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Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci

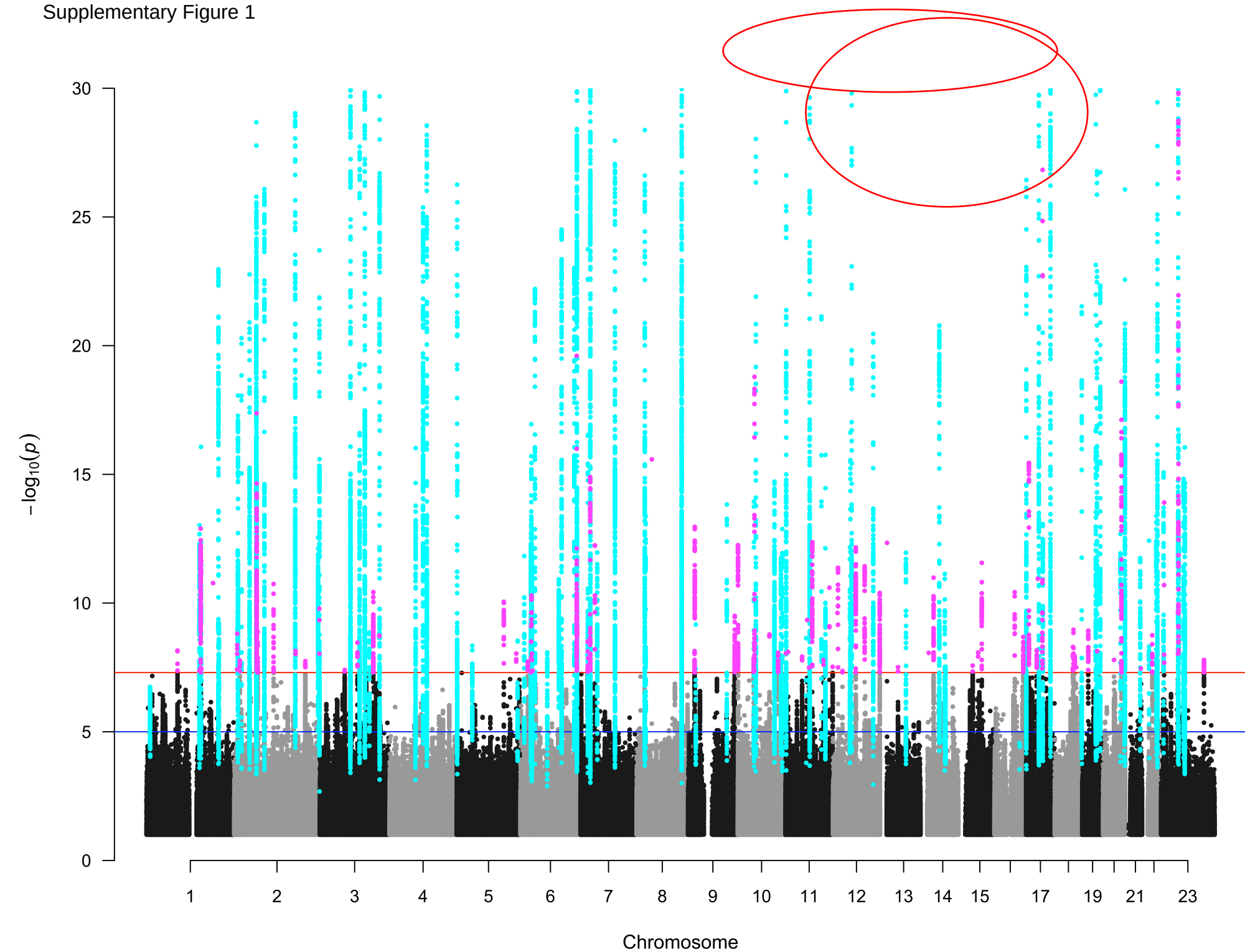
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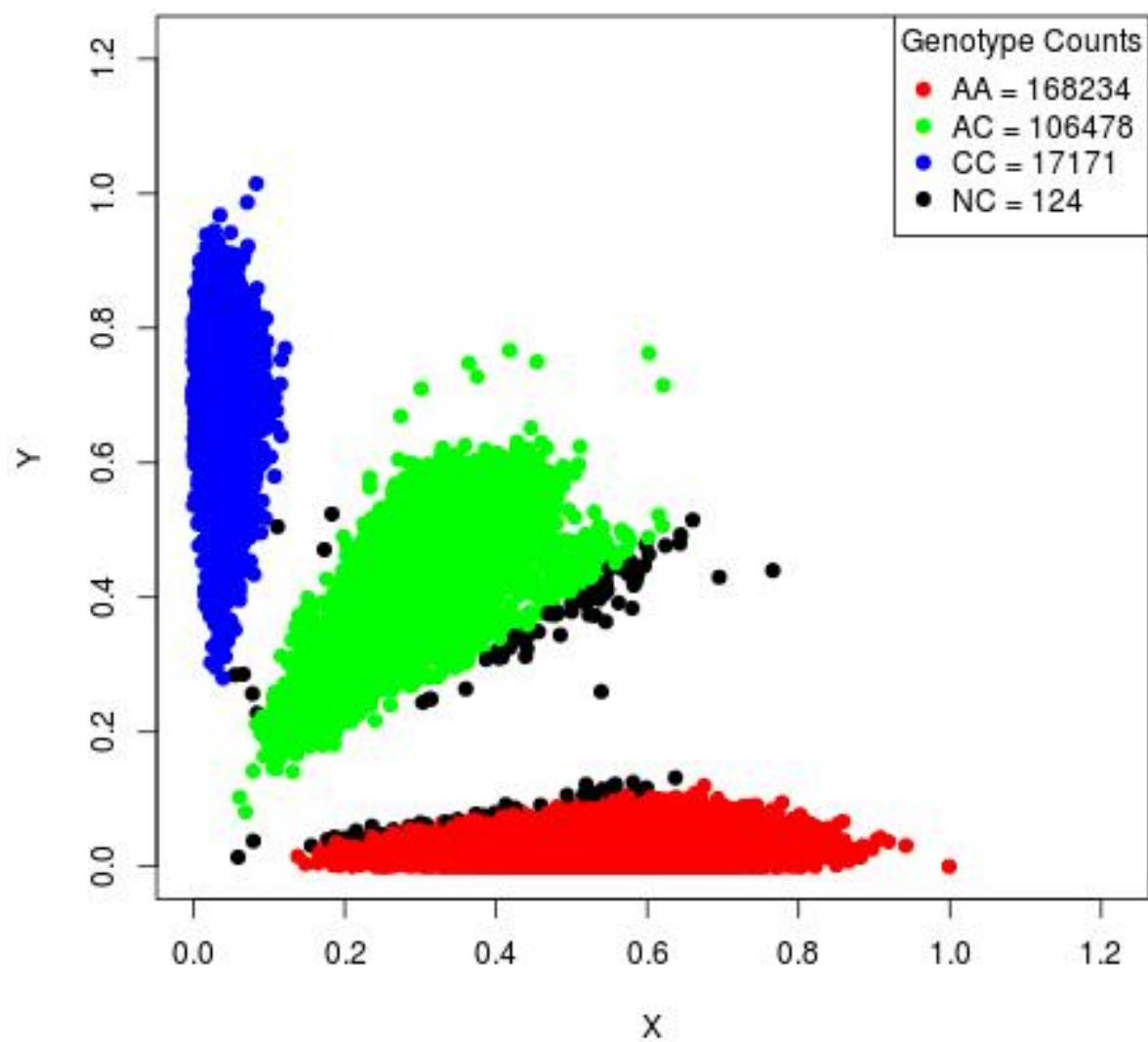
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Supplementary Figure 1



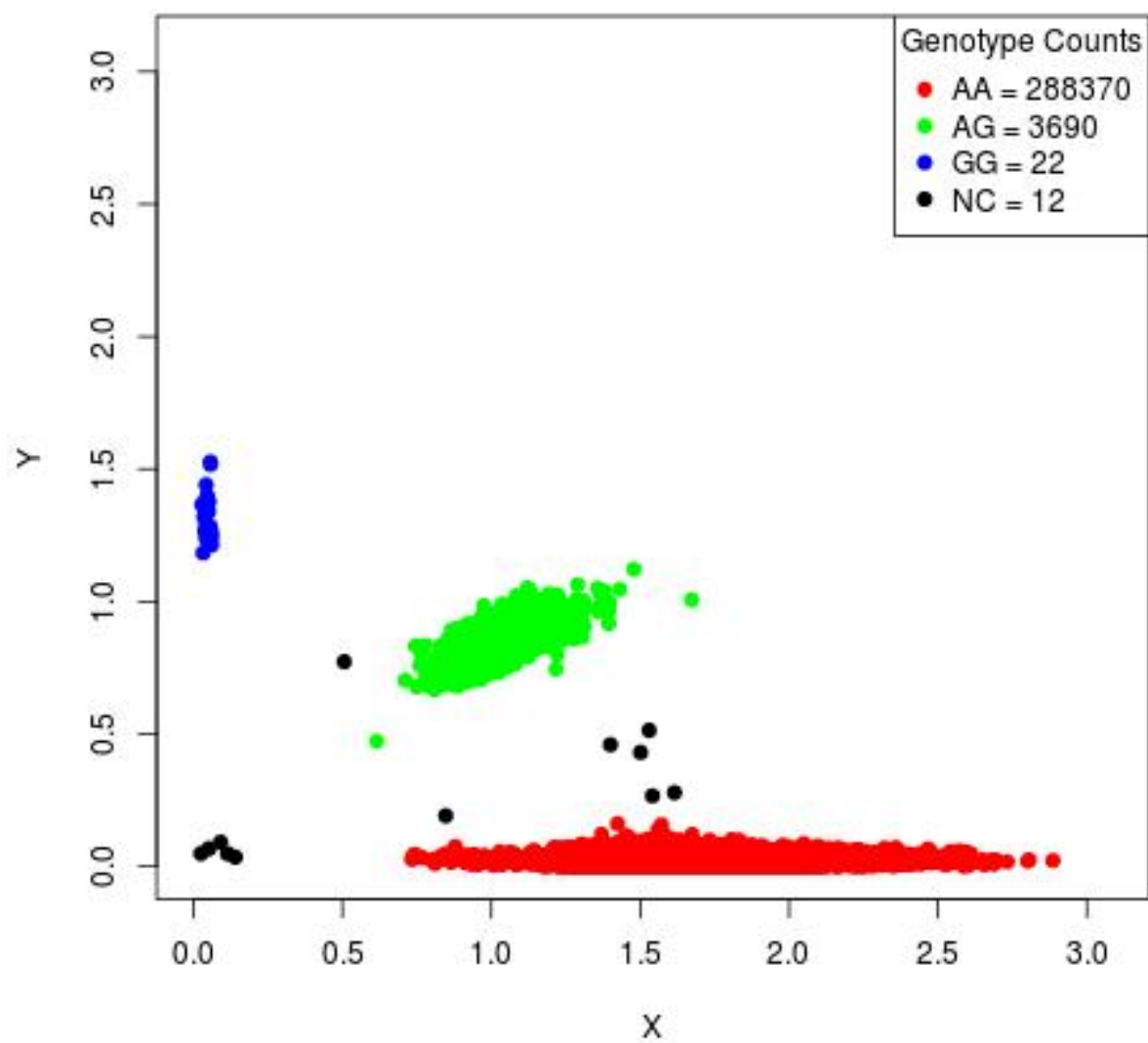
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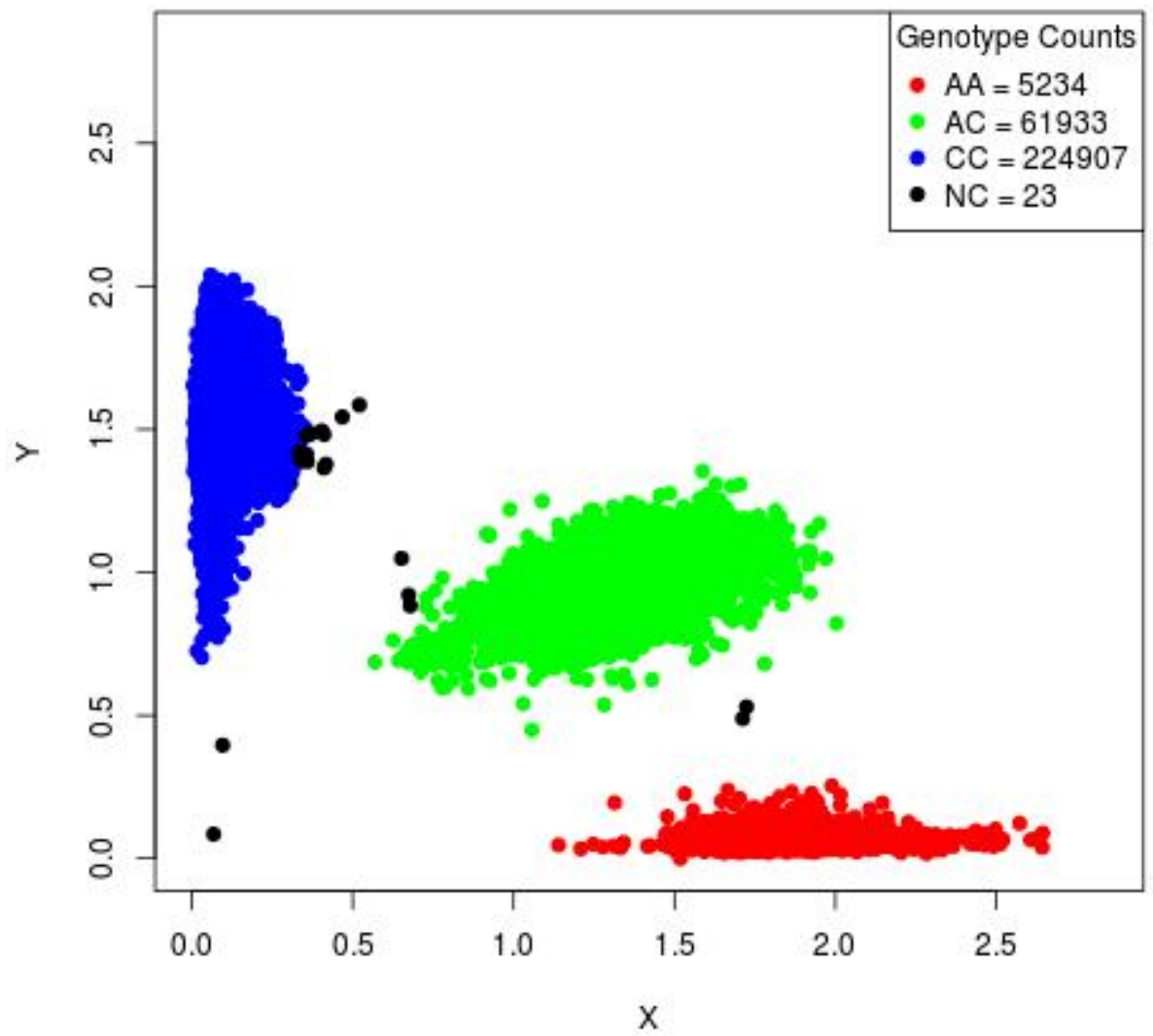
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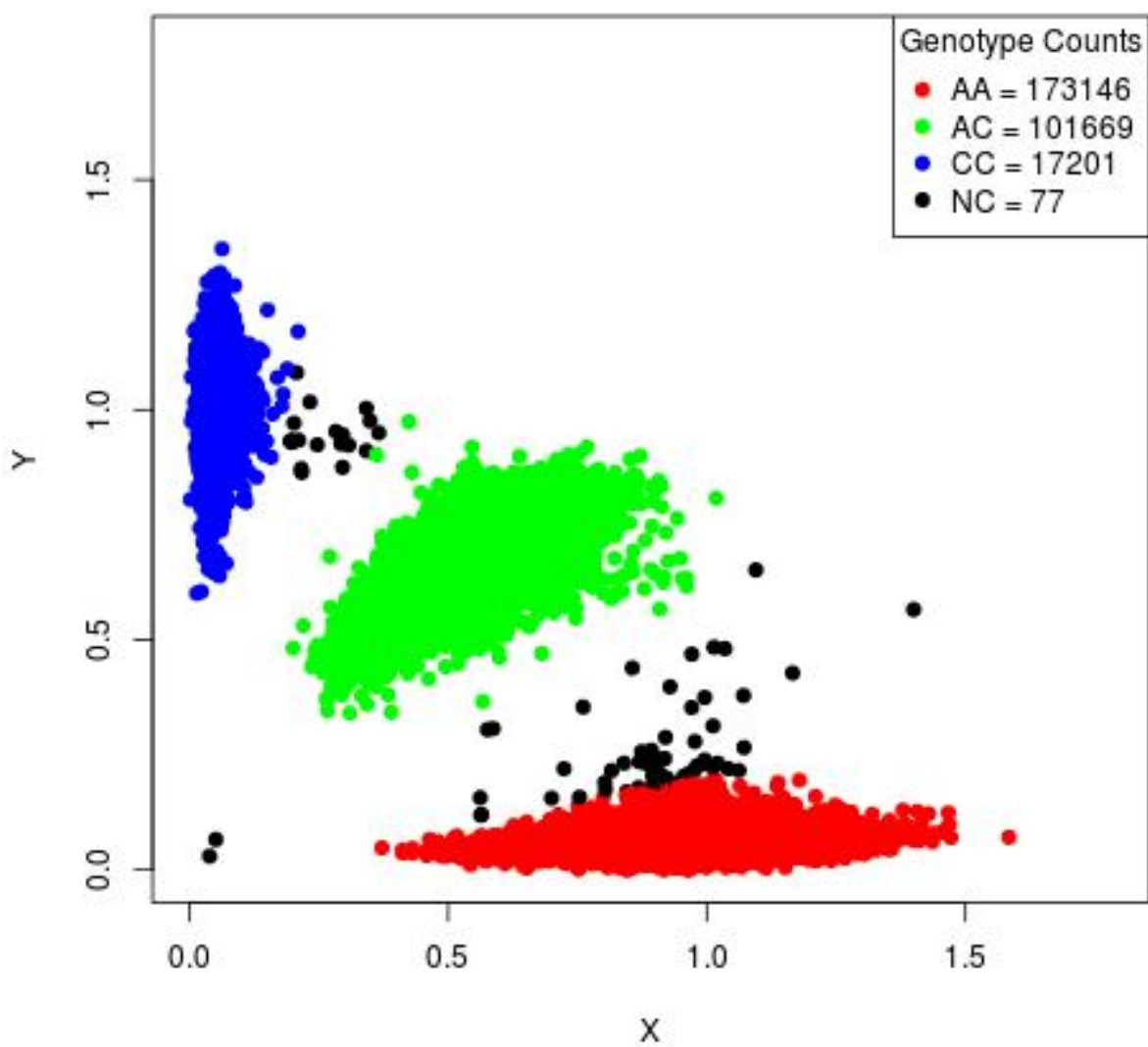
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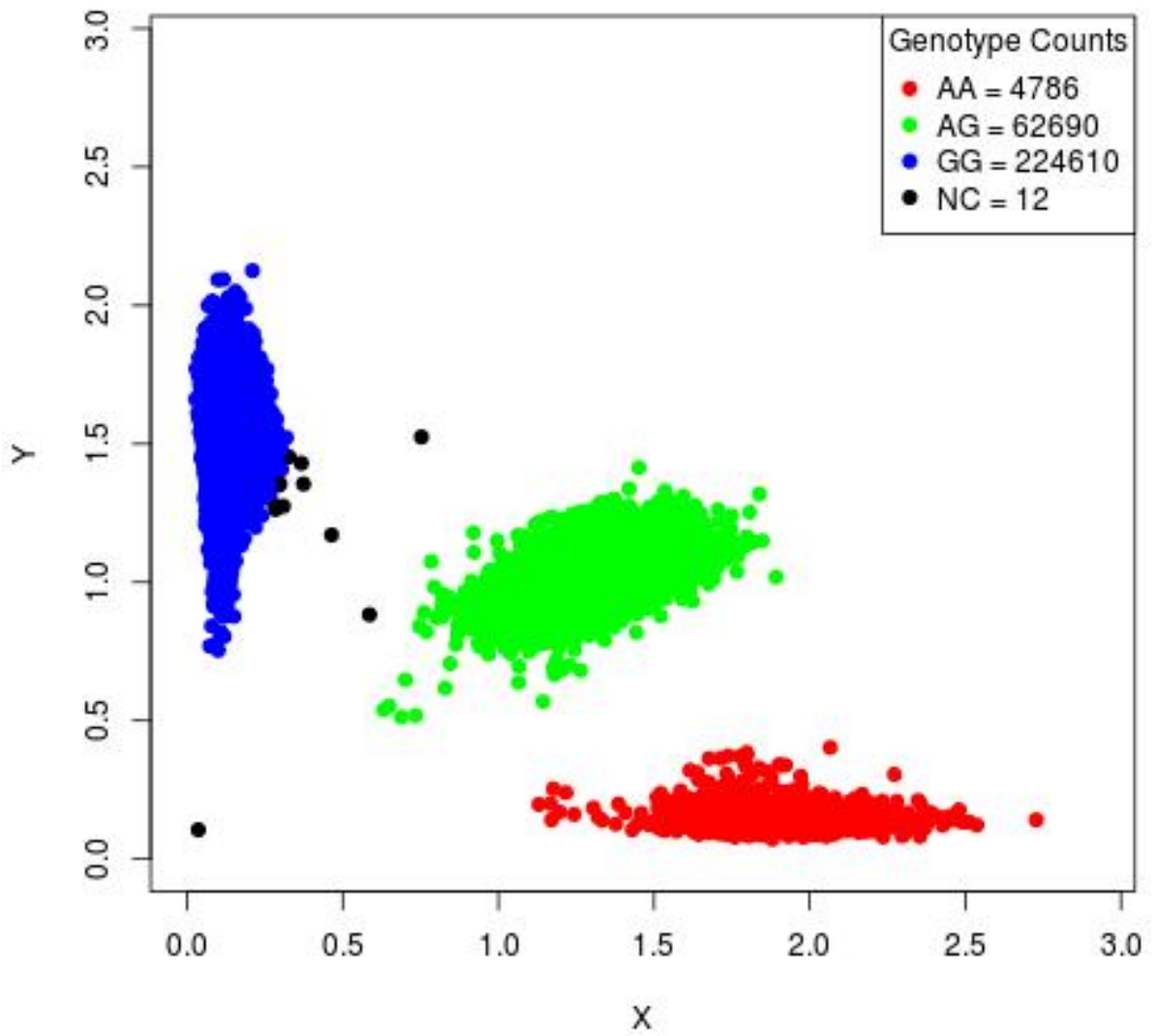
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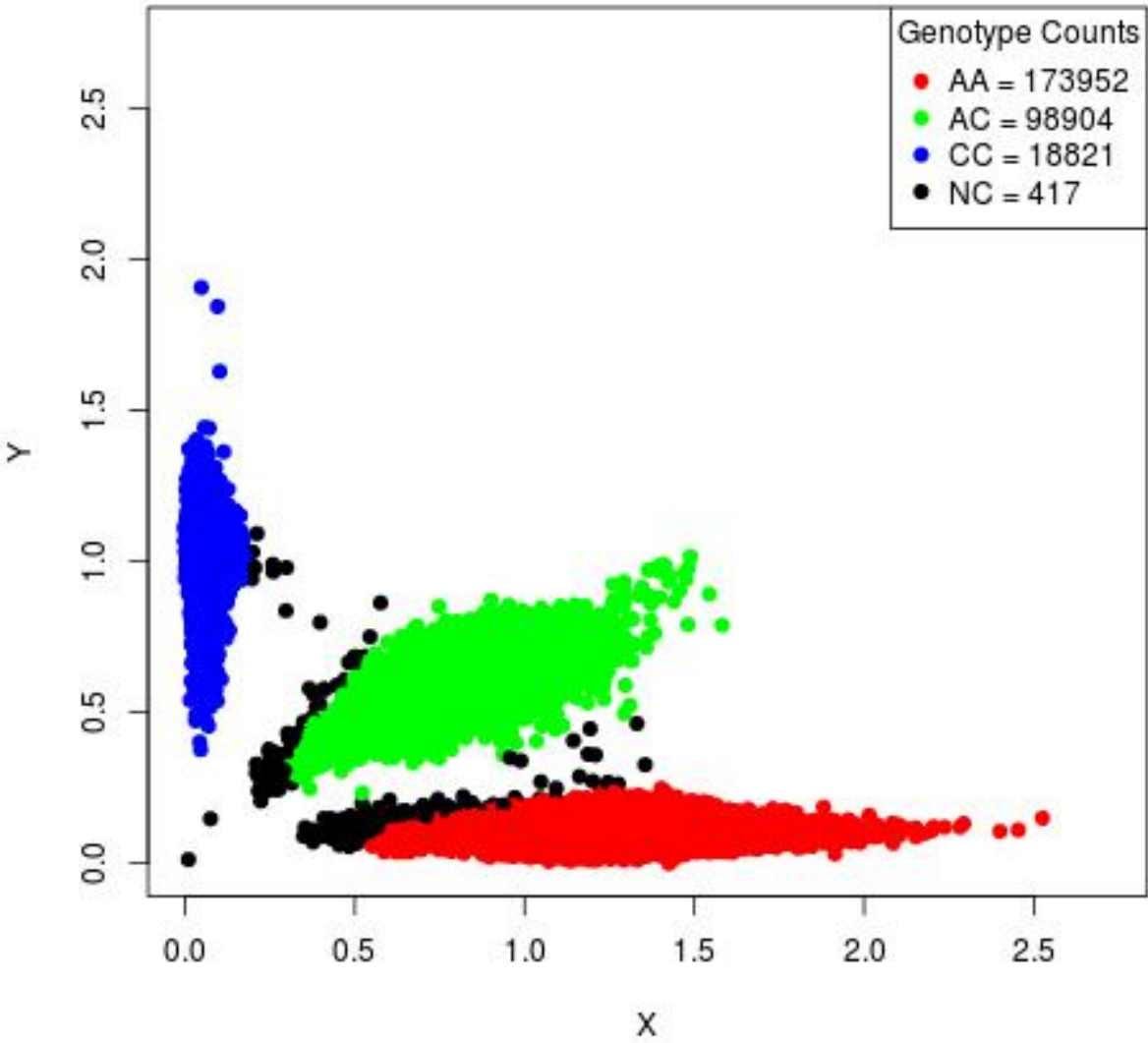
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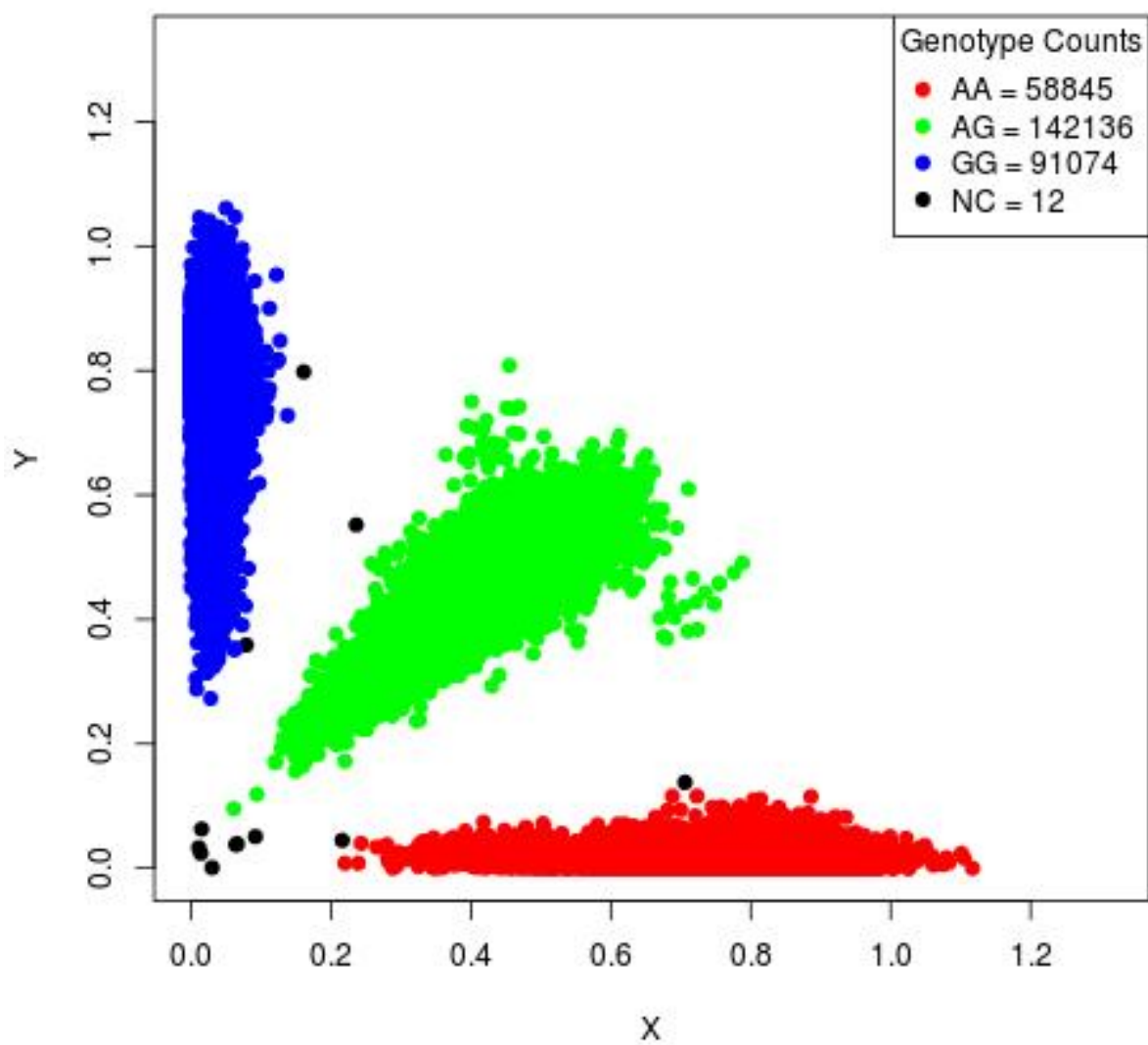


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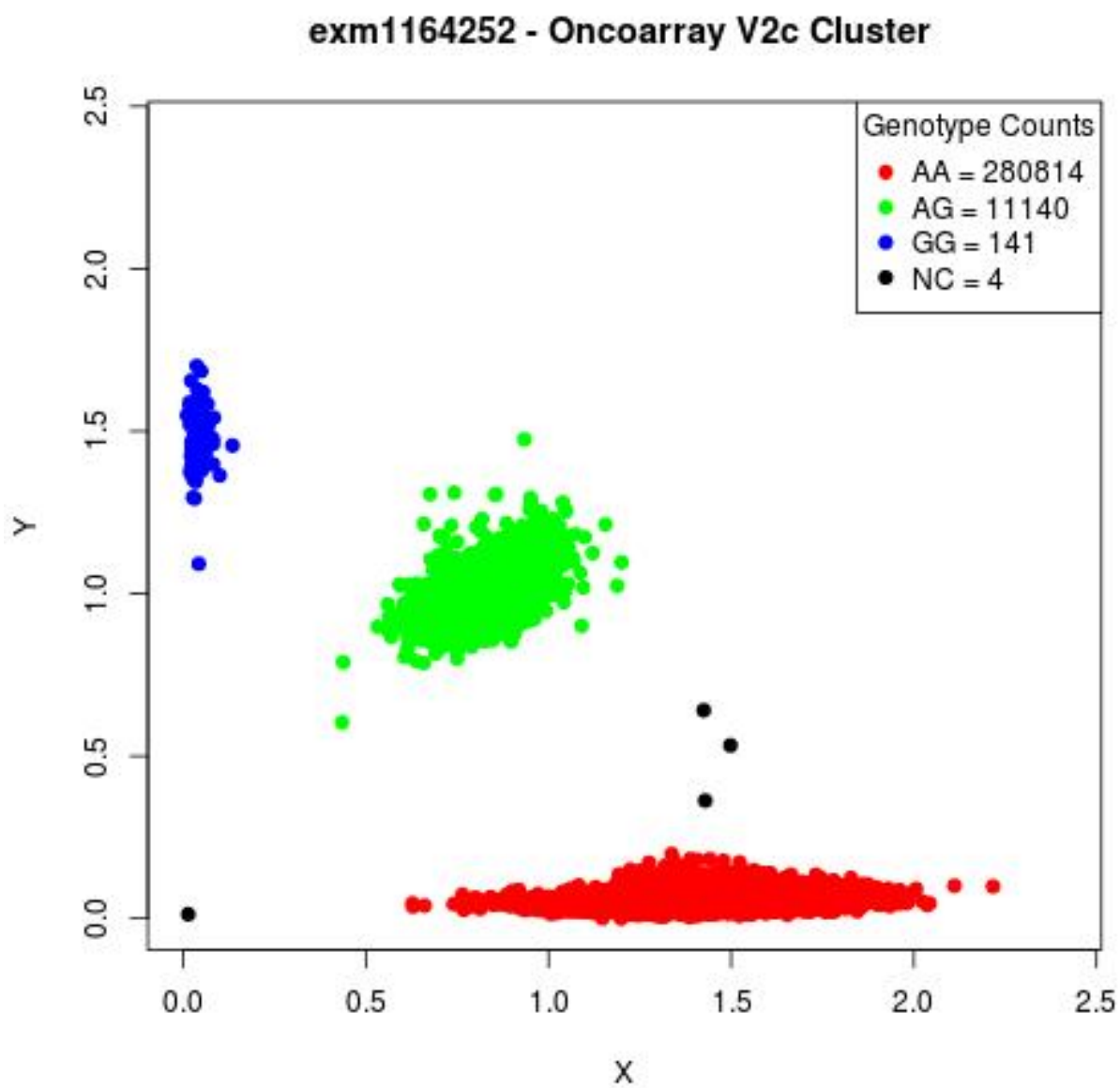
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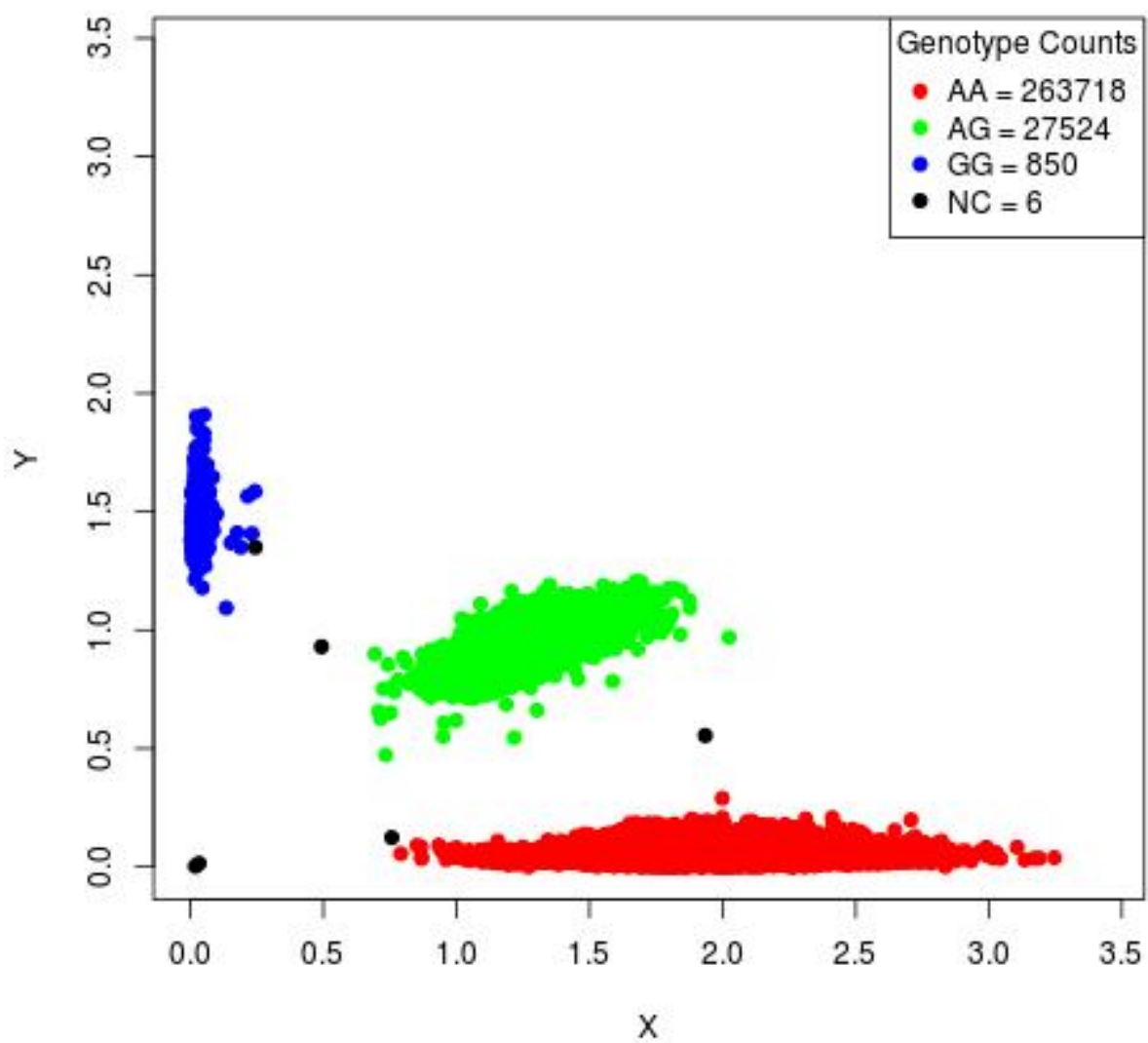


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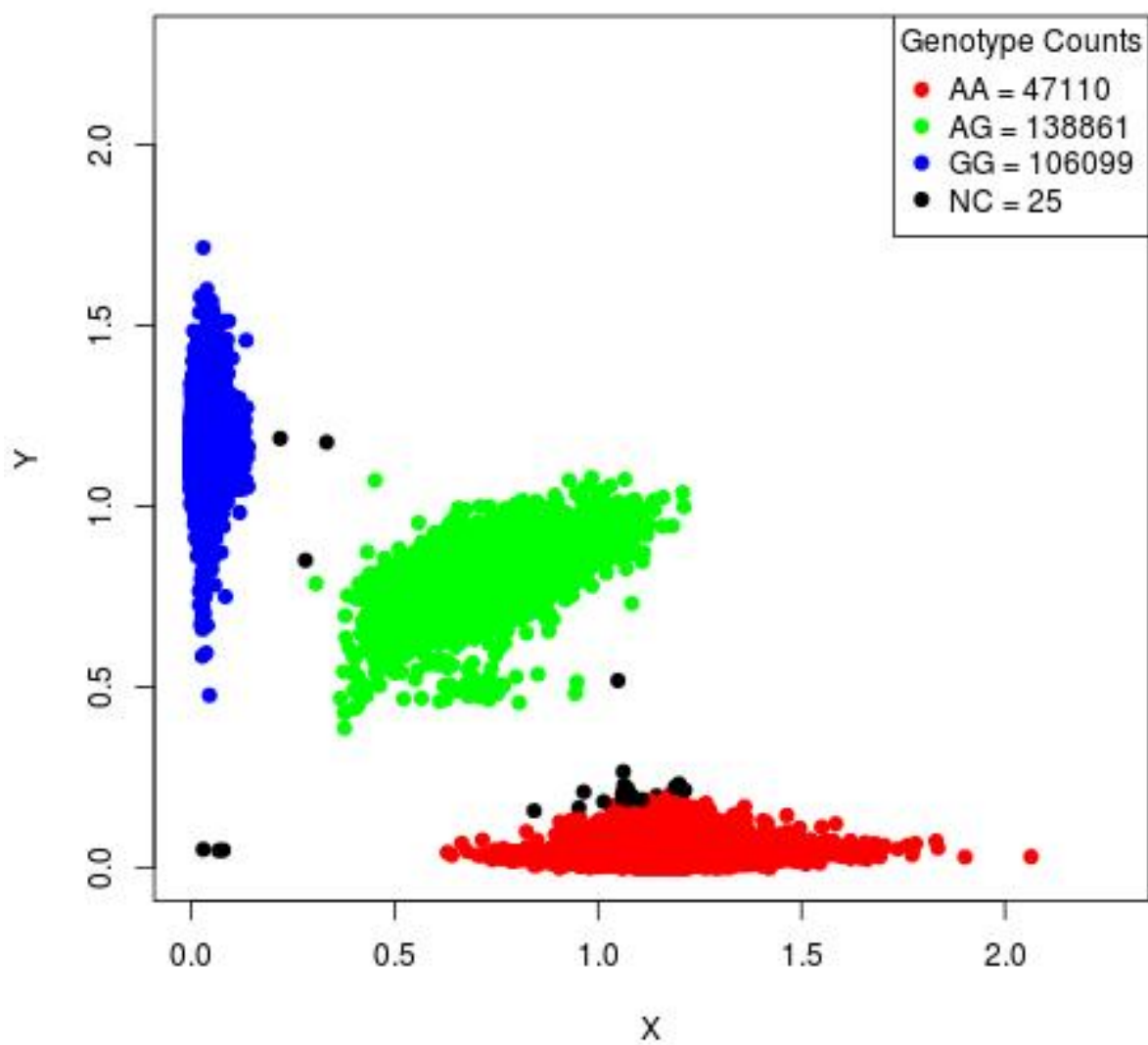
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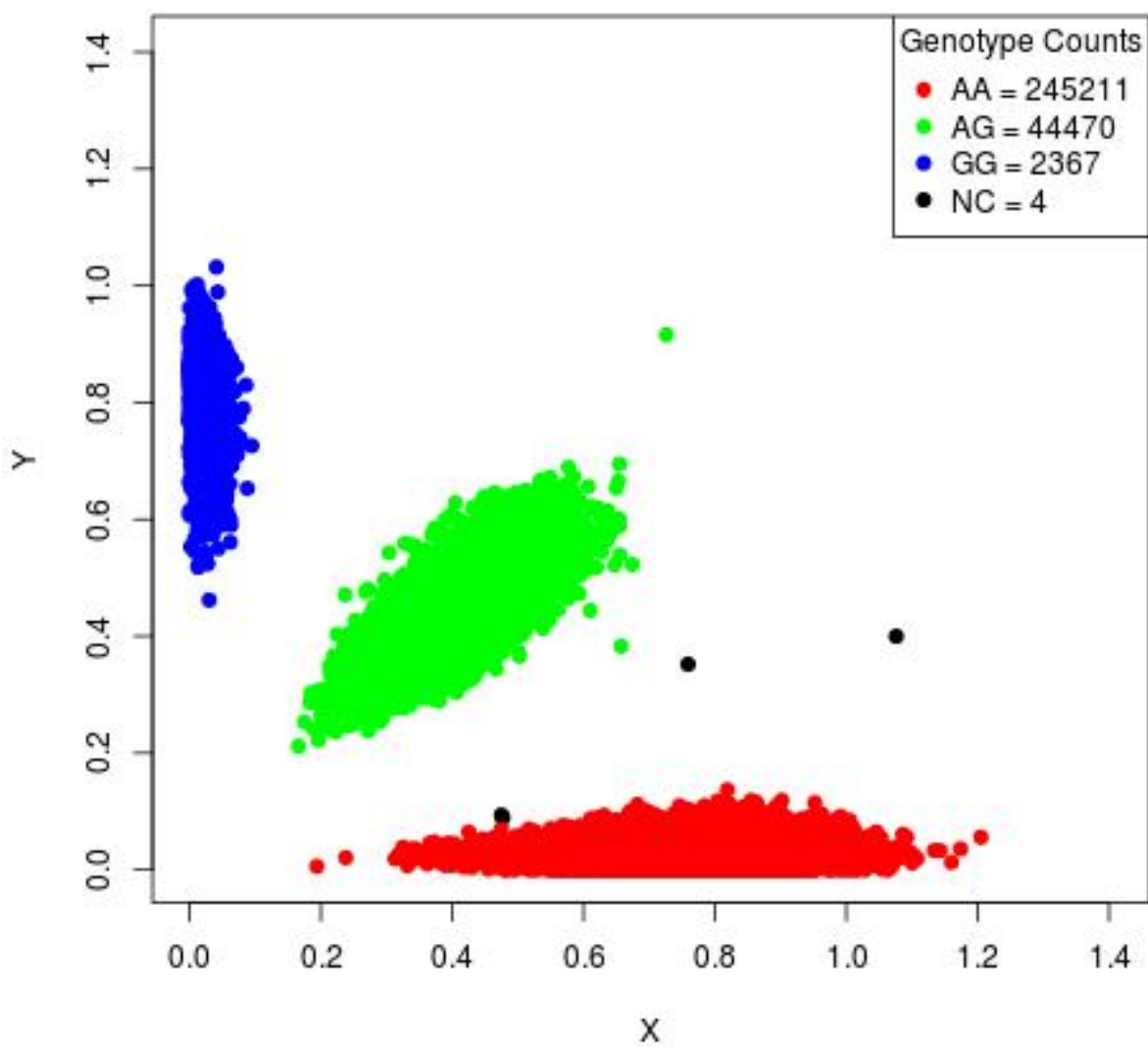
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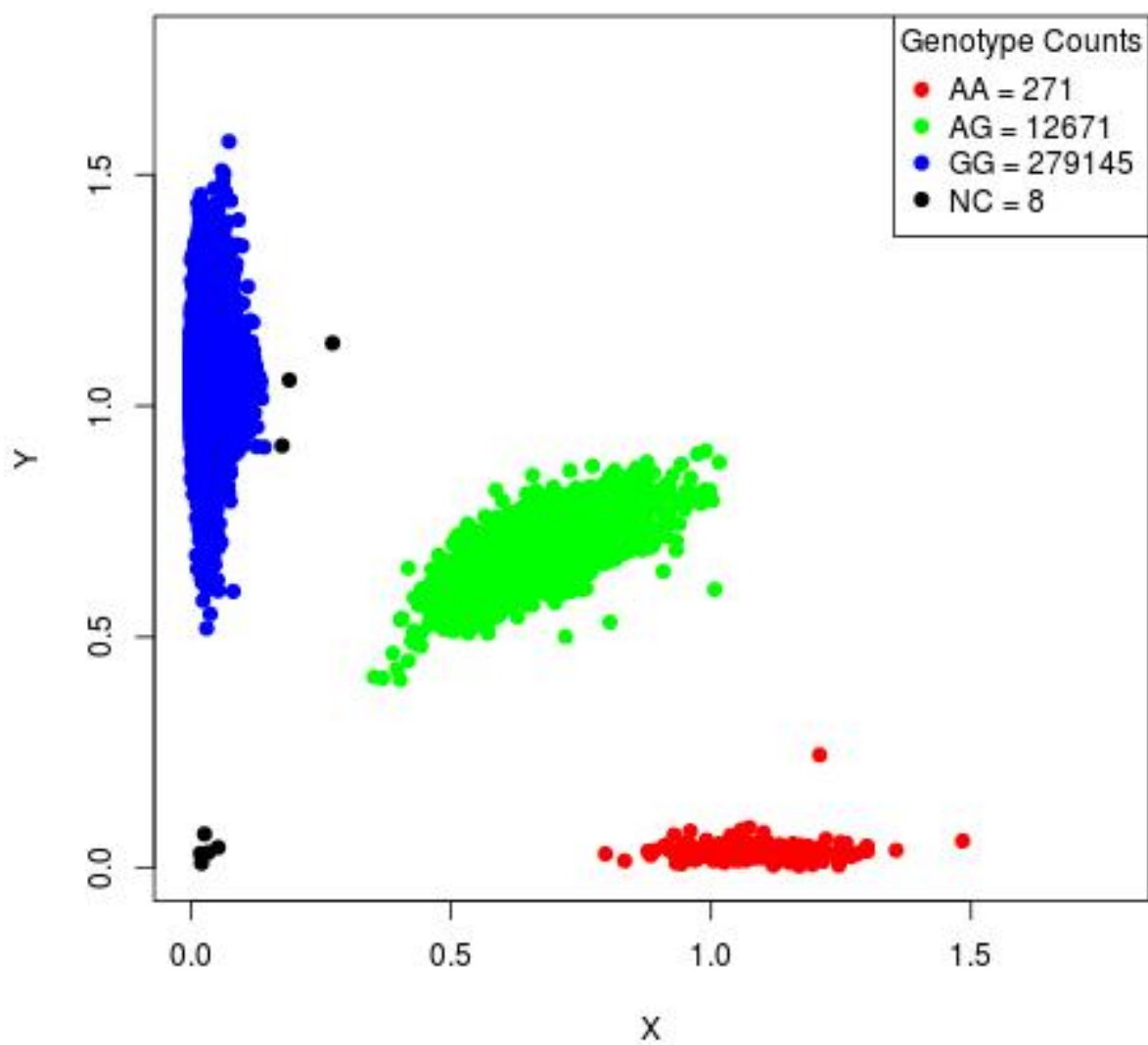
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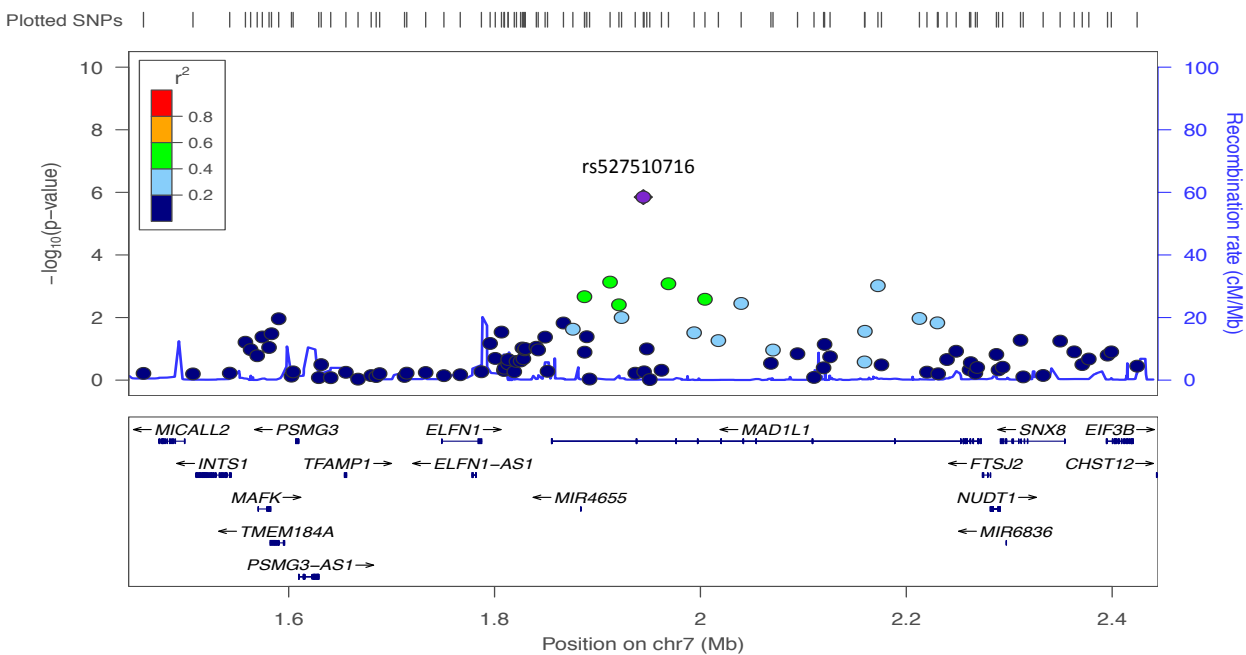


