Genomic Locus	IndSigSNP	chr	bp	snp	Date Added To Catalog	PMID	FirstAuth	Date	Journal	Link	Study	Trait	InitialN	Replicatio	Region	ReportedGene	MappedGene	UpGene	DownGene	SNP_Gene_ID	UpGeneDi	DownGene	Strongest	SNPs	marged	SNP_ID_cu	Context	intergenic	RiskAF	P	Pmlog	Ptext	OrBeta	95CI	Platform	CNV
1	1:32327685	1	32356815	rs34701865	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	1p35.2	RP11-84A19.4	SPOCD1 - PTP4A2	ENSG00000134668	ENSG00000184007		75163	15207	rs34701865-T	rs34701865	0	34701865	intron_variant	1	NR	1.00E-08	8		0.036605	[0.024-0.0	Affymetrix [323123] (imputed)	N
1	1:32327685	1	32397127	rs72665000	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist circumference adjusted for body mass index	457,690 Eu	NA	1p35.2	NR	PTP4A2			ENSG00000184007	NA	NA	rs72665000-?	rs72665000	0	72665000	intron_variant	0	NR	8.00E-10	9.09691		NA		Affymetrix [~ 8270000] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	29/06/2021	3.3E+07	Sinnott-Armstrong N	18/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33462484	Genetics of 35 blood and urine biomarkers in the UK Biobank.	Alanine aminotransferase levels	342,387 Eu	NA	1q21.2	NR	MCL1			ENSG00000143384	NA	NA	rs11580946-A	rs11580946	0	11580946	missense_variant	0	NR	1.00E-14	14		0.0737	[0.055-0.0	Affymetrix [9000000] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	29/06/2021	3.3E+07	Sinnott-Armstrong N	18/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33462484	Genetics of 35 blood and urine biomarkers in the UK Biobank.	Aspartate aminotransferase to alanine aminotransferase ratio	341,165 Eu	NA	1q21.2	NR	MCL1			ENSG00000143384	NA	NA	rs11580946-A	rs11580946	0	11580946	missense_variant	0	NR	2.00E-09	8.69897		0.0573	[0.039-0.0	Affymetrix [9000000] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	29/06/2021	3.3E+07	Sinnott-Armstrong N	18/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33462484	Genetics of 35 blood and urine biomarkers in the UK Biobank.	Gamma glutamyl transferase levels	342,339 Eu	NA	1q21.2	NR	MCL1			ENSG00000143384	NA	NA	rs11580946-A	rs11580946	0	11580946	missense_variant	0	NR	1.00E-19	19		0.0864	[0.068-0.1	Affymetrix [9000000] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Pulse pressure	810,865 Eu	354,096 Eu	1q21.2		MCL1			ENSG00000143384	NA	NA	rs11580946-A	rs11580946	0	11580946	missense_variant	0	0.015	3.00E-09	8.522879		0.388206	[0.26-0.52	Affymetrix, Illumina [242866] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Systolic blood pressure	810,865 Eu	354,096 Eu	1q21.2		MCL1			ENSG00000143384	NA	NA	rs11580946-A	rs11580946	0	11580946	missense_variant	0	0.0147	2.00E-08	7.69897		0.523103	[0.34-0.71	Affymetrix, Illumina [247314] (imputed)	N
2	1:150292561	1	1.51E+08	rs11580946	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Systolic blood pressure	approxima	NA	1q21.2		MCL1			ENSG00000143384	NA	NA	rs11580946-?	rs11580946	0	11580946	missense_variant	0	NR	1.00E-09	9		NA		NR [~ 8900000] (imputed)	N
2	1:150292561	1	1.5E+08	rs11581793	22/03/2021	3.3E+07	Nielsen JB	18/12/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/33339817	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease.	Alanine aminotransferase levels	76,081 Eur	NA	1q21.2	MRPS21, PRPF3	MRPS21 - PRPF3	ENSG00000266472	ENSG00000117360		11134	1366	rs11581793-?	rs11581793	1	11581793	regulatory_region_variant	1		2.00E-08	7.69897		0.1441	[0.094-0.1	Illumina [31500000] (imputed)	N
2	1:150292561	1	1.5E+08	rs187799739	21/05/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Height	approxima	NA	1q21.2		RPRD2			ENSG00000163125	NA	NA	rs187799739-?	rs187799739	0	1.88E+08	intron_variant	0	NR	1.00E-33	33		NA		NR [~ 8900000] (imputed)	N
2	1:150292561	1	1.5E+08	rs187799739	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Lung function (FVC)	approxima	NA	1q21.2		RPRD2			ENSG00000163125	NA	NA	rs187799739-?	rs187799739	0	1.88E+08	intron_variant	0	NR	8.00E-12	11.09691		NA		NR [~ 8900000] (imputed)	N
2	1:150292561	1	1.51E+08	rs190596489	16/11/2018	3E+07	Emilsson V	2/08/2018	Science	www.ncbi.nlm.nih.gov/pubmed/30072576	Co-regulatory networks of human serum proteins link genetics to disease.	Blood protein levels	3,200 Euro	NA	1q21.2	MCL1	MCL1 - ENSA	ENSG00000143384	ENSG00000143420		9829	11284	rs190596489-A	rs190596489	0	1.91E+08	intergenic_variant	1	0.992969	2.00E-07	6.69897	(MCL1, 102	0.778233	[0.48-1.07	Illumina [~ 1000000] (imputed)	N
2	1:150292561	1	1.51E+08	rs28521412	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Fat-free mass	70,700 Eur	NA	1q21.3	NR	CERS2 - ANXA9	ENSG00000143418	ENSG00000143412		7241	5	rs28521412-?	rs28521412	0	28521412	intergenic_variant	1	NR	1.00E-06	6	(female)	0.48049	[0.29-0.67	Affymetrix [7794483] (imputed)	N
2	1:150292561	1	1.51E+08	rs28521412	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Fat-free mass	70,700 Eur	NA	1q21.3	NR	CERS2 - ANXA9	ENSG00000143418	ENSG00000143412		7241	5	rs28521412-?	rs28521412	0	28521412	intergenic_variant	1	NR	2.00E-06	5.69897		0.41951	[0.25-0.59	Affymetrix [7794483] (imputed)	N
2	1:150292561	1	1.51E+08	rs28521412	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Bi	NA	1q21.3	ANXA9	CERS2 - ANXA9	ENSG00000143418	ENSG00000143412		7241	5	rs28521412-A	rs28521412	0	28521412	intergenic_variant	1	NR	1.00E-16	16		0.094603	[0.072-0.1	Affymetrix [321016] (imputed)	N
2	1:150292561	1	1.51E+08	rs6684154	13/08/2021	3.4E+07	Ward LD	27/07/2021	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/34315874	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms.	Alanine aminotransferase levels	387,859 Bi	NA	1q21.3	PRUNE1	PRUNE1			ENSG00000143363	NA	NA	rs6684154-?	rs6684154	0	6684154	intron_variant	0	NR	3.00E-15	14.52288		0.0142	[0.011-0.0	Affymetrix [21347608] (imputed)	N
2	1:150292561	1	1.51E+08	rs6684154	13/08/2021	3.4E+07	Ward LD	27/07/2021	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/34315874	GWAS of serum ALT and AST reveals an association of SLC30A10 Thr95Ile with hypermanganesemia symptoms.	Aspartate aminotransferase levels	386,570 Bi	NA	1q21.3	PRUNE1	PRUNE1			ENSG00000143363	NA	NA	rs6684154-?	rs6684154	0	6684154	intron_variant	0	NR	3.00E-08	7.522879		0.0061	[0.0037-0.	Affymetrix [21347608] (imputed)	N
2	1:150292561	1	1.51E+08	rs6684154	9/06/2021	3.4E+07	Pazoki R	10/05/2021	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/33972514	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes.	Liver enzyme levels (alanine transaminase)	437,267 Eu	315,572 Eu	1q21.3	PRUNE1	PRUNE1			ENSG00000143363	NA	NA	rs6684154-C	rs6684154	0	6684154	intron_variant	0	0.984478	1.00E-21	21		0.015071	[0.012-0.0	Affymetrix [13995440] (imputed)	N
2	1:150292561	1	1.51E+08	rs72704611	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist-to-hip ratio adjusted for BMI	457,690 Eu	NA	1q21.3	NR	CTSS			ENSG00000163131	NA	NA	rs72704611-?	rs72704611	0	72704611	intron_variant	0	NR	1.00E-08	8		NA		Affymetrix [~ 8270000] (imputed)	N
3	4:17942560	4	17792869	rs12640250	8/01/2020	3E+07	Mahajan A	8/10/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30297969	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps.	Type 2 diabetes	74,124 Eu	NA	4p15.31	LCORL	FAM184B - DCAF	ENSG00000047662	ENSG00000163257		9625	9409	rs12640250-C	rs12640250	0	12640250	intergenic_variant	1	0.7149	4.00E-08	7.39794		1.04	[1.03-1.05	Affymetrix, Illumina [~ 27000000] (imputed)	N
3	4:17942560	4	18015156	rs16896276	26/01/2021	3.2E+07	Fan Q	19/03/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32193507	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error.	Corneal curvature	29,580 Eur	88,218 Eur	4p15.31		LCORL			ENSG00000178177	NA	NA	rs16896276-A	rs16896276	0	16896276	intron_variant	0	0.26	1.00E-31	31		0.013	mm increa	Affymetrix, Illumina [8936601] (imputed)	N
3	4:17942560	4	18015156	rs16896276	26/01/2021	3.2E+07	Fan Q	19/03/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32193507	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error.	Corneal curvature	29,580 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs16896276-A	rs16896276	0	16896276	intron_variant	0	0.27	1.00E-07	7		0.014	mm increa	Affymetrix, Illumina [8936601] (imputed)	N
3	4:17942560	4	18015156	rs16896276	26/01/2021	3.2E+07	Fan Q	19/03/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32193507	Genome-wide association meta-analysis of corneal curvature identifies novel loci and shared genetic influences across axial length and refractive error.	Corneal curvature	35,422 ind	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs16896276-A	rs16896276	0	16896276	intron_variant	0	NR	9.00E-09	8.045757		0.0143	[0.0096-0.	Affymetrix, Illumina [8936601] (imputed)	N
3	4:17942560	4	18015156	rs16896276	16/11/2022	3.5E+07	Knot MJ	15/11/2021	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/34791242	Genetic architecture of orbital telorism.	Orbital telorism	34,130 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs16896276-?	rs16896276	0	16896276	intron_variant	0	NR	4.00E-09	8.39794		0.1431	[0.095-0.1	Affymetrix, Illumina [NR] (imputed)	N
3	4:17942560	4	18015156	rs16896276	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist circumference adjusted for body mass index	457,690 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs16896276-?	rs16896276	0	16896276	intron_variant	0	NR	8.00E-20	19.04576		NA		Affymetrix [~ 8270000] (imputed)	N
3	4:17942560	4	18025484	rs2011603	19/10/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Educational attainment (years of education)	up to 1,13	NA	4p15.31		LCORL - NA	ENSG00000178177			1985	NA	rs2011603-A	rs2011603	0	2011603	intergenic_variant	1	0.7359	1.00E-08	8		0.0091	[0.006-0.0	Affymetrix, Illumina [~ 10000000] (imputed)	N
3	4:17942560	4	18025484	rs2011603	7/03/2019	3.1E+07	Giri A	21/12/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30578418	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals.	Pulse pressure	365,998 Eu	299,024 Eu	4p15.31	intergenic	LCORL - NA	ENSG00000178177			1985	NA	rs2011603-A	rs2011603	0	2011603	intergenic_variant	1	0.7256	2.00E-11	10.69897		0.1432	[0.1-0.181	Affymetrix [NR] (imputed)	N
3	4:17942560	4	18025484	rs2011603	14/09/2020	3.3E+07	Vujkovic M	15/06/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/32541925	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis.	Type 2 diabetes	148,726 Eu	NA	4p15.31	NR	LCORL - NA	ENSG00000178177			1985	NA	rs2011603-G	rs2011603	0	2011603	intergenic_variant	1	0.2752	2.00E-13	12.69897		0.0383	[0.028-0.0	Affymetrix, Illumina [11987871] (imputed)	N
3	4:17942560	4	17998426	rs2061456	15/01/2020	3.1E+07	Plotnikov D	16/05/2019	Br J Ophthalmol	www.ncbi.nlm.nih.gov/pubmed/31097437	Association between birth weight and refractive error in adulthood: a Mendelian randomisation study.	Birth weight	188,039 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs2061456-A	rs2061456	0	2061456	intron_variant	0	0.25	4.00E-25	24.39794		0.038	[0.03-0.046	Affymetrix [up to 10400000] (imputed)	N
3	4:17942560	4	17998426	rs2061456	17/07/2019	2.9E+07	Tachmazidou I	1/06/2017	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/28552196	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits.	Height	1,249 who	205,003 Eu	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2061456-A	rs2061456	0	2061456	intron_variant	0	0.261	1.00E-19	19		0.0656	[0.051-0.0	Affymetrix, Illumina, Perlegen [15844966] (imputed)	N
3	4:17942560	4	17998426	rs2061456	5/08/2022	3.6E+07	Chiou JS	13/07/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35831902	Your height affects your health: genetic determinants and health-related outcomes in Taiwan.	Height	67,452 Ha	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2061456-A	rs2061456	0	2061456	intron_variant	0	NR	9.00E-57	56.04576		0.08	[0.07-0.09	Affymetrix [NR] (imputed)	N
3	4:17942560	4	17812615	rs2074974	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Bi	NA	4p15.31	NCAPG	NCAPG			ENSG00000109805	NA	NA	rs2074974-A	rs2074974	0	2074974	5_prime_UTR_variant	0	NR	1.00E-11	11		0.021246	[0.015-0.0	Affymetrix [321016] (imputed)	N
3	4:17942560	4	17917781	rs2174633	28/01/2019	3.1E+07	Morris JA	31/12/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30598549	An atlas of genetic influences on osteoporosis in humans and mice.	Heel bone mineral density	426,824 Bi	NA	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2174633-A	rs2174633	0	2174633	intron_variant	0	0.265235	5.00E-13	12.30103		0.015139	[0.011-0.0	NR [13737936] (imputed)	N
3	4:17942560	4	17917781	rs2174633	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Heel bone mineral density	approxima	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2174633-?	rs2174633	0	2174633	intron_variant	0	NR	2.00E-18	17.69897		NA		NR [~ 8900000] (imputed)	N
3	4:17942560	4	17917781	rs2174633	18/10/2018	3E+07	Kim SK	26/07/2018	PLoS One	www.ncbi.nlm.nih.gov/pubmed/30048462	Identification of 613 new loci associated with heel bone mineral density and a polygenic risk score for bone mineral density, osteoporosis and fracture.	Heel bone mineral density	394,929 Eu	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2174633-?	rs2174633	0	2174633	intron_variant	0	NR	2.00E-12	11.69897		0.016269	[0.012-0.0	Affymetrix [20259828] (imputed)	N
3	4:17942560	4	17917781	rs2174633	5/08/2019	3.1E+07	Warrington NM	1/05/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31043758	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors.	Offspring birth weight	210,267 Eu	NR	4p15.31	LCORL, DCAF16	LCORL			ENSG00000178177	NA	NA	rs2174633-A	rs2174633	0	2174633	intron_variant	0	0.267868	4.00E-12	11.39794		0.023908	[0.017-0.0	Affymetrix, Illumina [14869762] (imputed)	N
3	4:17942560	4	17972372	rs2320299	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Diastolic blood pressure	810,865 Eu	354,096 Eu	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2320299-A	rs2320299	0	2320299	intron_variant	0	0.7285	6.00E-11	10.22185		0.104971	[0.074-0.1	Affymetrix, Illumina [2428661] (imputed)	N
3	4:17942560	4	17972372	rs2320299	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Hypertension	810,865 Eu	354,096 Eu	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2320299-A	rs2320299	0	2320299	intron_variant	0	0.7265	1.00E-13	13		7.44408	z score incr	Affymetrix, Illumina [2398431] (imputed)	N
3	4:17942560	4	17972372	rs2320299	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Pulse pressure	810,865 Eu	354,096 Eu	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2320299-A	rs2320299	0	2320299	intron_variant	0	0.7285	8.00E-14	13.09691		0.134267	[0.099-0.1	Affymetrix, Illumina [2428661] (imputed)	N
3	4:17942560	4	17972372	rs2320299	21/09/2021	3.3E+07	Surendran P	23/11/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33230300	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals.	Systolic blood pressure	810,865 Eu	354,096 Eu	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2320299-A	rs2320299	0	2320299	intron_variant	0	0.7286	9.00E-21	20.04576		0.237589	[0.19-0.29	Affymetrix, Illumina [2428661] (imputed)	N
3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 1 year old	24,551 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.261018	2.00E-06	5.69897		0.054456	[0.033-0.0	Illumina [9200000] (imputed)	N
3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 1.5 years old	21,871 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.261342	6.00E-08	7.221849		0.059748	[0.039-0.0	Illumina [9200000] (imputed)	N
3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 2 years old	21,831 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.261779	1.00E-06	6		0.061031	[0.037-0.0	Illumina [9200000] (imputed)	N
3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 5 years old	16,902 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.262489	2.00E-06	5.69897		0.065286	[0.039-0.0	Illumina [9200000] (imputed)	N

3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 6 months old	11,095 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.261584	4.00E-06	5.39794		0.048107	[0.028-0.0	Illumina [9200000] (imputed)	N
3	4:17942560	4	18022834	rs2610989	20/06/2022	3.5E+07	Helgeland O	21/03/2022	Nat Metab	www.ncbi.nlm.nih.gov/pubmed/35315439	Characterization of the genetic architecture of infant and early childhood body mass index.	BMI at 8 months old	24,302 Eur	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610989-T	rs2610989	0	2610989	intron_variant	0	0.261319	3.00E-06	5.522879		0.051667	[0.031-0.0	Illumina [9200000] (imputed)	N
3	4:17942560	4	18008232	rs2610990	1/07/2022	3.5E+07	Okbay A	31/03/2022	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/35361970	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.	Educational attainment	3,037,499	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2610990-A	rs2610990	0	2610990	intron_variant	0	0.2583	3.00E-22	21.52288		0.011579	[0.0092-0.	Illumina [10675380] (imputed)	N
3	4:17942560	4	18008232	rs2610990	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Bi	NA	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2610990-A	rs2610990	0	2610990	intron_variant	0	NR	2.00E-19	18.69897		0.028798	[0.023-0.0	Affymetrix [321016] (imputed)	N
3	4:17942560	4	18008232	rs2610990	29/11/2018	3E+07	Evangelou E	17/09/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30224653	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits.	Systolic blood pressure	757,601 Eu	249,262 Eu	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2610990-A	rs2610990	0	2610990	intron_variant	0	0.2607	4.00E-20	19.39794		0.2573	[0.2-0.31]	Affymetrix, Illumina [~ 7100000] (imputed)	N
3	4:17942560	4	17942560	rs2707450	16/10/2019	3.2E+07	Akiyama M	27/09/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31562340	Characterizing rare and low-frequency height-associated variants in the Japanese population.	Height	159,095 Ja	32,692 Jap	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2707450-?	rs2707450	0	2707450	intron_variant	0	NR	5.00E-19	18.30103		0.030342	[0.024-0.0	Illumina [27896057] (imputed)	N
3	4:17942560	4	17942560	rs2707450	7/03/2019	3.1E+07	Giri A	21/12/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30578418	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals.	Systolic blood pressure	365,998 Eu	299,024 Eu	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2707450-T	rs2707450	0	2707450	intron_variant	0	0.7357	2.00E-12	11.69897		0.2125	[0.15-0.27	Affymetrix [NR] (imputed)	N
3	4:17942560	4	17946432	rs2724475	24/10/2012	2.1E+07	Lango Allen H	29/09/2010	Nature	www.ncbi.nlm.nih.gov/pubmed/20881960	Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height	133,653 Eu	50,074 Eur	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs2724475-?	rs2724475	0	2724475	intron_variant	0	NR	2.00E-09	8.69897	(Condition	NA	[NR]	Affymetrix, Illumina [2834208] (imputed)	N
3	4:17942560	4	17946432	rs2724475	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs2724475-?	rs2724475	0	2724475	intron_variant	0	NR	2.00E-26	25.69897		0.062986	[0.051-0.0	Illumina [34656550] (imputed)	N
3	4:17942560	4	17946432	rs2724475	26/04/2022	3.5E+07	Fernandez-Rhodes L	11/03/2022	HGG Adv	www.ncbi.nlm.nih.gov/pubmed/35399580	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.	Height	59,771 His	8,110 Hisp	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2724475-T	rs2724475	0	2724475	intron_variant	0	0.3383	6.00E-11	10.22185		0.0498	[0.038-0.0	Affymetrix, Illumina [8927938] (imputed)	N
3	4:17942560	4	17946432	rs2724475	14/12/2020	3.2E+07	Ruth KS	10/02/2020	Nat Med	www.ncbi.nlm.nih.gov/pubmed/32042192	Using human genetics to understand the disease impacts of testosterone in men and women.	Sex hormone-binding globulin levels	370,125 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs2724475-T	rs2724475	0	2724475	intron_variant	0	0.261619	5.00E-13	12.30103		0.007659	[0.0056-0.	Affymetrix [16582965] (imputed)	N
3	4:17942560	4	17946432	rs2724475	14/12/2020	3.2E+07	Ruth KS	10/02/2020	Nat Med	www.ncbi.nlm.nih.gov/pubmed/32042192	Using human genetics to understand the disease impacts of testosterone in men and women.	Sex hormone-binding globulin levels adjusted for BMI	368,929 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs2724475-T	rs2724475	0	2724475	intron_variant	0	0.261619	5.00E-14	13.30103		0.007273	[0.0054-0.	Affymetrix [16582909] (imputed)	N
3	4:17942560	4	17969698	rs2724485	24/08/2022	3.6E+07	Plotnikov D	1/06/2022	Invest Ophthalmol Vis Sci	www.ncbi.nlm.nih.gov/pubmed/35762941	High Blood Pressure and Intraocular Pressure: A Mendelian Randomization Study.	Systolic blood pressure	526,001 Eu	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs2724485-T	rs2724485	0	2724485	intron_variant	0	NR	2.00E-10	9.69897		0.2561	[0.18-0.34	NR [NR] (imputed)	N
3	4:17942560	4	17903654	rs4144829	5/08/2019	3.1E+07	Warrington NM	1/05/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31043758	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors.	Birth weight	298,142 Eu	NR	4p15.31	LCORL, DCAF16	LCORL			ENSG00000178177	NA	NA	rs4144829-C	rs4144829	0	4144829	intron_variant	0	0.267008	4.00E-34	33.39794		0.035507	[0.03-0.04	Affymetrix, Illumina [15144367] (imputed)	N
3	4:17942560	4	17903654	rs4144829	13/08/2021	3.4E+07	Liu Y	15/06/2021	Elife	www.ncbi.nlm.nih.gov/pubmed/34128465	Genetic architecture of 11 organ traits derived from abdominal MRI using deep learning.	Lung volume	32,860 Eur	NA	4p15.31	NCAPG	LCORL			ENSG00000178177	NA	NA	rs4144829-?	rs4144829	0	4144829	intron_variant	0	NR	1.00E-09	9		0.0466	NR L decre	Affymetrix [9390170] (imputed)	N
3	4:17942560	4	17903654	rs4144829	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist circumference adjusted for body mass index	186,825 Bi	NA	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs4144829-C	rs4144829	0	4144829	intron_variant	0	NR	3.00E-09	8.522879		0.020853	[0.014-0.0	Affymetrix [321114] (imputed)	N
3	4:17942560	4	17854055	rs6842303	16/12/2019	3.2E+07	Helgeland O	1/10/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31575865	Genome-wide association study reveals dynamic role of genetic variation in infant and early childhood growth.	BMI at 1 year old	6,970 Norw	3,839 Norw	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs6842303-T	rs6842303	0	6842303	intron_variant	0	0.27934	2.00E-08	7.69897		0.086	[0.057-0.1	Illumina [~ 8500000] (imputed)	N
3	4:17942560	4	17854055	rs6842303	16/12/2019	3.2E+07	Helgeland O	1/10/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31575865	Genome-wide association study reveals dynamic role of genetic variation in infant and early childhood growth.	BMI at 1.5 years old	6,800 Norw	3,780 Norw	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs6842303-T	rs6842303	0	6842303	intron_variant	0	0.27934	8.00E-09	8.09691		0.089	[0.06-0.11	Illumina [~ 8500000] (imputed)	N
3	4:17942560	4	17993410	rs724577	27/01/2020	3.2E+07	Yang XL	11/10/2019	Front Genet	www.ncbi.nlm.nih.gov/pubmed/31681408	Three Novel Loci for Infant Head Circumference Identified by a Joint Association Analysis.	Birth length (MTAG)	up to 182,9	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs724577-A	rs724577	0	724577	intron_variant	0	0.358	4.00E-16	15.39794		0.049361	[0.037-0.0	NR [1977400] (imputed)	N
3	4:17942560	4	17993410	rs724577	28/02/2013	2.3E+07	Horikoshi M	2/12/2012	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/23202124	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism.	Birth weight	Up to 26,8	Up to 42,5	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs724577-C	rs724577	0	724577	intron_variant	0	0.73	5.00E-11	10.30103		0.042	[0.030-0.0	Affymetrix, Illumina [~ 2700000] (imputed)	N
3	4:17942560	4	17993410	rs724577	27/01/2020	3.2E+07	Yang XL	11/10/2019	Front Genet	www.ncbi.nlm.nih.gov/pubmed/31681408	Three Novel Loci for Infant Head Circumference Identified by a Joint Association Analysis.	Birth weight (MTAG)	up to 182,9	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs724577-A	rs724577	0	724577	intron_variant	0	0.27	7.00E-17	16.1549		0.035029	[0.027-0.0	NR [1977400] (imputed)	N
3	4:17942560	4	17993410	rs724577	8/11/2011	2.2E+07	N'Diaye A	6/10/2011	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/21998595	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry.	Height	20,427 Afri	Up to 16,4	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs724577-A	rs724577	0	724577	intron_variant	0	0.31	1.00E-15	15		0.067	[0.051-0.0	Affymetrix, Illumina [3310998] (imputed)	N
3	4:17942560	4	17993410	rs724577	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs724577-?	rs724577	0	724577	intron_variant	0	NR	3.00E-26	25.52288		0.062901	[0.051-0.0	Illumina [34656550] (imputed)	N
3	4:17942560	4	17871012	rs73242122	1/07/2022	3.5E+07	Okbay A	31/03/2022	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/35361970	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.	Educational attainment	3,037,499	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs73242122-C	rs73242122	0	73242122	intron_variant	0	0.7774	7.00E-08	7.154902		0.006775	[0.0043-0.	Illumina [10675380] (imputed)	N
3	4:17942560	4	17798334	rs7679066	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	4p15.31	DCAF16	FAM184B - DCAF	ENSG00000047662	ENSG00000163257		15090	3944	rs7679066-G	rs7679066	0	7679066	intergenic_variant	1	NR	2.00E-14	13.69897		0.025864	[0.019-0.0	Affymetrix [323123] (imputed)	N
3	4:17942560	4	17919811	rs925098	15/01/2018	2.8E+07	Horikoshi M	13/10/2016	Nature	www.ncbi.nlm.nih.gov/pubmed/27680694	Genome-wide associations for birth weight and correlations with adult disease.	Birth weight	133,903 Eu	9,799 Euro	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.28	1.00E-15	15		0.0322	[0.024-0.0	Affymetrix, Illumina [at least 22434434] (imputed)	N
3	4:17942560	4	17919811	rs925098	25/11/2011	2.2E+07	Carty CL	21/10/2011	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/22021425	Genome-wide association study of body height in African Americans: the Women's Health Initiative SNP Health Association Resource (SHARe).	Height	8,149 Afric	Up to 20,8	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.35	3.00E-14	13.52288		0.056	[0.036-0.0	Affymetrix [855034]	N
3	4:17942560	4	17919811	rs925098	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs925098-?	rs925098	0	925098	intron_variant	0	NR	2.00E-23	22.69897		0.058421	[0.047-0.0	Illumina [34656550] (imputed)	N
3	4:17942560	4	17919811	rs925098	1/07/2021	3.4E+07	Graff M	5/03/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33713608	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry.	Height	41,389 Afri	11,364 Afri	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0		2.00E-59	58.69897		NA		Affymetrix, Illumina [17972582] (imputed)	N
3	4:17942560	4	17919811	rs925098	1/07/2021	3.4E+07	Graff M	5/03/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33713608	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry.	Height	25,369 Afri	8,449 Afric	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.351	6.00E-08	7.221849	(AA)	0.046	[0.028-0.0	Affymetrix, Illumina [19885954] (imputed)	N
3	4:17942560	4	17919811	rs925098	1/07/2021	3.4E+07	Graff M	5/03/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33713608	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry.	Height	16,021 Afri	2,915 Afric	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.347	1.00E-07	7	(AA)	0.059	[0.037-0.0	Affymetrix, Illumina [16055004] (imputed)	N
3	4:17942560	4	17919811	rs925098	1/07/2021	3.4E+07	Graff M	5/03/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33713608	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry.	Height	41,389 Afri	11,364 Afri	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.35	3.00E-13	12.52288	(AA)	0.05	[0.036-0.0	Affymetrix, Illumina [17972582] (imputed)	N
3	4:17942560	4	17919811	rs925098	14/12/2020	3.2E+07	Ruth KS	10/02/2020	Nat Med	www.ncbi.nlm.nih.gov/pubmed/32042192	Using human genetics to understand the disease impacts of testosterone in men and women.	Sex hormone-binding globulin levels	189,473 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.264724	8.00E-09	8.09691		0.00981	[0.0067-0.	Affymetrix [16585866] (imputed)	N
3	4:17942560	4	17919811	rs925098	13/06/2022	3.5E+07	Haas CB	22/02/2022	Endocrinology	www.ncbi.nlm.nih.gov/pubmed/35192695	Cross-ancestry genome-wide association studies of sex hormone concentrations in pre- and postmenopausal women.	Sex hormone-binding globulin levels	196,901 Eu	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.264593	1.00E-06	6		0.017685	[0.011-0.0	NR [NR] (imputed)	N
3	4:17942560	4	17919811	rs925098	13/06/2022	3.5E+07	Haas CB	22/02/2022	Endocrinology	www.ncbi.nlm.nih.gov/pubmed/35192695	Cross-ancestry genome-wide association studies of sex hormone concentrations in pre- and postmenopausal women.	Sex hormone-binding globulin levels	4,522 Afric	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs925098-?	rs925098	0	925098	intron_variant	0	NR	2.00E-07	6.69897		5.22	z score dec	NR [NR] (imputed)	N
3	4:17942560	4	17919811	rs925098	14/12/2020	3.2E+07	Ruth KS	10/02/2020	Nat Med	www.ncbi.nlm.nih.gov/pubmed/32042192	Using human genetics to understand the disease impacts of testosterone in men and women.	Sex hormone-binding globulin levels adjusted for BMI	188,908 Eu	NA	4p15.31	NR	LCORL			ENSG00000178177	NA	NA	rs925098-G	rs925098	0	925098	intron_variant	0	0.264724	3.00E-09	8.522879		0.00885	[0.0061-0.	Affymetrix [16585854] (imputed)	N
