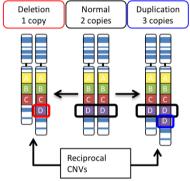
# The ENIGMA-CNV working group, 2<sup>nd</sup> wave

Copy number variant:

-high risk disease (son

-high risk, disease (somatic+psychiatric)



**Challenges:** 

**Genetics:** Low frequency, different SNP arrays

Imaging: Different scanner sites

#### **Aim**

identify CNVs with influence on brain structures



brain development & pathologies

osakasydneymas
ahus epigendublin
Sys lifespan big echodefindemgene hubin ship top
pafip gqtim haavik nesda
gobs imagenhunt
16p112europeanconsortium
neng ping ntr
betulastrokemi
1000brains
1000brains
1000brains

#### 1<sup>st</sup> wave (-2020)

~17,000 individuals (37 ENIGMA samples) supplemented with UK biobank **4 publications:** Brain structural effects of  $\underline{16p11.2 \text{ distal}}$  (*Mol Psych*),  $\underline{1q21.1 \text{ distal}}$  (*Trans Psych*) and  $\underline{15q11.2}$  (*JAMA Psych*) CNVs + 1  $\underline{\text{review}}$  (*HBM*, with ENIGMA-22q11)

# 2<sup>nd</sup> wave launch (2022-)

-Targeting a wider range of CNVs & broader range of brain measures

## Requirements

-item-level CNVs (genetic data), imaging data (starting with FreeSurfer-derived), covariates, both population+disease groups welcome MEGA-ANALYSIS



Protocols: <a href="https://github.com/ENIGMA-git/ENIGMA-CNV">https://github.com/ENIGMA-git/ENIGMA-CNV</a>

Help available for analysts. Data sharing agreements if necessary

### To join:

Contact ENIGMA-CNV chairs:

Ida E. Sønderby (<u>i.e.sonderby@medisin.uio.no</u>)
Ole A. Andreassen (<u>ole.andreassen@medisin.uio.no</u>)

Helpdesk (enigmacnvhelpdesk@gmail.com)