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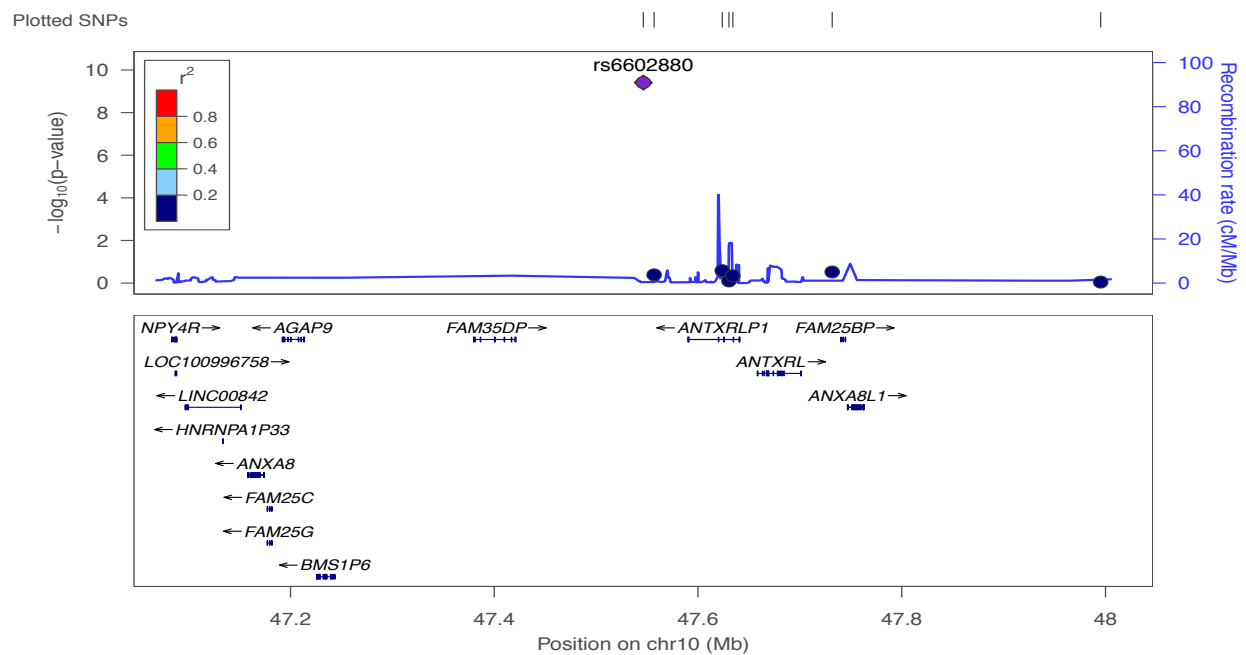
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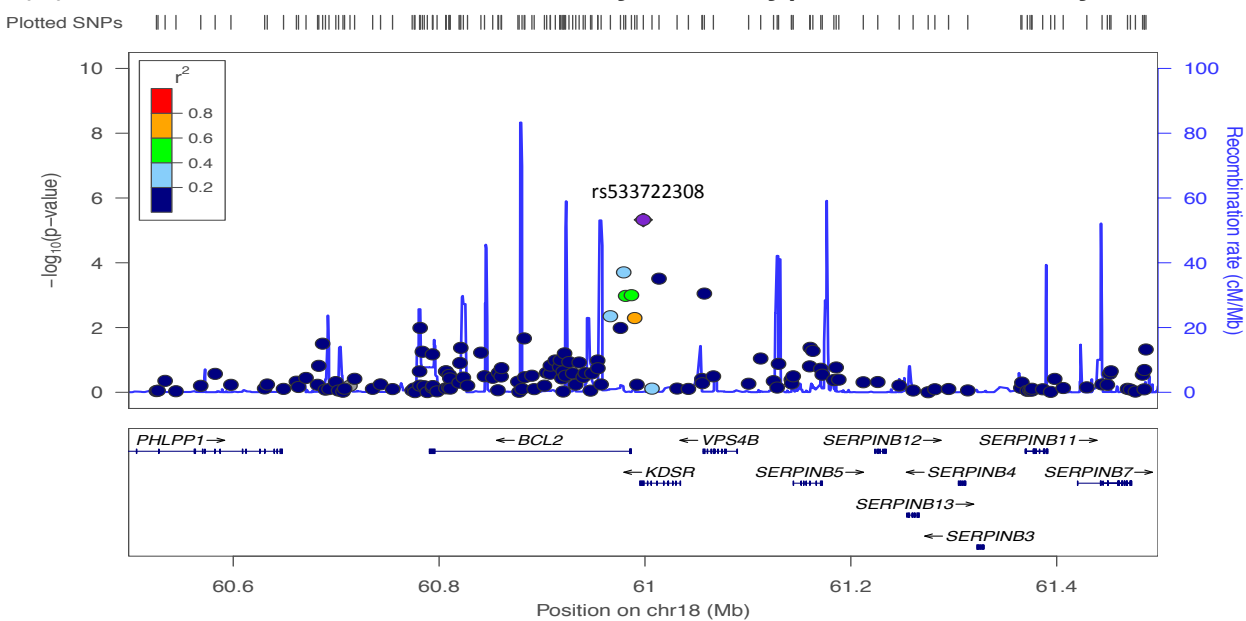
(a) rs527510716 – OncoArray Genotyped Meta-Analysis



(b) rs6602880 – OncoArray Genotyped Meta-Analysis

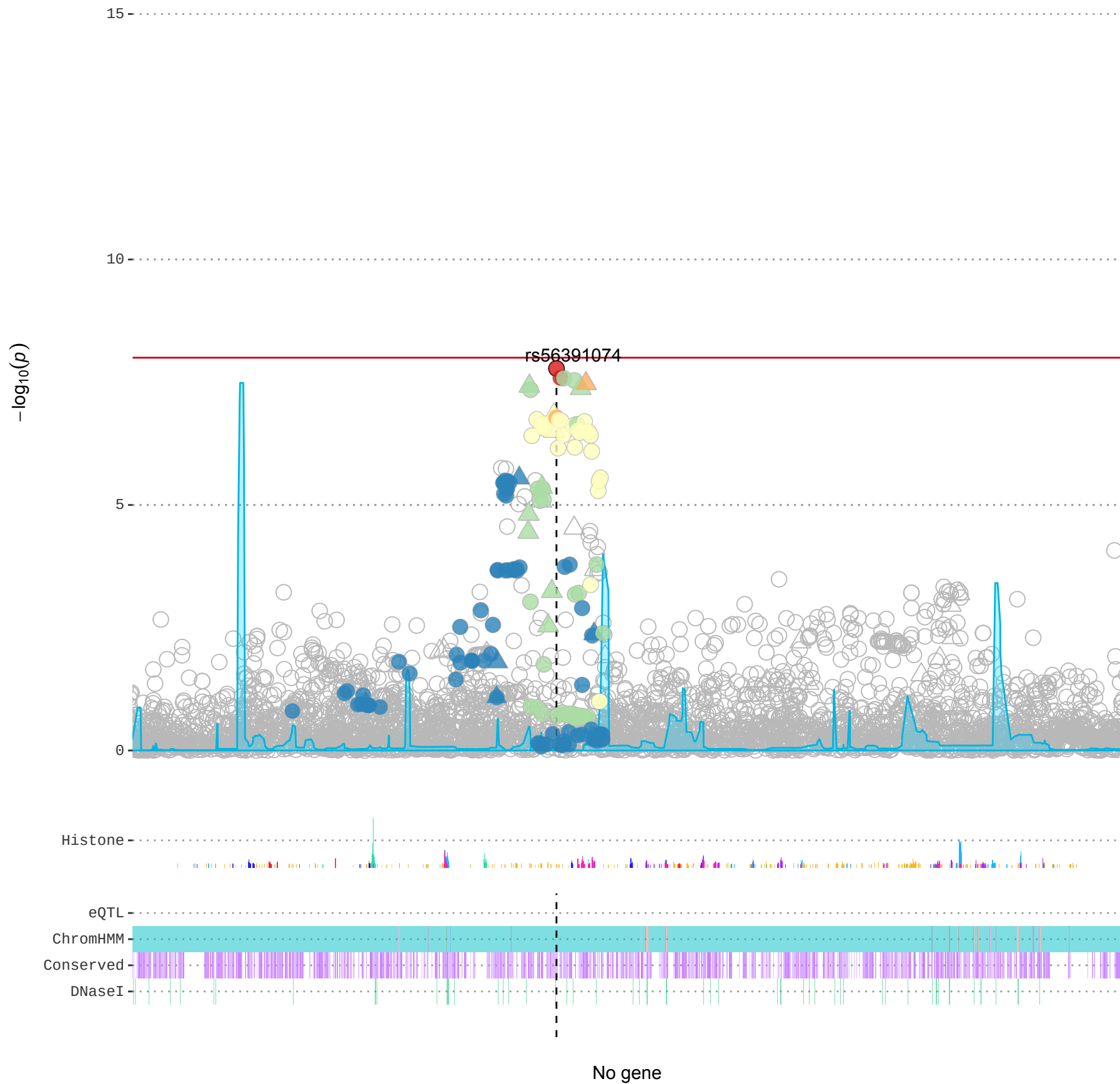


(c) rs533722308 – OncoArray Genotyped Meta-Analysis



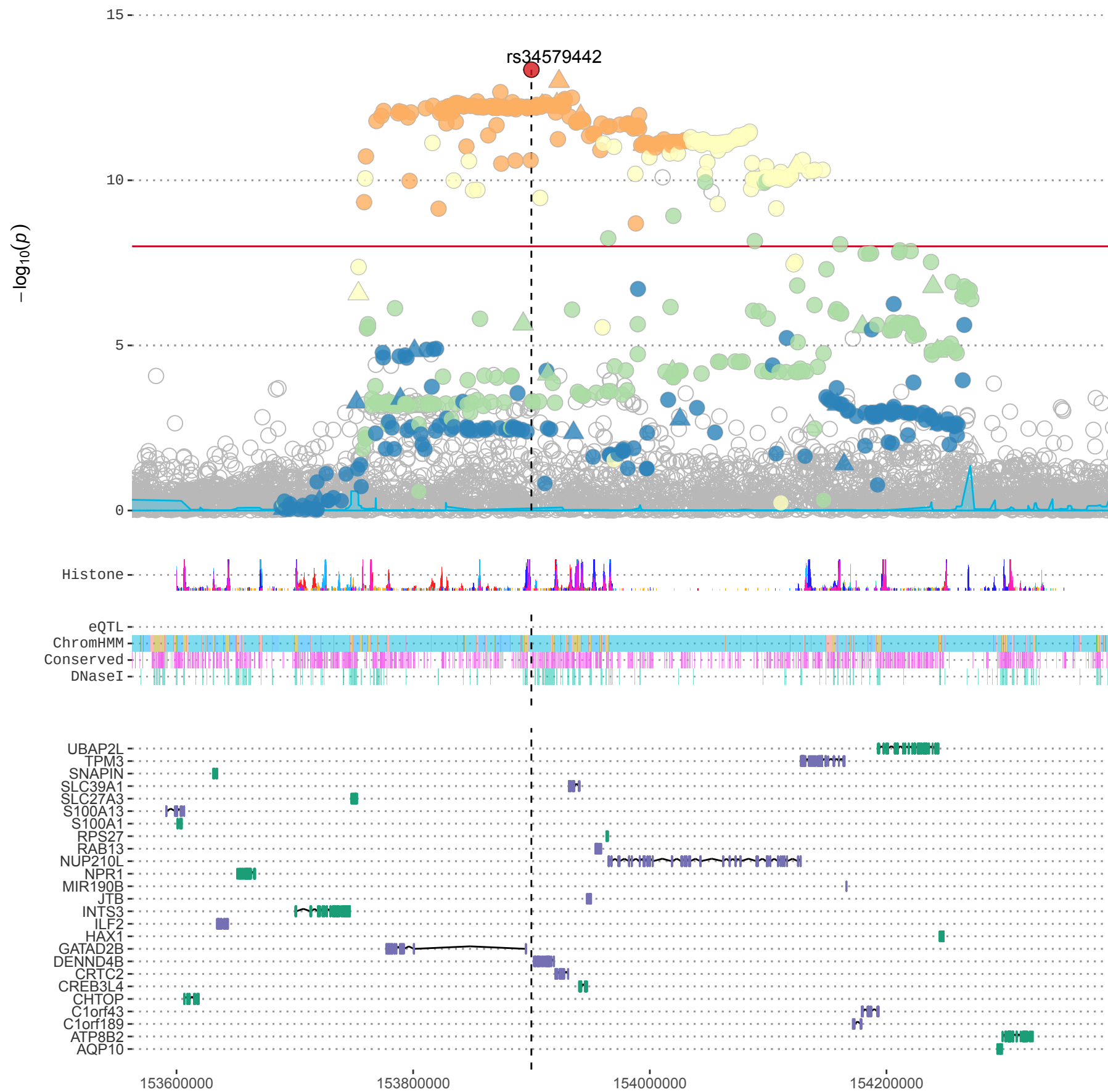
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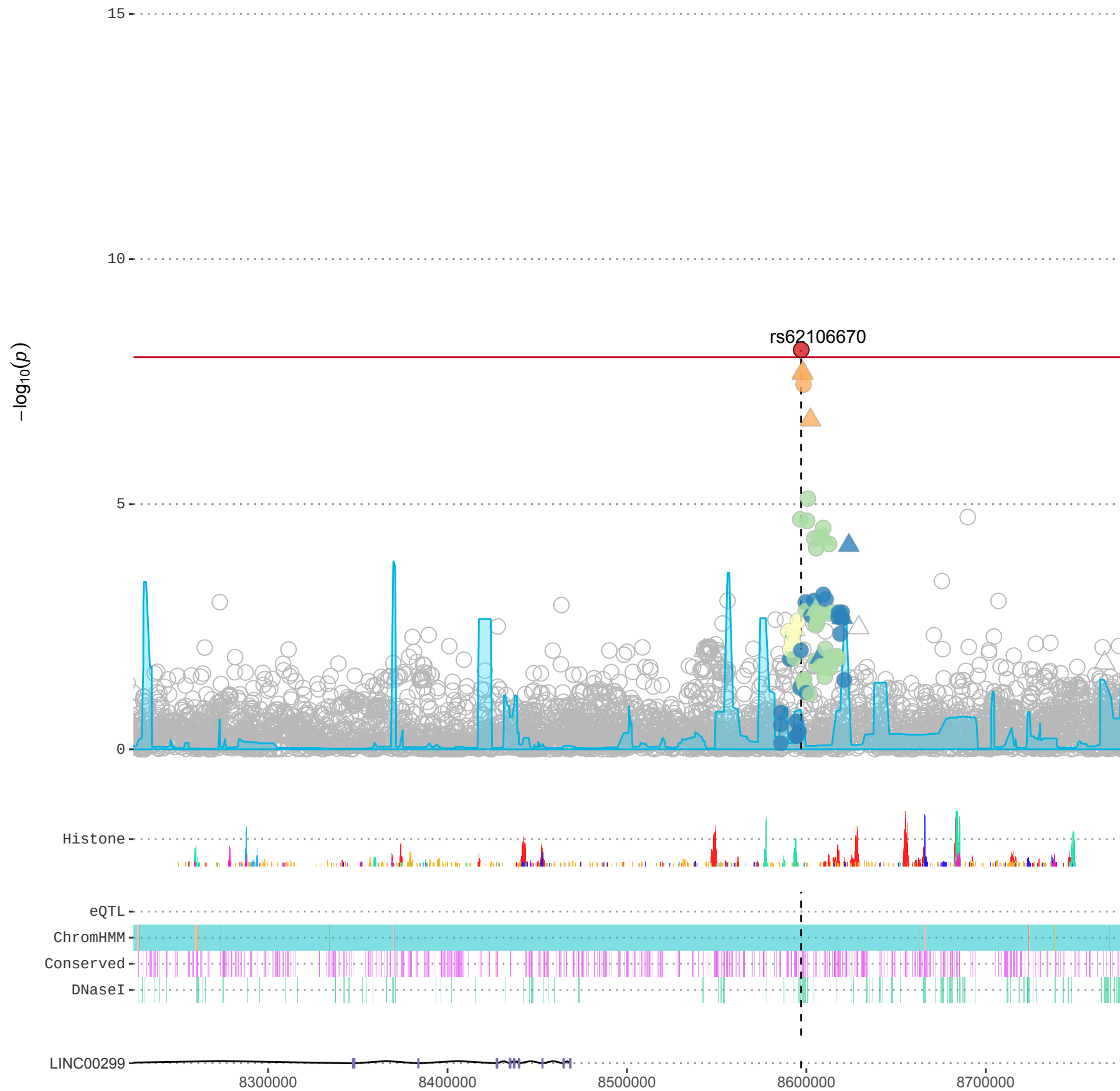


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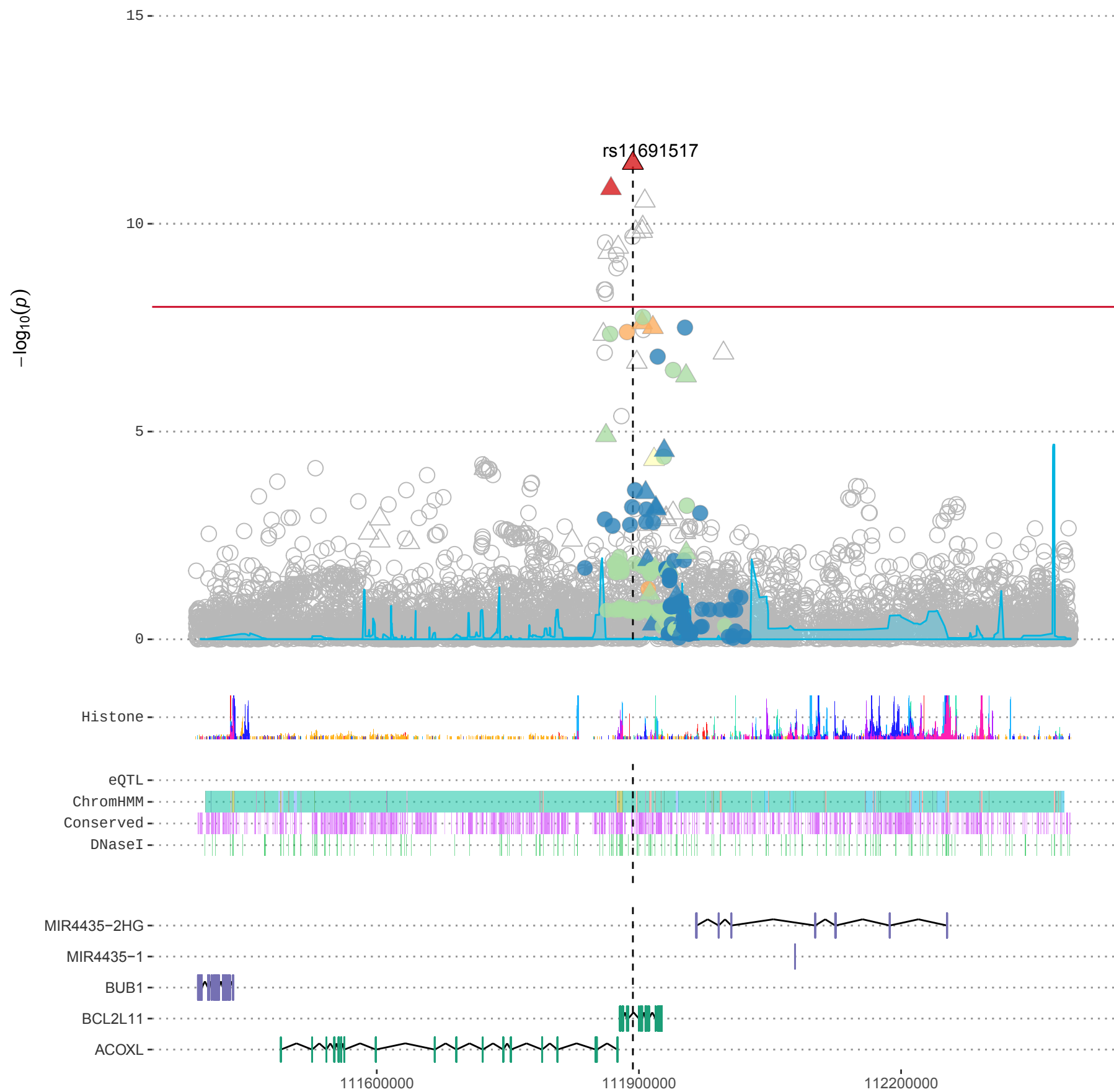
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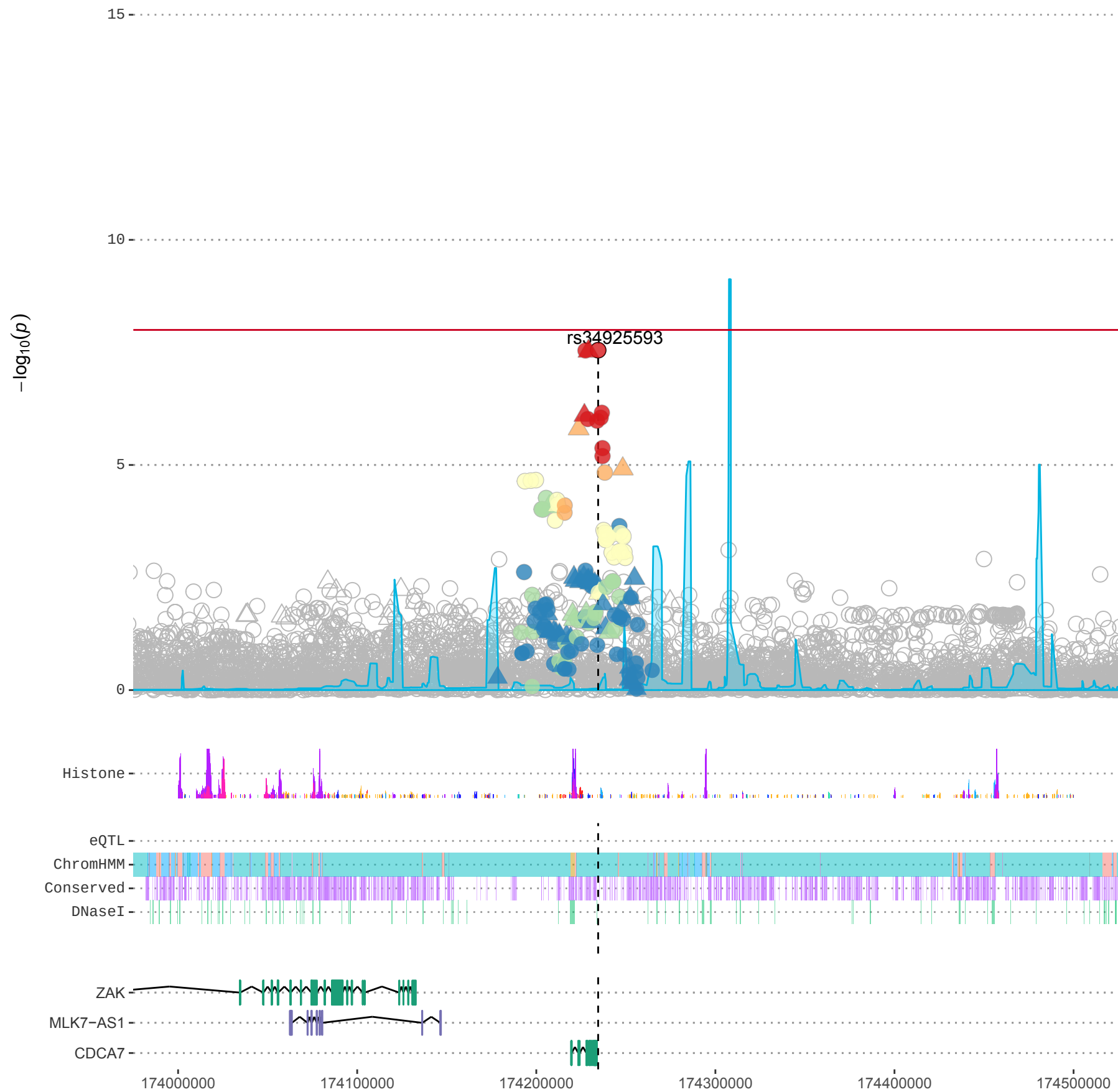
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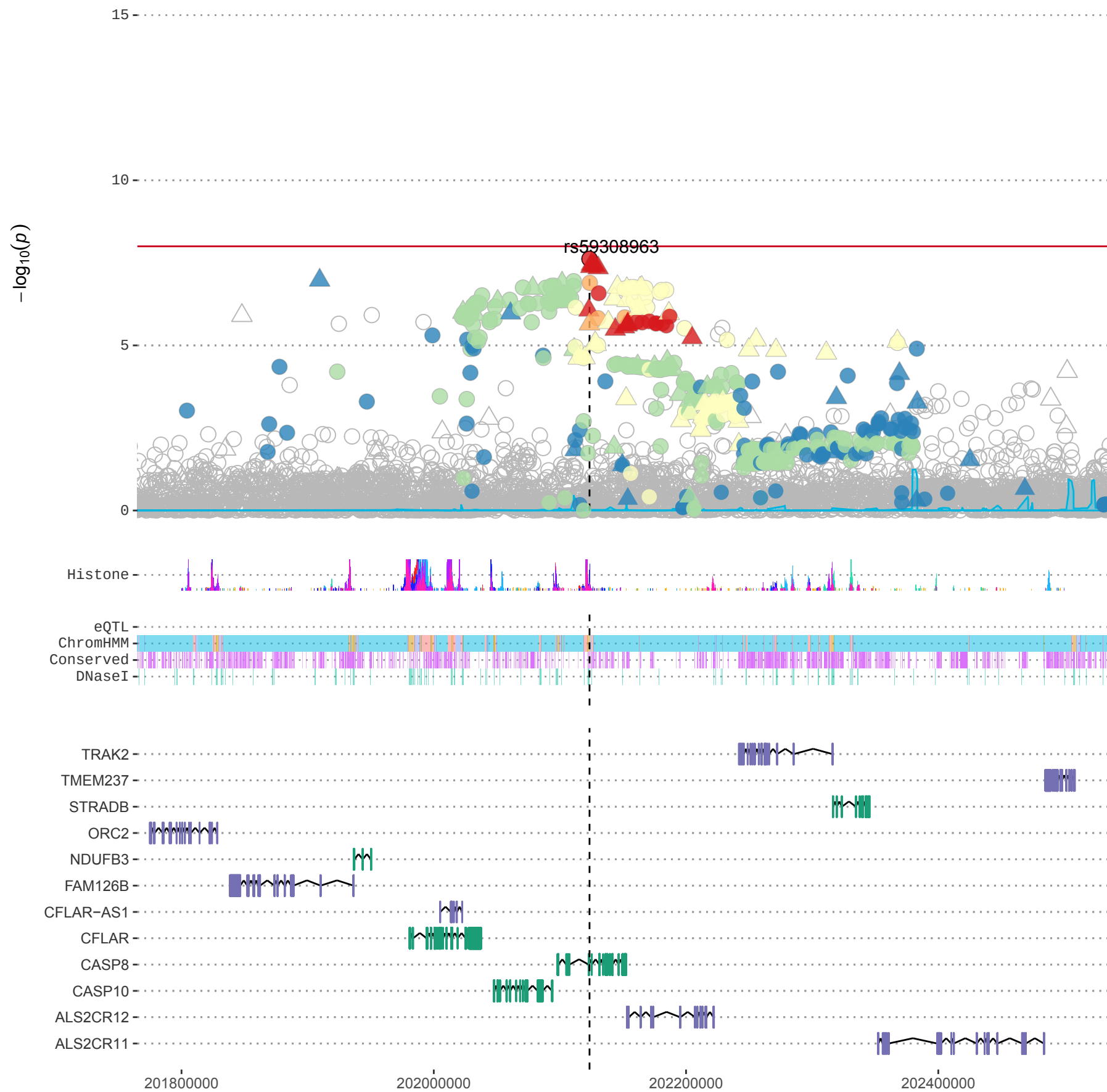
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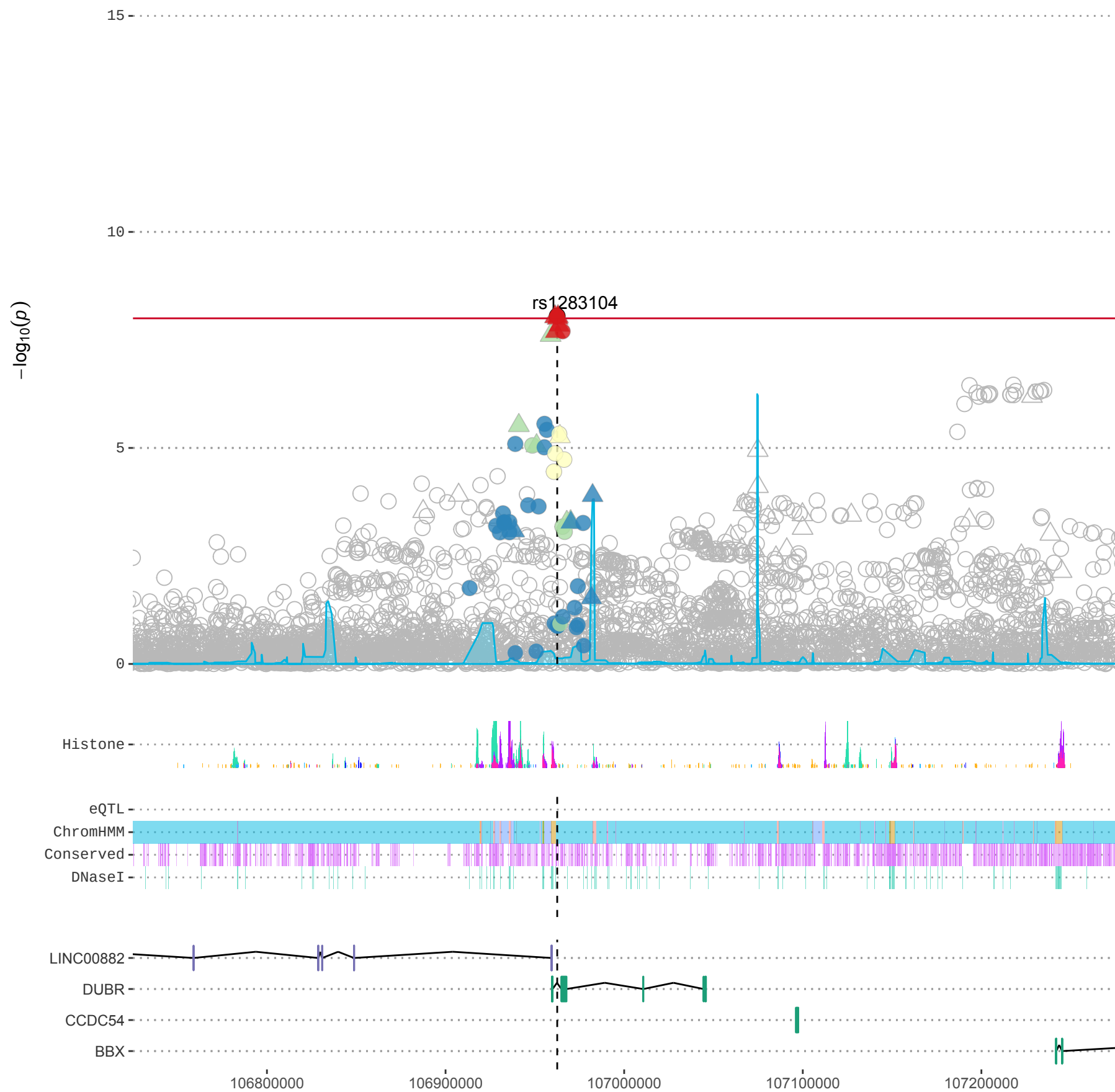
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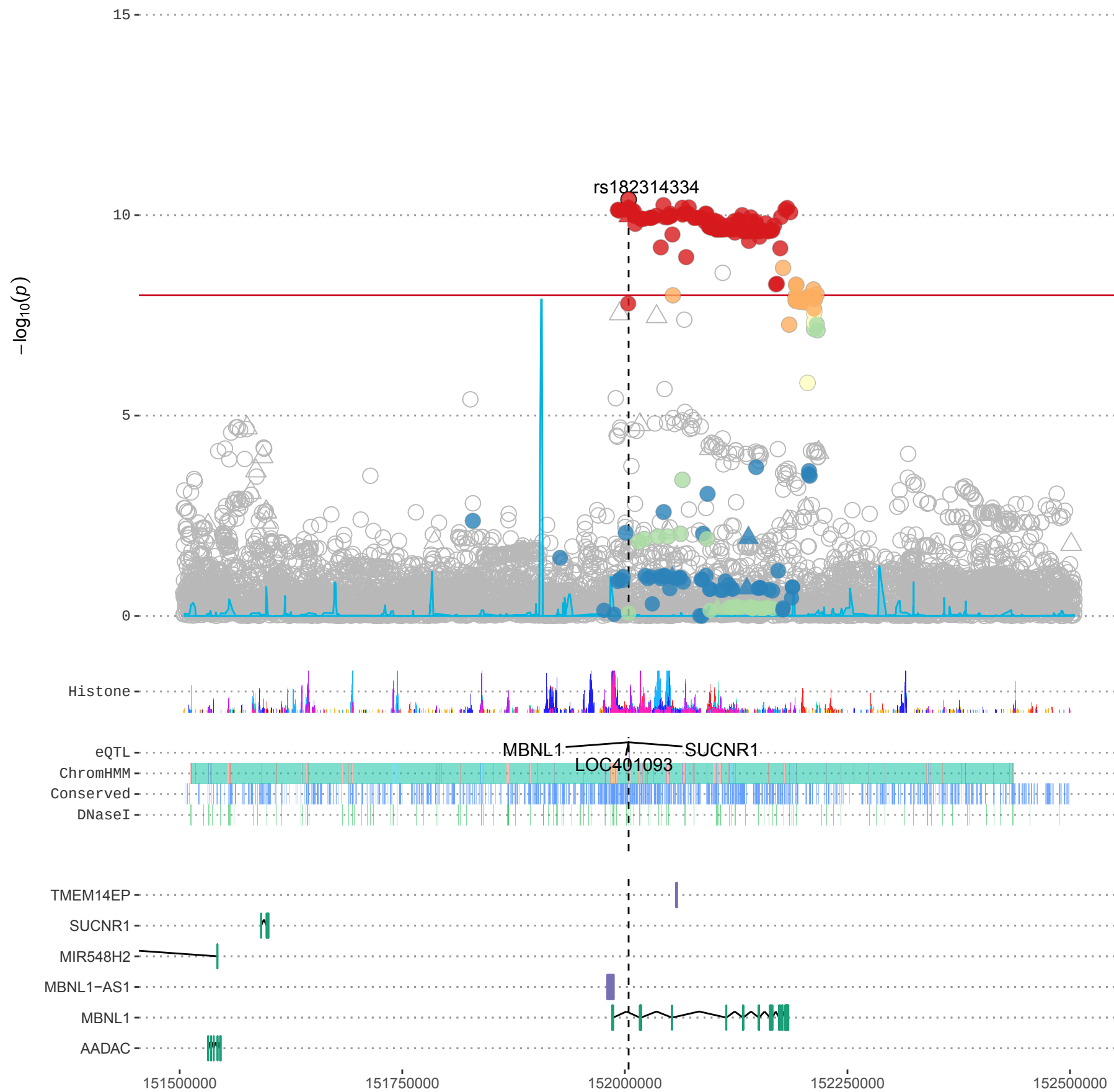
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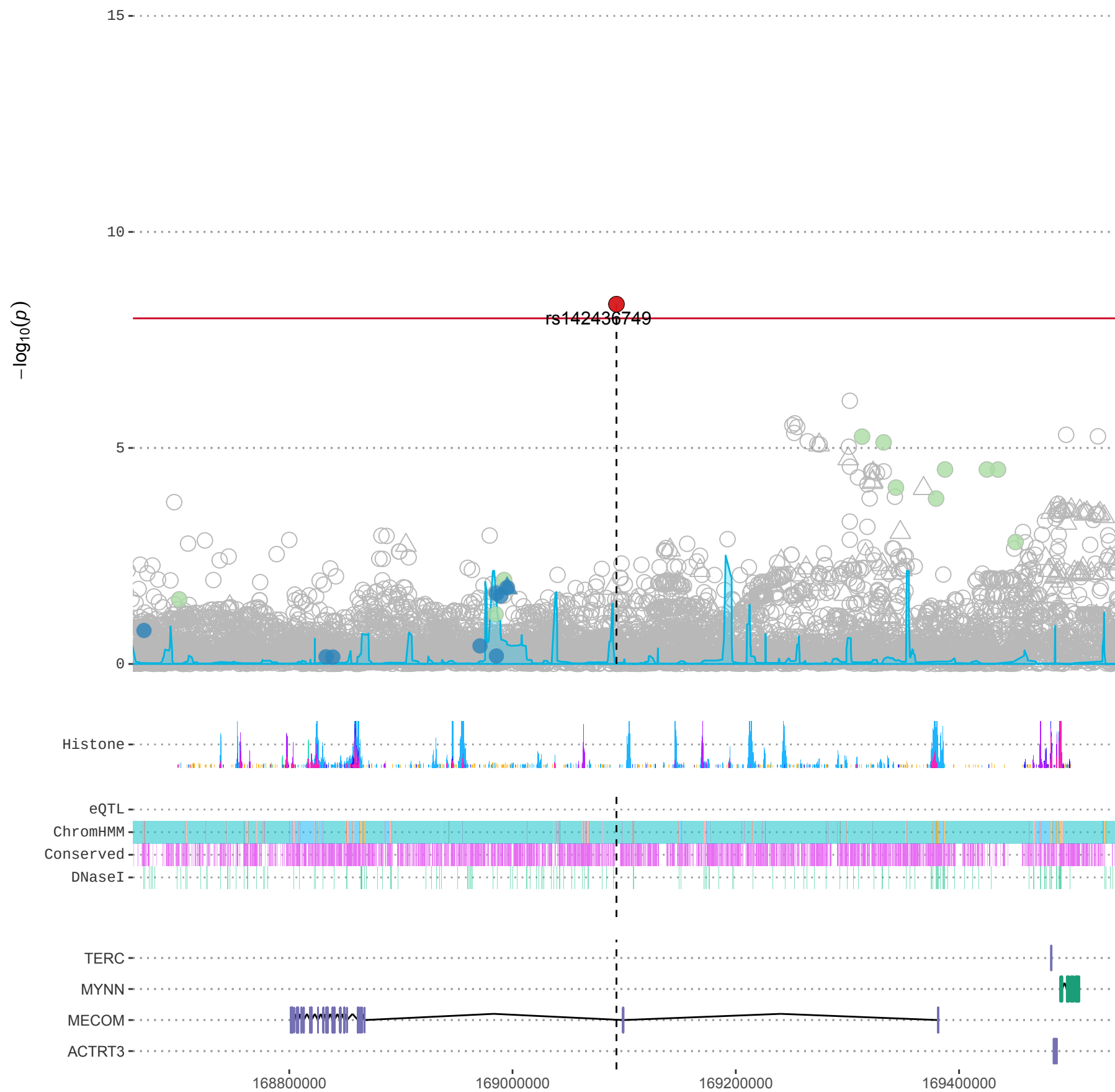
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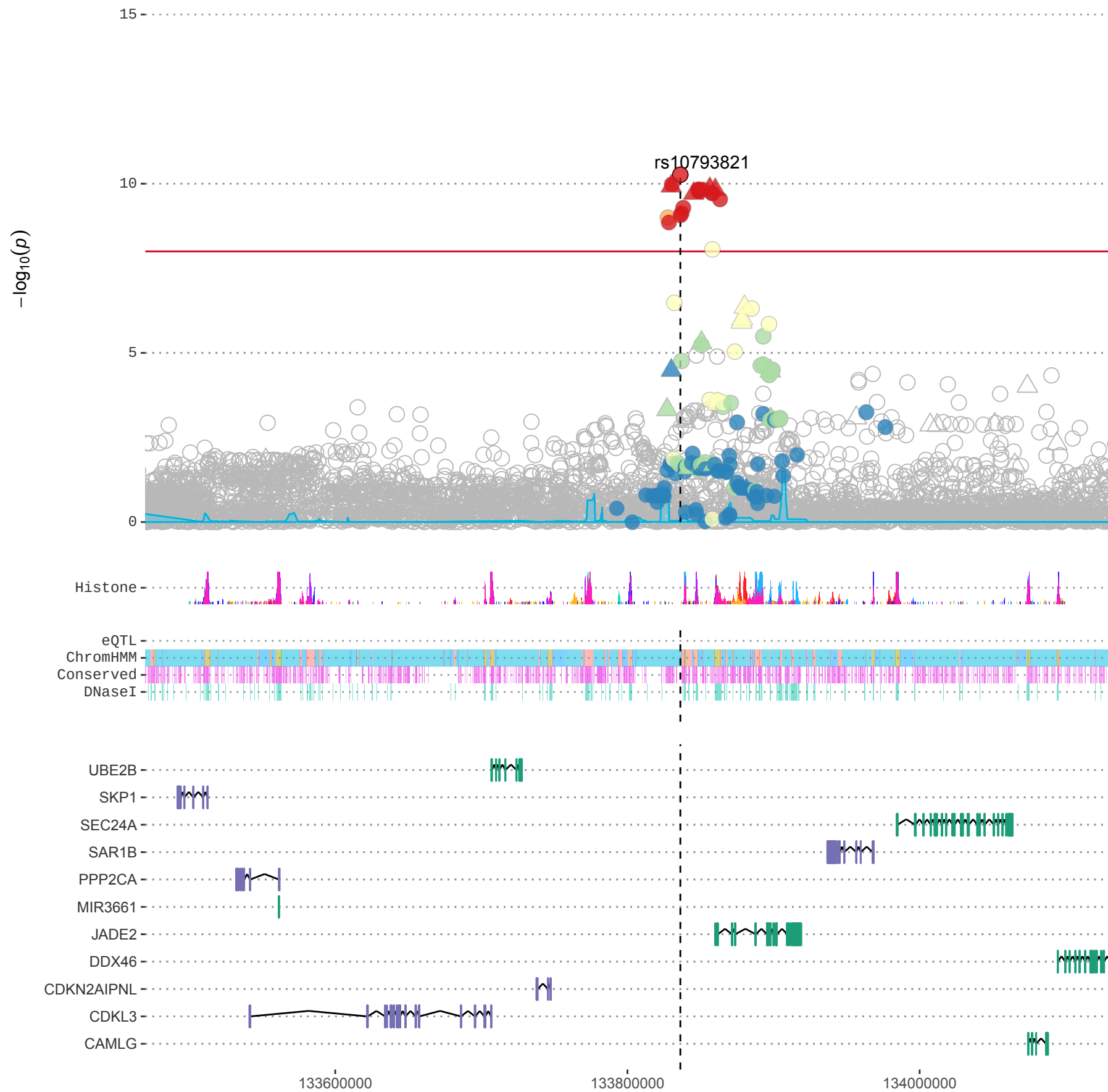
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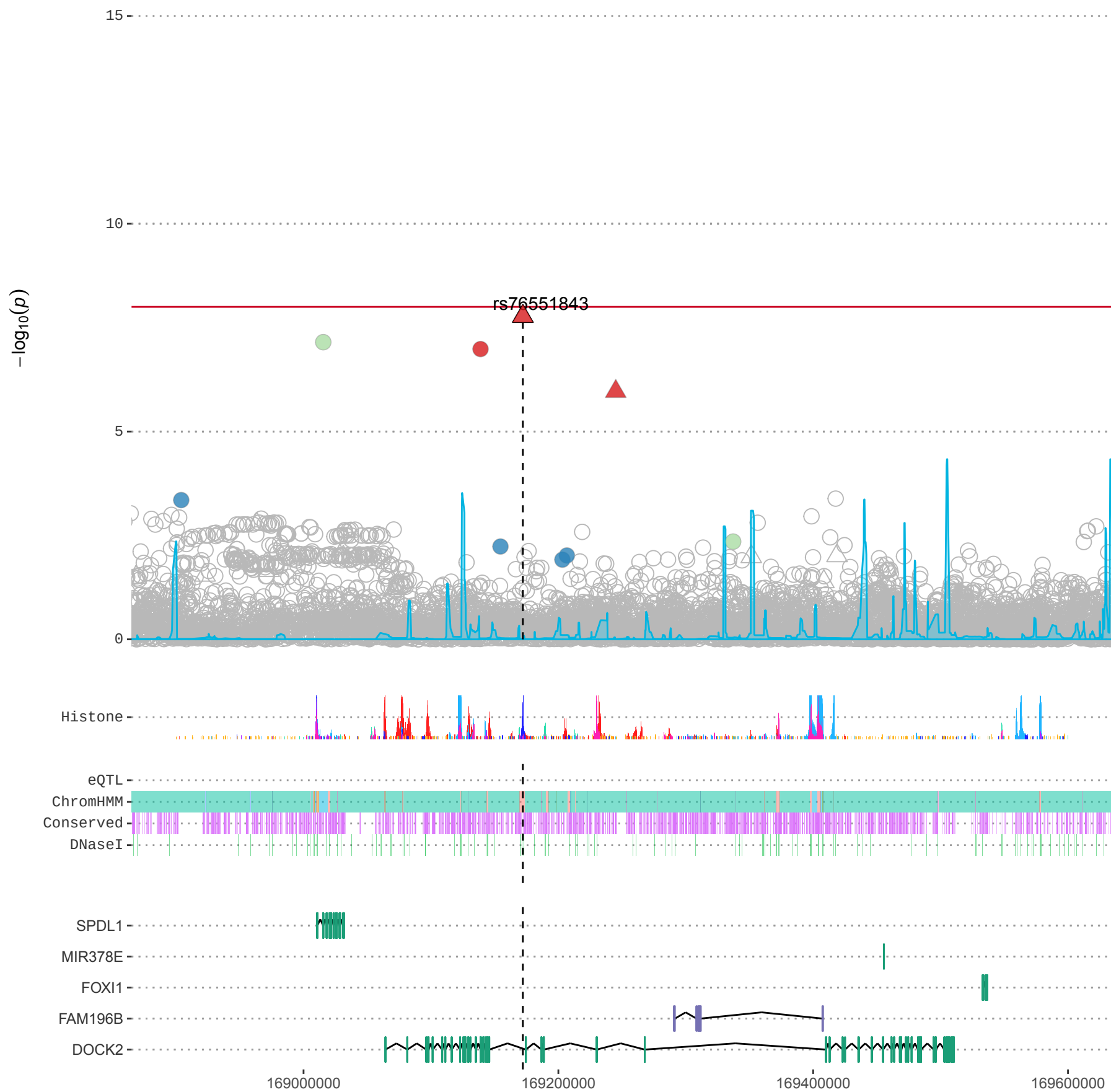


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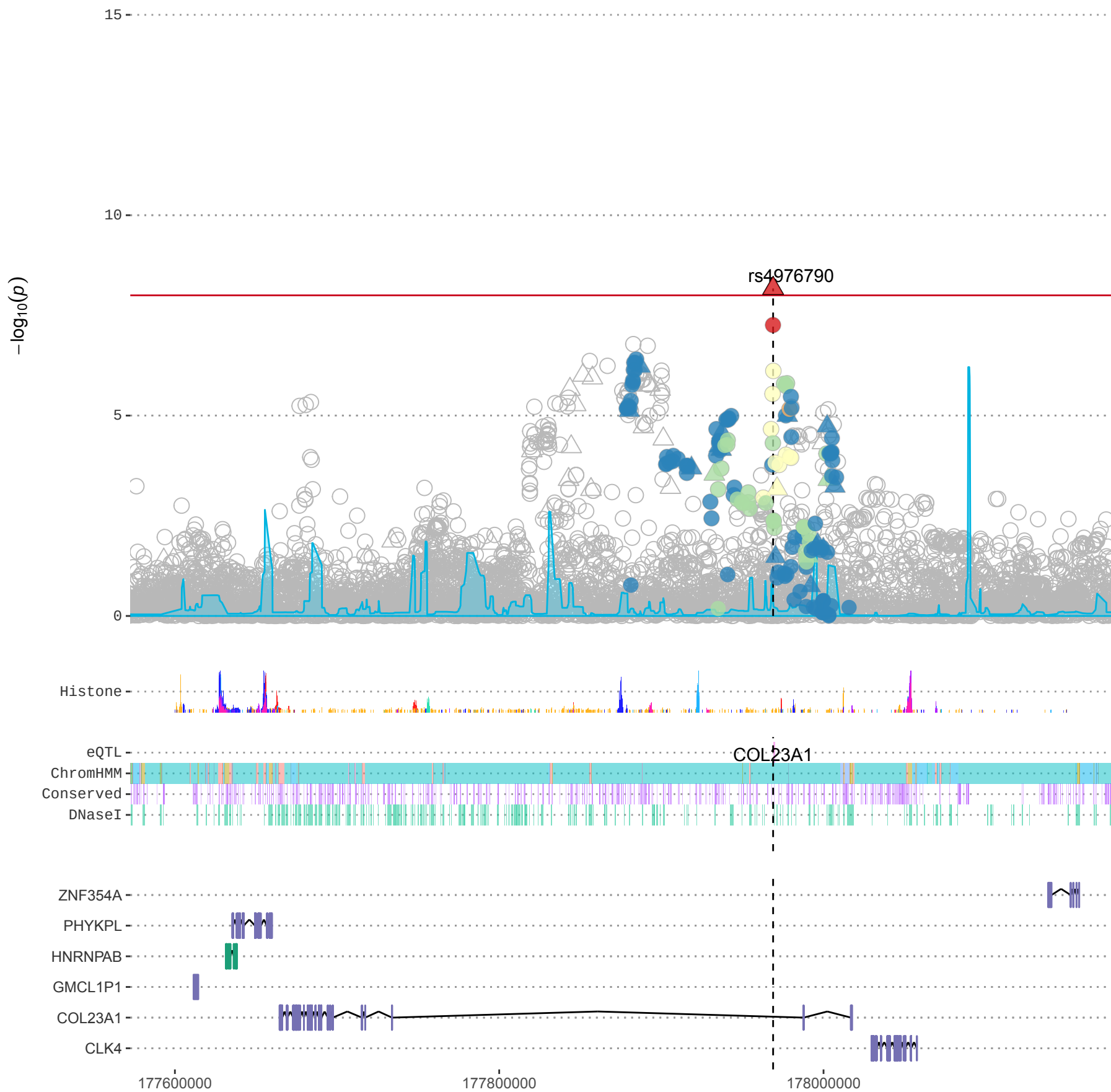