3	4:17942560	4	17901679	rs979532	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	4p15.31	LCORL	LCORL			ENSG00000178177	NA	NA	rs979532-C	rs979532	0	979532	intron_variant	0	NR	2.00E-21	20.69897		0.033283	[0.026-0.0	Affymetrix [323123] (imputed)	N
3	4:17942560	4	17901679	rs979532	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Systolic blood pressure	approxima	NA	4p15.31		LCORL			ENSG00000178177	NA	NA	rs979532-?	rs979532	0	979532	intron_variant	0	NR	4.00E-12	11.39794		NA		NR [~ 8900000] (imputed)	N
5	4:106215109	4	1.06E+08	rs200768290	29/06/2021	3.3E+07	de la Fuente J	7/09/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/32895543	A general dimension of genetic sharing across diverse cognitive traits inferred from molecular data.	Verbal-numerical reasoning	171,304 Bi	NA	4q24		RN7SL89P - PPA2	ENSG00000243383	ENSG00000138777		6	75125	rs200768290-?	rs200768290	0	2.01E+08	regulatory_region_variant	1	NR	8.00E-16	15.09691		NA		NR [7857346] (imputed)	N
5	4:106216800	4	1.06E+08	rs34104813	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Neutrophil count	349,856 Eu	NA	4q24		TET2			ENSG00000168769	NA	NA	rs34104813-T	rs34104813	0	34104813	intron_variant	0	NR	2.00E-21	20.69897		0.0214	[0.017-0.0	Affymetrix, Illumina [20526770] (imputed)	N
5	4:106216800	4	1.06E+08	rs34104813	24/08/2022	3.6E+07	Plotnikov D	1/06/2022	Invest Ophthalmol Vis Sci	www.ncbi.nlm.nih.gov/pubmed/35762941	High Blood Pressure and Intraocular Pressure: A Mendelian Randomization Study.	Pulse pressure	526,001 Eu	NA	4q24		TET2			ENSG00000168769	NA	NA	rs34104813-T	rs34104813	0	34104813	intron_variant	0	NR	5.00E-09	8.30103		0.1511	[0.1-0.2] u	NR [NR] (imputed)	N
5	4:106215109	4	1.06E+08	rs57692580	2/09/2019	3.1E+07	Adams MJ	1/07/2019	Int J Epidemiol	www.ncbi.nlm.nih.gov/pubmed/31263887	Factors associated with sharing e-mail information and mental health survey participation in large population cohorts.	Mental health study participation (completed survey)	122,647 Bi	NA	4q24	RN7SL89P	TET2 - RN7SL89P	ENSG00000168769	ENSG00000243383		13503	345	rs57692580-A	rs57692580	0	57692580	regulatory_region_variant	1	0.39	3.00E-08	7.522879		0.006151	[0.004-0.0	NR [16367095] (imputed)	N
5	4:106216800	4	1.06E+08	rs62332762	18/02/2021	3.3E+07	Said MA	8/12/2020	J Am Heart Assoc	www.ncbi.nlm.nih.gov/pubmed/33287642	Associations of Observational and Genetically Determined Caffeine Intake With Coronary Artery Disease and Diabetes Mellitus.	Caffeine consumption from coffee or tea	362,316 Eu	NA	4q24	TET2	TET2			ENSG00000168769	NA	NA	rs62332762-C	rs62332762	0	62332762	intron_variant	0	0.597585	1.00E-14	14		0.01828	[0.014-0.0	Affymetrix [19400838] (imputed)	N
6	4:145586459	4	1.46E+08	rs11100862	30/07/2021	3.3E+07	Lundtoft C	26/10/2020	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/33104735	Function of multiple sclerosis-protective HLA class I alleles revealed by genome-wide protein-quantitative trait loci mapping of interferon signalling.	interferon-related traits	303 Europ	NA	4q31.21	NR	KRT18P51 - HHIP	ENSG00000250504	ENSG00000248890		63516	6423	rs11100862-A	rs11100862	0	11100862	intron_variant	1	0.452	4.00E-06	5.39794	(IFNGR1_c	NA		Illumina [5084123] (imputed)	N
6	4:145905213	4	1.46E+08	rs11733300	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	4q31.21	OTUD4	OTUD4 - RPS23P	ENSG00000164164	ENSG00000240992		32085	57136	rs11733300-A	rs11733300	0	11733300	intergenic_variant	1	NR	2.00E-17	16.69897		0.026175	[0.02-0.03	Affymetrix [323123] (imputed)	N
6	4:145597759	4	1.46E+08	rs11946517	28/01/2019	3.1E+07	Morris JA	31/12/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30598549	An atlas of genetic influences on osteoporosis in humans and mice.	Heel bone mineral density	426,824 Bi	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs11946517-G	rs11946517	0	11946517	intron_variant	0	0.416446	6.00E-14	13.22185		0.014091	[0.01-0.01	NR [13737936] (imputed)	N
6	4:145597759	4	1.46E+08	rs11946517	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Heel bone mineral density	approxima	NA	4q31.21		HHIP			ENSG00000164161	NA	NA	rs11946517-?	rs11946517	0	11946517	intron_variant	0	NR	2.00E-22	21.69897		NA		NR [~ 8900000] (imputed)	N

6	4:145597759	4	1.46E+08	rs11946517	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 B	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs11946517-G	rs11946517	0	11946517	intron_variant	0	NR	1.00E-36	36		0.039349	[0.033-0.0	Affymetrix [323123] (imputed)	N
6	4:145586459	4	1.46E+08	rs12507427	1/08/2019	3.1E+07	Styrkarsdottir U	3/05/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31053729	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures.	Femoral neck size	28,954 Eur	9,383 Euro	4q31.21	HHIP	HHIP, HHIP-AS1			ENSG00000164161, E	NA	NA	rs12507427-A	rs12507427	0	12507427	5_prime_UTR_variant	0	0.431	8.00E-14	13.09691		0.054	[0.007-0.0	Illumina [33400000] (imputed)	N
6	4:145586459	4	1.46E+08	rs12507427	1/08/2019	3.1E+07	Styrkarsdottir U	3/05/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31053729	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures.	Hip bone size	28,900 Eur	7,912 Euro	4q31.21	HHIP	HHIP, HHIP-AS1			ENSG00000164161, E	NA	NA	rs12507427-A	rs12507427	0	12507427	5_prime_UTR_variant	0	0.43146	5.00E-09	8.30103		0.043	NR unit inc	Illumina [33400000] (imputed)	N
6	4:145586459	4	1.46E+08	rs13125694	16/10/2019	3.2E+07	Akiyama M	27/09/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31562340	Characterizing rare and low-frequency height-associated variants in the Japanese population.	Height	159,095 Ja	32,692 Jap	4q31.21	HHIP-AS1	HHIP-AS1			ENSG00000248890	NA	NA	rs13125694-?	rs13125694	0	13125694	intron_variant	0	NR	1.00E-29	29		0.044578	[0.037-0.0	Illumina [27896057] (imputed)	N
6	4:145586459	4	1.46E+08	rs13125694	5/08/2022	3.6E+07	Chiou JS	13/07/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35831902	Your height affects your health: genetic determinants and health-related outcomes in Taiwan.	Height	67,452 Ha	NA	4q31.21		HHIP-AS1			ENSG00000248890	NA	NA	rs13125694-T	rs13125694	0	13125694	intron_variant	0	NR	5.00E-21	20.30103		0.057	[0.045-0.0	Affymetrix [NR] (imputed)	N
6	4:145586459	4	1.46E+08	rs13125694	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Height	165,056 E	NA	4q31.21		HHIP-AS1			ENSG00000248890	NA	NA	rs13125694-T	rs13125694	0	13125694	intron_variant	0	0.191937	6.00E-27	26.22185		0.029849	[0.024-0.0	Illumina [13479295] (imputed)	N
6	4:145586459	4	1.46E+08	rs13125694	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 B	NA	4q31.21	HHIP-AS1	HHIP-AS1			ENSG00000248890	NA	NA	rs13125694-T	rs13125694	0	13125694	intron_variant	0	NR	6.00E-54	53.22185		0.047896	[0.042-0.0	Affymetrix [323123] (imputed)	N
6	4:145586459	4	1.46E+08	rs13125694	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip index	186,825 B	NA	4q31.21	HHIP-AS1	HHIP-AS1			ENSG00000248890	NA	NA	rs13125694-T	rs13125694	0	13125694	intron_variant	0	NR	5.00E-12	11.30103		0.022372	[0.016-0.0	Affymetrix [323858] (imputed)	N
6	4:145586459	4	1.46E+08	rs13146972	26/04/2022	3.5E+07	Fernandez-Rhodes L	11/03/2022	HGG Adv	www.ncbi.nlm.nih.gov/pubmed/35399580	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.	Height	59,771 His	8,110 Hisp	4q31.21		HHIP-AS1, HHIP			ENSG00000248890, E	NA	NA	rs13146972-T	rs13146972	0	13146972	non_coding_transcript_exon	0	0.4319	6.00E-14	13.22185		0.0406	[0.03-0.05	Affymetrix, Illumina [8927938] (imputed)	N
6	4:145655389	4	1.46E+08	rs1389029	4/08/2022	3.6E+07	Fan CC	3/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35505052	Multivariate genome-wide association study on tissue-sensitive diffusion metrics highlights pathways that shape the human brain.	Whole brain restricted isotropic diffusion (multivariate analysis)	23,543 Eur	11,555 Eur	4q31.21		HHIP			ENSG00000164161	NA	NA	rs1389029-?	rs1389029	0	1389029	intron_variant	0	NR	1.00E-22	22	(EA)	NA		NR [NR] (imputed)	N
6	4:145655389	4	1.46E+08	rs1492819	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist circumference adjusted for body mass index	186,825 B	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs1492819-T	rs1492819	0	1492819	intron_variant	0	NR	2.00E-08	7.69897		0.017354	[0.011-0.0	Affymetrix [321114] (imputed)	N
6	4:145655389	4	1.46E+08	rs1492820	12/09/2008	1.8E+07	Lettre G	6/04/2008	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/18391950	Identification of ten loci associated with height highlights new biological pathways in human growth.	Height	15,821 Eur	Up to 17,8	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs1492820-G	rs1492820	0	1492820	intron_variant	0	0.48	1.00E-11	11		0.29	[0.21-0.37	Affymetrix, Illumina [2260683] (imputed)	N
6	4:145655389	4	1.46E+08	rs1492820	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	4q31.21	NR	HHIP			ENSG00000164161	NA	NA	rs1492820-?	rs1492820	0	1492820	intron_variant	0	NR	2.00E-06	5.69897		0.027213	[0.016-0.0	Illumina [34656550] (imputed)	N
6	4:145586459	4	1.46E+08	rs17776795	15/01/2020	3.1E+07	Plotnikov D	16/05/2019	Br J Ophthalmol	www.ncbi.nlm.nih.gov/pubmed/31097437	Association between birth weight and refractive error in adulthood: a Mendelian randomisation study.	Birth weight	188,039 E	NA	4q31.21	NR	KRT18P51 - HHIP	ENSG00000250504	ENSG00000248890		50701	19238	rs17776795-A	rs17776795	0	17776795	intron_variant	1	0.42	6.00E-19	18.22185		0.029	[0.023-0.0	Affymetrix [up to 10400000] (imputed)	N
6	4:145905213	4	1.46E+08	rs200457388	7/02/2020	3.2E+07	Hernandez Cordero AI	21/11/2019	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/31761296	Genome-wide Associations Reveal Human-Mouse Genetic Convergence and Modifiers of Myogenesis, CPNE1 and STC2.	Appendicular lean mass	181,862 E	NA	4q31.21	NR	ANAPC10			ENSG00000164162	NA	NA	rs200457388-C	rs200457388	0	2E+08	intron_variant	0	0.423616	1.00E-12	12		0.04922	[0.036-0.0	Affymetrix [17914406] (imputed)	N
6	4:145905213	4	1.46E+08	rs200457388	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs200457388-C	rs200457388	0	2E+08	intron_variant	0	NR	4.00E-31	30.39794		0.035944	[0.03-0.04	Affymetrix [323123] (imputed)	N
6	4:145905213	4	1.46E+08	rs200457388	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-hip index	219,872 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs200457388-C	rs200457388	0	2E+08	intron_variant	0	NR	4.00E-09	8.39794		0.01677	[0.011-0.0	Affymetrix [319769] (imputed)	N
6	4:145905213	4	1.46E+08	rs200457388	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-to-hip ratio adjusted for BMI	219,872 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs200457388-C	rs200457388	0	2E+08	intron_variant	0	NR	4.00E-10	9.39794		0.017821	[0.012-0.0	Affymetrix [319769] (imputed)	N
6	4:145586459	4	1.46E+08	rs2131354	17/07/2019	2.9E+07	Tachmazidou I	1/06/2017	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/28552196	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits.	Height	1,249 who	205,003 E	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs2131354-A	rs2131354	0	2131354	intron_variant	0	0.5368	2.00E-19	18.69897		0.0599	[0.047-0.0	Affymetrix, Illumina, Perlegen [15844966] (imputed)	N
6	4:145586459	4	1.46E+08	rs2131354	18/05/2021	3.3E+07	Hebbar P	9/09/2020	Hum Genet	www.ncbi.nlm.nih.gov/pubmed/32902719	Genome-wide landscape establishes novel association signals for metabolic traits in the Arab population.	Height	2,732 Kuw	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs2131354-?	rs2131354	0	2131354	intron_variant	0	NR	8.00E-08	7.09691		5.358	NR unit inc	Illumina [up to 1520000] (imputed)	N
6	4:145586459	4	1.46E+08	rs2131354	17/07/2019	2.9E+07	Tachmazidou I	1/06/2017	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/28552196	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits.	Hip circumference adjusted for BMI	1,247 who	205,905 E	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs2131354-A	rs2131354	0	2131354	intron_variant	0	0.5421	2.00E-09	8.69897		0.0516	[0.035-0.0	Affymetrix, Illumina, Perlegen [15844966] (imputed)	N
6	4:145586459	4	1.46E+08	rs2131354	5/08/2019	3.1E+07	Warrington NM	1/05/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31043758	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors.	Offspring birth weight	210,267 E	NR	4q31.21	LOC646576, HHI	HHIP			ENSG00000164161	NA	NA	rs2131354-A	rs2131354	0	2131354	intron_variant	0	0.526791	3.00E-16	15.52288		0.025738	[0.02-0.03	Affymetrix, Illumina [14869762] (imputed)	N
6	4:145586459	4	1.46E+08	rs2131354	4/08/2022	3.6E+07	Fan CC	3/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35505052	Multivariate genome-wide association study on tissue-sensitive diffusion metrics highlights pathways that shape the human brain.	Whole brain restricted directional diffusion (multivariate analysis)	23,543 Eur	11,555 Eur	4q31.21		HHIP			ENSG00000164161	NA	NA	rs2131354-?	rs2131354	0	2131354	intron_variant	0	NR	3.00E-19	18.52288	(EA)	NA		NR [NR] (imputed)	N
6	4:145905213	4	1.46E+08	rs4576021	7/02/2020	3.2E+07	Hernandez Cordero AI	21/11/2019	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/31761296	Genome-wide Associations Reveal Human-Mouse Genetic Convergence and Modifiers of Myogenesis, CPNE1 and STC2.	Appendicular lean mass	181,862 E	NA	4q31.21	NR	HHIP - ANAPC10	ENSG00000164161	ENSG00000164162		47346	39291	rs4576021-T	rs4576021	0	4576021	intron_variant	1	0.42047	2.00E-11	10.69897		0.046526	[0.033-0.0	Affymetrix [17914406] (imputed)	N
6	4:145905213	4	1.46E+08	rs4576021	18/10/2018	3E+07	Kim SK	26/07/2018	PLoS One	www.ncbi.nlm.nih.gov/pubmed/30048462	Identification of 613 new loci associated with heel bone mineral density and a polygenic risk score for bone mineral density, osteoporosis and fracture.	Heel bone mineral density	394,929 E	NA	4q31.21		HHIP - ANAPC10	ENSG00000164161	ENSG00000164162		47346	39291	rs4576021-?	rs4576021	0	4576021	intron_variant	1	NR	1.00E-23	23		0.020726	[0.017-0.0	Affymetrix [20259828] (imputed)	N
6	4:145655389	4	1.46E+08	rs55817790	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-hip index	219,872 B	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs55817790-A	rs55817790	0	55817790	intron_variant	0	NR	4.00E-08	7.39794		0.015691	[0.01-0.02	Affymetrix [319769] (imputed)	N
6	4:145655389	4	1.46E+08	rs55817790	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-to-hip ratio adjusted for BMI	219,872 B	NA	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs55817790-A	rs55817790	0	55817790	intron_variant	0	NR	3.00E-09	8.522879		0.016937	[0.011-0.0	Affymetrix [319769] (imputed)	N
6	4:145905213	4	1.46E+08	rs6537315	28/05/2020	3.2E+07	Hysi PG	30/03/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/32231278	Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia.	Refractive error	542,934 E	NA	4q31.21	HHIP, OTUD4	HHIP - ANAPC10	ENSG00000164161	ENSG00000164162		58289	28348	rs6537315-?	rs6537315	0	6537315	intron_variant	1		5.00E-09	8.30103		NA		Affymetrix, Illumina [NR] (imputed)	N
6	4:145905213	4	1.46E+08	rs67365433	7/02/2020	3.2E+07	Hernandez Cordero AI	21/11/2019	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/31761296	Genome-wide Associations Reveal Human-Mouse Genetic Convergence and Modifiers of Myogenesis, CPNE1 and STC2.	Appendicular lean mass	181,862 E	NA	4q31.21	NR	ANAPC10			ENSG00000164162	NA	NA	rs67365433-A	rs67365433	0	67365433	intron_variant	0	0.423698	1.00E-12	12		0.049167	[0.036-0.0	Affymetrix [17914406] (imputed)	N
6	4:145905213	4	1.46E+08	rs67365433	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-hip index	186,825 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs67365433-A	rs67365433	0	67365433	intron_variant	0	NR	2.00E-09	8.69897		0.018861	[0.013-0.0	Affymetrix [127266] (imputed)	N
6	4:145905213	4	1.46E+08	rs67365433	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-to-hip ratio adjusted for BMI	186,825 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs67365433-A	rs67365433	0	67365433	intron_variant	0	NR	2.00E-10	9.69897		0.020219	[0.014-0.0	Affymetrix [323858] (imputed)	N
6	4:145655389	4	1.46E+08	rs6812830	14/02/2022	3.5E+07	Chambers T	25/01/2022	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/35079123	Genetic common variants associated with cerebellar volume and their overlap with mental disorders: a study on 33,265 individuals from the UK-Biobank.	Total cerebellar volume (excluding Crus I vermis)	33,265 Eur	NA	4q31.21		HHIP			ENSG00000164161	NA	NA	rs6812830-A	rs6812830	0	6812830	intron_variant	0	NR	2.00E-08	7.69897		0.0306	[0.02-0.04	Affymetrix [6193476] (imputed)	N
6	4:145655389	4	1.46E+08	rs6817771	26/04/2022	3.5E+07	Fernandez-Rhodes L	11/03/2022	HGG Adv	www.ncbi.nlm.nih.gov/pubmed/35399580	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.	Height	59,771 His	8,110 Hisp	4q31.21		HHIP			ENSG00000164161	NA	NA	rs6817771-C	rs6817771	0	6817771	intron_variant	0	0.4102	4.00E-10	9.39794		0.0363	[0.025-0.0	Affymetrix, Illumina [8927938] (imputed)	N
6	4:145655389	4	1.46E+08	rs6827641	4/08/2022	3.6E+07	Fan CC	3/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35505052	Multivariate genome-wide association study on tissue-sensitive diffusion metrics highlights pathways that shape the human brain.	Whole brain free water diffusion (multivariate analysis)	23,543 Eur	11,555 Eur	4q31.21		HHIP			ENSG00000164161	NA	NA	rs6827641-?	rs6827641	0	6827641	intron_variant	0	NR	3.00E-17	16.52288	(EA)	NA		NR [NR] (imputed)	N
6	4:145586459	4	1.46E+08	rs6845999	5/08/2019	3.1E+07	Warrington NM	1/05/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31043758	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors.	Birth weight	298,142 E	NR	4q31.21	LOC646576, HHI	HHIP-AS1			ENSG00000248890	NA	NA	rs6845999-T	rs6845999	0	6845999	intron_variant	0	0.431122	2.00E-24	23.69897		0.026255	[0.021-0.0	Affymetrix, Illumina [15144367] (imputed)	N
6	4:145586459	4	1.46E+08	rs6845999	15/07/2015	2.5E+07	He M	26/11/2014	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/25429064	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci.	Height	36,227 Eas	57,699 Eas	4q31.21	HHIP	HHIP-AS1			ENSG00000248890	NA	NA	rs6845999-T	rs6845999	0	6845999	intron_variant	0	0.22	4.00E-14	13.39794		0.037	[0.021-0.0	Affymetrix, Illumina [2704730] (imputed)	N
6	4:145586459	4	1.46E+08	rs6845999	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	4q31.21	NR	HHIP-AS1			ENSG00000248890	NA	NA	rs6845999-?	rs6845999	0	6845999	intron_variant	0	NR	3.00E-08	7.522879		0.036422	[0.024-0.0	Illumina [34656550] (imputed)	N
6	4:145586459	4	1.46E+08	rs6845999	26/04/2022	3.5E+07	Fernandez-Rhodes L	11/03/2022	HGG Adv	www.ncbi.nlm.nih.gov/pubmed/35399580	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits-The Hispanic/Latino Anthropometry Consortium.	Height	59,771 His	8,110 Hisp	4q31.21		HHIP-AS1			ENSG00000248890	NA	NA	rs6845999-T	rs6845999	0	6845999	intron_variant	0	0.4323	3.00E-16	15.52288		0.0431	[0.033-0.0	Affymetrix, Illumina [8927938] (imputed)	N
6	4:145586459	4	1.46E+08	rs6845999	5/08/2022	3.6E+07	Chiou JS	13/07/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35831902	Your height affects your health: genetic determinants and health-related outcomes in Taiwan.	Height	67,452 Ha	NA	4q31.21		HHIP-AS1			ENSG00000248890	NA	NA	rs6845999-T	rs6845999	0	6845999	intron_variant	0	NR	7.00E-22	21.1549		0.058	[0.046-0.0	Affymetrix [NR] (imputed)	N
6	4:145655389	4	1.46E+08	rs6854783	17/09/2008	1.8E+07	Weedon MN	6/04/2008	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/18391952	Genome-wide association analysis identifies 20 loci that influence adult height.	Height	13,665 Eur	16,482 Eur	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs6854783-A	rs6854783	0	6854783	intron_variant	0	0.43	2.00E-09	8.69897		0.06	[0.03-0.08	Affymetrix [402951]	N

6	4:145586459	4	1.46E+08	rs7675744	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 B	NA	4q31.21	HHIP-AS1, HHIP	HHIP-AS1, HHIP			ENSG00000248890, E	NA	NA	rs7675744-C	rs7675744	0	7675744	non_coding_transcript_exon	0	NR	2.00E-50	49.69897		0.04237	[0.037-0.0	Affymetrix [321016] (imputed)	N
6	4:145586459	4	1.46E+08	rs7692554	25/03/2022	3.4E+07	Lin E	16/07/2021	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/34270706	Genome-wide association study in the Taiwan biobank identifies four novel genes for human height: NABP2, RASA2, RNF41 and SLC39A5.	Height	14,571 Tai	20,506 Tai	4q31.21	HHIP-LOC10537	KRT18P51 - HHIP	ENSG00000250504	ENSG00000248890		42201	27735	rs7692554-?	rs7692554	0	7692554	intron_variant	1	NR	4.00E-08	7.39794		0.44	[0.28-0.6]	Affymetrix [5682219] (imputed)	N
6	4:145586459	4	1.46E+08	rs77362667	25/03/2022	3.4E+07	Lin E	16/07/2021	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/34270706	Genome-wide association study in the Taiwan biobank identifies four novel genes for human height: NABP2, RASA2, RNF41 and SLC39A5.	Height	14,571 Tai	20,506 Tai	4q31.21	HHIP	HHIP			ENSG00000164161	NA	NA	rs77362667-?	rs77362667	0	77362667	intron_variant	0	NR	3.00E-08	7.522879		0.45	[0.29-0.61	Affymetrix [5682219] (imputed)	N
6	4:145905213	4	1.46E+08	rs789351	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 B	NA	4q31.21	ANAPC10	ANAPC10			ENSG00000164162	NA	NA	rs789351-T	rs789351	0	789351	intron_variant	0	NR	3.00E-27	26.52288		0.030705	[0.025-0.0	Affymetrix [321016] (imputed)	N
6	4:145905213	4	1.46E+08	rs789351	4/11/2019	3E+07	Pulit SL	14/09/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30239722	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry.	Waist-hip ratio	697,734 E	NA	4q31.21	NA	ANAPC10			ENSG00000164162	NA	NA	rs789351-T	rs789351	0	789351	intron_variant	0	0.4202	8.00E-13	12.09691		0.0123	[0.009-0.0	NR [~ 27400000] (imputed)	N
6	4:145586459	4	1.46E+08	rs982903	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist circumference adjusted for body mass index	457,690 E	NA	4q31.21	NR	HHIP			ENSG00000164161	NA	NA	rs982903-?	rs982903	0	982903	intron_variant	0	NR	3.00E-13	12.52288		NA		Affymetrix [~ 8270000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/07/2020	3.2E+07	Richardson TG	23/03/2020	PLoS Med	www.ncbi.nlm.nih.gov/pubmed/32203549	Evaluating the relationship between circulating lipoprotein lipids and apolipoproteins with risk of coronary heart disease: A multivariable Mendelian randomisation analysis.	Apolipoprotein B levels	439,214 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.891606	3.00E-10	9.522879		0.021129	[0.015-0.0	Affymetrix [NR] (imputed)	N
7	10:71099109	10	71094504	rs17476364	10/06/2021	3.4E+07	Chen J	31/05/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34059833	The trans-ancestral genomic architecture of glycemic traits.	Glycated hemoglobin levels	146,806 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.9011	1E-314	314		0.0858	[0.081-0.0	Affymetrix, Illumina [33811881] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Hematocrit	173,039 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	#######	158.0969		0.151778	[0.14-0.16	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hematocrit	16,184 Afri	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.08	4.00E-26	25.39794		0.3706	[0.3-0.44]	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hematocrit	29,383 Eur	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.0946	1.00E-17	17		0.361	[0.28-0.44	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hematocrit	20,704 His	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.0651	7.00E-09	8.154902		0.3816	[0.25-0.51	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Hematocrit	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108758	5E-372	371.301		0.147147	[0.14-0.15	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Hematocrit	350,475 E	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	#######	282		0.1115	[0.11-0.12	Affymetrix, Illumina [20538534] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Hemoglobin	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108778	1E-368	368		0.146551	[0.14-0.15	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Hemoglobin	350,474 E	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	#######	288.5229		0.1098	[0.1-0.12]	Affymetrix, Illumina [20538521] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Hemoglobin A1c levels	344,182 E	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	4E-1745	1744.398		0.3256	[0.32-0.33	Affymetrix, Illumina [20525742] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Hemoglobin concentration	172,925 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	#######	156		0.151392	[0.14-0.16	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hemoglobin concentration	29,379 Eur	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.0946	9.00E-19	18.04576		0.126	[0.098-0.1	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hemoglobin concentration	20,692 His	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.0651	6.00E-10	9.221849		0.14	[0.096-0.1	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Hemoglobin concentration	16,186 Afri	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.08	1.00E-27	27		0.1301	[0.11-0.15	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	High light scatter reticulocyte count	170,761 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1104	3.00E-69	68.52288		0.100903	[0.09-0.11	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	High light scatter reticulocyte count	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108757	#######	194.2218		0.106568	[0.1-0.114	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	High light scatter reticulocyte percentage of red cells	170,763 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1104	3.00E-53	52.52288		0.08805	[0.077-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	High light scatter reticulocyte percentage of red cells	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108749	#######	151.699		0.094088	[0.087-0.1	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Immature fraction of reticulocytes	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.10878	6.00E-40	39.22185		0.047658	[0.041-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.4E+07	Bell S	3/02/2021	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/33536631	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis.	Iron status biomarkers (ferritin levels)	246,139 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108	4.00E-14	13.39794		0.043	[0.032-0.0	Affymetrix, Illumina [40000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/07/2020	3.2E+07	Richardson TG	23/03/2020	PLoS Med	www.ncbi.nlm.nih.gov/pubmed/32203549	Evaluating the relationship between circulating lipoprotein lipids and apolipoproteins with risk of coronary heart disease: A multivariable Mendelian randomisation analysis.	LDL cholesterol levels	440,546 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.891668	9.00E-11	10.04576		0.021785	[0.015-0.0	Affymetrix [NR] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Low density lipoprotein cholesterol levels	40,963 Sou	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	1.00E-26	26		NA		NR [52000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Low density lipoprotein cholesterol levels	1,320,016	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.098856	3.00E-23	22.52288		0.026846	[0.022-0.0	NR [52000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Mean corpuscular hemoglobin	172,332 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	4.00E-44	43.39794		0.078982	[0.068-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Mean corpuscular hemoglobin	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108777	#######	109.2218		0.079404	[0.072-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Mean corpuscular hemoglobin	486,823 E	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108072	#######	147.1549		0.080275	[0.074-0.0	Affymetrix, Illumina [50266654] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Mean corpuscular hemoglobin	630,125 A	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.104331	#######	144		NA		Affymetrix, Illumina [20825802] (imputed)	N
7	10:71099109	10	71094504	rs17476364	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Mean corpuscular hemoglobin	approxima	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	#######	127.301		NA		NR [~ 8900000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Mean corpuscular hemoglobin	350,472 E	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	3.00E-78	77.52288		0.0707	[0.063-0.0	Affymetrix, Illumina [20535878] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Mean corpuscular volume	172,433 E	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	7.00E-55	54.1549		0.088114	[0.077-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	22/03/2021	3.2E+07	Hodonsky CJ	14/03/2020	BMC Genomics	www.ncbi.nlm.nih.gov/pubmed/32171239	Ancestry-specific associations identified in genome-wide combined-phenotype study of red blood cell traits emphasize benefits of diversity in genomics.	Mean corpuscular volume	8,556 Afric	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	0.08	1.00E-06	6		0.3633	[0.22-0.51	Affymetrix, Illumina [21000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Mean corpuscular volume	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108777	#######	142		0.094037	[0.088-0.1	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Mean corpuscular volume	544,127 E	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.10674	#######	211		0.091405	[0.086-0.0	Affymetrix, Illumina [50615308] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Mean corpuscular volume	696,882 A	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.102938	#######	210		NA		Affymetrix, Illumina [24246363] (imputed)	N
