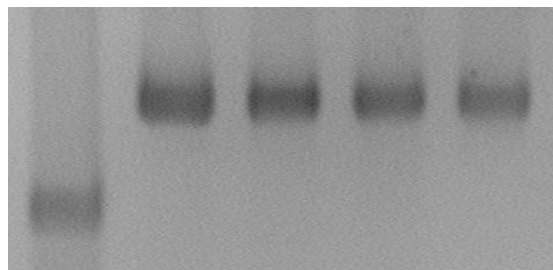


**A**

517/506 —



← Elk1

**B**

517/506 —

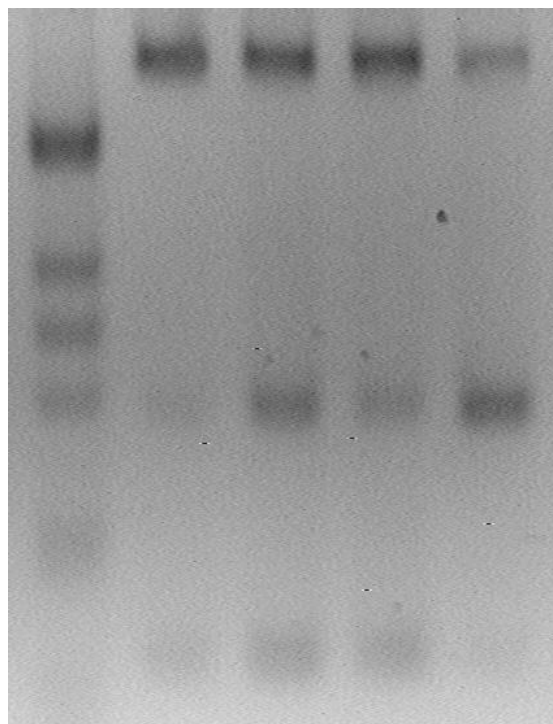
396 —

344 —

298 —

220 =

201 =



← Elk3

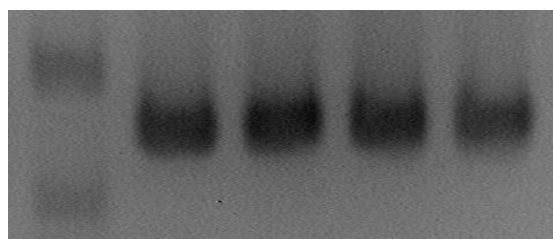
← Elk3b

← Elk3c

**C**

517/506 —

396 —



← Elk4

1 2 3 4 5

↓

E3/P2 \*\*\*\*\*  
 Elk3 AGAACATCATCAAGAAAGTGATCGGGCAGAAGTTTGTGTACAAGTTCGTC  
 Pctk2 AGAACATCATCAAGAAAGTGATCGGGCAGAAGTTTGTGTACAAGTTCGTC

E3/P2 \*\*\*\*\*  
 Elk3 TCTTTCCCGGATATCCTGAAAATGGATCCTCACGCGGTAGAGATCAGCCG  
 Pctk2 TCTTTCCCGGATATCCTGAAAATGGATCCTCACGCGGTAGAGATCAGCCG

E3/P2 \*\*\*\*\*  
 Elk3 GGAGAGCCTCCTGCTGCAGGACGGCGACTGTAAGGTGTCCCCGGAAGGCC  
 Pctk2 GGAGAGCCTCCTGCTGCAGGACGGCGACTGTAAGGTGTCCCCGGAAGGCC

E3/P2 \*\*\*\*\*  
 Elk3 GAGAGGTCCACAGGCACGGCTTGTCCCTCCCCTCAAAGTGCCAGCCGCAAC  
 Pctk2 GAGAGGTCCACAGGCACGGCTTGTCCCTCCCCTCAAAGTGCCAGCCGCAAC

