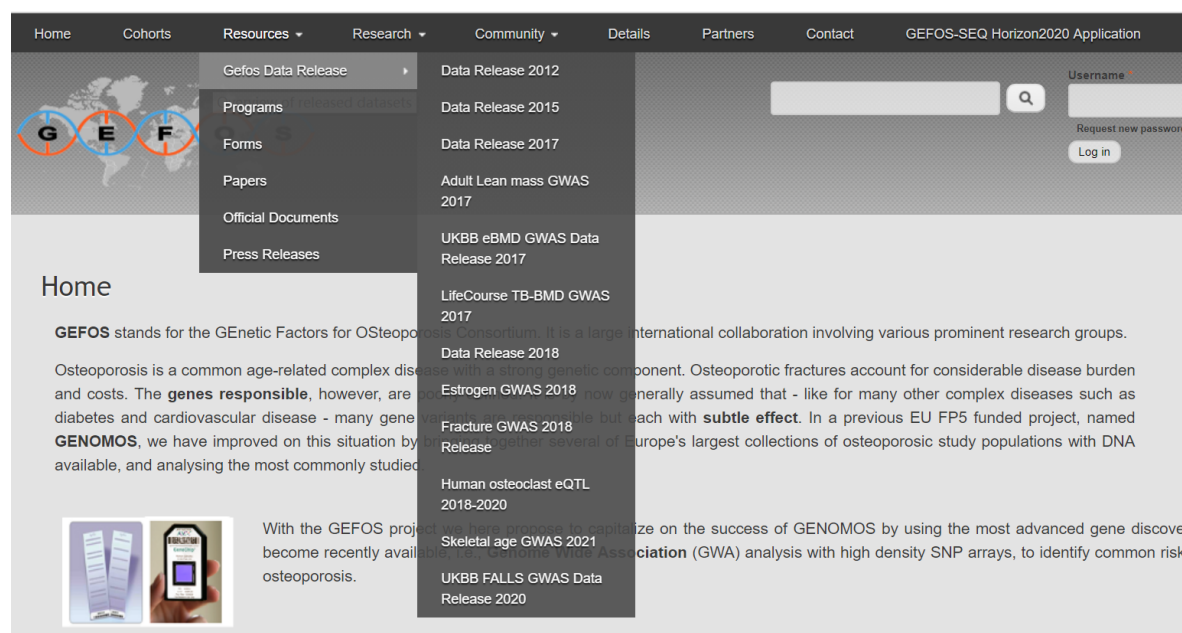


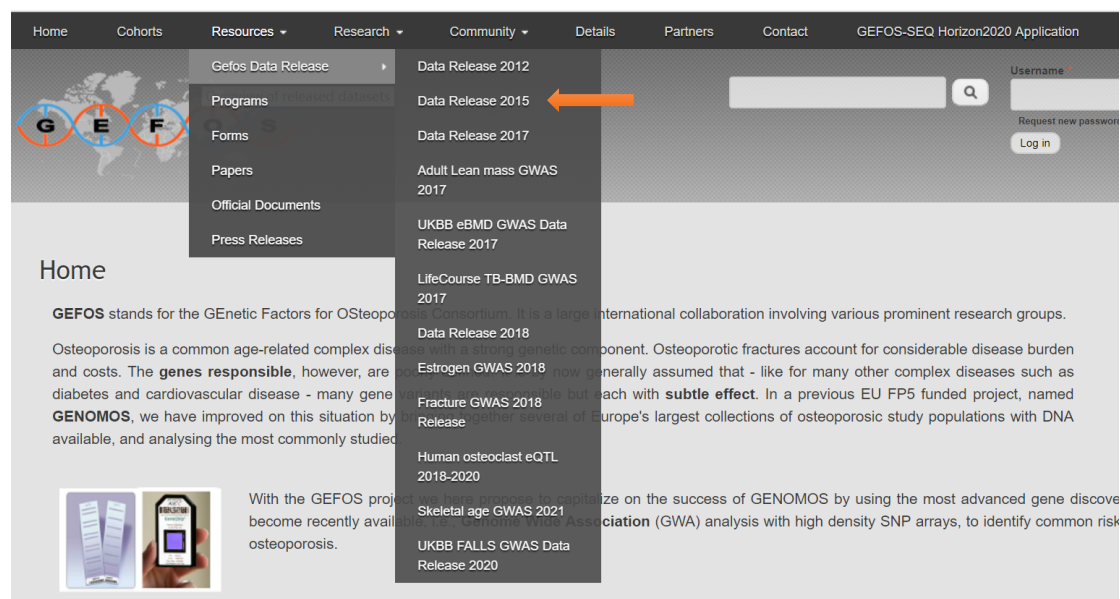
Detail procedures to download the GWAS summary data of all outcomes:

