Table S1. Associated slopes for the Figure 1. (c)

Feature	Sulcus	Hemisphere	Slope
Opening	Sylvian Fissure	left	0.0322
		right	0.0325
	Anterior Cingulate	left	0.0217
		right	0.0228
	Posterior Cingulate	left	0.0282
		right	0.0277
	Intraparietal	left	0.0252
		right	0.0232
	Central	left	0.029
		right	0.0293
	Inferior Frontal	left	0.0244
		right	0.0225
	Superior Frontal	left	0.0254
		right	0.0252
	Inferior Temporal	left	0.0145
		right	0.014
	Superior Temporal	left	0.0259
		right	0.0261
	Subparietal	left	0.02
		right	0.0206
Grey Matter Thickness	Sylvian Fissure	left	-0.019
		right	-0.0183
	Anterior Cingulate	left	-0.0181
		right	-0.0199
	Posterior Cingulate	left	-0.0125
		right	-0.0139
	Intraparietal	left	-0.0095
		right	-0.012
	Central	left	-0.0111
		right	-0.0105
	Inferior Frontal	left	-0.0145
		right	-0.0126
	Superior Frontal	left	-0.0105
		right	-0.0099
	Inferior Temporal	left	-0.0154
		right	-0.0156
	Superior Temporal	left	-0.0199
		right	-0.0194
	Subparietal	left	-0.0207
		right	-0.0244

Table S2. Heritability estimates and their associated p-values corresponding to Figure 2.

Feature	Sulcus	Left Hemisphere	Right Hemisphere
Opening	Sylvian Fissure	0.4 ± 0.048 ($5.3 \cdot 10^{-18}$)	0.423 ± 0.049 ($5.3 \cdot 10^{-19}$)
	Anterior Cingulate	0.23 ± 0.049 ($1.1 \cdot 10^{-6}$)	0.099 ± 0.048 (0.02)
	Posterior Cingulate	0.275 ± 0.049 ($7.2 \cdot 10^{-9}$)	0.19 ± 0.049 ($4.9 \cdot 10^{-5}$)
	Intraparietal	0.388 ± 0.049 ($1.6 \cdot 10^{-15}$)	0.345 ± 0.049 ($4.8 \cdot 10^{-13}$)
	Central	0.445 ± 0.049 ($1.7 \cdot 10^{-19}$)	0.349 ± 0.049 ($6.7 \cdot 10^{-13}$)
	Inferior Frontal	0.269 ± 0.049 ($1.2 \cdot 10^{-8}$)	0.317 ± 0.048 ($9.7 \cdot 10^{-12}$)
	Superior Frontal	0.246 ± 0.049 ($3.2 \cdot 10^{-7}$)	0.285 ± 0.049 ($2.4 \cdot 10^{-9}$)
	Inferior Temporal	0.151 ± 0.049 ($9.2 \cdot 10^{-4}$)	0.184 ± 0.049 ($6.6 \cdot 10^{-5}$)
	Superior Temporal	0.342 ± 0.048 ($2.4 \cdot 10^{-13}$)	0.318 ± 0.049 ($1.2 \cdot 10^{-11}$)
	Subparietal	0.198 ± 0.049 ($2.8 \cdot 10^{-5}$)	0.175 ± 0.048 ($1.1 \cdot 10^{-4}$)
Grey Matter Thickness	Sylvian Fissure	0.371 ± 0.048 ($2.8 \cdot 10^{-16}$)	0.323 ± 0.048 ($1.5 \cdot 10^{-12}$)
	Anterior Cingulate	0.218 ± 0.049 ($3.1 \cdot 10^{-6}$)	0.079 ± 0.048 (0.05)
	Posterior Cingulate	0.144 ± 0.049 ($1.3 \cdot 10^{-3}$)	0.127 ± 0.048 ($3.4 \cdot 10^{-3}$)
	Intraparietal	0.173 ± 0.048 ($1.0 \cdot 10^{-4}$)	0.239 ± 0.048 ($2.0 \cdot 10^{-7}$)
	Central	0.232 ± 0.048 ($4.2 \cdot 10^{-7}$)	0.253 ± 0.049 ($5.6 \cdot 10^{-8}$)
	Inferior Frontal	0.223 ± 0.048 ($1.2 \cdot 10^{-6}$)	0.224 ± 0.049 ($1.6 \cdot 10^{-6}$)
	Superior Frontal	0.151 ± 0.048 ($6.3 \cdot 10^{-4}$)	0.167 ± 0.048 ($2.0 \cdot 10^{-4}$)
	Inferior Temporal	0.1 ± 0.048 (0.02)	0.166 ± 0.049 ($2.6 \cdot 10^{-4}$)
	Superior Temporal	0.254 ± 0.048 ($2.9 \cdot 10^{-8}$)	0.266 ± 0.048 ($7.4 \cdot 10^{-9}$)
	Subparietal	0.159 ± 0.049 ($5.7 \cdot 10^{-4}$)	0.123 ± 0.048 ($4.9 \cdot 10^{-3}$)

