

Supplementary Figures

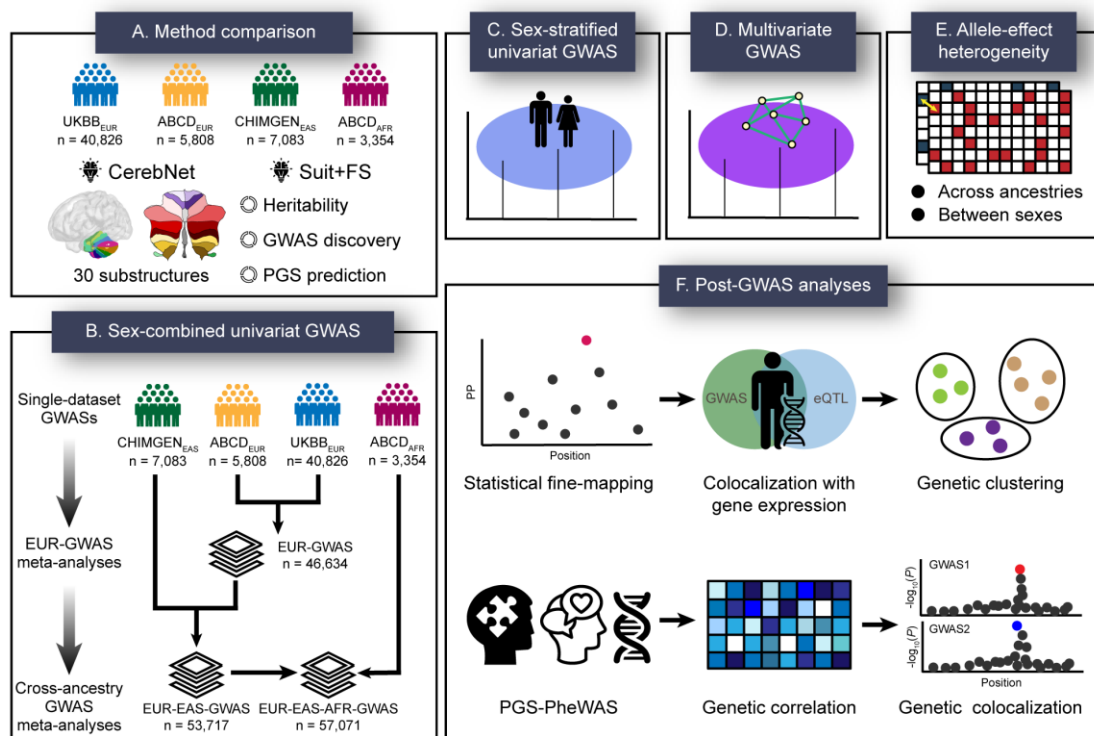


Fig. S1 | A schematic summary of study design. This study includes four independent subgroups with raw genetic and neuroimaging data (UKBB_{EUR}, ABCD_{EUR}, CHIMGEN_{EAS}, and ABCD_{AFR}). **(A)** To compare the cerebellar segmentation methods, we calculate the volumes of 30 cerebellar substructures using CerebNet and SUIT+FS, and we evaluate their differences in heritability estimation, GWAS discovery, and PGS prediction. **(B)** In the sex-combined univariate analyses, we further include total cerebellar volume as a trait and perform GWASs for the 31 cerebellar volumetric traits across the four subgroups, respectively. We also conduct one EUR-GWAS and two cross-ancestry (EUR-EAS and EUR-EAS-AFR) GWAS meta-analyses. **(C)** In the sex-stratified univariate analyses, we repeat the seven sets of GWASs in males and females, respectively. **(D)** Multivariate GWASs are performed in both sex-combined and sex-stratified populations. **(E)** We identify allelic-effect heterogeneity across ancestries

based on sex-combined EUR-GWASs, CHIMGEN_{EAS}-GWASs, and ABCD_{AFR}-GWASs, while we detect allelic-effect heterogeneity between sexes based on sex-stratified EUR-GWASs, CHIMGEN_{EAS}-GWASs, and ABCD_{AFR}-GWASs. (F) The post-GWAS analyses include statistical fine-mapping, genetic colocalization with cerebellar gene expression, genetic clustering for cerebellar subregions, PGS-PheWAS, and genetic correlation and colocalization with neuropsychiatric disorders. Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; FS, FreeSurfer; GWAS, genome-wide association study; PGS, polygenic score; PheWAS, phenome-wide association study; SUI, spatially unbiased infra-tentorial; FS, FreeSurfer; UKBB, the UK Biobank study.

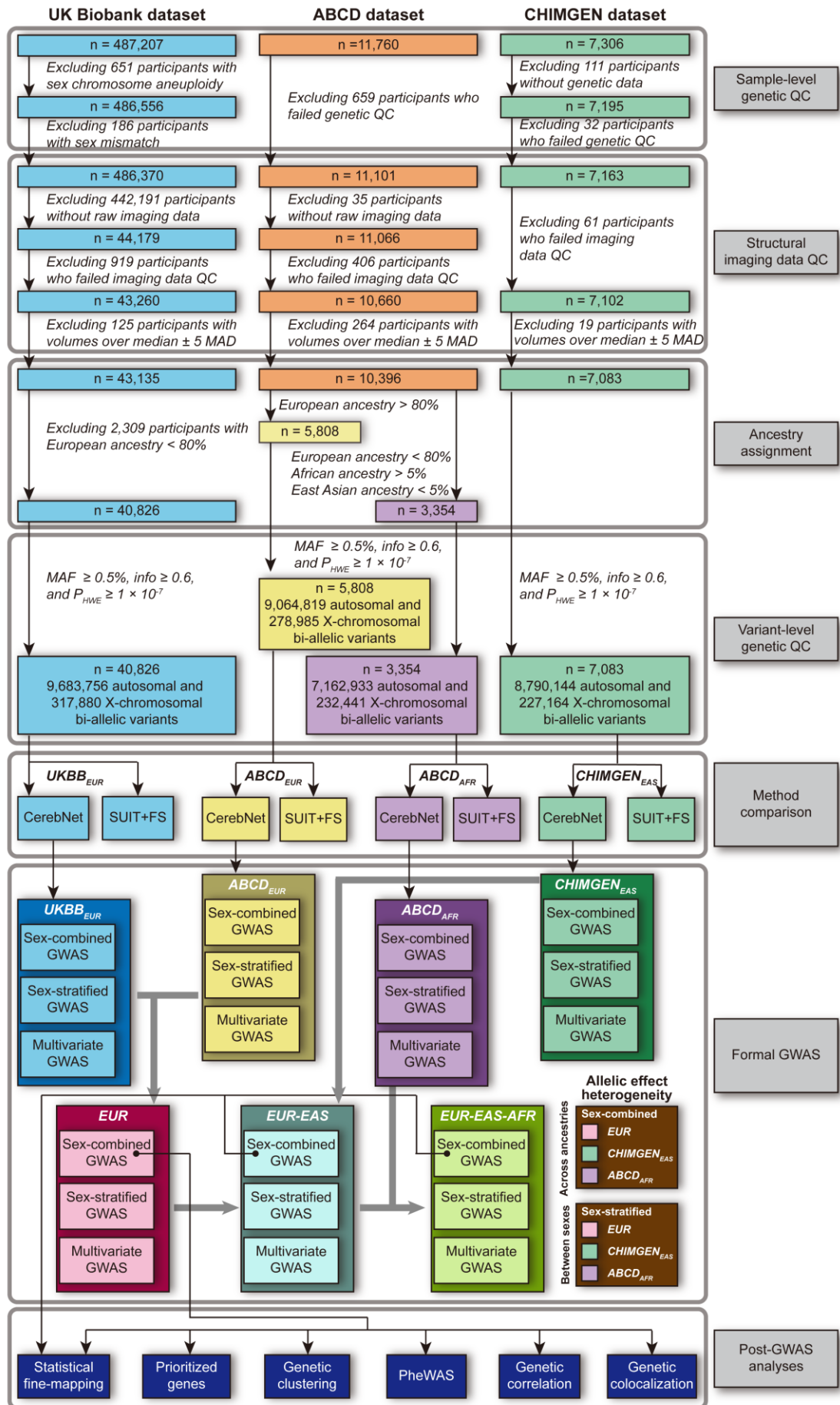
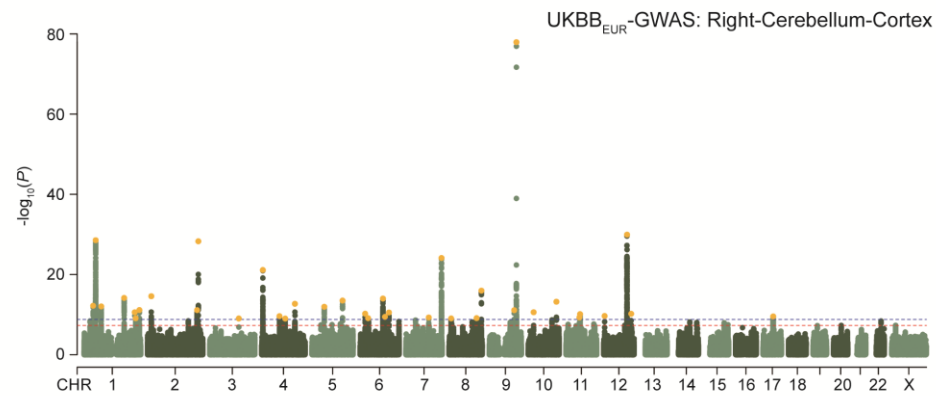
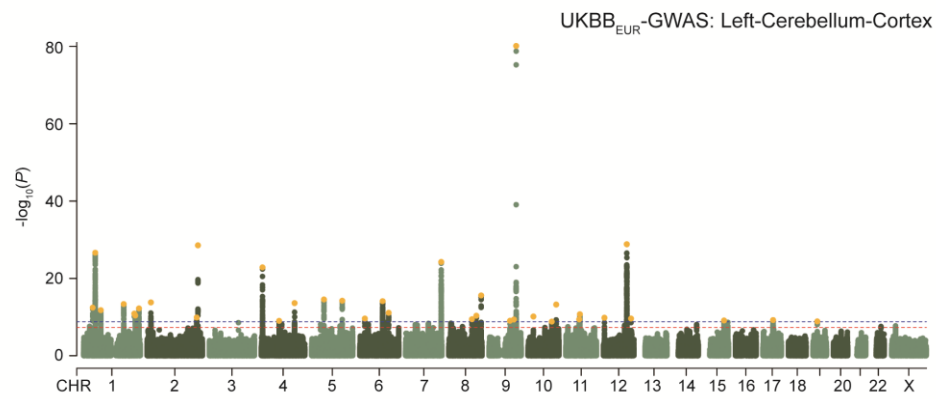
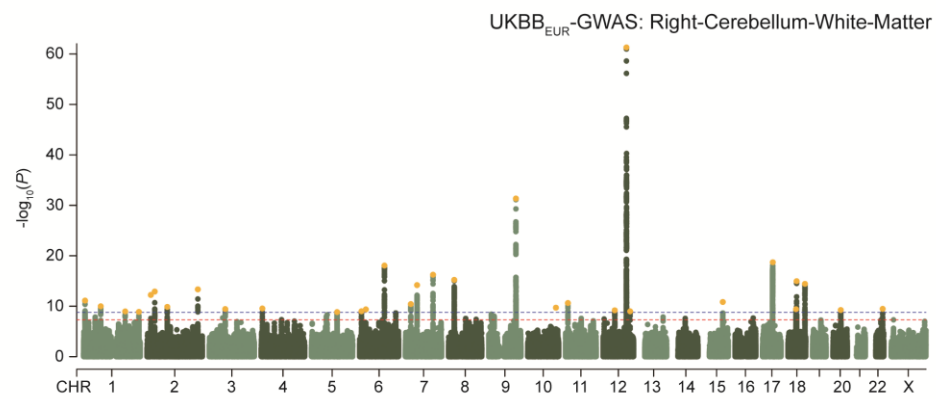
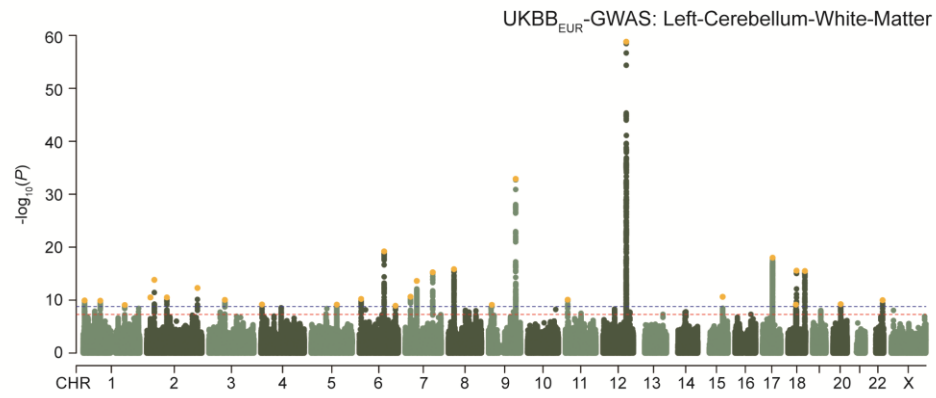
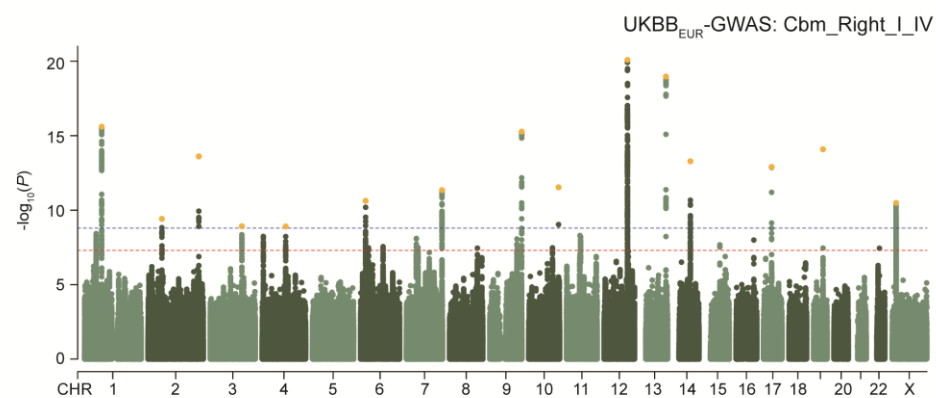
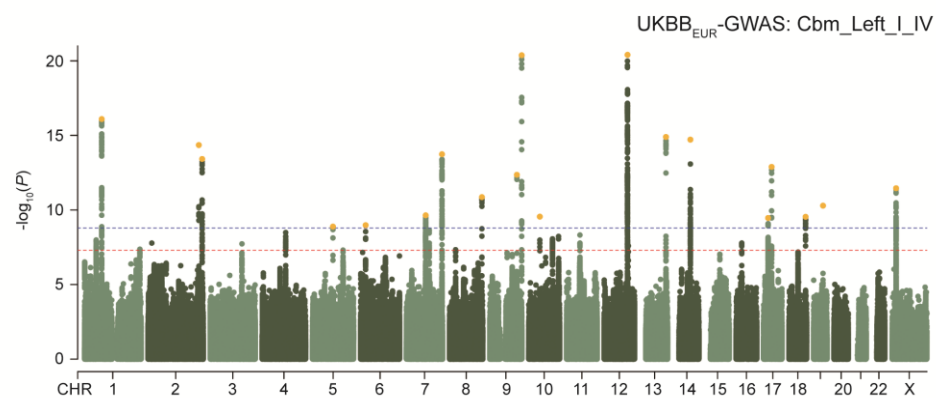
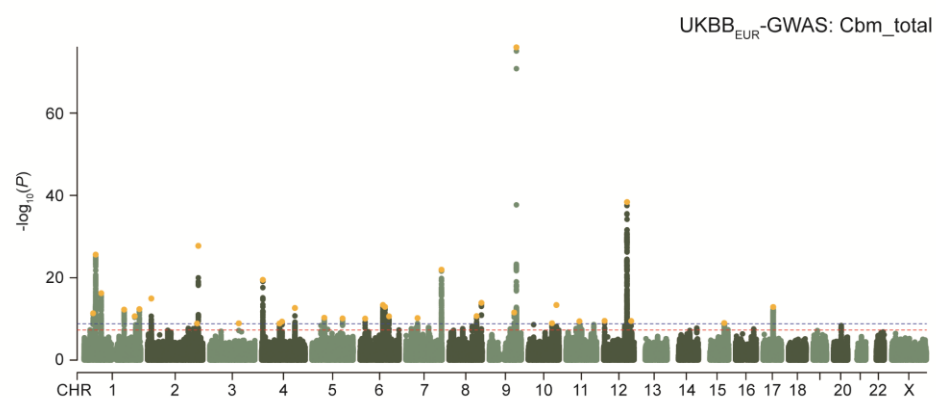
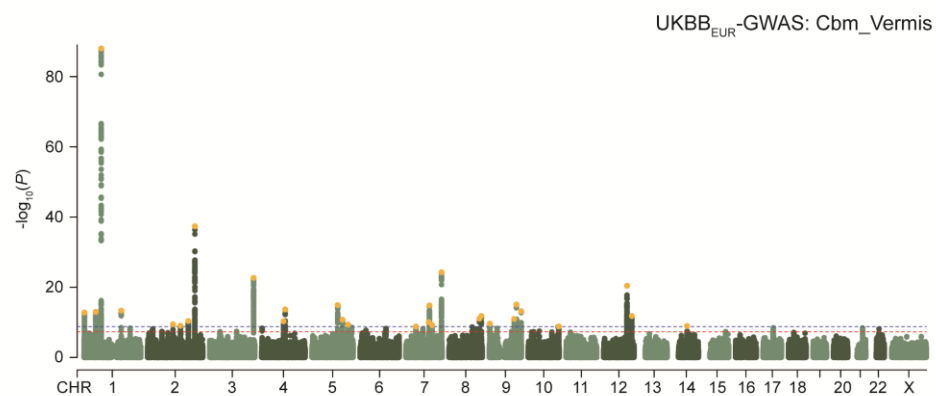
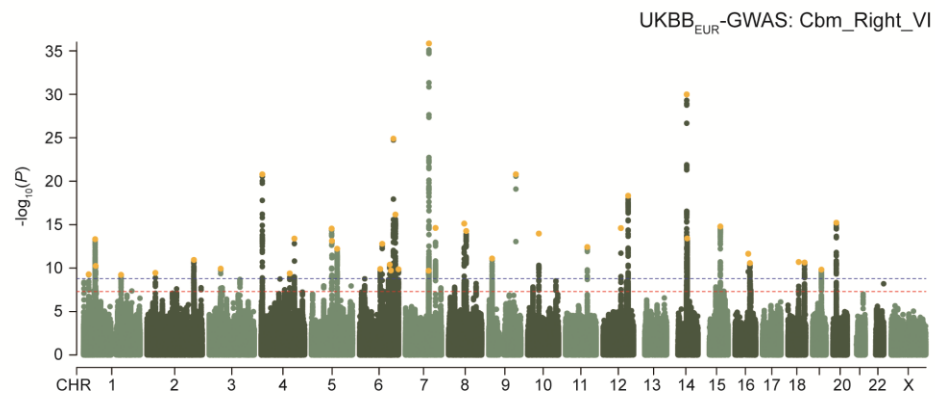
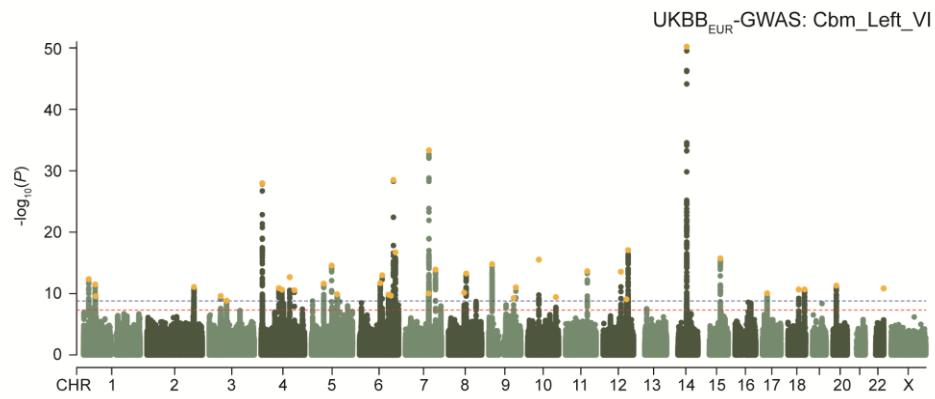
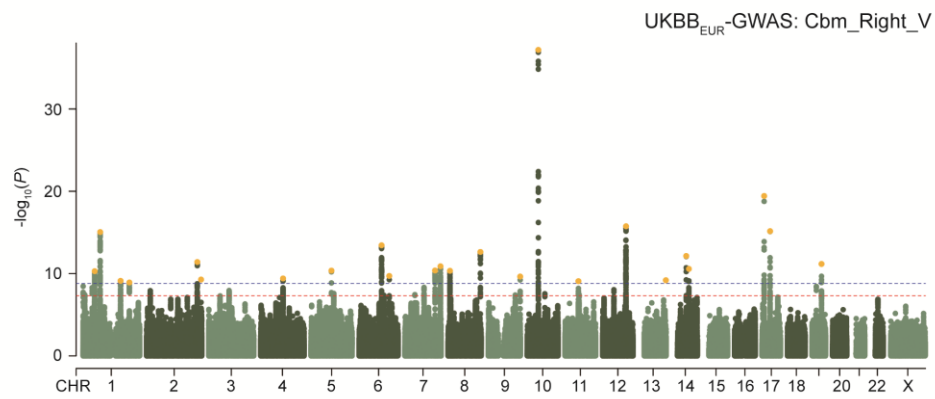
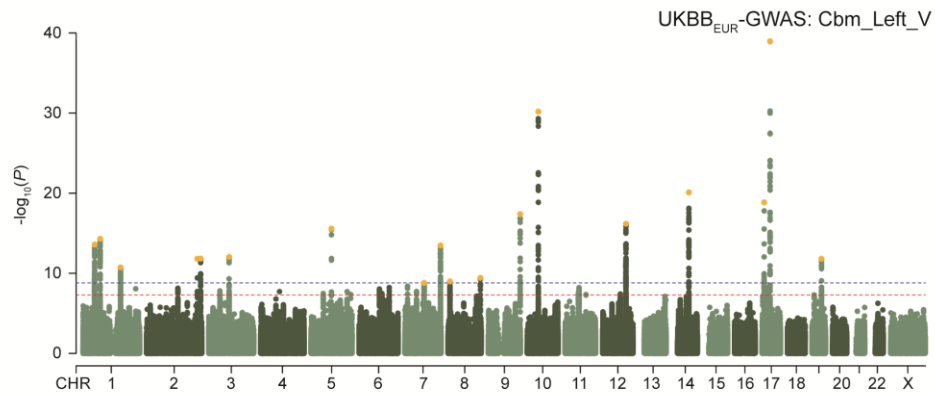


