

## GWAS Meta-Analysis of Neuroticism (N=449,484) Identifies Novel Genetic Loci and Pathways

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1 Neuroticism is an important risk factor for psychiatric traits including depression<sup>1</sup>, anxiety<sup>2,3</sup>,  
2 and schizophrenia<sup>4-6</sup>. Previous genome-wide association studies<sup>7-12</sup> (GWAS) reported 16  
3 genomic loci<sup>10-12</sup>. Here we report the largest neuroticism GWAS meta-analysis to date  
4 (N=449,484), and identify 136 independent genome-wide significant loci (124 novel),  
5 implicating 599 genes. Extensive functional follow-up analyses show enrichment in several  
6 brain regions and involvement of specific cell-types, including dopaminergic neuroblasts  
7 ( $P=3\times 10^{-8}$ ), medium spiny neurons ( $P=4\times 10^{-8}$ ) and serotonergic neurons ( $P=1\times 10^{-7}$ ). Gene-set  
8 analyses implicate three specific pathways: neurogenesis ( $P=4.4\times 10^{-9}$ ), behavioural response  
9 to cocaine processes ( $P=1.84\times 10^{-7}$ ), and axon part ( $P=5.26\times 10^{-8}$ ). We show that neuroticism's  
10 genetic signal partly originates in two genetically distinguishable subclusters<sup>13</sup> (*depressed*  
11 *affect* and *worry*, the former being genetically strongly related to depression,  $r_g=0.84$ ),  
12 suggesting distinct causal mechanisms for subtypes of individuals. These results vastly enhance  
13 our neurobiological understanding of neuroticism, and provide specific leads for functional  
14 follow-up experiments.

15

16 The neuroticism meta-analysis comprised data from the UK Biobank Study (UKB, full  
17 release<sup>14</sup>; N=372,903; **Online Methods; Supplementary Fig. 1**), 23andMe, Inc.<sup>15</sup>  
18 (N=59,206), and the Genetics of Personality Consortium (GPC1<sup>9</sup>; N=17,375; **Online**  
19 **Methods**, N=449,484 in total). In all samples, neuroticism was measured through (digital)  
20 questionnaires (**Online Methods; Supplementary Information**). SNP associations were  
21 meta-analyzed using METAL<sup>16</sup>, weighted by sample size (**Online Methods**). The quantile-  
22 quantile (Q-Q) plot of the genome-wide meta-analysis on 449,484 subjects and 14,978,477  
23 SNPs showed high inflation ( $\lambda=1.65$ ) and mean  $\chi^2$  statistic (1.91) (**Fig. 1a; Supplementary**  
24 **Table 1**). The LD score regression (LDSC)<sup>17,18</sup> intercept (1.02; SE=0.01) was consistent with

25 inflation due to true polygenicity and large sample size. The LDSC SNP-based heritability  
26 ( $h^2_{SNP}$ ) of neuroticism was 0.100 (SE=0.003).

27 The GWAS meta-analysis identified 9,745 genome-wide significant (GWS) SNPs ( $P < 5 \times 10^{-8}$ ),  
28 of which 157 and 2,414 were located in known associated inversions on chromosomes 8 and  
29 17<sup>10-12</sup>, respectively (**Supplementary Table 2; Fig. 1b; Supplementary Fig. 2**). FUMA<sup>19</sup>, a  
30 tool to functionally map and annotate GWAS results (**Online Methods**), extracted 170  
31 independent lead SNPs (158 novel; see **Supplementary information** for definition of lead  
32 SNPs), which mapped to 136 independent genomic loci (124 novel; **Online Methods**;  
33 **Supplementary information; Supplementary Table 3-8**). Of all lead SNPs, 4 were in exonic,  
34 88 in intronic, and 52 in intergenic regions. Of the 17,794 SNPs in high LD with one of the  
35 independent significant SNPs (see **Supplementary information** for definition of independent  
36 significant SNPs), most were intronic (9,147: 51,4%) or intergenic (5,460: 30,7%), and 3.8%  
37 was annotated as potentially having a functional impact, with 0.9% (155 SNPs) being exonic  
38 (**Fig. 1c, Supplementary Table 9**; see **Supplementary Tables 10-11** for an overview of  
39 chromatin state and regulatory functions of these SNPs). Of these, 37 were exonic non-  
40 synonymous (ExNS) (**Table 1, Supplementary Table 12**). The highest CADD score (34) of  
41 ExNS SNPs was for rs17651549, in exon 6 of *MAPT*, with a GWAS  $P$ -value of  $1.11 \times 10^{-28}$ , in  
42 high LD with the lead SNP in that region ( $r^2=0.97$ ). rs17651549 is a missense mutation leading  
43 to an Arginine to Tryptophan change with allele frequencies matching the inversion in that  
44 region. The ancestral allele C is associated with a lower neuroticism score (see **Table 1** and  
45 **Supplementary Table 12** for a detailed overview of all functional variants in genomic risk  
46 loci).

47 Stratified LDSC<sup>20</sup> (**Online Methods**), showed significant enrichment for  $h^2$  of SNPs located  
48 in conserved regions (enrichment=13.79,  $P=5.14 \times 10^{-16}$ ), intronic regions (enrichment=1.27,

49  $P=1.27\times 10^{-6}$ ), and in H3K4me3 (enrichment=2.14,  $P=1.02\times 10^{-5}$ ) and H3K9ac regions  
50 (enrichment=2.17,  $P=3.06\times 10^{-4}$ ) (**Fig. 1d; Supplementary Table 13**).

51 Polygenic scores (PGS) calculated using PRSice<sup>21</sup> (clumping followed by  $P$ -value  
52 thresholding) and LDpred<sup>22</sup> in three randomly drawn hold-out samples (UKB only, N=3,000  
53 each; **Online Methods**), explained up to 4.2% ( $P=1.49\times 10^{-30}$ ) of the variance in neuroticism  
54 (**Supplementary Fig. 3; Supplementary Table 14**).

55 We used four strategies to link our SNP results to genes: positional, eQTL, and chromatin  
56 interaction mapping (**Online Methods**) and genome-wide gene-association analysis  
57 (GWGAS; MAGMA<sup>23</sup>). GWGAS evaluates the joint association effect of all SNPs within a  
58 gene yielding a gene-based  $P$ -value. Based on our meta-analytic results, 283 genes were  
59 implicated through positional mapping, 369 through eQTL-mapping, and 119 through  
60 chromatin interaction-mapping (**Fig. 2a; Supplementary Table 15**). GWGAS identified 336  
61 GWS genes ( $P<2.75\times 10^{-6}$ , **Figs. 2b-c; Supplementary Table 16, Supplementary**  
62 **information**), of which 203 overlapped with genes implicated by FUMA, resulting in 599  
63 unique neuroticism-related genes. Of these, 50 were implicated by all four methods, of which  
64 49 had chromatin interaction and eQTL associations in the same tissue/cell type (**Fig. 2a,**  
65 **Supplementary Table 15**).

66  
67 19 of the 119 genes implicated through chromatin interaction mapping are especially  
68 interesting as they are implicated via interactions between two independent GWS genomic risk  
69 loci. There are several chromatin interactions in 7 tissue types (aorta, hippocampus, left  
70 ventricle, right ventricle, liver, spleen, pancreas) across two risk loci on chromosome 6 (**Fig.**  
71 **3a**). Two genes are located in locus 45 and are mapped by chromatin interactions from risk  
72 locus 46 (*HFE* and *HIST1H4C*), and another 16 genes are coding histones in locus 46 and are  
73 mapped by interactions from locus 45 (**Supplementary Table 15**). *XKRR6* is located on

74 chromosome 8 in risk locus 61, and is implicated by chromatin interactions in 5 tissue types  
75 (aorta, left ventricle, liver, pancreas and spleen) including cross locus interactions from locus  
76 60 (**Fig. 3b; Supplementary Table 15**). This gene is also mapped by eQTLs in blood and  
77 transformed fibroblasts. Out of the 19 genes mapped by two loci, 4 are located outside of the  
78 risk loci (*HIST1H2AI*, *HIST1H3H*, *HIST1H2AK* and *HIST1H4L*), and 7 are also implicated by  
79 eQTLs in several tissue types (*HFE* in adipose subcutaneous, aorta, esophagus muscularis,  
80 lung, tibial nerve, sub-exposed skin and thyroid; *HIST1H4J* in blood and adrenal gland;  
81 and *HIST1H4K*, *HIST1H2AK*, *HIST1H2BO* and *XKR6* in blood).

