Supplementary information S3 | miRNA dysregulation and altered gene expression in 22q11.2 animal models. Hemizygosity of the *Dgcr8* gene and *mir-185* gene (both located within the 1.5-Mb 22q11.2 deletion and the equivalent mouse deficiency) results in reduction in the levels of a subset of mature miRNAs (*red, blue*) in both PFC and HPC in *Del(Dgcr2-Hira)2Aam* mice. The combined effect on the levels of *mir-185* is predicted to be stronger than other miRNAs (indicated by a thicker arrow). Partial reduction in miRNA levels can have an effect on transcript or protein levels of target genes. Moreover, since target mRNAs can be simultaneously and synergistically bound and repressed by more than one miRNA, the level of repression achieved may be highly sensitive to the amount of available miRNA complexes and the number of affected miRNAs.

Target genes may be upregulated due to reduction of miRNAs affected by the *Dgcr8* deficiency (*bottom left*), due to reduction of miRNA genes removed by the 22q11.2 microdeletion (*mir-185* within the 1.5-MB minimal region is shown as an example here, *bottom right*), or due to a combination of both (*bottom middle*). miRNA dysregulation is one of the molecular pathways affected in 22q11.2DS, results in a number of phenotypic alterations and is predicted to change the levels of several downstream target transcripts and proteins.