Tissue Volume	Gene	Function (GeneCards®)	OMIM	NHGRI-EBI GWAS Catalog	KO Phenotype (MGI- behavioral, neurological, or nervous system phenotypes)	Expressed in prenatal murine nervous system (GXD)	Neuroimaging phenotype
ICV	***KLF13***	zinc-finger transcription factor	**chromosome 15q13.3 Deletion syndrome (ID, seizures, schizophrenia, ASD, ADHD)**	eosinophilic esophagitis[1], myasthenia gravis[2]		Y	
	EYA2	protein phosphatase and transcriptional coactivator for SIX1		Visceral adipose tissue/subcutaneous adipose tissue ratio[3], thiazide-induced adverse metabolic events in hypertensive patients[4]		Y	
	LMCD1	transcriptional co-factor				Y	
WM	***WWOX***	Putative oxidoreductase, tumor suppressor, plays a role in apoptosis.	**Epileptic encephalopathy, early infantile, 28; spinocerebellar ataxia, autosomal recessive 12**; esophageal squamous cell carcinoma, somatic	**Response to antipsychotic treatment in schizophrenia (reasoning)[5], 5-HIAA levels in CSF[6], anorexia[7], response to amphetamines[8], educational attainment[9], bipolar disorder(body mass index interaction)[10]**, obesity[11], cardiac structure and function[12], pulmonary function (interaction)[13], radiation response[14], forced vital capacity[15]	**Increased brain weight**	Y	**Rare mutations associated with multiple abnormalities including thin cerebral cortex, hippocampal dysplasia, hypoplasia of corpus callosum, hypotrophic temporal lobes, gyral pattern anomalies, hypomyelination and global brain atrophy[16]**
	SLC13A3	High-affinity sodium-dicarboxylate cotransporter		Glomerular filtration rate[17], chronic kidney disease[17]		Y	
	MEI4	Required for meiotic DNA double-strand break formation.		Blood pressure measurement[18]			
	HTR1B	**G-protein coupled receptor for 5-hydroxytryptamine (serotonin)**		Parasitemia in Tripanasoma cruzi seropositivity[19], menarche[20], capecitabine sensitivity[21], chemotherapy-induced neutropenia/leucopenia[22] , acute lymphoblastic leukemia[23]	**Mice homozygous for a knock-out allele exhibit an increase in aggression and drinking behavior, altered spatial learning and operant conditional behavior, reduced anxiety-related response and startle reflex.**	Y	
	MYOM1	Major component of the vertebrate myofibrillar M band		Symmetrical dimethylarginine levels[24]			
	USP44	cysteine protease, functions as deubiquitinating enzyme		Response to antidepressant treatment (sexual side effects)[25], breast size[26], breast cancer[27, 28]			
	IGFBP7	IGF-binding protein	Retinal arterial macroaneurysm with supravalvular pulmonic stenosis	IgG glycosylation[29], cotinine glucuronidation[30]			
	MPLKIP	Putative regulator of mitosis and cytokinesis	Trichothiodystrophy 4, nonphotosensitive				
	OPA1	Dynamin-related GTPase required for mitochondrial fusion and regulation of apoptosis	**Optic atrophy 1; Optic atrophy plus syndrome;** Glaucoma, normal tension, susceptibility to		**Mice homozygous for an ENU mutation exhibit embryonic lethality, embryonic growth retardation and morphological abnormalities. Mice heterozygous for an ENU mutation exhibit abnormal cellular morphology, altered optic nerve myelination, abnormal response to a new environment and decreased vision**	Y	**Rare variants associated cerebellar and cortical atrophies even in patients with normal neurological exam[31]**