7	10:71099109	10	71094504	rs17476364	12/11/2021	3.4E+07	Thompson A	8/06/2021	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/34104963	Assessing the impact of alcohol consumption on the genetic contribution to mean corpuscular volume.	Mean corpuscular volume	362,595 B	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.89	2.00E-92	91.69897		0.36	[-0.39--0.3	Affymetrix [NR] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Mean corpuscular volume	350,473 E	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	1.00E-98	98		0.0798	[0.072-0.0	Affymetrix, Illumina [20535844] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Mean reticulocyte volume	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108783	1.00E-59	59		0.058846	[0.052-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Mean spheric corpuscular volume	408,112 B	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108696	#######	158.5229		0.097074	[0.09-0.10	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Non-HDL cholesterol levels	1,320,016	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.099411	2.00E-15	14.69897		0.02536	[0.02-0.03	NR [52000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Non-HDL cholesterol levels	40,963 Sou	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	1.00E-17	17		NA		NR [52000000] (imputed)	N

7	10:71099109	10	71094504	rs17476364	13/12/2021	3.4E+07	Cade BE	26/08/2021	Genome Med	www.ncbi.nlm.nih.gov/pubmed/34446064	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program.	Obstructive sleep apnea trait (minimum oxyhemoglobin saturation across sleep episode)	5,173 Euro	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	2.00E-08	7.69897		1.129	[0.74-1.52	Affymetrix, Illumina [22105437] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Platelet count	542,827 Eu	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.106471	5.00E-11	10.30103		0.019617	[0.014-0.0	Affymetrix, Illumina [50241410] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Plateletcrit	408,112 Bi	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108814	1.00E-09	9		0.021964	[0.015-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Red blood cell count	172,952 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	2.00E-48	47.69897		0.083301	[0.072-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red blood cell count	727,624 Af	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.10294	#######	141		NA		Affymetrix, Illumina [24332387] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red blood cell count	545,203 Eu	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.106734	#######	145.0969		0.077124	[0.071-0.0	Affymetrix, Illumina [50628390] (imputed)	N
7	10:71099109	10	71094504	rs17476364	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Red blood cell count	approxima	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	#######	124.301		NA		NR [~ 8900000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Red blood cell count	408,112 Bi	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.10876	#######	115		0.081053	[0.074-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Red blood cell count	350,475 Eu	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	2.00E-87	86.69897		0.0646	[0.058-0.0	Affymetrix, Illumina [20538708] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Red cell distribution width	171,529 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1103	2.00E-11	10.69897		0.03798	[0.027-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red cell distribution width	563,352 Af	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.896569	1.00E-32	32		NA		Affymetrix, Illumina [22063850] (imputed)	N
7	10:71099109	10	71094504	rs17476364	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red cell distribution width	531,774 Eu	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs17476364-T	rs17476364	0	17476364	intron_variant	0	0.892832	6.00E-36	35.22185		0.038198	[0.032-0.0	Affymetrix, Illumina [49860007] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Red cell distribution width	408,112 Bi	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108735	3.00E-23	22.52288		0.035448	[0.028-0.0	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Red cell distribution width	approxima	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	2.00E-25	24.69897		NA		NR [~ 8900000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Reticulocyte count	170,641 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1104	2.00E-96	95.69897		0.119759	[0.11-0.13	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Reticulocyte count	408,112 Bi	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108807	#######	224.0969		0.115151	[0.11-0.12	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Reticulocyte fraction of red cells	170,690 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.1104	3.00E-72	71.52288		0.1033	[0.092-0.1	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Reticulocyte fraction of red cells	408,112 Bi	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.108802	#######	168.1549		0.099627	[0.093-0.1	Affymetrix [93095623] (imputed)	N
7	10:71099109	10	71094504	rs17476364	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Total bilirubin levels	342,829 Eu	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	NR	#######	111.699		0.0828	[0.076-0.0	Affymetrix, Illumina [20535842] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Total cholesterol levels	40,963 Sou	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-?	rs17476364	0	17476364	intron_variant	0	NR	4.00E-36	35.39794		NA		NR [52000000] (imputed)	N
7	10:71099109	10	71094504	rs17476364	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Total cholesterol levels	1,320,016	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs17476364-C	rs17476364	0	17476364	intron_variant	0	0.098904	2.00E-29	28.69897		0.030331	[0.026-0.0	NR [52000000] (imputed)	N
7	10:71099109	10	71099109	rs72805692	1/03/2022	3.5E+07	Downie CG	24/12/2021	Diabetologia	www.ncbi.nlm.nih.gov/pubmed/34951656	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study.	Glycated haemoglobin HbA1c levels adjusted for BMI	23,357 Eur	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-A	rs72805692	0	72805692	intron_variant	0	0.083	5.00E-44	43.30103		0.2647	[0.23-0.3]	Affymetrix, Illumina [23060038] (imputed)	N
7	10:71099109	10	71099109	rs72805692	1/03/2022	3.5E+07	Downie CG	24/12/2021	Diabetologia	www.ncbi.nlm.nih.gov/pubmed/34951656	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study.	Glycated haemoglobin HbA1c levels adjusted for BMI	9,228 Euro	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-A	rs72805692	0	72805692	intron_variant	0	0.1039	3.00E-25	24.52288		0.2682	[0.22-0.32	Affymetrix, Illumina [23060038] (imputed)	N
7	10:71099109	10	71099109	rs72805692	1/03/2022	3.5E+07	Downie CG	24/12/2021	Diabetologia	www.ncbi.nlm.nih.gov/pubmed/34951656	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study.	Glycated haemoglobin HbA1c levels adjusted for BMI	10,693 His	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-A	rs72805692	0	72805692	intron_variant	0	0.0635	3.00E-20	19.52288		0.2628	[0.21-0.32	Affymetrix, Illumina [23060038] (imputed)	N
7	10:71099109	10	71099109	rs72805692	12/08/2019	3.1E+07	Moon JY	18/06/2019	Diabetes Care	www.ncbi.nlm.nih.gov/pubmed/31213470	A Genome-Wide Association Study Identifies Blood Disorder-Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos.	Glycated hemoglobin levels	9,636 Hisp	4,777 Hisp	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	0.066	6.00E-26	25.22185		0.1	[0.08-0.12	Illumina [11510031] (imputed)	N
7	10:71099109	10	71099109	rs72805692	10/06/2021	3.4E+07	Chen J	31/05/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34059833	The trans-ancestral genomic architecture of glycemic traits.	Glycated hemoglobin levels	15,248 His	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-A	rs72805692	0	72805692	intron_variant	0	0.9293	2.00E-22	21.69897		0.0859	[0.069-0.1	Affymetrix, Illumina [29199641] (imputed)	N
7	10:71099109	10	71099109	rs72805692	21/07/2020	3.2E+07	Richardson TG	23/03/2020	PLoS Med	www.ncbi.nlm.nih.gov/pubmed/32203549	Evaluating the relationship between circulating lipoprotein lipids and apolipoproteins with risk of coronary heart disease: A multivariable Mendelian randomisation analysis.	HDL cholesterol levels	403,943 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-A	rs72805692	0	72805692	intron_variant	0	0.884869	9.00E-10	9.045757		0.018309	[0.012-0.0	Affymetrix [NR] (imputed)	N
7	10:71099109	10	71099109	rs72805692	28/01/2022	3.4E+07	Hu Y	21/04/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33887194	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program.	Hematocrit	33,324 Am	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	NR	5.00E-26	25.30103		0.39	[0.31-0.47	Illumina [110396782]	N
7	10:71099109	10	71099109	rs72805692	28/01/2022	3.4E+07	Hu Y	21/04/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33887194	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program.	Hemoglobin	33,325 Am	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	NR	3.00E-25	24.52288		0.13	[0.11-0.15	Illumina [110351653]	N
7	10:71099109	10	71099109	rs72805692	1/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Hemoglobin A1c levels	559 Africar	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-?	rs72805692	0	72805692	intron_variant	0	NR	1.00E-21	21		0.265	[0.21-0.32	Illumina [22871999] (imputed)	N
7	10:71099109	10	71099109	rs72805692	1/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Hemoglobin A1c levels	559 Africar	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-?	rs72805692	0	72805692	intron_variant	0	NR	6.00E-22	21.22185	(Hispanic/l	0.268372	[0.21-0.32	Illumina [22871999] (imputed)	N
7	10:71099109	10	71099109	rs72805692	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Hemoglobin concentration	563,946 Eu	NA	10q22.1	NR	HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	0.113894	2E-482	481.699		0.136402	[0.13-0.14	Affymetrix, Illumina [50638016] (imputed)	N
7	10:71099109	10	71099109	rs72805692	27/07/2021	3.4E+07	Page GP	20/05/2021	J Clin Invest	www.ncbi.nlm.nih.gov/pubmed/34014839	Multi-ancestry genome-wide association study identifies 27 loci associated with measures of hemolysis following blood storage.	hemolysis of donated blood (osmotic)	Up to 7,58	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-?	rs72805692	0	72805692	intron_variant	0	NR	5.00E-11	10.30103		1.8	NR unit inc	NR [14100000] (imputed)	N
7	10:71099109	10	71099109	rs72805692	27/07/2021	3.4E+07	Page GP	20/05/2021	J Clin Invest	www.ncbi.nlm.nih.gov/pubmed/34014839	Multi-ancestry genome-wide association study identifies 27 loci associated with measures of hemolysis following blood storage.	hemolysis of donated blood (osmotic)	Up to 7,58	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-?	rs72805692	0	72805692	intron_variant	0	NR	5.00E-08	7.30103		NA		NR [14100000] (imputed)	N
7	10:71099109	10	71099109	rs72805692	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Immature fraction of reticulocytes	170,548 Eu	NA	10q22.1	HK1	HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	0.1169	1.00E-11	11		0.037438	[0.027-0.0	Affymetrix [~ 2500000] (imputed)	N
7	10:71099109	10	71099109	rs72805692	28/01/2022	3.4E+07	Hu Y	21/04/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/33887194	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program.	Mean corpuscular volume	22,267 Am	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	NR	3.00E-09	8.522879		0.39	[0.25-0.53	Illumina [97506867]	N
7	10:71099109	10	71099109	rs72805692	22/02/2022	3.5E+07	Miao Z	24/08/2021	HGG Adv	www.ncbi.nlm.nih.gov/pubmed/35047847	Identification of 90 NAFLD GWAS loci and establishment of NAFLD PRS and causal role of NAFLD in coronary artery disease.	Nonalcoholic fatty liver disease (imputed)	28,396 Eur	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-?	rs72805692	0	72805692	intron_variant	0	NR	3.00E-09	8.522879		0.008334	[0.0056-0.	NR [NR]	N
7	10:71099109	10	71099109	rs72805692	15/03/2022	3.5E+07	Zekavat SM	8/11/2021	Circulation	www.ncbi.nlm.nih.gov/pubmed/34743558	Deep Learning of the Retina Enables Phenome- and Genome-wide Analyses of the Microvasculature.	Retinal vascular fractal density	38,932 Brit	NA	10q22.1		HK1			ENSG00000156515	NA	NA	rs72805692-G	rs72805692	0	72805692	intron_variant	0	0.11873	2.00E-07	6.69897		0.054727	[0.034-0.0	Affymetrix [15580782] (imputed)	N
8	13:50760125	13	50993083	rs143280072	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Bi	NA	13q14.3	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs143280072-C	rs143280072	0	1.43E+08	intron_variant	0	NR	2.00E-12	11.69897		0.058605	[0.042-0.0	Affymetrix [321016] (imputed)	N
8	13:50760125	13	50993083	rs143280072	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	13q14.3	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs143280072-C	rs143280072	0	1.43E+08	intron_variant	0	NR	2.00E-22	21.69897		0.088197	[0.07-0.10	Affymetrix [323123] (imputed)	N
8	13:50760125	13	50760125	rs182234180	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Lymphocyte count	408,112 Bi	NA	13q14.2	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs182234180-T	rs182234180	0	1.82E+08	non_coding_transcript_exon_	0	0.030056	3.00E-18	17.52288		0.057718	[0.045-0.0	Affymetrix [93095623] (imputed)	N
8	13:50760125	13	50760125	rs182234180	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Lymphocyte percentage of white cells	408,112 Bi	NA	13q14.2	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs182234180-T	rs182234180	0	1.82E+08	non_coding_transcript_exon_	0	0.03006	1.00E-09	9		0.040107	[0.027-0.0	Affymetrix [93095623] (imputed)	N
8	13:50760125	13	50771235	rs2703087	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Bi	NA	13q14.2	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs2703087-A	rs2703087	0	2703087	intron_variant	0	NR	1.00E-09	9		0.044012	[0.03-0.05	Affymetrix [321016] (imputed)	N
8	13:50760125	13	50771235	rs2703087	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 Bi	NA	13q14.2	DLEU1	DLEU1			ENSG00000176124	NA	NA	rs2703087-A	rs2703087	0	2703087	intron_variant	0	NR	7.00E-22	21.1549		0.075745	[0.06-0.09	Affymetrix [323123] (imputed)	N
9	17:44118848	17	43932789	rs10445365	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI ProbtrackX L2 atr l	20,860 Brit	10,495 Brit	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445365-T	rs10445365	0	10445365	intron_variant	0	0.184	3.00E-15	14.52288		0.103	[0.078-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43932789	rs10445365	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI ProbtrackX MD atr l	20,860 Brit	10,495 Brit	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445365-T	rs10445365	0	10445365	intron_variant	0	0.184	2.00E-16	15.69897		0.106	[0.081-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43932789	rs10445365	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Anterior corona radiata R	20,859 Brit	10,496 Brit	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445365-T	rs10445365	0	10445365	intron_variant	0	0.184	2.00E-19	18.69897		0.117	[0.092-0.1	Affymetrix [17103079] (imputed)	N

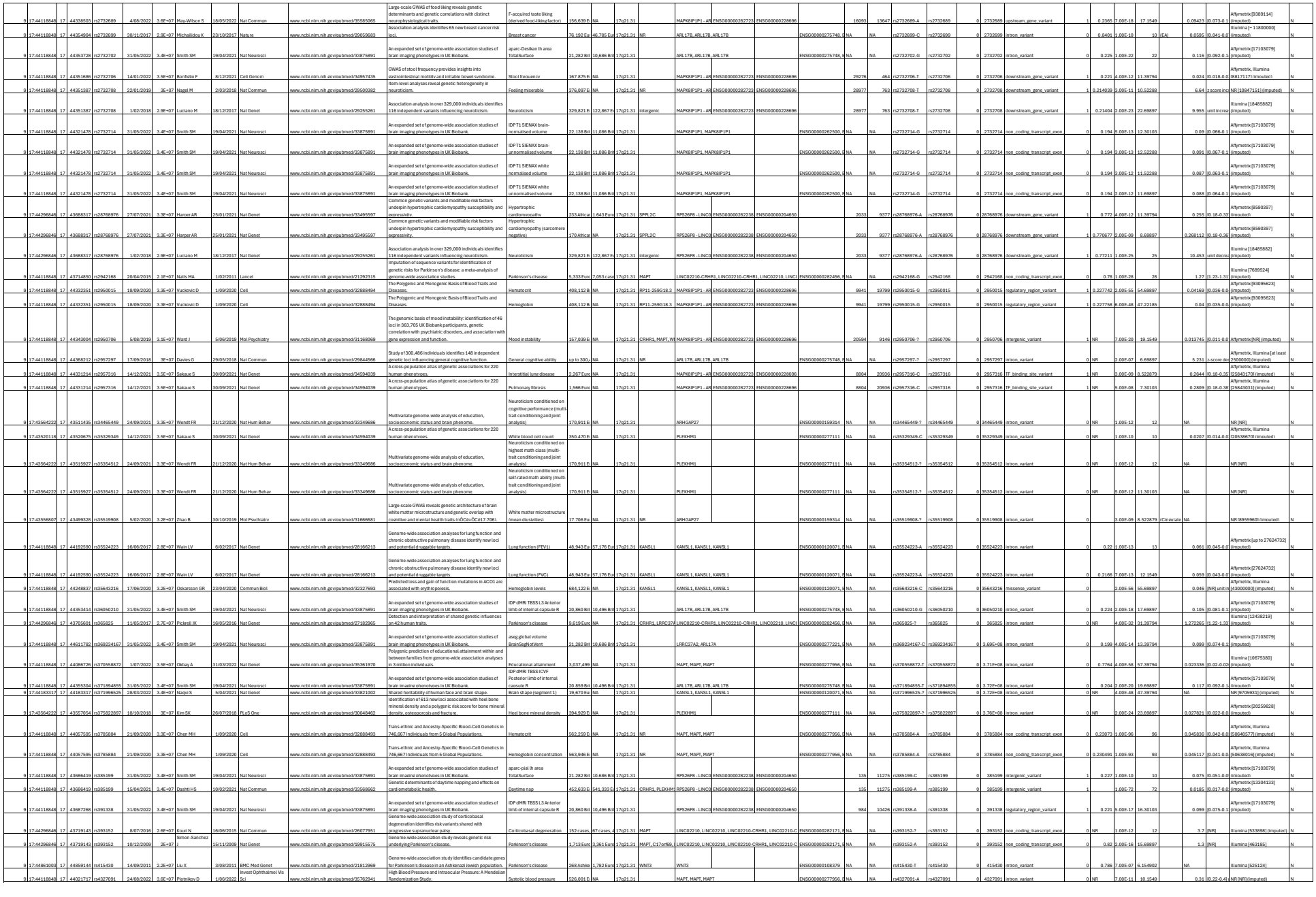
9	17:44118848	17	43932789	rs10445365	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Anterior limb of internal capsule R	20,859 Brit	10,496 Brit	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445365-T	rs10445365	0	10445365	intron_variant	0	0.184	2.00E-14	13.69897		0.1	[0.075-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43932789	rs10445365	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Retrolenticular part of internal capsule L	20,859 Brit	10,496 Brit	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445365-T	rs10445365	0	10445365	intron_variant	0	0.184	4.00E-15	14.39794		0.102	[0.077-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43932797	rs10445366	27/07/2021	3.4E+07	Mills MC	1/07/2021	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/34211149	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour.	Age at first birth	542,901 Eu	NA	17q21.31	MAPT-AS1	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445366-C	rs10445366	0	10445366	intron_variant	0	0.1843	7.00E-11	10.1549		0.0886	[0.062-0.1	NR [9744772] (imputed)	N
9	17:44118848	17	43932798	rs10445367	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Neutrophil count	349,856 Eu	NA	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445367-T	rs10445367	0	10445367	intron_variant	0	NR	1.00E-18	18		0.0282	[0.022-0.0	Affymetrix, Illumina [20526770] (imputed)	N
9	17:44118848	17	43932798	rs10445367	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔÇë=ÔÇë17,706).	White matter microstructure (fractional anisotropy)	17,706 Eur	NA	17q21.31	NR	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445367-?	rs10445367	0	10445367	intron_variant	0		1.00E-09	9	(Genu of c	NA		NR [8955960] (imputed)	N
9	17:44118848	17	43933171	rs10445368	23/10/2020	3.3E+07	van der Meer D	14/07/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32665545	Understanding the genetic determinants of the brain with MOSTest.	Cortical surface area (MOSTest)	26,502 Eur	NA	17q21.31	VCAN	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10445368-?	rs10445368	0	10445368	intron_variant	0		2.00E-38	37.69897		NA		NR [7428630] (imputed)	N
9	17:44118848	17	43950976	rs10491140	18/10/2018	3E+07	Kim SK	26/07/2018	PLoS One	www.ncbi.nlm.nih.gov/pubmed/30048462	Identification of 613 new loci associated with heel bone mineral density and a polygenic risk score for bone mineral density, osteoporosis and fracture.	Heel bone mineral density	394,929 Eu	NA	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs10491140-?	rs10491140	0	10491140	intron_variant	0	NR	3.00E-26	25.52288		0.025714	[0.021-0.0	Affymetrix [20259828] (imputed)	N
9	17:44118848	17	44073889	rs1052553	26/04/2018	2.6E+07	Onengut-Gumuscu S	1/04/2015	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/25751624	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers.	Type 1 diabetes	6,683 Euro	NA	17q21.31	Intergenic	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1052553-A	rs1052553	0	1052553	synonymous_variant	0	0.76	8.00E-08	7.09691		1.123596		Illumina [135870]	N
9	17:44118848	17	44073889	rs1052553	7/07/2021	3.4E+07	Robertson CC	14/06/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34127860	Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes.	Type 1 diabetes	20,065 Eur	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1052553-G	rs1052553	0	1052553	synonymous_variant	0	0.232	2.00E-15	14.69897		0.879		Illumina [715631] (imputed)	N
9	17:44118848	17	44073889	rs1052553	7/07/2021	3.4E+07	Robertson CC	14/06/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34127860	Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes.	Type 1 diabetes	20,065 Eur	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1052553-G	rs1052553	0	1052553	synonymous_variant	0	0.232	2.00E-15	14.69897		0.879		Illumina [715631] (imputed)	N
9	17:43564222	17	43513441	rs11012	5/02/2010	2E+07	Edwards TL	13/01/2010	Ann Hum Genet	www.ncbi.nlm.nih.gov/pubmed/20070850	Genome-wide association study confirms SNPs in SNCA and the MAPT region as common risk factors for Parkinson disease.	Parkinson's disease	1,752 Euro	NA	17q21.31	MAPT, PLEKHM1,	PLEKHM1			ENSG00000277111	NA	NA	rs11012-T	rs11012	0	11012	3_prime_UTR_variant	0	NR	6.00E-08	7.221849		1.43	[1.27-1.61	Illumina [495715] (imputed)	N
9	17:44118848	17	43839951	rs11079718	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Reticulocyte count	408,112 Bı	NA	17q21.31	RP11-105N13.4,	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs11079718-T	rs11079718	0	11079718	intron_variant	0	0.223963	5.00E-45	44.30103		0.0378	[0.033-0.0	Affymetrix [93095623] (imputed)	N
9	17:44118848	17	43857989	rs111433752	13/12/2016	2.7E+07	Smith DJ	12/04/2016	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/27067015	Genome-wide analysis of over 106ÔÇë000 individuals identifies 9 neuroticism-associated loci.	Neuroticism	91,370 Eur	NA	17q21.31	Intergenic	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs111433752-T	rs111433752	0	1.11E+08	intron_variant	0	0.79	9.00E-12	11.04576		0.12	[0.085-0.1	Affymetrix [7207648] (imputed)	N
9	17:44118848	17	44183403	rs111676341	13/01/2021	3.3E+07	Demange PA	7/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33414549	Investigating the genetic architecture of noncognitive skills using GWAS-by-subtraction.	Cognitive aspects of educational attainment	257,700 Eu	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs111676341-A	rs111676341	0	1.12E+08	intron_variant	0	0.240557	2.00E-11	10.69897		0.049242	[0.035-0.0	Affymetrix, Illumina, Perlegen [7305956] (imputed)	N
9	17:44118848	17	44019107	rs111825734	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Anterior corona radiata R	20,860 Brit	10,496 Brit	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs111825734-G	rs111825734	0	1.12E+08	intron_variant	0	0.232	9.00E-15	14.04576		0.09	[0.066-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43666492	rs112010353	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Self-reported math ability	564,698 Eu	NA	17q21.31	Intergenic	DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		2197	11743	rs112010353-C	rs112010353	0	1.12E+08	intergenic_variant	1	0.8237	2.00E-08	7.69897		0.0143	[0.0092-0.	Affymetrix, Illumina [10000000] (imputed)	N
9	17:44118848	17	43785098	rs112123127	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Anterior limb of internal capsule R	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs112123127-T	rs112123127	0	1.12E+08	intron_variant	0	0.221	8.00E-14	13.09691		0.088	[0.064-0.1	Affymetrix [17103079] (imputed)	N
9	17:43564222	17	43563304	rs112275793	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Aspartate aminotransferase levels	342,990 Eu	NA	17q21.31		PLEKHM1			ENSG00000277111	NA	NA	rs112275793-C	rs112275793	0	1.12E+08	intron_variant	0	NR	2.00E-19	18.69897		0.0277	[0.022-0.0	Affymetrix, Illumina [20538469] (imputed)	N
9	17:44118848	17	43669491	rs112327620	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Hemoglobin	350,474 Eu	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		5196	8744	rs112327620-G	rs112327620	0	1.12E+08	regulatory_region_variant	1	NR	3.00E-63	62.52288		0.0388	[0.034-0.0	Affymetrix, Illumina [20538521] (imputed)	N
9	17:44118848	17	44126673	rs112333322	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 Eu	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs112333322-A	rs112333322	0	1.12E+08	intron_variant	0	0.214965	4.00E-19	18.39794		8.94	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	44066172	rs112385572	3/12/2018	2.8E+07	Hagenaars SP	14/02/2017	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/28196072	Genetic prediction of male pattern baldness.	Male-pattern baldness	52,874 British ancestr		17q21.31	CRHR1, KANSL1,	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs112385572-G	rs112385572	0	1.12E+08	intron_variant	0	NR	8.00E-29	28.09691		0.076825	NR unit dec	NR [NR] (imputed)	N
9	17:44118848	17	44019103	rs112568425	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Immature fraction of reticulocytes	408,112 Bı	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs112568425-G	rs112568425	0	1.13E+08	intron_variant	0	0.279718	1.00E-14	14		0.020362	[0.015-0.0	Affymetrix [93095623] (imputed)	N
9	17:44118848	17	44072984	rs112572874	24/10/2022	3.4E+07	Harrison S	28/07/2021	Sci Adv	www.ncbi.nlm.nih.gov/pubmed/34321204	Testosterone and socioeconomic position: Mendelian randomization in 306,248 men and women in UK Biobank.	Free testosterone levels	148,248 Bı	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs112572874-G	rs112572874	0	1.13E+08	intron_variant	0	0.23	6.00E-09	8.221849		0	[0-0] nmol/	Affymetrix [NR] (imputed)	N
9	17:44118848	17	44348634	rs112665297	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔÇë=ÔÇë17,706).	White matter microstructure (axial diusivities)	17,706 Eur	NA	17q21.31	NR	MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		26224	3516	rs112665297-?	rs112665297	0	1.13E+08	intergenic_variant	1		1.00E-11	11	(Inferior fro	NA		NR [8955960] (imputed)	N
9	17:44118848	17	43695263	rs112997627	24/08/2021	3.4E+07	Simcoe M	10/03/2021	Sci Adv	www.ncbi.nlm.nih.gov/pubmed/33692100	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color.	Eye color	157,485 Eu	35,501 Eur	17q21.31		RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		8979	2431	rs112997627-T	rs112997627	0	1.13E+08	intergenic_variant	1	0.801	3.00E-08	7.522879	(EA)	5.56	NR z score	Illumina [11532091] (imputed)	N
9	17:44118848	17	43569245	rs113322852	13/01/2021	3.3E+07	Demange PA	7/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33414549	Investigating the genetic architecture of noncognitive skills using GWAS-by-subtraction.	Cognitive aspects of educational attainment	257,700 Eu	NA	17q21.31	NR	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		1130	14862	rs113322852-T	rs113322852	0	1.13E+08	regulatory_region_variant	1	0.198807	2.00E-12	11.69897		0.055314	[0.04-0.07	Affymetrix, Illumina, Perlegen [7305956] (imputed)	N
9	17:44118848	17	43569245	rs113322852	18/03/2019	3.1E+07	Baselmans BML	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643256	Multivariate genome-wide analyses of the well-being spectrum.	Neuroticism	523,783 Eu	59,206 Eur	17q21.31	NR	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		1130	14862	rs113322852-A	rs113322852	0	1.13E+08	regulatory_region_variant	1	0.190285	3.00E-19	18.52288		0.021022	[0.016-0.0	NR [NR]	N
9	17:44118848	17	43850932	rs113518470	11/05/2017	2.7E+07	Pickrell JK	16/05/2016	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/27182965	Detection and interpretation of shared genetic influences on 42 human traits.	Joint mobility (Beighton score)	64,143 Eur	NA	17q21.31	LRRC37A3, CRHR	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs113518470-?	rs113518470	0	1.14E+08	intron_variant	0	NR	6.00E-11	10.22185		0.09	[0.116-0.0	Illumina [12039492] (imputed)	N
9	17:44118848	17	43991272	rs113568679	15/03/2022	3.5E+07	Kulminski AM	6/11/2021	Geroscience	www.ncbi.nlm.nih.gov/pubmed/34743297	Pleiotropic predisposition to Alzheimer's disease and educational attainment: insights from the summary statistics analysis.	Alzheimer's disease or educational attainment (pleiotropy)	(see Lamb	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs113568679-A	rs113568679	1	17563986	intron_variant	0	0.7295	7.00E-09	8.154902		43.90281	z score inc	NR [6814003]	N
9	17:44091886	17	44228169	rs114974956	6/12/2019	3.2E+07	Alliey-Rodriguez N	17/09/2019	Transl Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31530798	NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis.	Ventral diencephalon volume	87 Europea	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs114974956-?	rs114974956	1	1918793	intron_variant	0		6.00E-06	5.221849		NA		Illumina [4322238] (imputed)	N
9	17:44118848	17	44699851	rs116956554	8/10/2020	3.3E+07	Zhou W	7/08/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32769997	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer.	Thyroid stimulating hormone levels	119,715 Eu	NA	17q21.31	NSFP1	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs116956554-A	rs116956554	0	1.17E+08	intron_variant	0	0.179849	3.00E-12	11.52288		0.0471	[0.034-0.0	Illumina [22400000] (imputed)	N
9	17:44118848	17	44051588	rs117124984	25/06/2019	3.1E+07	Jansen PR	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804565	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways.	Daytime nap	386,577 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs117124984-C	rs117124984	0	1.17E+08	5_prime_UTR_variant	0	0.7853	3.00E-13	12.52288		1.099626	[1.07-1.13	Affymetrix, Illumina [10858887] (imputed)	N
9	17:44118848	17	44051589	rs118087478	28/01/2020	3.2E+07	Zhao B	1/11/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31676860	Genome-wide association analysis of 19,629 individuals identifies variants influencing regional brain volumes and refines their genetic co-architecture with cognitive and mental health traits.	Brain region volumes	19,629 Brit	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs118087478-?	rs118087478	0	1.18E+08	5_prime_UTR_variant	0	NR	8.00E-14	13.09691	(total brain	NA		NR [9227495] (imputed)	N
