

Supplementary Material

Molecular beacons with a homo-DNA stems: improving target selectivity

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Best alignment of Cy5MB1-4 to selected target sequences of the array using the CLUSTAL W (1.82) multiple sequence alignment program of EMBL-EBI
<http://www.ebi.ac.uk/clustalw/#>

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B3734      GCAAGCTGAAAGGCATCCTCGATTCCCTTCAAAGCAACCCAATCCTGGTAA 50
Cy5MB1_anti -----CCGGCTTCAAAGCAACCCACCGG----- 23
                        *****

B3734      GCAAGCTGAAAGGCATCCTCGATTCCCTTCAAAGCAACCCAATCCTGGTAA 50
Cy5MB2_anti -----CCGGCTTCAATGCAACCCACCGG----- 23
                        *****

B3734      GCAAGCTGAAAGGCATCCTCGATTCCCTTCAAAGCAACCCAATCCTGGTAA 50
Cy5MB3_anti -----CCGCCTTCAATGCAACCCAGCGG----- 23
                        *****

B3734      GCAAGCTGAAAGGCATCCTCGATTCCCTTCAAAGCAACCCAATCCTGGTAA 50
Cy5MB4_anti -----GCGGCTTCAATGCAACCCACCGC----- 23
                        *****

B3734      GCAAGCTGAAAGGCATCCTCGATTCCCTTCAAAGCAACCCAATCCTGGTAA 50
Cy5MB5_anti -----GCGCCTTCAATGCAACCCAGCGC----- 23
                        *****

B1829     GCAGCGCCTGAAAACCAGCTATGAACCGCAAGAAGCAACCAGCATGATGG 50
Cy5MB1_anti --CCGGCTTCAAAGCAACCCACCGG----- 23
                ** * ** * * * *

B1829     GCAGCGCCTGAAAACCAGCTATGAACCGCAAGAAGCAACCAGCATGATGG 50
Cy5MB2_anti --CCGGCTTCAATGCAACCCACCGG----- 23
                ** * ** * * * *

B1829     GCAGCGCCTGAAAACCAGCTATGAACCGCAAGAAGCAACCAGCATGATGG 50
Cy5MB3_anti ---CCGCCTTCAATGCAACCCAGCGG----- 23
                ***** ** ** *

B1829     GCAGCGCCTGAAAACCAGCTATGAACCGCAAGAAGCAACCAGCATGATGG 50
Cy5MB4_anti ---GCGGCTTCAATGCAACCCACCGC----- 23
                *** ** ** ** *

B1829     GCAGCGCCTGAAAACCAGCTATGAACCGCAAGAAGCAACCAGCATGATGG 50
Cy5MB5_anti ---GCGCCTTCAATGCAACCCAGCGC----- 23
                ***** ** ** *

B0114     ACTGATGGCTTCGGTCGTTCCGACAGCCGTGAGAACCTGCGTCACCACTT 50
Cy5MB1_anti -----CCGGCTTCAAAGCAACCCACCGG----- 23
                        *** * * * *

B0114     ACTGATGGCTTCGGTCGTTCCGACAGCCGTGAGAACCTGCGTCACCACTT 50
Cy5MB2_anti -----CCGGCTTCAATGCAACCCACCGG----- 23
                        *** * * ** *

B0114     ACTGATGGCTTCGGTCGTTCCGACAGCCGTGAGAACCTGCGTCACCACTT 50
Cy5MB3_anti -----CCGCCTTCAATGCAACCCAGCGG----- 23
                        *** * * ** *

B0114     ACTGATGGCTTCGGTCGTTCCGACAGCCGTGAGAACCTGCGTCACCACTT 50
Cy5MB4_anti ----GCGGCTTCAATGCAACCCACCGC----- 23
                        ***** * ** **

B0114     ACTGATGGCTTCGGTCGTTCCGACAGCCGTGAGAACCTGCGTCACCACTT 50
Cy5MB5_anti -----GCGCCTTCAATGCAACCCAGCGC----- 23
                        ** * * ** *

B3399     ACGCCATCCGTCCTGAATGACTACCGCCGCTGATCCCCTCGCTAATGT 50
Cy5MB1_anti -----CCGGCTTCAAAGCAACCCACCGG--- 23
                        *** * * * *