Table S3. Summary GTEx information on the significant loci (GTEx Analysis Release V7 (dbGaP Accession phs000424.v7.p2))

chr	rsid	maf in ~12k subjects	Nearest gene(s)	eQTLs GTEx (meta p-val)
1	rs864736	0.45765	KCNK2	KCNK2 (multi-tissue 9.7*10^-6; significant tissue: ovary)
1	rs59084003	0.06957	KCNK2	No significant eQTLs (maf probably too low)
8	rs11774568	0.27672	DEFB136; DEFB135	Highly intergenic regions, notably significant eQTLs in brain tissues with genes ['CTSB', 'RP11-481A20.10', 'RP11-481A20.11', 'RP11-351I21.7', 'RP11-351I21.6', 'FAM66A']
9	rs10980645	0.29548	Intron of LPAR1	No significant eQTLs
12	rs12146713	0.09496	Intron of NUAK1	ENSG00000257890.1 (lincRNA) (multi-tissue 4.1*10^-28; significant tissues: skin-lower_leg; artery-tibial; adipose-subcutaneous)
16	rs9933149	0.37965	LOC101928708; C16orf95; FBXO31	ENSG00000261651.1 (antisense RNA) (p-val computed only in testis tissue 3.0*10^-7)

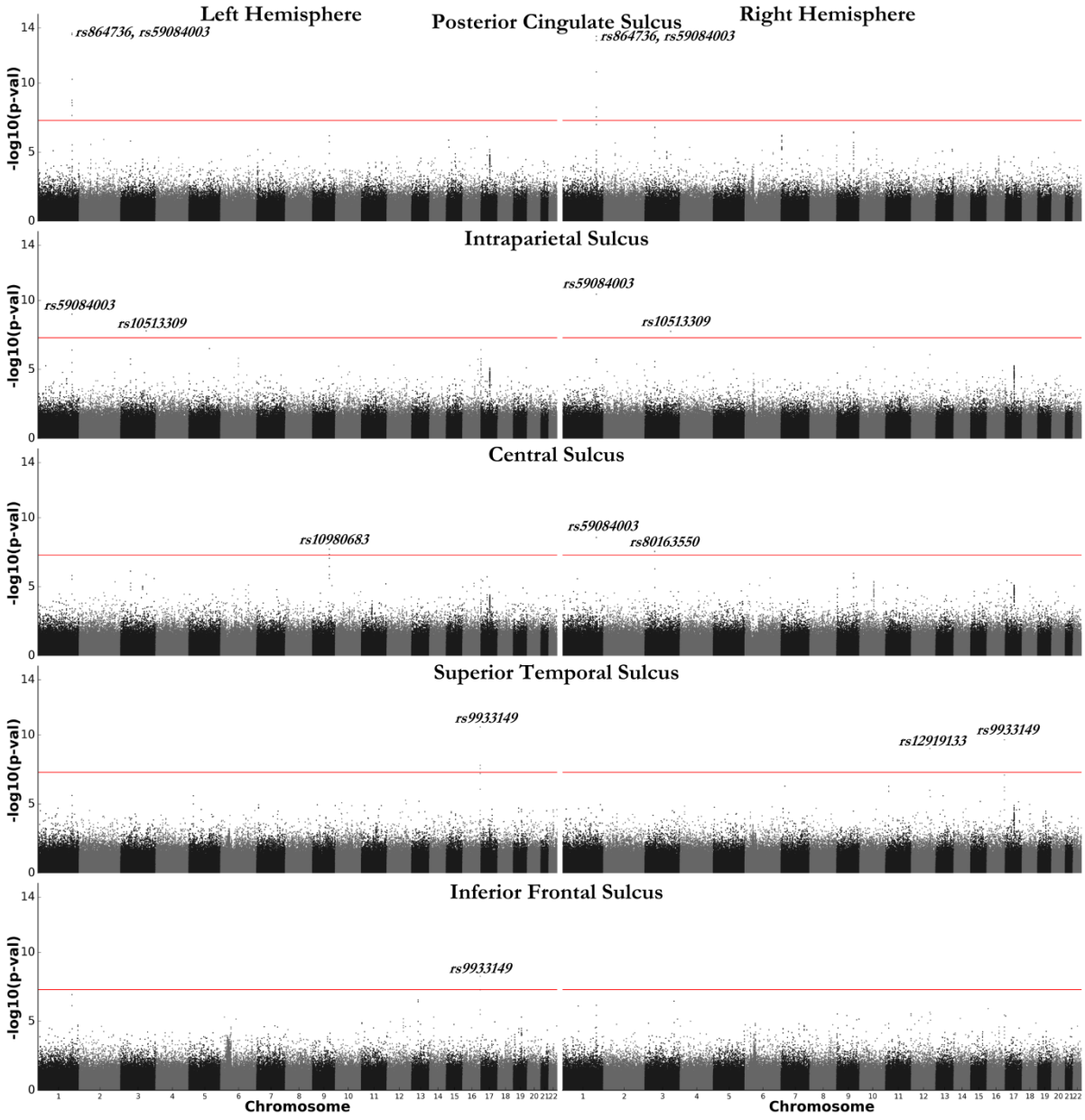

Figure S1. Manhattan plots for five sulci considering their opening as the phenotype for the GWAS.