E3/P2 \*\*\*\*\*  
 Elk3 GAGTACCTCCACTCGGGCCTCTACTCGTCCTTCACCATCAACTCCCTGCA  
 Pctk2 GAGTACCTCCACTCGGGCCTCTACTCGTCCTTCACCATCAACTCCCTGCA

E3/P2 \*\*\*\*\*  
 Elk3 GAACGCTCCAGAGGCCTTCAAGGCCATCAAGACGGAGAAGCTGGAGGAGC  
 Pctk2 GAACGCTCCAGAGGCCTTCAAGGCCATCAAGACGGAGAAGCTGGAGGAGC

E3/P2 \*\*\*\*\*  
 Elk3 CCTGTGATGACAGCCCCC  
 Pctk2 CCTGTGATGACAGCCCCC

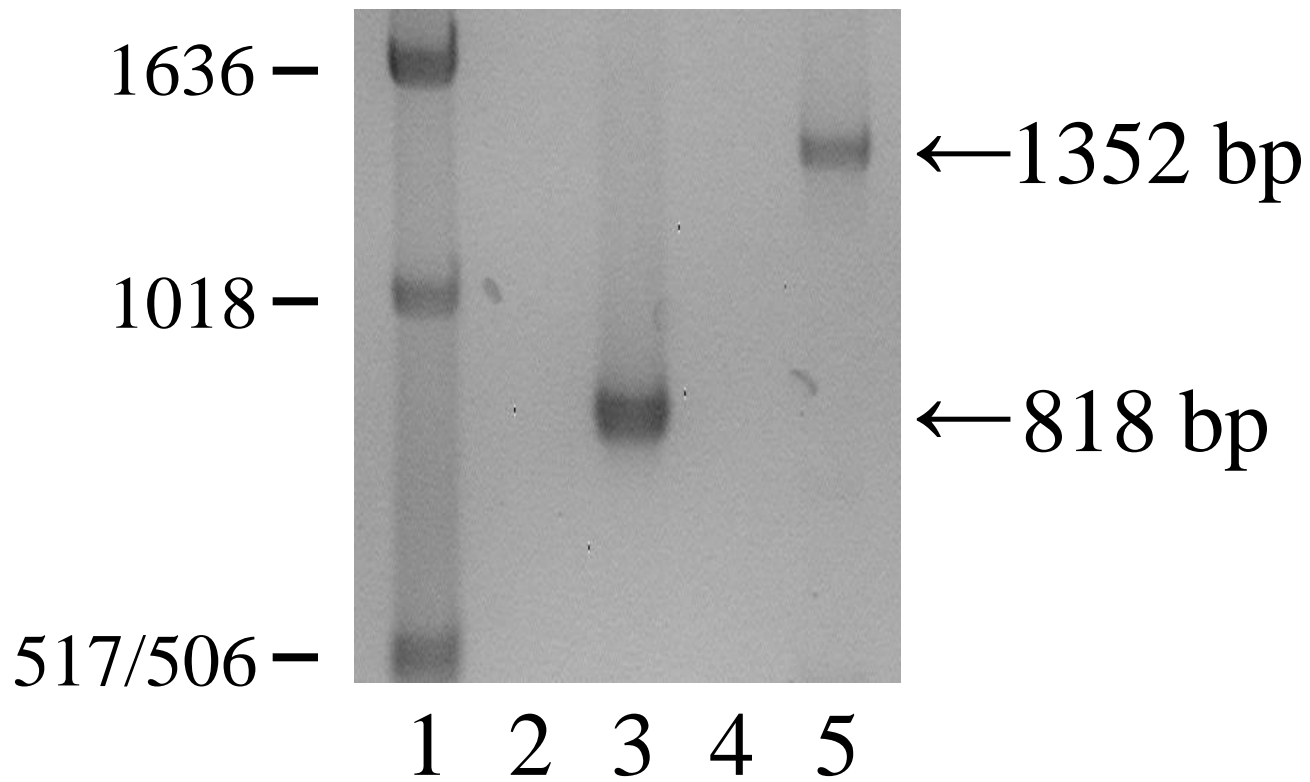
↑

↓

E4/Mf4 \*\*\*\*\*  
Elk4 CAGTTTCCCTCTGTACTCAACAGTCATGGCCCGTTCACTCTGTCAGGCCT  
Mfsd4 CAGTTTCCCTCTGTACTCAACAGTCATGGCCCGTTCACTCTGTCAGGCCT

