**Description of txt tables (Japanese quail, Vollmar et al.)**

**Phenotype\_Japanese\_quail\_Vollmar**

* Column Animal\_ID contains the individual ID of each animal
* Body\_weight\_gain contains the measurements of the difference between the life weights at day 10 and day 15 of each individual in g
* Feed\_intake contains the measurements of feed intake during the experimental period of each individual in g
* Feed\_per\_gain\_ratio describes the feed intake divided by body weight gain in g/g
* P\_utilization contains the measurements of the difference between absorbed and excreted quantity of phosphorus of each individual in %
* Ca\_utilization contains the measurements of the difference between absorbed and excreted quantity of phosphorus of each individual in %
* Test\_day contains the 12 different test-days

**Phylum\_Japanese\_quail\_Vollmar**

* Column Phylum\_ID contains individual phyla (sorted alphabetically)
* First row contains Animal\_IDs (1001, 1002,…)
* Values are abundances of phylum e.g. in one column all phyla for one animal

**Genus\_Japanese\_quail\_Vollmar**

* Column Genus\_ID contains individual genera (sorted alphabetically)
* First row contains Animal\_IDs (1001, 1002,…)
* Values are abundances of genera e.g. in one column all genera for one animal

**OTU\_Japanese\_quail\_Vollmar**

* Column OTU\_ID contains individual OTUs (sorted alphabetically)
* First row contains Animal\_IDs (1001, 1002,…)
* Values are abundances of OTUs e.g. in one column all OTUs for one animal