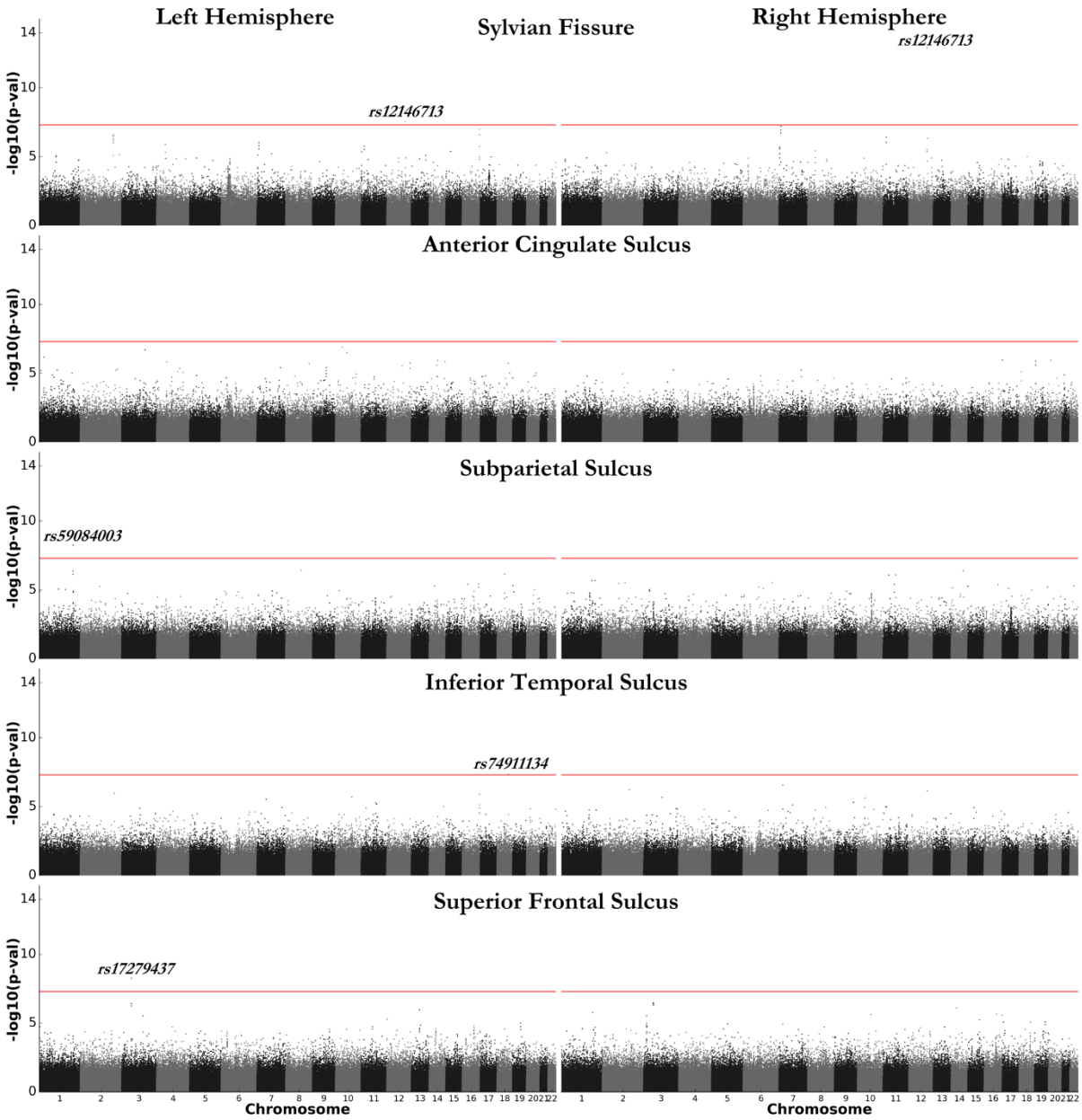

Figure S2. Manhattan plots for five sulci considering their opening as the phenotype for the GWAS.

