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SUPPLEMENTARY NOTE

Part 1: Discussion of novel loci.

The six novel loci we have identified (*SIPA1L2, INPP5F, MIR4697, GCH1, VPS13C*, and *DDRGK1*) in this meta-analysis include biologically plausible connections to PD etiology based on previous research. In the context of GWAS it is clear that the pathobiologically relevant gene is not always the closest or most obvious proximal candidate.[1] However, it is perhaps useful to discuss the potential pathobiological relevance of the candidate genes at our loci, with the caveat that further work is required to identify whether these are the true biological candidates. The signal-induced proliferation-associated 1 like 2 (SIPA1L2) locus has been implicated in inflammatory pathways by GWAS as well as in pharmacogenetic studies of smoking cessation and related behaviors.[2,3] INPP5F has been suggested as an initial candidate locus for late-onset alzheimer's disease from linkage studies.[4] *MIR4697* is a provisional microRNA identified in next generation sequencing studies of breast cancer.[5] GTP cyclohydrolase 1 (*GCH1*) is a likely biological candidate for future therapeutics and follow-up study, as SNPs at this locus are also associated with dopamine clearance in urine.[6] In addition, the *GCH1* locus has been offered as a risk locus in early onset and atypical PD, but results until this point have never been definitive.[7-9] The locus containing rs2414739 and the *VPS13C* gene possesses a likely connection to neurodegenerative disease etiology as alternative splicing of *VPS13C* contributes to risk of congenital myasthenic syndrome. [10] *DDRGK1* is also connected to neurodegenerative disease as it has been suggested as a candidate locus for spinocerebellar ataxias.[11]

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Part 2: Additional Acknowledgements and Funding

This work was supported in part by the Intramural Research Programs of the National Institute of Neurological Disorders and Stroke (NINDS), the National Institute on Aging (NIA), and the National Institute of Environmental Health Sciences both part of the National Institutes of Health, Department of Health and Human Services; project numbers Z01-AG000949-02 and Z01-ES101986. In addition this work was supported by the Department of Defense (award W81XWH-09-2-0128), and The Michael J Fox Foundation for Parkinson's Research. This work was supported by National Institutes of Health grants R01NS037167, R01CA141668, P50NS071674, American Parkinson Disease Association (APDA); Barnes Jewish Hospital Foundation; Greater St Louis Chapter of the APDA; Hersenstichting Nederland; Neuroscience Campus Amsterdam; and the section of medical genomics, the Prinses Beatrix Fonds. The KORA (Cooperative Research in the Region of Augsburg) research platform was started and financed by the Forschungszentrum für Umwelt und Gesundheit, which is funded by the German Federal Ministry of Education, Science, Research, and Technology and by the State of Bavaria. This study was also funded by the German National Genome Network (NGFNplus number 01GS08134, German Ministry for Education and Research); by the German Federal Ministry of Education and Research (NGFN 01GR0468, PopGen); and 01EW0908 in the frame of ERA-NET NEURON and Helmholtz Alliance Mental Health in an Ageing Society (HA-215), which was funded by the Initiative and Networking Fund of the Helmholtz Association. The French GWAS work was supported by the French National Agency of Research (ANR-08-MNP-012). This study was also funded by France-Parkinson Association, the French program "Investissements d'avenir" funding (ANR-10-IAIHU-06) and a grant from Assistance Publique-Hôpitaux de Paris (PHRC, AOR-08010) for the French clinical data. This study was also sponsored by the Landspitali University Hospital Research Fund (grant to SSv); Icelandic Research Council (grant to SSv); and European Community Framework Programme 7, People Programme, and IAPP on novel genetic and phenotypic markers of Parkinson's disease and Essential Tremor (MarkMD),

contract number PIAP-GA-2008-230596 MarkMD (to HP and JHu). This study utilized the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, Md. (http://biowulf.nih.gov), and DNA panels, samples, and clinical data from the National Institute of Neurological Disorders and Stroke Human Genetics Resource Center DNA and Cell Line Repository. People who contributed samples are acknowledged in descriptions of every panel on the repository website. We thank the French Parkinson's Disease Genetics Study Group and the Drug Interaction with genes (DIGPD) study group: Y Agid, M Anheim, A-M Bonnet, M Borg, A Brice, E Broussolle, J-C Corvol, P Damier, A Destée, A Dürr, F Durif, A Elbaz, D Grabil, S Klebe, P. Krack, E Lohmann, L. Lacomblez, M Martinez, V Mesnage, P Pollak, O Rascol, F Tison, C Tranchant, M Vérin, F Viallet, and M Vidailhet. We also thank the members of the French 3C Consortium: A Alpérovitch, C Berr, C Tzourio, and P Amouyel for allowing us to use part of the 3C cohort, and D Zelenika for support in generating the genome-wide molecular data. We thank P Tienari (Molecular Neurology Programme, Biomedicum, University of Helsinki), T Peuralinna (Department of Neurology, Helsinki University Central Hospital), L Myllykangas (Folkhalsan Institute of Genetics and Department of Pathology, University of Helsinki), and R Sulkava (Department of Public Health and General Practice Division of Geriatrics, University of Eastern Finland) for the Finnish controls (Vantaa85+ GWAS data). We used genome-wide association data generated by the Wellcome Trust Case-Control Consortium 2 (WTCCC2) from UK patients with Parkinson's disease and UK control individuals from the 1958 Birth Cohort and National Blood Service. Genotyping of UK replication cases on ImmunoChip was part of the WTCCC2 project, which was funded by the Wellcome Trust (083948/Z/07/Z). UK population control data was made available through WTCCC1. This study was supported by the Medical Research Council and Wellcome Trust disease centre (grant WT089698/Z/09/Z to NW, JHa, and ASc). As with previous IPDGC efforts, this study makes use of data generated by the Wellcome Trust Case-Control Consortium. A full list of the investigators who contributed to the generation of the data is available from www.wtccc.org.uk. Funding for the project was provided by the Wellcome Trust under award 076113, 085475 and 090355. This study was also supported by Parkinson's UK (grants 8047 and J-0804) and the Medical Research Council (G0700943). We thank Jeffrey Barrett for assistance with the design of the ImmunoChip. DNA extraction work that was done in the UK was undertaken at University College London Hospitals, University College London, who received a proportion of funding from the Department of Health's National Institute for Health Research Biomedical Research Centres funding. This study was supported in part by the Wellcome Trust/Medical Research Council Joint Call in Neurodegeneration award (WT089698) to the Parkinson's Disease Consortium (UKPDC), whose members are from the UCL Institute of Neurology, University of Sheffield, and the Medical Research Council Protein Phosphorylation Unit at the University of Dundee.

We would like to thank the NINDS sponsored Neurogenetics Repository hosted by Coriell Cell Repositories for the use of both case and control samples.

The work performed by the North American Brain Expression Consortium (NABEC) was supported in part by the Intramural Research Program of the National Institute on Aging, National Institutes of Health, part of the US Department of Health and Human Services; project number Z01 AG000932-04. In addition this work was supported by a Research Grant from the Department of Defense, W81XWH-09-2-0128. This study utilized the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, Md. (http://biowulf.nih.gov). This work performed by the UK Brain Expression Consortium (UKBEC) was supported by the MRC through the MRC Sudden Death Brain Bank (C.S.), by a Project Grant (G0901254 to J.H. and M.W.) and by a Fellowship award (G0802462 to M.R.). D.T. was supported by the King Faisal Specialist Hospital and Research Centre, Saudi Arabia. Computing facilities used at King's College London were supported by the National Institute for Health Research (NIHR) Biomedical Research Centre based at Guy's and St Thomas' NHS Foundation Trust and King's College London. We would like to thank AROS Applied Biotechnology AS company laboratories and Affymetrix for their valuable input.
This work was also supported by National Institutes of Health grants NS050487 (Clark), NS060113 (Clark) and NS036630 (Marder) ,2UL1 RR024156 (Marder) and the Parkinson's Disease Foundation (Clark/Marder).
This work has also been made possible by the kind support of The Michael J. Fox Foundation for Parkinson's Research with additional support from Cure Alzheimer's Fund (CAF), Prize4Life, the National Alliance for Research on Schizophrenia and Depression (NARSAD), and EMD Serono (to Lars Bertram). Christina M. Lill has been supported by the Fidelity Biosciences Research Initiative. Haydeh Payami was supported by National Institutes of Health R01-NS-36960.

This study was supported by the Parkinson's disease foundation (PDF) (GX, HH) We would like to thank Mark Gaskin for help with sample organisation and aliquoting.
This study was supported in part by Research Committee, University of Thessaly (code 2845; PI: GMH). We would like to thank Maria Dardioti for help with sample organisation and aliquoting. This study was supported by the Parkinson's disease foundation (PDF) (GX, HH). This study was supported by the Parkinson's disease foundation (PDF) (CS). This study was supported in part by Research Grant "Sinergasia" awarded to LS from the Hellenic Secretariat of Research and Technology, as well as a Research Grant from GlaxoSmithKline Greece.

This work was supported by the National Heart, Lung and Blood Institute's Framingham Heart Study (Contract No. N01-HC-25195) and its contract with Affymetrix, Inc for genotyping services (Contract No. N02-HL-6-4278) This study was also supported by grants from the National Institute of Neurological Disorders and Stroke (NS17950) and the National Institute of Aging (AG08122,

AG16495, AG033193, AG031287, P30AG013846, and AG025259) and an unrestricted grant to the Framingham study from the Bumpus foundation.

Cardiovascular Health Study (CHS): This CHS research was supported by NHLBI contracts HHSN268201200036C, HHSN268200800007C, N01HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086; and NHLBI grants HL080295, HL087652, HL105756, HL103612, and HL120393 with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through AG023629 and P30AG024826 from the National Institute on Aging (NIA), 1K23NS070867 (NINDS), and 1KL2RR024154 (National Center for Research Resources). A full list of principal CHS investigators and institutions can be found at CHS-NHLBI.org.
The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.
The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Funding was obtained through the Internationaal Parkinson Fonds, Netherlands Consortium for Healthy Aging, Netherlands Organization for Scientific Research (NWO), Netherlands Organization for Health Research and Development (ZonMW), Research Institute for Diseases in the Elderly (RIDE)

The Oxford Brain Bank is supported by grants form the Medical Research Council (OA), Brains for Dementia Research (Alzheimer Brain Bank UK) (OA) and in part by the National Institute for Health Research (NIHR) Oxford Biomedical Research Centre based at Oxford University Hospitals NHS Trust and University of Oxford (OA). The views expressed are those of the authors and not necessarily those of the NHS, the NIHR or the Department of Health. LP is supported by the Discovery Award from Parkinson's UK.

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50 - Department of Neurology, MEHT Broomfield Hospital, Chelmsford, Essex, UK
51 - Department of Neurology, Addenbrooke's Hospital, University of Cambridge, Cambridge, UK
52 - School of Social and Community Medicine, University of Bristol
53 - Department of Neurology and Alzheimer Center, VU University Medical Center
54 - Department of Motor Neuroscience, UCL Institute of Neurology
55 - Department of Neurology, Academic Medical Center, University of Amsterdam, Amsterdam, Netherlands
56 - Center for Human Genetic Research and Department of Neurology, Massachusetts General Hospital, Boston, MA, USA
57 - Department of Neurology, Radboud University Nijmegen Medical Centre, Nijmegen, Netherlands
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65 - INSERM U897, Université Victor Segalen, Bordeaux, France
66 - Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, UK
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70 - Cambridge Centre for Brain Repair, Cambridge, UK
71 - UCL Institute of Neurology
72 - University of Aberdeen
73 - Department of Neurology, Leiden University Medical Center, Leiden, Netherlands
74 - AARP, Washington DC, USA
75 - Queen Square Brain Bank for Neurological Disorders, UCL Institute of Neurology
76 - Department of Clinical Neurology, John Radcliffe Hospital, Oxford, UK
77 - Department of Neurology, Pennsylvania State University, Milton S Hershey Medical Center, Hershey, PA, USA
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101 - Medical Research Council, University of Cambridge
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107 - Neurosciences Department, Queen Elizabeth Hospital, University Hospitals Birmingham NHS Foundation Trust, Birmingham, UK
108 - Program in Medical and Population Genetics, Broad Institute, Cambridge, MA, USA
109 - DZNE, German Center for Neurodegenerative Diseases, Tübingen, Germany
110 - Albany Medical College
111 - Barrow Neurological Institute
112 - Baylor College of Medicine
113 - Beth Israel Deaconess Medical Center
114 - Brigham & Women's Hospital
115 - Brown University (Memorial Hospital of RI)
116 - Colorado Neurological Institute
117 - Columbia University Medical Center
118 - Creighton University
119 - Evanston Northwestern Healthcare
120 - Hotel-Dieu Hospital-Chum
121 - Hunter Homes McGuire Veterans Medical Center
122 - Indiana University School of Medicine
123 - Institute For Neurodegenerative Disorders
124 - Johns Hopkins University
125 - London Health Sciences Centre
126 - Mayo Clinic Jacksonville
127 - McFarland Neurosciences
128 - Medical College of Georgia
129 - Medical College of Wisconsin
130 - Medical University of Ohio
131 - Mount Sinai School of Medicine
132 - North Shore-LIJ Health System
133 - Northwestern University
134 - Ochsner Clinic Foundation
135 - Ohio State University
136 - Ottawa Hospital Civic Site
137 - Pacific Neuroscience Medical Group
138 - Saskatoon Dist Health Board Royal Univ Hosp
139 - Scott & White Hospital/Texas A&M University

140 - The Parkinson's & Movement Disorder Institute
141 - Toronto Western Hospital, University Health
142 - UMDNJ-School of Osteopathic Medicine
143 - University of Alabama at Birmingham
144 - University of Alberta
145 - University of Calgary
146 - University of California Irvine
147 - University of California San Diego
148 - University of California San Francisco
149 - University of Chicago
150 - University of Cincinnati
151 - University of Colorado Health Sciences Center
152 - University of Connecticut
153 - University of Iowa
154 - University of Kansas Medical Center
155 - University of Maryland School of Medicine
156 - University of Miami
157 - University of Minnesota
158 - University of New Mexico
159 - University of Puerto Rico School of Medicine
160 - University of Rochester
161 - University of South Florida
162 - University of Tennessee Health Science Center
163 - University of Texas Southwestern Medical Center
164 - Wake Forest University School of Medicine
165 - Washington University
166 - University Southern California School of Medicine
167 - University of Lübeck, Germany
168 - UMDNJ-Robert Wood Johnson Medical School
169 - Massachusetts General Hospital, Harvard Medical School
170 - University of Virginia Health System
171 - University of Toronto
172 - Sun Health Research Institute
173 - Parkinson Institute, Istituti Clinici di Perfezionamento, Milano, Italy
174 - Cleveland Clinic Foundation
175 - University of Louisville School of Medicine
176 - University of Sydney ANZAC Research Institute, Concord Hospital, Sydney, Australia
177 - Struthers Parkinson's Center, Minneapolis
178 - Port City Neurology, Scarborough, ME
179 - Parkinson's Disease and Movement Disorder Center of Boca Raton
180 - Newcastle University, Newcastle upon Tyne, UK
181 - General Regional Hospital Bolzano, Bolzano, Italy
182 - University of Arkansas for Medical Sciences
183 - Aarhus University Hospital, Aarhus, Denmark
184 - University of Arizona

185 - Auckland City Hospital, Auckland, New Zealand
186 - University of Kentucky College of Medicine
187 - VA Puget Sound Health Care System and University of Washington
188 - Oregon Health and Sciences University
189 - Evergreen Hospital Medical Center
190 - Virginia Mason Medical Center
191 - Samuel Stratton VA Medical Center and Albany Medical Center
192 - Emory University
193 - Department of Neurology, Gertrude H Sergievsky Center and Taub Institute for Alzheimer's Disease and the Aging Brain, Columbia University Medical Center
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209 - Clinical Research Branch, National Institute on Aging, Baltimore, MD, USA
210 - NICHD Brain and Tissue Bank for Developmental Disorders, University of Maryland Medical School, Baltimore, Maryland 21201, USA
211 - Lymphocyte Cell Biology Unit, Laboratory of Immunology, National Institute on Aging, National Institutes of Health, Baltimore, MD, USA
212 - Brain Resource Center, Johns Hopkins University, Baltimore, MD, USA
213 - Department of Neuroscience, Karolinska Institutet, 171 77 Stockholm, Sweden
214 - Department of Neuropathology, MRC Sudden Death Brain Bank Project, University of Edinburgh, Wilkie Building, Teviot Place, Edinburgh EH8 9AG)
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216 - Department of Neurology, Medical School, University of Crete, Heraklion, Crete, Greece
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226 - Department of Medical and Molecular Genetics, King’s College London, 8th Floor, Tower Wing, Guy¹s Hospital, London SE1 9RT, UK)
227 - CNRS, Paris, France
228 - Pitié-Salpêtrière Hospital
229 - Clinical neuroscience Center, 26400 West Twelve Mile Road, Suite 110, Southfield, MI 48034
230 - Department of Neurology, University Hospital of Larissa, Greece
231 - Queen Mary College, University of London, London, UK
232 - Neurology M4104, The Medical School, Newcastle upon Tyne, UK
233 - Boston University School of Medicine, Boston, MA, USA
234 - Washington University School of Medicine

Supplementary Table 1 (page 18): Studies contributing to the discovery phase meta- analysis.* denotes genomic inflation estimates (lambda) scaled to 1000 cases and 1000 controls.

Phase	*Study*	*Cases (N)*	*Controls (N)*	*Total sample size (N)*	*Lambda (raw)*	*Lambda (scaled)**	*Cases, % female*	*Controls, % female*	*Case, age at onset in years, mean (SD)*	*Control, age at ascertainment in years, mean (SD)*	*Case ascertainment criteria*	*Control ascertainment criteria*
	IPDGC-DC	604	4916	5520	1.061	1.05670092	47.8	56.9	62.2 (12.3)	80.2 (7.5)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	absence of self-report, ICD-9, and medications
	IPDGC-FR	985	1984	2969	0.854	0.88909397	41.2	33	48.9 (12.8)	73.7 (5.4)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-GE	667	937	1604	1.025	1.032081078	39.8	48	55.7 (11.5)	47.4 (12.4)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	Population controls
	IPDGC-NE	744	2019	2763	1.061	1.056101112	36	63.9	55.6 (11.8)	55.7 (5.8)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	Population controls
	IPDGC-NIA	937	1896	2833	1.035	1.027906585	40.5	52.8	57.8 (13.2)	63.3 (10.1)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-UK	1705	5200	6905	1.034	1.013239905	43.3	49.5	64.2 (12.4)	53 (0)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	Population controls
	23andMe.v2	3261	29499	32760	1.092	1.015665477	39.5	41.6	64.2 (11.2)	49.1 (14.9)	self-report of PD diagnosis by clinician	self-report of neurological disease, memory loss, tremor or family history of PD removed
	23andMe.v3	866	32538	33424	1.044	1.025506832	39	39.6	63.9 (10.9)	43.5 (15.9)	self-report of PD diagnosis by clinician	self-report of neurological disease, memory loss, tremor or family history of PD removed
	Ash Jewish	268	178	446	1.006	1.028047962	33.2	57.3	59.9 (12.1)	69.8 (8.8)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	medical records and self-report
	HIHG	574	619	1193	0.998	0.996642331	36.9	65.4	57.2 (12.03)	69.3 (9.9)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	NGRC	1956	1982	3938	1.013	1.006602624	33.2	61.3	58.6 (11.7)	70.3 (14.1)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	PGPD	828	852	1680	1.009	1.010716473	40.1	60.2	62.1 (10.7)	54.9 (13.1)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	CHARGE-CHS	107	3164	3271	1.009	1.043478325	44.9	61.4	73.0 (5.1)	72.3 (5.4)	self-report, ICD-9, and medications	absence of self-report, ICD-9, and medications
	CHARGE-FHS	60	3889	3949	0.995	0.957690495	41.7	54.6	76.2 (10.8)	64.2 (12.2)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	ongoing surveillance and periodic physician examination
	CHARGE-RSI	146	5609	5755	0.984	0.9437792	54.8	59	75.0 (8.2)	69.0 (8.9)	clinic visit; medication use; ICD codes	absence of self-report, ICD-9, and medications
Discovery	**Meta-analysis**	**13708**	**95282**	**109010**	**1.051**	1.0021	-	-	-	-	-	-
	IPDGC-FR	553	474	1027	-	-	37.4	63.3	55.8 (13.1)	58.0 (13.7)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-GE	1044	871	1915	-	-	37.9	41.2	57.5 (12.3)	60.1 (7.5)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-GK	944	877	1821	-	-	42.3	45.3	64.0 (10.9)	63.3 (12.0)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-NIA	2407	2782	5189	-	-	30.4	38.9	64.7 (11.8)	63.5 (18.7)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
	IPDGC-UK	405	547	952	-	-	39.3	54.5	51.5 (13.5)	74.8 (10.4)	clinic visit; standard UK Brain Bank criteria with a modification to allow the inclusion of cases that had a family history of PD	clinic visit and self-report
Replication	**Meta-analysis**	**5353**	**5551**	**10904**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**

SNP Information							Discovery phase (13,728 cases and 95,282 controls)					Replication phase (5,353 cases and 5,551 controls)					Joint phase (19,081 cases and 100,833 controls)				
SNP	C	Position (bp)	Nearest gene(s)	Effect allele	Alternate allele	Effect allele frequency	I2	Beta	Odds ratio	Standard error	P	I2	Beta	Odds ratio	Standard error	P	I2	Beta	Odds ratio	Standard error	P
Genome Wide Significant, Discovery Phase																					
rs35749011*	1	155,135,036	GBA/SYT11	a	g	0.017	0	0.566	1.762	0.057	6.09x10-23	0	0.836	2.307	0.148	7.48x10-09	65.5	0.601	1.824	0.053	1.37x-29
rs823118	1	205,723,572	RAB7L1/NUCKS1	t	c	0.559	55.7	0.119	1.126	0.016	1.36x10-13	0	0.104	1.109	0.029	1.43x10-04	0	0.116	1.122	0.014	1.66x-16
rs10797576	1	232,664,611	SIPA1L2	t	c	0.14	0	0.13	1.139	0.023	1.19x10-08	26	0.104	1.11	0.039	3.38x10-03	0	0.123	1.131	0.020	4.87x-10
rs6430538	2	135,539,967	ACMSD/TMEM163	t	c	0.43	0	-0.136	0.873	0.017	5.56x10-15	47.9	-0.126	0.882	0.029	9.42x10-06	0	-0.133	0.875	0.015	9.13x-20
rs1474055*	2	169,110,394	STK39	t	c	0.128	9.3	0.193	1.213	0.024	7.12x10-16	54.4	0.198	1.218	0.042	1.07x10-06	0	0.194	1.214	0.021	1.15x-20
rs115185635*	3	87,520,857	KRT8P25/APOOP2	c	g	0.035	91	0.582	1.789	0.104	2.18x10-08	30.4	-0.071	0.931	0.07	0.846	96.3	0.133	1.142	0.058	0.022
rs12637471	3	182,762,437	MCCC1	a	g	0.193	26.6	-0.17	0.844	0.021	3.32x10-16	59	-0.179	0.836	0.036	3.72x10-07	0	-0.172	0.842	0.018	2.14x-21
rs34311866	4	951,947	TMEM175/GAK/DGKQ	t	c	0.809	52.4	-0.243	0.784	0.02	3.58x10-33	55.4	-0.234	0.791	0.035	6.29x10-12	0	-0.241	0.786	0.017	1.02x-43
rs11724635	4	15,737,101	BST1	a	c	0.553	14.8	0.116	1.122	0.016	8.07x10-13	20.6	0.129	1.138	0.028	2.73x10-06	0	0.119	1.126	0.014	9.44x-18
rs6812193	4	77,198,986	FAM47E/SCARB2	t	c	0.364	29.5	-0.108	0.897	0.017	7.17x10-11	10.7	-0.067	0.935	0.029	0.011	32.8	-0.098	0.907	0.015	2.95x-11
rs356182	4	90,626,111	SNCA	a	g	0.633	48.5	-0.306	0.737	0.018	3.23x10-67	34.4	-0.196	0.822	0.028	1.75x10-12	90.8	-0.274	0.760	0.015	4.16x-73
rs9275326*	6	32,666,660	HLA-DQB1	t	c	0.094	2.1	-0.227	0.797	0.032	5.82x10-13	0	-0.105	0.9	0.05	0.018	76.3	-0.192	0.826	0.027	1.19x-12
rs199347	7	23,293,746	GPNMB	a	g	0.59	10	0.116	1.123	0.017	2.37x10-12	26.6	0.07	1.072	0.029	7.66x10-03	46.6	0.104	1.110	0.015	1.18x-12
rs117896735*	10	121,536,327	INPP5F	a	g	0.014	15.2	0.569	1.767	0.084	1.21x10-11	0	0.339	1.404	0.111	1.10x10-03	63.4	0.485	1.624	0.067	4.34x-13
rs3793947*	11	83,544,472	DLG2	a	g	0.443	0	-0.092	0.912	0.017	2.59x10-08	0	-0.024	0.976	0.028	0.201	76.8	-0.074	0.929	0.015	3.96x-07
rs329648	11	133,765,367	MIR4697	t	c	0.354	0	0.095	1.1	0.017	1.65x10-08	48.5	0.114	1.121	0.029	4.38x10-05	0	0.100	1.105	0.015	9.83x-12
rs76904798	12	40,614,434	LRRK2	t	c	0.143	0	0.157	1.17	0.022	1.33x10-12	26.4	0.104	1.11	0.039	3.69x10-03	28.6	0.144	1.155	0.019	5.24x-14
rs11060180	12	123,303,586	CCDC62	a	g	0.558	42.8	0.097	1.101	0.017	2.14x10-08	0	0.108	1.114	0.028	7.26x10-05	0	0.100	1.105	0.015	6.02x-12
rs11158026	14	55,348,869	GCH1	t	c	0.335	32.1	-0.118	0.889	0.018	7.13x10-11	0	-0.054	0.948	0.03	0.039	70.1	-0.101	0.904	0.015	5.85x-11
rs1555399*	14	67,984,370	TMEM229B	a	t	0.468	97.2	-0.138	0.872	0.017	5.53x10-16	0	-0.03	0.971	0.028	0.144	90.8	-0.109	0.897	0.015	6.63x-14
rs2414739	15	61,994,134	VPS13C	a	g	0.734	29	0.108	1.114	0.018	4.13x10-09	1.1	0.104	1.109	0.033	7.96x10-04	0	0.107	1.113	0.016	1.23x-11
rs14235	16	31,121,793	BCKDK/ STX1B	a	g	0.381	25.5	0.09	1.094	0.016	3.89x10-08	27.5	0.125	1.133	0.029	7.72x10-06	10.4	0.098	1.103	0.014	2.43x-12
rs17649553	17	43,994,648	MAPT	t	c	0.226	0	-0.261	0.771	0.021	4.86x10-37	0	-0.269	0.764	0.035	7.03x10-15	0	-0.263	0.769	0.018	2.37x-48
rs12456492	18	40,673,380	RIT2	a	g	0.693	11.2	-0.1	0.905	0.017	5.12x10-09	49.1	-0.105	0.9	0.03	2.16x10-04	0	-0.101	0.904	0.015	7.74x-12
rs62120679*	19	2,363,319	SPPL2B	t	c	0.314	47.1	0.132	1.141	0.022	2.53x10-09	40.3	-0.002	0.999	0.034	0.518	90.9	0.093	1.097	0.019	5.57x-07
rs8118008*	20	3,168,166	DDRGK1	a	g	0.657	32.8	0.105	1.111	0.019	2.32x10-08	0	0.107	1.113	0.029	1.18x10-04	0	0.106	1.111	0.016	3.04x-11
Previously Reported as Significant in Genome Wide Studies																					
rs34016896	3	160,992,864	NMD3	t	c	0.319	37.8	0.077	1.08	0.017	7.68x10-06	0	0.028	1.028	0.03	0.174	50.5	0.065	1.067	0.015	1.08x-05
rs591323	8	16,697,091	FGF20	a	g	0.275	0	-0.083	0.921	0.019	1.30x10-05	1.7	-0.103	0.902	0.032	6.16x10-04	0	-0.088	0.916	0.016	6.68x-08
rs60298754	8	89,373,041	MMP16	t	c	0.024	53.6	0.075	1.078	0.056	0.181	-	-	-	-	-	0	0.075	1.078	0.056	0.181
rs7077361	10	15,561,543	ITGA8	t	c	0.874	0	0.104	1.11	0.025	3.24x10-05	34.4	0.043	1.044	0.042	0.154	35.8	0.088	1.092	0.022	4.16x-05
rs11868035	17	17,715,101	SREBF/RAI1	a	g	0.298	56.2	-0.065	0.937	0.018	2.17x10-04	0	-0.055	0.947	0.031	0.036	0	-0.063	0.939	0.016	5.98x-05
rs2823357	21	16,914,905	USP25	a	g	0.37	57	0.035	1.036	0.016	0.032	55.9	0.018	1.018	0.029	0.267	0	0.031	1.031	0.014	0.027

Supplementary Table 2 (page 19): Additional details related to Table 1. C - Chromosome; OR - odds ratio; I2 – index of heterogeneity. *replication genotyping for these SNPs failed assay design or quality control and a suitable proxy variant was selected (rs35749011, proxy rs71628662; rs1474055, proxy rs1955337; rs115185635, proxy rs62267708; rs117896735, proxy rs118117788; rs3793947, proxy rs12283611; rs1555399, proxy rs1077989; rs62120679, proxy rs10402629; rs8118008, proxy rs55785911). Note, only replication phase p-values are one-sided. Nearest gene or previously published proximal gene names included in table.

Supplementary Table 3 (page 20): Additional details related to Table 2. Replication genotyping for these SNPs failed assay design or quality control and a suitable proxy variant was selected (rs1596117, proxy rs4859430; rs7681154, proxy rs3910105; rs13201101, proxy rs8192591; based on discovery series comparison, the minor allele for rs3910105 tags the major allele of rs7681154 therefore risk is consistent across proxy and discovery SNP). Note, only replication phase p-values are one-sided. Nearest gene or previously published proximal gene names included in table.

Significant conditional SNP, signifiying secondary locus	Most significant SNP from discovery phase, used as covariate	Nearest gene(s)	R2 between SNPs based on 1000 Genomes Project European ancestry samples	Conditional SNP information: C	Position (bp)	Effect allele	Alternate allele	Effect allele frequency
rs114138760	rs35749011	GBA/SYT11	0.000	1	154898185	c	g	0.012
rs79217002	rs12637471	MCCC1	0.003	3	183011072	a	g	0.9907
rs34884217	rs34311866	TMEM175/GAK/DGKQ	0.012	4	944210	a	c	0.9126
rs1596117*	rs6812193	FAM47E/SCARB2	0.028	4	77151490	t	c	0.2005
rs7681154*	rs356182	SNCA	0.209	4	90763703	a	c	0.5021
rs13201101*	rs9275326	HLA-DQB1	0.002	6	32343604	t	c	0.0529
rs10886515	rs117896735	INPP5F	0.000	10	121343589	t	c	0.7145

Significant conditional SNP	Summary statistics from conditional analyses: I2	Beta	Odds ratio	Standard error	P	Summary statistics from discovery phase: I2	Beta	Odds ratio	Standard error	P
rs114138760	0	0.454	1.574	0.089	3.80x10-07	0	0.403	1.497	0.085	2.18x10-06
rs79217002	16.4	-0.402	0.669	0.091	9.31x10-06	0	-0.375	0.688	0.087	1.69x10-05
rs34884217	0	0.220	1.247	0.045	1.10x10-06	19	0.296	1.344	0.042	1.56x10-12
rs1596117*	0	0.109	1.115	0.021	2.80x10-07	0	0.090	1.094	0.020	6.05x10-06
rs7681154*	5.6	-0.173	0.841	0.020	7.09x10-19	0	-0.003	0.997	0.016	0.854
rs13201101*	44.7	0.176	1.192	0.038	3.84x10-06	35.4	0.165	1.179	0.036	4.95x10-06
rs10886515	0	0.095	1.100	0.019	9.19x10-07	3.7	0.100	1.105	0.018	2.59x10-08

Significant conditional SNP	Summary statistics from replicaiton phase: I2	Beta	Odds ratio	Standard error	P	Summary statistics from combined discovery and replication phases: I2	Beta	Odds ratio	Standard error	P
rs114138760	25	0.461	1.586	0.142	5.72x10-04	0	0.418	1.519	0.073	9.73x-09
rs79217002	0	0.073	1.076	0.130	0.714	87.8	-0.236	0.789	0.072	1.08x-03
rs34884217	4.7	0.100	1.105	0.047	0.017	89.7	0.209	1.232	0.031	2.51x-11
rs1596117*	0	0.036	1.036	0.041	0.189	28.6	0.080	1.083	0.018	9.45x-06
rs7681154*	33.1	-0.068	0.934	0.028	8.02x10-03	75.4	-0.019	0.981	0.014	0.171
rs13201101*	15	0.196	1.217	0.082	8.33x10-03	0	0.170	1.185	0.033	2.50x-07
rs10886515	28.6	0.023	1.023	0.031	0.234	78.3	0.081	1.084	0.016	2.26x-07

Supplementary Table 4 (page 21): Summary statistics for risk profile scoring analyses.

			Trend (1 SD of change from mean)		1st quintile		2nd quintile		3rd quintile		4th quintile		5th quintile	
Study	Trend p-value	AUC	OR	95% CI	OR	95% CI	OR	95% CI	OR	95% CI	OR	95% CI	OR	95% CI
USA	<2x10-16	0.61	1.5	1.41-1.59	1	-	1.47	1.23-1.76	1.66	1.39-1.99	2.14	1.79-2.56	3.16	2.64-3.79
Germany	6.35x10-12	0.59	1.4	1.27-1.54	1	-	1.34	1-1.78	1.7	1.27-2.27	1.86	1.38-2.49	2.66	1.97-3.59
Greece	5.12x10-11	0.58	1.38	1.25-1.52	1	-	1.38	1.03-1.85	1.47	1.09-1.97	1.61	1.2-2.17	2.48	1.83-3.36
UK	6.36x10-05	0.61	1.51	1.23-1.85	1	-	1.48	0.78-2.83	2.38	1.15-4.93	2.52	1.28-4.95	4.13	2.03-8.39
France	<2x10-16	0.67	1.92	1.65-2.22	1	-	1.43	0.93-2.18	2.24	1.48-3.39	3.01	1.96-4.62	5.97	3.79-9.38
Combined	<2x10-16	0.63	1.51	1.38-1.66	1	-	1.42	1.25-1.61	1.7	1.5-1.93	2.07	1.72-2.48	3.31	2.55-4.3
% Cases					*36.14*		*43.92*		*48.44*		*53.62*		*63.34*	

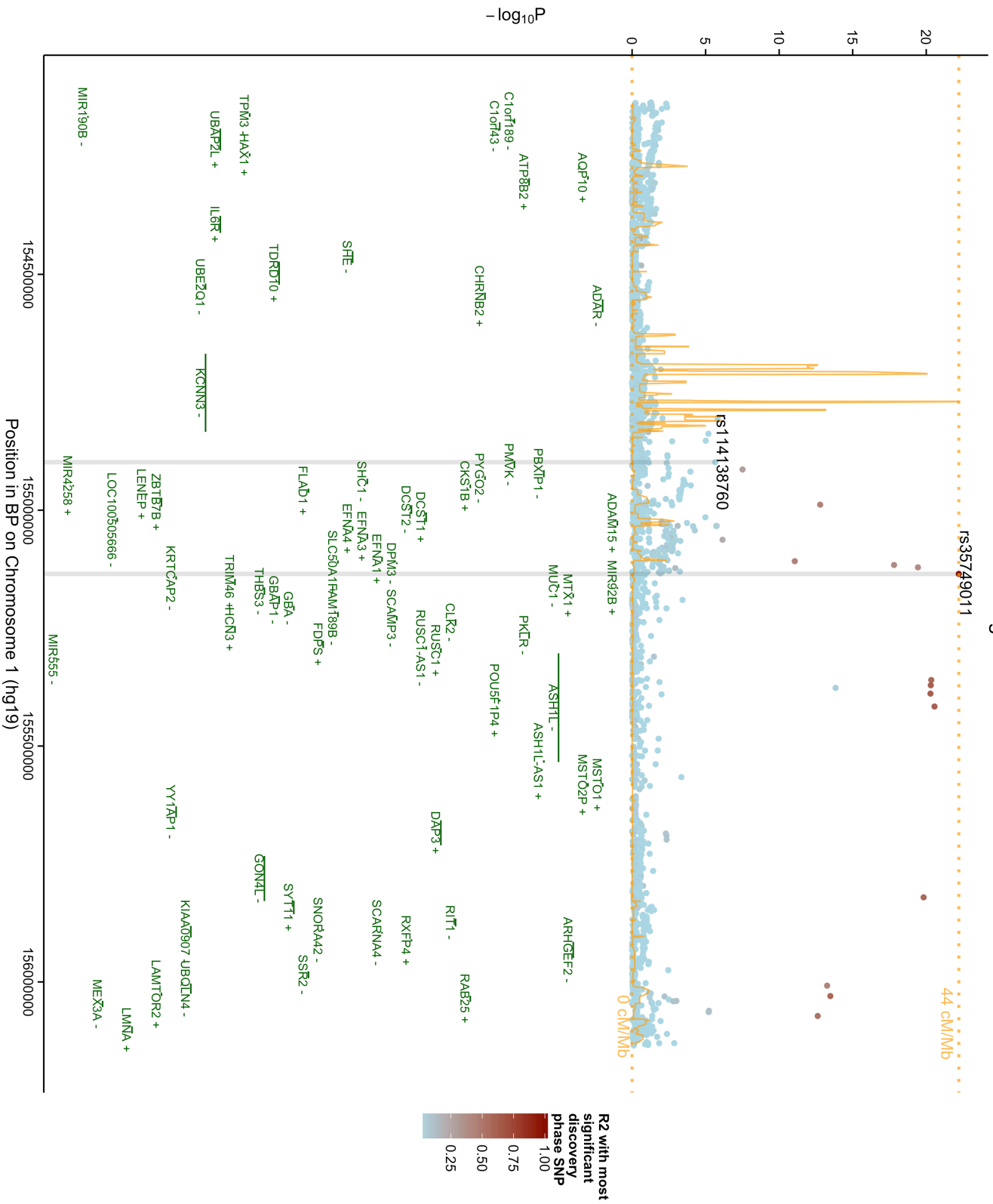
Supplementary Table 5 (page 22): Genome-wide significant SNPs are associated with distinct changes in methylation and expression levels in proximal genomic regions across multiple brain regions.