GM	***ZMAT4***	Function unclear		**Inattentive symptoms[32], Parkinson's disease (motor and cognitive)[33]**, fasting plasma glucose[34], refractive error[35]		Y	
	CNDP1	homodimeric dipeptidase identified as human carnosinase					
	TOX3	Transcriptional coactivator of the p300/CBP-mediated transcription complex. **Required for depolarization-induced transcription activation of the C-FOS promoter in neurons.**		PCOS[36], breast cancer[37]		Y	
	CAAP1	Anti-apoptotic protein		Smoking behavior[38], drug-induced liver injury[39], gallbladder cancer[40], age-related hearing impairment[41], visceral adipose tissue/subcutaneous adipose tissue ratio[3]			
	C16orf62	copper-dependent ATP7A trafficking between trans-Golgi network and vesicles in cell periphery					
	SLC35F4	Putative solute transporter		**Bipolar disorder[42, 43], bipolar disorder and schizophrenia[44], ADHD (time to onset)[32]**, HIV-1 control[45], pulmonary function[46]			
	CACNB2	beta subunit of voltage-dependent calcium channel	Brugada syndrome	**Schizophrenia[47, 48] bipolar disorder and schizophrenia[44], ASD, ADHD, Bipolar, and schizophrenia (combined)[49], response to antipsychotic treatment[50], metabolite levels (HVA/MHPG ratio)[6]**, protein QTL[51], systolic blood pressure[52-54], diastolic blood pressure[52, 54], primary tooth development[55], obesity-related traits[56], blood pressure[57], hypertension[54]	**Delayed brain development**	Y	
	CTH	Catalyzes the last step in the trans-sulfuration pathway from methionine to cysteine	Cystathioninuria, Homocysteine, total plasma, elevated	Antipsychotic-induced QTc interval prolongation[50], chemotherapy-induced alopecia[58], inflammatory bowel disease[59]	**paralysis**	Y	
	SEC14L5	Function unclear		**Metabolite levels (HVA/MHPG ratio)[6]**, lung-cancer asbestos exposure interaction[60]			
CSF	***RBFOX1***	RNA-binding protein that regulates alternative splicing events		**Bipolar disorder and schizophrenia[44], ADHD and conduct disorder[61], conduct disorder (interaction)[62], response to antipsychotic therapy (extrapyramidal side effects)[63], sleep time[64]**, refractive error[35, 65], obesity-related traits[56], hyperopia[66], myopia[66], glaucoma[67], allergic rhiniti[68]s, diabetic retinopathy[69], metabolite levels (PC)[70], phospholipid levels[71], intraocular pressure[72], periodontitis[73], Dengue shock syndrome[74], visceral adipose tissue adjusted for BMI[3]	**Mice homozygous for a conditional allele activated in the brain exhibit infrequent spontaneous seizures, increased susceptibility to kainic acid-induced seizures and lethality, and increased neuronal excitation**	Y	**Common variants associated with temporal lobe volume[75, 76]**
	TBX4	Transcription factor	Small patella syndrome	Height[77-82]		Y	**17q23.1–q23.2 microduplication involving TBX4 shows microcephaly, generalized volume loss, and simplified gyral pattern**

	FRG1	May play a role in regulation of pre-mRNA splicing, the assembly of rRNA into ribosomal subunits, or mRNA transport.	Possible role in facioscapulohumeral muscular dystrophy-1	Testosterone levels[83]			
	METTL4	Probable methyltransferase		**Heschl's gyrus morphology**[84], exercise (leisure time)[85], PR interval in Tripanosoma cruzi seropositivity[19], QRS duration in Tripanasoma cruzi seropositivity[19], very long-chain saturated fatty acid levels[86], acute lymphoblastic leukemia (childhood)[87]			Suggestive association for right HG area[84]

Supplementary Table 5. Bioinformatics integration for loci exceeding the threshold of $p < 1.25 \times 10^{-6}$. The nearest protein coding gene within 500kb for each LD-independent SNP is included. Column 3 is a brief functional description based on GeneCards® (http://www.genecards.org/). Column 4 (OMIM) shows entries in the Online Mendelian Inheritance in Man (http://www.omim.org, accessed October 2015). Column 5 shows all intersections with the NHGRI-EBI GWAS catalog (https://www.ebi.ac.uk/gwas/, accessed October 2015). Column 6 provides phenotype information for genes where mouse knock-outs were reported to have behavioral, neurological, or nervous system phenotypes (http://www.informatics.jax.org).

Abbreviations: ASD=autism spectrum disorder, ADHD=attention deficit hyperactivity disorder, ID=intellectual disability, VBP=variable by probe, NFD=not found in database.