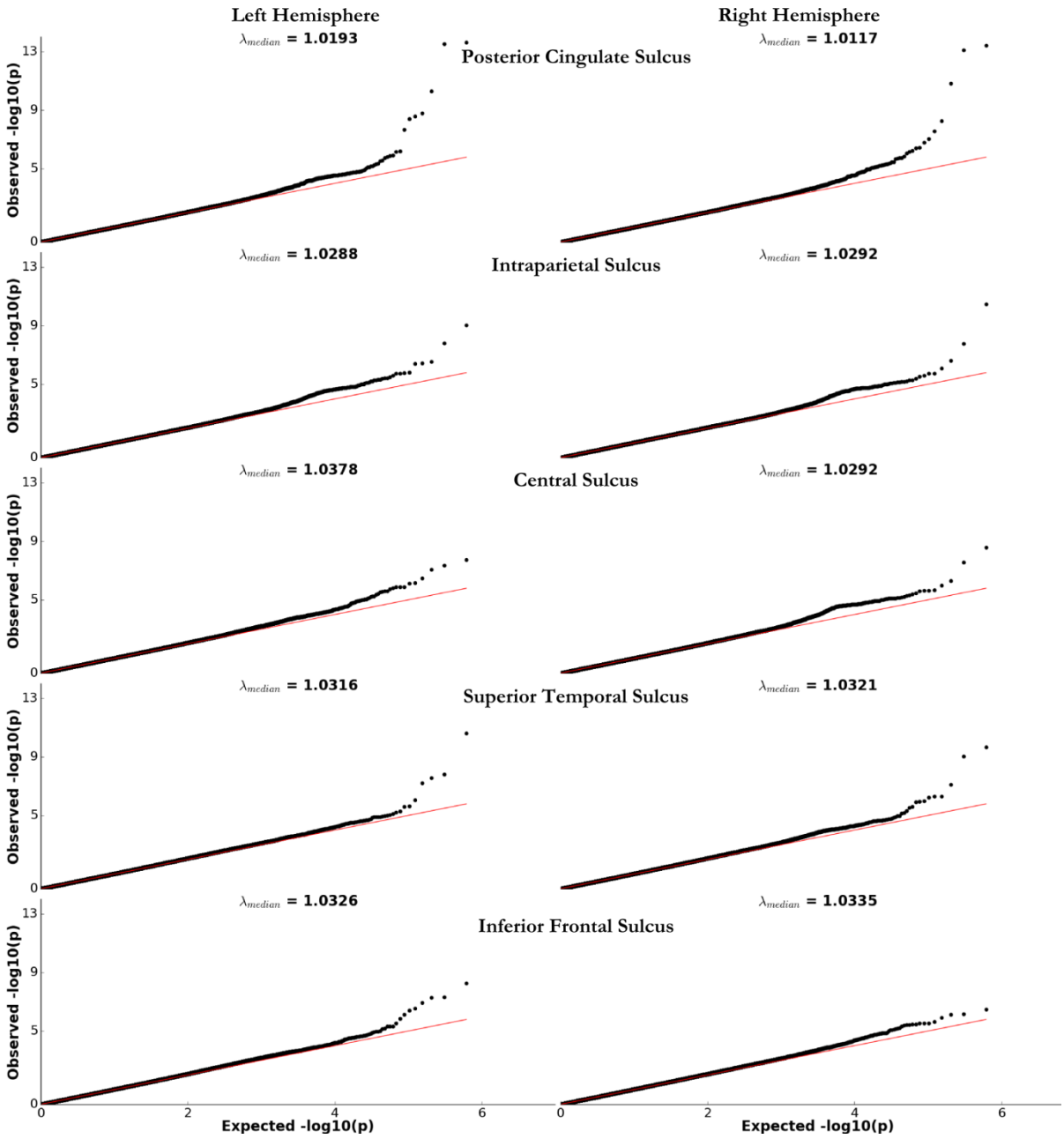

Figure S3. QQ plots for five sulci considering their opening as the phenotype for the GWAS.

