

Supplementary Table S4. Genomic organization of *R. dominica* Bt-R1-like cadherin gene. The number and length of the deduced exons and their encoding cadherin domains are shown. All the intron-exon borders provided were followed the GT-AG rule for RNA 5' acceptor and 3' donor splice sites. The exon sequences are shown in upper case, coding regions for the first and last exons are shown in parentheses, asterisk indicate that the lengths provided for 5'- and 3'-UTRs were only approximate. The start and stop codon (TGA) were underlined and shaded grey, respectively. The transposable elements (TE) predicted by Censor (www.girinst.org/censor/) inside the introns of cadherin gene are provided.

Exon		Protein domain	Intron/exon junction	Exon/Intron junction	Intron	
No	Size (bp)		5'-Acceptor	3'-Donor	Size (bp)	TE classes
-1 (5'-UTR)	134*			ATTTTATAG <u>gt</u> atacaaat	803	nd
1	67 (64)	SP	tttttttc <u>ag</u> GATATGGACA	TTCAAGGGT <u>g</u> taagtatgt	52	nd
2	135	EC1	aacatgac <u>ag</u> TACATAGCTG	AATTATGAT <u>g</u> taagtttat	15 217	LTR/Gypsy; DNA/Transib
3	266	EC1, EC2	aatttttc <u>ag</u> GGTCGTCAAC	CCAAATTGAG <u>g</u> taagtaaac	17 337	LTR/Gypsy
4	90	EC2	tttcttgc <u>ag</u> GAAAACTACG	TTCTGGAAC <u>g</u> taagtataa	623	nd
5	147	EC2	ttatttttc <u>ag</u> AGAAACGAAA	GACGGTAAC <u>g</u> taagttaat	23 227	DNA/Mariner; LTR/Gypsy
6	120	EC2, EC3	acttttttc <u>ag</u> GACAGCGGCA	AACCGAACAG <u>g</u> tttgtataa	51	nd
7	73	EC3	tgtgttttc <u>ag</u> CACTTTTCCG	GAGTCTGAAT <u>g</u> taatatata	55	nd
8	281	EC3, EC4	gcgatttc <u>ag</u> ATGACGATCT	TAGAGACTCG <u>g</u> taagtattt	2 115	nd
9	371	EC4, EC5	ttcttttc <u>ag</u> ATAGAAAACG	ACGAAATTAG <u>g</u> taagtattag	3 821	nd
10	229	EC5	tatcttttc <u>ag</u> GTACAGTCTA	GATCAGAGTT <u>g</u> taagtaact	3 021	nd
11	173	EC6	atacttttc <u>ag</u> GAATCACTAA	ACTATAGAGA <u>g</u> taagtacat	15 511	LTR/Bel, LTR/Gypsy
12	179	EC6	tatattgt <u>ag</u> CTGCATACTG	ACTGCTGCAG <u>g</u> taacacaaat	143	nd
13	172	EC6, EC7	catcttct <u>ag</u> TTACTGTTAC	ATTCCATTGAG <u>g</u> taagtaact	8 981	LTR/Gypsy
14	160	EC7	taaattttc <u>ag</u> GCCAGCAGGC	CACTGCAGAA <u>g</u> taagaagtt	2 402	Non-LTR/RTE
15	136	EC7, EC8	cgttatgc <u>ag</u> ATCCAGATTT	GACCGTGATAG <u>g</u> taagtatat	590	nd
16	192	EC8	cttttgtt <u>ag</u> GTCCTTACAA	TACTCAACAG <u>g</u> taaaatagg	69	nd
17	113	EC8, EC9	tataccct <u>ag</u> GTGGCATACA	TACATCTAAT <u>g</u> taagtaaata	357	nd
18	219	EC9	atgttcac <u>ag</u> AATACTCAAA	GATCATTCAG <u>g</u> tatttttagt	87	nd
19	132	EC9, EC10	caatttttc <u>ag</u> GTGAACGATT	CCTTAGAAAG <u>g</u> taagaagaa	77	nd
20	112	EC10	gcttttttc <u>ag</u> ACCCAAAACG	ATCGACTCTG <u>g</u> ttagtaata	4 647	LTR/Gypsy
21	110	EC10	atttttgt <u>ag</u> ATGATTCAGA	TCAATATACC <u>g</u> taagttact	54	nd
22	399	EC10, EC11	atgggttgc <u>ag</u> TTGAATATAA	TACTATTAA <u>g</u> taaaacatt	1 129	nd
23	102	EC11, EC12	tacattttc <u>ag</u> GTAATTGATG	TACAGTTTCAG <u>g</u> taagttttt	54	nd
24	196	EC12	ttgcttta <u>ag</u> GCGTACGATC	ACTGACCCAC <u>g</u> taagtaacg	5 106	DNA/Mariner, LTR/Gypsy
25	113	EC12, MPED	tcccttac <u>ag</u> CTCCATATCA	TCAGTCCGAG <u>g</u> ttcactttt	53	nd
26	164	MPED	tttgttttc <u>ag</u> GTAAAAGATG	CAATACAGAG <u>g</u> tactaatgc	65	nd

27	201	MPED, TM	atcatttt ag CAAACCTTAGT	AGCTACAAAC gt aagttaac	295	nd
28	165	CYT	aatggttac ag ATTGAAACGA	ATCGATCAAG gt acgttttt	61	nd
29	270* (82)	CYT	gtgtatac ag TATTCATAGT	AAGATACT TGA CAAAGTGAAT	-	