meba

# The Zyg001 data product

Original number of biological samples*	618
Number of samples (per 08.01.2024)	614
Number of unique participants	614
Biological sample type	DNA (cord blood)
Participant type(s)	MoBa children
Collection timepoint	Birth
Selection criteria	Twins
Variable type(s)	Zygosity
Original reference article	Not available
Analytical method(s)	MassARRAY
Related MoBaBIO product(s)	None
FHI Project number(s)	PDB1316

\*In addition to analysis results for biological samples from same-sex MoBa twins (N=614), this data product also contains zygosity results from questionnaire data from 1,116 same-sex MoBa twins. In addition, information for 1,438 opposite-sex MoBa twins are included. The entire dataset thus comprises zygosity data for a total of 3,168 individual participants (1,584 twin pairs).



# Zyg001

# The project that generated these data

#### **Zygosity of MoBa Twins**

#### Project lead: Eivind Ystrøm

The purpose of this study was to make the Norwegian Mother, Father and Child Cohort Study (MoBa) data resource more attractive for family studies by making information on zygosity available for same-sex twins who were born and are included in MoBa. Characterizing zygosity makes it possible to address important research questions that need to take familial and genetic effects into account across psychic and somatic health.

# Study population

The original Zyg001 data source is based on **3,194 child participants** (1,597 pairs of twins) that were live-born and are currently part of MoBa. The Zyg001 data product provides information on zygosity derived from genotyping results on biological samples from 309 pairs of same-sex twins (for a total of 618 genotyped child participants), questionnaire data from 1,120 same-sex twins (560 twin pairs) as well as zygosity information for 1,456 opposite-sex twins (728 twin pairs).

## Available measures (variable names in bold)

The Zyg001 data source provides two variables with information relevant to zygosity:

c\_zyg: Zygosity
c\_zyg\_method: Method used to determine zygosity

#### Value interpretation index

#### Zygosity:

1: monozygotic
 2: dizygotic same sex
 3: dizygotic opposite sex

#### Method used to determine zygosity:

geno: genotyping quest: self-reported questionnaire NA: not applicable (neither method was required for characterizing opposite-sex dizygotic twins)



# Biological sampling and processing

Cord blood samples were drawn at the time of delivery or, in cases where cord blood was unavailable, a capillary sample was taken from the newborn child simultaneous to phenylketonuria (PKU) screening (approximately 3–4 days after birth). Cord blood samples were collected in two 7-ml ethylenediaminetetraacetic acid (EDTA) tubes. These were shipped from the collecting hospital overnight to MoBa's biobank at the Norwegian Institute of Public Health (NIPH). The samples usually arrived at the biobank within 1–2 days of blood donation, where whole blood was aliquoted into two polypropylene deep-well plates (930 µl in each, ABgene, Surrey, UK).

DNA extraction was performed manually using a FlexiGene DNA extraction kit (Qiagen, Hilden, Germany), and DNA content was quality controlled using a spectrophotometer (Spectramax 190, Molecular Devices, Sunnyvale, CA). DNA is stored at –20 °C at NIPH's biobank.

For more information on biological sampling, processing and storage, please refer to the original reference articles for NIPH's biobank by <u>Rønningen *et al.* 2006</u> and <u>Paltiel *et al.*</u> 2014.

## Analytical methodology

The genotyping methodology used in this study is based on a panel of 47 extensively validated SNPs, and zygosity is calculated as the likelihood of being monozygotic (identical) versus dizygotic (fraternal) given the genotyping data. Genotyping was performed on the **MassARRAY Platform from Agena** (www.agenabio.com).

For more information related to the validation of this SNP panel and/or determination of zygosity please refer to the original reference article for this method by <u>Hannelius *et al.*</u>.

# Published articles using Zyg001

This section also includes articles related to study design, sampling, and data collection.

Not available.

## **Restrictions for use**

None currently known.

## Acknowledgements recommended for use

We recommend that any use of these data in analyses that are presented in peer-review publications acknowledges the original article describing sampling and data collection:



None currently available.

## Disclaimer

The data in Zyg001 that are available for use are provided by MoBa on an *as is* basis as they were received from the generating laboratory and have not been curated or quality controlled prior to release. FHI does not provide any guarantees related to data quality and assurance of the original dataset. We reserve the right to periodically remove samples from the dataset belonging to participants who have retracted their consent to participate in this cohort study, and may alter the contents of the associated documentation accordingly.