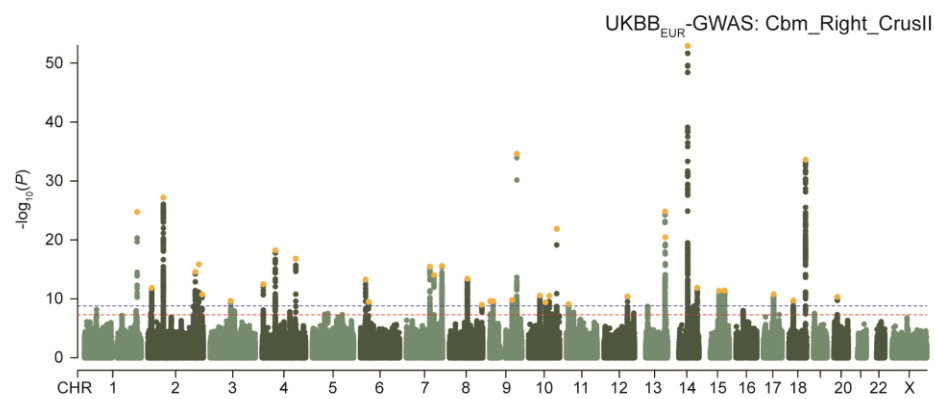
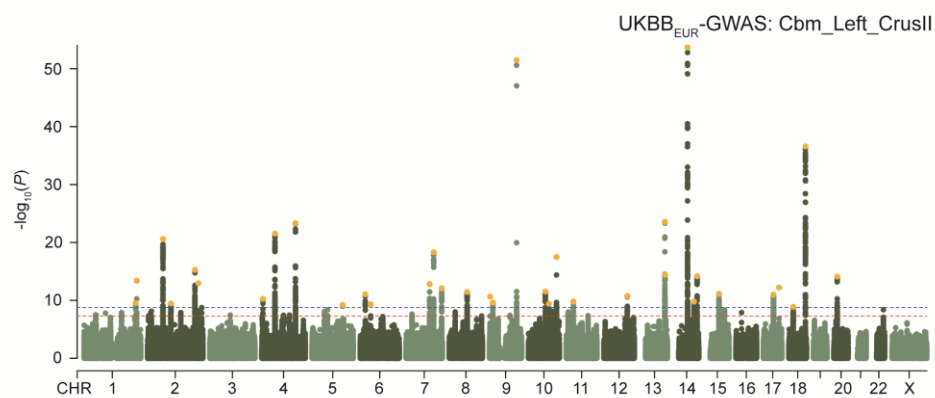
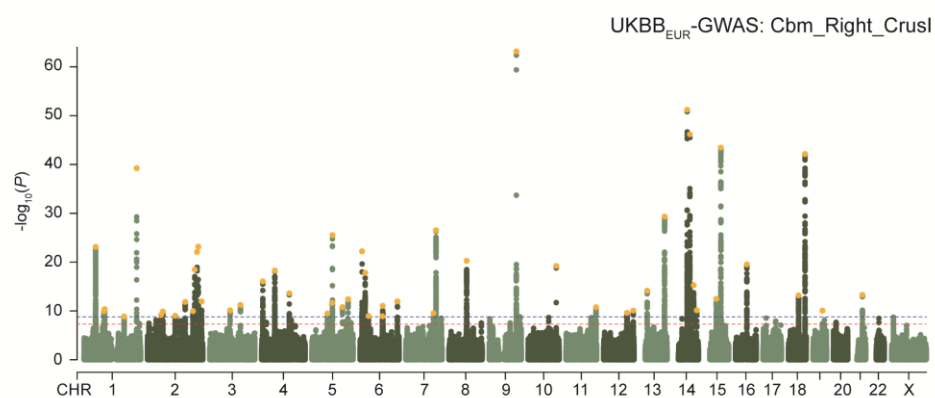
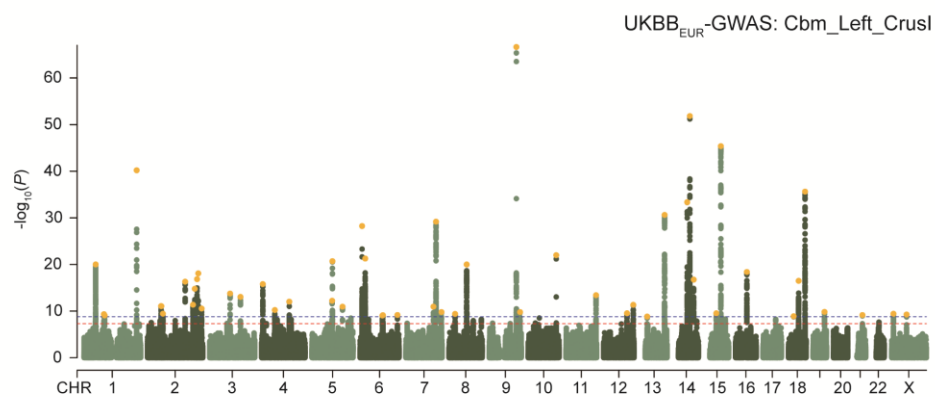
Fig. S2 | Participant selection, quality control, and analysis workflow.

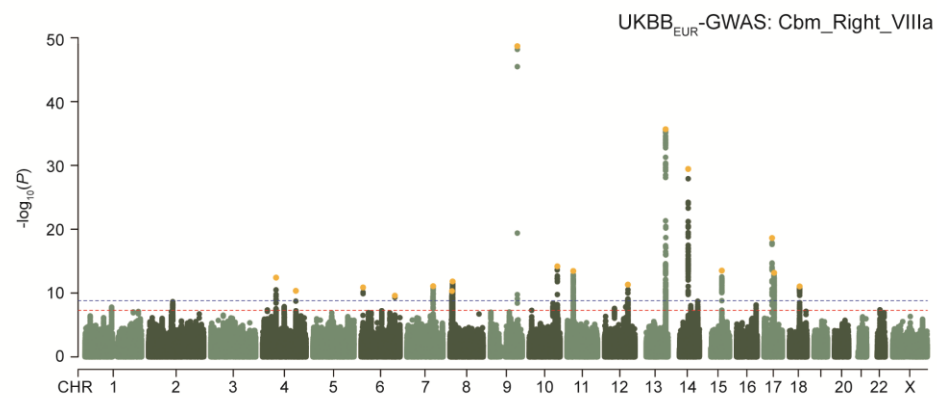
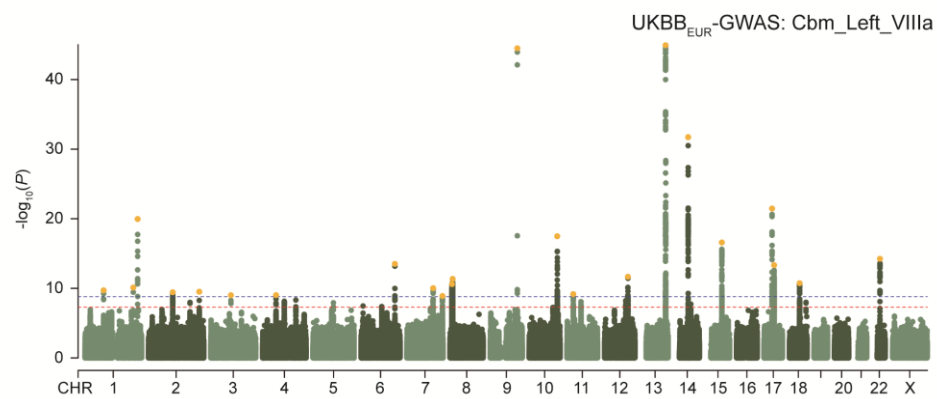
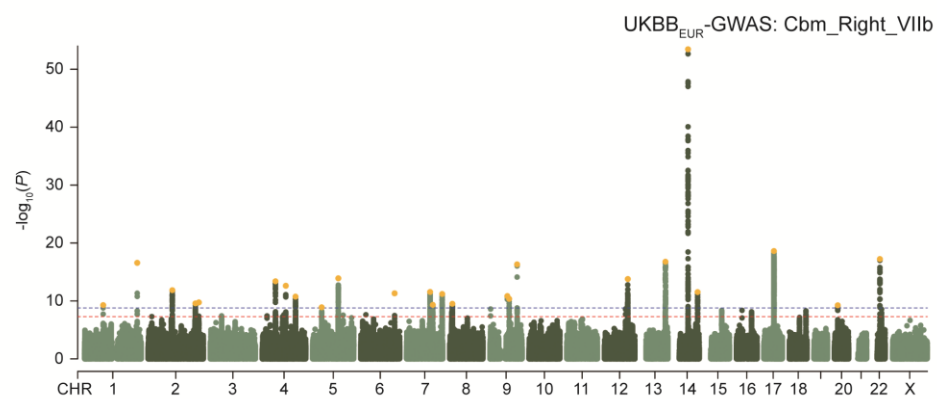
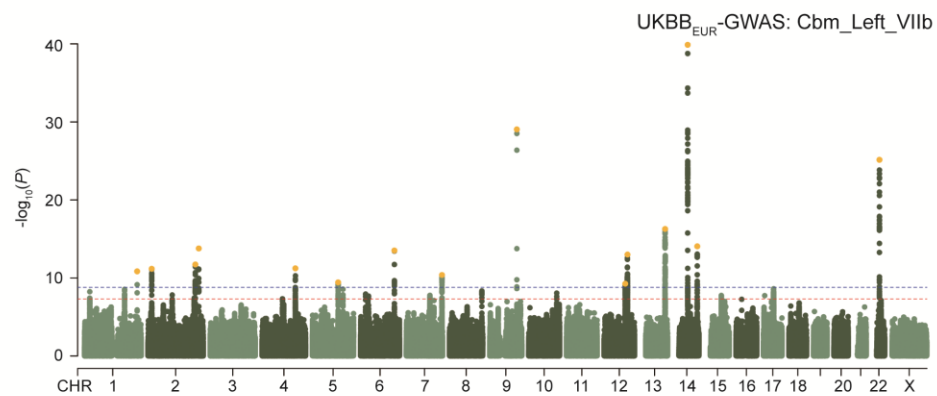
Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; FS, FreeSurfer; GWAS, genome-wide association study; HWE, Hardy-Weinberg equilibrium; info, imputation information score; MAD, median absolute deviation; MAF, minor allele frequency; PheWAS, phenome-wide association study; QC, quality control; SUIT, spatially unbiased infra-tentorial; UKBB, the UK Biobank study.

