

Supplemental File 1 (S01) for

Integration of microscopy and multi-omic data reveals pathology of a coral disease outbreak

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Methodology	WP	SCTLD
Gross morphology	Borger (2003) Brandt et al. (2012)	Precht et al. (2016) Aeby et al. (2019) Alvarez-Filip et al. (2019) Landsberg et al. (2020) Aeby et al. (2021) Brandt et al. (2021) Meiling et al. (2021)

		Work et al. (2025)
Histopathology	--	Landsberg et al. (2020) Work et al. (2025) Rossin et al. (2026)
TEM	Richardson et al. (1998) Soffer et al. (2014) ^c	Work et al. (2021)^{c, s} Work et al. (2025)^{c, s}
Amplicon sequencing: 16S	Richardson et al. (1998) Pantos et al. (2003) Cárdenas et al. (2012) Roder et al. (2013) MacKnight et al. (2021)	Meyer et al. (2019) Rosales et al. (2020) Becker et al. (2021) Clark et al. (2021) Evans et al. (2022) Huntley et al. (2022) Evans et al. (2023) Rosales et al. (2023) Arriaga-Piñon et al. (2024) Becker et al. (2024) Rosales et al. (2025)
Amplicon sequencing: ITS-2	--	Dennison et al. (2021) Titus et al. (2022) Karp et al. (2023) Karrick et al. (in review)
Comparative metagenomics	Garcia et al. (2013) ^{b, e}	Traylor-Knowles et al. (2021) ^c Rosales et al. (2022) ^{b, e} Heinz et al. (2024) ^{b, c, s, v} Nandi et al. (2025) ^{b, s, v}
Comparative metatranscriptomics	MacKnight et al. (2022) ^c Silva-Lima et al. (2021) ^{b, c, s, v}	Beavers et al. (2023)^{c, s} Beavers et al. (2025) ^{c, s} Veglia et al. (in prep)^v

Supplemental Table 1: Papers that have used gross morphology, histopathology, transmission electron microscopy (TEM), amplicon sequencing of the 16S rRNA gene, amplicon sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA, comparative metagenomics, and comparative metatranscriptomics to study white plague (WP) and stony coral tissue loss disease (SCTLD). **Bolded studies** included *Pseudodiploria strigosa*; superscripts indicate that a given study: ^b - analyzed bacterial sequences, ^c - analyzed coral sequences/cells, ^e - analyzed non-Symbiodiniaceae microeukaryotic sequences, ^s - analyzed Symbiodiniaceae sequences/cells, and ^v - analyzed viral sequences. -- indicates that no applicable published studies exist.

Feature	Proportion HH cells with feature	Proportion HD cells with feature	Proportion DD cells with feature	ANOVA χ^2	ANOVA p
Indistinct organelles	~52.1% (62 of 119)	~49.3% (67 of 136)	~43.6% (75 of 172)	2.22	3.303×10^{-1}
Abnormal cell membrane	~39.5% (47 of 119)	~28.7% (39 of 136)	~32.6% (56 of 172)	3.39	1.840×10^{-1}
Indistinct thylakoid membranes	~58.8% (70 of 119)	~72.8% (99 of 136)	~63.4% (109 of 172)	5.93	5.164×10^{-2}
Large cavities	~49.6% (59 of 119)	~52.9% (72 of 136)	~62.2% (107 of 172)	5.20	7.412×10^{-2}
Overall degraded	~62.2% (74 of 119)	~63.2% (86 of 136)	~64.5% (111 of 172)	0.17	9.176×10^{-1}
Pyrenoid body absent	~68.9% (82 of 119)	~66.9% (91 of 136)	~64.5% (111 of 172)	0.62	7.337×10^{-1}
Starch granules present	~73.9% (88 of 119)	~73.5% (100 of 136)	~85.5% (147 of 172)	8.702	*** 1.289×10^{-2}
Filamentous VLPs	~10.9% (13 of 119)	~5.9% (8 of 136)	~12.2% (21 of 172)	3.94	1.396×10^{-1}
Mass of filamentous VLPs	~0.8% (1 of 119)	~0.7% (1 of 136)	~1.2% (2 of 172)	0.16	9.210×10^{-1}
Spherical/ico sahedral VLPs	~8.4% (10 of 119)	~28.7% (39 of 136)	~25.6% (44 of 172)	20.32	*** 3.865×10^{-6}
Crystalline arrays of spherical/icos ahedral VLPs	0% (0 of 119)	0% (0 of 136)	~1.2% (2 of 172)	3.65	1.611×10^{-1}
Crystal structures	~9.2% (11 of 119)	~5.9% (8 of 136)	~8.7% (5 of 172)	1.26	5.319×10^{-1}
Viroplasms	~11.8% (14)	~11.8% (16)	~13.4% (23)	0.24	8.858×10^{-1}

