- Число публикаций, упоминающих метод полногеномного анализа ассоциации (Genome-Wide Association, GWA) по годам
- База данных PubMed
- Запрос ("genome-wide association" OR "whole-genome association") AND 2011[dp]


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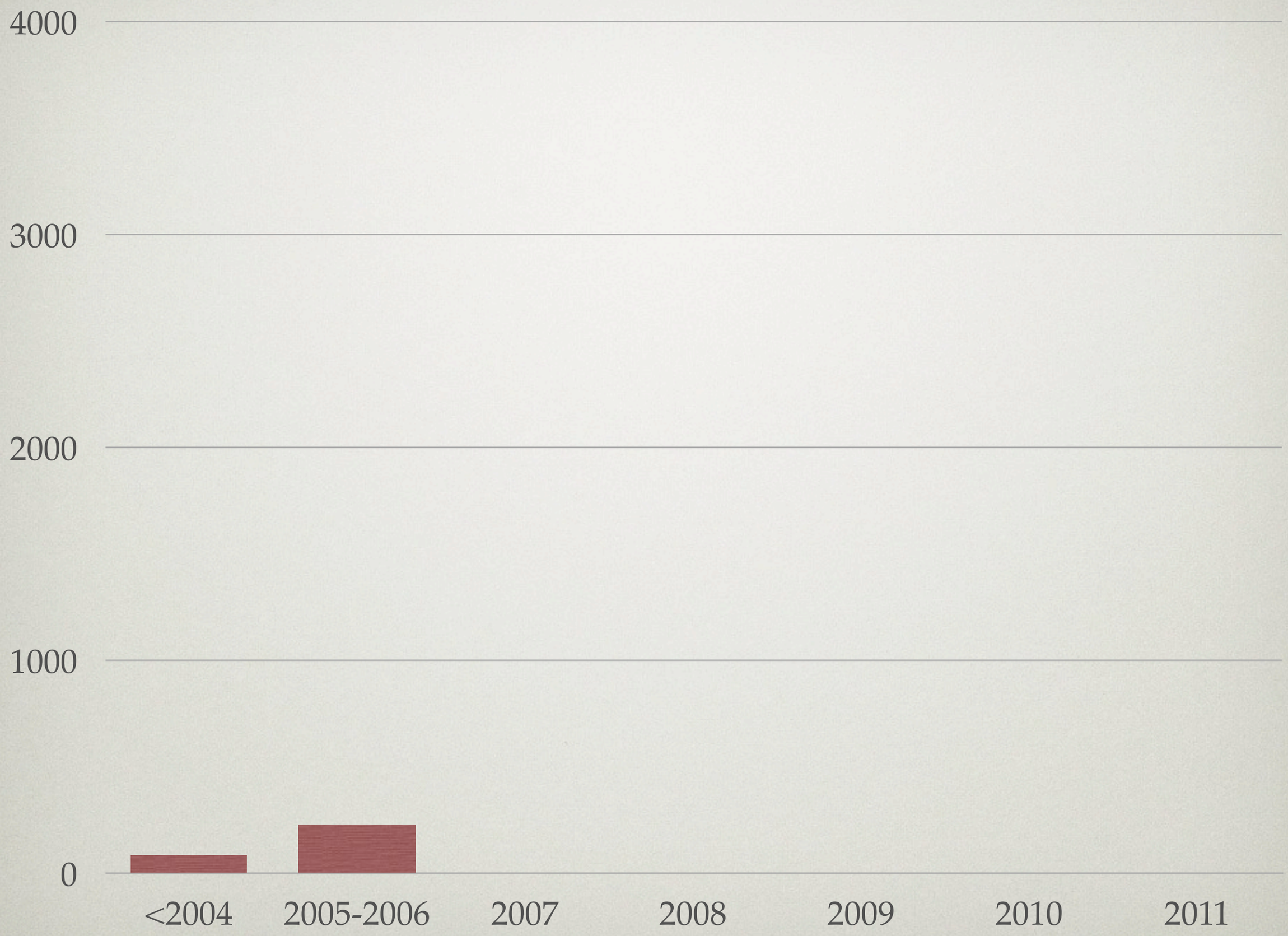