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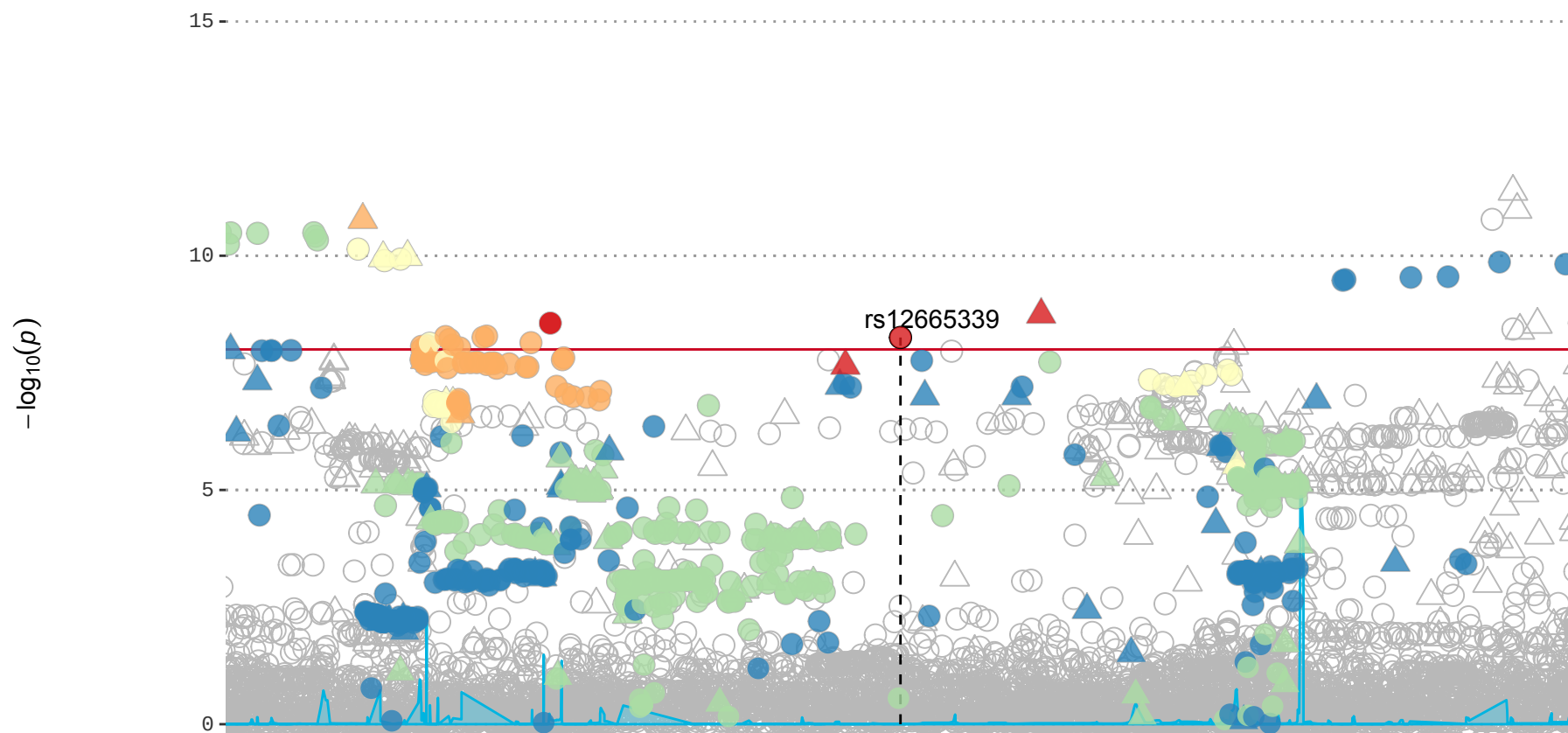
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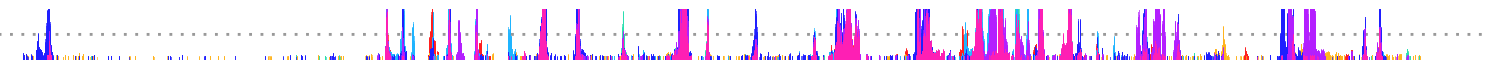


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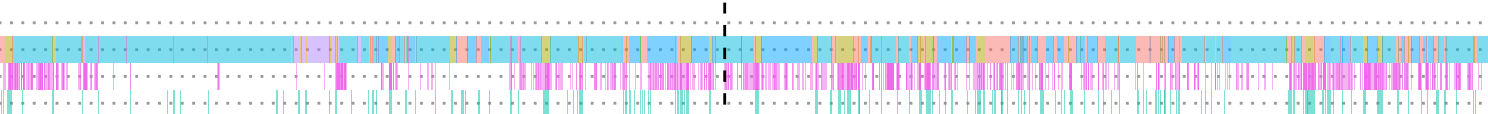


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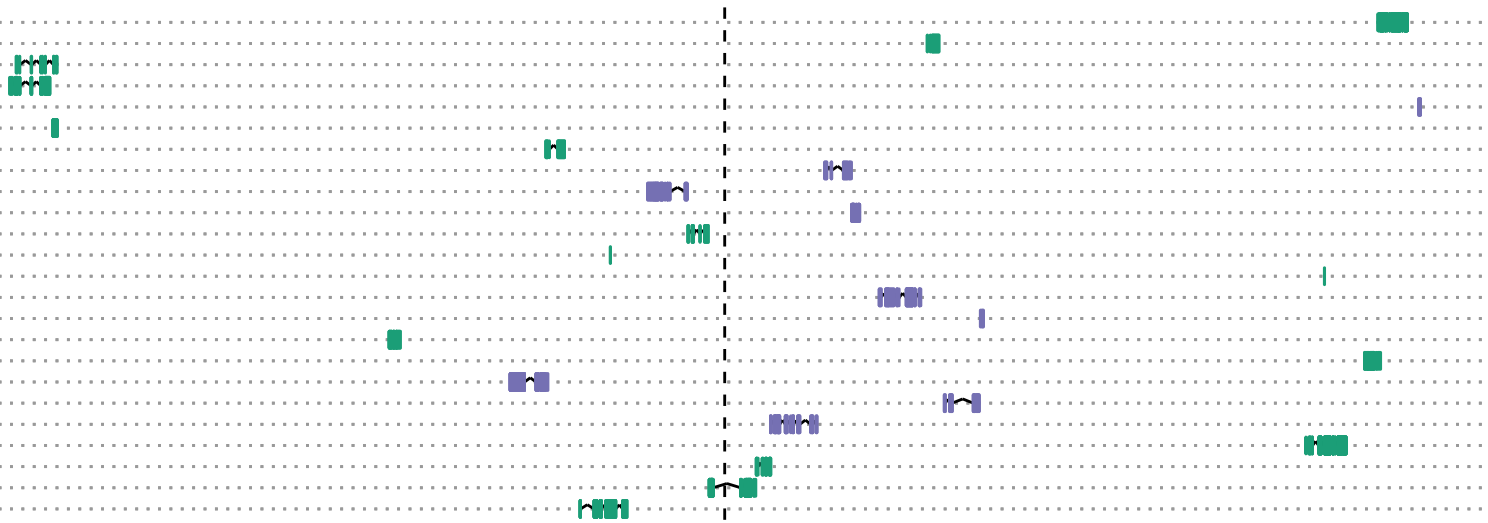
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Conserved

DNaseI



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NRM
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MIR877
MIR4640
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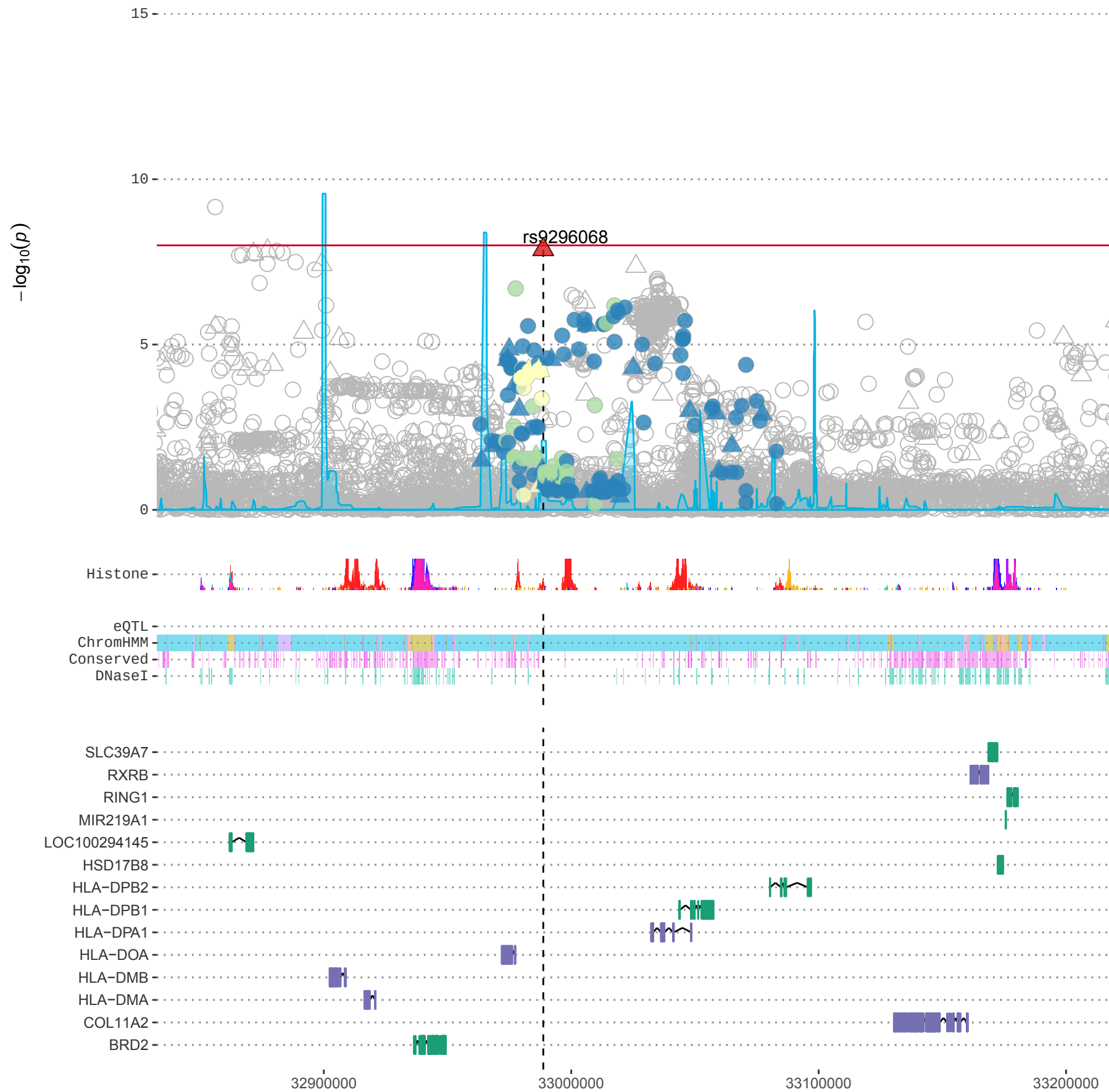
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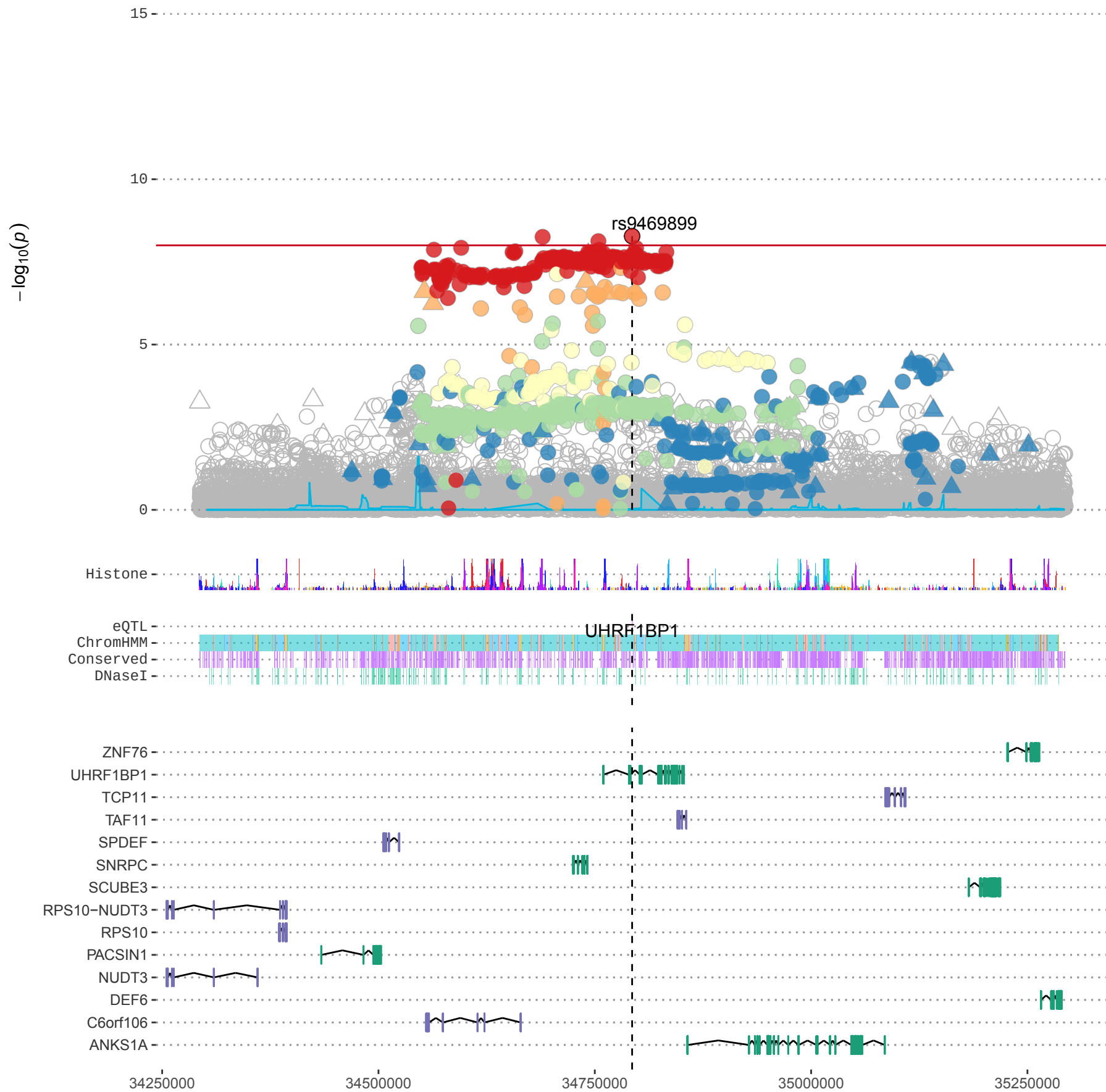
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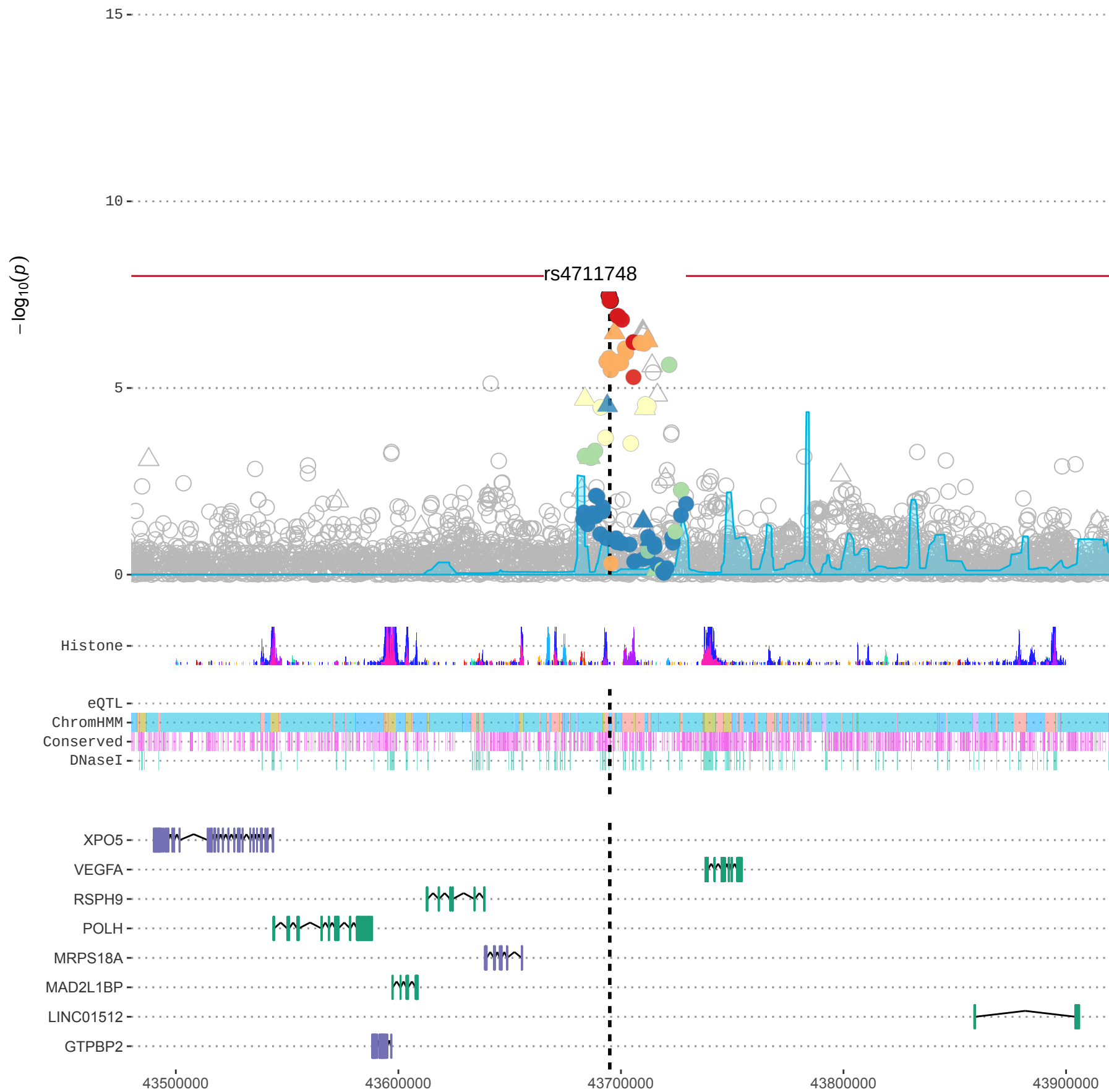
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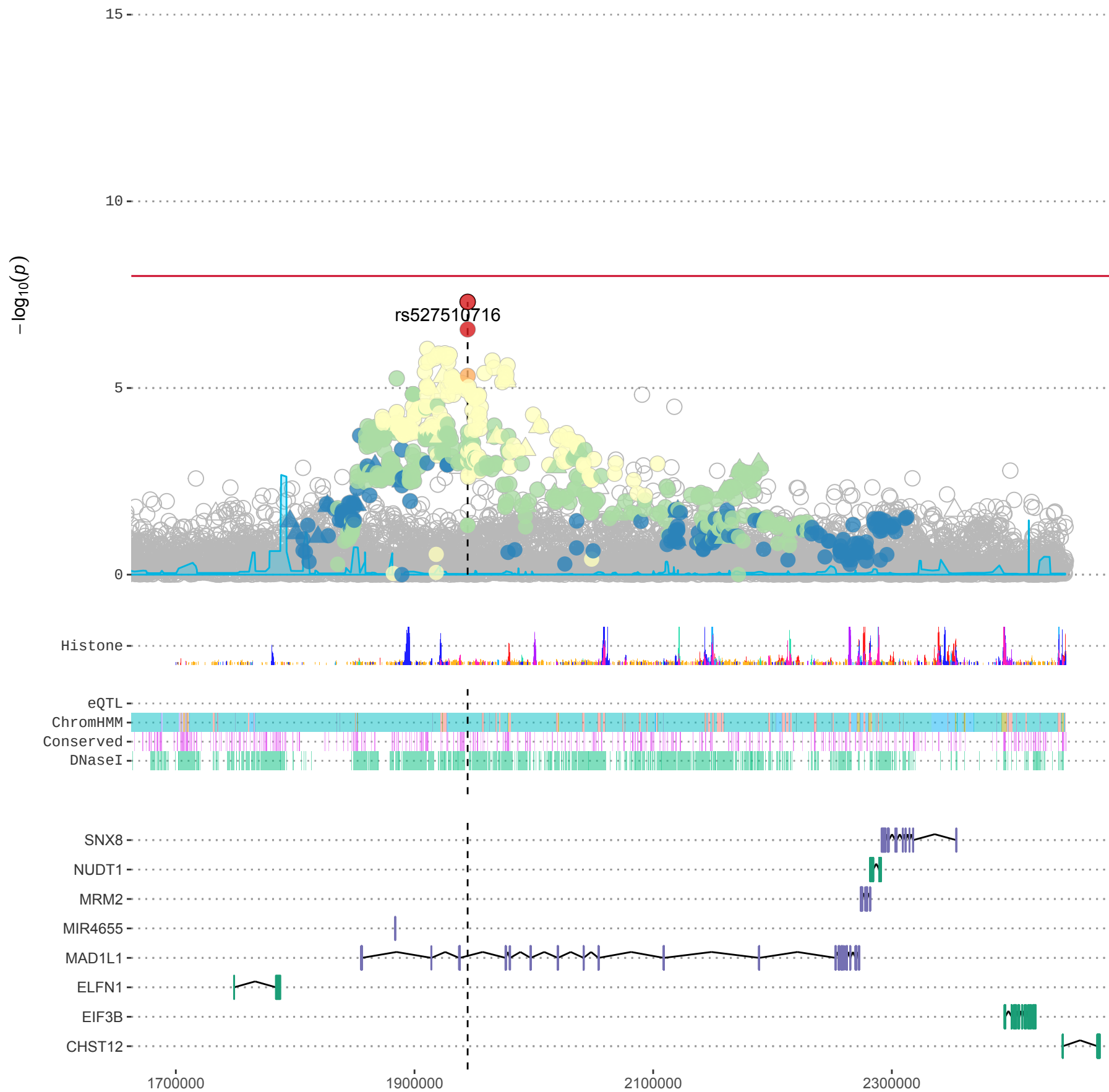
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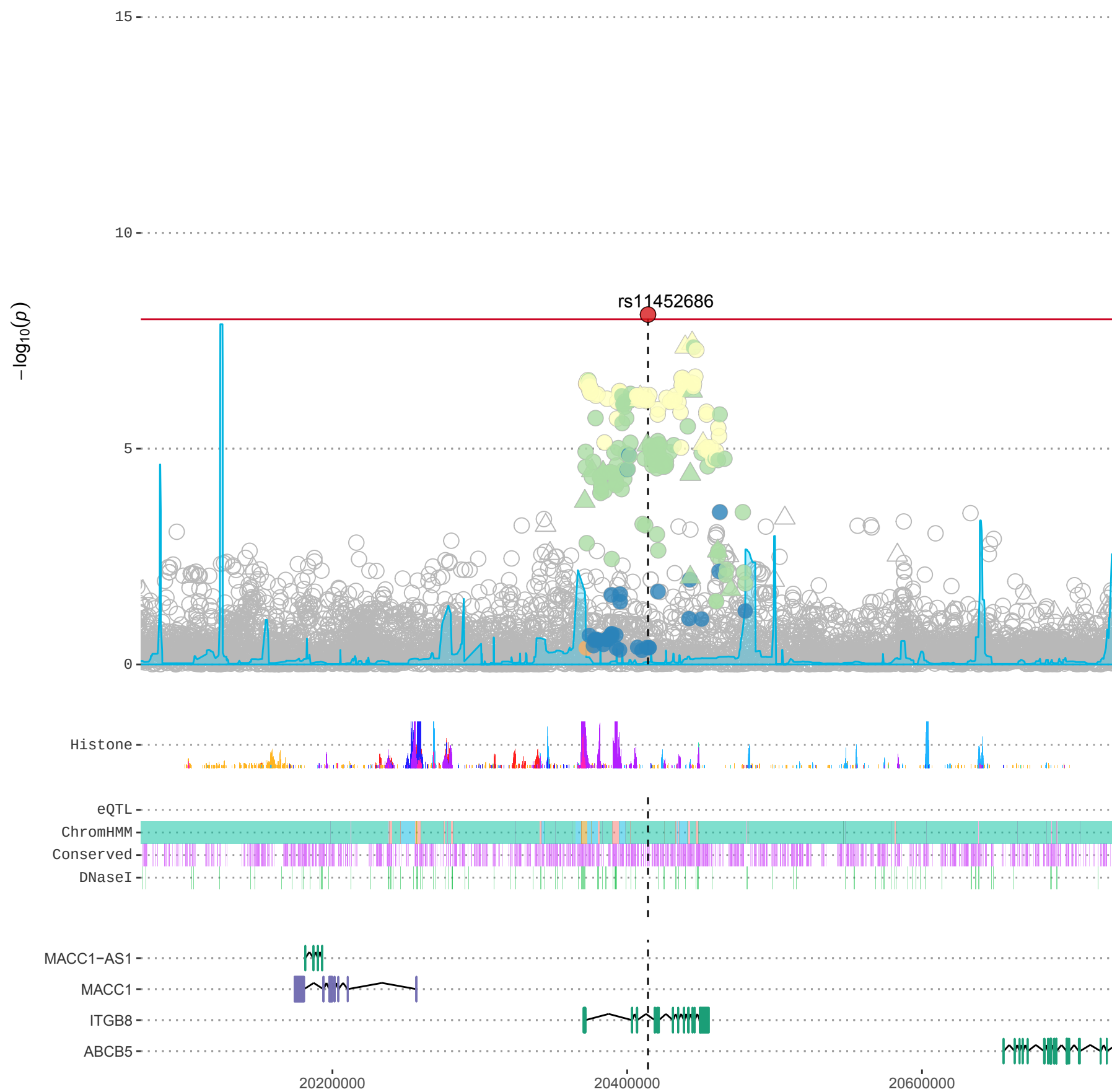
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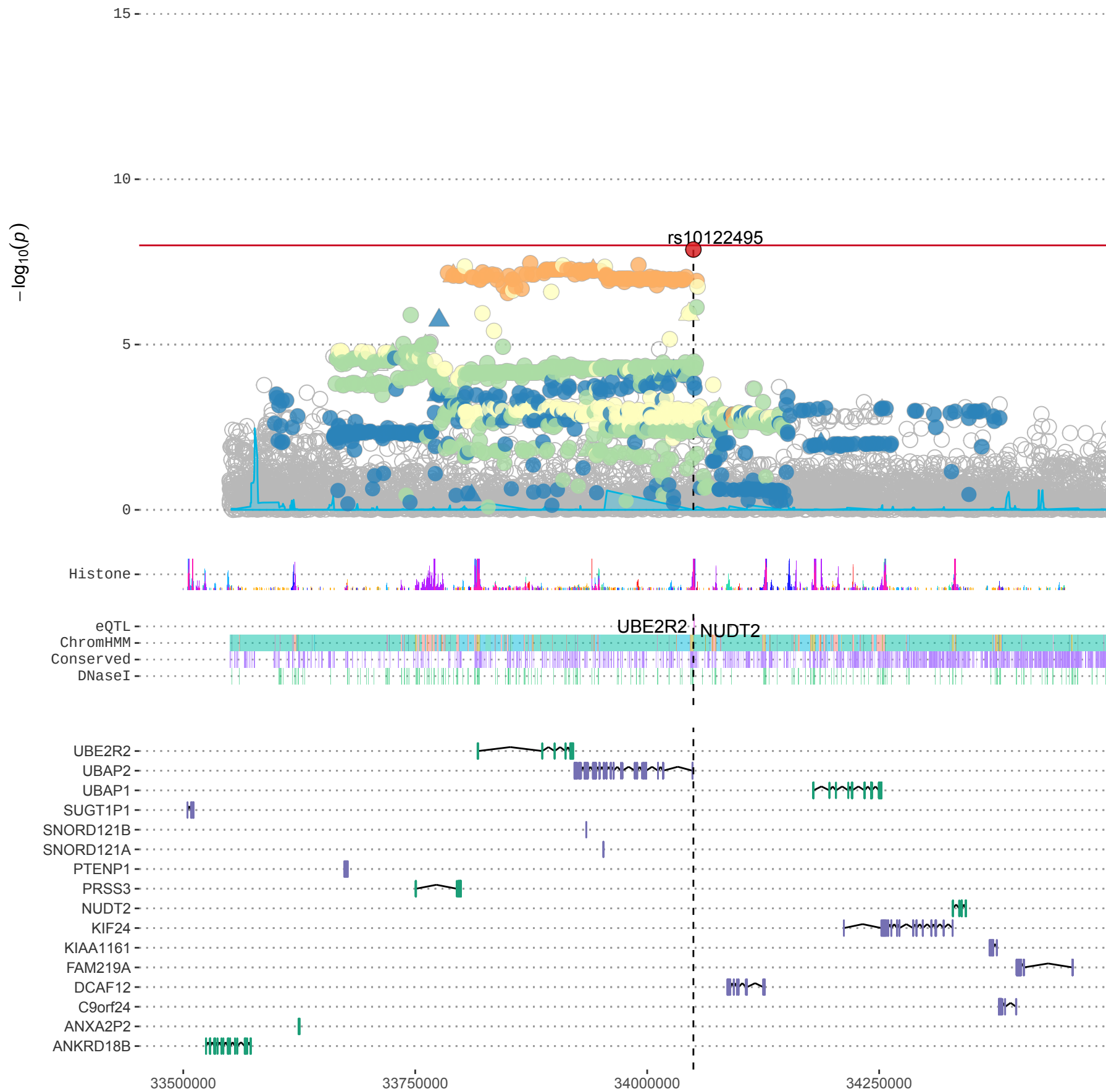
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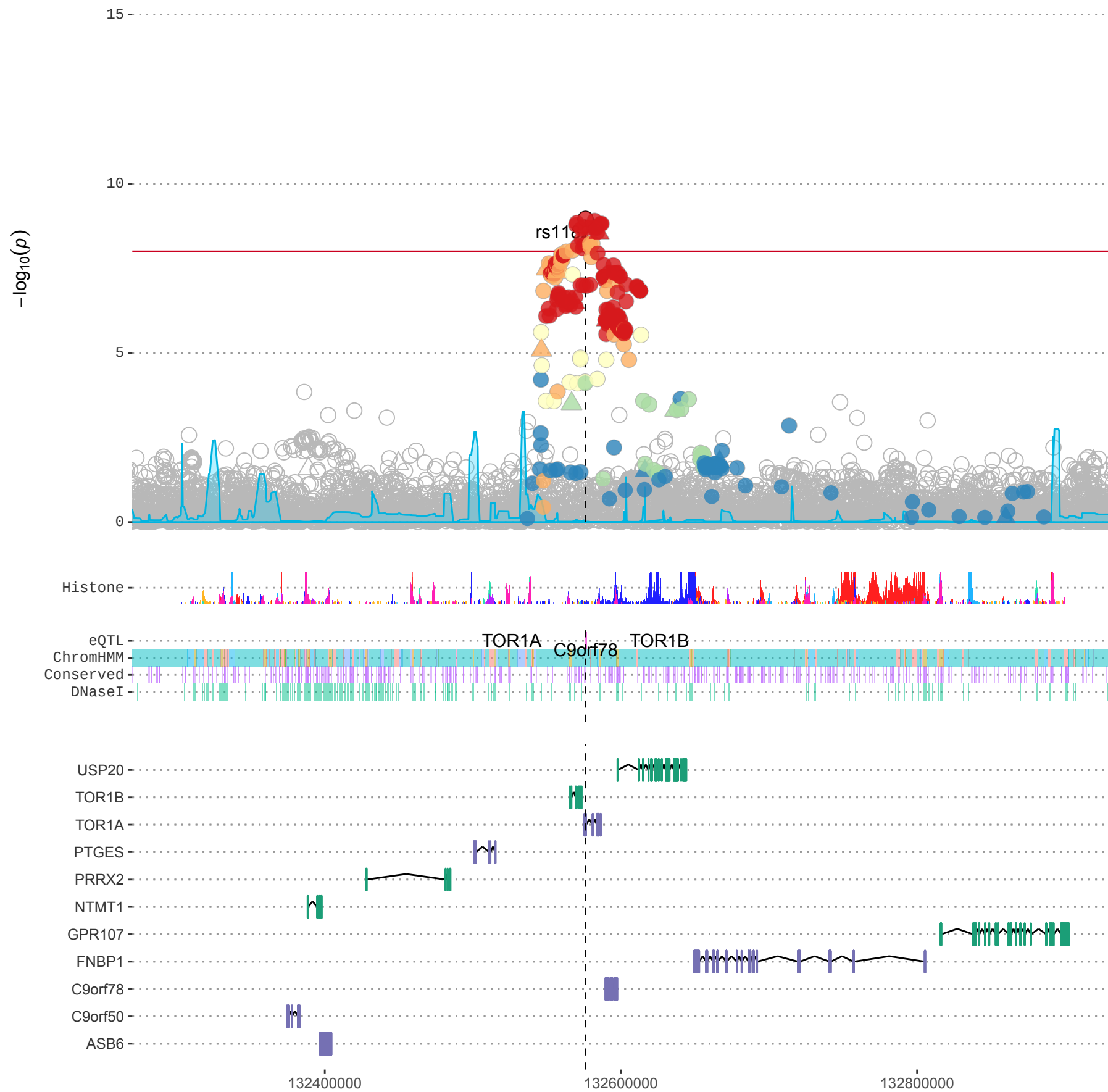
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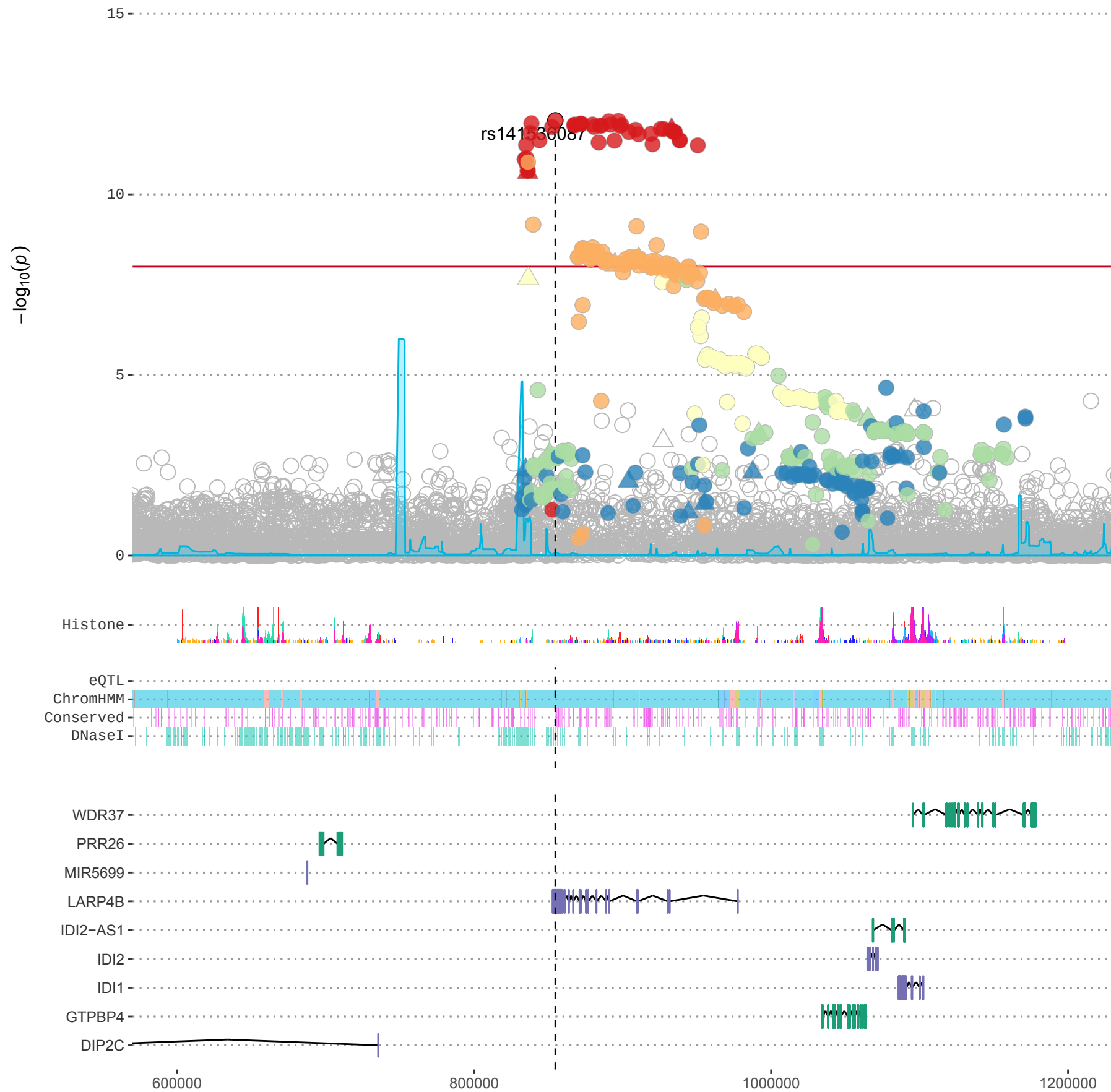
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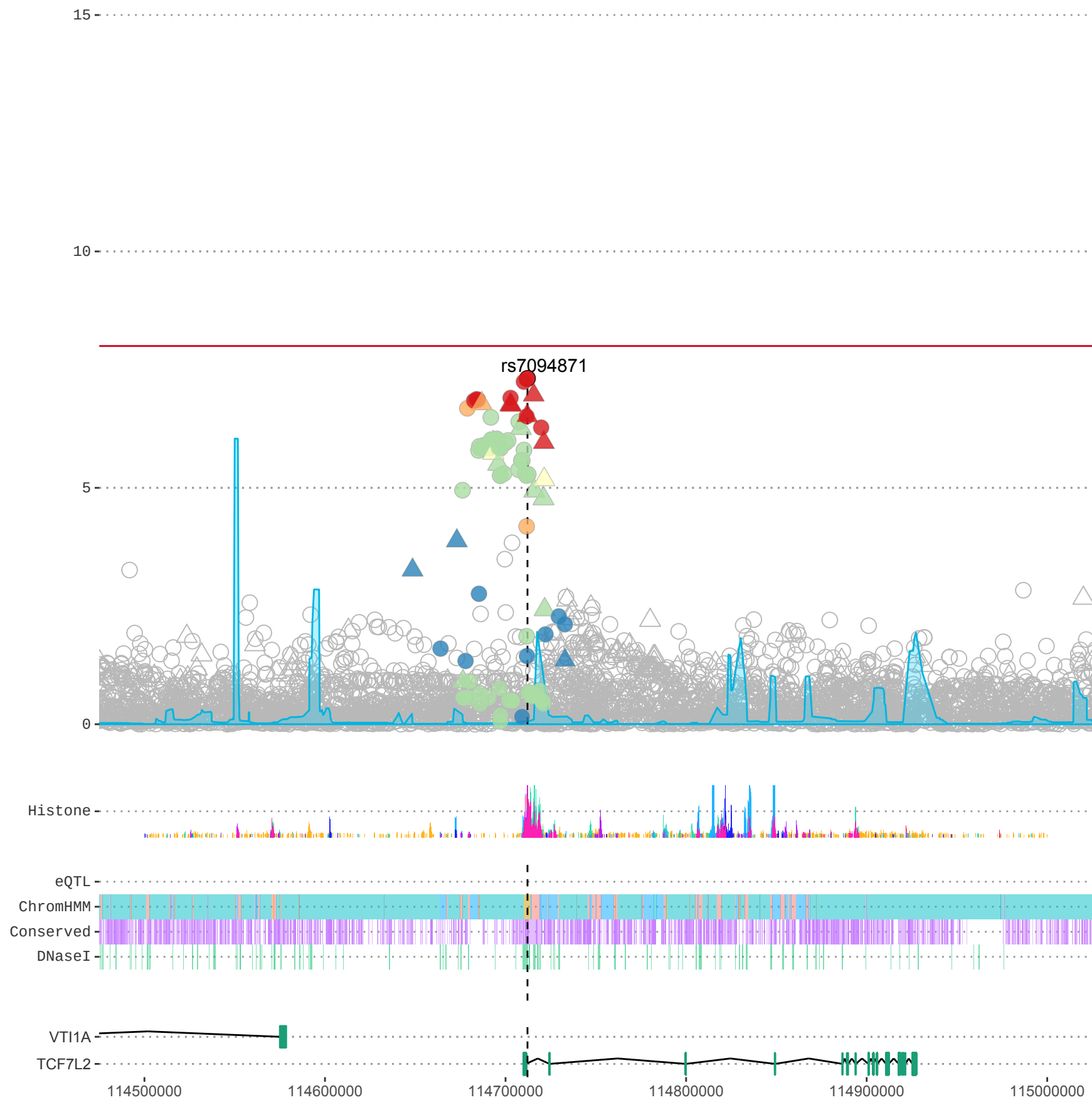
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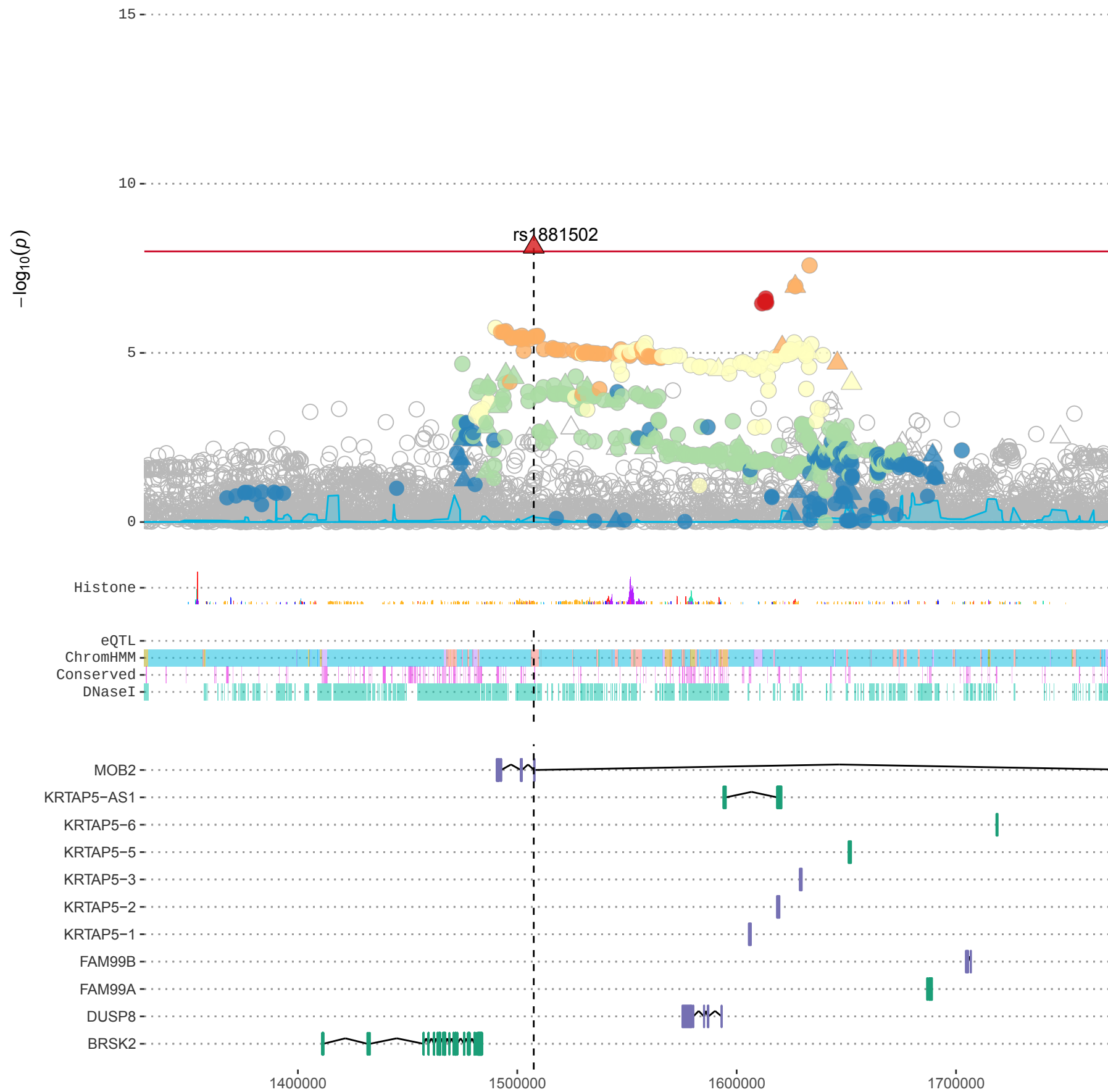
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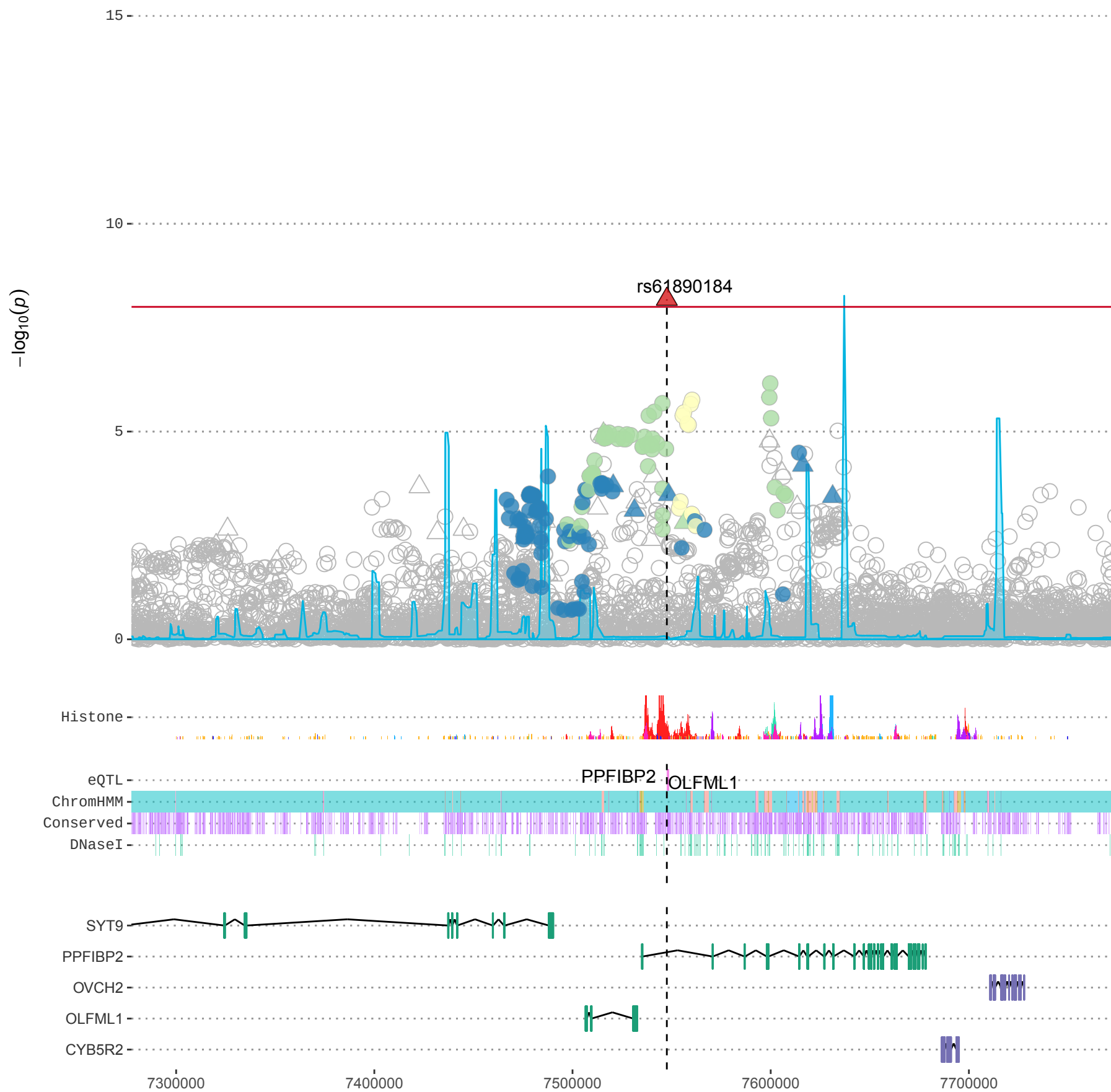
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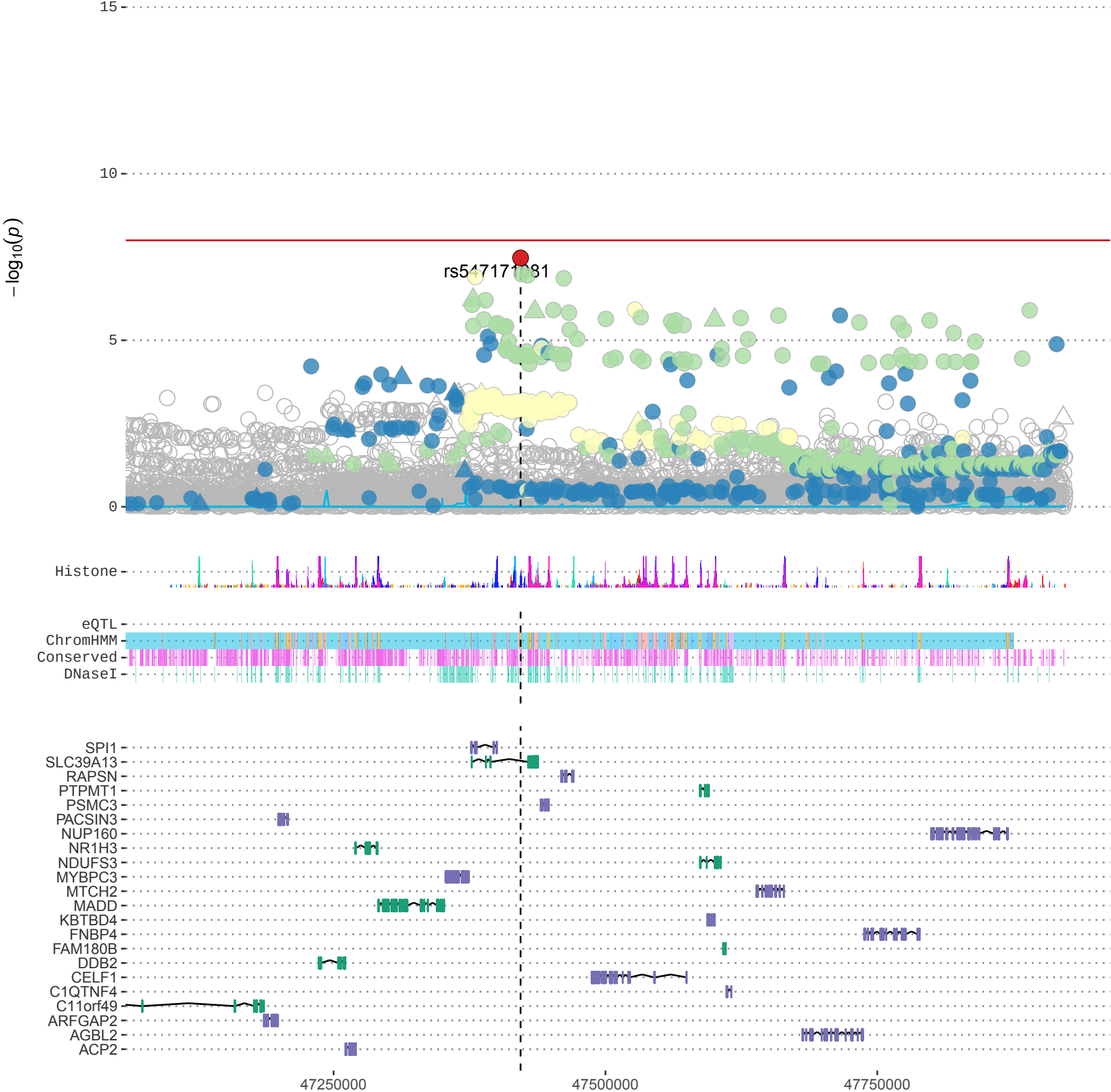
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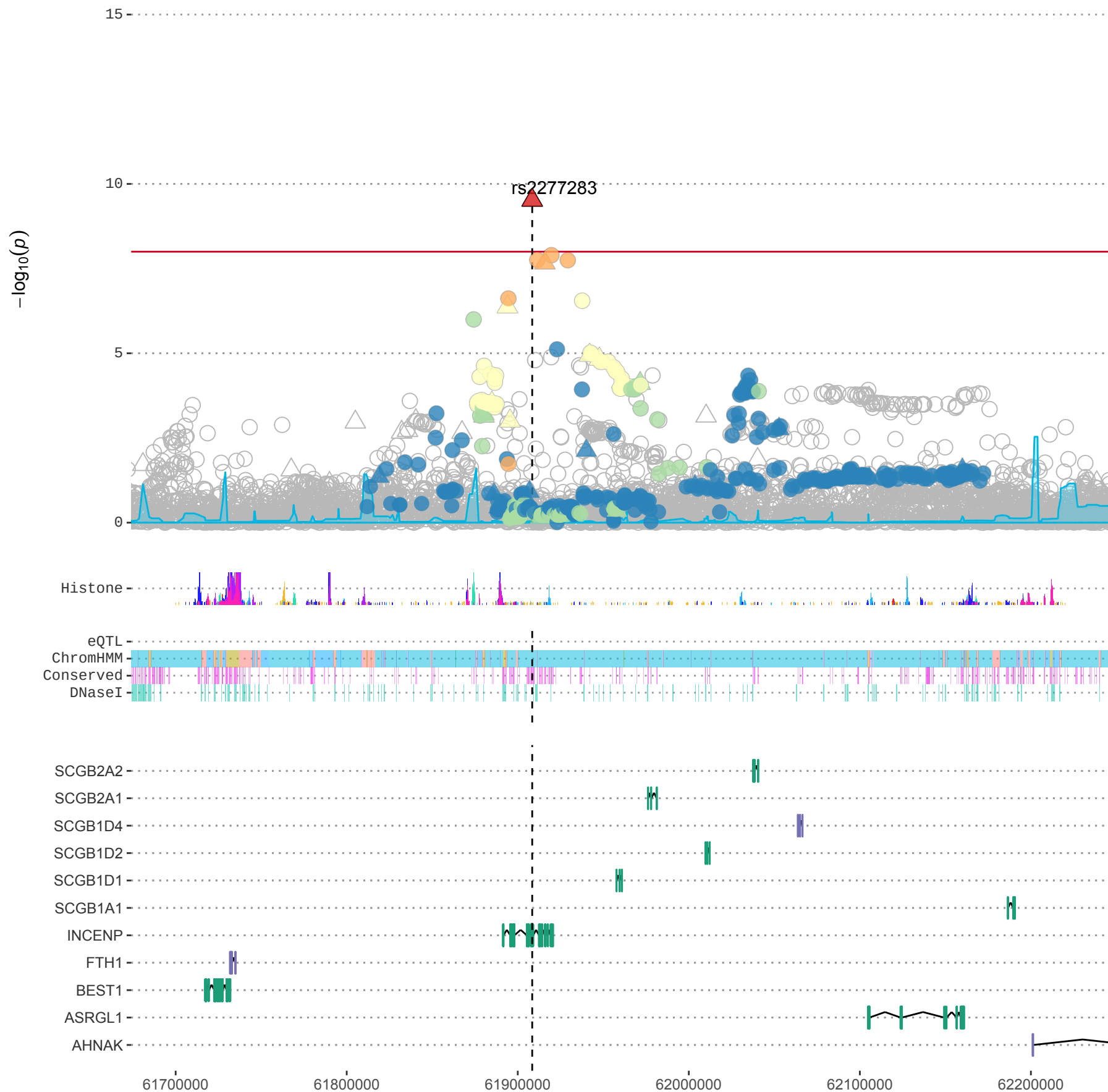




