

Figure	Sample Size	Statistical test	Values
1B	<p>wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<p>trial: <math>F_{(3.512, 157.2)} = 8.760</math>, <math>P &lt; 0.0001</math>  genotype: <math>F_{(2, 45)} = 4.735</math>, <math>P = 0.0136</math>  trial <math>\times</math> genotype interaction: <math>F_{(8, 179)} = 0.8201</math>, <math>P = 0.5858</math></p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: <math>P = 0.1996</math>  Trial2: <math>P = 0.4601</math>  Trial3: <math>P = 0.8604</math>  Trial4: <math>P = 0.1793</math>  Trial5: <math>P = 0.2983</math></p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: <math>P = 0.0500</math>  Trial2: <math>P = 0.1476</math>  Trial3: <math>P = 0.2713</math>  Trial4: <math>P = 0.0609</math>  Trial5: <math>P = 0.2653</math></p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: <math>P = 0.9361</math>  Trial2: <math>P = 0.7916</math>  Trial3: <math>P = 0.0967</math>  Trial4: <math>P = 0.9844</math>  Trial5: <math>P = 0.9880</math></p>
1C	<p>wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<p>trial: <math>F_{(3.318, 148.5)} = 0.5512</math>, <math>P = 0.6658</math>  genotype: <math>F_{(2, 45)} = 6.569</math>, <math>P = 0.0031</math>  trial <math>\times</math> genotype interaction: <math>F_{(8, 179)} = 0.9465</math>, <math>P = 0.4797</math></p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: <math>P = 0.0226</math>  Trial2: <math>P = 0.0063</math>  Trial3: <math>P = 0.5086</math>  Trial4: <math>P = 0.7346</math>  Trial5: <math>P = 0.066</math></p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: <math>P = 0.2453</math>  Trial2: <math>P = 0.1319</math>  Trial3: <math>P = 0.2567</math>  Trial4: <math>P = 0.1472</math>  Trial5: <math>P = 0.598</math></p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: <math>P = 0.6477</math>  Trial2: <math>P = 0.3311</math>  Trial3: <math>P = 0.8572</math>  Trial4: <math>P = 0.5895</math></p>

			Trial5: P=0.4593
1D	<p>wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<p>trial: F<sub>(2.703, 121.0)</sub> = 3.131, P=0.0328 genotype: F<sub>(2, 45)</sub> = 13.24, P&lt;0.0001 trial × genotype interaction: F<sub>(8, 179)</sub> = 1.357, P=0.2183</p> <p>wild-type vs MNK1<sup>KO</sup> Trial1: P=0.357 Trial2: P=0.0155 Trial3: P=0.2736 Trial4: P=0.0188 Trial5: P=0.0886</p> <p>wild-type vs MNK2<sup>KO</sup> Trial1: P=0.0004 Trial2: P=0.0001 Trial3: P=0.0351 Trial4: P=0.3417 Trial5: P=0.0667</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup> Trial1: P=0.2773 Trial2: P=0.6374 Trial3: P=0.4472 Trial4: P=0.2077 Trial5: P=0.9735</p>
1E	<p>wild-type=17 MNK1<sup>KO</sup>=15 MNK2<sup>KO</sup>=17</p>	RM two-way ANOVA	<p>trials: F<sub>(3.882, 178.6)</sub> = 41.79, P&lt;0.0001 genotype: F<sub>(2, 46)</sub> = 1.825, P=0.1727 trials × genotype: F<sub>(22, 506)</sub> = 1.265, P=0.1887</p>
1F	<p>wild-type=17 MNK1<sup>KO</sup>=15 MNK2<sup>KO</sup>=17</p>	RM two-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>trial: F<sub>(2.514, 115.6)</sub> = 37.21, P&lt;0.0001 genotype: F<sub>(2, 46)</sub> = 10.58, P=0.0002 trial × genotype: F<sub>(8, 184)</sub> = 6.180, P&lt;0.0001</p> <p>wild-type vs MNK1<sup>KO</sup> Trial1: P=0.0037 Trial2: P=0.0155 Trial3: P=0.1663 Trial4: P=0.0127 Trial5: P=0.0005</p> <p>wild-type vs MNK2<sup>KO</sup> Trial1: P=0.8023 Trial2: P=0.8813 Trial3: P=0.7782</p>

			<p>Trial4: P=0.9338 Trial5: P=0.2891</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup> Trial1: P=0.0066 Trial2: P=0.0309 Trial3: P=0.3216 Trial4: P=0.0086 Trial5: P&lt;0.0001</p>
1G	wild-type=17 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =17	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	<p>K<sub>(3)</sub>=19.25, P&lt;0.0001</p> <p>wild-type vs MNK1<sup>KO</sup>: P=0.0073 wild-type vs MNK2<sup>KO</sup>: P=0.5720 MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P&lt;0.0001</p>
1H	wild-type=17 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =17	RM two-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>object: F<sub>(1, 46)</sub> = 20.08, P&lt;0.0001 genotype: F<sub>(2, 46)</sub> = 13.48, P&lt;0.0001 object × genotype: F<sub>(2, 46)</sub> = 4.183, P=0.0214</p> <p>familiar vs novel wild-type: P=0.0006 MNK1<sup>KO</sup>: P=0.9973 MNK2<sup>KO</sup>: P=0.0017</p>
1I	wild-type=17 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =17	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>F<sub>(2, 46)</sub> = 4.843, P=0.0123</p> <p>wild-type vs MNK1<sup>KO</sup>: P= 0.0407 wild-type vs MNK2<sup>KO</sup>: P= 0.9177 MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P= 0.0158</p>
1J	<p>wild-type=16 MNK1<sup>KO</sup>=15 MNK2<sup>KO</sup>=17</p> <p><i>Last three minutes are missing from one MNK1<sup>KO</sup> mouse</i></p>	Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<p>time: F<sub>(4.129, 183.0)</sub> = 20.74, P&lt;0.0001 genotype: F<sub>(2, 45)</sub> = 3.984, P=0.0255 time × genotype: F<sub>(18, 399)</sub> = 3.815, P&lt;0.0001</p> <p>wild-type vs MNK1<sup>KO</sup> Minute 1: P=0.0640 Minute 2: P=0.0006 Minute 3: P=0.0652 Minute 4: P=0.1525 Minute 5: P=0.0203 Minute 6: P=0.3122 Minute 7: P=0.7071 Minute 8: P=0.8076 Minute 9: P=0.6218 Minute 10: P=0.2908</p> <p>wild-type vs MNK2<sup>KO</sup> Minute 1: P=0.1390 Minute 2: P=0.4599</p>

