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   1 : TTCAAAATGATGAACAGATGCATCTCAAGTCAGCACTAGACCATCTTCTAAAATAGGAAGAT :   62
  63 : CTATGGAAGCAACACTCCCAAATGCAGTGGCTTCAAAATGGGGATTGCAATACGAAGTTTAT :  124
 125 : CCATGTTTGGGCAAGTAACAGGAAAAAAAGAATACTATCACTGAACTCTAGCAAGGCGATCA :  186
 187 : GAAGATTATCGAATAGCAGCAAATCCAATCCACATTCTACAACTTTTTTTCTACCCTACTAG :  248
 249 : GCTCGACTGAGGAATGACTCATCCAAGCTGATTAGAAGATTCTTTATCCAGAAGGACCTCTG :  310
 311 : GATCTTGCTGACATTGAGTATCCATTTATGGAGAAAGAAATCCATGATACAGTGTATGACTT :  372
 373 : GGCTTTGGAAAAGTCACCCGGATGATATTTTCCCATTCTCCTTCTATATGCACTTCTAGTGT :  434
 435 : ATCATCAAACATGACCTGATGAACCTACTGTAAAATCAGCTAATGTAGACCATCTGAACTAC :  496
 497 : TTGTTCATCACCCTTATCCCAAAAAAAAATTGGTGTGTATTCAGTTAGAGACTTCAGGCCAA :  558
 559 : TAAGCCTGATTAATGGAGTAATAAAAAATATTTCAAAAACTCTATCGAAAAGGCTCTCACAG :  620
 621 : AAAATGAATTTGTTAATTTTATCCACAGAGCTTGCTTTCAACAAAGGAAGAAATATCTCTGA :  682
 683 : ATATTTTGTAATGACTATGGAAACTATACACTTCTGCAAAGCTGAAGTACACAAGGATCTCA :  744
 745 : ATTATAAAGTCGACTTCGAGAAAGCTTTTGACAATGTGGATTGGAGCTTTCTATTGAAATTG :  806
 807 : CTATCCAGCACGGGGCTTTGATTCGAGGTGGTGTCAATGGATAGAATATCTGATTTATACAG :  868
 869 : CTAAATTCTCAGTCCTTATTAATGGTGATAAAGGTAAACTTTTTAAATTGAGGAAAGATCTC :  930
 931 : AGGCAAGGAGATCCTCTATTCGCCTAGCTCTTTCTCTTAGTTGTTGATATAGAATGATCAAG :  992
 993 : GGAGCAAGTAGGTTCAATCTTTTTGTTGGAATTGGATCATATAATATCATGGGATAACTTCA : 1054
1055 : AAGCTTTTAGTTCACTGATGACACACTTATATTTTGCAGATATGATCTAAAATACATCAAAA : 1116
1117 : CTCTTAAATTTTTACTCTATAGTTATGAGCTACTGATGGGTCTCAAAATTAACTTTGAAAAA : 1178
1179 : TTCCAATTTTTTGGCTTGAGAATTGCAAAGATGTCAGTACAGCAAGTTGCATCTATCCTAGA : 1240
1241 : AAGCAAGGTGGCTACATTTTCCATTACTTATTTGGGTCTCCCACTCCATCATTCTAAACTGA : 1302
1303 : GGAAAACTTATTGGAATCCACTCCTTGAGAAGGTTCAGAAGAAATTGATCGGGTAGAAAGGT : 1364
1365 : AAACTTCTTAACCTCTAGGGTAGGCTTATACTAACTAATGCAGTGCTTACAGGGATCCCACT : 1426
1427 : ACTCTGGAGGGATACATTCCTTCTCCCTCAATTCATTATCAAATAAATTGATAAAATCCATC : 1488
1489 : GATCATTCATTTGGAGAGGAAACGAGGAGTATAACTAAGGGCACTCTAGAATATGTTGGTCG : 1550
1551 : AATATTTGTCGATCAAAAAAATTTGGAGGACTGGGGGTTCCTCAATCTAAAAATTTTCAATA : 1612
1613 : CAATTCTTCTTTGTAAATGGTGGTGGAAGCTCTACTCTAATGCTGGTGACCCGTGGTGTAGT : 1674
1675 : TTTATTGCCACTATCCACCCAACTTCACACTAGAGATCTAAAGGTATACACAAATCAACCTC : 1736
1737 : TTCATTTTGGAATGGTTTACAGCACACATGAAATATTTCTACTCCTAATCCACTTTCAAGTT : 1798
1799 : AGCAACTAGTATTATTTTGGAAAGATAGTTGGTTACATAATCATCCACTGAAGGATCGATTT : 1860
