**Supplementary data:**

**Hunter-gatherer oral microbiomes are shaped by contact network structure**

Federico Musciotto1,2+, Begoña Dobon3,4+, Alex Mira5, Michael Greenacre6,7, Abigail E Page8, Mark Dyble9, Sylvain Viguier9, Daniel Smith10, Nikhil Chaudhary11, Gul Deniz Salali9, Pascale Gerbault12, Rodolph Schlaepfer3, Jesus Gomez-Gardenes13,14, Vito Latora15,16,17, Federico Battiston2,3, Jaume Bertranpetit4+, Lucio Vinicius3,9=, Andrea Bamberg Migliano3,9=\*

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**Figure S1. Number of socially and non-socially transmitted ASVs per Agta individual.** Plot shows that around 50 (out of 137) socially transmitted ASVs were found in only one Agta individual (out of 138); very few were found in more than 25 individuals. For non-socially transmitted ASVs, about 800 (out of 1843) were found in only one individual; overall, only 36 bacteria were found in more than 100 individuals.



**Figure S2.** **Rarefaction curves calculated at an interval step of 50 for each sample.** Each line shows the cumulative number of different ASVs found in a sample based on the number of sequences sampled.

**Table S1. The social microbiome.** List of 137 ASVs whose presence was significantly higher in the set of strong social dyads. For each ASV we indicate the ID, assignment to the lowest taxonomic level possible, score *s* , and P-values adjusted for multiple testing correction by FDR.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ASV ID** | **Taxonomy** | **score** | **P-value** | **Pathogen** | **Oral** |
| b25c829862abd4562b2fabce02efe7f9 | *Absconditabacteriales (SR1)* | 0.8 | 1.953E-07 | - | - |
| 9a656f2c05098299287b32b2e6f13761 | *Absconditabacteriales (SR1)* | 0.66 | 0.000003929 | - | - |
| cd0cd3aabdbac40539a75cbbd044fddb | *Actinobacillus* | 0.61 | 0.0002761 | yes | yes |
| 7bcbdca610fb5b00d8f5d6981e4ccfd2 | *Actinomyces* | 0.84 | 0.00006402 | no | yes |
| f286725317b52a9b2ba02911fb43fb74 | *Actinomyces* | 0.74 | 0.00006549 | no | yes |
| 36ee23e5fb8e520ff8ab3a712fe62103 | *Actinomyces* | 0.58 | 0.00005728 | no | yes |
| aea92ec7459b1c6e56da664f437e5eb4 | *Aggregatibacter* | 1 | 1.616E-20 | yes | yes |
| bdbbe305d476fc32349d0f9d7acc1f3e | *Aggregatibacter* | 1 | 8.315E-08 | yes | yes |
| dfc2bc8dd378c88b687d07b971908422 | *Aggregatibacter* | 1 | 8.315E-08 | yes | yes |
| f5be277e1cedbf3e9d1da2cca8e5b3fe | *Aggregatibacter* | 1 | 8.315E-08 | yes | yes |
| 17505f5c0a3bd9db87c889d58c44d91e | *Aggregatibacter* | 0.62 | 0.000111 | yes | yes |
| 4e15e6c595af34bcff84ecc611652853 | *Alloprevotella* | 1 | 8.315E-08 | yes | yes |
| 60454192547174a30de06730e332a018 | *Alloprevotella* | 1 | 8.315E-08 | yes | yes |
| 7edd6744ca56724e25206e58b8eb31e4 | *Alloprevotella* | 1 | 8.315E-08 | yes | yes |
| 6c7df48453603f14fea2d0df78054fc8 | *Alloprevotella* | 0.9 | 4.589E-26 | yes | yes |
| 036b52b252c3d12c9d67cb5b92ad3b8f | *Alloprevotella* | 0.87 | 0.00004631 | yes | yes |