			<p>Minute 3: P=0.2032  Minute 4: P=0.4710  Minute 5: P=0.0012  Minute 6: P=0.1773  Minute 7: P=0.9988  Minute 8: P=0.8445  Minute 9: P=0.6583  Minute 10: P=0.2778</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Minute 1: P=0.0003  Minute 2: P=0.0266  Minute 3: P=0.6507  Minute 4: P=0.5080  Minute 5: P=0.6591  Minute 6: P=0.8818  Minute 7: P=0.6743  Minute 8: P=0.3860  Minute 9: P=0.9824  Minute 10: P=0.9967</p>
1K	<p>wild-type=16  MNK1<sup>KO</sup>=15  MNK2<sup>KO</sup>=17</p> <p><i>Last three minutes are missing from one MNK1<sup>KO</sup> mouse</i></p>	Mixed-effects model	<p>time: F<sub>(5,368, 238.0)</sub> = 2.066, P=0.0655  genotype: F<sub>(2, 45)</sub> = 0.08049, P=0.9228  time × genotype interaction: F<sub>(18, 399)</sub> = 1.324, P=0.1684</p>
3B	<p>Mean log<sub>2</sub> value relative to wild-type from 4 mice per genotype.  Number of pairs: 9114 proteins / genotype</p>	Pearson r	<p>MNK1<sup>KO</sup> logFC vs MNK2<sup>KO</sup>  logFC: r = 0.5574 (95% confidence interval 0.5430 – 0.5713), P&lt;0.0001</p> <p>MNK1<sup>KO</sup> logFC vs MNK1/2<sup>DKO</sup>  logFC: r = 0.5186 (95% confidence interval 0.5034 – 0.5334), P&lt;0.0001</p> <p>MNK2<sup>KO</sup> logFC vs MNK1/2<sup>DKO</sup>  logFC: r = 0.4770 (95% confidence interval 0.4610 – 0.4927), P&lt;0.0001</p>
4A	<p>Mean log<sub>2</sub> value relative to wild-type from 4 mice per genotype.  Number of pairs: 9114 proteins / genotype</p>	Pearson r	<p>MNK1<sup>KO</sup> logFC vs MNK2<sup>KO</sup>  logFC: r = 0.05323 (95% confidence interval 0.03273 – 0.07368), P&lt;0.0001</p> <p>MNK1<sup>KO</sup> logFC vs MNK1/2<sup>DKO</sup>  logFC: r = 0.2309 (95% confidence interval 0.2114 – 0.2502), P&lt;0.0001</p> <p>MNK2<sup>KO</sup> logFC vs MNK1/2<sup>DKO</sup>  logFC: r = 0.6062 (95%</p>

			confidence interval 0.5930 – 0.6190), $P < 0.0001$
4E	Mean log <sub>2</sub> value relative to wild-type from 4 mice per genotype. Ribosomes: 73 All: 73 randomly selected proteins	Kolmogorov-Smirnov test	<p>MNK1<sup>KO</sup> CX: D= 0.3699, <math>P &lt; 0.0001</math></p> <p>MNK2<sup>KO</sup> CX: D= 0.3288, <math>P = 0.0007</math></p> <p>MNK1/2<sup>DKO</sup> CX: D= 0.4110, <math>P &lt; 0.0001</math></p> <p>MNK1<sup>KO</sup> SYP: D= 0.6849, <math>P &lt; 0.0001</math></p> <p>MNK2<sup>KO</sup> SYP: D= 0.3288, <math>P = 0.0007</math></p> <p>MNK1/2<sup>DKO</sup> SYP: D= 0.6164, <math>P &lt; 0.0001</math></p>
6B	wild-type=18 MNK1 <sup>KO</sup> =12 MNK2 <sup>KO</sup> =12	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	<p><math>K_{(3)} = 10.77</math>, <math>P = 0.0046</math></p> <p>wild-type vs MNK1<sup>KO</sup>: <math>P = 0.0142</math>  wild-type vs MNK2<sup>KO</sup>: <math>P = 0.0234</math>  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: <math>P &gt; 0.9999</math></p>
6D	wild-type=21 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =16	Kruskal-Wallis test	$K_{(3)} = 2.754$ , $P = 0.2523$
6F	wild-type=5 MNK1 <sup>KO</sup> =5 MNK2 <sup>KO</sup> =5 MNK1/2 <sup>DKO</sup> =4	Two-way ANOVA	<p>Subcellular region: <math>F_{(1, 30)} = 210.9</math>, <math>P &lt; 0.0001</math>  genotype: <math>F_{(3, 30)} = 0.4374</math>, <math>P = 0.7279</math>  Subcellular region <math>\times</math> genotype: <math>F_{(3, 30)} = 0.3395</math>, <math>P = 0.7969</math></p>
6H	wild-type=165 synapses (2 mice) MNK1 <sup>KO</sup> =178 synapses (3 mice) MNK2 <sup>KO</sup> =157 synapses (3 mice)	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	<p><math>K_{(3)} = 8.594</math>, <math>P = 0.0136</math></p> <p>wild-type vs MNK1<sup>KO</sup>: <math>P = 0.0699</math>  wild-type vs MNK2<sup>KO</sup>: <math>P = 0.0181</math>  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: <math>P &gt; 0.9999</math></p>
6I	wild-type=165 synapses (2 mice) MNK1 <sup>KO</sup> =178 synapses (3 mice)	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	<p><math>K_{(3)} = 46.83</math>, <math>P &lt; 0.0001</math></p> <p>wild-type vs MNK1<sup>KO</sup>: <math>P = 0.0202</math>  wild-type vs MNK2<sup>KO</sup>: <math>P &lt; 0.0001</math>  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: <math>P &lt; 0.0001</math></p>

