

**Publication****Common epigenetic variation in a European population of mentally healthy young adults****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 3671814**Author(s)** Milnik, Annette; Vogler, Christian; Demougin, Philippe; Egli, Tobias; Freytag, Virginie; Hartmann, Francina; Heck, Angela; Peter, Fabian; Spalek, Klara; Stetak, Attila; de Quervain, Dominique J.-F.; Papassotiropoulos, Andreas; Vukojevic, Vanja**Author(s) at UniBasel** [Milnik, Annette](#) ; [Vogler, Christian](#) ; [Demougin, Philippe](#) ; [Egli, Tobias](#) ; [Freytag, Virginie](#) ; [Hartmann, Francina](#) ; [Heck, Angela](#) ; [Peter, Fabian](#) ; [Stetak, Attila](#) ; [Papassotiropoulos, Andreas](#) ; [Vukojevic, Vanja](#) ; [de Quervain, Dominique](#) ;**Year** 2016**Title** Common epigenetic variation in a European population of mentally healthy young adults**Journal** Journal of Psychiatric Research**Volume** 83**Pages / Article-Number** 260-268

DNA methylation represents an important link between structural genetic variation and complex phenotypes. The study of genome-wide CpG methylation and its relation to traits relevant to psychiatry has become increasingly important. Here, we analyzed quality metrics of 394,043 CpG sites in two samples of 568 and 319 mentally healthy young adults. For 25% of all CpGs we observed medium to large common epigenetic variation. These CpGs were overrepresented in open sea and shore regions, as well as in intergenic regions. They also showed a strong enrichment of significant hits in association analyses. Furthermore, a significant proportion of common DNA methylation is at least partially genetically driven and thus may be observed similarly across tissues. These findings could be of particular relevance for studies of complex neuropsychiatric traits, which often rely on proxy tissues.

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