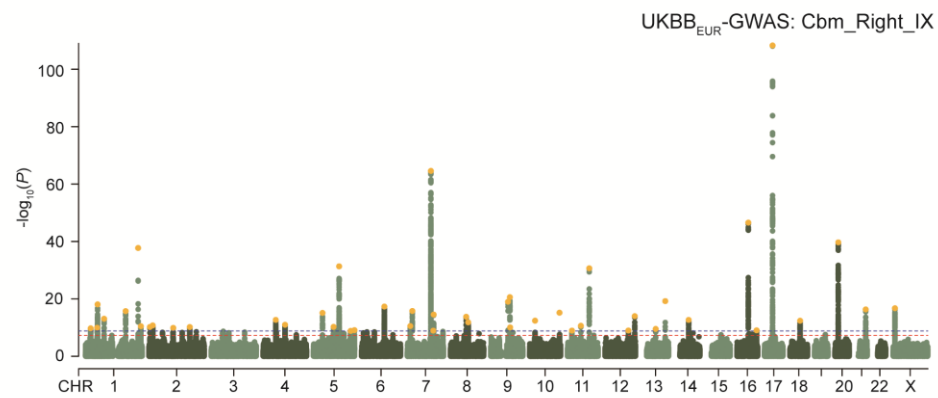
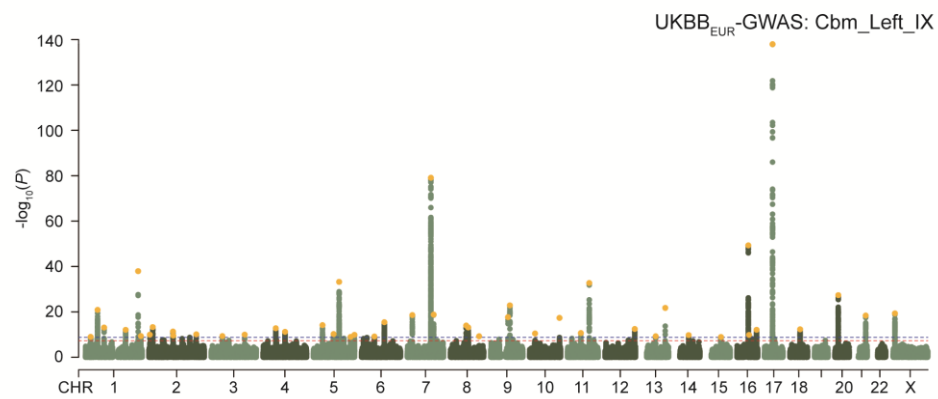
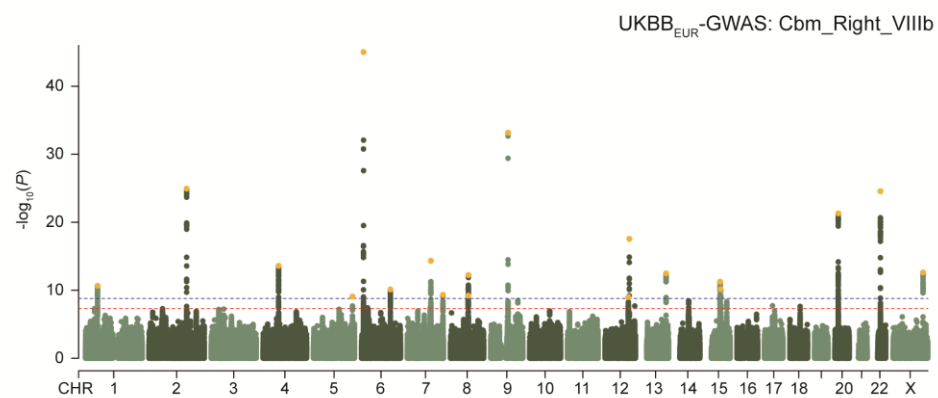
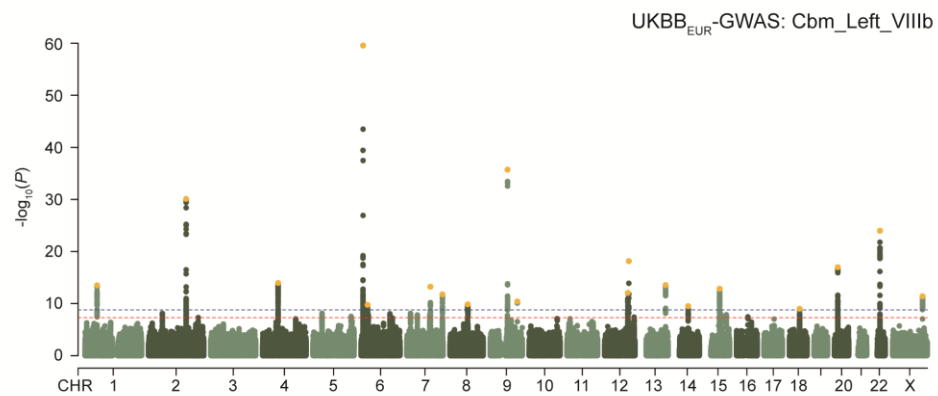


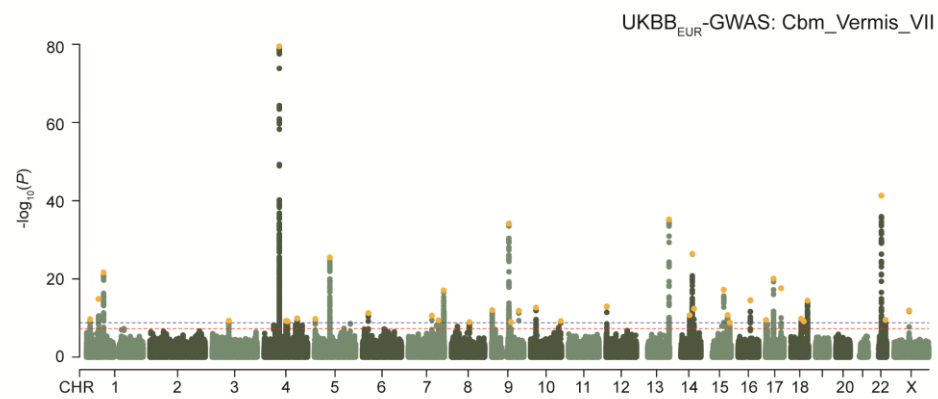
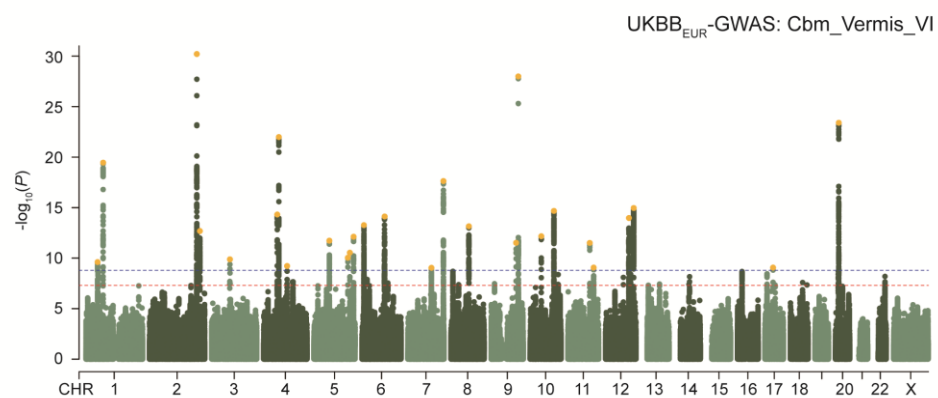
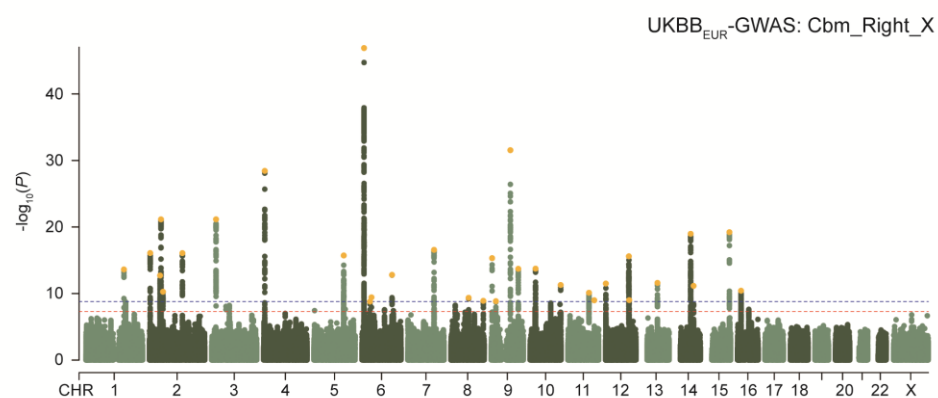
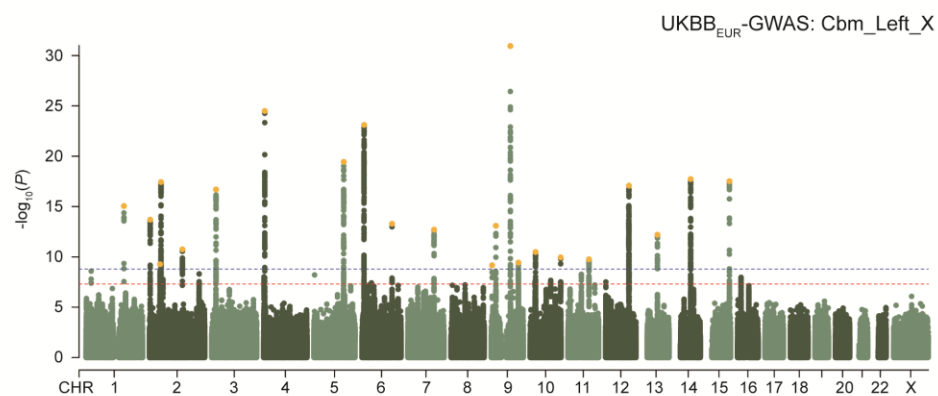


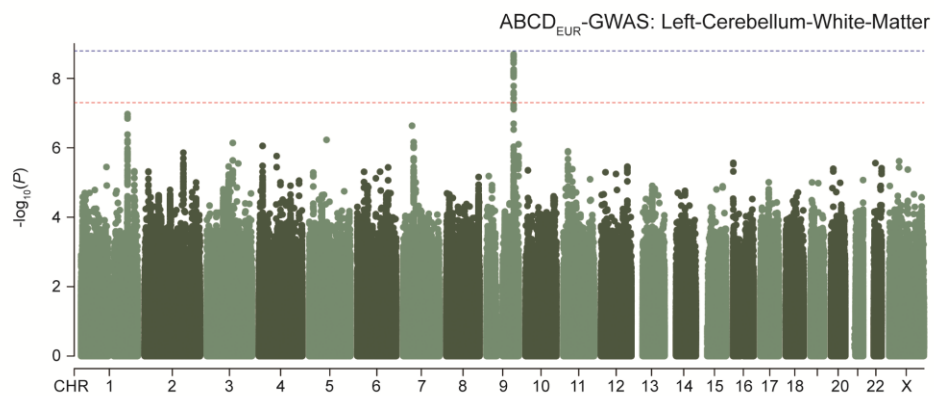
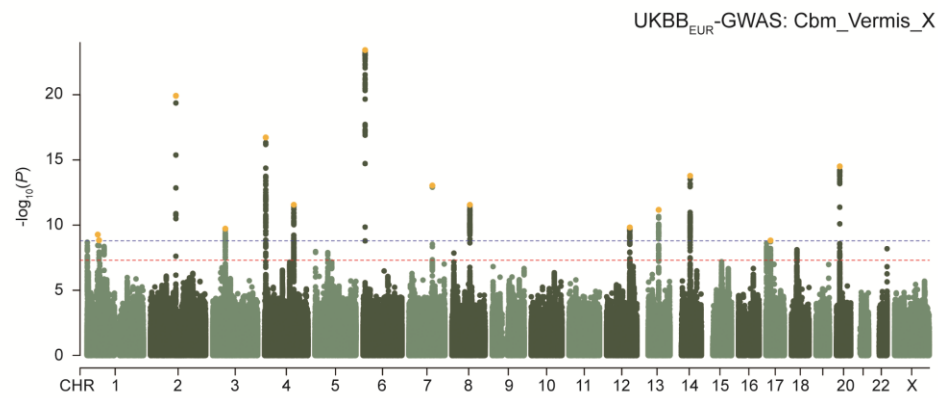
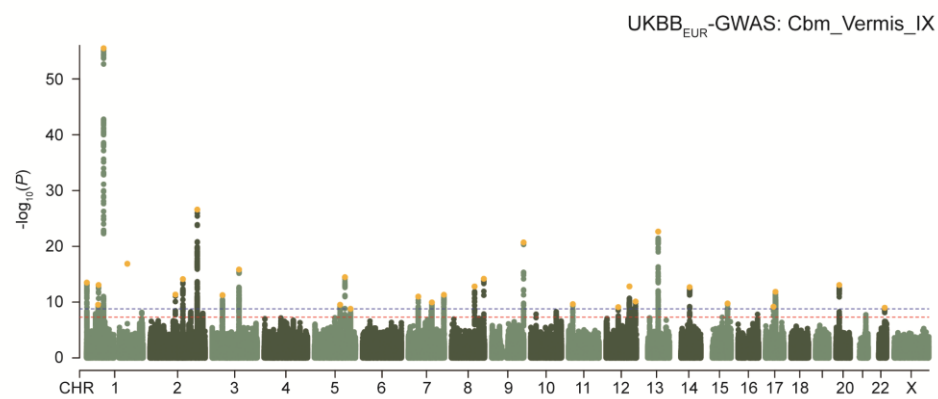
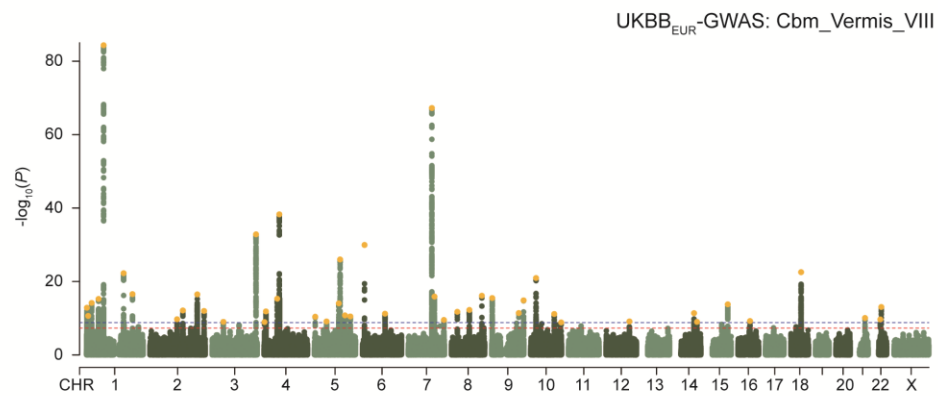


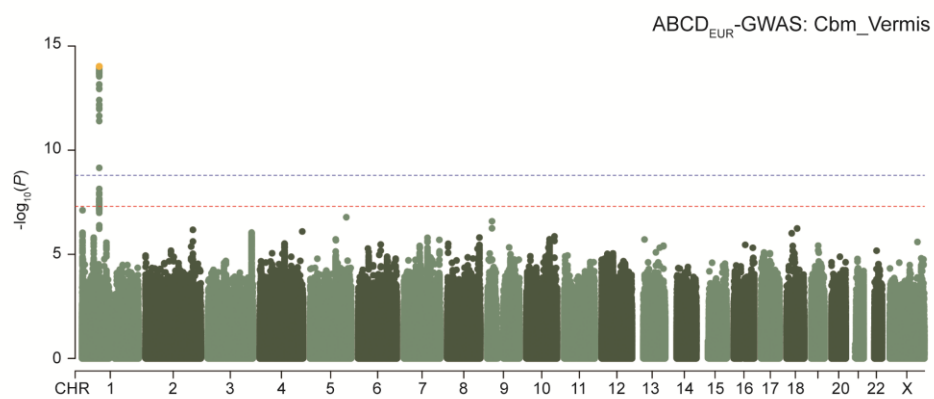
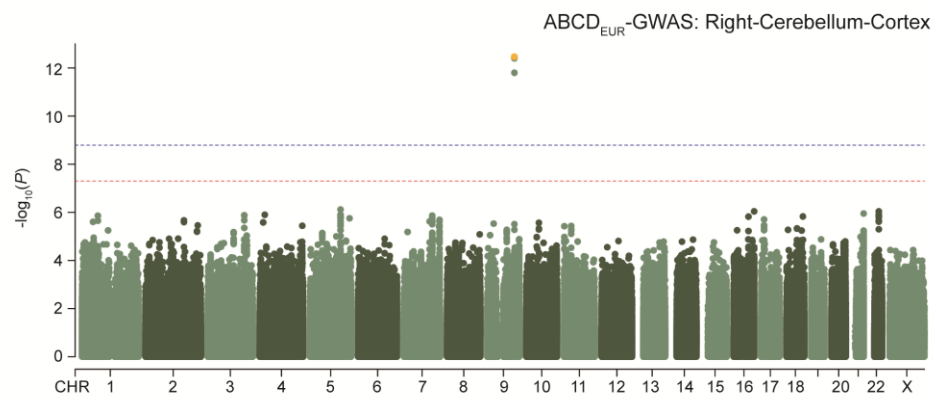
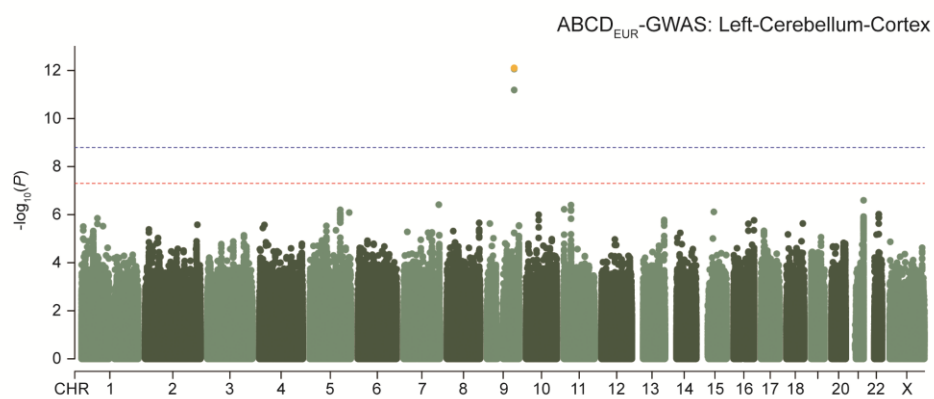
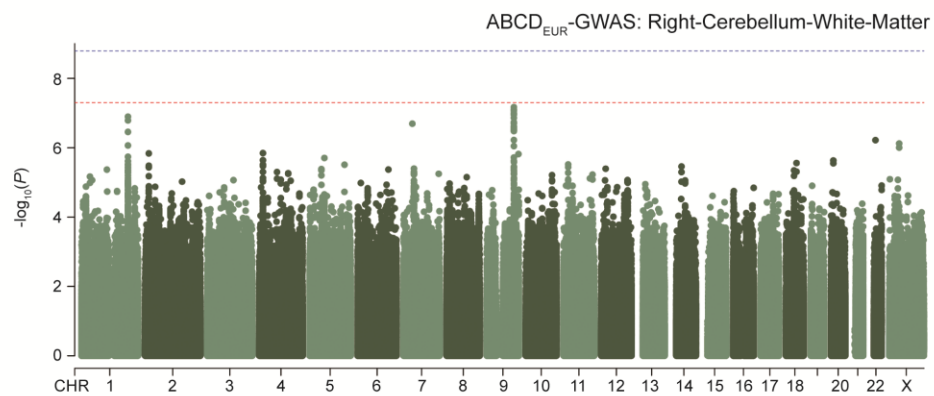


