S2 Table: **Microsatellite and mtDNA population genetic distances (FST) without suspected hybrids.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Localities | GME\_Faeroe I. | GME\_Iberian P. | GMA\_Canary I. | GMA\_Azores I. | GMA\_ F. Polynesia |
| GME\_Faeroe I. | - | **-0.0239** | 0.1601 | 0.1829 | 0.1160 |
| GME\_Iberian P. | **0.0739** | - | 0.1713 | 0.1957 | 0.1425 |
| GMA\_Canary I. | 0.9627 | 0.9284 | - | **0.0088** | 0.1028 |
| GMA\_Azores I. | 0.9666 | 0.9273 | **-0.0221** | - | 0.0937 |
| GMA\_ F. Polynesia | 0.9513 | 0.8900 | 0.3954 | 0.4017 | - |

Pairwise FST estimates based on mtDNA (below diagonal) and microsatellite loci (above diagonal). Significant P values are in bold. GME: *Globicephala melas*; GMA: *G. macrorhynchus*.