9	17:44118848	17	44015446	rs12150229	25/06/2019	3.1E+07	Jansen PR	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804565	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways.	Ease of getting up in the morning	385,949 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs12150229-G	rs12150229	0	12150229	intron_variant	0	0.2236	4.00E-09	8.39794		0.0122	[0.0081-0.	Affymetrix, Illumina [10862568] (imputed)	N
9	17:44118848	17	43826637	rs12150672	11/05/2017	2.8E+07	van Rooij FJA	22/12/2016	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/28017375	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis.	Red blood cell count	up to 40,2!	16,389 ind	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs12150672-?	rs12150672	0	12150672	intron_variant	0	NR	4.00E-09	8.39794		NA		NR [2500000] (imputed)	N
9	17:44118848	17	43923654	rs12185233	4/11/2019	3E+07	Pulit SL	14/09/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30239722	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry.	Waist-to-hip ratio adjusted for BMI	379,501 Eu	NA	17q21.31	NR	SPPL2C, SPPL2C, SPPL2C, MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000277106, E	NA	NA	rs12185233-C	rs12185233	0	12185233	missense_variant	0	0.2133	2.00E-14	13.69897		0.0159	[0.012-0.0	NR [~ 27400000] (imputed)	N
9	17:44118848	17	43923683	rs12185268	8/07/2016	2.6E+07	Kouri N	16/06/2015	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/26077951	Genome-wide association study of corticobasal degeneration identifies risk variants shared with progressive supranuclear palsy.	Corticobasal degeneration	152 cases,	NA	17q21.31	MAPT	MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12185268-?	rs12185268	0	12185268	missense_variant	0	NR	1.00E-09	9		3.46	[2.27-5.28	Illumina [533898] (imputed)	N
9	17:44118848	17	43923683	rs12185268	20/07/2011	2.2E+07	Do CB	23/06/2011	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/21738487	Web-based genome-wide association study identifies two novel loci and a substantial genetic component for Parkinson's disease.	Parkinson's disease	3,426 Euro	NA	17q21.31	MAPT	MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12185268-A	rs12185268	0	12185268	missense_variant	0	0.79	3.00E-14	13.52288		1.3	[1.22-1.39	Illumina [522782]	N
9	17:44118848	17	43924073	rs12373123	24/01/2022	3.4E+07	He L	26/02/2021	Transl Psychiatry	www.ncbi.nlm.nih.gov/pubmed/33637690	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease.	Alzheimer's disease (age of onset) in APOE e4 non-carriers	7,185 Euro	5,416 Euro	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12373123-?	rs12373123	0	12373123	missense_variant	0	NR	7.00E-08	7.154902		0.861		NR [98334]	N
9	17:44118848	17	43924073	rs12373123	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 Eu	NA	17q21.31	SPPL2C	MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12373123-C	rs12373123	0	12373123	missense_variant	0		2.00E-61	60.69897		0.044	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:44118848	17	43924219	rs12373124	15/08/2012	2.3E+07	Li R	31/05/2012	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/22693459	Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases.	Male-pattern baldness	3,891 Euro	NA	17q21.31	intergenic	SPPL2C, SPPL2C, SPPL2C, MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000277106, E	NA	NA	rs12373124-T	rs12373124	0	12373124	synonymous_variant	0	0.438	5.00E-10	9.30103		1.33	[1.21-1.45	Affymetrix, Illumina [2391230] (imputed)	N
9	17:44118848	17	43924219	rs12373124	3/12/2018	2.8E+07	Hagenaars SP	14/02/2017	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/28196072	Genetic prediction of male pattern baldness.	Male-pattern baldness	52,874 British ancestr		17q21.31	NR	SPPL2C, SPPL2C, SPPL2C, MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000277106, E	NA	NA	rs12373124-C	rs12373124	0	12373124	synonymous_variant	0	NR	1.00E-27	27		0.08	NR unit dec	NR [NR] (imputed)	N
9	17:44118848	17	43924200	rs12373142	1/05/2019	3.1E+07	Sakornsakolpat P	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804561	Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations.	Chronic obstructive pulmonary disease	35,735 cas	NA	17q21.31	SPPL2C	MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12373142-G	rs12373142	0	12373142	missense_variant	0	0.22	1.00E-09	9		1.08	[1.05-1.10	Affymetrix, Illumina [6224355] (imputed)	N
9	17:44118848	17	43924200	rs12373142	1/06/2021	3.4E+07	Moll M	28/04/2021	Am J Physiol Lung Cell Mol Physiol	www.ncbi.nlm.nih.gov/pubmed/33909500	A Systematic Analysis of Protein-altering Exonic Variants in Chronic Obstructive Pulmonary Disease.	Chronic obstructive pulmonary disease	up to 31,4(	NA	17q21.31	SPPL2C	MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12373142-G	rs12373142	0	12373142	missense_variant	0	0.22	2.00E-10	9.69897		1.08	[1.05 -1.1]	Illumina [at least 109036]	N
9	17:43924337	17	43924337	rs12373168	5/09/2022	3.6E+07	Rao S	28/06/2022	Neuropsychobiology	www.ncbi.nlm.nih.gov/pubmed/35764056	Genetic Relationships between Attention-Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, and Intelligence.	Attention deficit hyperactivity disorder or autism spectrum disorder or intelligence (pleiotropy)	20,183 Eur	NA	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1, SPPL2C, SPPL2C, SPPL2C			ENSG00000264589, E	NA	NA	rs12373168-?	rs12373168	0	12373168	3_prime_UTR_variant	0	NR	5.00E-10	9.30103		NA		NR [6307410] (imputed)	N

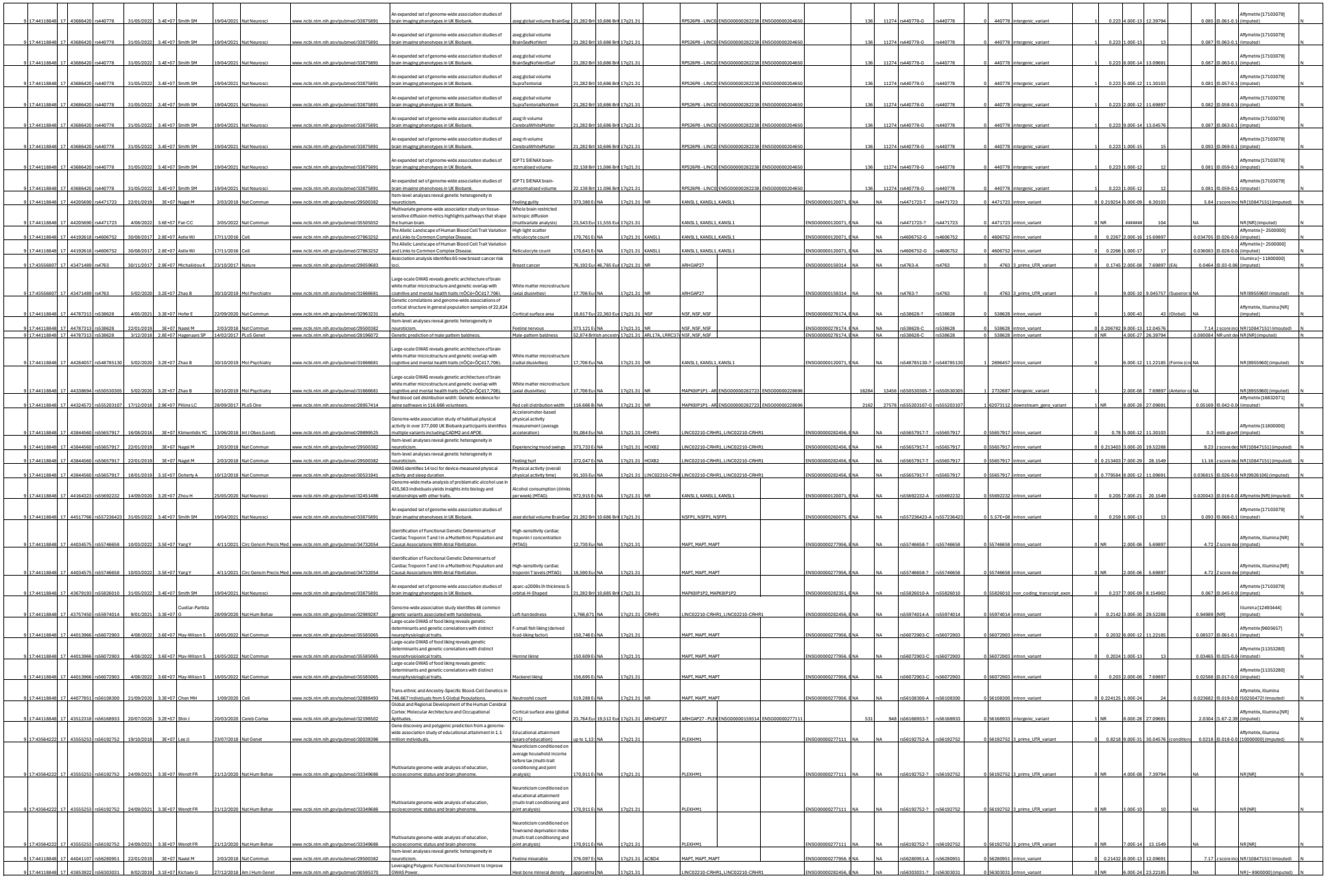
9	17:43520118	17	43495420	rs12936645	3/08/2020	3.2E+07	Han X	30/04/2020	JAMA Ophthalmol	www.ncbi.nlm.nih.gov/pubmed/32352494	Association of Myopia and Intraocular Pressure With Retinal Detachment in European Descent Participants of the UK Biobank Cohort: A Mendelian Randomization Study.	Spherical equivalent	95,827 Eur	NA	17q21.31	NR	ARHGAP27			ENSG00000159314	NA	NA	rs12936645-T	rs12936645	0	12936645	intron_variant	0		5.00E-09	8.30103		0.09	[0.051-0.1	NR [NR]	N
9	17:43564222	17	43507297	rs12949256	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 Eu	NA	17q21.31	ARHGAP27	ARHGAP27			ENSG00000159314	NA	NA	rs12949256-T	rs12949256	0	12949256	missense_variant	0		3.00E-51	50.52288		0.043	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:43803189	17	43803189	rs1358071	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 Superior longitudinal fasciculus R	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs1358071-A	rs1358071	0	1358071	intron_variant	0	0.731	4.00E-16	15.39794		0.09	[0.068-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44787312	rs1378358	20/07/2020	3.2E+07	Shin J	20/03/2020	Cereb Cortex	www.ncbi.nlm.nih.gov/pubmed/32198502	Global and Regional Development of the Human Cerebral Cortex: Molecular Architecture and Occupational Aptitudes.	Cortical surface area (global PC1)	23,784 Eur	19,512 Eur	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-?	rs1378358	0	1378358	intron_variant	0	NR	1.00E-31	31		2.0049	[1.67-2.34	Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	44787312	rs1378358	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling miserable	376,097 Eu	NA	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.206287	2.00E-11	10.69897		6.69	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44787312	rs1378358	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling worry	372,869 Eu	NA	17q21.31	GOSR2	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.206287	2.00E-08	7.69897		5.619	unit increa	NR [10847151] (imputed)	N
9	17:44118848	17	44787312	rs1378358	5/03/2021	3.3E+07	Tadros R	25/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33495596	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect.	Hypertrophic cardiomyopathy	1,733 Euro	2,694 Euro	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.2314	7.00E-16	15.1549		1.281355	1.21-1.36	Illumina [6530233] (imputed)	N
9	17:44118848	17	44787312	rs1378358	5/03/2021	3.3E+07	Tadros R	25/01/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33495596	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect.	Hypertrophic cardiomyopathy (MTAG)	1,733 Euro	NA	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.2314	5.00E-13	12.30103		1.337631	1.22-1.47	Illumina [6530233] (imputed)	N
9	17:44118848	17	44787312	rs1378358	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Neurociticism	380,506 Eu	NA	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.206287	2.00E-27	26.69897		10.86	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44787312	rs1378358	18/03/2019	3.1E+07	Baselmans BML	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643256	Multivariate genome-wide analyses of the well-being spectrum.	Neuroticism	523,783 Eu	59,206 Eur	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs1378358-T	rs1378358	0	1378358	intron_variant	0	0.217293	2.00E-18	17.69897		0.019632	[0.015-0.0	NR [NR]	N
9	17:44118848	17	44335579	rs139077859	1/02/2022	3.5E+07	Hanscombe KB	9/11/2021	Genome Med	www.ncbi.nlm.nih.gov/pubmed/34753499	The genetic case for cardiorespiratory fitness as a clinical vital sign and the routine prescription of physical activity in healthcare.	Cardiorespiratory fitness (vo2 max)	70,783 Eur	NA	17q21.31		MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		13169	16571	rs139077859-G	rs139077859	0	1.39E+08	intergenic_variant	1	0.79	2.00E-08	7.69897		0.033	[0.021-0.0	Affymetrix [8918919] (imputed)	N
9	17:44118848	17	44335579	rs139077859	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 Superior longitudinal fasciculus L	20,860 Brit	10,496 Brit	17q21.31		MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		13169	16571	rs139077859-A	rs139077859	0	1.39E+08	intergenic_variant	1	0.206	5.00E-14	13.30103		0.093	[0.069-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43933790	rs142955985	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Eosinophil counts	349,856 Eu	NA	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs142955985-T	rs142955985	0	1.43E+08	intron_variant	0	NR	2.00E-24	23.69897		0.0218	[0.018-0.0	Affymetrix, Illumina [20529668] (imputed)	N
9	17:44118848	17	43685698	rs143246821	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FEV1)	60,552 European ance		17q21.31	LOC644172, CRH	MAPK8IP1P2 - RP	ENSG00000263503	ENSG00000282238		5992	239	rs143246821-A	rs143246821	1	444967	upstream_gene_variant	1	0.79	9.00E-10	9.045757	(EA)	30.58	[20.8-40.3	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	43685698	rs143246821	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FVC)	60,552 European ance		17q21.31		MAPK8IP1P2 - RP	ENSG00000263503	ENSG00000282238		5992	239	rs143246821-?	rs143246821	1	444967	upstream_gene_variant	1	NR	7.00E-08	7.154902	(EA)	30.54	[19.45-41.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	44132458	rs143364530	15/03/2022	3.5E+07	Kulminski AM	6/11/2021	Geroscience	www.ncbi.nlm.nih.gov/pubmed/34743297	Pleiotropic predisposition to Alzheimer's disease and educational attainment: insights from the summary statistics analysis.	Alzheimer's disease or educational attainment (pleiotropy)	(see Lamb	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs143364530-A	rs143364530	1	62063686	intron_variant	0	0.278	3.00E-08	7.522879		40.49891	z score inc	NR [6814003]	N
9	17:44118848	17	43546057	rs143982995	15/03/2022	3.5E+07	Kulminski AM	6/11/2021	Geroscience	www.ncbi.nlm.nih.gov/pubmed/34743297	Pleiotropic predisposition to Alzheimer's disease and educational attainment: insights from the summary statistics analysis.	Alzheimer's disease or educational attainment (pleiotropy)	(see Lamb	NA	17q21.31		PLEKHM1			ENSG00000277111	NA	NA	rs143982995-T	rs143982995	1	62065399	intron_variant	0	0.222	6.00E-07	6.221849		34.3468	z score inc	NR [6814003]	N
9	17:43564222	17	43564222	rs144733372	3/12/2018	2.8E+07	Hagenaars SP	14/02/2017	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/28196072	Genetic prediction of male pattern baldness.	Male-pattern baldness	52,874 British ancestr		17q21.31	ACBD4, ARHGAP2	PLEKHM1			ENSG00000277111	NA	NA	rs144733372-G	rs144733372	1	9899111	intron_variant	0	NR	2.00E-22	21.69897		0.076714	NR unit de	NR [NR] (imputed)	N
9	17:43564222	17	43564222	rs144733372	10/07/2018	3E+07	Amare AT	6/03/2018	Front Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29559929	Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder.	Remission after SSRI treatment in MDD or neuroticism	865 individ	NA	17q21.31	PLEKHM1	PLEKHM1			ENSG00000277111	NA	NA	rs144733372-G	rs144733372	1	9899111	intron_variant	0	NR	3.00E-11	10.52288		NA		NR [NR] (imputed)	N
9	17:44118848	17	43569909	rs146746174	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Cognitive performance	257,841 Eu	NA	17q21.31	Intergenic	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		1794	14198	rs146746174-T	rs146746174	1	62065449	intergenic_variant	1	0.815	1.00E-12	12		0.0263	[0.019-0.0	Affymetrix, Illumina [10100000] (imputed)	N
9	17:44118848	17	43569909	rs146746174	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Cognitive performance (MTAG)	402,382 Eu	NA	17q21.31	Intergenic	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		1794	14198	rs146746174-T	rs146746174	1	62065449	intergenic_variant	1	0.815	1.00E-23	23	(MTAG)	0.0297	[0.024-0.0	Affymetrix, Illumina [7100000] (imputed)	N
9	17:44118848	17	43569909	rs146746174	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Self-reported math ability (MTAG)	670,471 Eu	NA	17q21.31	Intergenic	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		1794	14198	rs146746174-T	rs146746174	1	62065449	intergenic_variant	1	0.8153	3.00E-15	14.52288	(MTAG)	0.0182	[0.014-0.0	Affymetrix, Illumina [7100000] (imputed)	N
9	17:44118848	17	44335635	rs147431626	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔÇë=ÔÇë17,706).	White matter microstructure (radial diusivities)	17,706 Eur	NA	17q21.31	NR	MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		13225	16515	rs147431626-?	rs147431626	0	1.47E+08	intergenic_variant	1		4.00E-13	12.39794	(Anterior li	NA		NR [8955960] (imputed)	N
9	17:44118848	17	43549608	rs149366495	4/05/2021	3.3E+07	Hofer E	22/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32963231	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults.	Cortical volume	22,824 Eur	NA	17q21.31	PLEKHM1	PLEKHM1			ENSG00000277111	NA	NA	rs149366495-?	rs149366495	0	1.49E+08	intron_variant	0		8.00E-13	12.09691	(Global)	NA		Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	43687072	rs150180355	15/03/2022	3.5E+07	Kulminski AM	6/11/2021	Geroscience	www.ncbi.nlm.nih.gov/pubmed/34743297	Pleiotropic predisposition to Alzheimer's disease and educational attainment: insights from the summary statistics analysis.	Alzheimer's disease or educational attainment (pleiotropy)	(see Lamb	NA	17q21.31		RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		788	10622	rs150180355-A	rs150180355	1	2949997	downstream_gene_variant	1	0.2519	4.00E-07	6.39794		35.50565	z score inc	NR [6814003]	N
9	17:44874453	17	44874453	rs1563304	17/10/2018	3E+07	Nielsen JB	30/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30061737	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology.	Atrial fibrillation	60,620 Eur	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	0.178	3.00E-12	11.52288		1.07	[1.05-1.09	Illumina [34740186] (imputed)	N
9	17:44874453	17	44874453	rs1563304	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 Eu	NA	17q21.31	MAPT	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	0.172485	2.00E-10	9.69897		6.37	z score inc	NR [10847151] (imputed)	N
9	17:44874453	17	44874453	rs1563304	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling hurt	372,047 Eu	NA	17q21.31	MAPT	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	0.172485	1.00E-11	11		6.76	z score inc	NR [10847151] (imputed)	N
9	17:44874453	17	44874453	rs1563304	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Neuroticism	449,484 Eu	NA	17q21.31	NR	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	NR	5.00E-12	11.30103		6.9	z score inc	Affymetrix [10847151] (imputed)	N
9	17:44874453	17	44874453	rs1563304	1/02/2018	2.9E+07	Luciano M	18/12/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29255261	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism.	Neuroticism	329,821 Eu	122,867 Eu	17q21.31	intergenic	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	0.17248	3.00E-10	9.522879		6.281	unit increa	Illumina [18485882] (imputed)	N
9	17:44874453	17	44874453	rs1563304	25/06/2019	3.1E+07	Jansen PR	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804565	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways.	Snoring	359,916 Eu	NA	17q21.31	NR	WNT3			ENSG00000108379	NA	NA	rs1563304-T	rs1563304	0	1563304	intron_variant	0	0.1782	4.00E-08	7.39794		1.04	[1.03-1.05	Affymetrix, Illumina [10862568] (imputed)	N
9	17:44118848	17	43675489	rs1614886	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Anterior limb of internal capsule L	20,860 Brit	10,496 Brit	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		11194	2746	rs1614886-T	rs1614886	0	1614886	regulatory_region_variant	1	0.258	3.00E-18	17.52288		0.1	[0.076-0.1	Affymetrix [17103079] (imputed)	N
9	17:43750921	17	43756969	rs1635288	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-a2009s lh area S-collat-transv-ant	21,282 Brit	10,686 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs1635288-G	rs1635288	0	1635288	intron_variant	0	0.754	7.00E-11	10.1549		0.073	[0.051-0.0	Affymetrix [17103079] (imputed)	N
9	17:43750921	17	43751913	rs1635291	30/03/2020	3.2E+07	Thompson A	15/01/2020	Sci Adv	www.ncbi.nlm.nih.gov/pubmed/31998841	Functional validity, role, and implications of heavy alcohol consumption genetic loci.	Alcohol consumption (heavy vs. light/non-drinkers)	21,967 Brit	47,967 Eur	17q21.31	CRHR1	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs1635291-A	rs1635291	0	1635291	intron_variant	0	0.754	7.00E-09	8.154902		5.803	NR z score	Affymetrix [11141077] (imputed)	N
9	17:43750921	17	43744344	rs1635298	1/06/2021	3.3E+07	Bigdeli TB	10/11/2020	Schizophr Bull	www.ncbi.nlm.nih.gov/pubmed/33169155	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans.	Schizophrenia	37,759 Eur	NA	17q21.31	CRHR1	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs1635298-A	rs1635298	0	1635298	intron_variant	0	NR	3.00E-08	7.522879		1.07	[1.05-1.09	Affymetrix [up to 49134253] (imputed)	N
9	17:44118848	17	44790203	rs169201	4/05/2021	3.3E+07	Hofer E	22/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32963231	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults.	Cortical volume	22,824 Eur	NA	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs169201-?	rs169201	0	169201	intron_variant	0		2.00E-13	12.69897	(Global)	NA		Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	43908152	rs16940672	29/01/2020	3.2E+07	Hill WD	16/12/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31844048	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income.	Household income (MTAG)	505,541 Bi	NA	17q21.31	CRHR1	MAPT-AS1, MAPT-AS1, MAPT-AS1, LINC02210-CRHR1, LINC(			ENSG00000264589, E	NA	NA	rs16940672-T	rs16940672	0	16940672	non_coding_transcript_exon	0	0.218	2.00E-16	15.69897		0.020259	[0.015-0.0	Affymetrix [up to 18485882] (imputed)	N
9	17:44091886	17	44186063	rs16940904	31/08/2022	3.6E+07	Borges MC	13/06/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35692035	Role of circulating polyunsaturated fatty acids on cardiovascular diseases risk: analysis using Mendelian randomization and fatty acid genetic association data from over 114,000 UK Biobank participants.	Circulating docosahexaenoic acid levels	114,999 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.77	2.00E-16	15.69897		0.04	[0.031-0.0	NR [12321876] (imputed)	N
9	17:44091886	17	44186063	rs16940904	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Docosahexaenoic acid levels	115,006 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.773434	1.00E-16	16		0.038987	[0.03-0.04	NR [11722792] (imputed)	N
9	17:44091886	17	44186063	rs16940904	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Omega-3 fatty acid levels	115,006 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.773434	4.00E-13	12.39794		0.034508	[0.025-0.0	NR [11722792] (imputed)	N
9	17:44091886	17	44186063	rs16940904	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Ratio of docosahexaenoic acid to total fatty acid levels	115,006 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.773434	4.00E-16	15.39794		0.038921	[0.03-0.04	NR [11722792] (imputed)	N
9	17:44091886	17	44186063	rs16940904	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Ratio of omega-3 fatty acids to total fatty acids	115,006 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.773434	5.00E-18	17.30103		0.041183	[0.032-0.0	NR [11722792] (imputed)	N
9	17:44091886	17	44186063	rs16940904	31/08/2022	3.6E+07	Borges MC	13/06/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35692035	Role of circulating polyunsaturated fatty acids on cardiovascular diseases risk: analysis using Mendelian randomization and fatty acid genetic association data from over 114,000 UK Biobank participants.	Total omega-3 fatty acid levels	114,999 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs16940904-C	rs16940904	0	16940904	intron_variant	0	0.77	3.00E-13	12.52288		0.036	[0.026-0.0	NR [12321876] (imputed)	N

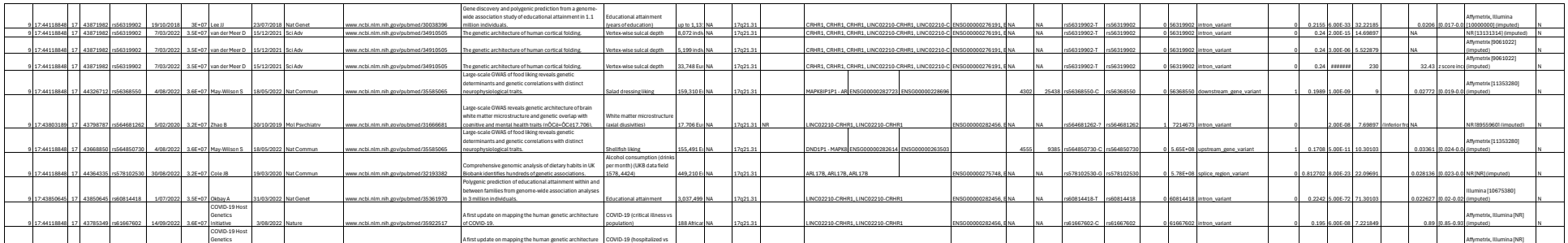
9	17:44118848	17	43672118	rs1724417	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Baked/steamed fish liking	158,335 E	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7823	6117	rs1724417-G	rs1724417	0	1724417	downstream_gene_variant	1	0.1726	2.00E-08	7.69897		0.02836	[0.018-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	43672118	rs1724417	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-fish liking (derived food-liking factor)	155,344 E	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7823	6117	rs1724417-G	rs1724417	0	1724417	downstream_gene_variant	1	0.1727	9.00E-14	13.04576		0.10025	[0.074-0.1	Affymetrix [9578548] (imputed)	N
9	17:44118848	17	43672118	rs1724417	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-oily fish liking (derived food-liking factor)	158,547 E	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7823	6117	rs1724417-G	rs1724417	0	1724417	downstream_gene_variant	1	0.1727	5.00E-09	8.30103		0.10055	[0.067-0.1	Affymetrix [9609308] (imputed)	N
9	17:44118848	17	43672118	rs1724417	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-seafood liking (derived food-liking factor)	156,740 E	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7823	6117	rs1724417-G	rs1724417	0	1724417	downstream_gene_variant	1	0.1727	2.00E-11	10.69897		0.08833	[0.063-0.1	Affymetrix [9618964] (imputed)	N
9	17:44118848	17	43662020	rs1724429	14/09/2020	3.2E+07	Zhou H	25/05/2020	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/32451486	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits.	Problematic alcohol use (MTAG)	972,915 E	NA	17q21.31	NR	RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		25584	1217	rs1724429-G	rs1724429	0	1724429	intron_variant	1	0.2	7.00E-16	15.1549		0.024308	[0.018-0.0	Affymetrix [10613246] (imputed)	N
9	17:44118848	17	43656176	rs1724438	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Eosinophil counts	474,237 E	NA	17q21.31	NR	RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		19740	7061	rs1724438-A	rs1724438	0	1724438	intron_variant	1	0.206005	6.00E-44	43.22185		0.035496	[0.03-0.04	Affymetrix, Illumina [50000174] (imputed)	N
9	17:44118848	17	43656176	rs1724438	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Eosinophil counts	583,850 A	NA	17q21.31	NR	RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		19740	7061	rs1724438-A	rs1724438	0	1724438	intron_variant	1	0.198341	4.00E-41	40.39794		NA		Affymetrix, Illumina [19872809] (imputed)	N
9	17:44118848	17	43656176	rs1724438	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Cingulum cingulate gyrus R	20,860 Bri	10,496 Bri	17q21.31		RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		19740	7061	rs1724438-A	rs1724438	0	1724438	intron_variant	1	0.205	4.00E-11	10.39794		0.081	[0.057-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43830938	rs17426174	17/11/2022	3.6E+07	Baselmans B	6/10/2021	Biol Psychiatry Glob Open Sci	www.ncbi.nlm.nih.gov/pubmed/36324656	The Genetic and Neural Substrates of Externalizing Behavior.	Disruptive behavior (multivariate analysis)	523,150 E	NA	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs17426174-?	rs17426174	0	17426174	intron_variant	0	NR	1.00E-13	13		NA		Affymetrix [NR]	N
9	17:44118848	17	43830938	rs17426174	23/02/2018	2.9E+07	Hill WD	11/01/2018	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29326435	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence.	Intelligence (MTAG)	120,934 B	NA	17q21.31	RP11-105N13.4	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs17426174-C	rs17426174	0	17426174	intron_variant	0	NR	6.00E-11	10.22185		0.023149	[0.016-0.0	Affymetrix [NR]	N
9	17:44118848	17	43811072	rs17563683	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Hematocrit	173,039 E	NA	17q21.31	CRHR1, RP11-10	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs17563683-G	rs17563683	0	17563683	intron_variant	0	0.2333	2.00E-28	27.69897		0.045156	[0.037-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43811072	rs17563683	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Hemoglobin concentration	172,925 E	NA	17q21.31	CRHR1, RP11-10	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs17563683-G	rs17563683	0	17563683	intron_variant	0	0.2333	3.00E-26	25.52288		0.043442	[0.035-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43811072	rs17563683	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 E	NA	17q21.31	MGC57346-CRH	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs17563683-G	rs17563683	0	17563683	intron_variant	0		4.00E-61	60.39794		0.043	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:44118848	17	43991272	rs17563986	12/01/2018	2.9E+07	Lam M	28/11/2017	Cell Rep	www.ncbi.nlm.nih.gov/pubmed/29186694	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets.	Cognitive ability	107,207 E	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17563986-?	rs17563986	0	17563986	intron_variant	0	NR	8.00E-08	7.09691		5.368	z score inc	Affymetrix, Illumina [7357080] (imputed)	N
9	17:44118848	17	43991272	rs17563986	12/01/2018	2.9E+07	Lam M	28/11/2017	Cell Rep	www.ncbi.nlm.nih.gov/pubmed/29186694	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets.	Cognitive ability (MTAG)	436,124 E	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17563986-?	rs17563986	0	17563986	intron_variant	0	NR	5.00E-12	11.30103		6.905	z score inc	Affymetrix, Illumina, Perlegen [7333576] (imputed)	N
9	17:44118848	17	44006601	rs17564829	14/05/2018	2.3E+07	Liu JZ	1/10/2012	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/22961000	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis.	Primary biliary cirrhosis	2,861 Briti	NA	17q21.31	CRHR1, MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17564829-G	rs17564829	0	17564829	intron_variant	0	0.24	2.00E-09	8.69897		1.25	[1.16-1.35	Illumina [237619] (imputed)	N
9	17:44118848	17	44187492	rs17577094	5/12/2014	2.5E+07	Vacic V	19/05/2014	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/24842889	Genome-wide mapping of IBD segments in an Ashkenazi PD cohort identifies associated haplotypes.	Parkinson's disease	1,130 Ashk	306 Ashke	17q21.31	MAPT	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs17577094-?	rs17577094	0	17577094	intron_variant	0	0.74	8.00E-09	8.09691		1.56	[1.39-1.79	Affymetrix, Illumina [1069161] (imputed)	N
9	17:44118848	17	44192923	rs17577369	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling miserable	376,097 E	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs17577369-A	rs17577369	0	17577369	intron_variant	0	0.2157	4.00E-12	11.39794		6.96	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	43516402	rs17631303	2/08/2013	2.4E+07	Couch FJ	27/03/2013	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/23544013	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk.	Ovarian cancer in BRCA1 mutation carriers	683 Europ	1,706 Euro	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs17631303-?	rs17631303	0	17631303	intron_variant	0	NR	1.00E-08	8		NA		Illumina [2568349] (imputed)	N
9	17:44118848	17	43516402	rs17631303	2/08/2013	2.4E+07	Couch FJ	27/03/2013	PLoS Genet	www.ncbi.nlm.nih.gov/pubmed/23544013	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk.	Ovarian cancer in BRCA1 mutation carriers	683 Europ	1,706 Euro	17q21.31	intergenic	PLEKHM1			ENSG00000277111	NA	NA	rs17631303-G	rs17631303	0	17631303	intron_variant	0	0.19	1.00E-08	8		1.27	[1.17-1.38	Illumina [2568349] (imputed)	N
9	17:44118848	17	43994648	rs17649553	9/05/2015	2.5E+07	Nalls MA	27/07/2014	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/25064009	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease.	Parkinson's disease	13,708 Eu	5,353 Euro	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17649553-C	rs17649553	0	17649553	intron_variant	0	0.774	2.00E-48	47.69897		1.3	[1.27-1.34	Illumina [7893274] (imputed)	N
