



Figure S1. Diagram Showing ClustalW Alignment of Top BlastP Hits to *CNTNAP2*

Unique variants identified in the case (dark blue) and control groups (black) are highlighted. Amino acids marked with gray are identical to human sequence. Those marked in light blue fall into the same broad physico-chemical group. Red indicates that the amino acid was the same as the change caused by the rare variant. An asterisk (*) identifies residues or nucleotides that are identical in all sequences in the

alignment. A colon (:) designates conserved substitutions. A period (.) denotes semiconserved substitutions. *Homo sapiens*, NP_054860.1; *Pan troglodytes*, XP_519462.2; *Macaca mulatta*, XP_001094652.1 ; *Pongo pygmaeus*, Q5RD64; *Mus musculus*, NP_001004357.1; *Monodelphis domestica*, XP_001368218.1 ; *Ornithorhynchus anatinus*, XP_001505555.1; *Xenopus tropicalis*, NP_001072732.1; *Danio rerio*, XP_691801.2; *Tetraodon nigroviridis*, CAG11627.1.