	of 119)	of 136)	of 172)		
Multi-membrane vesicles (MMVs)	~3.4% (4 of 119)	~3.7% (5 of 136)	~17.4% (30 of 172)	23.93	***6.358 x 10 ⁻⁶

Supplemental Table 2: The proportion of cells per health state containing each cell abnormality and viral characteristic identified in Symbiodiniaceae electron micrographs. χ^2 and p-values are shown from ANOVA of binomial logistic regression. Asterisks (*) indicate $p < 0.05$. VLP: virus-like particle.

Sample	A2b	B1-B1co-B1x-B1j-B1gz-B1l-B1do-B1ha-B14d	B1-B1co-B1x-B14d	B1-B14d-B1x-B1ao-B1co-B1l-B1j	B1-B1l-B1x	B1-B1co-B1x-B1j-B14d
001_HD	0	6316	0	0	0	0
001_DD	0	16019	0	0	0	0
002_HH	0	12180	0	0	0	0
003_HD	0	0	0	0	0	13490
003_DD	244	15856	0	0	0	0
004_HH	0	0	0	40225	0	0
005_HD	0	14032	0	0	0	0
005_DD	0	0	4394	0	0	0
006_HH	0	5186	0	0	0	0
007_HD	0	0	1603	0	0	0
007_DD	0	0	4657	0	0	0
008_HH	0	0	0	0	14639	0
009_HD	0	461	0	0	0	0
009_DD	0	474	0	0	0	0
010_HH	0	0	0	5728	0	0

Supplemental Table 3: Absolute counts of Symbiodiniaceae internal transcribed spacer-2 (ITS-2) type profiles after running ITS-2 sequences through SymPortal. HH: apparently healthy tissue on an apparently healthy coral; HD: apparently healthy tissue on a diseased coral; DD: lesion-adjacent tissue.

Species	Region	Number of Contigs	BUSCO %	Complete & Single Copy	Complete & Duplicate	Fragments	Missing	N50	Percent Annotated
<i>P. strigosa</i>	Flower Garden Banks	14424	69.10%	59.20%	9.90%	3.00%	27.90%	3635	75%

Supplemental Table 4: *Pseudodiploria strigosa* de novo transcriptome assembly statistics from BUSCO. All fifteen samples were used in de novo transcriptome assembly.

