

Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci

Xianyong Yin¹, Lap Sum Chan¹, Debraj Bose¹, Anne U. Jackson¹, Peter VandeHaar¹, Adam E. Locke², Christian Fuchsberger^{1,3}, Heather M. Stringham¹, Ryan Welch¹, Ketian Yu¹, Lilian Fernandes Silva⁴, Susan K. Service⁵, Daiwei Zhang^{1,6}, Emily C. Hector⁷, Erica Young^{2,8}, Liron Ganel², Indrani Das², Haley Abel⁹, Michael R. Erdos¹⁰, Lori L. Bonnycastle¹⁰, Johanna Kuusisto^{4,11}, Nathan O. Stitzel^{2,8,12}, Ira M. Hall¹³, Gregory R. Wagner¹⁴, FinnGen*, Jian Kang¹, Jean Morrison¹, Charles F. Burant¹⁵, Francis S. Collins¹⁰, Samuli Ripatti^{16,17,18}, Aarno Palotie^{16,17,19}, Nelson B. Freimer⁵, Karen L. Mohlke²⁰, Laura J. Scott¹, Xiaoquan Wen¹, Eric B. Fauman^{21,22}, Markku Laakso^{4,22}, Michael Boehnke^{1,22}

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Supplementary Table 1: Ten biochemical classes of the assayed metabolites

Class	Abbreviation
Amino acid	AA
Carbohydrate	CA
Cofactors and vitamins	CV
Energy	EN
Lipid	LI
Nucleotide	NU
Partially characterized	PC
Peptide	PE
Xenobiotics	XE
Unnamed	UN

Class: biochemical class of the metabolites.

Supplementary Table 2: Characteristics of METSIM participants and those with Metabolon metabolomics data

Characteristic	All	Metabolon	Analysis
Sample size	10,197	6,490	6,136
Age at baseline (years, mean \pm SD)	57.8 \pm 7.1	58.0 \pm 7.0	58.1 \pm 7.0
BMI (kg/m ² , mean \pm SD)	27.3 \pm 4.2	26.8 \pm 3.7	26.7 \pm 3.6
Waist circumference (cm, mean \pm SD)	98.8 \pm 11.5	97.4 \pm 10.5	97.1 \pm 10.1
Fasting glucose (mmol/l, mean \pm SD)	6.0 \pm 1.1	5.8 \pm 0.8	5.7 \pm 0.5
Diabetics at baseline %	14.1	4.1	0.0
Current smoker %	18.1	16.1	16.0
Blood pressure medication use %	39.2	35.5	34.5
Lipid lowering medication use %	28.2	26.2	25.4

SD: standard deviation. Analysis: the analysis set after quality control.

Supplementary Table 3a: Numbers of genetic variants by variant type in the METSIM imputation reference panel

Variant type	Rare (MAF<1%)	Common (MAF≥1%)	All
Single nucleotide variant	14,765,788	8,528,549	23,294,337
Insertion/deletion	1,752,855	1,098,993	2,851,848
Total	16,518,643	9,627,542	26,146,185

MAF: minor allele frequency.

Supplementary Table 3b: Numbers of genetic variants by variant annotation in the METSIM imputation reference panel

Variant annotation	Rare (MAF<1%)	Common (MAF≥1%)	All
Intron	8,998,202	5,172,297	14,170,499
Intergenic	5,101,805	3,117,352	8,219,157
Downstream/upstream	1,902,347	1,109,324	3,011,671
3' UTR	165,893	82,936	248,829
Non-coding transcript exon	123,505	72,800	196,305
Missense	108,023	25,100	133,123
Synonymous	56,499	25,162	81,661
5' UTR	32,858	13,216	46,074
Splice region	16,632	7,384	24,016
Frameshift	3,642	340	3,982
Stop gained	3,143	225	3,368
Inframe deletion	1,951	443	2,394
Splice donor	1,534	356	1,890
Splice acceptor	1,230	243	1,473
Inframe insertion	901	260	1,161
Start lost	276	45	321
Stop lost	135	39	174
Others	67	20	87
Total	16,518,643	9,627,542	26,146,185

MAF: minor allele frequency. Others includes incomplete_terminal_codon_variant, transcript_ablation, protein_altering_variant, mature_miRNA_variant, and coding_sequence_variant annotations in Variant Effect Predictor (VEP).

Supplementary Table 4a: Numbers of genetic variants with genotype imputation $r^2 \geq 0.3$ by variant type in the 6,490 METSIM participants with Metabolon metabolomics data

Variant type	Rare (MAF<1%)	Common (MAF\geq1%)	All
Single nucleotide variant	10,656,966	8,526,031	19,182,997
Insertion/deletion	1,306,701	1,098,016	2,404,717
Total	11,963,667	9,624,047	21,587,714

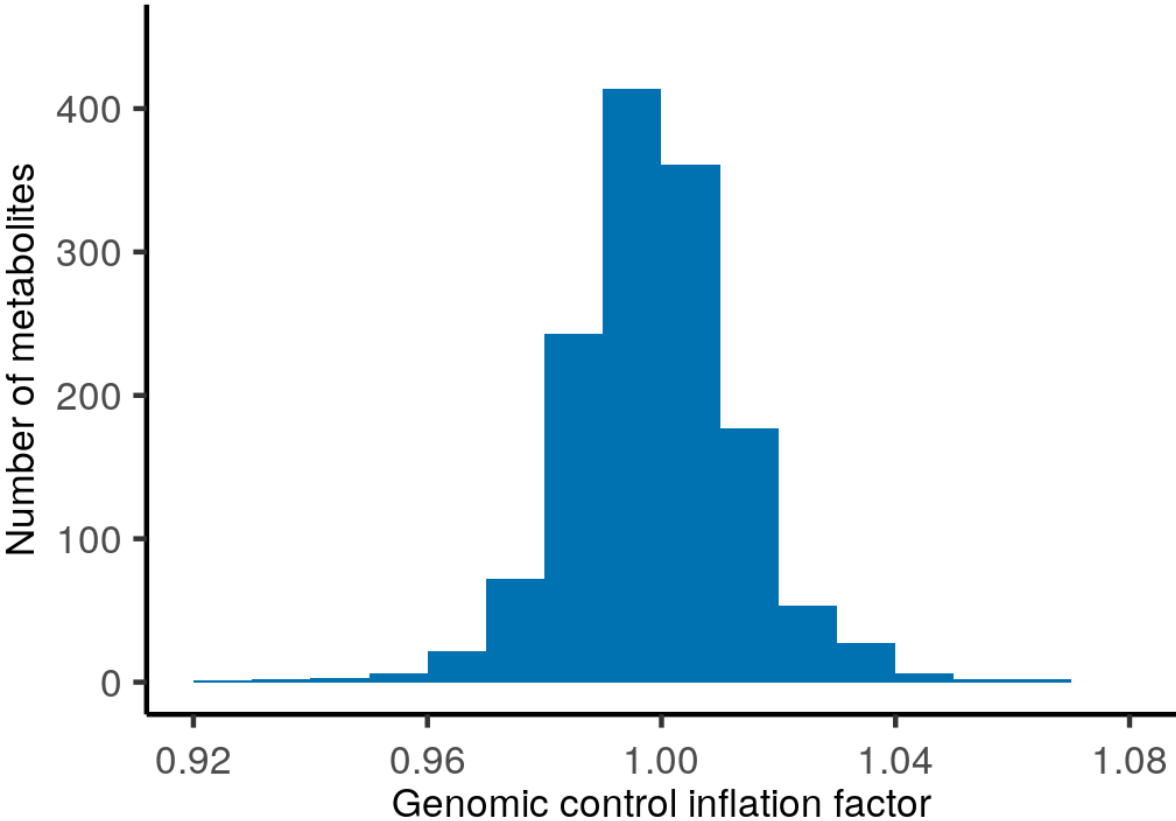
MAF: minor allele frequency.

Supplementary Table 4b: Numbers of genetic variants with genotype imputation $r^2 \geq 0.3$ by variant annotation in the 6,490 METSIM participants with Metabolon metabolomics data

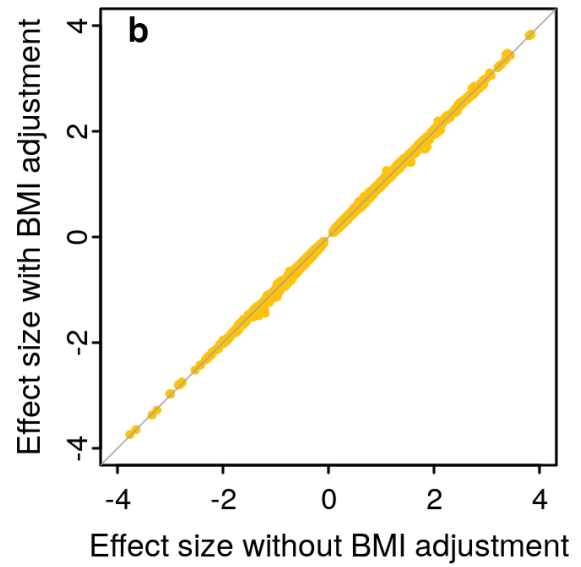
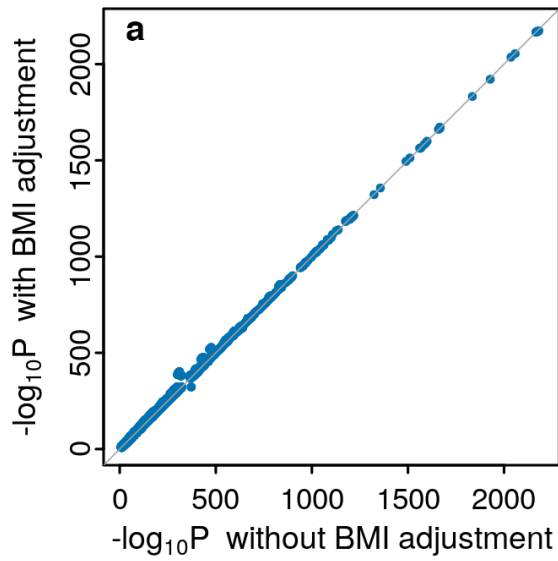
Variant annotation	Rare (MAF<1%)	Common (MAF\geq1%)	All
Intron	7,010,536	5,575,203	12,585,739
Intergenic	3,099,351	2,619,219	5,718,570
Downstream/upstream	1,456,125	1,174,576	2,630,701
Non-coding transcript exon	116,862	95,642	212,504
3' UTR	121,829	84,387	206,216
Missense	73,393	25,394	98,787
Synonymous	40,008	25,316	65,324
5' UTR	24,437	14,079	38,516
Splice region	12,516	8,096	20,612
Frameshift	2,379	364	2,743
Stop gained	1,924	239	2,163
Inframe deletion	1,332	437	1,769
Splice donor	1,114	419	1,533
Splice acceptor	886	311	1,197
Inframe insertion	648	262	910
Start lost	201	44	245
Stop lost	76	40	116
Others	50	19	69
Total	11,963,667	9,624,047	21,587,714

