Table S1 – Species Chao1 richness estimation for a controlled sample size (100 - 1000 sequences) using resampling of bacterial 16S rRNA gene sequences from Xestospongia testudinaria (Xt), sediment (Sd) and seawater (Wt) samples.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Groups | Sample | Sample size | Chao1 | SD |
| Xt | BSin13Xt001 | 100 | 74,66 | 34,59 |
| BSin13Xt011 | 102,03 | 38,71 |
| BSin13Xt021 | 80,89 | 35,52 |
| Sd | BSin13Sd040 | 350,54 | 192,10 |
| BSin13Sd042 | 343,35 | 140,91 |
| BSin13Sd043 | 289,77 | 100,85 |
| Wt | BSin13Wt036 | 140,79 | 51,61 |
| Xt | BSin13Xt001 | 200 | 86,35 | 22,87 |
| BSin13Xt011 | 116,83 | 21,57 |
| BSin13Xt021 | 95,53 | 26,35 |
| Sd | BSin13Sd040 | 421,90 | 105,68 |
| BSin13Sd042 | 432,65 | 97,67 |
| BSin13Sd043 | 374,61 | 80,69 |
| Wt | BSin13Wt036 | 187,66 | 46,30 |
| Xt | BSin13Xt001 | 300 | 96,45 | 19,73 |
| BSin13Xt011 | 125,74 | 18,25 |
| BSin13Xt021 | 105,97 | 22,42 |
| Sd | BSin13Sd040 | 503,84 | 98,83 |
| BSin13Sd042 | 501,16 | 85,98 |
| BSin13Sd043 | 436,99 | 71,40 |
| Wt | BSin13Wt036 | 230,58 | 48,23 |
| Xt | BSin13Xt001 | 400 | 106,09 | 22,61 |
| BSin13Xt011 | 133,75 | 16,97 |
| BSin13Xt021 | 112,80 | 21,24 |
| Sd | BSin13Sd040 | 574,52 | 97,56 |
| BSin13Sd042 | 557,75 | 75,69 |
| BSin13Sd043 | 491,38 | 69,52 |
| Wt | BSin13Wt036 | 266,86 | 49,34 |
| Xt | BSin13Xt001 | 500 | 114,18 | 22,02 |
| BSin13Xt011 | 138,12 | 15,90 |
| BSin13Xt021 | 119,13 | 20,69 |
| Sd | BSin13Sd040 | 627,48 | 95,64 |
| BSin13Sd042 | 600,76 | 72,56 |
| BSin13Sd043 | 538,73 | 69,89 |
| Wt | BSin13Wt036 | 296,09 | 49,83 |
| Xt | BSin13Xt001 | 600 | 119,48 | 20,57 |
| BSin13Xt011 | 143,47 | 14,49 |
| BSin13Xt021 | 124,62 | 19,62 |
| Sd | BSin13Sd040 | 669,87 | 86,95 |
| BSin13Sd042 | 635,34 | 71,76 |
| BSin13Sd043 | 569,46 | 66,14 |
| Wt | BSin13Wt036 | 316,34 | 47,89 |
| Xt | BSin13Xt001 | 700 | 125,32 | 21,05 |
| BSin13Xt011 | 148,40 | 13,16 |
| BSin13Xt021 | 130,46 | 19,89 |
| Sd | BSin13Sd040 | 716,53 | 89,10 |
| BSin13Sd042 | 670,65 | 69,24 |
| BSin13Sd043 | 606,19 | 64,00 |
| Wt | BSin13Wt036 | 331,69 | 42,88 |
| Xt | BSin13Xt001 | 800 | 130,52 | 21,96 |
| BSin13Xt011 | 152,21 | 12,36 |
| BSin13Xt021 | 136,30 | 20,34 |
| Sd | BSin13Sd040 | 748,11 | 84,63 |
| BSin13Sd042 | 698,74 | 67,52 |
| BSin13Sd043 | 636,00 | 67,08 |
| Wt | BSin13Wt036 | 344,31 | 38,82 |
| Xt | BSin13Xt001 | 900 | 135,35 | 23,07 |
| BSin13Xt011 | 156,17 | 10,40 |
| BSin13Xt021 | 140,32 | 19,99 |
| Sd | BSin13Sd040 | 785,36 | 83,97 |
| BSin13Sd042 | 724,72 | 64,75 |
| BSin13Sd043 | 658,84 | 61,30 |
| Wt | BSin13Wt036 | 357,15 | 35,85 |
| Xt | BSin13Xt001 | 1000 | 139,04 | 23,02 |
| BSin13Xt011 | 159,02 | 8,18 |
| BSin13Xt021 | 145,07 | 20,70 |
| Sd | BSin13Sd040 | 811,05 | 79,67 |
| BSin13Sd042 | 751,43 | 64,14 |
| BSin13Sd043 | 681,39 | 60,62 |
| Wt | BSin13Wt036 | 368,22 | 29,85 |



Fig. S1 - Relative abundance of the most abundant bacterial classes (a-g) and orders (h-o) and the most abundant OTU (p) for samples from Xestospongia testudinaria (Xt) and sediment (Sd). Error bars represent a single standard deviation. The dominant OTU represents the mean abundance for the single most dominant OTU in each biotope, thus not necessarily the same OTU.