B3399     ACGCCATCCGTCCTGAATGACTACCGCCGCTGATCCCCTCGCTAATGT 50
Cy5MB2_anti -----CCGGCTTCAATGCAACCCACCGG--- 23
                        *** * * * *

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B1531      TACCGGATGACCAATATGCAGGGCGAATCGCGCTTTTTACATCCATTAAA 50
Cy5MB4_anti -----GCGGCTTCAATGCAACCCACCGC----- 23
                ** *   ***   *   *

B1531      TACCGGATGACCAATATGCAGGGCGAATCGCGCTTTTTACATCCATTAAA-- 50
Cy5MB5_anti -----GCGCCTTCAATGCAACCCACCGC 23
                ***** ** *   *

B2610      AAGAAAATGAAGAAGGGCGGAATGGCGAAGATGATGAGAAGCATGAAGGG 50
Cy5MB1_anti --CCGGCTTCAAAGCAACCCACCGG----- 23
                * * *   * * **

B2610      AAGAAAATGAAGAAGGGCGGAATGGCGAAGATGATGAGAAGCATGAAGGG 50
Cy5MB2_anti -----CCGGCTTCAATGCAACCCACCGG--- 23
                **   *** * **

B2610      AAGAAAATGAAGAAGGGCGGAATGGCGAAGATGATGAGAAGCATGAAGGG 50
Cy5MB3_anti -----CCGCCTTCAATGCAACCCAGCGG--- 23
                **   *** * **

B2610      AAGAAAATGAAGAAGGGCGGAATGGCGAAGATGATGAGAAGCATGAAGGG 50
Cy5MB4_anti -----GCGGCTTCAATGCAACCCACCGC--- 23
                ***   *** * **

B2610      AAGAAAATGAAGAAGGGCGGAATGGCGAAGATGATGAGAAGCATGAAGGG 50
Cy5MB5_anti -----GCGCCTTCAATGCAACCCAGCGC--- 23
                ***   *** * **

B2278      CTGAACTCAATGATGAACATCCCGGCTGTCCTTTCCCGCTTTGCAGGTAA 50
Cy5MB1_anti -----CCGGCTTCAAAGCAACCCACCGG----- 23
                * *   * ** ** * *

B2278      CTGAACTCAATGATGAACATCCCGGCTGTCCTTTCCCGCTTTGCAGGTAA 50
Cy5MB2_anti CCGGCTTCAATGCAACCCACCGG----- 23
* *   ***** ** *

B2278      CTGAACTCAATGATGAACATCCCGGCTGTCCTTTCCCGCTTTGCAGGTAA 50
Cy5MB3_anti CCGCCTTCAATGCAACCCAGCGG----- 23
* *   ***** ** *

B2278      CTGAACTCAATGATGAACATCCCGGCTGTCCTTTCCCGCTTTGCAGGTAA 50
Cy5MB4_anti GCGGCTTCAATGCAACCCACCGC----- 23
*   ***** ** * *

B2278      CTGAACTCAATGATGAACATCCCGGCTGTCCTTTCCCGCTTTGCAGGTAA 50
Cy5MB5_anti GCGCCTTCAATGCAACCCAGCGC----- 23
*   ***** ** * *

B0431      ACCAGCATTTTCGATGAGATTACTAAGGCAGGGCTGAAAAATGGCAACTGA 50
Cy5MB1_anti -----CCGGCTTCAAAGCAACCCACCGG 23
                * ** * ** * ** *

B0431      ACCAGCATTTTCGATGAGATTACTAAGGCAGGGCTGAAAAATGGCAACTGA 50
Cy5MB2_anti -----CCGGCTTCAATGCAACCCACCGG 23
                * ** * ** * ** *

B0431      ACCAGCATTTTCGATGAGATTACTAAGGCAGGGCTGAAAAATGGCAACTGA 50
Cy5MB3_anti --CCGCCTTCAATGCAACCCAGCGG----- 23
                * ** * *   *

B0431      ACCAGCATTTTCGATGAGATTACTAAGGCAGGGCTGAAAAATGGCAACTGA 50
Cy5MB4_anti ---GCGGCTTCAATGCAACCCACCGC----- 23
                *** ** *

B0431      ACCAGCATTTTCGATGAGATTACTAAGGCAGGGCTGAAAAATGGCAACTGA 50
Cy5MB5_anti -----GCGCCTTCAATGCAACCCAGCGC----- 23
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