	MNK2 <sup>KO</sup> =157 synapses (3 mice)		
6K	wild-type=14 MNK1 <sup>KO</sup> =14 MNK2 <sup>KO</sup> =16	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	$F_{(2, 41)} = 17.27$ , $P < 0.0001$  wild-type vs MNK1 <sup>KO</sup> : $P = 0.0026$ wild-type vs MNK2 <sup>KO</sup> : $P < 0.0001$ MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : $P = 0.0932$
6L	wild-type=14 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =15	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	$K_{(3)} = 22.14$ , $P < 0.0001$  wild-type vs MNK1 <sup>KO</sup> : $P < 0.0001$ wild-type vs MNK2 <sup>KO</sup> : $P = 0.0166$ MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : $P = 0.1545$
6M	Mean log <sub>2</sub> value relative to wild- type from 4 mice per genotype. Number of pairs: 10230 phosphosites / genotype	Pearson r	<i>cortex</i> : MNK1 <sup>KO</sup> logFC vs MNK2 <sup>KO</sup> logFC: $r = 0.4523$ (95% confidence interval 0.4368 – 0.4676), $P < 0.0001$  <i>synaptoneurosome</i> : MNK1 <sup>KO</sup> logFC vs MNK2 <sup>KO</sup> logFC: $r = 0.2254$ (95% confidence interval 0.2069 – 0.2437), $P < 0.0001$
<b>Supplementary Figures</b>	<b>Sample Size</b>	<b>Statistical test</b>	<b>Values</b>
S1B	wild-type=17 MNK1 <sup>KO</sup> =14 MNK2 <sup>KO</sup> =17	RM two-way ANOVA	trial: $F_{(4, 180)} = 85.86$ , $P < 0.0001$ genotype: $F_{(2, 45)} = 0.7987$ , $P = 0.4562$ trial $\times$ genotype: $F_{(8, 180)} = 1.933$ , $P = 0.0577$
S1C	wild-type=17 MNK1 <sup>KO</sup> =14 MNK2 <sup>KO</sup> =17	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	$F_{(2, 45)} = 6.565$ , $P = 0.0031$ wild-type vs MNK1 <sup>KO</sup> : $P = 0.0038$ wild-type vs MNK2 <sup>KO</sup> : $P = 0.8385$ MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : $P = 0.0164$
S1D	wild-type=17 MNK1 <sup>KO</sup> =14 MNK2 <sup>KO</sup> =17  <i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i>	<i>Nose to tail</i> Mixed-effects model          <i>Nose to body</i> Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<i>Nose to tail</i> trial: $F_{(2.676, 119.8)} = 30.94$ , $P < 0.0001$ genotype: $F_{(2, 45)} = 2.411$ , $P = 0.1012$ trial $\times$ genotype: $F_{(8, 179)} =$ $0.1849$ , $P = 0.9927$          <i>Nose to body</i> trial: $F_{(3.757, 168.1)} = 4.985$ , $P = 0.0010$

			<p>genotype: <math>F_{(2, 45)} = 4.599</math>,  <math>P=0.0152</math>  trial <math>\times</math> genotype: <math>F_{(8, 179)} = 0.8569</math>,  <math>P=0.5541</math></p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: <math>P= 0.0520</math>  Trial2: <math>P= 0.4134</math>  Trial3: <math>P= 0.9037</math>  Trial4: <math>P= 0.6319</math>  Trial5: <math>P= 0.3153</math></p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: <math>P= 0.0155</math>  Trial2: <math>P= 0.0752</math>  Trial3: <math>P= 0.4734</math>  Trial4: <math>P= 0.1237</math>  Trial5: <math>P= 0.0995</math></p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: <math>P= 0.9999</math>  Trial2: <math>P= 0.6942</math>  Trial3: <math>P= 0.3563</math>  Trial4: <math>P= 0.5535</math>  Trial5: <math>P= 0.9831</math></p> <p><i>Nose to nose</i>  Mixed-effects model</p> <p><i>Nose to nose</i>  trial: <math>F_{(2.235, 100.0)} = 5.231</math>,  <math>P=0.0052</math>  genotype: <math>F_{(2, 45)} = 1.827</math>,  <math>P=0.1726</math>  trial <math>\times</math> genotype: <math>F_{(8, 179)} = 1.186</math>,  <math>P=0.3099</math></p>
S1E	<p>wild-type=17  MNK1<sup>KO</sup>=14  MNK2<sup>KO</sup>=17</p> <p><i>Trial 5 is missing  from one MNK2<sup>KO</sup>  mouse</i></p>	<p><i>Side by side</i>  Mixed-effects model,  Tukey's post-hoc test for  multiple comparisons</p>	<p><i>Side by side</i>  trial: <math>F_{(2.492, 111.5)} = 3.214</math>,  <math>P=0.0336</math>  genotype: <math>F_{(2, 45)} = 3.387</math>,  <math>P=0.0426</math>  trial <math>\times</math> genotype: <math>F_{(8, 179)} = 0.7083</math>, <math>P=0.6840</math></p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: <math>P= 0.0714</math>  Trial2: <math>P= 0.0610</math>  Trial3: <math>P= 0.9046</math>  Trial4: <math>P= 0.7391</math>  Trial5: <math>P= 0.1718</math></p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: <math>P= 0.2334</math>  Trial2: <math>P= 0.4526</math></p>

		<p>Side by side reverse Mixed-effects model, Tukey's post-hoc test for multiple comparisons</p>	<p>Trial3: P= 0.5697 Trial4: P= 0.3383 Trial5: P= 0.9498</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup> Trial1: P= 0.7469 Trial2: P= 0.6209 Trial3: P= 0.7352 Trial4: P= 0.7417 Trial5: P= 0.2276</p> <p>Side by side reverse trial: F<sub>(3.672, 164.3)</sub> = 1.060, P=0.3753 genotype: F<sub>(2, 45)</sub> = 5.983, P=0.0050 trial × genotype: F<sub>(8, 179)</sub> = 0.5915, P=0.7841</p> <p>wild-type vs MNK1<sup>KO</sup> Trial1: P= 0.2486 Trial2: P= 0.0274 Trial3: P= 0.3846 Trial4: P= 0.9537 Trial5: P= 0.1072</p> <p>wild-type vs MNK2<sup>KO</sup> Trial1: P= 0.3977 Trial2: P= 0.1633 Trial3: P= 0.2106 Trial4: P= 0.4885 Trial5: P= 0.4039</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup> Trial1: P= 0.8071 Trial2: P= 0.3965 Trial3: P= 0.9997 Trial4: P= 0.7163 Trial5: P= 0.8183</p>
S1F	<p>wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	<p>Sniffing test Mixed-effects model, Tukey's post-hoc test for multiple comparisons</p>	<p>Sniffing test trial: F<sub>(2.962, 132.5)</sub> = 3.233, P=0.0250 genotype: F<sub>(2, 45)</sub> = 12.11, P&lt;0.0001 trial × genotype: F<sub>(8, 179)</sub> = 1.633, P= 0.1182</p> <p>wild-type vs MNK1<sup>KO</sup> Trial1: P= 0.5450 Trial2: P= 0.0354 Trial3: P= 0.3064 Trial4: P= 0.0154 Trial5: P= 0.2479</p>



