Figure S1 ***Clustering of bacterial communities based on T-RFLP profile using Bray-Curtis similarity.*** Samples are clustered by Group average algorithm. Blue, healthy group; yellow, intermediate group; red, necrotic group.

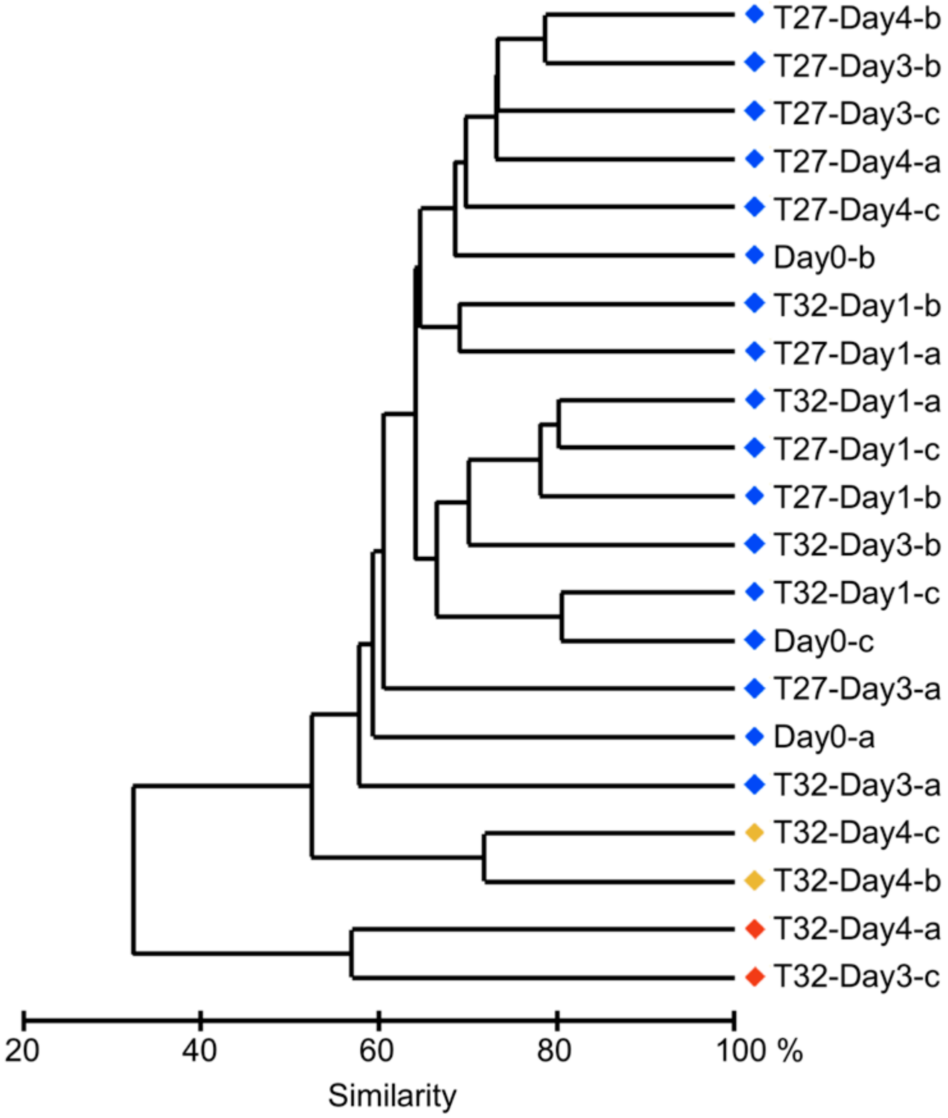

Figure S2 ***Sample clustering based on community functional composition and community expression.*** (A) Metagenomes annotated by Pfam. (B) Metagenomes annotated by Subsystem. (C) Metaproteomes annotated by Pfam. (D) Metaproteomes annotated by Subsystem.