| 61d261ad17a704d3d229d0496fba9e97 | *Alloprevotella* | 0.68 | 0.00000539 | yes | yes |
| b8020fc6e528e89bafe954b34f69274b | *Alloprevotella* | 0.63 | 1.737E-07 | yes | yes |
| 6c2744ef88823b8d0b5fdd828a1453d3 | *Alloprevotella tannerae* | 1 | 8.315E-08 | yes | yes |
| d09d418c3e2b81c4a46662603dc54b1f | *Alloprevotella tannerae* | 1 | 8.315E-08 | yes | yes |
| 1d9ba470f99d53770f6473ae481a5cc3 | *Alphaproteobacteria* | 0.81 | 6.955E-07 | - | - |
| 76d2465e9a710bb2e488d385edb22d17 | *Alphaproteobacteria bacterium canine oral taxon 081* | 0.98 | 5.519E-90 | no | yes |
| 120ccaea0a052ab1f8b0baf7ffcb39a6 | *Bacteroidales* | 0.81 | 2.006E-10 | - | - |
| 99875da18febf2481d929455749c8503 | *Bacteroidia bacterium feline oral taxon 115* | 1 | 8.315E-08 | no | yes |
| 3b6c7d236810be54ec3dd91d33c30455 | *Bergeyella* | 0.85 | 0.000002938 | no | yes |
| 8a6f6e0af66418d7fa87950f534478a8 | *Campylobacter* | 0.5 | 0.00005724 | no | yes |
| a01841648577830b64c254d8dd08fcf3 | *Capnocytophaga* | 1 | 8.315E-08 | no | yes |
| bac498e2637e542824bf7b1bc8e28b24 | *Capnocytophaga* | 1 | 8.315E-08 | no | yes |
| d1a9e0fe590b656651169d84e57809b4 | *Capnocytophaga* | 1 | 8.315E-08 | no | yes |
| d2fc9bc158ba9aff203bd217f2f545a4 | *Capnocytophaga* | 1 | 8.315E-08 | no | yes |
| d4d4576ada9fd36d2cc41ea0957d50c9 | *Capnocytophaga* | 0.87 | 0.00004631 | no | yes |
| 0c658276c6d993cc01766afc18f7afbe | *Cardiobacterium* | 1 | 8.315E-08 | yes | yes |
| 547c6f945f05cf12835a3d6973cd04ca | *Cardiobacterium* | 0.65 | 0.0004462 | yes | yes |
| 4f24b4bf4eef612f489f7a4038865283 | *Clostridiales vadinBB60 group* | 0.59 | 4.324E-08 | - | - |
| 6171427c1a227174358a9a87e40a4ae2 | *Comamonas* | 0.85 | 0.000002938 | yes | no |
| 42ae4b093c67013ddf62f40807f49fa0 | *Corynebacterium 1* | 1 | 8.315E-08 | no | yes |
| 1739a3f1e983a966d734f530d37eefac | *Desulfobulbus* | 0.71 | 0.00002376 | yes | yes |
| 9b269bc964583400b329a49cafa1e3bc | *Eikenella* | 0.6 | 0.000000277 | yes | yes |
| f600213584dbb9514dd959a3205ee75e | *Family XIII* | 0.9 | 1.277E-10 | - | - |
| 17fff0e5de7356d0f0550b1aca93ee78 | *Fretibacterium* | 1 | 8.171E-27 | yes | yes |
| 4ec2702d8dd22de789fd3a09cf12915a | *Fusobacterium* | 1 | 8.315E-08 | yes | yes |
| cb5675d64323623f3d4b5bd78080a04f | *Fusobacterium* | 0.78 | 1.208E-19 | yes | yes |
| 09298163bbf43ab3455ecc8889a8a4fb | *Gemella* | 0.85 | 0.000002938 | no | yes |
| 73c36bda51565bb80fa330526300db1a | *Granulicatella* | 1 | 8.315E-08 | no | yes |
| 50a81506ffbe40f7d237efdc5e298313 | *Haemophilus* | 1 | 8.315E-08 | no | yes |
| 99bba9b5380c4a6649ebc36672104cb8 | *Haemophilus* | 0.9 | 1.277E-10 | no | yes |
| 947cdb60bfbbbcc302bdccee2cbbd446 | *Haemophilus* | 0.85 | 0.000002938 | no | yes |
| ea1e95399e4fde2510758c450eae3860 | *Haemophilus* | 0.56 | 0.00004969 | no | yes |
| 182242c7388a1731ebad95813e48cd67 | *Haemophilus* | 0.53 | 4.678E-12 | no | yes |
