Figure S1. Maximum likelihood tree based on mitochondrial cytochrome oxidase I COI gene sequences of species of *Donax* using the Atlantic surf clam *Spisula solidissima* as an outgroup. Numbers in internal nodes, reported as percentages, indicate maximum-likelihood bootstrap support values (500 replicates).

Donax trunculus (Praia América 44)

ggtcaacaaatcataaagatattggaagtctttatttcgttttaggtttatgatccggccttgtggggctggtctatagagtaataatgcggactgagttaatacatccgggcgcctttt atgggagagtctgtgtataatgtgttggtcacttcgcatgggttactaatgattttcttcatagtaatacctctaataattgggttttttggtaattgggctgttcccttactgctagcagccc ctgatatagtttttgcgcggctgaacaatctaaggttctgattacttccggccgcaactgtcctcctacttatgtctaacgaagtggaagagggtgttgggactgggtgaactctttaccct ccgctatcggcttggcttggacaccccgcgcccgcgatggaattcatgatttttagggcttcatattgcaggattatcatctattttgctagtattaattttgtaactactggcgctaacatac gcccggagggagttgcccccagcgtactactttgttcgtagtatccgttgttattacgtctttcctgttggtggctgctatgcctgttttagctgcaggcttaactatactgttaacagatcga aattttaacacttctttttttcgaccctgtaggggggaggagatccggtgttactcattcacctattctgattttttggtcacctgaagttta

| Expected patterns: | 582/124 | 58/236/412 | 56/53/183/201/165/48 | 706 bp |
| Nantón et al. [14]: | 505/91 | 217/379 | 31/183/201/166/15 | 596 bp |

Donax vittatus (Praia América 01)

ggtcaacaaatcataaagatattggtagtctttattttgttcttggactatgatctggccttgttgggctggtctacagagttataatacgtactgaactaatacatcctggtgccctttatg gtgagtctgtatataatgtttttagttacgtcacatggcctacttataattttttttatagttataccactaataattggttttttggtaattgagctgtgcccctcctattagcggccccggatat ggtttctcgcccgtcttaataatcttagattttggttattaccagctgctacagttcttctacttatatcaaatgaagttgaggaaggagtaggaactggttggactttatatcctcctctttct gcttgattaggacaccctgcccctgctatagagtttataattttaggggcttcatattgctggcctatcttctattttgctagtattaattttgttacaacagggggctaatatgcggcctgag gggagtggcccctcagcgaactacccttttgtagtgtctgtagtaattacttcatttcttctcgtagctgctataccagttctagctgctggactgacgatacttctaacagatcgtaacttta atacttcctttttgacccagtaggggggggagacccgtattatttattcacctcttttgatttttggtcacctgaagttta

| Expected patterns: | 219/75/270/18/124 | 58/102/80/196/55/13/202 | 244/462 | 706 bp |
| Nantón et al. [14]: | 142/75/270/18/91 | 83/80/196/55/13/169 | 166/430 | 596 bp |

Figure S2. Compatibility between the expected restriction fragment patterns for *Donax trunculus* and *Donax vittatus* mitochondrial cytochrome oxidase I COI gene sequences obtained in this work and those described by Nanton et al. [14]. The sequences display both the primers used in this work (red) and those used in [14] (bold, underlined) and the restriction targets for *Alu*I (yellow), *Hae*III (green) and *Msp*I (blue). The combination of restriction fragment sizes expected from our 706 bp sequences and those described in [14] (596-bp sequences) for each restriction enzyme is displayed in the corresponding colors.