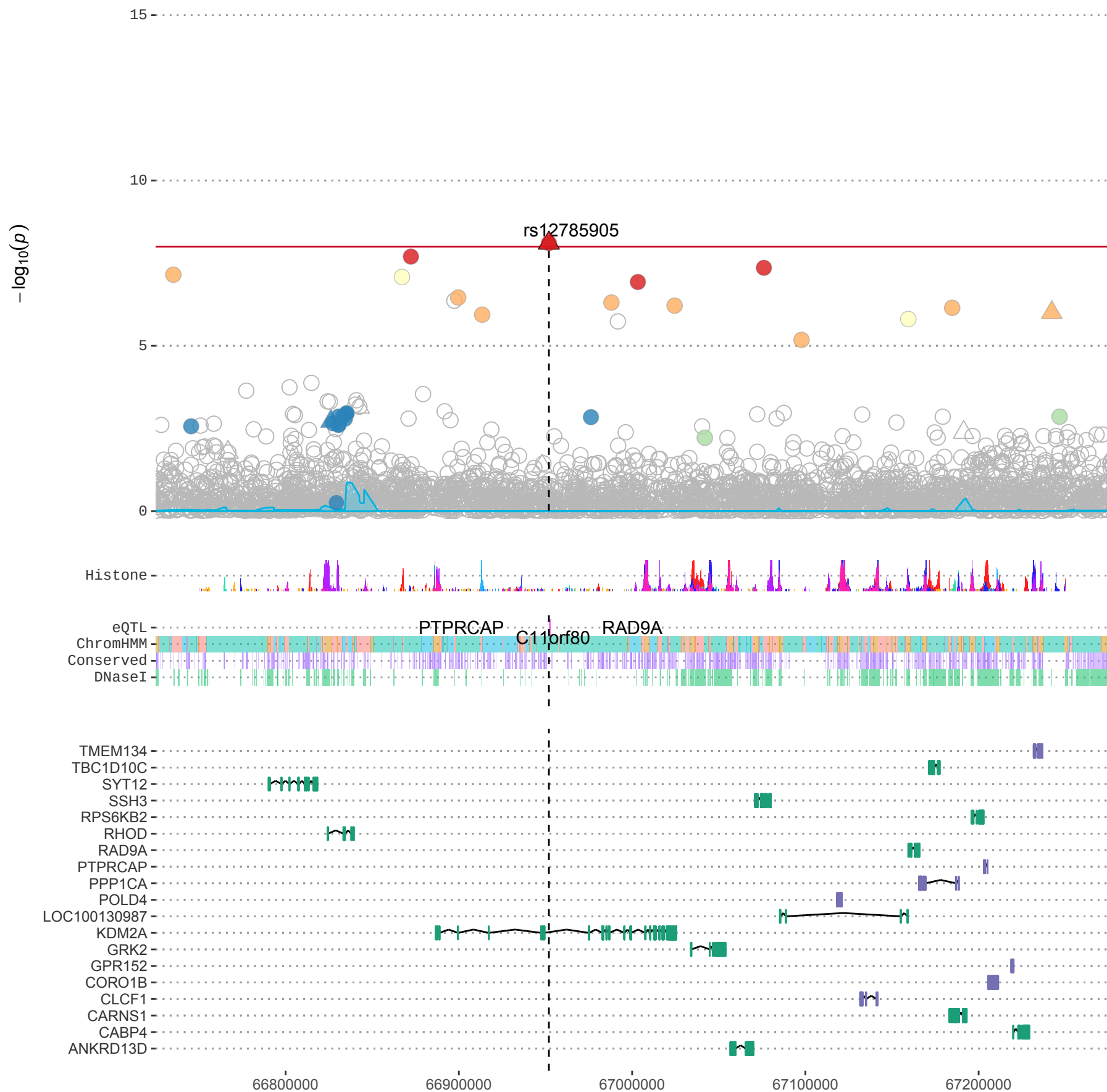


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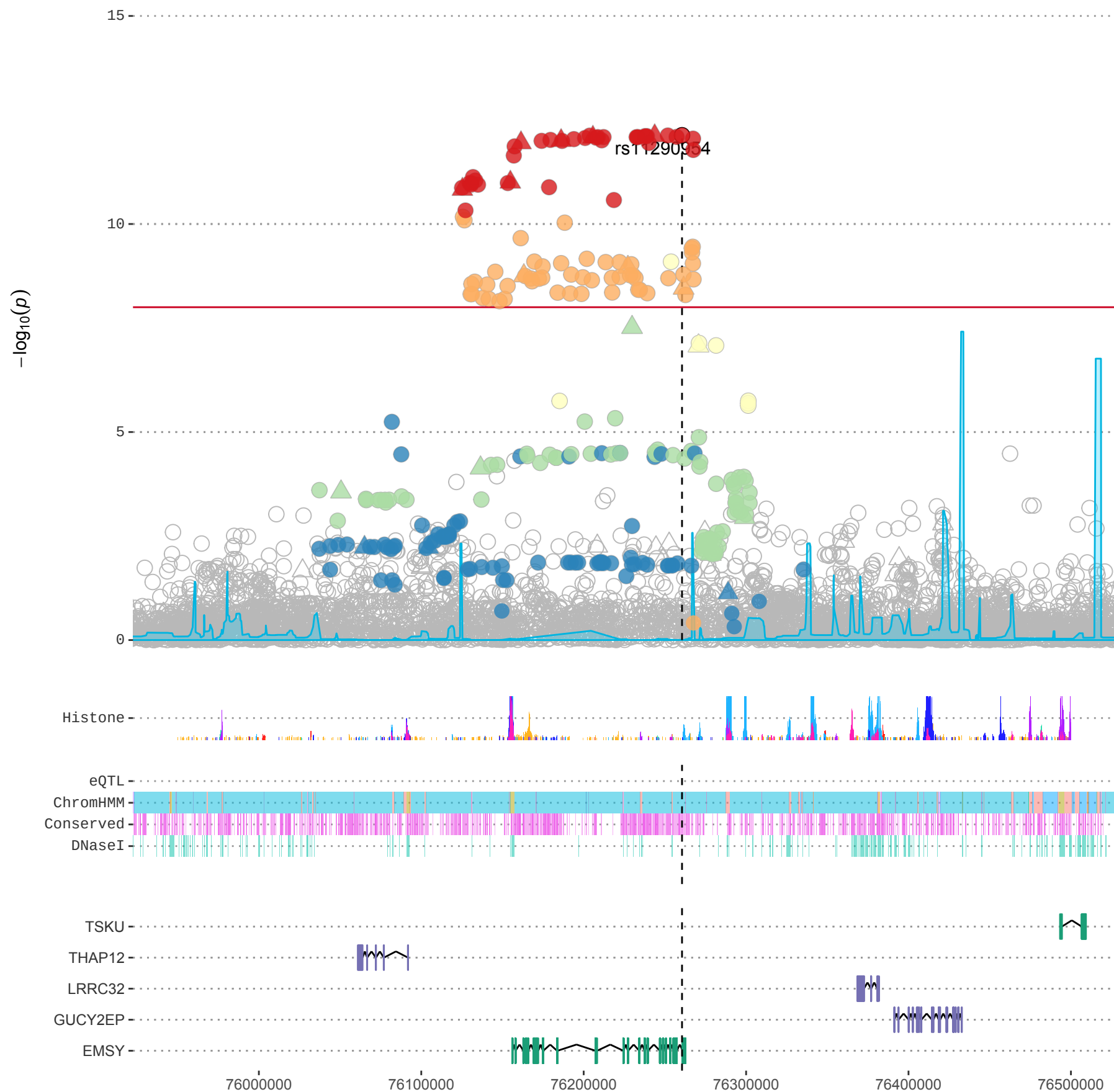
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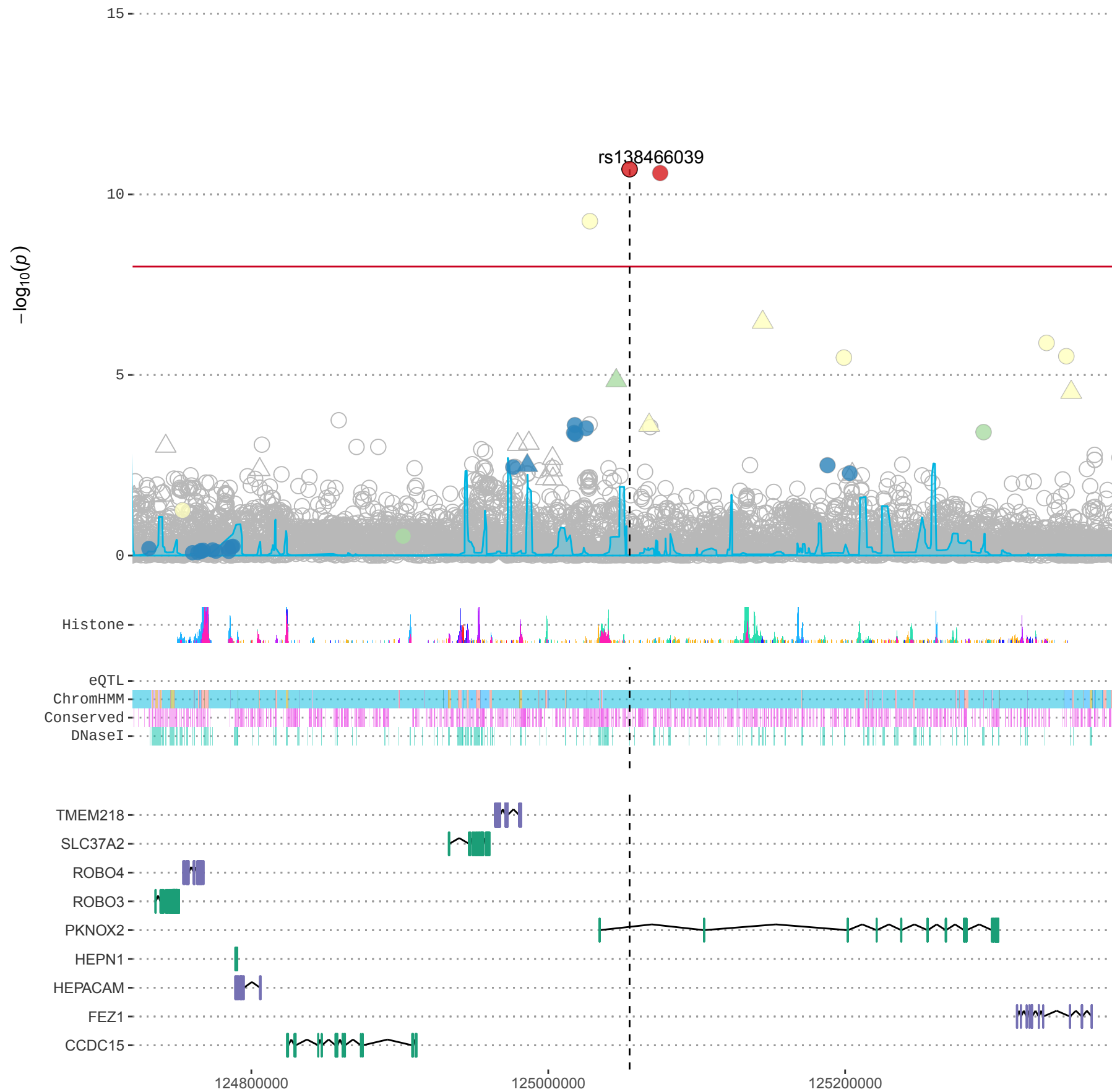


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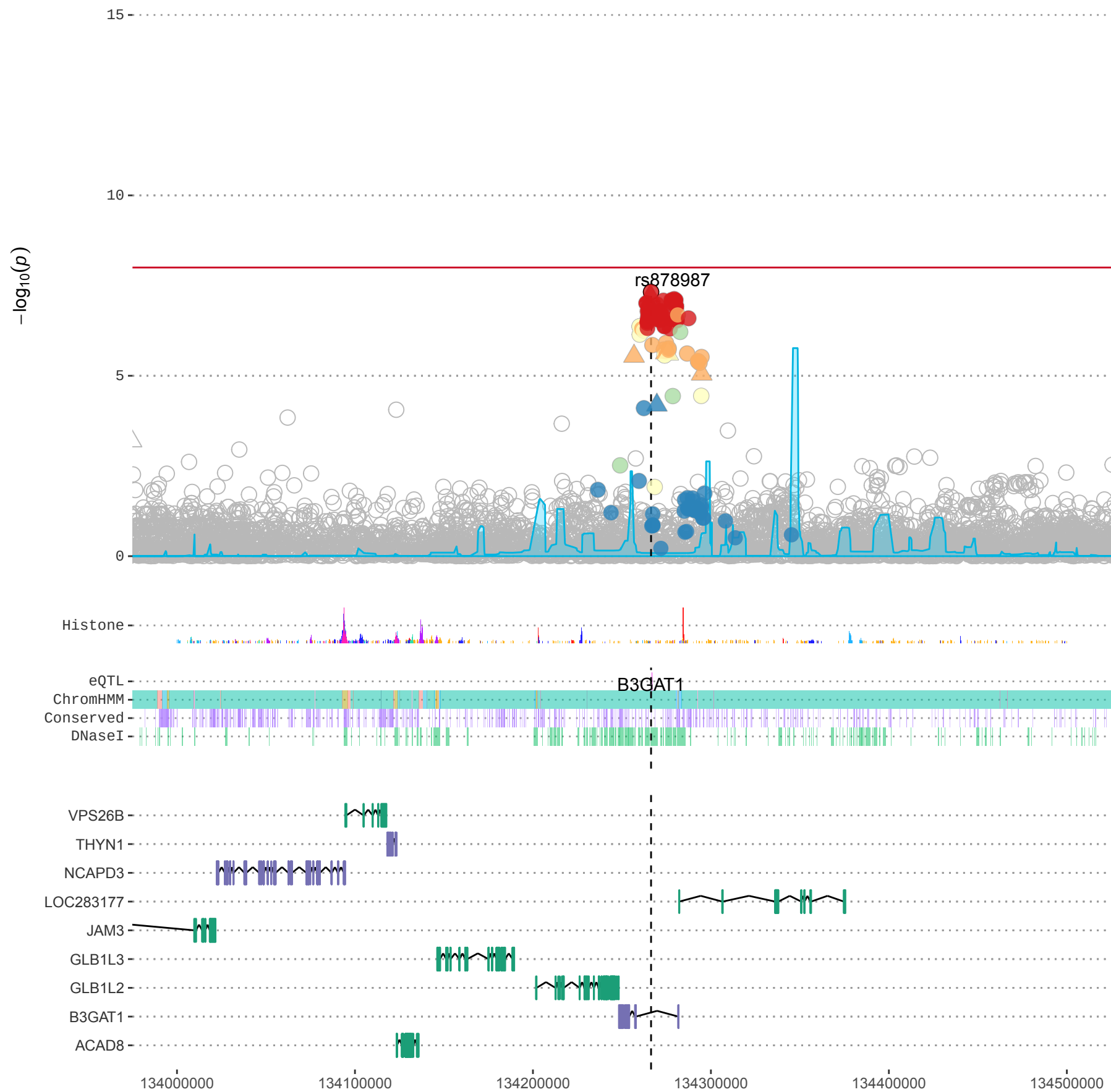


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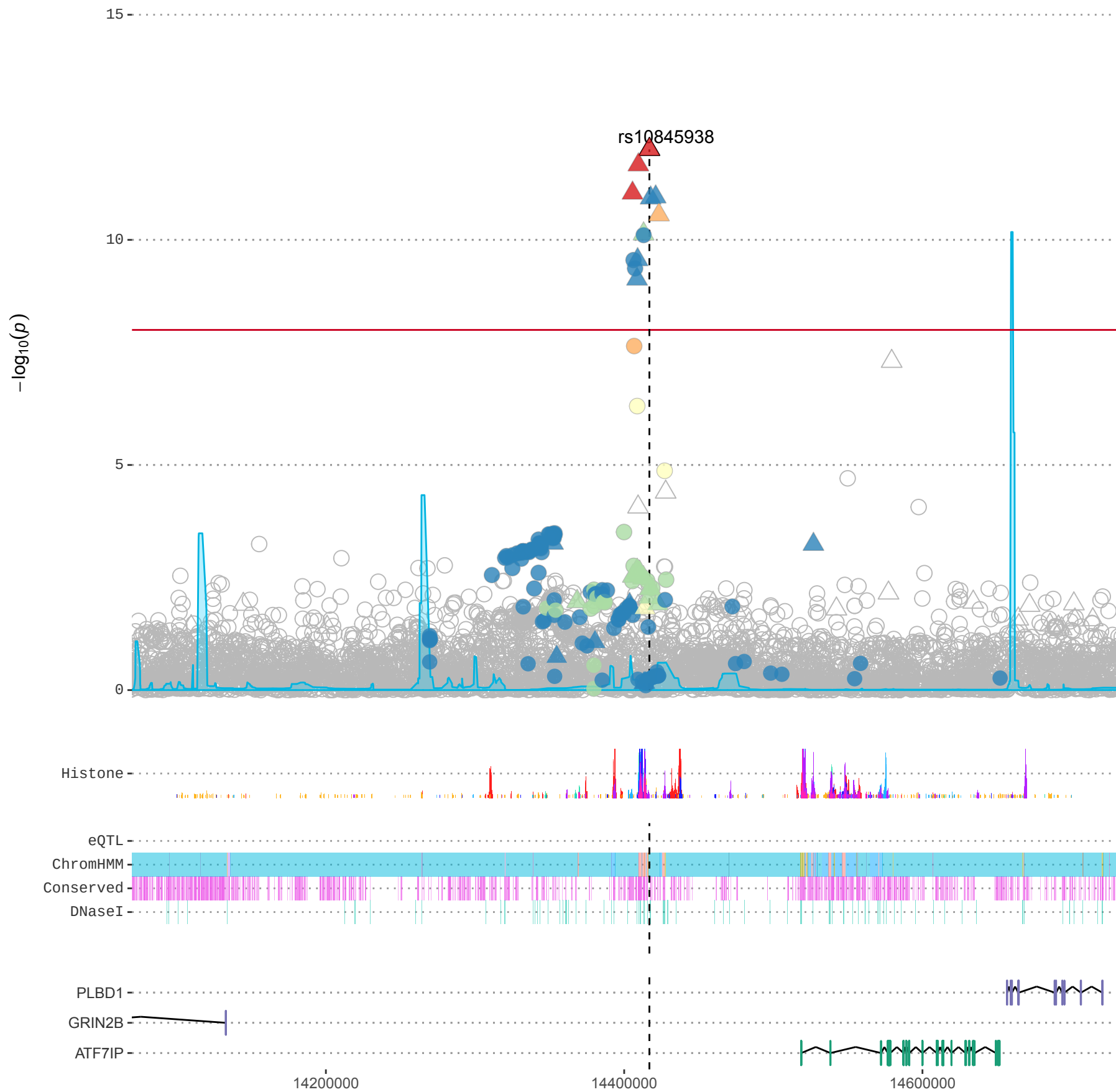
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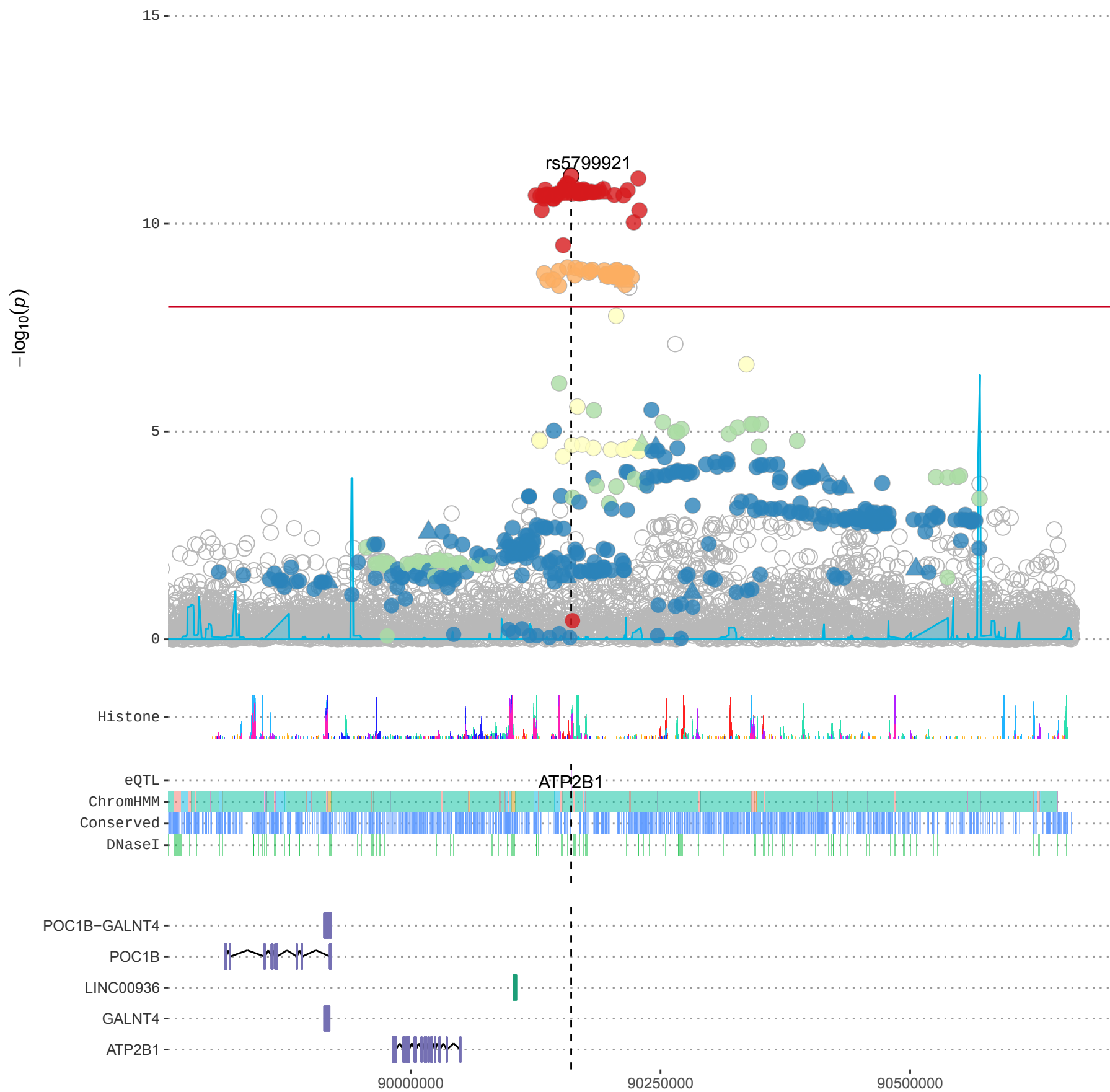
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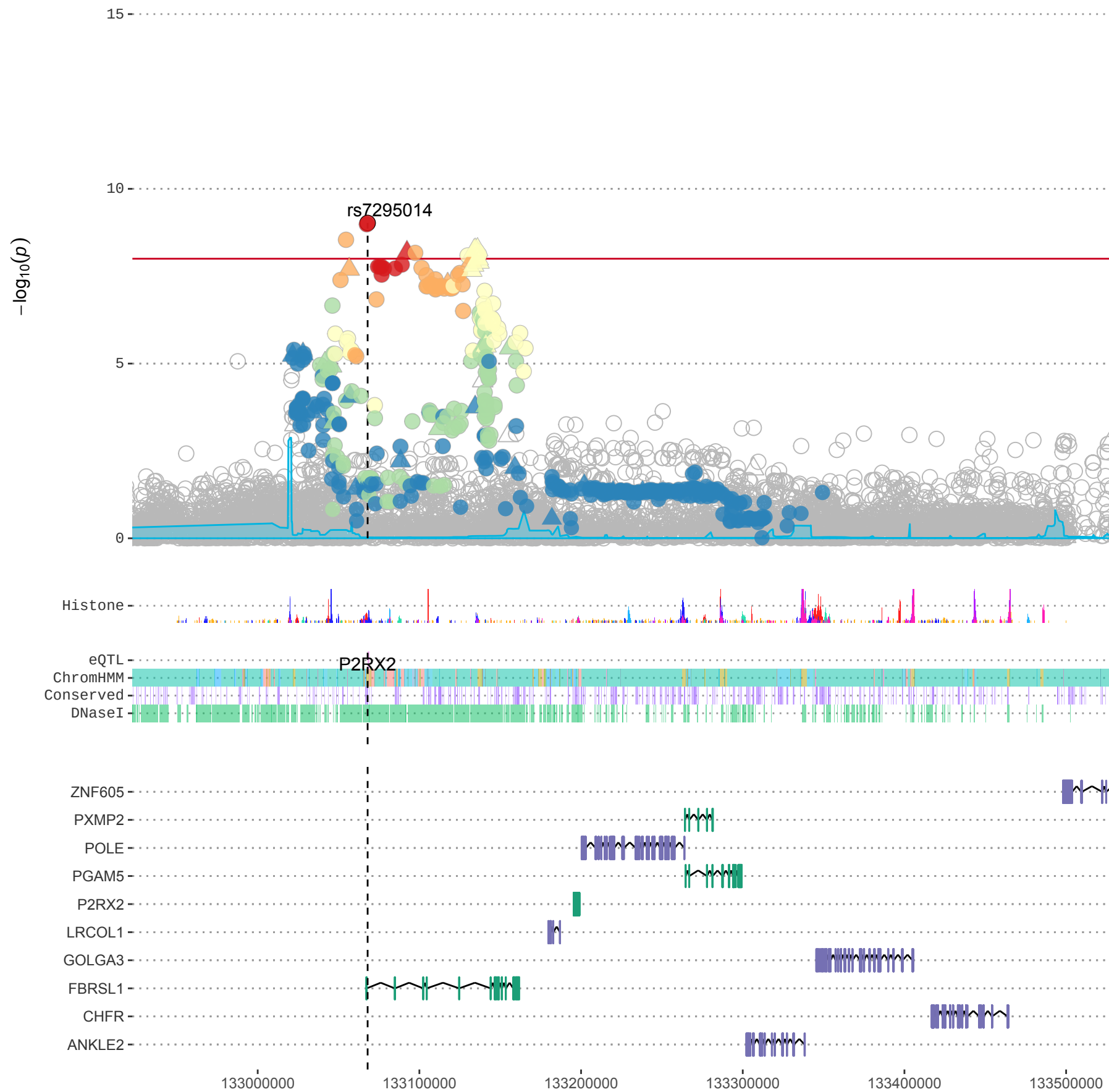
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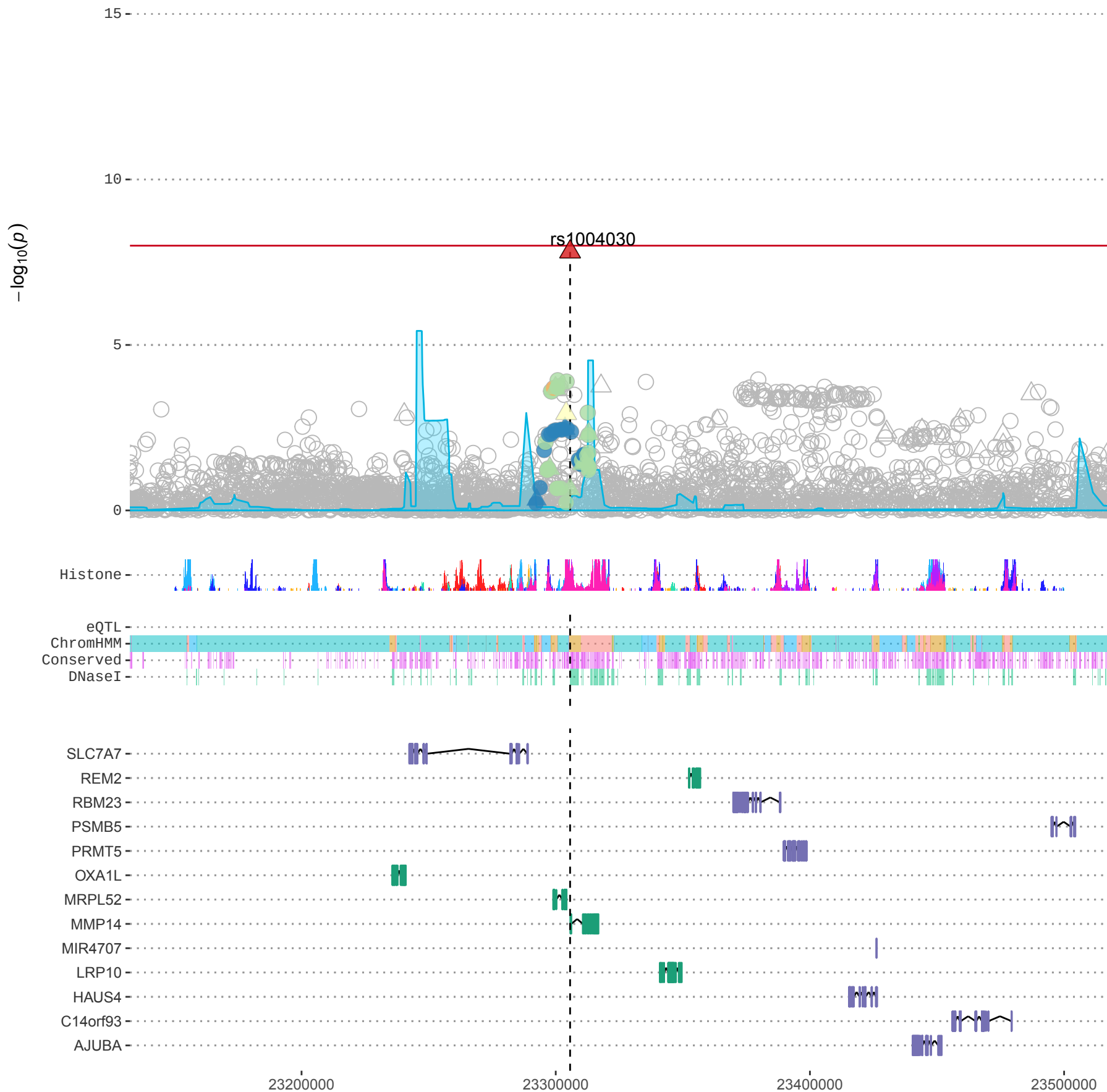


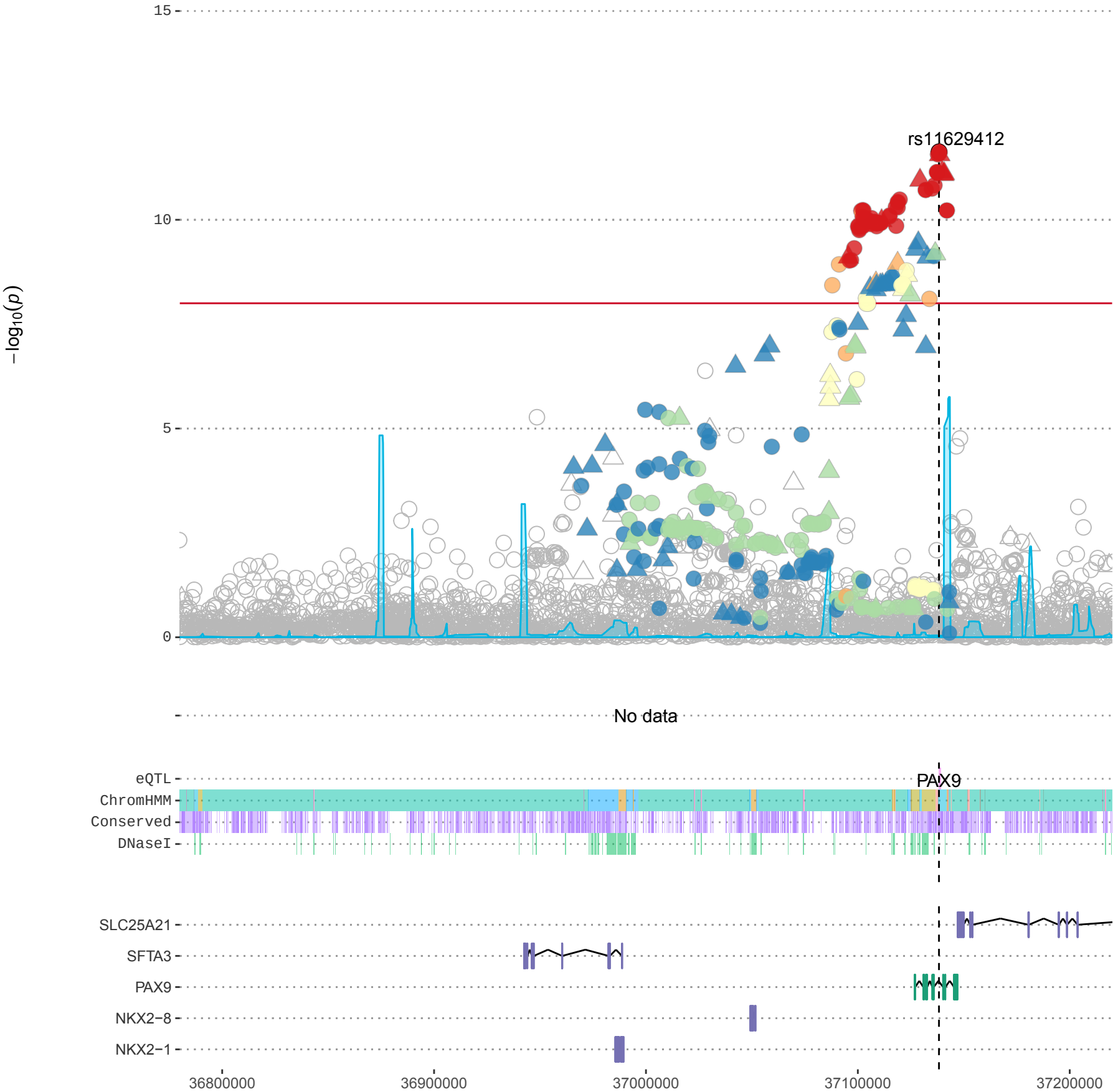
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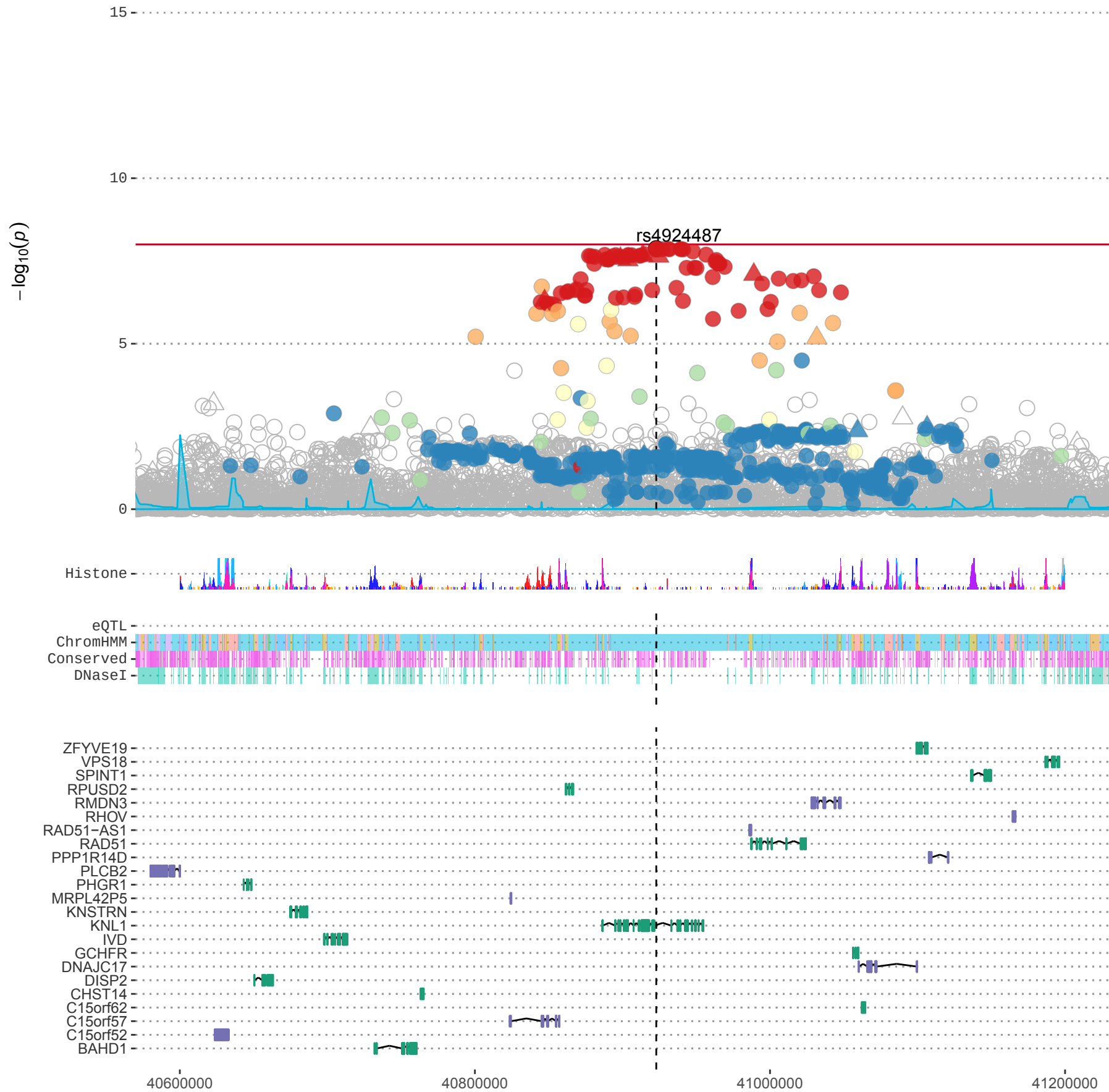
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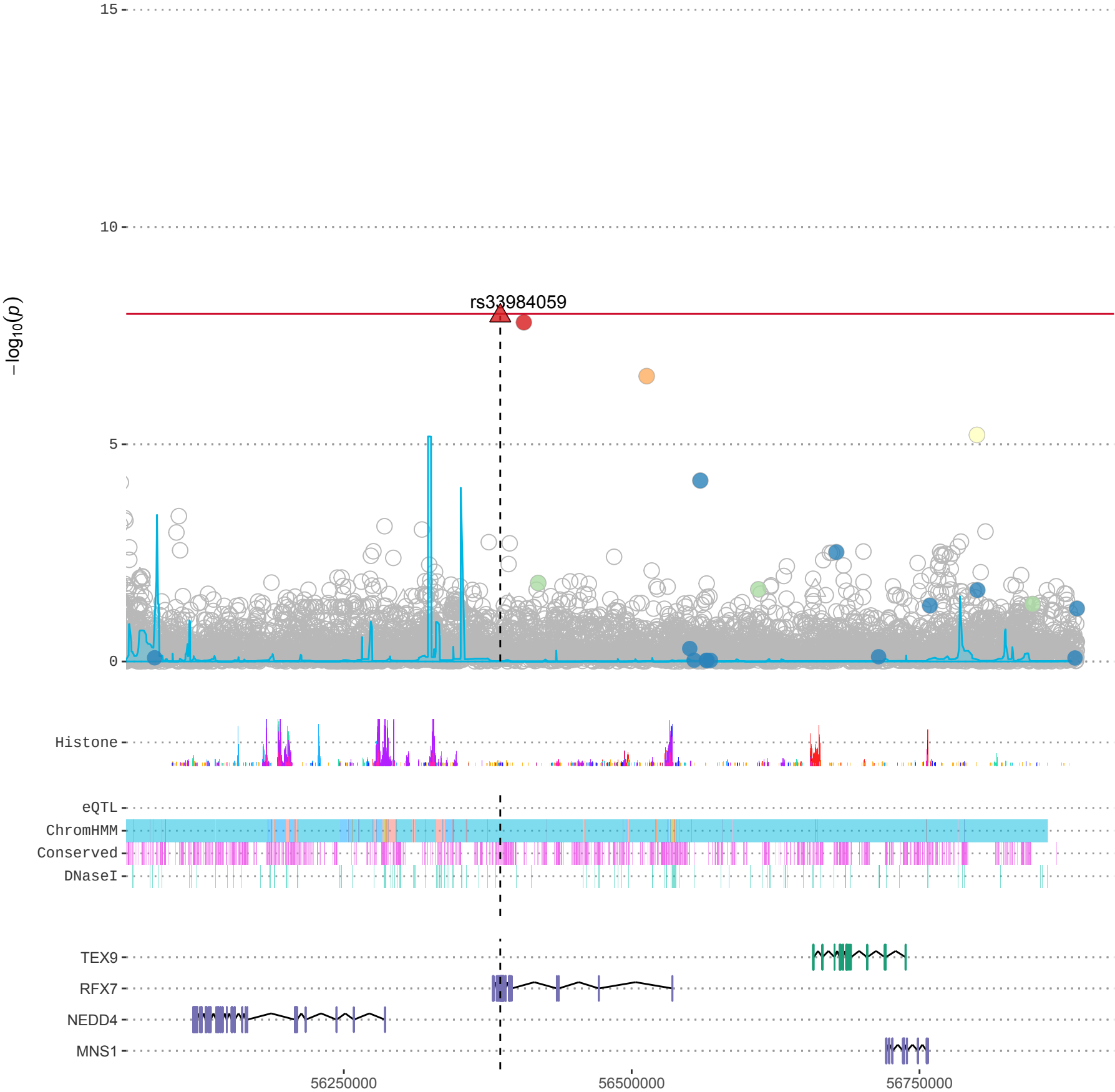




