.00	24.00	42.00
PM3B	F11	Uridine	37.50	24.00	23.00	43.00
PM3B	F12	Inosine	53.50	35.50	36.50	86.00
PM3B	G01	Xanthine	74.50	85.00	71.50	158.50
PM3B	G02	Xanthosine	34.50	24.50	21.00	36.00
PM3B	G03	Uric acid	106.00	141.50	104.00	190.50
PM3B	G04	Alloxan	54.00	25.50	48.50	33.00
PM3B	G05	Allantoin	46.00	17.50	9.50	135.50
PM3B	G06	Parabanic acid	53.50	71.00	70.50	104.50
PM3B	G07	D,L-a-Amino-N-Butyric acid	51.50	13.50	6.00	36.00
PM3B	G08	g-Amino-N-Butyric acid	22.50	9.50	4.00	207.00
PM3B	G09	e-Amino-N-Caproic acid	30.00	17.50	18.50	36.00
PM3B	G10	D,L-a-Amino-Caprylic acid	69.50	27.00	36.50	40.00
PM3B	G11	d-Amino-N-Valeric acid	41.50	24.50	25.50	43.50

PM3B	G12	a-Amino-N-Valeric acid	119.00	37.50	32.00	60.50
PM3B	H01	Ala-Asp	54.50	46.00	37.00	52.50
PM3B	H02	Ala-Gln	152.50	89.00	28.00	45.50
PM3B	H03	Ala-Glu	98.50	28.00	55.50	40.00
PM3B	H04	Ala-Gly	101.00	26.00	138.00	39.50
PM3B	H05	Ala-His	112.50	23.50	17.50	57.50
PM3B	H06	Ala-Leu	118.50	24.00	14.50	39.50
PM3B	H07	Ala-Thr	51.00	27.00	18.50	42.00
PM3B	H08	Gly-Asn	135.50	38.50	16.50	41.00
PM3B	H09	Gly-Gln	119.00	79.00	19.50	42.00
PM3B	H10	Gly-Glu	48.50	29.50	54.50	46.00
PM3B	H11	Gly-Met	63.50	32.00	26.50	49.50
PM3B	H12	Met-Ala	136.00	45.00	36.50	67.50
PM4A	A01	Negative Control	64.00	39.50	50.50	90.00
PM4A	A02	Phosphate	184.50	88.00	64.50	175.50
PM4A	A03	Pyrophosphate	168.00	89.00	23.00	160.00
PM4A	A04	Trimetaphosphate	175.50	86.50	14.50	167.50
PM4A	A05	Tripolyphosphate	62.50	75.50	10.50	152.50
PM4A	A06	Triethyl Phosphate	47.50	20.00	9.00	99.00
PM4A	A07	Hypophosphite	50.00	21.50	18.50	87.50
PM4A	A08	Adenosine 2`-Monophosphate	152.00	78.50	155.50	173.00
PM4A	A09	Adenosine 3`-Monophosphate	151.50	80.50	103.00	176.00
PM4A	A10	Adenosine 5`-Monophosphate	154.50	83.50	114.00	182.50
PM4A	A11	Adenosine 2`,3`-Cyclic Monophosphate	131.00	88.50	26.50	167.00
PM4A	A12	Adenosine 3`,5`-Cyclic Monophosphate	169.00	104.00	90.50	181.50
PM4A	B01	Thiophosphate	191.50	45.00	25.00	154.00
PM4A	B02	Dithiophosphate	156.50	44.50	10.50	153.00
PM4A	B03	D,L-a-Glycerol Phosphate	150.00	69.00	8.00	165.00
PM4A	B04	b-Glycerol Phosphate	152.00	74.00	64.50	170.50
PM4A	B05	Carbamyl Phosphate	182.50	76.50	44.50	166.00
PM4A	B06	D-2-Phospho-Glyceric acid	163.50	75.00	76.50	168.50
PM4A	B07	D-3-Phospho-Glyceric acid	142.00	84.00	154.00	166.50
PM4A	B08	Guanosine 2`-Monophosphate	146.50	72.00	9.50	160.50
PM4A	B09	Guanosine 3`-Monophosphate	135.00	72.00	13.00	167.00
PM4A	B10	Guanosine 5`-Monophosphate	143.00	73.50	57.00	167.00
PM4A	B11	Guanosine 2`,3`-Cyclic	114.50	74.50	20.00	161.00

