

Product datasheet for SC115052

MTCH2 (NM_014342) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	MTCH2 (NM_014342) Human Untagged Clone
Tag:	Tag Free
Symbol:	MTCH2
Synonyms:	HSPC032; MIMP; SLC25A50
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)
Fully Sequenced ORF:	>OriGene ORF within SC115052 sequence for NM_014342 edited (data generated by NextGen Sequencing) <pre> ATGGCGGACGCGCCAGTCAGGTGCTCCTGGGCTCCGGTCTCACCATCCTGTCCCAGCCG CTCATGTACGTGAAAGTGCTCATCCAGGTGGGATATGAGCCTCTTCCTCCAACAATAGGA CGAAATATTTTTGGGCGGCAAGTGTCAGCTTCTGGTCTCTTTAGTTATGCTCAGCAC ATTGCCAGTATCGATGGGAGGCGCGGTTGTTACAGGCTTAACCTCAAGACTGTGTTG GGAGTCTTGGAAGTGTGGTCCATGGTAAAGTTTTACAGCATTACCAGGAGAGTGACAAG GGTGAGGAGTTAGGACCTGGAAATGTACAGAAAGAAGTCTCATCTTCCTTTGACCACGTT ATCAAGGAGACAACCTCGAGAGATGATCGCTCGTTCTGCTGCTACCCTCATCACACATCCC TTCCATGTGATCACTCTGAGATCTATGGTACAGTTCATTGGCAGAGAATCCAAGTACTGT GGACTTTGTGATTCCATAATAACCATCTATCGGGAAGAGGGCATTCTAGGATTTTTTCGCG GGTCTTGTTCTCGCCTTCTAGGTGACATCCTTTCTTTGTGGCTGTGTAACCTCACTGGCC TACCTCGTCAATACCTATGCACTGGACAGTGGGTTTTCTACCATGAATGAAATGAAGAGT TATTCTCAAGCTGTCACAGGATTTTTTGCAGATATGTTGACCTATCCCTTTGTGCTTGTC TCCAATCTTATGGCTGTCAACAAGTGTGGTCTTGCTGGTGGATGCCCTCCTTACTCCCCA ATATATACGTCTTGATAGACTGTTGGTGCATGCTACAAAAGAGGGGAATATGAGCCGA GGAAATAGCTTATTTTTCCGGAAGGTCCCCTTTGGGAAGACTTATTGTTGTGACCTGAAA ATGTTAATTTGA </pre>

Clone variation with respect to NM_014342.3



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5' Read Nucleotide Sequence:

>OriGene 5' read for NM_014342 unedited
 GTGTCAAATTTGTATACGACTCCTATAGCGGCCCGCAATCGGCACGAGGTGACCTAGG
 ACCGGCTACCGGGTCGCTTGGTGGCTCCGTCTGTCTGTCGTCGCCCGCGGGTGCCAT
 CATGGCGGACGCGGCCAGTCAGGTGCTCCTGGGCTCCGGTCTCACCATCCTGTCCAGCC
 GCTCATGTACGTAAAGTGCTCATCCAGGTGGGATATGAGCCTCTTCTCCAACAATAGG
 ACGAAATATTTTTGGGCGCAAGTGTGTGAGCTTCCTGGTCTCTTTAGTTATGCTCAGCA
 CATTGCCAGTATCGATGGGAGGCGGGTTGTTACAGGCTTAACCCAAGACTGTGTTT
 GGGAGTCCTTGGAAGTGTGGTCCATGGTAAAGTTTTACAGCATTACCAGGAGAGTGACAA
 GGGTGAGGAGTTAGGACCTGAAATGTACAGAAAGAGTCTCATCTTCTTTGACCACGT
 TATCAAGGAGACAACCTCGAGAGATGATCGCTCGTTCTGCTGCTACCCTCATCACACATCC
 CTTCCATGTGATCACTCTGAGATCTATGGTACAGTTTCATTGGCAGAGAATCCAAGTACTG
 TGGACTTTGTGATTCCATAATAACCATCTATCGGAAGAGGGCATTCTAGGATTTTTCGC
 GGGTCTTGTTCTCGCTTCTANGTGACATCCTTTCTTTGTGGCTGTGAACTACTGGC
 CTACCTCGTCAATACCTATGCACTGGACAGTGGGGTTCTACCATGAATGAAATGAAGAG
 CTATTCTCAAGCTGTACAGGATTTTTGCGAGTATGTTGACCTATCCTTTGTGCTTGGCT
 CCAATCTTATGGCTGTCAACAACCTGGGGCTTGCTGTTGGATGCCCTCCCTACTCCCCA