82

83 Gene-based *P*-values were used for gene-set analysis in MAGMA<sup>23,26</sup>, testing 7,246 pre-  
84 defined gene-sets derived from MsigDB<sup>24</sup>, gene expression profiles in 53 tissue types obtained  
85 from the GTEx Project<sup>25</sup>, and 24 cell-type specific expression profiles using RNAseq  
86 information<sup>26</sup> (**Online Methods**). Neuroticism was significantly associated with genes  
87 predominantly expressed in 11 brain tissue types (**Fig. 2d; Supplementary Table 17-18**) and  
88 with 7 gene ontology (GO) gene-sets, with the strongest association for neurogenesis  
89 ( $P=0.0004$ ) and neuron differentiation ( $P=0.002$ ) (**Supplementary Table 17**). Conditional  
90 gene-set analyses (**Online Methods**) suggested that 3 of the 7 gene-sets (neurogenesis,  
91  $P=4.4\times 10^{-9}$ ; behavioral response to cocaine,  $P=1.84\times 10^{-7}$ ; axon part,  $P=5.26\times 10^{-8}$ ) had largely  
92 independent associations, implying a role in neuroticism (**Supplementary Table 19**).  
93 Conditional analyses of the tissue-specific expression ascertained general involvement of  
94 (frontal) cortex expressed genes (**Supplementary Table 20; Supplementary Fig. 4**).  
95 Cell type specific gene-set analysis showed significant association with genes expressed in  
96 multiple brain cell types (**Fig. 2e; Supplementary Table 21**), with dopaminergic neuroblasts  
97 ( $P=3\times 10^{-8}$ ), medium spiny neurons ( $P=4\times 10^{-8}$ ) and serotonergic neurons ( $P=1\times 10^{-7}$ ) showing

98 the strongest associations, and conditional analysis indicated that these three cell types were  
99 also independently associated with neuroticism.

100 Aiming to further specify neuroticism's neurobiological interpretation, we compared the  
101 genetic signal of the full neuroticism trait to that of two genetically distinguishable neuroticism  
102 subclusters *depressed affect* and *worry*<sup>13</sup> (**Online Methods**). As a validation of the *depressed*  
103 *affect* dimension, we also compare with GWAS results for depression. GWA analyses of the  
104 subclusters were conducted on the UKB-data only (dictated by item-level data availability;  
105 **Online Methods**; *depressed affect*, N=357,957; *worry*, N=348,219). For depression, our meta-  
106 analysis comprised data from the UKB<sup>14</sup> (N=362,696; **Supplementary Fig. 5**), 23andMe<sup>15</sup>  
107 (N=307,354), and the Psychiatric Genetics Consortium (PGC<sup>27</sup>; N=18,759) (total N=688,809,  
108 not previously published;  $r_g$  between samples: 0.61-0.80; **Online Methods**; **Supplementary**  
109 **Table 22, Supplementary Information**). Genetic correlations of neuroticism with all three  
110 phenotypes were considerable (depression:  $r_g=0.79$ ; *depressed affect*:  $r_g=0.88$ , *worry*:  $r_g=0.87$ ;  
111 **Supplementary Table 23**).

112 The subclusters showed notable differences in genetic signal (e.g., exclusive GWS associations  
113 on chromosomes 2 and 19 for *depressed affect*, and chromosomes 3 and 22 for *worry*;  
114 **Supplementary Figs. 6-12; Supplementary Tables 24-26**). Of the 136 genetic loci associated  
115 with neuroticism, 32 were also GWS for *depressed affect* (7 shared with depression) but not  
116 for *worry*, and 26 were also GWS for *worry* (3 shared with depression) but not for *depressed*  
117 *affect* (**Supplementary Table 27; Supplementary Fig. 12**). These results were mirrored by  
118 gene-based analyses (**Supplementary information; Supplementary Tables 28-30;**  
119 **Supplementary Fig. 13**), suggesting that part of neuroticism's genetic signal originates  
120 specifically in one of the two subclusters, possibly implicating different causal genetic  
121 mechanisms .

122 To test specificity of the gene-sets implicated in neuroticism in the conditional analyses, we  
123 repeated the analyses, but now corrected for *depressed affect*, and *worry* scores, respectively  
124 (**Supplementary Table 31; Supplementary Fig. 14**). The association with ‘axon-part’ was  
125 markedly lower after correction for *worry* scores (uncorrected  $P=5.26\times 10^{-8}$ ; corrected for  
126 *depressed affect*  $P=2.42\times 10^{-6}$ ; corrected for *worry*  $P=.0013$ ), suggesting that the involvement  
127 of ‘axon-part’ in neuroticism originates predominantly from the *worry*-component.

128

129 To examine the genetic correlational pattern of neuroticism, and to compare it to the patterns  
130 observed for depression, *depressed affect* and *worry*, we used LDSC to calculate genetic  
131 correlations with 35 traits for which large-scale GWAS summary statistics were available  
132 (**Supplementary Table 32; Online Methods**). We observed 11 Bonferroni-corrected  
133 significant genetic correlations for neuroticism ( $\alpha=0.05/(4\times 35)$ ;  $P<3.6\times 10^{-4}$ ) (**Fig. 4;**  
134 **Supplementary Table 33**), covering previously reported psychiatric traits ( $r_g$  range: .20-.82)  
135 and subjective well-being ( $r_g= -.68$ ). These correlations were supported by enrichment of  
136 neuroticism genes in sets of genes previously implicated in psychiatric traits (**Supplementary**  
137 **Table34**). The  $r_g$ 's of depression and *depressed affect* strongly mirrored each other (correlation  
138 between their  $r_g$ 's is  $r=.98$ ; **Supplementary information**), validating the *depressed affect*  
139 cluster. The correlational patterns for *depressed affect* and *worry* were markedly different and  
140 sometimes antipodal, with the genetic signal of the full neuroticism trait being a blend of both.

141

142 In conclusion, we identified 119 novel genetic loci for neuroticism. Extensive functional  
143 annotations highlighted several genes being implicated through multiple routes. We  
144 demonstrated the involvement of specific neuronal cell types and three independently  
145 associated genetic pathways, and established the genetic multidimensionality of the  
146 neuroticism phenotype, and its link with depression. The current study provides new leads, and

147 testable functional hypotheses for unraveling the neurobiology of neuroticism, its subtypes,  
148 and genetically associated traits.  
149



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256 <https://github.com/bulik/ldsc>

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270

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287

288 **Table 1. Exonic non-synonymous (ExNS) variants in the genomic loci associated with neuroticism and in LD ( $r^2>0.6$ ) with one of the**  
 289 **independent GWS SNPs.**

290 CADD: CADD score; rdb: regulome DB score; MAF: minor allele frequency; Z-score: z-score from the GWAS meta-analysis in METAL. Results  
 291 are reported on hg19 coordinates (NCBI b37). Genes containing multiple ExNS are annotated in red.  
 292