REFERENCES

1 Kottyan, L.C., *et al.* Genome-wide association analysis of eosinophilic esophagitis provides insight into the tissue specificity of this allergic disease. *Nat. Genet.* **46**, 895-900 (2014).
2 Gregersen, P.K., *et al.* Risk for myasthenia gravis maps to a (151) Pro-->Ala change in TNIP1 and to human leukocyte antigen-B*08. *Ann. Neurol.* **72**, 927-935 (2012).
3 Fox, C.S., *et al.* Genome-wide association for abdominal subcutaneous and visceral adipose reveals a novel locus for visceral fat in women. *Plos Genet* **8**, e1002695 (2012).
4 Del-Aguila, J.L., *et al.* Genome-wide association analyses suggest NELL1 influences adverse metabolic response to HCTZ in African Americans. *Pharmacogenomics J* **14**, 35-40 (2014).
5 McClay, J.L., *et al.* Genome-wide pharmacogenomic study of neurocognition as an indicator of antipsychotic treatment response in schizophrenia. *Neuropsychopharmacology* **36**, 616-626 (2011).
6 Luykx, J.J., *et al.* Genome-wide association study of monoamine metabolite levels in human cerebrospinal fluid. *Mol. Psychiatry* **19**, 228-234 (2014).
7 Wade, T.D., *et al.* Genetic variants associated with disordered eating. *Int. J. Eat. Disord.* **46**, 594-608 (2013).
8 Hart, A.B., *et al.* Genome-wide association study of d-amphetamine response in healthy volunteers identifies putative associations, including cadherin 13 (CDH13). *PLoS ONE* **7**, e42646 (2012).
9 Rietveld, C.A., *et al.* Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. *Proc. Natl. Acad. Sci. U. S. A.* **111**, 13790-13794 (2014).
10 Winham, S.J., *et al.* Genome-wide association study of bipolar disorder accounting for effect of body mass index identifies a new risk allele in TCF7L2. *Mol. Psychiatry* **19**, 1010-1016 (2014).
11 Wang, K., *et al.* A genome-wide association study on obesity and obesity-related traits. *PLoS ONE* **6**, e18939 (2011).
12 Vasan, R.S., *et al.* Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA* **302**, 168-178 (2009).
13 Hancock, D.B., *et al.* Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. *Plos Genet* **8**, e1003098 (2012).
14 Niu, N., *et al.* Radiation pharmacogenomics: a genome-wide association approach to identify radiation response biomarkers using human lymphoblastoid cell lines. *Genome Res.* **20**, 1482-1492 (2010).
15 Loth, D.W., *et al.* Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nat. Genet.* **46**, 669-677 (2014).
16 Tabarki, B., Al Mutairi, F. & Al Hashem, A. The fragile site WWOX gene and the developing brain. *Exp Biol Med (Maywood)* **240**, 400-402 (2015).
17 Nanayakkara, S., *et al.* An integrative study of the genetic, social and environmental determinants of chronic kidney disease characterized by tubulointerstitial damages in the North Central Region of Sri Lanka. *J Occup Health* **56**, 28-38 (2014).
18 He, J., *et al.* Genome-wide association study identifies 8 novel loci associated with blood pressure responses to interventions in Han Chinese. *Circ Cardiovasc Genet* **6**, 598-607 (2013).
19 Deng, X., *et al.* Genome wide association study (GWAS) of Chagas cardiomyopathy in Trypanosoma cruzi seropositive subjects. *PLoS ONE* **8**, e79629 (2013).
20 Perry, J.R., *et al.* Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature* **514**, 92-97 (2014).
21 O'Donnell, P.H., *et al.* Identification of novel germline polymorphisms governing capecitabine sensitivity. *Cancer* **118**, 4063-4073 (2012).
22 Low, S.K., *et al.* Genome-wide association study of chemotherapeutic agent-induced severe neutropenia/leucopenia for patients in Biobank Japan. *Cancer Sci* **104**, 1074-1082 (2013).
23 Ellinghaus, E., *et al.* Identification of germline susceptibility loci in ETV6-RUNX1-rearranged childhood acute lymphoblastic leukemia. *Leukemia* **26**, 902-909 (2012).
24 Seppala, I., *et al.* Genome-wide association study on dimethylarginines reveals novel AGXT2 variants associated with heart rate variability but not with overall mortality. *Eur. Heart J.* **35**, 524-531 (2014).
25 Clark, S.L., *et al.* Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. *Psychol. Med.* **42**, 1151-1162 (2012).
26 Eriksson, N., *et al.* Genetic variants associated with breast size also influence breast cancer risk. *Bmc Med Genet* **13**, 53 (2012).
27 Michailidou, K., *et al.* Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nat. Genet.* **45**, 353-361, 361e351-352 (2013).
28 Garcia-Closas, M., *et al.* Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nat. Genet.* **45**, 392-398, 398e391-392 (2013).
29 Lauc, G., *et al.* Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. *Plos Genet* **9**, e1003225 (2013).
30 Patel, Y.M., *et al.* The contribution of common genetic variation to nicotine and cotinine glucuronidation in multiple ethnic/racial populations. *Cancer Epidemiol. Biomarkers Prev.* **24**, 119-127 (2015).
31 Roubertie, A., *et al.* Neuroradiological findings expand the phenotype of OPA1-related mitochondrial dysfunction. *J. Neurol. Sci.* **349**, 154-160 (2015).