3' Read Nucleotide Sequence:

>OriGene 3' read for NM_014342 unedited
 TTACCGCGGCCGCAATCTAGAGTCGAGTTTTTTTTTTTTTTTTTTTAAACATTTTCCAGAC
 ATCTTTACTTAAAGATTTTTTGGGAGAAAAGGTAGGCAGCAAACATTTTATATTTAAAC
 AAATGCAGATAGTAATATTGAAATAGTATATAAAATTGACATTACTTTTTGAGACAAAGG
 AAGAGACATCAAAGACATTTTAAGCCGAGCTCCTCATGAGCTTCCTAAACCCAGGGGAG
 GGAAGAGACCCCTGCATTCTCGTTCTGTCTAATATTATCAGTGGGGCTGTTTTGACAGAG
 AAGTCTCAGAAGCAGCAATTAAGTGCTTACTCATTTGGCAATGTCCAGTGAGTTATAT
 AAATAAGTGAAACACAGGCTTTCTCATTTTAGAGCATTTTAACTGCTTTTTAAAGGC
 CTGAGTAAACAGAAGCTTTATGCTTGAGTTGAATTTTATTTTCTCCCAAAGTGATTTTTT
 TCCTCCTATAATGTAAACATGCTTAACTGAGGGTATGGCATGTGAGGTGGTCAGTGTC
 TAAGACCCATGTCGACTTGGGTTGGCATTACCAGACATGGAGTTACAAATATACTTTCCA
 AGGCTGTCATCAGAAATGCAAACTACTCACCTTCGGCAACAATAACAAAAGGAAACAA
 AACANAACTGAAGAACAAAAGATTATATATAATTAGAACGGTATGGTGAATTTAAGC
 ACTGGNCAATACTTGGCTCTTAAAGAAAGGGTTACTCCTGCAGGATCTGCTTTTCATAT
 TTTATGTGAAAAACAGAACCTCTTTGAGGAAAAAAGTGCAATTATACTTCTTTTCCAAAA
 CTTGCTTATTTCTGTAATGGCCTTTTCTTTGGTGTGCTGACCCTTATCCTATTATTNTT
 TTCAGGAAGCTTTGAN

Restriction Sites:

ECorI-NOT

ACCN:

NM_014342

Insert Size:

2600 bp

OTI Disclaimer:

Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).

Components:

The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:	1. Centrifuge at 5,000xg for 5min. 2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA. 3. Close the tube and incubate for 10 minutes at room temperature. 4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom. 5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	<u>NM_014342.2, NP_055157.1</u>
RefSeq Size:	2524 bp
RefSeq ORF:	912 bp
Locus ID:	23788
UniProt ID:	<u>Q9Y6C9</u>
Cytogenetics:	11p11.2
Domains:	mito_carr
Gene Summary:	This gene encodes a member of the SLC25 family of nuclear-encoded transporters that are localized in the inner mitochondrial membrane. Members of this superfamily are involved in many metabolic pathways and cell functions. Genome-wide association studies in human have identified single-nucleotide polymorphisms in several loci associated with obesity. This gene is one such locus, which is highly expressed in white adipose tissue and adipocytes, and thought to play a regulatory role in adipocyte differentiation and biology. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. A recent study showed this gene to be an authentic stop codon readthrough target that can produce two isoforms from the same mRNA by use of alternative in-frame translation termination codons. [provided by RefSeq, Dec 2017] Transcript Variant: This variant (1) represents the predominant transcript and encodes two isoforms, which result from the use of alternative in-frame translation termination codons. The shorter isoform (1) results from translation termination at the upstream UGA stop codon, while the longer isoform (1x) results from UGA stop codon readthrough to the downstream UAG termination codon. This RefSeq represents the shorter isoform (1). Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.