		Monophosphate				
PM4A	B12	Guanosine 3`,5`-Cyclic Monophosphate	72.00	75.50	33.50	174.50
PM4A	C01	Phosphoenol Pyruvate	174.50	88.50	25.00	168.50
PM4A	C02	Phospho-Glycolic acid	171.50	51.00	75.00	157.00
PM4A	C03	D-Glucose-1-Phosphate	141.50	60.00	77.50	157.00
PM4A	C04	D-Glucose-6-Phosphate	140.00	67.00	80.50	162.50
PM4A	C05	2-Deoxy-D-Glucose 6-Phosphate	144.00	71.00	84.50	168.50
PM4A	C06	D-Glucosamine-6-Phosphate	149.00	70.00	89.50	165.50
PM4A	C07	6-Phospho-Gluconic acid	147.00	74.00	7.00	163.50
PM4A	C08	Cytidine 2`-Monophosphate	140.00	65.50	92.50	165.50
PM4A	C09	Cytidine 3`-Monophosphate	134.00	65.50	181.50	172.50
PM4A	C10	Cytidine 5`-Monophosphate	142.50	74.50	15.50	161.50
PM4A	C11	Cytidine 2`,3`-Cyclic Monophosphate	86.00	71.50	18.00	161.50
PM4A	C12	Cytidine 3`,5`-Cyclic Monophosphate	137.50	90.50	33.50	179.00
PM4A	D01	D-Mannose-1-Phosphate	156.00	76.00	24.00	167.00
PM4A	D02	D-Mannose-6-Phosphate	142.00	49.50	153.50	153.00
PM4A	D03	Cysteamine-S-Phosphate	197.00	13.50	14.50	131.00
PM4A	D04	Phospho-L-Arginine	174.00	82.00	60.50	175.00
PM4A	D05	O-Phospho-D-Serine	159.00	67.50	42.00	158.50
PM4A	D06	O-Phospho-L-Serine	148.00	78.50	80.50	172.00
PM4A	D07	O-Phospho-L-Threonine	135.00	69.00	63.50	178.00
PM4A	D08	Uridine 2`-Monophosphate	142.50	67.00	79.00	163.50
PM4A	D09	Uridine 3`-Monophosphate	138.50	68.00	8.00	166.00
PM4A	D10	Uridine 5`-Monophosphate	138.50	71.50	91.00	163.00
PM4A	D11	Uridine 2`,3`-Cyclic Monophosphate	51.00	69.50	9.50	158.50
PM4A	D12	Uridine 3`,5`-Cyclic Monophosphate	146.00	89.00	33.00	178.50
PM4A	E01	O-Phospho-D-Tyrosine	130.50	76.50	74.50	162.50
PM4A	E02	O-Phospho-L-Tyrosine	159.00	72.50	73.00	176.50
PM4A	E03	Phosphocreatine	179.00	76.00	10.00	164.50
PM4A	E04	Phosphoryl Choline	155.50	77.50	178.00	189.00
PM4A	E05	O-Phosphoryl-Ethanolamine	143.00	65.50	56.00	161.00
PM4A	E06	Phosphono Acetic acid	39.00	11.50	56.00	118.50

PM4A	E07	2-Aminoethyl Phosphonic acid	38.00	7.00	111.00	94.50
PM4A	E08	Methylene Diphosphonic acid	34.50	10.00	45.00	88.50
PM4A	E09	Thymidine 3`-Monophosphate	160.50	67.50	161.50	165.00
PM4A	E10	Thymidine 5`-Monophosphate	130.50	64.50	11.00	176.00
PM4A	E11	Inositol Hexaphosphate	51.50	27.50	13.50	152.00
PM4A	E12	Thymidine 3`,5`-Cyclic Monophosphate	150.00	84.00	33.00	169.00
PM4A	F01	Negative Control	76.00	32.50	34.50	113.50
PM4A	F02	Sulfate	174.50	77.50	63.00	166.50
PM4A	F03	Thiosulfate	156.00	63.50	9.00	157.00
PM4A	F04	Tetrathionate	180.50	46.00	14.50	169.00
PM4A	F05	Thiophosphate	97.00	75.00	10.00	156.50
PM4A	F06	Dithiophosphate	106.50	75.50	8.50	168.50
PM4A	F07	L-Cysteine	69.00	61.00	52.00	171.00
PM4A	F08	D-Cysteine	67.50	19.00	13.50	111.50
PM4A	F09	Cys-Gly	77.00	50.00	82.50	133.00
PM4A	F10	L-Cysteic acid	67.00	23.50	28.50	142.50
PM4A	F11	Cysteamine	85.00	47.00	26.50	128.00
PM4A	F12	L-Cysteine Sulfinic acid	108.50	96.50	110.00	186.00
PM4A	G01	N-Acetyl-L-Cysteine	78.50	35.00	61.50	130.00
PM4A	G02	S-Methyl-L-Cysteine	77.00	62.00	13.00	134.00
PM4A	G03	Cystathionine	67.00	20.50	84.50	156.50
PM4A	G04	Lanthionine	66.00	19.50	39.00	150.00
PM4A	G05	Glutathione	71.50	18.50	106.50	109.50
PM4A	G06	D,L-Ethionine	66.00	11.50	18.50	99.50
PM4A	G07	L-Methionine	91.00	48.50	10.50	171.00
PM4A	G08	D-Methionine	93.00	58.50	69.50	173.00
PM4A	G09	Gly-Met	89.00	22.00	89.50	166.00
PM4A	G10	N-Acetyl-D,L-Methionine	66.00	21.50	79.00	145.50
PM4A	G11	L-Methionine Sulfoxide	86.50	34.00	70.50	165.00
PM4A	G12	L-Methionine Sulfone	86.50	43.00	41.50	168.00
PM4A	H01	L-Djenkolic acid	76.00	31.50	65.50	141.00
PM4A	H02	Thiourea	100.00	31.00	18.00	114.50
PM4A	H03	1-Thio-b-D-Glucose	71.50	23.50	42.50	128.00
PM4A	H04	D,L-Lipoamide	140.50	19.50	86.50	117.50
PM4A	H05	Taurocholic acid	62.00	9.00	12.00	179.50
PM4A	H06	Taurine	59.50	14.50	27.50	167.00
PM4A	H07	Hypotaurine	80.50	26.00	29.50	175.00
PM4A	H08	p-Aminobenzene Sulfonic acid	77.50	25.00	40.50	96.50
PM4A	H09	Butane Sulfonic acid	68.50	24.50	31.50	165.50