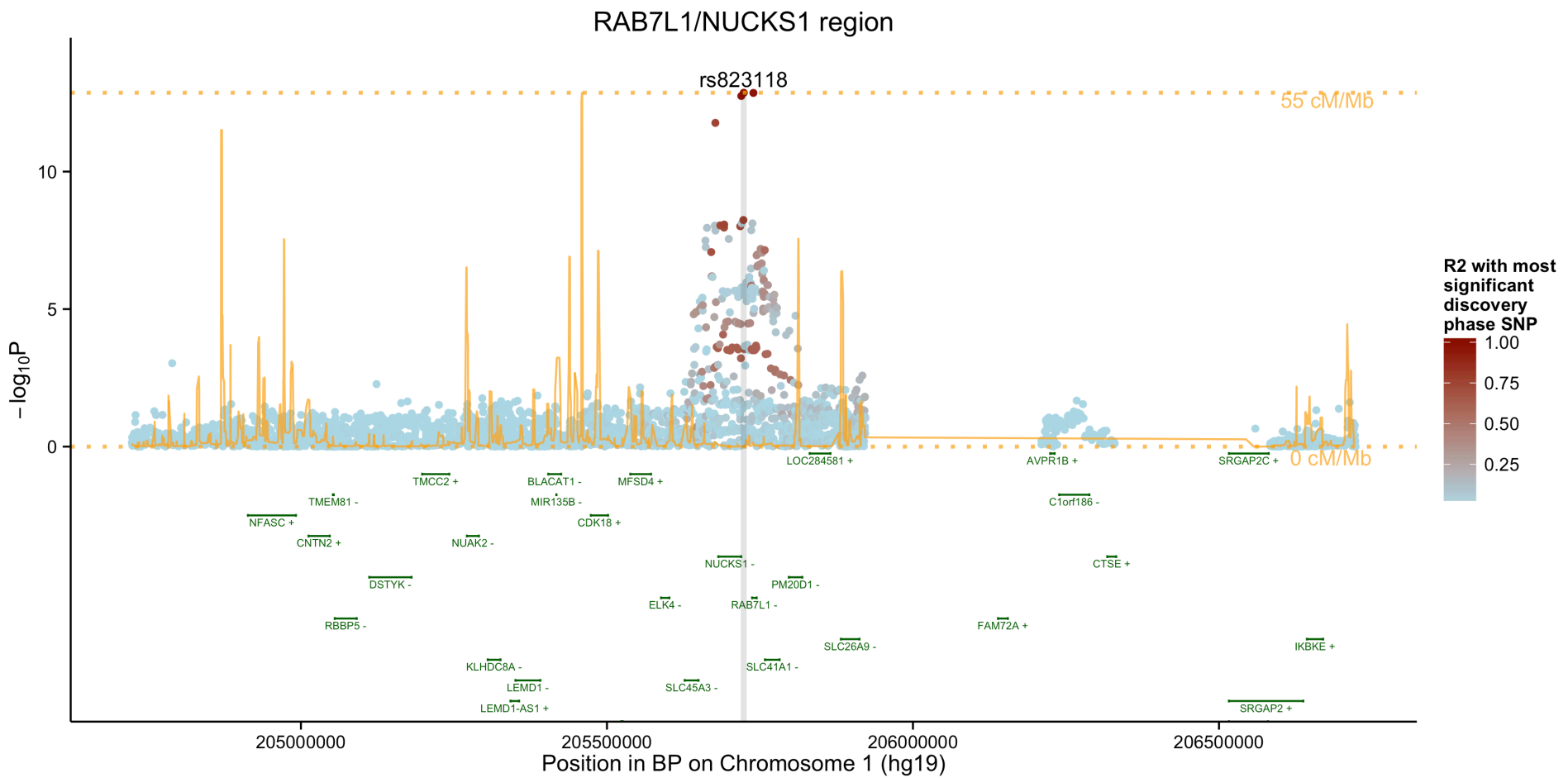
Methylation or expression	Brain region	SNP	Probe	Chromosome	SNP position (BP)	Reference allele	Alternate allele	Reference allele frequency	Imputation quality for SNP (RSQ from minimac)	Effect of alternate allele dosage (in Z units)	Standard error	P-value	FDR adjusted p-value	Probe start (BP)	Probe end (BP)	CpG or mRNA gene symbol
Expression	Cerebellum	rs823118	ILMN_1680692	1	205723572	T	C	0.545	0.994	0.31	0.069	7.72x10-06	4.28x10-04	205687394	205687443	NUCKS1
		rs823118	ILMN_1813685	1	205723572	T	C	0.545	0.994	-0.347	0.07	6.57x10-07	4.37x10-05	205738374	205738423	RAB7L1
		rs13201101	ILMN_1800461	6	32343604	C	T	0.949	0.998	-0.589	0.188	4.48x10-04	2.13x10-02	31637261	31637285	CSNK2B
		rs199347	ILMN_1789816	7	23293746	A	G	0.591	0.87	-0.414	0.079	1.65x10-07	1.37x10-05	23240107	23240156	NUPL2
		rs199347	ILMN_2115154	7	23293746	A	G	0.591	0.87	-0.44	0.079	2.66x10-08	2.96x10-06	23240192	23240241	NUPL2
		rs17649553	ILMN_1709549	17	43994648	C	T	0.738	0.965	-0.471	0.082	7.90x10-09	1.32x10-06	43513445	43513494	PLEKHM1
		rs17649553	ILMN_2393693	17	43994648	C	T	0.738	0.965	-1.241	0.09	1.41x10-43	4.69x10-41	43584483	43584532	MGC57346
		rs8118008	ILMN_1797828	20	3168166	A	G	0.602	0.985	-0.235	0.072	1.00x10-03	4.80x10-02	3171228	3171277	DDRGK1
	Frontal cortex	rs823118	ILMN_1680692	1	205723572	T	C	0.545	0.994	0.373	0.069	6.85x10-08	1.15x10-05	205687394	205687443	NUCKS1
		rs823118	ILMN_1813685	1	205723572	T	C	0.545	0.994	-0.251	0.068	2.25x10-04	1.90x10-02	205738374	205738423	RAB7L1
		rs199347	ILMN_1789816	7	23293746	A	G	0.591	0.87	-0.427	0.079	1.15x10-07	1.05x10-05	23240107	23240156	NUPL2
		rs199347	ILMN_2115154	7	23293746	A	G	0.591	0.87	-0.404	0.079	3.20x10-07	3.59x10-05	23240192	23240241	NUPL2
		rs14235	ILMN_1739236	16	31121793	G	A	0.62	0.642	0.325	0.092	2.60x10-04	2.60x10-02	31072258	31072307	ZNF668
		rs14235	ILMN_1804679	16	31121793	G	A	0.62	0.642	-0.308	0.092	7.93x10-04	3.30x10-02	31142528	31142577	KAT8
		rs17649553	ILMN_1698680	17	43994648	C	T	0.738	0.965	-0.278	0.082	6.99x10-04	3.30x10-02	44594196	44594245	ARL17A
		rs8118008	ILMN_1797828	20	3168166	A	G	0.602	0.985	-0.25	0.072	5.15x10-04	2.90x10-02	3171228	3171277	DDRGK1
Methylation	Cerebellum	rs823118	cg14159672	1	205723572	T	C	0.545	0.996	-0.844	0.079	1.03x10-26	4.46x10-24	205819179	205819229	FLJ32569
		rs823118	cg14893161	1	205723572	T	C	0.545	0.996	-0.863	0.079	5.25x10-28	4.54x10-25	205819201	205819251	FLJ32569
		rs13201101	cg09973262	6	32343604	C	T	0.949	0.997	-0.663	0.186	3.73x10-04	4.60x10-02	32191845	32191895	NOTCH4
		rs13201101	cg07363637	6	32343604	C	T	0.949	0.997	-0.664	0.186	3.67x10-04	4.60x10-02	31846946	31846996	SLC44A4
		rs13201101	cg14700707	6	32343604	C	T	0.949	0.997	-0.765	0.186	3.97x10-05	6.88x10-03	32191840	32191890	NOTCH4
		rs199347	cg17274742	7	23293746	A	G	0.578	0.903	0.404	0.092	1.17x10-05	2.53x10-03	23286489	23286539	GPNMB
		rs17649553	cg19832721	17	43994648	C	T	0.745	0.998	0.496	0.099	5.91x10-07	1.70x10-04	44594196	44594245	KIAA1267
		rs8118008	cg11004890	20	3168166	A	G	0.596	0.99	-0.293	0.083	4.43x10-04	4.80x10-02	3218500	3218550	SLC4A11
		rs823118	cg14159672	1	205723572	T	C	0.545	0.996	-0.798	0.079	3.62x10-24	1.57x10-21	205819179	205819229	FLJ32569
		rs823118	cg14893161	1	205723572	T	C	0.545	0.996	-0.811	0.079	6.58x10-25	5.69x10-22	205819201	205819251	FLJ32569
		rs13201101	cg07363637	6	32343604	C	T	0.949	0.997	-0.798	0.186	1.82x10-05	2.62x10-03	31846946	31846996	SLC44A4
		rs199347	cg17274742	7	23293746	A	G	0.578	0.903	0.494	0.092	8.46x10-08	1.83x10-05	23286489	23286539	GPNMB
	Frontal cortex	rs199347	cg22832819	7	23293746	A	G	0.578	0.903	0.496	0.092	7.55x10-08	1.83x10-05	23285742	23285792	GPNMB
		rs14235	cg25033993	16	31121793	G	A	0.611	0.743	0.441	0.1	1.12x10-05	1.93x10-03	31022372	31022422	STX1B2

Supplementary Table 6 (page 23): Minor allele frequencies for all SNPs in meta-analysis stratified by case-control status for discovery and replication phases. All replication samples
were included in these estimates. Discovery phase estimates include all 23andMe samples, PGPD, HIHG, NGRC and all IPDGC samples except those from the UK and Iceland.

SNP	*C*	*Position (bp)*	*Minor allele*	*Discovery and conditional phases, minor allele frequency (cases)*	*Discovery and conditional phases, minor allele frequency (controls)*	*Replication phase, minor allele frequency (cases)*	*Replication phase, minor allele frequency (controls)*
rs114138760	1	154898185	C	0.015	0.011	0.013	0.009
rs35749011	1	155135036	A	0.026	0.014	NA	NA
rs71628662	1	155359992	C	0.028	0.018	0.015	0.007
rs823118	1	205723572	C	0.416	0.444	0.405	0.435
rs10797576	1	232664611	T	0.152	0.134	0.163	0.146
rs6430538	2	135539967	T	0.408	0.436	0.480	0.497
rs1474055	2	169110394	T	0.145	0.123	NA	NA
rs1955337	2	169129145	T	0.147	0.125	0.142	0.121
rs62267708	3	87489314	T	0.021	0.021	0.042	0.043
rs115185635	3	87520857	C	0.022	0.022	NA	NA
rs34016896	3	160992864	T	0.331	0.312	0.335	0.326
rs12637471	3	182762437	A	0.177	0.200	0.174	0.199
rs79217002	3	183011072	G	0.011	0.008	0.011	0.012
rs34884217	4	944210	C	0.062	0.073	0.096	0.105
rs34311866	4	951947	C	0.226	0.183	0.236	0.195
rs11724635	4	15737101	C	0.422	0.455	0.421	0.456
rs4859430	4	77149099	A	0.150	0.132	0.142	0.133
rs1596117	4	77151490	T	0.218	0.198	NA	NA
rs6812193	4	77198986	T	0.342	0.370	0.348	0.363
rs356182	4	90626111	G	0.421	0.355	0.397	0.337
rs3910105	4	90682571	G	0.427	0.457	0.444	0.459
rs7681154	4	90763703	C	0.502	0.500	NA	NA
rs8192591	6	32185796	T	0.039	0.036	0.033	0.028
rs13201101	6	32343604	T	0.057	0.050	NA	NA
rs9275326	6	32666660	T	0.083	0.097	0.083	0.093
rs199347	7	23293746	G	0.385	0.413	0.396	0.416
rs591323	8	16697091	A	0.261	0.279	0.252	0.272
rs60298754	8	89373041	T	0.025	0.023	NA	NA
rs7077361	10	15561543	C	0.116	0.130	0.124	0.131
rs10886515	10	121343589	C	0.270	0.291	0.281	0.284
rs117896735	10	121536327	A	0.017	0.012	NA	NA
rs118117788	10	121710488	T	0.013	0.008	0.021	0.015
rs12283611	11	83487277	A	0.398	0.415	0.418	0.426
rs3793947	11	83544472	A	0.428	0.446	NA	NA
rs329648	11	133765367	T	0.372	0.346	0.388	0.359
rs76904798	12	40614434	T	0.162	0.141	0.159	0.144
rs11060180	12	123303586	G	0.426	0.444	0.420	0.446
rs11158026	14	55348869	T	0.309	0.334	0.307	0.318
rs1077989	14	67975822	C	0.484	0.486	0.480	0.487
rs1555399	14	67984370	A	0.478	0.481	NA	NA
rs2414739	15	61994134	G	0.244	0.269	0.240	0.264
rs14235	16	31121793	A	0.400	0.374	0.427	0.395
rs11868035	17	17715101	A	0.287	0.301	0.303	0.314
rs17649553	17	43994648	T	0.189	0.231	0.187	0.228
rs12456492	18	40673380	G	0.328	0.300	0.337	0.316
rs117022814	19	2209647	T	0.027	0.023	0.022	0.022
rs10402629	19	2324458	G	0.244	0.225	0.217	0.218
rs62120679	19	2363319	T	0.321	0.300	NA	NA
rs55785911	20	3153503	A	0.357	0.374	0.368	0.386
rs8118008	20	3168166	G	0.341	0.359	NA	NA
rs2823357	21	16914905	A	0.382	0.375	0.383	0.378

Supplementary Figure 1 (pages 24 - 55): Regional association plots. 32 regional association plots for SNPs from discovery phase analyses +/- 1 Mb from most significant SNP per locus in Table 1. The r2 pattern is based on most significant SNP per locus, based on the 283 European ancestry samples from the August 2010 release of the 1000 genomes project dataset.
Secondary signals are annotated in text as per their description in the conditional analysis section of Table 2. Recombination rates are as per HapMap phase 2 European ancestry samples. Nearest gene or previously published proximal gene names included in table.




RAB7L1/NUCKS1 region
rs823118
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0 cM/Mb
10
5
0
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TMCC2 +
BLACAT1 -
MFSD4 +
TMEM81 -
MIR135B -
NFASC +
CDK18 +
CNTN2 +
NUAK2 -
NUCKS1 -
DSTYK -
PM20D1 -
ELK4 -
RAB7L1 -
RBBP5 -
KLHDC8A -
SLC41A1 -
LEMD1 -
SLC45A3 -
LEMD1-AS1 +
LOC284581 +
AVPR1B +
SRGAP2C +
C1orf186 -
CTSE +
FAM72A +
SLC26A9 -
IKBKE +
SRGAP2 +
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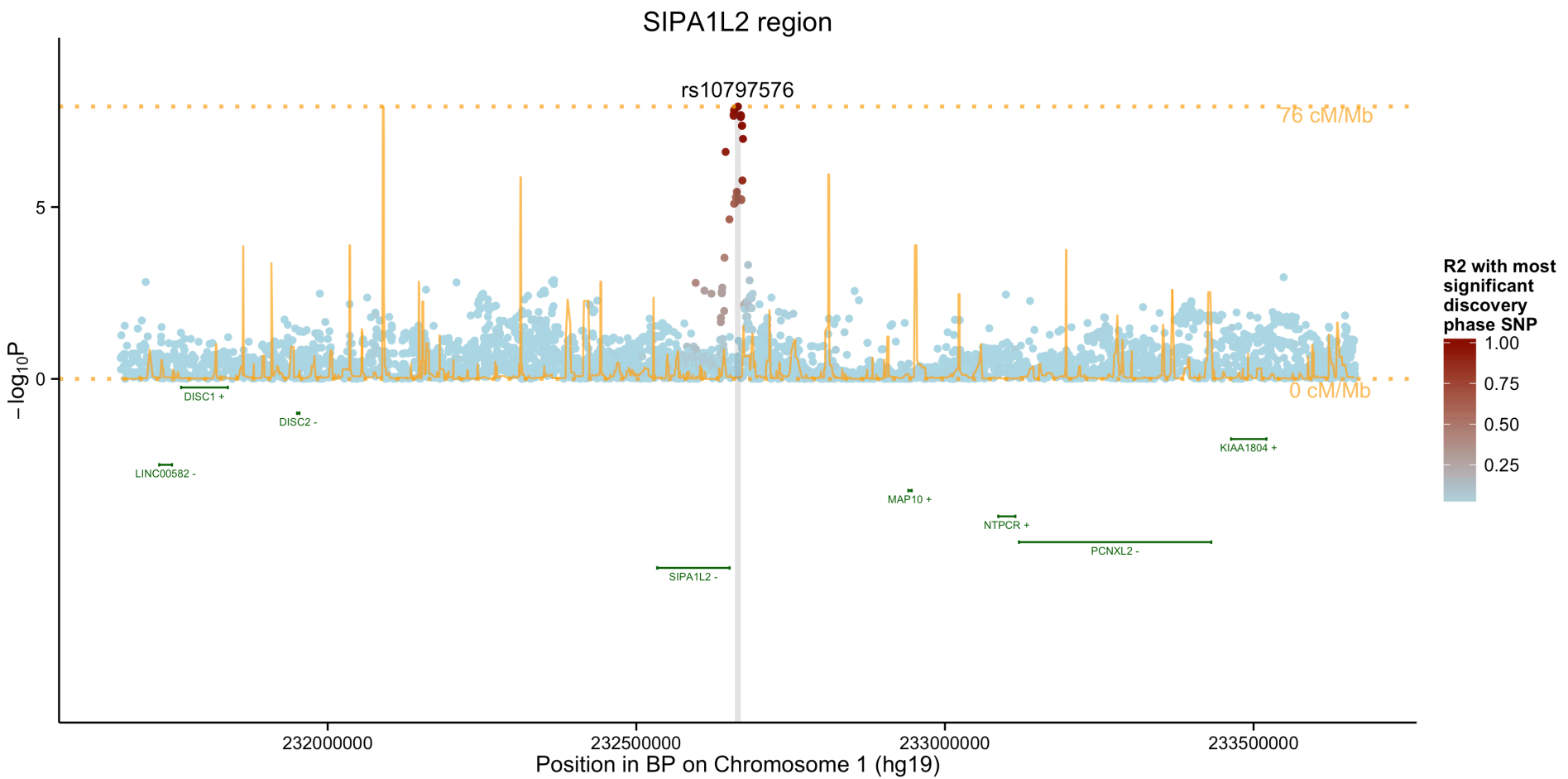
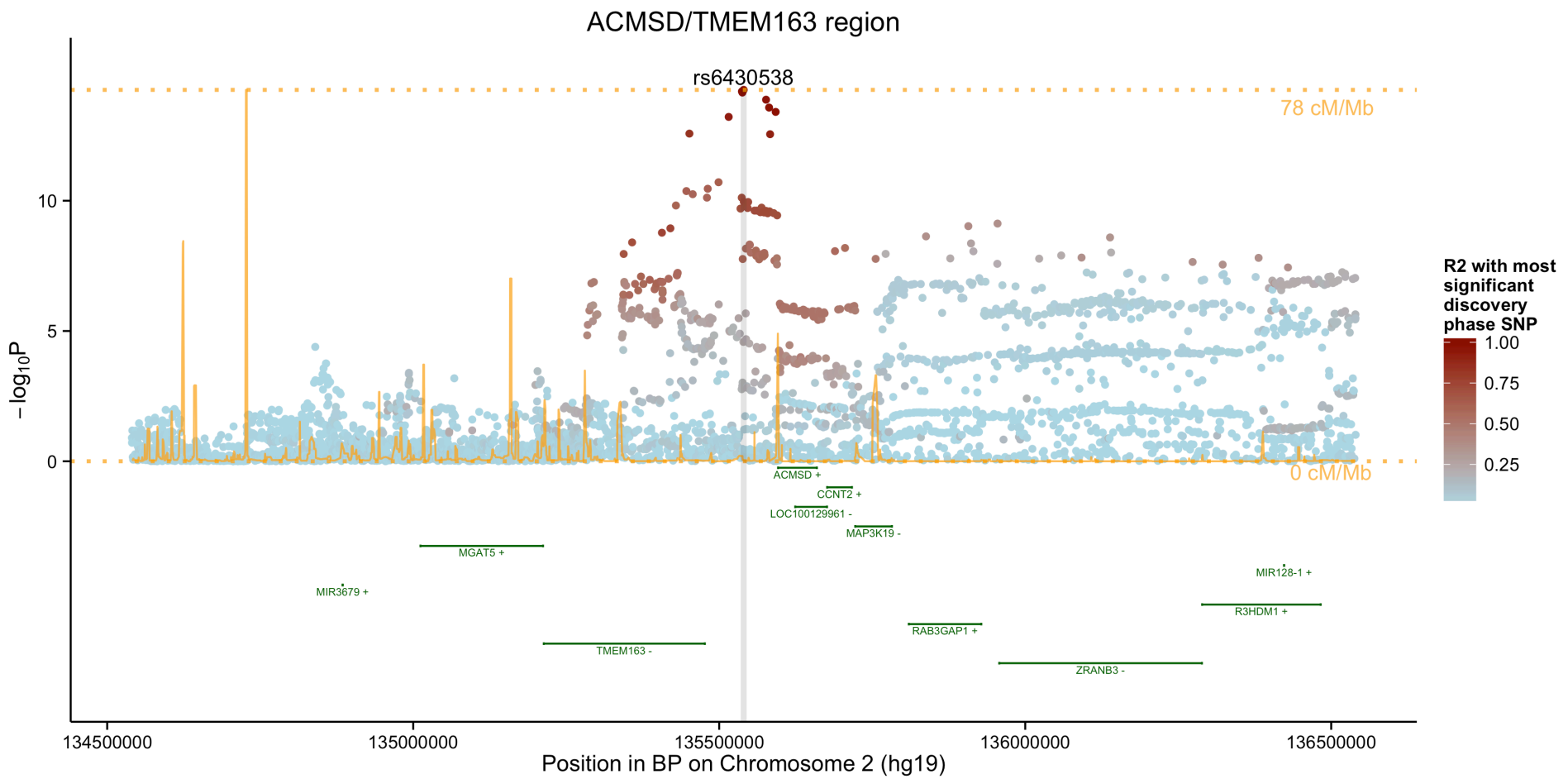
206500000
Position in BP on Chromosome 1 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25


SIPA1L2 region
rs10797576
75 cM/Mb
0 cM/Mb
5
0
– log10P
DISC1 +
DISC2 -
LINC00582 -
KIAA1804 +
MAP10 +
NTPCR +
PCNXL2 -
SIPA1L2 -
232000000
232500000
233000000
233500000
Position in BP on Chromosome 1 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25


ACMSD/TMEM163 region
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78 cM/Mb
0 cM/Mb
10
5
0
$-\log_{10}P$
ACMSD +
CCNT2 +
LOC100129961 -
MAP3K19 -
MGAT5 +
MIR3679 +
TMEM163 -
MIR128-1 +
R3HDM1 +
RAB3GAP1 +
ZRANB3 -
134500000
135000000
135500000
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136500000
Position in BP on Chromosome 2 (hg19)
R2 with most significant discovery phase SNP
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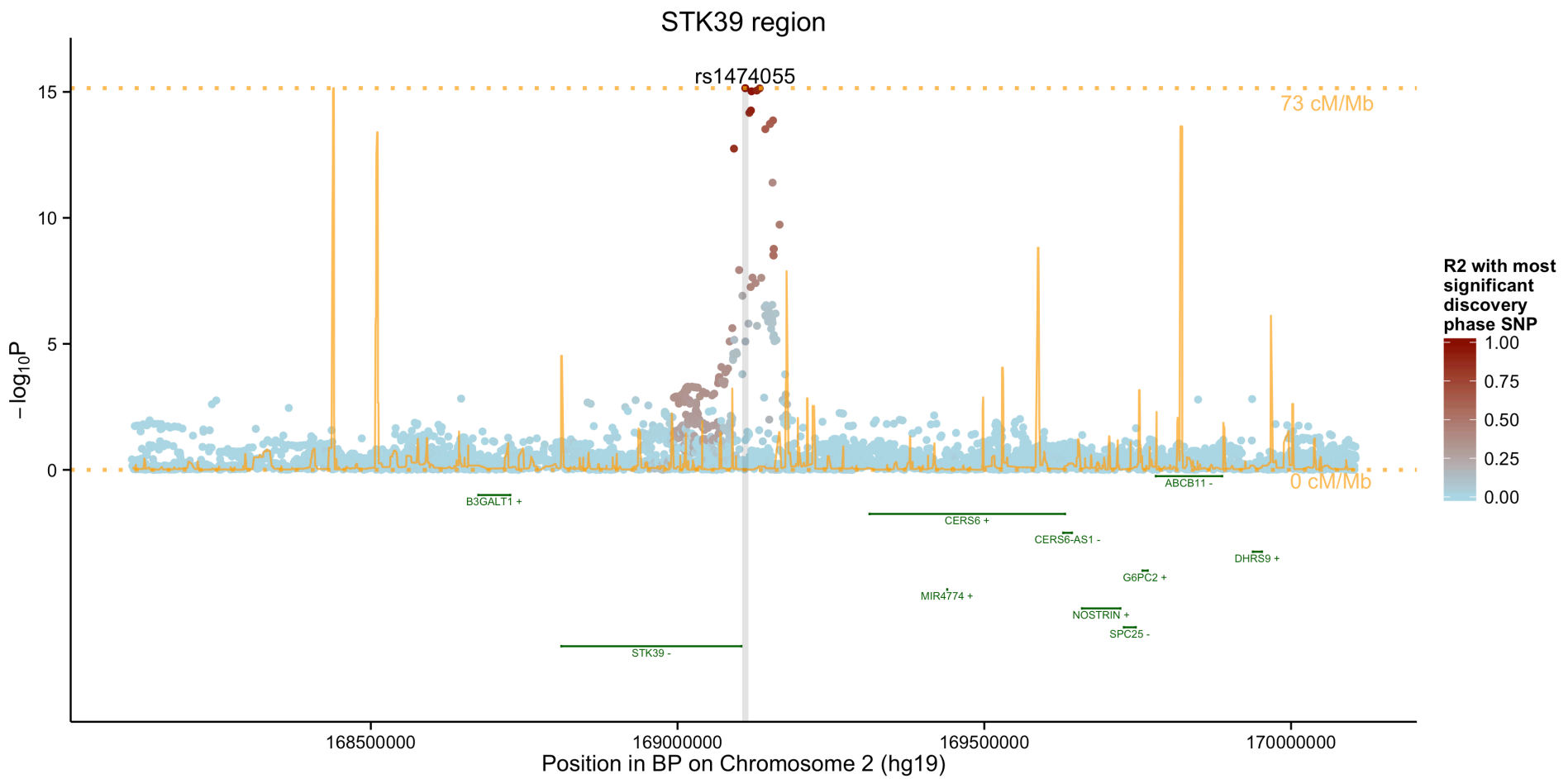
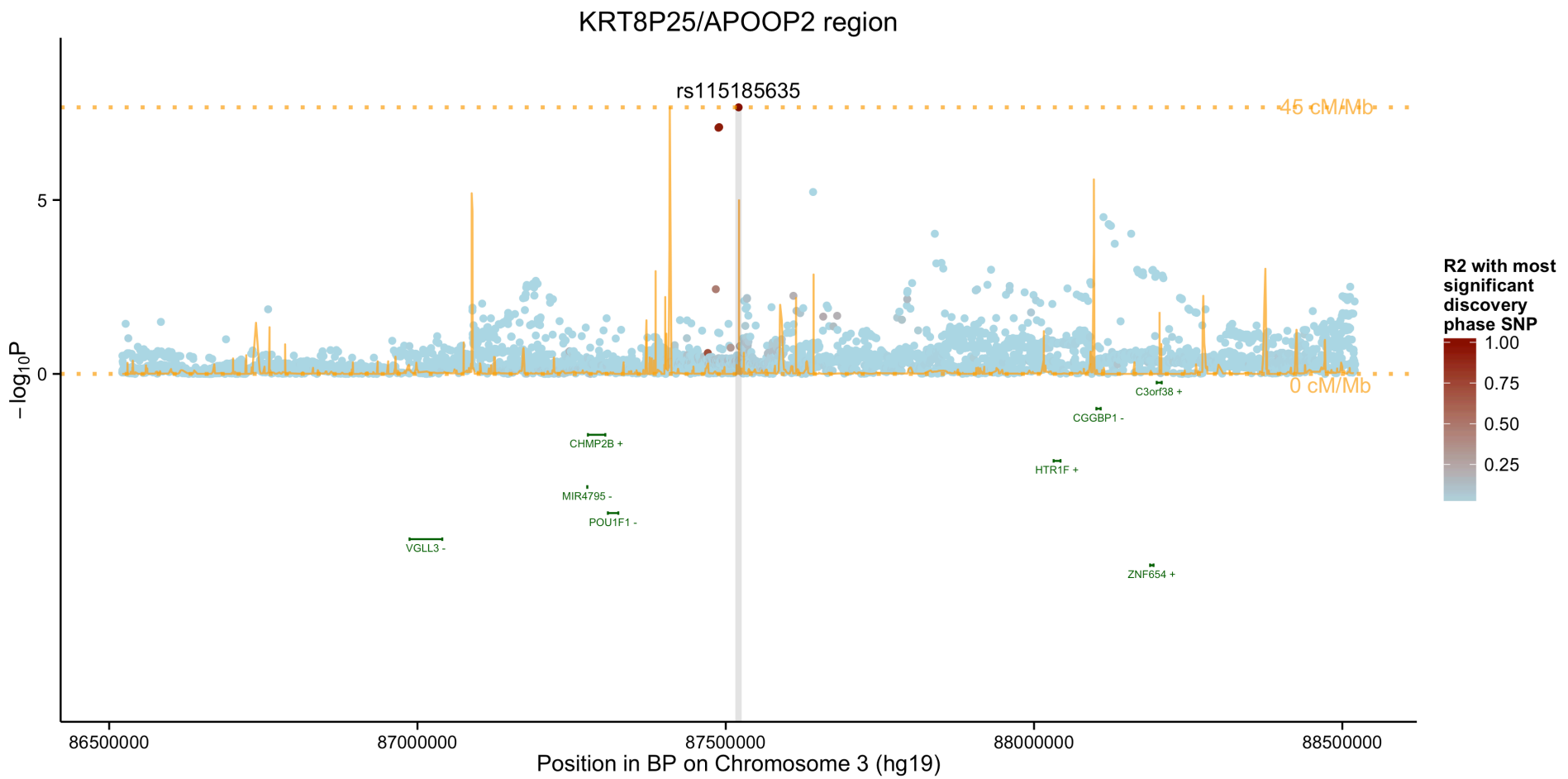
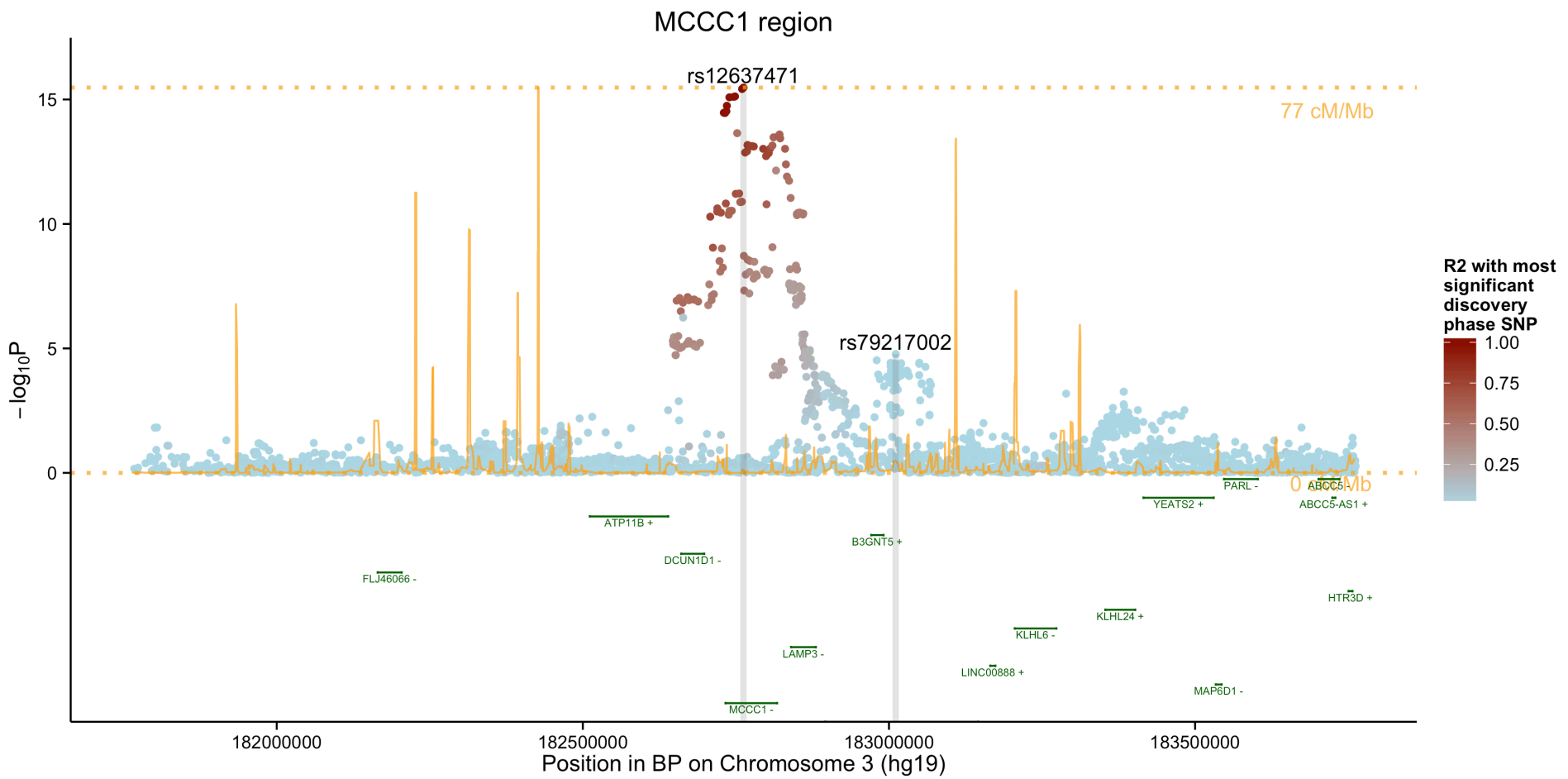
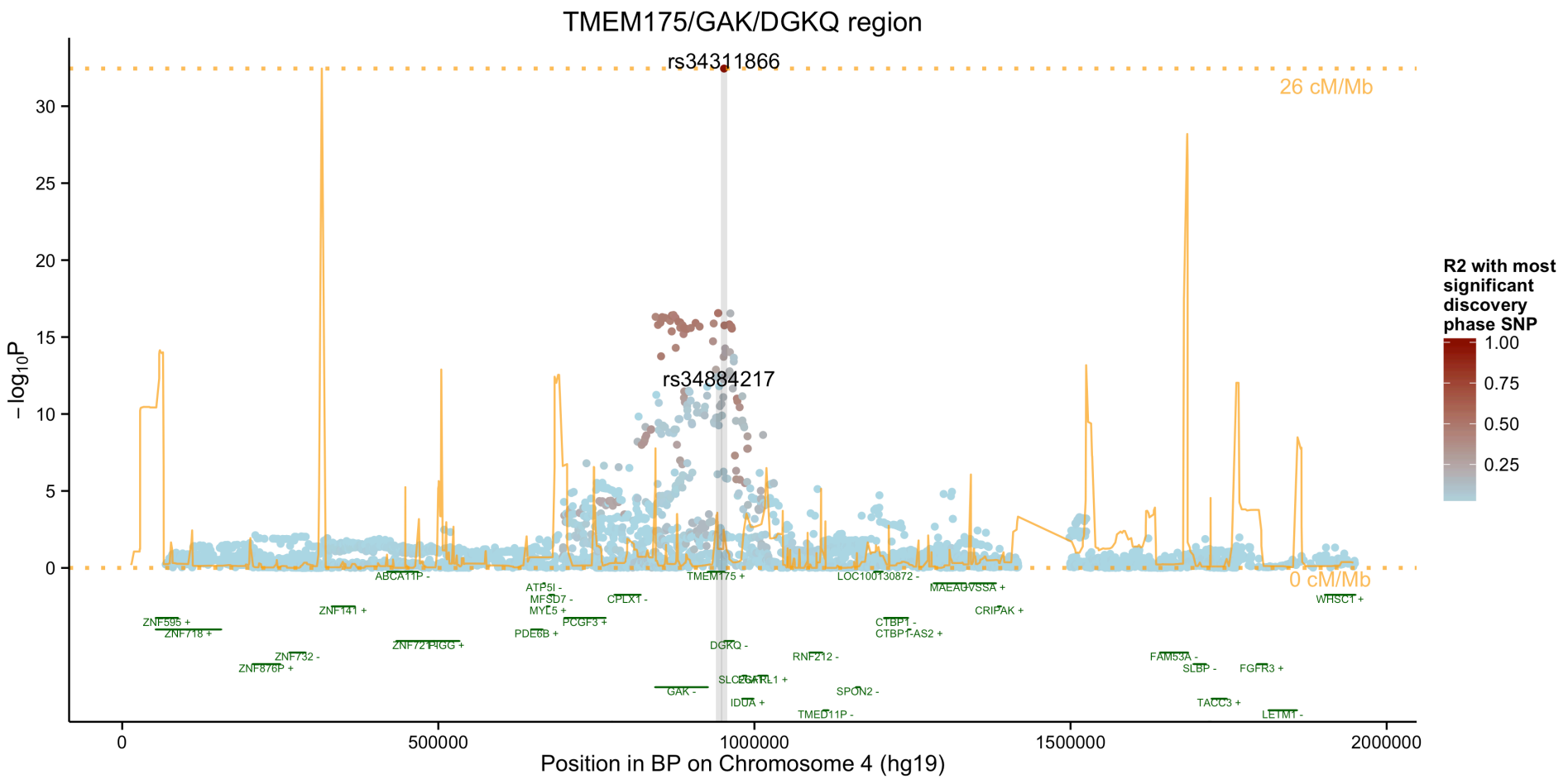
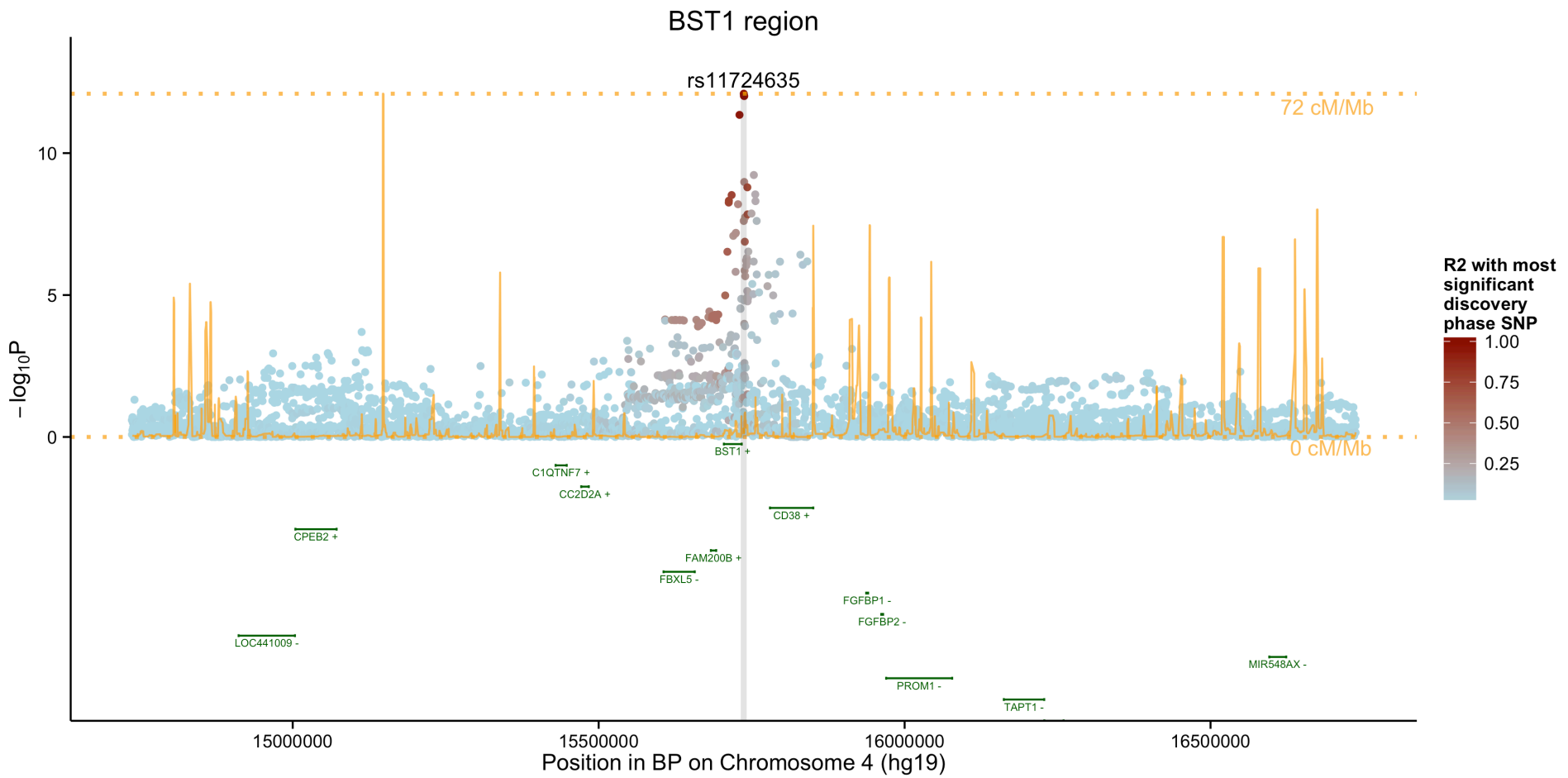
0.75
0.50
0.25

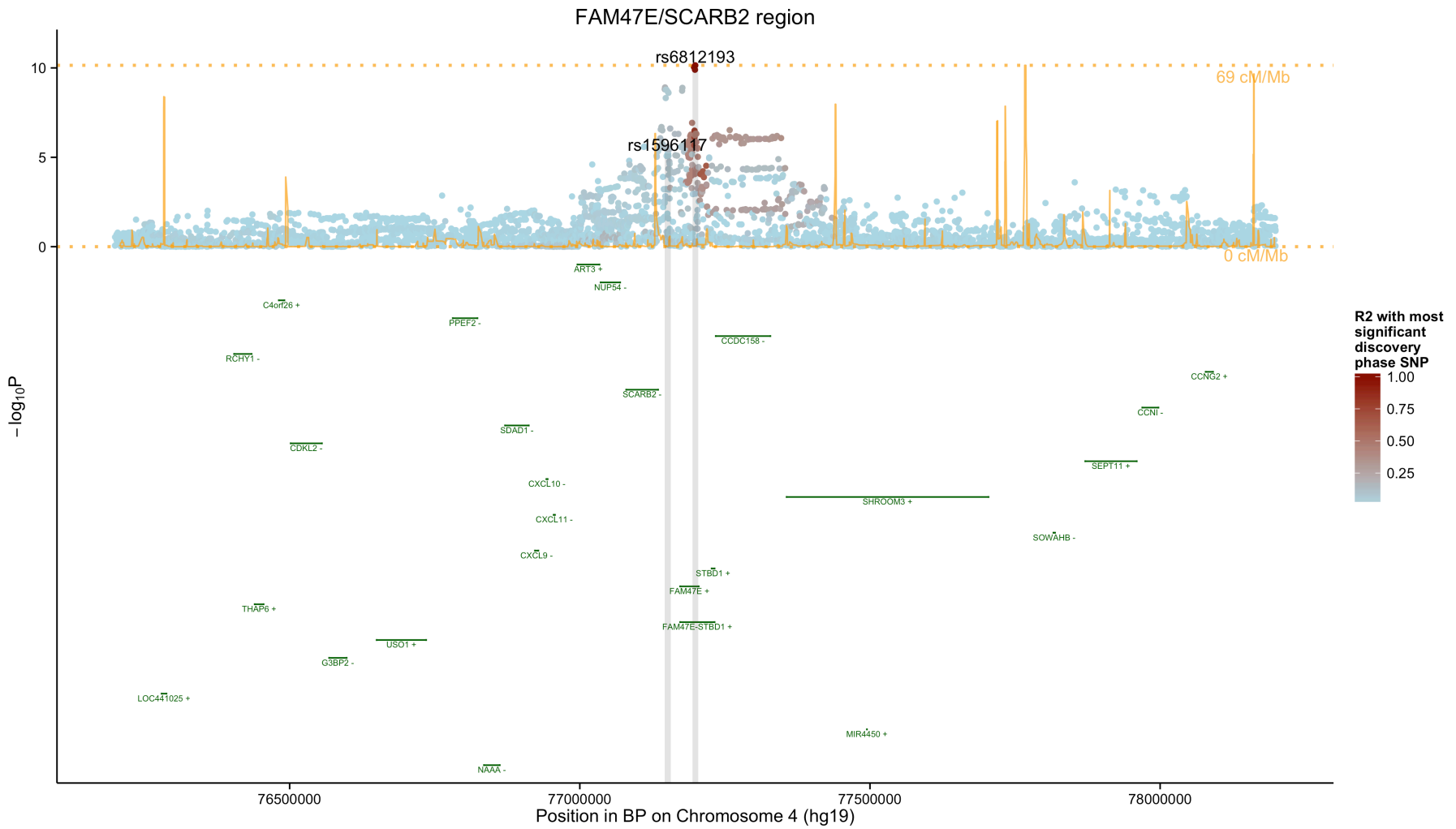

STK39 region
rs1474055
73 cM/Mb
0 cM/Mb
15
10
5
0
$-\log_{10}P$
B3GALT1 +
STK39 -
CERS6 +
CERS6-AS1 -
MIR4774 +
G6PC2 +
DHRS9 +
NOSTRIN +
SPC25 -
ABCB11 -
168500000
169000000
169500000
170000000
Position in BP on Chromosome 2 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
0.00