			<p>wild-type vs MNK2<sup>KO</sup>  Trial1: P= 0.0001  Trial2: P= 0.0008  Trial3: P= 0.0182  Trial4: P= 0.2998  Trial5: P= 0.0304</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: P= 0.0472  Trial2: P= 0.3948  Trial3: P= 0.3763  Trial4: P= 0.1547  Trial5: P= 0.8933</p> <p><i>Climbing test</i>  Mixed-effects model,  Tukey's post-hoc test for  multiple comparisons</p> <p><i>Climbing test</i>  trial: F<sub>(3.078, 137.8)</sub> = 1.141,  P=0.3355  genotype: F<sub>(2, 45)</sub> = 5.391,  P=0.0080  trial × genotype: F<sub>(8, 179)</sub> =  0.5523, P= 0.8157</p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: P= 0.3453  Trial2: P= 0.1734  Trial3: P= 0.4833  Trial4: P= 0.2026  Trial5: P= 0.0955</p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: P= 0.0298  Trial2: P= 0.0693  Trial3: P= 0.2653  Trial4: P= 0.6798  Trial5: P= 0.7745</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: P= 0.9522  Trial2: P= 0.9916  Trial3: P= 0.8581  Trial4: P= 0.5523  Trial5: P= 0.3675</p>
		<p><i>Speed test</i>  Mixed-effects model,  Tukey's post-hoc test for  multiple comparisons</p>	<p><i>Speed test</i>  trial: F<sub>(3.629, 162.4)</sub> = 17.83,  P&lt;0.0001  genotype: F<sub>(2, 45)</sub> = 1.410,  P=0.2548  trial × genotype: F<sub>(8, 179)</sub> =  0.9646, P= 0.4652</p>

S1G	<p><i>Trial 1-4</i> wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17</p> <p><i>Trial 5</i> wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=16</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	<p><i>Nose to tail stimulus</i> <i>Trial 1-4</i> RM two-way ANOVA Tukey's post-hoc test for multiple comparisons</p> <p><i>Trial 5</i> Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons</p> <p><i>Nose to body stimulus</i> <i>Trial 1-4</i> RM two-way ANOVA Tukey's post-hoc test for multiple comparisons</p> <p><i>Trial 5</i> Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons</p>	<p><i>Nose to tail stimulus</i> trial: <math>F_{(2.405, 108.2)} = 9.880</math>, <math>P &lt; 0.0001</math> genotype: <math>F_{(2, 45)} = 0.1016</math>, <math>P = 0.9036</math> trial <math>\times</math> genotype: <math>F_{(6, 135)} = 0.2036</math>, <math>P = 0.9752</math></p> <p><i>Trial 5</i> <math>K_{(3)} = 1.752</math>, <math>P = 0.4164</math></p> <p><i>Nose to body stimulus</i> trial: <math>F_{(1.831, 82.39)} = 1.237</math>, <math>P = 0.2933</math> genotype: <math>F_{(2, 45)} = 1.049</math>, <math>P = 0.3587</math> trial <math>\times</math> genotype: <math>F_{(6, 135)} = 0.7871</math>, <math>P = 0.5815</math></p> <p><i>Trial 5</i> <math>K_{(3)} = 1.133</math>, <math>P = 0.5676</math></p>
S1H	<p><i>Trial 1-4</i> wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=17 <i>Trial 5</i> wild-type=17 MNK1<sup>KO</sup>=14 MNK2<sup>KO</sup>=16</p> <p><i>Trial 5 is missing from one MNK2<sup>KO</sup> mouse</i></p>	<p><i>Sniffing stimulus</i> <i>Trial 1-4</i> RM two-way ANOVA Tukey's post-hoc test for multiple comparisons</p> <p><i>Trial 5</i> Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons</p>	<p><i>Sniffing stimulus</i> trial: <math>F_{(2.726, 122.7)} = 0.8485</math>, <math>P = 0.4608</math> genotype: <math>F_{(2, 45)} = 4.349</math>, <math>P = 0.0188</math> trial <math>\times</math> genotype: <math>F_{(6, 135)} = 1.347</math>, <math>P = 0.2405</math></p> <p>wild-type vs MNK1<sup>KO</sup> Trial1: <math>P = 0.2406</math> Trial2: <math>P = 0.0848</math> Trial3: <math>P = 0.8704</math> Trial4: <math>P = 0.5397</math></p> <p>wild-type vs MNK2<sup>KO</sup> Trial1: <math>P = 0.0840</math> Trial2: <math>P = 0.0009</math> Trial3: <math>P = 0.1845</math> Trial4: <math>P = 0.7983</math></p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup> Trial1: <math>P = 0.8235</math> Trial2: <math>P = 0.5235</math> Trial3: <math>P = 0.4831</math> Trial4: <math>P = 0.8956</math></p> <p><i>Trial 5</i> <math>K_{(3)} = 7.106</math>, <math>P = 0.0286</math> wild-type vs MNK1<sup>KO</sup>: <math>P = 0.1021</math></p>

		<p><i>Climbing stimulus</i>  <i>Trial 1-4</i>  RM two-way ANOVA  Tukey's post-hoc test for multiple comparisons</p> <p><i>Trial 5</i>  Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons</p>	<p>wild-type vs MNK2<sup>KO</sup>: P= 0.0465  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P &gt;0.9999</p> <p><i>Climbing stimulus</i>  trial: F<sub>(2,199, 98.94)</sub> = 13.31, P&lt;0.0001  genotype: F<sub>(2, 45)</sub> = 9.062, P=0.0005  trial × genotype: F<sub>(6, 135)</sub> = 1.747, P=0.1149</p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: P= 0.0098  Trial2: P= 0.0122  Trial3: P= 0.0029  Trial4: P= 0.3759</p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: P= 0.1692  Trial2: P= 0.1393  Trial3: P= 0.0425  Trial4: P&gt;0.9999</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: P= 0.6840  Trial2: P= 0.2173  Trial3: P= 0.5598  Trial4: P= 0.2081</p> <p><i>Trial 5</i>  K<sub>(3)</sub>= 8.680, P= 0.0130  wild-type vs MNK1<sup>KO</sup>: P= 0.0100  wild-type vs MNK2<sup>KO</sup>: P= 0.7436  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P = 0.2177</p>
		<p><i>Speed stimulus</i>  <i>Trial 1-4</i>  RM two-way ANOVA  Tukey's post-hoc test for multiple comparisons</p> <p><i>Trial 5</i>  Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons</p>	<p><i>Speed stimulus</i>  trial: F<sub>(2,267, 102.0)</sub> = 48.06, P&lt;0.0001  genotype: F<sub>(2, 45)</sub> = 3.162, P=0.0519  trial × genotype: F<sub>(6, 135)</sub> = 3.638, P=0.0022</p> <p>wild-type vs MNK1<sup>KO</sup>  Trial1: P= 0.0014  Trial2: P= 0.0247  Trial3: P= 0.0725  Trial4: P= 0.7854</p> <p>wild-type vs MNK2<sup>KO</sup>  Trial1: P= 0.9622  Trial2: P= 0.9987  Trial3: P= 0.6026</p>

