Application number/Title: 11559 - Enhancing Neuro Imaging Genetics through Meta Analysis

Applicant PI: Associate Professor Sarah Medland

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Quantitative Genetics

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Keywords provided by the Applicant PI to describe the research project:

Brain, Depression, Aging, Dementia,

Application Lay Summary:

1a: The ENIGMA Network brings together researchers in imaging genomics, to understand brain structure, function, and disease, based on brain imaging and genetic data.

ENIGMA is an international effort, we seek to identify genetic, age and disease driven variation in brain structure and function.

By combining imaging data through meta-analysis we can achieve the large samples necessary to have sufficient power to detect small effects.

1b: Our research seeks to identify how brain structure and function is influenced by genetics, aging and disease.

A major focus of our research is the identification of genetic markers which may aid in the prevention, diagnosis and treatment of mental health conditions such as depression and age related diseases including dementia.

We will use cross-sectional self-report data and the data contained in the Episodes and Diagnoses variables to ascertain these conditions.

1c: We will use several methods including:

• Genomewide association studies (GWAS) that aim to identify individual genetic variants associated with a particular outcome.

• GCTA and LDscore analyses to estimate the genetic correlations between traits. To allow these analyses we request access to the data from the full cohort.

• Polygenic risk score analyses that aim to predict brain traits or diseases based on large numbers of genetic variables.

• Regression analyses to identify the effects of age on the brain.

• T-tests and ANOVAs to identify differences between individuals with a condition or trait, such as depression, and those without.

1d: We will typically use all available observations in the UK Biobank that have measures of the phenotype(s) under investigation. For genetic analyses we will typically restrict the data to the subset of participants that are of European descent and have been successfully genotyped.