1 Click "<http://www.gefos.org/>"

2 Then, click "Resources"---"Gefos Data Release"



3 For GWAS summary data of forearm BMD, femoral neck BMD and lumbar spine BMD, please click "Data release 2015".



4 Then, click "fa2stu.MAF0\_.005.pos\_.out\_.gz",

"fn2stu.MAF0\_.005.pos\_.out\_.gz",

"ls2stu.MAF0\_.005.pos\_.out\_.gz"

at the bottom of webpage to down the GWAS summary data of forearm BMD, femoral neck BMD and lumbar spine BMD, separately.

beta Overall beta value for meta-analysis

se standard error

beta\_95L Lower 95% CI for BETA

beta\_95U Upper 95% CL for BETA

z Z-score

p-value Meta-analysis p-value

log10\_p-value Absolute value of logarithm of meta-analysis p-value to the base of 10

q\_statistic Cochran's heterogeneity statistic

q\_p-value Cochran's heterogeneity statistic's p-value

i2 Heterogeneity index I2 by Higgins et al 2003

n\_studies Number of studies with marker present

n\_samples Number of samples with marker present (will be NA if marker is present in any input file where N column is not present)

effects Summary of effect directions ('+' - positive effect of reference allele, '-' - negative effect of reference allele, '0' - no effect (or non-significant) effect of reference allele, '?' - missing data)

For further information on this format please refer to GWAMA by visiting <http://www.well.ox.ac.uk/gwama/>

Publications

Zheng HF, et al. Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature 2015.

Terms of Use

The UK10K, AOGC and GEFOS-seq Consortia require appropriate attribution for use of data in a product, service, or publication by citing the article generating this set of results (Zheng et al, Nature 2015) and acknowledging its use.

Download

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Files:

- README.txt
- fa2stu.MAF0\_005\_pos\_out.gz
- fn2stu.MAF0\_005\_pos\_out.gz
- ls2stu.MAF0\_005\_pos\_out.gz

5 For GWAS summary data of fall, please click “UKBB FALLS GWAS Data Release 2020”.

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GEFOS

Home

GEFOS stands for the GEneTic Factors for Osteoporosis Consortium. It is a large international collaboration involving various prominent research groups. Osteoporosis is a common age-related complex disease with a strong genetic component. Osteoporotic fractures account for considerable disease burden and costs. The genes responsible, however, are still largely unknown. It is now generally assumed that - like for many other complex diseases such as diabetes and cardiovascular disease - many genes are involved, but each with subtle effect. In a previous EU FP5 funded project, named GENOMOS, we have improved on this situation by bringing together several of Europe's largest collections of osteoporotic study populations with DNA microarrays, and analysing the most commonly studied SNPs.

With the GEFOS project we here propose to capitalize on the success of GENOMOS by using the most advanced gene discovery technology available, the Genome Wide Association (GWA) analysis with high density SNP arrays, to identify common risk variants for osteoporosis.

Resources

- GeFos Data Release
  - Data Release 2012
  - Data Release 2015
  - Data Release 2017
  - Adult Lean mass GWAS 2017
  - UKBB eBMD GWAS Data Release 2017
  - LifeCourse TB-BMD GWAS 2017
  - Data Release 2018
  - Estrogen GWAS 2018
  - Fracture GWAS 2018 Release
  - Human osteoclast eQTL 2018-2020
  - Skeletal age GWAS 2021
  - UKBB FALLS GWAS Data Release 2020
- Programs
- Forms
- Papers
- Official Documents
- Press Releases

6 Then, click “UKBB\_falls\_gwas\_MAF001\_INF003.txt.gz” at the bottom of webpage to download the GWAS summary data of fall.

