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 ATTTCTTCAGTTCTCAATATCTCGATCGAGTATGTAGATACAGAAAACTGTAGACATTTTTATAGGA 136
 TATGGACAAAGCAATTCGCTTTTATTATATGTTTAAATAATAGCTCTTTTACCTTCAAGGGTGTAC 204
 M D K A I R F Y L Y G L I I A L F T F K G V 22

 ATAGCTGGAGCTTCATACATTCCGATGACGACAGAGTTGACACAACCTGACGTCATCACTACAAATAAT 272
 H S W S F I H S D D D R V D T T D V I T T N N 45

 ATCCTAGTATATATGGATGAAGAACTGGAACCTAATATTATACTAGCATACGTGAATTATGATGGGTC 340
 I L V Y M D E E L E P N I I L A Y V N Y D G S 68

 GTC AACACCAGAAATAGCACAGATTAATCCAGACAACAGTATTATAGGAGCAGTATTACAAGAAGAAT 408
 S T P E I A Q I N P D N S I I G A V L Q E E 90

 CACTTGAAGGCGAATCTTATTGGGCAGTTGTAATAACTAACAAAATTGATTATGAATCCATCCCAGAA 476
 S L E G E S Y W A V V I T N K I D Y E S I P E 113

 GATGTGATGGTGTTCGAAATAGAAATATCAGTTGAAGGTGACAGCAATACAATATTTCTTTACGTACA 544
 D V M V F E I E I S V E G D S N T I F L Y V Q 136

 GAACATAGATGATAATGCACCAATAATAGTTGTTGTACAAACCCATGCCAAATTGAGGAAAACCTACG 612
 N I D D N A P I I V V V T N P C Q I E E N Y 158

 CTGGTCCTTCCAACCTGTACATACAACATACAAGATGCTGATGGATGGCTACAATATATGAAAATGGAT 680
 A G P S N C T Y N I Q D A D G W L Q Y M K M D 181

 GTTTCTGGAACAAGAAACGAAACGGAACCTCTCAAATTTGAATACGAAGATCTAAATGAGATAACTAA 748
 V S G T R N E T E L F K F E Y E D L N E I T N 204

 TACAACAAAATCAGCATCATTGCTGCTACATACTATAGCAGAACTGGACTATGAAACAATAACTCTCC 816
 T T K S A S L L L H T I A E L D Y E T I T L 226

 ATCTGATTAACTGGACGGTAACGGACAGCGCAATCATTCTGTATCACAAACGGTGGTTGTAAATGTT 884
 H L I N W T V T D S G N H S V S Q T V V V N V 249

 ATTGACCTACCTGATACTCCACCTAGATGGACGACAATTTTTGCAACTCAACAGTTTGACGAAAAAAC 952
 I D L P D T P P R W T T I F A T Q Q F D E K T 272

 CGAACAGCACTTTTCCGTTGCAGCTATAGACGGAGACATTGGAGTAAATGACGATATAAAATATTCCT 1020
 E Q H F S V A A I D G D I G V N D D I K Y S 294

 TAGAGTCTGAATATGACGATCTGTTTTCTATCGACAGCACTACAGGTGACCTCTATGTTAATGAAATT 1088
 L E S E Y D D L F S I D S T T G D L Y V N E I 317

 GACCGTGATACATTGAACATGCAAATTTTACATTCTTATATTTGCAACAGAGGAAAATGACCCATG 1156
 D R D T L N M Q I F T F L I F A T E E N D P W 340

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 Y S T N Q T I T F V V N D V N D H A P N V T 362

 ATCCTGATCCAAAACAAATACACTTTTTACTGTTAGAAGAAAGGGTAACGCAACTGAATGATACGATT 1292
 D P D P K Q I H F L L L E E R V T Q L N D T I 385