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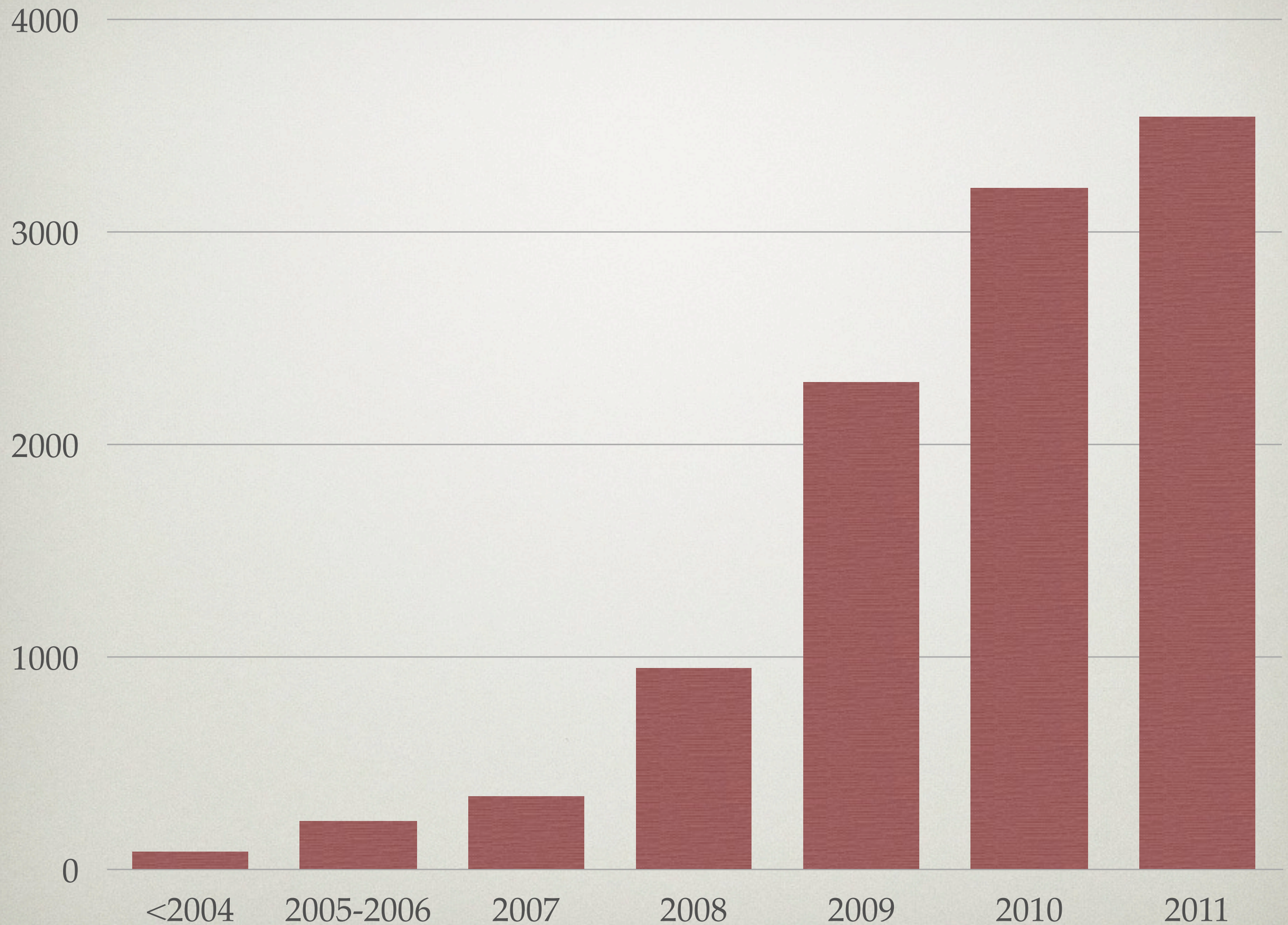
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Теоретическое обсуждение, разработка технологии и ресурсов


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Показано, что метод работает на практике

