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| Table S2. All Rare Variants Seen, Including In Both Cases And Controls\* |
| Gene | Number in cases (n=1030) | Number in controls (n=942) | OR | OR 95% CI lower | OR 95% CI upper | One-tailed Fisher exact p-value |
| *CNTN1* | 15 | 6 | 2.305 | 0.836 | 6.673 | 0.059 |
| *CNTN2* | 62 | 52 | 1.096 | 0.738 | 1.63 | 0.353 |
| *CNTN3* | 50 | 53 | 0.856 | 0.565 | 1.296 | 0.252 |
| *CNTN4* | 28 | 23 | 1.117 | 0.618 | 2.022 | 0.404 |
| *CNTN5* | 44 | 50 | 0.796 | 0.515 | 1.23 | 0.165 |
| *CNTN6* | 23 | 27 | 0.774 | 0.425 | 1.406 | 0.226 |
| *CNTNAP1* | 17 | 11 | 1.42 | 0.627 | 3.255 | 0.238 |
| *CNTNAP2* | 38 | 39 | 0.887 | 0.549 | 1.432 | 0.344 |
| *CNTNAP4* | 39 | 25 | 1.444 | 0.843 | 2.479 | 0.098 |
| *CNTNAP5* | 33 | 35 | 0.858 | 0.515 | 1.429 | 0.309 |

\*Because our focus was rare variants unique to cases or controls, variants predicted to be in both were only subject to PCR confirmation until the point that the variant was confirmed in at least one case and at least one control, at which point no further PCR of additional instances of that variant was done. Therefore, though our confirmation rate was very high, it was not 100%, and the above numbers do involve some unconfirmed variant predictions and should be regarded as close approximations rather than exact.