

## Assay Summary

### TM4SF2 Gene Mutation Analysis

#### Non-Syndromic X-Linked Mental Retardation

##### *Synopsis*

X-linked mental retardation (XLMR) has a prevalence of 2.6 cases per 1,000 in the general population, accounting for over 10% of all cases of mental retardation<sup>1</sup>. It is estimated that 2/3 of X-linked mental retardation is non-syndromic (mental retardation without other distinguishing features). Recently, mutations in the transmembrane 4 superfamily member 2 (TM4SF2) gene have been found in non-syndromic X-linked mental retardation patients.<sup>2-4</sup>

##### *Indications for testing*

Individuals with a diagnosis of non-syndromic mental retardation, especially those in whom Fragile X disease has been ruled out, are candidates for testing. After a specific mutation is identified in a family, carrier testing can be performed for appropriate at-risk females and presymptomatic males. With appropriate genetic counseling, prenatal testing can be performed for females with an identified mutation.

##### *Methodology*

**Full Mutation Analysis of TM4SF2:** All coding exons and associated intron junctions of the TM4SF2 gene are analyzed by direct DNA sequence analysis using an automated fluorescent sequencing machine. When a mutation is detected, confirmation is carried out by sequencing in the opposite direction, in an independent PCR amplification. If no mutation is found sequence analysis is performed in both directions. At-risk family members can be offered DNA sequence analysis of only the region of the gene with the previously identified mutation.

##### *Limitations*

For mutation analysis, the method will not detect mutations located in regions of the genes that are not analyzed (non-coding exon regions, intron regions other than the splice junctions, and upstream and downstream regions). The method also will not detect gross genetic alterations including most deletions in females, duplications, and inversions. Some sequence alterations that may be detected (such as those causing missense or synonymous changes) will be of unknown clinical significance. Interpretation of test results should be in the context of the patient's ethnicity, clinical and family histories, and other laboratory test results.

##### *Specimen Requirements*

(a) Blood samples: 2 tubes with a total of 6 ccs in ACD (yellow top) or EDTA (lavender top) tubes.

Keep at ambient temperature and ship by overnight courier. Samples must be received in our laboratory within 72 hours of draw.

**Note:**

- i) for infants, a minimum of 3 ccs is sufficient.
- ii) we accept DNA; at least 10 micrograms is required.

(b) Prenatal samples: 2 T25 flasks of confluent cells sent padded to arrive on M/Tu/W.

A blood sample from the mother maybe required (2 tubes with a total of 6 ccs in ACD (yellow top) or EDTA (lavender top) tubes) for use as positive control. Maternal cell contamination studies are not done here but are required for autosomal disorders and dosage analysis on X-linked disorders. We would be happy to assist in coordinating sending out a specimen for this purpose.

**Test Request Form (TRF)**

A completed MDL [TRF](#) is required for each specimen. Please submit the completed TRF with the specimen. Complete testing and billing information must be provided before the specimen is processed.

<b>Order Codes</b>	<b>CPT Codes</b>	<b>TAT</b>
TM4SF2-SEQ (TM4SF2 gene, full gene sequencing)	83890, 83898(x7), 83894, 83904(x7), 83912	5 wks
TM4SF2-CAS (TM4SF2 gene, targeted mutation analysis, known mutation)	83890, 83898, 83894, 83904, 83912	3 wks
TM4SF2-PD (TM4SF2 gene, known mutation detection, prenatal)	83890, 83898, 83894, 83904, 83912	2 wks

**References**

1. Stevenson RE, Schwartz CE (2002). *Cytogenet Genome Res* 99(1-4):265-75.
2. Abidi FE et al. (2002). *J. Med Genet* 39: 430-433.
3. Zemni R et al. (2000). *Nature Genet* 24: 167-170.
4. Maranduba CM et al. (2004). *Am J Med Genet* 124A(4):413-5.

NOTE: This test is performed pursuant to a license agreement with Roche Molecular Systems, Inc.