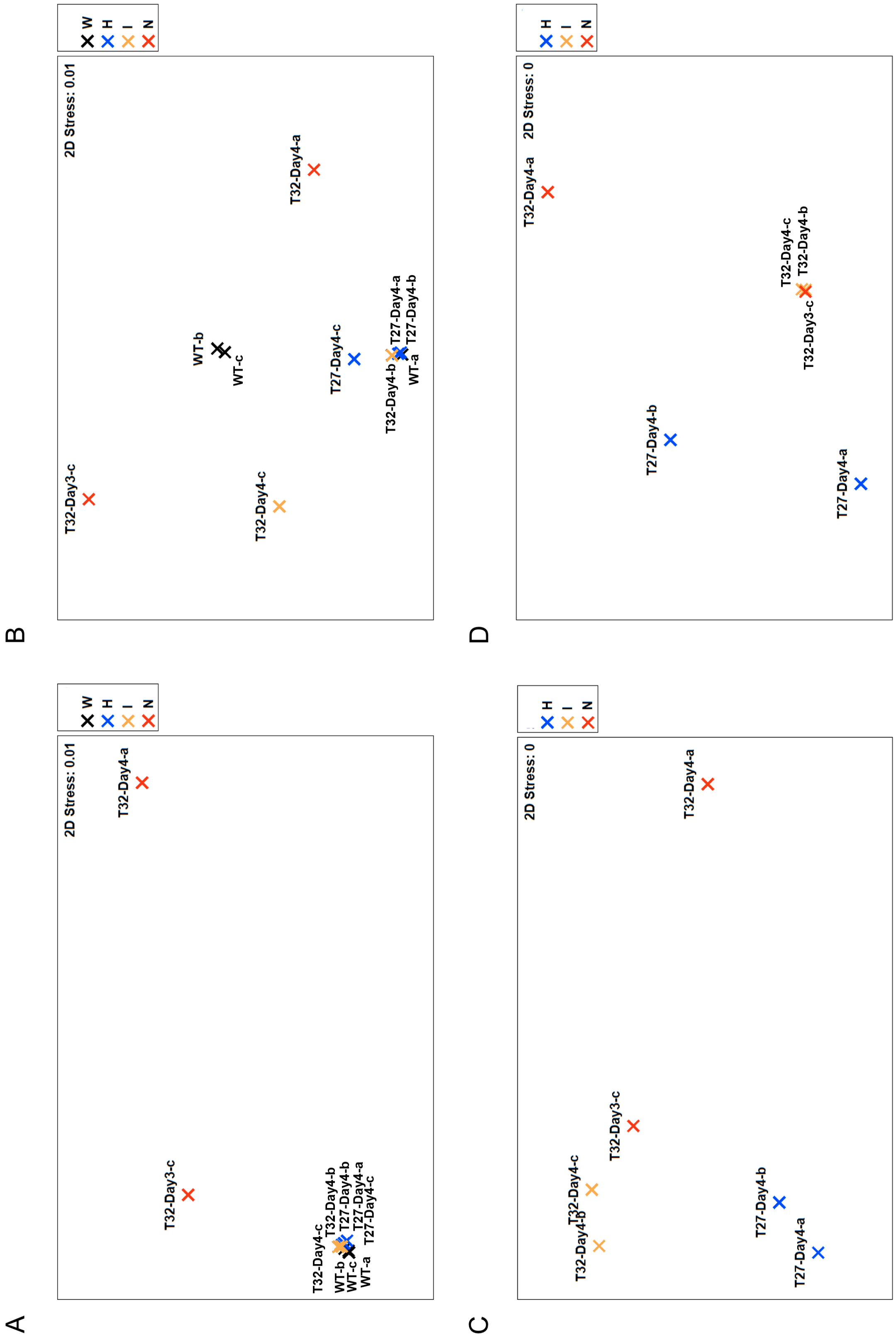

Figure S3 ***Specific functions and expressions abundant in normal and stressed sponge microbial communities annotated with Pfam and Subsystem.*** (A) Metagenome with Pfam annotation. (B) Metagenome with Subsystem annotation. (C) Metaproteome with Pfam annotation. (D) Metaproteome with Subsystem annotation. Samples are clustered using Bray-Curtis similarity and group averages. The heatmap is plotted according to the abundance of each function (copy per genome for metagenome and percentage in all peptides for metaproteome) per sample. Black, wild-type group; blue, healthy group; orange, intermediate group; red, necrotic group.