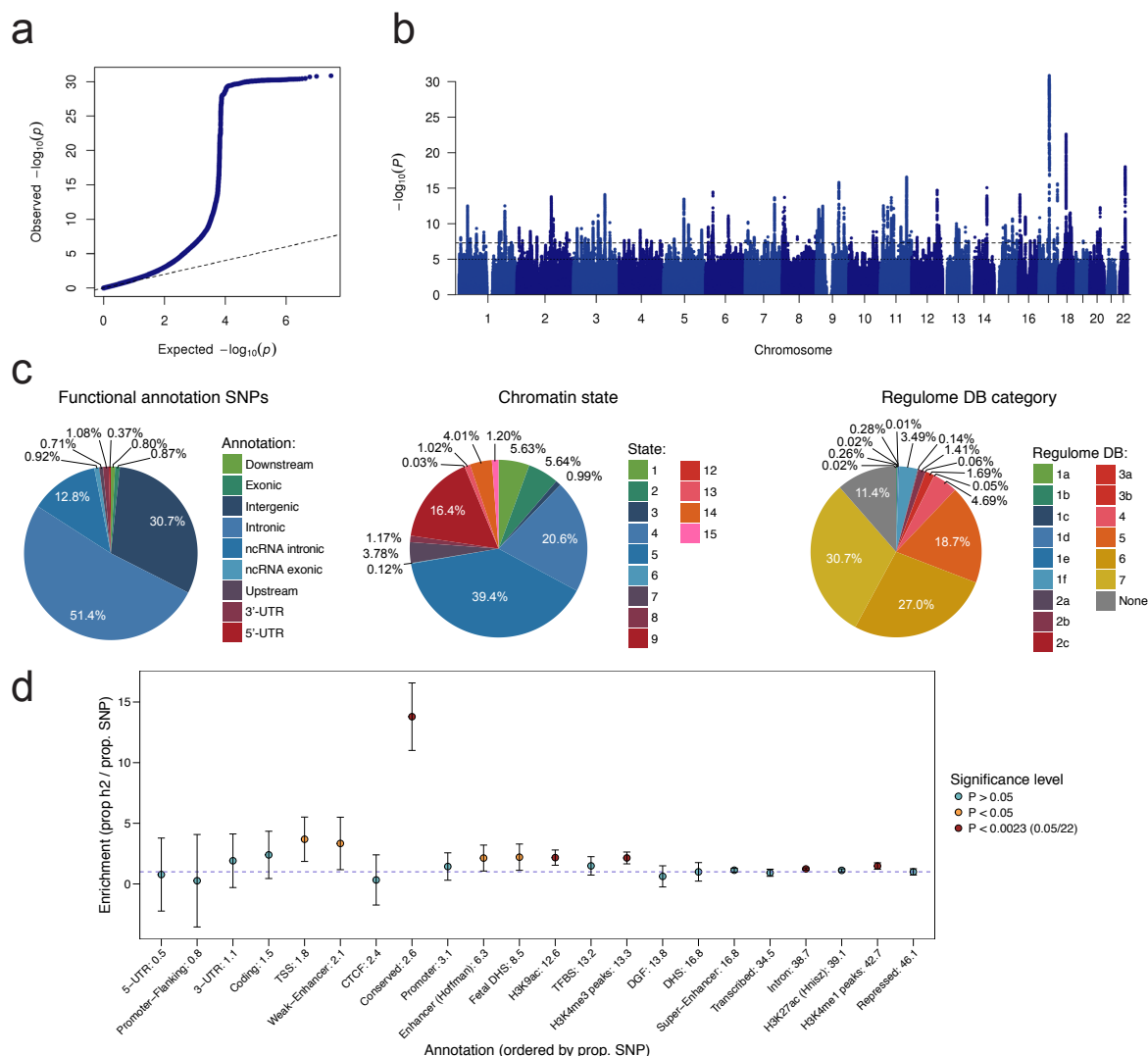
rsID	Exon	Gene	A1	MAF	gwas P	beta	$r^2$	Independent Sign. SNP	Locus	CADD	RDB	Min. Chromatin state
rs41266050	14	RABGAP1L	T	0.25	5.65E-06	-4.54	0.84	rs7536102	6	2.85	7	5
rs2073498	2	RASSF1	A	0.11	2.71E-08	5.56	0.98	rs6776145	25	19.43	7	3
rs111177	3	<b>GNL3</b>	A	0.38	2.49E-07	-5.16	0.75	rs2015971	26	22.90	NA	1
rs2289247	11	<b>GNL3</b>	A	0.41	2.28E-06	-4.73	0.65	rs2015971	26	12.82	NA	3
rs1029871	4	NEK4	C	0.38	2.29E-07	-5.17	0.75	rs2015971	26	24.10	1f	2
rs240780	39	ASCC3	C	0.43	3.01E-08	5.54	0.96	rs240769	49	19.95	7	4
rs11765552	11	LMTK2	A	0.46	7.68E-08	5.38	0.98	rs34320230	55	12.24	6	4
rs41274386	2	<b>FAM120AOS</b>	T	0.08	1.10E-07	5.31	0.66	rs78046549	71	2.36	4	1
rs1055710	1	<b>FAM120AOS</b>	A	0.33	1.11E-09	-6.09	0.99	rs10821129	71	0.05	NA	1
rs3816614	33	LRP4	T	0.23	5.69E-07	5.00	0.90	rs7940441	84	22.70	NA	4
rs2030166	5	NDUFS3	T	0.35	2.02E-10	-6.36	0.93	rs11039389	84	3.13	6	4
rs1064608	13	MTCH2	C	0.35	1.15E-10	-6.45	0.93	rs11039389	84	25.40	6	4
rs12286721	13	AGBL2	A	0.45	7.81E-08	-5.37	0.78	rs7107356	84	14.22	1f	5
rs4926	8	SERPING1	A	0.27	6.12E-07	4.99	0.86	rs73480560	85	23.50	5	4
rs11604671	6	<b>ANKK1</b>	A	0.49	2.57E-10	-6.32	0.64	rs2186800	88	1.39	5	4
rs1800497	8	<b>ANKK1</b>	A	0.20	8.45E-06	4.45	0.69	rs11214607	88	0.81	NA	4
rs7298565	12	UBE3B	A	0.48	2.24E-10	6.34	0.76	rs2111216	94	22.70	6	4
rs8007859	10	EXD2	T	0.39	2.28E-08	5.59	0.80	rs1275411	108	3.95	5	4
rs2286913	4	<b>RPS6KL1</b>	A	0.37	1.46E-07	5.26	0.89	rs3213716	110	12.96	5	2
rs7156590	3	<b>RPS6KL1</b>	T	0.37	2.79E-07	5.14	0.86	rs3213716	110	19.46	5	4
rs12443627	1	ENSG00000268863	C	0.37	1.28E-10	6.43	0.77	rs3751855	119	3.58	2b	1
rs35713203	2	<b>ZNF646</b>	C	0.38	3.67E-11	-6.62	0.98	rs3751855	119	0.05	2b	3
rs7196726	2	<b>ZNF646</b>	A	0.38	1.29E-11	-6.77	1.00	rs3751855	119	0.00	2b	3
rs7199949	8	PRSS53	C	0.38	1.32E-11	-6.77	1.00	rs3751855	119	0.00	2b	2
rs3748400	12	ZCCHC14	T	0.23	8.83E-09	-5.75	0.98	rs2042395	122	24.00	5	4
rs12949256	1	ARHGAP27	T	0.19	1.47E-23	10.00	0.73	rs77804065	126	11.97	4	1
rs16940674	6	<b>CRHR1</b>	T	0.23	5.24E-29	11.18	0.97	rs77804065	126	12.86	1f	5
rs16940681	13	<b>CRHR1</b>	C	0.23	2.18E-30	11.46	0.97	rs77804065	126	1.76	4	5
rs242944	1	<b>SPPL2C</b>	A	0.44	2.88E-12	-6.98	1.00	rs242947	126	0.00	NA	5
rs62054815	1	<b>SPPL2C</b>	A	0.23	1.74E-30	11.48	0.97	rs77804065	126	0.00	5	5
rs12185233	1	<b>SPPL2C</b>	C	0.23	6.76E-29	11.16	0.96	rs77804065	126	25.60	1f	5
rs12373139	1	<b>SPPL2C</b>	A	0.23	2.19E-30	11.46	0.97	rs77804065	126	0.53	1f	5
rs63750417	6	<b>MAPT</b>	T	0.23	4.89E-30	11.39	0.97	rs77804065	126	8.68	5	4

rsID	Exon	Gene	A1	MAF	gwas P	beta	r <sup>2</sup>	Independent Sign. SNP	Locus	CADD	RDB	Min. Chromatin state
rs62063786	6	MAPT	A	0.23	1.05E-29	11.32	0.97	rs77804065	126	7.65	5	4
rs17651549	6	MAPT	T	0.23	1.11E-28	11.11	0.97	rs77804065	126	34.00	1f	4
rs17522826	1	TCF4	A	0.18	2.17E-10	6.35	0.60	rs10503002	133	14.22	NA	1
rs139431	2	L3MBTL2	T	0.37	9.45E-07	-4.90	0.63	rs7289932	138	10.26	7	4