9	17:44118848	17	43994648	rs17649553	24/10/2017	2.9E+07	Chang D	11/09/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28892059	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci.	Parkinson's disease	20,184 Eu	5,851 Euro	17q21.31	ARHGAP27, CRH	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17649553-C	rs17649553	0	17649553	intron_variant	0	0.779	1.00E-68	68		1.282051	[1.25-1.32	Illumina [11933700] (imputed)	N
9	17:44118848	17	44037491	rs17650842	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 E	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17650842-A	rs17650842	0	17650842	intron_variant	0	0.21663	2.00E-12	11.69897		7.01	z score dec	NR [~ 10847151] (imputed)	N
9	17:44118848	17	44098967	rs17652520	29/01/2020	3.2E+07	Hill WD	16/12/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31844048	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income.	Household income	286,301 B	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17652520-A	rs17652520	0	17652520	intron_variant	0	NR	5.00E-12	11.30103		0.013847	[0.0099-0.	Affymetrix [18485882] (imputed)	N
9	17:44118848	17	44098967	rs17652520	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Lager liking	156,958 E	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17652520-A	rs17652520	0	17652520	intron_variant	0	0.2287	8.00E-10	9.09691		0.02614	[0.018-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	44098967	rs17652520	21/06/2019	3.1E+07	Wu Y	23/04/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31015401	Genome-wide association study of medication-use and associated disease in the UK Biobank.	Medication use (anilides)	83,218 Eu	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17652520-A	rs17652520	0	17652520	intron_variant	0	0.231386	8.00E-13	12.09691		0.05571	[0.04-0.07	Affymetrix [7288503] (imputed)	N
9	17:44118848	17	44098967	rs17652520	1/02/2018	2.9E+07	Luciano M	18/12/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29255261	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism.	Neuroticism	329,821 E	122,867 E	17q21.31	intergenic	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17652520-A	rs17652520	0	17652520	intron_variant	0	0.2216	1.00E-25	25		10.472	unit increa	Illumina [18485882] (imputed)	N
9	17:44118848	17	44098967	rs17652520	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Neuroticism	approxima	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs17652520-?	rs17652520	0	17652520	intron_variant	0	NR	2.00E-27	26.69897		NA		NR [~ 8900000] (imputed)	N
9	17:44118848	17	44192957	rs17661015	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling hurt	372,047 E	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs17661015-T	rs17661015	0	17661015	intron_variant	0	0.215131	3.00E-28	27.52288		11.02	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	44192957	rs17661015	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 E	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs17661015-T	rs17661015	0	17661015	intron_variant	0	0.215131	4.00E-12	11.39794		6.93	z score dec	NR [~ 10847151] (imputed)	N
9	17:44118848	17	44357351	rs17665188	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 E	NA	17q21.31	NR	ARL17B, ARL17B, ARL17B			ENSG00000275748, E	NA	NA	rs17665188-T	rs17665188	0	17665188	intron_variant	0	0.213949	1.00E-18	18		8.79	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	43906828	rs17689882	3/11/2015	2.6E+07	Hibar DP	21/01/2015	Nature	www.ncbi.nlm.nih.gov/pubmed/25607358	Common genetic variants influence human subcortical brain structures.	Subcortical brain region volumes	up to 13,1	up to 15,1	17q21.31	CRHR1	CRHR1, CRHR1, CRHR1, LINC02210-CRHR1, LINC02210-C			ENSG00000276191, E	NA	NA	rs17689882-A	rs17689882	0	17689882	intron_variant	0	0.22	8.00E-09	8.09691	(Intracrani	13460.47	[8891.61-1	Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	43927290	rs17769552	13/09/2022	3.6E+07	Hoglund J	22/07/2022	Front Immunol	www.ncbi.nlm.nih.gov/pubmed/35935937	Gene-Based Variant Analysis of Whole-Exome Sequencing in Relation to Eosinophil Count.	Eosinophil counts	365,954 B	NA	17q21.31		MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs17769552-A	rs17769552	0	17769552	intron_variant	0	0.198	1.00E-17	17		0.038	[0.03-0.04	Affymetrix [6661079] (imputed)	N
9	17:44118848	17	43927290	rs17769552	9/07/2018	3E+07	Tikkanen E	24/04/2018	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/29691431	Biological Insights Into Muscular Strength: Genetic Findings in the UK Biobank.	Hand grip strength	334,825 B	NA	17q21.31	SPPL2C	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs17769552-A	rs17769552	0	17769552	intron_variant	0	0.2235	2.00E-08	7.69897		0.002	[0.0014-0.	Affymetrix [15275733] (imputed)	N
9	17:44118848	17	44219831	rs1819040	14/03/2022	3.4E+07	COVID-19 Host Genetics Initiative	8/07/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34237774	Mapping the human genetic architecture of COVID-19.	COVID-19 (hospitalized vs population)	790 Africa	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs1819040-A	rs1819040	0	1819040	intron_variant	0	0.1855	2.00E-10	9.69897		0.879018	[0.844849	Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	44219831	rs1819040	14/03/2022	3.4E+07	COVID-19 Host Genetics Initiative	8/07/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34237774	Mapping the human genetic architecture of COVID-19.	SARS-CoV-2 infection	2,544 Afric	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs1819040-A	rs1819040	0	1819040	intron_variant	0	0.184	5.00E-06	5.30103		0.957168	[0.939337	Affymetrix, Illumina, Perlegen [NR] (imputed)	N
9	17:44118848	17	44359783	rs184837332	12/11/2021	3.4E+07	Thompson A	8/06/2021	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/34104963	Assessing the impact of alcohol consumption on the genetic contribution to mean corpuscular volume.	Mean corpuscular volume	362,595 B	NA	17q21.31		ARL17B, ARL17B, ARL17B			ENSG00000275748, E	NA	NA	rs184837332-G	rs184837332	0	1.85E+08	intron_variant	0	0.775	9.00E-14	13.04576		0.1	[0.07-0.13	Affymetrix [NR] (imputed)	N
9	17:44118848	17	44408004	rs1863114	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 E	NA	17q21.31	LRRC37A	ARL17B, ARL17B, ARL17B, LRRC37A, LRRC37A			ENSG00000275748, E	NA	NA	rs1863114-C	rs1863114	0	1863114	missense_variant	0		2.00E-50	49.69897		0.045	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:44118848	17	43977827	rs1864325	11/04/2013	2.3E+07	Estrada K	15/04/2012	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/22504420	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture.	Lumbar spine bone mineral density	Up to 32,9	Up to 50,9	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1864325-T	rs1864325	0	1864325	intron_variant	0	0.22	5.00E-11	10.30103		0.04	[NR] unit d	Affymetrix, Illumina [~ 2500000] (imputed)	N
9	17:44118848	17	43682323	rs186806998	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FEV1)	60,552 European ance		17q21.31	CRHR1	MAPK8IP1P2 - RP	ENSG00000263503	ENSG00000282238		2617	3614	rs186806998-T	rs186806998	1	56383763	upstream_gene_variant	1	0.79	1.00E-09	9	(EA)	36.39	[24.71-48.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	43682323	rs186806998	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FEV1)	60,552 European ance		17q21.31	LOC644172, CRH	MAPK8IP1P2 - RP	ENSG00000263503	ENSG00000282238		2617	3614	rs186806998-T	rs186806998	1	56383763	upstream_gene_variant	1	0.82	3.00E-10	9.522879		29.5	[20.29-38.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	43682323	rs186806998	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FVC)	60,552 European ance		17q21.31		MAPK8IP1P2 - RP	ENSG00000263503	ENSG00000282238		2617	3614	rs186806998-?	rs186806998	1	56383763	upstream_gene_variant	1	NR	1.00E-08	8		30.52	[20.01-41.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	43911443	rs1876829	22/09/2019	3.1E+07	Lotta LA	1/12/2018	JAMA	www.ncbi.nlm.nih.gov/pubmed/30575882	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors.	Waist-hip ratio	663,598 E	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1, MAPT-AS1, MAPT-A			ENSG00000282456, E	NA	NA	rs1876829-C	rs1876829	0	1876829	intron_variant	0	0.22	5.00E-08	7.30103		NA		Affymetrix [2446094] (imputed)	N
9	17:44118848	17	43911443	rs1876829	22/09/2019	3.1E+07	Lotta LA	1/12/2018	JAMA	www.ncbi.nlm.nih.gov/pubmed/30575882	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors.	Waist-to-hip ratio adjusted for BMI	660,648 E	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1, MAPT-AS1, MAPT-A			ENSG00000282456, E	NA	NA	rs1876829-C	rs1876829	0	1876829	intron_variant	0	0.22	7.00E-17	16.1549		0.019	[0.015-0.0	Affymetrix [2446094] (imputed)	N
9	17:44118848	17	43567337	rs1879586	4/08/2017	2.8E+07	Phelan CM	27/03/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28346442	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.	Epithelial ovarian cancer	16,924 Eu	NA	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs1879586-G	rs1879586	0	1879586	intron_variant	0	0.181254	2.00E-19	18.69897		1.161137	[1.123966	Illumina [11595112] (imputed)	N
9	17:44118848	17	43567337	rs1879586	7/08/2017	2.8E+07	Phelan CM	27/03/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28346442	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.	High-grade serous ovarian cancer	13,037 Eu	NA	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs1879586-G	rs1879586	0	1879586	intron_variant	0	0.181254	3.00E-13	12.52288		1.158558	[1.113784	Illumina [11595112] (imputed)	N
9	17:44118848	17	43567337	rs1879586	3/08/2017	2.8E+07	Phelan CM	27/03/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28346442	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.	Invasive epithelial ovarian cancer	22,406 Eu	NA	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs1879586-G	rs1879586	0	1879586	intron_variant	0	0.181254	2.00E-13	12.69897		1.133901	[1.096609	Illumina [11595112] (imputed)	N
9	17:44118848	17	43567337	rs1879586	3/08/2017	2.8E+07	Phelan CM	27/03/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28346442	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.	Ovarian cancer in BRCA1 mutation carriers	2,933 Euro	NA	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs1879586-G	rs1879586	0	1879586	intron_variant	0	0.181254	7.00E-06	5.154902		1.180455	[1.098309	Illumina [11595112] (imputed)	N

9	17:44118848	17	43567337	rs1879586	7/08/2017	2.8E+07	Phelan CM	27/03/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/28346442	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer.	Serous invasive ovarian cancer	14,049 Eu	NA	17q21.31	NR	PLEKHM1			ENSG00000277111	NA	NA	rs1879586-G	rs1879586	0	1879586	intron_variant	0	0.181254	3.00E-12	11.52288		1.147209	[1.104061-	Illumina [11595112] (imputed)	N
9	17:44118848	17	44248769	rs1881193	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 Eu	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs1881193-T	rs1881193	0	1881193	missense_variant	0	0.21737	1.00E-18	18		8.84	z score dec	NR [10847151] (imputed)	N
9	17:44091886	17	44228169	rs1918793	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L3 Genu of corpus callosum	20,860 Brit	10,496 Brit	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs1918793-T	rs1918793	0	1918793	intron_variant	0	0.227	2.00E-15	14.69897		0.093	[0.069-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44218138	rs1918800	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	ThalamNuclei lh volume VAmc	21,282 Brit	10,686 Brit	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs1918800-T	rs1918800	0	1918800	intron_variant	0	0.182	9.00E-11	10.04576		0.087	[0.062-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43991515	rs192818565	25/02/2017	2.7E+07	Okbay A	26/05/2016	Nature	www.ncbi.nlm.nih.gov/pubmed/27225129	Genome-wide association study identifies 74 loci associated with educational attainment.	Educational attainment (college completion)	280,007 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs192818565-T	rs192818565	1	62056842	intron_variant	0	0.8097	5.00E-11	10.30103		1.053487	[NR]	Affymetrix, Illumina, Perlegen [~ 9300000] (imputed)	N
9	17:44118848	17	43991515	rs192818565	24/02/2017	2.7E+07	Okbay A	26/05/2016	Nature	www.ncbi.nlm.nih.gov/pubmed/27225129	Genome-wide association study identifies 74 loci associated with educational attainment.	Educational attainment (years of education)	405,072 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs192818565-T	rs192818565	1	62056842	intron_variant	0	0.7988	2.00E-12	11.69897		0.020457	NR unit inc	Affymetrix, Illumina, Perlegen [~ 9300000] (imputed)	N
9	17:44118848	17	44142332	rs193236081	17/03/2017	2.7E+07	Okbay A	18/04/2016	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/27089181	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses.	Neuroticism	170,911 Eu	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs193236081-T	rs193236081	1	77184207	intron_variant	0	0.774	6.00E-11	10.22185		0.028413	[0.02-0.03	Affymetrix [up to 6544775] (imputed)	N
9	17:44118848	17	43539437	rs1971631	3/10/2022	3.4E+07	Merino J	23/08/2021	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/34426670	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits.	Dietary macronutrient intake (multi-trait analysis)	282,271 Eu	NA	17q21.31		PLEKHM1			ENSG00000277111	NA	NA	rs1971631-C	rs1971631	0	1971631	intron_variant	0	0.825	2.00E-10	9.69897		NA		Affymetrix [11800000] (imputed)	N
9	17:44118848	17	44056767	rs1981997	1/11/2013	2.4E+07	Fingerlin TE	14/04/2013	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/23583980	Genome-wide association study identifies multiple susceptibility loci for pulmonary fibrosis.	Interstitial lung disease	1,161 Euro	876 Europ	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1981997-G	rs1981997	0	1981997	non_coding_transcript_exon	0	0.77	9.00E-14	13.04576		1.41	[1.28-1.56	Illumina [439828]	N
9	17:44118848	17	44083402	rs1991556	24/09/2019	3.1E+07	Evangelou E	29/07/2019	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/31358974	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders.	Alcohol consumption	480,842 Eu	NA	17q21.31	MAPT, STH	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1991556-A	rs1991556	0	1991556	intron_variant	0	0.22	5.00E-23	22.30103		0.012	[0.01-0.01	Affymetrix, Illumina [~ 7100000] (imputed)	N
9	17:44118848	17	44083402	rs1991556	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Lung function (FVC)	approxima	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1991556-?	rs1991556	0	1991556	intron_variant	0	NR	1.00E-53	53		NA		NR [~ 8900000] (imputed)	N
9	17:44118848	17	44083402	rs1991556	18/01/2019	3.1E+07	Doherty A	10/12/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30531941	GWAS identifies 14 loci for device-measured physical activity and sleep duration.	Sleep duration	91,105 Eu	NA	17q21.31	STH	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs1991556-G	rs1991556	0	1991556	intron_variant	0	0.774711	3.00E-09	8.522879		0.032805	[0.022-0.0	NR [9926106] (imputed)	N
9	17:44118848	17	44819565	rs199443	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling fed-up	374,971 Eu	NA	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199443-T	rs199443	0	199443	intron_variant	0	0.20675	4.00E-13	12.39794		7.26	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44819565	rs199443	27/09/2016	2.7E+07	Dong J	1/11/2015	Medicine (Baltimore)	www.ncbi.nlm.nih.gov/pubmed/26632684	Genome-wide Meta-analysis on the Sense of Smell Among US Older Adults.	Sense of smell	6,252 Euro	NA	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199443-T	rs199443	0	199443	intron_variant	0	0.2	3.00E-06	5.522879	(Ajusted fo	0.03	[0.01-0.05	Affymetrix, Illumina [2543887] (imputed)	N
9	17:44118848	17	44819565	rs199443	27/09/2016	2.7E+07	Dong J	1/11/2015	Medicine (Baltimore)	www.ncbi.nlm.nih.gov/pubmed/26632684	Genome-wide Meta-analysis on the Sense of Smell Among US Older Adults.	Sense of smell	6,252 Euro	NA	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199443-T	rs199443	0	199443	intron_variant	0	0.2	4.00E-06	5.39794		0.03	[0.01-0.05	Affymetrix, Illumina [2543887] (imputed)	N
9	17:44118848	17	44812188	rs199447	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Neuroticism	449,484 Eu	NA	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199447-T	rs199447	0	199447	intron_variant	0	NR	2.00E-26	25.69897		10.659	z score inc	Affymetrix [10847151] (imputed)	N
9	17:44118848	17	44797919	rs199456	28/01/2019	3.1E+07	Gao XR	7/12/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30535121	Genome-wide association analyses identify 139 loci associated with macular thickness in the UK Biobank cohort.	Macular thickness	59,814 Eu	8,609 Euro	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199456-?	rs199456	0	199456	intron_variant	0	NR	3.00E-28	27.52288		0.86	[0.7-1.02]	Affymetrix [11100000] (imputed)	N
9	17:44874453	17	44866602	rs199497	19/08/2022	3.6E+07	Carcel-Marquez J	8/07/2022	Front Cardiovasc Med	www.ncbi.nlm.nih.gov/pubmed/35872910	A Polygenic Risk Score Based on a Cardioembolic Stroke Multitrait Analysis Improves a Clinical Prediction Model for This Stroke Subtype.	Atrial fibrillation (MTAG)	1,030,836	NA	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199497-T	rs199497	0	199497	intron_variant	0	NR	1.00E-10	10		0.012	[0.0081-0.	Illumina [6808676] (imputed)	N
9	17:44874453	17	44866602	rs199497	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Cognitive performance (MTAG)	402,382 Eu	NA	17q21.31	Intergenic	WNT3			ENSG00000108379	NA	NA	rs199497-T	rs199497	0	199497	intron_variant	0	0.8232	6.00E-10	9.221849	(MTAG)	0.0189	[0.013-0.0	Affymetrix, Illumina [7100000] (imputed)	N
9	17:44874453	17	44866602	rs199497	2/05/2019	3.1E+07	Hill WD	13/03/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30867560	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life.	General factor of neuroticism	270,059 Br	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199497-T	rs199497	0	199497	intron_variant	0	NR	2.00E-10	9.69897		0.010905	[0.0076-0.	Affymetrix [18485882] (imputed)	N
9	17:44874453	17	44866602	rs199497	27/09/2022	3.5E+07	Trubetskoy V	8/04/2022	Nature	www.ncbi.nlm.nih.gov/pubmed/35396580	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.	Schizophrenia	53,386 Eu	1,979 Euro	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199497-T	rs199497	0	199497	intron_variant	0	0.866	7.00E-06	5.154902		1.05559	[1.03-1.08	Affymetrix [7585078] (imputed)	N
9	17:44118848	17	44865498	rs199499	30/08/2022	3.2E+07	Cole JB	19/03/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32193382	Comprehensive genomic analysis of dietary habits in UK Biobank identifies hundreds of genetic associations.	Alcohol consumption (drinks per month) (UKB data field 1578, 4424)	449,210 Eu	NA	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199499-C	rs199499	0	199499	intron_variant	0	0.794081	2.00E-17	16.69897		0.023427	[0.018-0.0	NR [NR] (imputed)	N
9	17:44118848	17	44865498	rs199499	3/02/2016	2.6E+07	Jun G	17/03/2015	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/25778476	A novel Alzheimer disease locus located near the gene encoding tau protein.	Alzheimer's disease in APOE e4- carriers	7,184 case	718 Europ	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199499-C	rs199499	0	199499	intron_variant	0	0.81	6.00E-06	5.221849		1.162791	[1.09-1.23	NR [NR]	N
9	17:44118848	17	44862162	rs199503	15/03/2022	3.5E+07	Kulminski AM	6/11/2021	Geroscience	www.ncbi.nlm.nih.gov/pubmed/34743297	Pleiotropic predisposition to Alzheimer's disease and educational attainment: insights from the summary statistics analysis.	Alzheimer's disease or educational attainment (pleiotropy)	(see Lamb	NA	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199503-A	rs199503	0	199503	intron_variant	0	0.2481	2.00E-08	7.69897		42.19048	z score inc	NR [6814003]	N
9	17:44118848	17	44862162	rs199503	27/04/2021	3.4E+07	Peyrot WJ	8/03/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/33686288	Identifying loci with different allele frequencies among cases of eight psychiatric disorders using CC-GWAS.	Schizophrenia vs autism spectrum disorder (ordinary least squares (OLS))	40,675 sch	NA	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199503-?	rs199503	0	199503	intron_variant	0	NR	3.00E-09	8.522879		0.0179	NR unit de	NR [4484088] (imputed)	N
9	17:44118848	17	44862162	rs199503	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-hip index	219,872 Br	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199503-A	rs199503	0	199503	intron_variant	0	NR	1.00E-10	10		0.022195	[0.015-0.0	Affymetrix [319769] (imputed)	N
9	17:44118848	17	44862162	rs199503	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist-to-hip ratio adjusted for BMI	219,872 Br	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199503-A	rs199503	0	199503	intron_variant	0	NR	1.00E-10	10		0.022073	[0.015-0.0	Affymetrix [319769] (imputed)	N
9	17:44861003	17	44861003	rs199504	4/05/2021	3.3E+07	Hofer E	22/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32963231	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults.	Cortical thickness	22,163 Eu	22,363 Eu	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199504-?	rs199504	0	199504	intron_variant	0		6.00E-13	12.22185	(Superior t	NA		Affymetrix, Illumina [NR] (imputed)	N
9	17:44861003	17	44859410	rs199505	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Depressed affect	357,957 Eu	NA	17q21.31	NR	WNT3			ENSG00000108379	NA	NA	rs199505-?	rs199505	0	199505	intron_variant	0	NR	1.00E-18	18		0.02469	[0.019-0.0	Affymetrix [10847151] (imputed)	N
9	17:44861003	17	44857929	rs199510	2/11/2021	3.4E+07	Karlsson Linner R	26/08/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/34446935	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction.	Externalizing behaviour (multivariate analysis)	up to 53,29	NA	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199510-A	rs199510	0	199510	intron_variant	0	0.238	3.00E-10	9.522879		0.01	[0.0061-0.	NR [NR] (imputed)	N
9	17:44861003	17	44857352	rs199512	8/10/2019	3.2E+07	Wiberg A	5/09/2019	Brain	www.ncbi.nlm.nih.gov/pubmed/31504236	Handedness, language areas and neuropsychiatric diseases: insights from brain imaging and genetics.	Handedness (Left-handed vs. non-left-handed)	38,322 Eu	NA	17q21.31	WNT3, MAPT, MAI	WNT3			ENSG00000108379	NA	NA	rs199512-?	rs199512	0	199512	intron_variant	0	NR	5.00E-08	7.30103		NA		NR [~ 11000000] (imputed)	N
9	17:44861003	17	44857352	rs199512	8/10/2019	3.2E+07	Wiberg A	5/09/2019	Brain	www.ncbi.nlm.nih.gov/pubmed/31504236	Handedness, language areas and neuropsychiatric diseases: insights from brain imaging and genetics.	Handedness (left-handed vs. right-handed)	38,322 Eu	NA	17q21.31	WNT3, MAPT, MAI	WNT3			ENSG00000108379	NA	NA	rs199512-C	rs199512	0	199512	intron_variant	0	0.791	4.00E-09	8.39794		1.06	[1.04-1.07	NR [~ 11000000] (imputed)	N
9	17:44861003	17	44857352	rs199512	8/10/2019	3.2E+07	Wiberg A	5/09/2019	Brain	www.ncbi.nlm.nih.gov/pubmed/31504236	Handedness, language areas and neuropsychiatric diseases: insights from brain imaging and genetics.	Handedness (non-right-handed vs right-handed)	44,631 Eu	NA	17q21.31	WNT3, MAPT, MAI	WNT3			ENSG00000108379	NA	NA	rs199512-?	rs199512	0	199512	intron_variant	0	NR	5.00E-08	7.30103		NA		NR [~ 11000000] (imputed)	N
9	17:44861003	17	44856641	rs199515	6/04/2022	3.5E+07	Bellenguez C	4/04/2022	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/35379992	New insights into the genetic etiology of Alzheimer's disease and related dementias.	Alzheimer's disease	39,106 Eu	25,392 cas	17q21.31		WNT3			ENSG00000108379	NA	NA	rs199515-G	rs199515	0	199515	intron_variant	0	0.2194	9.00E-13	12.04576		0.94	[0.93-0.96	Affymetrix, Illumina [21101114] (imputed)	N
9	17:44861003	17	44856641	rs199515	20/04/2012	2.2E+07	Pankratz N	1/03/2012	Ann Neurol	www.ncbi.nlm.nih.gov/pubmed/22451204	Meta-analysis of Parkinson's disease: identification of a novel locus, RIT2.	Parkinson's disease	4,238 Euro	3,738 Euro	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199515-?	rs199515	0	199515	intron_variant	0	NR	3.00E-17	16.52288		1.32	[NR]	Illumina [2500000] (imputed)	N
9	17:44118848	17	44847834	rs199525	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling guilty	373,380 Eu	NA	17q21.31	GOSR2	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	0.207235	4.00E-08	7.39794		5.51	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	44847834	rs199525	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	219,872 Br	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199525-G	rs199525	0	199525	intron_variant	0	NR	2.00E-08	7.69897		0.019361	[0.013-0.0	Affymetrix [321016] (imputed)	N
9	17:44118848	17	44847834	rs199525	17/04/2019	3.1E+07	Klein M	1/03/2019	Am J Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30818988	Genetic Markers of ADHD-Related Variations in Intracranial Volume.	Intracranial volume	24,024 Eu	NA	17q21.31	NR	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	NR	2.00E-20	19.69897		9.262	NR z score	NR [9186920] (imputed)	N
9	17:44118848	17	44847834	rs199525	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FEV1)	60,552 European ance		17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	0.8	1.00E-09	9		18.85	[12.81-24.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	44847834	rs199525	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FEV1)	60,552 European ance		17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	0.79	2.00E-08	7.69897	(EA)	19.16	[12.46-25.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	44847834	rs199525	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FVC)	60,552 European ance		17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	0.8	8.00E-09	8.09691		20.32	[13.42-27.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	44847834	rs199525	1/11/2018	3E+07	Wyss AB	30/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30061609	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function.	Lung function (FVC)	60,552 European ance		17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199525-T	rs199525	0	199525	intron_variant	0	0.79	3.00E-07	6.522879	(EA)	20.03	[12.41-27.	Affymetrix, Illumina [10900000] (imputed)	N
9	17:44118848	17	44843136	rs199528	4/10/2019	3.1E+07	Brazel DM	6/12/2018	Biol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30679032	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol┬áUse.	Alcohol consumption (drinks per week)	up to 357,8	NA	17q21.31	WNT3	WNT3			ENSG00000108379	NA	NA	rs199528-T	rs199528	0	199528	intron_variant	0	0.223	5.00E-21	20.30103		0.0286	[0.023-0.0	Illumina [~ 250000] (imputed)	N
9	17:44118848	17	44828931	rs199533	24/01/2022	3.4E+07	He L	26/02/2021	Transl Psychiatry	www.ncbi.nlm.nih.gov/pubmed/33637690	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease.	Alzheimer's disease (age of onset) (adjusted for APOE e4 carrier status)	10,216 Eu	9,261 Euro	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-?	rs199533	0	199533	synonymous_variant	0	NR	4.00E-07	6.39794		0.896		NR [110450]	N
9	17:44118848	17	44828931	rs199533	24/01/2022	3.4E+07	He L	26/02/2021	Transl Psychiatry	www.ncbi.nlm.nih.gov/pubmed/33637690	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease.	Alzheimer's disease (age of onset) in APOE e4 non-carriers	7,185 Euro	5,416 Euro	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-?	rs199533	0	199533	synonymous_variant	0	NR	1.00E-07	7		0.859		NR [98334]	N
9	17:44118848	17	44828931	rs199533	13/11/2020	3.3E+07	Rashkin SR	4/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32887889	Pan-cancer study detects genetic risk variants and shared genetic basis in two large cohorts.	Breast cancer	17,881 Eu	NA	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-G	rs199533	0	199533	synonymous_variant	0	NR	5.00E-08	7.30103		1.078	NR	Affymetrix [7846216] (imputed)	N

9	17:44118848	17	44828931	rs199533	13/11/2020	3.3E+07	Rashkin SR	4/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32887889	Pan-cancer study detects genetic risk variants and shared genetic basis in two large cohorts.	Cancer (pleiotropy)	64,962 Eu	NA	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-G	rs199533	0	199533	synonymous_variant	0	NR	4.00E-07	6.39794		1.06	[1.036-1.0	Affymetrix [7846216] (imputed)	N
9	17:44118848	17	44828931	rs199533	10/12/2009	2E+07	Simon-Sanchez J	15/11/2009	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/19915575	Genome-wide association study reveals genetic risk underlying Parkinson's disease.	Parkinson's disease	1,713 Euro	3,361 Euro	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-C	rs199533	0	199533	synonymous_variant	0	0.83	1.00E-14	14		1.28	[NR]	Illumina [463185]	N
9	17:44118848	17	44828931	rs199533	22/09/2010	2.1E+07	Hamza TH	15/08/2010	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/20711177	Common genetic variation in the HLA region is associated with late-onset sporadic Parkinson's disease.	Parkinson's disease	2,000 Euro	Up to 1,44	17q21.31	MAPT	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-C	rs199533	0	199533	synonymous_variant	0	0.78	1.00E-06	6		1.35	[1.19-1.52	Illumina [811597]	N