E4/Mf4 \*\*\*\*\*  
Elk4 GGACGGACCTTCCACTCCGGGCCCATTTTCTCCAGAC  
Mfsd4 GGACGGACCTTCCACTCCGGGCCCATTTTCTCCAGAC

↑



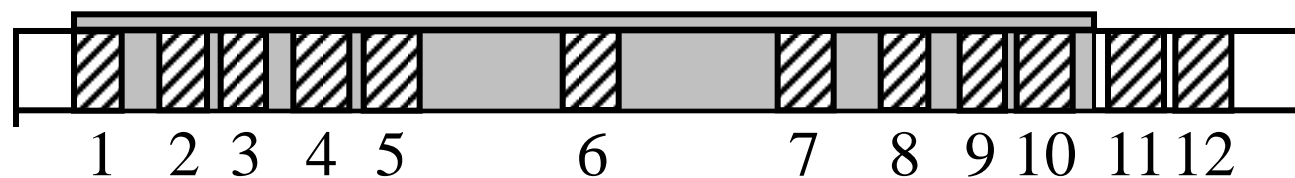
Supplemental Fig. S4.

mRNAs

proteins

MFS domain

Mfsd4a,  
Mfsf4c



Mfsd4b



Mfsd4d



nucleotide substitution, this study	amino acid change, this study	substitution, Giovane <i>et al</i> , 1994	substitution, Lopez <i>et al</i> , 1994
<b>G524C</b>	silent	<b>G524C</b>	<b>G524C</b>
<b>T794C</b>	silent	<b>T794C</b>	<b>T794C</b>
-	-	C833G	-
-	-	C864G	-
<b>T929C</b>	silent	<b>T929C</b>	<b>T929C</b>
-	-	G1005A	G1005A
-	-	G1064A	G1064A
<b>A1113G</b>	Ile → Val	<b>A1113G</b>	<b>A1113G</b>
-	-	C1123T	-
<b>C1217G</b>	Asp → Glu	<b>C1217G</b>	<b>C1217G</b>
G1401A	Ala → Thr	-	-
C1481T	silent	-	-
<b>T1490G</b>	silent	<b>T1490G</b>	<b>T1490G</b>
T1508C	silent	-	-

Supplemental Table S1.

<b><i>Gene, mRNA</i></b>	<b>Donor site</b>	<b>Acceptor site</b>
<i>Elk1</i> , Elk1	GATAAG/ <u>g</u> tatgg- intron 2	-cacttctc <u>a</u> g/AATATC
Elk1b	GATAAG/ <u>g</u> tatgg- (within ex3)	-accctgc <u>a</u> g/GAGTAC
<i>Elk3</i> , Elk3	GCACAG/ <u>g</u> taagc- intron 3	-tgtcttct <u>a</u> g/ACACCA
Elk3d	GACAAG/ <u>g</u> taaag- (skip ex3)	-tgtcttct <u>a</u> g/ACACCA
<i>Elk4</i> , Elk4	TCACAG/ <u>g</u> tagct- intron 3	-tgtgttgc <u>a</u> g/ACTCCC
Elk4c	ACTCTG/ <u>g</u> tttgt- (within ex3)	-tgtgttgc <u>a</u> g/ACTCCC
Elk4d	GTAAAG/ <u>g</u> taaat- (skip ex3)	-tgtgttgc <u>a</u> g/ACTCCC
Elk4e	CTGACG/ <u>g</u> taggc- (within ex3)	-tgtgttgc <u>a</u> g/ACTCCC

Supplemental Table S2.