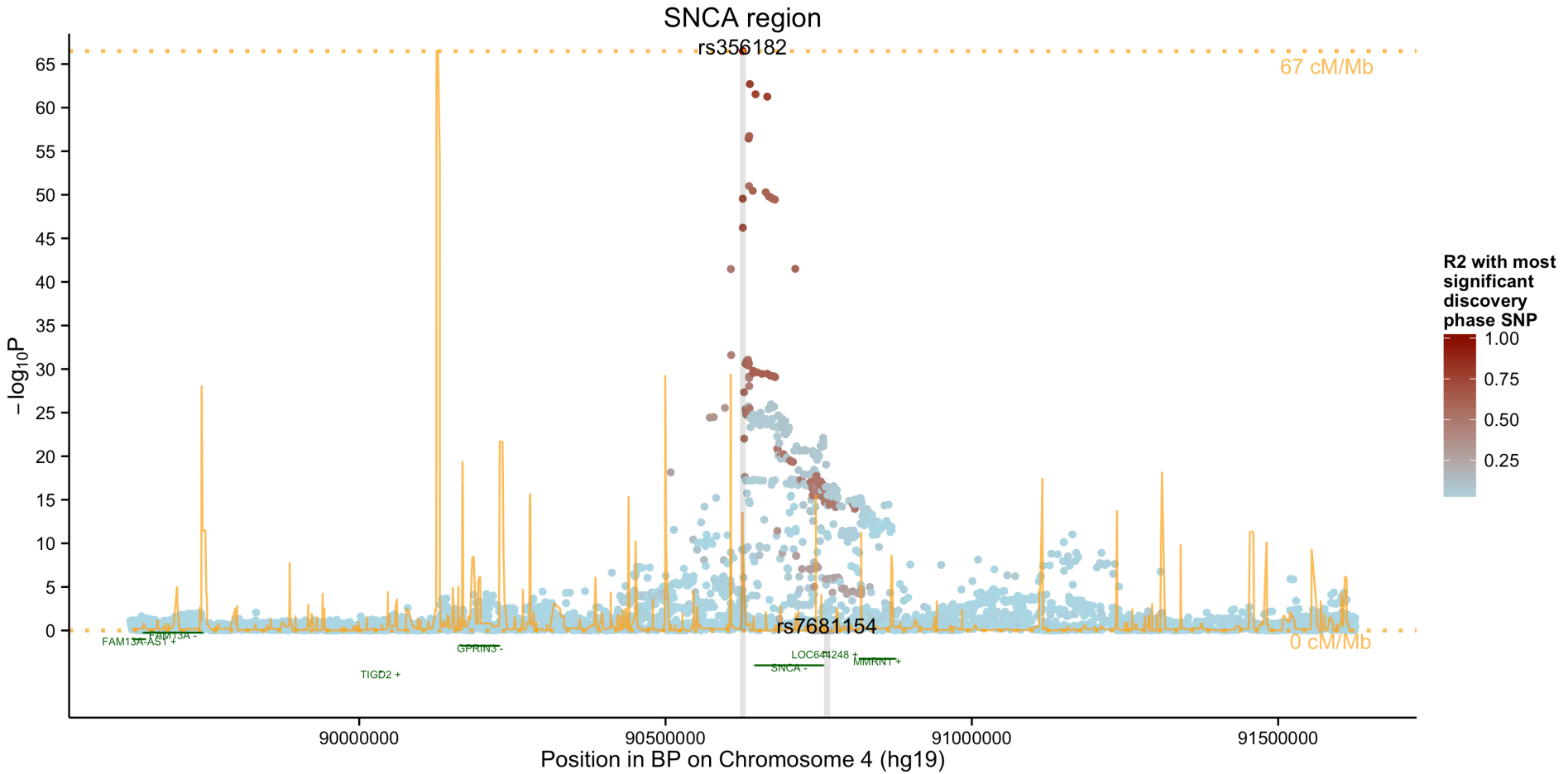

KRT8P25/APOOP2 region
rs115185635
45 cM/Mb
0 cM/Mb
5
0
– log10P
C3orf38 +
CGGBP1 -
CHMP2B +
HTR1F +
MIR4795 -
POU1F1 -
VGLL3 -
ZNF654 +
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
86500000
87000000
87500000
88000000
88500000
Position in BP on Chromosome 3 (hg19)

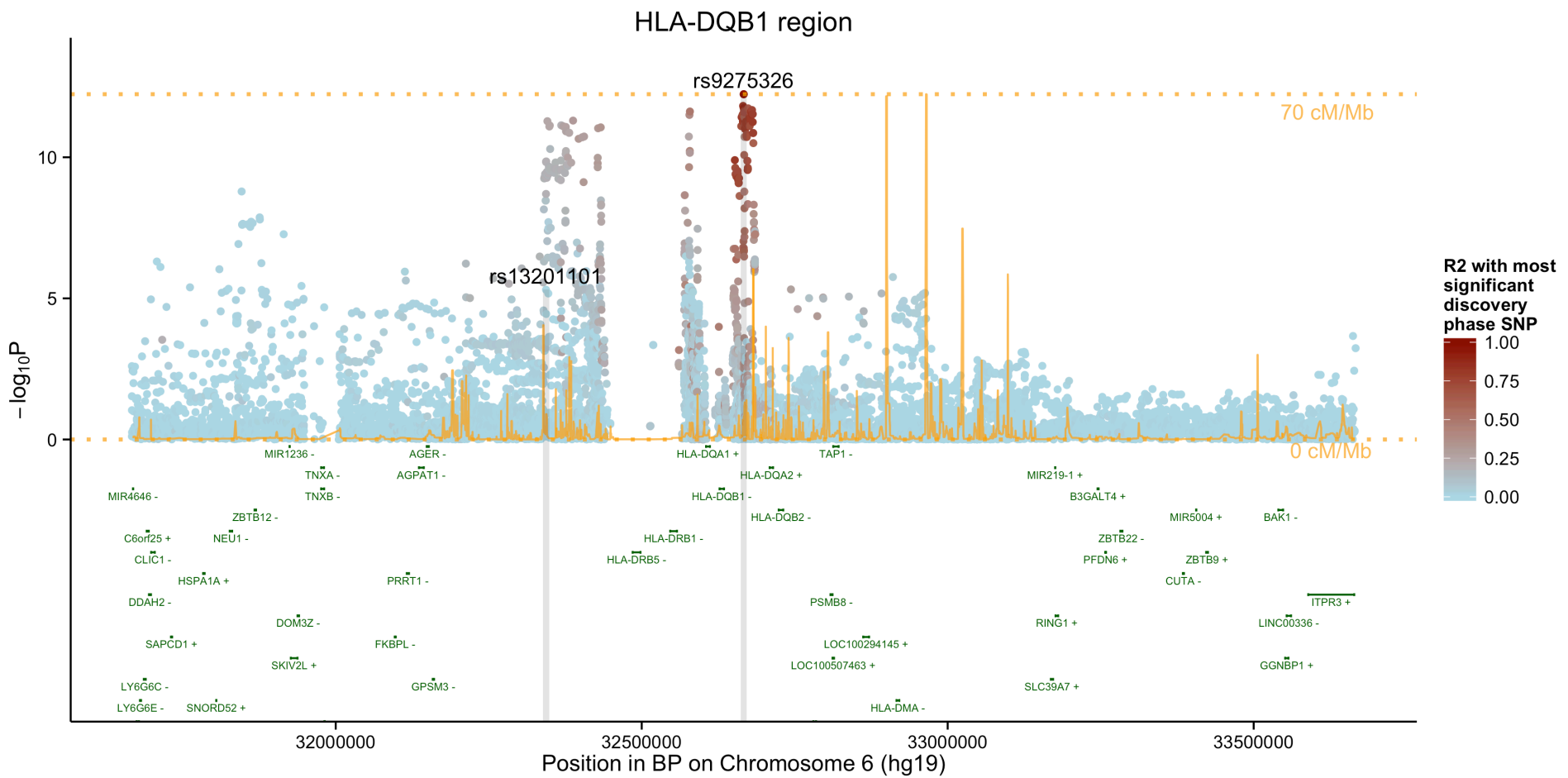

MCCC1 region
rs12637471
rs79217002
77 cM/Mb
0 cM/Mb
15
10
5
0
– log10P
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
ATP11B +
DCUN1D1 -
FLJ46066 -
B3GNT5 +
LAMP3 -
MCCC1 -
KLHL6 -
LINC00888 +
KLHL24 +
MAP6D1 -
YEATS2 +
PARL -
ABCC5 -
ABCC5-AS1 +
HTR3D +
182000000
182500000
183000000
183500000
Position in BP on Chromosome 3 (hg19)

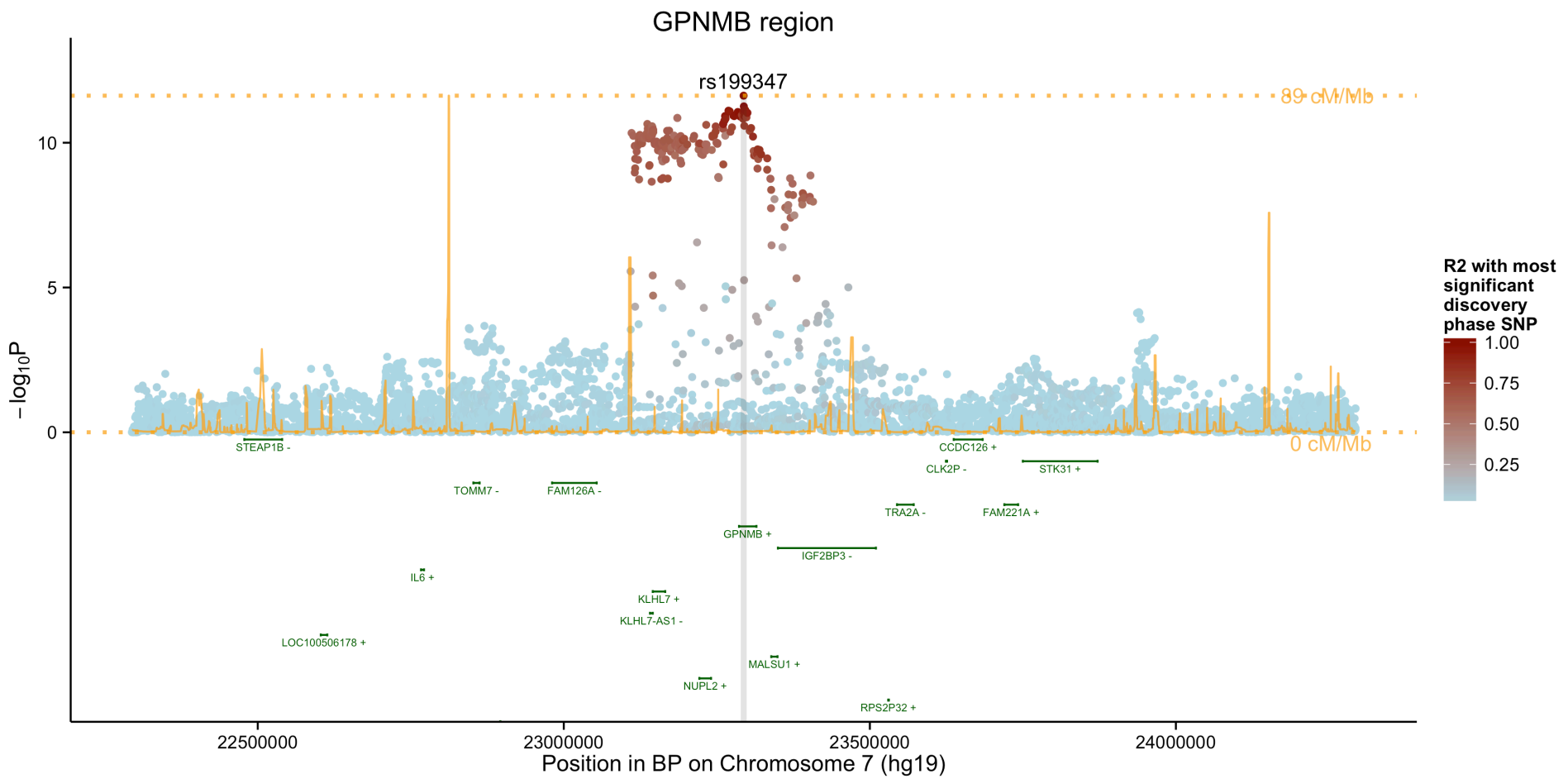

TMEM175/GAK/DGKQ region
rs34311866
rs34884217
26 cM/Mb
0 cM/Mb
– log10P
30
25
20
15
10
5
0
0
500000
1000000
1500000
2000000
Position in BP on Chromosome 4 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
ABCA11P -
ATP5I -
MFSD7 -
MYL5 +
CPLX1 -
TMEM175 +
LOC100130872 -
MAEA/VSSA +
WHSC1 +
ZNF595 +
ZNF718 +
ZNF141 +
PCGF3 +
PDE6B +
CTBP1 -
CTBP1-AS2 +
CRIPAK +
ZNF721
PIGG +
DGKQ -
RNF212 -
ZNF732 -
ZNF876P +
FAM53A -
SLBP -
FGFR3 +
GAK -
SLC2A4RG
GARL1 +
SPON2 -
IDUA +
TMED11P -
TACC3 +
LETM1 -

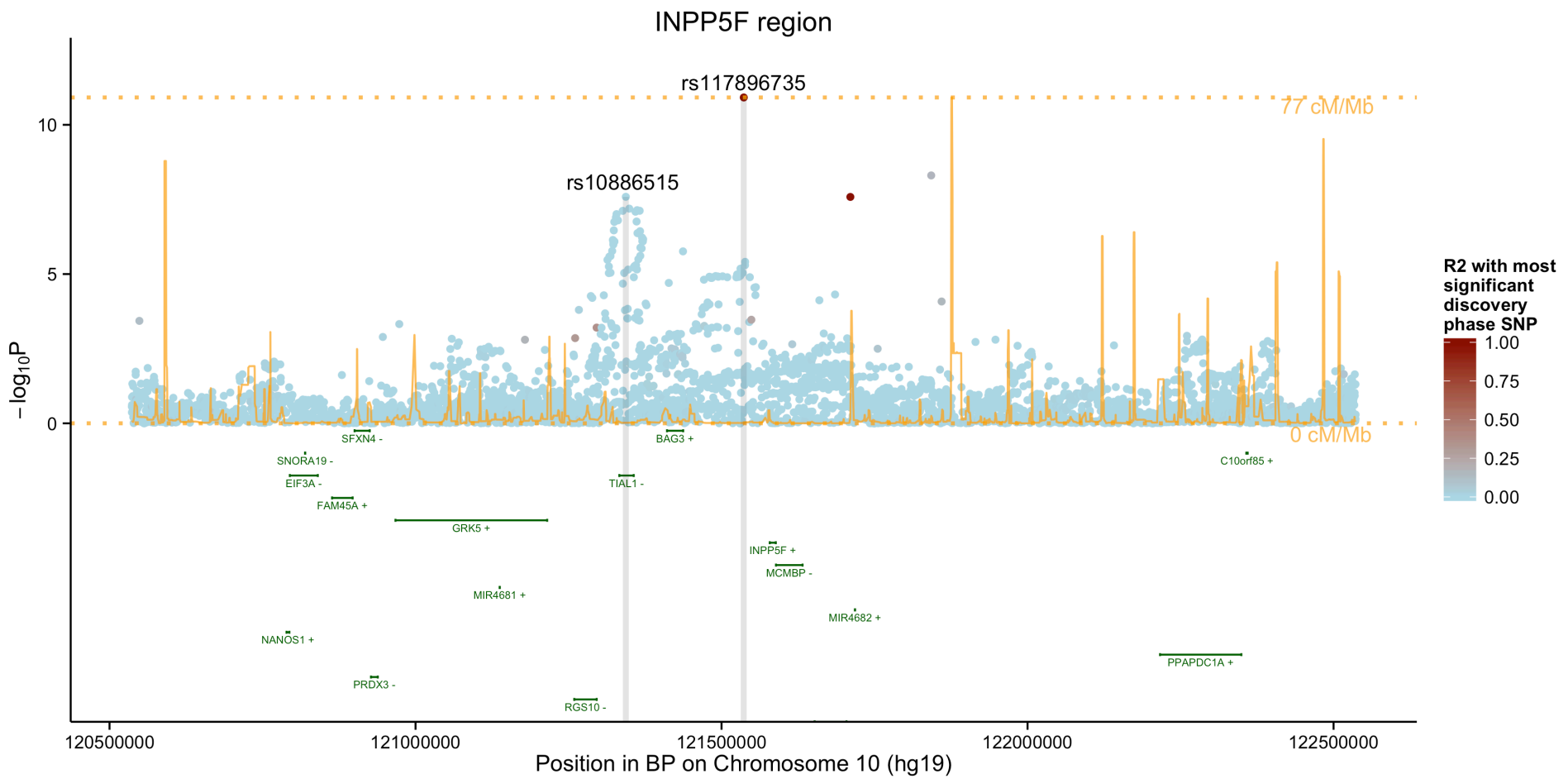

BST1 region
rs11724635
72 cM/Mb
0 cM/Mb
10
5
0
$-\log_{10}P$
BST1 +
C1QTNF7 +
CC2D2A +
CD38 +
CPEB2 +
FAM200B +
FBXL5 -
FGFBP1 -
FGFBP2 -
LOC441009 -
MIR548AX -
PROM1 -
TAPT1 -
15000000
15500000
16000000
16500000
Position in BP on Chromosome 4 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

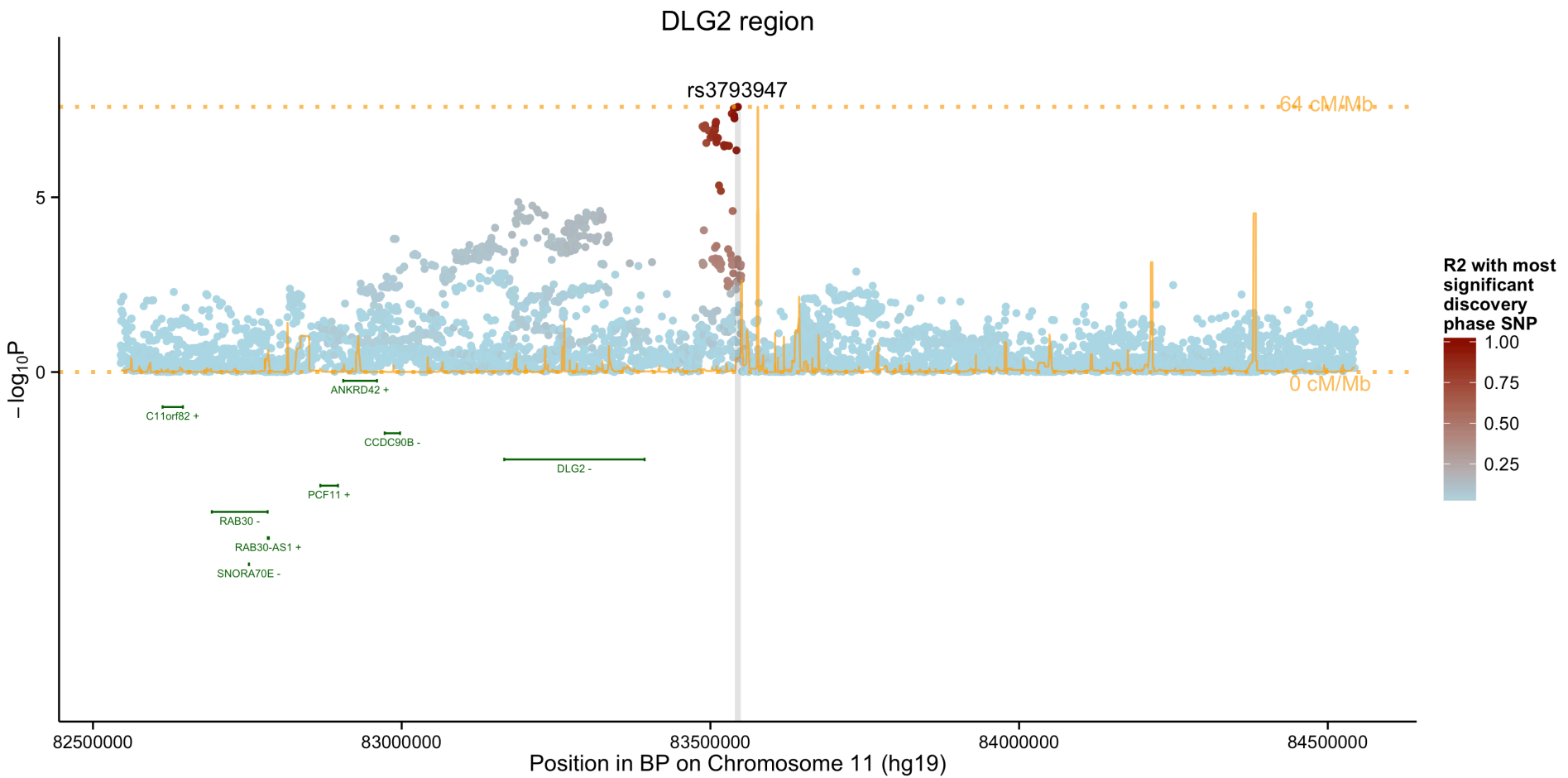

FAM47E/SCARB2 region
rs6812193
rs1596117
69 cM/Mb
0 cM/Mb
10
5
0
– log10P
ART3 +
NUP54 -
C4orf26 +
PPEF2 -
CCDC158 -
RCHY1 -
SCARB2 -
CCNG2 +
CCNI -
SDAD1 -
CDKL2 -
SEPT11 +
CXCL10 -
SHROOM3 +
CXCL11 -
SOWAHB -
CXCL9 -
STBD1 +
FAM47E +
THAP6 +
FAM47E-STBD1 +
USO1 +
G3BP2 -
LOC441025 +
MIR4450 +
NAAA -
76500000
77000000
77500000
78000000
Position in BP on Chromosome 4 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

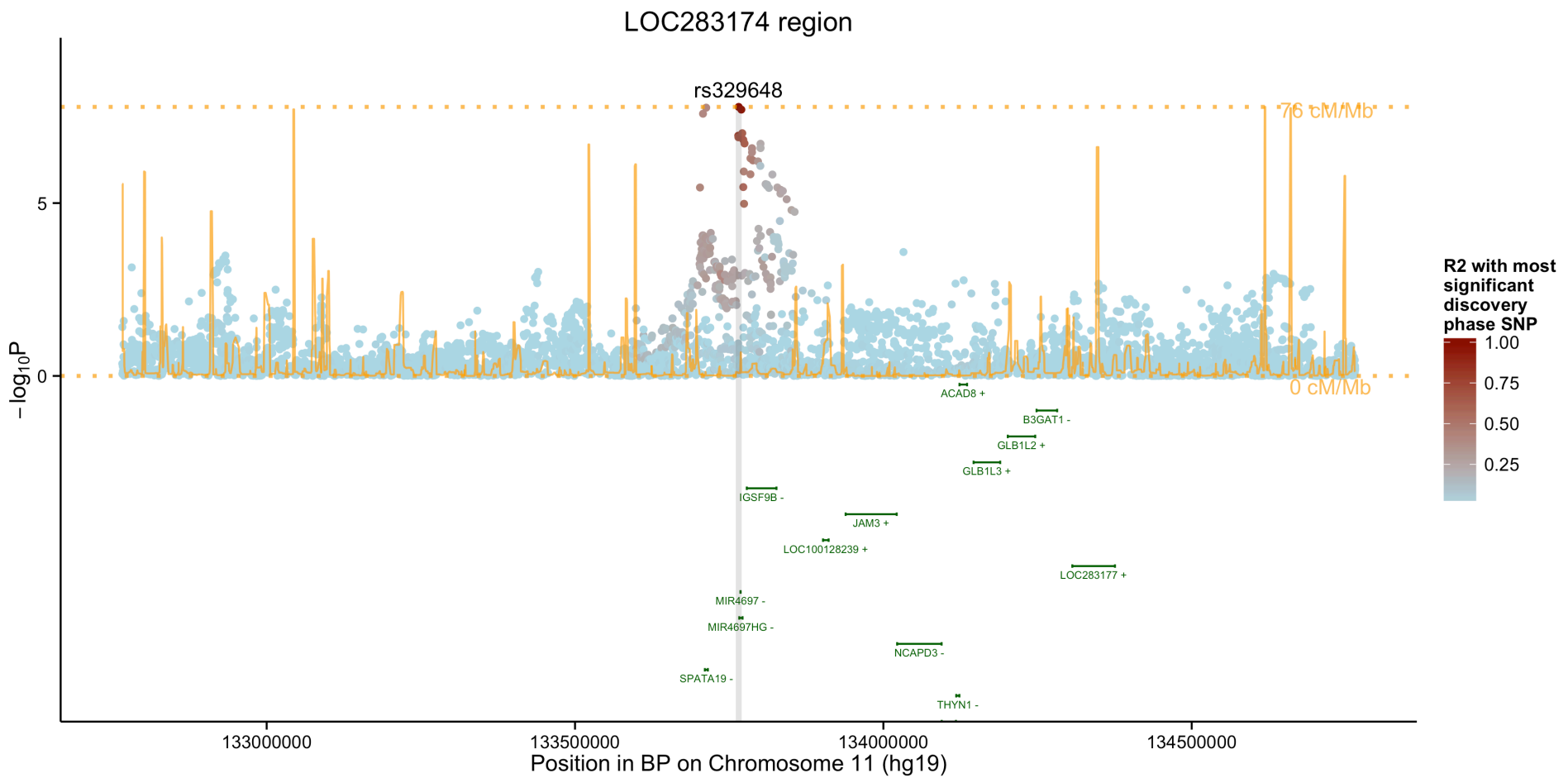

SNCA region
rs356182
67 cM/Mb
rs7681154
0 cM/Mb
– log10P
65
60
55
50
45
40
35
30
25
20
15
10
5
0
FAM13A-AS1 +
FAM13A -
GPRIN3 -
TIGD2 +
LOC644248 +
SNCA -
MIMRN1 +
90000000
90500000
91000000
91500000
Position in BP on Chromosome 4 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

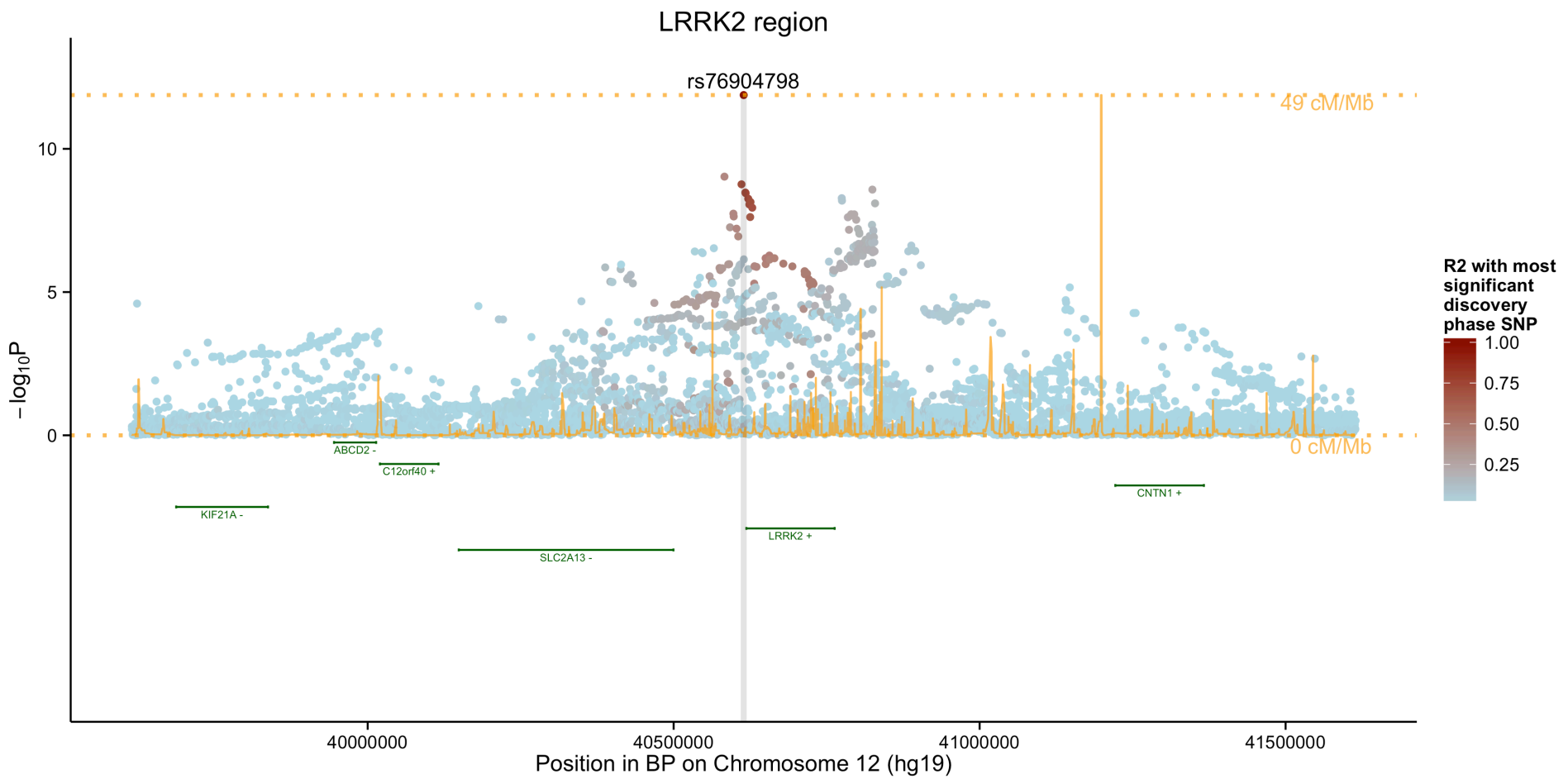

HLA-DQB1 region
rs9275326
rs13201101
70 cM/Mb
0 cM/Mb
10
5
0
$-\log_{10}P$
MIR1236 -
AGER -
TNXA -
AGPAT1 -
MIR4646 -
TNXB -
ZBTB12 -
C6orf25 +
NEU1 -
CLIC1 -
HSPA1A +
PRRT1 -
DDAH2 -
DOM3Z -
SAPCD1 +
FKBPL -
SKIV2L +
LY6G6C -
GPSM3 -
LY6G6E -
SNORD52 +
HLA-DQA1 +
TAP1 -
HLA-DQA2 +
HLA-DQB1 -
HLA-DQB2 -
HLA-DRB1 -
HLA-DRB5 -
PSMB8 -
LOC100294145 +
LOC100507463 +
HLA-DMA -
MIR219-1 +
B3GALT4 +
MIR5004 +
BAK1 -
ZBTB22 -
PFDN6 +
ZBTB9 +
CUTA -
ITPR3 +
RING1 +
LINC00336 -
GGNBP1 +
SLC39A7 +
32000000
32500000
33000000
33500000
Position in BP on Chromosome 6 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
0.00

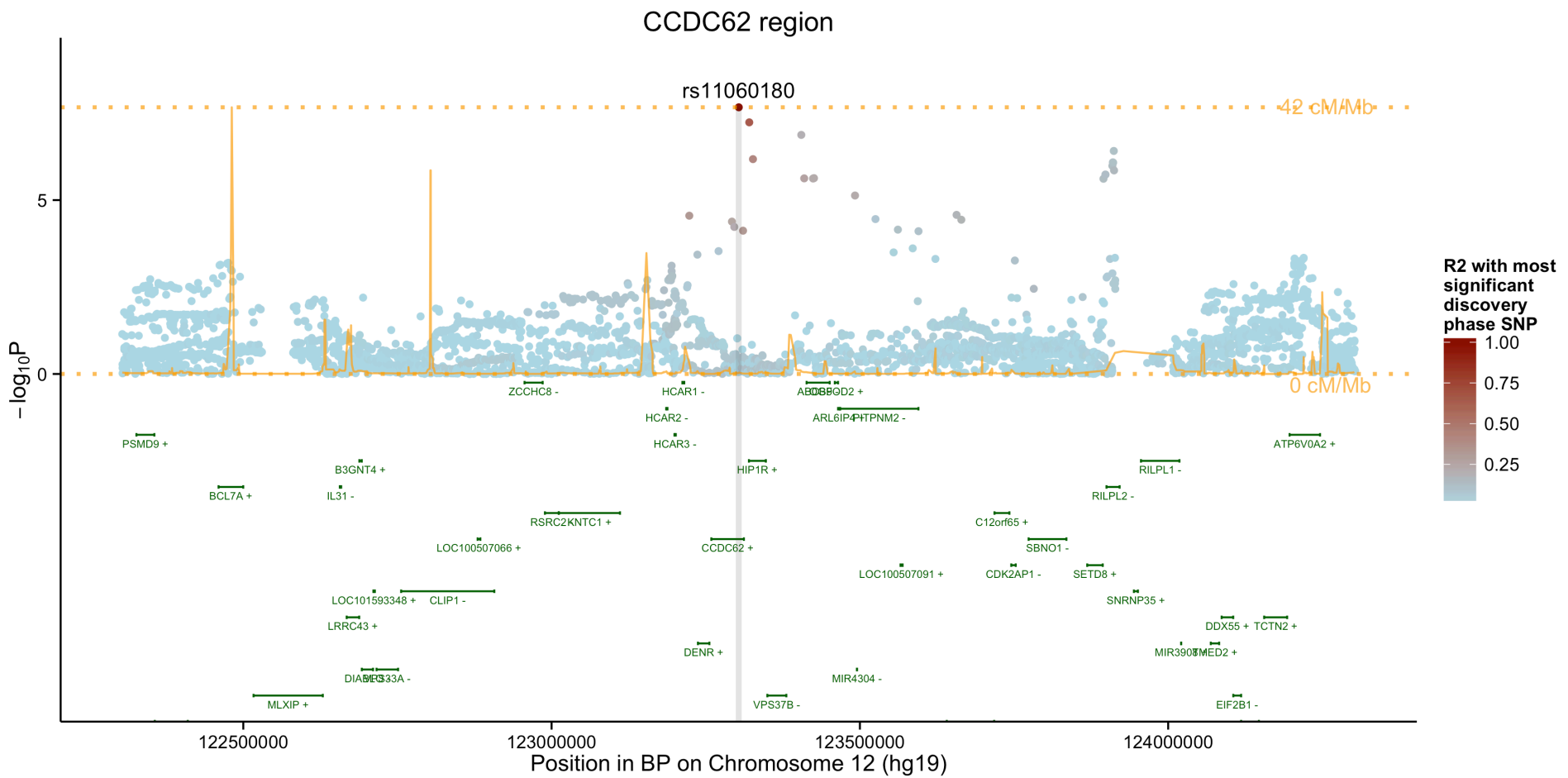

GPNMB region
rs199347
89 cM/Mb
0 cM/Mb
10
5
0
$-\log_{10}P$
STEAP1B -
TOMM7 -
FAM126A -
GPNMB +
IGF2BP3 -
IL6 +
KLHL7 +
KLHL7-AS1 -
LOC100506178 +
MALSU1 +
NUPL2 +
RPS2P32 +
TRA2A -
CLK2P -
CCDC126 +
FAM221A +
STK31 +
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
22500000
23000000
23500000
24000000
Position in BP on Chromosome 7 (hg19)

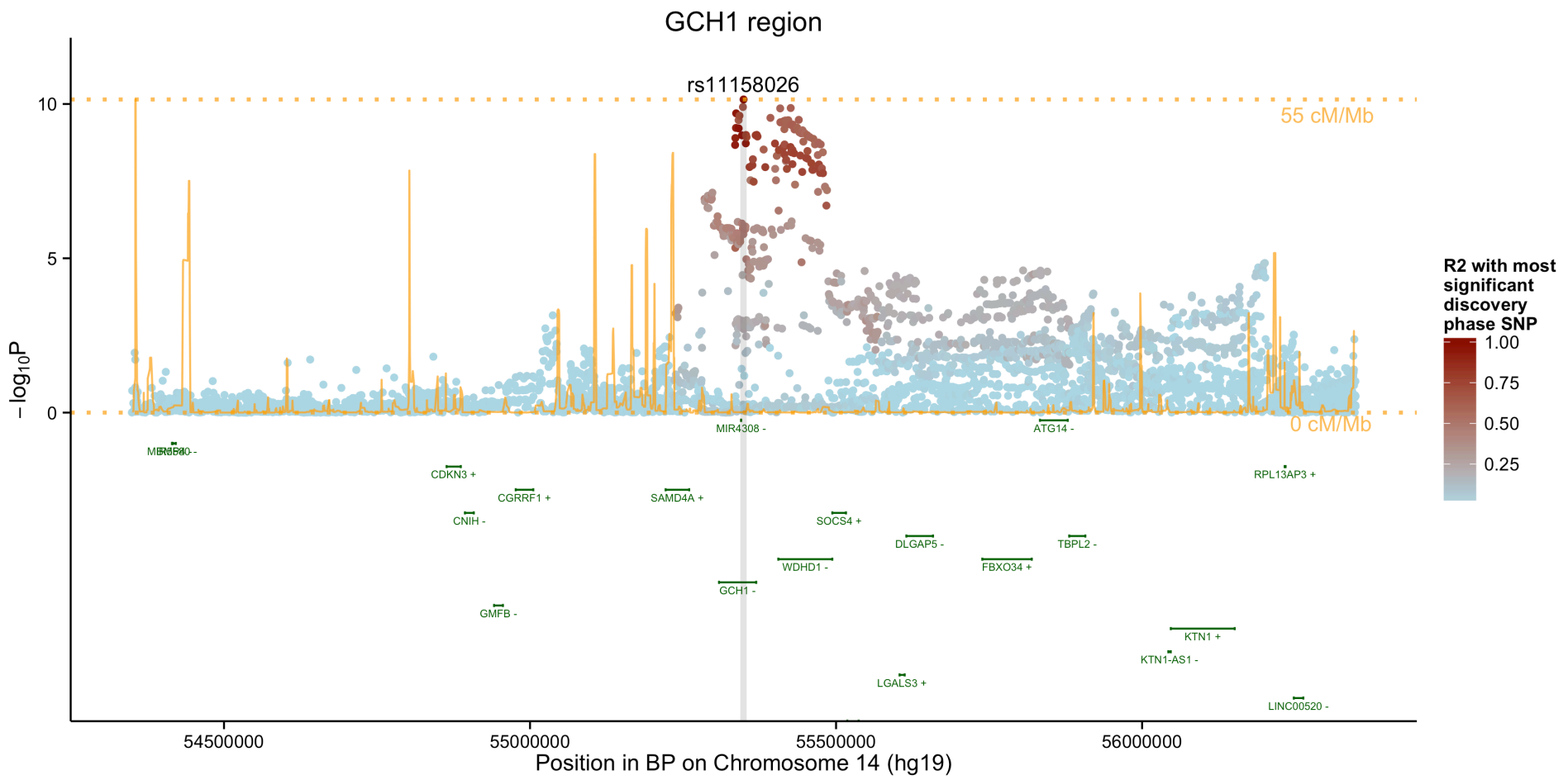

INPP5F region
rs117896735
rs10886515
77 cM/Mb
0 cM/Mb
10
5
0
– log10P
SFXN4 -
BAG3 +
SNORA19 -
C10orf85 +
EIF3A -
TIAL1 -
FAM45A +
GRK5 +
INPP5F +
MCMBP -
MIR4681 +
MIR4682 +
NANOS1 +
PPAPDC1A +
PRDX3 -
RGS10 -
120500000
121000000
121500000
122000000
122500000
Position in BP on Chromosome 10 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
0.00

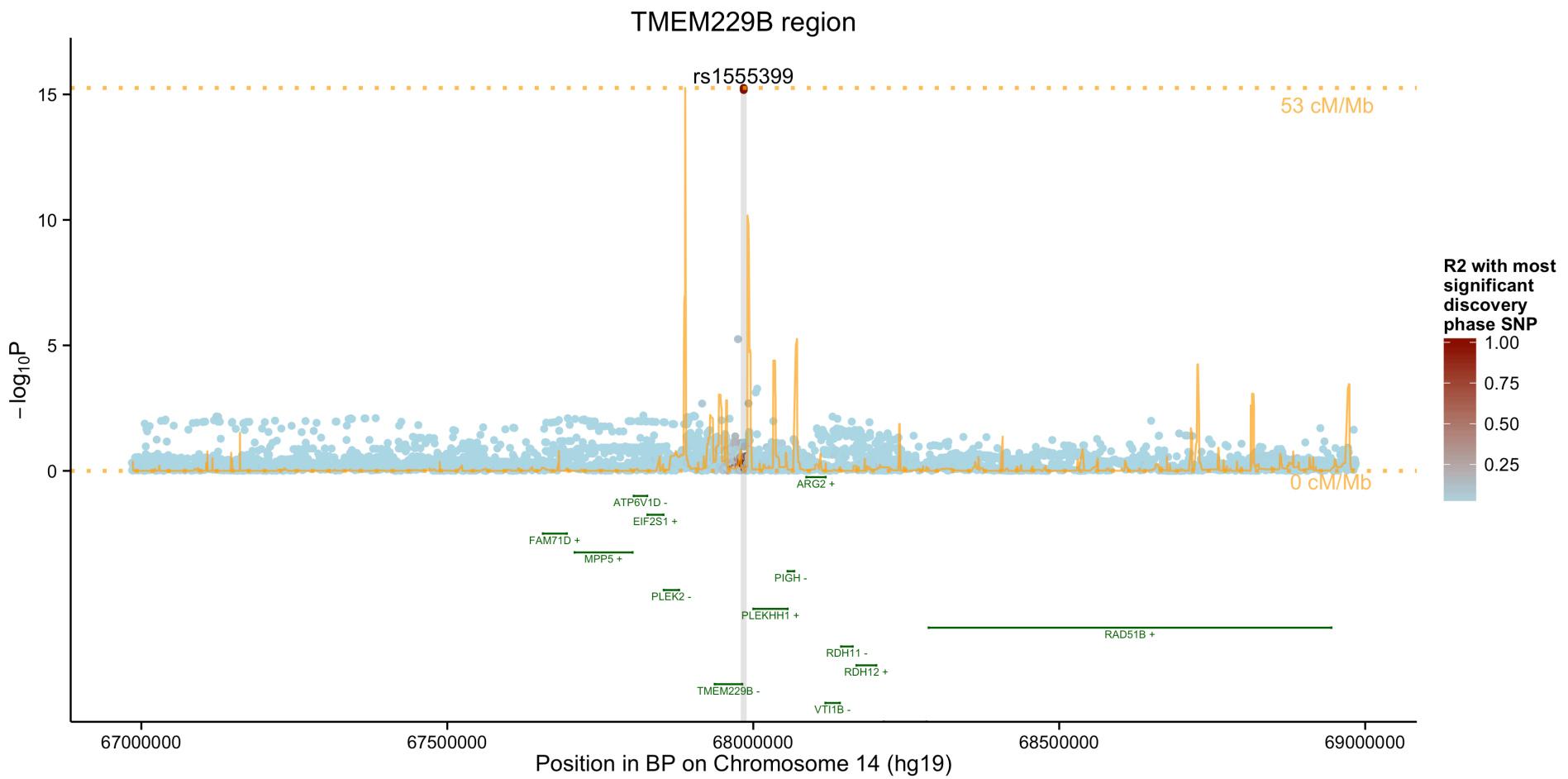

DLG2 region
rs3793947
64 cM/Mb
0 cM/Mb
5
0
– log10P
ANKRD42 +
C11orf82 +
CCDC90B -
DLG2 -
PCF11 +
RAB30 -
RAB30-AS1 +
SNORA70E -
82500000
83000000
83500000
84000000
84500000
Position in BP on Chromosome 11 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