| 82153eacad3cd51d6b3a159316faacd0 | *Haemophilus* | 0.52 | 0.000008254 | no | yes |
| 0d83f4e669c8bd5592b7d903f0f5b6a5 | *Kingella* | 0.85 | 0.000002938 | no | yes |
| c513e87eadeac410d5a85b1adbaf687e | *Lachnospiraceae* | 0.97 | 1.183E-09 | - | - |
| ab7763a264bbba1ebec32976b7c0fea6 | *Lentimicrobiaceae* | 0.85 | 0.000002938 | - | - |
| a82fe8651f12b22d44287be0774dbeb1 | *Leptotrichia* | 1 | 8.315E-08 | yes | yes |
| 9f3a649b43c68dab34628e2c0e857086 | *Leptotrichia* | 0.9 | 1.277E-10 | yes | yes |
| fe8befdd8666043c68ff20636a5aeda3 | *Moraxella* | 0.76 | 0.0003467 | yes | no |
| 3c434d1d0d35300e374391d6b49b87e8 | *Mycoplasma lipophilum* | 0.66 | 1.413E-07 | yes | no |
| 24fca62514bf0da1127bdcf65818c0fb | *Mycoplasmataceae genomosp. P1 oral clone MB1\_G23* | 0.94 | 1.044E-35 | - | - |
| 7b20f2e3370c92fe959c209e07077e42 | *Neisseria* | 1 | 8.315E-08 | no | yes |
| fda19216097fb3e23f463150767139d1 | *Neisseria* | 1 | 8.315E-08 | no | yes |
| 99f2f195389420c40b7940b63a3e2afb | *Neisseria* | 0.97 | 1.183E-09 | no | yes |
| a31d12203f88ae6f4281390954df6d97 | *Neisseria* | 0.97 | 7.743E-18 | no | yes |
| aba19a479824efbb05cb189c0da965ad | *Neisseria* | 0.85 | 0.000002938 | no | yes |
| f95ad0bf6012f19e14e99bef9ead4786 | *Neisseria* | 0.84 | 1.405E-10 | no | yes |
| 9226c61d7469c72143028153ad5523b1 | *Neisseria* | 0.8 | 1.518E-17 | no | yes |
| 371dc646bafa5255d74849f1f6442edd | *Neisseria* | 0.76 | 0.0003467 | no | yes |
| 1f541546376584432877fd483ca0222f | *Neisseria* | 0.72 | 0.0000203 | no | yes |
| f0f53626664dd2a6878f2e216360c30d | *Neisseriaceae* | 1 | 8.315E-08 | - | - |
| 539eb13db08b519c4c3d1af5f011b375 | *Peptococcus* | 1 | 8.315E-08 | no | yes |
| eec404a3a25d07d29d000c9f41e5b821 | *Peptostreptococcaceae* | 0.91 | 9.174E-24 | - | - |
| e6bc3076efad3a48311b27ad3b6a6048 | *Porphyromonas* | 1 | 8.315E-08 | yes | yes |
| 0b8e3ecb05c7d142675988a41dd7e2fd | *Porphyromonas* | 0.97 | 1.183E-09 | yes | yes |
| 168feac872e7eec19953b81b0345541f | *Porphyromonas* | 0.93 | 2.321E-10 | yes | yes |
| dfc9cdd227fee71a949b4addc2d85009 | *Porphyromonas* | 0.83 | 0.000003909 | yes | yes |
| 00fe295123cdb7e4e72217b89c29a43a | *Porphyromonas* | 0.81 | 5.37E-13 | yes | yes |
| 133bbdf823df539e546ce0576ae5c8bc | *Porphyromonas* | 0.77 | 1.089E-07 | yes | yes |
| 8f796084de02bbaab0ac802a490810e3 | *Porphyromonas* | 0.76 | 0.0003467 | yes | yes |
| 9f35d7353336bf13d1903922c24d1902 | *Porphyromonas* | 0.76 | 0.0003467 | yes | yes |
| b160a4086c4ca8a975b039fb636a4612 | *Porphyromonas* | 0.72 | 0.0000203 | yes | yes |
| 072b53f9fa81f68b79a69a304dc4967e | *Porphyromonas* | 0.67 | 1.099E-07 | yes | yes |
| bbf801a56fa41789f1360c7b23d20d37 | *Porphyromonas* | 0.63 | 0.000199 | yes | yes |
| 55c7b957ee7c3cda77ae0cad7a917008 | *Porphyromonas* | 0.62 | 0.00000325 | yes | yes |
| 45b54192fc6849a4f4c427c49dbc54f4 | *Prevotella* | 1 | 8.315E-08 | yes | yes |
| ebb0df96eac28526a676b240e63480ef | *Prevotella* | 1 | 1.616E-20 | yes | yes |