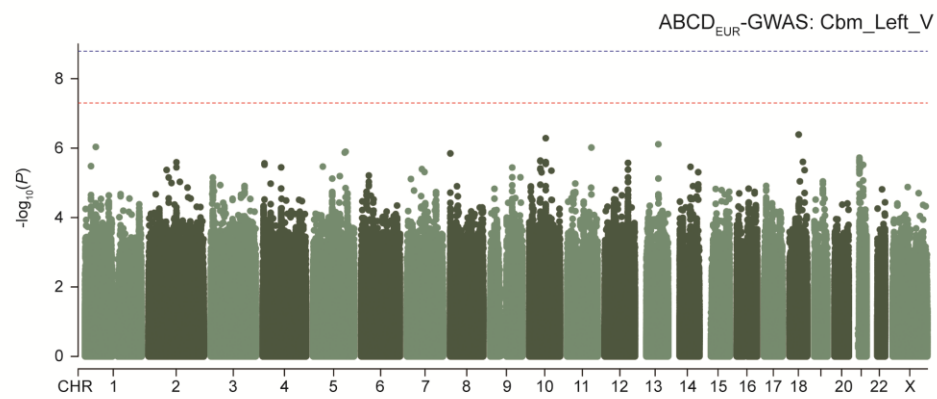
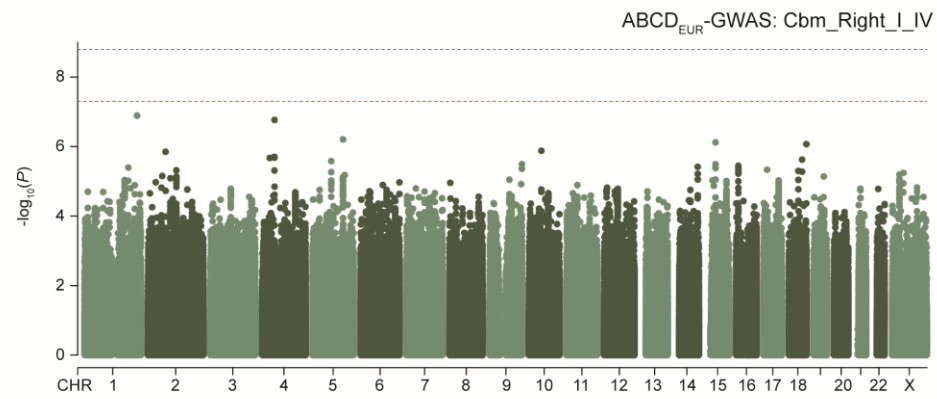
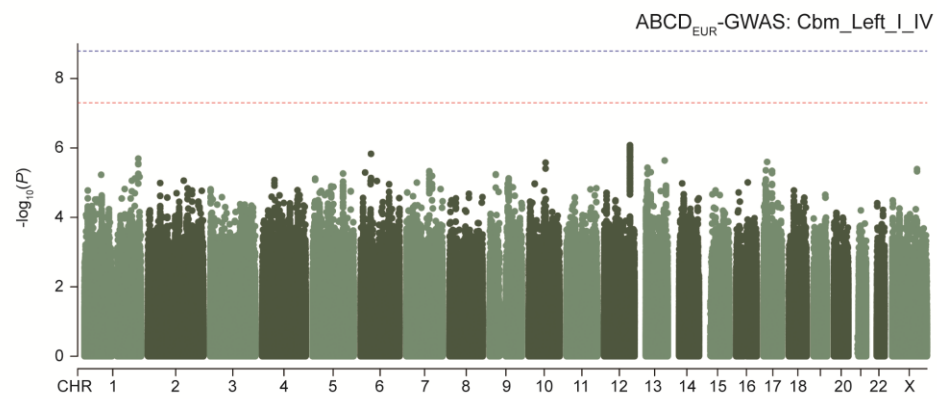
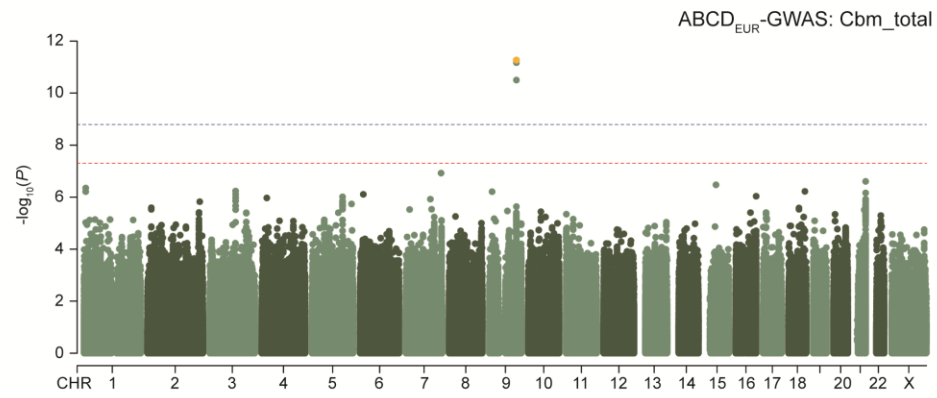


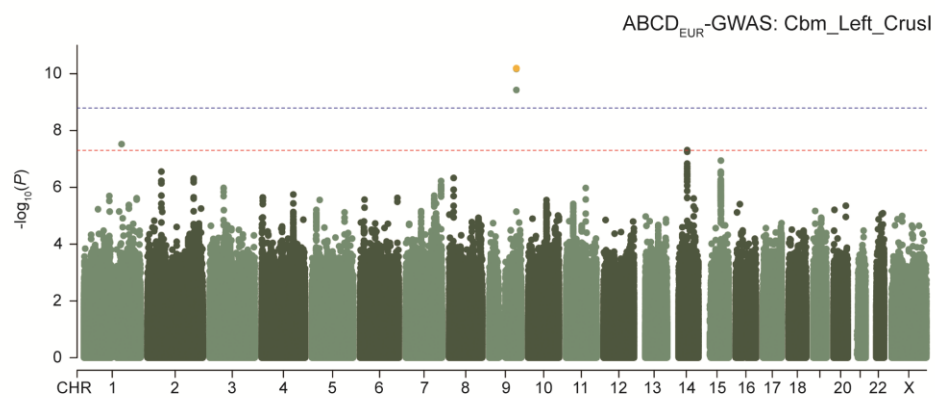
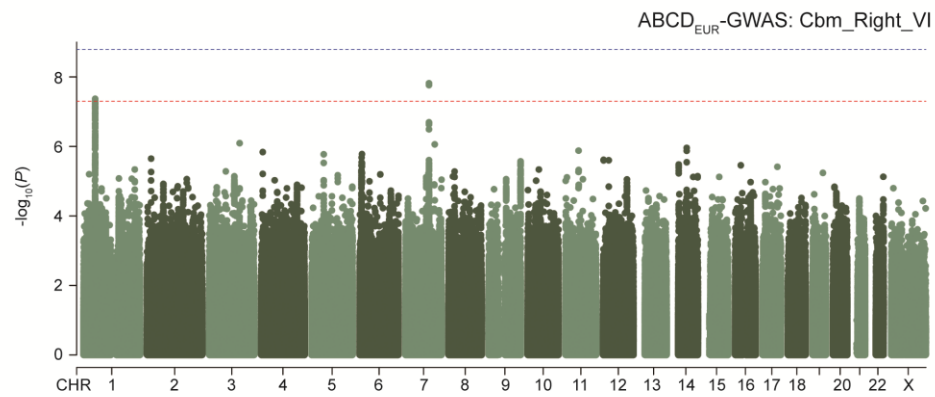
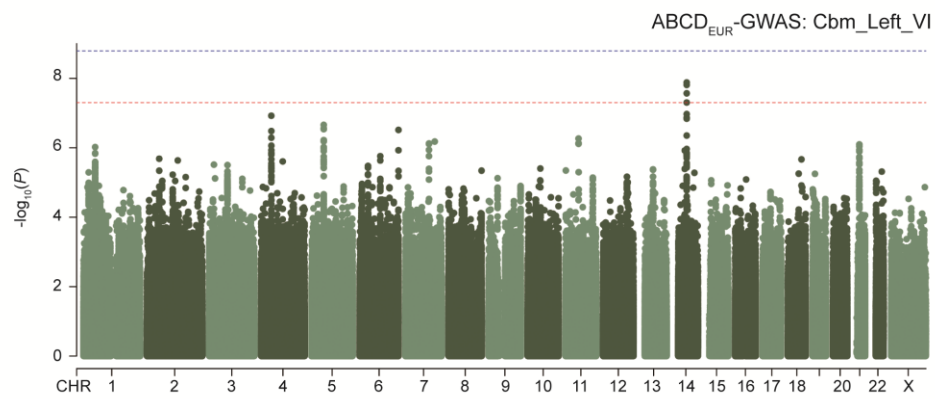
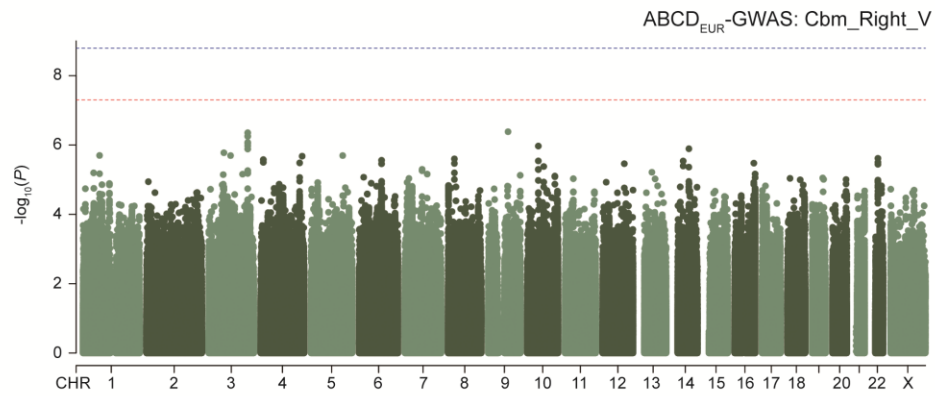


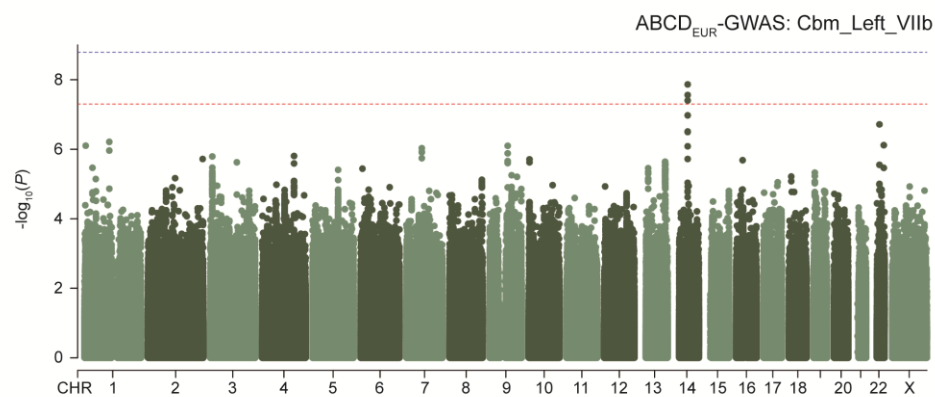
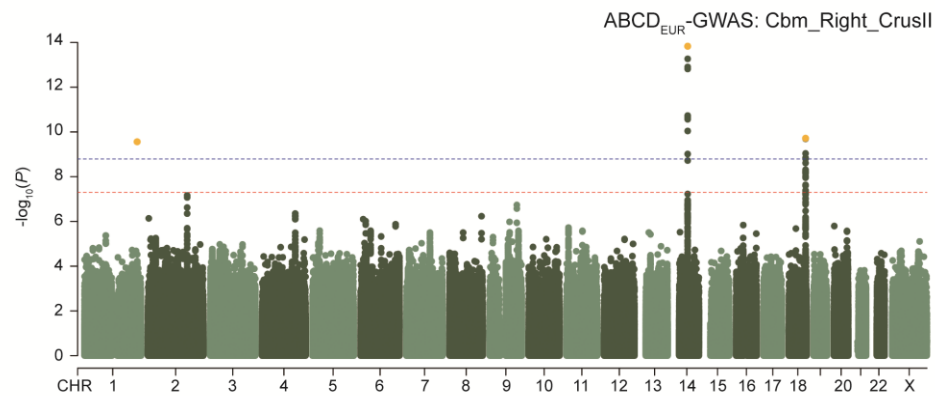
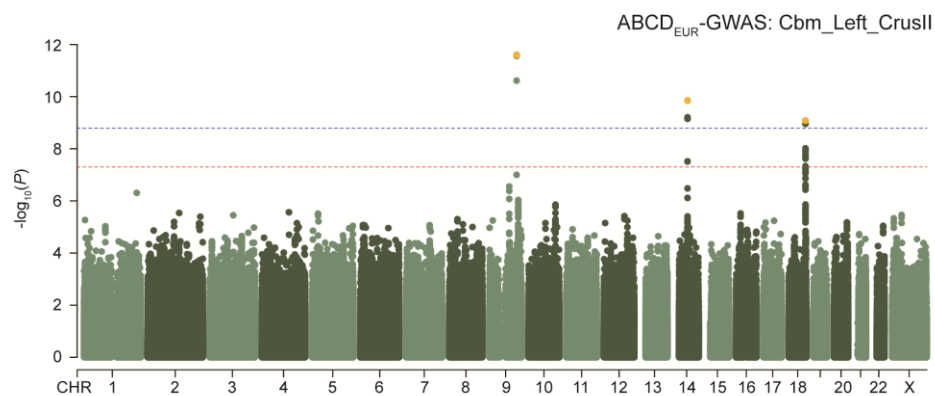
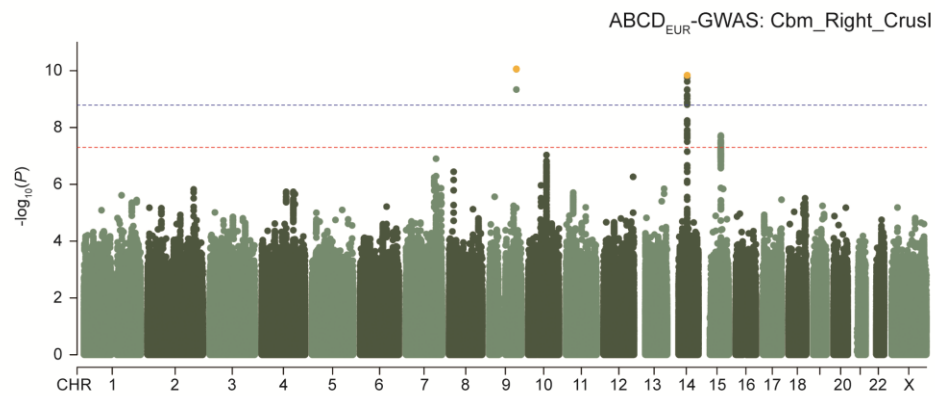


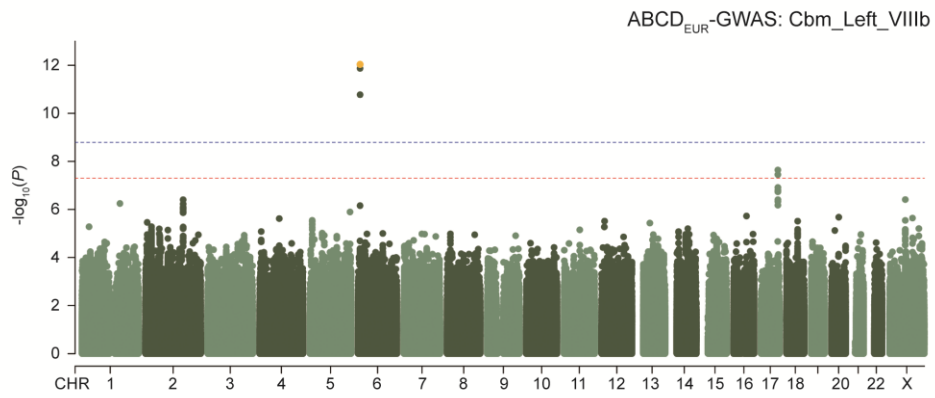
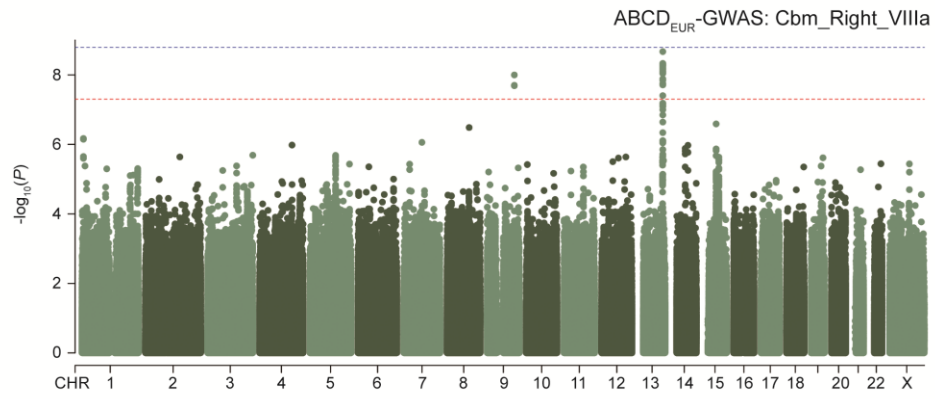
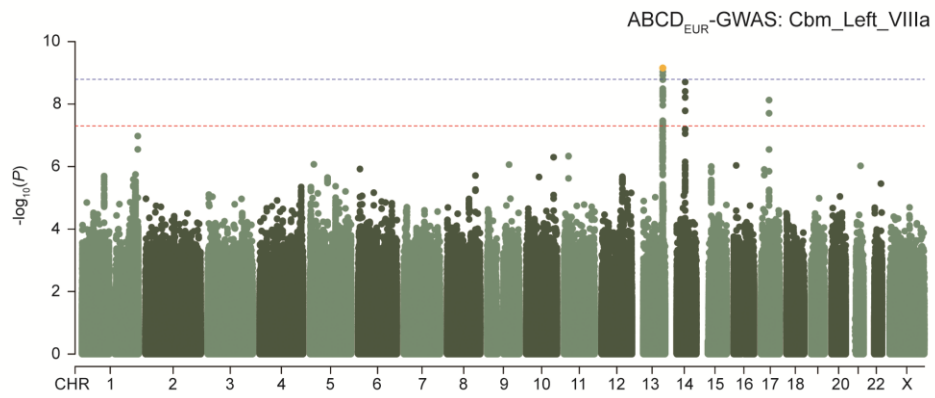
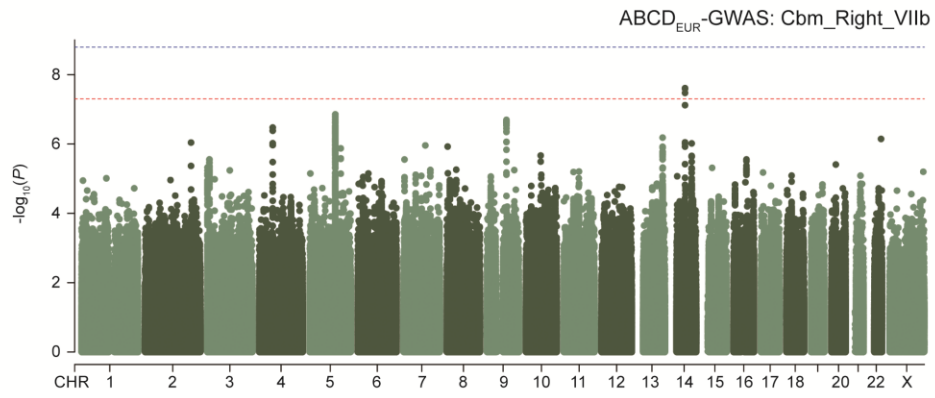


