

**Supplementary Material to Johansson et al. “*Genetic predisposition to mosaic chromosomal loss is associated with functional outcome after ischemic stroke*” (Neurology: Genetics MS ID#: NG/2021/017066)**

**Supplemental Methods**

The Genetics of Ischemic Stroke Functional Outcome (GISCOME) network was initiated with the aim to identify genetic factors with influence on ischemic stroke outcome. The present study was based on data from the first GISCOME GWAS on stroke outcome<sup>1</sup>. Cases were recruited retrospectively from 12 centers in Europe, USA and Australia. Inclusion criteria were ischemic stroke cases over 18 years of age with GWAS genotype data, data on initial stroke severity and functional outcome assessed by the modified Rankin Scale (mRS) 60-190 days after index stroke (the majority of the included studies ( $\approx 80\%$ ) assessed mRS at 3 months  $\pm$  2 weeks). This resulted in a study population of 6165 cases of mainly European ancestry. Genotyping at the different sites, quality control and imputation was performed as described<sup>1, 2</sup>. In brief, quality control was performed in several cohorts before inclusion and complementary quality control steps were performed for all cohorts at entry into the study. Imputation to the 1000 Genomes Phase 3 reference panel was performed for all cohorts individually. Further, five principal components were calculated for each cohort.

1. Soderholm M, Pedersen A, Lorentzen E, et al. Genome-wide association meta-analysis of functional outcome after ischemic stroke. *Neurology* 2019;92:e1271-e1283.
2. Maguire JM, Bevan S, Stanne TM, et al. GISCOME – Genetics of Ischaemic Stroke Functional Outcome network: A protocol for an international multicentre genetic association study. *European Stroke Journal* 2017;2:229-237.