MAF: minor allele frequency. Others includes incomplete_terminal_codon_variant, transcript_ablation, protein_altering_variant, mature_miRNA_variant, and coding_sequence_variant annotations in Variant Effect Predictor (VEP).

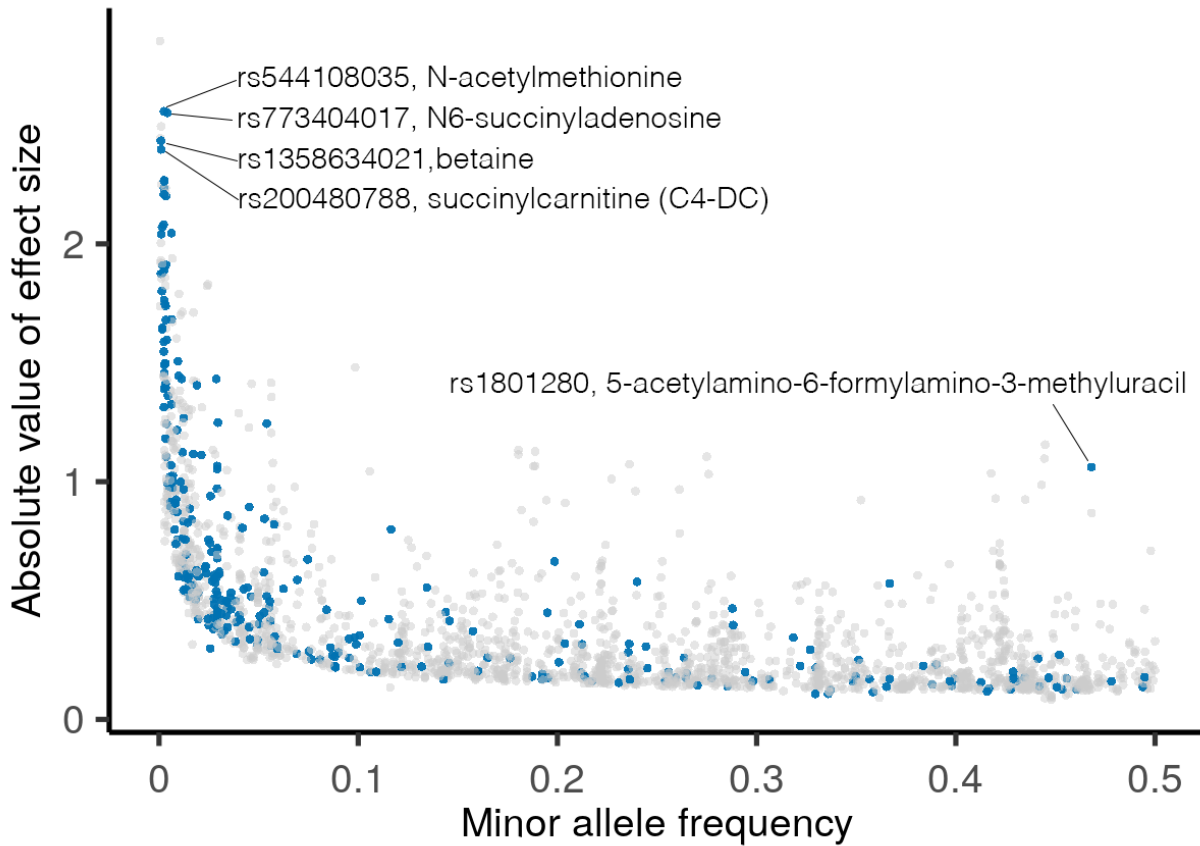
Supplementary Figure 1: Distribution of genomic control inflation factors for the 1,391 metabolite GWAS (median=1.00).



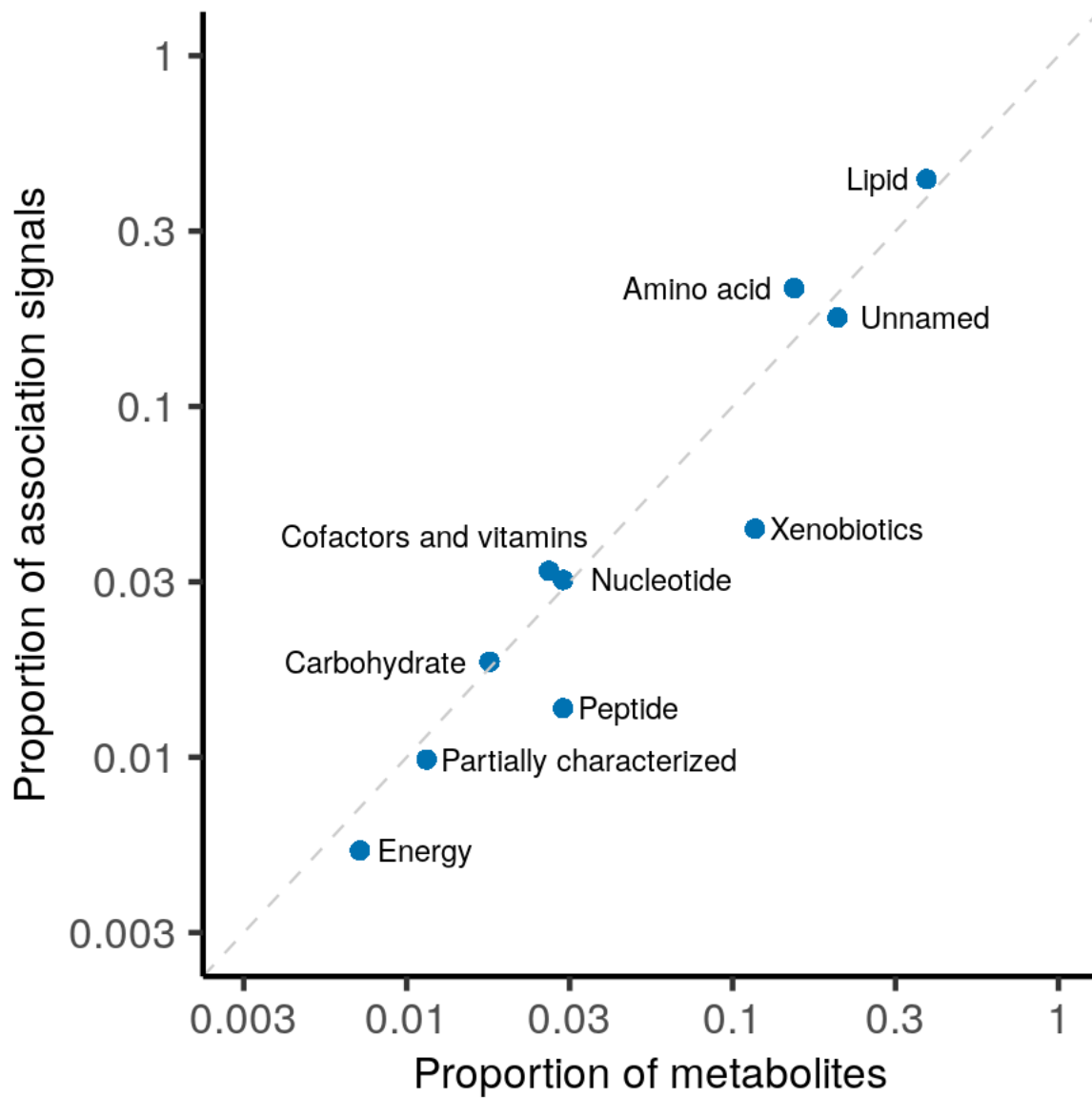
Supplementary Figure 2: Comparison of significant single-variant association results ($P < 7.2 \times 10^{-11}$) with or without adjustment for BMI: **a** $-\log_{10}P$ and **b** effect size estimate. For each comparison, the Pearson correlation coefficient $r = 0.999$. Each dot represents a genetic variant-metabolite pair.