Lasky-Su, J., *et al.* Genome-wide association scan of quantitative traits for attention deficit hyperactivity disorder identifies novel associations and confirms candidate gene associations. *Am J Med Genet B Neuropsychiatr Genet* **147B**, 1345-1354 (2008).

Chung, S.J., *et al.* Genomic determinants of motor and cognitive outcomes in Parkinson's disease. *Parkinsonism Relat Disord* **18**, 881-886 (2012).

Meigs, J.B., *et al.* Genome-wide association with diabetes-related traits in the Framingham Heart Study. *Bmc Med Genet* **8 Suppl 1**, S16 (2007).

Verhoeven, V.J., *et al.* Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nat. Genet.* **45**, 314-318 (2013).

Shi, Y., *et al.* Genome-wide association study identifies eight new risk loci for polycystic ovary syndrome. *Nat. Genet.* **44**, 1020-1025 (2012).

Ahsan, H., *et al.* A genome-wide association study of early-onset breast cancer identifies PFKM as a novel breast cancer gene and supports a common genetic spectrum for breast cancer at any age. *Cancer Epidemiol. Biomarkers Prev.* **23**, 658-669 (2014).

Caporaso, N., *et al.* Genome-wide and candidate gene association study of cigarette smoking behaviors. *PLoS ONE* **4**, e4653 (2009).

Daly, A.K., *et al.* HLA-B*5701 genotype is a major determinant of drug-induced liver injury due to flucloxacillin. *Nat. Genet.* **41**, 816-819 (2009).

Cha, P.C., *et al.* A genome-wide association study identifies SNP in DCC is associated with gallbladder cancer in the Japanese population. *J. Hum. Genet.* **57**, 235-237 (2012).

Fransen, E., *et al.* Genome-wide association analysis demonstrates the highly polygenic character of age-related hearing impairment. *Eur. J. Hum. Genet.* **23**, 110-115 (2015).

Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature* **447**, 661-678 (2007).

Jiang, Y. & Zhang, H. Propensity score-based nonparametric test revealing genetic variants underlying bipolar disorder. *Genet. Epidemiol.* **35**, 125-132 (2011).

Wang, K.S., Liu, X.F. & Aragam, N. A genome-wide meta-analysis identifies novel loci associated with schizophrenia and bipolar disorder. *Schizophr. Res.* **124**, 192-199 (2010).

Fellay, J., *et al.* Common genetic variation and the control of HIV-1 in humans. *Plos Genet* **5**, e1000791 (2009).

Wilk, J.B., Walter, R.E., Laramie, J.M., Gottlieb, D.J. & O'Connor, G.T. Framingham Heart Study genome-wide association: results for pulmonary function measures. *Bmc Med Genet* **8 Suppl 1**, S8 (2007).

Ripke, S., *et al.* Biological insights from 108 schizophrenia-associated genetic loci. *Nature* **511**, 421-+ (2014).

Ripke, S., *et al.* Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nat. Genet.* **45**, 1150-1159 (2013).

PGC. Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. *Lancet* **381**, 1371-1379 (2013).

Aberg, K., *et al.* Genome-wide association study of antipsychotic-induced QTc interval prolongation. *Pharmacogenomics J* **12**, 165-172 (2012).

Melzer, D., *et al.* A genome-wide association study identifies protein quantitative trait loci (pQTLs). *Plos Genet* **4**, e1000072 (2008).

Levy, D., *et al.* Genome-wide association study of blood pressure and hypertension. *Nat. Genet.* **41**, 677-687 (2009).

Lowe, J.K., *et al.* Genome-wide association studies in an isolated founder population from the Pacific Island of Kosrae. *Plos Genet* **5**, e1000365 (2009).

Ehret, G.B., *et al.* Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* **478**, 103-109 (2011).

Fatemifar, G., *et al.* Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. *Hum. Mol. Genet.* **22**, 3807-3817 (2013).

Comuzzie, A.G., *et al.* Novel genetic loci identified for the pathophysiology of childhood obesity in the Hispanic population. *PLoS ONE* **7**, e51954 (2012).

Wain, L.V., *et al.* Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nat. Genet.* **43**, 1005-1011 (2011).

Chung, S., *et al.* A genome-wide association study of chemotherapy-induced alopecia in breast cancer patients. *Breast Cancer Res* **15**, R81 (2013).

Jostins, L., *et al.* Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature* **491**, 119-124 (2012).