9	17:44118848	17	44828931	rs199533	1/02/2022	3.5E+07	Hanscombe KB	9/11/2021	Genome Med	www.ncbi.nlm.nih.gov/pubmed/34753499	The genetic case for cardiorespiratory fitness as a clinical vital sign and the routine prescription of physical activity in healthcare.	Physical activity	89,683 Eu	NA	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199533-G	rs199533	0	199533	synonymous_variant	0	0.79	4.00E-08	7.39794		0.25	[0.16-0.34	Affymetrix [8918919] (imputed)	N
9	17:44118848	17	44822662	rs199535	4/05/2021	3.3E+07	Hofer E	22/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32963231	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults.	Cortical surface area	18,617 Eu	22,363 Eu	17q21.31	NSF	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199535-?	rs199535	0	199535	intron_variant	0		8.00E-18	17.09691	(Fusiform)	NA		Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	44822662	rs199535	3/10/2022	3.4E+07	Merino J	23/08/2021	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/34426670	Genetic analysis of dietary intake identifies new loci and functional links with metabolic traits.	Dietary macronutrient intake (multi-trait analysis)	282,271 Eu	NA	17q21.31		NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs199535-A	rs199535	0	199535	intron_variant	0	0.79	1.00E-10	10		NA		Affymetrix [11800000] (imputed)	N
9	17:44118848	17	44625866	rs199913382	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 Eu	NA	17q21.31	LRRC37A2	ARL17A, LRRC37A2			ENSG00000185829, E	NA	NA	rs199913382-C	rs199913382	0	2E+08	missense_variant	0		3.00E-54	53.52288		0.043	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:44118848	17	44214888	rs2077551	9/03/2020	3.2E+07	Allen RJ	11/11/2019	Am J Respir Crit Care Med	www.ncbi.nlm.nih.gov/pubmed/31710517	Genome-Wide Association Study of Susceptibility to Idiopathic Pulmonary Fibrosis.	Idiopathic pulmonary fibrosis	2,668 Euro	1,456 Euro	17q21.31	MAPT	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2077551-T	rs2077551	0	2077551	intron_variant	0	0.814	3.00E-16	15.52288		1.408451	[1.3-1.54]	Affymetrix, Illumina [10790934] (imputed)	N
9	17:44118848	17	44214888	rs2077551	26/08/2022	3.6E+07	Allen RJ	10/06/2022	Thorax	www.ncbi.nlm.nih.gov/pubmed/35688625	Genome-wide association study across five cohorts identifies five novel loci associated with idiopathic pulmonary fibrosis.	Idiopathic pulmonary fibrosis	4,125 Euro	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2077551-T	rs2077551	0	2077551	intron_variant	0	0.807	2.00E-20	19.69897		1.42	[1.32-1.53	Illumina [7554248] (imputed)	N
9	17:44118848	17	43919105	rs2106785	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 Eu	NA	17q21.31	ACBD4	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs2106785-T	rs2106785	0	2106785	non_coding_transcript_exon_	0	0.213768	3.00E-13	12.52288		7.29	z score inc	NR [~ 10847151] (imputed)	N
9	17:44118848	17	43919096	rs2106786	28/01/2020	3.2E+07	Zhao B	1/11/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/31676860	Genome-wide association analysis of 19,629 individuals identifies variants influencing regional brain volumes and refines their genetic co-architecture with cognitive and mental health traits.	Brain region volumes	19,629 Bri	NA	17q21.31	NR	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs2106786-?	rs2106786	0	2106786	non_coding_transcript_exon	0	NR	3.00E-08	7.522879	(right pallid	NA		NR [9227495] (imputed)	N
9	17:44118848	17	43919096	rs2106786	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Red blood cell count	172,952 Eu	NA	17q21.31	SPPL2C	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs2106786-G	rs2106786	0	2106786	non_coding_transcript_exon	0	0.2242	3.00E-36	35.52288		0.053745	[0.045-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43953719	rs2214258	1/02/2018	2.9E+07	Luciano M	18/12/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29255261	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism.	Neuroticism	329,821 Eu	122,867 Eu	17q21.31	intergenic	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs2214258-C	rs2214258	0	2214258	intron_variant	0	0.21533	2.00E-25	24.69897		10.415	unit increa	Illumina [18485882] (imputed)	N
9	17:44118848	17	44222019	rs2222746	10/12/2020	3.2E+07	Hollis B	24/03/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32210231	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan.	Male puberty timing (age at voice breaking MTAG)	205,354 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2222746-T	rs2222746	0	2222746	intron_variant	0	NR	9.00E-28	27.04576		0.047722	[0.039-0.0	NR [7400000] (imputed)	N
9	17:44118848	17	44222019	rs2222746	10/12/2020	3.2E+07	Hollis B	24/03/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32210231	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan.	Male puberty timing (early vs. average onset facial hair)	13,226 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2222746-T	rs2222746	0	2222746	intron_variant	0	NR	4.00E-06	5.39794		0.00525	[0.003-0.0	NR [7400000] (imputed)	N
9	17:44118848	17	44222019	rs2222746	10/12/2020	3.2E+07	Hollis B	24/03/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32210231	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan.	Male puberty timing (late vs. average onset facial hair)	26,066 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2222746-T	rs2222746	0	2222746	intron_variant	0	NR	2.00E-30	29.69897		0.016454	[0.014-0.0	NR [7400000] (imputed)	N
9	17:44118848	17	44222019	rs2222746	10/12/2020	3.2E+07	Hollis B	24/03/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32210231	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan.	Male puberty timing (late vs. average onset voice breaking)	11,334 Eu	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2222746-T	rs2222746	0	2222746	intron_variant	0	NR	2.00E-11	10.69897		0.006902	[0.0049-0.	NR [7400000] (imputed)	N
9	17:44118848	17	44354549	rs2261201	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 Eu	NA	17q21.31	NR	ARL17B, ARL17B, ARL17B			ENSG00000275748, E	NA	NA	rs2261201-C	rs2261201	0	2261201	intron_variant	0	0.214631	5.00E-12	11.30103		6.91	z score dec	NR [~ 10847151] (imputed)	N
9	17:44118848	17	44304884	rs2261497	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-a2009s lh area S-orbital-H-Shaped	21,282 Bri	10,685 Bri	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		2129	16088	rs2261497-T	rs2261497	0	2261497	TF_binding_site_variant	1	0.258	5.00E-10	9.30103		0.071	[0.049-0.0	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43919068	rs2316766	21/07/2020	3.2E+07	Grasby KL	1/03/2020	Science	www.ncbi.nlm.nih.gov/pubmed/32193296	The genetic architecture of the human cerebral cortex.	Cortical thickness	33,992 Eu	14,727 Eu	17q21.31	NR	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs2316766-T	rs2316766	0	2316766	non_coding_transcript_exon	0	0.2061	3.00E-07	6.522879	(average)	0.003726	[0.0023-0.	Affymetrix, Illumina [NR]	N
9	17:44118848	17	43733983	rs241033	24/08/2022	3.6E+07	Plotnikov D	1/06/2022	Invest Ophthalmol Vis Sci	www.ncbi.nlm.nih.gov/pubmed/35762941	High Blood Pressure and Intraocular Pressure: A Mendelian Randomization Study.	Systolic blood pressure	526,001 Eu	NA	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs241033-A	rs241033	0	241033	intron_variant	0	NR	5.00E-10	9.30103		0.2944	[0.2-0.39]	NR [NR] (imputed)	N
9	17:44118848	17	43731719	rs241036	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 Eu	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1, LINC02210, LINC			ENSG00000282456, E	NA	NA	rs241036-A	rs241036	0	241036	non_coding_transcript_exon	0	0.217056	8.00E-20	19.09691		9.11	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	43731719	rs241036	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Menarche (age at onset)	approxima	NA	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1, LINC02210, LINC			ENSG00000282456, E	NA	NA	rs241036-?	rs241036	0	241036	non_coding_transcript_exon	0	NR	7.00E-13	12.1549		NA		NR [~ 8900000] (imputed)	N
9	17:44118848	17	44327370	rs2458185	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Salami liking	154,673 Eu	NA	17q21.31		MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		4960	24780	rs2458185-A	rs2458185	0	2458185	downstream_gene_variant	1	0.2116	1.00E-16	16		0.03706	[0.028-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	43665468	rs2458198	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan lh area TotalSurface	21,282 Bri	10,686 Bri	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1173	12767	rs2458198-G	rs2458198	0	2458198	intron_variant	1	0.228	3.00E-22	21.52288		0.112	[0.088-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43665468	rs2458198	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan rh area TotalSurface	21,282 Bri	10,686 Bri	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1173	12767	rs2458198-G	rs2458198	0	2458198	intron_variant	1	0.228	3.00E-24	23.52288		0.118	[0.094-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43665468	rs2458198	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-pial rh area TotalSurface	21,282 Bri	10,686 Bri	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1173	12767	rs2458198-G	rs2458198	0	2458198	intron_variant	1	0.228	1.00E-12	12		0.082	[0.058-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43665468	rs2458198	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP T1 SIENAX white normalised volume	22,138 Bri	11,086 Bri	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1173	12767	rs2458198-G	rs2458198	0	2458198	intron_variant	1	0.228	4.00E-12	11.39794		0.079	[0.057-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43665468	rs2458198	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP T1 SIENAX white unnormalised volume	22,138 Bri	11,086 Bri	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1173	12767	rs2458198-G	rs2458198	0	2458198	intron_variant	1	0.228	2.00E-12	11.69897		0.08	[0.058-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43671737	rs2463523	13/11/2020	3.3E+07	Rashkin SR	4/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32887889	Pan-cancer study detects genetic risk variants and shared genetic basis in two large cohorts.	Breast cancer	17,881 Eu	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7442	6498	rs2463523-A	rs2463523	0	2463523	regulatory_region_variant	1	NR	3.00E-10	9.522879		1.0887	NR	Affymetrix [7846216] (imputed)	N
9	17:44118848	17	43671737	rs2463523	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Ratio of omega-6 fatty acids to omega-3 fatty acids	115,006 Eu	NA	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		7442	6498	rs2463523-A	rs2463523	0	2463523	regulatory_region_variant	1	0.76521	3.00E-17	16.52288		0.040145	[0.031-0.0	NR [11722792] (imputed)	N
9	17:44118848	17	44285531	rs2469933	4/10/2019	3.1E+07	Brazel DM	6/12/2018	Biol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30679032	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol┬áUse.	Alcohol consumption (drinks per week)	up to 357,8	NA	17q21.31	KIAA1267	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2469933-A	rs2469933	0	2469933	intron_variant	0	0.225	2.00E-22	21.69897		0.0295	[0.024-0.0	Illumina [~ 250000] (imputed)	N
9	17:44091886	17	44257783	rs2532252	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan rh area TotalSurface	21,282 Bri	10,686 Bri	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532252-G	rs2532252	0	2532252	intron_variant	0	0.23	2.00E-24	23.69897		0.118	[0.094-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44256296	rs2532253	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Red cell distribution width	408,112 Bi	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532253-A	rs2532253	0	2532253	intron_variant	0	0.196735	2.00E-18	17.69897		0.03246	[0.025-0.0	Affymetrix [93095623] (imputed)	N
9	17:44118848	17	44252468	rs2532263	30/11/2017	2.9E+07	Michailidou K	23/10/2017	Nature	www.ncbi.nlm.nih.gov/pubmed/29059683	Association analysis identifies 65 new breast cancer risk loci.	Breast cancer	76,192 Eu	46,785 Eu	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532263-G	rs2532263	0	2532263	intron_variant	0	0.81	7.00E-13	12.1549	(EA)	1.052632	[1.03-1.08	Illumina [~ 11800000] (imputed)	N
9	17:44118848	17	44252468	rs2532263	2/05/2019	3.1E+07	Hill WD	13/03/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30867560	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life.	General factor of neuroticism	270,059 Bi	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532263-G	rs2532263	0	2532263	intron_variant	0	NR	4.00E-20	19.39794		0.015798	[0.012-0.0	Affymetrix [18485882] (imputed)	N
9	17:44118848	17	44229986	rs2532300	7/06/2022	3.5E+07	Kousathanas A	7/03/2022	Nature	www.ncbi.nlm.nih.gov/pubmed/35255492	Whole genome sequencing reveals host factors underlying critical Covid-19.	COVID-19 (critical illness vs population or mild symptoms)	5,989 Euro	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532300-T	rs2532300	0	2532300	intron_variant	0	NR	2.00E-08	7.69897		NA		Illumina [NR]	N
9	17:44118848	17	44229986	rs2532300	7/06/2022	3.5E+07	Kousathanas A	7/03/2022	Nature	www.ncbi.nlm.nih.gov/pubmed/35255492	Whole genome sequencing reveals host factors underlying critical Covid-19.	COVID-19 (critical illness vs population or mild symptoms)	5,989 Euro	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs2532300-T	rs2532300	0	2532300	intron_variant	0	0.77	4.00E-09	8.39794		1.2	[1.1-1.22]	Illumina [8121457]	N
9	17:44118848	17	44339473	rs2532349	13/09/2019	2.6E+07	Wain LV	27/09/2015	Lancet Respir Med	www.ncbi.nlm.nih.gov/pubmed/26423011	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank.	Lung function in never smokers (low FEV1 vs high FEV1)	9,745 Euro	NA	17q21.31	KANSL1	MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		17063	12677	rs2532349-G	rs2532349	0	2532349	intergenic_variant	1	0.242	2.00E-10	9.69897		1.22	[1.15-1.29	Affymetrix [28509962] (imputed)	N
9	17:44118848	17	44317210	rs2532384	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Goat cheese liking	150,875 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		14455	3762	rs2532384-A	rs2532384	0	2532384	upstream_gene_variant	1	0.2237	2.00E-17	16.69897		0.03695	[0.028-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	44313757	rs2532386	26/11/2020	3.3E+07	Bi W	23/06/2020	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/32589924	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank.	Osteoarthrosis (time to event)	29,071 Bri	NA	17q21.31	KANSL1, LRRC37	KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		11002	7215	rs2532386-?	rs2532386	0	2532386	regulatory_region_variant	1	NR	4.00E-08	7.39794		NA		NR [~ 24000000] (imputed)	N
9	17:44118848	17	44313522	rs2532387	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-sharp flavour liking (derived food-liking factor)	152,547 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		10767	7450	rs2532387-T	rs2532387	0	2532387	regulatory_region_variant	1	0.2169	5.00E-25	24.30103		0.11162	[0.09-0.13	Affymetrix [9605914] (imputed)	N
9	17:44118848	17	44313522	rs2532387	13/12/2021	3.4E+07	Kachuri L	26/08/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/34469753	Genetic determinants of blood-cell traits influence susceptibility to childhood acute lymphoblastic leukemia.	Lymphocyte-to-monocyte ratio	234,184 Eu	100,284 Eu	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		10767	7450	rs2532387-G	rs2532387	0	2532387	regulatory_region_variant	1	0.781	1.00E-19	19		NA		Affymetrix [10369434] (imputed)	N
9	17:44118848	17	44311107	rs2532389	13/11/2020	3.3E+07	Rashkin SR	4/09/2020	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/32887889	Pan-cancer study detects genetic risk variants and shared genetic basis in two large cohorts.	Cancer (pleiotropy)	64,962 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		8352	9865	rs2532389-G	rs2532389	0	2532389	intergenic_variant	1	NR	1.00E-09	9		1.074	[1.05-1.09	Affymetrix [7846216] (imputed)	N
9	17:44118848	17	44307193	rs2532395	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Brussel sprout liking	159,493 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		4438	13779	rs2532395-T	rs2532395	0	2532395	upstream_gene_variant	1	0.2126	1.00E-22	22		0.04292	[0.034-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	44304130	rs2532402	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Horseradish liking	152,847 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		1375	16842	rs2532402-G	rs2532402	0	2532402	upstream_gene_variant	1	0.2226	1.00E-14	14		0.03378	[0.025-0.0	Affymetrix [11353280] (imputed)	N







9	17:44118848	17	44018488	rs62061734	30/11/2017	2.9E+07	Michailidou K	23/10/2017	Nature	www.ncbi.nlm.nih.gov/pubmed/29059683	Association analysis identifies 65 new breast cancer risk loci.	Breast cancer	76,192 Eur	46,785 Eur	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62061734-C	rs62061734	0	62061734	intron_variant	0	0.2103	8.00E-12	11.09691	(EA)	0.0526	[0.038-0.0	Illumina [~ 11800000] (imputed)	N
9	17:44118848	17	44018488	rs62061734	25/06/2019	3.1E+07	Jansen PR	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804565	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways.	Sleep duration	384,317 Eu	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62061734-C	rs62061734	0	62061734	intron_variant	0	0.2205	2.00E-09	8.69897		0.01775	[0.012-0.0	Affymetrix, Illumina [10862567] (imputed)	N
9	17:44118848	17	44096553	rs62062288	14/12/2018	3E+07	Sanchez-Roige S	19/10/2018	Am J Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30336701	Genome-Wide Association Study Meta-Analysis of the Alcohol Use Disorders Identification Test (AUDIT) in Two Population-Based Cohorts.	Alcohol use disorder (consumption score)	121,604 Bi	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	NR	2.00E-09	8.69897		0.008	[0.006-0.0	NR [16213998]	N
9	17:44118848	17	44096553	rs62062288	7/09/2021	3.4E+07	Dao C	16/04/2021	Addiction	www.ncbi.nlm.nih.gov/pubmed/33861876	The Impact of Removing Former Drinkers from Genome-wide Association Studies of AUDIT-C.	Alcohol use disorder (consumption score)	5,135 Euro	NR	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-?	rs62062288	0	62062288	intron_variant	0	NR	2.00E-14	13.69897		0.097	[0.072-0.1	NR [7682250] (imputed)	N
9	17:44118848	17	44096553	rs62062288	14/12/2018	3E+07	Sanchez-Roige S	19/10/2018	Am J Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30336701	Genome-Wide Association Study Meta-Analysis of the Alcohol Use Disorders Identification Test (AUDIT) in Two Population-Based Cohorts.	Alcohol use disorder (total score)	141,932 Eu	NA	17q21.31	CRHR1, DND1P1,	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	NR	5.00E-10	9.30103		6.21	[NR] z scor	NR [16213998]	N
9	17:44118848	17	44096553	rs62062288	18/03/2019	3.1E+07	Karlsson Linner R	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643258	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences.	Automobile speeding propensity	404,291 Eu	NA	17q21.31	KANSL1	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.2196	1.00E-12	12		0.019352	[0.014-0.0	Affymetrix [11514463] (imputed)	N
9	17:44118848	17	44096553	rs62062288	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling guilty	373,380 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.211505	7.00E-10	9.154902		6.17	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44096553	rs62062288	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling worry	372,869 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.211505	1.00E-09	9		6.079	unit increa	NR [10847151] (imputed)	N
9	17:44118848	17	44096553	rs62062288	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Neurociticism	380,506 Eu	NA	17q21.31	STH	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.211505	6.00E-32	31.22185		11.77	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44096553	rs62062288	29/05/2020	3.2E+07	Cai N	30/03/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/32231276	Minimal phenotyping yields genome-wide association signals of low specificity for major depression.	Neuroticism	274,107 Bi	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.2181	7.00E-22	21.1549		0.01863	[0.015-0.0	NR [8968716] (imputed)	N
9	17:44118848	17	44096553	rs62062288	18/03/2019	3.1E+07	Karlsson Linner R	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643258	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences.	Risk-taking tendency (4-domain principal component model)	315,894 Eu	NA	17q21.31	KANSL1	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.2207	1.00E-29	29		0.035171	[0.029-0.0	Affymetrix [~ 11515000] (imputed)	N
9	17:44118848	17	44096553	rs62062288	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Worry too long after an embarrassing experience	367,725 Eu	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062288-A	rs62062288	0	62062288	intron_variant	0	0.211505	4.00E-08	7.39794		5.5	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44027366	rs62062797	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔÇë=ÔÇë17,706).	White matter microstructure (fractional anisotropy)	17,706 Eur	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62062797-?	rs62062797	0	62062797	intron_variant	0		5.00E-11	10.30103	(Anterior li	NA		NR [8955960] (imputed)	N
9	17:44118848	17	44038785	rs62063281	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-strong vegetable liking (derived food-liking factor)	147,344 Eu	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063281-G	rs62063281	0	62063281	intron_variant	0	0.2192	8.00E-13	12.09691		0.08345	[0.061-0.1	Affymetrix [9601173] (imputed)	N
9	17:44118848	17	44038785	rs62063281	18/03/2019	3.1E+07	Karlsson Linner R	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643258	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences.	Number of sexual partners	370,711 Eu	NA	17q21.31	STH	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063281-A	rs62063281	0	62063281	intron_variant	0	0.7784	4.00E-15	14.39794		0.02236	[0.017-0.0	Affymetrix [11515109] (imputed)	N
9	17:44118848	17	44038785	rs62063281	8/02/2019	3.1E+07	Tachmazidou I	21/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30664745	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data.	Osteoarthritis (hip)	15,704 Eur	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063281-G	rs62063281	0	62063281	intron_variant	0	0.22	5.00E-12	11.30103		1.1	[1.07-1.13	Affymetrix, Illumina [up to 17000000] (imputed)	N
9	17:44118848	17	44038785	rs62063281	26/11/2020	3.3E+07	Bi W	23/06/2020	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/32589924	A Fast and Accurate Method for Genome-Wide Time-to-Event Data Analysis and Its Application to UK Biobank.	Osteoarthrosis (time to event)	29,071 Brit	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063281-?	rs62063281	0	62063281	intron_variant	0	NR	3.00E-08	7.522879		NA		NR [~ 24000000] (imputed)	N
9	17:44118848	17	44038785	rs62063281	17/11/2022	3.6E+07	Baselmans B	6/10/2021	Biol Psychiatry Glob Open Sci	www.ncbi.nlm.nih.gov/pubmed/36324656	The Genetic and Neural Substrates of Externalizing Behavior.	Risk-taking behavior (multivariate analysis)	1,506,537	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063281-?	rs62063281	0	62063281	intron_variant	0	NR	3.00E-26	25.52288		NA		NR [NR]	N
9	17:44118848	17	44061023	rs62063786	17/06/2020	3.2E+07	Oskarsson GR	23/04/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/32327693	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis.	Hemoglobin levels	684,122 Eu	NA	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62063786-A	rs62063786	0	62063786	missense_variant	0		1.00E-61	61		0.044	[NR] unit in	Affymetrix, Illumina [43000000] (imputed)	N
9	17:44118848	17	43654468	rs62064364	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L3 Anterior limb of internal capsule L	20,860 Brit	10,496 Brit	17q21.31		RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		18032	8769	rs62064364-T	rs62064364	0	62064364	intron_variant	1	0.22	2.00E-28	27.69897		0.132	[0.11-0.16	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43654468	rs62064364	28/01/2019	3.1E+07	Gao XR	7/12/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30535121	Genome-wide association analyses identify 139 loci associated with macular thickness in the UK Biobank cohort.	Macular thickness	59,814 Eur	8,609 Euro	17q21.31	LRRC37A4P, MAF	RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		18032	8769	rs62064364-?	rs62064364	0	62064364	intron_variant	1	NR	4.00E-35	34.39794		0.978	[0.81-1.14	Affymetrix [11100000] (imputed)	N
9	17:44118848	17	43654468	rs62064364	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔÇë=ÔÇë17,706).	White matter microstructure (axial diusivities)	17,706 Eur	NA	17q21.31	NR	RDM1P1 - DND1P	ENSG00000266504	ENSG00000282614		18032	8769	rs62064364-?	rs62064364	0	62064364	intron_variant	1		5.00E-10	9.30103	(External c	NA		NR [8955960] (imputed)	N
9	17:44118848	17	43666001	rs62064395	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI ProbtrackX MD str l	20,860 Brit	10,495 Brit	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1706	12234	rs62064395-C	rs62064395	0	62064395	intergenic_variant	1	0.233	4.00E-14	13.39794		0.088	[0.064-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43666001	rs62064395	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L2 Genu of corpus callosum	20,860 Brit	10,496 Brit	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1706	12234	rs62064395-C	rs62064395	0	62064395	intergenic_variant	1	0.233	3.00E-15	14.52288		0.092	[0.068-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43666001	rs62064395	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L3 Genu of corpus callosum	20,860 Brit	10,496 Brit	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1706	12234	rs62064395-C	rs62064395	0	62064395	intergenic_variant	1	0.233	5.00E-15	14.30103		0.091	[0.067-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43666001	rs62064395	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Anterior corona radiata L	20,860 Brit	10,496 Brit	17q21.31		DND1P1 - MAPK8	ENSG00000282614	ENSG00000263503		1706	12234	rs62064395-C	rs62064395	0	62064395	intergenic_variant	1	0.233	1.00E-16	16		0.096	[0.072-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43473307	rs62064597	24/08/2022	3.6E+07	Plotnikov D	1/06/2022	Invest Ophthalmol Vis Sci	www.ncbi.nlm.nih.gov/pubmed/35762941	High Blood Pressure and Intraocular Pressure: A Mendelian Randomization Study.	Systolic blood pressure	526,001 Eu	NA	17q21.31		ARHGAP27			ENSG00000159314	NA	NA	rs62064597-C	rs62064597	0	62064597	intron_variant	0	NR	6.00E-10	9.221849		0.2971	[0.2-0.39]	NR [NR] (imputed)	N
9	17:43556807	17	43474668	rs62064598	2/05/2019	3.1E+07	Hill WD	13/03/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/30867560	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life.	General factor of neuroticism	270,059 Bi	NA	17q21.31	ENSG000002673	ARHGAP27			ENSG00000159314	NA	NA	rs62064598-C	rs62064598	0	62064598	intron_variant	0	NR	3.00E-15	14.52288		0.013541	[0.01-0.01	Affymetrix [18485882] (imputed)	N
9	17:43556807	17	43488792	rs62064641	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	White blood cell count	approxima	NA	17q21.31		ARHGAP27			ENSG00000159314	NA	NA	rs62064641-?	rs62064641	0	62064641	intron_variant	0	NR	1.00E-13	13		NA		NR [~ 8900000] (imputed)	N
9	17:43556807	17	43488792	rs62064641	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Worry	348,219 Eu	NA	17q21.31	NR	ARHGAP27			ENSG00000159314	NA	NA	rs62064641-C	rs62064641	0	62064641	intron_variant	0	NR	2.00E-11	10.69897		0.02055	[0.015-0.0	Affymetrix [10847151] (imputed)	N
9	17:44118848	17	44082528	rs62064667	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 Anterior corona radiata L	20,860 Brit	10,496 Brit	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs62064667-T	rs62064667	0	62064667	intron_variant	0	0.224	2.00E-13	12.69897		0.087	[0.063-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43573061	rs62065452	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan rh area lateraloccipital	21,282 Brit	10,686 Brit	17q21.31		PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		4946	11046	rs62065452-C	rs62065452	0	62065452	intergenic_variant	1	0.223	3.00E-14	13.52288		0.088	[0.064-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43573061	rs62065452	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan rh volume fusiform	21,282 Brit	10,686 Brit	17q21.31		PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		4946	11046	rs62065452-C	rs62065452	0	62065452	intergenic_variant	1	0.223	6.00E-10	9.221849		0.072	[0.048-0.0	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43573061	rs62065452	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-DKTatlas rh area lateraloccipital	21,282 Brit	10,686 Brit	17q21.31		PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		4946	11046	rs62065452-C	rs62065452	0	62065452	intergenic_variant	1	0.223	2.00E-14	13.69897		0.089	[0.065-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43573419	rs62065453	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling nervous	373,121 Eu	NA	17q21.31	NR	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		5304	10688	rs62065453-T	rs62065453	0	62065453	intron_variant	1	0.217174	6.00E-15	14.22185		7.81	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	43573419	rs62065453	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 Eu	NA	17q21.31	NR	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		5304	10688	rs62065453-T	rs62065453	0	62065453	intron_variant	1	0.217174	3.00E-12	11.52288		6.99	z score inc	NR [~ 10847151] (imputed)	N