**UKBB FALLS GWAS Data Release 2020**

The Genetic Factors for Osteoporosis (GEFOS) Consortium is a large international collaboration comprising numerous research groups. Osteoporosis is a common age-related complex disease with a strong genetic component. The UK Biobank is a health resource from the United Kingdom that has genetic data and phenotype measurements in 500,000 individuals, representative of the general population. We analyzed the full batch of genetic data, including genotyping and imputed data in up to 451,179 participants. We performed genome-wide association studies full history.

**Release**

This release comprises the summary data from our 2020 GWAS on falls in the full batch of genetic data from the UK Biobank. Analyses were performed based on the HRC imputation panel (hg19) including ~7,500,000 SNPs with MAF > 1% and acceptable imputation quality (info score > 0.3).

**Data file description**

Each file contains the following information:

- SNP** Descriptive ID for each variant
- RSID** rs ID for each variant
- CHR** Chromosome
- BP** Position (hg19)
- EA (ALLELE1)** Effect allele
- NEA (ALLELE0)** Non-effect allele
- EAF** Effect allele frequency
- INFO** Imputation quality score
- BETA** Effect estimate (logOR)
- SE** Standard error of the effect estimate (logOR, SE)
- P** P-value

**Publications**

**Terms of Use**

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**Download**

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**Files:**

- UKBB\_falls\_gwas\_MAF001\_INF003.tar.gz

7 For GWAS summary data of fracture, please click “Data Release 2018”.

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GEFOS Data Release Programs Forms Papers Official Documents Press Releases

Data Release 2012  
Data Release 2015  
Data Release 2017  
Adult Lean mass GWAS 2017  
UKBB eBMD GWAS Data Release 2017  
LifeCourse TB-BMD GWAS 2017  
Data Release 2018  
Estrogen GWAS 2018  
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Human osteoclast eQTL 2018-2020  
Skeletal age GWAS 2021  
UKBB FALLS GWAS Data Release 2020

**Home**

**GEFOS** stands for the Genetic Factors for Osteoporosis Consortium. It is a large international collaboration involving various prominent research groups. Osteoporosis is a common age-related complex disease with a strong genetic component. Osteoporotic fractures account for considerable disease burden and costs. The genes responsible, however, are generally assumed that - like for many other complex diseases such as diabetes and cardiovascular disease - many genes are involved, each with subtle effect. In a previous EU FP5 funded project, named GENOMOS, we have improved on this situation by identifying and validating a set of common genetic variants in each of Europe's largest collections of osteoporotic study populations with DNA microarrays. We will build on the success of GENOMOS by using the most advanced gene discovery technology (Genome-wide Association (GWA) analysis with high density SNP arrays, to identify common risk

With the GEFOS project, we will become recently available osteoporosis.

8 Then, click “Morrisetal2018.NatGen.SumStats.tar.gz” at the bottom of webpage to download GWAS summary data of fracture.

**Data file description**

Each file contains the following information:

- SNPID** Descriptive ID for each SNP
- RSID** rs ID for each SNP
- CHR** Chromosome
- BP** Position (hg19)
- EA (ALLELE1 for fracture data)** Effect allele
- NEA (ALLELE0 for fracture data)** Non-effect allele
- EAF** Effect allele frequency
- INFO** Imputation quality score
- BETA (logOR for fracture data)** Effect estimate
- SE (logOR,SE for fracture data)** Standard error of the effect estimate
- P** P-value
- PJ** P-value from infinitesimal model (recommended for fracture data)
- PNI** P-value from non-infinitesimal model (recommended for eBMD data)
- N** Sample size

**Publications**

[Morris, Kemp, et al. An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics 2018.](#)

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We require appropriate attribution for use of data in a product, service, or publication by citing the article generating this set of results (Morris et al., Nature Genetics 2018) and acknowledging its use.

**Download**

By downloading the files below, you explicitly agree to the Terms of Use stipulated above.

**Files:**

- Morrisetal2018.NatGen.SumStats.tar.gz