	HH			HD			DD		
Average similarity percent	9.78%			6.52%			8.79%		
ASVs contributing more than 1% to Bray-Curtis similarity	% contribution	ASV	Taxonomy (genus or last highest known taxonomic rank)	% contribution	ASV	Taxonomy (genus or last highest known taxonomic rank)	% contribution	ASV	Taxonomy (genus or last highest known taxonomic rank)
	7.41	ASV11	Synechococcus CC9902	5.43	ASV2	Ruegeria	11.39	ASV2	Ruegeria
	6.47	ASV2	Ruegeria	4.73	ASV6	Rhodobacteraceae	4.49	ASV10	Gastranaerophilales
	4.28	ASV17	Cyanobium PCC-6307	4.69	ASV14	Amoebophilaceae	4.24	ASV14	Amoebophilaceae
	3.58	ASV1	Pseudovibrio	3.13	ASV30	Romboutsia	4.1	ASV6	Rhodobacteraceae
	3.55	ASV7	Caldilineaceae	3.1	ASV1	Pseudovibrio	3.71	ASV11	Synechococcus CC9902
	2.79	ASV59	Paramedivibacter	2.93	ASV11	Synechococcus CC9902	3.41	ASV17	Cyanobium PCC-6307
	2.2	ASV21	Synechococcus CC9902	2.93	ASV18	Romboutsia	3.37	ASV4	Anaerolineaceae
	2.19	ASV34	Microbulbifer	2.81	ASV140	Pseudahrensia	2.81	ASV9	Desulforhopalus
	2.14	ASV25	Ruegeria	2.26	ASV152	Phormidiaceae	2.54	ASV255	Hungateiclostridiaceae
	1.87	ASV24	Defluviitalea	2.11	ASV17	Cyanobium PCC-6307	2.51	ASV35	Rubritalea
	1.85	ASV6	Rhodobacteraceae	1.99	ASV256	Alphaproteobacteria	2.04	ASV69	Mycobacterium
	1.44	ASV220	Hoeflea	1.59	ASV91	Bythopirellula	1.93	ASV21	Synechococcus CC9902
	1.39	ASV5	Microbulbifer	1.56	ASV51	Caldilineaceae	1.82	ASV25	Ruegeria
	1.32	ASV15	Subgroup 10	1.53	ASV4	Anaerolineaceae	1.72	ASV52	Synechococcus CC9902
	1.28	ASV49	Sva0996 marine group	1.44	ASV123	Haloferula	1.52	ASV61	Hyphomicrobiaceae
	1.2	ASV13	Candidatus Nitrosopumilus	1.4	ASV29	Rubritalea	1.32	ASV29	Rubritalea
	1.16	ASV130	Cyanobiaceae	1.28	ASV303	Dadabacteriales	1.2	ASV65	Ascidiaeihabitans
	1.06	ASV18	Romboutsia	1.21	ASV33	A4b (Anaerolineae, order SBR2031)	1.16	ASV109	Desulfocarbo
	1.05	ASV75	Rhodobacteraceae	1.13	ASV98	PAUC43f marine benthic group	1.07	ASV96	Rhodobacteraceae
	1.01	ASV36	Caldilineaceae				1.02	ASV81	Winogradskyella
	1	ASV173	Filomicrobium						

Supplemental Table 5: Average similarity percent analysis (SIMPER) indicates low similarity of bacterial/archaeal communities between samples within the same tissue state based on sequencing of the 16S rRNA gene. Amplicon sequence variants (ASVs) that contribute more than 1% to Bray-Curtis similarity and their associated percent contribution and taxonomy are listed for each tissue health state. HH: apparently healthy tissue on an apparently healthy coral; HD: apparently healthy tissue on a diseased coral; DD: lesion-adjacent tissue.

Total vOTUs	# low quality vOTUs	# medium quality vOTUs	# high quality vOTUs	# complete vOTUs	# undetermined quality vOTUs	# Duplodnaviria vOTUs	# Varidnaviria vOTUs	# Monodnaviria vOTUs	# Riboviria vOTUs	# unclassified vOTUs	Top 5 Classes of vOTUs
49	41	2	2	0	4	16	4	0	2	27	Caudoviricetes (n = 15) Megaviricetes (n = 3) Herviviricetes (n = 1) Revtraviricetes (n = 1) Polintoviricetes (n = 1)

Supplemental Table 6: After filtering and clustering, the total number of viral operational taxonomic units (vOTUs) and their associated CheckV quality scores and annotated taxonomy.

Sample ID	16S ASV Shannon diversity index	ITS-2 type profile Shannon diversity index	vOTU Shannon diversity index
001_HD	2.9202920017004	0	3.56016744098729
001_DD	2.97445216290151	0	3.49829660084376
002_HH	2.45812997173507	0	3.5110746960712
003_HD	1.44740202258056	0	2.96217294713671
003_DD	2.91464038342938	0.0785314774854859	3.1744453137836
004_HH	2.54540203238456	0	3.14927799106253
005_HD	3.16991322878206	0	3.39290884569713
005_DD	2.70320064282229	0	3.50597532765296
006_HH	2.73265537311187	0	3.54541279708284
008_HH	3.37482129075585	0	3.49898627661517
009_HD	3.31605467737271	0	3.16655439820604
009_DD	3.06815107317555	0	3.51113965093328
010_HH	2.9475911334777	0	3.52840483101666

Supplemental Table 7: Per-sample Shannon diversity indices of each microbial group generated from sequencing of the v4 region of the 16S rRNA gene, sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA, and mining of viral operational taxonomic units (vOTUs) from bulk RNA-Seq data. ASV: amplicon sequence variant.

