**S1 Appendix**

**Alignment of MHC class II DRβ1 alleles from Magellanic and Galápagos samples analyzed.** Magellanic alleles are designated as Smag\_# and Galápagos alleles are designated as Smen\_#. The starting and ending positions, bases 93 and 362, of exon 2 are marked with > and < signs above them, respectively. Putative peptide-binding codons (based on [85]) are marked with asterisks (\*) above the corresponding base positions.

**> \*\*\* \*\*\* \*\*\***

Smag\_01 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCTTAAGGCCGA

Smag\_02 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGGCCGA

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Smag\_05 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGTTCGA

Smag\_06 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCTTAAGGCCGA

Smag\_07 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCTTAAGGCCGA

Smag\_08 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGGCCGA

Smag\_09 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCTTAAGTTCGA

Smag\_11 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGTTCGA

Smag\_12 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGTTCGA

Smag\_15 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGTCCGA

Smag\_18 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGGCCGA

Smag\_20 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCATAAGTCCAA

Smag\_23 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCATAAGGCCGA

Smag\_24 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGGCCGA

Smag\_27 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCATAAGTCCAA

Smag\_37 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGGTAAGGCCGA

Smag\_39 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGCTTAAGGCCGA

Smen\_01 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGAGGATGCTTAAGTTCGA

Smen\_02 GCCATGGGGGGGGCTGGGAGGAGAGCGGCAACGGGGAGGGGGCTCCACGGTGCCTCCCTGCCCACCCACGACTTGCCTCCCTGCGCAAACAGGGTATTTCCAGGAGATGGTTAAGGCCGA

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Smag\_01 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGTGAGGGACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_02 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGAGAGGTACCTCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_03 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_04 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGGAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_05 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_06 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGTGAGGGACATCTACAACCGGCAGCAGAACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_07 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGTGAGGGACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_08 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGGAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_09 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGTGAGGGACATCTACAACCGGCAGCAGAACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_11 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_12 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

Smag\_15 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_18 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGAGAGGTACATCTACAACCGGCAGGAGTACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_20 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGAGAGGTACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_23 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGCTTGTGGAGAGGTACATCTACAACCGGCAGCAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

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Smag\_27 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGAGAGGTACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smag\_37 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGACAGGTACATCTACAACCGGCAGGAGTACGTGCACTTCGACAGCGACGTGGGGCAGTTTGTGGCCGACACCCCCCTGGG

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Smen\_01 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTATGTGGAGAGGGACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

Smen\_02 GTGTCATTTCCTCAACGGCACCGAGCGGGTGAGGTTTGTGGTGAGGGACATCTACAACCGGCAGCAGGACGTGCACTTCGACAGCGACGTGGGGTACTATGTGGCCGACACCCCCCTGGG

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Smag\_01 TGAGCCTGATGCCAAGTACTGGAACAGCCAGACGGACTTCCTGGAGCAGAGCCGGGCTGCGGTGGACACGATCTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

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Smag\_08 TGAGCTTATTGCCAAGTACTTGAACAGCCAGACGGACTTACTGGAGCAGAGACGGGCTGAGGTGGACAGGTACTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

Smag\_09 TGAGCTTATTGCCAAGTACTGGAACAGCCAGACGGACTTCCTGGAGCAGAAACGGGCTGAGGTGGACACGGTCTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

Smag\_11 TGAGCCTTCTGCCAAGTACTTGAACAGCCAGACGGACTTACTGGAGCAGAGACGGGCTGAGGTGGACACGTACTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

Smag\_12 TGAGCTTATTGCCAAGTACTTGAACAGCCAGACGGACTTACTGGAGCAGAGACGGGCTGCGGTGGACACGTACTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

Smag\_15 TGAGCCTTCTGCCAAGTACTTGAACAGCCAGACGGACTTACTGGAGCAGAGACGGGCTGAGGTGGACACGTACTGCCGACACAACTACGGGGTGGTGACCCCTTTCACTGTGGAGAGGAG

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Smen\_02 TGAGCCTGATGCCAAGTACTGGAACAGCCAGACGGACATACTGGAGCAGAGACGGGCTGAGGTGGACACGTACTGCCGACACAACTACGGGGTGGGGACCCCTTTCACTGTGGAGAGGAG

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Smag\_06 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

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Smag\_08 AGGTGAGTGCGTGGCAGAACATCTCCCTGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

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Smag\_11 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_12 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_15 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_18 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_20 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_23 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_24 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_27 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_37 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smag\_39 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smen\_01 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT

Smen\_02 AGGTGAGTGCGTGGCAGAACATCTCCCCGGGGGACGGGCGCAAGCCAAGCCCCGGGGCT