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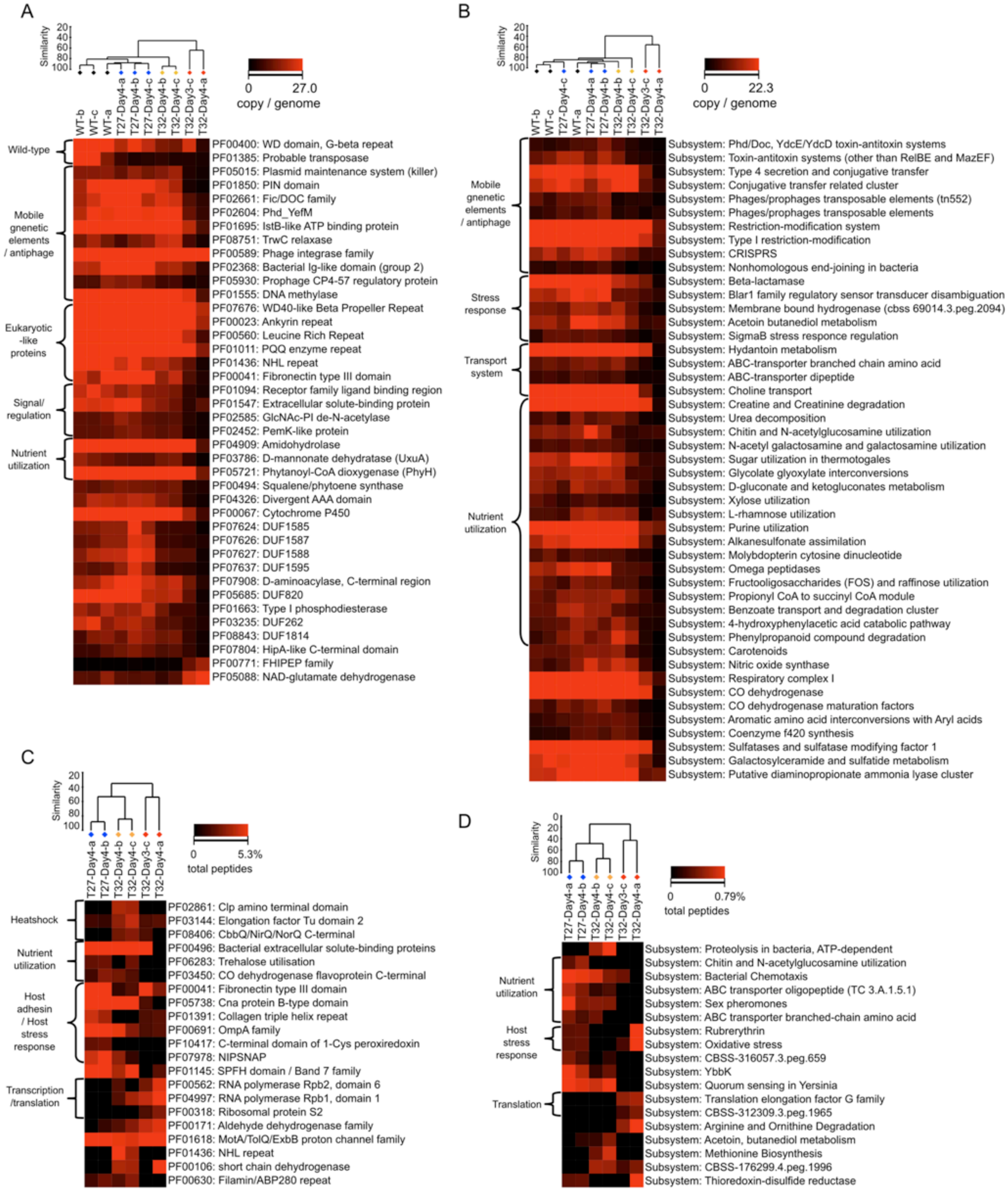
A
Similarity
20
40
60
80
100
0
27.0
copy / genome
WT-b
WT-c
WT-a
T27-Day4-a
T27-Day4-b
T27-Day4-c
T32-Day4-b
T32-Day4-c
T32-Day3-c
T32-Day4-a
Wild-type
Mobile gnenetic elements / antiphage
Eukaryotic -like proteins
Signal/ regulation
Nutrient utilization
PF00400: WD domain, G-beta repeat
PF01385: Probable transposase
PF05015: Plasmid maintenance system (killer)
PF01850: PIN domain
PF02661: Fic/DOC family
PF02604: Phd_YefM
PF01695: IstB-like ATP binding protein
PF08751: TrwC relaxase
PF00589: Phage integrase family
PF02368: Bacterial Ig-like domain (group 2)
PF05930: Prophage CP4-57 regulatory protein
PF01555: DNA methylase
PF07676: WD40-like Beta Propeller Repeat
PF00023: Ankyrin repeat
PF00560: Leucine Rich Repeat
PF01011: PQQ enzyme repeat
PF01436: NHL repeat
PF00041: Fibronectin type III domain
PF01094: Receptor family ligand binding region
PF01547: Extracellular solute-binding protein
PF02585: GlcNAc-PI de-N-acetylase
PF02452: PemK-like protein
PF04909: Amidohydrolase
PF03786: D-mannonate dehydratase (UxuA)
PF05721: Phytanoyl-CoA dioxygenase (PhyH)
PF00494: Squalene/phytoene synthase
PF04326: Divergent AAA domain
PF00067: Cytochrome P450
PF07624: DUF1585
PF07626: DUF1587
PF07627: DUF1588
PF07637: DUF1595
PF07908: D-aminoacylase, C-terminal region
PF05685: DUF820
PF01663: Type I phosphodiesterase
PF03235: DUF262
PF08843: DUF1814
PF07804: HipA-like C-terminal domain
PF00771: FHIPEP family
PF05088: NAD-glutamate dehydrogenase
B
Similarity
20
40
60
80
100
0
22.3
copy / genome
WT-b
WT-c
T27-Day4-c
WT-a
T27-Day4-a
T27-Day4-b
T32-Day4-b
T32-Day4-c
T32-Day3-c
T32-Day4-a
Mobile gnenetic elements / antiphage
Stress response
Transport system
Nutrient utilization
Subsystem: Phd/Doc, YdcE/YdcD toxin-antitoxin systems
Subsystem: Toxin-antitoxin systems (other than RelBE and MazEF)
Subsystem: Type 4 secretion and conjugative transfer
Subsystem: Conjugative transfer related cluster
Subsystem: Phages/prophages transposable elements (tn552)
Subsystem: Phages/prophages transposable elements