Dataset	Comparison	S	rho	p-value
Global	vOTU-ASV	326	0.1043956	0.737
HH-only	vOTU-ASV	18	0.1	0.95
HD-only	vOTU-ASV	8	0.2	0.9167
DD-only	vOTU-ASV	6	0.4	0.75
Global	vOTU-ITS2	448.25	-0.231455	0.4467
HH-only	vOTU-ITS2	NA	NA	NA
HD-only	vOTU-ITS2	NA	NA	NA
DD-only	vOTU-ITS2	17.746	-0.7745967	0.2254

Supplemental Table 8: The results of Spearman correlations between Shannon diversity indices of viral operational taxonomic units (vOTUs) mined from bulk RNA-Seq data and amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene (vOTU-ASV) or sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA (vOTU-ITS2). Correlations were run including all samples (i.e., globally) and in subsets of the data containing samples belonging to one tissue health state (i.e., HH-, HD-, or DD-only). HH: apparently healthy tissue from an apparently healthy coral; HD: apparently healthy tissue from a diseased coral; DD: lesion-adjacent tissue from a diseased coral.

Sample	ASV_PC1	ASV_PC2	ITS2_PC1	ITS2_PC2	vOTU_PC1	vOTU_PC2
001_HD	0.247482662277133	0.064671058556114	-0.306193155796415	-0.0304117448800576	-0.142427521063212	-0.0198509927966984
001_DD	0.300094741402311	0.304445947136803	-0.306193155796415	-0.0304117448800577	-0.104725745222357	-0.00568481935155246
002_HH	-0.465875994401494	0.164990593525535	-0.306193155796415	-0.0304117448800578	-0.0463013043840957	-0.010684923761823
003_HD	-0.506540065135118	0.193194295607076	0.408234830131494	0.364880215046424	0.239808333510272	-0.0847890877700079
003_DD	0.324243514881223	0.290591081424761	-0.3060876549507	-0.0303844990665678	0.18452356247765	-0.0384697897922045
004_HH	0.242279588798048	0.0128967580939773	0.612367627565562	-0.42568696595615	0.192754907799467	0.102655793322199
005_HD	-0.136916326278968	-0.0401469942295794	-0.306193155796415	-0.0304117448800576	0.0514506168868904	-0.00185270961520588
005_DD	0.0017529493640395	-0.461162157066017	0.408234830131494	0.364880215046424	-0.104382581286914	0.0438535014567782
006_HH	-0.138513503144699	0.136273740900512	-0.306193155796415	-0.0304117448800576	-0.109705429794275	-0.0490923361970085
008_HH	-0.0941968447240247	-0.0492987156625435	0.408234830131494	0.364880215046424	-0.120982150398009	-0.0865471423704287
009_HD	0.137117328506971	-0.245159309479262	-0.306193155796415	-0.0304117448800576	0.156108288680945	0.0500391114533283
009_DD	0.201843511169892	-0.0912263029597479	-0.306193155796415	-0.0304117448800576	-0.0648232332346252	-0.0313314276343821
010_HH	-0.11277156271531	-0.280069995847629	0.612367627565562	-0.42568696595615	-0.131297743971737	0.131754823057005

Supplemental Table 9: Per-sample PC1 and PC2 for principal coordinate analysis (PCoA) ordinations of Bray-Curtis dissimilarity matrices generated from three data types: (1) amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene, (2) ITS-2 type profiles from sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA, and (3) viral operational taxonomic units (vOTUs) mined from bulk RNA-Seq data.