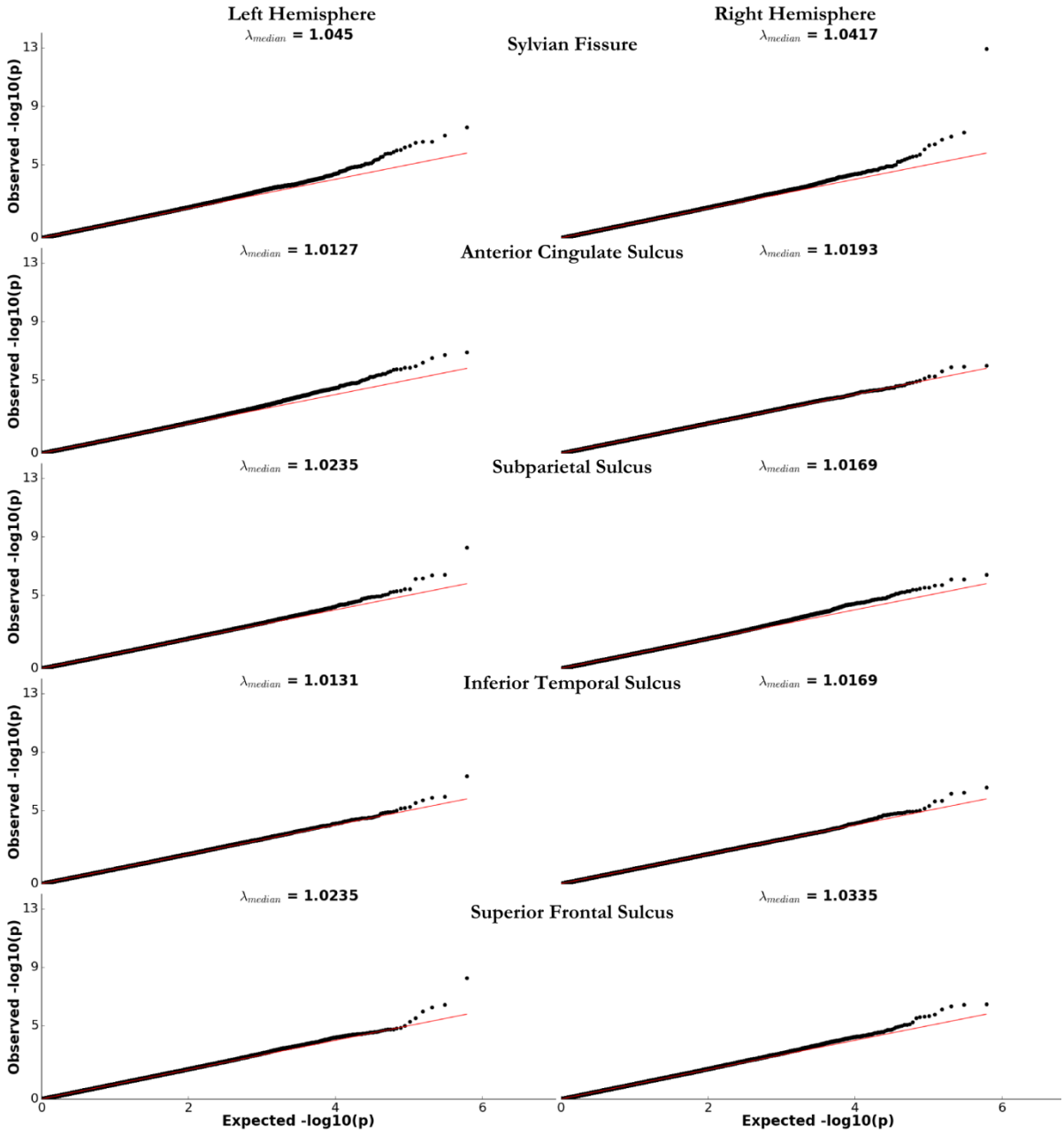

Figure S4. QQ plots for five sulci considering their opening as the phenotype for the GWAS.