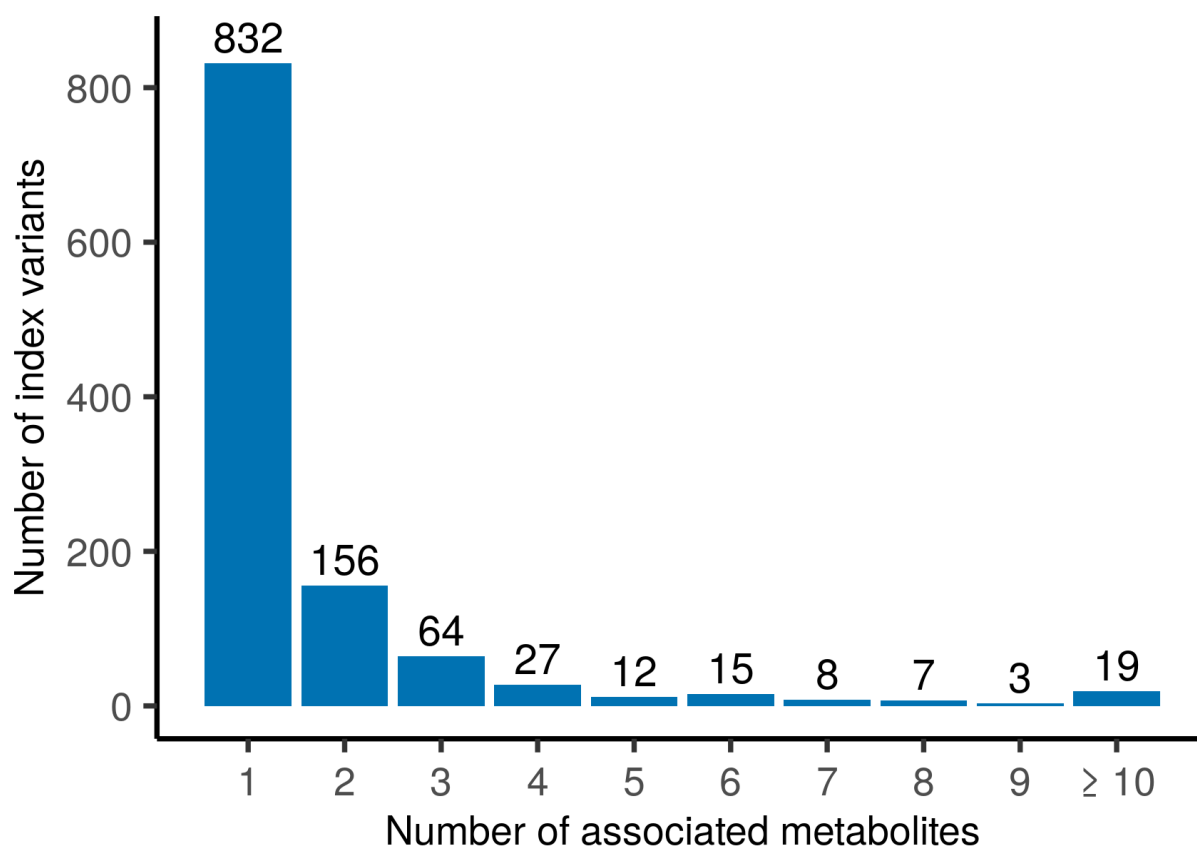
Supplementary Figure 3: Absolute value of the effect size estimate is inversely correlated with minor allele frequency (MAF) for the 2,030 conditional association signals (1,143 index variants; $P < 7.2 \times 10^{-11}$). Each dot represents an association signal. Novel signals are colored in blue. Effect size was estimated for inverse normalized metabolite level residuals after regression on covariates. Four novel association signals at rare variants and one at a common variant are labeled.



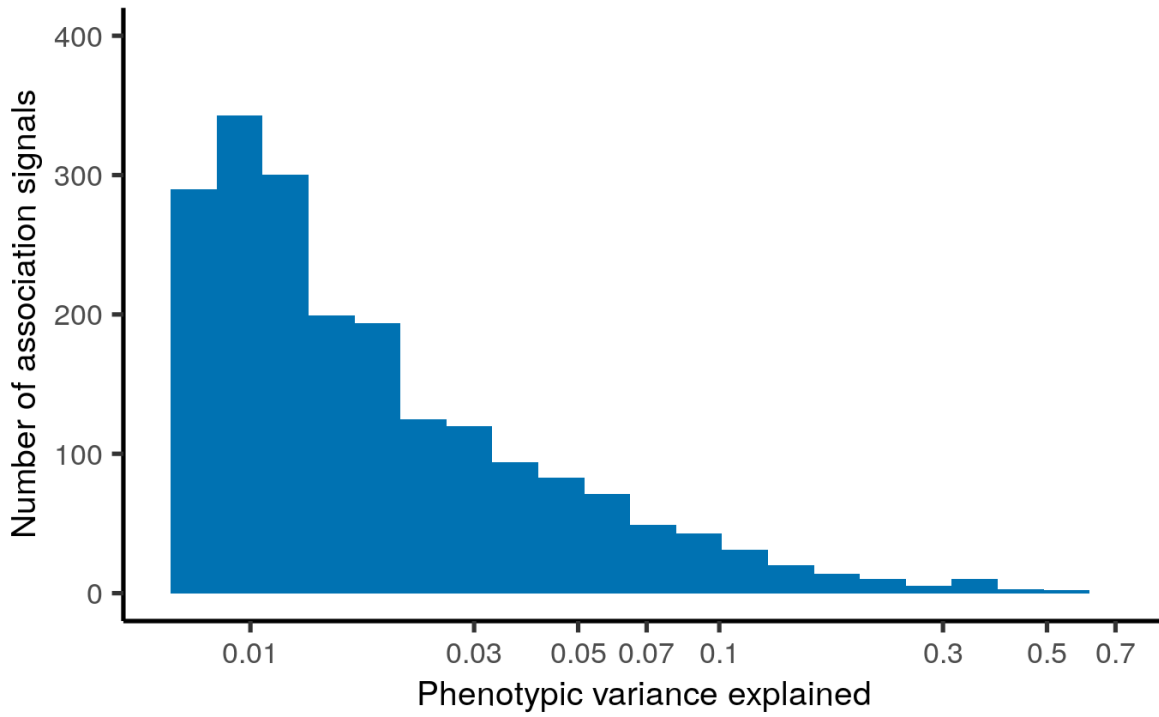
Supplementary Figure 4: Relationship between the number of metabolites and the number of significant conditional association signals at $P < 7.2 \times 10^{-11}$ for the ten metabolite biochemical classes. The proportion of metabolites and association signals are plotted on the log scale.



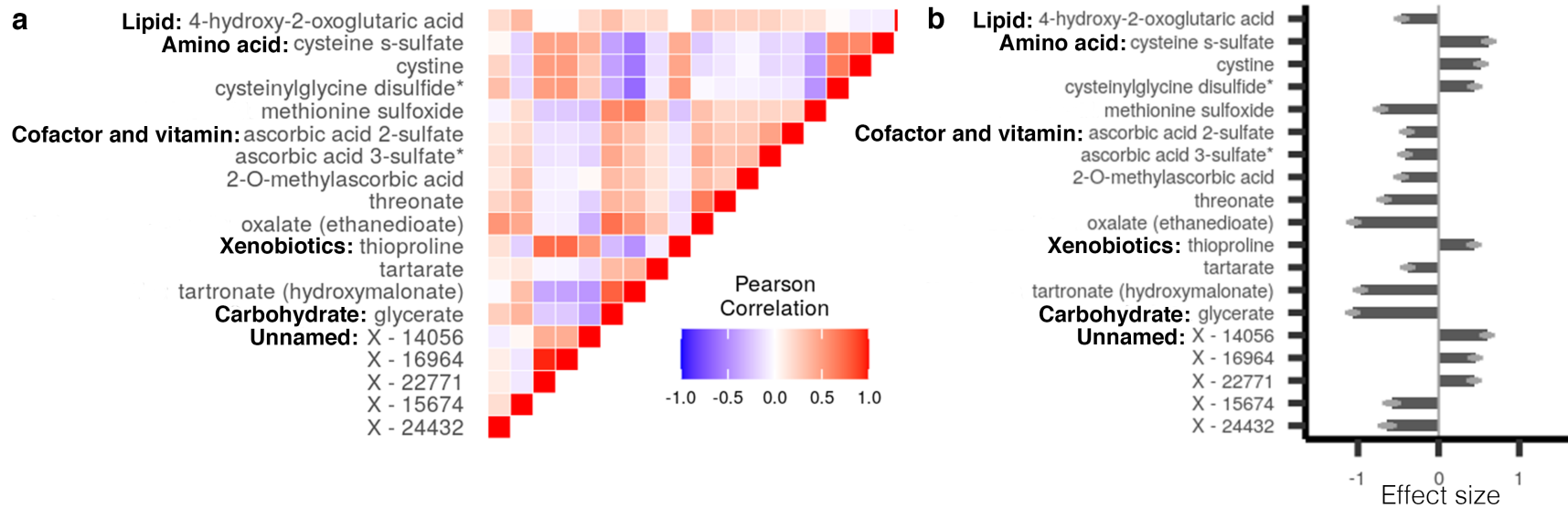
Supplementary Figure 5: Number of metabolites associated with each of the 1,143 index variants.