Dataset	Comparison	Mantel statistic r	p-value
Global	vOTU-ASV	-0.1646	0.885
HH-only	vOTU-ASV	-0.09091	0.625
HD-only	vOTU-ASV	-0.2571	0.41667
DD-only	vOTU-ASV	-0.6	1
Global	vOTU-ITS2	0.2693	0.057
HH-only	vOTU-ITS2	0.08704	0.4
HD-only	vOTU-ITS2	0.09759	0.5
DD-only	vOTU-ITS2	-0.09258	0.41667

Supplemental Table 10: The results of Mantel tests of Spearman correlations between Bray-Curtis dissimilarity matrices of viral operational taxonomic units (vOTUs) mined from bulk RNA-Seq data and amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene (vOTU-ASV) or sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA (vOTU-ITS2). Tests were run with 999 permutations including all samples (i.e., globally) and in subsets of the data containing samples belonging to one tissue health state (i.e., HH-, HD-, or DD-only). HH: apparently healthy tissue from an apparently healthy coral; HD: apparently healthy tissue from a diseased coral; DD: lesion-adjacent tissue from a diseased coral.

Dataset	Comparison	Procrustes sum of squares (m ²)	Correlation in a symmetric Procrustes rotation (r)	p-value
Global	vOTU-ASV	0.892	0.3287	0.717
HH-only	vOTU-ASV	0.3814	0.7865	0.28333
HD-only	vOTU-ASV	0.2155	0.8857	0.125
DD-only	vOTU-ASV	0.6865	0.5599	0.54167
Global	vOTU-ITS2	0.8072	0.4391	0.234
HH-only	vOTU-ITS2	0.5679	0.6574	0.5
HD-only	vOTU-ITS2	0.5938	0.6373	0.5
DD-only	vOTU-ITS2	0.82	0.4243	0.5

Supplemental Table 11: The results of Procrustes analyses of principal coordinate analysis (PCoA) ordinations of Bray-Curtis dissimilarity matrices of viral operational taxonomic units (vOTUs) mined from bulk RNA-Seq data and amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene (vOTU-ASV) or sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA (vOTU-ITS2). Tests were run with 999 permutations including all samples (i.e., globally) and in subsets of the data containing samples belonging to one tissue health state (i.e., HH-, HD-, or DD-only). HH: apparently healthy tissue from an apparently healthy coral; HD: apparently healthy tissue from a diseased coral; DD: lesion-adjacent tissue from a diseased coral.

rho cutoff	randcounts	truecounts	FDR
2.88539150664624E-05	10085.6056056056	9571	1.05376717225009
0.00205093832847693	10011.3993993994	9475	1.05661207381524
0.0044115733589442	9925.65565565566	9378	1.05839791593684
0.00770860602495061	9805.05305305305	9281	1.05646514955857
0.0105629331214836	9701.45445445446	9185	1.05622802988072
0.0128125448219238	9619.96396396396	9088	1.05853476716153
0.0156239676872751	9518.95295295295	8991	1.05872015937637
0.0183672398146725	9421.42942942943	8895	1.05918262275766
0.0210485900460325	9325.85785785786	8798	1.0599974832755
0.0232654099538217	9247.4994994995	8701	1.0628088150212
0.0256932369349596	9162.34134134134	8605	1.06476947604199