PM4A	H10	2-Hydroxyethane Sulfonic acid	66.50	20.50	31.50	167.50
PM4A	H11	Methane Sulfonic acid	74.00	29.00	52.50	172.50
PM4A	H12	Tetramethylene Sulfone	83.50	41.50	53.00	121.50
PM9	A01	1% NaCl	191.00	42.00	46.00	164.00
PM9	A02	2% NaCl	182.50	30.00	126.50	153.50
PM9	A03	3% NaCl	183.50	30.50	117.00	124.50
PM9	A04	4% NaCl	180.00	25.00	228.50	101.50
PM9	A05	5% NaCl	161.00	20.50	38.00	66.50
PM9	A06	5.5 %NaCl	159.00	21.50	29.00	50.00
PM9	A07	6% NaCl	163.50	34.00	33.50	42.50
PM9	A08	6.5% NaCl	158.00	34.00	45.50	37.50
PM9	A09	7% NaCl	149.50	30.00	34.00	35.00
PM9	A10	8% NaCl	133.50	38.00	40.50	30.50
PM9	A11	9% NaCl	133.50	45.50	53.00	40.50
PM9	A12	10% NaCl	127.00	55.50	60.50	41.00
PM9	B01	6% NaCl	174.00	41.50	47.00	47.00
PM9	B02	6% NaCl + Betaine	168.00	24.00	110.50	47.00
PM9	B03	6% NaCl + N,N Dimethyl Glycine	164.50	26.00	32.00	47.50
PM9	B04	6% NaCl + Sarcosine	170.00	13.00	27.50	45.00
PM9	B05	6% NaCl + Dimethyl Sulphonyl Propionate	161.00	19.00	29.00	45.00
PM9	B06	6% NaCl + MOPS	156.50	16.50	37.00	48.50
PM9	B07	6% NaCl + Ectoine	150.50	20.00	24.50	42.50
PM9	B08	6% NaCl + Choline	145.50	18.50	105.50	48.50
PM9	B09	6% NaCl + Phosphorylcholine	138.50	25.50	98.50	37.00
PM9	B10	6% NaCl + Creatine	136.00	29.00	36.50	38.00
PM9	B11	6% NaCl + Creatinine	136.50	32.50	46.00	44.50
PM9	B12	6% NaCl + L-Carnitine	152.50	55.50	53.00	47.50
PM9	C01	6% NaCl + KCl	178.00	42.00	48.00	47.50
PM9	C02	6% NaCl + L-Proline	173.00	19.00	30.50	39.00
PM9	C03	6% NaCl + N-Acetyl-L-Glutamine	159.00	19.50	26.00	41.00
PM9	C04	6% NaCl + b-Glutamic acid	148.00	16.00	23.50	50.50
PM9	C05	6% NaCl + g-Amino-N-Butyric acid	154.00	17.50	19.00	53.00
PM9	C06	6% NaCl + Glutathione	149.50	19.00	19.00	40.00
PM9	C07	6% NaCl + Glycerol	139.00	12.00	22.50	38.50
PM9	C08	6% NaCl + Trehalose	138.00	22.50	18.50	39.00
PM9	C09	6% NaCl + Trimethylamine-N-Oxide	133.50	16.50	25.50	30.50
PM9	C10	6% NaCl + Trimethylamine	133.00	27.00	31.00	42.00