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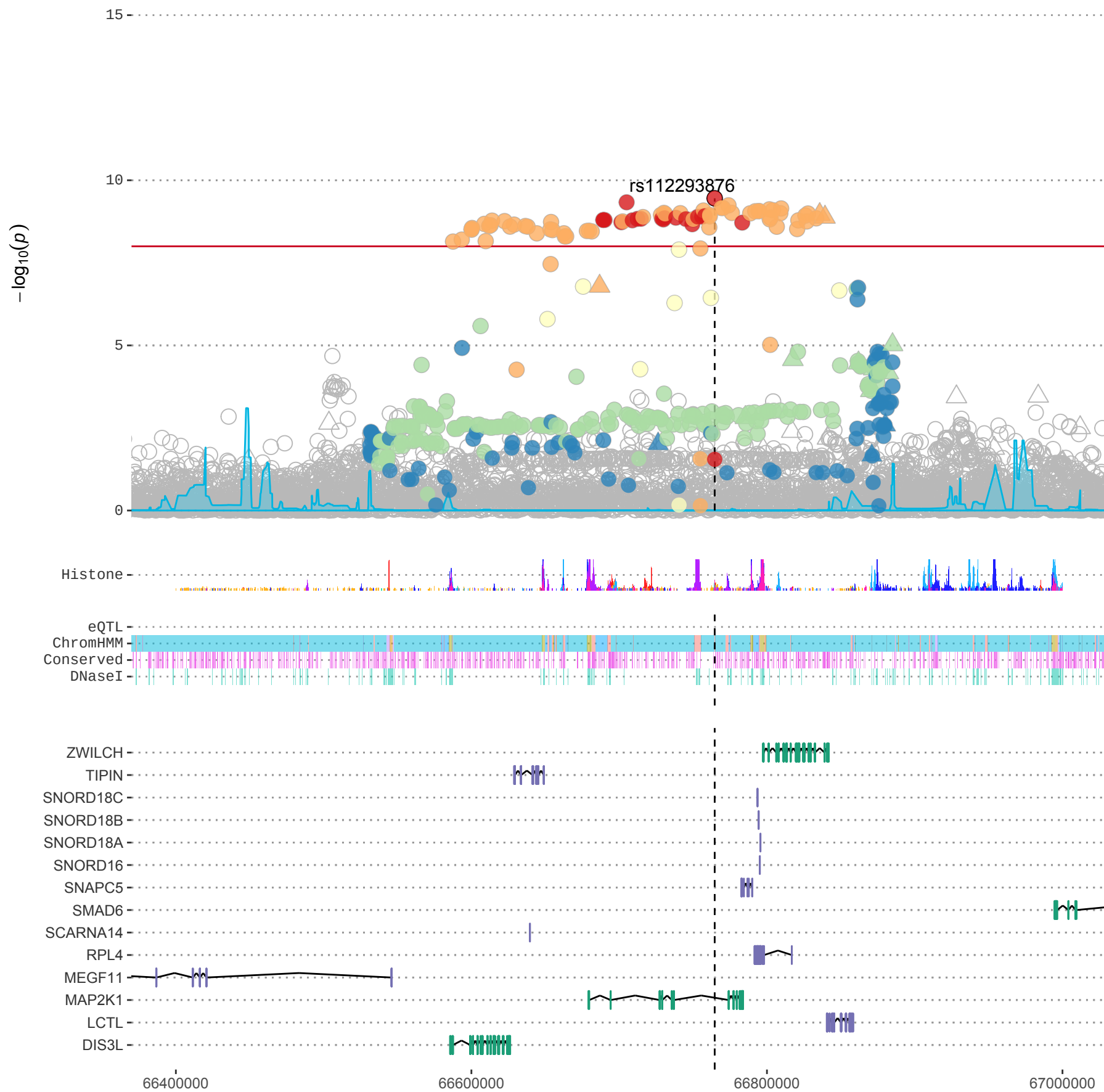
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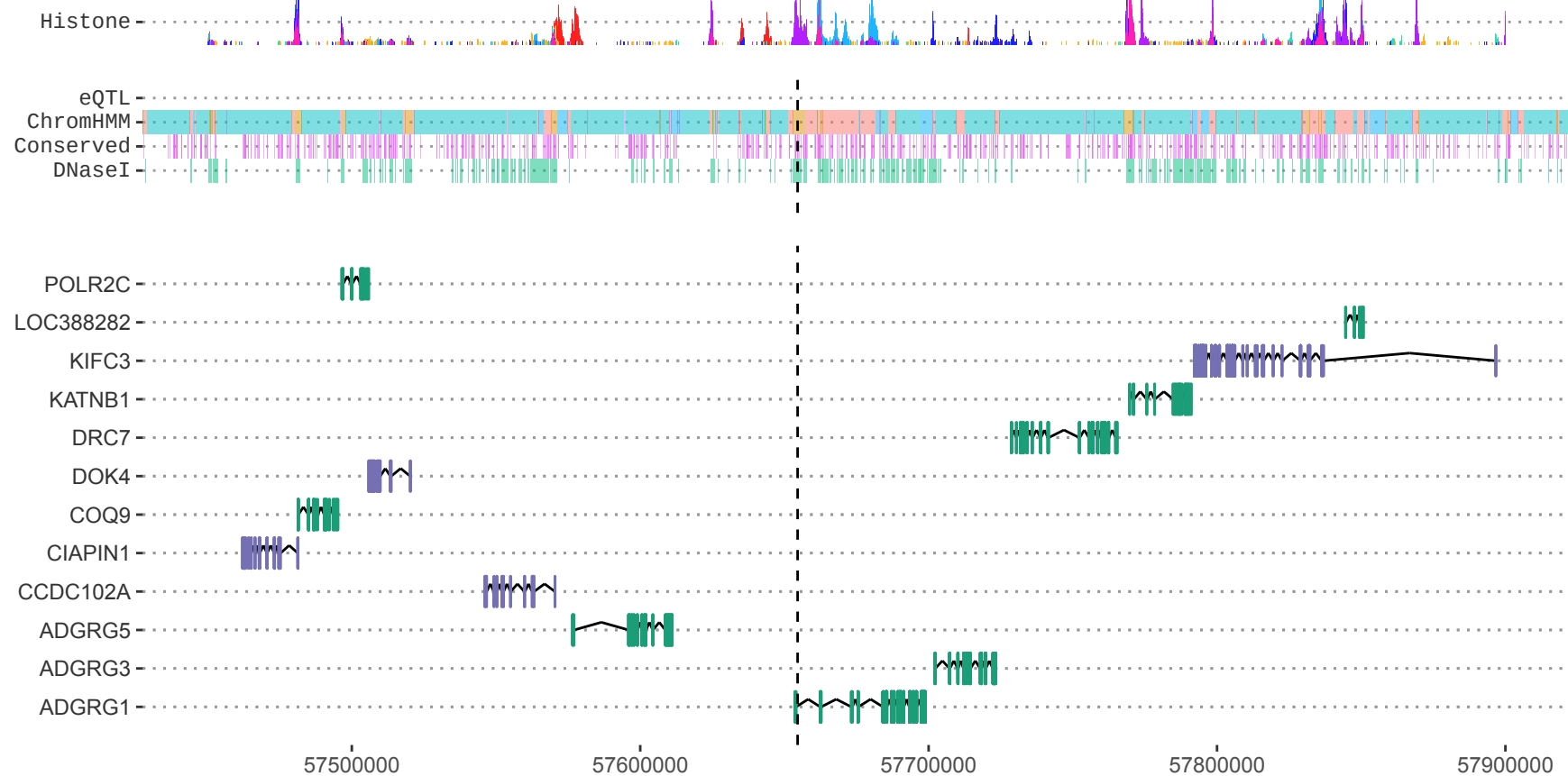
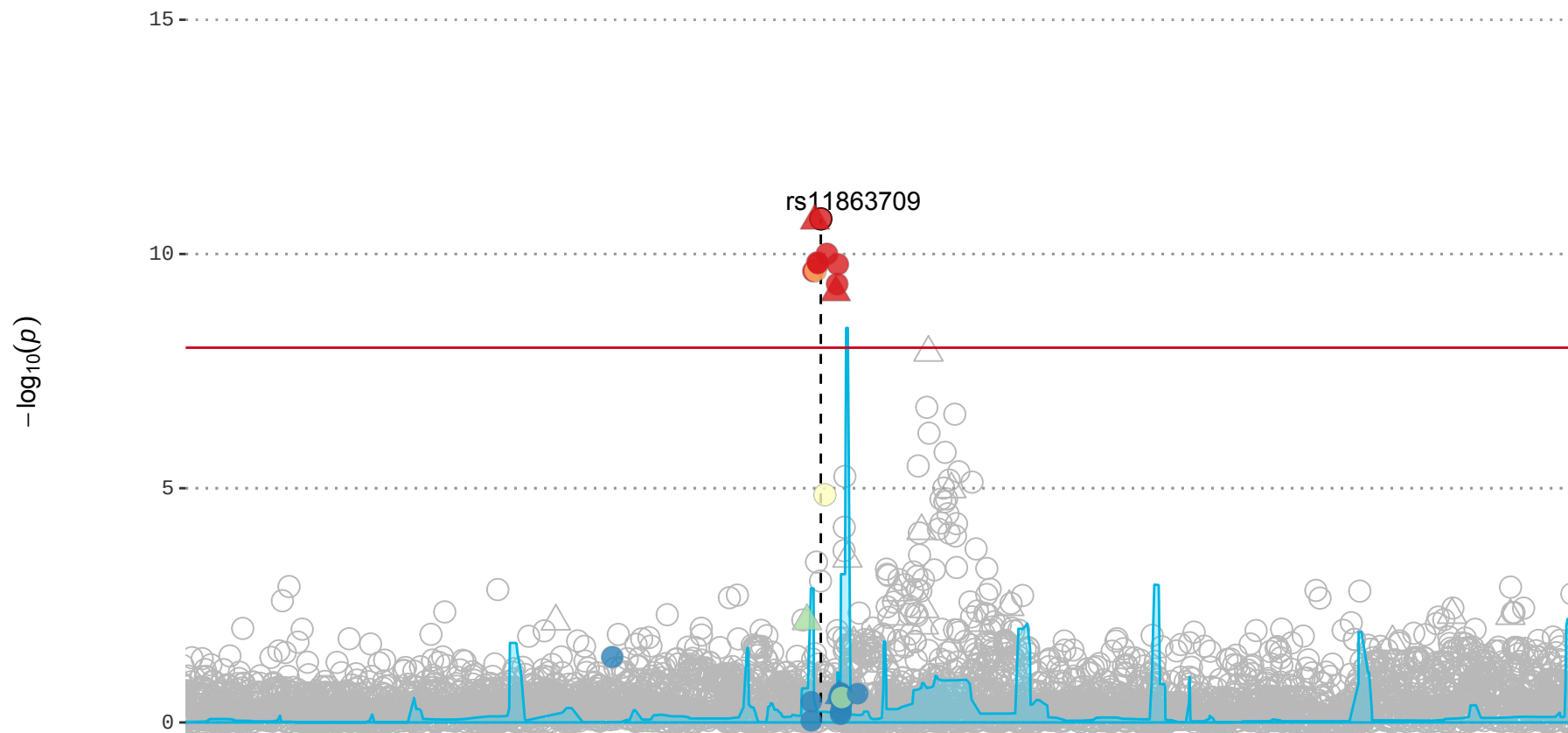
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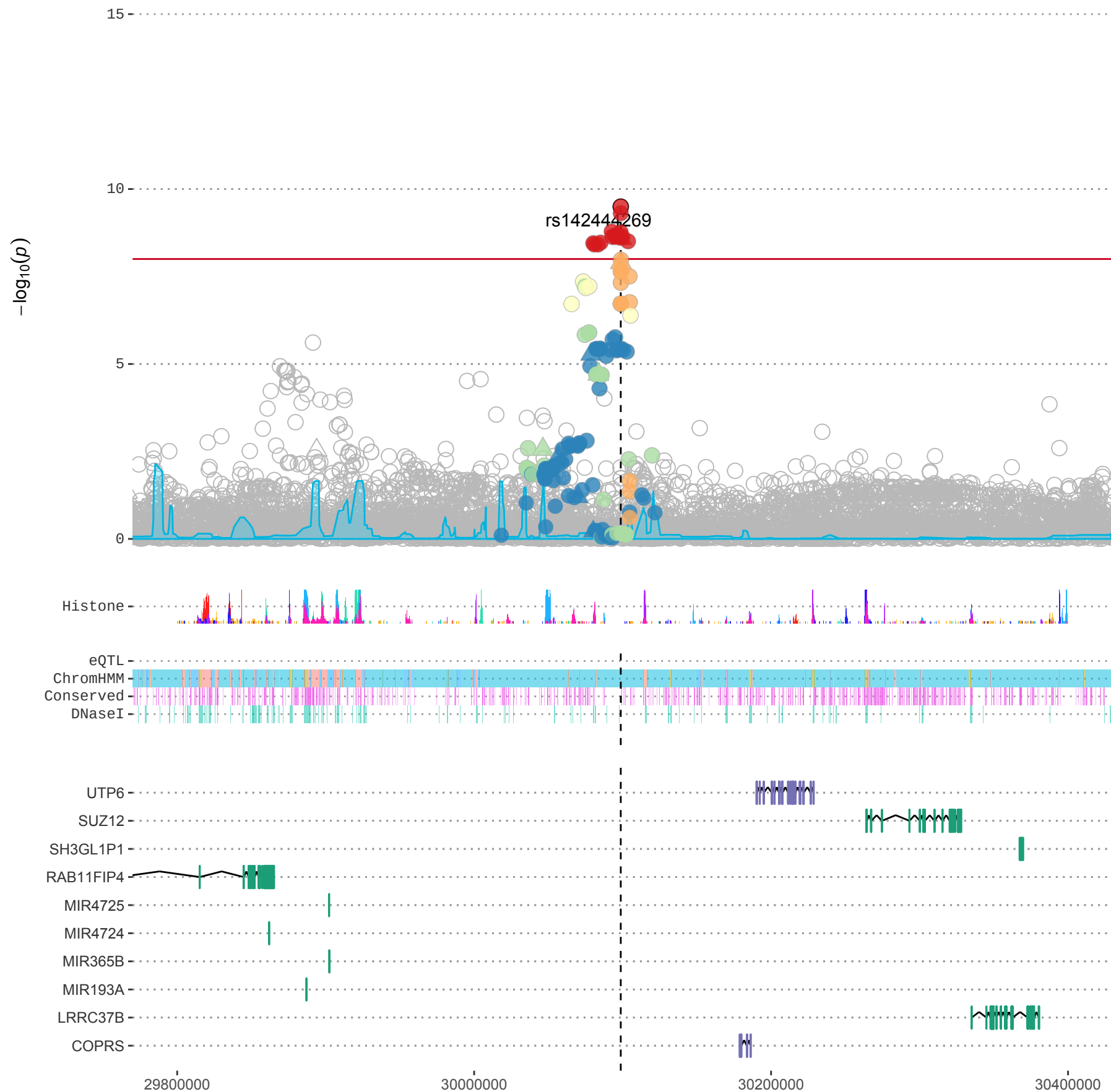


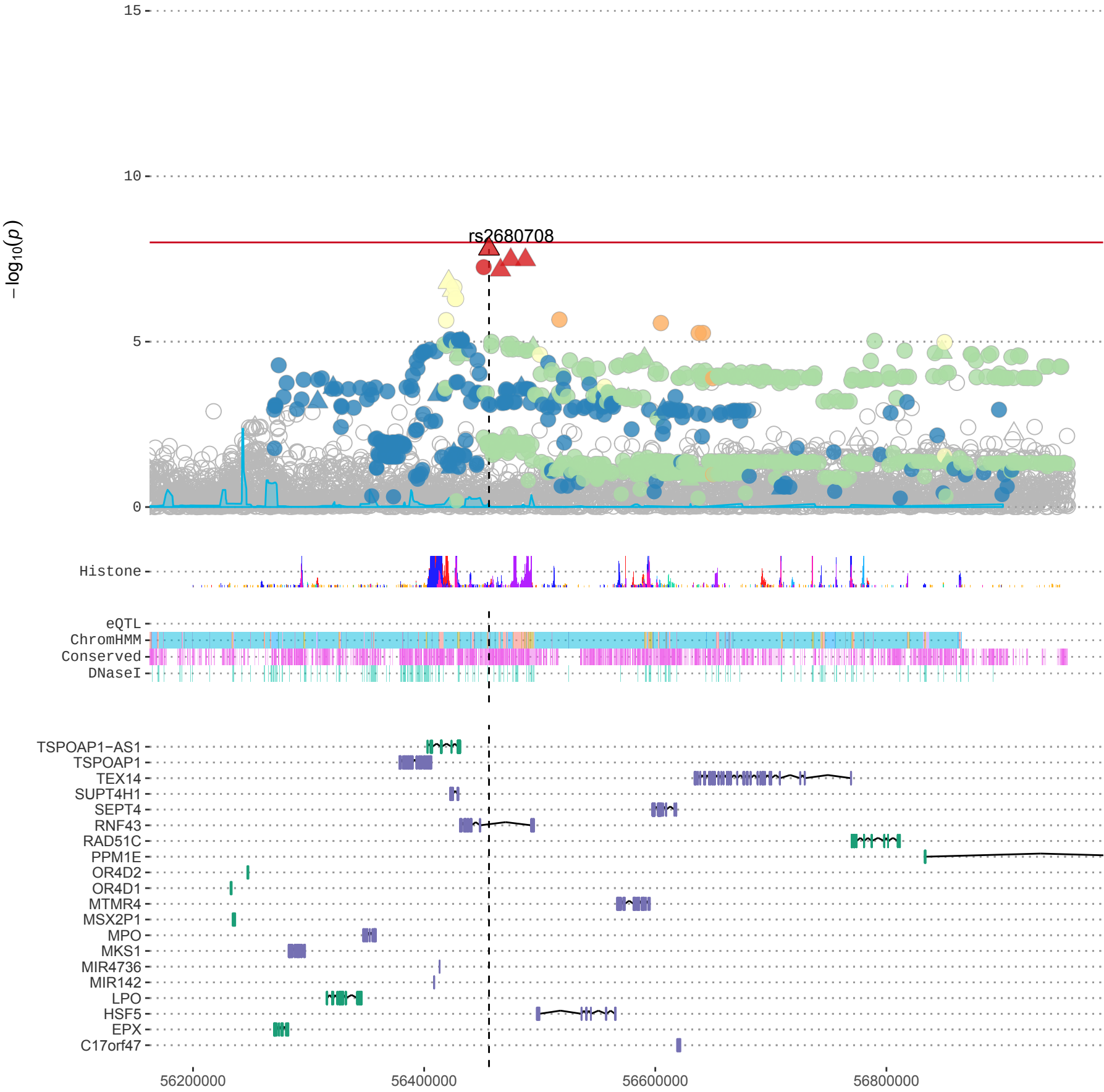
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15

10

5

0

rs8093601

POL1

Histone

eQTL

ChromHMM

Conserved

DNaseI

STARD6

SNORA37

POL1

MBD2

C18orf54

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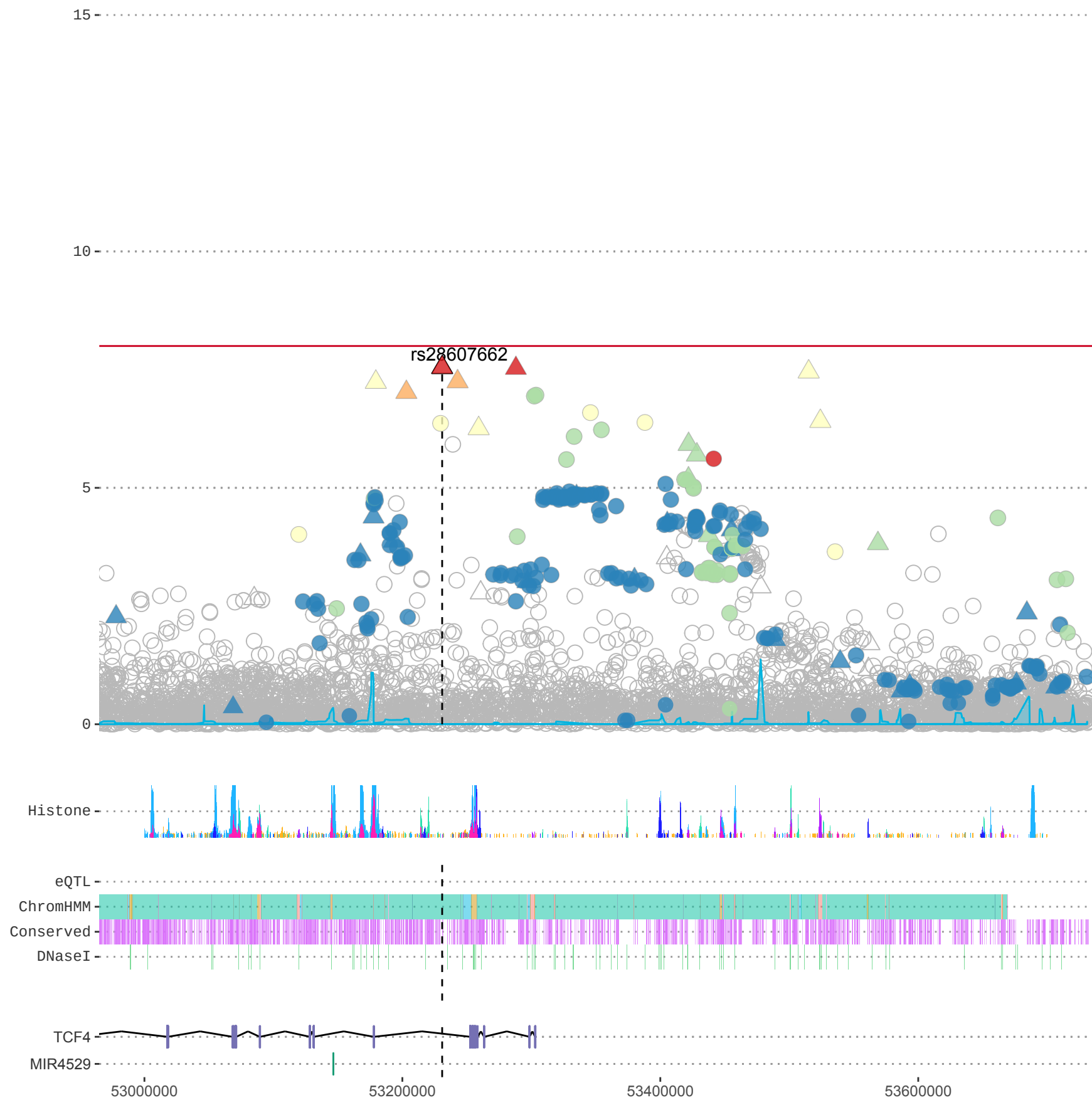
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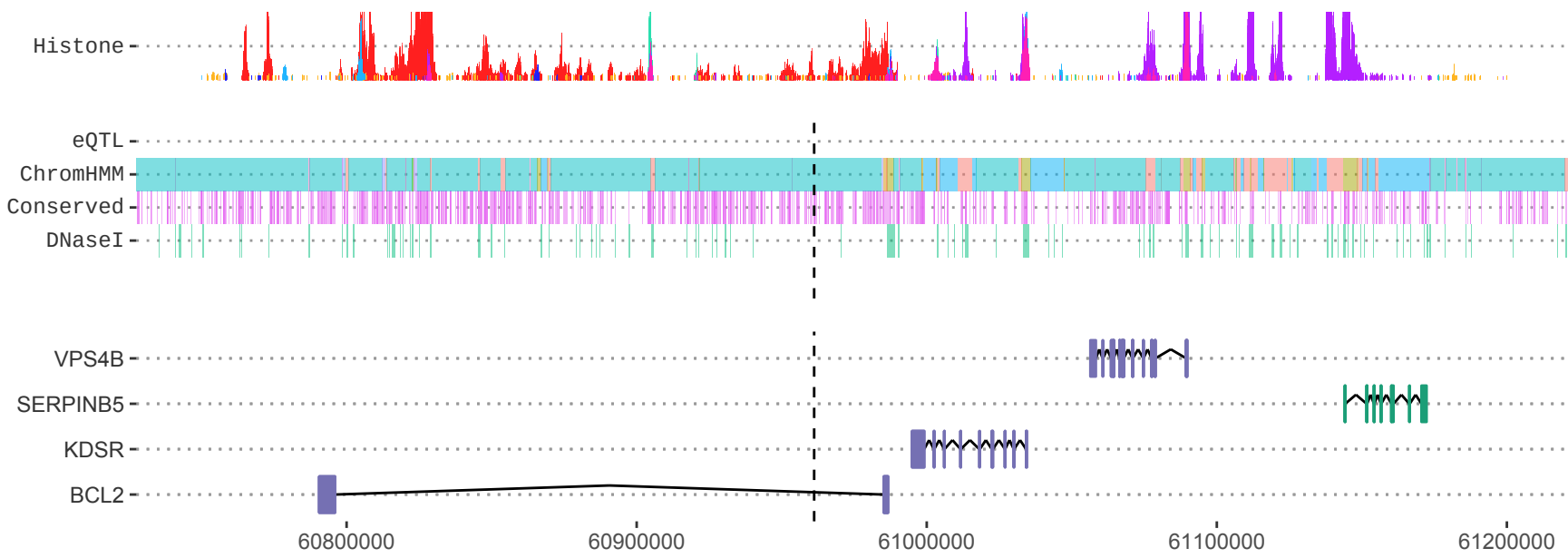
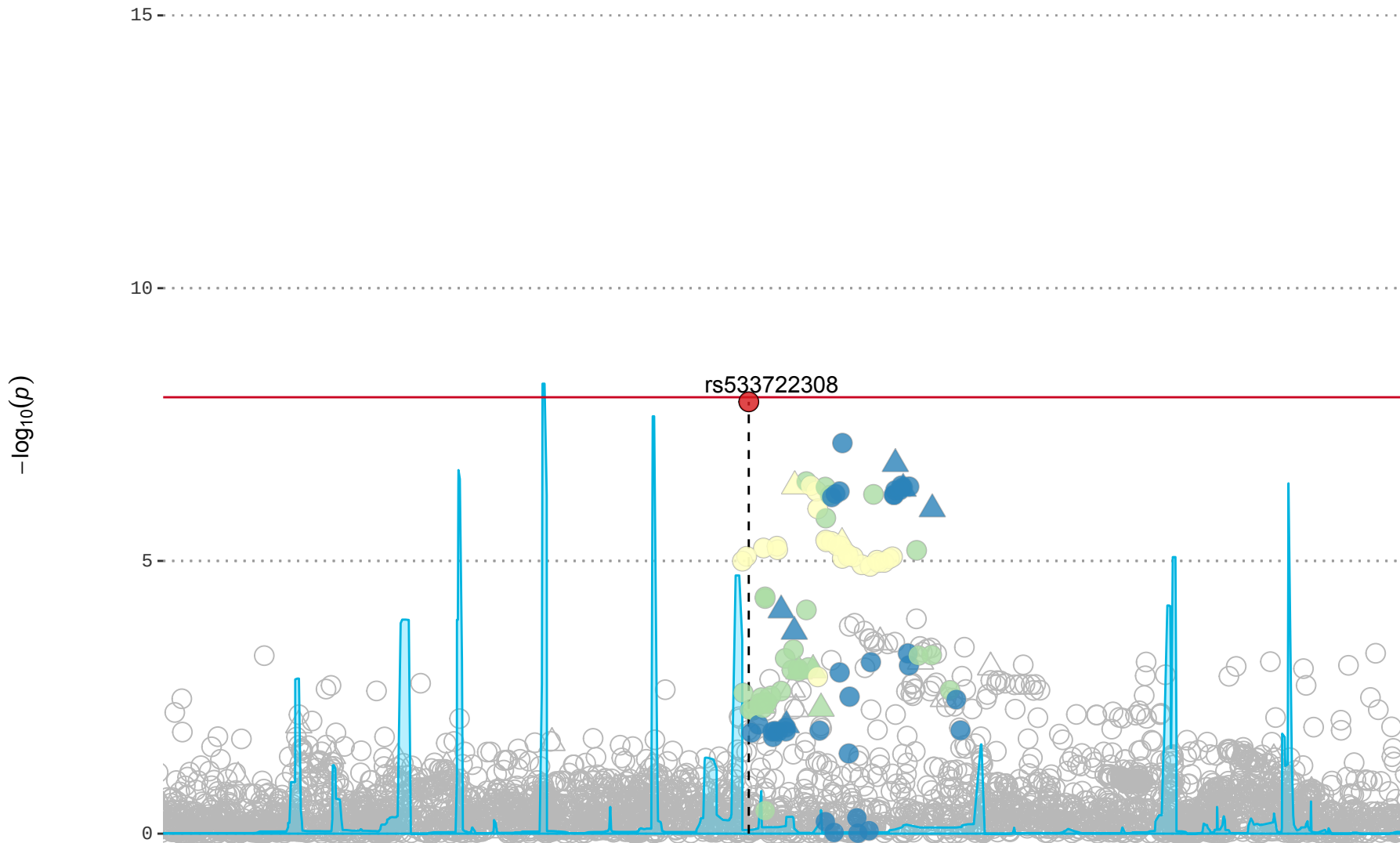
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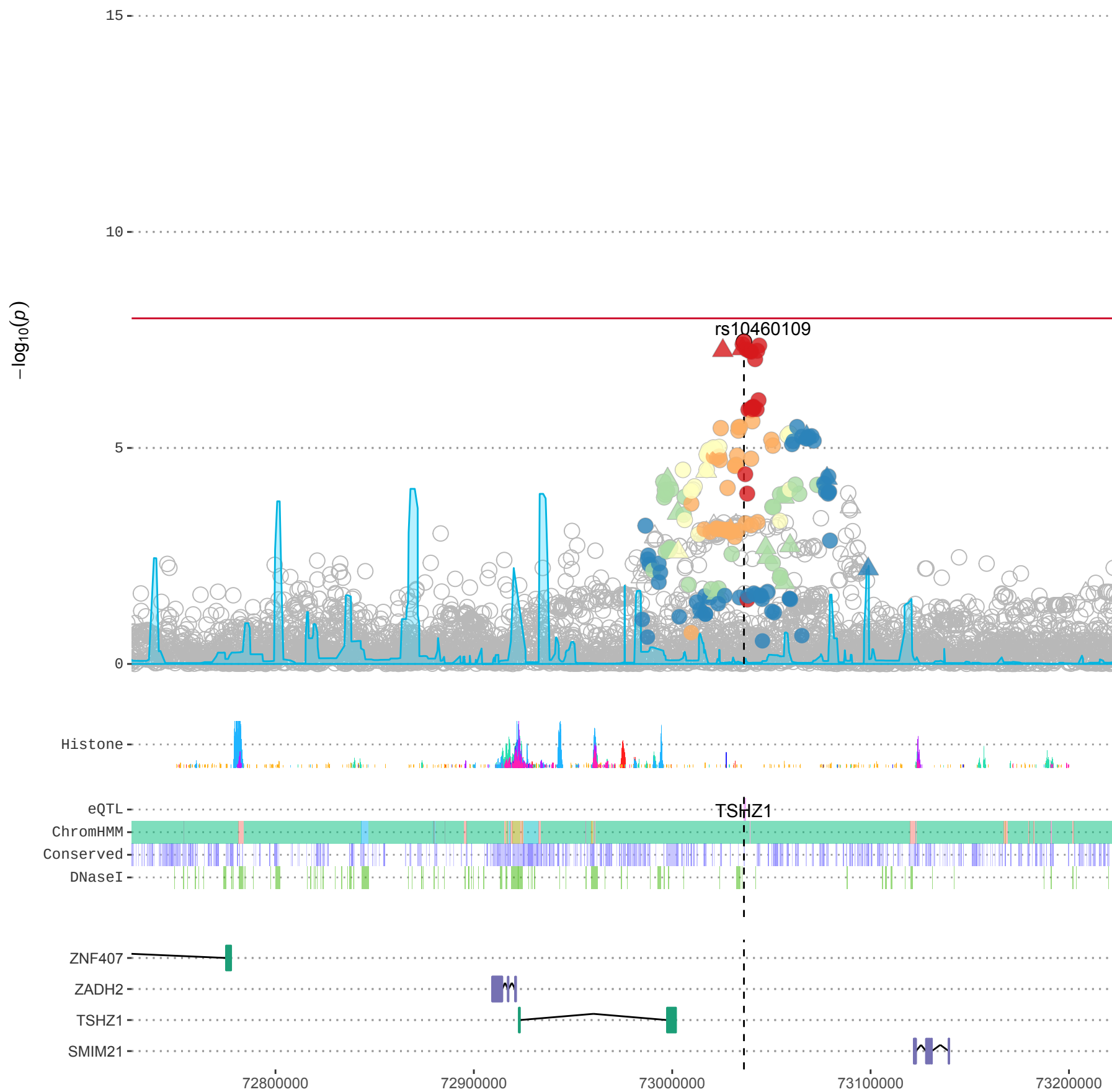
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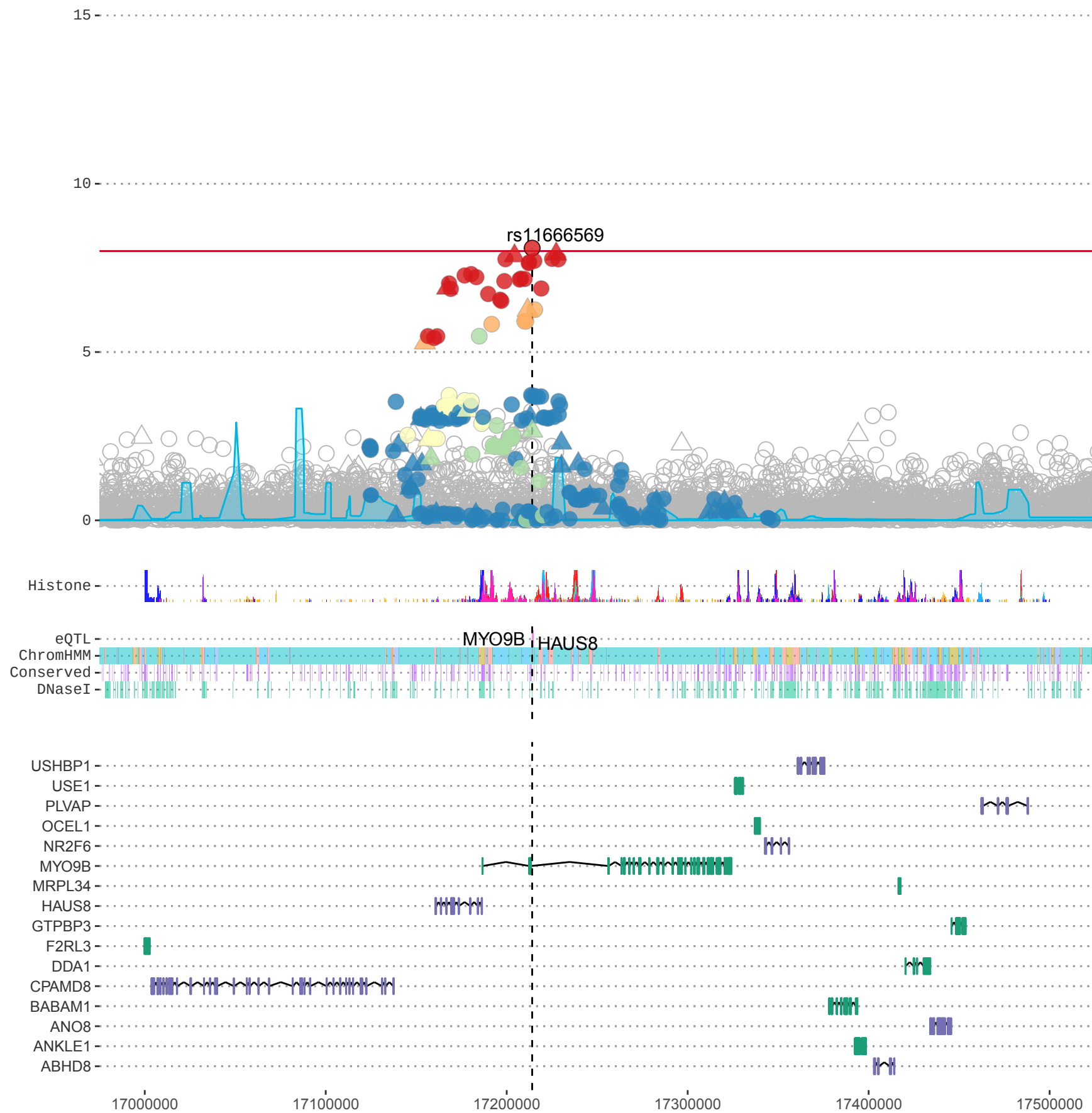
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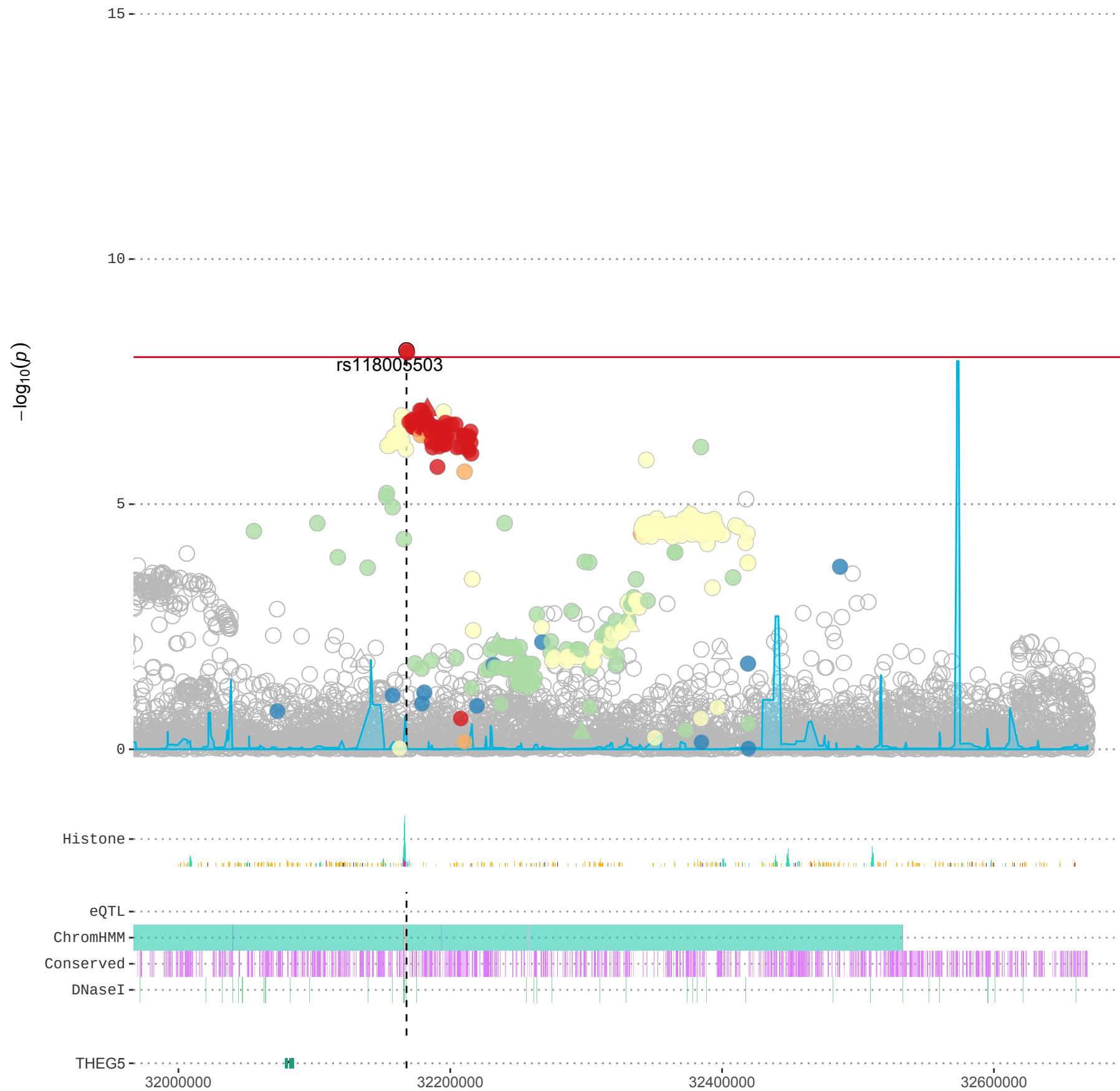


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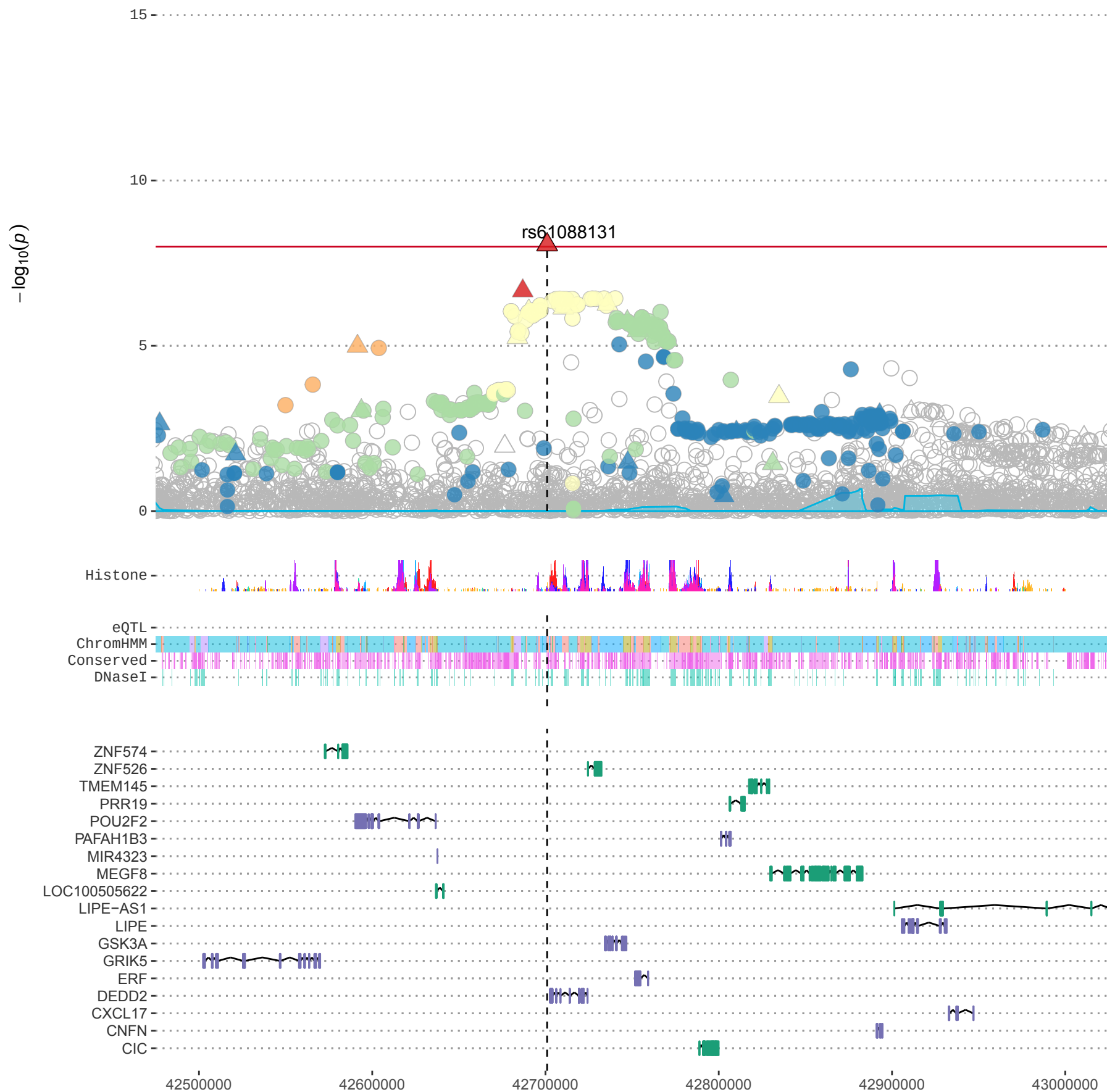
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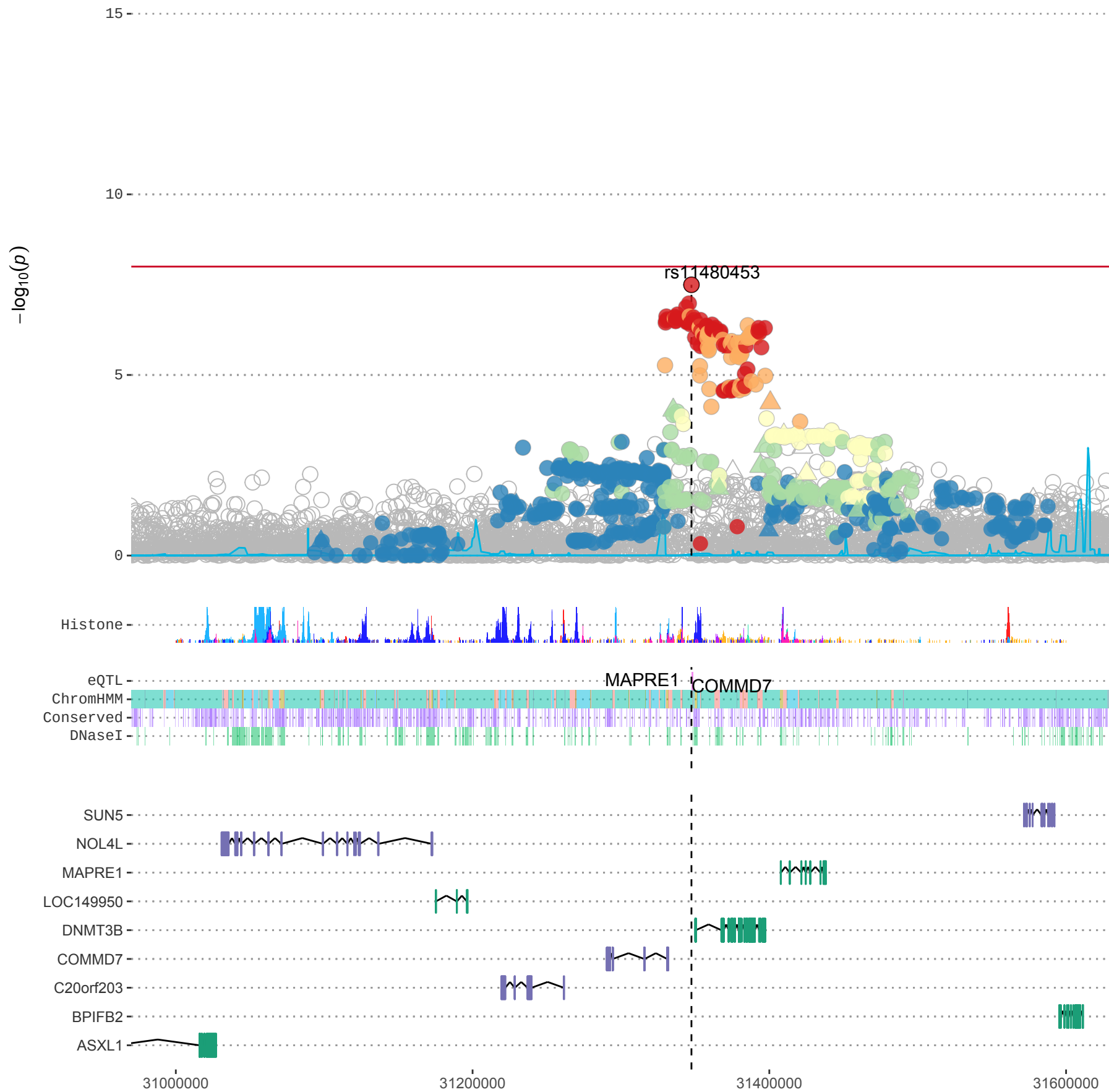
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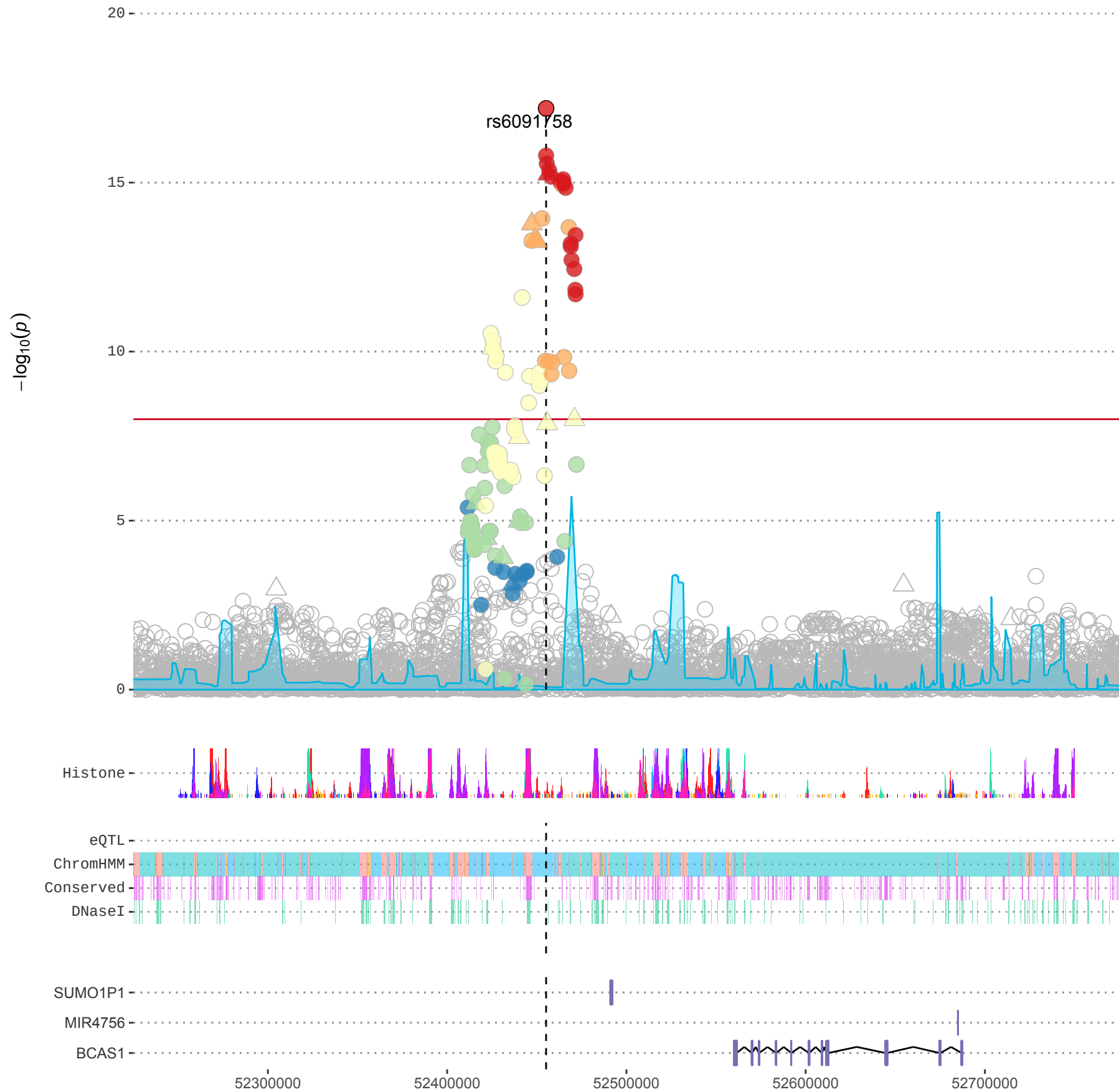
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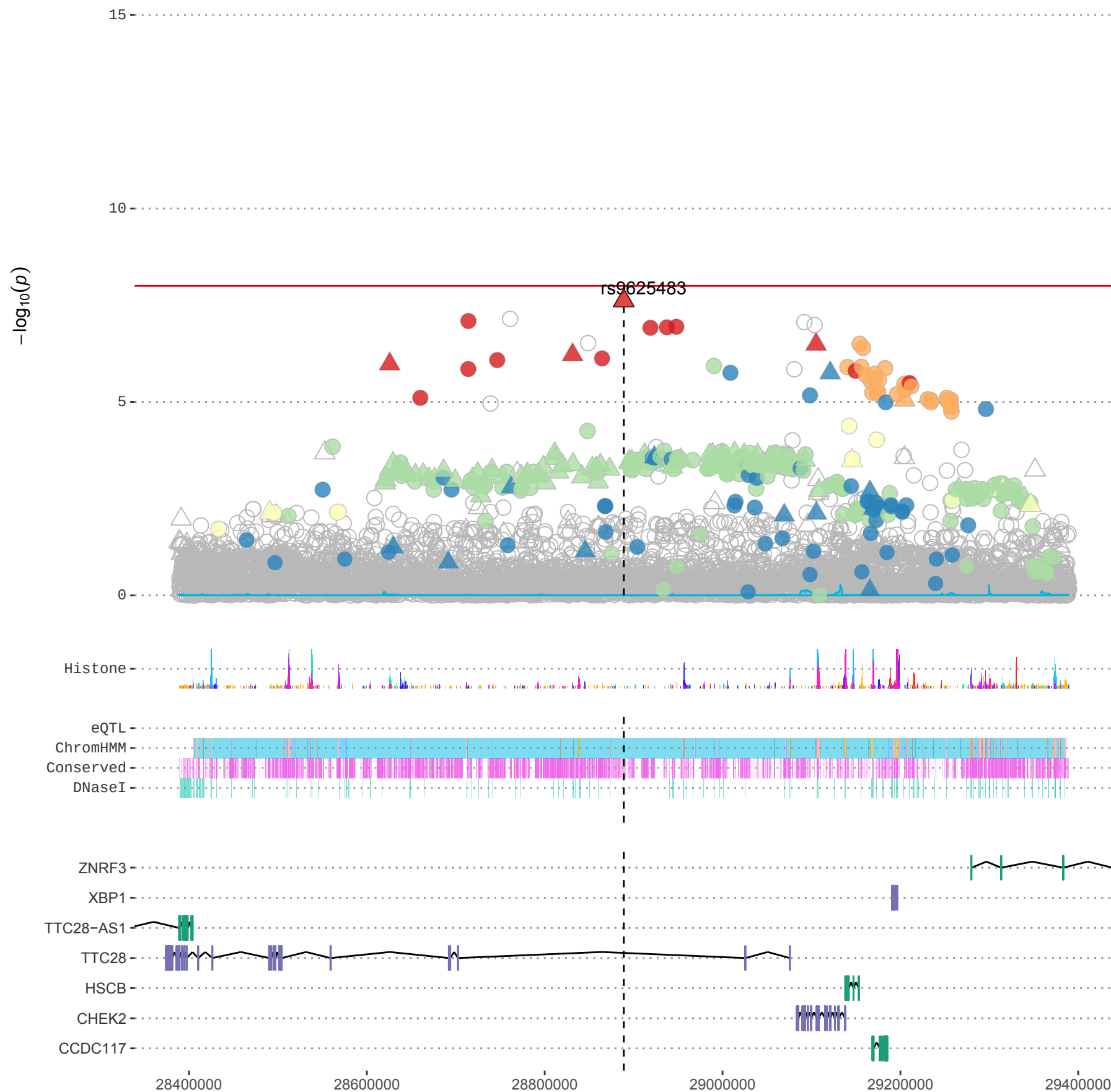