0.0285394223979278	9062.72372372372	8508	1.06520024961492
0.0312746906171875	8967.95695695696	8411	1.0662176860013
0.0345561573094535	8855.23423423423	8315	1.0649710444058
0.0379869721693642	8738.96196196196	8218	1.06339279167218
0.0407378546183659	8645.83183183183	8121	1.0646265031193
0.0438578729950623	8541.45045045045	8025	1.06435519631781
0.0469216220394117	8440.12312312312	7928	1.06459676124156
0.0501996582663175	8332.9059059059	7831	1.06409218566031
0.0533034139151339	8232.43343343343	7735	1.06430942901531
0.0556504561736159	8157.22722722723	7638	1.06797947463043
0.0585510590720216	8065.2002002002	7541	1.06951335369317
0.061358025087292	7976.72672672673	7445	1.07142064831789
0.0646451659551991	7875.57757757758	7348	1.07179879934371
0.0679268355142047	7775.51551551552	7251	1.07233699014143
0.0717149704089176	7661.72072072072	7155	1.07082050604063
0.0743662637208279	7582.32232232232	7058	1.07428766255629
0.0777243656510494	7483.78278278278	6961	1.07510167831961
0.0812100982007896	7382.08508508508	6865	1.07532193519084
0.0851122680623874	7270.6006006006	6768	1.07426131805564
0.0899630337558532	7133.44044044044	6671	1.06932100741125
0.0926788930248132	7058.31031031031	6575	1.07350727153009
0.0965276652822993	6952.2952952953	6478	1.07321631603817
0.100457519724713	6846.1001001001	6381	1.07288827771511
0.104128544312462	6747.98598598599	6284	1.07383608943125
0.109764496635182	6600.1041041041	6188	1.06659730189142
0.114881728768303	6467.06506506507	6091	1.06174110409868
0.118564794739901	6371.68868868869	5994	1.06301112590736
0.122499514839339	6270.57357357357	5898	1.06316947669949
0.126012464575028	6181.59259259259	5801	1.06560810077445
0.130890961589851	6058.46746746747	5704	1.06214366540453
0.135265494558839	5949.74474474474	5608	1.06093879185891
0.140465239499103	5821.35335335335	5511	1.05631525192403
0.145018554836179	5710.83883883884	5414	1.05482800865143
0.149791089360523	5597.05805805806	5318	1.05247424935278
0.154118803052919	5495.93493493493	5221	1.05265943975004
0.159333575850908	5375.4044044044	5124	1.04906409141382
0.163428932676098	5282.08708708709	5028	1.05053442463944
0.16869312732309	5164.5015015015	4931	1.04735378249878

0.174019425357673	5046.33133133133	4834	1.04392456171521
0.178203160229839	4954.19019019019	4738	1.04562899750743
0.183502868212798	4838.25825825826	4641	1.04250339544457
0.189433390233976	4709.07007007007	4544	1.03632704006824
0.193673268484928	4618.05705705706	4448	1.03823225203621
0.197562869483945	4535.80980980981	4351	1.04247524932425
0.202957914893845	4422.36136136136	4254	1.03957718884846
0.208979200999229	4297.66066066066	4158	1.03358842247731
0.213860349826695	4198.13713713714	4061	1.03376930242234
0.220213635972648	4071.65865865866	3964	1.02715909653347
0.229548087902634	3891.77477477477	3868	1.00614652915584
0.23590417124008	3773.74974974975	3771	1.00072918317416
0.24186837879648	3665.94594594595	3674	0.99780782415513
0.24841613238934	3551.16716716717	3578	0.992500605692333
0.253888930356333	3458.08508508509	3481	0.993417145959519
0.262010423837149	3324.30630630631	3384	0.982360019594062
0.269244896864603	3208.70770770771	3288	0.975884339327162
0.276645327322911	3094.08908908909	3191	0.969629924503005
0.285098746910566	2967.73173173173	3094	0.959189312130489
0.292815094439356	2856.72972972973	2997	0.953196439682926
0.301369217915983	2739.72472472472	2901	0.944407006109867
0.310620704579309	2620.31931931932	2804	0.934493337845692
0.318130034155095	2527.96896896897	2707	0.933863675274831
0.329014754990418	2402.13613613614	2611	0.920006180059799
0.339555186728934	2288.59159159159	2514	0.910338739694348
0.352146533053519	2162.70670670671	2417	0.8947897007475
0.36294930661159	2062.96196196196	2321	0.888824628161121
0.376603924125995	1947.24324324324	2224	0.87555901224966
0.391075667272105	1834.49049049049	2127	0.862477898679121
0.409723955578995	1701.37737737738	2031	0.837704272465474
0.424802789214389	1602.85585585586	1934	0.828777588343255
0.442359792128515	1496.28028028028	1837	0.814523832487904
0.462271485535754	1383.29129129129	1741	0.79453836375146
0.479015773572571	1288.51351351351	1644	0.783767343986322
0.496997051447836	1186.04204204204	1547	0.766672296084061
0.516922527303813	1078.22122122122	1451	0.743088367485335
0.536015462717277	984.97997997998	1354	0.727459364830118
0.55873929945997	886.847847847848	1257	0.70552732525684