9	17:44118848	17	43573419	rs62065453	9/06/2021	3.4E+07	Pazoki R	10/05/2021	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/33972514	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes.	Liver enzyme levels (alkaline phosphatase)	437,438 Eu	315,572 Eu	17q21.31	PLEKHM1	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		5304	10688	rs62065453-C	rs62065453	0	62065453	intron_variant	1	0.774564	2.00E-17	16.69897		0.002322	[0.0018-0.	Affymetrix [13995440] (imputed)	N
9	17:44118848	17	43573419	rs62065453	1/02/2018	2.9E+07	Luciano M	18/12/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29255261	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism.	Neuroticism	329,821 Eu	122,867 Eu	17q21.31	intergenic	PLEKHM1 - LRRC	ENSG00000277111	ENSG00000282331		5304	10688	rs62065453-T	rs62065453	0	62065453	intron_variant	1	0.21717	2.00E-24	23.69897		10.227	unit increa	Illumina [18485882] (imputed)	N
9	17:44118848	17	43688042	rs62066084	4/08/2022	3.6E+07	Fan CC	3/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35505052	Multivariate genome-wide association study on tissue-sensitive diffusion metrics highlights pathways that shape the human brain.	Whole brain free water diffusion (multivariate analysis)	23,543 Eur	11,555 Eur	17q21.31		RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		1758	9652	rs62066084-?	rs62066084	0	62066084	downstream_gene_variant	1	NR	4.00E-57	56.39794		NA		NR [NR] (imputed)	N
9	17:44118848	17	44308053	rs62070949	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan rh area fusiform	21,282 Brit	10,686 Brit	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		5298	12919	rs62070949-G	rs62070949	0	62070949	intergenic_variant	1	0.157	5.00E-26	25.30103		0.155	[0.13-0.18	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44308053	rs62070949	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-DKTatlas rh area fusiform	21,282 Brit	10,686 Brit	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		5298	12919	rs62070949-G	rs62070949	0	62070949	intergenic_variant	1	0.157	3.00E-24	23.52288		0.15	[0.12-0.18	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44308053	rs62070949	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-pial rh area fusiform	21,282 Brit	10,686 Brit	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		5298	12919	rs62070949-G	rs62070949	0	62070949	intergenic_variant	1	0.157	3.00E-18	17.52288		0.128	[0.099-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44316491	rs62073099	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-bitter food liking (derived food-liking factor)	157,485 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		13736	4481	rs62073099-C	rs62073099	0	62073099	upstream_gene_variant	1	0.1997	2.00E-10	9.69897		0.02904	[0.02-0.03	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	44316491	rs62073099	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-strong flavour liking (derived food-liking factor)	153,924 Eu	NA	17q21.31		KANSL1 - MAPK8I	ENSG00000278458	ENSG00000282723		13736	4481	rs62073099-C	rs62073099	0	62073099	upstream_gene_variant	1	0.1996	1.00E-16	16		0.09416	[0.072-0.1	Affymetrix [9535166] (imputed)	N
9	17:44118848	17	44388912	rs62073233	27/04/2022	3.5E+07	Richardson TG	25/02/2022	PLoS Biol	www.ncbi.nlm.nih.gov/pubmed/35213538	Characterising metabolomic signatures of lipid-modifying therapies through drug target mendelian randomisation.	Glucose levels	114,870 Eu	NA	17q21.31		LRRC37A, LRRC37A, ARL17B, ARL17B, ARL17B			ENSG00000176681, E	NA	NA	rs62073233-G	rs62073233	0	62073233	intron_variant	0	0.78721	2.00E-09	8.69897		0.033992	[0.023-0.0	NR [11722792] (imputed)	N

9	17:44118848	17	43696159	rs675600	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Granulocyte count	169,822 E	NA	17q21.31	CRHR1-IT1, CRHI	RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		9875	1535	rs675600-T	rs675600	0	675600	intergenic_variant	1	0.2046	5.00E-09	8.30103		0.026739	[0.018-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43696159	rs675600	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Myeloid white cell count	169,219 E	NA	17q21.31	CRHR1-IT1, CRHI	RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		9875	1535	rs675600-T	rs675600	0	675600	intergenic_variant	1	0.2046	3.00E-09	8.522879		0.027331	[0.018-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43696159	rs675600	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Neutrophil count	170,702 E	NA	17q21.31	CRHR1-IT1, CRHI	RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		9875	1535	rs675600-T	rs675600	0	675600	intergenic_variant	1	0.2045	3.00E-11	10.52288		0.030358	[0.021-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43696159	rs675600	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Sum basophil neutrophil counts	170,143 E	NA	17q21.31	CRHR1-IT1, CRHI	RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		9875	1535	rs675600-T	rs675600	0	675600	intergenic_variant	1	0.2046	2.00E-11	10.69897		0.030561	[0.022-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43696159	rs675600	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Sum neutrophil eosinophil counts	170,384 E	NA	17q21.31	CRHR1-IT1, CRHI	RPS26P8 - LINC0	ENSG00000282238	ENSG00000204650		9875	1535	rs675600-T	rs675600	0	675600	intergenic_variant	1	0.2045	6.00E-09	8.221849		0.026524	[0.018-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	44860021	rs70600	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Irritable mood	366,726 E	NA	17q21.31	NR	WNT3			ENSG00000108379	NA	NA	rs70600-T	rs70600	0	70600	intron_variant	0	0.20718	3.00E-11	10.52288		6.65	z score inc	NR [~ 10847151] (imputed)	N
9	17:44118848	17	44332793	rs71375338	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Neutrophil count	408,112 B	NA	17q21.31	RP11-259G18.3	MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		10383	19357	rs71375338-A	rs71375338	0	71375338	intergenic_variant	1	0.268548	3.00E-20	19.52288		0.023167	[0.018-0.0	Affymetrix [93095623] (imputed)	N
9	17:44118848	17	44332793	rs71375338	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Neutrophil count	627,215 A	NA	17q21.31	NR	MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		10383	19357	rs71375338-A	rs71375338	0	71375338	intergenic_variant	1	0.259541	3.00E-22	21.52288		NA		Affymetrix, Illumina [23114412] (imputed)	N
9	17:44118848	17	44332793	rs71375338	13/12/2021	3.4E+07	Kachuri L	26/08/2021	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/34469753	Genetic determinants of blood-cell traits influence susceptibility to childhood acute lymphoblastic leukemia.	Neutrophil-to-lymphocyte ratio	234,502 E	100,442 E	17q21.31		MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		10383	19357	rs71375338-G	rs71375338	0	71375338	intergenic_variant	1	0.73	3.00E-16	15.52288		NA		Affymetrix [10369434] (imputed)	N
9	17:43520118	17	43484598	rs73984391	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L3 Anterior corona radiata L	20,860 Brit	10,496 Brit	17q21.31		ARHGAP27			ENSG00000159314	NA	NA	rs73984391-T	rs73984391	0	73984391	intron_variant	0	0.182	2.00E-10	9.69897		0.081	[0.056-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44260845	rs74693982	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI ProbtrackX L1 slf l	20,860 Brit	10,495 Brit	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs74693982-A	rs74693982	0	74693982	intron_variant	0	0.19	9.00E-09	8.045757		0.076	[0.051-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43810873	rs75022332	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Worry too long after an embarrassing experience	367,725 E	NA	17q21.31	ACBD4	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs75022332-A	rs75022332	0	75022332	non_coding_transcript_exon	0	0.213608	2.00E-08	7.69897		5.62	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	44357654	rs75067210	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Beans liking	159,014 E	NA	17q21.31		ARL17B, ARL17B, ARL17B			ENSG00000275748, E	NA	NA	rs75067210-T	rs75067210	0	75067210	intron_variant	0	0.1805	1.00E-09	9		0.09898	[0.067-0.1	Affymetrix [9618863] (imputed)	N
9	17:44118848	17	44357654	rs75067210	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	Broad bean liking	158,921 E	NA	17q21.31		ARL17B, ARL17B, ARL17B			ENSG00000275748, E	NA	NA	rs75067210-T	rs75067210	0	75067210	intron_variant	0	0.1805	3.00E-10	9.522879		0.03108	[0.021-0.0	Affymetrix [11353280] (imputed)	N
9	17:44118848	17	43973233	rs76324150	28/05/2020	3.2E+07	Hysi PG	30/03/2020	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/32231278	Meta-analysis of 542,934 subjects of European ancestry identifies new genes and mechanisms predisposing to refractive error and myopia.	Refractive error	542,934 E	NA	17q21.31	ARHGAP27, MAPT	MAPT-IT1, MAPT-IT1, MAPT-IT1, MAPT, MAPT, MAPT			ENSG00000281284, E	NA	NA	rs76324150-?	rs76324150	0	76324150	non_coding_transcript_exon	0		8.00E-16	15.09691		NA		Affymetrix, Illumina [NR] (imputed)	N
9	17:44118848	17	43758887	rs76539714	24/10/2022	3.4E+07	Harrison S	28/07/2021	Sci Adv	www.ncbi.nlm.nih.gov/pubmed/34321204	Testosterone and socioeconomic position: Mendelian randomization in 306,248 men and women in UK Biobank.	Albumin levels	158,000 B	NA	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs76539714-G	rs76539714	0	76539714	intron_variant	0	0.23	4.00E-10	9.39794		0.09	[0.061-0.1	Affymetrix [NR] (imputed)	N
9	17:44118848	17	43758887	rs76539714	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-Desikan lh area fusiform	21,282 Brit	10,686 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs76539714-G	rs76539714	0	76539714	intron_variant	0	0.224	1.00E-22	22		0.114	[0.09-0.13	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43758887	rs76539714	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-DKTatlas lh area fusiform	21,282 Brit	10,686 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs76539714-G	rs76539714	0	76539714	intron_variant	0	0.224	4.00E-23	22.39794		0.116	[0.092-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43758887	rs76539714	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 External capsule R	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs76539714-G	rs76539714	0	76539714	intron_variant	0	0.224	6.00E-15	14.22185		0.092	[0.068-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44189858	rs76640332	30/08/2017	2.8E+07	Astle WJ	17/11/2016	Cell	www.ncbi.nlm.nih.gov/pubmed/27863252	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease.	Lymphocyte percentage of white cells	171,748 E	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs76640332-A	rs76640332	0	76640332	intron_variant	0	0.222	5.00E-13	12.30103		0.030675	[0.022-0.0	Affymetrix [~ 2500000] (imputed)	N
9	17:44118848	17	43776741	rs76761706	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Neurociticism	380,506 E	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs76761706-T	rs76761706	0	76761706	intron_variant	0	0.215553	7.00E-32	31.1549		11.76	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	43658409	rs769375	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L3 Superior fronto-occipital fasciculus L	20,860 Brit	10,496 Brit	17q21.31		LRRC37A4P, LRRC37A4P			ENSG00000214425, E	NA	NA	rs769375-A	rs769375	0	769375	intron_variant	0	0.211	7.00E-11	10.1549		0.078	[0.054-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43810896	rs77804065	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Feeling guilty	373,380 E	NA	17q21.31	ACBD4	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs77804065-T	rs77804065	0	77804065	splice_region_variant	0	0.217158	6.00E-10	9.221849		6.18	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	43810896	rs77804065	1/03/2018	2.9E+07	Meng W	31/01/2018	EBioMedicine	www.ncbi.nlm.nih.gov/pubmed/29397368	A Genome-Wide Association Study Finds Genetic Associations with Broadly-Defined Headache in UK Biobank (N=223,773).	Headache	74,461 Brit	NA	17q21.31	LINC02210, CRH	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs77804065-T	rs77804065	0	77804065	splice_region_variant	0	NR	6.00E-15	14.22185		0.013	[0.0097-0.	Affymetrix [9304965] (imputed)	N
9	17:44118848	17	43810896	rs77804065	18/09/2019	3.1E+07	Gelernter J	8/04/2019	Biol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31151762	Genome-wide Association Study of Maximum Habitual Alcohol Intake in >140,000 U.S. European and African American Veterans Yields Novel Risk Loci.	Maximum habitual alcohol consumption	126,936 E	NA	17q21.31	CRHR1	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs77804065-T	rs77804065	0	77804065	splice_region_variant	0	NR	2.00E-12	11.69897	(EA)	0.0711	NR unit dec	Affymetrix [up to 6007810] (imputed)	N
9	17:44118848	17	43810896	rs77804065	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Neuroticism	449,484 E	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs77804065-T	rs77804065	0	77804065	splice_region_variant	0	NR	1.00E-31	31		11.693	z score inc	Affymetrix [10847151] (imputed)	N
9	17:44118848	17	43810896	rs77804065	1/02/2018	2.9E+07	Luciano M	18/12/2017	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29255261	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism.	Neuroticism	329,821 E	122,867 E	17q21.31	ARHGAP27, CRHI	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs77804065-T	rs77804065	0	77804065	splice_region_variant	0	0.21716	8.00E-26	25.09691		10.503	unit increa	Illumina [18485882] (imputed)	N
9	17:44118848	17	44051612	rs77875796	29/04/2022	3.5E+07	Ko H	6/10/2021	Brain	www.ncbi.nlm.nih.gov/pubmed/34613391	Genome-wide association study of occupational attainment as a proxy for cognitive reserve.	Occupational attainment	248,847 E	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs77875796-G	rs77875796	0	77875796	5_prime_UTR_variant	0	0.241	5.00E-09	8.30103		0.049	[0.033-0.0	Affymetrix [9575249] (imputed)	N
9	17:44118848	17	44339607	rs77917260	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 External capsule L	20,860 Brit	10,496 Brit	17q21.31		MAPK8IP1P1 - AR	ENSG00000282723	ENSG00000228696		17197	12543	rs77917260-T	rs77917260	0	77917260	regulatory_region_variant	1	0.212	1.00E-16	16		0.1	[0.076-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44290850	rs78826239	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	aparc-a2009s rh area G-oc-temp-lat-fusifor	21,282 Brit	10,686 Brit	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs78826239-A	rs78826239	0	78826239	intron_variant	0	0.202	2.00E-11	10.69897		0.084	[0.059-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44189910	rs78929339	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Medication use (anilides)	83,218 Eur	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs78929339-G	rs78929339	0	78929339	intron_variant	0	NR	9.00E-13	12.04576		0.0559	[0.041-0.0	Affymetrix, Illumina [15248280] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Superior fronto-occipital fasciculus L	20,859 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	2.00E-23	22.69897		0.126	[0.1-0.15]	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Superior fronto-occipital fasciculus R	20,859 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	3.00E-27	26.52288		0.137	[0.11-0.16	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L1 Superior fronto-occipital fasciculus R	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	8.00E-13	12.09691		0.091	[0.066-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS L2 Superior fronto-occipital fasciculus L	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	1.00E-11	11		0.086	[0.061-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Superior corona radiata L	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	2.00E-12	11.69897		0.089	[0.064-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Superior fronto-occipital fasciculus L	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	3.00E-13	12.52288		0.092	[0.067-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43828764	rs79172804	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS MD Superior fronto-occipital fasciculus R	20,860 Brit	10,496 Brit	17q21.31		LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79172804-A	rs79172804	0	79172804	intron_variant	0	0.189	2.00E-18	17.69897		0.111	[0.086-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	44207932	rs79301522	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Neurociticism	380,506 E	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs79301522-A	rs79301522	0	79301522	intron_variant	0	0.217029	1.00E-30	30		11.51	z score dec	NR [10847151] (imputed)	N
9	17:44118848	17	43940021	rs79412431	27/03/2019	3.1E+07	Shrine N	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804560	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries.	FEV1	321,047 E	79,005 Eur	17q21.31	MAPT-AS1	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs79412431-A	rs79412431	0	79412431	intron_variant	0	0.2161	3.00E-49	48.52288		0.0426	[0.037-0.0	Affymetrix [19819130] (imputed)	N
9	17:44118848	17	43940021	rs79412431	27/03/2019	3.1E+07	Shrine N	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804560	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries.	Lung function (FVC)	321,047 E	79,005 Eur	17q21.31	MAPT-AS1	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs79412431-A	rs79412431	0	79412431	intron_variant	0	0.2161	3.00E-46	45.52288		0.0415	[0.036-0.0	Affymetrix [19819130] (imputed)	N
9	17:44118848	17	43940021	rs79412431	27/03/2019	3.1E+07	Shrine N	25/02/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30804560	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries.	Peak expiratory flow	321,047 E	24,218 Eur	17q21.31	MAPT-AS1	MAPT-AS1, MAPT-AS1, MAPT-AS1			ENSG00000264589, E	NA	NA	rs79412431-A	rs79412431	0	79412431	intron_variant	0	0.2161	6.00E-15	14.22185		0.0239	[0.018-0.0	Affymetrix [19819130] (imputed)	N
9	17:44118848	17	43897722	rs79600142	21/07/2020	3.2E+07	Grasby KL	1/03/2020	Science	www.ncbi.nlm.nih.gov/pubmed/32193296	The genetic architecture of the human cerebral cortex.	Cortical surface area	33,992 Eur	14,727 Eur	17q21.31	NR	MAPT-AS1, MAPT-AS1, MAPT-AS1, CRHR1, CRHR1, CRHR1, L			ENSG00000264589, E	NA	NA	rs79600142-T	rs79600142	0	79600142	intron_variant	0	0.79	1.00E-43	43	(total)	1414.626	[1214.65-1	Affymetrix, Illumina [NR]	N
9	17:44118848	17	43463493	rs79724577	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI ProbtrackX MD atr l	20,860 Brit	10,495 Brit	17q21.31		RNA5SP443 - ARI	ENSG00000199953	ENSG00000159314		58630	7775	rs79724577-C	rs79724577	0	79724577	regulatory_region_variant	1	0.181	9.00E-13	12.04576		0.091	[0.066-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43463493	rs79724577	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Anterior corona radiata R	20,859 Brit	10,496 Brit	17q21.31		RNA5SP443 - ARI	ENSG00000199953	ENSG00000159314		58630	7775	rs79724577-C	rs79724577	0	79724577	regulatory_region_variant	1	0.181	1.00E-14	14		0.099	[0.074-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43463493	rs79724577	31/05/2022	3.4E+07	Smith SM	19/04/2021	Nat Neurosci	www.ncbi.nlm.nih.gov/pubmed/33875891	An expanded set of genome-wide association studies of brain imaging phenotypes in UK Biobank.	IDP dMRI TBSS ICVF Retrolenticular part of internal capsule L	20,859 Brit	10,496 Brit	17q21.31		RNA5SP443 - ARI	ENSG00000199953	ENSG00000159314		58630	7775	rs79724577-C	rs79724577	0	79724577	regulatory_region_variant	1	0.181	3.00E-13	12.52288		0.093	[0.068-0.1	Affymetrix [17103079] (imputed)	N
9	17:44118848	17	43849415	rs79730878	28/01/2019	3.1E+07	Morris JA	31/12/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30598549	An atlas of genetic influences on osteoporosis in humans and mice.	Heel bone mineral density	426,824 B	NA	17q21.31	CRHR1-IT1-CRHF	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs79730878-T	rs79730878	0	79730878	intron_variant	0	0.771203	6.00E-20	19.22185		0.020214	[0.016-0.0	NR [13737936] (imputed)	N

9	17:44118848	17	43657257	rs79742625	20/05/2019	3.1E+07	Dudding T	5/03/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/30837455	Genome wide analysis for mouth ulcers identifies associations at immune regulatory loci.	Mouth ulcers	47,079 Brit	98,298 cas	17q21.31		RDM1P1 - DND1F	ENSG00000266504	ENSG00000282614		20821	5980	rs79742625-T	rs79742625	0	79742625	intron_variant	1	0.192862	3.00E-18	17.52288		1.060499	[1.04-1.08]	Affymetrix, Illumina [9851866] (imputed)	N
9	17:44118848	17	44013475	rs79857651	22/01/2019	3E+07	Nagel M	2/03/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29500382	Item-level analyses reveal genetic heterogeneity in neuroticism.	Experiencing mood swings	373,733 E	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs79857651-A	rs79857651	0	79857651	intron_variant	0	0.215594	9.00E-20	19.04576		9.1	z score inc	NR [10847151] (imputed)	N
9	17:44118848	17	44161470	rs80028338	4/08/2022	3.6E+07	May-Wilson S	18/05/2022	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/35585065	Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.	F-savoury food liking (derived food-liking factor)	157,915 E	NA	17q21.31		KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs80028338-C	rs80028338	0	80028338	intron_variant	0	0.2051	1.00E-12	12		0.10169	[0.074-0.1	Affymetrix [9551341] (imputed)	N
9	17:44118848	17	44161470	rs80028338	5/02/2020	3.2E+07	Zhao B	30/10/2019	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/31666681	Large-scale GWAS reveals genetic architecture of brain white matter microstructure and genetic overlap with cognitive and mental health traits (nÔCë=ÔCë17,706).	White matter microstructure (fractional anisotropy)	17,706 Eur	NA	17q21.31	NR	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs80028338-?	rs80028338	0	80028338	intron_variant	0		4.00E-08	7.39794	(Average a	NA		NR [8955960] (imputed)	N
9	17:44118848	17	44224940	rs80103986	2/02/2018	2.9E+07	Willems SM	12/07/2017	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29313844	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness.	Hand grip strength	142,035 E	53,145 Eur	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs80103986-A	rs80103986	0	80103986	intron_variant	0	0.805	1.00E-09	9		0.171	[0.12-0.23]	Affymetrix [at least 17000000] (imputed)	N
9	17:44118848	17	43776742	rs80143279	7/07/2020	3.2E+07	Nagel M	23/01/2020	Acta Psychiatr Scand	www.ncbi.nlm.nih.gov/pubmed/31972866	Genome-wide association study of the sensitivity to environmental stress and adversity (SESA) neuroticism cluster.	Sensitivity to environmental stress and adversity	351,827 E	NA	17q21.31	NR	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs80143279-C	rs80143279	0	80143279	intron_variant	0	NR	8.00E-22	21.09691		0.02682	NR unit inc	NR [7259579]	N
9	17:44118848	17	44081064	rs8070723	5/04/2022	3.5E+07	Pasman JA	2/12/2021	Behav Genet	www.ncbi.nlm.nih.gov/pubmed/34855049	Genetic Risk for Smoking: Disentangling Interplay Between Genes and Socioeconomic Status.	Lifetime smoking	272,943 E	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs8070723-?	rs8070723	0	8070723	intron_variant	0	NR	5.00E-08	7.30103		NA		NR [1300000]	N
9	17:44118848	17	44081064	rs8070723	5/04/2022	3.5E+07	Pasman JA	2/12/2021	Behav Genet	www.ncbi.nlm.nih.gov/pubmed/34855049	Genetic Risk for Smoking: Disentangling Interplay Between Genes and Socioeconomic Status.	Lifetime smoking (without educational attainment)	272,943 E	NA	17q21.31		MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs8070723-?	rs8070723	0	8070723	intron_variant	0	NR	5.00E-10	9.30103		NA		NR [1300000]	N
9	17:44118848	17	44081064	rs8070723	3/01/2011	2.1E+07	Spencer CC	2/11/2010	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/21044948	Dissection of the genetics of Parkinson's disease identifies an additional association 5' of SNCA and multiple associated haplotypes at 17q21.	Parkinson's disease	1,705 Euro	1,039 Euro	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs8070723-?	rs8070723	0	8070723	intron_variant	0	0.76	7.00E-12	11.1549		1.3	[1.19-1.43]	Illumina [532616]	N
9	17:44118848	17	44081064	rs8070723	14/07/2011	2.2E+07	Hoglinger GU	19/06/2011	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/21685912	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy.	Progressive supranuclear palsy	1,069 Euro	1,051 Euro	17q21.31	MAPT	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs8070723-?	rs8070723	0	8070723	intron_variant	0	0.23	#######	117.699		5.11	[4.43-5.91]	Illumina [531451]	N
9	17:44118848	17	44081064	rs8070723	4/11/2019	3E+07	Pulit SL	14/09/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30239722	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry.	Waist-hip ratio	381,152 E	NA	17q21.31	NR	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs8070723-A	rs8070723	0	8070723	intron_variant	0	0.7848	4.00E-15	14.39794		0.0162	[0.012-0.0	NR [~ 27400000] (imputed)	N
9	17:44118848	17	43893716	rs8072451	3/11/2015	2.6E+07	Hibar DP	21/01/2015	Nature	www.ncbi.nlm.nih.gov/pubmed/25607358	Common genetic variants influence human subcortical brain structures.	Subcortical brain region volumes	up to 13,1	up to 15,1	17q21.31	MAPT, GRN, CRHI	CRHR1, CRHR1, CRHR1, LINC02210-CRHR1, LINC02210-C			ENSG00000276191, E	NA	NA	rs8072451-?	rs8072451	0	8072451	intron_variant	0	NR	1.00E-08	8	(Intracrani	14489.99	[9539.28-1	Affymetrix, Illumina [NR] (imputed)	N
9	17:44091886	17	44162597	rs8080583	12/01/2018	2.9E+07	Lam M	28/11/2017	Cell Rep	www.ncbi.nlm.nih.gov/pubmed/29186694	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets.	Cognitive ability	107,207 E	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs8080583-?	rs8080583	0	8080583	intron_variant	0	NR	1.00E-08	8		5.717	z score dec	Affymetrix, Illumina [7357080] (imputed)	N
9	17:44118848	17	44065740	rs919462	12/01/2018	2.9E+07	Pirastu N	17/11/2017	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29146897	GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk.	Male-pattern baldness	25,662 Brit	13,367 Eur	17q21.31	WNT3, MAPT, PLE	MAPT, MAPT, MAPT			ENSG00000277956, E	NA	NA	rs919462-C	rs919462	0	919462	intron_variant	0	NR	1.00E-26	26		0.168393	[0.14-0.2]	Affymetrix [27512692] (imputed)	N
9	17:44091886	17	44187257	rs9303525	1/06/2012	2.3E+07	Ikram MA	15/04/2012	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/22504418	Common variants at 6q22 and 17q21 are associated with intracranial volume.	Intracranial volume	8,175 Euro	1,752 Euro	17q21.31	MAPT, GRN, CRHI	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs9303525-G	rs9303525	0	9303525	intron_variant	0	0.22	8.00E-15	14.09691		14.9	[NR] ml de	Affymetrix, Illumina [2229753] (imputed)	N
9	17:44118848	17	44150152	rs974295	29/01/2020	3.2E+07	Hill WD	16/12/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31844048	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income.	Household income	286,301 B	NA	17q21.31	KANSL1	KANSL1, KANSL1, KANSL1			ENSG00000120071, E	NA	NA	rs974295-T	rs974295	0	974295	intron_variant	0	NR	3.00E-11	10.52288		0.013331	[0.0094-0.	Affymetrix [18485882] (imputed)	N
9	17:44826056	17	44826056	rs9896243	31/10/2018	3E+07	Nagel M	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942085	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways.	Worry	348,219 E	NA	17q21.31	NR	NSF, NSF, NSF			ENSG00000278174, E	NA	NA	rs9896243-G	rs9896243	0	9896243	intron_variant	0	NR	2.00E-11	10.69897		0.01934	[0.014-0.0	Affymetrix [10847151] (imputed)	N
9	17:44118848	17	43822772	rs9906974	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Eosinophil percentage of white cells	408,112 B	NA	17q21.31	RP11-105N13.4,	LINC02210-CRHR1, LINC02210-CRHR1			ENSG00000282456, E	NA	NA	rs9906974-C	rs9906974	0	9906974	intron_variant	0	0.218668	1.00E-45	45		0.038293	[0.033-0.0	Affymetrix [93095623] (imputed)	N
10	17:62017421	17	61996255	rs2005172	7/02/2020	3.2E+07	Hernandez Cordero AI	21/11/2019	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/31761296	Genome-wide Associations Reveal Human-Mouse Genetic Convergence and Modifiers of Myogenesis, CPNE1 and STC2.	Appendicular lean mass	85,750 Eur	NA	17q23.3	NR	GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-C	rs2005172	0	2005172	intron_variant	1	0.641109	2.00E-15	14.69897		0.080328	[0.06-0.1]	Affymetrix [21375087] (imputed)	N
10	17:62017421	17	61996255	rs2005172	4/11/2020	3.3E+07	Pei YF	23/10/2020	Commun Biol	www.ncbi.nlm.nih.gov/pubmed/33097823	The genetic architecture of appendicular lean mass characterized by association analysis in the UK Biobank study.	Appendicular lean mass	450,243 E	NA	17q23.3	GH1	GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-A	rs2005172	0	2005172	intron_variant	1	0.3603	#######	127.699		0.048	[0.044-0.0	Affymetrix [18391927] (imputed)	N