293

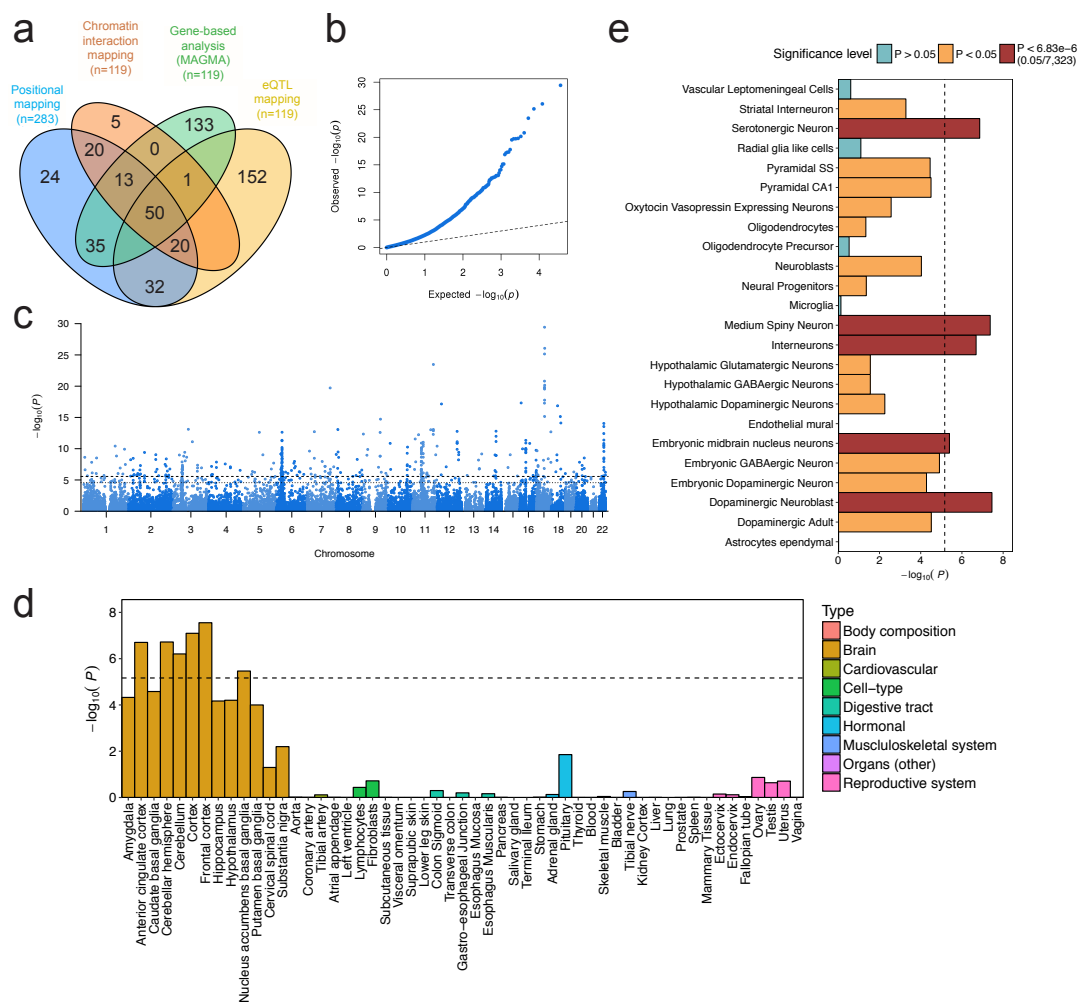


294



295

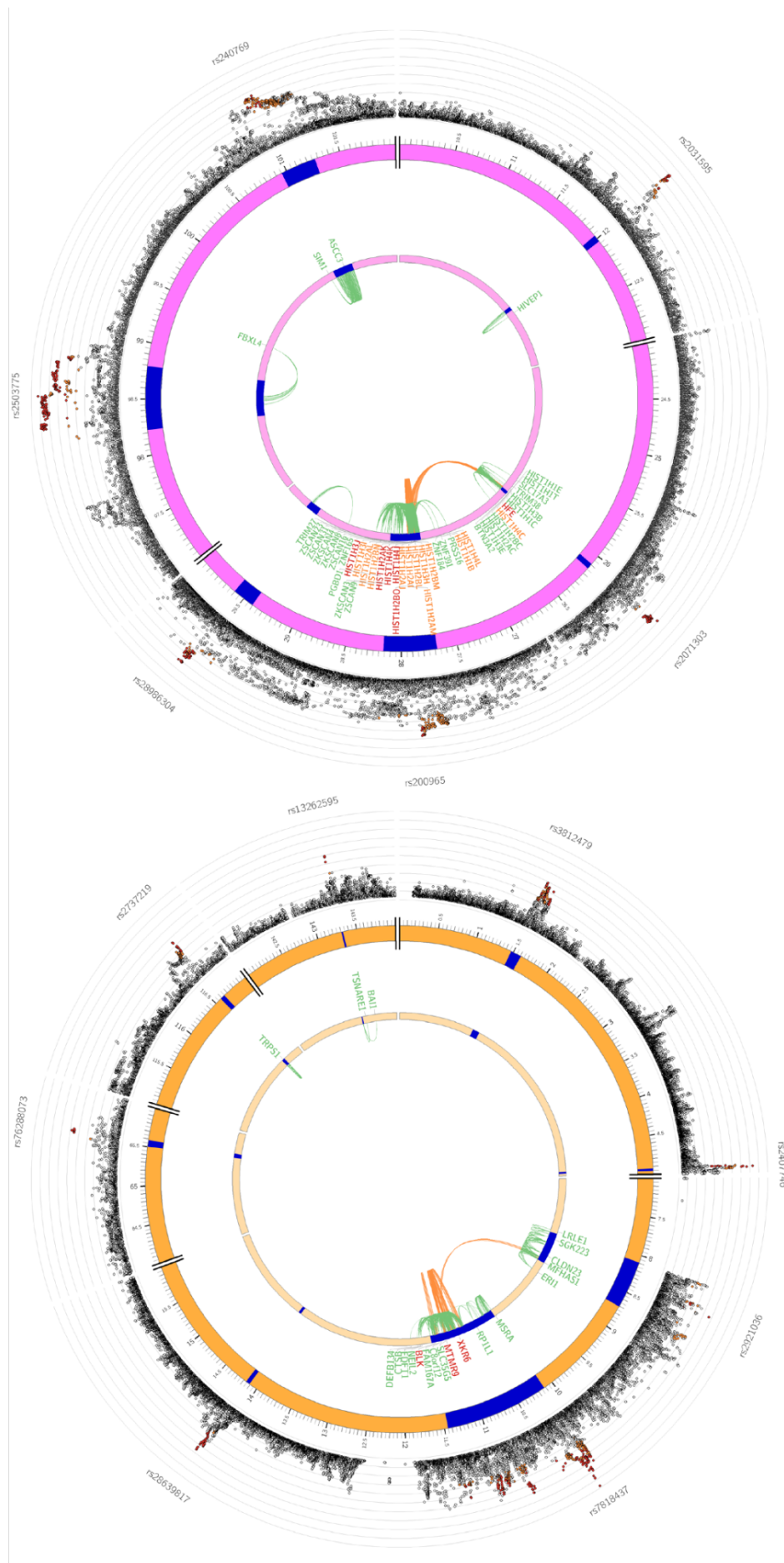
296 **Fig. 1. SNP-based associations with neuroticism in the GWAS meta-analysis.**  
 297 **(a)** Quantile-quantile plot of the SNP-based associations with neuroticism. **(b)** Manhattan plot  
 298 showing the  $-\log_{10}$  transformed  $P$ -value of each SNP on the y-axis and base pair positions  
 299 along the chromosomes on the x-axis. The dashed line indicates genome-wide significance  
 300 ( $P < 5 \times 10^{-8}$ ), the dotted line the threshold for suggestive associations ( $P < 1 \times 10^{-5}$ ). **(c)** Pie charts  
 301 showing the distribution of functional consequences of SNPs in linkage disequilibrium (LD)  
 302 with genome-wide significant lead SNPs in the meta-analysis, the minimum chromatin state  
 303 across 127 tissue and cell types and the distribution of regulome DB score, a categorical score  
 304 between 1a and 7, indicating biological evidence of a SNP being a regulatory element, with a  
 305 low score denoting a higher likelihood of being regulatory. **(d)** Heritability enrichment of 22  
 306 functional SNP annotations calculated with stratified LD score regression.  
 307