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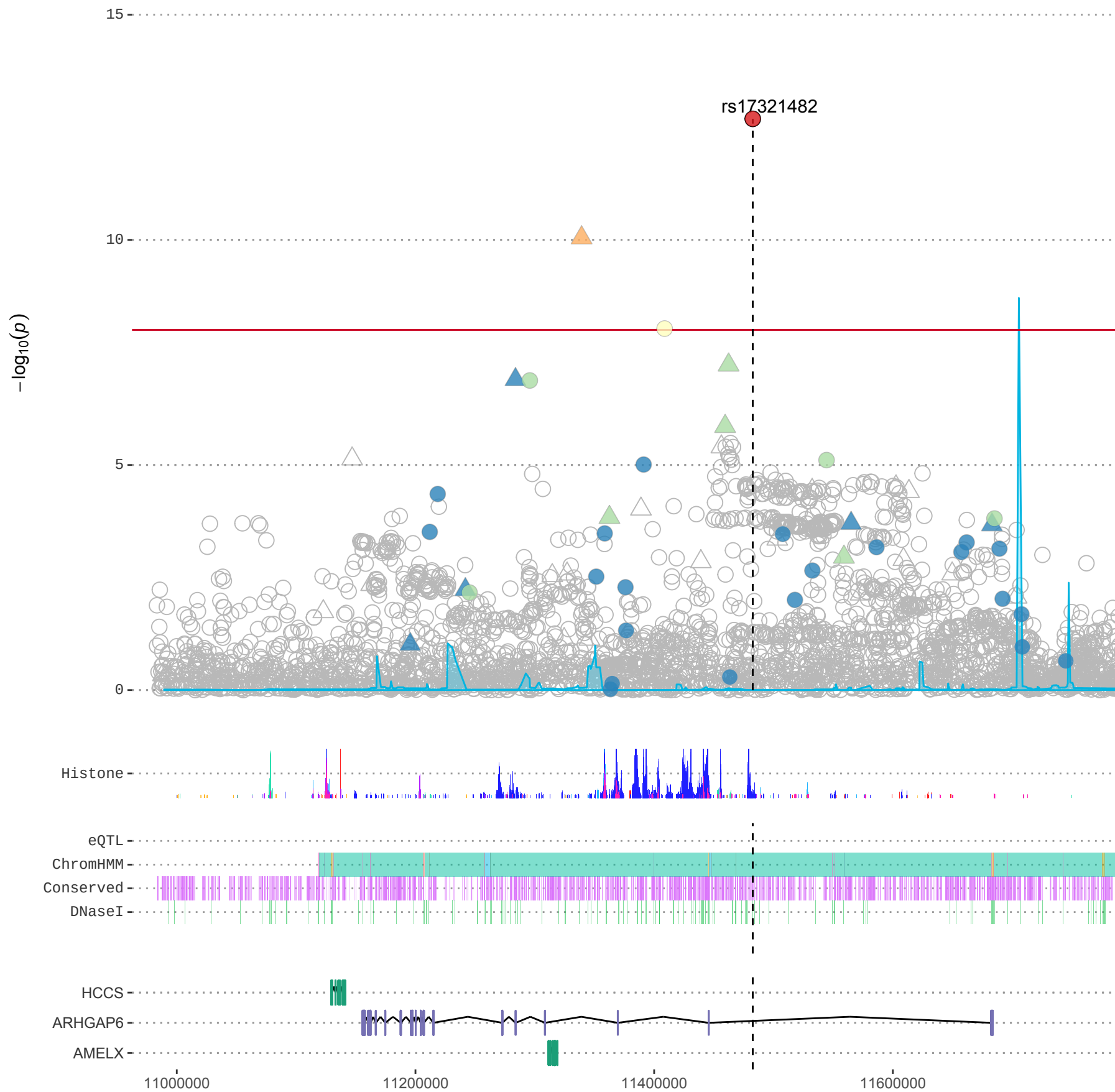
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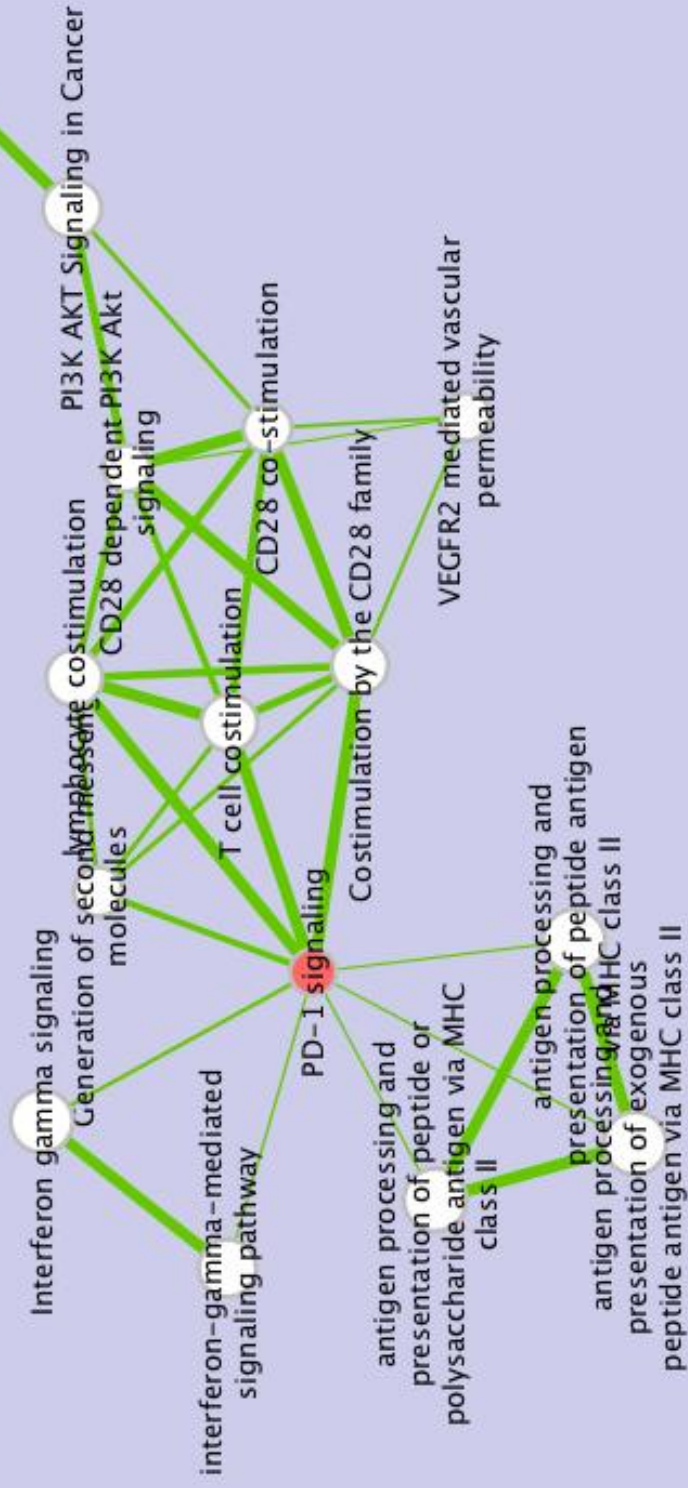
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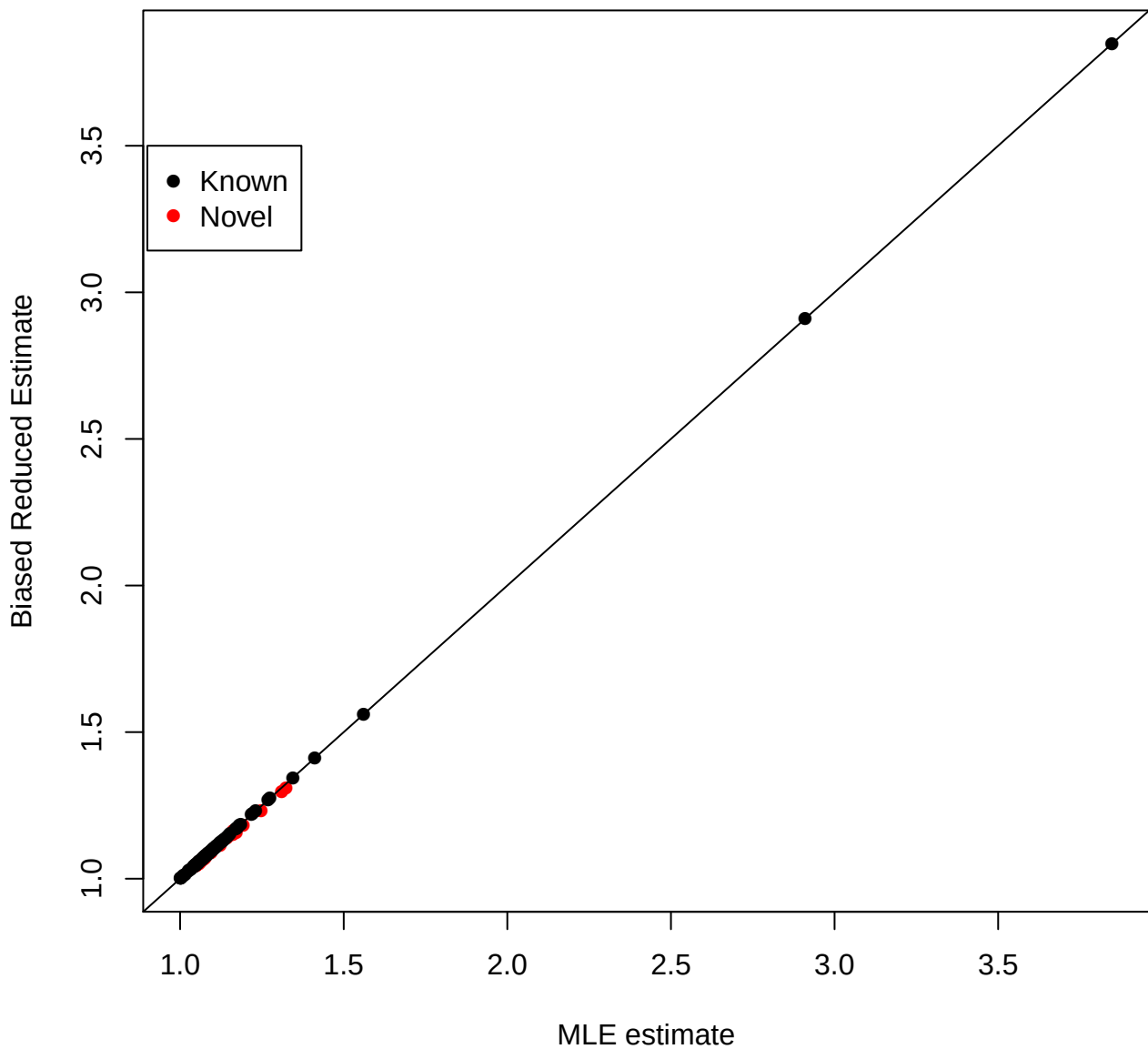


bf) chr23_10983000_11984000



Constitutive Signaling by AKT1
E17K in Cancer





Supplementary Table 1. Brief overview and details of studies included in the prostate cancer OncoArray project ².

Study Abbreviation	Study Name	Study Site	Country	Study Design	Principal Investigator(s)	Ancestry	No. of Cases ^a	No. of Controls ^a	No. of Cases in Analysis ^b	No. of Controls in Analysis ^b	Case Source	Control Source	Study Reference
Aarhus	Aarhus Prostate Cancer Study	Aarhus	Denmark	Hospital-based, Retrospective, Observational	Karina Dalsgaard Sorensen, Torben Falck Orntoft	European	1140	670	1079	550	Patients treated for prostate adenocarcinoma at Department of Urology, Aarhus University Hospital, Skejby (Aarhus, Denmark)	Age-matched males treated for myocardial infarction or undergoing coronary angioplasty, but with no prostate cancer diagnosis based on information retrieved from the Danish Cancer Register and the Danish Cause of Death Register.	PMID: 12891190
AHS	Agricultural Health Study	Maryland	USA	Nested case-control study within prospective cohort	Laura E. Beane-Freeman, Michael Alavanja, Stella Koutros	European	514	1314	471	1179	linkage to cancer registries in study states	matched controls from cohort	PMID: 8732939
ATBC	Alpha-Tocopherol Beta-Carotene	Maryland	USA	Prospective, nested case-control	Demetrius Albanes	Finnish	1474	2205	1205	1910	Finnish male smokers aged 50-69 years at baseline	Finnish male smokers aged 50-69 years at baseline	PMID: 8205268
Canary PASS	Prostate Active Surveillance Study	FHCRC (coordinating center)	USA	Prospective, Multi-site, Observational Active Surveillance Study	Daniel W. Lin	European	380	0	371	0	clinic based from Beth Israel Deaconess Medical Center, Eastern Virginia Medical School, University of California at San Francisco, University of Texas Health Sciences Center San Antonio, University of Washington, VA Puget Sound	N/A	PMID: 19758683
CCI	CCI Prostate	Alberta	Canada	Case series, Hospital-based	Matthew Parliament, Nawaid Usmani		285	0	270	0	Cases identified through clinics at the Cross Cancer Institute	N/A	PMID: 24656733
CeRePP (ProGene)	French Prostate Case Control Study	Paris	France	Case-Control, Prospective, Observational, Hospital-based	Olivier Cussenot, Géraldine Cance-Tassin	European	1064	881	923	694	Patients, treated in French departments of Urology, who had histologically confirmed prostate cancer	Controls were recruited as participating in a systematic health screening program and found unaffected (normal digital rectal examination and total PSA < 4 ng/ml, or negative biopsy if PSA > 4 ng/ml).	PMID: 18264096
COH	City Of Hope	Duarte	USA	Hospital-based cases and controls from outside	Susan L. Neuhausen	non-Hispanic Caucasian	263	269	260	259	Consented prostate cancer cases at City of Hope	Consented unaffected males that were part of other studies where they consented to have their DNA used for other research studies.	
COSM	Cohort of Swedish Men	Stockholm	Sweden	Population-based cohort	Alicja Wolk	Caucasian	2406	1204	2051	1121	General population	General population	PMID: 23508823
CPCS1	Copenhagen Prostate Cancer Study 1 & 2	Copenhagen	Denmark	Case-control - Denmark	Berge G. Nordestgaard	European	552	269	533	256	Hospital referrals	Copenhagen General Population Study	PMID: 23468462
CPCS2	Copenhagen Prostate Cancer Study 1 & 2	Copenhagen	Denmark			European	461	238	439	227	Hospital referrals	Copenhagen General Population Study	PMID: 22563304
CPS-II	American Cancer Society (CPS-II)	Atlanta	USA	Nested case-control derived from a prospective cohort study	Susan M. Gapstur, Victoria L. Stevens	European	4743	4508	4425	4085	Identified through self-report on follow-up questionnaires and verified through medical records or cancer registries, identified through cancer registries or the National Death Index (with prostate cancer as the primary cause of death).	Cohort participants who were cancer-free at the time of diagnosis of the matched case, also matched on age (±6 mo) and date of biospecimen donation (±6 mo).	PMID: 11900235
EPIC	European Prospective Investigation Into Cancer and Nutrition (BPC3)	EU	Multi Center in EU	Case-control - Germany, Greece, Italy, Netherlands, Spain, Sweden, UK	Tim J. Key, Ruth C. Travis, Elio Riboli	European	697	739	632	696	Identified through record linkage with population-based cancer registries in Italy, the Netherlands, Spain, Sweden and UK. In Germany and Greece, follow-up is active and achieved through checks of insurance records and cancer and pathology registries as well as via self-reported questionnaires; self-reported incident cancers are verified through medical records.	Cohort participants without a diagnosis of cancer.	PMID: 12639222
ERSPC	Erasmus Medical Centre	Rotterdam	The Netherlands	Population-based randomised trial	Christopher Bangma, Monique J. Roobol	European	75	75	71	66	Men with Pca from screening arm ERSPC Rotterdam	Men without Pca from screening arm ERSPC Rotterdam	PMID: 19297566
ESTHER	Epidemiological investigations of the chances of preventing, recognizing early and optimally treating chronic diseases in an elderly population	Heidelberg	Germany	Case-control, Prospective, Observational, Population-based	Hermann Brenner	European	341	333	14	3	Prostate cancer cases in all hospitals in the state of Saarland, from 2001-2003	Random sample of participants from routine health check-up in Saarland, in 2000-2002	PMID: 19383895
FHCRC	Fred Hutchinson Cancer Research Centre	Seattle	USA	Population-based, case-control, ages 35-74 years at diagnosis, King County, WA, USA	Janet L. Stanford	European-American	434	421	409	391	Identified through the Seattle-Puget Sound SEER cancer registry	Randomly selected, age-frequency matched residents from the same county as cases	PMID: 10548316; PMID: 18556686
Gene-PARE	Genetic Predictors of Adverse Radiotherapy Effects	New York, Tokyo and Chiba	USA and Japan	Hospital-based	Barry Rosenstein, Harry Ostrer	European	1330	0	1231	0	Patients that received radiotherapy for treatment of prostate cancer	n/a	
Hamburg-Zagreb		Hamburg	Germany	Hospital-based, Prospective	Marija Gamulin, Davor Lessel	European	154	154	146	149	Prostate cancer cases seen at the Department of Oncology, University Hospital Center Zagreb, Croatia	Population-based (Croatia), healthy men, older than 50, with no medical record of cancer, and no family history of cancer (1st&2nd degree relatives)	

HPFS	Health Professionals Follow-up Study	Harvard	USA	Nested case-control	Sara Lindstrom, Edward Giovannucci, Kathryn L. Penney, Lorelei Mucci	European	1233	1095	1170	1050	Participants of the HPFS cohort	Participants of the HPFS cohort	
IMPACT	Identification of Men with a genetic predisposition to Prostate Cancer	The Institute of Cancer Research, London	UK	Observational	Rosalind A. Eeles	European	60	993	50	875	Carriers and non carriers (with a known mutation in the family) of the BRCA1 and BRCA2 genes, aged between 40 and 69, who are undergoing prostate screening with annual PSA testing. This cohort have been diagnosed with prostate cancer during the study.	Carriers and non carriers (with a known mutation in the family) of the BRCA1 and BRCA2 genes, aged between 40 and 69, who are undergoing prostate screening with annual PSA testing. This cohort have not been diagnosed with prostate cancer during the study.	PMID: 24484606; PMID 20840664; PMID 17419707
IPO-Porto	Portuguese Oncology Institute, Porto	Porto	Portugal	Hospital-based	Manuel R. Teixeira	European	386	190	371	180	Early onset and/or familial prostate cancer	Blood donors	PMID: 26176944; PMID 26289772
KULEUVEN	Katholieke Universiteit Leuven	Leuven	Belgium	Hospital-based, Prospective, Observational	Frank Claessens, Thomas Van den Broeck, Steven Joniau	European	175	103	166	103	Prostate cancer cases recruited at the University Hospital Leuven.	Healthy males with no history of prostate cancer recruited at the University Hospitals, Leuven.	
LAAPC	Los Angeles Study of Aggressive Prostate Cancer	California	USA	Population-based, Case-control	Sue Ann Ingles	European	789	621	443	287			
MCC-Spain	Multi Case Control Study-Spain	Barcelona	Spain	Case-control	Manolis Kogevinas, Gemma Castaño-Vinyals, Javier Llorca Diaz	European	542	443	523	399	Identified through the urology departments of the participating hospitals	Population-based, frequency age and region matched, ascertained through the rosters of the primary health care centers	PMID: 25613680
MCCS	Melbourne Collaborative Cohort Study	Melbourne	Australia	Nested case-control, Melbourne, Victoria	Graham G. Giles, Melissa C. Southey	European	780	334	401	303	Identified by linkage to the Victorian Cancer Registry	Cohort participants without a diagnosis of cancer	PMID: 12484128
MDACC_AS	MD Anderson Cancer Center, active surveillance trial	Texas	USA	A prospective cohort study	Christopher J. Logothetis, Jeri Kim	European	633	0	535	0	Men with clinically organ-confined prostate cancer meeting eligibility criteria for a prospective cohort study of active surveillance at MD Anderson Cancer Center	N/A	PMID: 26059275
MEC	Multiethnic Cohort Study MEC, Non-MEC	California & Hawaii	USA	Population-based	Christopher A. Haiman, Brian E. Henderson, Fredrick Schumacher	European	1310	1396	100	120			
MOFFITT	Moffitt Prostate Cancer Study	Florida	USA	Hospital-based	Jong Y. Park	European	602	346	400	205	clinic based from Moffitt Cancer Center	Moffitt Cancer Center affiliated Lifetime cancer screening center	PMID: 21802122
Oslo	Oslo University Hospital / General Cohort of Adults in Norway (CONOR)	Oslo	Norway	Population-based, Retrospective, Observational	Lovise Maehle, Eli Marie Grindedal, Johanna Schleutker, Fredrik Wiklund	European	1513	0	1453	0	Prostate cancer cases were selected from the following cohorts: The Tromsø Health Study (Tromsø IV and V), The Troms and Finnmark Health Study (TROFINN), The Nord-Trøndelag Health Study (HUNT 2 and 3), The Oslo Health Study (Oslo I, HUBRO, The Immigrant Study, The Health Study in Romsås and Furuset (MoRo), Oslo II), The Oppland and Hedmark Health Study (OPPHED), and the Hordaland Health Study (HUSK).	N/A	PMID: 17984119
PCMUS	Prostate Cancer study Medical University Sofia	Sofia	Bulgaria	Case-control - Sofia, Bulgaria	Radka Kaneva, Vario Mitev, Chavdar Slavov	European	195	90	192	89	Patients of Clinic of Urology, Alexandrovska University Hospital, Sofia, Bulgaria, PrCa histopathologically confirmed	72 patients with verified BPH and PSA<3.5; 78 healthy controls from the MMC Biobank, no history of PrCa	PMID: 19767753
PHS	Physicians Health Study	Harvard	USA	Nested case-control	Meir Stampfer, Sara Lindstrom, Peter Kraft, Kathryn L. Penney	European	664	286	631	267	Participants of the PHS1 trial/cohort	Participants of the PHS1 trial/cohort	PMID: 2664509
PLCO	Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial	Bethesda	USA	Nested case-control	Sonja I. Berndt, Stephen Chanock, Gerald Andriole	European	1010	1275	677	980	Men with a confirmed diagnosis of prostate cancer from the PLCO Cancer Screening Trial.	Controls were men enrolled in the PLCO Cancer Screening Trial without a diagnosis of cancer at the time of case ascertainment.	PMID: 19297565
Poland	The Poland Group	Szczecin	Poland	Case-control	Cezary Cybulski	European	510	345	484	317	men with unselected prostate cancer, diagnosed in north-western Poland at the University Hospital in Szczecin	cancer-free men from the same population, taken from the healthy adult patients of family doctors in the Szczecin region	
PRAGGA	PRostate cAncer Genetics in Galicia	Galicia	Spain	Case-control	Manuela Gago Dominguez, Jose Esteban Castelao Henrik Gronberg, Fredrik Wiklund	European	133	104	130	102	Population-based	Population-based	
PROCAP	PROgression in Cancer of the Prostate	Stockholm	Sweden	Population-based, Retrospective, Observational		European	677	339	613	241	Cases were ascertained from the National Prostate Cancer Register of Sweden Follow-Up Study, a retrospective nationwide cohort study of patients with localized prostate cancer.	Controls were selected among men referred for PSA testing in laboratories in Stockholm County, Sweden, between 2010 and 2012.	PMID: 21520160
PROFILE	Genetic prostate cancer risk stratification for targeted screening	The Institute of Cancer Research, London	UK	Hospital-based, Prospective, Observational	Rosalind A. Eeles	European	32	88	12	22	Men with a family history of prostate cancer who are screened for prostate cancer with PSA testing, MRI and biopsy. This cohort have been diagnosed with cancer	Men with a family history of prostate cancer who are screened for prostate cancer with PSA testing, MRI and biopsy. This cohort do not have cancer	
PROGRES	Prostate cancer : Mechanisms of progression and Treatment	Santiago de Compostela	Spain	Hospital-based, Prospective, Observational	Ana Vega	European	696	349	674	322	Prostate cancer cases from the Hospital Clínico Universitario de Santiago de Compostela, Galicia, Spain	Cancer-free men from the same population	PMID: 24674847; PMID: 23075580; PMID: 22385796

ProMPT	Prostate testing for cancer and Treatment	Cambridge	UK	A study to collect samples and data from subjects with and without prostate cancer. Retrospective, Experimental Trial of treatment. Samples taken from subjects invited for PSA testing from the community at nine centres across United Kingdom	David E. Neal	European	1002	12	782	12	Subjects attending outpatient clinics in hospitals	Subjects attending outpatient clinics in hospitals	
ProtecT	Prostate testing for cancer and Treatment	Oxford, Bristol and Cambridge	UK	Retrospective, Experimental Trial of treatment. Samples taken from subjects invited for PSA testing from the community at nine centres across United Kingdom	Jenny L. Donovan, Freddie C. Hamdy, David E. Neal, Richard Martin	European	4	1448	4	1414	Subjects who have a proven diagnosis of prostate cancer following testing.	Identified through invitation of subjects in the community.	PMID: 27415448
QLD & APCB	QLD = Retrospective Queensland Study & APCB = Australian Prostate Cancer BioResource	QLD = Brisbane APCB = Multi Center in Australia	Australia	QLD = Case-control APCB = Hospital based, prospective study	Jyotsna Batra, Suzanne Chambers, Amanda Spurdle, Judith Clements, Lisa Horvath, Wayne Tilley	European	3489	1356	3299	1252	QLD = A longitudinal cohort study (Prostate Cancer Supportive Care and Patient Outcomes Project: ProCan) conducted in Queensland, through which men newly diagnosed with prostate cancer from 26 private practices and 10 public hospitals were directly referred to ProCan at the time of diagnosis by their treating clinician (age range 43-88 years). All cases had histopathologically confirmed prostate cancer, following presentation with an abnormal serum PSA and/or lower urinary tract symptoms. APCB = Acquired through the Australian Prostate Cancer BioResource (APCB), where cases were recruited through local urologists at the time of diagnosis. Prostate cancer patients enrolled in radiotherapy trials: CHHIP, RT01, Dose Escalation, RADICALS, Pelvic IMRT, PIVOTAL	QLD = Controls comprised healthy male blood donors with no personal history of prostate cancer, recruited through (i) the Australian Red Cross Blood Services in Brisbane (age range 19-76 years) and (ii) the Australian Electoral Commission (AEC) (age and post-code/area matched to ProCan, age range 54-90 years). APCB = n/a	QLD = PMID: 22970239; PMID: 21791109 APCB = www.apcbresource.org.au
RAPPER	Radiogenomics: Assessment of Polymorphisms for Predicting the Effects of Radiotherapy	Manchester	UK	Multi-centre, hospital based blood sample collection study in patients enrolled in clinical trials with prospective collection of radiotherapy toxicity data	Alison Dunning, Catharine West, Neil Burnet	European	2350	0	2113	0	N/A		PMID: 23642504; PMID: 16969982
SEARCH	Study of Epidemiology and Risk factors in Cancer Heredity	Cambridge	UK	Case-control - East Anglia, UK	Paul Pharoah, Nora Pashayan, Alison Dunning	European	2932	1520	2431	232	Men < 70 years of age registered with prostate cancer at the population-based cancer registry, Eastern Cancer Registration and Information Centre, East Anglia, UK	Men attending general practice in East Anglia with no known prostate cancer diagnosis, frequency matched to cases by age and geographic region	PMID: 11044354
SFPCS	San Francisco Prostate Cancer Study	California	USA	Population-based case-control study, Retrospective, Observational	Esther M. John	European	378	249	279	205	non-Hispanic white and African-American men ages 40-79 years diagnosed with advanced prostate cancer from 1997-2000. Cases were identified through the Greater Bay Area Cancer Registry.	non-Hispanic white and African-American men ages 40-79 years without a history of prostate cancer, identified through random-digit dialling. Men ages 65-69 years were also identified through random selections from the rosters of beneficiaries of the Health Care Financing Administration (HCFA). Controls were frequency matched to cases on race and 5-year age group.	PMID: 15958597
SNP_Prostate_Ghent	Serum Proteomic analysis for biomarkers of Aggressive prostate disease in the Guernsey population	Ghent	Belgium	Hospital-based, Retrospective, Observational	Kim De Ruycck, Piet Ost	European	334	141	316	135	Men treated with IMRT as primary or postoperative treatment for prostate cancer at the Ghent University Hospital between 2000 and 2010.	Employees of the University hospital and members of social activity clubs, without a history of any cancer.	PMID: 22658438
SPAG	Serum Proteomic analysis for biomarkers of Aggressive prostate disease in the Guernsey population	Manchester, Southampton	UK	Hospital-based, Retrospective, Observational	Claire Aukim-Hastie, Samantha Larkin, Paul A. Townsend	European	47	192	40	171	Guernsey	Guernsey	
STHM2	Stockholm 2	Stockholm	Sweden	Population-based, Retrospective, Observational	Henrik Gronberg, Fredrik Wiklund	European	3148	1576	3028	1490	Cases were selected among men referred for PSA testing in laboratories in Stockholm County, Sweden, between 2010 and 2012. Randomized clinical trial	Controls were selected among men referred for PSA testing in laboratories in Stockholm County, Sweden, between 2010 and 2012. Randomized clinical trial	PMID: 23891454
SWOG-PCPT	Prostate Cancer Prevention Trial	Seattle	USA	Case-control from a randomized clinical trial	Catherine M. Tangen, Ian M. Thompson	European	1211	1424	1092	1152	Randomized clinical trial	Randomized clinical trial	PMID: 12824459
SWOG-SELECT	Selenium and Vitamin E Cancer Prevention Trial	Seattle	USA	Case-cohort from a randomized clinical trial	Catherine M. Tangen, Ian M. Thompson	European	1877	3295	1508	2138	Randomized clinical trial	Randomized clinical trial	PMID: 19068370
TAMPERE	Finnish Genetic Predisposition to Prostate Cancer Study	Tampere	Finland	Case-control - Finland, Retrospective, Observational, Population-based	Johanna Schleutker	European	2544	1226	2409	1179	Identified through linkage to the Finnish Cancer Registry and patient records; and the Finnish arm of the ERSPC study	Cohort participants without a diagnosis of cancer	PMID: 23535732
Toronto		Toronto	Canada	Prospective hospital-based biopsy cohort	Robert J. Hamilton, Neil E. Fleshner, Antonio Finelli	European	821	599	732	544	Positive biopsies in our database	No prior history of prostate cancer; negative biopsy (or biopsies) in our database	PMID: 24568896
UKGPCS	U.K. Genetic Prostate Cancer Study and The Prostate Cancer Research Foundation Study		UK	ICR, UK	Kenneth Muir, Rosalind A. Eeles, ZSofia Kote-Jarai	European	14107	7601	5790	946	Cases identified through clinics at the Royal Marsden hospital and nationwide NCRN hospitals	Ken Muir's control- 2000	

ULM	Institut fuer Humangenetik Ulm	Ulm	Germany	Case-control - Germany	Christiane Maier	European	475	190	403	3	familial cases (n=162): identified through questionnaires for family history by collaborating urologists all over Germany; sporadic cases (n=308): prostatectomy series performed in the Clinic of Urology Ulm between 2012 and 2014	age-matched controls (n=188): age-matched men without prostate cancer and negative family history collected in hospitals of Ulm	PMID: 19861517
WUGS/WUPCS	Washington University Genetics Study	St. Louis	USA	Cases Series, USA	Bettina Drake, Adam S. Kibel, Aleksandra Klim, Graeme Colditz	European	930	153	674	0	Identified through clinics at Washington University in St. Louis	Men diagnosed and managed with prostate cancer in University based clinic	PMID: 23535732

^a Number of cases/controls denotined before quality control
^b Number of cases/controls including in analysis after quality control
^c The analyses were performed stratified by country and those countries with less than 50 samples (cases or controls) were excluded from analysis. We analysed the OncoArray data with and without overlap with the previous GWAS. This table shows the number without overlap used for the meta-analysis.

Supplementary Table 2. Study-specific descriptive statistics for studies included in the analysis.

Study	Cases			Controls			Cases ^c			
	N ^a	Mean Age	SD ^b	N ^a	Mean Age	SD ^b	N Advanced ^d	N High Aggressive ^e	N Intermediate Aggressive ^e	N Low Aggressive ^e
Aarhus	1079	63.97	6.38	550	64.73	7.55	208	435	565	-
AHS	471	67.34	8.19	1179	56.90	8.72	80	116	138	-
ATBC	1205	72.30	5.55	1910	57.83	4.85	265	183	360	-
Canary PASS	371	62.01	6.74	0	-	-	-	-	-	-
CCI	270	63.71	6.94	0	-	-	-	-	176	94
CeRePP	923	65.78	8.06	694	65.42	8.17	211	415	504	-
COH	260	60.33	6.01	259	57.71	6.76	-	63	197	-
COSM	2051	70.83	8.00	1121	62.16	8.05	495	779	767	497
CPCS1	533	68.25	7.12	256	57.93	11.05	166	272	187	-
CPCS2	439	63.83	5.56	227	57.01	11.85	-	91	263	-
CPSII	4425	71.42	5.87	4085	64.20	5.40	84	359	1009	-
EPIC	632	66.73	6.16	696	57.03	6.45	71	121	212	-
ERSPC	71	71.16	2.26	66	71.27	2.25	-	-	-	-
ESTHER	14	67.04	3.52	3	60.36	3.20	-	-	-	-
FHCRC	409	60.26	7.25	391	60.13	7.81	51	121	112	-
Gene-PARE	1231	67.72	6.95	0	-	-	-	279	565	163
Hamburg_Zagreb	146	68.10	7.41	149	55.36	4.93	-	73	59	-
HPFS	1170	69.77	7.58	1050	54.77	8.03	151	253	664	188
IMPACT	50	63.67	5.70	875	53.14	8.34	-	-	-	-
IPO-Porto	371	56.25	5.71	180	53.12	7.26	65	181	159	-
KULEUVEN	166	65.84	7.36	103	68.54	6.94	69	114	-	-
LAAPC	443	67.19	9.39	287	64.21	10.64	-	-	-	-
MCC-Spain	523	66.76	7.44	399	66.90	8.29	90	118	266	113
MCCS	401	71.08	7.27	303	58.89	7.17	109	89	148	-
MDACC-AS	535	64.55	8.33	0	-	-	-	-	181	345
MEC	100	71.49	8.08	120	60.77	7.98	-	-	-	-
MOFFITT	400	64.66	8.08	205	62.05	9.20	50	58	183	157
Oslo	1453	72.22	8.59	0	-	-	764	51	490	-
PCMUS	192	68.18	7.65	89	66.42	9.21	68	111	93	-
PHS	631	68.62	7.21	267	58.86	8.40	159	147	332	128
PLCO	677	72.39	5.49	980	61.76	4.80	101	115	274	-
Poland	484	69.06	8.28	317	64.38	7.26	152	236	180	56
PRAGGA	130	68.07	6.24	102	61.21	15.91	-	56	-	-
PROCAP	613	64.39	5.01	241	66.03	8.44	-	-	368	132
PROFILE	12	59.85	7.90	22	51.53	7.73	-	-	-	-
PROReSS	674	69.74	6.75	322	61.14	12.03	95	193	380	93
ProMPT	782	64.55	7.93	12	58.54	9.52	184	412	321	-
ProtecT	4	64.50	7.05	1414	60.91	5.61	-	-	-	-
QLD/APCB	3299	62.72	7.04	1252	59.24	10.73	360	1027	1750	88
RAPPER	2113	70.19	6.16	0	-	-	-	-	-	-
SEARCH	2431	63.20	4.72	232	54.38	7.74	468	827	865	291
SFPCS	279	64.78	8.01	205	64.93	8.21	50	-	-	-
SNP_Prostate_Ghent	316	65.28	6.90	135	66.44	9.48	62	140	140	-
SPAG	40	65.21	7.07	171	-	-	-	-	-	-
STHM2	3028	65.29	6.97	1490	65.91	7.80	417	650	1266	661
SWOG-PCPT	1092	69.84	5.79	1152	63.86	5.69	66	77	360	618
SWOG-SELECT	1508	67.40	6.03	2138	63.98	6.27	107	107	700	602
TAMPERE	2409	67.16	6.59	1179	65.99	3.23	349	532	743	404

TORONTO	732	64.78	7.92	544	61.84	8.40	54	106	350	156
UKGPCS	5790	60.13	7.32	946	61.82	7.01	1324	2218	2070	539
ULM	403	64.69	7.08	3	50.67	12.50	69	161	228	-
WUGS/WUPCS	674	61.25	7.88	0	-	-	-	164	363	-
Previous Genome-Wide Association Studies										
BPC3	2068	68.6	6.9	2993	69.2	7	2068	-	-	-
CAPS 1 GWAS	474	67.8	7.5	482	66.3	7.6	443	442	-	-
CAPS 2 GWAS	1458	65.6	7.2	512	67.2	7.4	648	715	393	339
iCOGS	20219	64.3	8	20440	60.4	11.1	3666	6247	7739	2397
Pegasus	4600	68.79	5.8	2941	67.87	5.8	950	911	3263	1382
UK GWAS stage1	1854	57.6	7	1894	59.5	3.5	663	810	500	172
UK GWAS stage 2	3650	63.5	8.6	3940	57.4	6.9	1204	1567	1486	376

*Numbers are based on samples who passed the quality control with no overlap with previous GWAS. Only individuals of European ancestry ethnicities are included.

^bStandard deviation

^cEmpty cell indicate unavailable data or insufficient number of cases (<50) .

^dIdentification of advanced disease cases was based on previous definition of aggressiveness (iCOGS) and available phenotype information: Gleason score 8+, metastatic disease, PSA>100 or death from PrCa.

^eDisease aggressiveness is defined as Low: (T0 or T1) and Gleason Score<=6 and PSA<10; Intermediate: T2 or Gleason Score=7 or PSA between 10 and 20; High: (T3,T4) or (N1) or (M1) or Gleason Score>=8 or PSA>20.

Supplementary Table 3. Information on genotyping methods, quality control, imputation, and statistical analysis.

Study (Consortium)	Sample QC										Imputation (1KGP)		Association analyses		
	Contributed to Previous Meta-Analysis	Inclusion/exclusion criteria										SNPs Inclusion Criteria	Software	SNPs in meta-analysis ^b	Software
		No. of cases in file (with overlap)	No. of controls in file (with overlap)	Minimum sample call rate for inclusion	Exclusions ^a	No. of cases after exclusions (with overlap)	No. of controls after exclusions (with overlap)	Geno-typing platform	SNP Call rate	P, HWE	SNPs that met QC criteria				
OncoArray (European)	No	48889 (57580)	29293 (37927)	≥95%	1–9	46939 (55147)	27910 (36224)	Illumina OncoArray	≥95%	In controls: ≥1x10 ⁻⁷ In cases: ≥1x10 ⁻¹²	498417	Rsq>0.3,	Impute2	20370935	In-house C++ program
BPC3	Yes	2137	3101	≥95%	2,5-7	2068	2993	Illumina Human610 Illumina 610K	≥95%	≥1x10 ⁻⁵	525766	MAF>0.01, Rsq>0.3,	Impute2	9674516	SNPtest
CAPS 1 GWAS	Yes	498	502	≥95%	1, 2, 4-7	474	482	Affymetrix GeneChip 500K	≥95%	≥1x10 ⁻⁶	369025	MAF≥0.01, Info>0.3	Impute2	9614577	In-house C++ program
CAPS 2 GWAS	Yes	1483	519	≥95%	1, 2, 4-7	1458	512	Affymetrix GeneChip 5.0K	≥95%	≥1x10 ⁻⁶	369610	MAF≥0.01, Info>0.3	Impute2	9585491	In-house C++ program
iCOGS	Yes	24198	23994	≥95%	1–9	20219	20440	Custom Illumina Infinium (iCOGS)	≥95%	≥1x10 ⁻⁷	201598	MAF≥0.005, Info>0.3	Impute2	10894742	In-house C++ program
Pegasus	Yes	4622	2954	≥94%	4,6,7	4600	2941	Human Omni 2.5	≥90%	≥1x10 ⁻⁶	1675706	Info>0.3	Impute2	16852405	SNPtest
UK GWAS stage1	Yes	1906	1934	≥97%	1, 2, 4-7	1854	1894	Illumina Infinium HumanHap 550 Array	≥95%	≥1x10 ⁻⁵	541129	MAF≥0.01, Info>0.3	Impute2	9491560	In-house C++ program
UK GWAS stage 2	Yes	3888	3956	≥97%	1, 2, 4-7	3650	3940	Illumina iSELECT	≥95%	≥1x10 ⁻⁵	43671	MAF≥0.01, Info>0.3	Impute2	5904519	In-house C++ program

^aExclusion criteria = 1) XX or XXY; 2) heterozygosity lower/higher than 4.89 SD from mean; 3) low concordance with previous genotypes; 4) false duplicates; 5) cryptic duplicates; 6) relatives; 7) ancestry outliers; 8) UK, CAPS or BPC3 GWAS overlap; 9) only case study from case/control analyses.

^bThese SNPs were filtered by imputation $r^2 < 0.3$

Supplementary Table 4. Prostate cancer definitions and classifications for aggressiveness.

OncoArray Stratified Analyses				
	Analysis Title	Outcome Group	Reference Group	Model
	Overall	PrCa Cases	Non-PrCa Controls	Logistic
	High vs Low	High Aggressive	Low Aggressive	Logistic
	High vs Low/Intermediate	High Aggressive	Low/Intermediate Aggressive	Logistic
	Gleason Score	Continuous score	-	Linear
	Advanced vs Non-advanced	Advanced PrCa	Non Advanced PrCa	Logistic
	Advanced	Advanced PrCa	Non-PrCa Controls	Logistic
	Early-onset	PrCa Age at Dx <= 55	Non-PrCa Controls	Logistic
Classification	Low Aggressive	Intermediate Aggressive	High Aggressive	Advanced
	<=T1 and GS<=6 and PSA<10	T2 or GS7 or PSA 10-20	T3/T4 or N1 or M1 or GS>=8 or PSA>20	Metastatic disease or GS>=8 or PSA>100 or PrCa Death

Supplementary Table 5. Study sample sizes by consortia/GWAS and prostate cancer clinical definitions in the overall and stratified meta-analyses.

	Overall		High vs Low ^a		High vs Low/Intermediate ^a		Advanced vs Non-Advanced ^a		Advanced ^a		Early-onset		Gleason Score
	PrCa Cases	Non-PrCa Controls	High PrCa ^b	Low PrCa ^b	High PrCa ^b	Low/Intermediate PrCa ^b	High PrCa (+death) ^b	Low/Intermediate PrCa ^b	High PrCa (+death) ^b	Non-PrCa Controls ^b	PrCa Age at Dx ≤ 55	Non-PrCa Controls ^b	Cases
OncoArray European	44825	27904	8449	5136	10609	21710	7095	38704	6263	27235	3359	26353	32852
BPC3	2068	2993	-	-	-	-	-	-	1918	3007	-	-	1316
CAPS1	474	482	-	-	-	-	301	189	301	466	-	-	412
CAPS2	1458	512	715	339	715	733	491	999	491	480	110	480	1382
iCOGS	20219	20440	3190	2334	6046	10002	3456	15544	3377	18469	2142	12636	16989
Pegasus	4600	2941	911	1382	911	3263	950	3230	950	2941	-	-	4544
UK1	1854	1894	810	172	810	672	663	1191	663	1894	684	1894	1356
UK2	3650	3940	1486	376	1567	1713	1204	2564	1204	3816	693	2893	3127
Total	79148	61106	15561	9739	20658	38093	14160	62421	15167	58308	6988	44256	61978

^a Case/control definitions provided in Supplementary Table 4.

^b Case and control sample sizes may differ based on the criteria of a minimum of 50 cases were needed for a study to contribute to the analysis.

Supplementary Table 6. Inflation statistics (λ) in the overall analysis (SNPs with MAF $\geq$ 1%).

Study/Population	No. SNPs	λ	λ_{1000}^a	No. SNPs ^b	λ	λ_{1000}^a
BPC3	10695315	0.9390	0.9751	10320462	0.9390	0.9751
CAPS1	10103646	1.0410	1.0858	9750405	1.0380	1.0795
CAPS2	10080045	1.0499	1.0658	9726753	1.0465	1.0614
iCOGS	10144365	1.1065	1.0051	9789222	1.0839	1.0040
Pegasus	10061233	1.0085	1.0024	9708196	1.0027	1.0008
UK1	9982351	1.0448	1.0239	9642575	1.0354	1.0189
UK2	9356389	1.0340	1.0095	9022466	1.0219	1.0061
OncoArray (European) ^c	10109934	1.1622	1.0038	9757757	1.1335	1.0031
European (Meta-analysis)	10387995	1.2027	1.0029	10025514	1.1700	1.0024

^a λ_{1000} : Inflation for a study with 1000 cases and 1000 controls.

^bAfter excluding SNPs/indels within ± 500 kb of the known prostate cancer risk loci.

^cOncoArray analysis applied a logistic regression model stratified by country. Analyses of iCOGS, BPC3, and UK2 used a logistic regression model stratified by study.

Supplementary Table 7. Known prostate cancer SNP associations in the overall meta-analysis and the OncoArray.