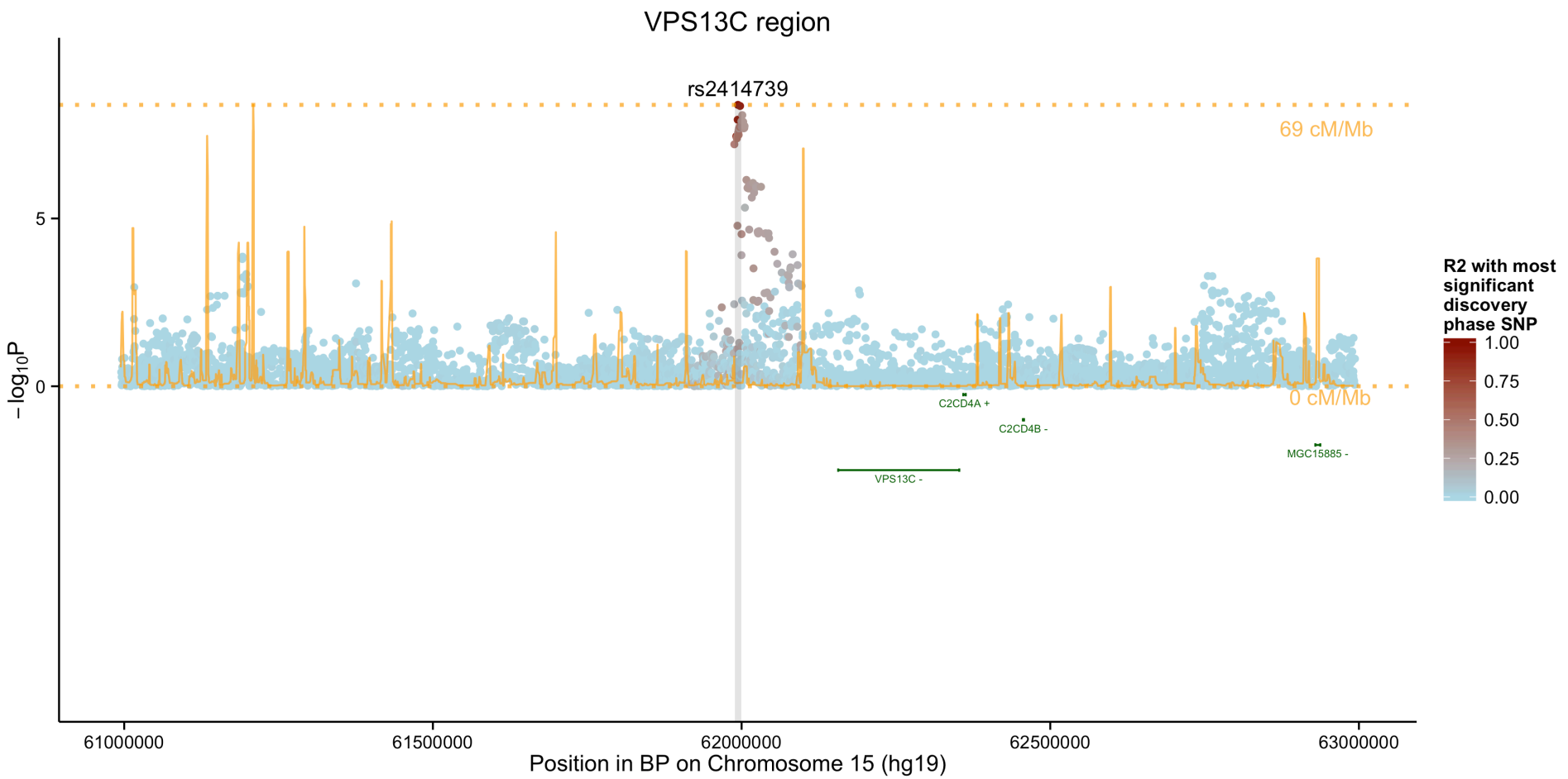

LOC283174 region
rs329648
76 cM/Mb
0 cM/Mb
5
0
$-\log_{10}P$
ACAD8 +
B3GAT1 -
GLB1L2 +
GLB1L3 +
IGSF9B -
JAM3 +
LOC100128239 +
LOC283177 +
MIR4697 -
MIR4697HG -
NCAPD3 -
SPATA19 -
THYN1 -
133000000
133500000
134000000
134500000
Position in BP on Chromosome 11 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

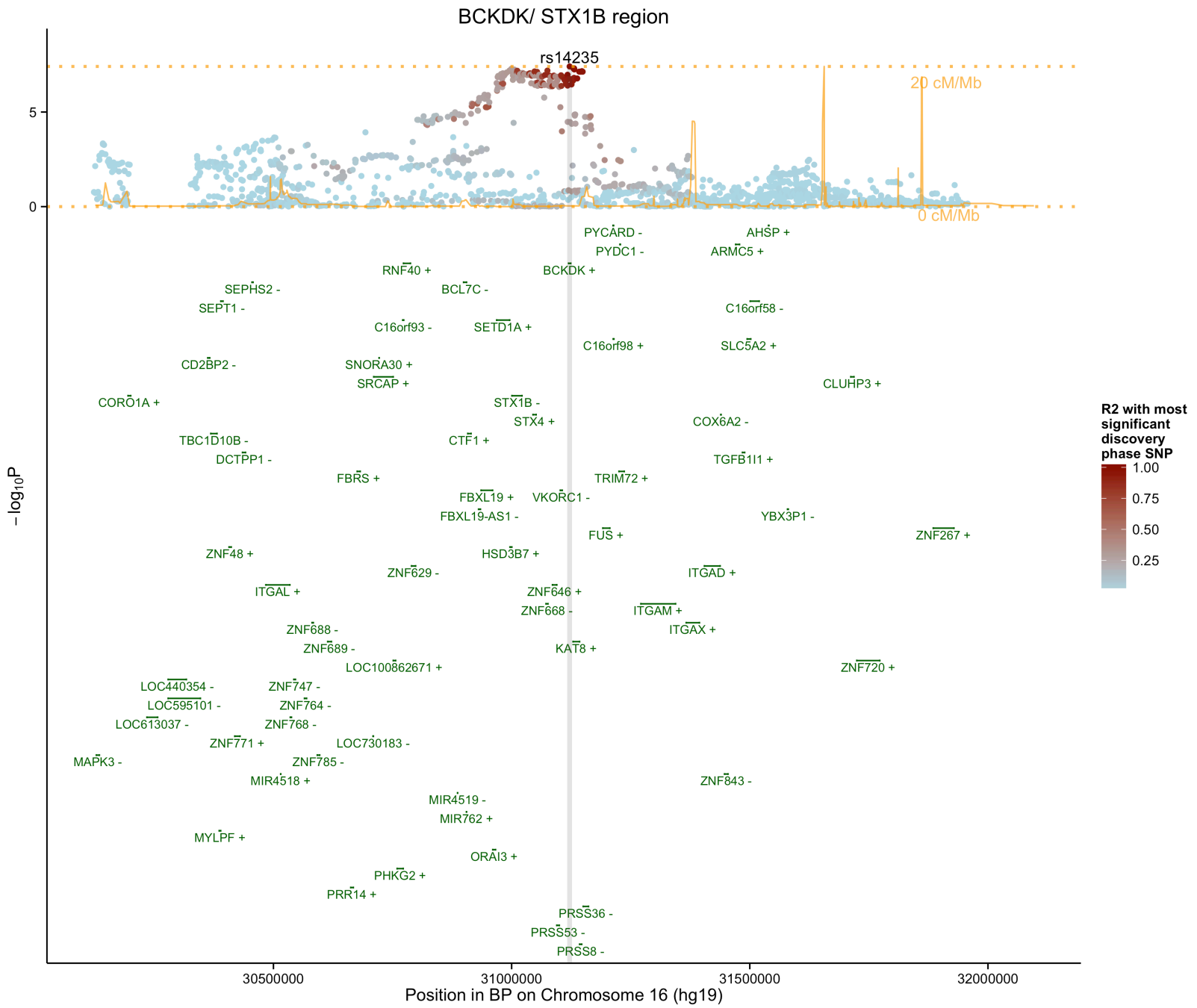

LRRK2 region
rs76904798
49 cM/Mb
0 cM/Mb
10
5
0
$-\log_{10}P$
ABCD2 -
C12orf40 +
KIF21A -
SLC2A13 -
LRRK2 +
CNTN1 +
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
40000000
40500000
41000000
41500000
Position in BP on Chromosome 12 (hg19)

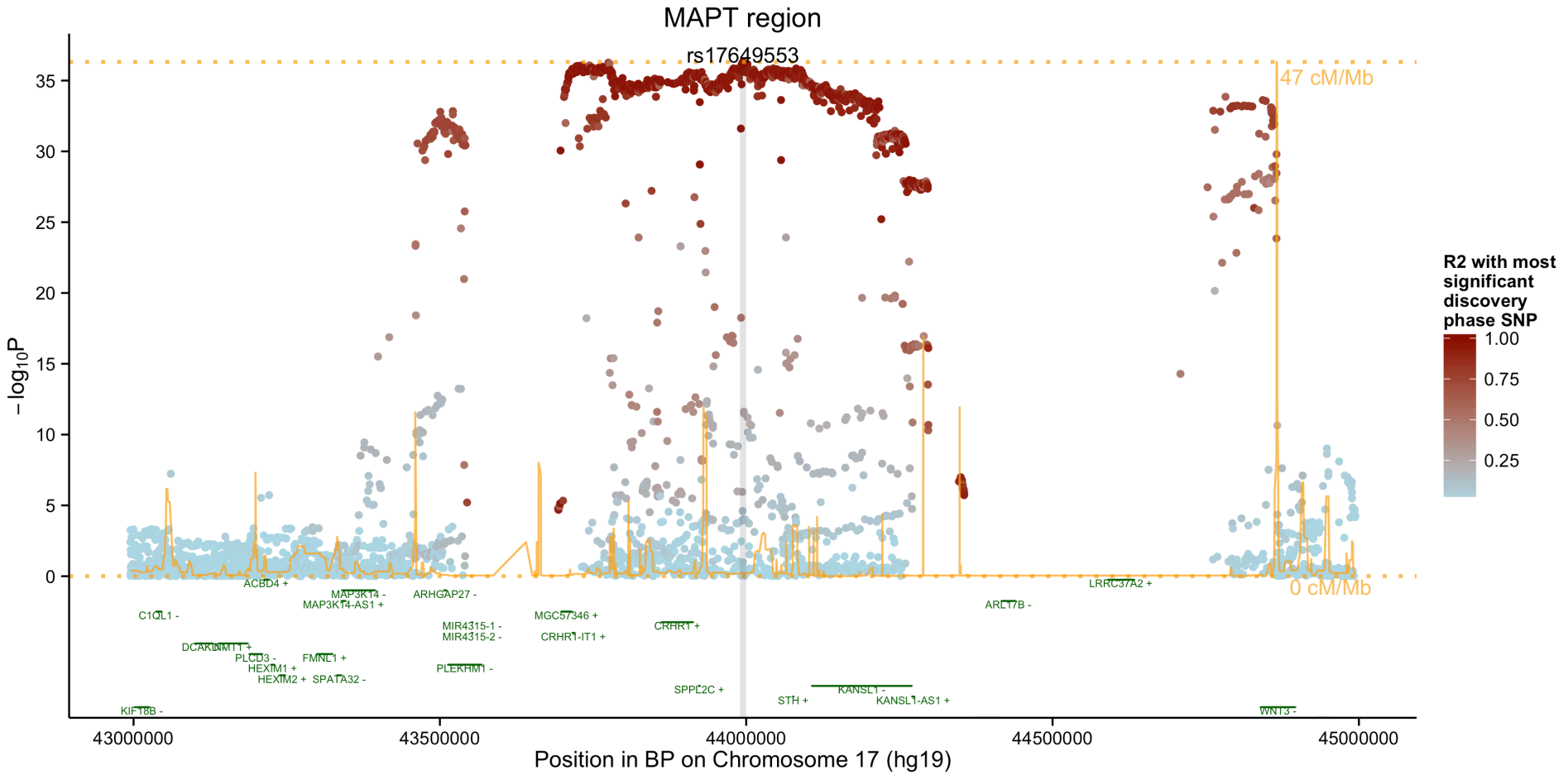

CCDC62 region
rs11060180
42 cM/Mb
0 cM/Mb
5
0
– log10P
ZCCHC8 -
HCAR1 -
HCAR2 -
HCAR3 -
ARL6IP4 +
PITPNM2 -
PSMD9 +
B3GNT4 +
BCL7A +
IL31 -
HIP1R +
RILPL1 -
RILPL2 -
ATP6V0A2 +
RSRC2
KNTC1 +
C12orf65 +
LOC100507066 +
CCDC62 +
SBNO1 -
LOC100507091 +
CDK2AP1 -
SETD8 +
LOC101593348 +
CLIP1 -
SNRNP35 +
LRRC43 +
DDX55 +
TCTN2 +
DENR +
MED2 +
MIR4304 -
MLXIP +
VPS37B -
EIF2B1 -
122500000
123000000
123500000
124000000
Position in BP on Chromosome 12 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

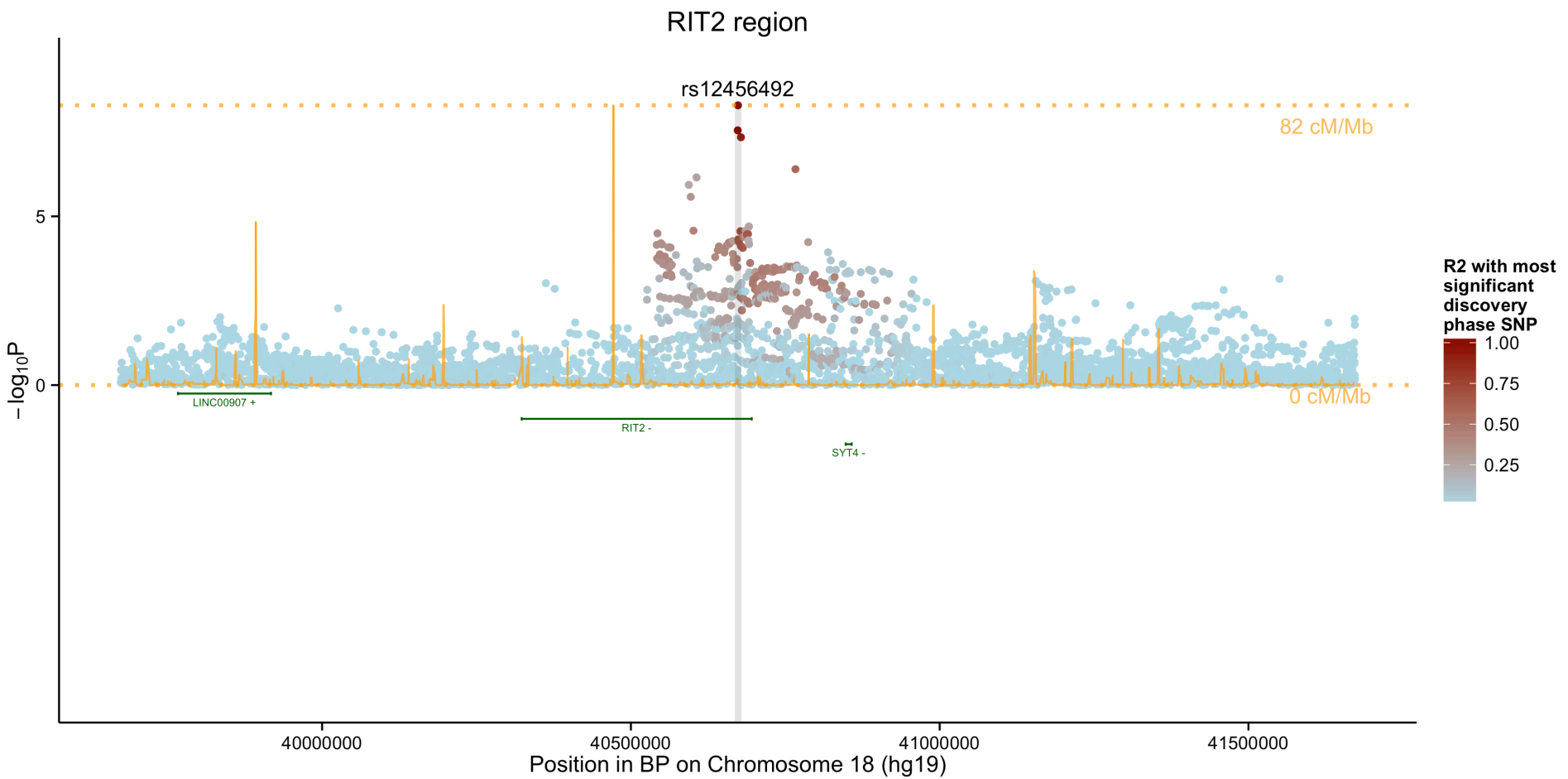

GCH1 region
rs11158026
55 cM/Mb
0 cM/Mb
10
5
0
– log10P
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
MIR4308 -
ATG14 -
CDKN3 +
CGRRF1 +
SAMD4A +
CNIH -
SOCS4 +
DLGAP5 -
TBPL2 -
WDHD1 -
FBXO34 +
GCH1 -
GMFB -
RPL13AP3 +
KTN1 +
KTN1-AS1 -
LGALS3 +
LINC00520 -
54500000
55000000
55500000
56000000
Position in BP on Chromosome 14 (hg19)


TMEM229B region
rs1555399
53 cM/Mb
0 cM/Mb
15
10
5
0
– log10P
ATP6V1D -
EIF2S1 +
FAM71D +
MPP5 +
ARG2 +
PIGH -
PLEK2 -
PLEKHH1 +
RAD51B +
RDH11 -
RDH12 +
TMEM229B -
VTI1B -
67000000
67500000
68000000
68500000
69000000
Position in BP on Chromosome 14 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

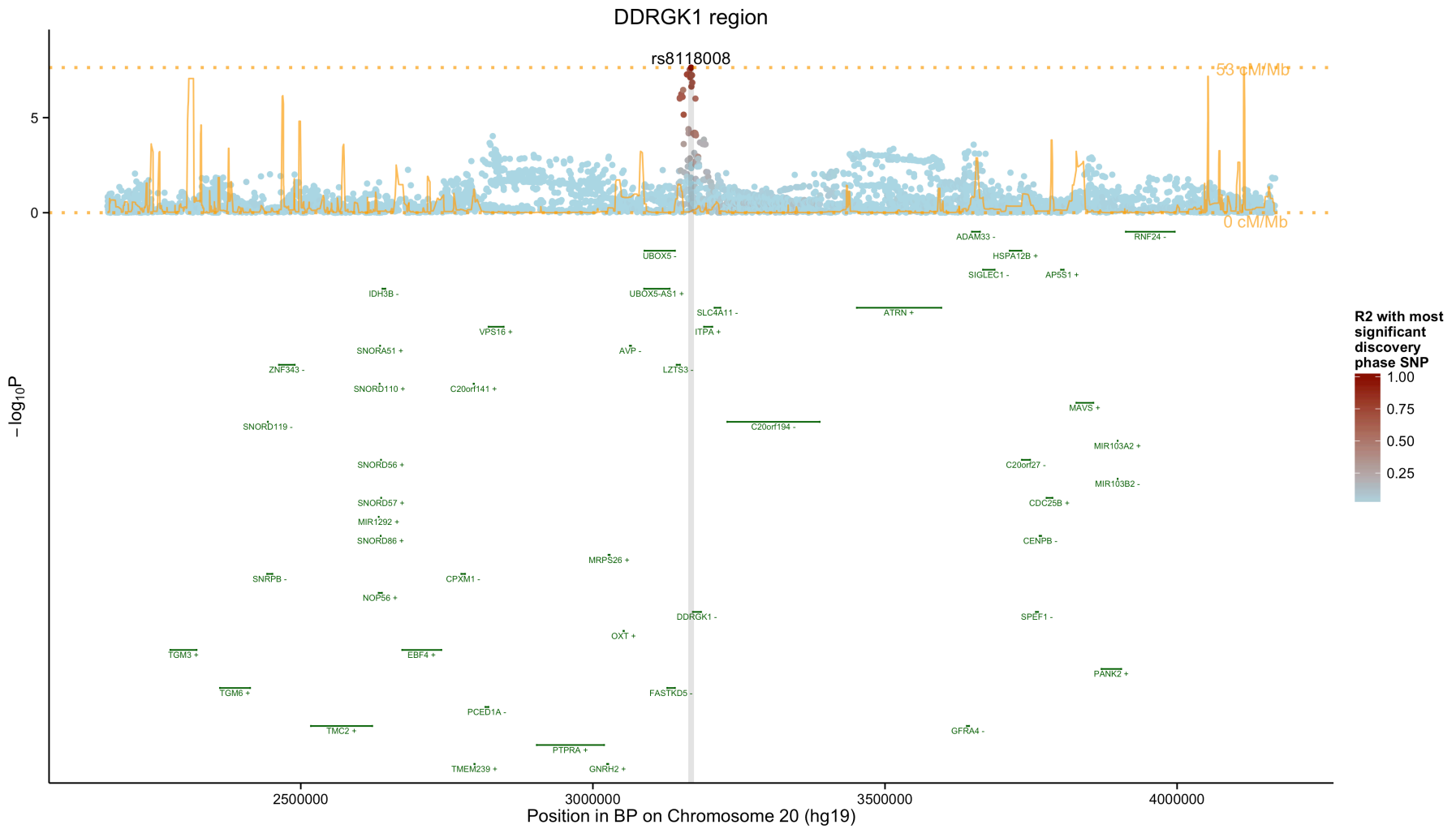

VPS13C region
rs2414739
69 cM/Mb
0 cM/Mb
5
0
– log10P
C2CD4A +
C2CD4B -
MGC15885 -
VPS13C -
61000000
61500000
62000000
62500000
63000000
Position in BP on Chromosome 15 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
0.00

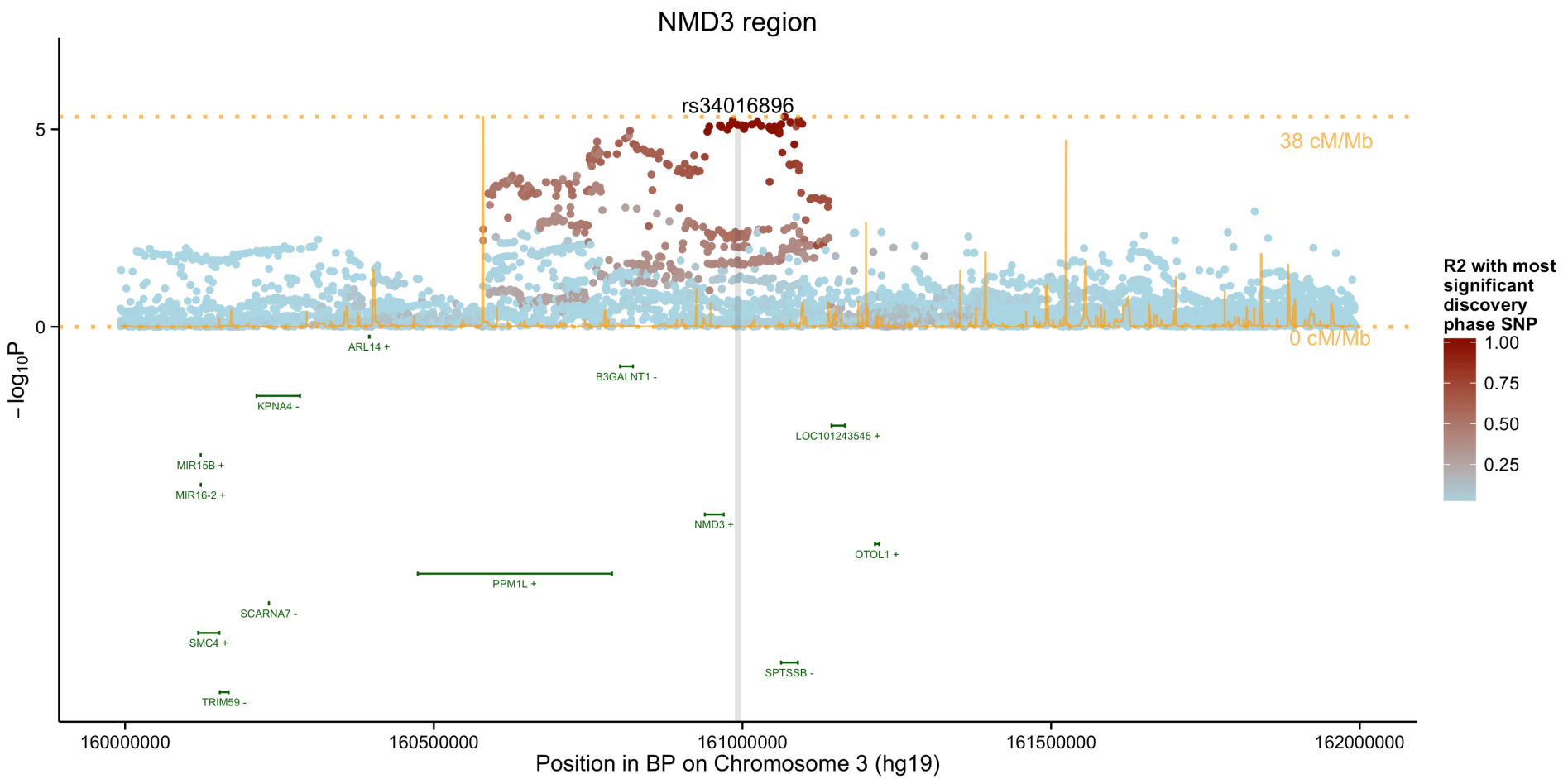

BCKDK/ STX1B region
rs14235
20 cM/Mb
0 cM/Mb
5
0
– log10P
PYCARD -
AHSP +
PYDC1 -
ARMC5 +
RNF40 +
BCKDK +
SEPHS2 -
BCL7C -
SEPT1 -
C16orf58 -
C16orf93 -
SETD1A +
C16orf98 +
SLC5A2 +
CD2BP2 -
SNORA30 +
SRCAP +
CLUHP3 +
CORO1A +
STX1B -
STX4 +
COX6A2 -
TBC1D10B -
CTF1 +
DCTPP1 -
TGFB1I1 +
FBRS +
TRIM72 +
FBXL19 +
VKORC1 -
FBXL19-AS1 -
YBX3P1 -
FUS +
ZNF267 +
ZNF48 +
HSD3B7 +
ZNF629 -
ITGAD +
ITGAL +
ZNF646 +
ZNF668 -
ITGAM +
ITGAX +
ZNF688 -
ZNF689 -
KAT8 +
LOC100862671 +
ZNF720 +
LOC440354 -
ZNF747 -
LOC595101 -
ZNF764 -
LOC613037 -
ZNF768 -
ZNF771 +
LOC730183 -
MAPK3 -
ZNF785 -
MIR4518 +
ZNF843 -
MIR4519 -
MIR762 +
MYLPF +
ORAI3 +
PHKG2 +
PRR14 +
PRSS36 -
PRSS53 -
PRSS8 -
30500000
31000000
31500000
32000000
Position in BP on Chromosome 16 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

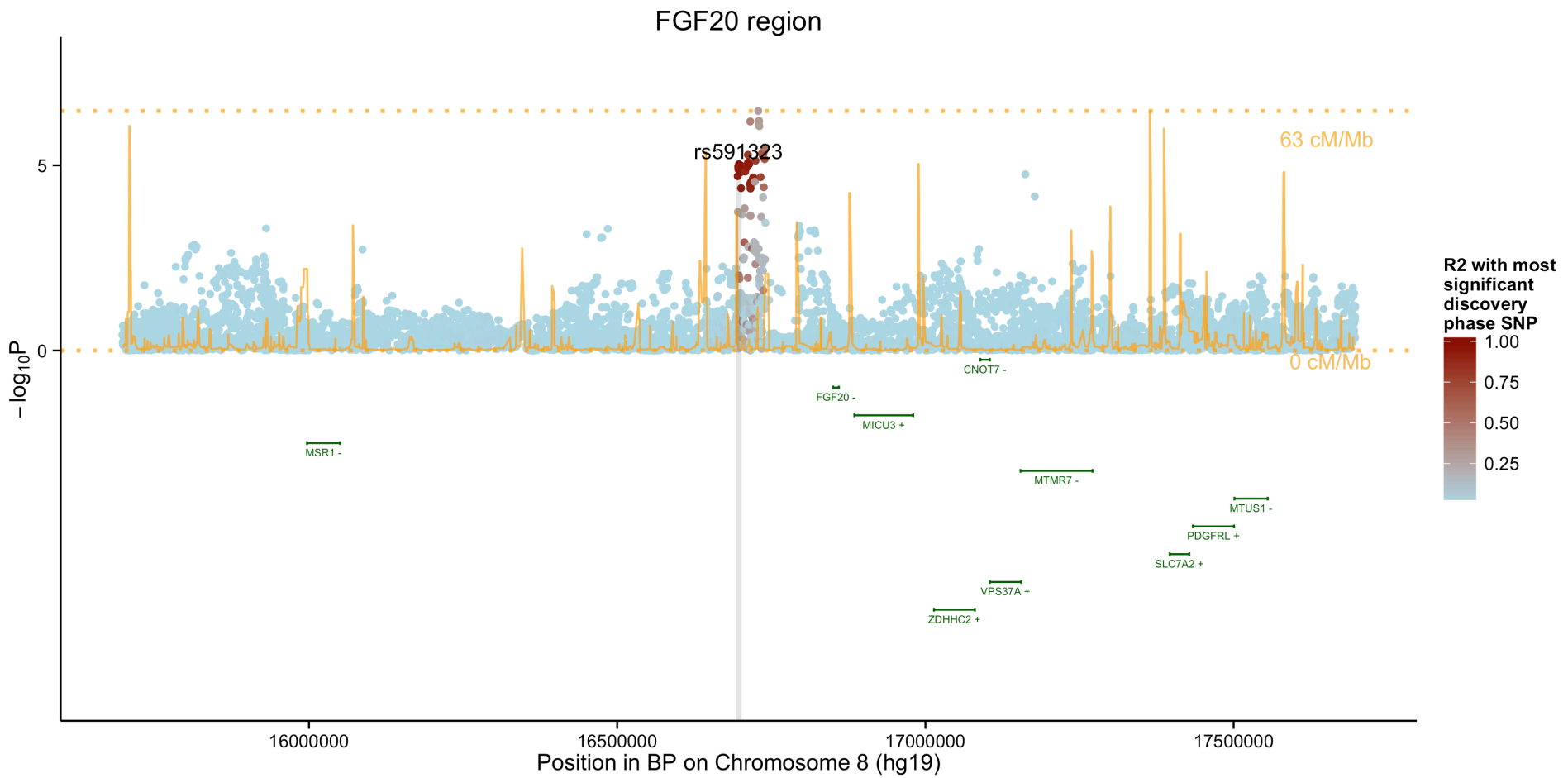

MAPT region
rs17649553
47 cM/Mb
0 cM/Mb
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
−log10P
35
30
25
20
15
10
5
0
43000000
43500000
44000000
44500000
45000000
Position in BP on Chromosome 17 (hg19)
ACBD4 +
MAP3K14 -
MAP3K14-AS1 +
ARHGAP27 -
C1QL1 -
MIR4315-1 -
MIR4315-2 -
MGC57346 +
CRHR1-IT1 +
CRHR1 +
LRRC37A2 +
ARL17B -
DCAKD +
PLCD3 -
HEXIM1 +
HEXIM2 +
SPATA32 -
FMNL1 +
PLEKHM1 -
SPPL2C +
STH +
KANSL1 -
KANSL1-AS1 +
KIF18B -
WNT3 -

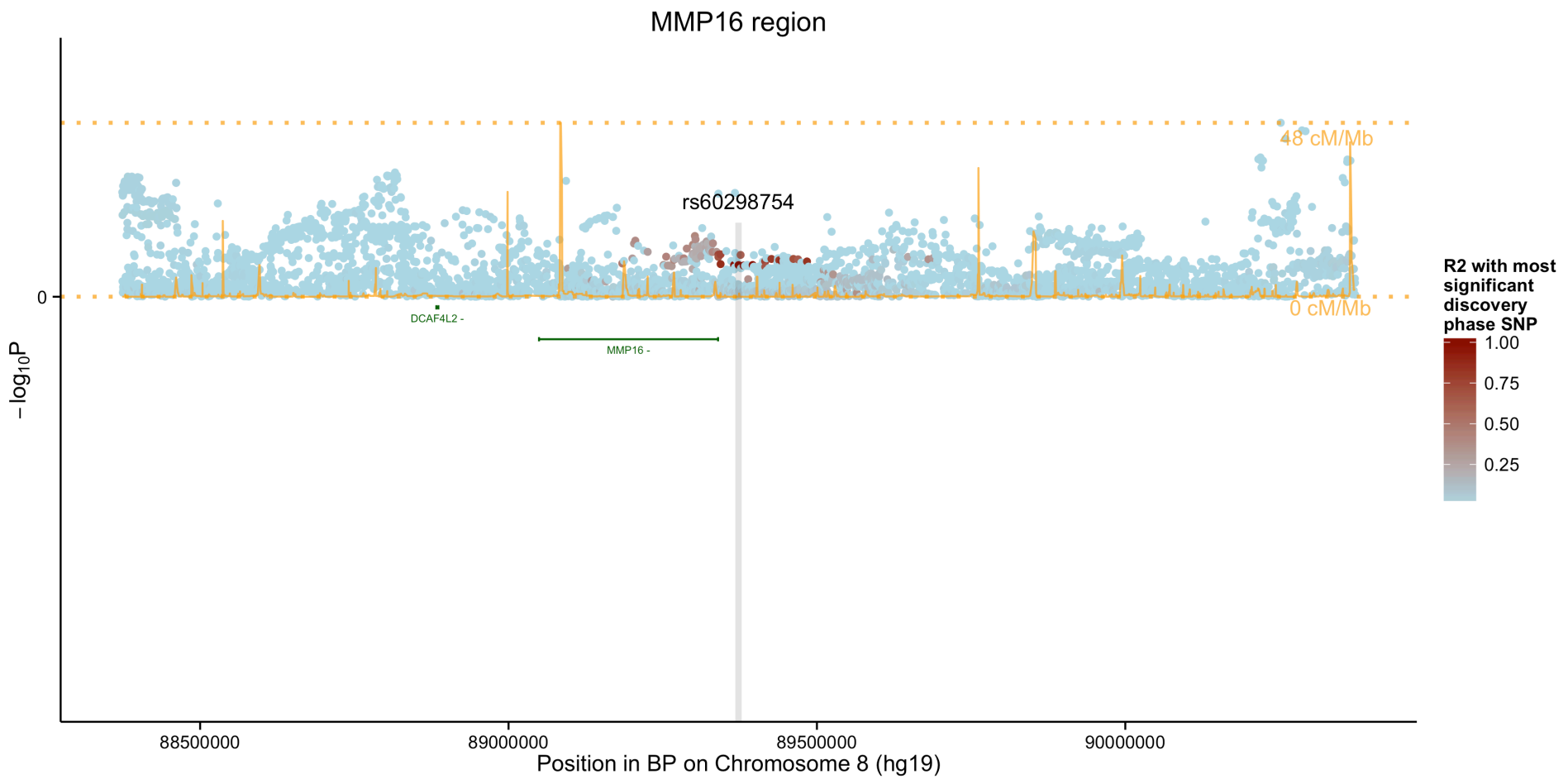

RIT2 region
rs12456492
82 cM/Mb
0 cM/Mb
5
0
$-\log_{10}P$
LINC00907 +
RIT2 -
SYT4 -
40000000
40500000
41000000
41500000
Position in BP on Chromosome 18 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

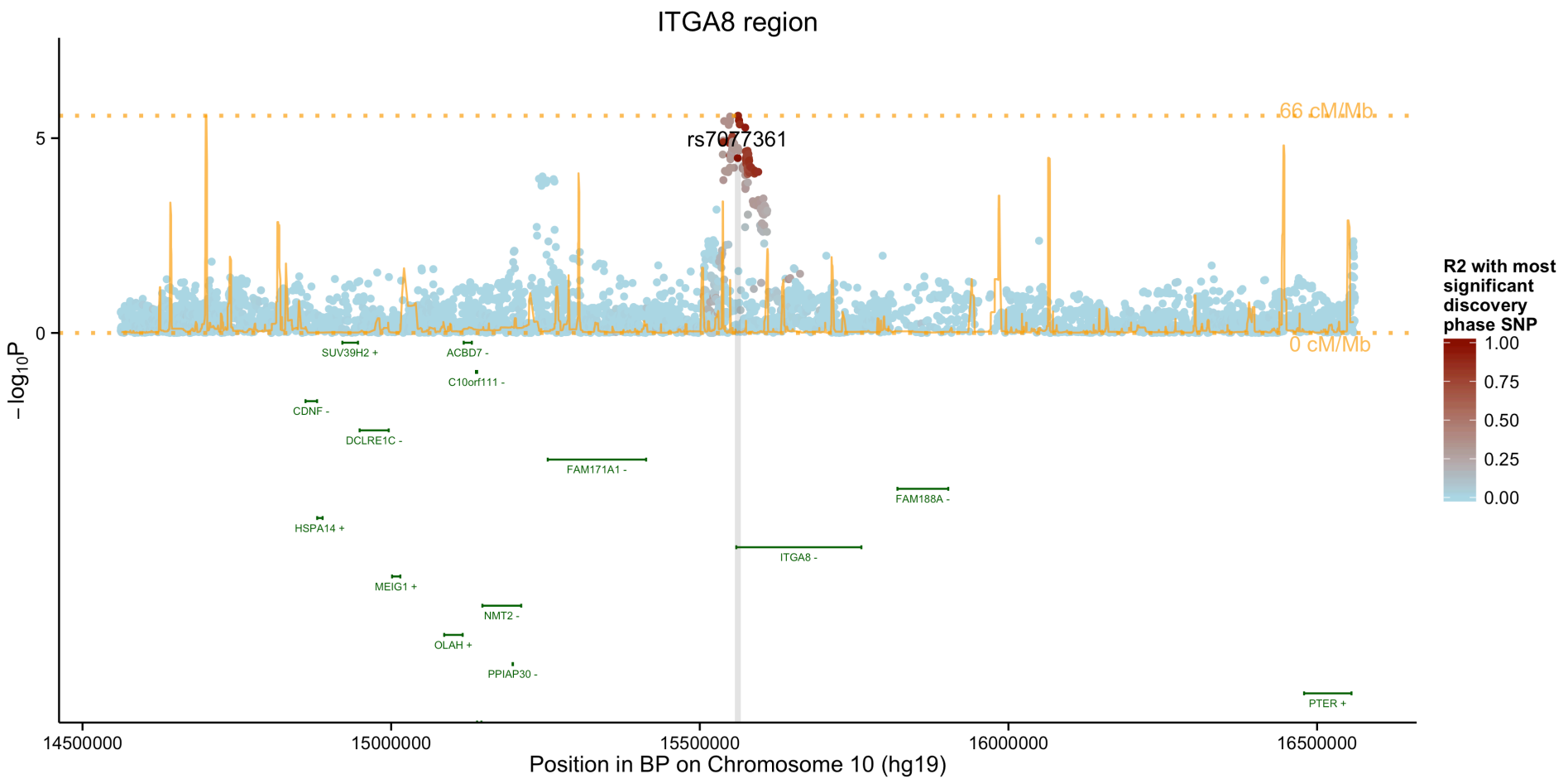

SPPL2B region
rs62120679
rs117022814
72 cM/Mb
0 cM/Mb
5
0
− log10P
ONECUT3
ABHD17A -
ADAT3 +
PLEKHJ1 -
PLK5 +
REEP6 +
AMH +
AES -
REXO1 -
AP3D1 -
ATP8B3 -
S1PR4 +
SCAMP4
BTBD2 -
C19orf25 -
SF3A2 +
C19orf35 -
SGTA -
SLC39A3 -
CELF5 +
CSNK1G2 +
SPPL2B +
TCF3 -
CSNK1G2-AS1 -
DAZAP1 +
THOP1 +
TIMM13 -
DIRAS1 -
DOT1L +
TLE2 -
GADD45B +
TLE6 +
GAMT -
TMPRSS9 +
UQCR11 -
GNA11 +
ZNF554 +
GNA15 +
GNG7 -
ZNF555 +
IZUMO4 +
ZNF556 +
JSRP1 -
ZNF57 +
KLF16 -
ZNF77 -
LINGO3 -
LMNB2 -
LOC100288123 +
LSM7 -
MBD3 -
MEX3D -
MIR1227 -
MIR1909 -
MIR4321 +
MKNK2 -
MOB3A -
NCLN +
NDUFS7 +
OAZ1 +
1500000
2000000
2500000
3000000
Position in BP on Chromosome 19 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

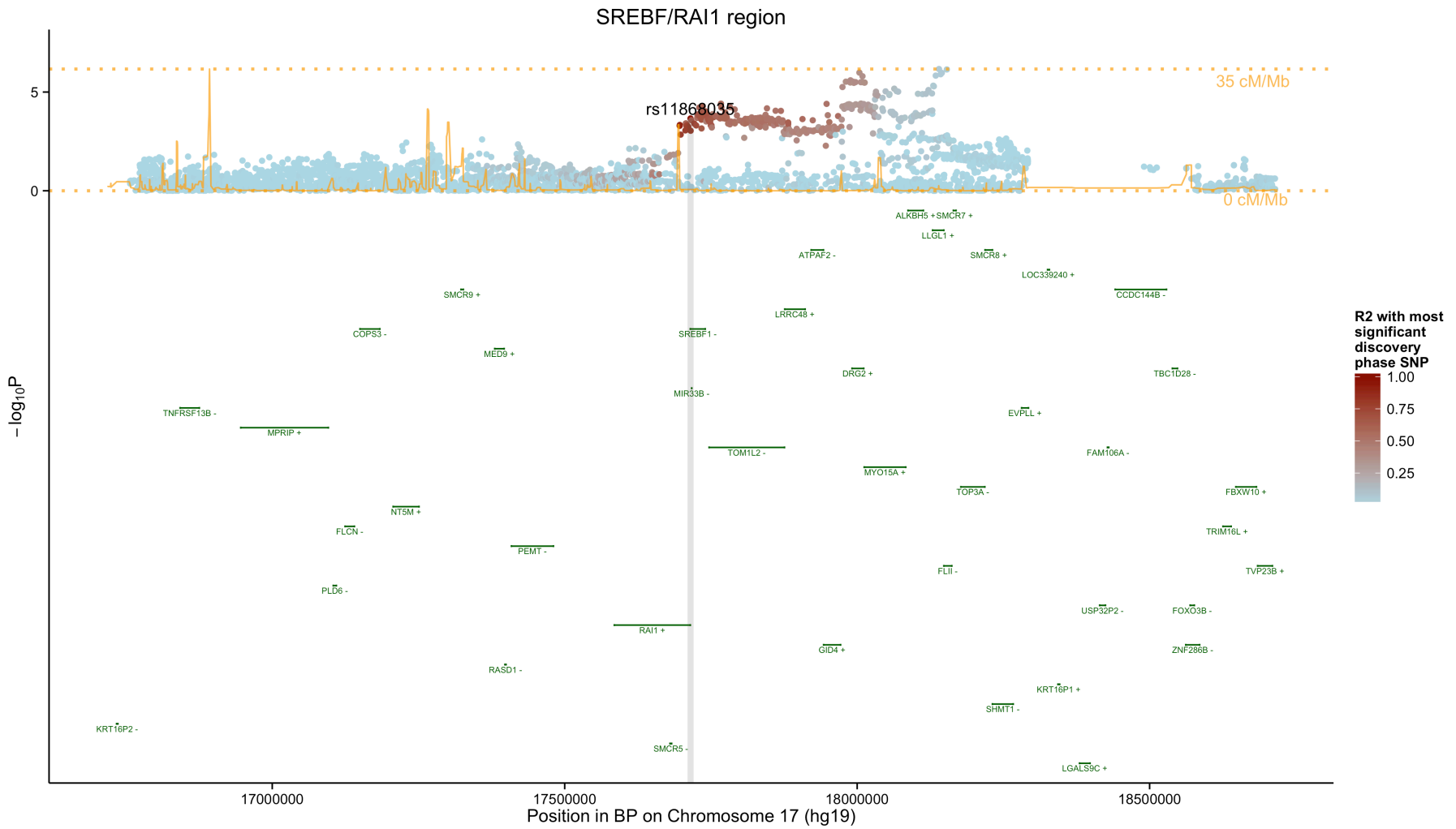

DDRGK1 region
rs8118008
53 cM/Mb
0 cM/Mb
5
0
– log10P
ADAM33 -
RNF24 -
UBOX5 -
HSPA12B +
SIGLEC1 -
AP5S1 +
IDH3B -
UBOX5-AS1 +
SLC4A11 -
ATRN +
VPS16 +
ITPA +
SNORA51 +
AVP -
ZNF343 -
LZTS3 -
SNORD110 +
C20orf141 +
MAVS +
SNORD119 -
C20orf194 -
MIR103A2 +
SNORD56 +
C20orf27 -
MIR103B2 -
SNORD57 +
CDC25B +
MIR1292 +
SNORD86 +
CENPB -
MRPS26 +
SNRPB -
CPXM1 -
NOP56 +
DDRGK1 -
SPEF1 -
OXT +
TGM3 +
EBF4 +
PANK2 +
TGM6 +
FASTKD5 -
PCED1A -
TMC2 +
GFRA4 -
PTPRA +
TMEM239 +
GNRH2 +
2500000
3000000
3500000
4000000
Position in BP on Chromosome 20 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