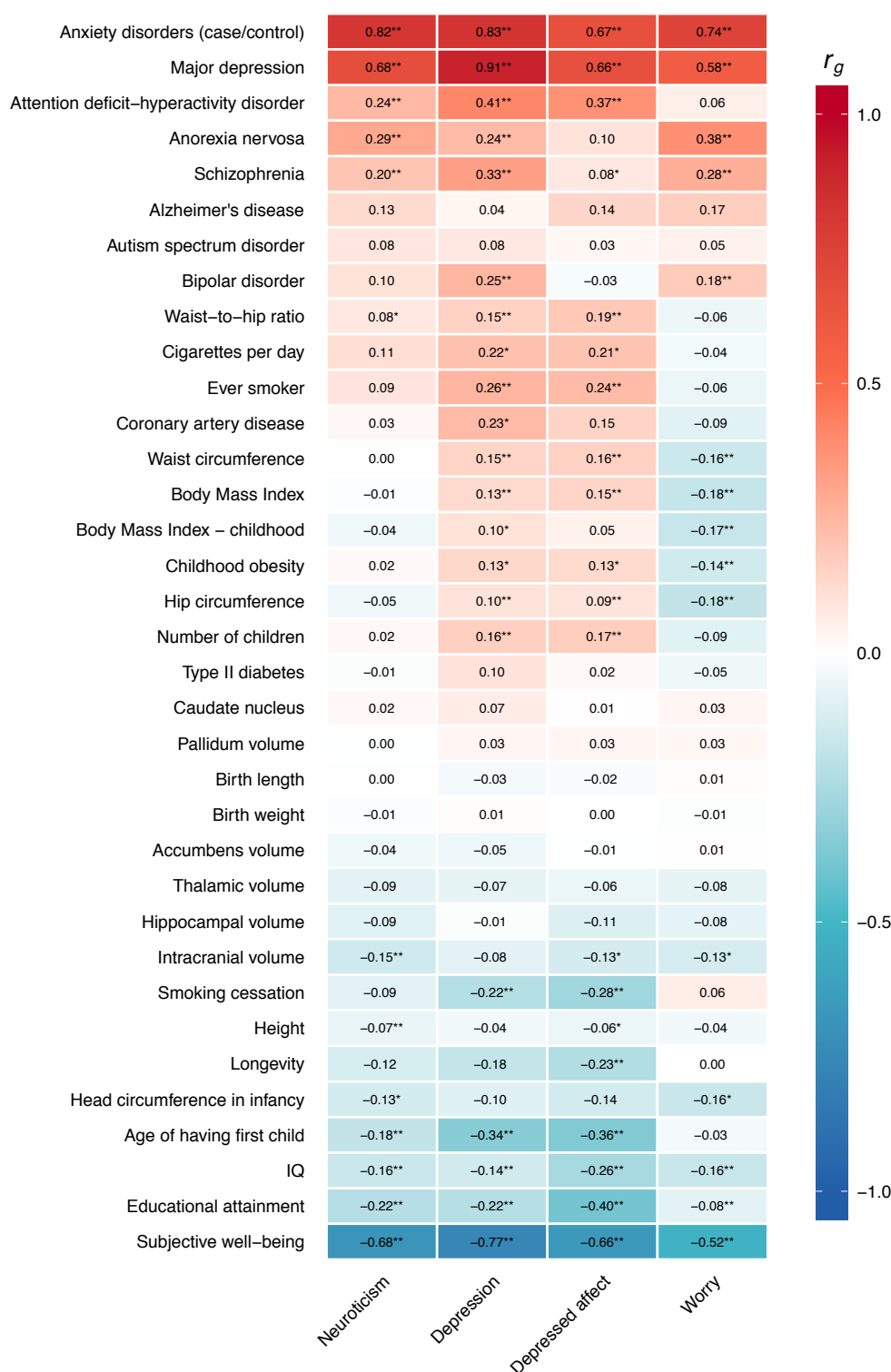
308

309 **Fig. 2. Mapping of genes and tissue- and cell expression profiles.**

310 (a) Venn diagram showing overlap of genes implicated by positional mapping, eQTL mapping,  
 311 chromatin interaction mapping, and gene-based genome-wide association (GWGAS). (b)  
 312 Quantile-quantile plot of the GWGAS. (c) Manhattan plot of the genome-wide gene-based  
 313 association analysis (GWGAS) on neuroticism. The y-axis shows the  $-\log_{10}$  transformed  $P$ -  
 314 value of each gene, and the chromosomal position (start position) on the x-axis. The dashed  
 315 line indicates the threshold for genome-wide significance of the gene-based test ( $P < 2.76 \times 10^{-6}$ ;  
 316 0.05/18,128), and the dotted line indicates the suggestive threshold ( $P < 2.76 \times 10^{-5}$ ;  
 317 0.5/18,128). (d) Gene expression profiles of identified genes for 53 tissue types. Expression  
 318 data were extracted from the Genotype-Tissue Expression (GTEx) database. Expression values  
 319 (RPKM) were  $\log_2$  transformed with pseudocount 1 after winsorization at 50 and averaged per  
 320 tissue. Gene-set tests for tissue expressions were calculated using MAGMA (**Online**  
 321 **Methods**). (e) Enrichment of genetic signal for neuroticism in 24 brain cell types. The dashed  
 322 line indicates the Bonferroni-corrected significance threshold ( $P = 0.05/7,323 = 6.83 \times 10^{-6}$ ).  
 323



325 **Fig 3. Genomic risk loci, eQTL associations and chromatin interaction for chromosome**  
326 **6 and 8, containing cross-locus interactions.**  
327 Circos plot showing genes on **(a)** chromosome 6 and **(b)** chromosome 8 that were implicated  
328 by the genomic risk (blue areas) loci by chromatin interaction (CTI; orange), eQTL (green) or  
329 implicated by both eQTL and CTI mapping (red). The outer layer shows a Manhattan plot  
330 containing the  $-\log_{10}$  transformed  $P$ -value of each SNP in the GWAS meta-analysis. Empty  
331 regions in the Manhattan plot layer indicate regions where no SNPs with  $P < 0.05$  are situated.  
332



333

334 **Fig. 4. Genetic correlations between neuroticism and other traits.**

335 Genetic correlations of neuroticism, depression, *depressed* affect and worry with various traits  
 336 and diseases. LD score regression (**Online Methods**) tested genome-wide SNP associations  
 337 for the neuroticism score against previously published results for 35 neuropsychiatric  
 338 outcomes, antropometric and health-related traits, and brain morphology (**Supplementary**  
 339 **Table 32-33**).