SNP ID	Chr	Pos	Effect Allele	Overall Meta-Analysis			OncoArray			Fine-Mapped Regions		
				EAF	OR (95% CI)	P	EAF	OR (95% CI)	P	Start	Finish	PMID
SNPs discovered in European populations												
rs636291	1	10556097	A	0.68	1.04 (1.03-1.06)	5.9E-07	0.68	1.03 (1.01-1.06)	1.4E-02	10056097	11056097	25217961
rs17599629	1	150658287	G	0.22	1.07 (1.05-1.09)	9.9E-12	0.22	1.05 (1.02-1.07)	1.3E-03	150158287	151158287	25217961
rs1218582	1	154834183	G	0.45	1.05 (1.03-1.06)	9.6E-09	0.45	1.04 (1.01-1.06)	3.0E-03	154334183	155411798	23535732
rs4245739	1	204518842	A	0.74	1.10 (1.08-1.12)	3.2E-24	0.74	1.10 (1.07-1.13)	1.2E-12	203991549	205018842	20197460, 23535732
rs11902236	2	10117868	T	0.27	1.05 (1.03-1.06)	5.2E-07	0.27	1.03 (1.00-1.06)	2.5E-02	9611973	11210730	23535732
rs9287719	2	10710730	C	0.47	1.07 (1.05-1.09)	6.0E-17	0.47	1.08 (1.05-1.10)	8.7E-11	9611973	11210730	25217961
rs9306895 ^a	2	20878153	C	0.36	1.08 (1.06-1.10)	3.1E-21	0.37	1.07 (1.05-1.10)	1.0E-09	20388265	21388265	26025378
rs1465618	2	43553949	T	0.21	1.09 (1.07-1.11)	2.1E-18	0.21	1.09 (1.06-1.12)	1.2E-09	43053949	44137998	19767753
rs721048	2	63131731	A	0.18	1.10 (1.08-1.12)	5.0E-22	0.18	1.10 (1.07-1.13)	5.0E-11	62263347	63777843	18264098
rs10187424	2	85794297	T	0.57	1.08 (1.06-1.09)	1.3E-20	0.57	1.07 (1.05-1.10)	3.7E-10	85267735	86294297	21743467
rs12621278	2	173311553	A	0.94	1.27 (1.23-1.32)	2.2E-42	0.94	1.26 (1.20-1.32)	1.2E-19	172809618	173915560	19767753
rs2292884 ^b	2	238443226	G	0.24	1.06 (1.04-1.08)	3.7E-11	0.24	1.05 (1.03-1.08)	1.4E-04	237940449	238943226	21743057
rs3771570	2	242382864	T	0.15	1.09 (1.06-1.11)	1.2E-14	0.15	1.09 (1.05-1.12)	1.7E-07	241657087	242920971	23535732
rs2660753	3	87110674	T	0.10	1.13 (1.10-1.16)	6.3E-21	0.11	1.12 (1.08-1.16)	3.3E-10	86610674	87967332	18264097
rs7611694	3	113275624	A	0.58	1.09 (1.07-1.10)	4.5E-25	0.58	1.08 (1.06-1.11)	2.9E-12	112775624	113782326	23535732
rs10934853	3	128038373	A	0.28	1.10 (1.09-1.12)	1.1E-29	0.28	1.10 (1.07-1.12)	2.5E-13	127419046	128752313	19767754
rs6763931	3	141102833	A	0.44	1.04 (1.03-1.06)	7.4E-08	0.44	1.04 (1.01-1.06)	2.4E-03	140602833	141610074	21743467
rs10936632	3	170130102	A	0.51	1.10 (1.08-1.12)	3.4E-34	0.50	1.10 (1.07-1.12)	2.4E-16	169574517	170630102	21743467
rs10009409	4	73855253	T	0.31	1.06 (1.04-1.08)	4.3E-10	0.31	1.03 (1.00-1.05)	2.9E-02	73355253	74849158	25217961
rs1894292	4	74349158	G	0.52	1.06 (1.05-1.08)	5.2E-15	0.52	1.05 (1.02-1.07)	1.5E-04	73355253	74849158	23535732
rs12500426	4	95514609	A	0.46	1.07 (1.05-1.09)	5.1E-18	0.47	1.05 (1.03-1.07)	2.2E-05	95005592	96062877	19767753
rs17021918	4	95562877	C	0.65	1.09 (1.07-1.11)	1.4E-24	0.65	1.07 (1.05-1.10)	2.3E-09	95005592	96062877	19767753
rs7679673	4	106061534	C	0.59	1.13 (1.11-1.15)	1.2E-49	0.59	1.11 (1.09-1.14)	4.6E-20	105561534	106564626	19767753
rs2242652	5	1280028	G	0.79	1.17 (1.15-1.20)	3.5E-52	0.79	1.19 (1.16-1.22)	9.6E-34	780028	2395829	21743467
rs2121875	5	44365545	C	0.33	1.05 (1.03-1.07)	1.4E-08	0.33	1.02 (1.00-1.05)	4.4E-02	43865545	44885415	21743467
rs6869841	5	172939426	T	0.21	1.04 (1.02-1.06)	2.0E-05	0.21	1.02 (1.00-1.05)	1.1E-01	172439426	173444400	23535732
rs4713266	6	11219030	C	0.52	1.05 (1.04-1.07)	9.5E-11	0.52	1.04 (1.02-1.07)	3.0E-04	10719030	11719030	25217961
rs7767188 ^c	6	30073776	A	0.21	1.06 (1.04-1.08)	2.0E-08	0.20	1.04 (1.02-1.07)	2.6E-03	29573776	30573776	25217961
rs130067	6	31118511	G	0.20	1.05 (1.03-1.07)	1.6E-07	0.20	1.04 (1.01-1.07)	5.3E-03	30618511	32900939	21743467
rs3096702	6	32192331	A	0.38	1.06 (1.04-1.07)	9.5E-12	0.37	1.05 (1.02-1.07)	8.2E-05	30618511	32900939	23535732
rs3129859 ^d	6	32400939	G	0.67	1.06 (1.04-1.08)	1.3E-12	0.68	1.05 (1.02-1.08)	1.2E-04	30618511	32900939	25217961
rs2273669	6	109285189	G	0.15	1.07 (1.05-1.10)	3.2E-10	0.15	1.06 (1.03-1.09)	3.5E-04	108779211	109785189	23535732
rs1933488	6	153441079	A	0.58	1.08 (1.06-1.10)	4.0E-21	0.58	1.07 (1.04-1.09)	3.5E-08	152932566	153941079	23535732
rs9364554	6	160833664	T	0.28	1.11 (1.09-1.13)	4.6E-33	0.28	1.10 (1.07-1.12)	3.7E-13	160081543	161382029	18264097
rs12155172	7	20994491	A	0.22	1.10 (1.08-1.12)	9.1E-23	0.22	1.08 (1.06-1.11)	2.0E-09	20494491	21496953	23535732
rs10486567	7	27976563	G	0.76	1.14 (1.12-1.16)	2.0E-45	0.76	1.15 (1.12-1.18)	1.3E-25	27091215	28476563	18264096
rs56232506	7	47437244	A	0.45	1.06 (1.04-1.07)	1.3E-11	0.45	1.04 (1.02-1.07)	4.1E-04	46937244	47937244	25217961
rs6465657	7	97816327	C	0.46	1.11 (1.09-1.12)	7.0E-37	0.46	1.10 (1.08-1.13)	2.0E-17	97307882	98316327	18264097
rs2928679	8	23438975	A	0.44	1.05 (1.04-1.07)	1.9E-11	0.44	1.05 (1.03-1.07)	3.6E-05	22938975	24028511	19767753
rs11135910	8	25892142	T	0.15	1.08 (1.06-1.10)	9.2E-13	0.15	1.06 (1.03-1.10)	1.5E-04	25392142	26410156	23535732
rs12543663	8	127924659	C	0.29	1.12 (1.10-1.14)	2.6E-38	0.29	1.11 (1.08-1.14)	3.8E-17	127333841	129040776	19767752
rs10086908	8	128011937	T	0.70	1.13 (1.11-1.15)	1.8E-47	0.70	1.12 (1.10-1.15)	9.4E-21	127333841	129040776	19767752
rs183373024	8	128104117	G	0.01	2.91 (2.69-3.14)	3.7E-160	0.01	2.89 (2.58-3.22)	2.1E-79	127333841	129040776	23104005
rs16901979	8	128124916	A	0.03	1.56 (1.50-1.62)	1.4E-105	0.03	1.51 (1.43-1.60)	1.1E-46	127333841	129040776	17401366
rs620861	8	128335673	G	0.63	1.15 (1.13-1.17)	4.9E-63	0.63	1.16 (1.13-1.18)	5.8E-36	127333841	129040776	19767752
rs6983267	8	128413305	G	0.51	1.22 (1.20-1.24)	2.8E-141	0.51	1.21 (1.18-1.24)	1.2E-64	127333841	129040776	17401363
rs1447295	8	128485038	A	0.11	1.41 (1.38-1.45)	1.2E-179	0.10	1.43 (1.38-1.48)	3.3E-96	127333841	129040776	17401363, 17401366
rs17694493	9	22041998	G	0.14	1.08 (1.05-1.10)	2.3E-10	0.14	1.05 (1.02-1.09)	2.5E-03	21541998	22541998	25217961
rs1571801	9	124427373	T	0.27	1.03 (1.01-1.04)	3.8E-03	0.27	1.01 (0.99-1.02)	3.2E-01	123927373	125154402	18073375
rs76934034	10	46082985	T	0.92	1.12 (1.09-1.16)	2.0E-14	0.92	1.11 (1.06-1.16)	1.1E-06	45582985	46582985	25217961
rs10993994	10	51549496	T	0.38	1.23 (1.21-1.25)	2.3E-147	0.38	1.24 (1.21-1.26)	1.1E-78	51049496	52049496	18264096, 18264097
rs3850699	10	104414221	A	0.70	1.07 (1.05-1.09)	6.0E-16	0.70	1.06 (1.03-1.08)	9.0E-06	103914221	104915094	23535732
rs4962416	10	126698672	C	0.27	1.06 (1.04-1.08)	2.4E-11	0.27	1.06 (1.03-1.09)	5.2E-06	126140936	127196872	18264096
rs7127900	11	2233574	A	0.20	1.19 (1.16-1.21)	4.9E-68	0.20	1.18 (1.15-1.21)	1.2E-32	1733574	2734093	19767753
rs7931342	11	68994497	G	0.50	1.17 (1.15-1.19)	9.7E-87	0.51	1.16 (1.14-1.19)	3.6E-40	68484602	69953985	18264097
rs11568818	11	102401661	T	0.55	1.08 (1.06-1.09)	1.7E-19	0.55	1.08 (1.05-1.10)	7.4E-11	101901661	102901661	23535732
rs11214775	11	113807181	G	0.71	1.07 (1.05-1.09)	3.9E-15	0.70	1.08 (1.05-1.10)	4.4E-09	113307181	114307181	25217961
rs80130819	12	48419618	A	0.91	1.10 (1.07-1.13)	1.9E-11	0.91	1.10 (1.05-1.14)	6.3E-06	47919618	48919618	25217961
rs10875943	12	49676010	C	0.29	1.07 (1.05-1.09)	2.3E-15	0.29	1.06 (1.03-1.08)	9.9E-06	49176010	50176010	21743467
rs902774	12	53273904	A	0.15	1.13 (1.11-1.16)	1.7E-31	0.15	1.13 (1.10-1.17)	1.3E-15	52773904	53816821	21743057
rs1270884	12	114685571	A	0.48	1.07 (1.06-1.09)	1.2E-18	0.48	1.07 (1.05-1.10)	1.5E-09	114185571	115584059	23535732
rs8008270	14	53372330	C	0.81	1.09 (1.07-1.11)	6.4E-16	0.81	1.07 (1.03-1.10)	2.3E-05	5287		

rs4844289	23	70407983	G	0.38	1.04 (1.03-1.05)	2.9E-12	0.39	1.04 (1.02-1.06)	8.0E-06	69639850	70907983	25217961
<i>SNPs discovered in multi-ancestry populations</i>												
rs1775148	1	205757824	C	0.36	1.04 (1.03-1.06)	1.47E-07	0.36	1.03 (1.01-1.06)	9.2E-03	205257824	206257824	25217961
rs9443189	6	76495882	A	0.86	1.07 (1.04-1.09)	4.68E-08	0.86	1.07 (1.03-1.10)	1.6E-04	75995882	76995882	25217961
rs7153648	14	61122526	C	0.08	1.03 (1.01-1.07)	2.14E-02	0.08	1.02 (0.99-1.05)	3.0E-01	60622526	61622526	25217961
rs12051443	16	71691329	A	0.34	1.03 (1.01-1.05)	6.86E-04	0.34	1.02 (0.99-1.04)	1.3E-01	71191329	72191329	25217961
rs12480328	20	49527922	T	0.93	1.11 (1.08-1.15)	6.67E-12	0.93	1.11 (1.06-1.16)	4.7E-06	49027922	50027922	25217961
rs1041449	21	42901421	G	0.43	1.05 (1.04-1.07)	2.94E-10	0.43	1.04 (1.02-1.07)	3.9E-04	42401421	43401421	25217961
rs2238776	22	19757892	G	0.80	1.05 (1.03-1.08)	7.61E-07	0.80	1.04 (1.01-1.07)	5.0E-03	19257892	20257892	25217961
<i>SNPs discovered in non-European populations</i>												
rs2055109	3	87467332	T	0.76	1.02 (1.00-1.03)	8.99E-02	0.76	1.02 (1.00-1.05)	7.2E-02	86610674	87967332	22366784
rs12653946	5	1895829	T	0.42	1.08 (1.06-1.10)	9.58E-22	0.43	1.08 (1.06-1.11)	4.8E-12	780028	2395829	20676098
rs1983891	6	41536427	T	0.28	1.09 (1.07-1.10)	1.13E-20	0.28	1.09 (1.07-1.12)	3.9E-13	41036427	42043793	20676098
rs339331	6	117210052	T	0.69	1.09 (1.07-1.11)	5.35E-22	0.70	1.09 (1.06-1.12)	6.9E-12	116666036	117710052	20676098
rs1512268	8	23526463	T	0.43	1.14 (1.12-1.15)	6.33E-58	0.43	1.14 (1.12-1.17)	4.6E-32	22938975	24028511	20676098
rs817826	9	110156300	T	0.86	1.00 (0.98-1.03)	8.96E-01	0.86	1.00 (1.01-0.98)	3.8E-01	109651379	110656300	23023329
rs2252004	10	122844709	A	0.10	1.00 (0.98-1.03)	8.69E-01	0.10	1.03 (0.99-1.07)	1.3E-01	122283141	123344709	22366784
rs12791447	11	7556577	G	0.07	1.05 (1.02-1.08)	1.54E-03	0.07	1.08 (1.03-1.13)	5.3E-04	7056577	8056577	26443449
rs1938781	11	58915110	G	0.23	1.03 (1.01-1.05)	1.05E-02	0.21	1.03 (1.00-1.06)	3.3E-02	58415110	59610571	22366784
rs9600079	13	73728139	T	0.44	1.01 (0.99-1.03)	2.14E-01	0.44	1.02 (1.00-1.04)	1.1E-01	73228139	74468916	20676098
rs58262369	14	64693912	C	0.998	1.27 (1.03-1.57)	2.61E-02	0.999	1.26 (0.92-1.73)	1.4E-01	64193912	65193912	26443449
rs7210100	17	47436749	A	0.0001	1.34 (0.33-5.41)	6.77E-01	0.0001	1.34 (0.71-2.55)	3.7E-01	46302314	47952263	21602798
rs103294	19	54797848	C	0.78	1.00 (0.98-1.02)	9.17E-01	0.78	1.00 (0.99-1.00)	3.9E-01	54204670	55297848	23023329

^a Original index signal was rs13385191; rs13385191-rs9306895 r^2 (EUR) =0.45; rs9306895 is used to compare polygenic risk score

^b A better marker was reported, rs7584330; rs2292884 is used to compare polygenic risk score

^c Formerly known as rs115457135

^d Formerly known as rs115306967

^e Original index signal was rs9623117; rs58133635 is used to compare polygenic risk score

Supplementary Table 8. Imputation quality score for 63 novel prostate cancer loci by GWAS and OncoArray consortia.

SNP ID	Chr	Position	OncoArray	UK Stage 1	UK Stage 2	CAPS 1	CAPS 2	iCOGS	BPC3	PEGASUS	Average* (Min, Max)
rs56391074	1	88210715	0.99	0.99	0.97	0.98	0.99	0.94	0.99	1.00	0.98 (0.94, 1.00)
rs34579442	1	153899900	0.93	0.93	0.85	0.94	0.93	0.91	0.93	0.95	0.92 (0.85, 0.95)
rs62106670	2	8597123	0.91	0.87	-	0.86	0.87	0.75	0.85	1.00	0.87 (0.75, 1.00)
rs74702681	2	66652885	0.98	0.99	0.73	0.87	0.96	0.97	0.96	0.97	0.93 (0.73, 0.99)
rs11691517	2	111893096	1.00	0.98	0.95	0.92	0.91	0.99	0.98	0.99	0.96 (0.91, 1.00)
rs34925593	2	174234547	1.00	0.99	0.54	0.94	0.89	0.70	1.00	1.00	0.88 (0.54, 1.00)
rs59308963	2	202123479	1.00	0.99	0.70	0.97	0.98	1.00	1.00	0.99	0.95 (0.7, 1.00)
rs1283104	3	106962521	1.00	0.99	0.99	0.85	0.84	0.99	0.99	1.00	0.96 (0.84, 1.00)
rs182314334	3	152004202	0.99	0.98	0.48	0.98	0.98	0.98	0.98	1.00	0.92 (0.48, 1.00)
rs142436749	3	169093100	0.93	0.92	0.50	0.80	0.82	0.77	0.89	0.94	0.82 (0.5, 0.94)
rs10793821	5	133836209	0.99	1.00	0.99	0.87	0.92	1.00	1.00	1.00	0.97 (0.87, 1.00)
rs76551843	5	169172133	1.00	0.90	0.39	0.81	0.90	0.81	0.89	0.93	0.83 (0.39, 1.00)
rs4976790	5	177968915	1.00	1.00	0.47	0.83	0.86	0.92	1.00	1.00	0.89 (0.47, 1.00)
rs12665339	6	30601232	0.99	1.00	1.00	0.98	0.97	1.00	1.00	1.00	0.99 (0.97, 1.00)
rs9296068	6	32988695	1.00	1.00	1.00	0.97	0.97	0.95	1.00	1.00	0.99 (0.95, 1.00)
rs9469899	6	34793124	0.99	0.98	0.97	0.97	0.97	0.97	0.99	0.99	0.98 (0.97, 0.99)
rs4711748	6	43695371	0.99	1.00	1.00	0.78	0.79	1.00	1.00	1.00	0.95 (0.78, 1.00)
rs138004030	6	170475879	1.00	0.98	-	-	0.98	0.45	-	-	0.85 (0.45, 1.00)
rs527510716	7	1944537	0.79	0.76	-	0.75	0.76	0.75	0.78	0.77	0.77 (0.75, 0.79)
rs11452686	7	20414110	0.88	0.88	0.42	0.89	0.90	0.86	0.89	0.94	0.83 (0.42, 0.94)
rs17621345	7	40875192	1.00	0.98	0.87	0.93	0.94	0.73	0.98	1.00	0.93 (0.73, 1.00)
rs1048169	9	19055965	1.00	1.00	0.96	0.99	0.99	1.00	1.00	1.00	0.99 (0.96, 1.00)
rs10122495	9	34049779	0.97	0.97	0.85	0.97	0.97	0.94	0.97	0.98	0.95 (0.85, 0.98)
rs1182	9	132576060	1.00	1.00	1.00	0.99	0.99	0.97	1.00	1.00	0.99 (0.97, 1.00)
rs141536087	10	854691	0.97	0.97	0.87	0.96	0.96	0.88	0.97	0.98	0.95 (0.87, 0.98)
rs1935581	10	90195149	1.00	1.00	0.92	1.00	1.00	1.00	1.00	1.00	0.99 (0.92, 1.00)
rs7094871	10	114712154	1.00	0.96	0.80	1.00	1.00	1.00	0.97	1.00	0.96 (0.8, 1.00)
rs1881502	11	1507512	1.00	1.00	0.83	0.99	0.98	0.99	1.00	1.00	0.97 (0.83, 1.00)
rs61890184	11	7547587	1.00	0.97	0.52	0.91	0.90	0.94	0.98	1.00	0.9 (0.52, 1.00)
rs547171081	11	47421962	0.92	0.91	0.37	0.90	0.91	0.87	0.91	0.93	0.84 (0.37, 0.93)
rs2277283	11	61908440	0.95	0.91	0.46	0.94	0.92	0.91	0.93	1.00	0.88 (0.46, 1.00)
rs12785905	11	66951965	0.89	0.84	0.64	0.82	0.82	0.74	0.87	0.96	0.82 (0.64, 0.96)
rs11290954	11	76260543	1.00	1.00	0.99	1.00	1.00	1.00	1.00	1.00	1 (0.99, 1.00)
rs1800057	11	108143456	0.99	0.87	0.65	0.93	0.94	0.94	0.92	0.99	0.9 (0.65, 0.99)
rs138466039	11	125054793	0.98	0.90	0.73	0.94	0.96	0.89	0.95	0.97	0.92 (0.73, 0.98)
rs878987	11	134266372	0.99	1.00	0.39	0.92	0.90	0.80	1.00	1.00	0.87 (0.39, 1.00)
rs2066827	12	12871099	1.00	1.00	0.40	0.58	0.58	1.00	1.00	1.00	0.82 (0.4, 1.00)
rs10845938	12	14416918	1.00	0.98	0.96	0.83	0.82	0.99	0.98	1.00	0.94 (0.82, 1.00)
rs7968403	12	65012824	0.99	0.99	0.33	0.98	0.97	0.99	0.99	0.99	0.9 (0.33, 0.99)
rs5799921	12	90160530	0.99	1.00	0.44	0.99	0.99	0.97	0.99	1.00	0.92 (0.44, 1.00)

rs7295014	12	133067989	0.98	1.00	0.92	0.86	0.84	0.98	0.99	1.00	0.94 (0.84, 1.00)
rs1004030	14	23305649	0.99	0.99	0.58	0.77	0.76	0.99	0.99	1.00	0.88 (0.58, 1.00)
rs11629412	14	37138294	1.00	0.97	0.37	0.94	0.94	1.00	0.97	1.00	0.9 (0.37, 1.00)
rs4924487	15	40922915	1.00	1.00	0.56	0.99	1.00	1.00	1.00	1.00	0.94 (0.56, 1.00)
rs33984059	15	56385868	1.00	0.61	0.39	0.48	0.43	0.67	0.59	0.56	0.59 (0.39, 1.00)
rs112293876	15	66764641	0.92	0.92	0.65	0.93	0.92	0.92	0.92	0.91	0.89 (0.65, 0.93)
rs11863709	16	57654576	0.93	0.90	0.43	0.57	0.57	0.87	0.90	0.99	0.77 (0.43, 0.99)
rs201158093	16	82178893	0.88	0.87	0.85	0.88	0.89	0.88	0.89	0.91	0.88 (0.85, 0.91)
rs28441558	17	7803118	1.00	0.88	0.56	0.91	0.87	0.66	0.89	0.98	0.84 (0.56, 1.00)
rs142444269	17	30098749	0.97	0.96	0.38	0.83	0.79	0.61	0.96	0.97	0.81 (0.38, 0.97)
rs2680708	17	56456120	1.00	0.99	0.89	0.99	0.99	0.97	0.99	1.00	0.98 (0.89, 1.00)
rs8093601	18	51772473	1.00	1.00	0.71	0.92	0.92	0.95	0.99	1.00	0.93 (0.71, 1.00)
rs28607662	18	53230859	1.00	0.99	0.61	0.98	0.98	0.97	0.99	1.00	0.94 (0.61, 1.00)
rs12956892	18	56746315	0.99	0.99	0.98	0.99	0.98	0.98	0.99	1.00	0.99 (0.98, 1.00)
rs533722308	18	60961193	0.77	0.76	0.35	0.73	0.74	0.81	0.76	0.85	0.72 (0.35, 0.85)
rs10460109	18	73036165	1.00	1.00	1.00	1.00	0.99	1.00	1.00	1.00	1 (0.99, 1.00)
rs11666569	19	17214073	1.00	0.99	0.40	0.98	0.85	1.00	0.99	1.00	0.9 (0.4, 1.00)
rs118005503	19	32167803	0.97	0.97	0.83	0.97	0.97	0.50	0.97	0.99	0.9 (0.5, 0.99)
rs61088131	19	42700947	1.00	0.97	0.55	0.83	0.84	0.89	0.97	0.98	0.88 (0.55, 1.00)
rs11480453	20	31347512	0.96	0.97	0.46	0.96	0.96	0.96	0.97	0.98	0.9 (0.46, 0.98)
rs6091758	20	52455205	0.97	0.94	0.36	0.98	0.97	0.86	0.94	0.98	0.87 (0.36, 0.98)
rs9625483	22	28888939	1.00	0.93	0.73	0.96	0.96	0.95	0.97	0.97	0.94 (0.73, 1.00)
rs17321482	23	11482634	0.96	0.93	-	0.92	0.93	0.75	0.86	0.94	0.9 (0.75, 0.96)

* The average was calculated using studies with $r^2 \geq 0.3$

Supplementary Table 9. Concordance values for novel prostate cancer variants with low imputation quality scores ($r^2 < 0.80$) in the OncoArray sample series. The calculations were based on an imputation validation experiment using 259 samples from the 1000 Genomes Project.

SNP		Imputed ^a			Concordance ^b
rs527510716	Reference ^c	CC	CG	GG	
$r^2=0.79$	CC	15	1	0	0.911
	CG	2	88	3	
	GG	0	8	142	
rs6602880		CC	CT	TT	
$r^2=0.53$	CC	21	4	3	0.812
	CT	2	92	9	
	TT	0	12	116	
rs533722308		C	C CT	CT CT	
$r^2=0.77$	C	67	3	0	0.931
	C CT	12	142	12	
	CT CT	0	2	21	
rs144166867		A	G		
$r^2=0.38$	A	257	1		0.665
	G	0	1		

^aGenotypes were imputed utilizing a mixed population reference panel of 2,504 samples from the 1000 Genomes Project.

^bA linear weighted Kappa statistic based on the needed categories.

^cAmong a random sample of 259 individuals of European ancestry in the 1000 Genomes Project were imputed using the variants available on the OncoArray.

Supplementary Table 10. OncoArray and GWAS summary statistics for 63 novel prostate cancer associations.

SNP ID	Band	Chromosome	Position	Effect	Baseline	OncoArray			UK1			UK2			CAPS1			CAPS2			ICOGS			BPC3			Pegasus			P _{GW}
						EAF	OR	P	EAF	OR	P	EAF	OR	P	EAF	OR	P	EAF	OR	P	EAF	OR	P	EAF	OR	P	EAF	OR	P	
rs56391074	1q22.3	1	88210715	AT	A	0.37	1.05	8.70E-05	0.36	1.16	3.10E-03	0.37	1.05	1.55E-01	0.40	0.98	3.91E-01	0.39	1.07	2.75E-01	0.37	1.05	4.09E-03	0.37	0.99	7.89E-01	0.37	1.03	4.37E-01	0.41
rs34579442	1q23.1	1	153899900	C	CT	0.34	1.07	2.27E-07	0.32	1.13	2.53E-02	0.34	1.04	2.53E-01	0.36	0.93	3.12E-01	0.35	1.11	1.71E-01	0.34	1.07	2.53E-05	0.34	1.04	3.97E-01	0.33	1.07	5.32E-02	0.76
rs2106670	2p25.1	2	8597123	T	C	0.38	1.05	1.96E-05	0.38	1.05	2.54E-01	-	-	-	0.35	0.99	3.98E-01	0.35	1.02	3.91E-01	0.37	1.08	6.94E-05	0.36	1.00	9.43E-01	0.41	1.01	7.57E-01	0.58
rs74702081	2p14	2	66652885	T	C	0.02	1.15	1.97E-04	0.02	1.32	6.21E-02	0.02	1.10	3.36E-01	0.01	1.18	3.67E-01	0.01	1.50	1.47E-01	0.02	1.23	4.01E-05	0.03	0.95	7.23E-01	0.02	1.12	3.03E-01	0.66
rs11691517	2q13	2	11189096	T	G	0.74	1.05	7.57E-05	0.74	1.12	4.29E-02	0.75	1.04	2.35E-01	0.72	0.97	3.84E-01	0.72	1.13	1.52E-01	0.74	1.07	6.97E-05	0.75	1.03	5.98E-01	0.74	1.16	1.07E-04	0.26
rs34925593	2q31.1	2	174234547	C	T	0.49	1.06	5.00E-07	0.49	0.97	3.42E-01	0.46	1.08	1.06E-01	0.50	1.07	3.14E-01	0.50	1.05	3.24E-01	0.47	1.03	1.35E-01	0.50	0.99	7.92E-01	0.48	1.08	1.77E-02	0.33
rs59308963	2q33.1	2	202123479	T	TATTCTGTC	0.73	1.05	5.89E-04	0.75	1.01	3.96E-01	0.77	0.97	3.05E-01	0.70	1.28	2.11E-02	0.69	1.43	2.41E-05	0.73	1.05	2.34E-03	0.71	1.02	6.76E-01	0.73	1.09	2.15E-02	1.39E-03
rs1283104	3q13.12	3	106962521	G	C	0.38	1.04	2.26E-03	0.36	1.17	2.05E-03	0.38	1.02	3.42E-01	0.40	1.17	1.18E-01	0.38	1.04	3.48E-01	0.38	1.07	1.33E-05	0.40	0.98	6.62E-01	0.38	1.03	4.17E-01	0.09
rs182314334	3q25.1	3	152004202	T	C	0.89	1.10	2.40E-07	0.90	1.05	3.29E-01	0.92	0.93	2.82E-01	0.91	1.21	2.13E-01	0.90	1.00	3.99E-01	0.90	1.12	2.01E-05	0.90	1.15	5.79E-02	0.89	0.96	5.01E-01	0.13
rs142436749	3q26.2	3	169093100	G	A	0.01	1.23	1.33E-04	0.01	1.48	4.78E-02	0.01	1.54	1.44E-01	0.01	0.84	3.72E-01	0.02	0.91	3.81E-01	0.01	1.30	4.75E-04	0.02	0.91	6.25E-01	0.01	1.35	3.60E-02	0.50
rs10793821	5q31.1	5	133836209	T	C	0.58	1.05	7.10E-05	0.55	1.15	3.44E-03	0.57	1.08	3.54E-02	0.63	0.99	3.98E-01	0.60	1.13	1.22E-01	0.58	1.06	1.94E-04	0.59	1.04	3.48E-01	0.59	1.01	7.57E-01	0.41
rs76551843	5q35.1	5	169172133	A	G	0.99	1.33	1.00E-05	0.99	3.86	4.74E-05	1.00	0.95	3.96E-01	1.00	0.55	2.91E-01	0.99	1.27	3.45E-01	0.99	1.26	1.53E-02	0.99	1.17	5.64E-01	0.99	1.04	8.44E-01	0.03
rs4976790	5q35.3	5	177968915	T	G	0.11	1.09	1.83E-06	0.12	0.97	3.64E-01	0.10	1.02	3.85E-01	0.10	1.09	3.52E-01	0.09	1.26	8.42E-02	0.11	1.06	1.86E-02	0.11	1.14	5.14E-02	0.12	1.06	2.81E-01	0.58
rs12665339	6p21.33	6	30601232	G	A	0.16	1.06	2.79E-04	0.14	1.12	8.02E-02	0.15	1.04	2.64E-01	0.22	0.96	3.71E-01	0.20	1.05	3.48E-01	0.17	1.09	1.47E-05	0.18	0.96	4.35E-01	0.17	1.05	2.91E-01	0.41
rs9296068	6p21.32	6	32988695	T	G	0.65	1.05	3.67E-05	0.66	1.09	9.24E-02	0.67	1.05	1.82E-01	0.68	0.92	2.85E-01	0.68	1.02	3.91E-01	0.65	1.05	1.75E-03	0.64	0.96	3.49E-01	0.65	1.07	5.90E-02	0.45
rs9469889	6p21.31	6	34793124	A	G	0.36	1.05	1.77E-05	0.35	1.17	2.80E-03	0.35	1.01	3.78E-01	0.32	1.14	1.73E-01	0.35	1.02	3.83E-01	0.35	1.03	3.52E-02	0.36	1.10	3.77E-02	0.36	1.04	2.25E-01	0.30
rs4711748	6p21.1	6	43694598	T	C	0.23	1.05	4.86E-04	0.21	1.21	1.26E-03	0.22	1.10	2.72E-02	0.21	1.03	3.91E-01	0.25	0.95	3.38E-01	0.23	1.05	8.43E-03	0.24	1.03	5.61E-01	0.22	1.03	3.98E-01	0.26
rs18004030	6p27	6	170475879	G	A	0.92	1.28	1.63E-05	0.92	1.04	3.99E-01	-	-	-	-	-	-	0.88	1.62	6.97E-02	0.89	1.34	1.55E-03	-	-	-	-	-	-	0.25
rs527510716	7p22.3	7	1944537	C	G	0.24	1.07	3.45E-06	0.25	1.08	1.76E-01	-	-	-	0.23	1.10	3.00E-01	0.23	1.12	2.04E-01	0.24	1.04	4.38E-02	0.24	0.93	2.09E-01	0.24	1.10	3.04E-02	0.25
rs11452686	7p21.1	7	20414110	T	TA	0.56	1.04	1.45E-03	0.57	0.98	3.64E-01	0.46	1.08	1.20E-01	0.59	0.99	3.96E-01	0.55	1.13	1.20E-01	0.55	1.06	1.84E-04	0.57	1.03	5.86E-01	0.56	1.11	2.53E-03	0.36
rs17621345	7p14.1	7	40875192	A	C	0.74	1.07	8.72E-07	0.74	1.09	1.19E-01	0.73	1.10	3.15E-02	0.73	1.14	1.86E-01	0.75	1.07	3.00E-01	0.75	1.09	1.44E-05	0.74	1.06	2.32E-01	0.74	1.04	2.87E-01	0.93
rs1048169	9p22.1	9	19055965	C	T	0.38	1.07	2.04E-09	0.38	1.09	6.85E-02	0.38	0.96	2.13E-01	0.38	0.91	2.44E-01	0.37	1.03	3.68E-01	0.38	1.07	4.59E-06	0.39	1.00	9.83E-01	0.38	1.07	5.74E-02	0.05
rs10122495	9p13.1	9	34049779	T	A	0.29	1.05	3.42E-04	0.27	1.11	3.35E-02	0.31	1.08	7.23E-02	0.30	1.08	2.98E-01	0.32	0.97	3.73E-01	0.30	1.04	1.29E-02	0.30	1.09	6.55E-02	0.29	1.07	5.70E-02	0.83
rs1182	9q34.11	9	132576060	A	C	0.22	1.07	1.75E-06	0.22	1.18	4.45E-03	0.22	1.02	3.65E-01	0.21	1.13	2.19E-01	0.21	1.06	3.35E-01	0.22	1.05	4.24E-03	0.23	1.05	3.73E-01	0.22	0.99	8.58E-01	0.32
rs141536087	10p15.3	10	1841349	-	GCGCA	0.15	1.10	1.34E-09	0.16	1.18	1.15E-02	0.15	0.98	3.78E-01	0.15	1.03	3.91E-01	0.15	1.11	2.44E-01	0.15	1.06	1.35E-02	0.14	1.11	9.79E-02	0.15	1.08	9.90E-02	0.30
rs1935581	10q23.31	10	90195149	C	T	0.62	1.06	5.37E-06	0.65	1.01	3.88E-01	0.63	1.10	1.42E-02	0.61	1.03	3.83E-01	0.61	1.10	1.65E-01	0.64	1.03	6.15E-02	0.63	1.00	9.13E-01	0.62	1.09	1.40E-02	0.42
rs7094871	10q25.2	10	114712154	G	C	0.54	1.04	2.15E-04	0.52	1.10	4.55E-02	0.58	1.03	2.92E-01	0.51	1.03	3.82E-01	0.49	1.16	4.88E-02	0.54	1.05	2.96E-03	0.54	1.03	5.47E-01	0.55	1.01	7.62E-01	0.69
rs1881502	11p15.5	11	1507512	T	C	0.19	1.06	1.61E-04	0.18	1.06	2.40E-01	0.20	1.01	3.95E-01	0.19	1.07	3.42E-01	0.19	1.08	2.77E-01	0.19	1.07	4.11E-04	0.19	1.04	4.19E-01	0.19	1.08	7.27E-02	0.96
rs61890184	11p15.4	11	7547587	A	G	0.12	1.08	1.31E-05	0.12	1.17	3.07E-02	0.13	1.08	2.06E-01	0.15	1.11	2.88E-01	0.15	1.17	1.22E-01	0.13	1.05	2.33E-02	0.12	1.00	1.00E+00	0.12	1.08	1.35E-01	0.74
rs547171081	11p11.2	11	47421962	CGG	C	0.47	1.05	1.91E-05	0.46	1.13	1.99E-02	0.46	0.95	2.77E-01	0.46	0.94	3.22E-01	0.47	0.94	2.90E-01	0.47	1.06	5.67E-04	0.47	1.02	5.81E-01	0.48	1.00	8.95E-01	0.15
rs12277281	11q12.3	11	61908440	C	T	0.31	1.06	2.87E-06	0.32	1.00	3.99E-01	0.28	0.97	3.38E-01	0.28	1.44	5.86E-04	0.28	1.17	6.06E-02	0.32	1.07	1.22E-04	0.32	1.03	5.69E-01	0.32	1.00	9.66E-01	0.01
rs12785905	11q13.2	11	66951965	C	G	0.05	1.09	2.64E-03	0.05	1.12	2.30E-01	0.05	1.41	7.22E-04	0.04	1.39	1.63E-01	0.03	1.66	2.09E-02	0.04	1.13	5.02E-03	0.04	1.12	3.38E-01	0.05	1.15	6.43E-02	0.13
rs11290594	11q13.5	11	76280543	AC	A	0.68	1.07	7.40E-08	0.66	1.14	1.07E-02	0.68	1.03	2.76E-01	0.70	1.15	1.55E-01	0.69	1.03	3.80E-01	0.68	1.06	3.45E-04	0.69	1.02	6.37E-01	0.67	1.04	2.92E-01	0.66
rs1800057	11q22.3	11	108143456	G	C	0.02	1.13	8.09E-04	0.02	1.35	6.54E-02	0.02	1.15	2.36E-01	0.03	1.08	3.84E-01	0.03	1.17	3.10E-01	0.02	1.18	2.75E-03	0.03	1.13	3.96E-01	0.02	1.35	2.91E-03	0.79
rs138466039	11																													

Supplementary Table 11. Clinically significant prostate cancer variants.

SNP ID	EA	EAF	Overall PrCa		Advanced PrCa		Advanced vs Non-Advanced PrCa		Early-onset PrCa	
			OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value	OR (95%CI)	P-value
rs111599055 ^a	C	0.69	1.05 (1.03-1.07)	8.34E-08	1.02 (0.99-1.05)	0.108	0.97 (1.00-0.94)	0.04649	1.13 (1.08-1.18)	1.47E-08
rs11859370 ^b	T	0.95	1.13 (1.09-1.17)	1.60E-10	1.21 (1.13-1.29)	2.24E-08	1.08 (1.00-1.15)	0.03565	1.19 (1.08-1.30)	0.0003307
rs2788524 ^c	G	0.15	1.06 (1.04-1.07)	9.03E-11	1.10 (1.07-1.13)	3.52E-10	1.05 (1.02-1.08)	0.001144	1.08 (1.04-1.12)	0.000126
rs56366063 ^d	C	0.11	1.08 (1.05-1.11)	1.77E-08	1.14 (1.09-1.19)	1.32E-08	1.07 (1.02-1.12)	0.005577	1.08 (1.01-1.15)	0.02493
rs77777548	G	0.02	1.07 (0.94-1.23)	0.3143	1.09 (0.85-1.40)	0.5042	1.05 (0.81-1.35)	0.7227	2.94 (2.01-4.29)	2.92E-08

^a rs111599055-rs7295014 $r^2=0.54$

^b rs11859370-rs11863709 $r^2=0.82$

^c rs2788524-rs17321482 $r^2=0.64$

^d rs56366063-rs11691517 $r^2=0.33$

Supplementary Table 12. Functional annotation of the novel risk regions.

SNP Information																							
SNP ID	Band	Position	Alleles ^a	OR	Gm12878	ChromHMM	H1hesC	ChromHMM	Huvec	ChromHMM	PC3	ChromHMM	PrEC	ChromHMM	GSM1008595	RWPE1	DNaseI	1024742	PrEC	DN	GSM736565	LNcap	DNaseI
rs56391074	1p22.3	88210715	AT/A	1.05	Quies		Quies		Quies		Heterochromatin		Heterochromatin										
rs34579442	1q21.3	153899900	C/CT	1.07	Gen5'		Pol2		Pol2		Transcribed		Heterochromatin										
rs62106670	2p25.1	8597123	T/C	1.05	PromF		DnaseD		Quies		Promoter		Heterochromatin										
rs74702681	2p14	66652885	T/C	1.17	Repr		PromP		PromP		Heterochromatin		Promoter		1							1	
rs11691517	2q13	111893096	T/G	1.07	Elon		Low		Elon		Heterochromatin		Heterochromatin										
rs34925593	2q31.1	174234547	C/T	1.05	EnhWF		Pol2		ElonW		Heterochromatin		Heterochromatin										
rs59308963	2q33.1	202123479	T/TATTCTGTC	1.05	Tss		EnhW		Tss		Promoter		Promoter		1								
rs1283104	3q13.12	106962521	G/C	1.05	Quies		Low		Low		Heterochromatin		Heterochromatin										
rs182314334	3q25.1	152004202	T/C	1.09	ElonW		Low		Gen5'		Transcribed		Transcribed										
rs142436749	3q26.2	169093100	G/A	1.25	Quies		Quies		Low		Heterochromatin		Heterochromatin										
rs10793821	5q31.1	133836209	T/C	1.05	Low		Low		Low		Heterochromatin		Transcribed										
rs76551843	5q35.1	169172133	A/G	1.31	Gen5'		Low		Quies		Heterochromatin		Enhancer										
rs4976790	5q35.3	177968915	T/G	1.08	Quies		Low		Low		Heterochromatin		Heterochromatin										
rs12665339	6p21.33	30601232	G/A	1.06	Pol2		Pol2		Elon		Heterochromatin		Heterochromatin										
rs9296068	6p21.32	32988695	T/G	1.05	Low		Low		ReprW		Heterochromatin		Heterochromatin										
rs9469899	6p21.31	34793124	A/G	1.05	Elon		Low		ElonW		Heterochromatin		Heterochromatin										
rs4711748	6p21.1	43694598	T/C	1.05	Low		Low		Low		Heterochromatin		Enhancer									1	
rs527510716	7p22.3	1944537	C/G	1.06	ElonW		Low		Low		Heterochromatin		Heterochromatin										
rs11452686	7p21.1	20414110	T/TA	1.05	Low		Low		Low		Heterochromatin		Heterochromatin										
rs17621345	7p14.1	40875192	A/C	1.07	Low		Quies		Low		Heterochromatin		Transcribed										
rs1048169	9p22.1	19055965	C/T	1.06	ElonW		Pol2		ElonW		Heterochromatin		Heterochromatin										
rs10122495	9p13.3	34049779	T/A	1.05	Tss		Tss		Tss		Promoter		Promoter										
rs1182	9q34.11	132576060	A/C	1.06	Gen3'		Gen3'		Gen3'		Transcribed		Heterochromatin										
rs141536087	10p15.3	854691	GCGCA/G	1.08	Elon		ElonW		Elon		Transcribed		Heterochromatin									1	
rs1935581	10q23.31	90195149	C/T	1.05	Quies		Quies		Quies		Heterochromatin		Heterochromatin										
rs7094871	10q25.2	114712154	G/C	1.04	PromP		Tss		Tss		Promoter		Promoter		1								
rs1881502	11p15.5	1507512	T/C	1.06	DnaseD		DnaseD		DnaseD		Promoter		Enhancer										
rs61890184	11p15.4	7547587	A/G	1.07	EnhWF		Low		ReprW		Heterochromatin		Heterochromatin										
rs547171081	11p11.2	47421962	CGG/C	1.05	Tss		Tss		TssF		Heterochromatin		Promoter										
rs2277283	11q12.3	61908440	C/T	1.06	Gen3'		Elon		Elon		Heterochromatin		Heterochromatin										
rs12785905	11q13.2	66951965	C/G	1.12	Elon		Elon		Gen3'		Heterochromatin		Heterochromatin										
rs11290954	11q13.5	76260543	AC/A	1.06	ElonW		ElonW		Low		Heterochromatin		Heterochromatin										
rs1800057	11q22.3	108143456	G/C	1.16	Elon		Elon		ElonW		Heterochromatin		Heterochromatin										
rs138466039	11q24.2	125054793	T/C	1.32	ReprW		Low		Repr		Heterochromatin		Heterochromatin										
rs878987	11q25	134266372	G/A	1.07	ReprW		DnaseD		Low		Heterochromatin		Heterochromatin										
rs2066827	12p13.1	12871099	T/G	1.06	Tss		PromP		Tss		Promoter		Promoter										
rs10845938	12p13.1	14416918	G/A	1.06	Low		Low		Low		Heterochromatin		Heterochromatin										
rs7968403	12q14.2	65012824	T/C	1.06	Tss		Low		Enh		Enhancer		Heterochromatin										
rs5799921	12q21.33	90160530	GA/G	1.06	EnhW		Quies		Quies		Transcribed		Heterochromatin										
rs7295014	12q24.33	133067989	G/A	1.05	TssF		PromP		PromP		Promoter		Promoter					1					1
rs1004030	14q11.2	23305649	T/C	1.05	Pol2		Tss		Tss		CTCF+Promoter		Promoter		1								
rs11629412	14q13.3	37138294	C/G	1.06	Quies		Repr		ReprW		Heterochromatin		Transcribed										
rs4924487	15q15.1	40922915	C/G	1.06	Elon		Low		Elon		Heterochromatin		Heterochromatin										
rs33984059	15q21.3	56385868	A/G	1.19	Elon		Gen3'		Elon		Heterochromatin		Heterochromatin										
rs112293876	15q22.31	66764641	C/CA	1.06	Enh		EnhF		EnhF		Enhancer		Enhancer										
rs11863709	16q21	57654576	C/T	1.16	Low		EnhW		Low		Promoter		Promoter		1								
rs201158093	16q23.3	82178893	TAA/TA	1.05	Quies		Low		Low		Heterochromatin		Heterochromatin										
rs28441558	17p13.1	7803118	C/T	1.16	Gen3'		Low		Gen3'		Heterochromatin		Heterochromatin										
rs142444269	17q11.2	30098749	C/T	1.07	ReprW		DnaseU		Repr		Heterochromatin		Heterochromatin										
rs2680708	17q22	56456120	G/A	1.05	Low		Low		ReprW		Enhancer		Transcribed										
rs8093601	18q21.2	51772473	C/G	1.05	Low		EnhWF		Low		Heterochromatin		Heterochromatin										
rs28607662	18q21.2	53230859	C/T	1.08	Quies		H4K20		ElonW		Heterochromatin		Heterochromatin										
rs12956892	18q21.32	56746315	T/G	1.05	ReprW		Quies		Repr		Heterochromatin		Heterochromatin										
rs533722308	18q21.33	60961193	CT/C	1.05	Gen5'		Low		Low		Heterochromatin		Heterochromatin										
rs10460109	18q22.3	73036165	T/C	1.05	Quies		Quies		ReprW		Heterochromatin		Heterochromatin										
rs11666569	19p13.11	17214073	C/T	1.05	Gen5'		CtcfO		CtcfO		CTCF		CTCF										
rs118005503	19q12	32167803	G/C	1.09	Quies		Low		Quies		Heterochromatin		Heterochromatin										
rs61088131	19q13.2	42700947	T/C	1.06	Gen3'		EnhW		ElonW		Promoter		Enhancer										
rs11480453	20q11.21	31347512	C/CA	1.05	Quies		Low		Low		Heterochromatin		Heterochromatin										
rs6091758	20q13.2	52455205	G/A	1.07	EnhF		Low		Low		Promoter		Transcribed										
rs9625483	22q12.1	28888939	A/G	1.14	ReprW		Quies		Low		Heterochromatin		Heterochromatin										
rs17321482	23p22.2	11482634	C/T	1.07	Quies		Quies		Low		Heterochromatin		Heterochromatin									1	

^a Effect allele/Reference allele

ICR Annotation													
GSM736603	LNCaP_DNasel	1816634_LNCaP+androgen_DN	GSM816637_LNCaP_DNasel	merged_ENCODE_DNasel	GERP++	SiPhy_Omega	SiPhy_Pi	PhastCons	Cons_Elem_merged	MirBasev20	TCGA_eQTL_gene	TCGA_eQTL_P	
					1	1	1	1	1				15
1	1	1	1	1									
				1									
											MBNL1 4154	6.08172E-11	
											COL23A1 91522	1.89625E-05	
1			1	1							UHRF1BP1 54887	3.69723E-17	
					1				1		HAUS6 54801	1.4466E-11	
	1		1	1							UBE2R2 54926	7.99215E-05	
1		1	1	1							TOR1B 27348	4.20864E-16	
	1		1	1	1	1	1		1				
	1		1	1							OLFML1 283298	0.000254262	
			1	1	1	1	1	1	1				
					1	1	1	1	1		RAD9A 5883	0.000056896	
	1	1	1	1	1	1	1	1	1		B3GAT1 27087	2.4025E-06	
	1		1	1	1	1	1	1	1				
											WIF1 11197	0.00181921	
1	1	1	1	1			1		1		ATP2B1 490	5.78894E-05	
		1	1	1	1		1		1		P2RX2 22953	5.77526E-05	
											PAX9 5083	0.00114077	
					1	1	1	1	1				
	1	1	1	1									
					1				1		GUCY2D 3000	2.52336E-05	2.
											POLJ 11201	1.3725E-13	
					1	1	1	1	1		TSHZ1 10194	0.00139519	
											MYO9B 4650	4.45961E-10	
											MAPRE1 22919	3.05543E-05	
1	1		1	1	1	1	1	1	1				

Supplementary Table 12. Functional annotation of the novel risk regions.

GENCODE genes		dbSNP func annot	GERP cons	SiPhy cons	motomer histone	maricr histone	DNase	Proteins bound	Haploreg Annotation		Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	Regulomedb score	CADD PHRED
55kb 3' of RP5-102701.1			y	y		BRST, SKIN				2fp105					5	11.68
2.1kb 3' of DENND4B						SKIN, BLD				HDAC2, Pax-4, p300					5	6.669
73kb 5' of LINC00299						BLD, GI	BLD, BLD			Ets, STAT, Znf143					5	3.581
981bp 3' of MEIS1-AS3					18 tissues	5 tissues	26 tissues			6 altered motifs					4	10.12
BCL2L11	intronic					16 tissues	BLD	ELF1		EBF					4	0.589
821bp 3' of CDCA7						BLD, VAS				HNFI					6	2.02
CASP8	intronic				23 tissues	ESC, ESDR	24 tissues	4 bound proteins		NF-1				38 hits	2b	10.98
RP11-446H18.3	intronic				BRN	6 tissues				5 altered motifs					6	5.265
MBNL1	intronic					BLD, VAS, SKIN				18 altered motifs					6	0.749
MECOM	intronic									Tel2					n/a	10.88
233bp 5' of U6										BHLHE40, TCF12				1 hit	n/a	1.786
DOCK2	intronic				BLD	14 tissues	iKIN, BLD, SKIN			Ik-2					4	0.952
COL23A1	intronic					5 tissues				4 altered motifs				1 hit	6	1.392
ATAT1	intronic									8 altered motifs		4 hits		17 hits	5	13.8
11kb 5' of HLA-DOA						BLD				4 altered motifs		6 hits		4 hits	6	0.192
UHRF1BP1	intronic									AhR, Irf, Nanog				58 hits	n/a	0.096
RP1-261G23.5						SKIN				CTCF, RBP, Jkappa		1 hit		3 hits	3a	0.407
n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a		n/a	n/a	n/a	n/a	n/a	n/a	1.142
ITGB8	intronic									5 altered motifs					6	1.911
C7orf10	intronic					ESC, IPSC, BR	OVRY			6 altered motifs				2 hits	6	3.261
HAUSE	3'-UTR	y								Barhl1, Nkx2, Nkx3		1 hit		10 hits	6	0.7
184bp 5' of 7SK						19 tissues		HAE2F1, GATA1, POL2		6 altered motifs				2 hits	4	4.323
TOR1A	3'-UTR					ESDR, LIV	BRN, MUS			CHD2, ZBTB33				46 hits	4	6.909
792bp 3' of LARP4B						HRT	SKIN, LNG			7 altered motifs					5	1.451
RNLS	intronic									BDP1, Pou2f2, STAT					n/a	2.382
TCF7L2	intronic	y	y		24 tissues	BRN	27 tissues	POL2, HAE2F1		10 altered motifs				18 hits	4	17.86
MOB2	intronic				9 tissues	19 tissues	13 tissues	ERALPHA_A, PAX5C2		AhR				3 hits	2b	0.053
PPFIBP2	intronic				LIV	4 tissues				Hoxa5					5	4.543
n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a		n/a	n/a	n/a	n/a	n/a	2b	8.038
INCENP	missense	y	y		n/a	4 tissues						1 hit		2 hits	5	23.5
KDM2A	intronic									6 altered motifs			1 hit	19 hits	6	0.248
C11orf30	intronic									8 altered motifs					6	0.446
ATM	missense	y	y							4 altered motifs					n/a	26.5
PKNOX2	intronic					LIV				Sin3Ak-20					5	2.016
B3GAT1	intronic					ESDR, SKIN				6 altered motifs				3 hits	5	4.208
CDKN1B	missense	y	y		24 tissues	IPSC, BRN	32 tissues	ELF1, POL2		10 altered motifs				1 hit	2b	11.36
14kb 5' of U6						6 tissues		STAT1, FOXA1		11 altered motifs					2b	3.756
RASSF3	intronic				FAT, BLD, CRVX	18 tissues	5 tissues			Pou2f2					4	3.139
13kb 3' of U6					BLD	BLD	GI	NFKB							5	1.944
FBRSL1	intronic	y			24 tissues	ESDR, IPSC	14 tissues	4 bound proteins		6 altered motifs				13 hits	3a	5.146
116bp 5' of MMP14						39 tissues				8 altered motifs					3a	0.289
PAX9	intronic									4 altered motifs					5	0.187
CASC5	intronic						KID			12 altered motifs				6 hits	n/a	0.329
REFX7	missense	y	y				ESDR, BLD			Foxa					5	25
MAP2K1	intronic				ESDR, BLD	17 tissues	14 tissues	BATF, PBX3, TCF12		4 altered motifs					3a	5.191
GPR56	intronic				8 tissues	10 tissues	8 tissues			13 altered motifs					2b	6.286
2.5kb 3' of MPHOSPH6										7 altered motifs					6	0.056
CHD3	intronic														n/a	0.081
7kb 3' of RP11-805L22.3										Irf, Nrf-2, PRDM1					5	5.801
RP5-1171110.4	intronic					6 tissues				Maf				21 hits	n/a	4.836
21kb 5' of MBD2						4 tissues	IPSC			RFK5, SREBP				35 hits	5	0.271
TCF4	intronic						IPSC, ADRL								n/a	5.569
61kb 5' of SEC11C										5 altered motifs					5	0.703
BCL2	intronic				MUS, GI	8 tissues	4 tissues			4 altered motifs					5	2.905
34kb 3' of TSHZ1		y	y				MUS, MUS			10 altered motifs					5	21
MYO9B	intronic														4	3.045
21kb 5' of RN55471						BLD, SPLN	7 tissues	CTCF, RAD21		10 altered motifs		1 hit		10 hits	6	0.005
209bp 5' of POU2F2					BLD	BRST, MUS	8 tissues	5 bound proteins		BDP1				2 hits	4	0.665
2.7kb 5' of DNMT3B						BLD				4 altered motifs					6	1.242
37kb 5' of AC006076.1					BLD	4 tissues	8 tissues			5 altered motifs					3a	1.561
TTC28	intronic					BLD				5 altered motifs				1 hit	5	10.67
ARHGAP6	intronic	y	y		BLD		BLD			Ets, GR, STAT					2c	15.92

Supplementary Table 13. PSA associations among disease-free controls (N=9,090) with the novel prostate cancer SNPs.