Subsystem: Restriction-modification system
Subsystem: Type I restriction-modification
Subsystem: CRISPRS
Subsystem: Nonhomologous end-joining in bacteria
Subsystem: Beta-lactamase
Subsystem: Blar1 family regulatory sensor transducer disambiguation
Subsystem: Membrane bound hydrogenase (cbss 69014.3.peg.2094)
Subsystem: Acetoin butanediol metabolism
Subsystem: SigmaB stress responce regulation
Subsystem: Hydantoin metabolism
Subsystem: ABC-transporter branched chain amino acid
Subsystem: ABC-transporter dipeptide
Subsystem: Choline transport
Subsystem: Creatine and Creatinine degradation
Subsystem: Urea decomposition
Subsystem: Chitin and N-acetylglucosamine utilization
Subsystem: N-acetyl galactosamine and galactosamine utilization
Subsystem: Sugar utilization in thermotogales
Subsystem: Glycolate glyoxylate interconversions
Subsystem: D-gluconate and ketogluconates metabolism
Subsystem: Xylose utilization
Subsystem: L-rhamnose utilization
Subsystem: Purine utilization
Subsystem: Alkanesulfonate assimilation
Subsystem: Molybdopterin cytosine dinucleotide
Subsystem: Omega peptidases
Subsystem: Fructooligosaccharides (FOS) and raffinose utilization
Subsystem: Propionyl CoA to succinyl CoA module
Subsystem: Benzoate transport and degradation cluster
Subsystem: 4-hydroxyphenylacetic acid catabolic pathway
Subsystem: Phenylpropanoid compound degradation
Subsystem: Carotenoids
Subsystem: Nitric oxide synthase
Subsystem: Respiratory complex I
Subsystem: CO dehydrogenase
Subsystem: CO dehydrogenase maturation factors
Subsystem: Aromatic amino acid interconversions with Aryl acids
Subsystem: Coenzyme f420 synthesis
Subsystem: Sulfatases and sulfatase modifying factor 1
Subsystem: Galactosylceramide and sulfatide metabolism
Subsystem: Putative diaminopropionate ammonia lyase cluster
C
Similarity
20
40
60
80
100
0
5.3%
total peptides
T27-Day4-a
T27-Day4-b
T32-Day4-b
T32-Day4-c
T32-Day3-c
T32-Day4-a
Heatshock
Nutrient utilization
Host adhesin / Host stress response
Transcription /translation
PF02861: Clp amino terminal domain
PF03144: Elongation factor Tu domain 2
PF08406: CbbQ/NirQ/NorQ C-terminal