| 7935b791c24c4cf3fa8a93e050911b61 | *Prevotella* | 0.84 | 1.405E-10 | yes | yes |
| 68b9a5f481efce8c7b663affba05bc46 | *Prevotella* | 0.74 | 0.00006549 | yes | yes |
| 9cb69417458318e7a5788962ed460823 | *Prevotella 2* | 1 | 8.315E-08 | yes | yes |
| 0b023b14031f0c1437238531f61b840c | *Prevotella 6* | 0.9 | 1.277E-10 | yes | yes |
| 0752c07579f161763a14b35807e652dc | *Prevotella 7* | 1 | 8.315E-08 | yes | yes |
| a58e730355612ddb3774b7ac5b45f553 | *Prevotella 7* | 1 | 8.315E-08 | yes | yes |
| f39ff4d55317cb4503dd5ac0f22da429 | *Prevotella 7* | 0.93 | 2.301E-09 | yes | yes |
| d2b9ec42c67c014e5cb6b90dd769d332 | *Prevotella 7* | 0.87 | 0.00004631 | yes | yes |
| 6312cc2aa05385884bc3e37e03a098ab | *Prevotella 7* | 0.85 | 0.000002938 | yes | yes |
| d0e01ad29b194e56e51d6b04c5af5035 | *Prevotella 7* | 0.84 | 6.148E-14 | yes | yes |
| 1c9a0321e8682b034026b25d5827ed0f | *Prevotella 7* | 0.79 | 0.000000243 | yes | yes |
| b7faca61f48c3bbf0e855a2368228c3e | *Prevotella 7* | 0.79 | 0.000000243 | yes | yes |
| 375751ab097bd7a719f0227f5078b167 | *Prevotella 7* | 0.76 | 0.0003467 | yes | yes |
| 7b2c9a5c2a49dac61d7e9e8f54cdfbfd | *Prevotella 7* | 0.76 | 0.0003467 | yes | yes |
| 502099d689a6216f8994165629ed7583 | *Prevotella 7* | 0.74 | 9.699E-08 | yes | yes |
| 1353e32e91379a898e6ae897d476654a | *Prevotella 7* | 0.68 | 0.00001399 | yes | yes |
| 888f4f33031fe98dd0835ce5522b2732 | *Prevotella 7* | 0.63 | 0.000199 | yes | yes |
| c341fcd5f0a8071fd1d1523ed7a5fb69 | *Prevotella 7* | 0.62 | 0.000111 | yes | yes |
| a464e0c7c280de0b62e480f593cd83d5 | *Prevotella denticola* | 1 | 8.315E-08 | yes | yes |
| b00bb5c5753a7497c8cb65c0c6e9026b | *Prevotella denticola* | 1 | 8.315E-08 | yes | yes |
| 86fd4b50470ba3fb481d6767165e8302 | *Prevotellaceae* | 1 | 8.315E-08 | - | - |
| 22e718b73ca663ece8c0640369074d10 | *Rikenellaceae RC9 gut group* | 1 | 8.315E-08 | no | no |
| 4f7068054843a928a53d46d22e9c84bf | *Rikenellaceae RC9 gut group* | 0.76 | 0.0003467 | no | no |
| f106b7d2b39369fe6607d602261b69e4 | *Saccharimonadaceae* | 0.93 | 2.321E-10 | - | - |
| a2d4c1ada677d53277070f5908ea71aa | *Selenomonas 3* | 1 | 8.171E-27 | yes | yes |
| 4c7c966561749540e4da0a8da2926577 | *Selenomonas 3* | 0.97 | 1.183E-09 | yes | yes |
| d6def8480a6d8c3e0b9b98b4a2dd102e | *Selenomonas 3* | 0.8 | 1.953E-07 | yes | yes |
| fe83f9ca205205232d74bbbd2e161c38 | *Selenomonas 3* | 0.74 | 9.183E-10 | yes | yes |
| c317c61db783a68f608ca5f4ddc6036a | *Selenomonas 3* | 0.68 | 0.00000539 | yes | yes |
| 6da15ce884d82b5da6e35dce02a5bb12 | *Staphylococcus* | 0.72 | 0.0000203 | yes | no |
| 4b596386776da049d8b6c150318ec667 | *Streptobacillus* | 0.7 | 0.000009111 | yes | yes |
| aa61647189cbff68249bb1899d6f12f9 | *Streptococcus* | 1 | 8.315E-08 | yes | yes |
| c5695e12335bcfbf910273bce1f781cb | *Streptococcus* | 1 | 8.315E-08 | yes | yes |
| d74bdb359c7e158570d073c578497131 | *Streptococcus* | 0.63 | 1.191E-08 | yes | yes |