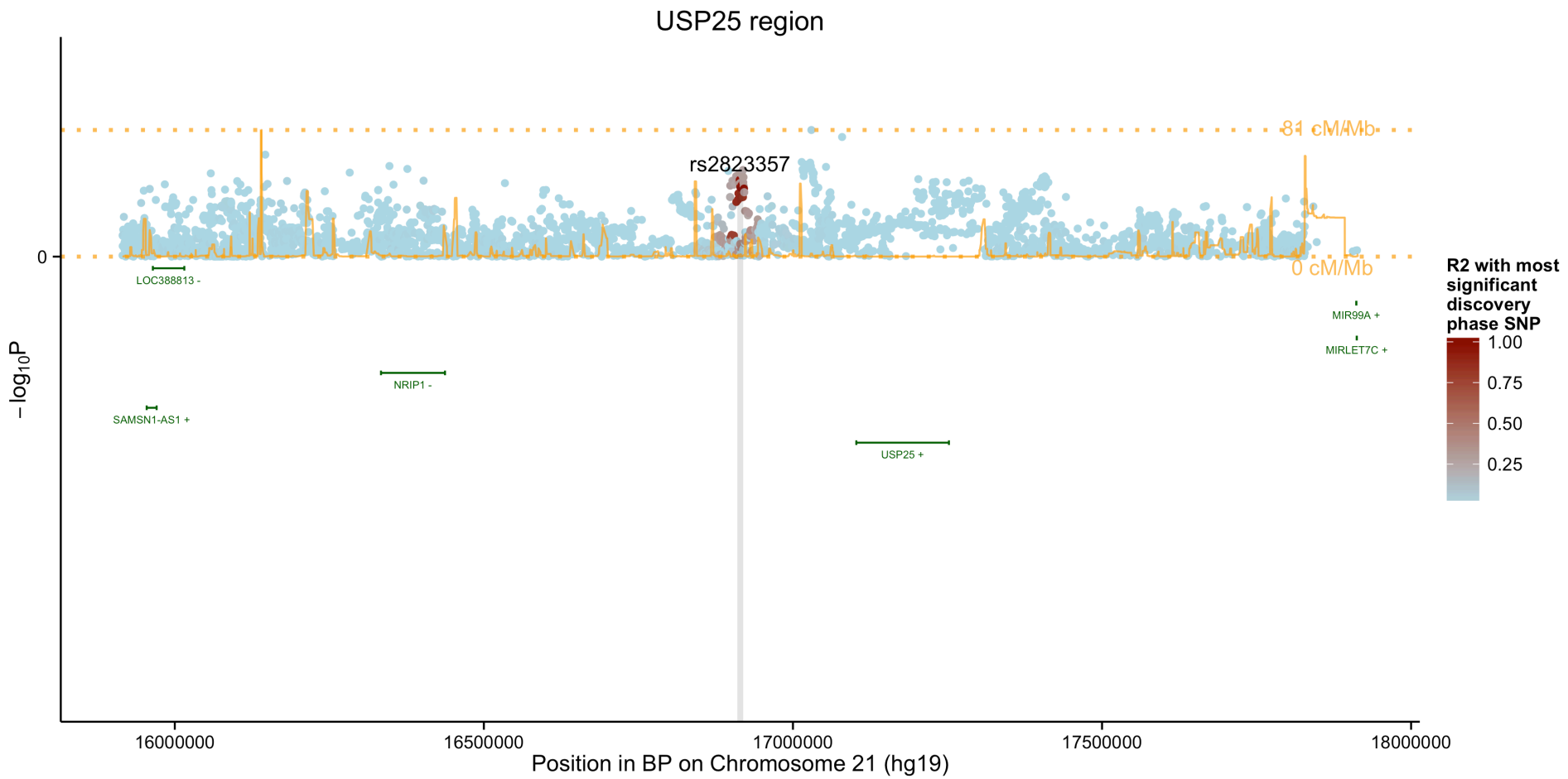

NMD3 region
rs34016896
38 cM/Mb
0 cM/Mb
5
0
– log10P
ARL14 +
B3GALNT1 -
KPNA4 -
LOC101243545 +
MIR15B +
MIR16-2 +
NMD3 +
OTOL1 +
PPM1L +
SCARNA7 -
SMC4 +
SPTSSB -
TRIM59 -
160000000
160500000
161000000
161500000
162000000
Position in BP on Chromosome 3 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25


FGF20 region
rs591323
63 cM/Mb
0 cM/Mb
5
0
$-\log_{10}$P
CNOT7 -
FGF20 -
MICU3 +
MSR1 -
MTMR7 -
MTUS1 -
PDGFRL +
SLC7A2 +
VPS37A +
ZDHHC2 +
16000000
16500000
17000000
17500000
Position in BP on Chromosome 8 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

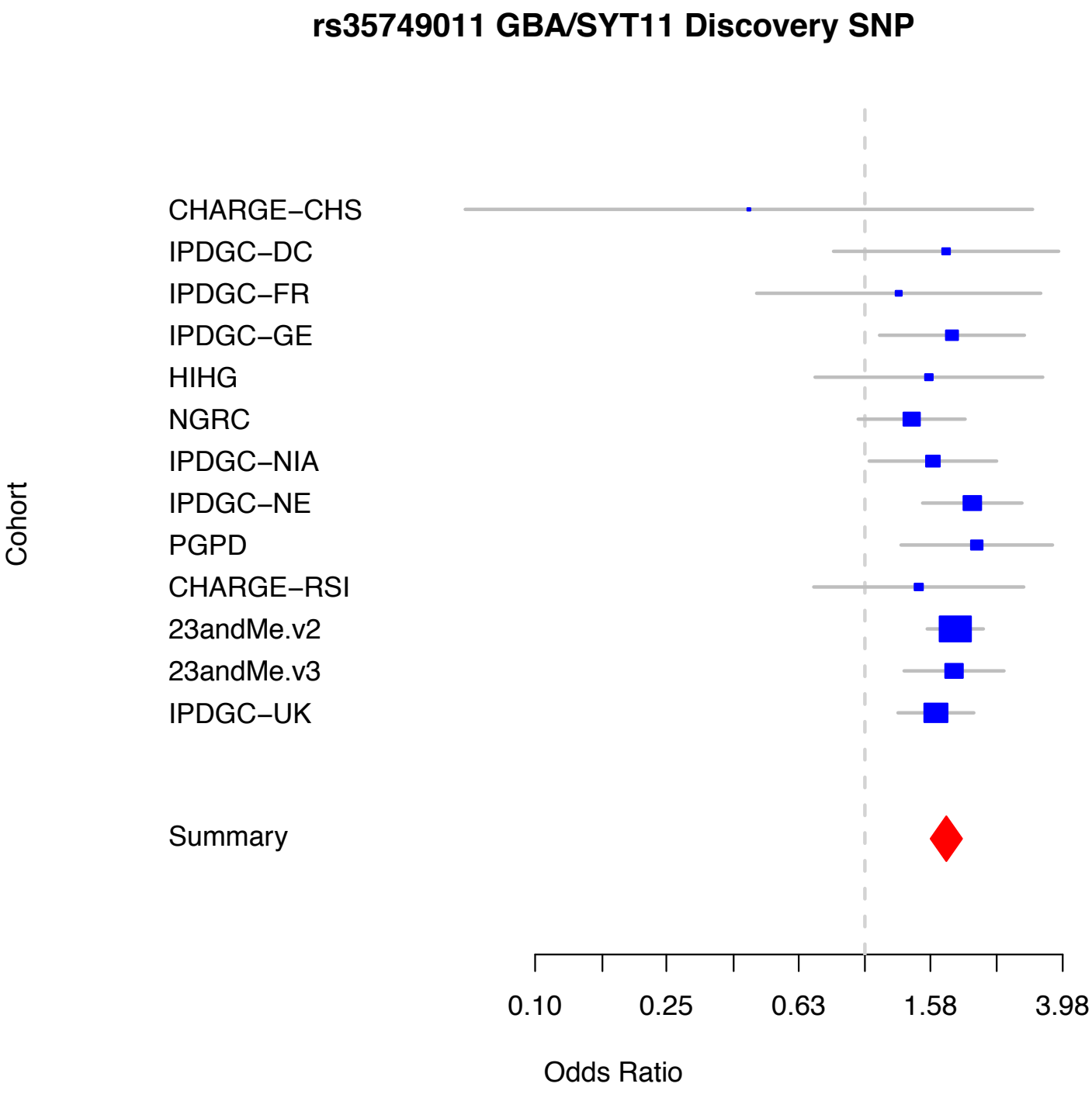

MMP16 region
48 cM/Mb
rs60298754
0
0 cM/Mb
DCAF4L2 -
MMP16 -
– log10P
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
88500000
89000000
89500000
90000000
Position in BP on Chromosome 8 (hg19)

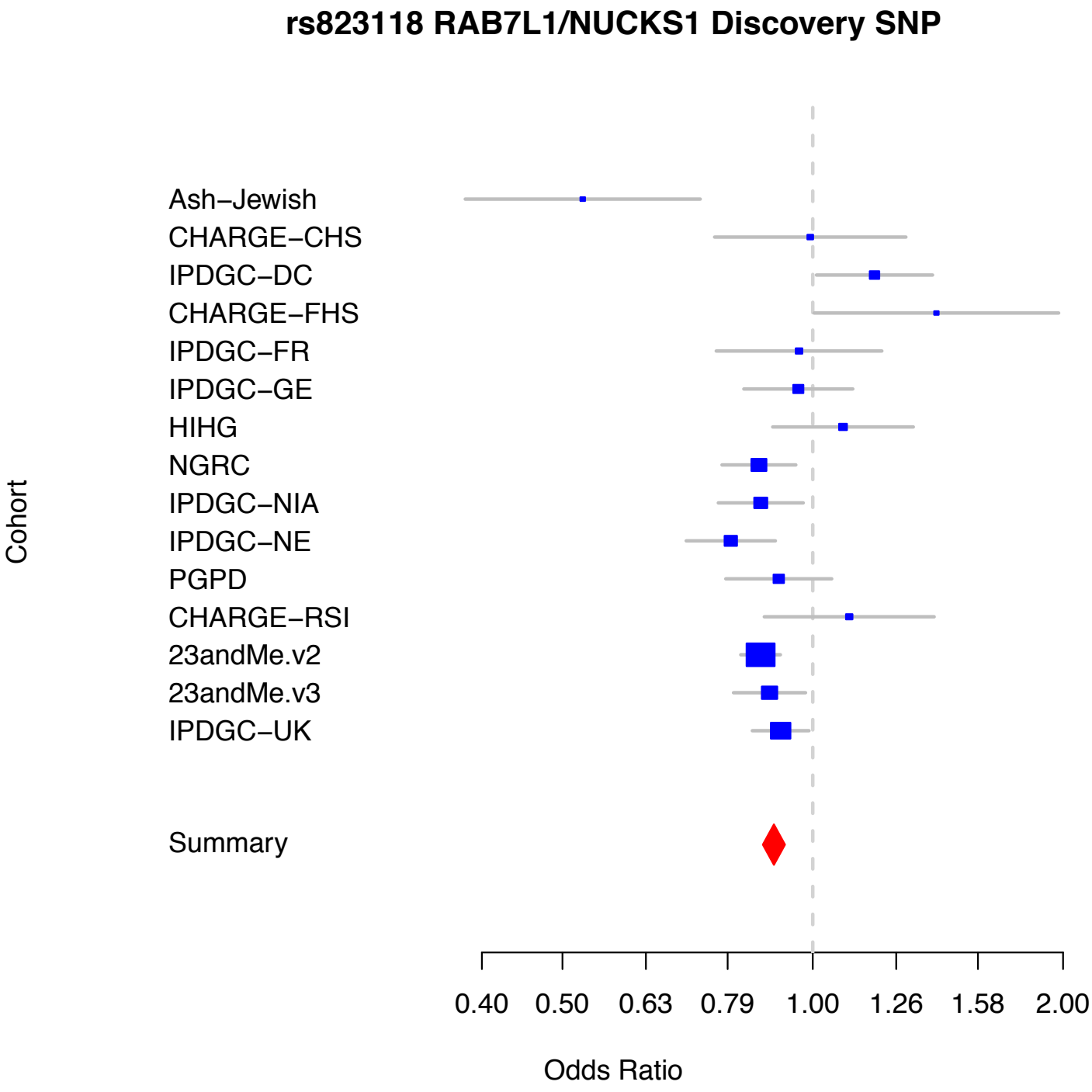

ITGA8 region
rs7077361
66 cM/Mb
0 cM/Mb
5
0
$-\log_{10}P$
SUV39H2 +
ACBD7 -
C10orf111 -
CDNF -
DCLRE1C -
FAM171A1 -
FAM188A -
HSPA14 +
ITGA8 -
MEIG1 +
NMT2 -
OLAH +
PPIAP30 -
PTER +
14500000
15000000
15500000
16000000
16500000
Position in BP on Chromosome 10 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
0.00

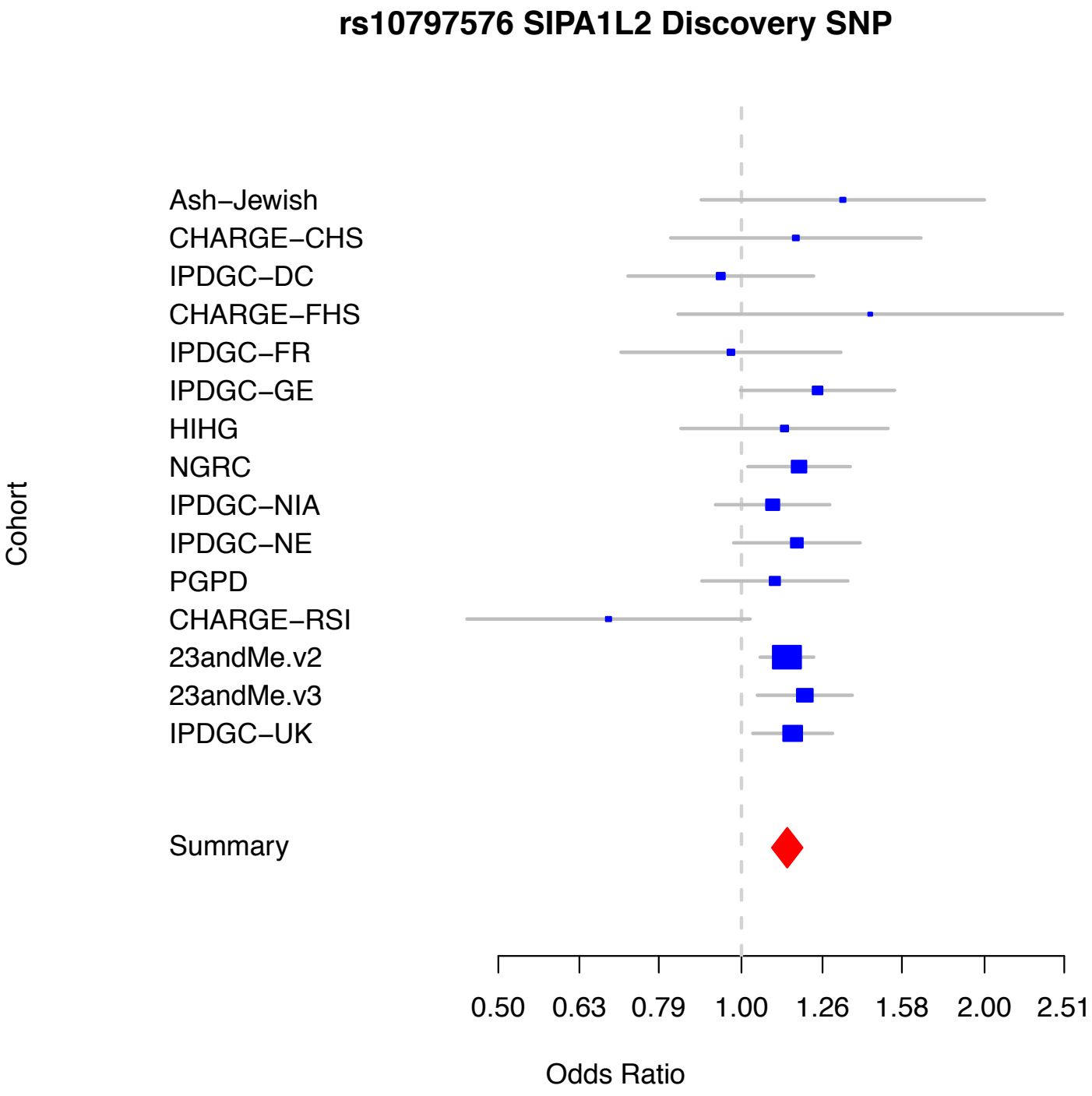

SREBF/RAI1 region
rs11868035
35 cM/Mb
0 cM/Mb
5
0
− log10P
ALKBH5 + SMCR7 +
LLGL1 +
ATPAF2 -
SMCR8 +
LOC339240 +
CCDC144B -
SMCR9 +
LRRC48 +
COPS3 -
SREBF1 -
MED9 +
DRG2 +
TBC1D28 -
MIR33B -
TNFRSF13B -
EVPLL +
MPRIP +
TOM1L2 -
FAM106A -
MYO15A +
TOP3A -
FBXW10 +
NT5M +
FLCN -
TRIM16L +
PEMT -
FLII -
TVP23B +
PLD6 -
USP32P2 -
FOXO3B -
RAI1 +
GID4 +
ZNF286B -
RASD1 -
KRT16P1 +
SHMT1 -
KRT16P2 -
SMCR5 -
LGALS9C +
17000000
17500000
18000000
18500000
Position in BP on Chromosome 17 (hg19)
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25

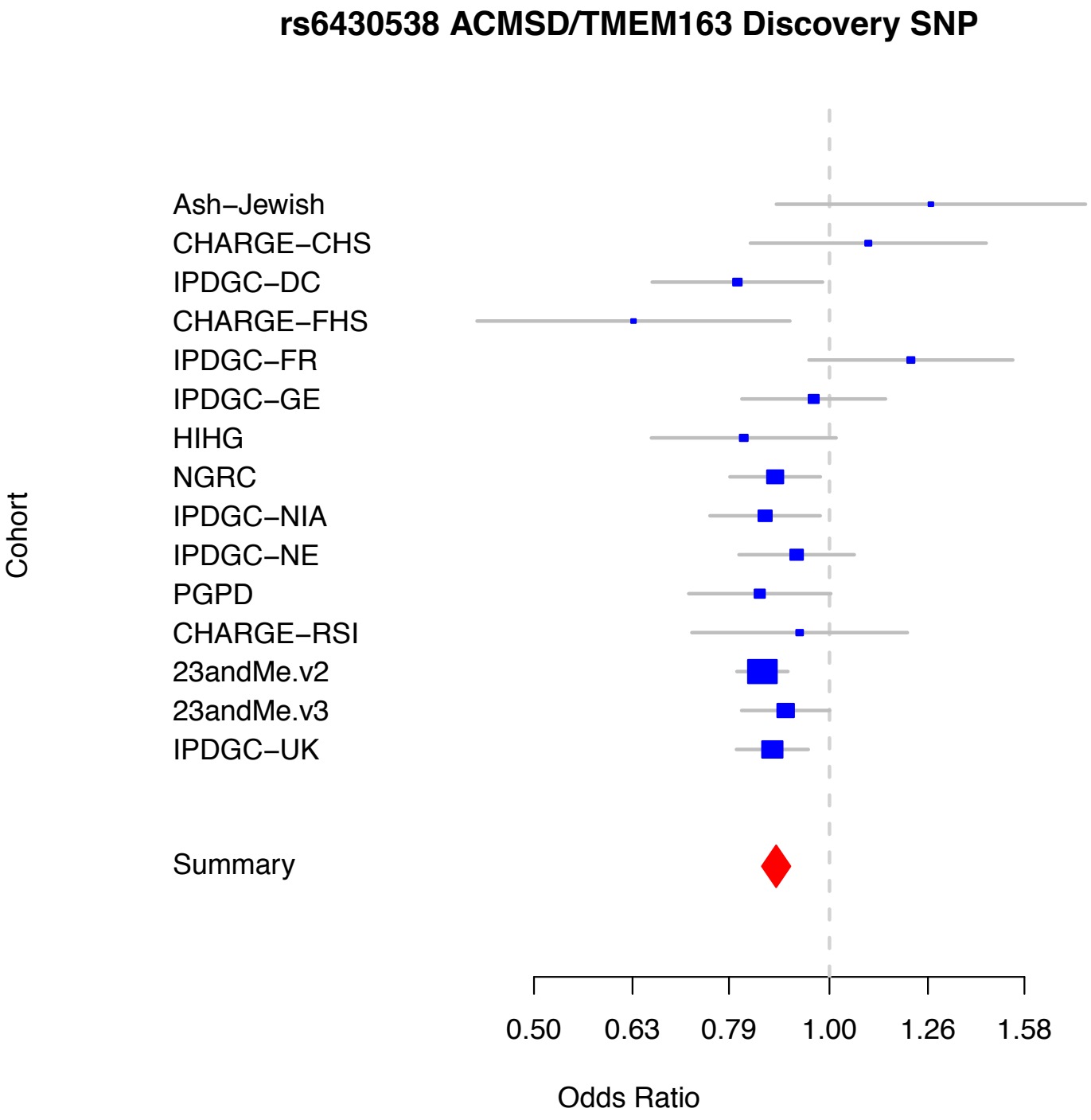

USP25 region
81 cM/Mb
0 cM/Mb
rs2823357
0
LOC388813 -
NRIP1 -
SAMSN1-AS1 +
USP25 +
MIR99A +
MIRLET7C +
R2 with most significant discovery phase SNP
1.00
0.75
0.50
0.25
– log10P
16000000
16500000
17000000
17500000
18000000
Position in BP on Chromosome 21 (hg19)

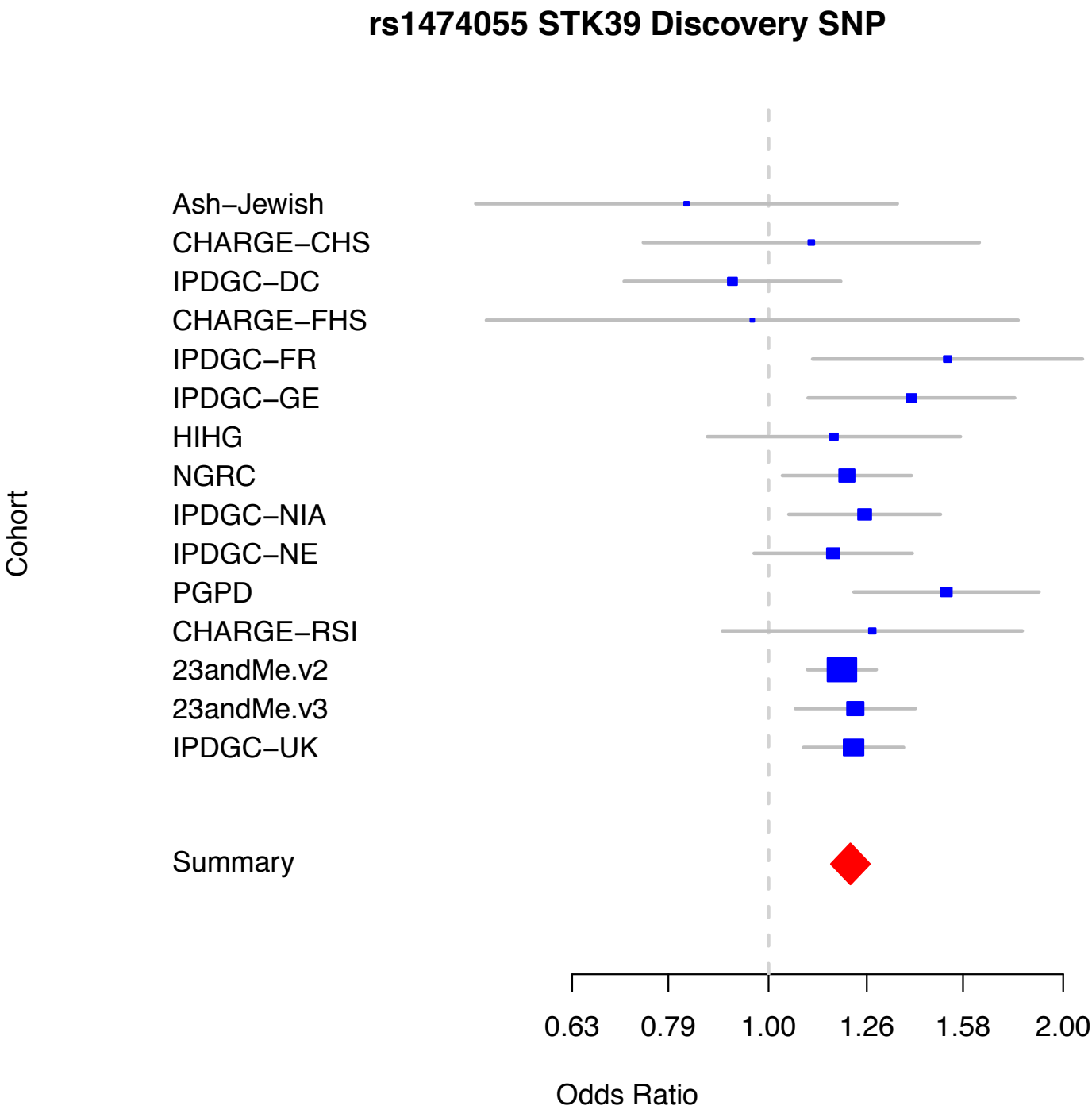
Supplementary Figure 2 (page 56 - 95): Forest plots. 40 Forest plots of SNPs from discovery and conditional phases described in Tables 1 and 2. Nearest gene or previously published proximal gene names included in table.

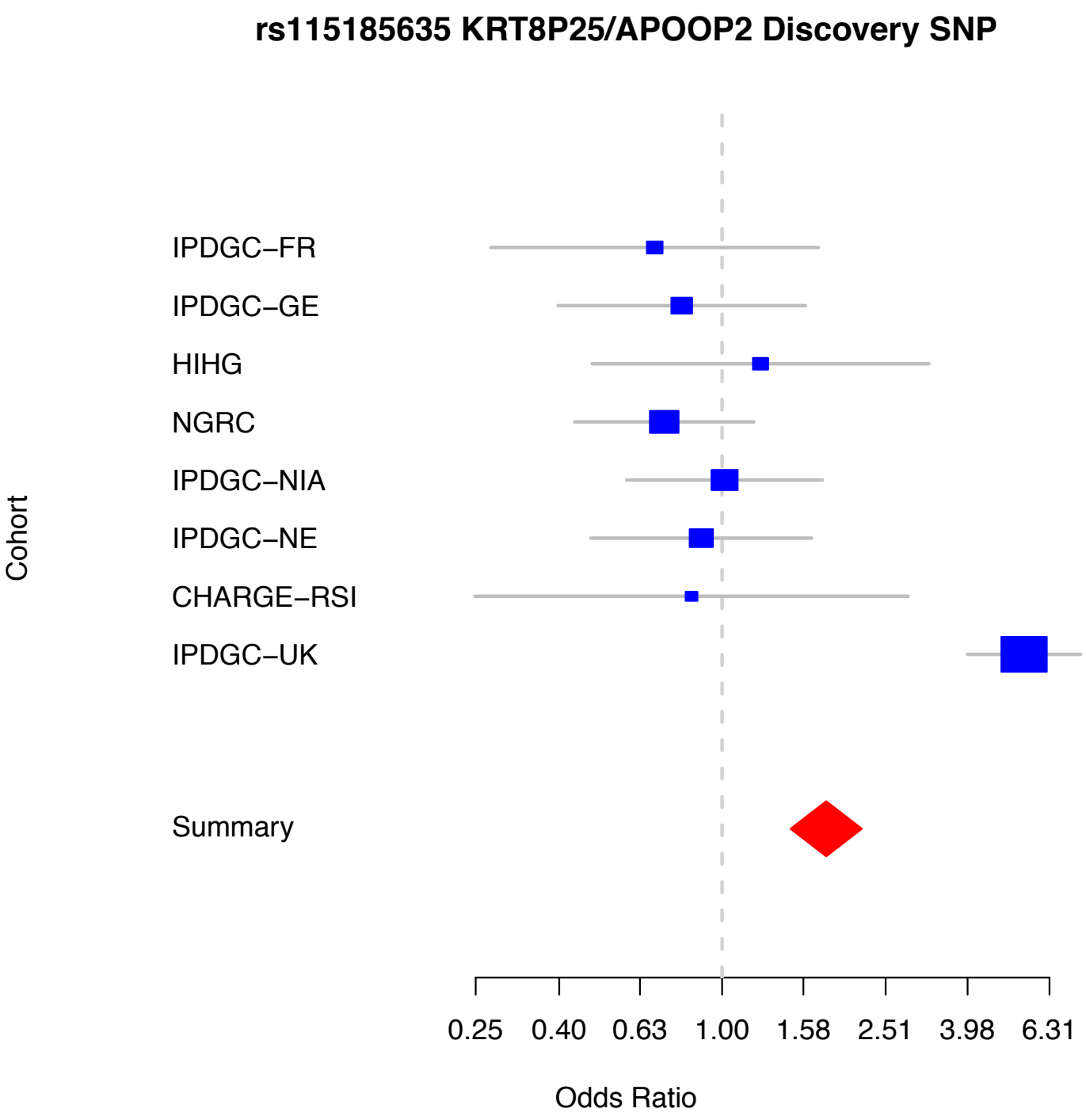


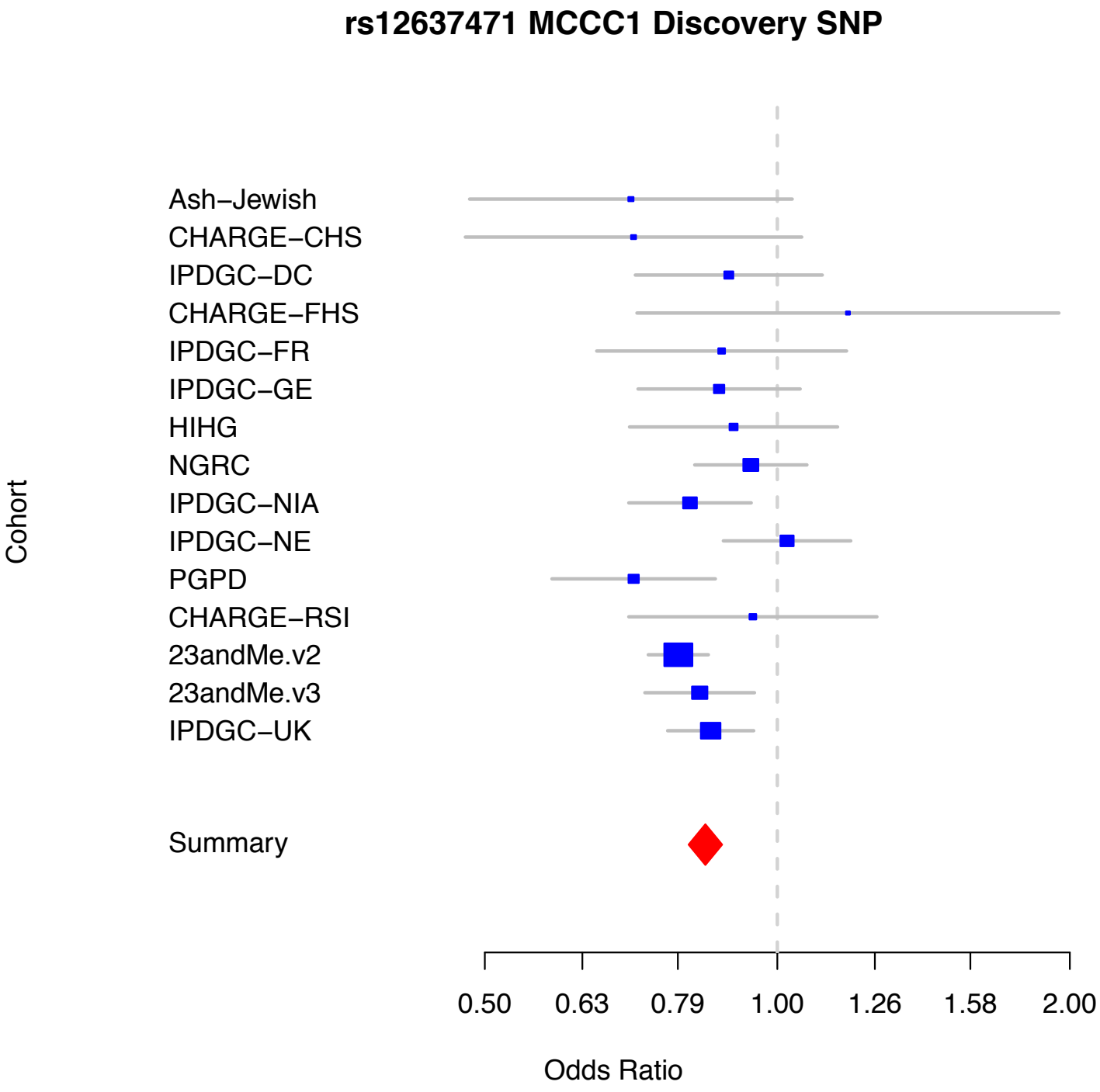

rs823118 RAB7L1/NUCKS1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.40
0.50
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

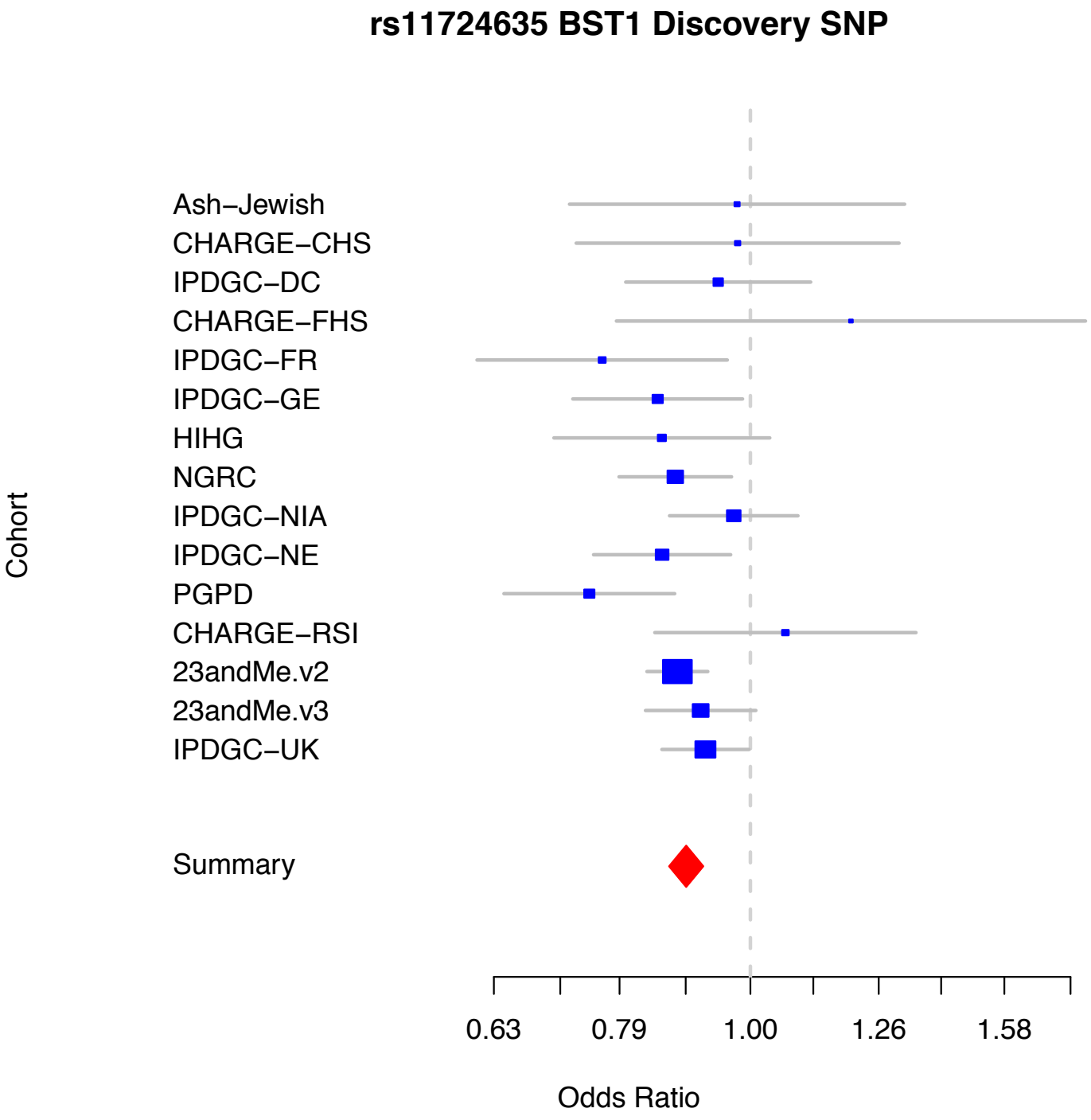

rs10797576 SIPA1L2 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
2.51
Odds Ratio

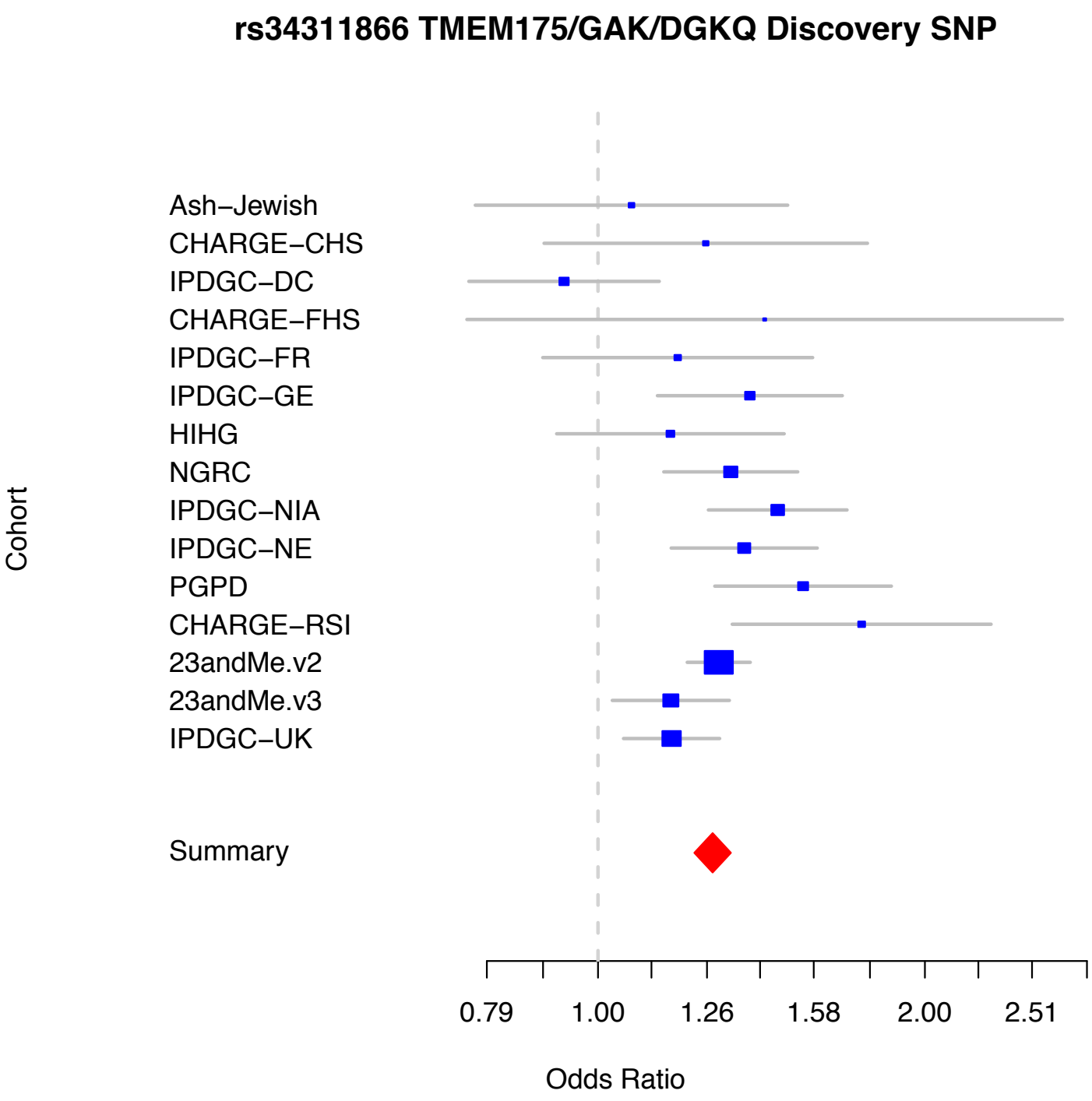

rs6430538 ACMSD/TMEM163 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
Odds Ratio

