Approved BIOS data requests (until October, 2018)

1) Eline Slagboom The ageing genome: consistent changes in gene regulation and loss of transcriptional control (BIOS RNA, methylation and GWAS data)

2) Erik van Zwet & Bas Heijmans Development and evaluation of statistical methods for meQTL detection (BIOS RNA, methylation and GWAS data)

3) Silvère van der Maarel & Bas Heijmans Genetics of X inactivation (sex chromosome RP3 RNA, methylation and GWAS data)

4) Peter A.C. ’t Hoen Private and exogenous RNAs (BIOS & GONL RNA data)

5) Dorret Boomsma 
   1) Heritability of epigenetic marks: a twin study (BIOS methylation data)
   2) Epigenetic markers in (discordant) MZ twins (BIOS methylation data, BMI, depression phenotypes)

6) Rick Jansen, Brenda Penninx & Dorret Boomsma Transcriptomic biomarkers for major depressive disorder (BIOS RNA data, depression phenotypes)

7) Jacqueline Vink, Rick Jansen, Dorret Boomsma Smoking effects on the transcriptome and methylation: an integrative study (BIOS RNA and methylation data)

8) Rick Jansen & Dorret Boomsma Estimating Heritability of Gene Expression in RNA-sequencing data (BIOS RNA data)

9) Cisca Wijmenga Functional genomics of autoimmune disease risk SNPs using the LifeLines deep cohort (LifeLines Methylation and RNA-seq data)

10) Aaron Isaacs Functional genomics of electrocardiographic parameters

11) Kai Ye Transcriptome and epigenome signature in samples with de novo structural variants (GONL methylation and RNA-seq)

12) Peter-Bram ’t Hoen Medical RNA-sequencing: aberrant RNA expression in patients BIOS RNA-seq
13) Alexandra Zhernakova  
**Functional genomics of biological aging in immune cell types**  
(Lifelines RNA & methylation data, additional data is telomere length)

14) Lude Franke  
**Identification of bacterial and viral signatures in human transcriptomic data**  
(BIOS BIOS RNA and GWAS data)

15) Lude Franke  
**Replication of CpG sites that correlate with BMI**  
(278 CpG methylation sites, BMI)

16) Wouter Jukema & Bas Heijmans  
**An Epigenome-Wide Association Study of LDL cholesterol in circulating cells**  
(RNA relevant for differential methylation observed in BIOS cohorts, BIOS Methylation data, 47 SNPs to construct LDL GRS and SNPs recapitulating LDL-associated differential methylation, LDL + covariates)

17) Lude Franke  
**Mendelian randomization of 38 blood pressure loci and their corresponding CpG sites**  
(38 SNPs and CpG methylation sites, BP)

18) Wouter Jukema & Bas Heijmans  
**An Epigenome-Wide Association Study of blood lipids in circulating cells**  
(BIOS methylation data, transcripts relevant for differential methylation observed in BIOS cohorts, 47 SNPs to construct LDL GRS and SNPs recapitulating LDL-associated differential methylation)

19) Marjolein J. Peters & Joyce B.J. van Meurs  
**The impact of SNPs in micro and macro non-coding RNAs on genome-wide gene expression profiles**  
(BIOS RNA-seq and methylation data)

20) Pooja R. Mandaviya  
**An Epigenome-wide association of Homocysteine**  
(BIOS RNA-seq and methylation data, 18 homocysteine-associated SNPs)

21) Vinod Kumar  
**Systems genetics approach to identify genetic susceptibility factors to candidemia**  
(Lifelines RNA-seq)

22) Peter Visscher  
**Prediction of phenotypes from methylation and genotype data**  
(Lifelines methylation and RNA-seq)

23) Cisca Wijmenga  
**Replication of eQTL effect of autoimmune disease risk SNPs using the RNA sequencing data of Rotterdam samples**  
(Rotterdam RNA-seq)