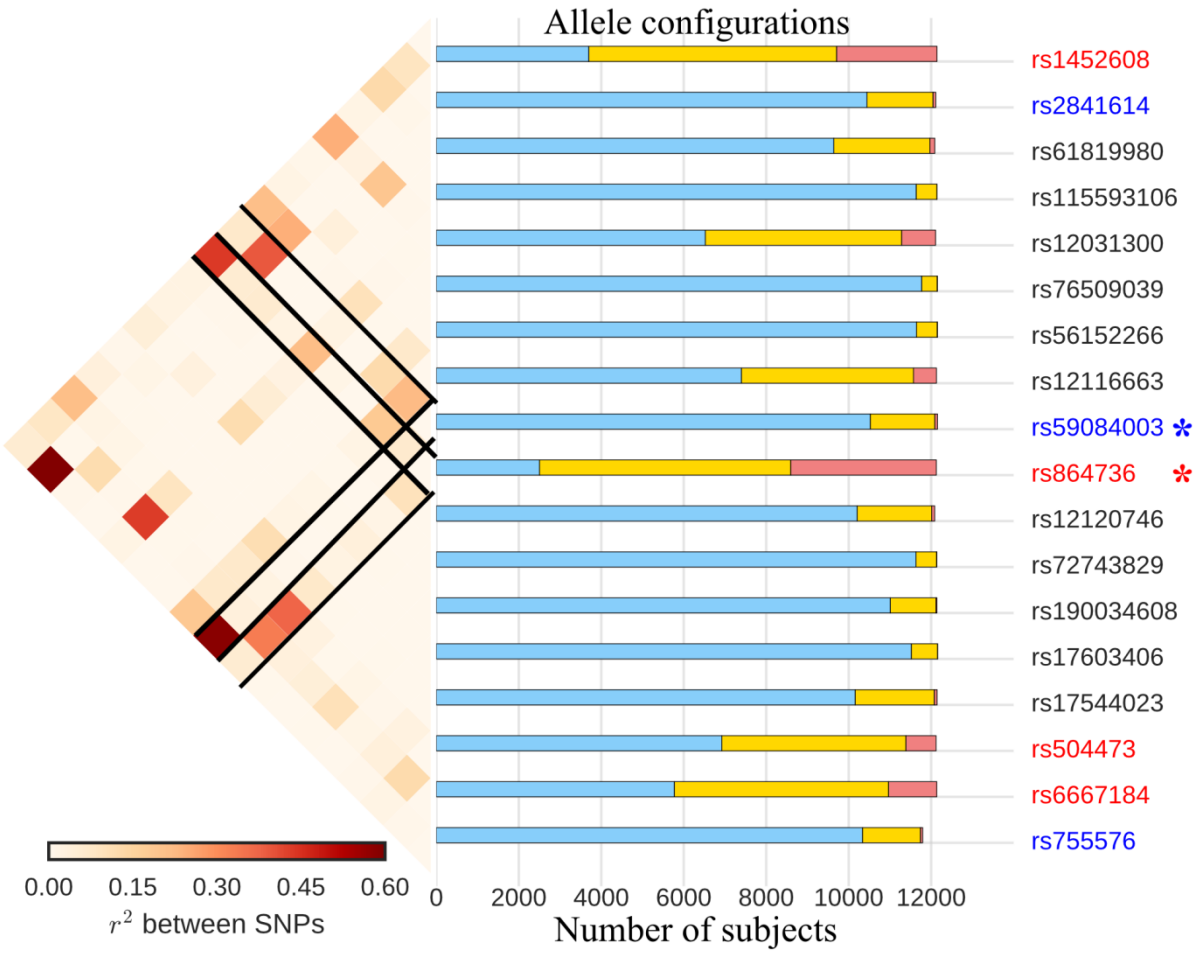

Figure S5. Linkage disequilibrium (r^2 computed with PLINK) for SNPs in the significant locus upward of *KCNK2*. The number of subjects for the different allelic configurations is displayed (number of subjects homozygote major allele in blue, heterozygote in yellow, homozygote minor allele in red). The significant variants in GWAS (**Tab. 1**) in LD with rs864736 and rs59084003 are in red and blue, respectively.