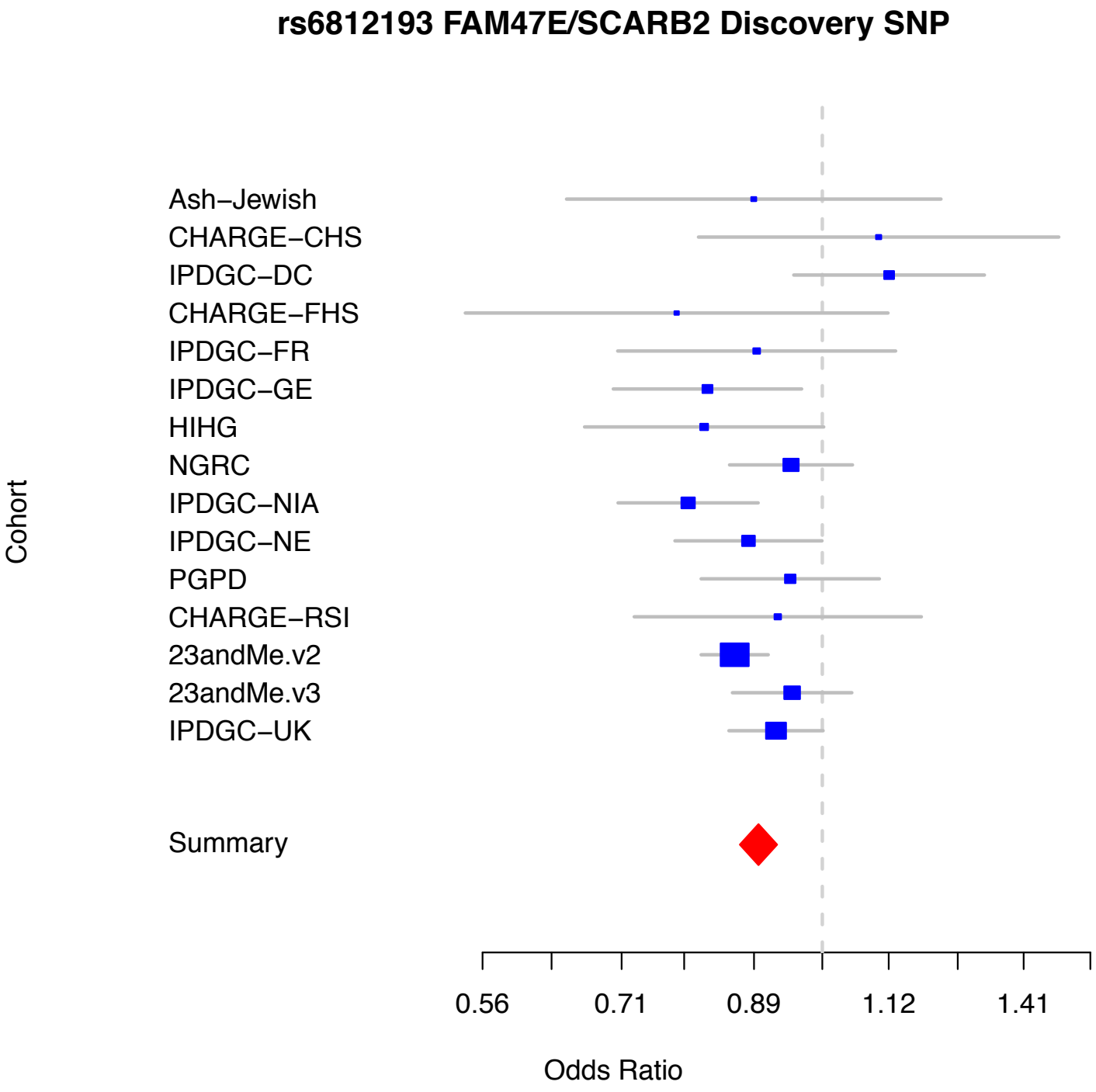

rs1474055 STK39 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

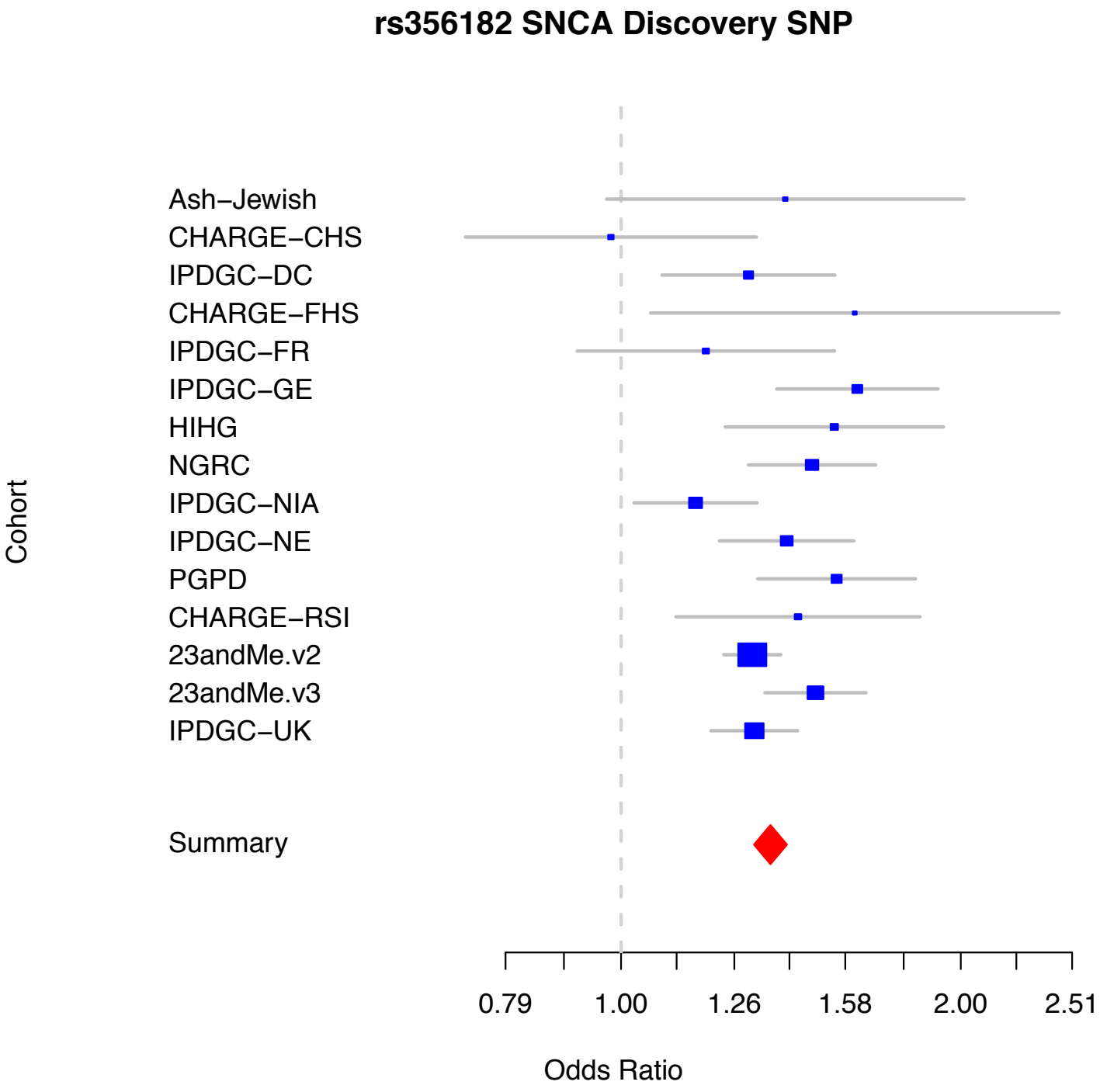

rs115185635 KRT8P25/APOOP2 Discovery SNP
Cohort
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
CHARGE−RSI
IPDGC−UK
Summary
0.25
0.40
0.63
1.00
1.58
2.51
3.98
6.31
Odds Ratio

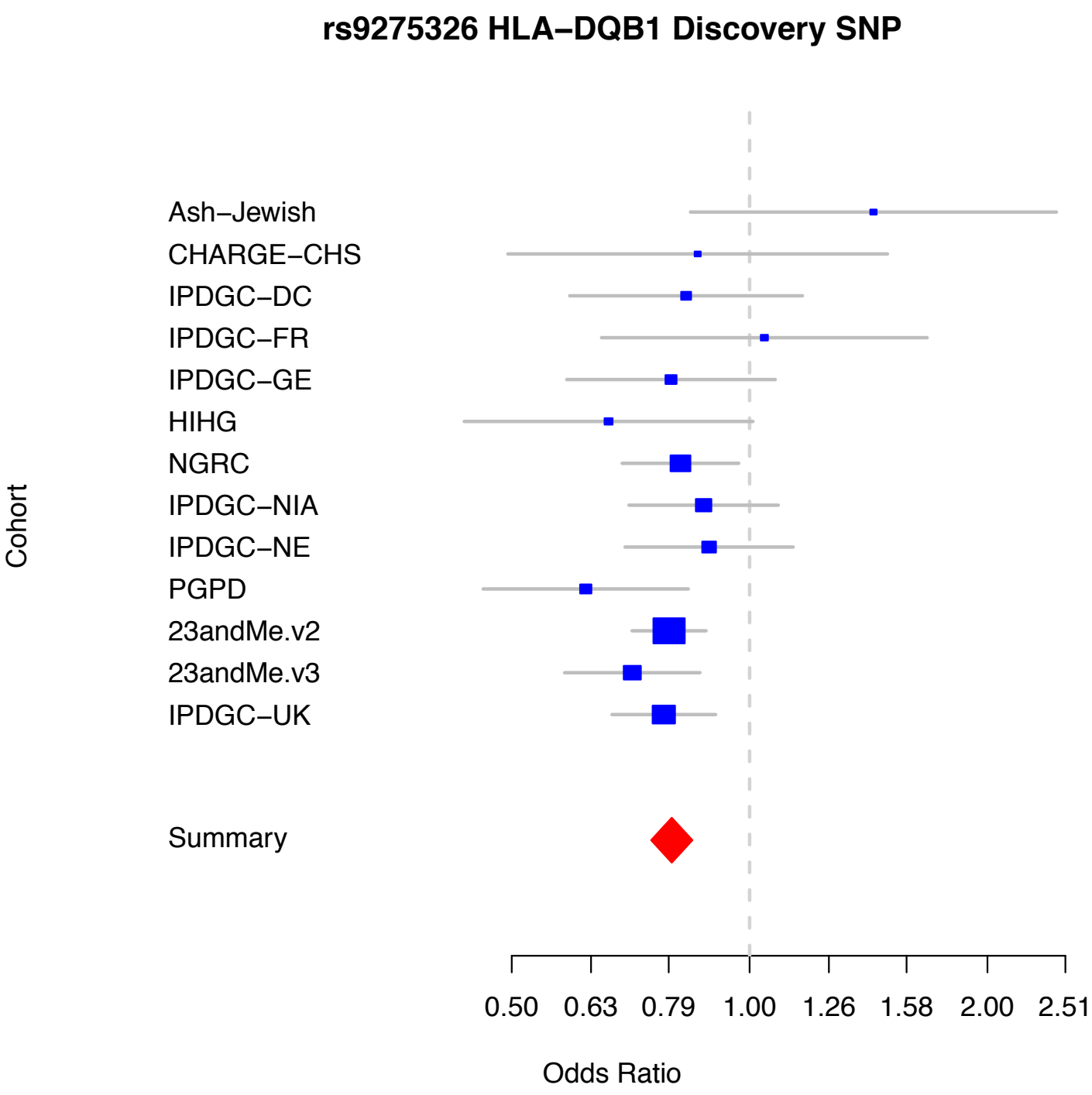

rs12637471 MCCC1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

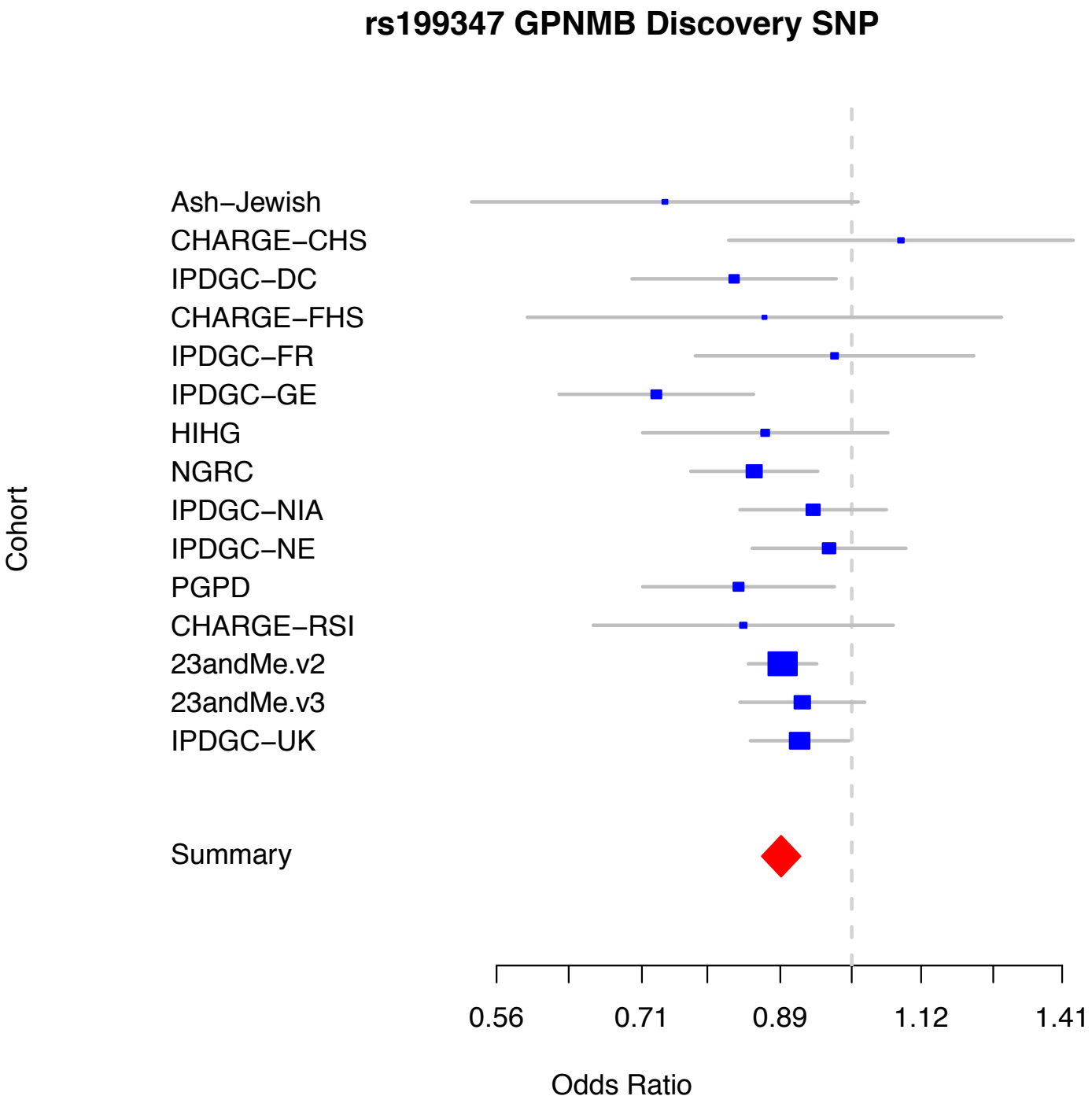

rs11724635 BST1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
Odds Ratio

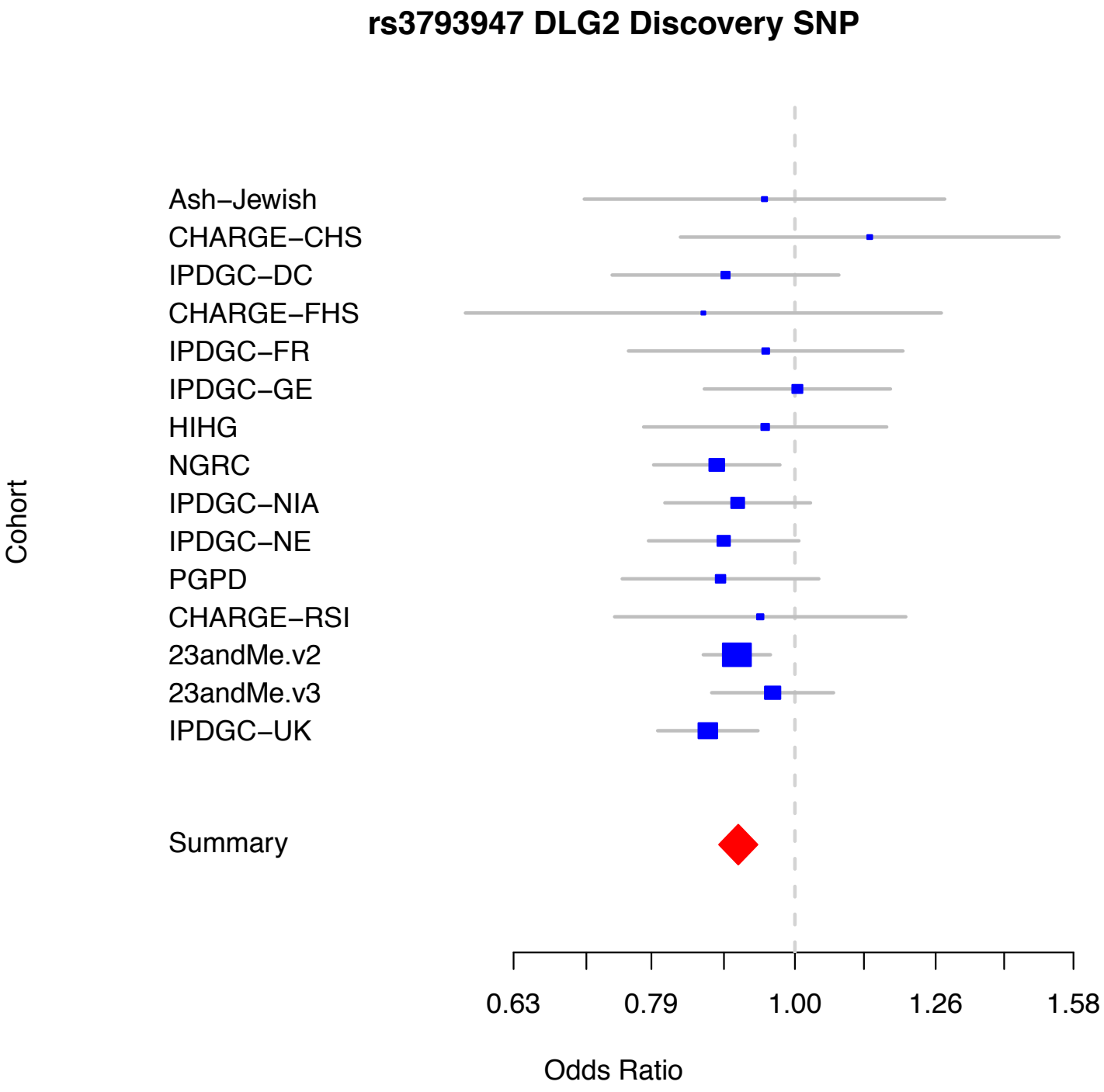

rs34311866 TMEM175/GAK/DGKQ Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.79
1.00
1.26
1.58
2.00
2.51
Odds Ratio

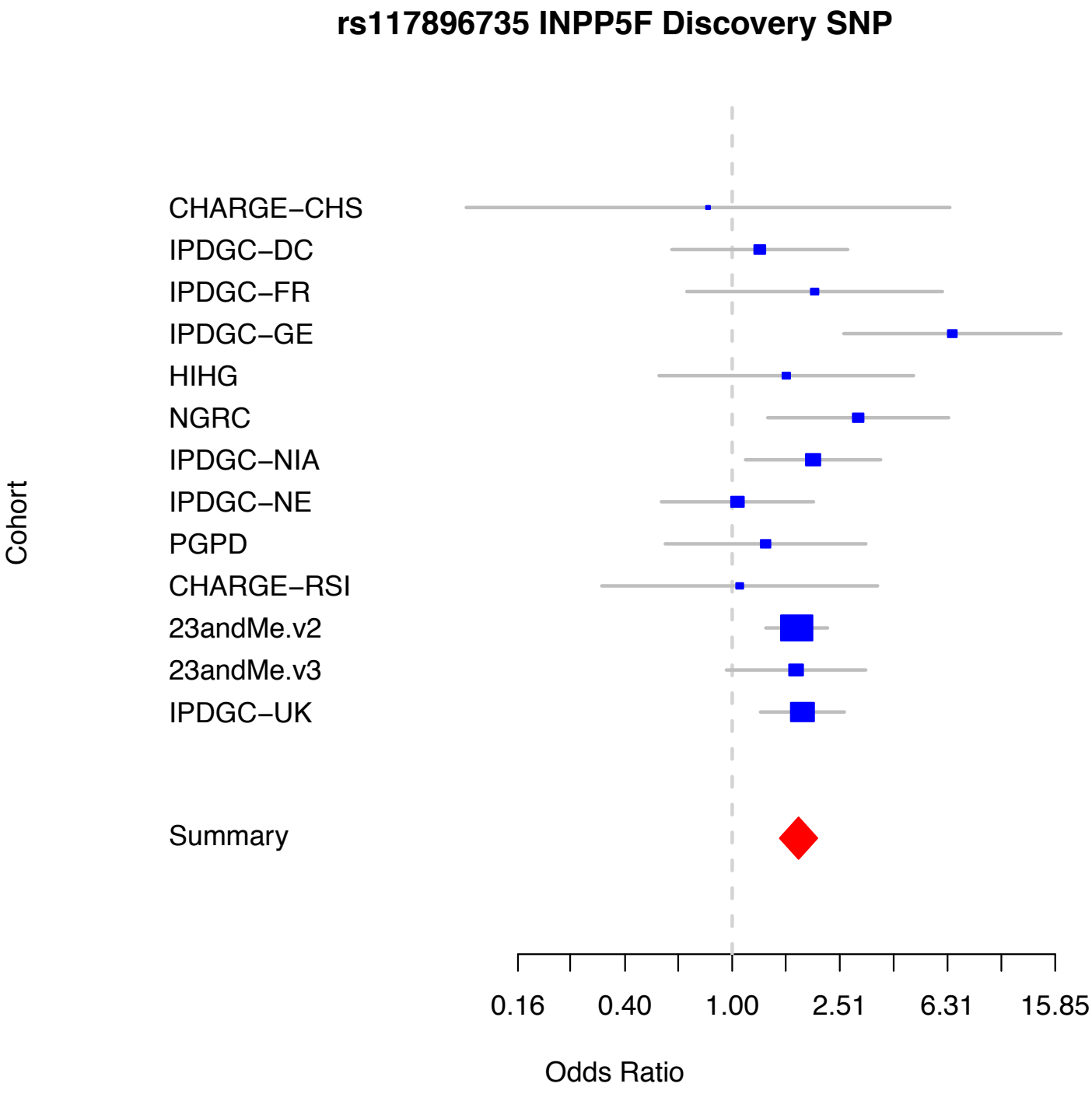

rs6812193 FAM47E/SCARB2 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.56
0.71
0.89
1.12
1.41
Odds Ratio

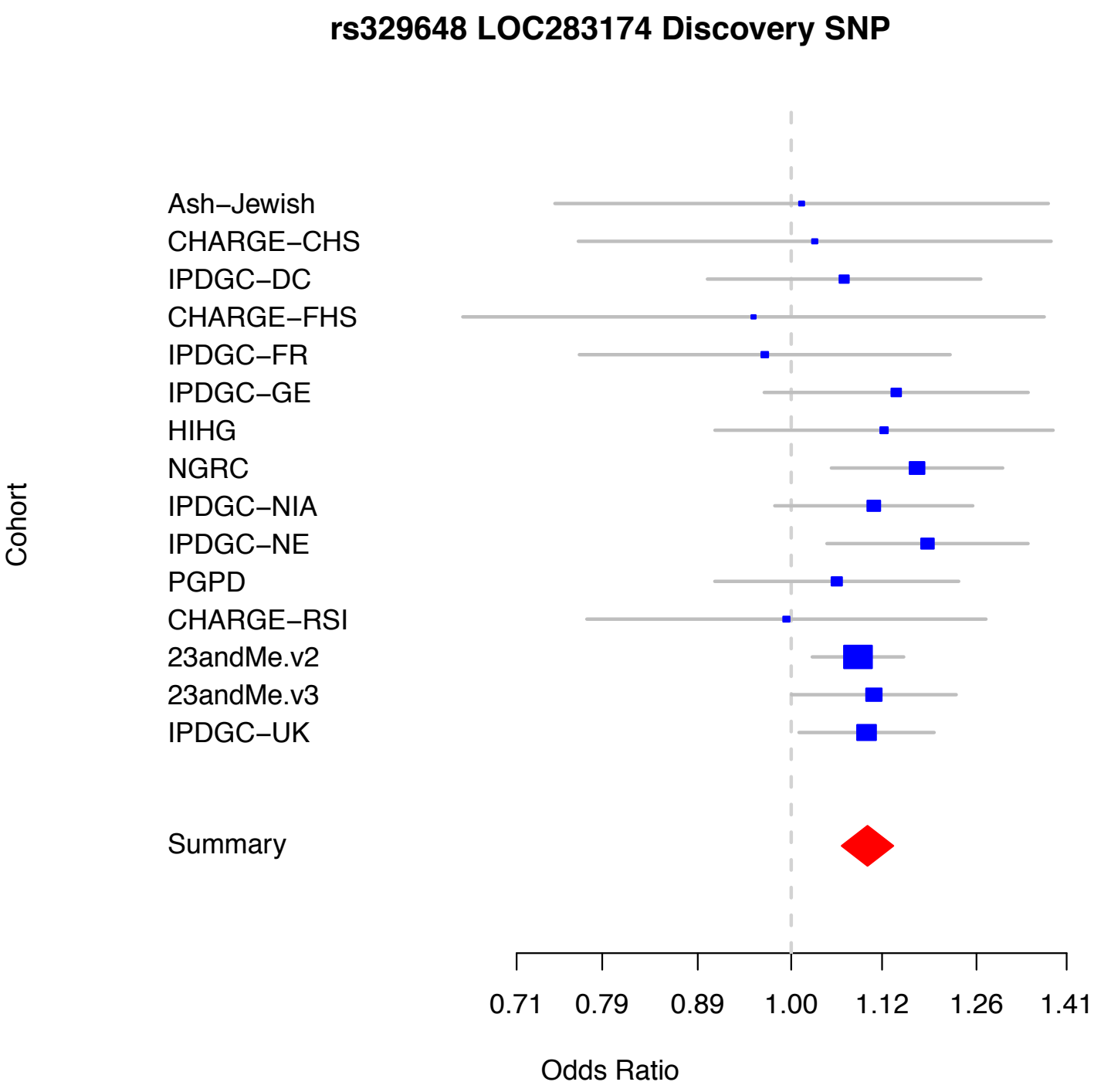

rs356182 SNCA Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.79
1.00
1.26
1.58
2.00
2.51
Odds Ratio

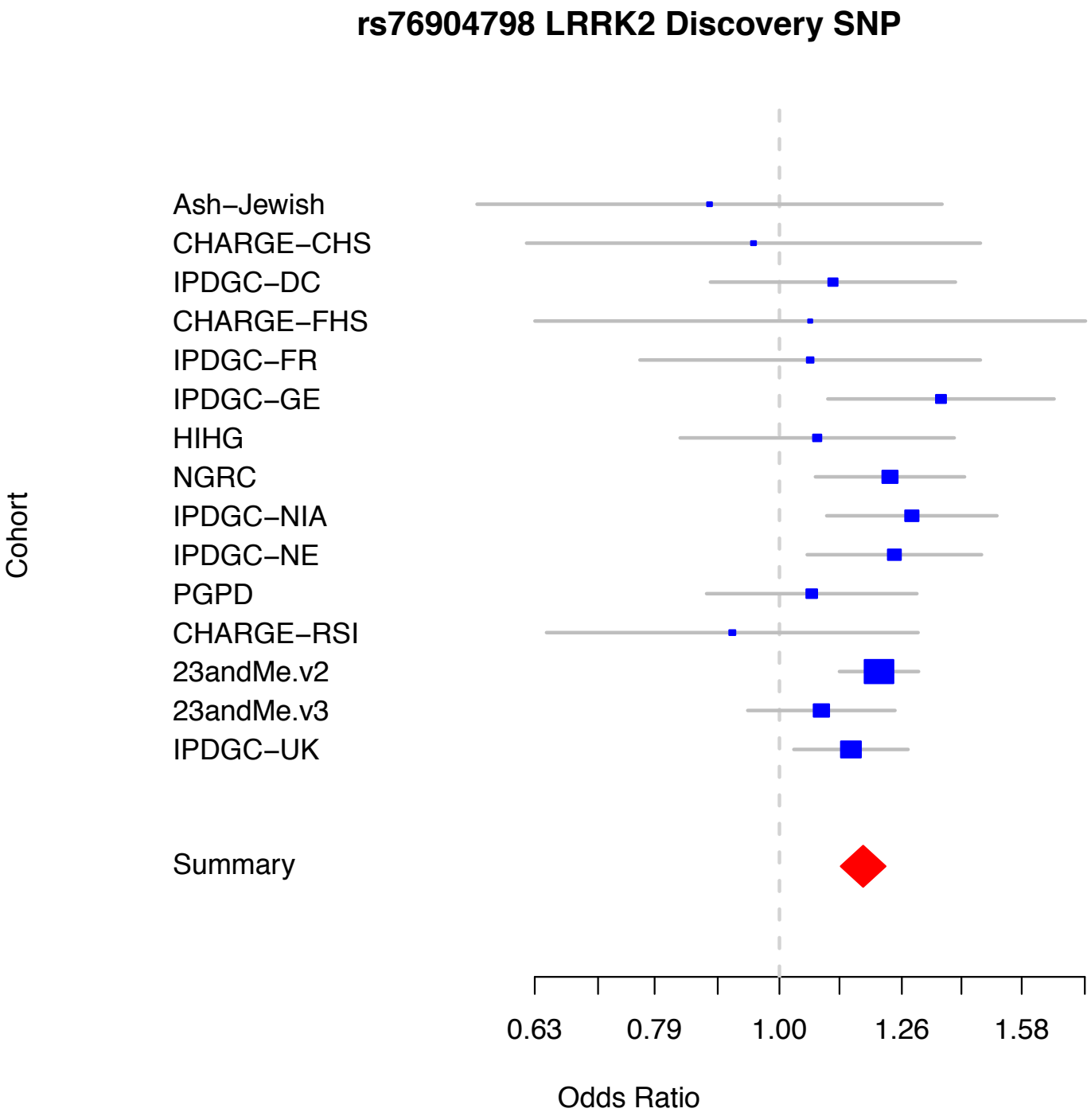

rs9275326 HLA−DQB1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
2.51
Odds Ratio

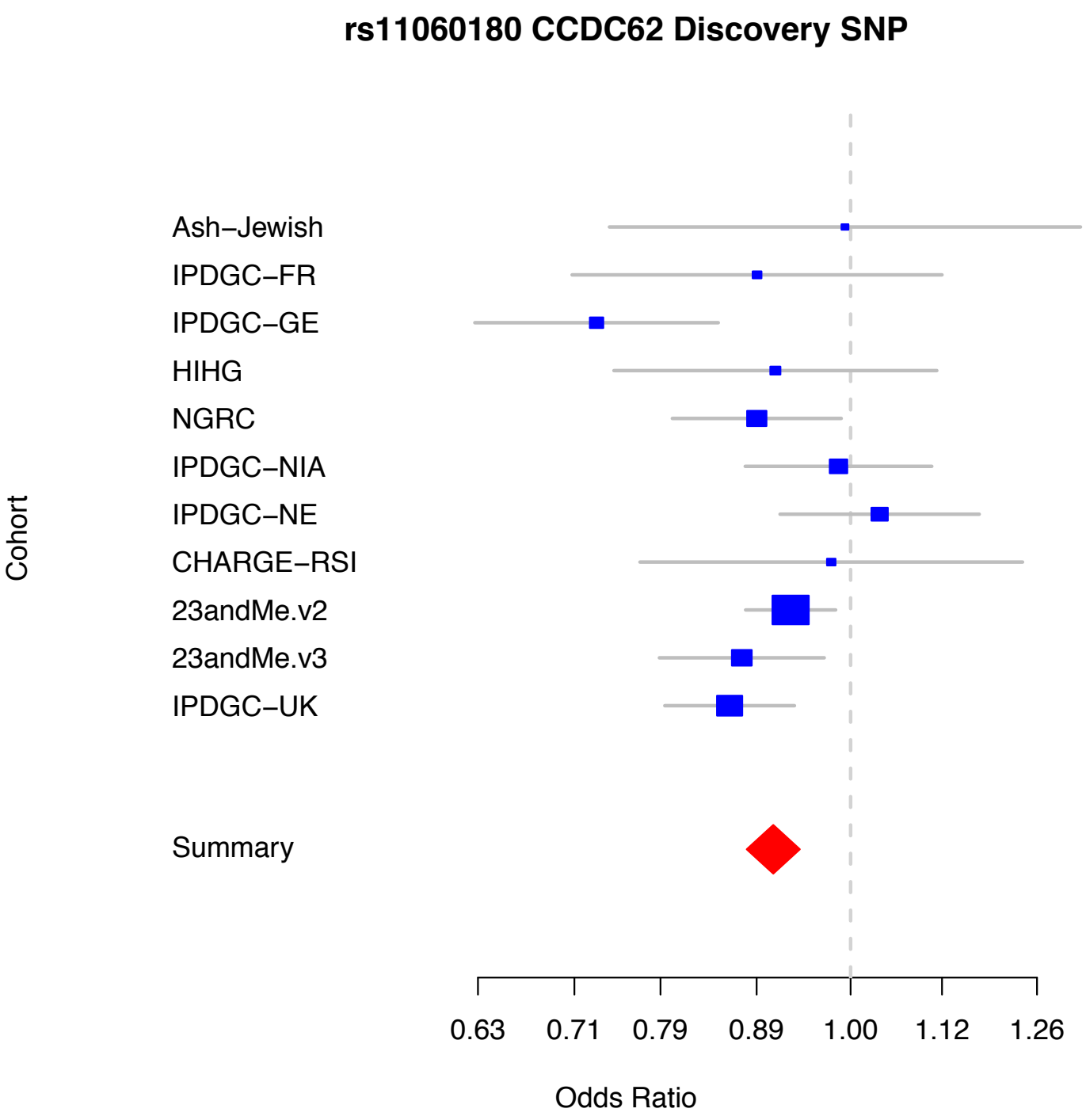

rs199347 GPNMB Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.56
0.71
0.89
1.12
1.41
Odds Ratio

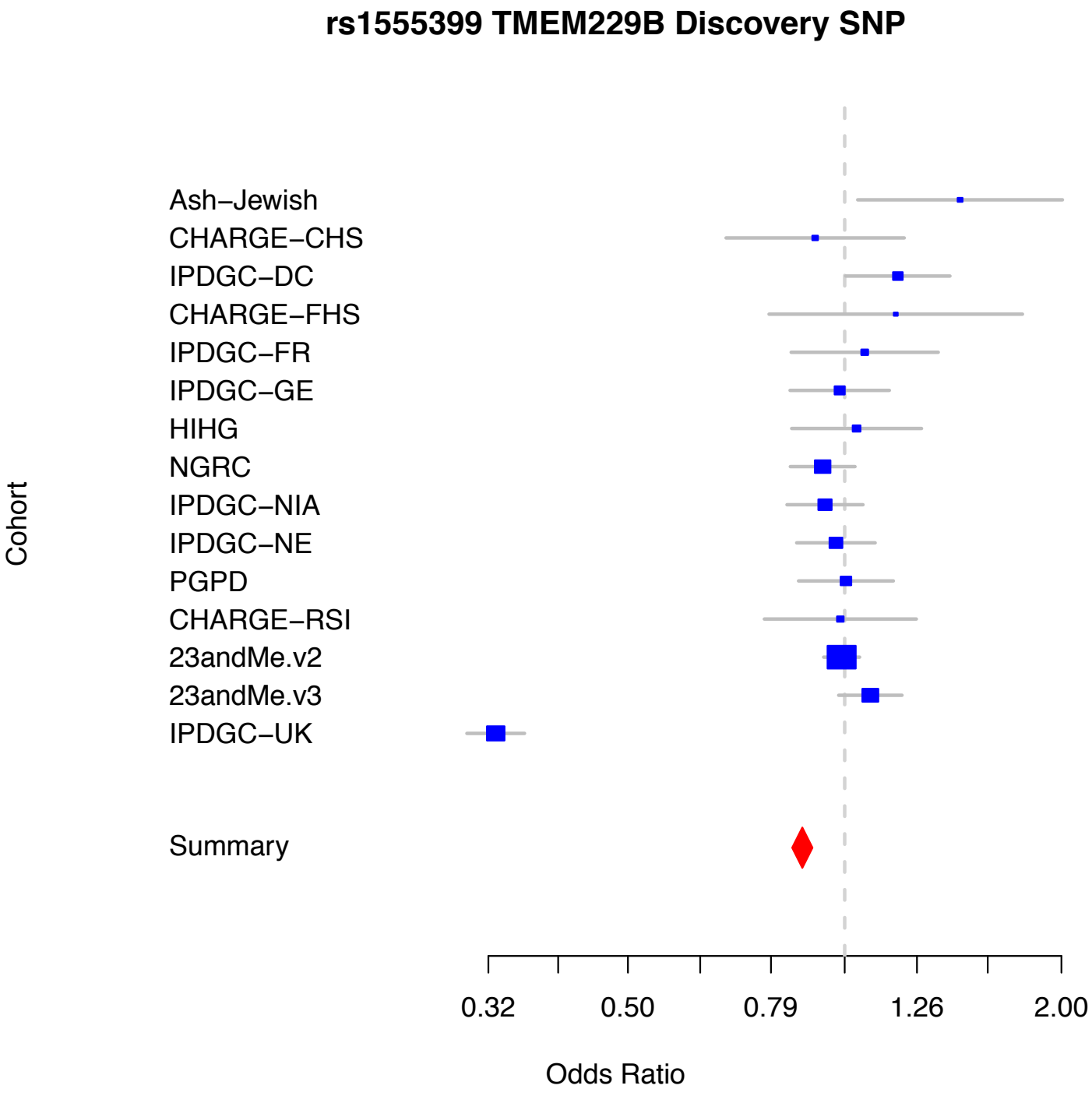

rs3793947 DLG2 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
Odds Ratio

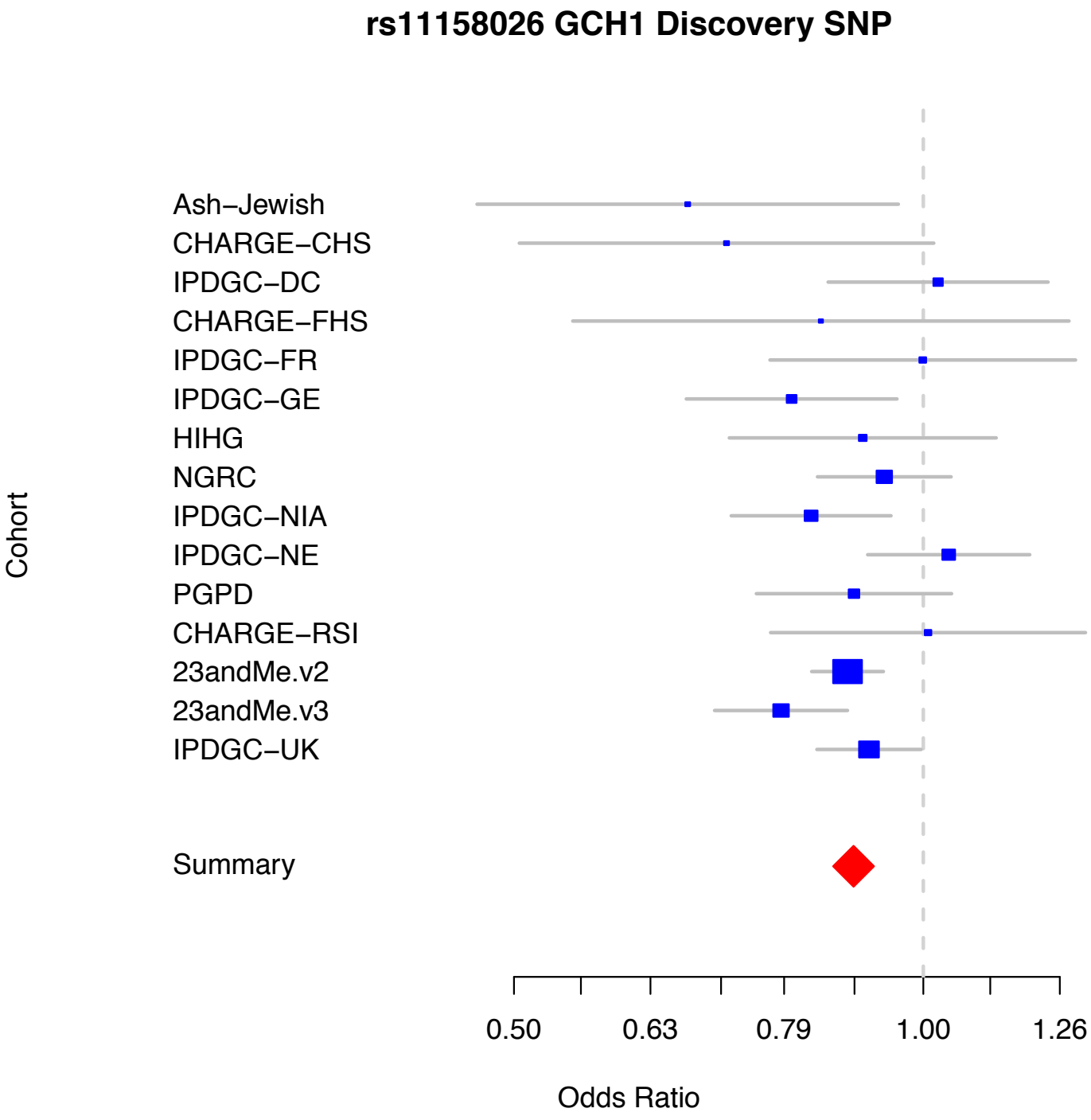

rs117896735 INPP5F Discovery SNP
Cohort
CHARGE−CHS
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.16
0.40
1.00
2.51
6.31
15.85
Odds Ratio