 TCTGTACTAGATAGAGACTCGATAGAAAACGCCATGTTTACTATATCTTTGCAAGATACATCCGATAA 1360
 S V L D R D S I E N A M F T I S L Q D T S D N 408

TGGCATT TTTGTACACCGAGGCTTTTCAAGTTCCTTCGCAAGGGTATCAGAATTACACGTTTTCTTTAT 1428
 G I L Y T E A F Q V P S Q G Y Q N Y T F S L 430
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 S I I D S S L L D Y D D E N W Q N F N F K V F 452
 ATAGAAGAAACGGTAGACCCATCGCATACTGATGAAGTCGAAATTACCGTAAATCTAATAAACTGGAA 1564
 I E E T V D P S H T D E V E I T V N L I N W N 476
 TGACGAAACTCCCATATTTGAAAATGAGGAATATGATGCCGAAATTTATGAAAACGTCAGCATAACATA 1632
 D E T P I F E N E E Y D A E I Y E N V S I H 498
 EC5 → *
 CCTTCATCCAACAGGTATATGCAACCGACAGAGACGTGGACGACGAAATTAGGTACAGTCTAGTAGGA 1700
 T F I Q Q V Y A T D R D V D D E I R Y S L V G 521
 GCATCGGTAAATACAATTCTTGCGGTCAATTCAAGTGGGATTGTTTCGACGACTGTTGACGGAGCATT 1768
 A S V N T I L A V N S S G I V S T T V D G A F 544
 *
 TGATTACGAGCGTCAAACAGAATACATTATTCAAATTGCTGCACAAGACACGCTGCAAGTTATAAACG 1836
 D Y E R Q T E Y I I Q I A A Q D T L Q V I N 566
 AATCTCTCCATACAGCATAACGCTCAACTGACGATAAATATTCTGGATGTCAACGATGAAACGCCATCG 1904
 E S L H T A Y A Q L T I N I L D V N D E T P S 589
 ATCAGAGTTGAATCACTAATAAGTGTTGAAGAAAACAGGCCAAATGGCACAGAGATAGATTCTACTAT 1972
 I R V E S L I S V E E N R P N G T E I D S T I 612
 EC6 → *
 TACAGCAACCGATGATGACACTACAGCCGAGTTATTATTCTATATAGATTGGGATTCAACTTACGCTA 2040
 T A T D D D T T A E L L F Y I D W D S T Y A 634
 CAAAAAGTGGGCGAATGTATGATGACCTTCTAGAGTACTATAGAGACTGCATACTGGTAGAAACCGAA 2108
 T K S G R M Y D D L L E Y Y R D C I L V E T E 657
 GACATTTTCAGACACATCATCAGGTTATGCTAAAGCAAAGCTTTTTATAACGATGTGGTGGAAGGAAA 2176
 D I S D T S S G Y A K A K L F I N D V V E G N 680
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 T P D Y E K F D T L Y I R L I V E D L N Q E 702
 AAGGAGAAGCTACTGCTGCAGTTACTGTTACAATTGTGGTTGAGGACCTGAATGACAATTATCCAGTT 2312
 E G E A T A A V T V T I V V E D L N D N Y P V 725
 TTTACGGACAGTGTTAATAACAAATAATACAGTCACAGAAGCTGCGGTTCTGTGGTGTTACTATAGGAAC 2380
 F T D S V N T N N T V T E A A V R G V T I G T 748
 EC7 → *
 CATTACTGCAACAGATGATGACGGACCAGGCTTCAATACTGTAACATATTCCATTGAGCCAGCAGGCA 2448
 I T A T D D D G P G F N T V T Y S I E P A G 770
 GTACTCCGCAAGGACTGGTCACGATTAATTCAACAACCTGGACTACTCACTGTGCGATGAGGATGGTGCA 2516
 S T P Q G L V T I N S T T G L L T V D E D G A 793