- Основной результат метода GWA - определение геномных районов (локусов), вариация последовательности которых связана с болезнями и другими признаками (человека)

- Число идентифицированых локусов (база данных GWAS Integrator)


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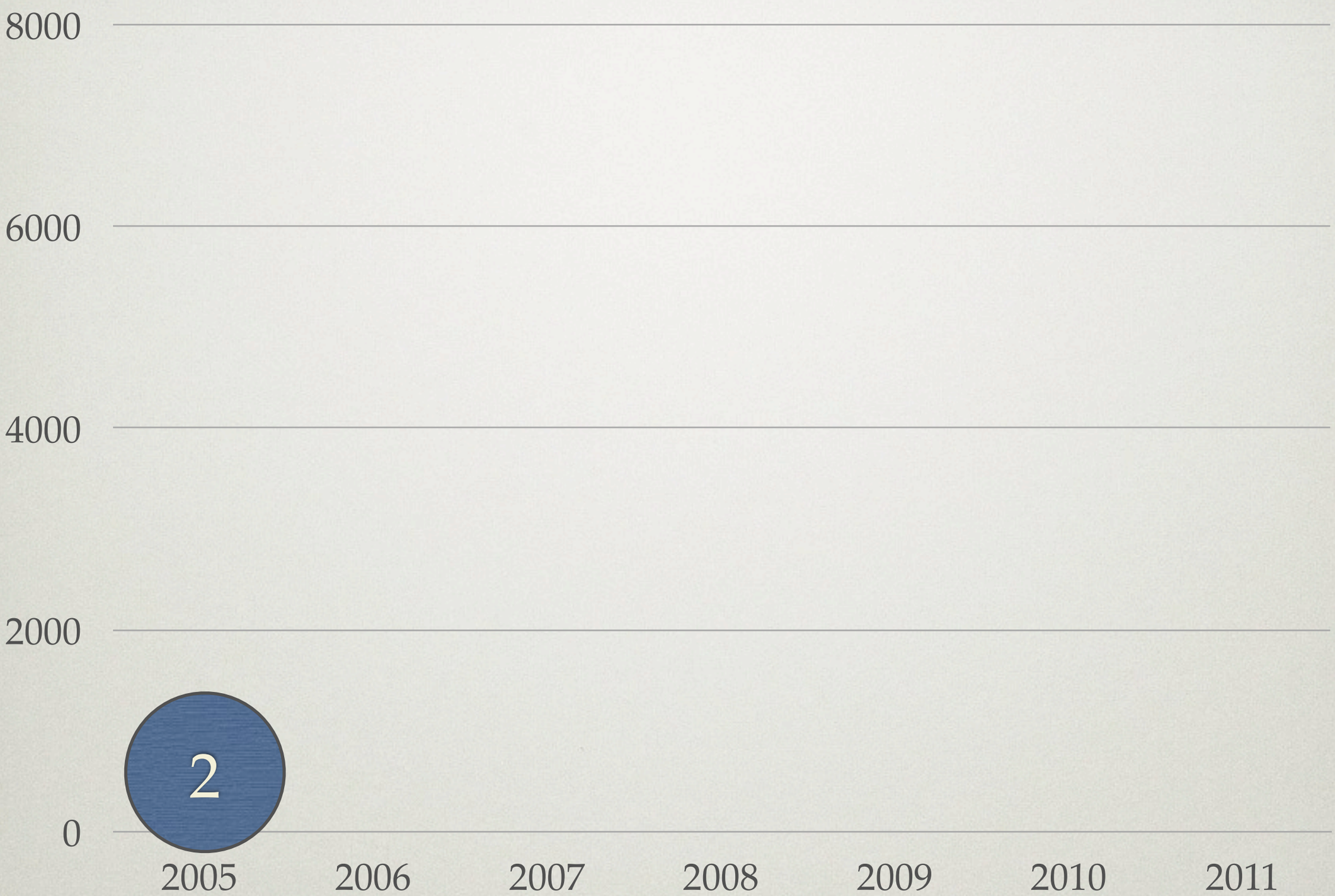
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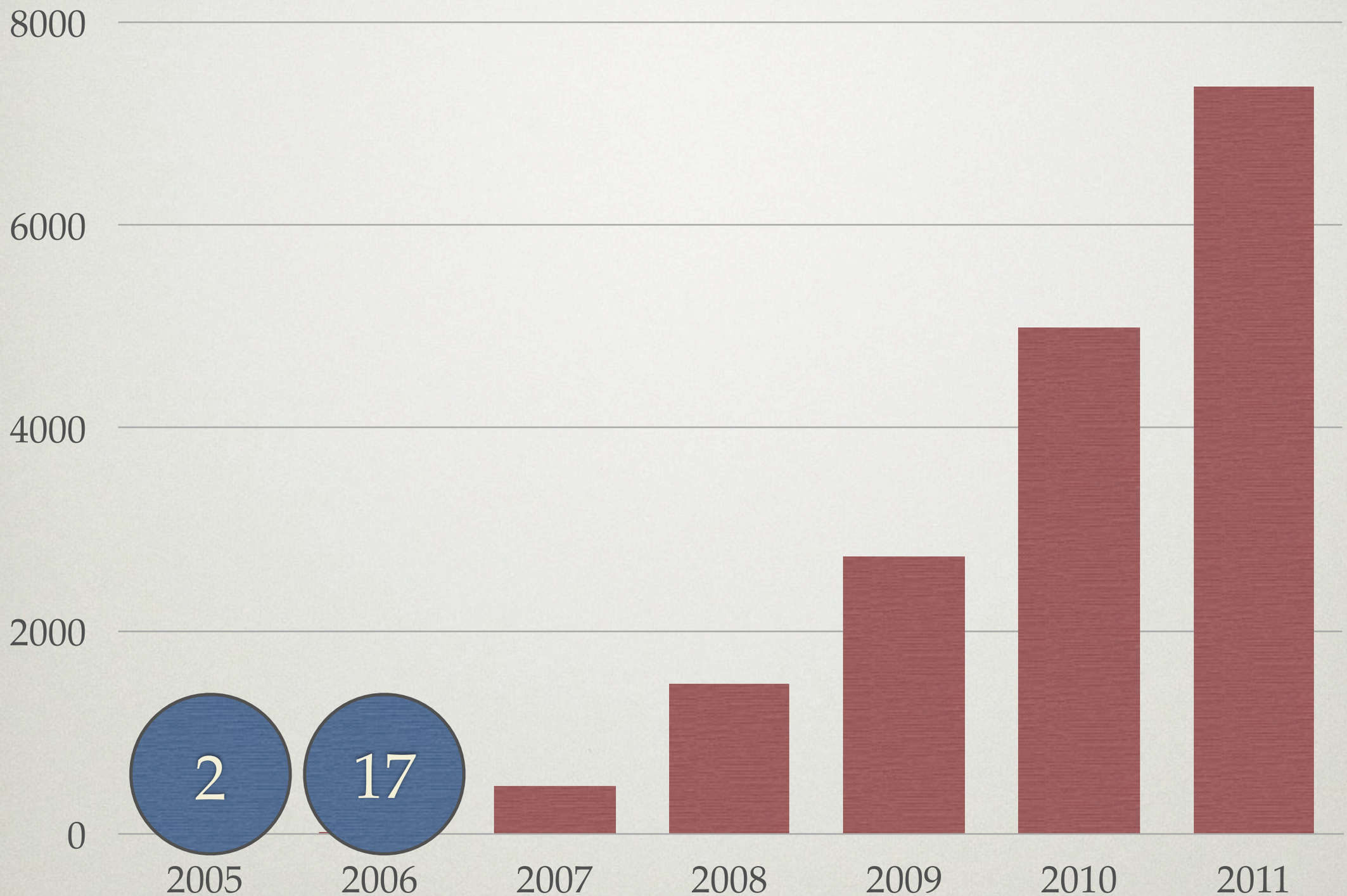
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A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol