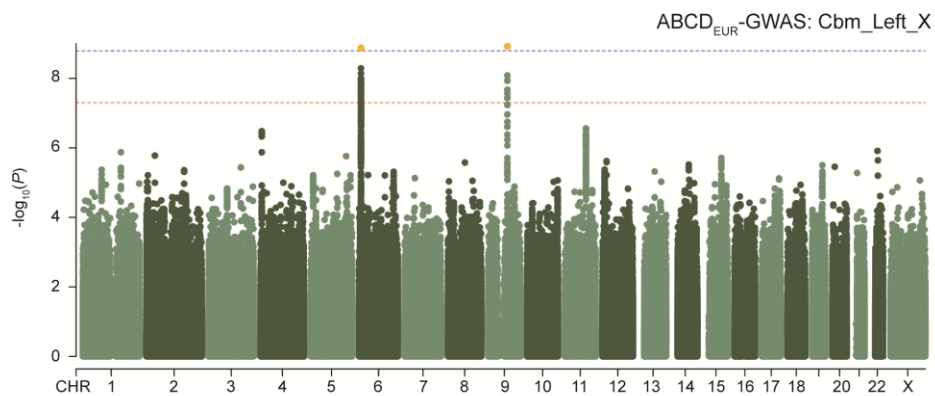
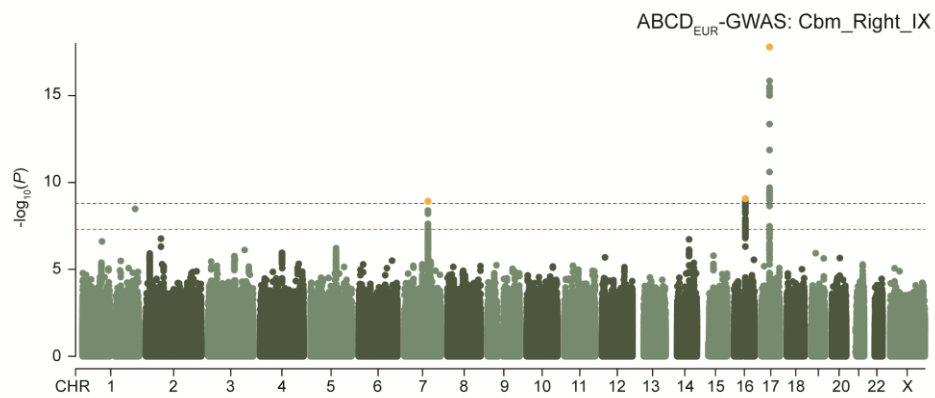
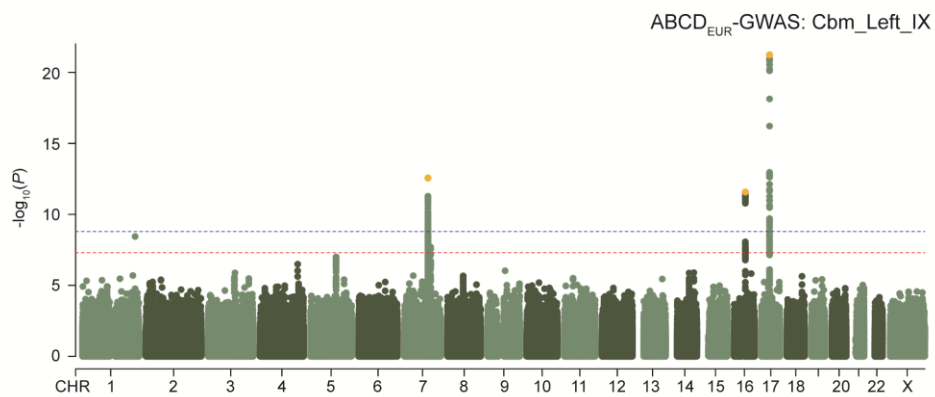
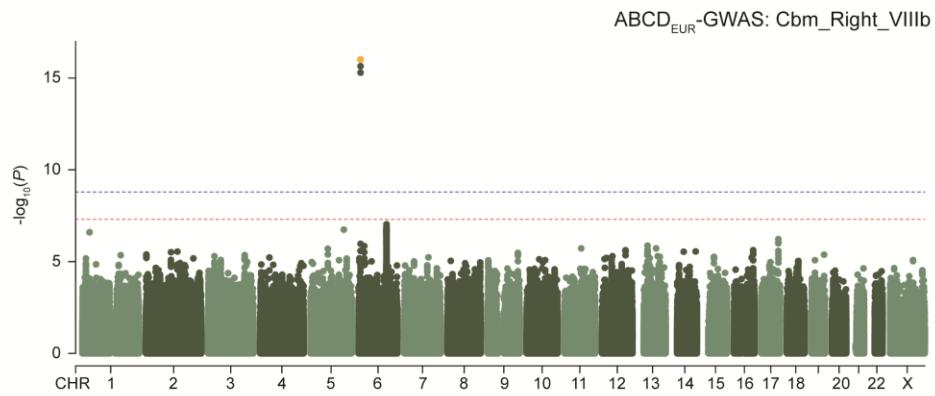


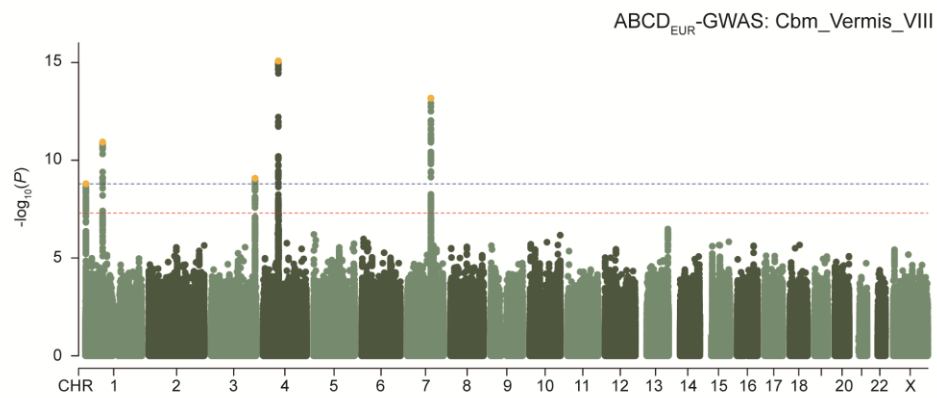
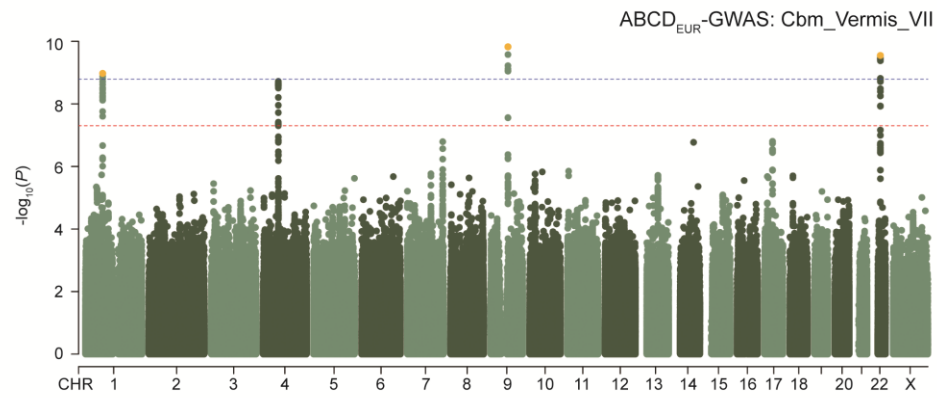
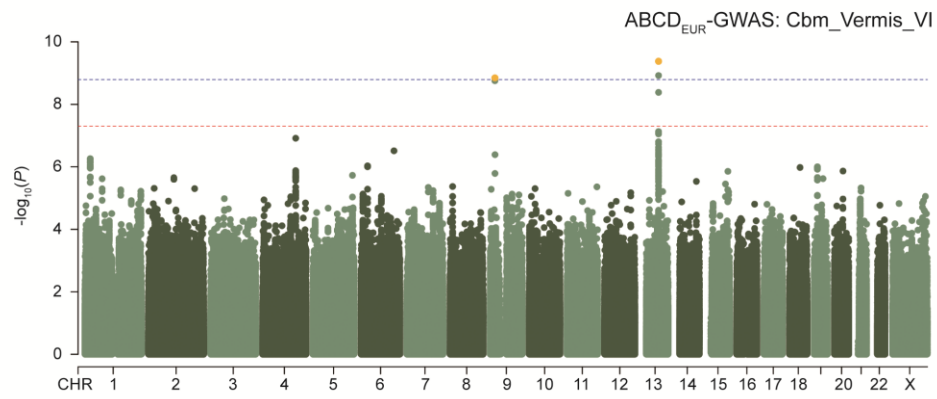
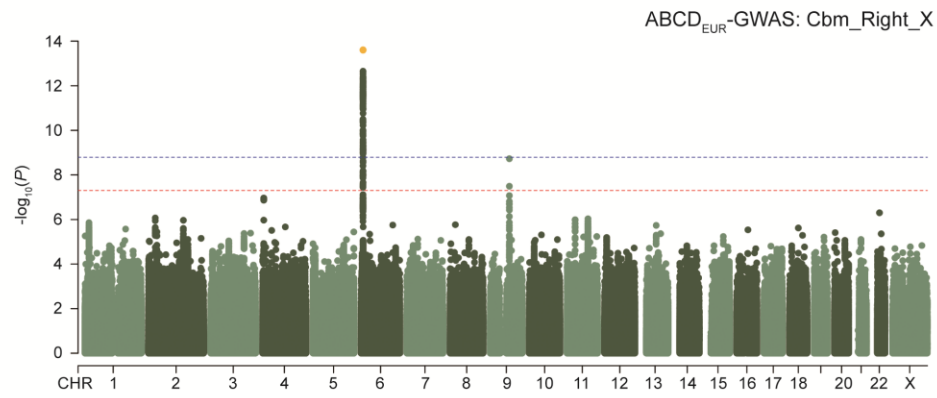


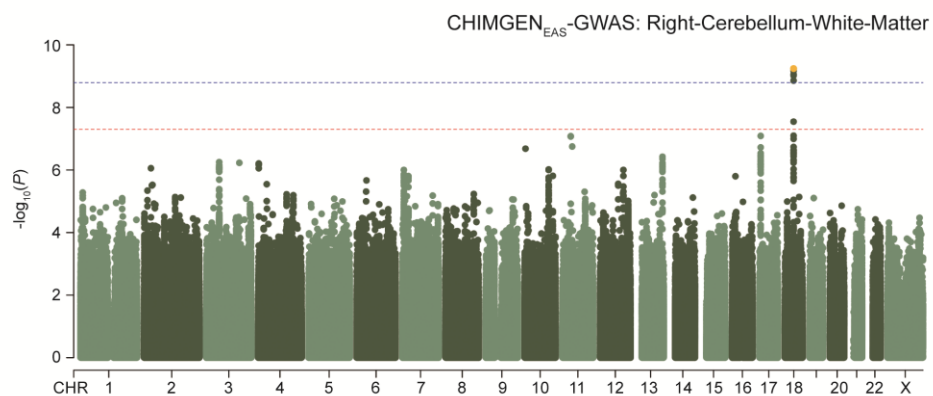
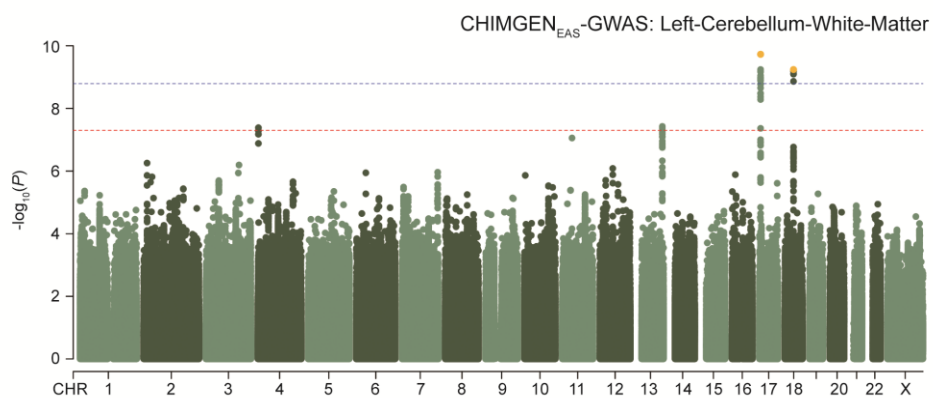
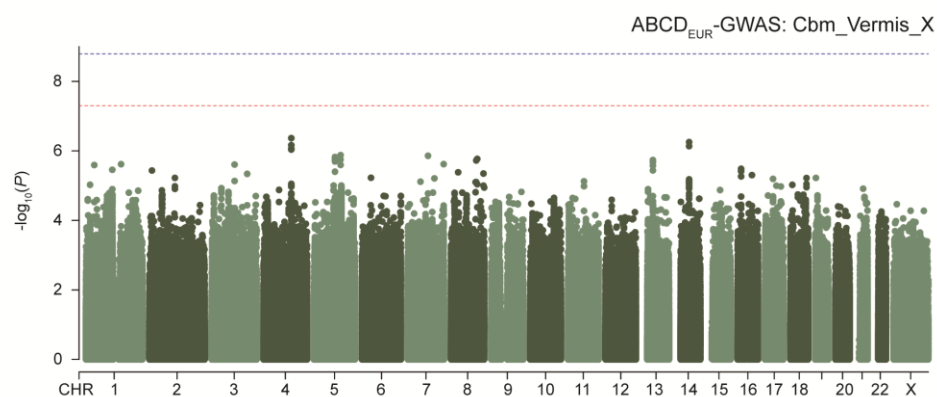
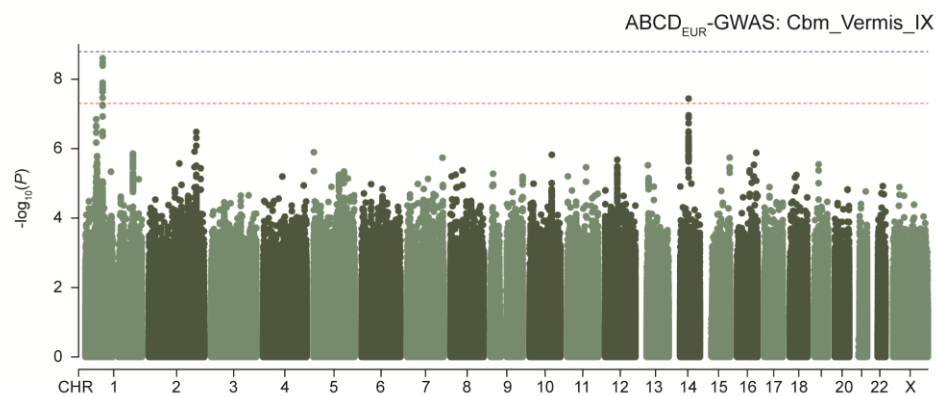