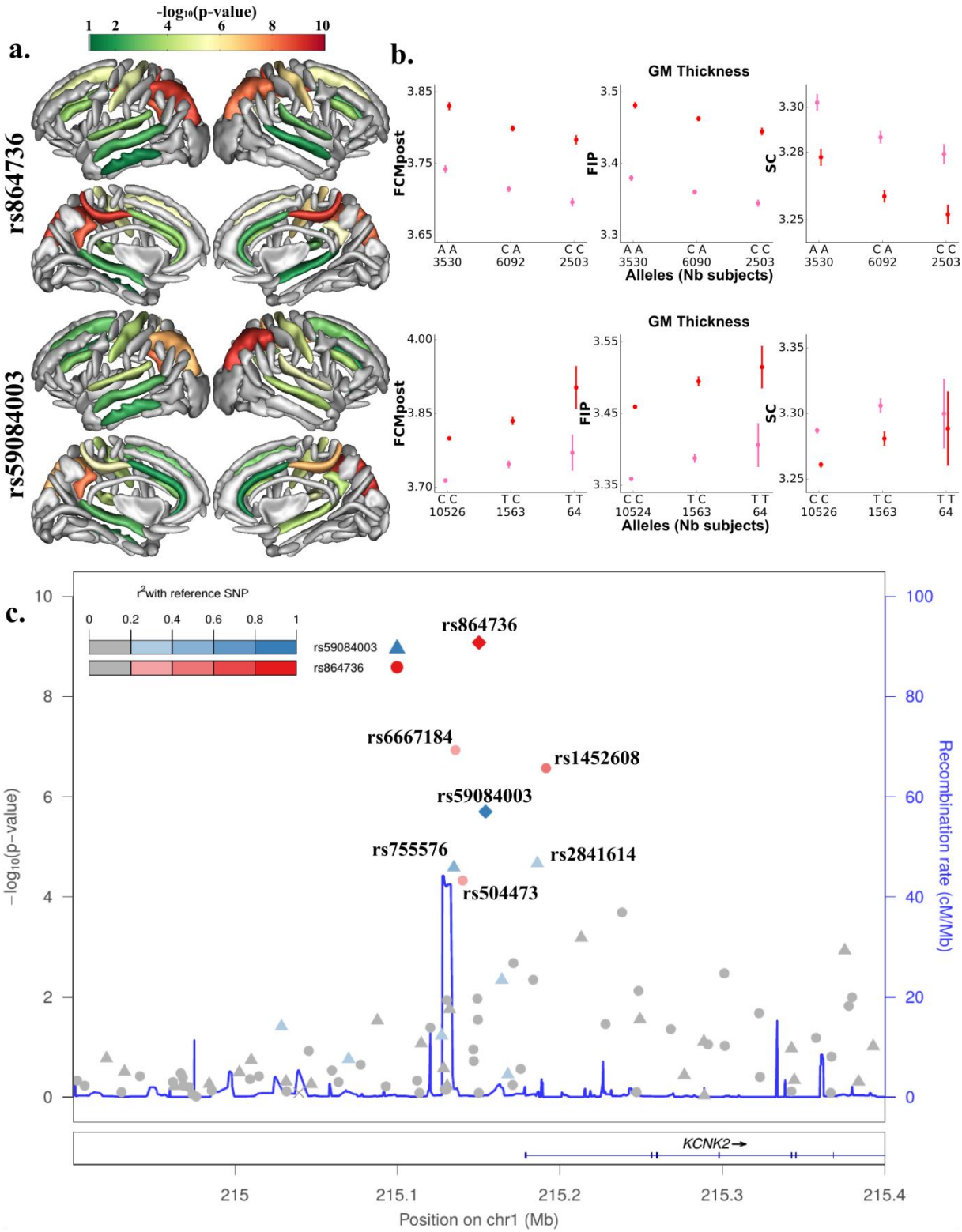

Figure S6. Most significant GWAS hits on KCNK2 regulating the GM thickness. First and second lines correspond to rs864736 and rs59084003, respectively. Lines represents respectively: **a.** the log10(p-value) of each SNPs mapped onto the nominally significant sulci among the ten considered; **b.** the mean GM thickness and standard error for each configuration of variants in the most significant sulci; **c.** Locuszoom display (Pruim et al. 2011) of the phenotype-variants association for the region upward to KCNK2 with the left posterior cingulate sulcus opening as a phenotype..

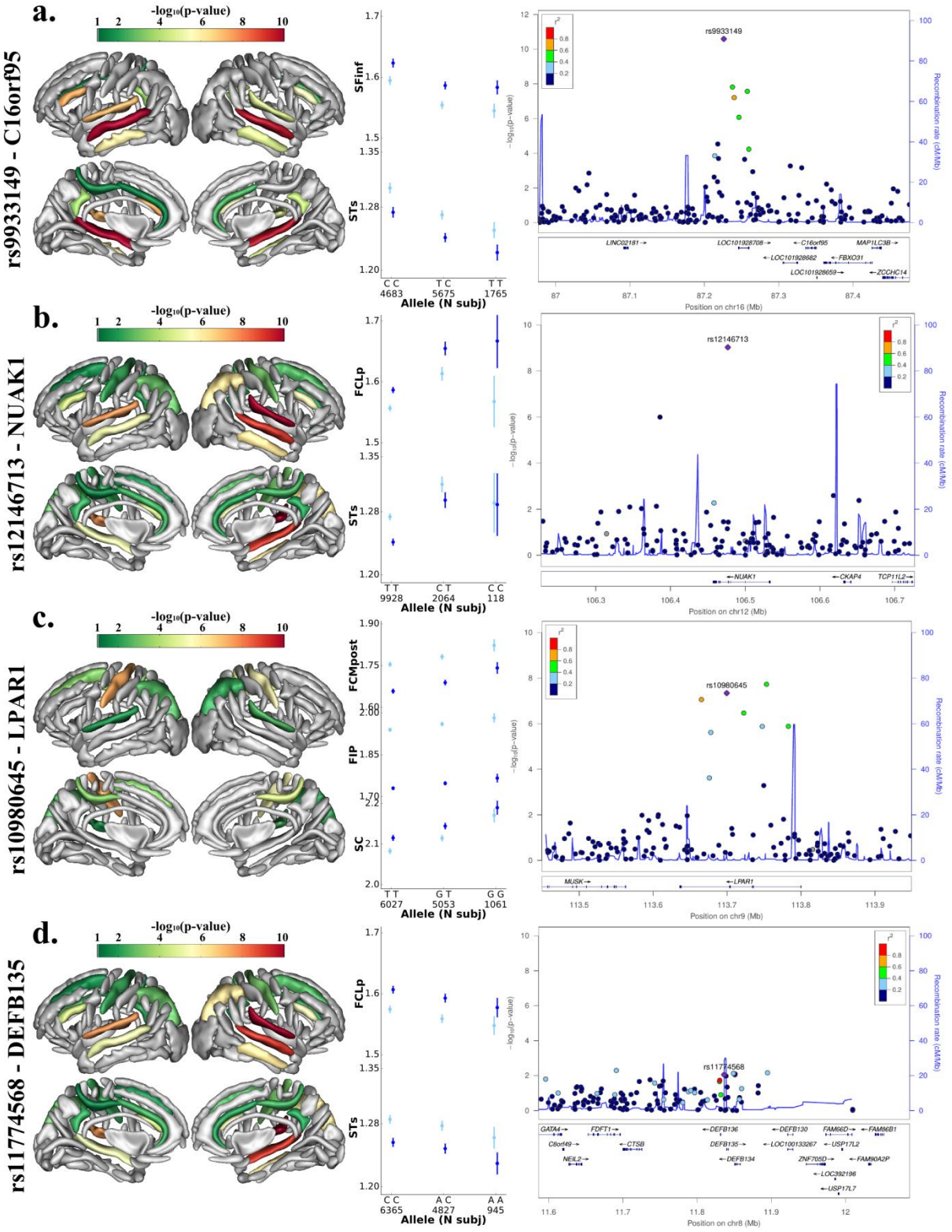

Figure S7. Four significant GWAS hits on the sulcal opening. Lines correspond to the SNPs presented in the following order rs9933149 (**a.**), rs12146713 (**b.**) rs10980645 (**c.**) rs11774568 (**d.**). Columns represents respectively the log10(p-value) of each SNPs mapped onto the nominally significant sulci among the ten considered; the mean sulcal opening and standard error for each configuration of variants in the most significant sulci; Locuszoom display (Pruim et al. 2011) for each variant with the associated most significant phenotype.