Ida Surakka[1,2], Aaron Isaacs[3,4], Lennart C. Karssen[3], Pirkka-Pekka P. Laurila[1,2,5], Rita P. S. Middelberg[6,7], Emmi Tikkanen[1,2], Janina S. Ried[8], Claudia Lamina[9], Massimo Mangino[10], Wilmar Igl[11], Jouke-Jan Hottenga[12], Vasiliki Lagou[13,14], Pim van der Harst[15], Irene Mateo Leach[15], Tõnu Esko[16,17], Zoltán Kutalik[18,19], Nicholas W. Wainwright[20,21], Maksim V. Struchalin[3], Antti-Pekka Sarin[1,2], Antti J. Kangas[22], Jorma S. Viikari[23], Markus Perola[1,2,16], Taina Rantanen[24], Ann-Kristin Petersen[8], Pasi Soininen[25], Åsa Johansson[11], Nicole Soranzo[10,20], Andrew C. Heath[26], Theodore Papamarkou[20,21], Inga Prokopenko[13,14], Anke Tönjes[27,28], Florian Kronenberg[9], Angela Döring[29,30], Fernando Rivadeneira[31,32,33], Grant W. Montgomery[6], John B. Whitfield[6], Mika Kähönen[34,35], Terho Lehtimäki[35,36], Nelson B. Freimer[37,38], Gonneke Willemsen[12], Eco J. C. de Geus[12], Aarno Palotie[1,5,20,39], Manj S. Sandhu[20,21], Dawn M. Waterworth[40], Andres Metspalu[16,17,41], Michael Stumvoll[42], André G. Uitterlinden[31,32,33], Antti Jula[43], Gerjan Navis[44], Cisca Wijmenga[45], Bruce H. R. Wolffenbuttel[46], Marja-Riitta Taskinen[47], Mika Ala-Korpela[22,25,48], Jaakko Kaprio[1,49,50], Kirsten O. Kyvik[51,52], Dorret I. Boomsma[12], Nancy L. Pedersen[53], Ulf Gyllensten[11], James F. Wilson[54], Igor Rudan[54,55], Harry Campbell[54], Peter P. Pramstaller[56,57,58,59], Tim D. Spector[10], Jacqueline C. M. Witteman[31,32,33], Johan G. Eriksson[60,61,62,63,64], Veikko Salomaa[65], Ben A. Oostra[66], Olli T. Raitakari[67,68], H.-Erich Wichmann[29,69,70], Christian Gieger[8], Marjo-Riitta Järvelin[71], Nicholas G. Martin[6], Albert Hofman[31,32,33], Mark I. McCarthy[13,14,72], Leena Peltonen[1,2,5,18,39]†, Cornelia M. van Duijn[3,4,33], Yurii S. Aulchenko[3]¶, Samuli Ripatti[1,2,20]¶*, for the ENGAGE Consortium

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IF ~ 10

nature genetics

Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts

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ARTICLES

nature genetics

Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts

IF ~ 36

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LETTER

doi:10.1038/nature09410

Hundreds of variants clustered in genomic loci and biological pathways affect human height

A full list of authors and their affiliations appears at the end of the paper.

LETTER

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IF ~ 36

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A full list of authors and their affiliations appears at the end of the paper.