PM9	C11	6% NaCl + Octopine	130.00	26.50	47.00	42.50
PM9	C12	6% NaCl + Trigonelline	138.50	46.00	47.00	42.50
PM9	D01	3% Potassium Chloride	169.00	50.00	32.50	180.00
PM9	D02	4% Potassium chloride	95.50	29.50	18.00	157.50
PM9	D03	5% Potassium Chloride	45.50	24.00	22.00	115.00
PM9	D04	6% Potassium chloride	32.00	19.00	12.50	98.00
PM9	D05	2% Sodium Sulfate	150.00	13.50	15.50	129.00
PM9	D06	3% Sodium Sulfate	149.00	14.00	24.50	126.50
PM9	D07	4% Sodium Sulfate	145.00	10.00	10.50	122.50
PM9	D08	5% Sodium Sulfate	136.00	12.50	34.00	123.00
PM9	D09	5% Ethylene Glycol	138.00	23.00	219.50	191.00
PM9	D10	10% Ethylene Glycol	113.50	22.00	218.00	136.50
PM9	D11	15% Ethylene Glycol	78.50	17.50	121.00	117.50
PM9	D12	20% Ethylene Glycol	97.50	32.00	214.50	122.00
PM9	E01	1% Sodium Formate	145.50	58.00	42.50	168.00
PM9	E02	2% Sodium Formate	60.00	24.50	24.00	132.50
PM9	E03	3% Sodium Formate	30.50	19.50	22.00	95.00
PM9	E04	4% Sodium Formate	21.00	12.50	18.50	39.00
PM9	E05	5% Sodium Formate	20.50	6.50	15.50	27.50
PM9	E06	6% Sodium Formate	22.50	20.00	26.50	22.50
PM9	E07	2% Urea	112.00	14.00	18.50	180.50
PM9	E08	3% Urea	30.00	14.00	16.00	172.50
PM9	E09	4% Urea	31.00	16.00	28.50	124.00
PM9	E10	5% Urea	30.50	20.00	27.00	57.50
PM9	E11	6% Urea	36.00	31.50	33.50	24.50
PM9	E12	7% Urea	60.00	59.00	50.50	48.00
PM9	F01	1% Sodium Lactate	61.50	52.00	52.00	90.00
PM9	F02	2% Sodium Lactate	40.50	35.50	22.00	30.50
PM9	F03	3% Sodium Lactate	22.00	15.50	33.00	23.50
PM9	F04	4% Sodium Lactate	24.50	7.50	32.00	18.00
PM9	F05	5% Sodium Lactate	24.50	25.00	33.00	32.00
PM9	F06	6% Sodium Lactate	22.50	4.00	31.50	23.50
PM9	F07	7% Sodium Lactate	30.50	5.50	27.00	21.00
PM9	F08	8% Sodium Lactate	18.00	3.50	24.50	8.50
PM9	F09	9% Sodium Lactate	35.50	6.50	30.00	13.00
PM9	F10	10% Sodium Lactate	34.00	17.00	34.50	30.50
PM9	F11	11% Sodium Lactate	47.50	25.00	29.50	26.50
PM9	F12	12% Sodium Lactate	58.50	46.00	41.00	36.50
PM9	G01	20mM Sodium Phosphate pH 7	168.50	46.50	41.00	173.00
PM9	G02	50mM Sodium Phosphate pH 7	93.50	30.00	30.00	136.00
PM9	G03	100mM Sodium Phosphate pH 7	54.50	23.00	34.50	136.50
PM9	G04	200mM Sodium Phosphate pH 7	32.00	26.00	16.00	144.00

PM9	G05	20mM Sodium Benzoate pH 5.2	40.50	16.00	18.50	132.00
PM9	G06	50mM Sodium Benzoate pH 5.2	19.00	14.00	27.00	26.00
PM9	G07	100mM Sodium Benzoate pH 5.2	21.00	11.50	16.50	16.50
PM9	G08	200mM Sodium Benzoate pH 5.2	26.00	9.50	13.00	23.00
PM9	G09	10mM Ammonium Sulfate pH 8	33.00	24.00	224.50	166.00
PM9	G10	20mM Ammonium Sulfate pH 8	42.00	30.50	204.00	167.00
PM9	G11	50mM Ammonium Sulfate pH 8	43.00	38.50	114.50	147.00
PM9	G12	100mM Ammonium Sulfate pH 8	57.50	54.00	126.50	154.00
PM9	H01	10mM Sodium Nitrate	173.00	48.00	238.00	179.50
PM9	H02	20mM Sodium Nitrate	144.00	36.50	237.50	182.00
PM9	H03	40mM Sodium Nitrate	124.50	27.50	219.00	178.50
PM9	H04	60mM Sodium Nitrate	119.50	27.50	222.50	209.00
PM9	H05	80mM Sodium Nitrate	118.50	25.00	122.00	190.50
PM9	H06	100mM Sodium Nitrate	119.00	21.50	119.50	188.00
PM9	H07	10mM Sodium Nitrite	157.50	27.50	28.00	180.50
PM9	H08	20mM Sodium Nitrite	137.50	24.00	20.50	175.50
PM9	H09	40mM Sodium Nitrite	72.50	29.00	27.50	168.50
PM9	H10	60mM Sodium Nitrite	39.00	31.50	43.00	145.50
PM9	H11	80mM Sodium Nitrite	44.50	45.00	39.50	119.50
PM9	H12	100mM Sodium Nitrite	55.00	47.50	56.00	67.50