| 82d0ab08bfd8c78e3273176d2d7f55b4 | *Streptococcus agalactiae* | 1 | 8.315E-08 | yes | yes |
| 7a71b6c59201f0c4d0905636f5a4291c | *Streptococcus anginosus subsp. anginosus* | 1 | 8.315E-08 | yes | yes |
| ceda3c3fe01b6063e5cff7b7037bb8cd | *Streptococcus pneumoniae* | 0.87 | 0.00004631 | yes | no |
| b1df9daebace21a760c18d9f6b0e4cae | *Streptococcus salivarius subsp. thermophilus* | 1 | 8.315E-08 | no | yes |
| 19ce44c4330d456b253e2cdee3aa3e1c | *Tannerella* | 1 | 8.315E-08 | yes | yes |
| 03130f5f63fbb08e367e495108725101 | *Tetragenococcus halophilus subsp. halophilus* | 1 | 8.315E-08 | no | no |
| 49bf26ff1d63a85bcf394b15312148b6 | *Tetragenococcus halophilus subsp. halophilus* | 1 | 8.315E-08 | no | no |
| 0134de3d2f4469b2fabc44c6798d9641 | *Treponema 2* | 1 | 3.35E-35 | yes | yes |
| 15ed671b76d15a74b96014d8fe5d7c4f | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| 3701b97ea929ba9173dbd5cbc3e746af | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| 4317f558afcf25ecd8a971d9ab4e4f8d | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| 7c7973a8ba3f5c853a28443ac5b81d3c | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| b840bceb156406769aace3276ce755ae | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| eba7f1369b1e48c88e4ecf7584bee4e5 | *Treponema 2* | 1 | 8.315E-08 | yes | yes |
| f88b4bfedbf55516ab0f73ca153a8d0c | *Treponema 2* | 0.87 | 5.172E-29 | yes | yes |
| 7d2eb8b10cc6962443ab06c55d316c52 | *Treponema 2* | 0.75 | 1.493E-13 | yes | yes |
| 71fa3dd57665727b7d7e4451bc847ac6 | *Treponema 2* | 0.68 | 0.00001399 | yes | yes |
| 3832fe923c7767291484ea4004dc250f | *Veillonella* | 0.93 | 2.301E-09 | no | yes |
| 5f2ddaf156d728f5c72def7dc74168ab | *Veillonella* | 0.58 | 1.164E-12 | no | yes |

**Table S2. Comparison of dyadic link weights from the social bacterial sharing network and randomised networks of the same size and topology (n=1000) by dyad type.** Mean weights are the sum of weights from dyads in a category divided by number of dyads in category. Z-score is the standardised ratio of real to mean link weight in randomised networks. P-values from non-parametric two-tailed one-sample tests (test value=0) after FDR correction for multiple testing.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Dyadic type** | **Mean weight (real network)** | **Mean weight (randomised networks)** | **Ratio** | **SD** | **z-score** | ***P* value** |
| Mother-Offspring | 2.81 | 0.36 | 7.72 | 0.17 | 14.06 | <10-44 |
| Siblings | 2.46 | 0.36 | 6.84 | 0.14 | 15.47 | <10-53 |
| Other kin | 1.72 | 0.37 | 4.69 | 0.13 | 10.75 | <10-26 |
| Spouses | 1.6 | 0.36 | 4.46 | 0.19 | 6.51 | <10-10 |
| Friends | 1.05 | 0.36 | 2.95 | 0.1 | 7.29 | <10-10 |
| Friends, same camp | 1.05 | 0.36 | 2.95 | 0.1 | 6.84 | <10-11 |
| Friends, different camps | 1.04 | 0.36 | 2.91 | 0.21 | 3.18 | 0.0014 |
| Father offspring | 0.96 | 0.35 | 2.73 | 0.19 | 3.24 | 0.0012 |