			<p>Trial4: P= 0.8590</p> <p>MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>  Trial1: P= 0.0272  Trial2: P= 0.0407  Trial3: P= 0.4160  Trial4: P= 0.9713</p> <p><i>Trial 5</i>  K<sub>(3)</sub>= 6.324, P= 0.0423  wild-type vs MNK1<sup>KO</sup>: P= 0.1265  wild-type vs MNK2<sup>KO</sup>: P&gt;0.9999  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P = 0.0570</p>
S1I	wild-type=17 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =17	RM two-way ANOVA	<p>trial: F<sub>(3.039, 136.8)</sub> = 67.06,  P&lt;0.0001  genotype: F<sub>(2, 45)</sub> = 0.8909,  P=0.4174  trial × genotype: F<sub>(8, 180)</sub> = 1.699,  P=0.1013</p>
S1J	wild-type=17 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =17	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>F<sub>(2, 45)</sub> = 6.475, P=0.0034  wild-type vs MNK1<sup>KO</sup>: P= 0.0423  wild-type vs MNK2<sup>KO</sup>: P= 0.5220  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P = 0.0027</p>
S2A-B	<i>females:</i> wild-type=10 MNK1 <sup>KO</sup> =8 MNK2 <sup>KO</sup> =12  <i>males:</i> wild-type=7 MNK1 <sup>KO</sup> =6 MNK2 <sup>KO</sup> =5	Three-way Repeated Measures ANOVA	<p>Genotype: F<sub>(2, 42)</sub>=0.28, P=0.760  Sex: F<sub>(1, 42)</sub>=1.19, P=0.2820  genotype x Sex F<sub>(2, 42)</sub>=1.63,  P=0.2080  trials: F<sub>(3.35, 140.79)</sub>=81.16,  P&lt;0.0001  genotype x trials:  F<sub>(6.7, 140.79)</sub>=1.887, P=0.0820  Sex x trials<sub>(3.35, 140.79)</sub>: F=0.86,  P=0.4720  Sex x trials x genotype<sub>(6.7, 140.79)</sub>:  F=0.67, P=0.6880</p>
S2C	<i>females:</i> wild-type=10 MNK1 <sup>KO</sup> =8 MNK2 <sup>KO</sup> =12  <i>males:</i> wild-type=7 MNK1 <sup>KO</sup> =6 MNK2 <sup>KO</sup> =5	Two-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>Interaction: F<sub>(2, 42)</sub> = 0.2222,  P=0.8017  Sex: F<sub>(1, 42)</sub> = 0.2822, P=0.5980  Genotype: F<sub>(2, 42)</sub> = 6.141,  P=0.0046</p> <p>wild-type vs MNK1<sup>KO</sup>: P= 0.0060  wild-type vs MNK2<sup>KO</sup>: P= 0.9260  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P = 0.0209</p>
S2D-E	<i>females:</i> wild-type=10 MNK1 <sup>KO</sup> =8	Three-way Repeated Measures ANOVA	<p>Genotype: F<sub>(2, 43)</sub> =2.48,  P=0.0950  Sex: F<sub>(1, 43)</sub> =2.23, P=0.1430</p>

	<p>MNK2<sup>KO</sup>=12</p> <p><i>males:</i> wild-type=7 MNK1<sup>KO</sup>=7 MNK2<sup>KO</sup>=5</p>		<p>genotype x sex: <math>F_{(2, 42)} = 2.06</math>, <math>P = 0.139</math>  trials: <math>F_{(3.87, 166.45)} = 42.84</math>, <math>P &lt; 0.0001</math>  genotype x trials: <math>F_{(7.74, 166.45)} = 1.47</math>, <math>P = 0.175</math>  Sex x trials: <math>F_{(3.87, 166.45)} = 0.58</math>, <math>P = 0.669</math>  Sex x trials x genotype: <math>F_{(7.74, 166.45)} = 1.62</math>, <math>P = 0.125</math></p>
S2F-G	<p><i>females:</i> wild-type=10 MNK1<sup>KO</sup>=8 MNK2<sup>KO</sup>=12</p> <p><i>males:</i> wild-type=7 MNK1<sup>KO</sup>=7 MNK2<sup>KO</sup>=5</p>	Three-way Repeated Measures ANOVA	<p>Genotype: <math>F_{(2, 43)} = 9.80</math>, <math>P &lt; 0.0001</math>  Sex: <math>F_{(1, 43)} = 0.54</math>, <math>P = 0.465</math>  genotype x sex: <math>F_{(2, 43)} = 1.74</math>, <math>P = 0.188</math>  trials: <math>F_{(2.43, 104.6)} = 34.96</math>, <math>P &lt; 0.0001</math>  genotype x trials: <math>F_{(4.86, 104.6)} = 5.89</math>, <math>P &lt; 0.0001</math>  Sex x trials: <math>F_{(2.43, 104.6)} = 0.83</math>, <math>P = 0.461</math>  Sex x trials x genotype: <math>F_{(4.86, 104.6)} = 0.61</math>, <math>P = 0.689</math></p>
S2H	<p><i>females:</i> wild-type=10 MNK1<sup>KO</sup>=8 MNK2<sup>KO</sup>=12</p> <p><i>males:</i> wild-type=7 MNK1<sup>KO</sup>=7 MNK2<sup>KO</sup>=5</p>	Two-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>Interaction: <math>F_{(2, 43)} = 0.9540</math>, <math>P = 0.3932</math>  Sex: <math>F_{(1, 43)} = 0.6882</math>, <math>P = 0.4114</math>  Genotype: <math>F_{(2, 43)} = 14.51</math>, <math>P &lt; 0.0001</math></p> <p>Wild-type vs MNK1<sup>KO</sup> : <math>P = 0.0221</math>  Wild-type vs MNK2<sup>KO</sup>: <math>P = 0.0211</math>  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: <math>P &lt; 0.0001</math></p>
S2I	<p><i>females:</i> wild-type=10 MNK1<sup>KO</sup>=8 MNK2<sup>KO</sup>=12</p> <p><i>males:</i> wild-type=7 MNK1<sup>KO</sup>=7 MNK2<sup>KO</sup>=5</p>	Three-way Repeated Measures ANOVA, Bonferroni's post-hoc test for multiple comparisons	<p>Genotype: <math>F_{(2, 43)} = 11.66</math>, <math>P &lt; 0.0001</math>  Sex: <math>F_{(1, 43)} = 0.51</math>, <math>P = 0.479</math>  Novelty: <math>F_{(1, 43)} = 21.05</math>, <math>P &lt; 0.0001</math>  genotype x sex: <math>F_{(2, 43)} = 3.23</math>, <math>P = 0.049</math>  genotype x novelty: <math>F_{(2, 43)} = 4.62</math>, <math>P = 0.015</math>  Sex x novelty: <math>F_{(1, 43)} = 0.70</math>, <math>P = 0.409</math>  Sex x novelty x genotype: <math>F_{(2, 43)} = 0.52</math>, <math>P = 0.596</math></p> <p><u>Post-hoc: Novelty x genotype</u>  <u>Familiar vs novel object</u>  Wild-type: <math>P = 0.004</math>  MNK1<sup>KO</sup>: <math>P = 0.772</math></p>