Wei, S., *et al.* Genome-wide gene-environment interaction analysis for asbestos exposure in lung cancer susceptibility. *Carcinogenesis* **33**, 1531-1537 (2012).

Anney, R.J., *et al.* Conduct disorder and ADHD: evaluation of conduct problems as a categorical and quantitative trait in the international multicentre ADHD genetics study. *Am J Med Genet B Neuropsychiatr Genet* **147B**, 1369-1378 (2008).

Sonuga-Barke, E.J., *et al.* Does parental expressed emotion moderate genetic effects in ADHD? An exploration using a genome wide association scan. *Am J Med Genet B Neuropsychiatr Genet* **147B**, 1359-1368 (2008).

Aberg, K., *et al.* Genomewide association study of movement-related adverse antipsychotic effects. *Biol. Psychiatry* **67**, 279-282 (2010).

Byrne, E.M., *et al.* A genome-wide association study of sleep habits and insomnia. *Am J Med Genet B Neuropsychiatr Genet* **162B**, 439-451 (2013).

Stambolian, D., *et al.* Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. *Hum. Mol. Genet.* **22**, 2754-2764 (2013).

Simpson, C.L., *et al.* Genome-wide meta-analysis of myopia and hyperopia provides evidence for replication of 11 loci. *PLoS ONE* **9**, e107110 (2014).

Hoffmann, T.J., *et al.* Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. *Hum. Mol. Genet.* **23**, 6634-6643 (2014).

Bunyavanich, S., *et al.* Integrated genome-wide association, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathway in allergic rhinitis. *BMC Med Genomics* **7**, 48 (2014).

Grassi, M.A., *et al.* Genome-wide meta-analysis for severe diabetic retinopathy. *Hum. Mol. Genet.* **20**, 2472-2481 (2011).

Gieger, C., *et al.* Genetics meets metabolomics: a genome-wide association study of metabolite profiles in human serum. *Plos Genet* **4**, e1000282 (2008).

Demirkan, A., *et al.* Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *Plos Genet* **8**, e1002490 (2012).

Ozel, A.B., *et al.* Genome-wide association study and meta-analysis of intraocular pressure. *Hum. Genet.* **133**, 41-57 (2014).

Teumer, A., *et al.* Genome-wide association study of chronic periodontitis in a general German population. *J. Clin. Periodontol.* **40**, 977-985 (2013).

Khor, C.C., *et al.* Genome-wide association study identifies susceptibility loci for dengue shock syndrome at MICB and PLCE1. *Nat. Genet.* **43**, 1139-1141 (2011).

Kohannim, O., *et al.* Discovery and Replication of Gene Influences on Brain Structure Using LASSO Regression. *Front Neurosci* **6**, 115 (2012).

Kohannim, O., *et al.* Predicting Temporal Lobe Volume on Mri from Genotypes Using L(1)-L(2) Regularized Regression. *Proc IEEE Int Symp Biomed Imaging* , 1160-1163 (2012).

Gudbjartsson, D.F., *et al.* Many sequence variants affecting diversity of adult human height. *Nat. Genet.* **40**, 609-615 (2008).

Kim, J.J., *et al.* Identification of 15 loci influencing height in a Korean population. *J. Hum. Genet.* **55**, 27-31 (2010).

He, M., *et al.* Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. *Hum. Mol. Genet.* **24**, 1791-1800 (2015).

Lango Allen, H., *et al.* Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature* **467**, 832-838 (2010).

Wood, A.R., *et al.* Defining the role of common variation in the genomic and biological architecture of adult human height. *Nat. Genet.* **46**, 1173-1186 (2014).

Berndt, S.I., *et al.* Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nat. Genet.* **45**, 501-512 (2013).

83 Prescott, J., *et al.* Genome-wide association study of circulating estradiol, testosterone, and sex hormone-binding globulin in postmenopausal women. *PLoS ONE* **7**, e37815 (2012).
84 Cai, D.C., *et al.* A genome-wide search for quantitative trait loci affecting the cortical surface area and thickness of Heschl's gyrus. *Genes Brain Behav* **13**, 675-685 (2014).
85 De Moor, M.H., *et al.* Genome-wide association study of exercise behavior in Dutch and American adults. *Med. Sci. Sports Exerc.* **41**, 1887-1895 (2009).
86 Lemaitre, R.N., *et al.* Genetic loci associated with circulating levels of very long-chain saturated fatty acids. *J. Lipid Res.* **56**, 176-184 (2015).
87 Trevino, L.R., *et al.* Germline genomic variants associated with childhood acute lymphoblastic leukemia. *Nat. Genet.* **41**, 1001-1005 (2009).