10	17:62017421	17	61996255	rs2005172	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Fat-free mass	70,700 Eur	NA	17q23.3	NR	GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-?	rs2005172	0	2005172	intron_variant	1	NR	2.00E-15	14.69897	(male)	0.29124	[0.22-0.36]	Affymetrix [7794483] (imputed)	N
10	17:62017421	17	61996255	rs2005172	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Fat-free mass	70,700 Eur	NA	17q23.3	NR	GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-?	rs2005172	0	2005172	intron_variant	1	NR	8.00E-14	13.09691	(female)	0.18928	[0.14-0.24]	Affymetrix [7794483] (imputed)	N
10	17:62017421	17	61996255	rs2005172	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Fat-free mass	70,700 Eur	NA	17q23.3	NR	GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-?	rs2005172	0	2005172	intron_variant	1	NR	3.00E-26	25.52288		0.2464	[0.2-0.29]	Affymetrix [7794483] (imputed)	N
10	17:62017421	17	61996255	rs2005172	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Weight	360,116 E	NA	17q23.3		GH1 - CD79B	ENSG00000259384	ENSG00000007312		56	9845	rs2005172-C	rs2005172	0	2005172	intron_variant	1	NR	3.00E-16	15.52288		0.014	[0.011-0.0	Affymetrix, Illumina [20539548] (imputed)	N
10	17:62017421	17	62007498	rs2070776	24/09/2015	2.5E+07	Wood AR	5/10/2014	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/25282103	Defining the role of common variation in the genomic and biological architecture of adult human height.	Height	253,288 E	80,067 Eur	17q23.3	CD79B	CD79B			ENSG00000007312	NA	NA	rs2070776-A	rs2070776	0	2070776	stop_gained	0	0.346	6.00E-41	40.22185		0.042	[0.036-0.0	Affymetrix, Illumina, Perlegen [2550858] (imputed)	N
10	17:62017421	17	62007498	rs2070776	24/10/2012	2.1E+07	Lango Allen H	29/09/2010	Nature	www.ncbi.nlm.nih.gov/pubmed/20881960	Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height	133,653 E	50,074 Eur	17q23.3	GH region	CD79B			ENSG00000007312	NA	NA	rs2070776-?	rs2070776	0	2070776	stop_gained	0	NR	9.00E-09	8.045757	(Condition	NA	[NR]	Affymetrix, Illumina [2834208] (imputed)	N
10	17:62017421	17	62007498	rs2070776	2/07/2019	3.1E+07	Wojcik GL	19/06/2019	Nature	www.ncbi.nlm.nih.gov/pubmed/31217584	Genetic analyses of diverse populations improves discovery for complex traits.	Height	17,286 Afri	NA	17q23.3	NR	CD79B			ENSG00000007312	NA	NA	rs2070776-?	rs2070776	0	2070776	stop_gained	0	NR	8.00E-06	5.09691		0.025638	[0.014-0.0	Illumina [34656550] (imputed)	N
10	17:62017421	17	62007498	rs2070776	5/08/2022	3.6E+07	Chiou JS	13/07/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35831902	Your height affects your health: genetic determinants and health-related outcomes in Taiwan.	Height	67,452 Ha	NA	17q23.3		CD79B			ENSG00000007312	NA	NA	rs2070776-G	rs2070776	0	2070776	stop_gained	0	NR	7.00E-20	19.1549		0.046	[0.036-0.0	Affymetrix [NR] (imputed)	N
10	17:62017421	17	62008318	rs2320125	5/08/2022	3.6E+07	Chiou JS	13/07/2022	BMC Med	www.ncbi.nlm.nih.gov/pubmed/35831902	Your height affects your health: genetic determinants and health-related outcomes in Taiwan.	Height	67,452 Ha	NA	17q23.3		CD79B			ENSG00000007312	NA	NA	rs2320125-C	rs2320125	0	2320125	intron_variant	0	NR	5.00E-20	19.30103		0.046	[0.036-0.0	Affymetrix [NR] (imputed)	N
10	17:62017421	17	62008318	rs2320125	22/09/2019	3.1E+07	Lotta LA	1/12/2018	JAMA	www.ncbi.nlm.nih.gov/pubmed/30575882	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors.	Waist-hip ratio	663,598 E	NA	17q23.3	NR	CD79B			ENSG00000007312	NA	NA	rs2320125-T	rs2320125	0	2320125	intron_variant	0	0.35	5.00E-08	7.30103		NA		Affymetrix [2446094] (imputed)	N
10	17:62017421	17	62008318	rs2320125	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist-to-hip ratio adjusted for BMI	457,690 E	NA	17q23.3	NR	CD79B			ENSG00000007312	NA	NA	rs2320125-?	rs2320125	0	2320125	intron_variant	0	NR	1.00E-08	8		NA		Affymetrix [~ 8270000] (imputed)	N
10	17:62017421	17	62008318	rs2320125	4/11/2019	3E+07	Pulit SL	14/09/2018	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/30239722	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry.	Waist-to-hip ratio adjusted for BMI	379,501 E	NA	17q23.3	NR	CD79B			ENSG00000007312	NA	NA	rs2320125-T	rs2320125	0	2320125	intron_variant	0	0.3502	5.00E-12	11.30103		0.013	[0.0093-0.	NR [~ 27400000] (imputed)	N
10	17:62017421	17	62008318	rs2320125	22/09/2019	3.1E+07	Lotta LA	1/12/2018	JAMA	www.ncbi.nlm.nih.gov/pubmed/30575882	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors.	Waist-to-hip ratio adjusted for BMI	660,648 E	NA	17q23.3	NR	CD79B			ENSG00000007312	NA	NA	rs2320125-T	rs2320125	0	2320125	intron_variant	0	0.35	2.00E-10	9.69897		0.012	[0.0083-0.	Affymetrix [2446094] (imputed)	N
10	17:62017421	17	62017421	rs2532111	17/07/2019	2.9E+07	Tachmazidou I	1/06/2017	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/28552196	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits.	Height	1,249 who	205,003 E	17q23.3	SCN4A	SCN4A			ENSG00000007314	NA	NA	rs2532111-A	rs2532111	0	2532111	3_prime_UTR_variant	0	0.3539	7.00E-09	8.154902		0.0389	[0.026-0.0	Affymetrix, Illumina, Perlegen [15844966] (imputed)	N
10	17:62017421	17	62017421	rs2532111	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Hip circumference adjusted for BMI	186,825 B	NA	17q23.3	SCN4A	SCN4A			ENSG00000007314	NA	NA	rs2532111-A	rs2532111	0	2532111	3_prime_UTR_variant	0	NR	5.00E-14	13.30103		0.024271	[0.018-0.0	Affymetrix [323123] (imputed)	N
10	17:62017421	17	62017421	rs2532111	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Waist-hip ratio	approxima	NA	17q23.3		SCN4A			ENSG00000007314	NA	NA	rs2532111-?	rs2532111	0	2532111	3_prime_UTR_variant	0	NR	6.00E-10	9.221849		NA		NR [~ 8900000] (imputed)	N
11	20:47627095	20	47648856	rs1022688	21/01/2019	3E+07	Day FR	3/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29970889	Elucidating the genetic basis of social interaction and isolation.	Loneliness	80,134 Eur	NA	20q13.13	PREX1, ARFGEF2,	ARFGEF2			ENSG00000124198	NA	NA	rs1022688-G	rs1022688	0	1022688	3_prime_UTR_variant	0	0.67	3.00E-08	7.522879		0.0048	[0.003-0.0	NR [NR] (imputed)	N
11	20:47627095	20	47648856	rs1022688	21/01/2019	3E+07	Day FR	3/07/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29970889	Elucidating the genetic basis of social interaction and isolation.	Loneliness (MTAG)	487,647 E	NA	20q13.13	PREX1, ARFGEF2,	ARFGEF2			ENSG00000124198	NA	NA	rs1022688-G	rs1022688	0	1022688	3_prime_UTR_variant	0	0.669916	3.00E-09	8.522879		0.012942	[0.0087-0.	NR [NR] (imputed)	N
11	20:47746974	20	47817815	rs13036715	30/11/2018	3E+07	Baselmans BML	2/10/2018	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/30279531	A genetic perspective on the relationship between eudaimonic -and hedonic well-being.	Eudaimonic well-being	108,154 B	NA	20q13.13	NR	STAU1 - DDX27	ENSG00000124214	ENSG00000124228		12911	18069	rs13036715-A	rs13036715	0	13036715	intergenic_variant	1	0.241067	3.00E-07	6.522879		5.11717	[NR] z scor	Affymetrix [~ 8600000] (imputed)	N
11	20:47746974	20	47849216	rs13038866	17/04/2020	3.2E+07	Zhu Z	24/10/2019	J Allergy Clin Immunol	www.ncbi.nlm.nih.gov/pubmed/31669095	Shared Genetic and Experimental Links between Obesity-Related Traits and Asthma Subtypes in UK Biobank.	Waist circumference adjusted for body mass index	457,690 E	NA	20q13.13	NR	DDX27			ENSG00000124228	NA	NA	rs13038866-?	rs13038866	0	13038866	intron_variant	0	NR	3.00E-12	11.52288		NA		Affymetrix [~ 8270000] (imputed)	N
11	20:47746974	20	47800829	rs13041213	23/02/2018	2.9E+07	Hill WD	11/01/2018	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29326435	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence.	Intelligence (MTAG)	120,934 B	NA	20q13.13	STAU1	STAU1			ENSG00000124214	NA	NA	rs13041213-A	rs13041213	0	13041213	intron_variant	0	NR	7.00E-12	11.1549		0.024944	[0.018-0.0	Affymetrix [NR]	N
11	20:47627095	20	47705496	rs1538482	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Body fat percentage	70,700 Eur	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs1538482-?	rs1538482	0	1538482	intron_variant	0	NR	3.00E-10	9.522879		0.14468	[0.1-0.19]	Affymetrix [7794483] (imputed)	N
11	20:47627095	20	47705496	rs1538482	8/02/2019	3.1E+07	Hubel C	28/12/2018	Am J Med Genet B Neuropsychiatr Genet	www.ncbi.nlm.nih.gov/pubmed/30593698	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa.	Body fat percentage	70,700 Eur	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs1538482-?	rs1538482	0	1538482	intron_variant	0	NR	8.00E-06	5.09691	(male)	0.12586	[0.071-0.1	Affymetrix [7794483] (imputed)	N
11	20:47627095	20	47705496	rs1538482	17/03/2017	2.7E+07	Okbay A	18/04/2016	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/27089181	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses.	Positive affect	180,281 K	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs1538482-T	rs1538482	0	1538482	intron_variant	0	0.6958	1.00E-06	6		0.0177	[0.011-0.0	Affymetrix, Illumina, Perlegen [at least 5170349] (imputed)	N
11	20:47627095	20	47705496	rs1538482	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on cognitive performance (multi-trait conditioning and joint analysis)	298,420 E	NA	20q13.13		CSE1L			ENSG00000124207	NA	NA	rs1538482-?	rs1538482	0	1538482	intron_variant	0	NR	9.00E-11	10.04576		NA		NR [NR]	N

11	20:47627095	20	47603241	rs1569750	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Non-HDL cholesterol levels	1,320,016	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs1569750-G	rs1569750	0	1569750	intron_variant	0	0.303776	5.00E-10	9.30103		0.012993	[0.0095-0.	NR [52000000] (imputed)	N
11	20:47746974	20	47772264	rs17450430	24/09/2015	2.5E+07	Wood AR	5/10/2014	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/25282103	Defining the role of common variation in the genomic and biological architecture of adult human height.	Height	253,288 Eu	80,067 Eur	20q13.13	STAU1	STAU1			ENSG00000124214	NA	NA	rs17450430-A	rs17450430	0	17450430	intron_variant	0	0.761	2.00E-24	23.69897		0.035	[0.029-0.0	Affymetrix, Illumina, Perlegen [2550858] (imputed)	N
11	20:47627095	20	47701765	rs1885163	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Non-HDL cholesterol levels	40,963 Sou	NA	20q13.13		CSE1L			ENSG00000124207	NA	NA	rs1885163-?	rs1885163	0	1885163	intron_variant	0	NR	1.00E-11	11		NA		NR [52000000] (imputed)	N
11	20:47746974	20	47552467	rs189331311	24/08/2021	3.4E+07	Christakoudi S	21/05/2021	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/34021172	GWAS of allometric body-shape indices in UK Biobank identifies loci suggesting associations with morphogenesis, organogenesis, adrenal cell renewal and cancer.	Waist circumference adjusted for body mass index	186,825 Bi	NA	20q13.13	ARFGEF2	ARFGEF2			ENSG00000124198	NA	NA	rs189331311-C	rs189331311	0	1.89E+08	intron_variant	0	NR	5.00E-08	7.30103		0.019805	[0.013-0.0	Affymetrix [321114] (imputed)	N
11	20:47746974	20	47701024	rs2075677	18/03/2019	3.1E+07	Baselmans BML	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643256	Multivariate genome-wide analyses of the well-being spectrum.	Positive affect	410,603 Eu	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs2075677-G	rs2075677	0	2075677	intron_variant	0	0.238398	2.00E-14	13.69897		0.018965	[0.014-0.0	NR [NR]	N
11	20:47746974	20	47701024	rs2075677	17/03/2017	2.7E+07	Okbay A	18/04/2016	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/27089181	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses.	Subjective well-being	298,420 Ko	NA	20q13.13	CSE1L	CSE1L			ENSG00000124207	NA	NA	rs2075677-A	rs2075677	0	2075677	intron_variant	0	0.7603	2.00E-08	7.69897		0.0175	[0.011-0.0	Affymetrix, Illumina, Perlegen [at least 5170349] (imputed)	N
11	20:47746974	20	47701024	rs2075677	7/07/2022	3.6E+07	Kim S	19/05/2022	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/35589828	Shared genetic architectures of subjective well-being in East Asian and European ancestry populations.	Subjective well-being	110,919 Ko	NA	20q13.13		CSE1L			ENSG00000124207	NA	NA	rs2075677-A	rs2075677	0	2075677	intron_variant	0	NR	4.00E-10	9.39794		0.013317	unit increa	NR [NR] (imputed)	N
11	20:47627095	20	47582884	rs2295027	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Low density lipoprotein cholesterol levels	40,963 Sou	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs2295027-?	rs2295027	0	2295027	intron_variant	0	NR	1.00E-12	12		NA		NR [52000000] (imputed)	N
11	20:47627095	20	47582884	rs2295027	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Low density lipoprotein cholesterol levels	1,320,016	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs2295027-A	rs2295027	0	2295027	intron_variant	0	0.322025	6.00E-11	10.22185		0.011545	[0.0086-0.	NR [52000000] (imputed)	N
11	20:47627095	20	47582884	rs2295027	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Total cholesterol levels	1,320,016	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs2295027-A	rs2295027	0	2295027	intron_variant	0	0.321731	3.00E-11	10.52288		0.011737	[0.0089-0.	NR [52000000] (imputed)	N
11	20:47746974	20	47903019	rs237743	24/10/2012	2.1E+07	Lango Allen H	29/09/2010	Nature	www.ncbi.nlm.nih.gov/pubmed/20881960	Hundreds of variants clustered in genomic loci and biological pathways affect human height.	Height	133,653 Eu	50,074 Eur	20q13.13	ZNFX1	ZFAS1			ENSG00000177410	NA	NA	rs237743-A	rs237743	0	237743	intron_variant	0	0.21	1.00E-20	20		0.041	[NR] unit in	Affymetrix, Illumina [2834208] (imputed)	N
11	20:47746974	20	47851919	rs238150	7/07/2022	3.6E+07	Kim S	19/05/2022	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/35589828	Shared genetic architectures of subjective well-being in East Asian and European ancestry populations.	Subjective well-being	110,919 Ko	NA	20q13.13		DDX27			ENSG00000124228	NA	NA	rs238150-T	rs238150	0	238150	non_coding_transcript_exon	0	0.81	3.00E-11	10.52288		0.015	[0.011-0.0	NR [NR] (imputed)	N
11	20:47746974	20	47851919	rs238150	7/07/2022	3.6E+07	Kim S	19/05/2022	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/35589828	Shared genetic architectures of subjective well-being in East Asian and European ancestry populations.	Subjective well-being	563,176 Eu	NA	20q13.13		DDX27			ENSG00000124228	NA	NA	rs238150-T	rs238150	0	238150	non_coding_transcript_exon	0	0.784	5.00E-12	11.30103		0.016	[0.012-0.0	NR [NR] (imputed)	N
11	20:47746974	20	47844341	rs238164	16/10/2019	3.2E+07	Akiyama M	27/09/2019	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/31562340	Characterizing rare and low-frequency height-associated variants in the Japanese population.	Height	159,095 Ja	32,692 Jap	20q13.13	DDX27	DDX27			ENSG00000124228	NA	NA	rs238164-?	rs238164	0	238164	intron_variant	0	NR	2.00E-09	8.69897		0.029782	[0.02-0.03	Illumina [27896057] (imputed)	N
11	20:47627095	20	47780105	rs2426139	15/12/2021	3.5E+07	Shadrin AA	21/09/2021	Neuroimage	www.ncbi.nlm.nih.gov/pubmed/34560273	Vertex-wise multivariate genome-wide association study identifies 780 unique genetic loci associated with cortical morphology.	Cortical thickness	35,657 Wh	NA	20q13.13	NR	STAU1			ENSG00000124214	NA	NA	rs2426139-A	rs2426139	0	2426139	intron_variant	0	0.3008	5.00E-08	7.30103		NA		NR [9056863] (imputed)	N
11	20:47495794	20	47493894	rs34116853	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Highest math class taken (MTAG)	811,539 Eu	NA	20q13.13	Intergenic	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		49358	44354	rs34116853-A	rs34116853	0	34116853	regulatory_region_variant	1	0.6796	1.00E-12	12	(MTAG)	0.0125	[0.009-0.0	Affymetrix, Illumina [7100000] (imputed)	N
11	20:47495794	20	47493894	rs34116853	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Self-reported math ability	564,698 Eu	NA	20q13.13	Intergenic	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		49358	44354	rs34116853-A	rs34116853	0	34116853	regulatory_region_variant	1	0.6805	1.00E-09	9		0.0127	[0.0086-0.	Affymetrix, Illumina [10000000] (imputed)	N
11	20:47495794	20	47493894	rs34116853	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Self-reported math ability (MTAG)	670,471 Eu	NA	20q13.13	Intergenic	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		49358	44354	rs34116853-A	rs34116853	0	34116853	regulatory_region_variant	1	0.6805	9.00E-14	13.04576	(MTAG)	0.0143	[0.011-0.0	Affymetrix, Illumina [7100000] (imputed)	N
11	20:47627095	20	47768988	rs348258	21/01/2020	3.2E+07	Abdellaoui A	13/09/2019	Hum Mol Genet	www.ncbi.nlm.nih.gov/pubmed/31518406	Phenome-wide investigation of health outcomes associated with genetic predisposition to loneliness.	Loneliness	511,280 Eu	NA	20q13.13	STAU1	STAU1			ENSG00000124214	NA	NA	rs348258-?	rs348258	0	348258	intron_variant	0	NR	1.00E-08	8		0.02	[0.014-0.0	Affymetrix, Illumina [up to 14113458] (imputed)	N
11	20:47627095	20	47786190	rs348276	12/01/2018	2.9E+07	Lam M	28/11/2017	Cell Rep	www.ncbi.nlm.nih.gov/pubmed/29186694	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets.	Cognitive ability	107,207 Eu	NA	20q13.13	STAU1	STAU1			ENSG00000124214	NA	NA	rs348276-?	rs348276	0	348276	intron_variant	0	NR	1.00E-08	8		5.699	z score inc	Affymetrix, Illumina [7357080] (imputed)	N
11	20:47627095	20	47786190	rs348276	4/09/2019	3.1E+07	Lam M	1/08/2019	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/31374203	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways.	Cognitive ability, years of educational attainment or schizophrenia (pleiotropy)	328,917 in	NA	20q13.13	STAU1	STAU1			ENSG00000124214	NA	NA	rs348276-?	rs348276	0	348276	intron_variant	0	NR	5.00E-09	8.30103		0.012521	[0.0083-0.	NR [7306098]	N
11	20:47627095	20	47786190	rs348276	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on average household income before tax (multi-trait conditioning and joint analysis)	298,420 Eu	NA	20q13.13		STAU1			ENSG00000124214	NA	NA	rs348276-?	rs348276	0	348276	intron_variant	0	NR	9.00E-10	9.045757		NA		NR [NR]	N
11	20:47627095	20	47786190	rs348276	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on Townsend deprivation index (multi-trait conditioning and joint analysis)	298,420 Eu	NA	20q13.13		STAU1			ENSG00000124214	NA	NA	rs348276-?	rs348276	0	348276	intron_variant	0	NR	2.00E-10	9.69897		NA		NR [NR]	N
11	20:47746974	20	47746974	rs34841991	30/11/2018	3E+07	Baselmans BML	2/10/2018	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/30279531	A genetic perspective on the relationship between eudaimonic -and hedonic well-being.	Hedonic well-being	221,575 Bi	NA	20q13.13	NR	STAU1			ENSG00000124214	NA	NA	rs34841991-C	rs34841991	0	34841991	intron_variant	0	0.24	2.00E-10	9.69897		0.022	[0.014-0.0	Affymetrix [~ 8600000] (imputed)	N
11	20:47746974	20	47806092	rs3795075	14/12/2021	3.5E+07	Sakaue S	30/09/2021	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/34594039	A cross-population atlas of genetic associations for 220 human phenotypes.	Height	165,056 Ea	NA	20q13.13		STAU1 - DDX27	ENSG00000124214	ENSG00000124228		1188	29792	rs3795075-A	rs3795075	0	3795075	intergenic_variant	1	0.089743	1.00E-08	8		0.020327	[0.013-0.0	Illumina [13479295] (imputed)	N
11	20:47495794	20	47440220	rs4809728	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Mean reticulocyte volume	408,112 Bi	NA	20q13.13	PREX1	PREX1			ENSG00000124126	NA	NA	rs4809728-G	rs4809728	0	4809728	intron_variant	0	0.341007	7.00E-12	11.1549		0.016283	[0.012-0.0	Affymetrix [93095623] (imputed)	N
11	20:47495794	20	47495794	rs4810883	17/09/2018	3E+07	Davies G	29/05/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29844566	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function.	General cognitive ability	up to 300,4	NA	20q13.13	ARFGEF2	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		51258	42454	rs4810883-T	rs4810883	0	4810883	regulatory_region_variant	1	NR	1.00E-08	8		5.69	z-score inc	Affymetrix, Illumina [at least 2500000] (imputed)	N
11	20:47495794	20	47495794	rs4810883	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red blood cell count	545,203 Eu	NA	20q13.13	NR	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		51258	42454	rs4810883-T	rs4810883	0	4810883	regulatory_region_variant	1	0.329032	3.00E-13	12.52288		0.014533	[0.011-0.0	Affymetrix, Illumina [50628390] (imputed)	N
11	20:47495794	20	47495794	rs4810883	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Red blood cell count	727,624 Af	NA	20q13.13	NR	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		51258	42454	rs4810883-T	rs4810883	0	4810883	regulatory_region_variant	1	0.302151	1.00E-11	11		NA		Affymetrix, Illumina [24332387] (imputed)	N
11	20:47495794	20	47495794	rs4810883	18/09/2020	3.3E+07	Vuckovic D	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888494	The Polygenic and Monogenic Basis of Blood Traits and Diseases.	Red blood cell count	408,112 Bi	NA	20q13.13		PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		51258	42454	rs4810883-T	rs4810883	0	4810883	regulatory_region_variant	1	0.329974	3.00E-10	9.522879		0.014927	[0.01-0.02	Affymetrix [93095623] (imputed)	N
11	20:47495794	20	47477706	rs6012542	23/02/2018	2.9E+07	Hill WD	11/01/2018	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29326435	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence.	Intelligence (MTAG)	120,934 Bi	NA	20q13.13	PREX1	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		33170	60542	rs6012542-T	rs6012542	0	6012542	regulatory_region_variant	1	NR	8.00E-12	11.09691		0.021212	[0.015-0.0	Affymetrix [NR]	N
11	20:47627095	20	47541517	rs6019535	5/09/2022	3.6E+07	Rao S	28/06/2022	Neuropsychobiology	www.ncbi.nlm.nih.gov/pubmed/35764056	Genetic Relationships between Attention-Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, and Intelligence.	Attention deficit hyperactivity disorder or autism spectrum disorder or intelligence (pleiotropy)	20,183 Eur	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs6019535-?	rs6019535	0	6019535	intron_variant	0	NR	6.00E-20	19.22185		NA		NR [6307410] (imputed)	N
11	20:47627095	20	47541517	rs6019535	12/09/2018	3E+07	Savage JE	25/06/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/29942086	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence.	Intelligence	269,867 Eu	NA	20q13.13	NR	ARFGEF2			ENSG00000124198	NA	NA	rs6019535-A	rs6019535	0	6019535	intron_variant	0	NR	3.00E-17	16.52288		8.436	z-score inc	Affymetrix, Illumina [9295118] (imputed)	N
11	20:47627095	20	47541517	rs6019535	17/11/2022	3.5E+07	Graham SE	9/12/2021	Nature	www.ncbi.nlm.nih.gov/pubmed/34887591	The power of genetic diversity in genome-wide association studies of lipids.	Total cholesterol levels	40,963 Sou	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs6019535-?	rs6019535	0	6019535	intron_variant	0	NR	8.00E-15	14.09691		NA		NR [52000000] (imputed)	N
11	20:47627095	20	47685815	rs6019624	17/09/2018	3E+07	Davies G	29/05/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29844566	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function.	Reaction time	330,069 Eu	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs6019624-?	rs6019624	0	6019624	intron_variant	0	NR	1.00E-06	6		0.008534	[0.0051-0.	Affymetrix [805426] (imputed)	N
11	20:47627095	20	47666027	rs6090940	18/03/2019	3.1E+07	Baselmans BML	14/01/2019	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30643256	Multivariate genome-wide analyses of the well-being spectrum.	Life satisfaction	80,852 Eur	NA	20q13.13	NR	CSE1L			ENSG00000124207	NA	NA	rs6090940-T	rs6090940	0	6090940	intron_variant	0	0.322627	3.00E-08	7.522879		0.017017	[0.011-0.0	NR [NR]	N
11	20:47495794	20	47446556	rs6095319	26/10/2022	3.6E+07	Hatoum AS	14/07/2022	Biol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/36150907	Genome-wide Association Study Shows That Executive Functioning Is Influenced by GABAergic Processes and Is a Neurocognitive Genetic Correlate of Psychiatric Disorders.	Common executive function	427,037 Eu	NA	20q13.13		PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		2020	91692	rs6095319-?	rs6095319	0	6095319	intron_variant	1	NR	2.00E-14	13.69897		NA		Affymetrix [7391068] (imputed)	N
11	20:47627095	20	47532536	rs6095360	30/11/2018	3E+07	Baselmans BML	2/10/2018	Sci Rep	www.ncbi.nlm.nih.gov/pubmed/30279531	A genetic perspective on the relationship between eudaimonic -and hedonic well-being.	Eudaimonic well-being	108,154 Bi	NA	20q13.13	NR	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		88000	5712	rs6095360-G	rs6095360	0	6095360	intergenic_variant	1	0.324609	9.00E-07	6.045757		4.91741	[NR] z scor	Affymetrix [~ 8600000] (imputed)	N
11	20:47627095	20	47532536	rs6095360	6/02/2019	3E+07	Coleman JRI	8/03/2018	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29520040	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals.	Extremely high intelligence	1,247 Euro	NA	20q13.13	ARFGEF2, CSE1L	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		88000	5712	rs6095360-A	rs6095360	0	6095360	intergenic_variant	1	0.693	7.00E-10	9.154902		6.16	NR z-score	Illumina [up to 12595966] (imputed)	N
11	20:47627095	20	47532536	rs6095360	23/02/2018	2.9E+07	Hill WD	11/01/2018	Mol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/29326435	A combined analysis of genetically correlated traits identifies 187 loci and a role for neurogenesis and myelination in intelligence.	Intelligence (MTAG)	120,934 Bi	NA	20q13.13	ARFGEF2	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		88000	5712	rs6095360-A	rs6095360	0	6095360	intergenic_variant	1	NR	7.00E-16	15.1549		0.025381	[0.019-0.0	Affymetrix [NR]	N
11	20:47627095	20	47627095	rs6095395	7/03/2022	3.5E+07	van der Meer D	15/12/2021	Sci Adv	www.ncbi.nlm.nih.gov/pubmed/34910505	The genetic architecture of human cortical folding.	Vertex-wise cortical thickness	33,748 Eur	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs6095395-G	rs6095395	0	6095395	intron_variant	0	0.3	1.00E-09	9		6.05	z score inc	Affymetrix [9061022] (imputed)	N
11	20:47627095	20	47678201	rs6095417	17/09/2018	3E+07	Davies G	29/05/2018	Nat Commun	www.ncbi.nlm.nih.gov/pubmed/29844566	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function.	General cognitive ability	up to 300,4	NA	20q13.13	CSE1L	CSE1L			ENSG00000124207	NA	NA	rs6095417-A	rs6095417	0	6095417	intron_variant	0	NR	1.00E-14	14		7.724	z-score inc	Affymetrix, Illumina [at least 2500000] (imputed)	N
11	20:47495794	20	47481726	rs67021138	12/11/2018	3E+07	Lee JJ	23/07/2018	Nat Genet	www.ncbi.nlm.nih.gov/pubmed/30038396	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals.	Educational attainment (MTAG)	1,311,438	NA	20q13.13	Intergenic	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		37190	56522	rs67021138-T	rs67021138	0	67021138	TF_binding_site_variant	1	0.6814	9.00E-10	9.045757	(MTAG)	0.0086	[0.0059-0.	Affymetrix, Illumina [7100000] (imputed)	N

11	20:47627095	20	47652254	rs707533	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on educational attainment (multi-trait conditioning and joint analysis)	298.420	Ei	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs707533-?	rs707533	0	707533	3_prime_UTR_variant	0	NR	9.00E-11	10.04576		NA		NR (NR)	N
11	20:47627095	20	47652254	rs707533	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on highest math class (multi-trait conditioning and joint analysis)	298.420	Ei	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs707533-?	rs707533	0	707533	3_prime_UTR_variant	0	NR	1.00E-10	10		NA		NR (NR)	N
11	20:47627095	20	47652254	rs707533	24/09/2021	3.3E+07	Wendt FR	21/12/2020	Nat Hum Behav	www.ncbi.nlm.nih.gov/pubmed/33349686	Multivariate genome-wide analysis of education, socioeconomic status and brain phenome.	Subjective wellbeing conditioned on self-rated math ability (multi-trait conditioning and joint analysis)	298.420	Ei	NA	20q13.13		ARFGEF2			ENSG00000124198	NA	NA	rs707533-?	rs707533	0	707533	3_prime_UTR_variant	0	NR	7.00E-11	10.1549		NA		NR (NR)	N
11	20:47746974	20	47701309	rs7264419	18/10/2022	3.5E+07	Maihofer AX	28/09/2021	Biol Psychiatry	www.ncbi.nlm.nih.gov/pubmed/34865855	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information.	Post-traumatic stress disorder (MTAG)	217,491	Ei	NA	20q13.13		CSE1L			ENSG00000124207	NA	NA	rs7264419-A	rs7264419	0	7264419	intron_variant	0	NR	5.00E-09	8.30103		5.85	Z score deri	Affymetrix, Illumina [NR] (imputed)	N
11	20:47495794	20	47447870	rs7267607	21/09/2020	3.3E+07	Chen MH	1/09/2020	Cell	www.ncbi.nlm.nih.gov/pubmed/32888493	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations.	Mean corpuscular hemoglobin	486.823	Ei	NA	20q13.13	NR	PREX1 - ARFGEF2	ENSG00000124126	ENSG00000124198		3334	90378	rs7267607-C	rs7267607	0	7267607	intron_variant	1	0.341038	1.00E-22	22		0.019896	[0.016-0.0	Affymetrix, Illumina [502666541 (imputed)	N
11	20:47746974	20	47762249	rs8122757	8/02/2019	3.1E+07	Kichaev G	27/12/2018	Am J Hum Genet	www.ncbi.nlm.nih.gov/pubmed/30595370	Leveraging Polygenic Functional Enrichment to Improve GWAS Power.	Lung function (FVC)	approxima	NA	20q13.13			STAU1			ENSG00000124214	NA	NA	rs8122757-?	rs8122757	0	8122757	intron_variant	0	NR	7.00E-11	10.1549		NA		NR (~ 8900000) (imputed)	N