The Gtp001 data product

Original number of samples	3,000
Number of samples (per 07.03.2024)	2,897
Number of unique participants	2,897
Biological sample type	DNA
Participant type(s)	MoBa mothers
Collection timepoint	Gestational week ~17
Case-control selection criteria	None
Biomarker type(s)	SNPs related to one-carbon, folate or homocysteine metabolism
Original reference article	Not available
Analytical method(s)	MALDI-TOF Mass Spectrometry
Related MoBaBIO product(s)	Mab001, Mab004
FHI Project number(s)	PDB168

The project that generated these data

Pregnancy, one-carbon metabolism and related single nucleotide polymorphisms (SNPs)

Project lead: Stein Emil Vollset

The purpose of this study was to measure B-vitamins, B-vitamin markers, and related one-carbon metabolites in pregnancy, and study the potential associations and effects of these on adverse prenatal and postnatal health conditions and outcomes.

Study population

The original Gtp001 biomarker data source is based on DNA samples from **3,000 mothers** whose babies were born between July 2002 and December 2003. The mothers were selected at random, but inclusion required that mothers had donated a blood sample at the second trimester routine ultrasound appointment, were registered in the Medical Birth Registry of Norway (MBRN) and had completed and returned a baseline questionnaire and a Food Frequency Questionnaire (FFQ) administered during the second trimester.

Available biomarker measures (variable names in bold)

CBS_844I: 68 bp insertion in the coding region of exon 8
CBS_C699: C→T mutation at position 699
MTHFR_C6: C→T mutation at position 677
MTHFR_A1: A→C mutation at position 1298
MTR_A275: A→G mutation at position 2756
MTRR_A66: A→G mutation at position 66
MTRR_C52: C→T mutation at position 524
BHMT_G74: G→A mutation at position 742
TCII_C77: C→G mutation at position 776
TCII_A67: A→G mutation at position 67
RFC1_G80: G→A mutation at position 80
FOLR1_G1: G→A mutation at position 1314
MTHFD1_G: G→A mutation at position 1958
MTHFD1_R: T→C mutation at position –105 in the promoter region
CTH_G136: G→T mutation at position 1364
SHMT_C14: C→T mutation at position 1420
DHFR_19D: functional polymorphic 19-bp deletion within intron-1
NOS7_T78: T→C mutation at position −786 in the promoter region
NOS8_G89: G→T mutation at position 894
TYMS_DEL: 6-bp deletion in the 3'-untranslated region

Target loci abbreviations

Betaine-homocysteine methyltransferase (BHMT)
Cystathionase (Cystathionine gamma-Lyase) (CTH)
Cystathionine ß-synthase (CBS)
Dihydrofolate reductase (DHFR)
Folate receptor alpha (FOLR1)
Methionine synthase (MTR)
Methionine synthase reductase (MTRR)
Methylenetetrahydrofolate reductase (MTHFR)
Methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1 (MTHFD1)
Nitric oxide synthase 3 (NOS)
Serine hydroxymethyltransferase 1 (SHMT)
Solute carrier family 19 member 1 (SLC19A1) (also commonly referred to as Reduced folate carrier-1 (RFC1) in the literature)
Thymidylate synthase (TYMS)
Transcobalamin 2 (TCII)

Biological sampling and processing

Whole blood samples were collected from mothers at 17–18 weeks of gestation. 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

SNP data in Gtp001 were collected using high-level multiplex genotyping method based on **matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS)** for the detection of 20 polymorphisms in 14 genes with known associations and functional consequences for one-carbon, folate or homocysteine metabolism.

For more information related to the methodology used in this study, please refer to the original reference articles Meyer *et al*. 2004 and Meyer *et al*. 2009.

Value interpretation index:

For all mutations, except for CBS_844I:

0: wild type
1: heterozygous
2: homozygous

CBS_844I requires semiquantitative determination of the genotype:

< 0.25: wild type
0.25 < 0.8: heterozygous
≥ 0.8: homozygous

Published articles using Gtp001

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

- None currently known

Restrictions for use

None currently known.

Acknowledgements recommended for use

There is currently no original reference article available describing sampling and data collection for SNP data generated under Gtp001. We therefore recommend that any use of these data in analyses that are presented in peer-review publications acknowledges the original articles describing sampling and data collection for Mab001 and Mab004:

Nilsen RM, Vollset SE, Monsen AL, Ulvik A, Haugen M, Meltzer HM, Magnus P, Ueland PM. Infant birth size is not associated with maternal intake and status of folate during the second trimester in Norwegian pregnant women. J Nutr. 2010 Mar;140(3):572-9.

Disclaimer

The data in Gtp001 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.