			<p>MNK2<sup>KO</sup>: P=0.003</p> <p><u>Post-hoc: Novelty x sex</u></p> <p><i>female</i></p> <p>Wild-type vs MNK1<sup>KO</sup>: P=0.0056  Wild-type vs MNK2<sup>KO</sup>: P=0.056  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P&lt;0.0001</p> <p><i>male</i></p> <p>Wild-type vs MNK1<sup>KO</sup>: P=0.158  Wild-type vs MNK2<sup>KO</sup>: P&gt;0.9999  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P=0.687</p> <p><u>Post-hoc: Novelty x sex</u></p> <p><i>Female vs male</i></p> <p>Wild-type: P=0.38  MNK1<sup>KO</sup>: P=0.017  MNK2<sup>KO</sup>: P=0.115</p>
S2J	<p>females:  wild-type=10  MNK1<sup>KO</sup>=8  MNK2<sup>KO</sup>=12</p> <p>males:  wild-type=7  MNK1<sup>KO</sup>=7  MNK2<sup>KO</sup>=5</p>	Two-way ANOVA, Tukey's post-hoc test for multiple comparisons	<p>Interaction: F<sub>(2, 43)</sub> = 0.8828, P=0.4210  Sex: F<sub>(1, 43)</sub> = 1.423, P=0.2394  Genotype: F<sub>(2, 43)</sub> = 5.574, P=0.0070</p> <p>Wild-type vs MNK1<sup>KO</sup>: P=0.0497  Wild-type vs MNK2<sup>KO</sup>: P=0.6531  MNK1<sup>KO</sup> vs MNK2<sup>KO</sup>: P=0.0071</p>
S2K	<p>females:  wild-type=10  MNK1<sup>KO</sup>=6  MNK2<sup>KO</sup>=12</p> <p>males:  wild-type=6  MNK1<sup>KO</sup>=7  MNK2<sup>KO</sup>=5</p>	Two-way ANOVA	<p>Interaction: F<sub>(2, 40)</sub> = 2.049, P=0.1422  Sex: F<sub>(1, 40)</sub> = 0.01534, P=0.9020  Genotype: F<sub>(2, 40)</sub> = 2.453, P=0.0989</p>
S2L	<p>females:  wild-type=10  MNK1<sup>KO</sup>=6  MNK2<sup>KO</sup>=12</p> <p>males:  wild-type=6  MNK1<sup>KO</sup>=7  MNK2<sup>KO</sup>=5</p>	Two-way ANOVA	<p>Interaction: F<sub>(2, 40)</sub> = 0.1024, P=0.9029  Sex: F<sub>(1, 40)</sub> = 2.415, P=0.1281  Genotype: F<sub>(2, 40)</sub> = 0.1471, P=0.8637</p>
S3A	<p>wild-type= 13  MNK1/2<sup>DKO</sup>=15</p>	Two-way Repeated Measures ANOVA	<p>Genotype x trial: F<sub>(4, 104)</sub> = 0.2954, P=0.8804  Trial: F<sub>(2.730, 70.97)</sub> = 27.66, P&lt;0.0001</p>

			Genotype: $F_{(1, 26)} = 0.2456$ , $P=0.6243$
S3B	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	Unpaired t-test	$t=0.1726$ , $df=26$ $P=0.8635$
S3C	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Two-way Repeated Measures ANOVA	Genotype x trial: $F_{(11, 297)} = 0.3062$ , $P=0.9843$ Trial: $F_{(3.989, 107.7)} = 19.90$ , $P<0.0001$ Genotype: $F_{(1, 27)} = 0.6022$ , $P=0.4445$
S3D	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Two-way Repeated Measures ANOVA	Genotype x trial: $F_{(4, 108)} = 0.9991$ , $P=0.4114$ Trial: $F_{(2.182, 58.92)} = 21.69$ , $P<0.0001$ Genotype: $F_{(1, 27)} = 0.8417$ , $P=0.3670$
S3E	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Unpaired t-test	$t=0.09051$ , $df=27$ $P=0.9286$
S3F	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Two-way Repeated Measures ANOVA, Šídák's post-hoc test for multiple comparisons	Genotype x trial: $F_{(1, 27)} = 0.2934$ , $P=0.5925$ Trial: $F_{(1, 27)} = 27.39$ , $P<0.0001$ Genotype: $F_{(1, 27)} = 0.1725$ , $P=0.6812$  Familiar vs novel object: wild-type: $P=0.0078$ MNK1/2 <sup>DKO</sup> : $P=0.0004$
S3G	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Mann-Whitney test	$U=104$ $P>0.9999$
S3H	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Two-way Repeated Measures ANOVA, Tukey's post-hoc test for multiple comparisons	Genotype x time: $F_{(9, 243)} = 1.131$ , $P=0.3416$ Time: $F_{(4.908, 132.5)} = 6.144$ , $P<0.0001$ Genotype: $F_{(1, 27)} = 18.34$ , $P=0.0002$  wild-type vs MNK1/2 <sup>DKO</sup> Minute 1: $P=0.0035$ Minute 2: $P=0.0104$ Minute 3: $P=0.0437$ Minute 4: $P=0.0335$ Minute 5: $P=0.0343$ Minute 6: $P=0.0404$ Minute 7: $P=0.1042$ Minute 8: $P=0.4245$ Minute 9: $P=0.3170$ Minute 10: $P=0.1799$
S3I	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Two-way Repeated Measures ANOVA	Genotype x time: $F_{(9, 243)} = 0.4459$ , $P=0.9089$