24) Peter A.C ’t Hoen  
**Effect of rare genetic variants on gene expression**  
(BIOS RNA-seq)

25) Abbas Dehghan  
**Epigenome-wide association study of fasting glucose, fasting insulin and type 2 diabetes**  
(BIOS Methylation and genotype data)

26) Alexandra Zhernakova  
**Identification of individual expression profile for pathway analysis**  
(Lifelines methylation and RNA-seq data)
27) Marjolein J. Peters
Prediction of transcriptomic and epigenetic age and the correlation with biological ageing markers
(BIOS RNA-seq and Methylation)

28) Bas Heijmans
An Transcriptome-Wide Association Study of blood lipids in circulating cells
(BIOS RNA-seq and Methylation, LDL, HDL, triglycerides)

29) Maarten van Iterson
The impact of DNA helix deformation on transcriptional regulation
(BIOS RNA-seq, methylation and genotype data)

30) Cisca Wijmenga
A compendium of transcriptional knockouts in the human genome and their downstream consequences
(BIOS RNA-seq, methylation and genotype data)

31) Ivan Nedeljkovic
Epigenome wide association study of COPD and lung function
(BIOS RNA-seq, methylation and genotype data)

32) Michel Nivard
Genome wide enrichments of blood eQTLs and mQTLs in their effect on complex traits
(eQTL and mQTL results)

33) Ilja Arts
Identification of epigenetic and transcriptional biomarkers for Metabolic Syndrome and CVD in the
CODAM study
(CODAM RNA-seq, methylation and genotype data)

34) Noah Zaitlen (EGA)
Correction for cell type heterogeneity in epigenome-wide association studies

35) Dorret Boomsma
Realizing a complex behavior database (COMBA) to enhance large scale mega and meta-analyses projects using
BBMRI BIOS resources

36) Annique J. Claringbould
Genome-wide multi-phenotype analysis of omega fatty acids using multivariate analytical methods

37) Tuuli Lappalainen
Variation of genomic imprinting in humans uncovered by large-scale genomic and experimental analysis

38) Rick Jansen
Lookup of SNPs from Fertility GWAS in eQTL and mQTL database

39) Klaasjan Ouwens
Can RNA sequence / methylation information help to elucidate DNA differences within twin pairs?

40) Simone Wahl
Epigenome-wide association study of leptin

41) Caroline Relton
GoDMC meQTL meta-analysis

42) Eline Slagboom
Epigenome-wide association study of NMR metabolite levels

43) Zoltan Kutilik
Replication of parent-of-origin effects for 135 eQTLs
44) Zoltan Kutalik
Multi-instrument Mendelian randomization approach, applicable to association summary statistics

45) Rick Jansen
Building predictors for cis-methylation and cis-expression for association with phenotypes using GWAS summary statistics

46) Jeroen van Rooij
Interaction between Apoe-4 carrier status and the transcriptome with ageing

47) Jenny van Dongen
Epigenome-wide Association Study of Aggressive Behavior

48) Annique J. Claringbould
Effects of TOMM40 and APOE locus variants on susceptibility to Parkinson’s disease (PD) and associated late onset dementias

49) Bas Heijmans
Look-up of prenatal famine associated CpGs for their association with expression

50) Amanda G. Mason
Identification of blood biomarkers for FSHD1

51) Maaike de Vries
Epigenetic alterations upon environmental exposures in COPD

52) J.H. Veldink
Unraveling the methylome of amyotrophic lateral sclerosis.

53) Annique J. Claringbould
Dissecting the mechanisms of genetic effects through large-scale multi-phenotype analysis of BMI and three blood lipids within the ENGAGE consortium

54) P.E.M. Taschner
Monitoring effects of exercise using gene expression analysis

55) Rick Jansen
Replication of associations between asthma risk factors and methylation sites and expression markers

56) Alan Hodgkinson
Genomic Analysis of the Mitochondrial Transcriptome

57) Chengjian Xu
Functional annotation of asthma associated methylation CpG sites

58) Ayse Demirkan
Differential gene methylation related to glycemic traits and the role of gene expression in these relationships

59) Peter ‘t Hoen
X-inactivation in the general female population studied by RNA-seq

60) Oscar H. Franco
The development and validation of cumulative association models for lifestyle factors based on DNA methylation levels.