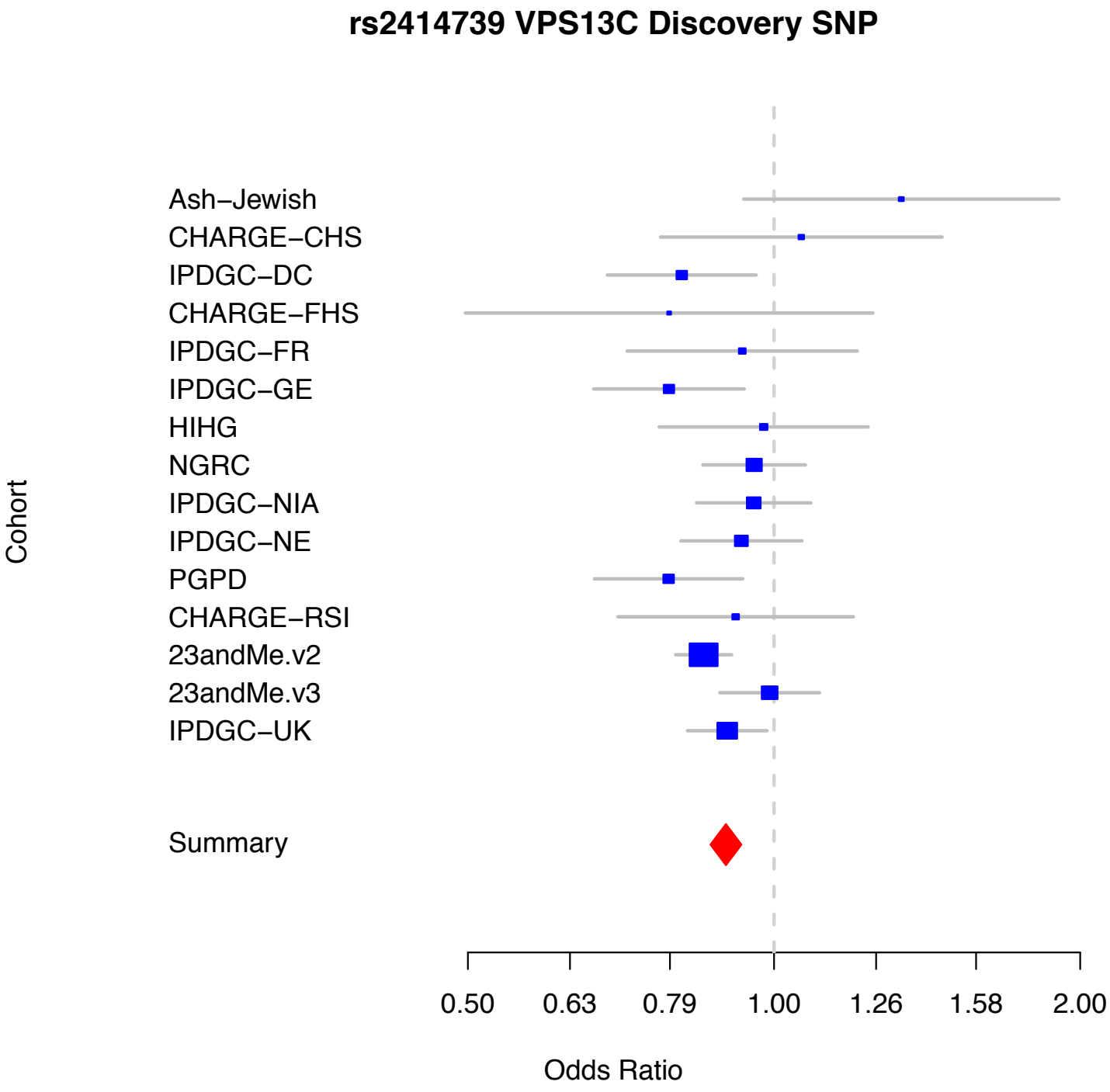

rs329648 LOC283174 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.71
0.79
0.89
1.00
1.12
1.26
1.41
Odds Ratio

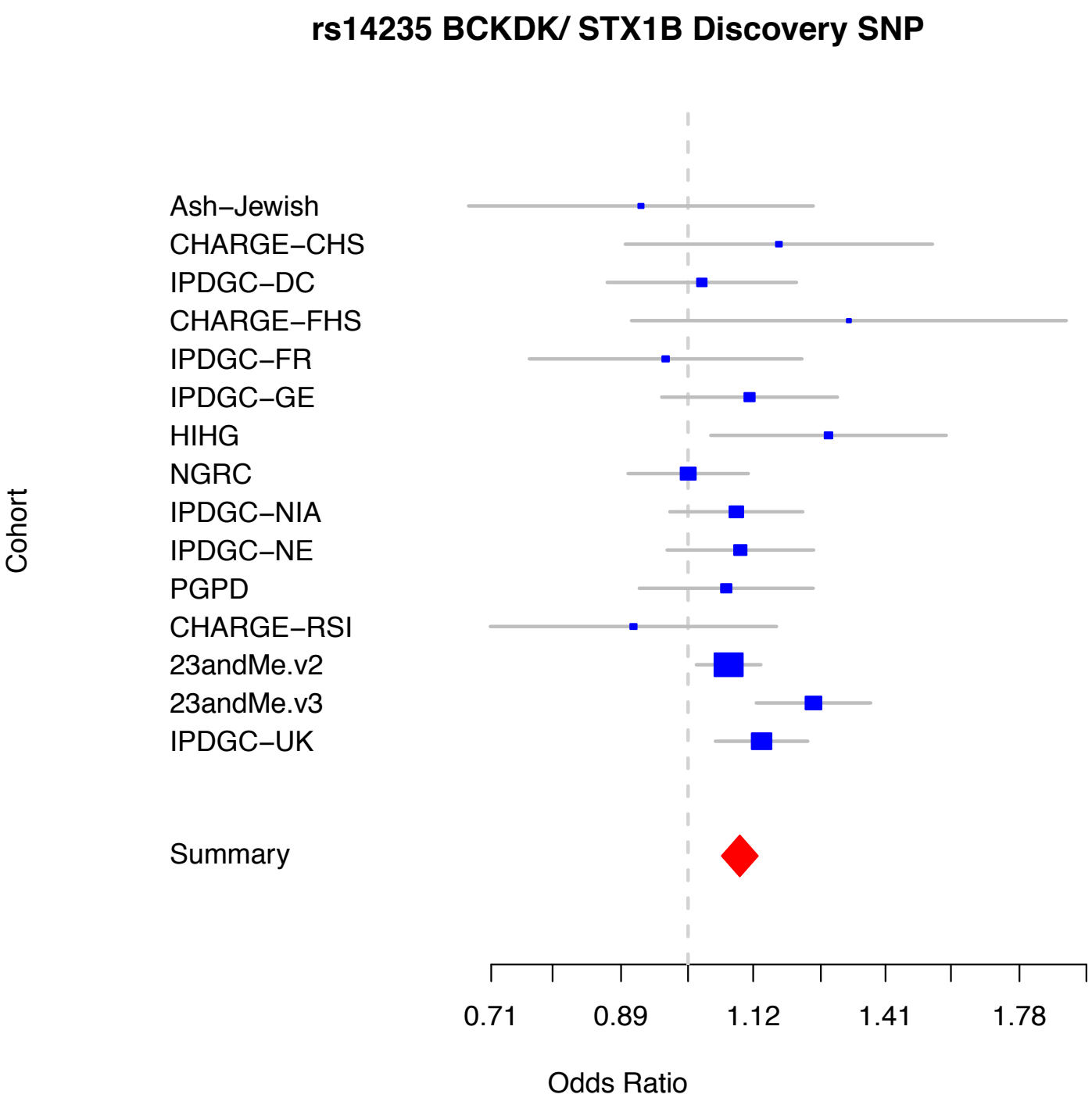

rs76904798 LRRK2 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
Odds Ratio

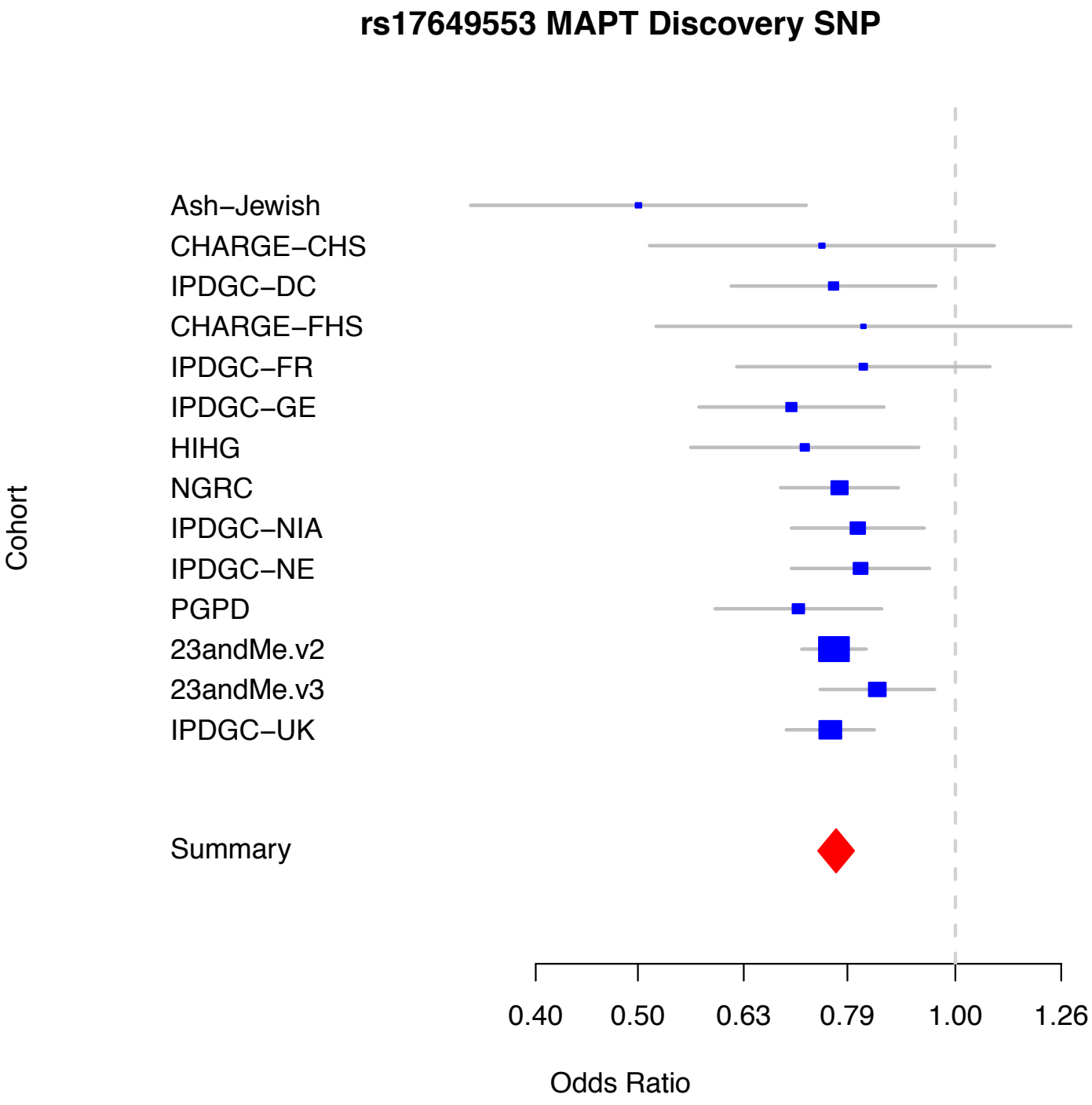

rs11060180 CCDC62 Discovery SNP
Cohort
Ash−Jewish
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.71
0.79
0.89
1.00
1.12
1.26
Odds Ratio

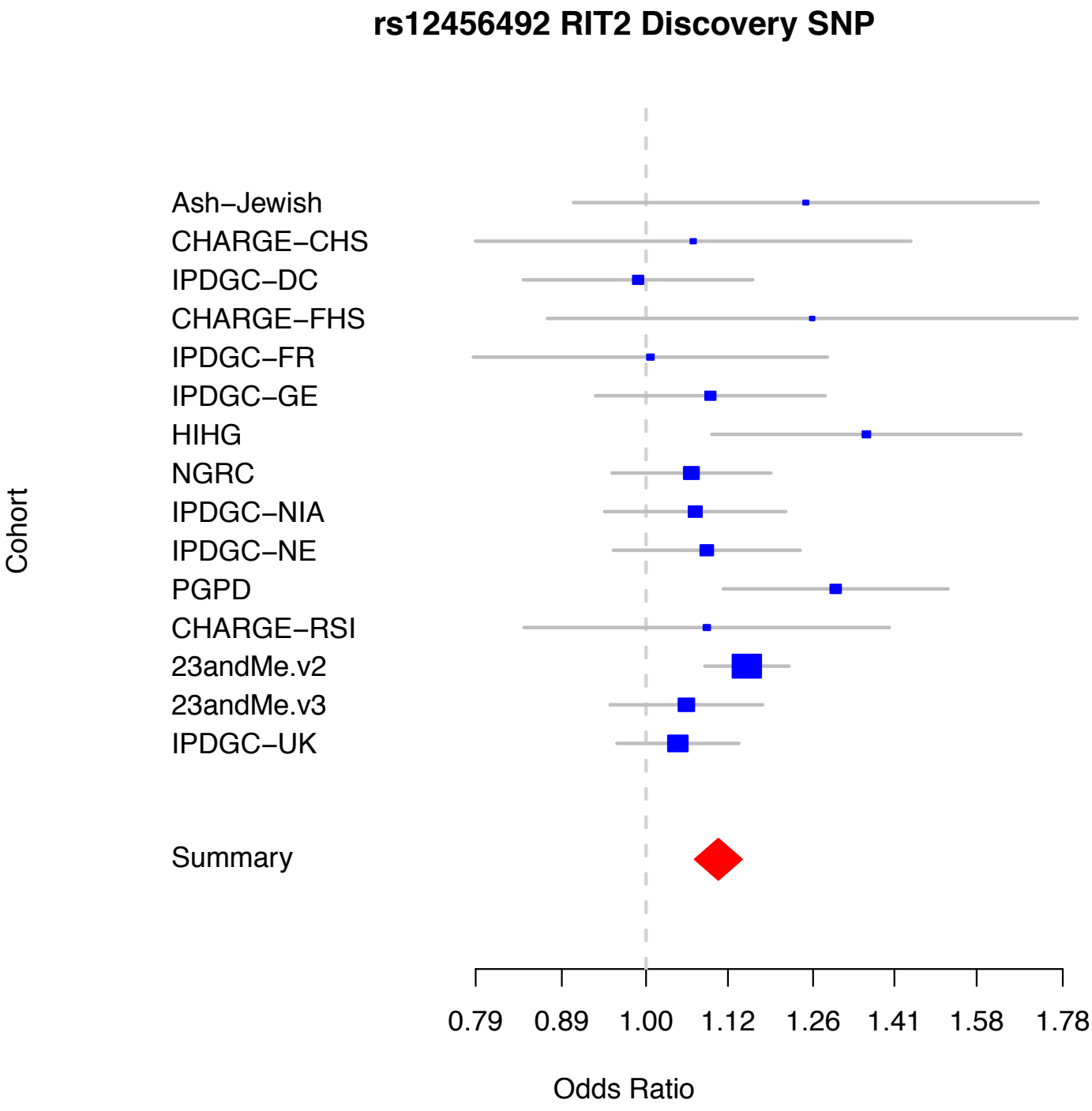

rs1555399 TMEM229B Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.32
0.50
0.79
1.26
2.00
Odds Ratio

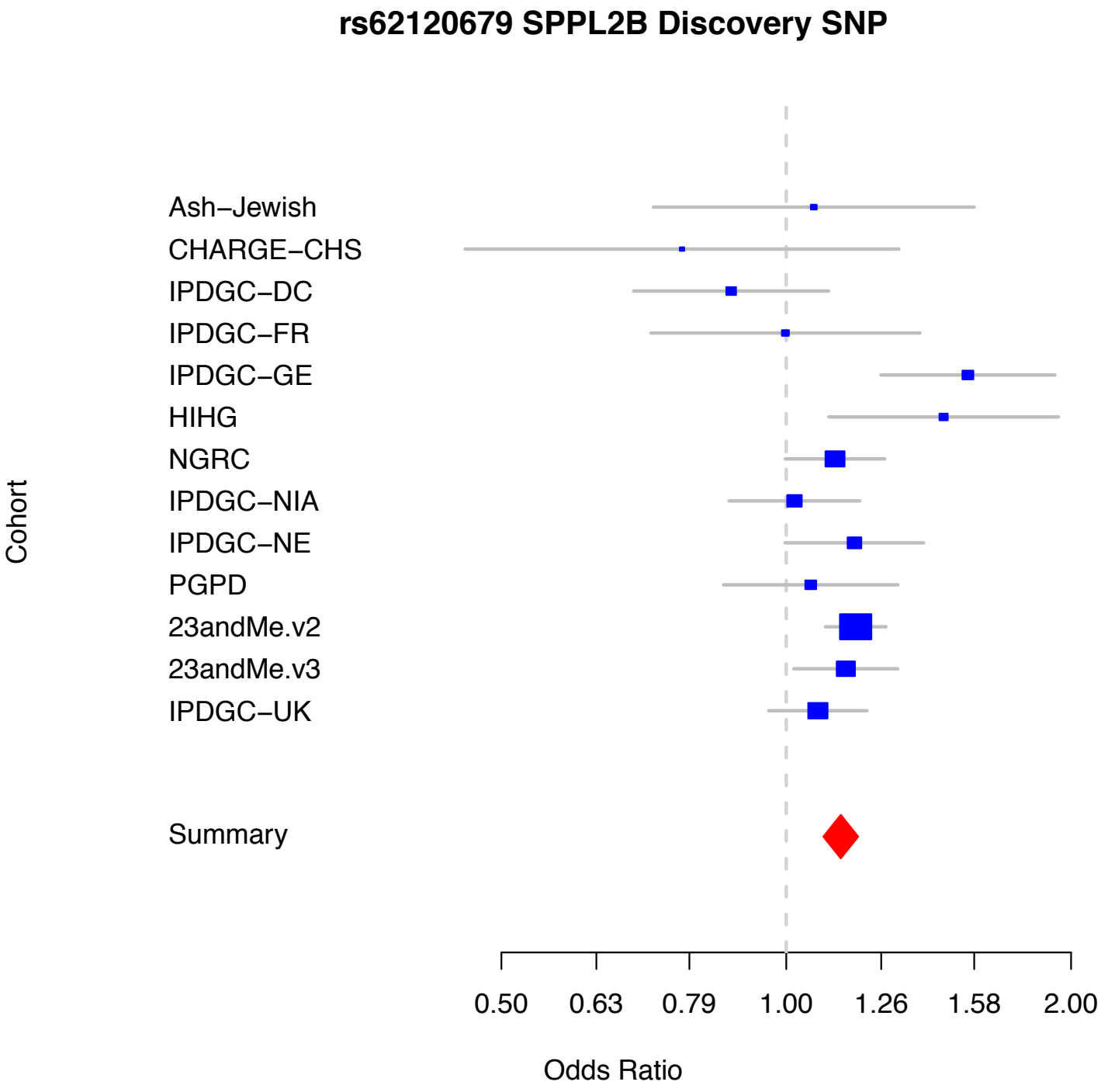

rs11158026 GCH1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
Odds Ratio

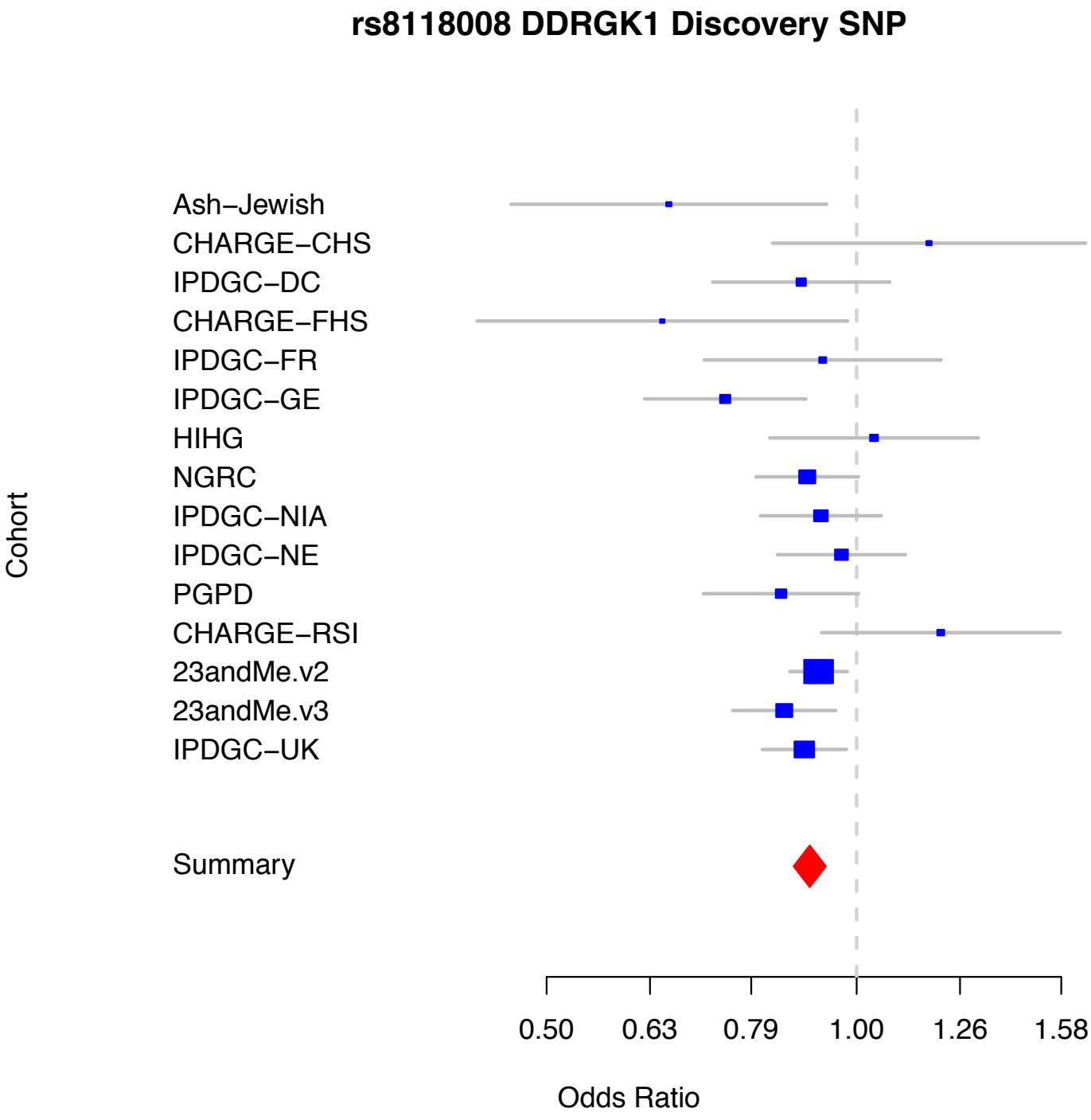

rs2414739 VPS13C Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

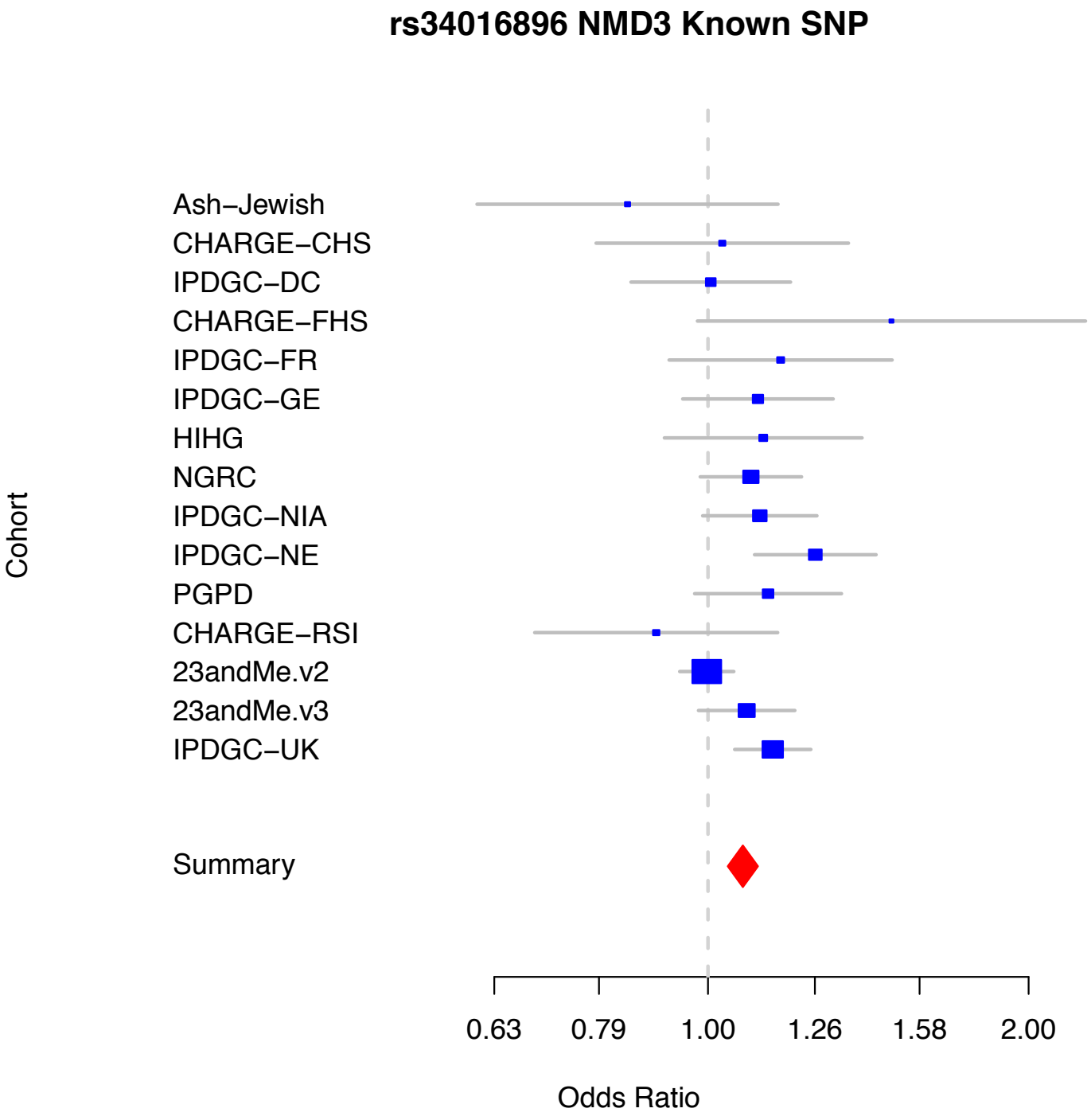

rs14235 BCKDK/ STX1B Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.71
0.89
1.12
1.41
1.78
Odds Ratio

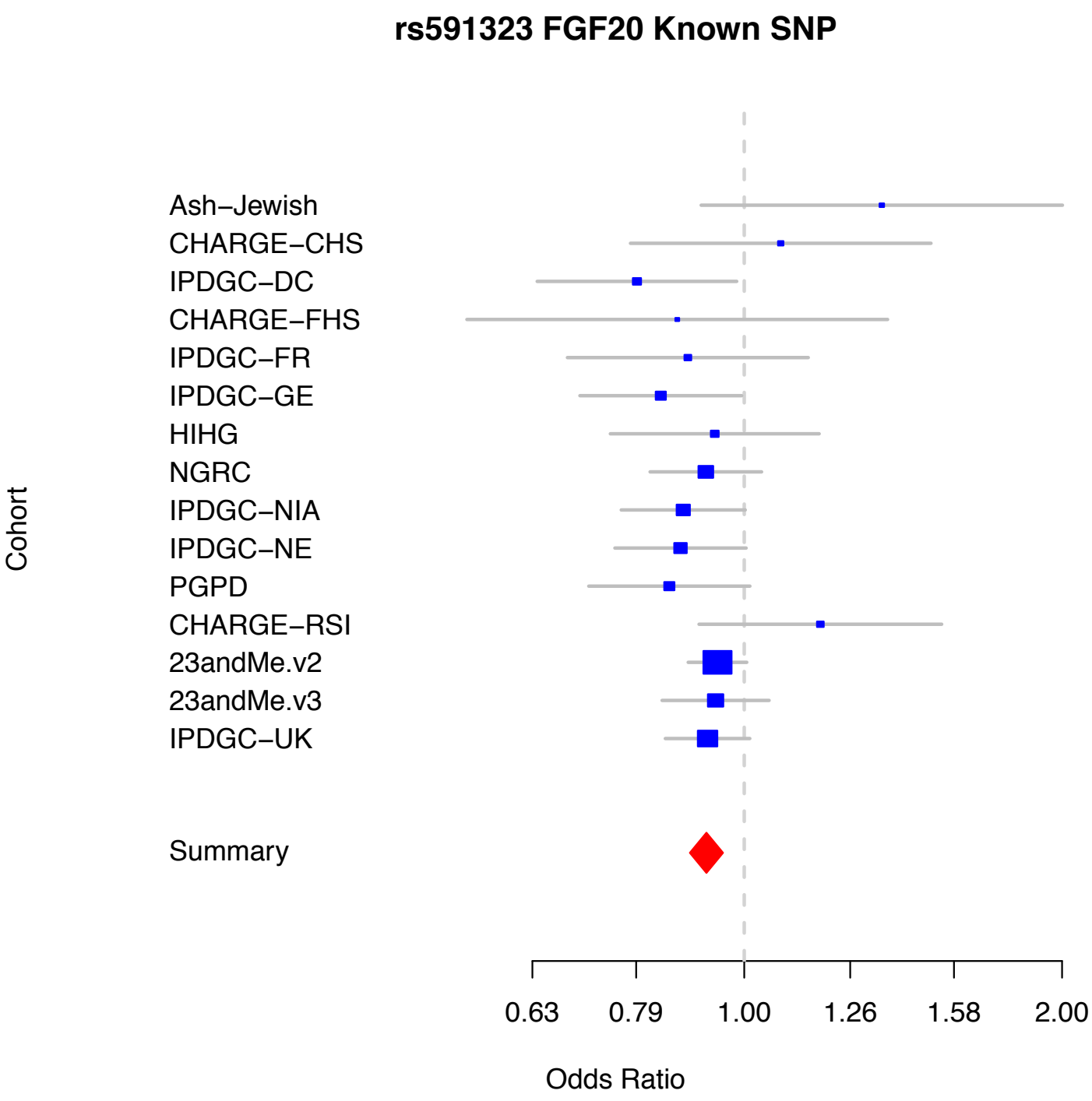

rs17649553 MAPT Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.40
0.50
0.63
0.79
1.00
1.26
Odds Ratio

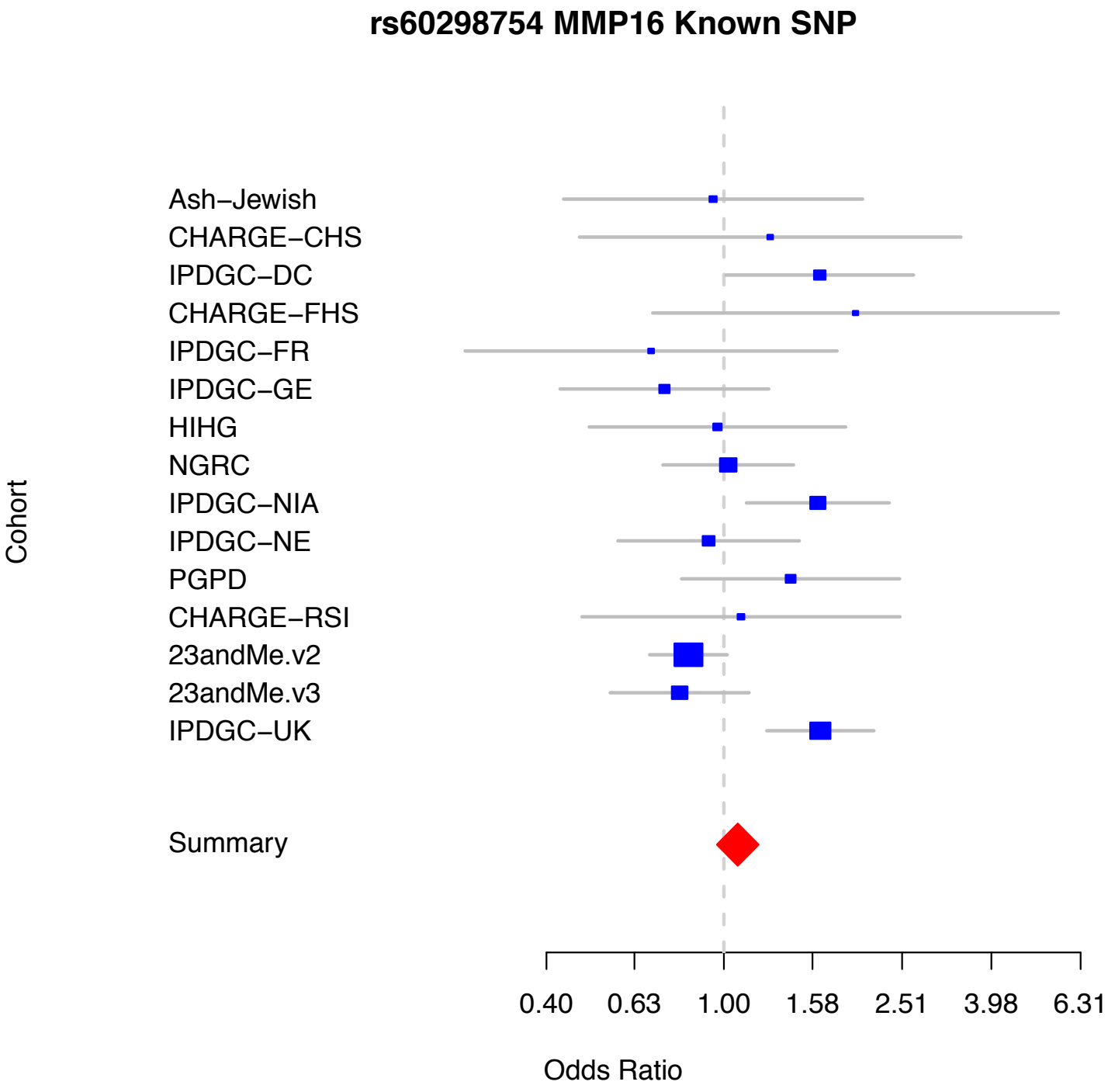

rs12456492 RIT2 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.79
0.89
1.00
1.12
1.26
1.41
1.58
1.78
Odds Ratio

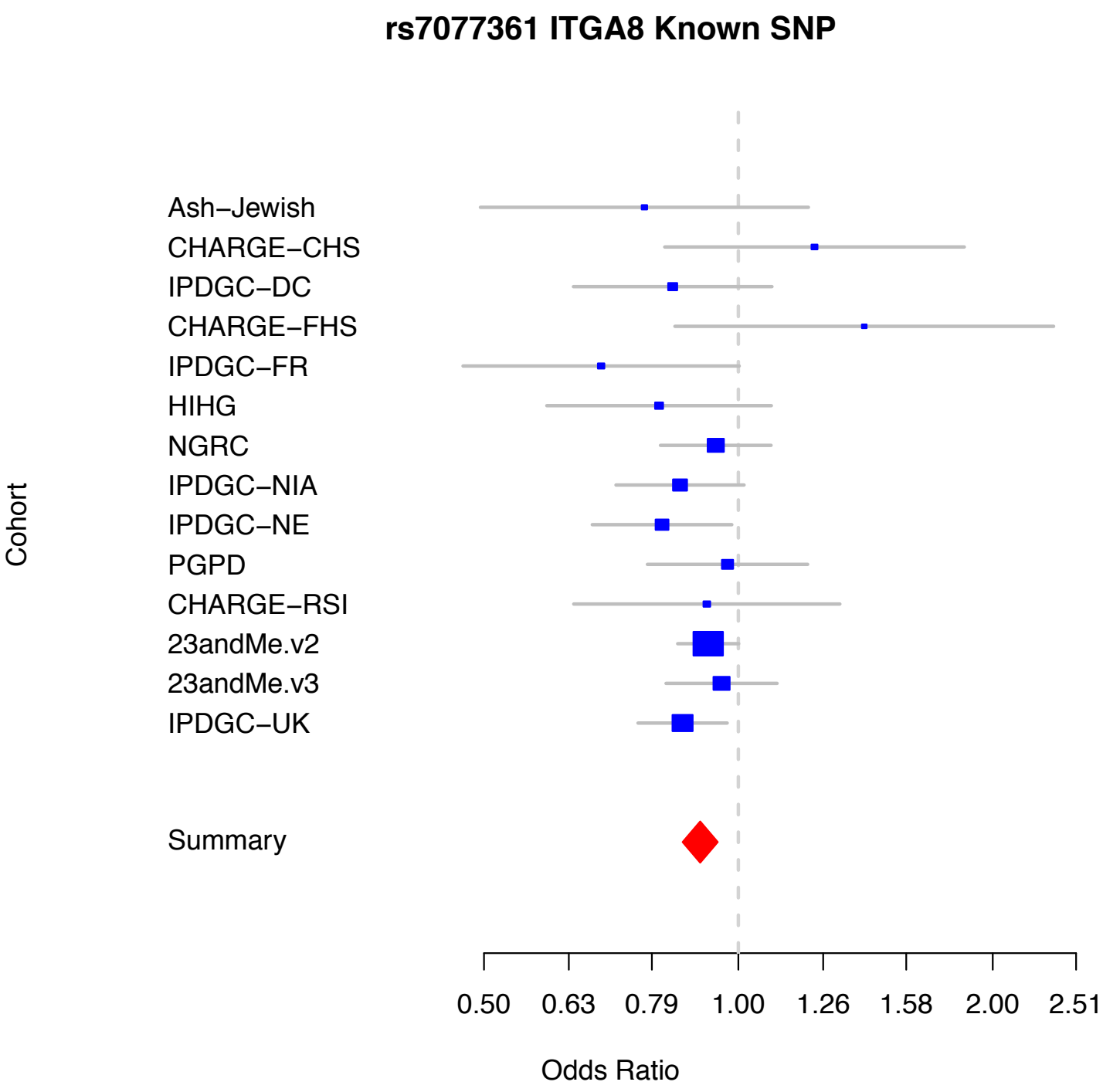

rs62120679 SPPL2B Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

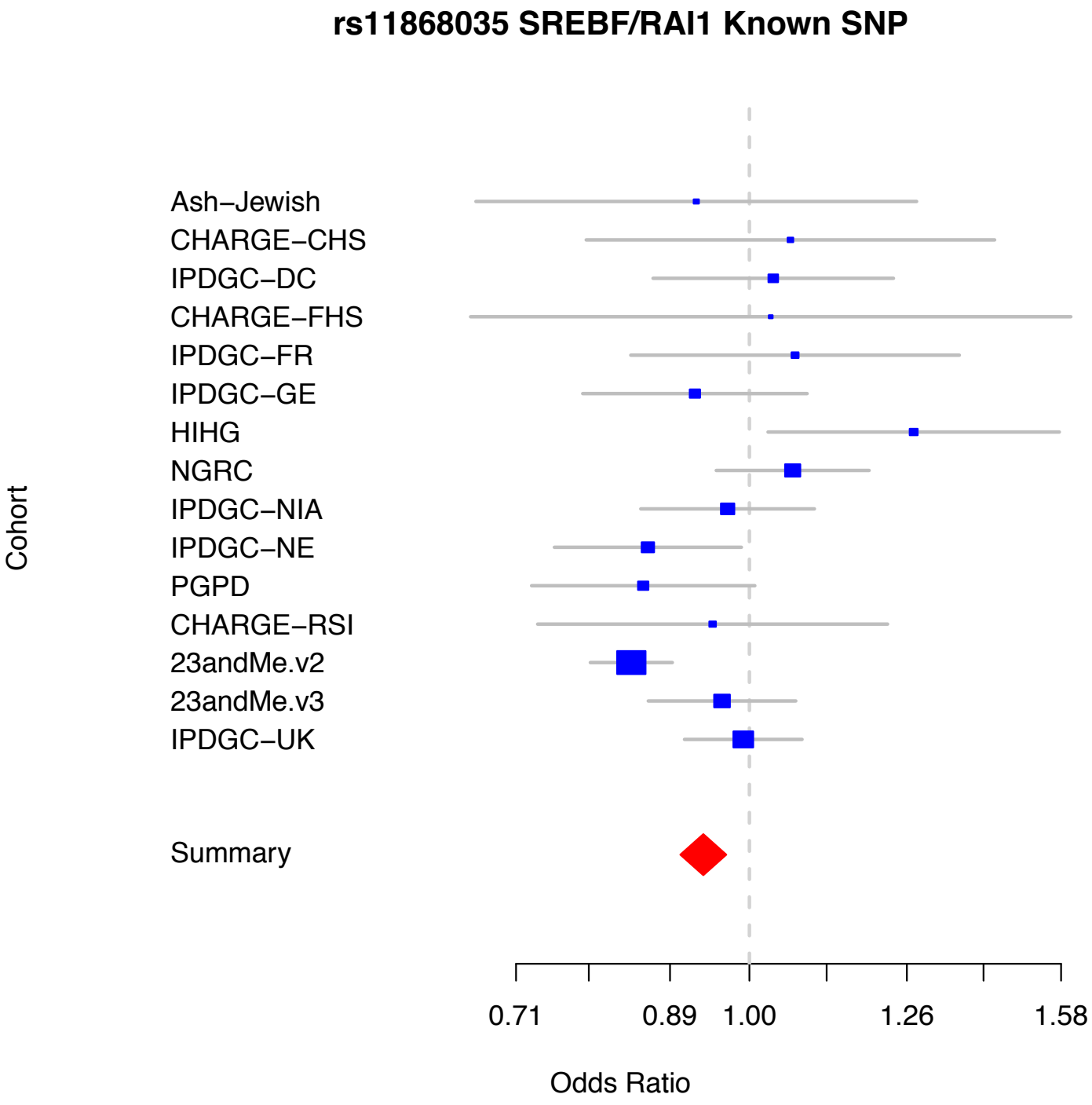

rs8118008 DDRGK1 Discovery SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
Odds Ratio

