Table S3.

Genome size of selected specimens of *V. epipsila*, *V. palustris* and their putative hybrids.

|  |  |  |  |
| --- | --- | --- | --- |
| Taxon | Samples name | 2C DNA (pg) | 1C/Cx (pg) |
| *V. epipsila* | BNP1 | 2.52 a |  |
| BNP6 | 2.50 a |  |
| BNP11 | 2.55 a |  |
| **Mean for the species (±SD)** | | **2.52 (±0.03)** | **1.26/0.63** |
| *V. palustris* | BNP8 | 4.27 a |  |
| BNP13 | 4.23 a |  |
| OST\_9 | 4.26 a |  |
| KR\_21 | 4.27 a |  |
| **Mean for the species (±SD)** | | **4.26 (±0.02)** | **2.13/0.53** |
| putative hybrids | BNP2 | 3.43 a |  |
| BNP3 | 3.39 a |  |
| BNP4 | 3.41 a |  |
| BNP5 | 3.37 a |  |
| BNP7 | 3.42 a |  |
| BNP9 | 3.39 a |  |
| BNP10 | 3.38 a |  |
| BNP12 | 3.43 a |  |
| BNP14 | 3.39 a |  |
| SZ\_5 | 3.38 a |  |
| KOZ\_14 | 3.45 a |  |
| KOZ\_15 | 3.45 a |  |
| OST\_6 | 3.35 a |  |
| OST\_7 | 3.34 a |  |
| OST\_8 | 3.43 a |  |
| **Mean for the hybrid (±SD)** | | **3.42 (±0.06)** | **1.71/0.57** |

Origin of samples: Poland (BNP, KR, KOZ, OST, SZ). Detailed information in Table S1.

Average values followed by the same letter do not differ significantly at P ≤ 0.05 in Kruskal-Wallis test