PF00496: Bacterial extracellular solute-binding proteins
PF06283: Trehalose utilisation
PF03450: CO dehydrogenase flavoprotein C-terminal
PF00041: Fibronectin type III domain
PF05738: Cna protein B-type domain
PF01391: Collagen triple helix repeat
PF00691: OmpA family
PF10417: C-terminal domain of 1-Cys peroxiredoxin
PF07978: NIPSNAP
PF01145: SPFH domain / Band 7 family
PF00562: RNA polymerase Rpb2, domain 6
PF04997: RNA polymerase Rpb1, domain 1
PF00318: Ribosomal protein S2
PF00171: Aldehyde dehydrogenase family
PF01618: MotA/TolQ/ExbB proton channel family
PF01436: NHL repeat
PF00106: short chain dehydrogenase
PF00630: Filamin/ABP280 repeat
D
Similarity
0
20
40
60
80
100
0
0.79%
total peptides
T27-Day4-a
T27-Day4-b
T32-Day4-b
T32-Day4-c
T32-Day3-c
T32-Day4-a
Nutrient utilization
Host stress response
Translation
Subsystem: Proteolysis in bacteria, ATP-dependent
Subsystem: Chitin and N-acetylglucosamine utilization
Subsystem: Bacterial Chemotaxis
Subsystem: ABC transporter oligopeptide (TC 3.A.1.5.1)
Subsystem: Sex pheromones
Subsystem: ABC transporter branched-chain amino acid
Subsystem: Rubrerythrin
Subsystem: Oxidative stress
Subsystem: CBSS-316057.3.peg.659
Subsystem: YbbK
Subsystem: Quorum sensing in Yersinia
Subsystem: Translation elongation factor G family
Subsystem: CBSS-312309.3.peg.1965
Subsystem: Arginine and Ornithine Degradation
Subsystem: Acetoin, butanediol metabolism
Subsystem: Methionine Biosynthesis
Subsystem: CBSS-176299.4.peg.1996
Subsystem: Thioredoxin-disulfide reductase

Figure S4 ***Protein expression for the microbial communities of healthy, intermediate and necrotic sponges as annotated by COG categories.*** COG category counts were normalized by the total peptides per proteome.

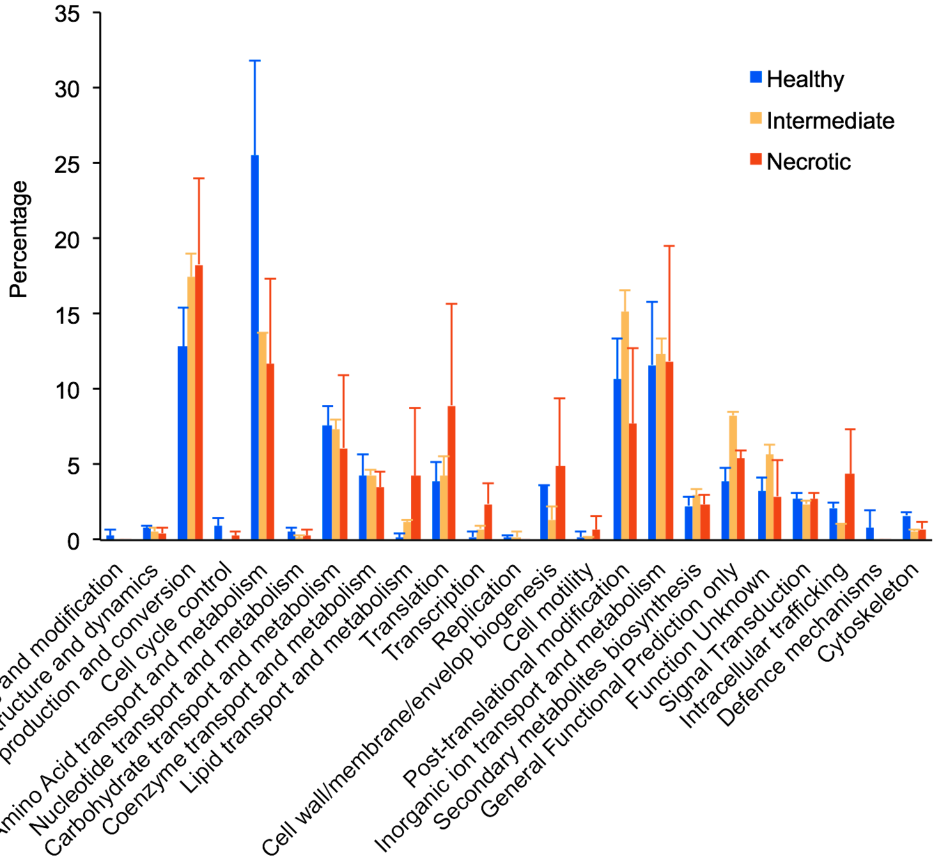

Figure S5 ***Rarefaction plot showing the dynamics of community diversity in different samples.*** (A) Diversity based on total phylogenetic distance. (B) Diversity based on OTU number. Black, wild-type group; blue, healthy group; yellow, intermediate group; red, necrotic group. Average values of 1 000 replications of Jackknife subsampling were plotted.