0.580738548436145	809.013013013013	1161	0.696824300614137
0.605326089046826	738.214214214214	1064	0.693810351705089
0.634713684590041	659.163163163163	967	0.681657872971213
0.663206881299452	588.888888888889	871	0.6761066462559
0.696557967843355	529.101101101101	774	0.683593153877392
0.737451114845017	468.855855855856	677	0.692549270097276
0.770465959862945	406.728728728729	581	0.700049447037399
0.807518782890237	351.867867867868	484	0.726999726999727
0.871816215758437	287.403403403403	387	0.742644453238768
0.929512711386464	215.817817817818	291	0.74164198562824
0.992552427375218	134.26026026026	194	0.692063197217836
0.998465063216889	71.2372372372372	97	0.734404507600384
0.99999992438447	0.421421421421	0	Inf

Supplemental Table 12: False discovery rate per tested rho threshold for pairwise proportional relationships between microbial taxa.

Dataset	n nodes	n edges	n communities	Edge density	Modularity	Transitivity
Global	30	24	7	0.05517241	0.7838542	0
HH-only	0	0	0	NA	NA	NA
HD-only	2	1	1	1	0	NA
DD-only	2	1	1	1	0	NA

Supplemental Table 13: A summary of network-level statistics for co-occurrence networks between amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene, ITS-2 type profiles from sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA, and mining of viral operational taxonomic units (vOTUs) from bulk RNA-Seq data. Networks were created with all samples (i.e., globally) and with HH-, HD-, and DD-only subsets of the samples. HH: apparently healthy tissue from an apparently healthy coral; HD: apparently healthy tissue from a diseased coral; DD: lesion-adjacent tissue from a diseased coral.

network	node1	node2	weight	sign
global	vOTU_3	vOTU_5	0.763468027114868	+
global	vOTU_4	vOTU_13	0.87660720257744	+
global	vOTU_15	vOTU_22	0.77277	+
global	vOTU_19	vOTU_22	0.948601543903351	+
global	vOTU_3	vOTU_23	0.866046058838676	+
global	vOTU_19	vOTU_26	0.945331321914883	+
global	vOTU_10	vOTU_27	0.673428416252136	+
global	vOTU_19	vOTU_29	0.896565471849903	+
global	vOTU_5	vOTU_30	0.915919952259656	+
global	vOTU_1	vOTU_32	0.95613832597322	+
global	vOTU_3	vOTU_33	0.713685750961304	+
global	vOTU_14	vOTU_33	0.923991907964082	+
global	vOTU_27	vOTU_34	0.894551025710443	+
global	vOTU_9	vOTU_36	0.698057472705841	+
global	vOTU_32	vOTU_36	0.833984673023224	+
global	vOTU_5	vOTU_37	0.891716327748376	+
global	vOTU_34	vOTU_39	0.876275892142206	+
global	vOTU_32	vOTU_40	0.93408362911577	+
global	vOTU_9	vOTU_41	0.887167835297037	+
global	vOTU_15	vOTU_42	0.876831976345857	+
global	vOTU_8	vOTU_43	0.867616628546023	+
global	vOTU_5	vOTU_45	0.804281134004974	+
global	vOTU_16	vOTU_45	0.954853594809661	+
global	vOTU_10	vOTU_46	0.805988634830968	+
HD-only	vOTU_3	vOTU_32	0.999878400011962	+
DD-only	vOTU_29	vOTU_30	-0.999709505366906	-

Supplemental Table 14: A summary of node-level statistics for co-occurrence networks between amplicon sequence variants (ASVs) from sequencing of the v4 region of the 16S rRNA gene, ITS-2 type profiles from sequencing of the internal transcribed spacer-2 (ITS-2) region of Symbiodiniaceae rDNA, and mining of viral operational taxonomic units (vOTUs) from bulk RNA-Seq data. Networks were created with all samples (i.e., globally) and with HH-, HD-, and DD-only subsets of the samples, but no nodes were significant in the HH-only network. HH: apparently healthy tissue from an apparently healthy coral; HD: apparently healthy tissue from a diseased coral; DD: lesion-adjacent tissue from a diseased coral.

