

Additional Data File 1.

The 5 *Sly* clones from the microarray in Clustal alignment with the cDNA clone BC049626. The original cDNAs were digested with Rsa1 (cut site GT'AC). MTnF_J16 extends further 3' because there is a single base change converting a GT'AC site to GTTC. MTnE_N09 lacks *Sly* exons 5 and 6.

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BC049626  -----ACAGAAGGGTGCGGTTTGAAGGTGTTCTCCTCTTAGATGAGCTACTACTGAGTTCTTATGAGAAGAATGGCTCTTAA 78
MtnH_K10  -----
MtnE_N09  GAGCTAAGCACAGAAGGGTGCGGTTTGAAGGTGTTCTCCTCTTAGATGAGCTACTACTGAGTTCTTATGAGAAGAATGGCTCTTAA 87
MtnF_J16  -----
MtnB_M09  -----
Mtn14_G18 -----
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GAAATTGAAGGTGATACCAAAGGAAGGTTACTTATTACTTTTGGACTTTGATGATGAGGACGATGACATAAAAGTTTCAGAGGAGGCTCTTTCGGAA 175
-----GATGAGGACGATGACATAAAAGTTTCAGAGGAGGCTCTTTCGGAA 45
GAAATTGAAGGTGATACCAAAGGAAGGTTACTTATTACTTTTGGACTTTGATGATGAGGACGATGACATAAAAGTTTCAGAGGAGGCTCTTTCGGAA 184
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GTAAAGAGCCCAGCATTGTGATAAAATGAGAATATATCGCCTCAAGCAGAAGCAGATGAAGATATGGGAGATGAAGTAGACAGTATGTTGGATAAAT 272
GTAAAGAGCCCAGCATTGTGATAAAATGAGAATATATCGCCTCAAGCAGAAGCAGATGAAGATATGGGAGATGAAGTAGACAGTATGTTGGATAAAT 142
GTAAAGAGCCCAGCATTGTGATAAAATGAGAATATATCGCCTCAAGCAGAAGCAGATGAAGATATGGGAGATGAAGTAGACAGTATGTTGGATAAAT 281
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CTGAAGTAAATAATCCAGCAATTGGTAAAGATGAAAATATATCGCCTCAAGTAAAAGGAGATGAAGACATGGGACATGAAGTAGGCAGTATGTTGGA 369
CTGAAGTAAATAATCCAGCAATTGGTAAAGATGAAAATATATCGCCTCAAGTAAAAGGAGATGAAGACATGGGACATGAAGTAGGCAGTATGTTGGA 239
CTGAAG----- 287

TAAATCTGGAGATGACATTTATAAGACGCTTCACATAAAGAGAAAAATGGATGGAACTTATGTCAAAGAATCTTTCAAAGGCAGCAACCAGAAATTA 466
TAAATCTGGAGATGACATTTATAAGACGCTTCACATAAAGAGAAAAATGGATGGAACTTATGTCAAAGAATCTTTCAAAGGCAGCAACCAGAAATTA 336
-----ATGACATTTATAAGACGCTTCACATAAAGAGAAAAATGGATGGAACTTATGTCAAAGAATCTTTCAAAGGCAGCAACCAGAAATTA 373

GAAAGATTTTGCAAAACGAACGAACGAGAGAGGAAGAACATCAACAACAAATTTTGTGAGCAGTATATAACTACATTTTCAGAAGTCTGATATGGATG 563
GAAAGATTTTGCAAAACGAACGAACGAGAGAGGAAGAACATCAACAACAAATTTTGTGAGCAGTATATATCTACATTTTCAGAAGTCTGATATGGATG 433
GAAAGATTTTGCAAAACGAACGAACGAGAGAGGAAGAACATCAACAACAAATTTTGTGAGCAGTATATAACTACATTTTCAGAAGTCTGATATGGATG 470

TACAGAAATTC AATGAAGAAAAAGAAAAATCAGTGAATAGTTGTCAAAAAGAACAACAAGCATTGAAACTGTCCAAATGTAGTCAGAACCAGACCCT 660
T----- 434
TACAGAAATTC AATGAAGAAAAAGAAAAATCAGTGAATAGTTGTCAAAAAGAACAACAAGCATTGAAACTGTCCAAATGTAGTCAGAACCAGACCCT 567
-ACAGAAATTC AATGAAGAAAAAGAAAAATCAGTGAATAGTTGTCAAAAAGAACAACAAGCATTGAAACTGTCCAAATGTAGTCAGAACCAGACCCT 96
-ACAGAAATTC AATGAAGAAAAAGAAAAATCAGTGAATAGTTGTCAAAAAGAACAACAAGCATTGAAACTGTCCAAATGTAGTCAGAACCAGACCCT 96
-ACAGAAATTC AATGAAGAAAAAGAAAAATCAGTGAATAGTTGTCAAAAAGAACAACAAGCATTGAAACTGTCCAAATGTAGTCAGAACCAGACCCT 96

GGAAGCAGTTAAAGAAATGCATGAGAAGTCCATGGAGGTTTTGATGAACTTGGGGACCAAGAAGTAAGAAATGCTTTTTGGTGTAGATGGTGAAGTG 757

GGAAGCAGTTAAAGAAATGCATGAGAAGTCCATGGAGGTTTTGATGAACTTGGGGACCAAGAAGTAAGAAATGCTTTTTGGTGTAGATGGTGAAGTG 664
GGAAGCAGTTAAAGAAATGCATGAGAAGTCCATGGAGGTTTTGATGAACTTGGGGACCAAGAAGTAAGATATGCTTTTTGGTGTAGATGGTGAAGTG 193
GGAAGCAGTTAAAGAAATGCATGAGAAGTCCATGGAGGTTTTGATGAACTTGGGGACCAAGAAGTAAGATATGCTTTTTGGTGTAGATGGTGAAGTG 193
GGAAGCAGTTAAAGAAATGCATGAGAAGTCCATGGAGGTTTTGATGAACTTGGGGACCAAGAAGTAAGATATGCTTTTTGGTGTAGATGGTGAAGTG 193

A-AAAAAAAAATGTCTATGTTTGAAAGAGCCATCATGGAGGATAATCTGAAGTACTCTTCTACTTTCCCATCTTCAGAAAAATGAAGCATGAAAAAT 853

AGAAAAAAAA-TGTCTATGTTTGAAAGAGCCATCATGGAGGATAATCTGAAGT----- 716

AGAAAAAAAAATGTCTATGTTTGAAAGAGCCATCATGGAGAATAATCTGAAGT----- 246

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TTTCACTTGCTGGTATATATATAAAACAAATAAAAAAATCTCTAACTTTTTTGTTCCTACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 946

TTTCACTTGCTGGTATATATATAAAACAAATAAAAAAATCTCTAACTTTTTTGTTCCTATGAAACAGAAAAAAAAAAAAAAAAAAAAAA-- 380
