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| Table S6. SIFT-or-PolyPhen2 deleterious\* singleton inheritance |
| Gene | Number paternal | Number maternal | One-tailed binomial p-value |
| *CNTN1* | 6 | 3 | 0.2539 |
| *CNTN2* | 4 | 6 | 0.3770 |
| *CNTN3* | 2 | 1 | 0.5 |
| *CNTN4* | 5 | 2 | 0.2266 |
| *CNTN5* | 4 | 5 | 0.5 |
| *CNTN6* | 4 | 6 | 0.3770 |
| *CNTNAP1* | 5 | 4 | 0.5 |
| *CNTNAP2* | 4 | 9 | 0.1334 |
| *CNTNAP4* | 4 | 7 | 0.2668 |
| *CNTNAP5* | 3 | 3 | 0.5 |

\*Deleterious mutations were defined as “damaging” in SIFT and/or “possibly damaging” or “probably damaging” in PolyPhen2, as well as all nonsense and splice site mutations which were not evaluated by these programs but were regarded as deleterious intrinsically