<b>mRNA</b>	<b>Donor site</b>	<b>Acceptor site</b>
Pctaire2a	AGACAG/ <u>gt</u> gtgt-(join ex16/17)-tatat <u>tttag</u> /GACATG	
2b/2c/2d	AGACAG/ <u>gt</u> gtgt-(join ex16/18)-gacg <u>tttcag</u> /CCTTAT	
2b	CTGAAG/ <u>gt</u> aaga-(join ex18/21)-tcttccac <u>ag</u> /GGGGAC	
2c	CTGAAG/ <u>gt</u> aaga-(join ex18/19)-ttt <u>cactcag</u> /TTCCTA	
2d	CTGAAG/ <u>gt</u> aaga-(join ex18/20)-ctctt <u>tgca</u> g/CTCCTG	
2c	CCACAG/ <u>gt</u> gggt-(join ex19/21)-tcttccac <u>ag</u> /GGGGAC	
2d	GACTGG/ <u>gt</u> tagt-(join ex20/21)-tcttccac <u>ag</u> /GGGGAC	



<b>Mfsd4 mRNA</b>	<b>Donor site</b>	<b>Acceptor site</b>
4a/4b/4c	GGCTTG/ <u>g</u> taggt-	(join ex8/9) -tctctggc <u>a</u> g/ATCTTT
4d	GGCTTG/ <u>g</u> taggt-	(join ex8/9*)-ttttccac <u>a</u> g/GATACA
4a/4c	CATCAG/ <u>g</u> taaga-	(join ex9/11)-gtgtttac <u>a</u> g/GTGAAA
4b/4d	CATCAG/ <u>g</u> taaga-	(join ex9/10)-tcttttg <u>t</u> ag/TTCTTA
4a	CCTTCA/ <u>g</u> taagt-	(join ex11/12)-tcaatgcc <u>a</u> g/GGACGC
4c	CCTTCA/ <u>g</u> taagt-	(join ex11/13)-tcttctg <u>c</u> ag/GTCTGG

Supplemental Table S4.

sequence	nt	start	Elk4 mRNA	exon
TGGAGCCAAGACCTCTAGTCGCAA	24	133,845,321	735-758	3
TAGCAGAGAAGAAAGCCCAGG	21	133,845,452	866-886	3
TCGAGCCTGTCGCTGCTGCC	20	133,845,527	941-960	3
TGAGAGACCAAGGGACTAGGAAACA	25	133,851,215	1656-1680	5
TCAGGAGTGGGAGAAACCTTAGGCCG	25	133,851,776	2217-2240	5
TGAGCTCTGACATGACAGTTCCA	23	133,851,831	2272-2294	5
TGAGCTCTGACATGACAGTTCCACA	25	133,851,831	2272-2296	5
TGGTGTGTGCTTTGAGTGGTGTG	23	133,852,035	2476-2498	5
CTTGCAGTTAGCTGGAGATGCA	22	133,852,338	2779-2808	5
TGCTAATTCACAGTGAATCTTGAA	26	133,852,541	2982-3007	5
TAATGGGCTTGCTTCTCATGGTG	23	133,852,893	3334-3356	5
TTGGAATTTCCCTCAGCAGCACTT	24	133,852,939	3380-3403	5
TTAGCACAGAGCTGCCTTGGGTCC	24	133,853,130	3571-3594	5
TAGCACAGAGCTGCCTTGGGTC	22	133,853,131	3572-3593	5
TGGAAGCACGTGCTTGGTCTGTGGA	25	133,853,388	not proven	-
AACAGATACTCAGGGAGA	18	133,853,560	not proven	-
TGAGGCAAGGGAGGAGCAGCCTGTCAG	27	133,853,657	not proven	-
TTGGTCCCCTGTGGTGGGTCTGGA	24	133,853,834	not proven	-

Supplemental Table S5.