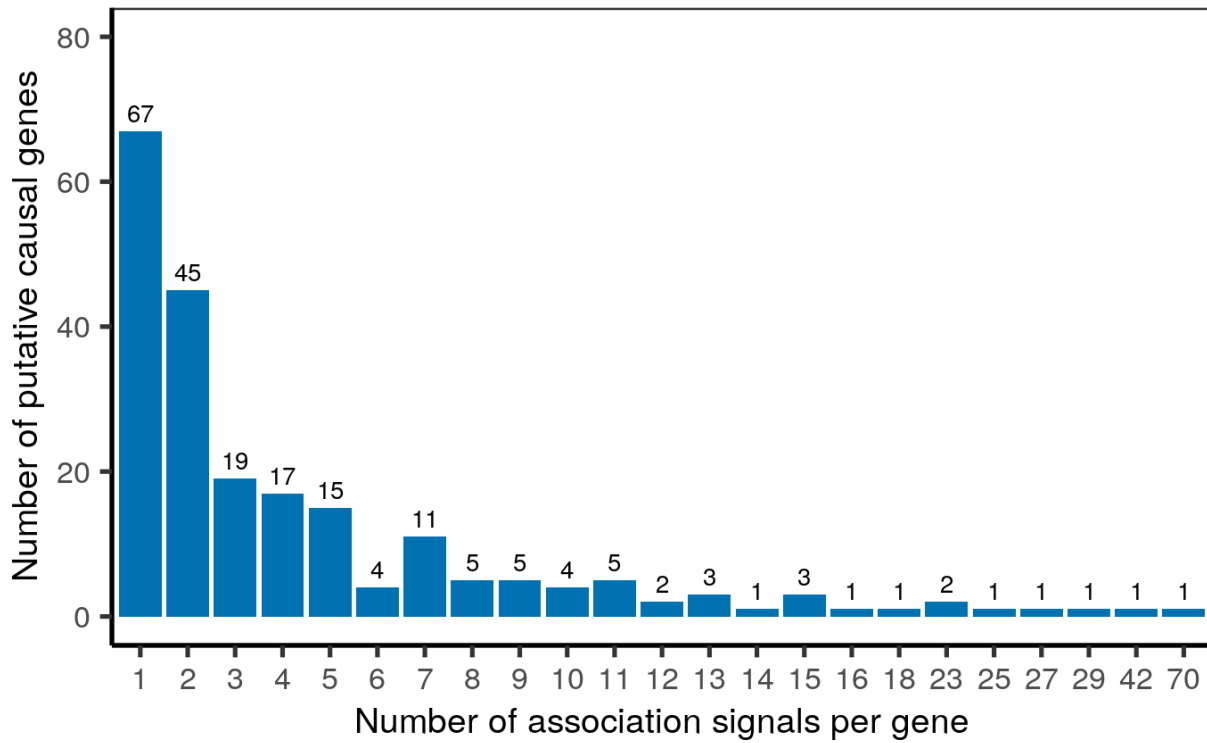
Supplementary Figure 6: Distribution of metabolite phenotypic variance explained by the index variant for each of the 2,030 significant association signals. The distribution is plotted on the log scale.



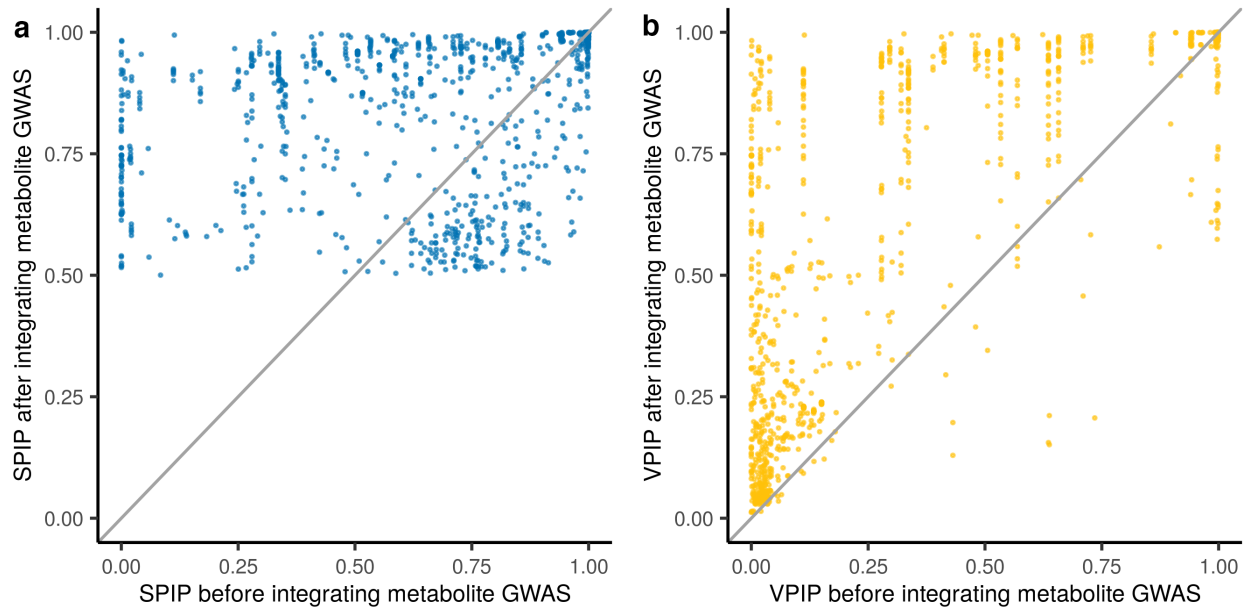
Supplementary Figure 7: Significant genetic associations ($P < 7.2 \times 10^{-11}$) between *SLC23A3* missense variant p.Asn336Lys (rs192756070) and 19 metabolites. **a** Phenotypic correlations between the 19 metabolites; and **b** Effect size estimates and standard errors for the 19 metabolite association signals sorted by biochemical class. Within each class, metabolites are sorted by their association effect sizes.



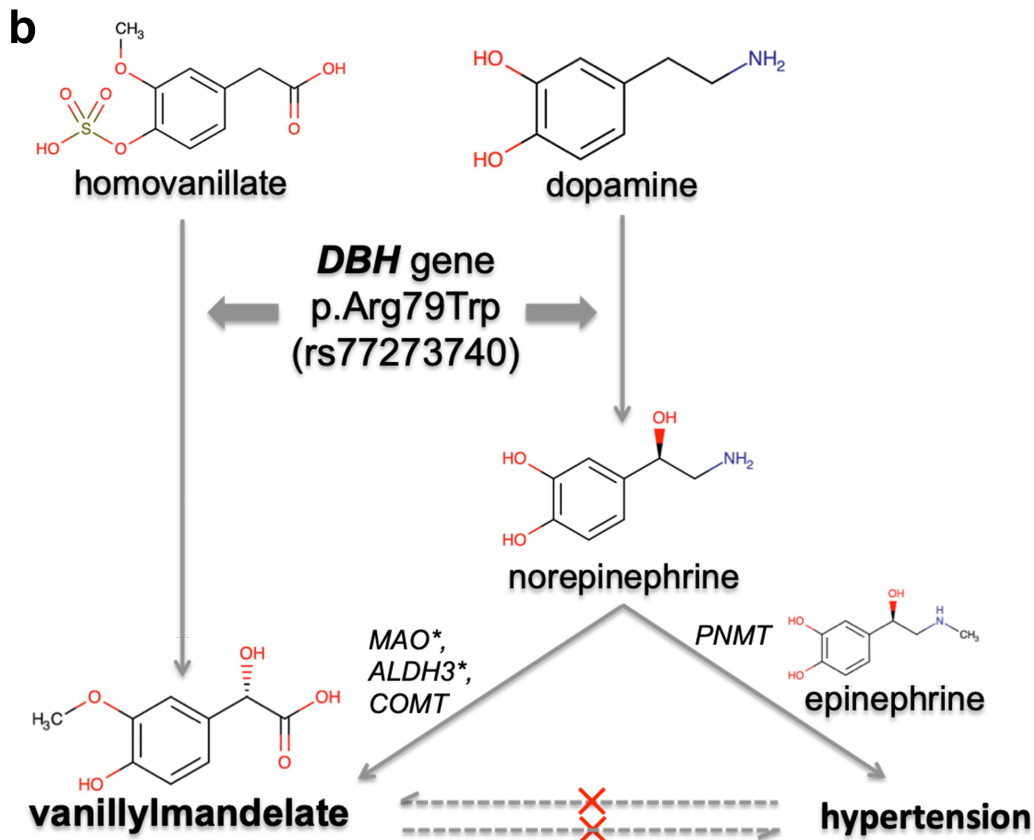
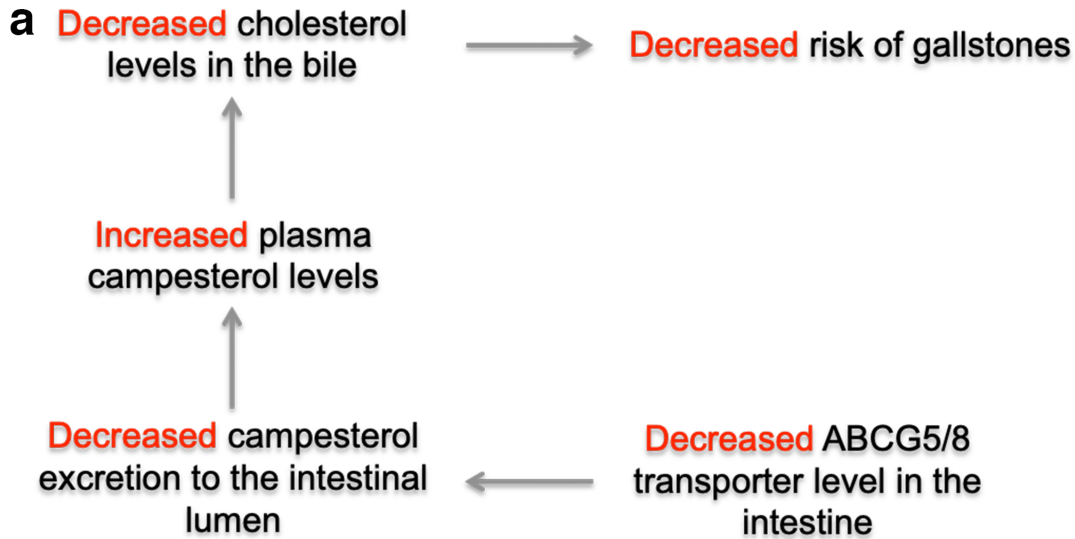
Supplementary Figure 8: Number of conditional association signals associated with each of the 215 putative causal genes.