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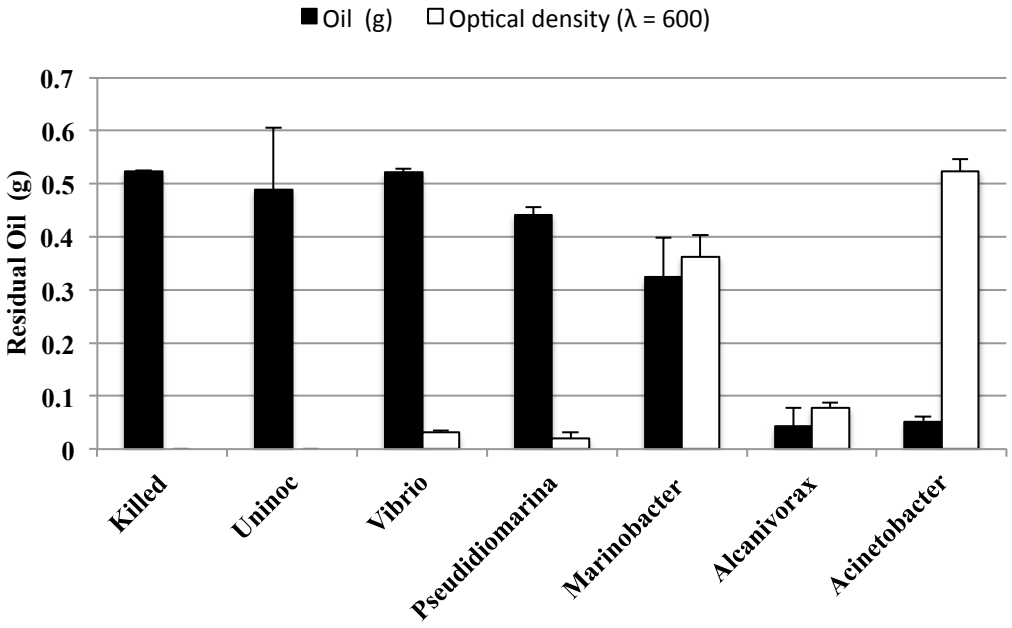


Figure S1: Degradation of crude oil by representative pure cultures isolated from oiled beach sands in this study. The proportion of residual oil is plotted along with the concomitant increase in cell biomass. Residual oil was extracted with chloroform and measured gravimetrically in pre-weighted glass vials. Values are the average of triplicates and error bars represent one standard deviation.