			Time: $F_{(4.466, 120.6)} = 2.781$ , $P=0.0250$ Genotype: $F_{(1, 27)} = 0.2810$ , $P=0.6004$
S3J	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	Two-way Repeated Measures ANOVA	<i>Nose to tail:</i> Genotype x trial: $F_{(4, 104)} = 2.360$ , $P=0.0581$ Trial: $F_{(2.535, 65.91)} = 19.31$ , $P<0.0001$ Genotype: $F_{(1, 26)} = 0.8639$ , $P=0.3612$  <i>Nose to body:</i> Genotype x trial: $F_{(4, 104)} = 0.7983$ , $P=0.5290$ Trial: $F_{(3.376, 87.78)} = 3.135$ , $P=0.0247$ Genotype: $F_{(1, 26)} = 0.9439$ , $P=0.3402$  <i>Nose to nose:</i> Genotype x trial: $F_{(4, 104)} = 0.8784$ , $P=0.4796$ Trial: $F_{(2.175, 56.56)} = 0.6077$ , $P=0.5615$ Genotype: $F_{(1, 26)} = 0.01554$ , $P=0.9018$
S3K	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	Two-way Repeated Measures ANOVA	<i>Side by side:</i> Genotype x trial: $F_{(4, 104)} = 0.3384$ , $P=0.8515$ Trial: $F_{(2.790, 72.53)} = 3.958$ , $P=0.0131$ Genotype: $F_{(1, 26)} = 0.002354$ , $P=0.9617$  <i>Side by side reverse:</i> Genotype x trial: $F_{(4, 104)} = 0.3721$ , $P=0.8281$ Trial: $F_{(3.338, 86.79)} = 4.022$ , $P=0.0077$ Genotype: $F_{(1, 26)} = 0.05315$ , $P=0.8195$
S3L	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	Two-way Repeated Measures ANOVA, Tukey's post-hoc test for multiple comparisons	<i>Sniffing test:</i> Genotype x trial: $F_{(4, 104)} = 0.7951$ , $P=0.5310$ Trial: $F_{(2.426, 63.09)} = 0.8449$ , $P=0.4537$ Genotype: $F_{(1, 26)} = 3.936$ , $P=0.0579$



			<p><i>Climbing test:</i>  Genotype x trial: <math>F_{(4, 104)} = 0.7891</math>, <math>P=0.5348</math>  Trial: <math>F_{(2.636, 68.55)} = 0.3906</math>, <math>P=0.7345</math>  Genotype: <math>F_{(1, 26)} = 5.317</math>, <math>P=0.0293</math></p> <p>wild-type vs MNK1/2<sup>DKO</sup>  Trial 1: <math>P=0.8295</math>  Trial 2: <math>P=0.3322</math>  Trial 3: <math>P=0.2598</math>  Trial 4: <math>P=0.0716</math>  Trial 5: <math>P=0.0336</math></p> <p><i>Speed:</i>  Genotype x trial: <math>F_{(4, 104)} = 0.7477</math>, <math>P=0.5617</math>  Trial: <math>F_{(3.310, 86.06)} = 7.521</math>, <math>P&lt;0.0001</math>  Genotype: <math>F_{(1, 26)} = 0.3190</math>, <math>P=0.5770</math></p>
S3M	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	<p><i>Trial 1-4</i>  RM two-way ANOVA  Tukey's post-hoc test for multiple comparisons  <i>Trial 5</i>  Mann Whitney test</p>	<p><i>Nose to tail stimulus:</i>  <i>Trial 1-4</i>  Genotype x trial: <math>F_{(3, 78)} = 1.480</math>, <math>P=0.2264</math>  Trial: <math>F_{(2.643, 68.71)} = 8.680</math>, <math>P=0.0001</math>  Genotype: <math>F_{(1, 26)} = 0.4082</math>, <math>P=0.5285</math></p> <p><i>Trial 5</i>  <math>U=58.50</math>, <math>P=0.0731</math></p> <p><i>Nose to body stimulus:</i>  <i>Trial 1-4</i>  Genotype x trial: <math>F_{(3, 78)} = 2.327</math>, <math>P=0.0811</math>  Trial: <math>F_{(2.684, 69.78)} = 1.908</math>, <math>P=0.1424</math>  Genotype: <math>F_{(1, 26)} = 0.6106</math>, <math>P=0.4416</math></p> <p><i>Trial 5</i>  <math>U=96</math>, <math>P=0.9639</math></p>
S3N	wild-type= 13 MNK1/2 <sup>DKO</sup> =15	<p><i>Sniffing stimulus:</i>  <i>Trial 1-4</i>  RM two-way ANOVA  Tukey's post-hoc test for multiple comparisons</p>	<p><i>Sniffing stimulus:</i>  <i>Trial 1-4</i>  Genotype x trial: <math>F_{(3, 78)} = 0.4744</math>, <math>P=0.7010</math>  Trial: <math>F_{(2.283, 59.36)} = 0.3091</math>,</p>

		<p><i>Trial 5</i> Unpaired t-test</p> <p><i>Climbing stimulus:</i> <i>Trial 1-4</i> RM two-way ANOVA Tukey's post-hoc test for multiple comparisons <i>Trial 5</i> Unpaired t-test</p> <p><i>Speed stimulus:</i> <i>Trial 1-4</i> RM two-way ANOVA Tukey's post-hoc test for multiple comparisons <i>Trial 5</i> Unpaired t-test</p>	<p>P=0.7635 Genotype: F<sub>(1, 26)</sub> = 1.249, P=0.2739</p> <p><i>Trial 5</i> t=0.2977, df=26, P=0.7683</p> <p><i>Climbing stimulus:</i> <i>Trial 1-4</i> Genotype x trial: F<sub>(3, 78)</sub> = 0.2593, P=0.8545 Trial: F<sub>(2.485, 64.62)</sub> = 3.488, P=0.0275 Genotype: F<sub>(1, 26)</sub> = 1.224, P=0.2786</p> <p><i>Trial 5</i> t=1.495, df=26, P=0.1469</p> <p><i>Speed stimulus:</i> <i>Trial 1-4</i> Genotype x trial: F<sub>(3, 78)</sub> = 0.06861, P=0.9765 Trial: F<sub>(2.731, 71.02)</sub> = 15.05, P&lt;0.0001 Genotype: F<sub>(1, 26)</sub> = 3.580, P=0.0697</p> <p><i>Trial 5</i> U=69, P=0.2005</p>
S3O	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Mixed-effects model, Tukey's post-hoc test for multiple comparisons	<p>Genotype x trial: F<sub>(4, 107)</sub> = 0.6498, P= 0.6282 Trial: F<sub>(2.370, 63.41)</sub> = 4.601, P=0.0097 Genotype: F<sub>(1, 27)</sub> = 14.24, P= 0.0008</p> <p>wild-type vs MNK1/2<sup>DKO</sup> Trial 1: P=0.0032 Trial 2: P=0.1093 Trial 3: P&lt;0.0001 Trial 4: P=0.0943 Trial 5: P=0.1019</p>
S3P	wild-type= 13 MNK1/2 <sup>DKO</sup> =16	Mann Whitney test	U=79, P=0.2875
S5B	Mean log <sub>2</sub> value of ETC-168 treated wild-type relative to vehicle-treated wild-type from 4	Kolmogorov-Smirnov test	WT ETC-168: D= 0.3506, P=0.0002

