

## Product datasheet for **SC335740**

### MAEL (NM\_001286378) Human Untagged Clone

#### Product data:

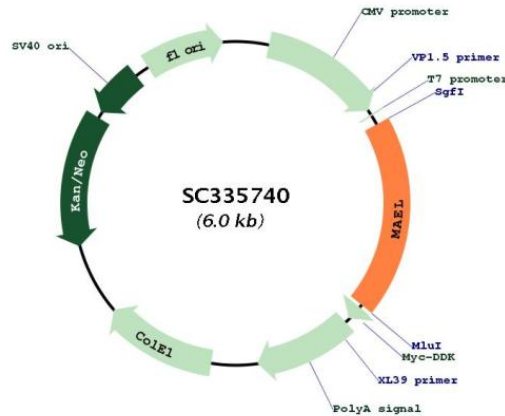
Product Type:	Expression Plasmids
Product Name:	MAEL (NM_001286378) Human Untagged Clone
Tag:	Tag Free
Symbol:	MAEL
Synonyms:	CT128; SPATA35
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC335740 representing NM_001286378. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTGTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGGCTCGAGAATGGAGGGCCGCTCAGGAAAGGACCCTGGGCCCTCAGAGAAGCAGAAACCTGTTTTT
ACACCACTGAGGAGGCCAGGCATGCTTGTACCAAAGCAGAATGTTTCACCTCCAGATATGTCAGCTTTG
TCTTTAAAGGTGATCAAGCTCTCCTGGAGGCATTTTTATTTTTTGAACATTTTAGCCATGGCGAG
CTACCTCCTCATTGTGAACAGCGCTTCCCTCCCTTGTGAAATTGGCTGTGTTAAGTATTCTCTCAAGAA
GGTATTATGGCAGATTTCCACAGTTTTATAAATCCTGGTAAATTCACGAGGATTCGATTTTCATTGT
CAGGCTGCAAGTATTCTAGTACAAGATTCCTATTTCAAATTTGAACGTGGGCATAACCAAGCAACT
GTGTTACAAAACCTTTATAGATTTATTCATCCCAACCCAGGGAACCTGGCCACCTATCTACTGCAAGTCT
GATGATAGAACCAGAGTCAACTGGTGTGTTGAAGCATATGGCAAAGGCATCAGAAATCAGGCAAGATCTA
CAACTTCTCACTGTAGAGGACCTTGTAGTGGGGATCTACCAACAAAAATTTCTCAAGGAGCCCTCTAAG
ACTTGGATTCTGAAGCCTCCTAGATGTGGCCATGTGGGATATTCTAGCAACACAAGGTGCAAGTGGCAT
GAAGAAAATGATATTCTCTTCTGTGCTTTAGCTGTTTGAAGAAGATTGCGTACTGCATCAGTAATTCT
CTGGCCACTCTCTTTGGAATCCAGCTCACAGAGGCTCATGTACCACTACAAGATTATGAGGCCAGCAAT
AGTGTGACACCCAAAATGGTTGTATTGGATGCAGGGCGTTACCAGAAGCTAAGGGTTGGGAGTTCAGGA
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GCAAAAATTTCTGGCAAAACAGCAGCGTTCGGGGAAGAGGAATTACCCGCTTACTAGAGAGCATTTC
AATTCTCCAGCAATATCCACAAATCTCCAACCTGTGACACTTCACTCTCACCTTACATGTCCAAAAA
GATGGATACAAATCTTTCTCTTCTTAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
```

Restriction Sites: SgfI-MluI



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**Plasmid Map:**


**ACCN:** NM\_001286378

**Insert Size:** 1137 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:** [NM\\_001286378.1](#)

**RefSeq Size:** 1715 bp

**RefSeq ORF:** 1137 bp

**Locus ID:** 84944

**UniProt ID:** [Q96JY0](#)

**Cytogenetics:** 1q24.1

**MW:** 42.6 kDa

**Gene Summary:**

Plays a central role during spermatogenesis by repressing transposable elements and preventing their mobilization, which is essential for the germline integrity. Acts via the piRNA metabolic process, which mediates the repression of transposable elements during meiosis by forming complexes composed of piRNAs and Piwi proteins and governs the methylation and subsequent repression of transposons. Its association with piP-bodies suggests a participation in the secondary piRNAs metabolic process. Required for the localization of germ-cell factors to the meiotic nuage (By similarity).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) differs in the 5' UTR and lacks a portion of the 5' coding region compared to variant 1. These differences cause translation initiation at a downstream start codon compared to variant 1. The encoded isoform (3) is shorter than 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.