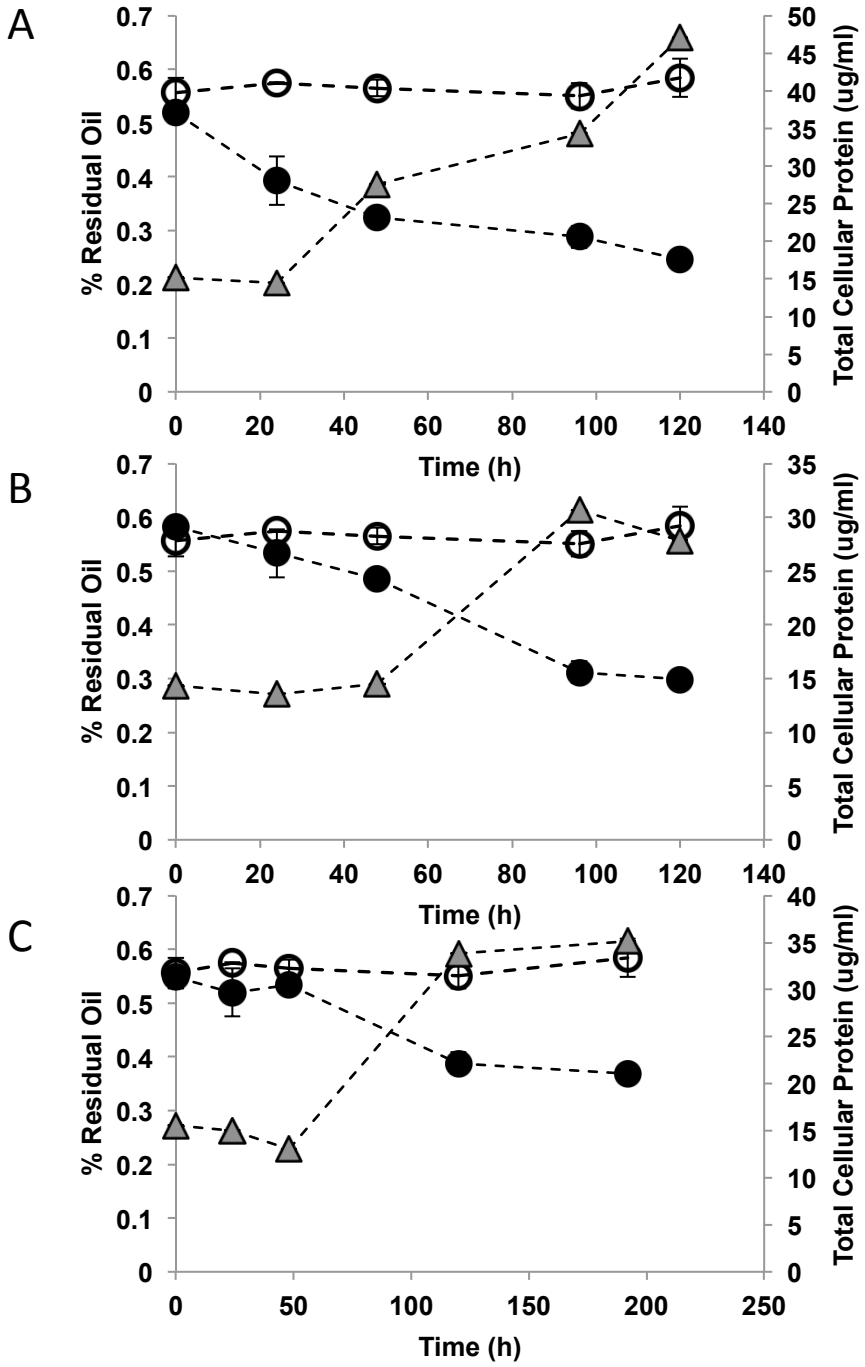
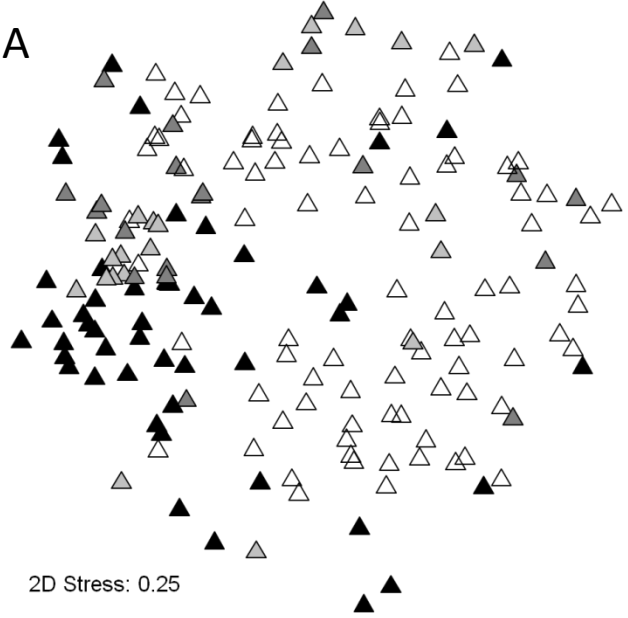


Figure S2: Growth response (∇) as total cellular protein, of *Marinobacter* (A), *Acinetobacter* (B) and *Alcanivorax* (C) strains with concomitant crude oil degradation (●) in comparison to uninoculated control cultures (ʘ). The concentration of residual oil was determined spectrophotometrically in chloroform extracts (λ=520) and total cellular protein was quantified using the Bradford method. Values represent the average of triplicates and error bars represent one standard deviation.

A



B

Analysis of Similarity				
	Clean	Low	Moderate	High
Clean				
Low	0.001			
Moderate	0.001	0.374		
High	0.001	0.029	0.036	

C

Similarity Percentages (SIMPER)			
Clean	**Low**	**Moderate**	**High**
661	729	661	729
804	804	729	600
470	661	804	844
977	571	571	661
38%	53%	54%	54%