	mice per treatment. Ribosomes: 77 All: 77 randomly selected proteins		
S5B	Ribosomal proteins: 30 All: 680	Wilcoxon-Mann-Whitney U test	$W = 6762$ , $P = 0.001379$
S6C	Mean $\log_2$ value relative to wild-type from 3 mice per genotype. Number of pairs: 18141 RNAs / genotype	Pearson r	$\text{MNK1}^{\text{KO}}$ logFC vs $\text{MNK2}^{\text{KO}}$ logFC: $r = 0.2649$ (95% confidence interval 0.2513 – 0.2784), $P < 0.0001$
S6D	logFC value of $\text{MNK1}^{\text{KO}}$ relative to wild-type from 3 (mRNA) or 4 (protein) mice per genotype. Number of pairs: 8294 genes/proteins	Pearson r	$\text{MNK1}^{\text{KO}}$ logFC protein vs $\text{MNK1}^{\text{KO}}$ logFC RNA: $r = -0.02401$ (95% confidence interval: -0.04551 to -0.002487), $P = 0.0288$
S6E	logFC value of $\text{MNK2}^{\text{KO}}$ relative to wild-type from 3 (mRNA) or 4 (protein) mice per genotype. Number of pairs: 8294 genes/proteins	Pearson r	$\text{MNK2}^{\text{KO}}$ logFC protein vs $\text{MNK2}^{\text{KO}}$ logFC RNA: $r = 0.09438$ (95% confidence interval: 0.07301 to 0.1157), $P < 0.0001$
S6H	wild-type= 18 $\text{MNK1}^{\text{KO}}$ =18 $\text{MNK2}^{\text{KO}}$ =18 $\text{MNK1/2}^{\text{DKO}}$ =18  N= mean fluorescent intensity of neurons per image. 5-7 images were analysed per animal, with 3 animals per genotype.	Kruskal-Wallis test	$K_{(4)} = 3.024$ , $P = 0.3880$
S6I	wild-type= 8 $\text{MNK1}^{\text{KO}}$ =7 $\text{MNK2}^{\text{KO}}$ =11 $\text{MNK1/2}^{\text{DKO}}$ =5	Kruskal-Wallis test	$K_{(4)} = 1.930$ , $P = 0.5870$

S6J	wild-type= 10 MNK1 <sup>KO</sup> =7 MNK2 <sup>KO</sup> =8 MNK1/2 <sup>DKO</sup> =7	Kruskal-Wallis test	K <sub>(4)</sub> = 2.694, P=0.4412
S7C	wild-type=6 MNK1 <sup>KO</sup> =7 MNK2 <sup>KO</sup> =7	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	K <sub>(3)</sub> =12.46, P=0.0002 wild-type vs MNK1 <sup>KO</sup> : P=0.0200 wild-type vs MNK2 <sup>KO</sup> : P=0.0023 MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : P>0.9999
S7D	wild-type=6 MNK1 <sup>KO</sup> =7 MNK2 <sup>KO</sup> =7	Kruskal-Wallis test, Dunn's post-hoc test for multiple comparisons	K <sub>(3)</sub> =15.43, P<0.0001 wild-type vs MNK1 <sup>KO</sup> : P=0.0003 wild-type vs MNK2 <sup>KO</sup> : P=0.0950 MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : P=0.1920
S7E	wild-type=14 MNK1 <sup>KO</sup> =14 MNK2 <sup>KO</sup> =16 MNK1/2 <sup>DKO</sup> =8	One-way ANOVA	F <sub>F (3, 48)</sub> = 2.378, P=0.0814
S7F	wild-type=14 MNK1 <sup>KO</sup> =15 MNK2 <sup>KO</sup> =15 MNK1/2 <sup>DKO</sup> =8	One-way ANOVA	F <sub>(3, 48)</sub> = 1.523, P=0.2204
S7G	wild-type=8 MNK1 <sup>KO</sup> =6 MNK2 <sup>KO</sup> =9 MNK1/2 <sup>DKO</sup> =9	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	F <sub>(3, 28)</sub> = 4.855, P=0.0076  wild-type vs MNK1 <sup>KO</sup> : P= 0.0038 wild-type vs MNK2 <sup>KO</sup> : P= 0.3164 wild-type vs MNK1/2 <sup>DKO</sup> : P= 0.1924 MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : P= 0.1274 MNK1 <sup>KO</sup> vs MNK1/2 <sup>DKO</sup> : P= 0.2121 MNK2 <sup>KO</sup> vs MNK1/2 <sup>DKO</sup> : P= 0.9893
S7H	wild-type=9 MNK1 <sup>KO</sup> =9 MNK2 <sup>KO</sup> =11 MNK1/2 <sup>DKO</sup> =7	One-way ANOVA, Tukey's post-hoc test for multiple comparisons	F <sub>(3, 32)</sub> = 7.421, P=0.0007  wild-type vs MNK1 <sup>KO</sup> : P= 0.0054 wild-type vs MNK2 <sup>KO</sup> : P= 0.0022 wild-type vs MNK1/2 <sup>DKO</sup> : P= 0.8317 MNK1 <sup>KO</sup> vs MNK2 <sup>KO</sup> : P= 0.9985 MNK1 <sup>KO</sup> vs MNK1/2 <sup>DKO</sup> : P= 0.0738 MNK2 <sup>KO</sup> vs MNK1/2 <sup>DKO</sup> : P= 0.0417
S7I	wild-type=8 MNK1 <sup>KO</sup> =8 MNK2 <sup>KO</sup> =9	One-way ANOVA	F <sub>(2, 22)</sub> = 0.9563, P=0.3997
S7J	wild-type=9 MNK1 <sup>KO</sup> =9	One-way ANOVA	F <sub>(3, 31)</sub> = 0.7150, P=0.5505

	MNK2 <sup>KO</sup> =10 MNK1/2 <sup>DKO</sup> =7		
S7K	wild-type=6 MNK1 <sup>KO</sup> =7 MNK2 <sup>KO</sup> =7 MNK1/2 <sup>DKO</sup> =4	One-way ANOVA	$F_{(3, 20)} = 1.050$ , $P=0.3922$
S7L	wild-type=14 MNK2 <sup>KO</sup> =16	Mann-Whitney test	Mann-Whitney U = 52, $P=0.0118$
S7M	wild-type=8 MNK2 <sup>KO</sup> =9	Mann-Whitney test	Mann-Whitney U = 19, $P=0.1139$