340

341 **Online methods**

342

343 ***Samples***

344 ***UK Biobank:*** The UK Biobank (UKB) Study is a major data resource, containing genetic and  
345 a wide range of phenotypic data of ~500,000 participants aged 40-69 at recruitment<sup>14</sup>. We used  
346 data released in July 2017, and selection (discussed below) resulted in final sample sizes of  
347 N=372,903 and N=362,696 individuals for neuroticism and depression, respectively  
348 (**Supplementary information**). The UKB received ethical approval from the National  
349 Research Ethics Service Committee North West–Haydock (reference 11/NW/0382), and all  
350 study procedures were performed in accordance with the World Medical Association for  
351 medical research. The current study was conducted under UKB application number 16406.

352 ***23andMe:*** 23andMe, Inc. is a large personal genomics company that provides genotype and  
353 health-related information to customers. For the neuroticism meta-analysis, we used  
354 neuroticism GWAS summary statistics from a subset of 23andMe research participants  
355 (N=59,206), described in more detail elsewhere<sup>10</sup>. For our depression meta-analysis, we used  
356 depression GWAS summary statistics from a subset of 23andMe research participants  
357 (N=307,354), described in detail elsewhere<sup>28</sup>. All included participants provided informed  
358 consent and were of European ancestry, and related individuals were excluded. Online data  
359 collection procedures were approved by the Ethical & Independent Review Services (E&I  
360 Review), an AAHRPP-accredited private institutional review board  
361 (<http://www.eandireview.com>).

362 ***Genetics of Personality Consortium:*** The Genetics of Personality Consortium (GCP) is a large  
363 body of cooperation concerning GWAS on personality. We used summary statistics of  
364 neuroticism from the first GCP personality meta-analysis (GPC1,  
365 <http://www.tweelingenregister.org/GPC/>)<sup>9</sup>, on 10 discovery cohorts (SardiNIA, NTR/NESDA,

366 ERF, SAGE, HBCS, NAG, IRPG, QIMR, LBC1936, BLSA, EGPOT), including in total  
367 N=17,375 participants of European descent. All included studies were approved by local ethic  
368 committees, and informed consent was obtained from all participants.

369 ***Psychiatric Genetics Consortium:*** The Psychiatric Genetics Consortium (PGC) unites  
370 investigators worldwide to conduct genetic meta- and mega-analyses for psychiatric disorders.  
371 We used summary statistics from the latest published PGC meta-analysis on depression  
372 (<http://www.med.unc.edu/pgc/results-and-downloads>)<sup>27</sup>, which included data from 8 cohorts  
373 (Bonn/Mannheim, GAIN, GenRED, GSK, MDD2000, MPIP, RADIANT, STAR\*D), covering  
374 N=18,759 participants of European descent. All included studies were approved by local ethic  
375 committees, and informed consent was obtained from all participants.

376

### 377 ***Phenotype assessment – Neuroticism***

378 ***UK Biobank:*** Neuroticism was measured with 12 dichotomous (yes/no) items of the Eysenck  
379 Personality Questionnaire Revised Short Form (EPQ-RS)<sup>29</sup>, using a touchscreen-questionnaire  
380 at the UKB assessment centers (**Supplementary Information 1.1**). Participants with valid  
381 responses to <10 items were excluded from analyses. A weighted neuroticism sum score was  
382 calculated by adding up individual valid item responses, and dividing that sum by the total  
383 number of valid responses. Scores on 4 EPQ-RS items (i.e., “Do you often feel lonely?”, “Do  
384 you ever feel ‘just miserable’ for no reason?”, “Does your mood often go up and down?”, and  
385 “Do you often feel ‘fed-up’?”) were summed to obtain scores for the cluster *depressed affect*.  
386 Similarly, scores on 4 other EPQ-RS items (i.e., “Are you a worried?”, “Do you suffer from  
387 nerves?”, “Would you call yourself a nervous person?”, and “Would you call yourself tense or  
388 highly strung”) were summed to obtain scores for the cluster *worry*. In the item-cluster  
389 analyses, only participants with complete scores on all 4 items were included, resulting in  
390 N=357,957 and N=348,219 for *depressed affect* and *worry*, respectively.



391 **23andMe**: Neuroticism was operationalized as of the sum of 8 neuroticism items (5-point  
392 Likert scale; ‘Disagree strongly’ to ‘Agree strongly’) from the Big Five Inventory (BFI<sup>30,31</sup>),  
393 as obtained in an online survey. Only participants with valid responses to all items were  
394 included in the analyses (**Supplementary Information 1.2**).

395 **Genetic Personality Consortium**: All 10 cohorts included in the first meta-analysis of the GPC  
396 used sums of the scores on 12 items (5-point Likert scale; ‘Strongly disagree’ to ‘Strongly  
397 agree’) of the NEO-FFI<sup>32</sup> to measure neuroticism. If <4 item scores were missing, data on  
398 invalid items were imputed by taking an individual’s average score on valid items. Participants  
399 were excluded from analyses if they had invalid scores on >3 items<sup>9</sup> (**Supplementary**  
400 **Information 1.3**).

401

#### 402 ***Phenotype assessment - Depression***

403 **UK Biobank**: Depression was operationalized by adding up the scores on two continuous items  
404 (“Over the past two weeks, how often have you felt down, depressed or hopeless?”, “Over the  
405 past two weeks, how often have you had little interest or pleasure in doing things?”; both  
406 evaluated on a 4-point Likert scale; ‘Not at all’ to ‘Nearly every day’), resulting in a continuous  
407 depression score (as used previously<sup>12</sup>). Only participants with scores on both items were  
408 included in the analyses, resulting in N=362,696 (**Supplementary Information 1.4**).

409

410 **23andMe**: This concerns a case-control sample. Four self-report survey items were used to  
411 determine case-control status. Cases were defined as replying affirmatively to at least one of  
412 these questions, and not replying negatively to previous ones. Controls replied negatively to at  
413 least one of the questions, and did not report being diagnosed with depression on previous ones  
414 (**Supplementary Information 1.5**).



415 ***Psychiatric Genetics Consortium:*** This concerns a case-control sample. Cases had a DSM-IV  
416 lifetime (sometimes (early onset) recurrent) major depressive disorder (MDD) diagnosis, either  
417 established through structured diagnostic interviews or clinician-administered DSM-IV  
418 checklists. Most cases were ascertained from clinical sources, while controls were randomly  
419 selected from population resources and screened for lifetime history of MDD<sup>27</sup>  
420 **(Supplementary Information 1.6).**

421

#### 422 ***Genotyping and imputation***

423 ***UK Biobank - Neuroticism:*** We used genotype data released by the UKB in July 2017. The  
424 genotype data collection and processing are described in detail by the responsible UKB  
425 group<sup>14</sup>. In short, 489,212 individuals were genotyped on two customized SNP arrays (the UK  
426 BiLEVE Axiom array (n=50,520) and UK Biobank Axiom array (n=438,692)), covering  
427 812,428 unique genetic markers (95% overlap in SNP content). After quality control  
428 procedures<sup>14</sup>, 488,377 individuals and 805,426 genotypes remained. Genotypes were phased  
429 and imputed by the coordinating team to approximately 96 million genotypes using a combined  
430 reference panel including the Haplotype Reference Consortium and the UK10K haplotype panel.  
431 Imputed and quality controlled genotype data was available for 487,422 individuals and  
432 92,693,895 genetic variants. As recommended by the UKB team, variants imputed from the  
433 UK10K reference panel were removed from the analyses due to technical errors in the  
434 imputation process.

