

High fusibility and chimera prevalence in an invasive colonial ascidian

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Supplementary dataset S3: ID number and sequence in fasta format of the 15 candidate loci with higher absolute difference between mean number of shared alleles per locus among fused and non-fused intercolony pairs.

>2126

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AAACASAACTTATTCCTTTTTAAACCAAGTGAAAAAAYGATCTTTTTGTAATATTGCAAAATATCCTTCTCTG
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WAATTGGAATTCGTACAAAATTTATGGTACTGTAAATTTTCGCTTTYTTCA
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>3784

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GAACTAAAAGCAAGAAAACGTTTTCTTTTTATTTGAGTTTGCAGTTGCTCAAAGTTAGGCGCATGAAAGA
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TTCCATGACTCCAACGAGASCCGAGAGGCACTTTTTGGCTCAGGAGTCAGTCATG
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>8985

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CTTAAAYGTTTGTA AAAACGCACGATATTGTAGTAATCAAACAATTGGATAACAGCTATAAATKGAAC TTC
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>9280

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ATTATAACGTCARGTGATAAATAATGAGAAAACTTGGTCATYTTCCATTCTTTTGATGAAAGATTTTCTTCT
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TTTGTTATAGGAACATAATAATAAACAGTAAATCAATCGGCAAGAAACGCAGG
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>11438

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GAAAATTTTGGTTAAACTTATTTTTGGTGTTTKYTTGCAAACCTATTAACCAAATTATGCAAAAAATTGCTGTC
AGAGATCATATTCCACGGAGTGAAAGCTGGTCGCAGAGCAAGATTTGTATGAAATTTGTTTTATTGTCCGAT
AGTGCAAAATGTATGCAYTATTTTTCACTTATATGTTTGAGATGTAAATGTTG
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>23738

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CCTGYACYACAAACCACAAATKCTATCGAGTACAGAAGTTCTAGCAGTTTCATATTCTTTGAGCAATCAAACA
CGGACTATAWTTWTTATCTGGGCTTCATGAGCAATCAAACACGGACTATAWTTWTTATCTGGGCTTCATGAA
TATTTTTRAAATGAAATAGCGTTTTTCATCTTCAATGTATCATAGTTTAGGATGACAGC
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>24274

CCAAAAGAACTCTGGGAAGATCCAAATCAATGGAATCAATGGAAGWAGGTGCTTTCGTKGTCCAAGTTTG
ACCGGATGAAAGYACGACCAATTTAGCCGCAATCAATGGAATCAATGGAAGWAGGTGCTTTCGTKGTCCA
AGTTTGACCGGATGAAAGYACGACCAATTTAGCCGCAAGAGGGCGYGCGTCCAACAAATC

>27281

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AAAGCGTAGTATTCGAKTTTTGTAAAAACAAAAAGCGTAGTATTCGAKTTTTGTAAAAACGATAAAATGCTT
AAAAGAAAAATGTAAAACTTGAAACCTCTATTCTTCTCCAGTTTGTACCATCAA

>27932

TGGTCAATTTTATTAAGAAAATAAATAAATTCAAAACTAAGAGCAGCACGAAGAAAAACACTACGAAGACA
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TGAAAGGAGAGCTGGTTTCTTTGAACTTGATAACGTCAGACGGGCCAAAGCATT

>33463

CAATGCCGTCACCAGAGCAAGCGAAGTGAARGAAAACCAAGTGAAAGGAAGGARCAACAARCATTTGATTG
ACCTTAGAGAGACATCGTCGTTCCGAGTCAATCAAGGGCGCTCGTAGACATTTTTGCAACGGGCAAATGTT
TTTTGGATAAAAAGAAAAGTGAAACTGRTGCTTTTGAAAACGCTATCATTGCAACAAC

>35804

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TCCTGTTTCGGCCTGATAAAATAGAAAACYTTCRTAAATAAGATAGAAAACMT

>36446

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>38223

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ATGAGTACAAAGTCAACATTACCACAGTTTATCACTGAAACAACAATGCCAACAA

>39173

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CGGAAGATCAAGCCTTGTTTCGAACTCAACTGAAAAGCAGATTTGTTGTTTTGAAACAAACGACTTTACT
CGGGCGGAARCAAAAGGAKACTGTTTCAGTTGGGTTATTTTTTGCCGAGTCGCT

>42739

TTGATTTTRGCTCTTTCGATGTGGATGGTTCAGCTTCCATTATTAATCAAACTTCACCTCTCTACACTAGGC
TACTAAGCTACTTTAGAATCAATTCAAGTTAGATAATGAAAACAAAACAACTAAACAAAACTCAACTCAA
TGTAATCATACTGATAACAATAATGTAACCTCTAAKTCTTGAATCATATCYC