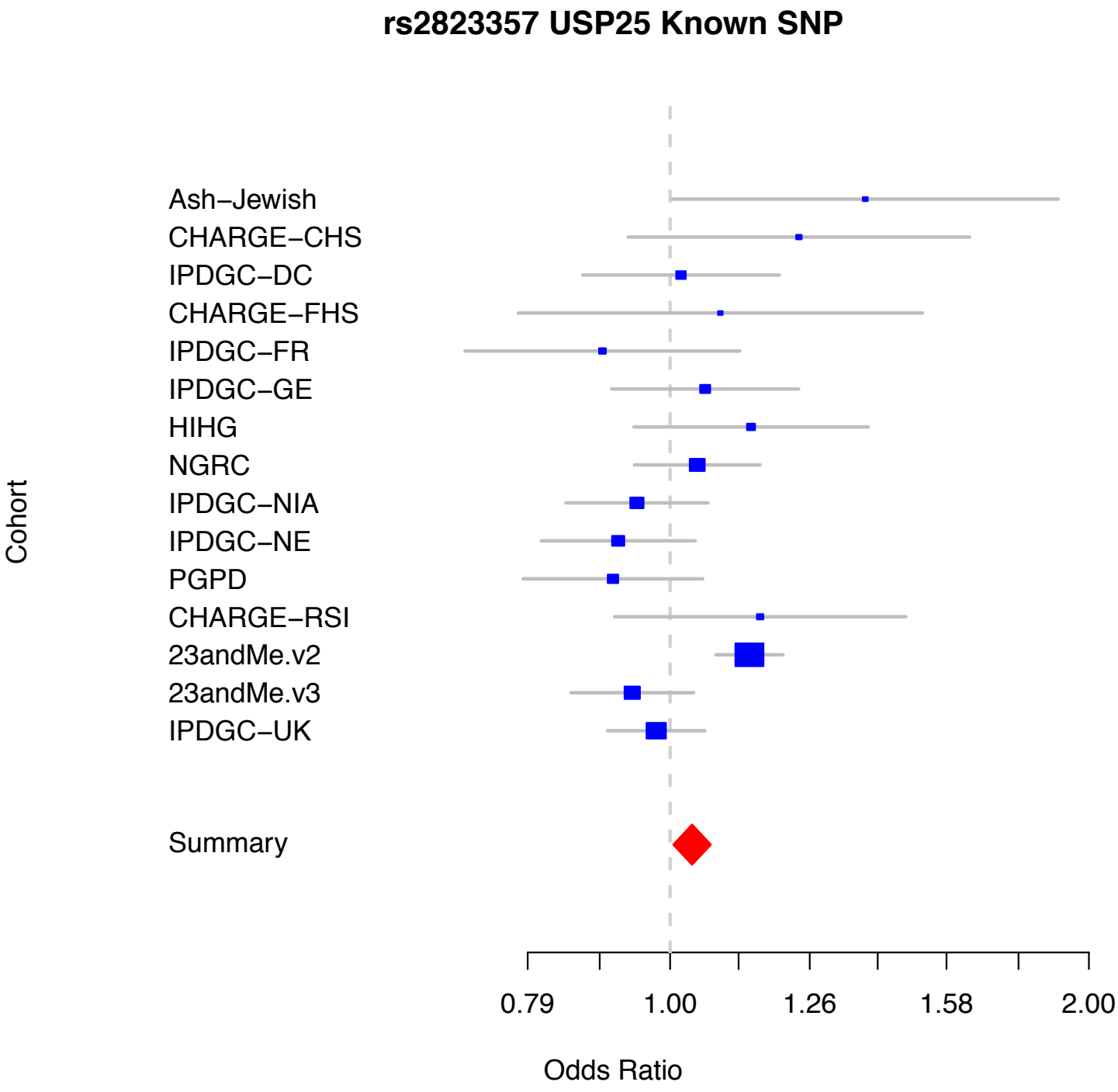

rs34016896 NMD3 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

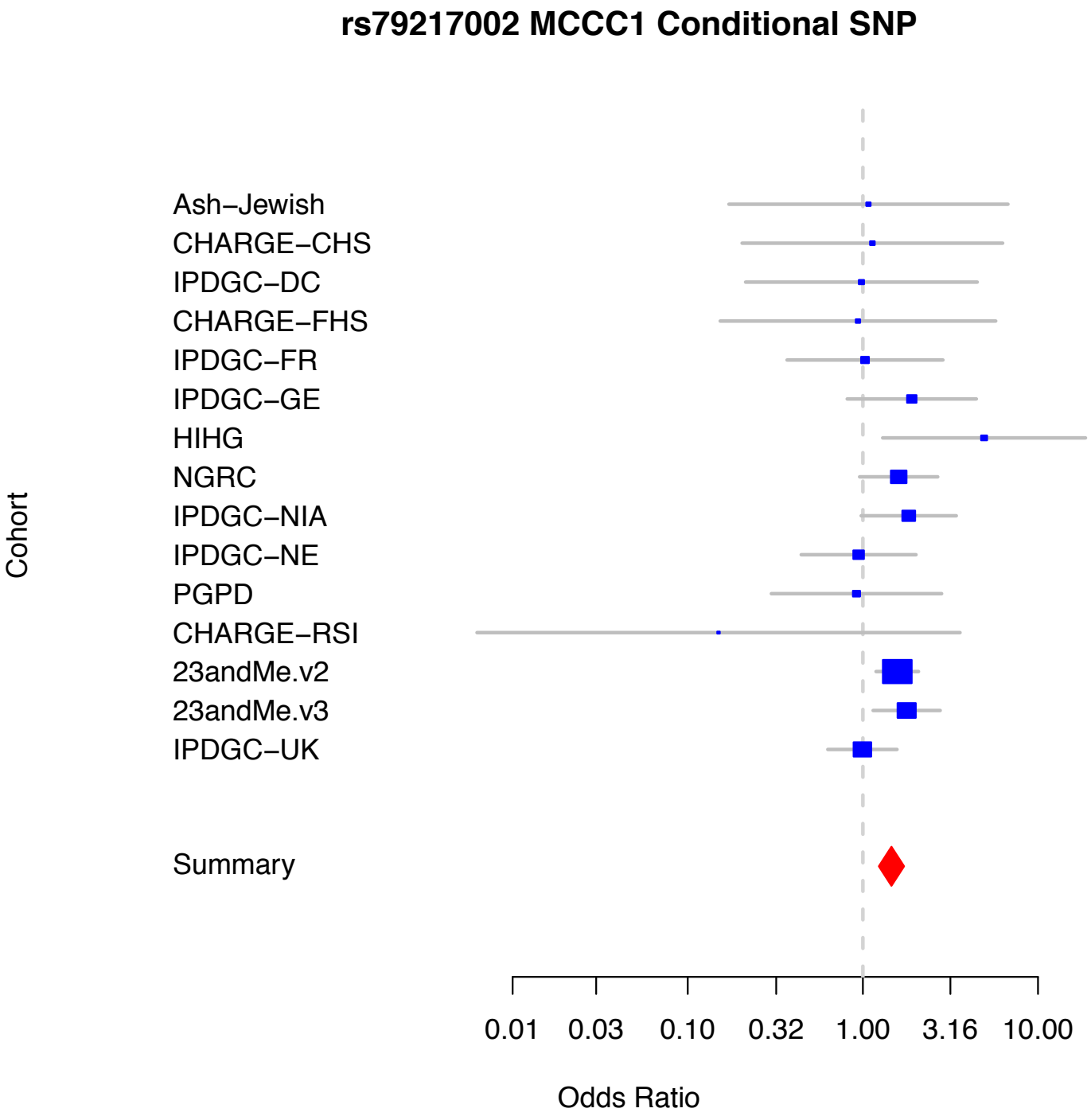

rs591323 FGF20 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
2.00
Odds Ratio

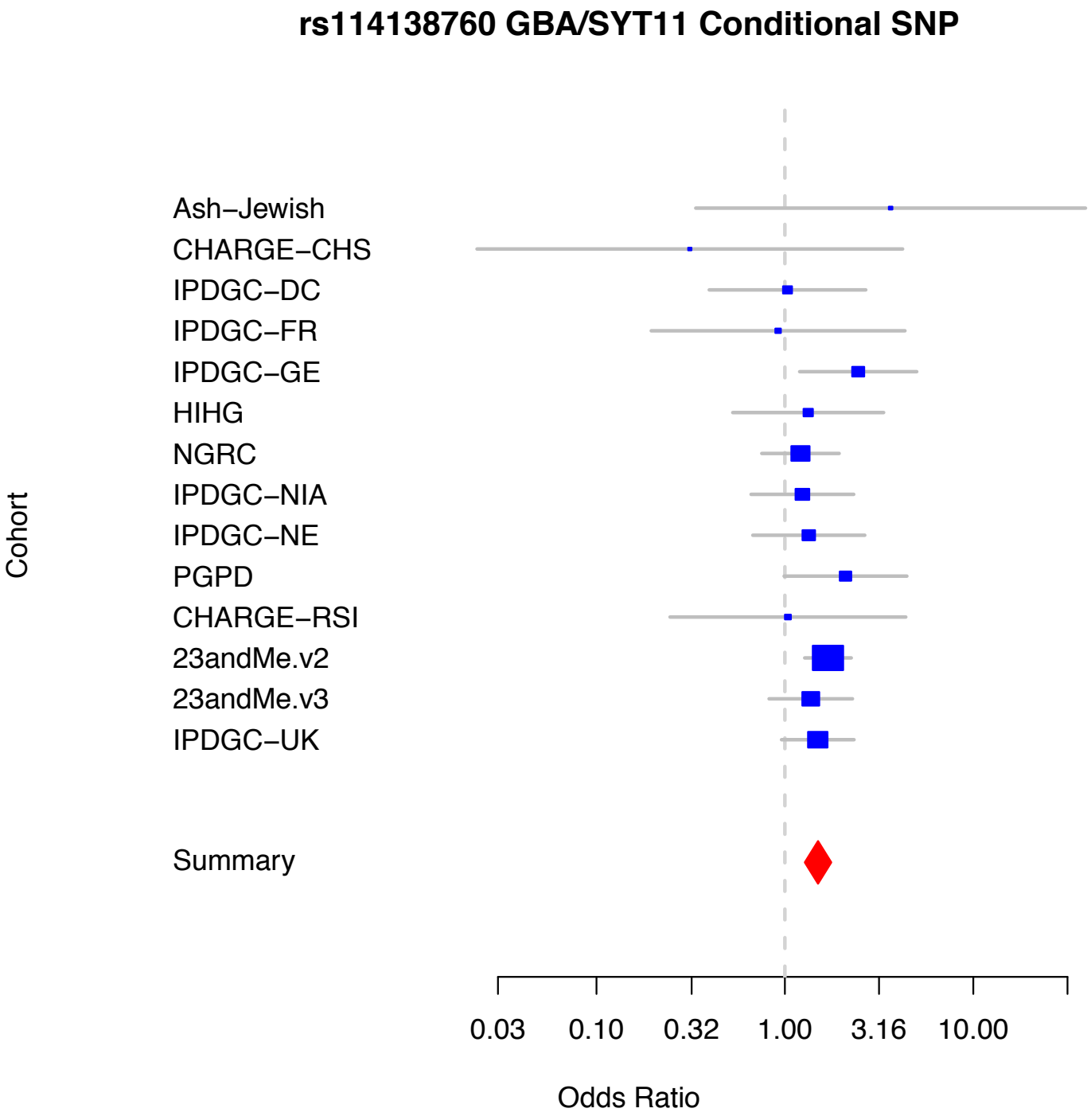

rs60298754 MMP16 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.40
0.63
1.00
1.58
2.51
3.98
6.31
Odds Ratio

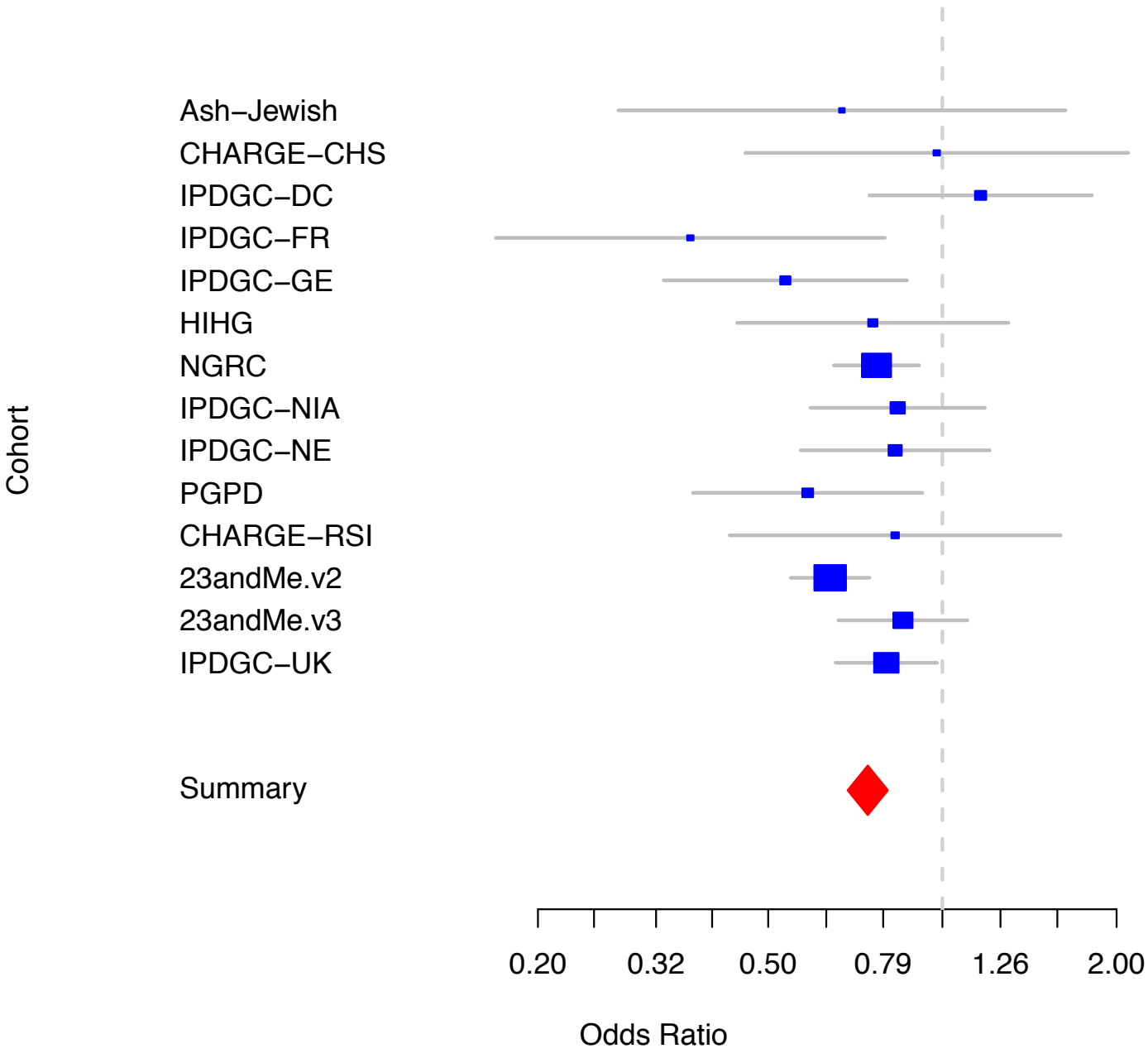

rs7077361 ITGA8 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.50
0.63
0.79
1.00
1.26
1.58
2.00
2.51
Odds Ratio

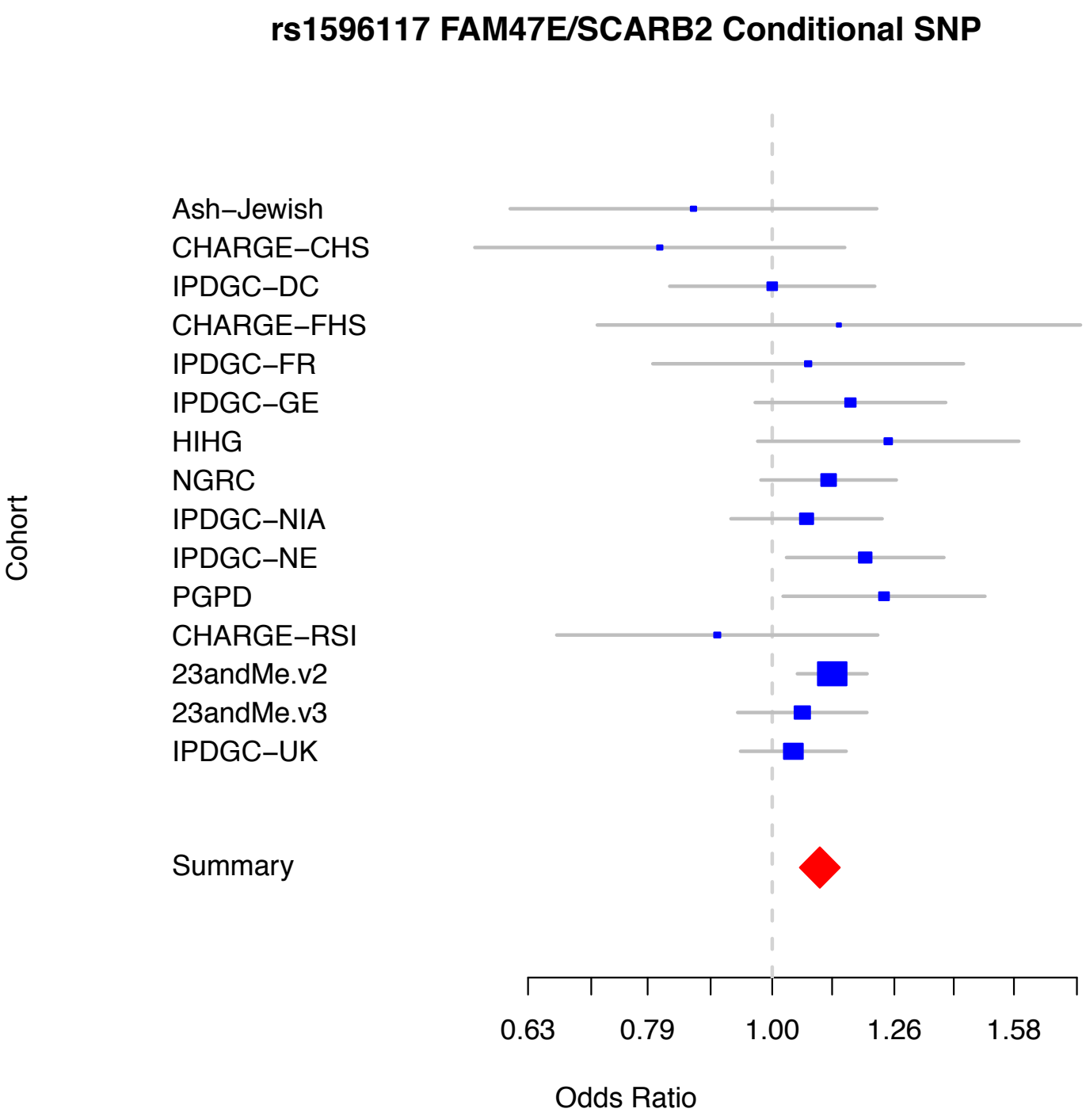

rs11868035 SREBF/RAI1 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.71
0.89
1.00
1.26
1.58
Odds Ratio

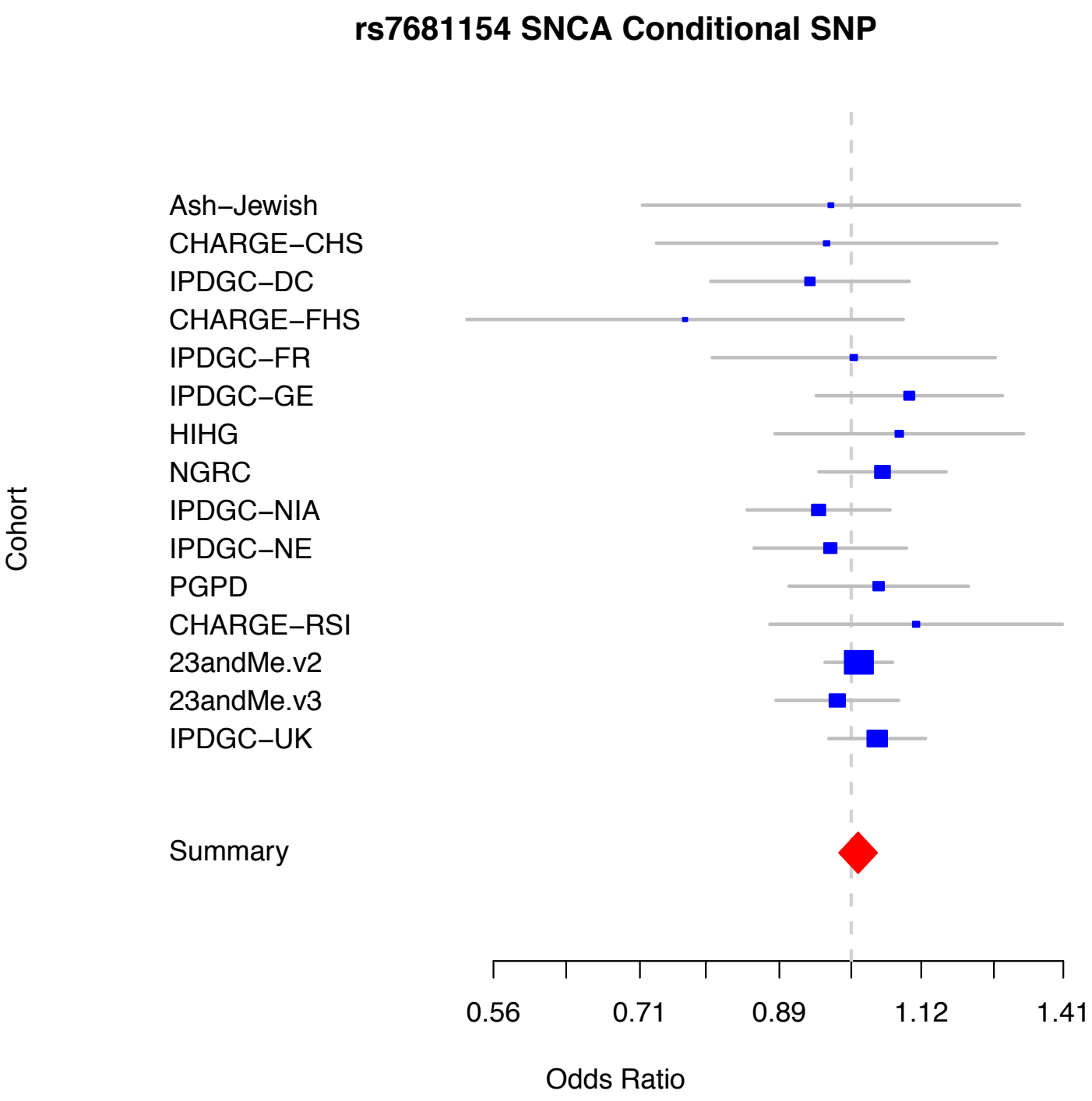

rs2823357 USP25 Known SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.79
1.00
1.26
1.58
2.00
Odds Ratio

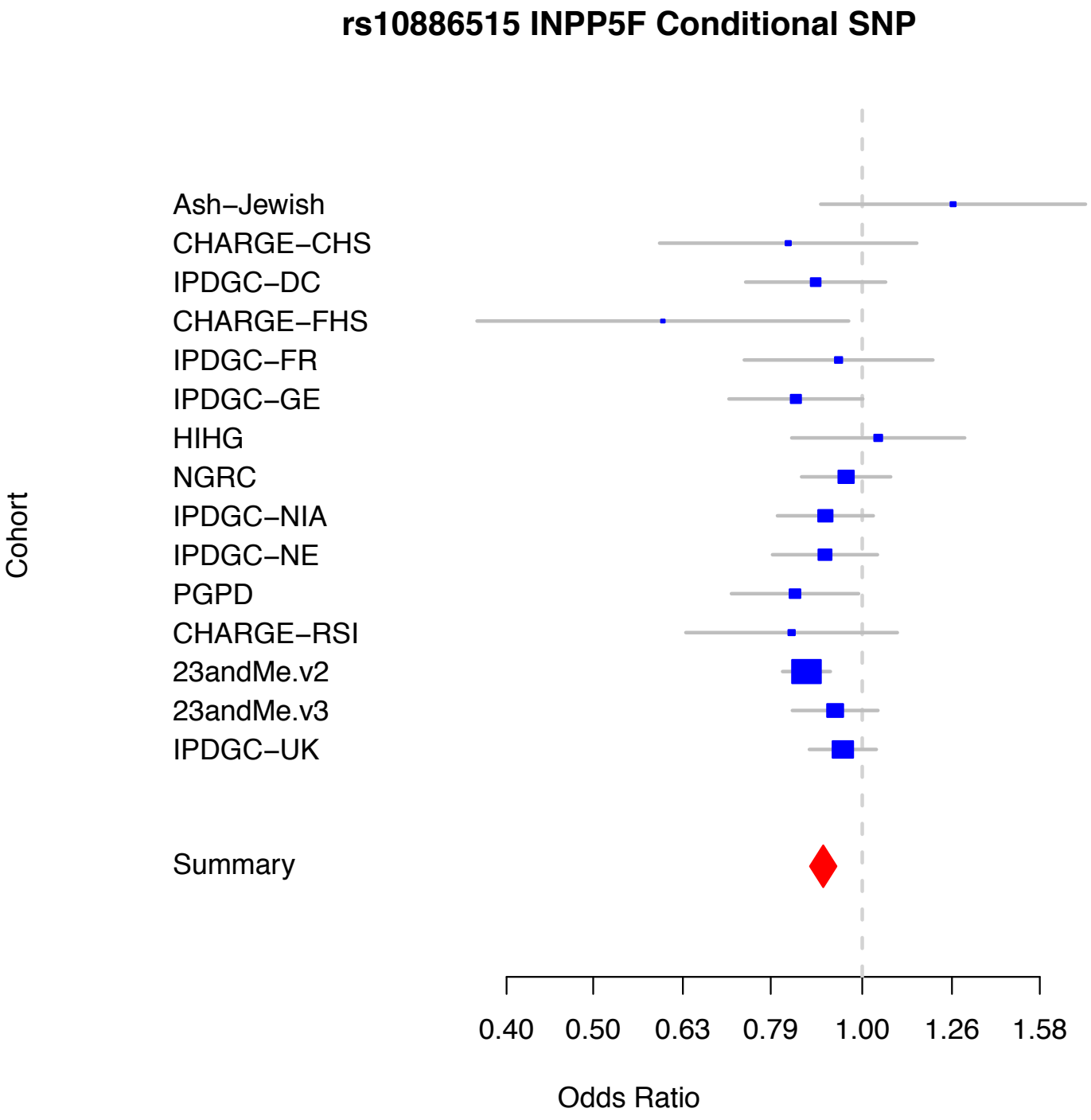

rs79217002 MCCC1 Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.01
0.03
0.10
0.32
1.00
3.16
10.00
Odds Ratio

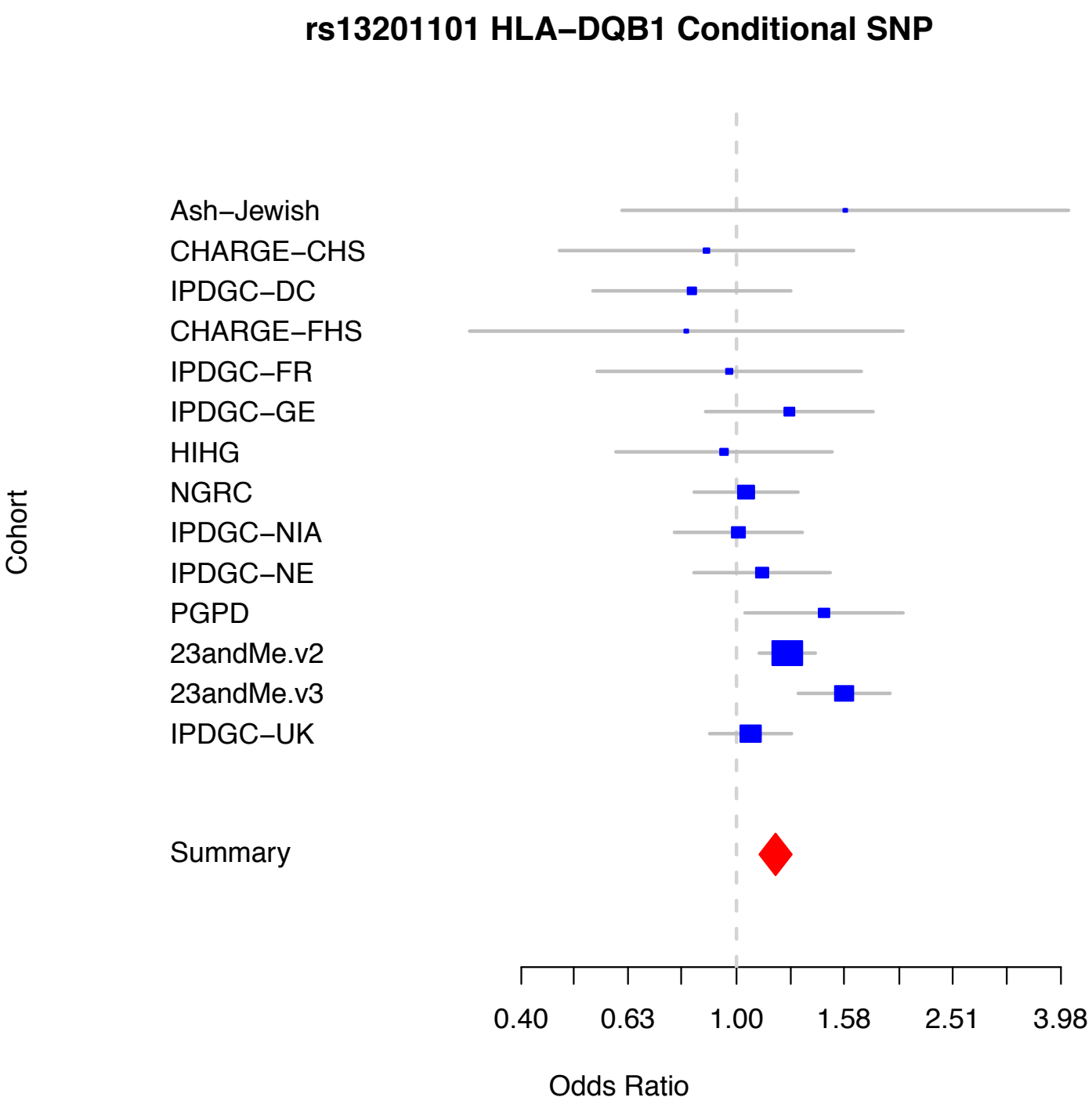

rs114138760 GBA/SYT11 Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.03
0.10
0.32
1.00
3.16
10.00
Odds Ratio

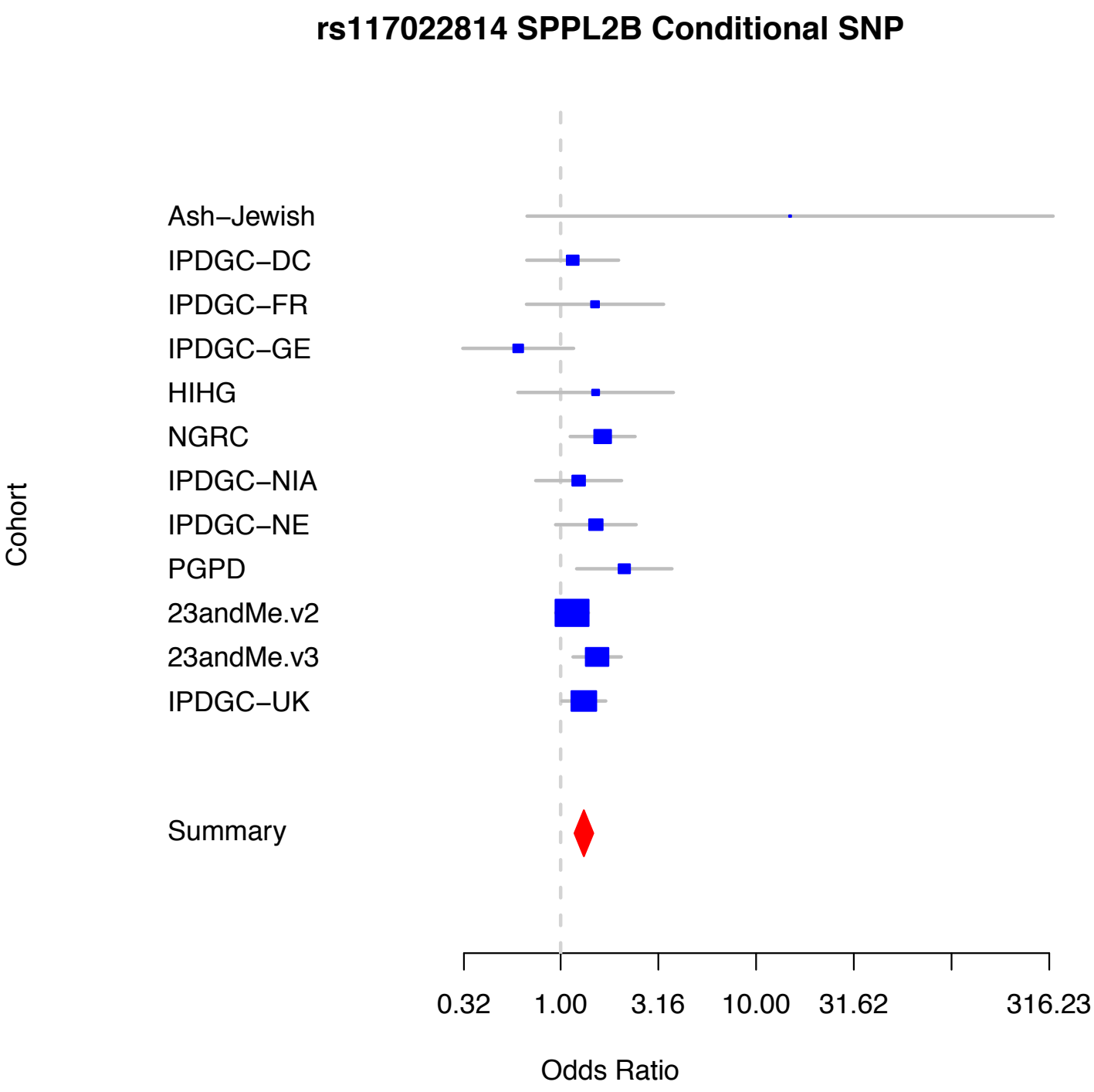

rs34884217 TMEM175/GAK/DGKQ Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.20
0.32
0.50
0.79
1.26
2.00
Odds Ratio


rs1596117 FAM47E/SCARB2 Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.63
0.79
1.00
1.26
1.58
Odds Ratio

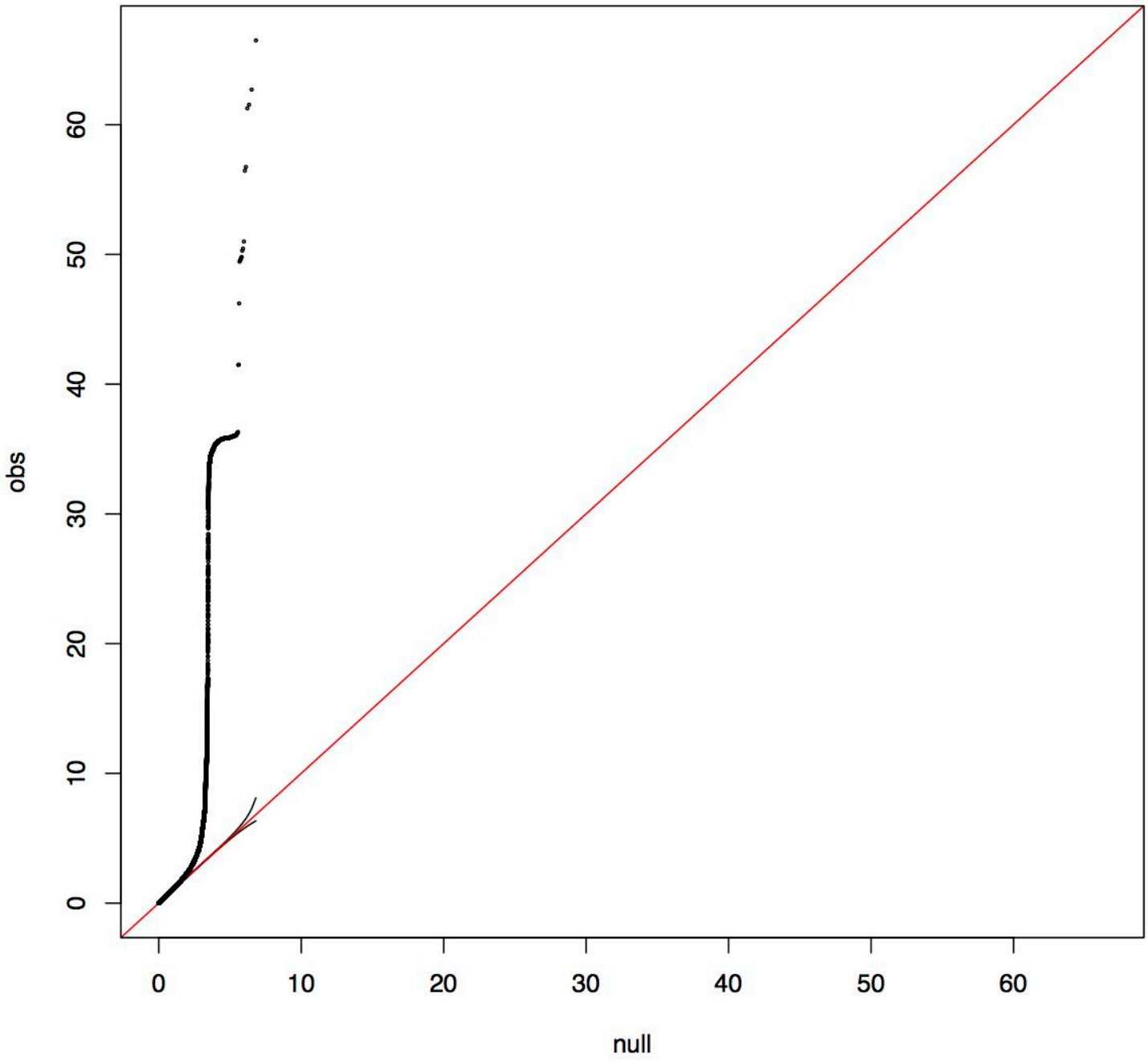

rs7681154 SNCA Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.56
0.71
0.89
1.12
1.41
Odds Ratio


rs10886515 INPP5F Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
CHARGE−RSI
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.40
0.50
0.63
0.79
1.00
1.26
1.58
Odds Ratio

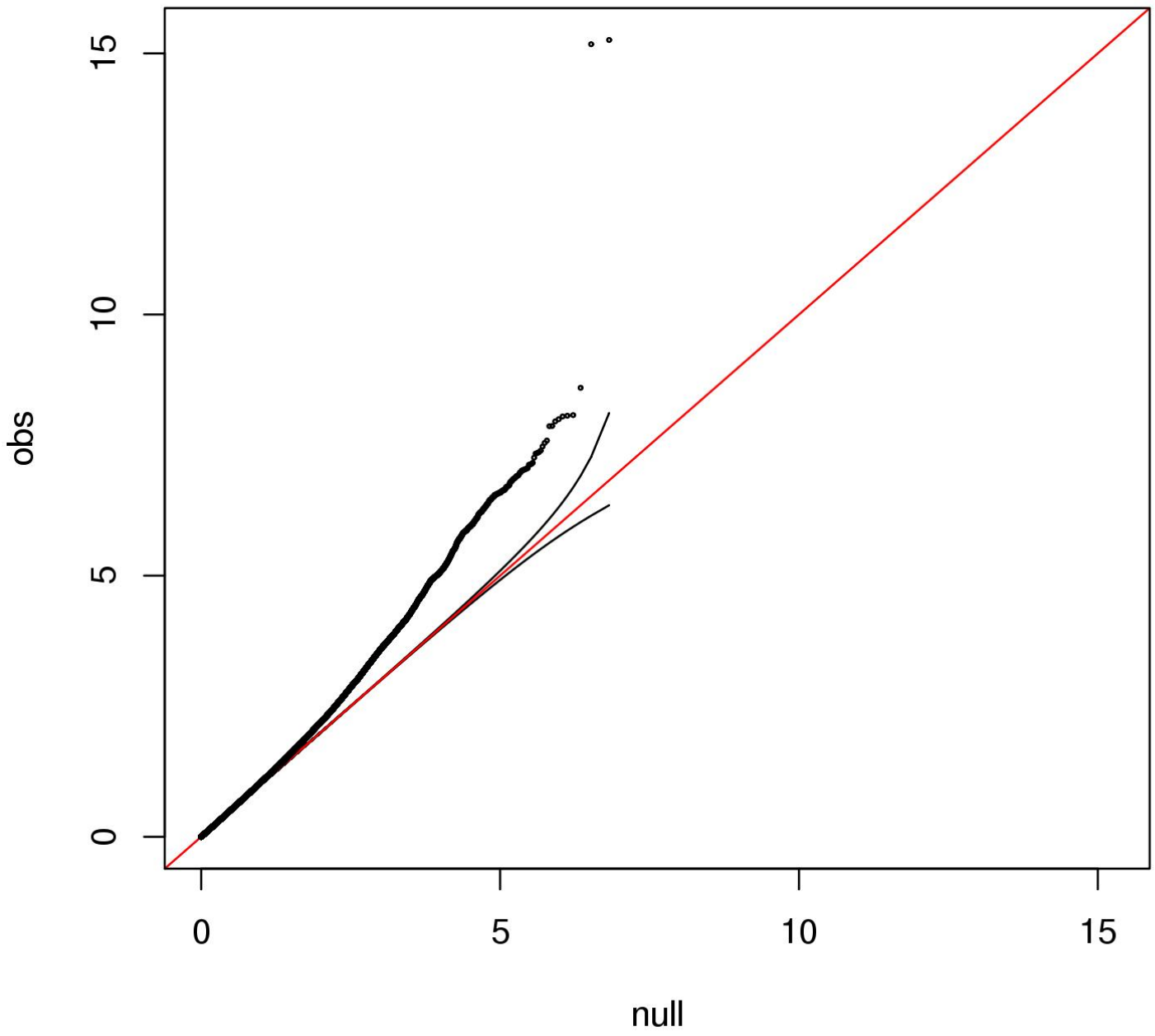

rs13201101 HLA−DQB1 Conditional SNP
Cohort
Ash−Jewish
CHARGE−CHS
IPDGC−DC
CHARGE−FHS
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.40
0.63
1.00
1.58
2.51
3.98
Odds Ratio


rs117022814 SPPL2B Conditional SNP
Cohort
Ash−Jewish
IPDGC−DC
IPDGC−FR
IPDGC−GE
HIHG
NGRC
IPDGC−NIA
IPDGC−NE
PGPD
23andMe.v2
23andMe.v3
IPDGC−UK
Summary
0.32
1.00
3.16
10.00
31.62
316.23
Odds Ratio

Supplementary Figure 3 (page 96):
QQ plot of p-values from discovery meta-analysis.



Supplementary Figure 4 (page 97): QQ plot of p-values from discovery meta-analysis excluding significant and replicated loci. All SNPs within +/- 1 megabase of a replicated genome-wide significant SNP were excluded (unadjusted lambda = 1.045).



Supplementary Figure 5 (page 98): ROC curve for genetic risk profiles across cohorts adjusting for cohort membership, age and gender.