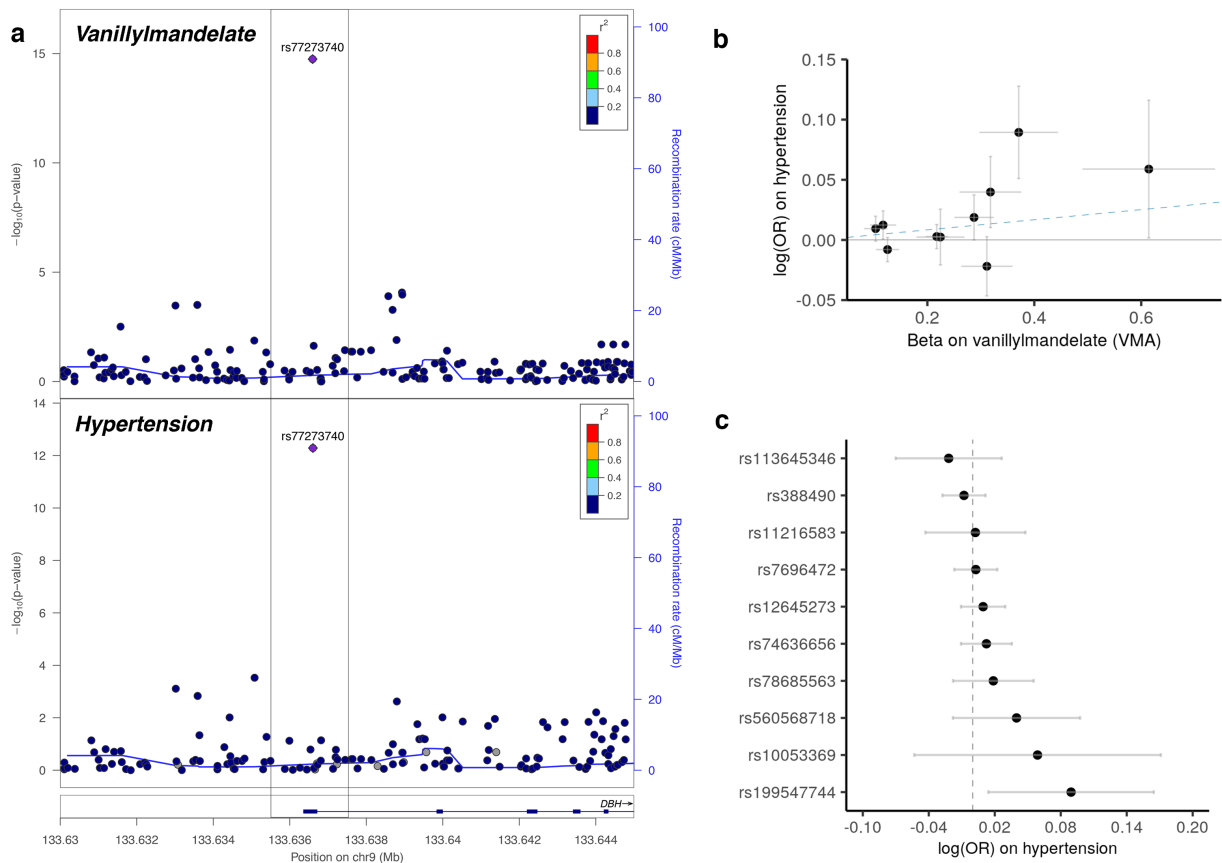
Supplementary Figure 9: Integrating metabolite GWAS into FinnGen disease genetic association results through colocalization analysis increases the posterior probabilities of **a** 64% of the disease association signals (SPIP); and **b** 90% of the putative causal variants (VIP). SPIP is the estimated probability that there is an association signal in the region. Here, VIP is the largest posterior probability that one of the genetic variants is causal. Each point denotes in **a** an association signal and in **b** a genetic variant.



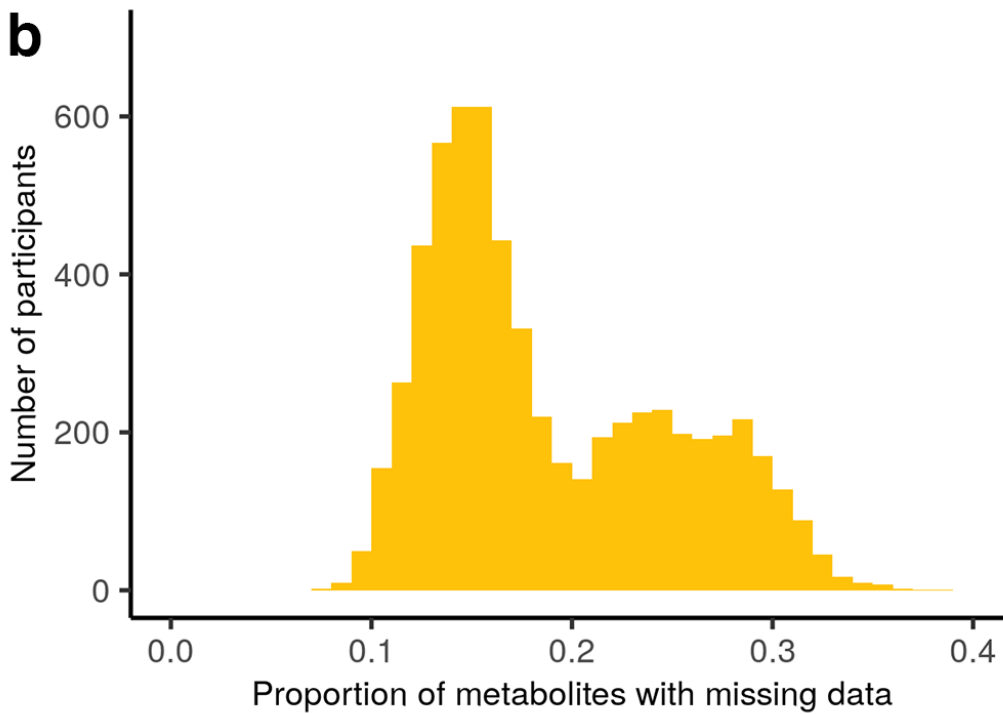
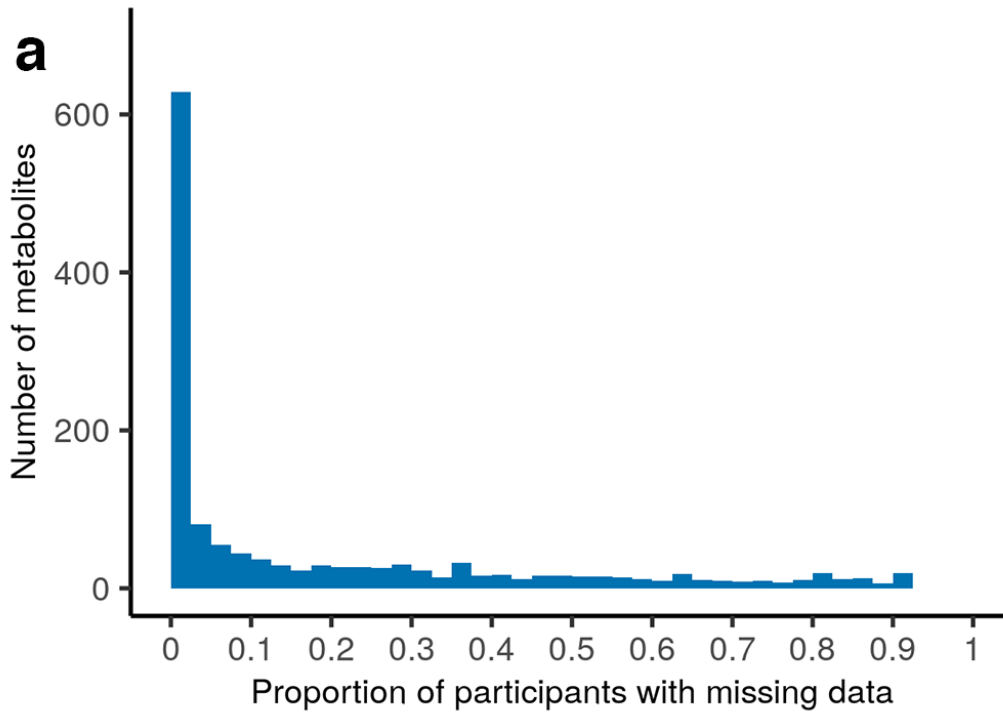
Supplementary Figure 10: Pathways from metabolite to diseases mediated by gene. **a** Potential causal pathway from plasma campesterol to the risk of gallstones at the *ABCG5/ABCG8* region; and **b** the potential distinct effects of the *DBH* gene on plasma vanillylmandelate (VMA) and the risk of hypertension.



Supplementary Figure 11: Dopamine beta hydroxylase (*DBH*) influence on vanillylmandelate and hypertension: distinct pathways. **a** Stacked regional association plots for vanillylmandelate and hypertension in the *DBH* region of chromosome 9. Genetic variants are colored by their linkage disequilibrium (LD) in METSIM to the index variant rs77273740; **b** Comparison of effect sizes of ten instrumental variables without significant heterogeneity ($P > 0.05$) in the genome used in the Mendelian randomization analysis between vanillylmandelate and hypertension. The slope of the blue dashed line depicts the estimated effect of vanillylmandelate on hypertension in Mendelian randomization analysis; and **c** Effects on hypertension of ten instrumental variables used in Mendelian randomization analysis. OR: odds ratio.



Supplementary Figure 12: Proportion of **a** METSIM participants with missing data for each of the 1,391 metabolites; and **b** metabolites with missing data among the 6,136 METSIM participants in the analysis dataset.