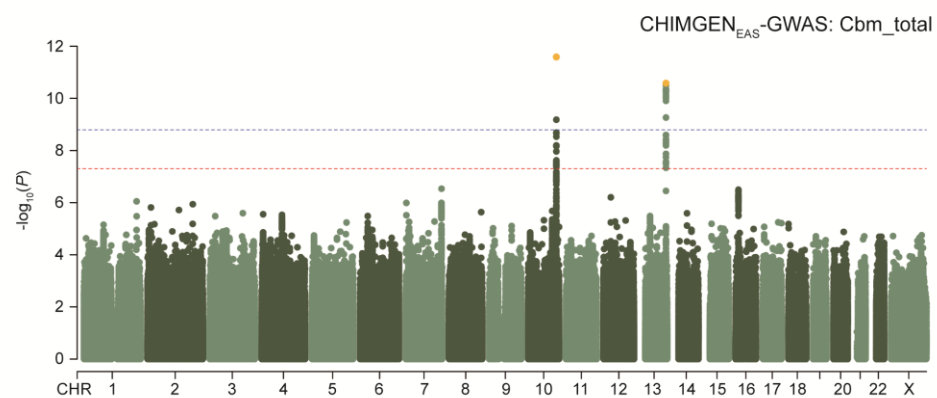
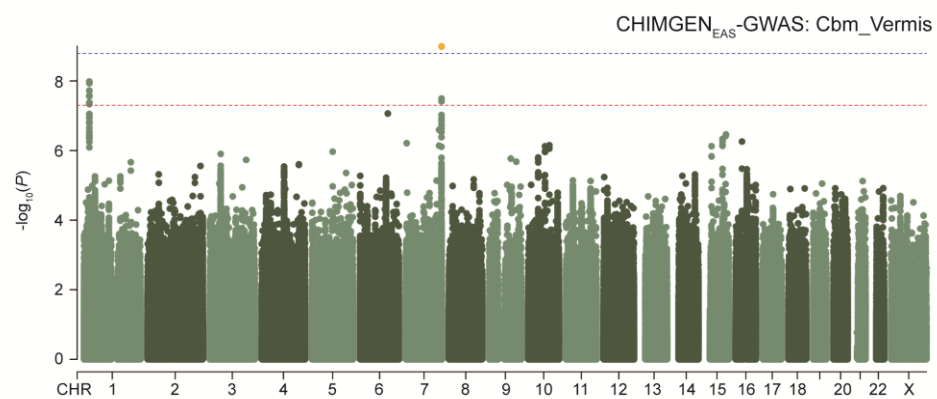
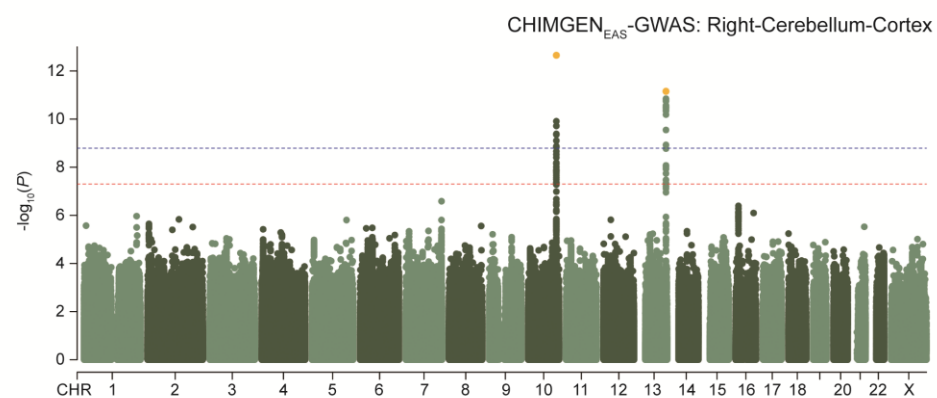
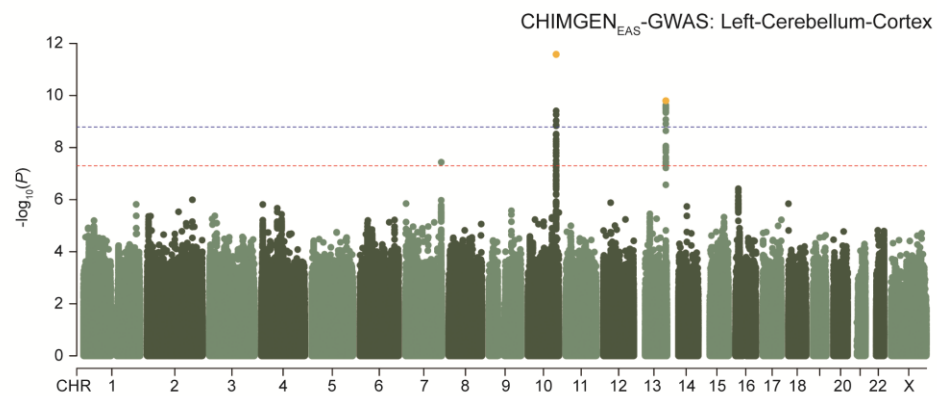


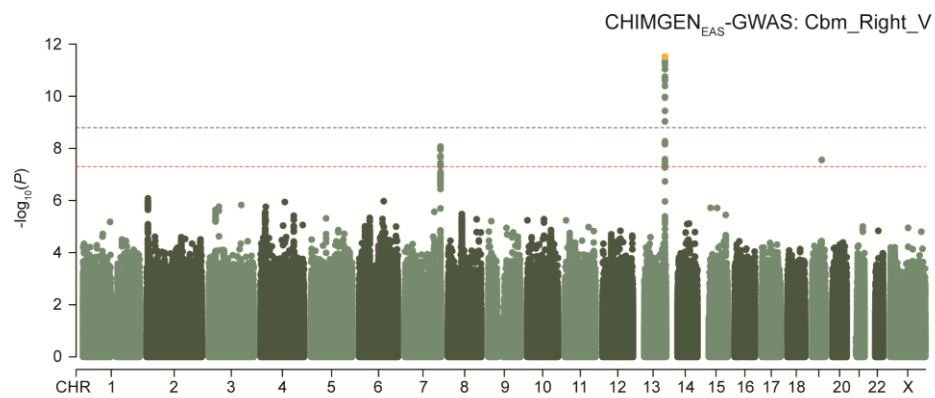
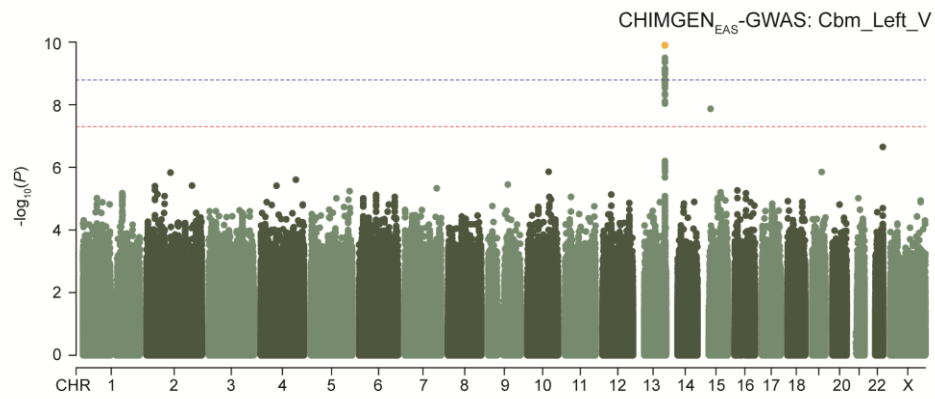
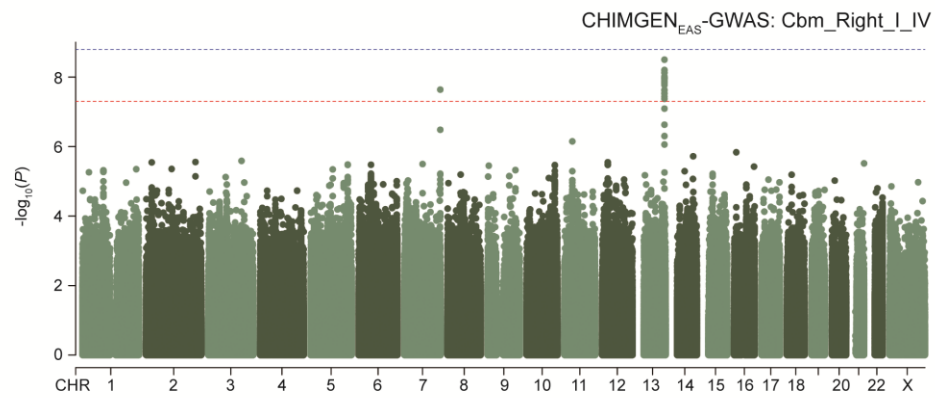
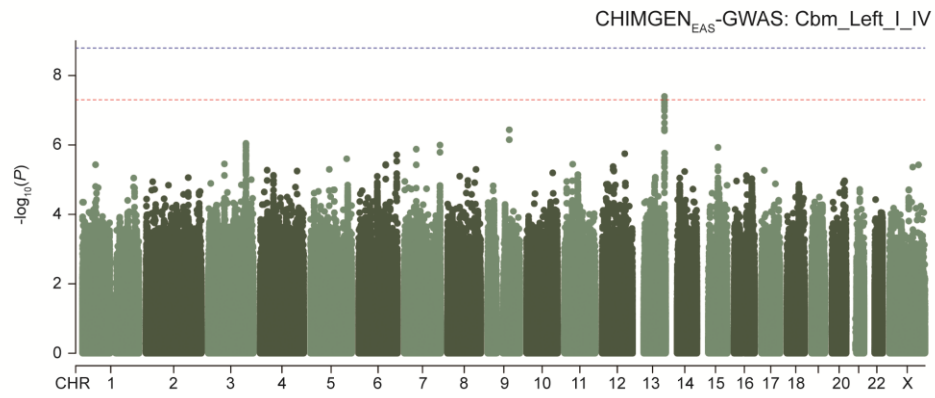


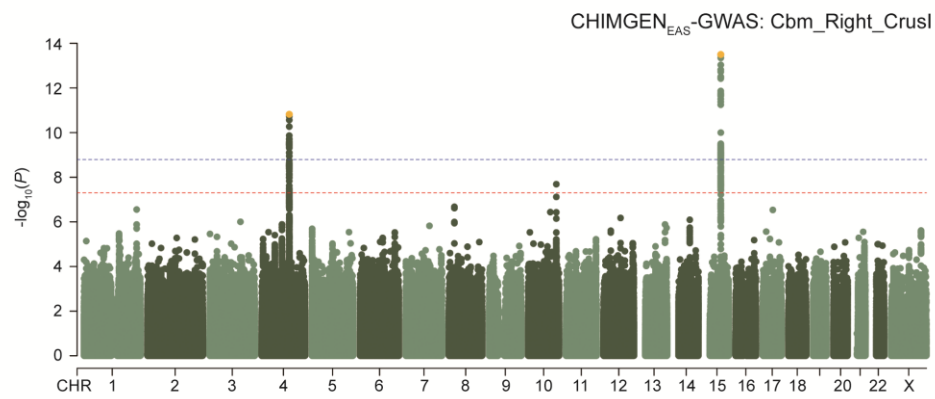
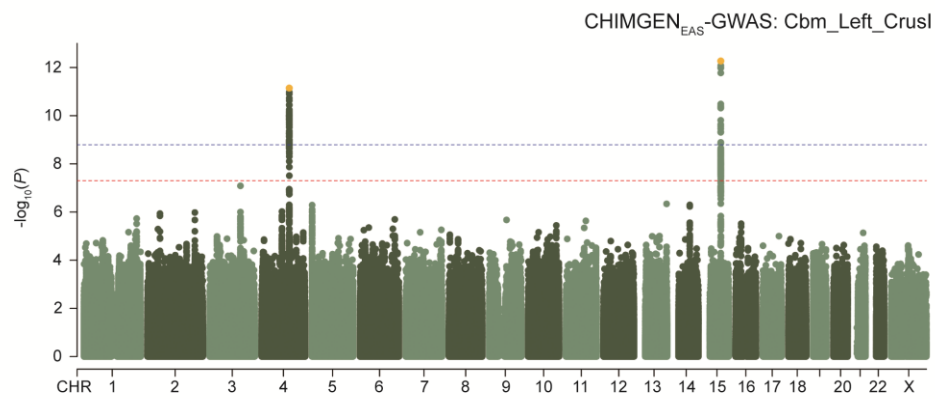
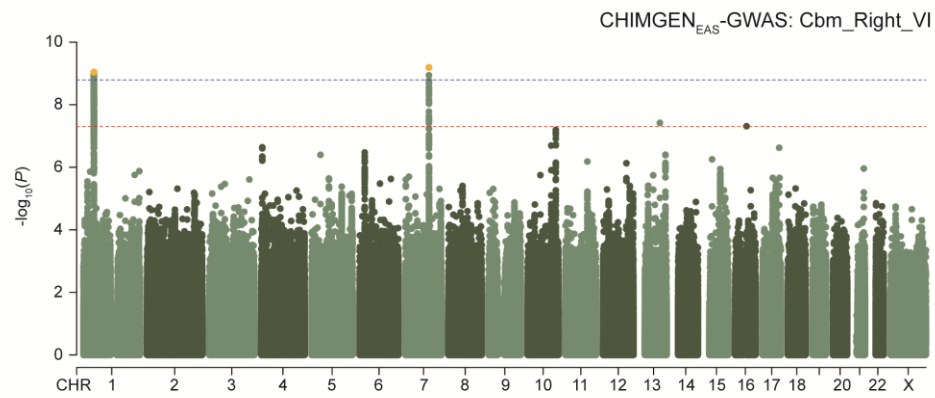
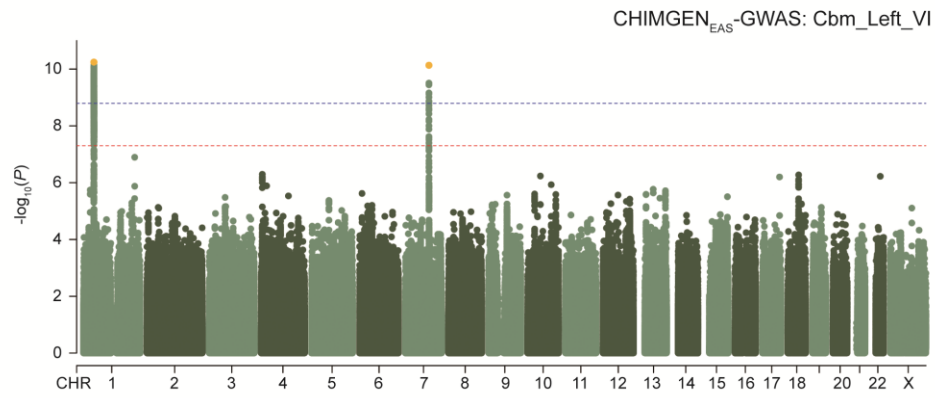


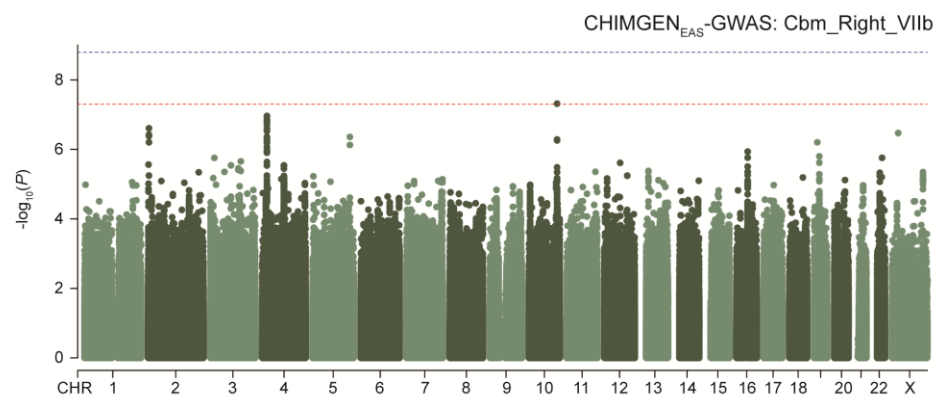
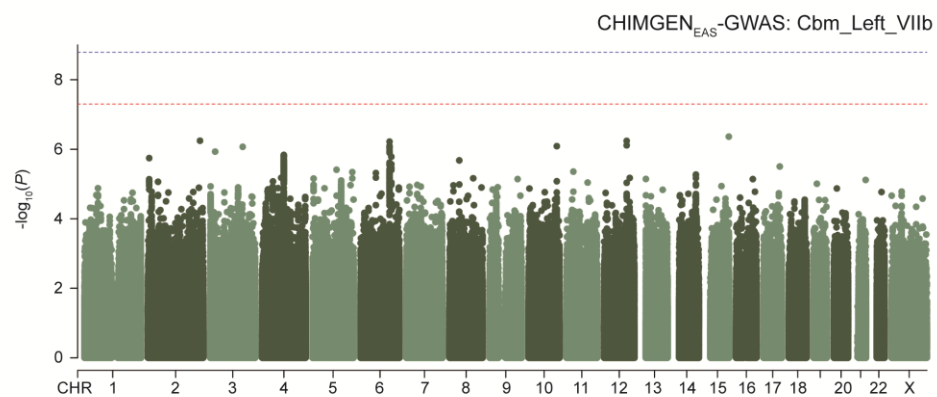
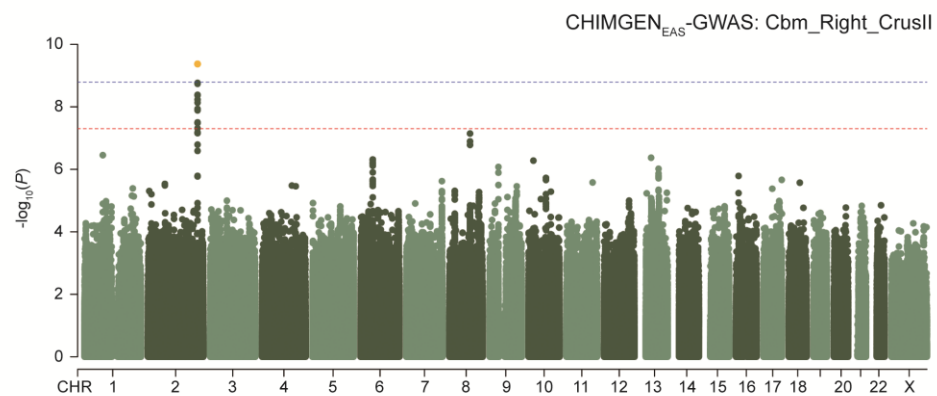
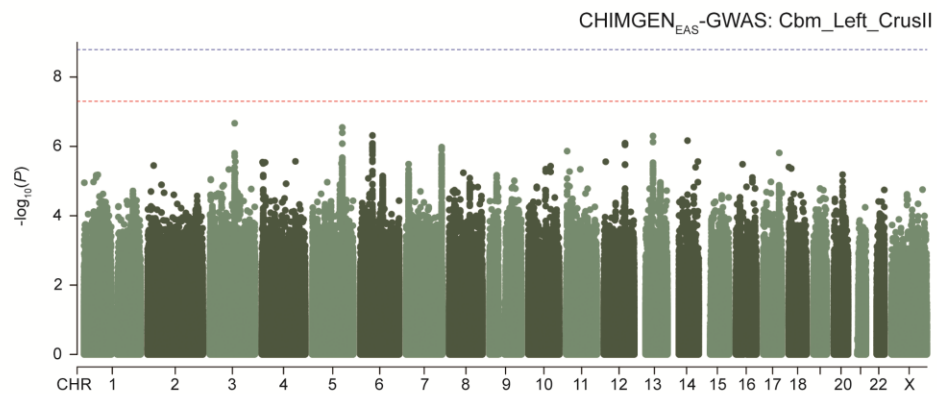


