

# Supplementary of “Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways”

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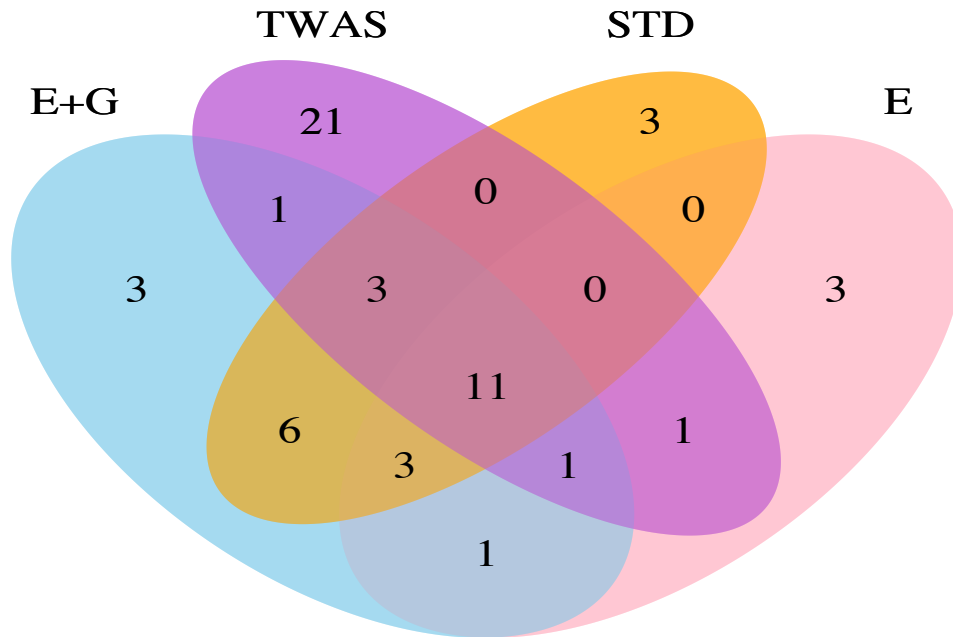


Figure 1: Venn diagram of the significant genes identified by the different methods applied to the 5,203 common genes in the SCZ1 data . “E+G” and “E” combine the results (take the union) of MCF7 and Hippo, while TWAS combine the results of YFS, NTR, METSIM, and CMC-based weights.

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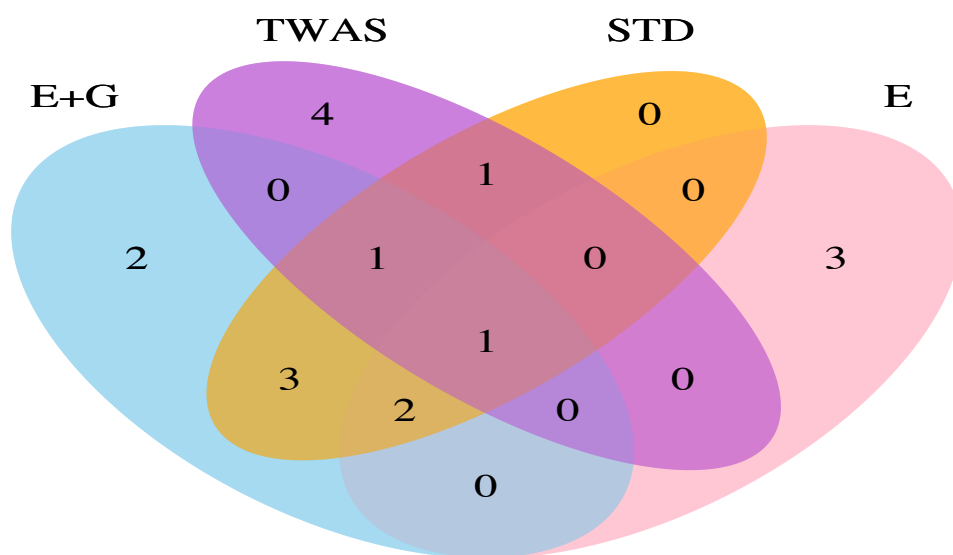


Figure 2: Venn diagram of the significant and novel genes identified by the different methods applied to the 2226 common genes in the SCZ1 data . “E+G” and “E” stand for the results of MCF7 data, while TWAS stands for the results of CMC-based weights.