61) Ayse Demirkan
Differential gene methylation related to glycemic traits and the role of gene expression in these relationships
62) Patrick Deelen  
Diagnosing unsolved patients by combining DNA sequencing with blood transcriptomics

63) Marc Jan Bonder  
Application of struct-LMM in identification of cis-eQTLs and eQTL module identification

64) Amy Webster  
Investigation into the DNA methylation landscape of RA discordant MZ twins

65) Pooja Mandaviya  
The creation of standardized catalogs of association between the functional genome (epigenetics/ RNA-expression) and available BBMRI phenotypes: Comparison of data analysis methodologies

66) Alkes Price  
Functional annotation of gene expression heritability and association with disease

67) Lude Franke  
Genomic Analysis of the Mitochondrial Transcriptome

68) Maartje Stutvoet  
Transcriptome wide association study (TWAS) on all BIOS phenotypes with special focus on age in order to discover gene expression-trait correlations as well as show the implications of data correction methods

69) Marian Beekman  
EWAS on plasma IgG glycosylation levels

70) Marian Beekman  
EWAS on CRP

71) Marian Beekman  
EWAS on freeT4 and plasma TSH levels

72) Adriaan van der Graaf  
Identification of causal genes at disease associated loci and their downstream effects

73) Phillip Koeffler  
Characterization of the B/T cel population and BCR/TCR repertoire in elderly individuals

74) Miina Ollikainen  
Prediction of smoking status based on DNA methylation profiles

75) Paolo Zanoni  
Alternative LDLR mRNA processing in the BIOS cohort

76) Lude Franke  
Identification of cis-eQTLs and correlation-QTLs in single-cell RNA-sequencing data

77) Niek de Klein  
Replication of GFI1 DNA methylation and cardio-metabolic phenotypes in adults

78) Lude Franke  
eQTLGen: Identifying downstream effects of genetic risk factors on gene expression levels

79) Urmo Võsa  
Investigation of the genetic architecture of metabolic coherence
80) Matthijs van der Zee
Molecular Transducers of Physical Activity and Sedentary Behavior in Humans

81) Paul Hop
Genome-wide identification of genes affecting DNA methylation in trans using genetic variants as causal anchors

82) Pooja Mandaviya
Meta-analysis of genome-wide DNA methylation and serum CRP levels

83) Jian Yang
Detecting SNPs associated with the variability of gene expression traits

84) Chengjian Xu
Functional annotation of methylation CpG sites in relation to air pollution exposure

85) Chengjian Xu
Functional annotation of smoking associated methylation CpG sites

86) Yun Li
Transcriptome-wide Association Study of Blood Cell Traits

87) Jan Oosting
Epimutation in familial melanoma

88) H Joosse
Cardiac disease and menopause: a study on methylation, gene expression and menopause in connection with cardiac disease

89) Twan Spelink
Linking the genetic basis for human immune variation to deep molecular phenotypes

90) Antoine Rimbert
Uncovering/refining genetic determinants involved in plasma lipid levels

91) Lude Franke
Deconvolution of blood eqtls

92) Olena Gruzieva
Prenatal particulate air pollution and DNA methylation in newborns

93) Jenny van Dongen
Bi-directional Mendelian randomization analysis of smoking and DNA methylation

94) Richard JLF Lemmers
Identification of epigenetic modifiers of somatic DUX4 expression and disease presentation in facioscapulohumeral dystrophy

95) Iris Jonkers
Identification and functional validation of genes genetically associated with celiac disease