

The Tel002 data product

Original number of samples	530
Number of samples (per 23.09.2026)	530
Number of unique participants	530
Biological sample type	DNA (whole blood)
Participant type(s)	MoBa children
Collection timepoint	Birth
Selection criteria	
Biomarker type(s)	Human terminal restriction fragments TRF1 and TRF2
Original reference article	Not yet available
Analytical method(s)	Southern Blot
Related MoBaBIO product(s)	
FHI Project number(s)	PDB3060

The project that generated these data

Revisiting and dissecting the maternal effect on childhood asthma

Project lead: Per Magnus

Asthma is a common disease in children. Currently, there are no measures to prevent the development of asthma. Our goal is to better understand the underlying biology of asthma, with the aim of offering improved preventive measures. The main purpose of this study is to investigate an unresolved mystery: children are more likely to develop asthma if the mother has the disease than if the father does. Identifying the reason for this could reveal a new mechanism underlying the development of the disease. The study aims to examine several hypotheses. One of these is to explore the potential effects of variation in the ends of chromosomes (telomeres), given that telomere length is more strongly inherited from the mother than from the father. The study will also examine postnatal environmental effects, based on the assumption that influences from the mother and father differ.

Study population

The Tel002 telomere data source is based on DNA samples from **530** MoBa children. 500 of these were randomly selected cord blood samples of children who fulfilled the following criteria:

- The mother has filled in Q7 and responded that the child has asthma, that it is confirmed by a physician, and that the child has had symptoms during the last year
- There is a completely genotyped trio (mother, father, child)
- A record in the medical birth registry of Norway (MBR) is available
- The mother has filled in questionnaire Q1
- The child is a singleton

The remaining **30** samples were randomly selected from samples that have been analyzed in the same laboratory earlier as part of another MoBa project, PDB2170

Available biomarker measures (variable names in bold)

- Terminal restriction fragment 1 (**TRF1**)
- Terminal restriction fragment 2 (**TRF2**)
- Mean Terminal restriction fragment length (**Mean_TRF**)
- Percent Coefficient of Variation (**CV_perc**)

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).

Whole blood samples were collected from mothers and fathers at 17–18 weeks of gestation, or after birth. 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 [Rønningen et al. 2006](#) and [Paltiel et al. 2014](#)

Analytical methodology

Terminal restriction fragment (TRF) length analysis of TRF1 and TRF2 was performed using **Southern blot**. For more information, refer to the original methodology reference article by [Kimura et al. 2010](#)

Measurement units:

Kilobase (kb)

Published articles using Tel002

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

❖ Not yet 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:

Not yet available

Disclaimer

The data in Tel002 that are available for use are provided on an *as is* basis, and FHI does not provide any guarantees related to data quality and assurance of the original dataset. MoBa participants can retract their consent to participate in the MoBa study at any time, and results generated using biological samples will be removed from MoBa datasets accordingly. The descriptive information regarding sample sizes and data content in this product sheet is correct and up-to-date as of **23.09.2026**.