ATAGATTGTGATAACCCACCTATATATTACCTTAACCTATACGGTGATTGCTACGGATGGTGAACCTAGA 2584
 I D C D N P P I Y Y L N Y T V I A T D G E L D 816
 *
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 S T A E I Q I Y V F D I N D N A P I I E S Y 838
 TBR1
 AGGACACAATAGAAATACCTGAGAAATCCGCCAATGGTACCAATGTTGTAGAAATAATAGCTATTGAT 2720
 E D T I E I P E K S A N G T N V V E I I A I D 861
 EC8
 GCCGACCGTGATAGTCCTTACAATGTCGTCTGGTATGAATTTACAACAGCATCTAACAGCGATGTAAG 2788
 A D R D S P Y N V V W Y E F T T A S N S D V R 884
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 S F F L M D M D T G V I S V R Y V S A E S T 906
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 L D R D Y G V S S F T V A F K A A D N Y Y S T 929
 GGTGGCATACAAAGGAGTGCGAAGGCGTATTTACGATTATTTTAACCGATATTAATGATAAGGTCCC 2992
 G G I Q R S A E G V F T I I L T D I N D K V P 952
 TGTGTGTACCACCAAATACATCAGTGTATCAGAAAATACATCTAATAATACTCAAATAAGCACTCGCA 3060
 V V T T K Y I S V S E N T S N N T Q I S T R 974
 EC9
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 I E A Y D D D E E G T D N S R I N F A V K G M 997
 ACAGACGAAGAAGGTGCTGAATATCAGTTATTTGAGATAGTAAATGACGAAGATGAGAACGGTGTAGC 3196
 T D E E G A E Y Q L F E I V N D E D E N G V A 1020
 ATACCTTTCCACGCTTGTTGATTTAGAGGGTTATTATGGCAACTATACTTTGATCATTGAGGTGAACG 3264
 Y L S T L V D L E G Y Y G N Y T L I I Q V N 1042
 ATTTTGGAGAACCCTATGAATACTGAAAATTATAGTGTAACCTTGGAATTTGAAAAGTATAGTTACTAT 3332
 D F G E P M N T E N Y S V T L E I E K Y S Y Y 1065
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 A P D Y L Y P E N P D G E R V Y L R K T Q N V 1088
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 N G Q L Y L Y D G R E L P N I Q A T D N Q G 1110
 EC10
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 E K W D I T F T I D S D D S D E A M I F Q I D 1133
 AATTCAGATTCTCTGGGTCAATCAACAGGAATGCTGCAATTAACCTACAATAGAAAACTGGGAAGATCA 3604
 N S D S L G Q S T G M L Q L T T I E N W E D Q 1156
 ATATACCTTGAATATAATAGCAAATGATAACGGAACCTCCACAACGCACTGCGAATGCTGTAATGTATA 3672
 Y T L N I I A N D N G T P Q R T A N A V M Y 1178
 TTCGATTCTTTGATTTAAATTCATTGCCATATTTTCCGAAAATGAAAGGCAACTAACAGCGCAGTTC 3740
 I R F F D L N S L P Y F P E N E R Q L T A Q F 1201
 EC11