435 In our analyses, only individuals from European descent (based on genetic principal  
436 components) were included. Therefore principal components from the 1000 Genomes  
437 reference populations<sup>33</sup> were projected onto the called genotypes available in UK Biobank.  
438 Subjects were identified as European if their projected principal component score was closest  
439 (based on the Mahalanobis distance) to the average score of the European 1000 Genomes

440 sample<sup>34</sup>. European subjects with a Mahalanobis distance > 6 S.D. were excluded. In addition,  
441 participants were excluded based on withdrawn consent, UKB provided relatedness (subjects  
442 with most inferred relatives, 3<sup>rd</sup> degree or closer, were removed until no related subjects were  
443 present), discordant sex, sex aneuploidy. After selecting individuals based on available  
444 neuroticism sum-score and active consent for participation, 372,903 individuals remained for  
445 the analyses.

446 To correct for population-stratification, 30 principal components were calculated on the subset  
447 of QC-ed unrelated European subjects based on 145,432 independent ( $r^2 < 0.1$ ) SNPs with  
448 MAF > 0.01 and INFO = 1 using FlashPC<sup>35</sup>. Subsequently, imputed variants were converted to  
449 hard call using a certainty threshold of 0.9. Multi-allelic SNPs, indels, and SNPs without unique  
450 rs id were excluded, as well as SNPs with a low imputation score (INFO score < 0.9), low minor  
451 allele frequency (MAF < 0.0001) and high missingness (> 0.05). This resulted in a total of  
452 10,847,151 SNPs used for downstream analysis.

453

454 **UK Biobank – Depression:** Similar genotyping/imputation/filtering procedures as described  
455 above for the UKB neuroticism GWAS were followed for the UKB depression GWAS,  
456 resulting in N=362,696.

457 **Other samples:** Summary statistics were used for 23andMe and PGC. Genotyping and  
458 imputation of these samples are described in detail elsewhere (23andMe depression<sup>28</sup>; PGC  
459 depression<sup>27</sup>).

460

#### 461 **Genome-wide association analyses**

462 **UK Biobank - Neuroticism:** Genome-wide association analyses were performed in PLINK<sup>36,37</sup>,  
463 using a linear regression model of additive allelic effects with age, sex, townsend deprivation  
464 index, genotype array, and 10 genetic European-based principal components as covariates.

465 **UK Biobank – Depression, depressed affect, worry:** The settings, covariates, and exclusion  
466 criteria for the UKB depression, UKB *depressed affect*, and UKB *worry* GWAS were the same  
467 as described above for UKB neuroticism GWAS, with 10,847,151 SNPs remaining after all  
468 exclusion steps.

469 **Other samples:** Summary statistics were used for 23andMe, GPC and PGC. Details on the  
470 genome-wide association analyses of these samples can be found elsewhere (23andMe  
471 neuroticism<sup>10</sup>; 23andMe depression<sup>28</sup>; GPC neuroticism<sup>9</sup>; PGC depression<sup>27</sup>).

472

### 473 **Meta-analysis**

474 **Neuroticism:** Meta-analysis of the neuroticism GWAS in UKB, 23andMe, and GPC was  
475 carried out in METAL<sup>16</sup>. The meta-analysis was performed on the *P*-value of each SNP using  
476 a sample size-weighted fixed-effects analysis. Bonferroni correction was applied to correct for  
477 multiple testing. The genetic signal correlated strongly between the three samples ( $r_g$  range:  
478 0.83 – 1.07; **Supplementary Table 1**), supporting the decision to meta-analyze.

479

480 **Depression:** Meta-analysis of the depression GWAS in UKB, 23andMe and PGC was carried  
481 out in METAL<sup>16</sup>. As the UKB GWAS concerned a continuous operationalization of the  
482 depression phenotype, while 23andMe and PGC used case-control phenotypes, the odds ratio  
483 from the 23andMe and PGC summary statistics were converted to log odds, reflecting the  
484 direction of the effect. The meta-analysis was then performed on the *P*-value of each SNP using  
485 a sample size-weighted fixed-effects analysis. Bonferroni correction was applied to correct for  
486 multiple testing. Genetic correlations between the three samples were moderate to strong ( $r_g$   
487 range: 0.61 – 0.80; **Supplementary Table 22**).

488

489

490 *Functional Annotation*

491 Functional annotation was performed using FUMA<sup>17</sup> (<http://fuma.ctglab.nl/>), an online  
492 platform for functional mapping of genetic variants. We first defined independent significant  
493 SNPs which have a genome-wide significant  $P$ -value ( $5 \times 10^{-8}$ ) and are independent at  $r^2 < 0.6$ .  
494 Lead SNPs were defined by retaining those independent significant SNPs that were  
495 independent from each other at  $r^2 < 0.1$  (based on LD information from UK Biobank genotypes;  
496 see **Supplementary Information** for a more detailed explanation). Subsequently, risk loci  
497 were defined by merging lead SNPs that physically overlapped or whose LD blocks were closer  
498 than 250kb apart. As a result, when analyzing multiple phenotypes, as in the current study, the  
499 same locus may be discovered for different phenotypes, whilst different lead SNPs are  
500 identified.

501 We selected all SNPs with  $r^2 > 0.6$  with one of the independent significant SNPs, a  $P$ -value  
502 lower than 0.05 and minor allele frequency (MAF) higher than 0.0001 for annotations.  
503 Functional consequences for all independent significant SNPs and SNPs in LD with them were  
504 obtained by performing ANNOVAR gene-based annotation using Ensembl genes. In addition,  
505 CADD scores (indicating the deleteriousness of SNP, with scores  $> 12.37$  seen as likely  
506 deleterious)<sup>38</sup> and RegulomeDB scores (with lower scores indicating a higher probability of  
507 having a regulatory function) were annotated to SNPs by matching chromosome, position,  
508 reference and alternative alleles.

509

510 *Gene-mapping*

511 SNPs in genomic risk loci that were GWS or were in LD ( $> 0.6$ ) with one of the independent  
512 GWS SNPs were mapped to genes in FUMA<sup>19</sup> using three strategies:

- 513 1. Positional mapping maps SNPs to genes based on the physical distances (i.e., within  
514 10kb window) from known protein coding genes in the human reference assembly  
515 (GRCh37/hg19).
- 516 2. eQTL mapping maps SNPs to genes with which they show a significant eQTL  
517 association (i.e. the expression of that gene is associated with allelic variation at the  
518 SNP). eQTL mapping uses information from 3 data repositories (GTEx, Blood eQTL  
519 browser BIOS QTL browser, and is based on cis-eQTLs which can map SNPs to genes  
520 up to 1Mb apart. A false discovery rate (FDR) of 0.05 was applied to define significant  
521 eQTL associations.
- 522 3. Chromatin interaction mapping was performed to map SNPs to genes based on a  
523 significant chromatin interaction between a genomic region in a risk locus and promoter  
524 regions of genes (250bp up and 500bp downstream of transcription start site (TSS)).  
525 Chromatin interaction mapping can involve long-range interactions as it does not have  
526 a distance boundary as in eQTL mapping. FUMA currently contains Hi-C data of 14  
527 tissue types from the study of<sup>39</sup>. Since chromatin interactions are often defined in a  
528 certain resolution, such as 40kb, an interacting region may span multiple genes. All  
529 SNPs within these regions would be mapped by this method to genes in the  
530 corresponding interaction region. To further prioritize candidate genes from chromatin  
531 interaction mapping, we integrated predicted enhancers and promoters in 111 tissue/cell  
532 types from the Roadmap Epigenomics Project<sup>40</sup>; chromatin interactions are selected in  
533 which one region involved in the interaction overlaps with predicted enhancers and the  
534 other region overlaps with predicted promoters in 250bp up- and 500bp downstream of  
535 TSS site of a gene. We used a FDR of  $1 \times 10^{-5}$  to define significant interactions.  
536  
537

