**Table S2:** Samples available in datasets A, B and C after sequence processing. For dataset A, values correspond to the number of samples obtained after rarefaction (1,455 or 4,000).

|  |  |  |
| --- | --- | --- |
| **DATASET A(Rarefaction: 1,455/4,000)** | **DATASET B (Rarefaction: 1,455)** | **DATASET C****(Rarefaction: 1,867)** |
| **Skin bacterial communities** | **Skin bacterial communities****(*Duttaphrynus melanostictus*)** | **Gut bacterial communities** |
| **Site** | ***Duttaphrynus melanostictus*** | ***Ptychadena mascareniensis*** | **Site** | **Males** | **Females** | **Site** | ***Duttaphrynus melanostictus*** | ***Ptychadena******mascareniensis*** |
| **S1** | 9/9 | 4/3 | **S1** | 3 | 6 | **S1** | Pool of 4 individuals | Pool of 4 individuals |
| **S2** | 10/9 | 3/2 | **S2** | 6 | 4 | **S2** | Pool of 4 individuals | Pool of 4 individuals |
| **S3** | 7/6 | 4/4 | **S3** | 6 | 1 **(a)** | **S3** | Pool of 4 individuals | Pool of 4 individuals |
| **Total of samples** | 26/24 | 11/9 | **Total of samples** | 15 | 11 | **Total of samples** | 3 pools | 3 pools |

**Notes: (a)** At site 3, only 1 female was collected, so this was excluded from the statistical analysis.