Supplementary Note 1

FinnGen Contributors

Steering Committee

Aarno Palotie Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mark Daly Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Pharmaceutical companies

Bridget Riley-Gills Abbvie, Chicago, IL, United States
Howard Jacob Abbvie, Chicago, IL, United States
Dirk Paul Astra Zeneca, Cambridge, United Kingdom
Heiko Runz Biogen, Cambridge, MA, United States
Sally John Biogen, Cambridge, MA, United States
Robert Plenge Celgene, Summit, NJ, United States/Bristol Myers Squibb, New York, NY, United States
Joseph Maranville Celgene, Summit, NJ, United States/Bristol Myers Squibb, New York, NY, United States
Mark McCarthy Genentech, San Francisco, CA, United States
Julie Hunkapiller Genentech, San Francisco, CA, United States
Meg Ehm GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro GlaxoSmithKline, Brentford, United Kingdom
Simonne Longereich Merck, Kenilworth, NJ, United States
Caroline Fox Merck, Kenilworth, NJ, United States
Anders Mälarstig Pfizer, New York, NY, United States
Katherine Klinger Sanofi, Paris, France
Deepak Raipal Sanofi, Paris, France
Eric Green Maze Therapeutics, San Francisco, CA, United States
Robert Graham Maze Therapeutics, San Francisco, CA, United States
Robert Yang Janssen Biotech, Beerse, Belgium
Richard Siegel Novartis, Basel, Switzerland

University of Helsinki & Biobanks

Tomi Mäkelä HiLIFE, University of Helsinki, Finland, Finland
Jaakko Kaprio Institute for Molecular Medicine Finland, HiLIFE, Helsinki, Finland, Finland
Petri Virolainen Auria Biobank/University of Turku/Hospital District of Southwest Finland, Turku, Finland
Antti Hakanen Auria Biobank/University of Turku/Hospital District of Southwest Finland, Turku, Finland
Terhi Kilpi THL Biobank / The National Institute of Health and Welfare Helsinki, Finland
Markus Perola THL Biobank / The National Institute of Health and Welfare Helsinki, Finland
Jukka Partanen Finnish Red Cross Blood Service / Finnish Hematology Registry and Clinical Biobank, Helsinki, Finland
Anne Pitkäranta Helsinki Biobank / Helsinki University and Hospital District of Helsinki and Uusimaa, Helsinki
Juhani Junttila Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia Hospital District, Oulu, Finland
Raisa Serpi Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia Hospital District, Oulu, Finland
Tarja Laitinen Finnish Clinical Biobank Tampere / University of Tampere / Pirkanmaa Hospital District, Tampere, Finland
Veli-Matti Kosma Biobank of Eastern Finland / University of Eastern Finland / Northern Savo Hospital District, Kuopio, Finland

Urho Kujala Central Finland Biobank / University of Jyväskylä / Central Finland Health Care
District, Jyväskylä, Finland
Marco Hautalahti FINBB - Finnish biobank cooperative

Other Experts/ Non-Voting Members

Outi Tuovila Business Finland, Helsinki, Finland
Raimo Pakkanen Business Finland, Helsinki, Finland

Scientific Committee

Pharmaceutical companies

Jeffrey Waring Abbvie, Chicago, IL, United States
Bridget Riley-Gillis Abbvie, Chicago, IL, United States
Ioanna Tachmazidou Astra Zeneca, Cambridge, United Kingdom
Chia-Yen Chen Biogen, Cambridge, MA, United States
Heiko Runz Biogen, Cambridge, MA, United States
Shameek Biswas Celgene, Summit, NJ, United States/Bristol Myers Squibb, New York, NY, United States
Sarah Pendergrass Genentech, San Francisco, CA, United States
Julie Hunkapiller Genentech, San Francisco, CA, United States
Meg Ehm GlaxoSmithKline, Brentford, United Kingdom
David Pulford GlaxoSmithKline, Brentford, United Kingdom
Neha Raghavan Merck, Kenilworth, NJ, United States
Adriana Huertas-Vazquez Merck, Kenilworth, NJ, United States
Anders Mälarstig Pfizer, New York, NY, United States
Xinli Hu Pfizer, New York, NY, United States
Katherine Klinger Sanofi, Paris, France
Matthias Gossel Sanofi, Paris, France
Robert Graham Maze Therapeutics, San Francisco, CA, United States
Eric Green Maze Therapeutics, San Francisco, CA, United States
Sahar Mozaffari Maze Therapeutics, San Francisco, CA, United States
Dawn Waterworth Janssen Biotech, Beerse, Belgium
Nicole Renaud Novartis, Basel, Switzerland
Ma' en Obeidat Novartis, Basel, Switzerland

University of Helsinki & Biobanks

Samuli Ripatti Institute for Molecular Medicine Finland, HiLIFE, Helsinki, Finland
Johanna Schleutker Auria Biobank / Univ. of Turku / Hospital District of Southwest Finland, Turku, Finland
Markus Perola THL Biobank / The National Institute of Health and Welfare Helsinki, Finland
Mikko Arvas Finnish Red Cross Blood Service / Finnish Hematology Registry and Clinical Biobank, Helsinki, Finland
Olli Carpén Helsinki Biobank / Helsinki University and Hospital District of Helsinki and Uusimaa, Helsinki
Reetta Hinttala Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia Hospital District, Oulu, Finland
Johannes Kettunen Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia Hospital District, Oulu, Finland
Arto Mannermaa Biobank of Eastern Finland / University of Eastern Finland / Northern Savo Hospital District, Kuopio, Finland
TBC Finnish Clinical Biobank Tampere / University of Tampere / Pirkanmaa Hospital District, Tampere, Finland
Jari Laukkanen Central Finland Biobank / University of Jyväskylä / Central Finland Health Care District, Jyväskylä, Finland
Urho Kujala Central Finland Biobank / University of Jyväskylä / Central Finland Health Care District, Jyväskylä, Finland

Johanna Mäkelä

FINBB - Finnish biobank cooperative

Clinical Groups

Neurology Group

Reetta Kälviäinen	Northern Savo Hospital District, Kuopio, Finland
Valtteri Julkunen	Northern Savo Hospital District, Kuopio, Finland
Hilkka Soininen	Northern Savo Hospital District, Kuopio, Finland
Anne Remes	Northern Ostrobothnia Hospital District, Oulu, Finland
Mikko Hiltunen	Northern Savo Hospital District, Kuopio, Finland
Jukka Peltola	Pirkanmaa Hospital District, Tampere, Finland
Pentti Tienari	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Juha Rinne	Hospital District of Southwest Finland, Turku, Finland
Roosa Kallionpää	Hospital District of Southwest Finland, Turku, Finland
Ali Abbasi	Abbvie, Chicago, IL, United States
Adam Ziemann	Abbvie, Chicago, IL, United States
Jeffrey Waring	Abbvie, Chicago, IL, United States
Sahar Esmaeeli	Abbvie, Chicago, IL, United States
Nizar Smaoui	Abbvie, Chicago, IL, United States
Anne Lehtonen	Abbvie, Chicago, IL, United States
Susan Eaton	Biogen, Cambridge, MA, United States
Heiko Runz	Biogen, Cambridge, MA, United States
Sanni Lahdenperä	Biogen, Cambridge, MA, United States
Janet van Adelsberg	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Shameek Biswas	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Julie Hunkapiller	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Edmond Teng	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Onuralp Soylemez	Merck, Kenilworth, NJ, United States
Kari Linden	Pfizer, New York, NY, United States
Fanli Xu	GlaxoSmithKline, Brentford, United Kingdom
David Pulford	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Laura Addis	GlaxoSmithKline, Brentford, United Kingdom
John Eicher	GlaxoSmithKline, Brentford, United Kingdom
Minna Raivio	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Beryl Cummings	Maze Therapeutics, San Francisco, CA, United States
Juulia Partanen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Gastroenterology Group

Martti Färkkilä	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Jukka Koskela	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Sampsa Pikkarainen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Airi Jussila	Pirkanmaa Hospital District, Tampere, Finland
Katri Kaukinen	Pirkanmaa Hospital District, Tampere, Finland
Timo Blomster	Northern Ostrobothnia Hospital District, Oulu, Finland
Mikko Kiviniemi	Northern Savo Hospital District, Kuopio, Finland
Markku Voutilainen	Hospital District of Southwest Finland, Turku, Finland
Ali Abbasi	Abbvie, Chicago, IL, United States
Graham Heap	Abbvie, Chicago, IL, United States
Jeffrey Waring	Abbvie, Chicago, IL, United States
Nizar Smaoui	Abbvie, Chicago, IL, United States
Fedik Rahimov	Abbvie, Chicago, IL, United States

Anne Lehtonen	Abbvie, Chicago, IL, United States
Keith Usiskin	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY,
United States	
Tim Lu	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Danny Oh	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Kirsi Kalpala	Pfizer, New York, NY, United States
Melissa Miller	Pfizer, New York, NY, United States
Xinli Hu	Pfizer, New York, NY, United States
Linda McCarthy	GlaxoSmithKline, Brentford, United Kingdom
Onuralp Soylemez	Merck, Kenilworth, NJ, United States
Mark Daly	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Rheumatology Group