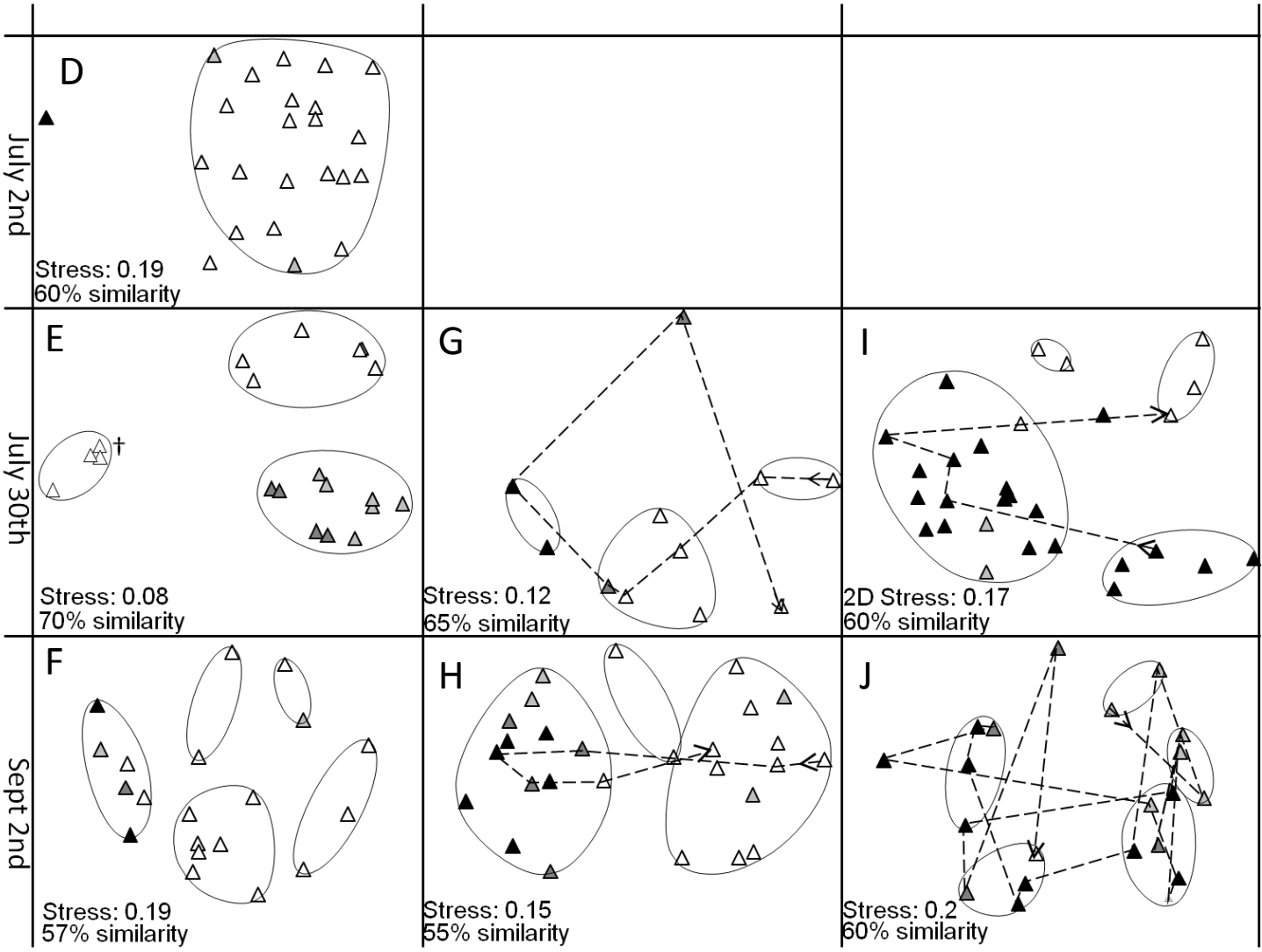


Figure S3. Community fingerprinting data generated through ARISA based analysis. These data represent 150 samples, spanning three sampling trips, that were collected from clean and oiled sands from Pensacola Beach. All NMDS plots were generated from a Bray-Curtis resemblance matrix calculated using log(X+1) transformed, normalized peak data. Shading corresponds to qualitative assessment of oil contamination (white = clean, light gray = low, gray = moderate, black = heavy). When present, clustering represents Bray-Curtis similarity between samples. (A) All samples collected from the study area to date. Clustering pattern indicates pronounced, if scattered, effect of oil contamination. (B) Analysis of similarity (ANOSIM) test performed on all samples to determine significance of grouping samples by qualitative oil contamination. The global R value was 0.21 corresponding to a global P value of 0.001. Pairwise p-values are indicated in the table and black cells are significant. (C) A similarity percentages (SIMPER) test was used to determine key fragments that lead to the significant grouping patterns. Note all 4 top peaks for the low and moderate groups are the same. (D-E) Sectioned core samples taken from all 3 sampling trips. † These samples were from the surface layer of the cores during an algal bloom are likely contaminated by chloroplast DNA (F,G) Vertical transect samples taken from beach surface, through the oil layer to clean underlying sediments. Trajectories are overlaid on both plots starting at the surface and preceding to the deepest samples. Note not all points were included in the trajectories. (H,I) Samples collected along a horizontal transect along the oil layer. Over laid trajectories began furthest from the beach and proceed to the water.

