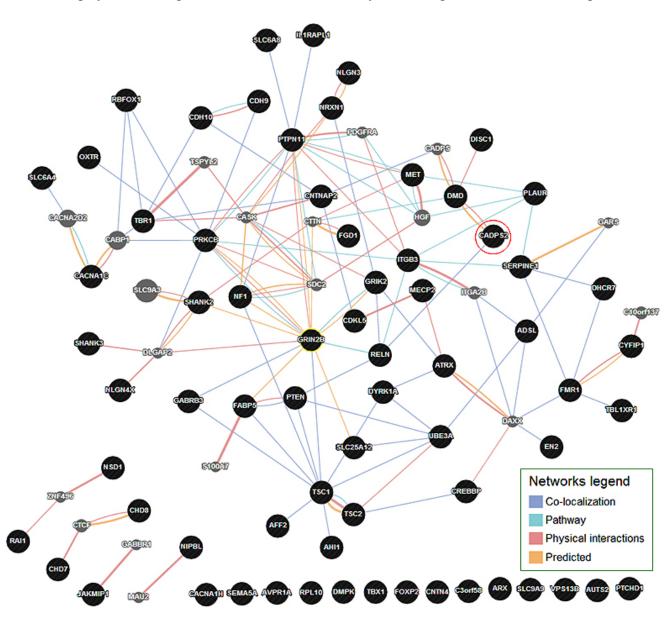
Mouse Models of Mutations and Variations in Autism Spectrum Disorder-Associated Genes: Mice Expressing Caps2/Cadps2 Copy Number and Alternative Splicing Variants

Figure S1. A predicted ASD-associated gene network. The network was predicted by the basic network weighting method of GeneMANIA [1] using information on co-localization, pathways, physical interactions and predicted relationships [2]. CADPS2 is highlighted by a red circle. ASD-associated genes are indicated by large black circles. Genes indicated by small gray circles are genes relevant to or functionally interacting with ASD-associated genes.



Reference

- 1. GeneMANIA. Availabel online: http://www.genemania.org (accessed on 15 November 2013).
- 2. Warde-Farley, D.; Donaldson, S.L.; Comes, O.; Zuberi, K.; Badrawi, R.; Chao, P.; Franz, M.; Grouios, C.; Kazi, F.; Lopes, C.T.; *et al.* The GeneMANIA prediction server: Biological network integration for gene prioritization and predicting gene function. *Nucl. Acid. Res.* **2010**, *38*, doi:10.1093/nar/gkq537.
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