Kari Eklund	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Antti Palomäki	Hospital District of Southwest Finland, Turku, Finland
Pia Isomäki	Pirkanmaa Hospital District, Tampere, Finland
Laura Pirilä	Hospital District of Southwest Finland, Turku, Finland
Olli Kaipiainen-Seppänen	Northern Savo Hospital District, Kuopio, Finland
Johanna Huhtakangas	Northern Ostrobothnia Hospital District, Oulu, Finland
Ali Abbasi	Abbvie, Chicago, IL, United States
Jeffrey Waring	Abbvie, Chicago, IL, United States
Fedik Rahimov	Abbvie, Chicago, IL, United States
Apinya Lertratanakul	Abbvie, Chicago, IL, United States
Nizar Smaoui	Abbvie, Chicago, IL, United States
Anne Lehtonen	Abbvie, Chicago, IL, United States
David Close	Astra Zeneca, Cambridge, United Kingdom
Marla Hochfeld	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY,
United States	
Natalie Bowers	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Onuralp Soylemez	Merck, Kenilworth, NJ, United States
Kirsi Kalpala	Pfizer, New York, NY, United States
Nan Bing	Pfizer, New York, NY, United States
Xinli Hu	Pfizer, New York, NY, United States
Jorge Esparza Gordillo	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Dawn Waterworth	Janssen Biotech, Beerse, Belgium
Nina Mars	Institute for Molecular Medicine Finland, HiLIFE, Helsinki, Finland

Pulmonology Group

Tarja Laitinen	Pirkanmaa Hospital District, Tampere, Finland
Margit Pelkonen	Northern Savo Hospital District, Kuopio, Finland
Paula Kauppi	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Hannu Kankaanranta	Pirkanmaa Hospital District, Tampere, Finland
Terttu Harju	Northern Ostrobothnia Hospital District, Oulu, Finland
Riitta Lahesmaa	Hospital District of Southwest Finland, Turku, Finland
Nizar Smaoui	Abbvie, Chicago, IL, United States
Alex Mackay	Astra Zeneca, Cambridge, United Kingdom
Glenda Lassi	Astra Zeneca, Cambridge, United Kingdom
Susan Eaton	Biogen, Cambridge, MA, United States
Steven Greenberg	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY,
United States	
Hubert Chen	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States

Natalie Bowers	Genentech, San Francisco, CA, United States
Joanna Betts	GlaxoSmithKline, Brentford, United Kingdom
Soumitra Ghosh	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Rajashree Mishra	GlaxoSmithKline, Brentford, United Kingdom
Sina Rüeger	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Cardiometabolic Diseases Group

Teemu Niiranen	The National Institute of Health and Welfare Helsinki, Finland
Felix Vaura	The National Institute of Health and Welfare Helsinki, Finland
Veikko Salomaa	The National Institute of Health and Welfare Helsinki, Finland
Markus Juonala	Hospital District of Southwest Finland, Turku, Finland
Kaj Metsärinne	Hospital District of Southwest Finland, Turku, Finland
Mika Kähönen	Pirkanmaa Hospital District, Tampere, Finland
Juhani Junttila	Northern Ostrobothnia Hospital District, Oulu, Finland
Markku Laakso	Northern Savo Hospital District, Kuopio, Finland
Jussi Pihlajmäki	Northern Savo Hospital District, Kuopio, Finland
Daniel Gordin	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Juha Sinisalo	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Marja-Riitta Taskinen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Tiinamaija Tuomi	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Jari Laukkanen	Central Finland Health Care District, Jyväskylä, Finland
Benjamin Challis	Astra Zeneca, Cambridge, United Kingdom
Dirk Paul	Astra Zeneca, Cambridge, United Kingdom
Julie Hunkapiller	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Onuralp Soylemez	Merck, Kenilworth, NJ, United States
Jaakko Parkkinen	Pfizer, New York, NY, United States
Melissa Miller	Pfizer, New York, NY, United States
Russell Miller	Pfizer, New York, NY, United States
Audrey Chu	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Keith Usiskin	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY,
United States	
Amanda Elliott	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
Broad Institute, Cambridge, MA, United States	
Joel Rämö	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Samuli Ripatti	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mary Pat Reeve	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Sanni Ruotsalainen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Oncology Group

Tuomo Meretoja	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Heikki Joensuu	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Olli Carpén	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Lauri Aaltonen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Johanna Mattson	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Annika Auranen	Pirkanmaa Hospital District, Tampere, Finland
Peeter Karihtala	Northern Ostrobothnia Hospital District, Oulu, Finland
Saila Kauppila	Northern Ostrobothnia Hospital District, Oulu, Finland
Päivi Auvinen	Northern Savo Hospital District, Kuopio, Finland
Klaus Elenius	Hospital District of Southwest Finland, Turku, Finland
Johanna Schleutker	Hospital District of Southwest Finland, Turku, Finland
Relja Popovic	Abbvie, Chicago, IL, United States
Jeffrey Waring	Abbvie, Chicago, IL, United States

Bridget Riley-Gillis	Abbvie, Chicago, IL, United States
Anne Lehtonen	Abbvie, Chicago, IL, United States
Jennifer Schutzman	Genentech, San Francisco, CA, United States
Julie Hunkapiller	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Andrey Loboda	Merck, Kenilworth, NJ, United States
Aparna Chhibber	Merck, Kenilworth, NJ, United States
Heli Lehtonen	Pfizer, New York, NY, United States
Stefan McDonough	Pfizer, New York, NY, United States
Marika Crohns	Sanofi, Paris, France
Sauli Vuoti	Sanofi, Paris, France
Diptee Kulkarni	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Esa Pitkänen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Nina Mars	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mark Daly	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Ophthalmology Group

Kai Kaarniranta	Northern Savo Hospital District, Kuopio, Finland
Joni A Turunen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Terhi Ollila	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Sanna Seitsonen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Hannu Uusitalo	Pirkanmaa Hospital District, Tampere, Finland
Vesa Aaltonen	Hospital District of Southwest Finland, Turku, Finland
Hannele Uusitalo-Järvinen	Pirkanmaa Hospital District, Tampere, Finland
Marja Luodonpää	Northern Ostrobothnia Hospital District, Oulu, Finland
Nina Hautala	Northern Ostrobothnia Hospital District, Oulu, Finland
Mengzhen Liu	Abbvie, Chicago, IL, United States
Heiko Runz	Biogen, Cambridge, MA, United States
Stephanie Loomis	Biogen, Cambridge, MA, United States
Erich Strauss	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Hao Chen	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Anna Podgornaia	Merck, Kenilworth, NJ, United States
Juha Karjalainen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
Broad Institute, Cambridge, MA, United States	
Esa Pitkänen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Dermatology Group

Kaisa Tasanen	Northern Ostrobothnia Hospital District, Oulu, Finland
Laura Huilaja	Northern Ostrobothnia Hospital District, Oulu, Finland
Katariina Hannula-Jouppi	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Teea Salmi	Pirkanmaa Hospital District, Tampere, Finland
Sirkku Peltonen	Hospital District of Southwest Finland, Turku, Finland
Leena Koulu	Hospital District of Southwest Finland, Turku, Finland
Kirsi Kalpala	Pfizer, New York, NY, United States
Ying Wu	Pfizer, New York, NY, United States
David Choy	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Nizar Smaoui	Abbvie, Chicago, IL, United States
Fedik Rahimov	Abbvie, Chicago, IL, United States
Anne Lehtonen	Abbvie, Chicago, IL, United States
Dawn Waterworth	Janssen Biotech, Beerse, Belgium

Odontology Group

Pirkko Pussinen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Aino Salminen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Tuula Salo	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
David Rice	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Pekka Nieminen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Ulla Palotie	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Juha Sinisalo	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Maria Siponen	Northern Savo Hospital District, Kuopio, Finland
Liisa Suominen	Northern Savo Hospital District, Kuopio, Finland
Päivi Mäntylä	Northern Savo Hospital District, Kuopio, Finland
Ulvi Gursoy	Hospital District of Southwest Finland, Turku, Finland
Vuokko Anttonen	Northern Ostrobothnia Hospital District, Oulu, Finland
Kirsi Sipilä	Northern Ostrobothnia Hospital District, Oulu, Finland
Sarah Pendergrass	Genentech, San Francisco, CA, United States

Women's Health and Reproduction Group

Hannele Laivuori	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Venla Kurra	Pirkanmaa Hospital District, Tampere, Finland
Oskari Heikinheimo	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Ilkka Kalliala	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Laura Kotaniemi-Talonen	Pirkanmaa Hospital District, Tampere, Finland
Kari Nieminen	Pirkanmaa Hospital District, Tampere, Finland
Päivi Polo	Hospital District of Southwest Finland, Turku, Finland
Kaarin Mäkikallio	Hospital District of Southwest Finland, Turku, Finland
Eeva Ekholm	Hospital District of Southwest Finland, Turku, Finland
Marja Vääräsmäki	Northern Ostrobothnia Hospital District, Oulu, Finland
Outi Uimari	Northern Ostrobothnia Hospital District, Oulu, Finland
Laure Morin-Papunen	Northern Ostrobothnia Hospital District, Oulu, Finland
Marjo Tuppurainen	Northern Savo Hospital District, Kuopio, Finland
Katja Kivinen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Elisabeth Widen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Taru Tukiainen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mary Pat Reeve	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mark Daly	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Liu Aoxing	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Eija Laakkonen	University of Jyväskylä, Jyväskylä, Finland
Niko Välimäki	University of Helsinki, Helsinki, Finland
Lauri Aaltonen	Hospital District of Helsinki and Uusimaa, Helsinki, Finland
Johannes Kettunen	Northern Ostrobothnia Hospital District, Oulu, Finland
Mikko Arvas	Finnish Red Cross Blood Service, Helsinki, Finland
Jeffrey Waring	Abbvie, Chicago, IL, United States
Bridget Riley-Gillis	Abbvie, Chicago, IL, United States
Mengzhen Liu	Abbvie, Chicago, IL, United States
Janet Kumar	GlaxoSmithKline, Brentford, United Kingdom
Kirsi Auro	GlaxoSmithKline, Brentford, United Kingdom
Andrea Ganna	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Sarah Pendergrass	Genentech, San Francisco, CA, United States