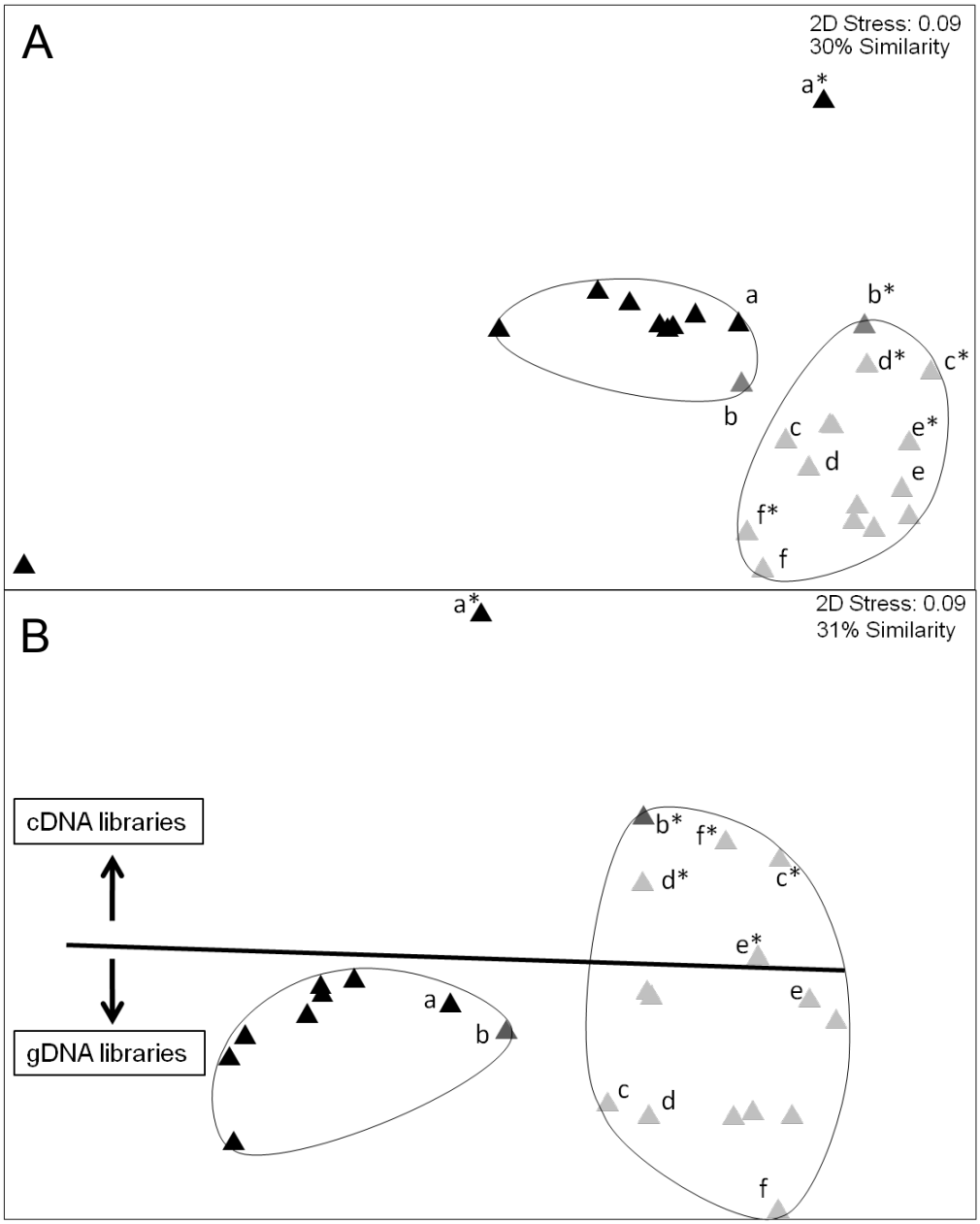


Figure S4. Bacterial community response to oil contamination in beach sands assessed using the weighted UniFrac metric and visualized with NMDS plots. Pensacola oiled samples are colored black, clean Pensacola and St. George Island samples are colored grey. Lowercase letters indicate samples derived from the same sand sample, asterisks (*) indicate RNA based sequence libraries. Subplot (A) includes all samples, while the outlier (dominated by Spirochaetes) is removed in subplot (B). Microbial communities reveal a strong response to oil contamination by grouping together on the left side of the plot. Notably, St. George Island samples (e,f) and clean Pensacola samples are not resolved using weighted UniFrac.