| Same household | 3.36 | 1.63 | 2.06 | 0.29 | 5.88 | <10-08 |
| Same camp | 2.48 | 1.62 | 1.54 | 0.12 | 7.25 | <10-12 |
| Different households | 1.59 | 1.62 | 0.98 | 0.04 | -0.85 | 0.39 |
| Non-kin | 0.31 | 0.36 | 0.88 | 0.02 | -2.43 | 0.015 |
| Different camps | 1.44 | 1.62 | 0.89 | 0.04 | -3.99 | <10-04 |

**Table S3. Comparison of dyadic link weights from the non-social bacterial sharing network and randomised networks of same size and topology (n=1000) by dyad type.** See Table S2 for details.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Dyadic type** | **Mean weight (real network)** | **Mean weight (randomised networks)** | **Ratio** | **SD** | **z-score** | ***P* value** |
| Father-offspring | 68.11 | 69.3 | 0.98 | 5.54 | -0.21 | 0.83 |
| Friends | 67.47 | 69.53 | 0.97 | 2.96 | -0.69 | 0.49 |
| Friends, different camps | 71.46 | 69.43 | 1.03 | 7.76 | 0.26 | 0.79 |
| Friends, same camp | 66.61 | 69.56 | 0.96 | 3.4 | -0.87 | 0.38 |
| Mother-offspring | 76.53 | 69.5 | 1.1 | 5.58 | 1.26 | 0.21 |
| Non-kin | 69.76 | 69.52 | 1 | 0.75 | 0.33 | 0.74 |
| Other kin | 74.67 | 69.75 | 1.07 | 4.06 | 1.21 | 0.22 |
| Siblings | 89.63 | 69.63 | 1.29 | 4.2 | 4.76 | <10-5 |
| Spouses | 80.76 | 69.29 | 1.17 | 4.29 | 2.68 | 0.0074 |
| Different households | 69.92 | 69.55 | 1.01 | 0.76 | 0.49 | 0.62 |
| Different camps | 69.71 | 69.52 | 1 | 0.79 | 0.23 | 0.81 |
| Same household | 75.47 | 69.41 | 1.09 | 2.52 | 2.4 | 0.016 |
| Same camp | 72.12 | 69.53 | 1.04 | 1.51 | 1.71 | 0.088 |
| Different camps | 1.44 | 1.62 | 0.89 | 0.04 | -3.99 | <10-4 |

**Table S4. Summary data on Agta social networks.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Location** | **Nodes** | **Edges** | **Maximum degree** | **Minimum degree** | **Mean degree** | **Maximum weight** | **Minimum weight** | **Mean weight** | **Largest component** |
| **Camps** |
| **1** | 20 | 177 | 19 | 12 | 17.7 | 3151 | 592 | 2173.9 | 20 |
| **2** | 19 | 142 | 18 | 3 | 14.95 | 12564 | 421 | 3181.96 | 19 |
| **3** | 21 | 202 | 20 | 17 | 19.24 | 3616 | 865 | 1897.71 | 21 |
| **4** | 25 | 259 | 24 | 11 | 20.72 | 3223 | 182 | 1835.28 | 25 |
| **Multi-camps** |
| **1** | 23 | 117 | 18 | 4 | 10.17 | 1572 | 48 | 494.7 | 23 |
| **2** | 29 | 291 | 26 | 3 | 20.07 | 1300 | 11 | 710.14 | 29 |

**Table S5. Summary data on Agta bacterial sharing networks.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Location** | **Nodes** | **Edges** | **Maximum degree** | **Minimum degree** | **Mean degree** | **Maximum weight** | **Minimum weight** | **Mean weight** | **Largest component** |
| **Camps** |
| **1** | 17 | 45 | 8 | 2 | 5.29 | 19 | 2 | 9.29 | 17 |
| **2** | 18 | 108 | 17 | 3 | 12 | 46 | 3 | 22.11 | 18 |
| **3** | 20 | 48 | 11 | 1 | 4.8 | 23 | 1 | 9 | 20 |
| **4** | 24 | 168 | 22 | 4 | 14 | 159 | 7 | 46.17 | 24 |
| **Multi-camps** |
| **1** | 19 | 59 | 12 | 1 | 6.21 | 35 | 1 | 12.21 | 19 |
| **2** | 27 | 95 | 16 | 2 | 7.04 | 30 | 2 | 10.89 | 27 |