ACAGAAAATACAACAGGAATGTCTGAGAGTGTTCATCCCAGGTGCTTCATATAGTGGCACTGAAGA 3808
T E N T T G M S E S V S I P G A S Y S G T E D 1224
CGAAGACTTTGATGTGTACTATTTATTGCTTGAAGGAAACAGCAGCATTTTAAATATCGATATTAATA 3876
E D F D V Y Y L L L E G N S S I F N I D I N 1246
CTGGACTAATTACCCTTTTGGAAATGTTAGACAGAGAAGAAACAGCATCACACGATATTACAATAATT 3944
T G L I T L L E M L D R E E T A S H D I T I I 1269
GCATCTAACAGTGATTCTGTTCCAACCAGTTATGATGAACAGTCCTTGCTTTTCGTTACTATTAAGGT 4012
A S N S D S V P T S Y D E Q S L L F V T I K V 1292
* TBR2
AATTGATGTAAATGACAATCCACCACAATTTAGCGAAAGTCGGTACACTGGAGGAATAAGTACTTCGA 4080
I D V N D N P P Q F S E S R Y T G G I S T S 1314
EC12
GTTCTTTGGATTATACTGTGACTACAGTTTCAGCGTACGATCCAGATATTAACGATACCTTAACCTTAC 4148
S S L D Y T V T T V S A Y D P D I N D T L T Y 1337
TCAATTAACACATCAAGTTTAACCGTTAGTGATTTCATCGCTCTCCAACATTGCTACACCTTTCAGAAT 4216
S I N T S S L T V S D S S L S N I A T P F R I 1360
TGATTCATCATCTGGTGCGGTAACATTAAACTTCGCAGTTCAAAGCAACATGCTTGGATATTTTGCCT 4284
D S S S G A V T L N F A V Q S N M L G Y F A 1382
TBR3
TCAATGTTGTTGTAAGTACCCACCTCCATATCATAACAGATACAGCACTCGTAGAGATTTATATAATC 4352
F N V V V T D P P P Y H T D T A L V E I Y I I 1405
ACGGATGAACATAGGGTGGAGTTTACTTTCCAGAATGATCTGAACACTGTAATAGCTCTTCAGTCCGA 4420
T D E H R V E F T F Q N D L N T V I A L Q S E 1428
GGTAAAAGATGTATTAGATGACGCGTTTGAATATTTATGCAACATTGAATCTATTCTTAGTGATACGG 4488
V K D V L D D A F E Y L C N I E S I L S D T 1450
ATGATGATGGCCAAACTTTGGATACTCAAAGTGTATGTACTGTACATTTTATTGATCCTGAATTAAT 4556
D D D G Q T L D T Q T V C T V H F I D P E L N 1473
GAACCAGTTAATAAACTACAATACAGAGCAAAGTCTAGTAGTCTAACATTCTATTCAAATCTGCGAAG 4624
E P V N K T T I Q S K L S S L T F Y S N L R S 1496
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S F S N I T L Y L L S Y S S G S T T T D N L 1518
*
AAGATCAATTAAGCTTGGCTAATAGGTGTGACTGTTGTACTAGGATCTCTCTGTATTACACTCCTA 4760
E D Q L K A W L I G V T V V L G S L C I T L L 1541
GTTGGATTTATCATCAAGCTACAACATTGAAACGACGCTTGAATAAGTTATCAGAAGTTAAATTTGG 4828
V G F I I K L Q T L K R R L N K L S E V K F G 1564
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S Q E S G L N R I G V A V P N T N K N A V E 1586
GTTCTAATCCAGTTTATAATGAGGAAAAGAAAATTCCAGATTTTGATCGATCAAGTATTCATAGTGGA 4964
G S N P V Y N E E K K I P D F D R S S I H S G 1609

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GACTCCGACCTTATTGGTGTGAAGACAATCCAGAATTTGACTATGGCATTAAAAATGAAAGATACTG 5032
D S D L I G V E D N P E F D Y G I K N E R Y 1631
.....
ACAAAGTGAATCATATATAGGTAATATAAGGTTTTAGCTGGCAAAGAAATTTGAGAGCATATAAATAA 5100
ATAAATAAATAAATAAATGT 5120

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Supplementary Figure S5. cDNA sequence and deduced open reading frame of the *R. dominica* BtR1-like cadherin gene (*RdCad1*). The predicted domains are underlined: the membrane signal peptide with a dashed line, the MPED domain with a solid line, and CYT domain with a dotted line. The start of each of the twelve cadherin repeat domains is marked with a solid arrow. The TM domain region is shaded gray. Predicted N- and O-glycosylation sites are marked by asterisks. The putative toxin binding regions (TBR1-3) are designated by the rounded rectangle below the sequence.