

Appendix 1 to Hayes JP, Logue MW, Reagan A, et al. COMT Val158Met polymorphism moderates the association between PTSD symptom severity and hippocampal volume. *J Psychiatry Neurosci* 2017.

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Supplementary Methods

Genotype data cleaning was performed using PLINK (Purcell et al., 2007). Heterozygosity of X-chromosome genotypes was concordant with self-reported sex for all genotyped subjects. Only self reported non-Hispanic white subjects were analyzed. Concordance between self-reported ancestry and genotype data was investigated using principal components (PC) analysis of 100,000 common SNPs using the EIGENSTRAT (Price et al., 2006) analysis program. First, PC analysis of the TRACTS subjects was performed together with 1,000 Genomes (Consortium, 2012) reference data for the EUR, AFR, ASN, and AMR samples. Of the 218 self-reported non-Hispanic subjects in TRACTS, 4 were more than 6 SD away from the non-Hispanic white group mean on the generated PC and were removed from the dataset, leaving 214 non-Hispanic white subjects for analysis. Next, PC were calculated for use as analysis covariates in the potential confounder analysis for the 214 remaining subjects. None of these 214 subjects were outliers (>6SD) in the PC analysis. A further 58 subjects were not included because they did not have available hippocampal volume data. Seven subjects were removed because of self-reported moderate or severe traumatic brain injury. Two participants were removed who did not agree to sharing data for the study, and an additional subject was removed who did not have available CAPS data. After these exclusions, the final sample was 146.

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