1

ggtttcacagagtccataggttcagcctaccatagattgaaaacatttgggggaagaaattatgtctatactaaacatgtacagacttttaagcttacag
aligned sequence mEGFP-ITSN1

--TCTATACTAAACATGTACAGACTTTTAAGCTTACAG
aligned sequence sequencing F

----
aligned sequence sequencing R

101

aataacagttgtttacatagcatttaccttgtattaaatattgtaagtaatctagagattatttgaagtatgcaagaggacgtgcttaggttatatgcaa
aligned sequence mEGFP-ITSN1

AATAACAGTTGTTTACATAGCATTTACCTTGTATTAAATATTGTAAGTAATCTAGAGATTATTTGAAGTATGCAAGAGGACGTGCTTAGGTTATATGCAA
aligned sequence sequencing F

----
aligned sequence sequencing R

201

atactgtgccattttatatcagggacttgaggatccacggattttttttttaatccatgggaggtcttggaaccagtgttcctgggataatgagggacaac
aligned sequence mEGFP-ITSN1

ATACTGTGCCATTTTATATCAGGGACTTGAGGATCCACGGATTTTTTTTTAATCCATGGGAGGTCTTGGAACCAGTGTTCCTGGGATAATGAGGGACAAC
aligned sequence sequencing F

----
aligned sequence sequencing R

301

tgtatacttaaaaagtaacacgtgaatgaatgaattccttaattgtagagctatgctctggctctagtattagtcctctgaccattaaagatagcatgtt
aligned sequence mEGFP-ITSN1

TGTATACTTAAAAAGTAACACGTGAATGAATGAATTCCTTAATTGTAGAGCTATGCTCTGGCTCTAGTATTAGTCCTCTGACCATTAAAGATAGCATGTT
aligned sequence sequencing F

--AGCATGTT
aligned sequence sequencing R

401

ggtgtgtttatgattatacaggaattaagttttcataaacttaaatgttgcattttcacttacaggcgtcgattagcaaggtaaaagtaacagaaccatg
aligned sequence mEGFP-ITSN1   ITSN1 start codon ▭▶

GGTGTGTTTATGATTATACAGGAATTAAGTTTTCATAAACTTAAATGTTGCATTTTCACTTACAGGCGTCGATTAGCAAGGTAAAAGTAACAGAACCATG
aligned sequence sequencing F

GGTGTGTTTATGATTATACAGGAATTAAGTTTTCATAAACTTAAATGTTGCATTTTCACTTACAGGCGTCGATTAGCAAGGTAAAAGTAACAGAACCATG
aligned sequence sequencing R

501

GTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
mEGFP »
aligned sequence mEGFP-ITSN1

GTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
aligned sequence sequencing F

GTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG
aligned sequence sequencing R

610

AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGG

mEGFP

aligned sequence mEGFP-ITSN1

AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGG

aligned sequence sequencing F

AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGG

aligned sequence sequencing R

701

CGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTC

mEGFP

aligned sequence mEGFP-ITSN1

CGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTC

aligned sequence sequencing F

CGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTC

aligned sequence sequencing R

801

AAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACG

mEGFP

aligned sequence mEGFP-ITSN1

AAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACG

aligned sequence sequencing F

AAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACG

aligned sequence sequencing R

901

GCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT

mEGFP

aligned sequence mEGFP-ITSN1

GCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT

aligned sequence sequencing F

GCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT

aligned sequence sequencing R

1001

CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC

mEGFP

aligned sequence mEGFP-ITSN1

CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGA---

aligned sequence sequencing F

CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTAC

aligned sequence sequencing R

1101

CTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGG

mEGFP

aligned sequence mEGFP-ITSN1

----

aligned sequence sequencing F

CTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGG

aligned sequence sequencing R

1201

ACGAGCTGTACAAGTCCGGAGGTACTCAGATCTCGAGGgctcagtttccaacaccttttggtggtaagttttcagaaatttctctttttaatgtactttg

mEGFP   linker   ITSN1 coding region

aligned sequence mEGFP-ITSN1

----

aligned sequence sequencing F

ACGAGCTGTACAAGTCCGGAGGTACTCAGATCTCGAGGGCTCAGTTTCCAACACCTTTTGGTGGTAAGTTTTCAGAAATTTCTCTTTTTAATGTACTTTG

aligned sequence sequencing R

1301

ggaccagatttttaaaaacttgatattatggcaaatttaaaattaaaaagtagagaaaataatataatcagcattcatgtattccatcatatagtttcatt

aligned sequence mEGFP-ITSN1

----

aligned sequence sequencing F

GGACCAGATTTTTAAAAACTTGATATTATGGCAAATTTAAAATTAAAAAGTAGAGAAAATAATATAATCAGCATTCATGTATTCCATCATATAGTTTCATT

aligned sequence sequencing R

1401

aattatcaactcatgcccaatattgtttcatctggattctttttggagcaactcccaggcatcatttcatctataa

aligned sequence mEGFP-ITSN1

----

aligned sequence sequencing F

AATTATCAACTCATGCCCAATAT---

aligned sequence sequencing R