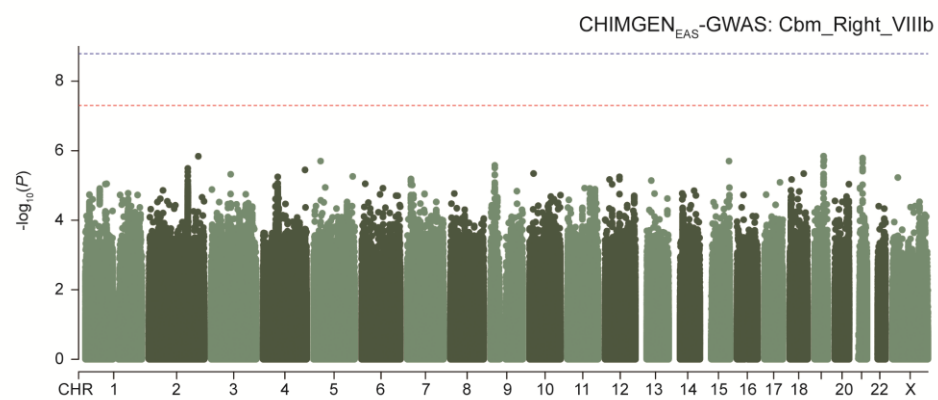
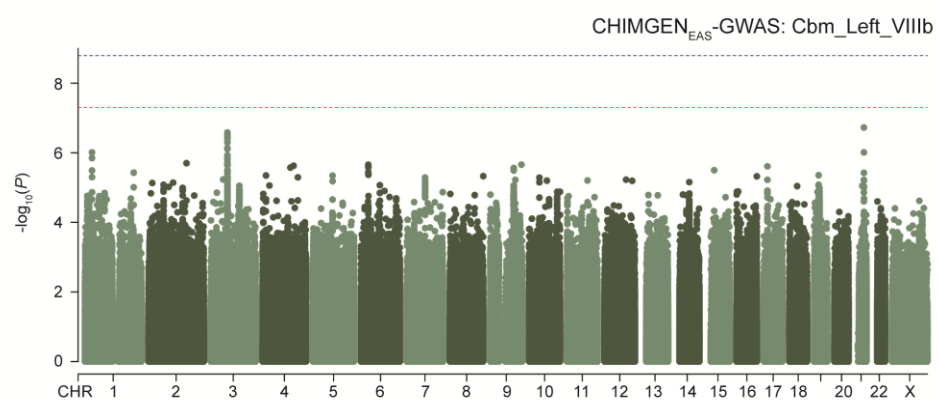
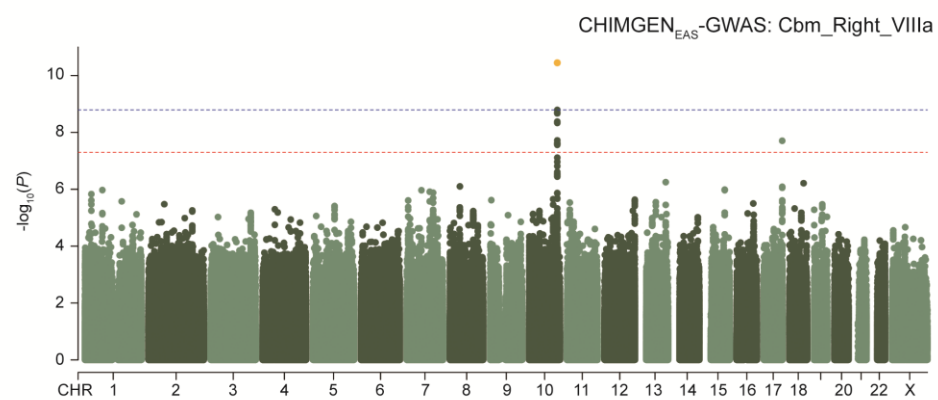
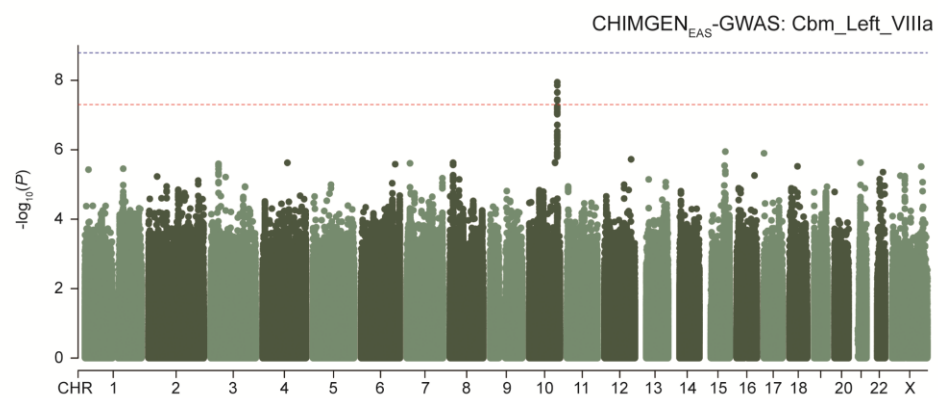


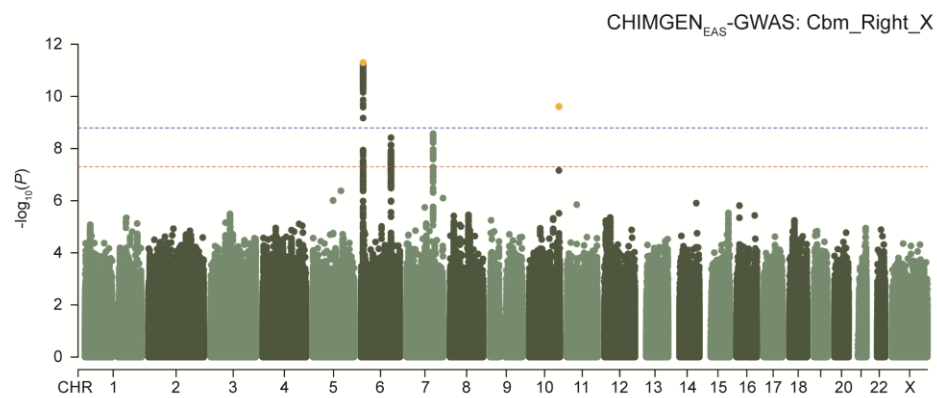
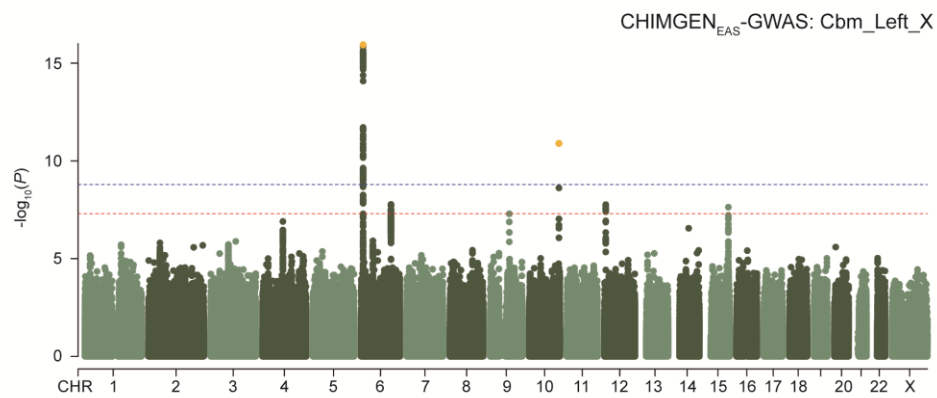
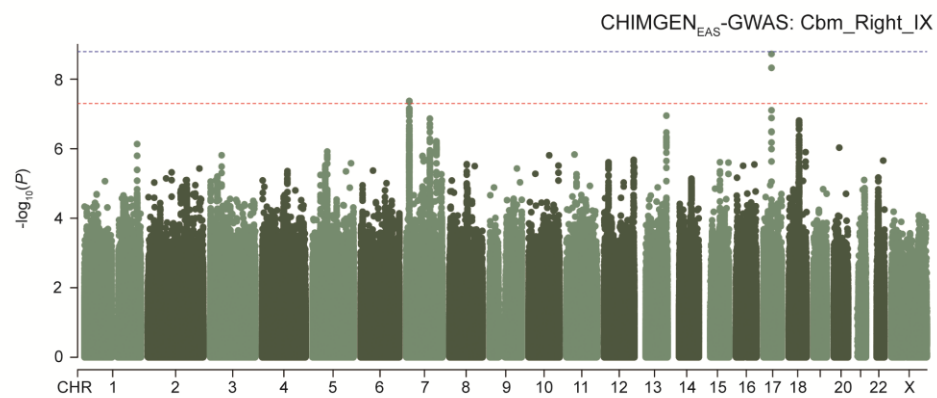
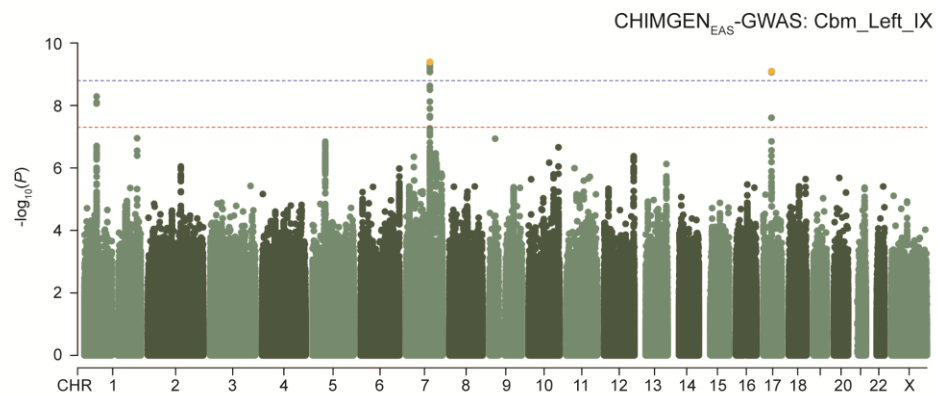


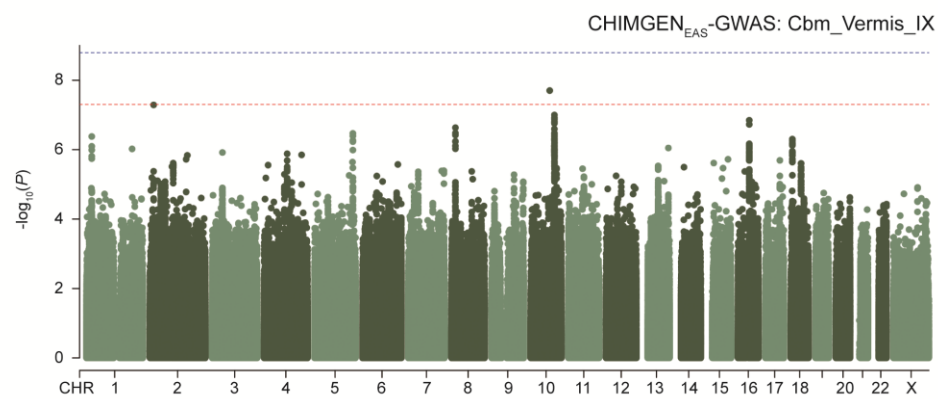
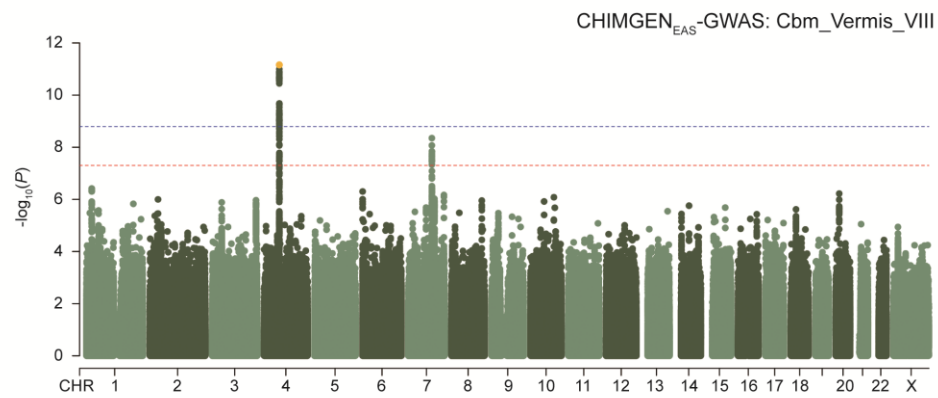
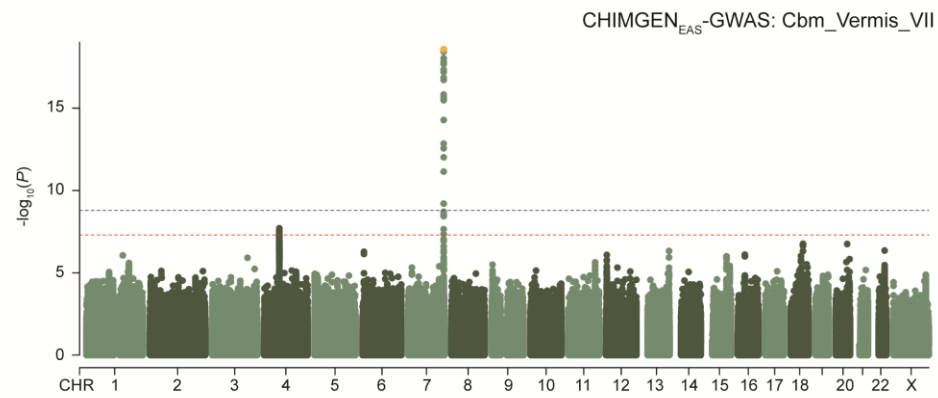
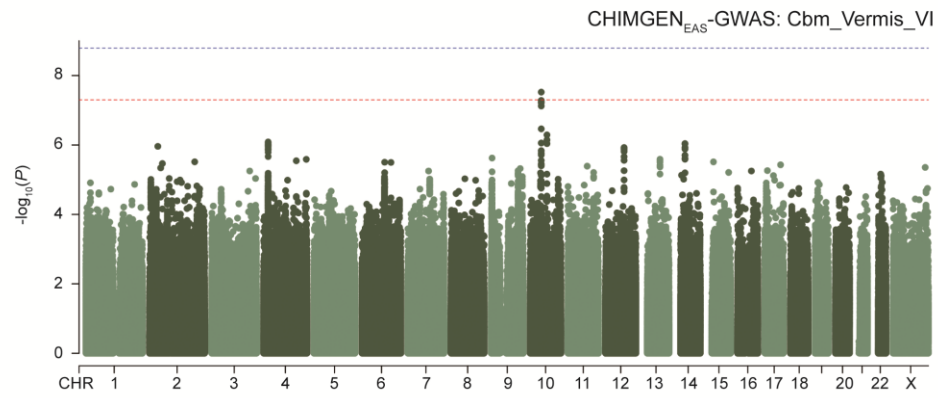