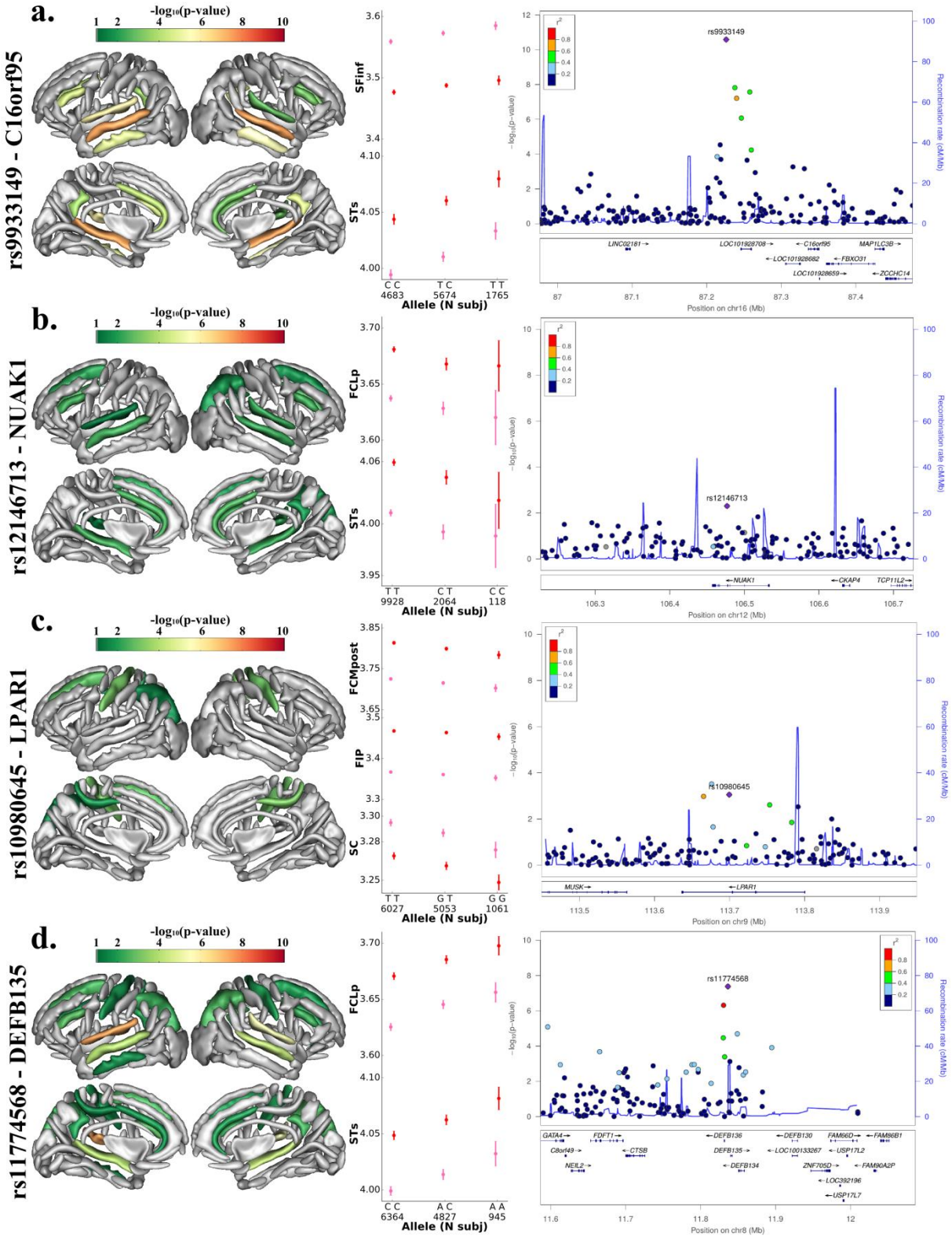

Figure S8. Four significant GWAS hits on the grey matter thickness of the sulci. Lines correspond to the SNPs presented in the following order rs9933149 (**a.**), rs12146713 (**b.**) rs10980645 (**c.**) rs11774568 (**d.**). Columns represents respectively: the log10(p-value) of each SNPs mapped onto the nominally significant sulci among the ten considered; the mean sulci grey matter thickness and standard error for each configuration of variants in the most significant sulci; Locuszoom display (Pruim et al. 2011) for each variant with the associated most significant phenotype.