FinnGen Analysis working group

Justin Wade Davis	Abbvie, Chicago, IL, United States
Bridget Riley-Gillis	Abbvie, Chicago, IL, United States
Reza Hammond	Abbvie, Chicago, IL, United States
Fedik Rahimov	Abbvie, Chicago, IL, United States
Sahar Esmaeeli	Abbvie, Chicago, IL, United States
Mengzhen Liu	Abbvie, Chicago, IL, United States

Slavé Petrovski	Astra Zeneca, Cambridge, United Kingdom
Eleonor Wigmore	Astra Zeneca, Cambridge, United Kingdom
Adele Mitchell	Biogen, Cambridge, MA, United States
Benjamin Sun	Biogen, Cambridge, MA, United States
Ellen Tsai	Biogen, Cambridge, MA, United States
Denis Baird	Biogen, Cambridge, MA, United States
Paola Bronson	Biogen, Cambridge, MA, United States
Ruoyu Tian	Biogen, Cambridge, MA, United States
Stephanie Loomis	Biogen, Cambridge, MA, United States
Yunfeng Huang	Biogen, Cambridge, MA, United States
Joseph Maranhville	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Shameek Biswas	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Elmutaz Mohammed	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Samir Wadhawan	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Erika Kvikstad	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Minal Caliskan	Celgene, Summit, NJ, United States/ Bristol Myers Squibb, New York, NY, United States
Diana Chang	Genentech, San Francisco, CA, United States
Julie Hunkapiller	Genentech, San Francisco, CA, United States
Tushar Bhangale	Genentech, San Francisco, CA, United States
Natalie Bowers	Genentech, San Francisco, CA, United States
Sarah Pendergrass	Genentech, San Francisco, CA, United States
Kirill Shkura	Merck, Kenilworth, NJ, United States
Victor Neduva	Merck, Kenilworth, NJ, United States
Xing Chen	Pfizer, New York, NY, United States
Åsa Hedman	Pfizer, New York, NY, United States
Karen S King	GlaxoSmithKline, Brentford, United Kingdom
Padhraig Gormley	GlaxoSmithKline, Brentford, United Kingdom
Jimmy Liu	GlaxoSmithKline, Brentford, United Kingdom
Clarence Wang	Sanofi, Paris, France
Ethan Xu	Sanofi, Paris, France
Franck Auge	Sanofi, Paris, France
Clement Chatelain	Sanofi, Paris, France
Deepak Rajpal	Sanofi, Paris, France
Dongyu Liu	Sanofi, Paris, France
Katherine Call	Sanofi, Paris, France
Tai-He Xia	Sanofi, Paris, France
Beryl Cummings	Maze Therapeutics, San Francisco, CA, United States
Matt Brauer	Maze Therapeutics, San Francisco, CA, United States
Huilei Xu	Novartis, Basel, Switzerland
Amy Cole	Novartis, Basel, Switzerland
Jonathan Chung	Novartis, Basel, Switzerland
Jaison Jacob	Novartis, Basel, Switzerland
Katrina de Lange	Novartis, Basel, Switzerland
Jonas Zierer	Novartis, Basel, Switzerland
Mitja Kurki	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland / Broad Institute, Cambridge, MA, United States
Samuli Ripatti	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mark Daly	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Juha Karjalainen	Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland / Broad Institute, Cambridge, MA, United States

Aki Havulinna Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Juha Mehtonen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Priit Palta Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Shabbeer Hassan Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Pietro Della Briotta Parolo Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Wei Zhou Broad Institute, Cambridge, MA, United States
 Mutaamba Maasha Broad Institute, Cambridge, MA, United States
 Shabbeer Hassan Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Susanna Lemmelä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Manuel Rivas University of Stanford, Stanford, CA, United States
 Aarno Palotie Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Arto Lehisto Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Andrea Ganna Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Vincent Llorens Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Hannele Laivuori Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Mari E Niemi Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Taru Tukiainen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Mary Pat Reeve Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Henrike Heyne Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Nina Mars Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Kimmo Palin University of Helsinki, Helsinki, Finland
 Javier Garcia-Tabuenca University of Tampere, Tampere, Finland
 Harri Siirtola University of Tampere, Tampere, Finland
 Tuomo Kiiskinen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
 Jiwoo Lee Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
 Broad Institute, Cambridge, MA, United States
 Kristin Tsuo Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
 Broad Institute, Cambridge, MA, United States
 Amanda Elliott Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
 Broad Institute, Cambridge, MA, United States
 Kati Kristiansson THL Biobank / The National Institute of Health and Welfare Helsinki, Finland
 Mikko Arvas Finnish Red Cross Blood Service / Finnish Hematology Registry and Clinical
 Biobank, Helsinki, Finland
 Kati Hyvärinen Finnish Red Cross Blood Service, Helsinki, Finland
 Jarmo Ritari Finnish Red Cross Blood Service, Helsinki, Finland
 Miika Koskinen Helsinki Biobank / Helsinki University and Hospital District of Helsinki and
 Uusimaa, Helsinki
 Olli Carpén Helsinki Biobank / Helsinki University and Hospital District of Helsinki and
 Uusimaa, Helsinki
 Johannes Kettunen Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia
 Hospital District, Oulu, Finland
 Katri Pylkäs University of Oulu, Oulu, Finland
 Eeva Sliz University of Oulu, Oulu, Finland
 Minna Karjalainen University of Oulu, Oulu, Finland
 Tuomo Mantere Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia
 Hospital District, Oulu, Finland
 Eeva Kangasniemi Finnish Clinical Biobank Tampere / University of Tampere / Pirkanmaa Hospital
 District, Tampere, Finland
 Sami Heikkinen University of Eastern Finland, Kuopio, Finland
 Arto Mannermaa Biobank of Eastern Finland / University of Eastern Finland / Northern Savo
 Hospital District, Kuopio, Finland
 Eija Laakkonen University of Jyväskylä, Jyväskylä, Finland
 Samuel Heron University of Turku, Turku, Finland
 Dhanaprakash Jambulingam University of Turku, Turku, Finland
 Venkat Subramaniam Rathinakannan University of Turku, Turku, Finland

Nina Pitkänen Auria Biobank / University of Turku / Hospital District of Southwest Finland,
Turku, Finland

Biobank directors

Lila Kallio Auria Biobank / University of Turku / Hospital District of Southwest Finland,
Turku, Finland
Sirpa Soini THL Biobank / The National Institute of Health and Welfare Helsinki, Finland
Jukka Partanen Finnish Red Cross Blood Service / Finnish Hematology Registry and Clinical
Biobank, Helsinki, Finland
Eero Punkka Helsinki Biobank / Helsinki University and Hospital District of Helsinki and
Uusimaa, Helsinki
Raisa Serpi Northern Finland Biobank Borealis / University of Oulu / Northern Ostrobothnia
Hospital District, Oulu, Finland
TBC Finnish Clinical Biobank Tampere / University of Tampere / Pirkanmaa Hospital
District, Tampere, Finland
Veli-Matti Kosma Biobank of Eastern Finland / University of Eastern Finland / Northern Savo
Hospital District, Kuopio, Finland
Teijo Kuopio Central Finland Biobank / University of Jyväskylä / Central Finland Health Care
District, Jyväskylä, Finland

FinnGen Teams

Administration

Anu Jalanko Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Huei-Yi Shen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Risto Kajanne Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Mervi Aavikko Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Analysis

Mitja Kurki Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
Broad Institute, Cambridge, MA, United States
Juha Karjalainen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland /
Broad Institute, Cambridge, MA, United States
Pietro Della Briotta Parolo Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki,
Finland
Arto Lehisto Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Juha Mehtonen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Wei Zhou Broad Institute, Cambridge, MA, United States
Masahiro Kanai Broad Institute, Cambridge, MA, United States
Mutaamba Maasha Broad Institute, Cambridge, MA, United States

Clinical Endpoint Development

Hannele Laivuori Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Aki Havulinna Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Susanna Lemmelä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Tuomo Kiiskinen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
L. Elisa Lahtela Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Communication

Mari Kaunisto Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

E-Science

Elina Kilpeläinen Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Timo P. Sipilä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland
Georg Brein Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Oluwaseun Alexander Dada Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Awaisa Ghazal Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Anastasia Shcherban Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Genotyping

Kati Donner Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Timo P. Sipilä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Sample Collection Coordination

Anu Loukola Helsinki Biobank / Helsinki University and Hospital District of Helsinki and Uusimaa, Helsinki

Sample Logistics

Päivi Laiho THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Tuuli Sistonen THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Essi Kaiharju THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Markku Laukkanen THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Elina Järvensivu THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Sini Lähteenmäki THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Lotta Männikkö THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Regis Wong THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Registry Data Operations

Hannele Mattsson THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Kati Kristiansson THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Susanna Lemmelä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Sami Koskelainen THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Tero Hiekkalinna THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Teemu Paajanen THL Biobank / The National Institute of Health and Welfare Helsinki, Finland

Sequencing Informatics

Priit Palta Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Kalle Pärn Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Mart Kals Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Shuang Luo Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Vishal Sinha Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Trajectory

Tarja Laitinen Pirkanmaa Hospital District, Tampere, Finland

Mary Pat Reeve Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

Harri Siirtola University of Tampere, Tampere, Finland

Javier Gracia-Tabuenca University of Tampere, Tampere, Finland

Mika Helminen University of Tampere, Tampere, Finland

Tiina Luukkaala University of Tampere, Tampere, Finland

Iida Vähätalo University of Tampere, Tampere, Finland

Data protection officer

Tero Jyrhämä Institute for Molecular Medicine Finland, HiLIFE, University of Helsinki, Finland

FINBB - Finnish biobank cooperative

Marco Hautalahti

Johanna Mäkelä

Laura Mustaniemi

Mirka Koivusalo
Sarah Smith
Tom Southerington

Bibliography for Supplementary Data 7. Each reference starts with the PMID before a colon. The references are sorted by their PMIDs.

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