1861 : CCTCACCTTTACACAATAGCATTGAAGTGCAACAACTCAGTGGCAAAGGTATTAAGCAATCT : 1922
1923 : ACTTGATAATAGCTCTTTTAGTACTCCTCTTCCTCAAAGATACCAAGAAGATTTTCAGAGTC : 1984
1985 : TATAGGAAAGCATTGAACAAATTACATTAACGGAACGACCTGATACTATACAATGGAAATGG : 2046
2047 : TTTAGTAGCAATATTTTTTTGGCATGAAGGATCTACTATTTTCTGCAAGATGGAGGAGTTTG : 2108
2109 : GCCTCTACTGAGTAATATTATATAAAAACTCCTAATACCAAAGAAAGCCAAGTTATTTGCTT : 2170
2171 : GGCTAAGTGCTCACAACAAAATCCCAATGAAAGCTAATCTTCTTAATAGAGGAATAATTGGA : 2232
2233 : ACTGATTACTGTACACTTTGCGATGACTTATCAGAAACTAATGATCATCTAATGCTCATCTA : 2294
2295 : TACTTTTTCAAAAGCAATTTGGAATCAAGTACTTTCAGACCTGCAATTGTCGAAACTTTTAT : 2356
2357 : GCATGCTTAACACCCTATGGGATACTTGGAGACTCATCAATATGCAACACGATAGAAGACCT : 2418
2419 : AAACTAGCTGCTCTATTCGTAATTGGTCAATGGTGTCTTTGGAAGGAAAGAAATAAAAGATT : 2480
2481 : ATTCGACTTCTATACTTTTTATCCACGATCGATTGCTGAAACTGTGTCACTTTTTCTTTCTT : 2542
2543 : GGGCATCACACCTAACAACGGAGCAACTAAAGATGTTAGCTCCTGTTCGAGAAGTTCTCTTA : 2604
2605 : TCTAAGAATGAAAACACACAATCTTTAGTGAGAATTACAGATGCTAACAGGCGCAGATGAAT : 2666
2667 : GTTTTATGAGCATTTTTATAGCTGCAGCTTATATGTGATCTATGGTGCAAGGAGTTAATTAT : 2728
2729 : AACCATGGATATTAGTTAGGTTGACTATCAGAAATCATCTCCAATACATTCTATGTAACCAC : 2790
2791 : TGATCAATTCCATGTTCAACTAGATAGGAACCTGCCTATATACAGGTATGTCCCTGATGTAA : 2852
2853 : CTATAGTATACTATTATTCATAAATAAATAACGAAGGTTTTACCTTCTTCTCATAAAAAAAA : 2914
2915 : AGTATCTTCATGTCATCCTATATGTCATGCATCTCCTTTGCTACTTCTTTTATTTACTTCTT : 2976
2977 : AAACTTGGTTCTACCATATATTATCAGCCCCTTTTAAATTTGCTTTTGGATATTGCATATTC : 3038
3039 : CACTCTTCAATCACCTCATGCCAAGCAAAACATTTATTCACACTTGAAAACCAATATAAGAA : 3100
3101 : TACCAAAGAATTTATCCATGAAATTCTAGAAACTTTGGTTTTACTCCTTTCTCCATCATTCA : 3162
3163 : AAAAGGTTCAAAATGATGA : 3181
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Supplementary Figure 1. Annotated *Karma* element DNA sequence. The 13 bp direct repeats defining the boundaries of the *Karma* element are highlighted gray. The splice site (GAACAG^ATGC, where ^ precedes the splice acceptor site) is in green font. The *Karma* sequence included in the *kDEF1* transcript is italicized and in bold font. The region of homology to rice *Karma* (Genbank accession AB081316.2) is in red font. The *Bbv* I, *Rsa* I and *Scr* FI restriction sites used for quantitative PCR DNA methylation assays are highlighted in yellow, blue and green, respectively. CHG sites are underlined.