SNP	Cytoband	Position	Effect Allele	Other Allele	EAF	Beta	StDev	P	P _{het}
rs56391074	1p22.3	88210715	AT	A	-	-	-	-	-
rs34579442	1q21.3	153899900	C	CT	-	-	-	-	-
rs62106670	2p25.1	8597123	T	C	0.36525	-0.032	0.018	0.07	0.12
rs74702681	2p14	66652885	T	C	0.01625	-0.047	0.066	0.48	0.47
rs11691517	2q13	111893096	T	G	0.7364	0.002	0.017	0.89	0.66
rs34925593	2q31.1	174234547	C	T	0.4882	-0.005	0.017	0.78	0.04
rs59308963	2q33.1	202123479	T	TATTCTGTC	-	-	-	-	-
rs1283104	3q13.12	106962521	G	C	0.3832	-0.007	0.015	0.63	0.40
rs182314334	3q25.1	152004202	T	C	0.9702	0.005	0.055	0.93	0.06
rs142436749	3q26.2	169093100	G	A	0.0135	-0.008	0.076	0.92	0.54
rs10793821	5q31.1	133836209	T	C	0.5714	0.034	0.015	0.02	0.29
rs76551843	5q35.1	169172133	A	G	-	-	-	-	-
rs4976790	5q35.3	177968915	T	G	0.0984	0.061	0.025	0.02	0.69
rs12665339	6p21.33	30601232	G	A	0.182	0.027	0.019	0.16	0.69
rs9296068	6p21.32	32988695	T	G	0.671	-0.003	0.015	0.84	0.13
rs9469899	6p21.31	34793124	A	G	0.3496	0.026	0.016	0.10	0.83
rs4711748	6p21.1	43694598	T	C	0.231	0.045	0.017	0.009	0.51
rs138004030	6q27	170475879	G	A	0.892	0.014	-	-	-
rs527510716	7p22.3	1944537	C	G	-	-	-	-	-
rs11452686	7p21.1	20414110	T	TA	-	-	-	-	-
rs17621345	7p14.1	40875192	A	C	0.7496	0.022	0.018	0.23	0.19
rs1048169	9p22.1	19055965	C	T	0.3802	0.002	0.015	0.87	0.89
rs10122495	9p13.3	34049779	T	A	0.3674	-0.002	0.017	0.90	0.19
rs1182	9q34.11	132576060	A	C	0.2172	-0.006	0.018	0.72	0.31
rs141536087	10p15.3	854691	GCGCA	G	-	-	-	-	-
rs1935581	10q23.31	90195149	C	T	0.627	0.001	0.015	0.94	0.58
rs7094871	10q25.2	114712154	G	C	0.5342	0.03	0.015	0.04	0.60
rs1881502	11p15.5	1507512	T	C	0.1918	0.011	0.019	0.55	0.73
rs61890184	11p15.4	7547587	A	G	0.134	-0.018	0.023	0.43	0.84
rs547171081	11p11.2	47421962	CGG	C	-	-	-	-	-
rs2277283	11q12.3	61908440	C	T	0.2996	-0.021	0.017	0.22	0.99
rs12785905	11q13.2	66951965	C	G	0.0372	-0.043	0.042	0.31	0.80
rs11290954	11q13.5	76260543	AC	A	0.6866	0.01	0.015	0.53	0.56
rs1800057	11q22.3	108143456	G	C	0.0266	0.048	0.05	0.34	0.60
rs138466039	11q24.2	125054793	T	C	0.0105	0.196	0.088	0.03	0.99
rs878987	11q25	134266372	G	A	0.13525	0.029	0.024	0.22	0.73
rs2066827	12p13.1	12871099	T	G	0.7602	-0.019	0.018	0.28	0.21
rs10845938	12p13.1	14416918	G	A	0.5588	-0.008	0.015	0.60	0.12
rs7968403	12q14.2	65012824	T	C	0.6385	-0.011	0.016	0.50	0.98
rs5799921	12q21.33	90160530	GA	G	0.6846	0.01	0.017	0.56	0.30
rs7295014	12q24.33	133067989	G	A	0.3604	0.019	0.016	0.23	0.44
rs1004030	14q11.2	23305649	T	C	0.5634	-0.002	0.015	0.89	0.35
rs11629412	14q13.3	37138294	C	G	0.5725	0.014	0.016	0.37	0.06
rs4924487	15q15.1	40922915	C	G	0.8316	-0.009	0.02	0.64	0.54
rs33984059	15q21.3	56385868	A	G	0.9845	0.183	0.107	0.09	0.80
rs112293876	15q22.31	66764641	C	CA	-	-	-	-	-
rs11863709	16q21	57654576	C	T	0.9544	0.069	0.041	0.09	0.43
rs201158093	16q23.3	82178893	TAA	TA	-	-	-	-	-
rs28441558	17p13.1	7803118	C	T	0.062	0.052	0.038	0.17	0.60
rs142444269	17q11.2	30098749	C	T	0.7665	0.017	0.022	0.45	0.89
rs2680708	17q22	56456120	G	A	0.606	0.034	0.015	0.02	0.43
rs8093601	18q21.2	51772473	C	G	0.4606	0.052	0.015	0.0005	0.86
rs28607662	18q21.2	53230859	C	T	0.099	0.016	0.026	0.54	0.79
rs12956892	18q21.32	56746315	T	G	0.3214	-0.006	0.016	0.72	0.25
rs533722308	18q21.33	60961193	CT	C	-	-	-	-	-
rs10460109	18q22.3	73036165	T	C	0.4102	0.001	0.015	0.96	0.87
rs11666569	19p13.11	17214073	C	T	0.71375	0.017	0.017	0.32	0.63
rs118005503	19q12	32167803	G	C	0.9116	0.004	0.031	0.91	0.51
rs61088131	19q13.2	42700947	T	C	0.7956	0.033	0.02	0.09	0.58
rs11480453	20q11.21	31347512	C	CA	-	-	-	-	-
rs6091758	20q13.2	52455205	G	A	-	-	-	-	-
rs9625483	22q12.1	28888939	A	G	0.0284	-0.01	0.053	0.85	0.22
rs17321482	23p22.2	11482634	C	T	-	-	-	-	-

Supplementary Table 14. Associations of novel SNPs by prostate cancer clinical features.

SNP ID	Band	Position	Nearest Gene	Alleles	High vs Low		High vs Low/Intermediate		Advanced vs Non-Advanced		Advanced		Age<55		Gleason Score	
					OR	P	OR	P	OR	P	OR	P	OR	P	Beta	P
rs56391074	1p22.3	88210715	RP11-60A14.1	AT/A	0.99	7.43E-01	0.99	3.02E-01	0.98	2.36E-01	1.03	2.06E-02	1.07	1.61E-03	-0.002	7.98E-01
rs34579442	1q21.3	153899900	DENND4B	C/CT	1.05	3.01E-02	1.03	2.32E-02	1.00	8.33E-01	1.08	7.71E-07	1.10	1.01E-05	0.012	6.68E-02
rs62106670	2p25.1	8597123	AC011747.3	T/C	1.04	6.34E-02	1.01	5.12E-01	1.01	4.93E-01	1.06	2.08E-04	1.06	1.48E-02	0.010	1.53E-01
rs74702681	2p14	66652885	MEIS1-AS3	T/C	0.89	8.20E-02	0.93	9.63E-02	0.87	1.77E-03	1.01	7.79E-01	1.19	6.41E-03	-0.042	3.14E-02
rs11691517	2q13	111893096	BCL2L11	T/G	1.04	1.09E-01	1.03	6.39E-02	1.02	3.38E-01	1.08	6.50E-07	1.10	3.73E-05	0.013	7.16E-02
rs34925593	2q31.1	174234547	CDC47	C/T	0.99	5.29E-01	0.99	3.17E-01	1.01	6.14E-01	1.05	1.86E-03	1.04	7.75E-02	-0.003	6.71E-01
rs59308963	2q33.1	202123479	CASP8	T/TATTCTGTC	1.00	9.41E-01	0.98	2.53E-01	1.01	4.49E-01	0.95	1.91E-03	0.94	9.95E-03	-0.006	4.17E-01
rs1283104	3q13.12	106962521	DUBR	G/C	0.98	4.21E-01	1.00	7.38E-01	1.02	2.05E-01	1.06	6.58E-05	1.07	9.08E-04	0.005	4.26E-01
rs182314334	3q25.1	152004202	MBNL1	T/C	0.96	2.12E-01	0.97	1.58E-01	0.97	2.17E-01	1.06	1.10E-02	1.14	8.19E-05	-0.008	4.14E-01
rs142436749	3q26.2	169093100	MECOM	G/A	1.12	2.15E-01	1.03	6.45E-01	1.12	7.19E-02	1.32	1.20E-05	1.37	4.10E-04	0.010	7.18E-01
rs10793821	5q31.1	133836209	RNU6-456P	T/C	1.02	4.09E-01	1.00	7.98E-01	1.02	1.65E-01	1.07	9.03E-07	1.06	3.24E-03	0.008	1.76E-01
rs76551843	5q35.1	169172133	DOCK2	A/G	1.02	8.92E-01	0.99	9.43E-01	0.90	2.54E-01	1.24	9.85E-03	1.54	1.06E-03	-0.009	8.17E-01
rs4976790	5q35.3	177968915	COL23A1	T/G	1.03	3.44E-01	1.04	7.72E-02	1.01	7.09E-01	1.09	4.81E-05	1.06	4.89E-02	-0.001	9.28E-01
rs12665339	6p21.33	30601232	ATAT1	G/A	1.01	5.88E-01	0.98	2.18E-01	0.97	7.21E-02	1.04	3.72E-02	1.10	5.13E-04	-0.009	2.81E-01
rs9296068	6p21.32	32988695	HLA-DOA	T/G	0.97	2.04E-01	0.98	1.88E-01	0.99	6.86E-01	1.04	6.04E-03	1.06	4.39E-03	0.002	7.82E-01
rs9469899	6p21.31	34793124	UHRF1BP1	A/G	1.02	4.10E-01	1.02	1.20E-01	1.01	3.16E-01	1.07	2.49E-06	1.09	4.37E-05	0.011	7.69E-02
rs4711748	6p21.1	43694598	RP1-261G23.5	T/C	0.96	9.79E-02	0.97	4.35E-02	0.99	3.69E-01	1.05	6.24E-03	1.05	3.15E-02	-0.014	4.91E-02
rs138004030	6q27	170475879	LOC154449	G/A	0.88	2.72E-04	1.02	3.90E-01	0.99	8.40E-01	1.03	3.11E-01	1.27	2.85E-08	0.010	4.66E-01
rs527510716	7p22.3	1944537	MAD1L1	C/G	1.05	6.21E-02	1.02	1.79E-01	1.03	7.91E-02	1.10	3.38E-07	1.10	3.14E-04	0.013	9.38E-02
rs11452686	7p21.1	20414110	ITGB8	T/TA	0.99	5.33E-01	0.99	4.73E-01	0.98	2.00E-01	1.04	1.55E-02	1.05	3.69E-02	-0.005	4.81E-01
rs17621345	7p14.1	40875192	SUGCT	A/C	0.96	1.21E-01	0.98	1.12E-01	0.99	4.93E-01	1.07	1.38E-05	1.09	1.76E-04	-0.004	5.72E-01
rs1048169	9p22.1	19055965	HAUS6	C/T	0.98	2.64E-01	0.98	1.00E-01	0.99	6.91E-01	1.05	1.38E-04	1.10	8.32E-07	-0.005	4.19E-01
rs10122495	9p13.3	34049779	RN7SKP114	T/A	0.99	6.63E-01	0.99	6.58E-01	1.00	9.65E-01	1.06	1.66E-04	1.08	4.10E-04	-0.001	9.16E-01
rs1182	9q34.11	132576060	TOR1A	A/C	1.07	2.65E-03	1.02	1.26E-01	1.03	5.86E-02	1.09	1.04E-07	1.13	1.15E-07	0.005	4.51E-01
rs141536087	10p15.3	854691	LARP4B	GCGCA/G	1.01	6.28E-01	1.00	7.83E-01	1.00	8.08E-01	1.09	5.23E-06	1.13	4.19E-06	0.008	3.22E-01
rs1935581	10q23.31	90195149	RNLS	C/T	0.98	2.54E-01	0.99	3.03E-01	1.00	9.23E-01	1.05	5.93E-04	1.07	6.57E-04	-0.004	5.77E-01
rs7094871	10q25.2	114712154	TCF7L2	G/C	1.06	5.66E-03	1.01	6.76E-01	0.99	5.07E-01	1.04	4.02E-03	1.05	1.40E-02	0.008	1.73E-01
rs1881502	11p15.5	1507512	MOB2	T/C	0.98	4.31E-01	1.00	8.66E-01	1.01	7.16E-01	1.07	4.57E-05	1.07	1.16E-02	-0.004	5.68E-01
rs1890184	11p15.4	7547587	PPFIBP2	A/G	1.04	1.80E-01	1.02	4.11E-01	1.05	2.90E-02	1.11	1.44E-07	1.09	5.52E-03	0.013	1.53E-01
rs457171081	11p11.2	47421962	RP11-750H9.5	CGG/C	1.00	9.02E-01	1.00	8.29E-01	0.98	2.39E-01	1.03	5.20E-02	1.07	6.59E-04	-0.004	5.45E-01
rs2277283	11q12.3	61908440	INCENP	C/T	1.04	1.21E-01	1.00	8.08E-01	1.01	5.67E-01	1.07	1.10E-05	1.07	1.20E-03	0.008	2.58E-01
rs12785905	11q13.2	66951965	KDM2A	C/G	0.99	7.56E-01	0.99	7.53E-01	0.99	7.67E-01	1.15	5.18E-05	1.19	2.27E-04	-0.015	3.04E-01
rs11290954	11q13.5	76260543	C11orf30	AC/A	0.97	9.97E-02	0.97	4.05E-02	0.97	1.65E-02	1.03	2.44E-02	1.05	2.40E-02	-0.023	3.16E-04
rs1800057	11q22.3	108143456	ATM	G/C	0.92	2.17E-01	0.98	6.48E-01	0.91	3.92E-02	1.10	4.29E-02	1.31	1.42E-05	0.005	8.09E-01
rs138466039	11q24.2	125054793	PKNOX2	T/C	1.02	8.42E-01	0.98	8.02E-01	0.97	6.64E-01	1.29	3.91E-04	1.25	2.00E-02	0.036	2.13E-01
rs878987	11q25	134266372	B3GAT1	G/A	1.04	2.03E-01	0.99	7.64E-01	0.99	5.81E-01	1.06	3.09E-03	1.11	1.71E-04	-0.004	6.48E-01
rs2066827	12p13.1	12871099	CDKN1B	T/G	1.04	1.13E-01	1.02	1.78E-01	1.01	6.96E-01	1.06	1.64E-04	1.08	6.25E-04	-0.001	9.48E-01
rs10845938	12p13.1	14416918	RNU6-491P	G/A	1.02	2.52E-01	1.02	2.40E-01	1.02	1.14E-01	1.07	8.55E-07	1.11	6.55E-08	0.011	7.43E-02
rs7968403	12q14.2	65012824	RASSF3	T/C	0.98	2.82E-01	1.00	8.46E-01	1.02	1.37E-01	1.06	1.76E-05	1.04	5.25E-02	0.001	8.72E-01
rs5799921	12q21.33	90160530	RNU6-148P	GA/G	1.03	2.67E-01	1.02	1.04E-01	1.02	1.86E-01	1.08	1.10E-06	1.07	1.30E-03	0.007	3.00E-01
rs7295014	12q24.33	133067989	FBRSL1	G/A	0.97	1.14E-01	0.99	4.03E-01	0.97	4.15E-02	1.03	3.90E-02	1.12	6.14E-08	-0.021	1.02E-03
rs1004030	14q11.2	23305649	MMP14	T/C	0.97	1.16E-01	0.98	1.50E-01	0.99	5.65E-01	1.04	1.27E-02	1.06	4.31E-03	-0.007	2.34E-01
rs11629412	14q13.3	37138294	PAX9	C/G	0.99	6.68E-01	0.99	2.90E-01	1.00	7.36E-01	1.06	5.47E-05	1.05	1.22E-02	-0.008	1.99E-01
rs4924487	15q15.1	40922915	CASC5	C/G	0.98	5.76E-01	1.00	8.56E-01	0.98	3.29E-01	1.05	7.67E-03	1.05	7.22E-02	-0.013	1.21E-01
rs33984059	15q21.3	56385868	RFK7	A/G	1.05	5.77E-01	1.03	5.32E-01	0.99	8.77E-01	1.19	2.01E-03	1.22	6.95E-03	-0.003	9.02E-01
rs112293876	15q22.31	66764641	MAP2K1	C/CA	1.03	2.43E-01	1.01	4.61E-01	0.99	5.01E-01	1.03	3.06E-02	1.10	4.92E-05	-0.010	1.37E-01
rs11863709	16q21	57654576	GPR56	C/T	1.15	1.14E-02	1.07	7.18E-02	1.04	2.85E-01	1.21	6.78E-07	1.21	5.79E-04	0.059	5.58E-04
rs201158093	16q23.3	82178893	RP11-510J16.5	TAA/TA	0.98	2.94E-01	1.00	9.77E-01	0.98	2.12E-01	1.03	2.33E-02	1.11	5.73E-07	-0.005	4.52E-01
rs28441558	17p13.1	7803118	CHD3	C/T	1.03	5.40E-01	0.98	5.60E-01	0.95	6.56E-02	1.13	1.01E-04	1.19	1.34E-04	-0.019	1.48E-01
rs142444269	17q11.2	30098749	RP11-805L22.3	C/T	1.01	6.07E-01	1.01	7.67E-01	0.99	6.09E-01	1.06	1.35E-03	1.06	3.34E-02	-0.007	4.02E-01
rs2680708	17q22	56456120	RNF43	G/A	1.00	8.98E-01	1.01	5.67E-01	1.01	5.64E-01	1.05	3.75E-04	1.09	4.74E-05	-0.006	3.69E-01
rs8093601	18q21.2	51772473	MBD2	C/G	0.99	7.05E-01	0.98	1.27E-01	1.00	9.97E-01	1.04	3.11E-03	1.05	2.56E-02	0.003	6.11E-01
rs28607662	18q21.2	53230859	TCF4	C/T	1.11	1.44E-03	1.04	7.27E-02	1.05	4.78E-02	1.11	4.97E-06	1.06	9.88E-02	0.019	5.39E-02
rs12956892	18q21.32	56746315	OACVLP	T/G	0.98	4.05E-01	0.99	4.69E-01	0.98	1.73E-01	1.03	3.05E-02	1.09	3.47E-05	-0.013	4.23E-02
rs533722308	18q21.33	60961193	BCL2	CT/C	0.99	5.33E-01	0.99	5.22E-01	0.97	8.25E-02	1.03	3.45E-02	1.10	4.48E-05	-0.021	2.47E-03
rs10460109	18q22.3	73036165	TSHZ1	T/C	1.01	7.14E-01	1.00	7.99E-01	0.99	5.07E-01	1.04	9.82E-03	1.07	3.15E-04	0.000	9.94E-01
rs11666569	19p13.11	17214073	MYO9B	C/T	0.95	2.24E-02	0.96	9.45E-03	0.96	9.09E-03	1.03	8.87E-02	1.11	2.77E-06	-0.014	4.16E-02
rs118005503	19q12	32167803	THEG5	G/C	1.03	4.18E-01	1.02	4.38E-01	1.02	4.70E-01	1.12	3.80E-05	1.18	3.13E-05	0.012	3.29E-01
rs61088131	19q13.2	42700947	POU2F2	C/T	1.07	1.86E-02	1.06	1.23E-03	1.03	1.00E-01	1.09	3.97E-06	1.07	6.96E-03	0.022	6.97E-03
rs11480453	20q11.21	31347512	DNMT3B	C/CA	0.99	7.93E-01	1.01	4.09E-01	1.01	6.84E-01	1.05	1.65E-03	1.06	8.28E-03	0.007	2.51E-01
rs6091758	20q13.2	52455205	BCAS1	G/A	1.01	7.57E-01	0.99	6.34E-01	1.01	3.43E-01	1.08	1.61E-07	1.10	5.88E-06	0.005	4.59E-01
rs9625483	22q12.1	28888939	TTCT8	A/G	0.95	3.23E-01	0.94	1.06E-01	0.97	4.58E-01	1.09	3.84E-02	1.12	8.25E-02	-0.013	4.56E-01
rs17321482																

Supplementary Table 15. Biological pathways enriched with prostate cancer susceptibility (enrichment score, ES>0.50).

Pathway	Database	Pathway ID	Enrichment Score	Pathway Size	Genes
PD-1 signaling	REACTOME: RELEASE 57	389948	0.761	22	CD3D, HLA-DRI1, PTPN6, HLA-DQA1, PDCD1, CSK, HLA-DQA2, LCK, HLA-DPA1, HLA-DQB2, HLA-DRE5, PTPN11, HLA-DRE4, HLA-DRE3, CD3E, HLA-DQA1, HLA-DQA1, PDCD1, CD274, HLA-DRA, CD4, CD3E
	REACTOME: RELEASE 57	425428	0.722	30	SLC44A1, SLC22A2, SLC44A2, SLC44A1, SLC44A2, SLC22A2, HMGCR, SLC6A1, SLC6A1, SLC6A7, SLC6A2, SLC44A4, SLC44A5, SLC44A6, SLC44A7, SLC44A8, SLC44A9, SLC44A10, SLC44A11, SLC44A12, SLC44A13, SLC44A14, SLC44A15, SLC44A16, SLC44A17, SLC44A18, SLC44A19, SLC44A20, SLC44A21, SLC44A22, SLC44A23, SLC44A24, SLC44A25, SLC44A26, SLC44A27, SLC44A28, SLC44A29, SLC44A30, SLC44A31, SLC44A32, SLC44A33, SLC44A34, SLC44A35, SLC44A36, SLC44A37, SLC44A38, SLC44A39, SLC44A40, SLC44A41, SLC44A42, SLC44A43, SLC44A44, SLC44A45, SLC44A46, SLC44A47, SLC44A48, SLC44A49, SLC44A50, SLC44A51, SLC44A52, SLC44A53, SLC44A54, SLC44A55, SLC44A56, SLC44A57, SLC44A58, SLC44A59, SLC44A60, SLC44A61, SLC44A62, SLC44A63, SLC44A64, SLC44A65, SLC44A66, SLC44A67, SLC44A68, SLC44A69, SLC44A70, SLC44A71, SLC44A72, SLC44A73, SLC44A74, SLC44A75, SLC44A76, SLC44A77, SLC44A78, SLC44A79, SLC44A80, SLC44A81, SLC44A82, SLC44A83, SLC44A84, SLC44A85, SLC44A86, SLC44A87, SLC44A88, SLC44A89, SLC44A90, SLC44A91, SLC44A92, SLC44A93, SLC44A94, SLC44A95, SLC44A96, SLC44A97, SLC44A98, SLC44A99, SLC44A100, SLC44A101, SLC44A102, SLC44A103, SLC44A104, SLC44A105, SLC44A106, SLC44A107, SLC44A108, SLC44A109, SLC44A110, SLC44A111, SLC44A112, SLC44A113, SLC44A114, SLC44A115, SLC44A116, SLC44A117, SLC44A118, SLC44A119, SLC44A120, SLC44A121, SLC44A122, SLC44A123, SLC44A124, SLC44A125, SLC44A126, SLC44A127, SLC44A128, SLC44A129, SLC44A130, SLC44A131, SLC44A132, SLC44A133, SLC44A134, SLC44A135, SLC44A136, SLC44A137, SLC44A138, SLC44A139, SLC44A140, SLC44A141, SLC44A142, SLC44A143, SLC44A144, SLC44A145, SLC44A146, SLC44A147, SLC44A148, SLC44A149, SLC44A150, SLC44A151, SLC44A152, SLC44A153, SLC44A154, SLC44A155, SLC44A156, SLC44A157, SLC44A158, SLC44A159, SLC44A160, SLC44A161, SLC44A162, SLC44A163, SLC44A164, SLC44A165, SLC44A166, SLC44A167, SLC44A168, SLC44A169, SLC44A170, SLC44A171, SLC44A172, SLC44A173, SLC44A174, SLC44A175, SLC44A176, SLC44A177, SLC44A178, SLC44A179, SLC44A180, SLC44A181, SLC44A182, SLC44A183, SLC44A184, SLC44A185, SLC44A186, SLC44A187, SLC44A188, SLC44A189, SLC44A190, SLC44A191, SLC44A192, SLC44A193, SLC44A194, SLC44A195, SLC44A196, SLC44A197, SLC44A198, SLC44A199, SLC44A200, SLC44A201, SLC44A202, SLC44A203, SLC44A204, SLC44A205, SLC44A206, SLC44A207, SLC44A208, SLC44A209, SLC44A210, SLC44A211, SLC44A212, SLC44A213, SLC44A214, SLC44A215, SLC44A216, SLC44A217, SLC44A218, SLC44A219, SLC44A220, SLC44A221, SLC44A222, SLC44A223, SLC44A224, SLC44A225, SLC44A226, SLC44A227, SLC44A228, SLC44A229, SLC44A230, SLC44A231, SLC44A232, SLC44A233, SLC44A234, SLC44A235, SLC44A236, SLC44A237, SLC44A238, SLC44A239, SLC44A240, SLC44A241, SLC44A242, SLC44A243, SLC44A244, SLC44A245, SLC44A246, SLC44A247, SLC44A248, SLC44A249, SLC44A250, SLC44A251, SLC44A252, SLC44A253, SLC44A254, SLC44A255, SLC44A256, SLC44A257, SLC44A258, SLC44A259, SLC44A260, SLC44A261, SLC44A262, SLC44A263, SLC44A264, SLC44A265, SLC44A266, SLC44A267, SLC44A268, SLC44A269, SLC44A270, SLC44A271, SLC44A272, SLC44A273, SLC44A274, SLC44A275, SLC44A276, SLC44A277, SLC44A278, SLC44A279, SLC44A280, SLC44A281, SLC44A282, SLC44A283, SLC44A284, SLC44A285, SLC44A286, SLC44A287, SLC44A288, SLC44A289, SLC44A290, SLC44A291, SLC44A292, SLC44A293, SLC44A294, SLC44A295, SLC44A296, SLC44A297, SLC44A298, SLC44A299, SLC44A300, SLC44A301, SLC44A302, SLC44A303, SLC44A304, SLC44A305, SLC44A306, SLC44A307, SLC44A308, SLC44A309, SLC44A310, SLC44A311, SLC44A312, SLC44A313, SLC44A314, SLC44A315, SLC44A316, SLC44A317, SLC44A318, SLC44A319, SLC44A320, SLC44A321, SLC44A322, SLC44A323, SLC44A324, SLC44A325, SLC44A326, SLC44A327, SLC44A328, SLC44A329, SLC44A330, SLC44A331, SLC44A332, SLC44A333, SLC44A334, SLC44A335, SLC44A336, SLC44A337, SLC44A338, SLC44A339, SLC44A340, SLC44A341, SLC44A342, SLC44A343, SLC44A344, SLC44A345, SLC44A346, SLC44A347, SLC44A348, SLC44A349, SLC44A350, SLC44A351, SLC44A352, SLC44A353, SLC44A354, SLC44A355, SLC44A356, SLC44A357, SLC44A358, SLC44A359, SLC44A360, SLC44A361, SLC44A362, SLC44A363, SLC44A364, SLC44A365, SLC44A366, SLC44A367, SLC44A368, SLC44A369, SLC44A370, SLC44A371, SLC44A372, SLC44A373, SLC44A374, SLC44A375, SLC44A376, SLC44A377, SLC44A378, SLC44A379, SLC44A380, SLC44A381, SLC44A382, SLC44A383, SLC44A384, SLC44A385, SLC44A386, SLC44A387, SLC44A388, SLC44A389, SLC44A390, SLC44A391, SLC44A392, SLC44A393, SLC44A394, SLC44A395, SLC44A396, SLC44A397, SLC44A398, SLC44A399, SLC44A400, SLC44A401, SLC44A402, SLC44A403, SLC44A404, SLC44A405, SLC44A406, SLC44A407, SLC44A408, SLC44A409, SLC44A410, SLC44A411, SLC44A412, SLC44A413, SLC44A414, SLC44A415, SLC44A416, SLC44A417, SLC44A418, SLC44A419, SLC44A420, SLC44A421, SLC44A422, SLC44A423, SLC44A424, SLC44A425, SLC44A426, SLC44A427, SLC44A428, SLC44A429, SLC44A430, SLC44A431, SLC44A43

Supplementary Table 16. Prostate cancer risk variants included in the Familial Relative Risk and Polygenic Risk Score calculations. The betas and standard errors are based on the overall meta-analysis (N=140,306 biologically independent samples).

SNP	Chr	Position	Source	Effect Allele	Beta ^a	Std Error ^b
rs56391074	1	88210715	Novel	AT	0.047	8.20E-03
rs34579442	1	153899900	Novel	C	0.066	8.70E-03
rs62106670	2	8597123	Novel	T	0.052	9.00E-03
rs74702681	2	66652885	Novel	T	0.159	2.64E-02
rs11691517	2	111893096	Novel	T	0.064	9.10E-03
rs34925593	2	174234547	Novel	C	0.047	8.40E-03
rs59308963	2	202123479	Novel	T	0.051	9.00E-03
rs1283104	3	106962521	Novel	G	0.047	8.20E-03
rs182314334	3	152004202	Novel	T	0.089	1.34E-02
rs142436749	3	169093100	Novel	G	0.221	3.78E-02
rs10793821	5	133836209	Novel	T	0.053	8.00E-03
rs76551843	5	169172133	Novel	A	0.271	4.80E-02
rs4976790	5	177968915	Novel	T	0.074	1.27E-02
rs12665339	6	30601232	Novel	G	0.062	1.06E-02
rs9296068	6	32988695	Novel	T	0.048	8.40E-03
rs9469899	6	34793124	Novel	A	0.048	8.30E-03
rs4711748	6	43694598	Novel	T	0.052	9.40E-03
rs527510716	7	1944537	Novel	C	0.059	1.07E-02
rs11452686	7	20414110	Novel	T	0.050	8.60E-03
rs17621345	7	40875192	Novel	A	0.072	9.50E-03
rs1048169	9	19055965	Novel	C	0.061	8.10E-03
rs10122495	9	34049779	Novel	T	0.050	8.80E-03
rs1182	9	132576060	Novel	A	0.058	9.50E-03
rs141536087	10	854691	Novel	GCGCA	0.081	1.13E-02
rs1935581	10	90195149	Novel	C	0.048	8.20E-03
rs7094871	10	114712154	Novel	G	0.044	8.00E-03
rs1881502	11	1507512	Novel	T	0.058	1.01E-02
rs61890184	11	7547587	Novel	A	0.071	1.22E-02
rs547171081	11	47421962	Novel	CGG	0.047	8.50E-03
rs2277283	11	61908440	Novel	C	0.056	8.90E-03
rs12785905	11	66951965	Novel	C	0.116	2.00E-02
rs11290954	11	76260543	Novel	AC	0.061	8.50E-03
rs1800057	11	108143456	Novel	G	0.150	2.60E-02
rs138466039	11	125054793	Novel	T	0.281	4.18E-02
rs878987	11	134266372	Novel	G	0.064	1.17E-02
rs2066827	12	12871099	Novel	T	0.056	9.40E-03
rs10845938	12	14416918	Novel	G	0.057	8.00E-03

rs7968403	12	65012824	Novel	T	0.059	8.50E-03
rs5799921	12	90160530	Novel	GA	0.061	8.90E-03
rs7295014	12	133067989	Novel	G	0.052	8.40E-03
rs1004030	14	23305649	Novel	T	0.046	8.20E-03
rs11629412	14	37138294	Novel	C	0.057	8.20E-03
rs4924487	15	40922915	Novel	C	0.062	1.09E-02
rs33984059	15	56385868	Novel	A	0.176	3.08E-02
rs112293876	15	66764641	Novel	C	0.057	9.10E-03
rs11863709	16	57654576	Novel	C	0.148	2.20E-02
rs201158093	16	82178893	Novel	TAA	0.049	8.50E-03
rs28441558	17	7803118	Novel	C	0.151	1.82E-02
rs142444269	17	30098749	Novel	C	0.067	1.06E-02
rs2680708	17	56456120	Novel	G	0.046	8.20E-03
rs8093601	18	51772473	Novel	C	0.045	8.10E-03
rs28607662	18	53230859	Novel	C	0.075	1.34E-02
rs12956892	18	56746315	Novel	T	0.050	8.60E-03
rs533722308	18	60961193	Novel	CT	0.052	9.10E-03
rs10460109	18	73036165	Novel	T	0.044	8.00E-03
rs11666569	19	17214073	Novel	C	0.052	9.00E-03
rs118005503	19	32167803	Novel	G	0.090	1.56E-02
rs61088131	19	42700947	Novel	T	0.062	1.08E-02
rs11480453	20	31347512	Novel	C	0.046	8.40E-03
rs6091758	20	52455205	Novel	G	0.072	8.30E-03
rs9625483	22	28888939	Novel	A	0.134	2.40E-02
rs17321482	23	11482634	Novel	C	0.067	9.10E-03
rs17599629	1	150658287	Known	G	0.065	9.60E-03
rs1218582	1	154834183	Known	G	0.046	8.00E-03
rs4245739	1	204518842	Known	A	0.092	9.10E-03
rs9287719	2	10710730	Known	C	0.066	7.90E-03
rs9306895	2	20878153	Known	C	0.077	8.20E-03
rs1465618	2	43553949	Known	T	0.083	9.50E-03
rs721048	2	63131731	Known	A	0.097	1.01E-02
rs10187424	2	85794297	Known	T	0.074	8.00E-03
rs12621278	2	173311553	Known	A	0.242	1.78E-02
rs2292884	2	238443226	Known	G	0.061	9.20E-03
rs3771570	2	242382864	Known	T	0.084	1.09E-02
rs2660753	3	87110674	Known	T	0.120	1.28E-02
rs7611694	3	113275624	Known	A	0.083	8.00E-03
rs10934853	3	128038373	Known	A	0.099	8.70E-03
rs6763931	3	141102833	Known	A	0.043	8.00E-03
rs10936632	3	170130102	Known	A	0.097	8.00E-03
rs10009409	4	73855253	Known	T	0.056	8.90E-03
rs1894292	4	74349158	Known	G	0.062	7.90E-03

rs12500426	4	95514609	Known	A	0.069	7.90E-03
rs17021918	4	95562877	Known	C	0.085	8.30E-03
rs7679673	4	106061534	Known	C	0.120	8.10E-03
rs2242652	5	1280028	Known	G	0.160	1.05E-02
rs12653946	5	1895829	Known	T	0.079	8.20E-03
rs2121875	5	44365545	Known	C	0.048	8.50E-03
rs4713266	6	11219030	Known	C	0.051	7.90E-03
rs7767188	6	30073776	Known	A	0.054	9.70E-03
rs3096702	6	32192331	Known	A	0.056	8.20E-03
rs3129859	6	32400939	Known	G	0.060	8.50E-03
rs1983891	6	41536427	Known	T	0.082	8.80E-03
rs9443189	6	76495882	Known	A	0.064	1.16E-02
rs2273669	6	109285189	Known	G	0.069	1.10E-02
rs339331	6	117210052	Known	T	0.084	8.70E-03
rs1933488	6	153441079	Known	A	0.076	8.10E-03
rs9364554	6	160833664	Known	T	0.104	8.70E-03
rs12155172	7	20994491	Known	A	0.093	9.40E-03
rs10486567	7	27976563	Known	G	0.134	9.40E-03
rs56232506	7	47437244	Known	A	0.054	8.00E-03
rs6465657	7	97816327	Known	C	0.101	7.90E-03
rs2928679	8	23438975	Known	A	0.053	8.00E-03
rs1512268	8	23526463	Known	T	0.128	8.00E-03
rs11135910	8	25892142	Known	T	0.078	1.10E-02
rs12543663	8	127924659	Known	C	0.111	8.60E-03
rs10086908	8	128011937	Known	T	0.126	8.70E-03
rs183373024	8	128104117	Known	G	1.068	3.96E-02
rs16901979	8	128124916	Known	A	0.445	2.04E-02
rs620861	8	128335673	Known	G	0.139	8.30E-03
rs6983267	8	128413305	Known	G	0.200	7.90E-03
rs1447295	8	128485038	Known	A	0.345	1.21E-02
rs17694493	9	22041998	Known	G	0.073	1.14E-02
rs76934034	10	46082985	Known	T	0.115	1.51E-02
rs10993994	10	51549496	Known	T	0.208	8.00E-03
rs3850699	10	104414221	Known	A	0.070	8.70E-03
rs4962416	10	126696872	Known	C	0.059	8.90E-03
rs7127900	11	2233574	Known	A	0.170	9.80E-03
rs7931342	11	68994497	Known	G	0.157	7.90E-03
rs11568818	11	102401661	Known	T	0.074	8.20E-03
rs11214775	11	113807181	Known	G	0.071	9.00E-03
rs80130819	12	48419618	Known	A	0.096	1.42E-02
rs10875943	12	49676010	Known	C	0.069	8.70E-03
rs902774	12	53273904	Known	A	0.126	1.08E-02
rs1270884	12	114685571	Known	A	0.070	7.90E-03

rs8008270	14	53372330	Known	C	0.083	1.03E-02
rs7141529	14	69126744	Known	C	0.051	7.90E-03
rs8014671	14	71092256	Known	G	0.047	8.30E-03
rs684232	17	618965	Known	C	0.083	8.20E-03
rs11649743	17	36074979	Known	G	0.122	1.02E-02
rs4430796	17	36098040	Known	A	0.197	8.10E-03
rs138213197	17	46805705	Known	T	1.348	8.06E-02
rs11650494	17	47345186	Known	A	0.099	1.45E-02
rs1859962	17	69108753	Known	G	0.161	7.90E-03
rs7241993	18	76773973	Known	C	0.076	8.70E-03
rs8102476	19	38735613	Known	C	0.090	8.00E-03
rs11672691	19	41985587	Known	G	0.092	9.20E-03
rs2735839	19	51364623	Known	G	0.167	1.15E-02
rs12480328	20	49527922	Known	T	0.107	1.56E-02
rs2427345	20	61015611	Known	C	0.045	8.20E-03
rs6062509	20	62362563	Known	T	0.078	8.90E-03
rs1041449	21	42901421	Known	G	0.051	8.10E-03
rs58133635	22	40471188	Known	T	0.068	9.90E-03
rs5759167	22	43500212	Known	G	0.142	8.00E-03
rs2405942	23	9814135	Known	A	0.049	6.90E-03
rs5945619	23	51241672	Known	C	0.104	5.70E-03
rs2807031	23	52896949	Known	C	0.058	7.20E-03
rs5919432	23	67021550	Known	T	0.043	7.10E-03
rs6625711	23	70139850	Known	A	0.008	8.20E-03

^aBeta values from the overall meta-analysis.

^bStandard error values from the overall meta-analysis.

Supplementary Table 17. Polygenetic Risk Score (PRS) and proportion of Familial Relative Risk (FRR) for novel and previously known prostate cancer susceptibility variants.

	OncoArray Analysis
Number of previous known SNPs	83
Rare SNPs reported on 8q24 and <i>HOXB13</i> ^a	2
Number of newly identified SNPs	62
Total number of SNPs	147
Total number of samples in analysis (co/ca)	72,729 (27,904/44,825)
Relative Risk (95%CI) of top 1% vs median risk group (85 known) ^b	4.93 (4.35-5.60)
Relative Risk (95%CI) of top 1% vs median risk group (147 new+known) ^b	5.71 (5.04-6.48)
FRR (83 known) ^c	19.5%
FRR (2 Rare SNPs reported on 8q24 and <i>HOXB13</i>) ^{a, c}	4.5%
FRR (62 new) ^c	4.4%
FRR (147 new+known) ^c	28.4%

^a 8q24:rs183373024; *HOXB13*:rs138213197

^b Polygenetic Risk Score (PRS) was computed for OncoArray European individuals using the beta coefficients computed from the European overall meta-analysis.

^c Familial relative risk (FRR) estimation based on allele frequencies and beta estimates computed in the European overall meta-analysis. We assumed a familial risk of 2.5 for first-degree relatives of individuals with prostate cancer (Kicinski *et al.* 2011)

Supplementary Table 18. Polygenetic risk score (PRS) for overall prostate cancer risk and by several sub-analyses.

	OR (95%CI)		P-value^c
Overall ^a	1.86 (1.83-1.89)		< 0.0001
Family History Status ^b	No - OR (95%CI)	Yes - OR (95%CI)	
	1.84 (1.80-1.88)	1.95 (1.85-2.05)	1.18E-24
Age of Disease Onset	Age > 55 - OR (95%CI)	Age ≤ 55 - OR (95%CI)	
	1.84 (1.81-1.87)	2.29 (2.20-2.39)	8.26E-33
Aggressivness (Previous Definition)	Non-advanced - OR (95%CI)	Advanced - OR (95%CI)	
	1.88 (1.85-1.91)	1.80 (1.75-1.86)	7.46E-06
Aggressivness (New Definition)	Low/Intermediate - OR (95%CI)	High - OR (95%CI)	
	1.89 (1.86-1.93)	1.88 (1.83-1.93)	0.01

^a We divided PRS by the overall standard deviation of PRS in the controls (Standardized PRS).

^b We used all controls versus cases for each sub-analysis (e.g. cases with family history or cases without family history); analyses were stratified by country and adjusted for 7 PCs in European OncoArray data set.

^c P-value for testing differences among effect sizes (by family history, age of disease onset, and aggressiveness of disease) were derived from a case-only analysis

Supplementary Table 19. OncoArray studies that will be available in dbGAP.

StudyAcronym	in_dbGap	PCT
Aarhus	1631	100.0%
AHS	1650	100.0%
ATBC	3194	100.0%
Canary PASS	373	100.0%
CCI	270	100.0%
CeRePP	1570	100.0%
COH	519	100.0%
COSM	3418	100.0%
CPCS1	795	100.0%
CPCS2	672	100.0%
CPS-II	8519	100.0%
EPIC	1332	100.0%
ERSPC	137	100.0%
ESTHER	639	100.0%
FHCRC	812	100.0%
Gene-PARE	253	20.6%
Hamburg-Zagreb	295	100.0%
HPFS	2221	100.0%
IMPACT	926	100.0%
IPO-Porto	554	100.0%
KULEUVEN	269	100.0%
LAAPC	732	100.0%
MCC-Spain	922	100.0%
MCCS	1033	100.0%
MDACC_AS	535	100.0%
MEC	1298	100.0%
MOFFITT	615	100.0%
Oslo	0	0.0%
PCMUS	281	100.0%
PHS	899	100.0%
PLCO	1658	100.0%
Poland	802	100.0%
PRAGGA	0	0.0%
PROCAP	901	100.0%
PROFILE	0	0.0%
PROGReSS	996	100.0%
ProMPT	858	100.0%
ProtecT	1419	100.0%
QLD	4583	100.0%

RAPPER	2155	100.0%
SEARCH	3985	100.0%
SFPCS	0	0.0%
SNP_Prostate_Ghent	451	100.0%
SPAG	211	100.0%
STHM2	4527	100.0%
SWOG-PCPT	2247	100.0%
SWOG-SELECT	3660	100.0%
TAMPERE	3610	100.0%
TORONTO	0	0.0%
UKGPCS	19045	100.0%
ULM	636	100.0%
WUGS	682	100.0%

Total studies	52	
in dbGAP	47	
Total samples	88790	88.9%

SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure 1. Manhattan plot of known (blue) and novel (magenta) prostate cancer loci (N=62) from the meta-analysis of overall prostate cancer risk.

Manhattan plot of genotyped and imputed results from the European-ancestry meta-analysis of overall prostate cancer risk (N=140,306 biologically independent samples). P-values were calculated from a two-sided likelihood ratio test implemented in a logistic regression framework. All SNPs within 500 kb of known and novel PrCa index SNPs are highlighted (known=blue; novel=magenta). The red line and blue line represents $P = 5 \times 10^{-8}$ and $P = 1 \times 10^{-5}$. The y-axis has been limited to $P > 1 \times 10^{-20}$.

Supplementary Figure 2. Cluster plots for twelve of the novel index SNPs. Panels a-l represent the cluster plots for all cancer samples genotyped using the OncoArray platform in the GAME-ON consortium. Twelve of the 63 novel prostate cancer susceptibility loci were genotyped and represented. The respective colored clusters represent the genotype, i.e. homozygote wild-type, heterozygote, homozygote variant-type. The genotype counts are listed in the upper right corner of each cluster plot.

Supplementary Figure 3. Linkage disequilibrium plots of novel prostate cancer variants with poor imputation quality scores ($r^2 < 0.80$). The index signal (purple diamond) is imputed whereas the remaining points are the genotyped markers from the OncoArray (N=74,849 biologically independent samples). The strength of the linkage disequilibrium (LD) between the imputed index signal and the genotyped markers is represented by the colors. The x-axis represents the genomic position ± 500 KB of the index signal. The y-axis is the $-\log P$ of the association with prostate cancer risk from the OncoArray analysis only. The bottom panel lists the known genes within the region. The OncoArray for the locus rs144166867 (Chr X) did not contain any genotyped SNPs. **(a)** LD region for rs527510716 (Chr 7); **(b)** LD region for rs6602880 (Chr 10); and **(c)** LD region for rs533722308 (Chr 18).

Supplementary Figure 4. LocusExplorer plots of the 63 novel prostate cancer loci. The index SNPs are labeled on the top portion of the plot. Clusters of correlated variants for each signal are distinguished using different colors in the plot and on the panel below. Stronger shading indicates greater correlation with the index SNP, with variants not correlated at $r^2 \geq 0.5$ with any index SNP uncolored. $\log_{10} P$ -values are shown on the Y-axis of the plot. The position of genes within the region and the genomic coordinates of the plot are shown on the lower panel, with genes on the positive strand in green and the negative strand in purple.

Supplementary Figure 5. Enrichment map of the PD-1 Signaling Pathway. Shaded circles represent pathways (darker red indicates higher enrichment score) and larger size denotes a greater number of genes in the pathway), as labelled. Edges connect similar pathways, as determined by gene set overlap. Green lines connect those that are most similar in terms of gene set overlap ($>70\%$) thicker lines denote greater similarity).

Supplementary Figure 6. Effect estimation bias of the overall meta-analysis. A correlation plot of the known PrCa (black) and novel PrCa (red) loci where the x-axis is the log odds ratio from the overall meta-analysis (N=140,306 biologically independent samples) and the y-axis is the Bayesian corrected estimate.

SUPPLEMENTARY NOTE

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Previously Reported PrCa Susceptibility Loci

Of the 104 previously reported loci for either overall or stratum-specific (*i.e.* aggressive, early-onset, etc.) PrCa risk, we observed associations at $P < 5.0 \times 10^{-8}$ for 84 markers and $P < 0.05$ for 97 markers in the overall meta-analysis (**Supplementary Table 7**). The effect sizes with the OncoArray were similar to those previously observed. Of the twenty markers failing to replicate at the genome-wide significance level ($P < 5.0 \times 10^{-8}$) nine were initially identified in non-European ancestral populations (8 Asian and 1 African American) and an additional four loci were identified in a multiethnic meta-analysis including European, African, Japanese and Latino populations. An index variant, rs636291, previously reported to be associated with early-onset failed to replicate with overall PrCa ($P = 5.87 \times 10^{-7}$) or our early-onset meta-analysis ($P = 3.57 \times 10^{-6}$). A similar null association was observed for rs1571801, a previously reported aggressive prostate cancer marker ($P = 3.78 \times 10^{-3}$). One previously reported PrCa marker (rs662571 on chromosome X) failed to replicate ($P = 0.55$; **Supplementary Table 7**), highlighting the likelihood of a false-positive result. The minor allele frequency (MAF) was initially reported as 41% among Europeans for rs662571 whereas our European OncoArray

subset observed a MAF of 18%, likely indicating a genotyping array design error. Limiting the association results to the OncoArray only, we replicated 75 of the 104 known PrCa loci ($P=0.05/104=4.8\times 10^{-4}$; **Supplementary Table 7**). Of the 29 loci failing to replicate, 16 were discovered in previous GWAS of individuals of European ancestry, 4 were reported in multi-ethnic meta-analyses, and 9 were discovered in populations of non-European ancestry. Fine-mapping is needed to determine if correlated markers within these regions can clarify this apparent inconsistency. These fine-mapping efforts are underway to address this discrepancy.

Novel PrCa Susceptibility Loci

The consortia specific associations were consistent across the eight contributing GWAS studies (**Supplementary Table 10**) as indicated by the effect estimates and the test for heterogeneity. Although several markers showed evidence for heterogeneity (P -values_{het}<0.05), these failed to reach statistical significance after correcting for multiple comparisons ($P=0.05/63=7.9\times 10^{-4}$).

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