Table S2. Classification of partial *Tas2rs* in the genome assemblies of Reptiles. Overlapping partial *Tas2rs* with similar orthologies in the multiple alignments were regarded as being derived from different loci. In contrast, non-overlapping *Tas2rs* were regarded as being derived from the same loci with gap(s).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Different orthologs | Overlapping TAS2Rs(potentially intact paralogs) | Non-overlapping TAS2Rs(potentially intact gene fromsame locus) | **Intact****TAS2Rs** | **Partial*TAS2R*s** | **Partial*TAS2R* loci** | **Potentially intact****TAS2Rs** |
| Japanese Gecko (*Gekko japonicas*) | - | Tas2r41\_P, Tas2r40\_P | - | 50 | 2 | 2 | 52 |
| Gharial(*Gavialis gangeticus*) | Tas2r9\_P | - | - | 8 | 1 | 1 | 9 |