### 538 ***Gene-based analysis***

539 A genome-wide gene association analysis (GWGAS) can identify genes in which multiple  
540 SNPs show moderate association to the phenotype of interest without reaching the stringent  
541 genome-wide significance level. At the same time, as a GWGAS takes all SNPs within a gene  
542 into account, a gene harbouring a genome-wide significant SNP may not be implicated by a  
543 GWGAS analyses when multiple other SNPs within that gene show only very weak association  
544 signal. The *P*-values from the SNP-based GWAS meta-analyses for neuroticism and  
545 depression, and the GWAS for *depressed affect* and *worry*, were used as input for the genome-  
546 wide gene association analysis (GWGAS) in MAGMA (<http://ctg.cncr.nl/software/magma>)<sup>23</sup>,  
547 and all 19,427 protein-coding genes from the NCBI 37.3 gene definitions were used. We  
548 annotated all SNPs in our GWA (meta-) analyses to these genes, resulting in 18,187, 18,187,  
549 18,182, and 18,182 genes that were represented by at least one SNP in the neuroticism meta-  
550 analysis, the depression meta-analysis, the *depressed affect* GWAS, and the *worry* GWAS,  
551 respectively. We included a window around each gene of 2 kb before the transcription start site  
552 and 1 kb after the transcription stop site. Gene association tests were performed taking into  
553 account the LD between SNPs, and a stringent Bonferroni correction was applied to correct for  
554 multiple testing (0.05/number of genes tested:  $P < 2.75 \times 10^{-6}$ ).

555

### 556 ***Gene-set analysis***

557 We used MAGMA<sup>23</sup> to test for association of predefined gene-sets with neuroticism,  
558 depression, *depressed affect*, and *worry*. A total of 7,246 gene-sets were derived from several  
559 resources, including BioCarta, KEGG, Reactome<sup>41</sup> and GO. All gene-sets were obtained from  
560 the MsigDB version 5.2 (<http://software.broadinstitute.org/gsea/msigdb/collections.jsp>). In  
561 addition, we performed gene-set analysis on 53 tissue expression profiles obtained from the  
562 GTEx portal (<https://www.gtexportal.org/home/>), and 24 cell-type specific expression profiles.

563 Definition and calculation of gene-sets for cell-type specific expression is described in detail  
564 elsewhere<sup>26,42</sup>. Briefly, brain cell-type expression data was drawn from scRNAseq data from  
565 mouse brain<sup>26</sup>. For each gene, the value for each cell-type was calculated by dividing the mean  
566 Unique Molecular Identifier (UMI) counts for the given cell type by the summed mean UMI  
567 counts across all cell types<sup>26</sup>. Associations between gene-wise  $P$ -values from the meta-analysis  
568 and cell-type specific gene expression were calculated using MAGMA<sup>23</sup>, by grouping genes  
569 into 40 equal bins by specificity of expression, and regressing bin-membership on gene-wise  
570 association with neuroticism in the meta-analysis. Results were considered significant if the  
571 association  $P$ -values were smaller than the relevant Bonferroni threshold.

572 For all gene-sets we computed competitive  $P$ -values, which result from the test whether the  
573 combined effect of genes in a gene-set is significantly larger than the combined effect of a same  
574 number of randomly selected genes (in contrast, self-contained  $P$ -values result from testing  
575 against the null hypothesis of no effect). We only report competitive  $P$ -values, which are more  
576 conservative compared to self-contained  $P$ -values. Competitive  $P$ -values were Bonferroni  
577 corrected ( $\alpha=0.05/7,323=6.83\times 10^{-6}$ ).

578 Conditional gene-set analyses were performed with MAGMA as a secondary analysis to test  
579 whether each observed enriched cell-type was independent of all others. Full details of the  
580 method implemented are provided in <sup>26</sup>.

581

## 582 ***Genetic correlations***

583 Genetic correlations ( $r_g$ ) were computed using LDscore regression<sup>17,18</sup>  
584 (<https://github.com/bulik/ldsc>). The significance of the genetic correlations of neuroticism,  
585 depression, *depressed affect* and *worry* with 35 behavioral, social and (mental) health  
586 phenotypes for which summary statistics were available was determined while correcting for

587 multiple testing through a stringent Bonferroni corrected threshold of  $P < 0.05 / (4 \times 35)$  ( $3.6 \times 10^{-4}$ ).  
588

589

### 590 *Partitioned heritability*

591 To investigate the relative contribution to the overall heritability of SNPs annotated to 22  
592 specific genomic categories, we partitioned SNP heritability by binary annotations using  
593 stratified LD score regression<sup>20,43</sup>. Information about binary SNP annotations were obtained  
594 from the LD score website (<https://github.com/bulik/ldsc>). Enrichment results reflect the X-  
595 fold increase in  $h^2$  proportional to the number of SNPs (e.g., enrichment=13.79 for SNPs in  
596 conserved regions implies that a 13,79-fold increase in  $h^2$  is carried by SNPs in these region,  
597 corrected for the proportion of SNPs in these regions compared to all tested SNPs).

598

### 599 *Polygenic risk scoring*

600 To test the predictive accuracy ( $\Delta R^2$ ) of the our meta-analytic results, we calculated a polygenic  
601 risk score (PGS) based on the SNP effect sizes of the current analysis. As independent samples  
602 we used holdout samples; we removed 3,000 individuals from the discovery sample (UKB  
603 only, as we only had access to raw data from this sample) and reran the genome-wide analyses.  
604 We repeated this three times, to create 3 randomly drawn, independent hold-out samples. Next,  
605 we calculated a PGS on the individuals in each of the 3 holdout samples. PGS were calculated  
606 using LDpred<sup>22</sup> and PRSice<sup>21</sup> (clumping followed by  $P$ -value thresholding).

607 For LDpred, PGS were calculated based on different LDpred priors ( $P_{LDpred} = 0.01, 0.05, 0.1,$   
608  $0.5, 1$  and infinitesimal). The explained variance ( $R^2$ ) was derived from the linear model, using  
609 the neuroticism summary score as the outcome, while correcting for age, gender, array, batch  
610 and genetic principal components.

611



612 ***Data availability***

613 Our policy is to make genome-wide summary statistics (sumstats) publically available.

614 Sumstats from our neuroticism meta-analysis, our depression meta-analysis, and the GWA

615 analyses for *depressed affect* and *worry* are available for download at <https://ctg.cncr.nl/>.

616 Note that our freely available meta-analytic sumstats concern results excluding the 23andMe

617 sample. This is a non-negotiable clause in the 23andMe data transfer agreement, intended to

618 protect the privacy of the 23andMe research participants. To fully recreate our meta-analytic

619 results for neuroticism: (a) obtain Lo et al. (2016) sumstats from 23andMe (see below); (b)

620 conduct a meta-analysis of our sumstats with the Lo et al. sumstats. To fully recreate our meta-

621 analytic results for depression: (a) obtain Hyde et al. (2016) sumstats from 23andMe (see

622 below); (b) conduct a meta-analysis of our sumstats with the Hyde et al. sumstats.

623 23andMe participant data are shared according to community standards that have been

624 developed to protect against breaches of privacy. Currently, these standards allow for the

625 sharing of summary statistics for at most 10,000 SNPs. The full set of summary statistics can

626 be made available to qualified investigators who enter into an agreement with 23andMe that

627 protects participant confidentiality. Interested investigators should contact David Hinds

628 ([dhinds@23andme.com](mailto:dhinds@23andme.com)) for more information.

629

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