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Feitosa[37], Tõnu Esko[38,39,40], Toby Johnson[41,42,43,44], Shamika Ketkar[37], Peter Kraft[45,46], Massimo Mangino[18], Inga Prokopenko[13,47], Devin Absher[48], Eva Albrecht[31], Florian Ernst[49], Nicole L. Glazer[50], Caroline Hayward[51], Jouke-Jan Hottenga[52], Kevin B. Jacobs[53], Joshua W. Knowles[54], Zoltán Kutalik[41,42], Keri L. Monda[55], Ozren Polasek[56,57], Michael Preuss[58], Nigel W. Rayner[13,47], Neil R. Robertson[13,47], Valgerdur Steinthorsdottir[20], Jonathan P. Tyrer[59], Benjamin F. Voight[11,14,15], Fredrik Wiklund[60], Jianfeng Xu[61], Jing Hua Zhao[32], Dale R. Nyholt[62], Niina Pellikka[63,64], Markus Perola[63,64], John R. B. Perry[1], Ida Surakka[63,64], Mari-Liis Tammesoo[38], Elizabeth L. Altmaier[9,10], Najaf Amin[2], Thor Aspelund[24,25], Tushar Bhangale[65], Gabrielle Boucher[5], Daniel I. Chasman[66,67], Constance Chen[68], Lachlan Coin[69], Matthew N. Cooper[70], Anna L. Dixon[71], Quince Gibson[72], Elin Grundberg[17,26,27], Ke Hao[73], M. 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Peters[3,4], Samuli Ripatti[63,64], Joyce B. J. van Meurs[2,3,4], Katja K. Aben[136], Kristin G. Ardlie[11], Jacques S. Beckmann[41,137], John P. Bellby[108,109,138], Richard N. Bergman[139], Sven Bergmann[41,42], Francis S. Collins[140], Daniele Cusi[95], Martin den Heijer[141], Gudny Eiríksdóttir[24], Pablo V. Gejman[97], Alistair S. Hall[92], Anders Hamsten[142], Heikki V. Huikuri[74], Carlos Infante[143,144], Mika Kähönen[145], Jaakko Kaprio[63,123,146], Sekar Kathiresan[11,14,147,148,149], Lambertus Kiemeney[136,150,151], Thomas Kocher[152], Lenore J. Launer[153], Terho Lehtimäki[154], Olle Melander[126], Tom H. Mosley Jr[155], Arthur W. Musk[108,156], Markku S. Nieminen[131], Christopher J. O'Donnell[140,157], Claes Ohlsson[77], Ben Oostra[158], Lyle J. Palmer[70,109], Olli Raitakari[159], Paul M. Ridker[66,67], John D. Rioux[56], Aila Rissanen[124], Carlo Rivolta[41], Heribert Schunkert[160], Alan R. Shuldiner[72,161], David S. 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Hayes[187], Marjo-Riitta Jarvelin[69,111,125,188], Vincent Mooser[183], Patricia B. Munroe[44], Willem H. Ouwehand[17,128,129], Brenda W. Penninx[136,189,190], Peter P. Pramstaller[95,191,192], Thomas Quertermous[54], Igor Rudan[51,116], Nilesh J. Samani[94,98], Timothy D. Spector[18], Henry Völzke[130], Hugh Watkins on behalf of the Procardis Consortium[13,121], James F. Wilson[93], Leif C. Groop[91], Talin Haritunians[127], Frank B. Hu[22,23,45], Robert C. Kaplan[193], Andres Metspalu[38,39,40], Kari E. North[55,194], David Schlessinger[195], Nicholas J. Wareham[32], David J. Hunter[22,23,45], Jeffrey R. O'Connell[72], David P. Strachan[196], H.-Erich Wichmann[31,80,197], Ingrid B. Borecki[37,175], Cornelia M. van Duijn[2,4], Eric E. Schadt[198,199], Unnur Thorsteinsdottir[20,200], Leena Peltonen[17,63,64,82,201], André G. Uitterlinden[2,3,4], Peter M. Visscher[19], Nilanjan Chatterjee[7], Ruth J. F. Loos[32], Michael Boehnke[8], Mark I. 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Методологические исследования

AJHG

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Article

Abundant Pleiotropy in Human Complex Diseases and Traits

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IF ~ 12

TECHNICAL REPORTS

nature genetics

Variance component model to account for sample structure in genome-wide association studies

Hyun Min Kang[1,2,8], Jae Hoon Sul[3,8], Susan K Service[4], Noah A Zaitlen[5], Sit-yee Kong[4], Nelson B Freimer[4], Chiara Sabatti[6] & Eleazar Eskin[3,7]

IF ~ 36

Временная структура курса

Временная структура курса

Основы генетики и популяционной генетики

Временная структура курса

Основы эпидемологии и исследования ассоциации

Основы генетики и популяционной генетики

Временная структура курса

Полногеномный анализ ассоциации

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Основы генетики и популяционной генетики

Временная структура курса

Современные проблемы статистической геномики

Полногеномный анализ ассоциации

Основы эпидемологии и исследования ассоциации

Основы генетики и популяционной генетики