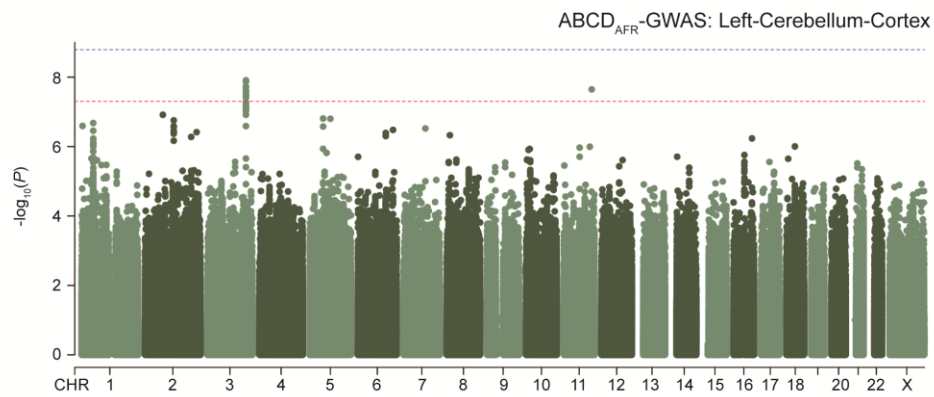
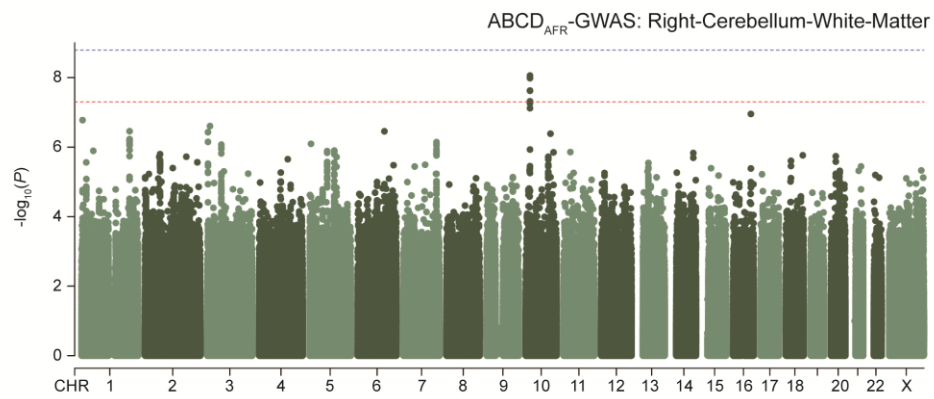
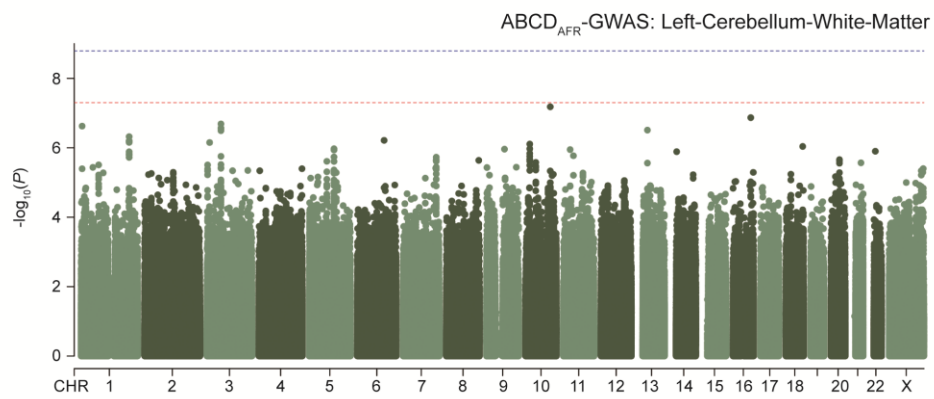
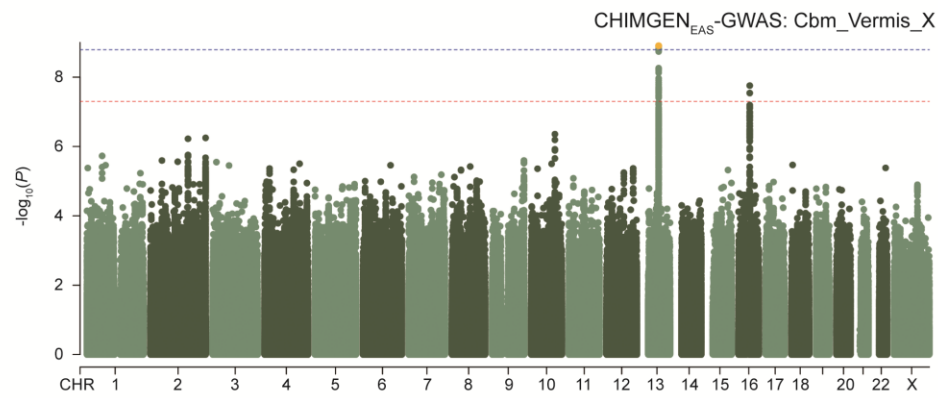


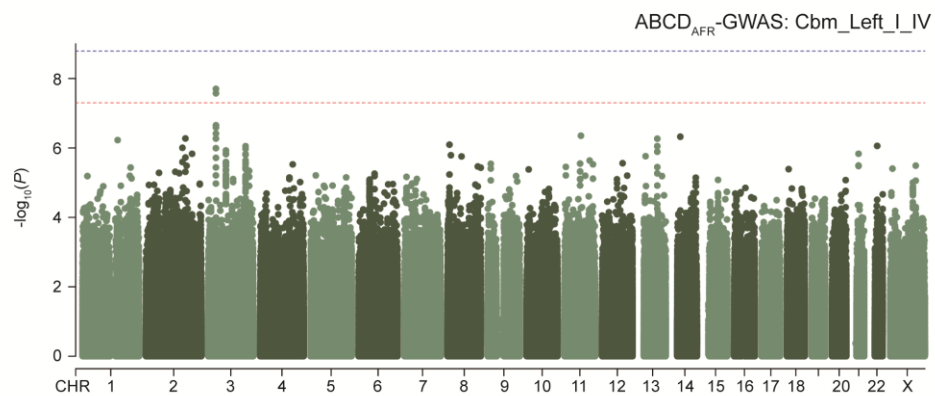
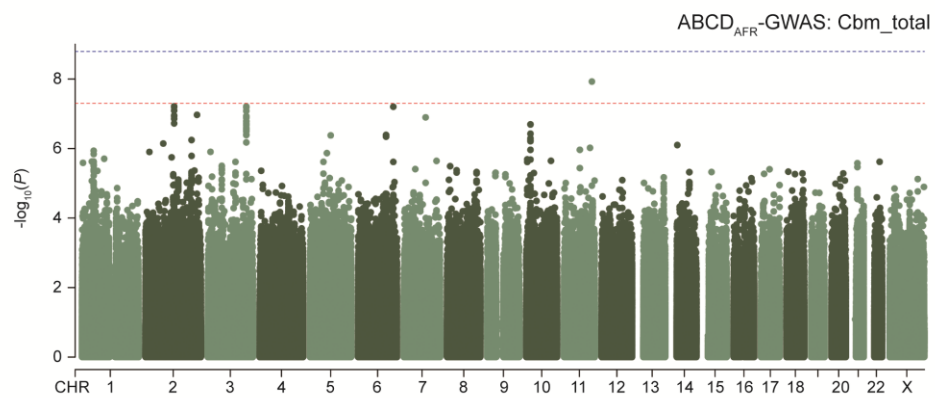
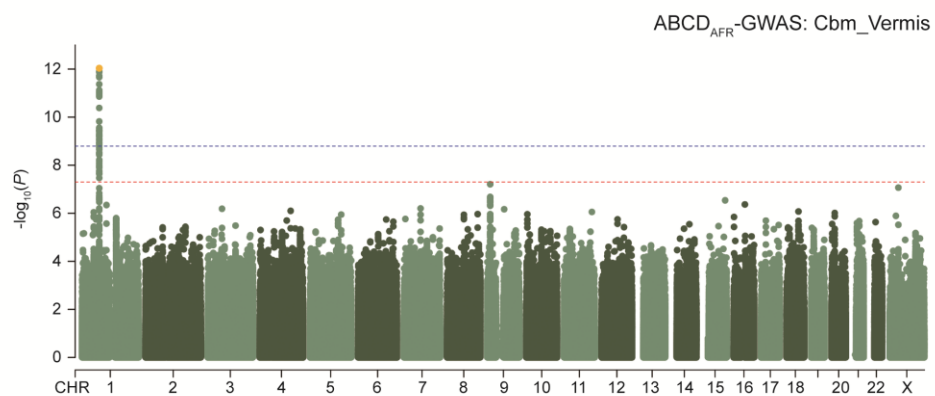
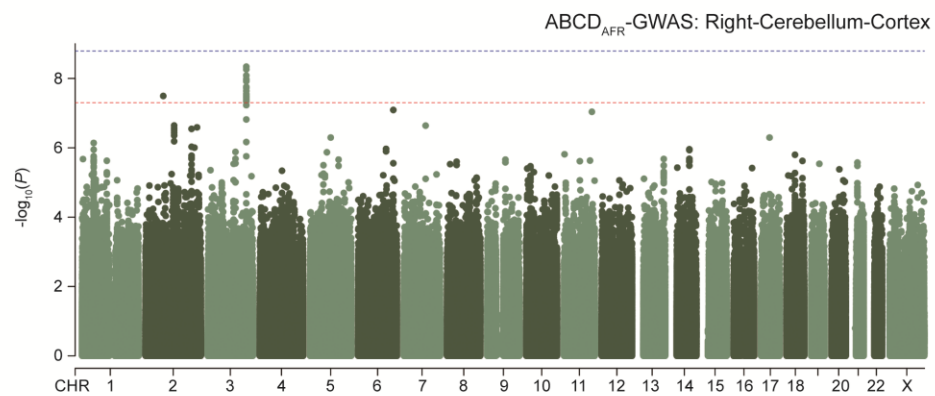


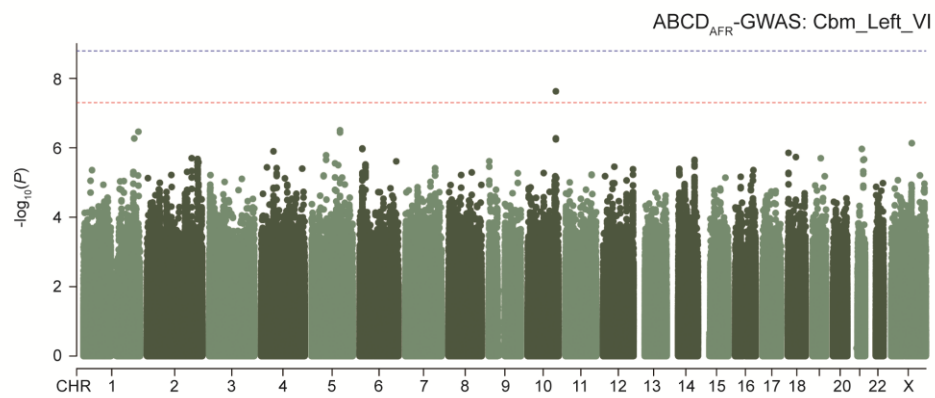
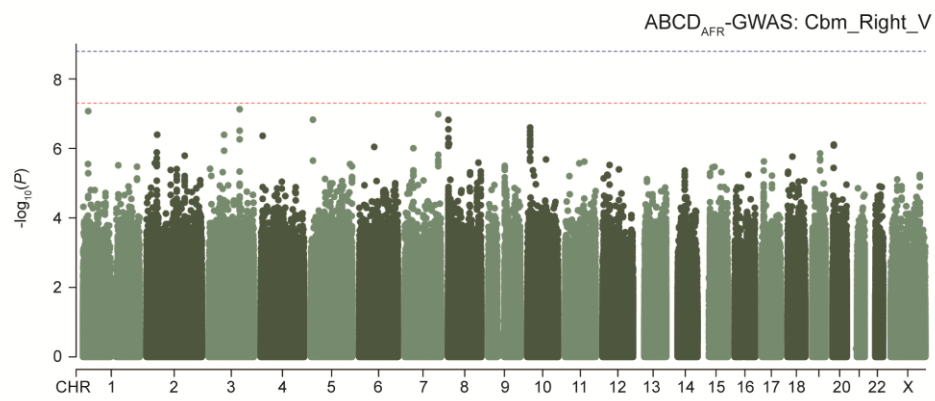
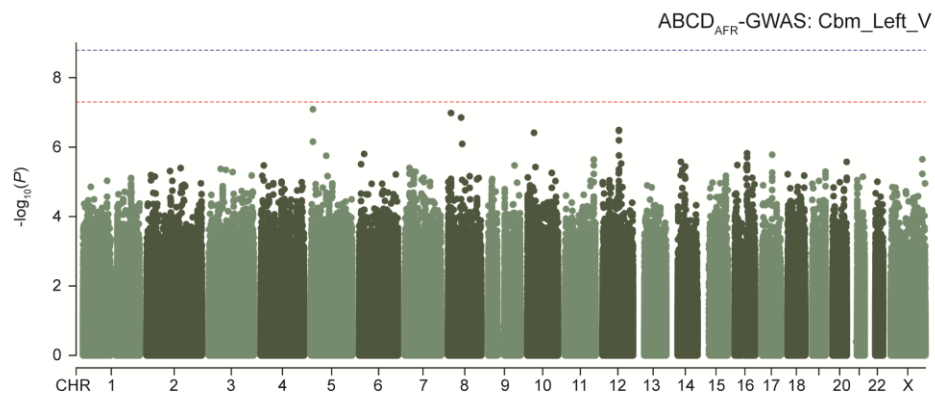
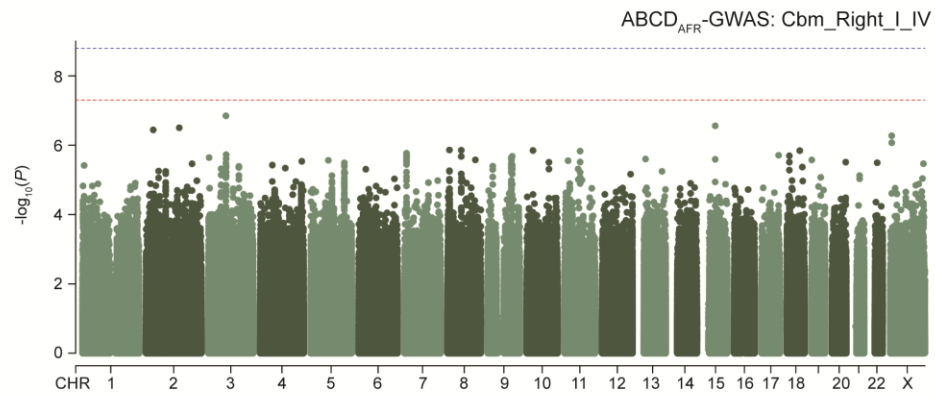


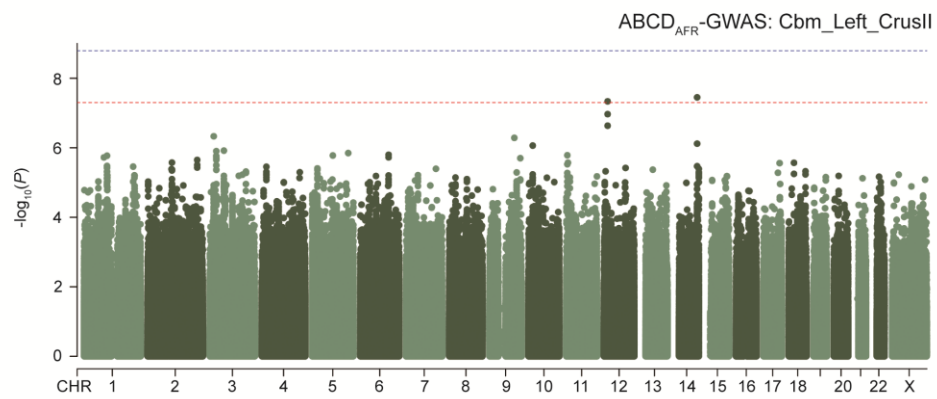
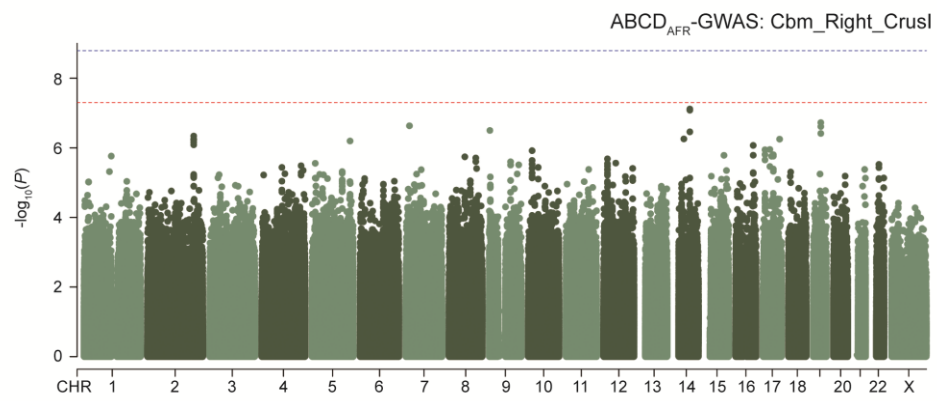
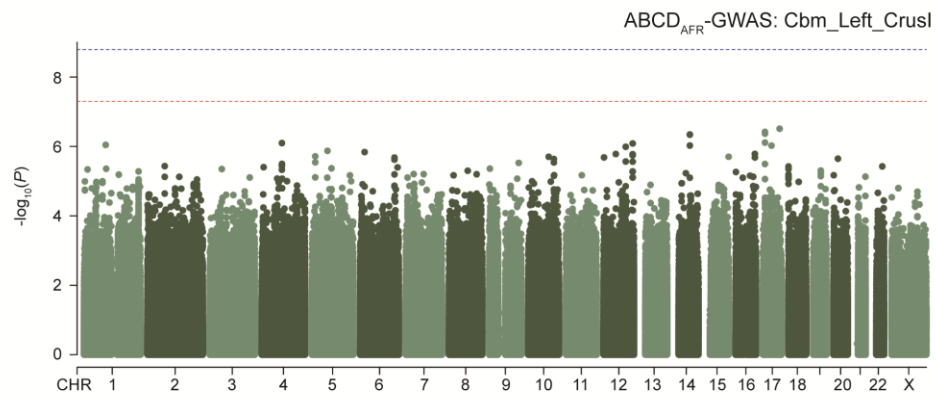
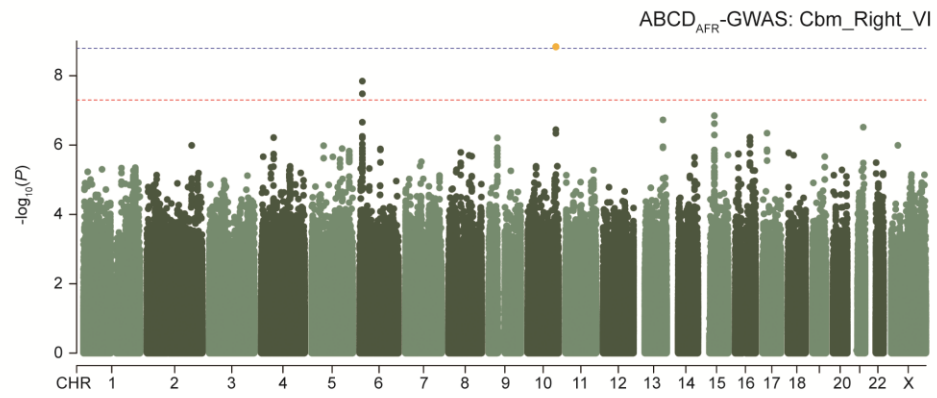


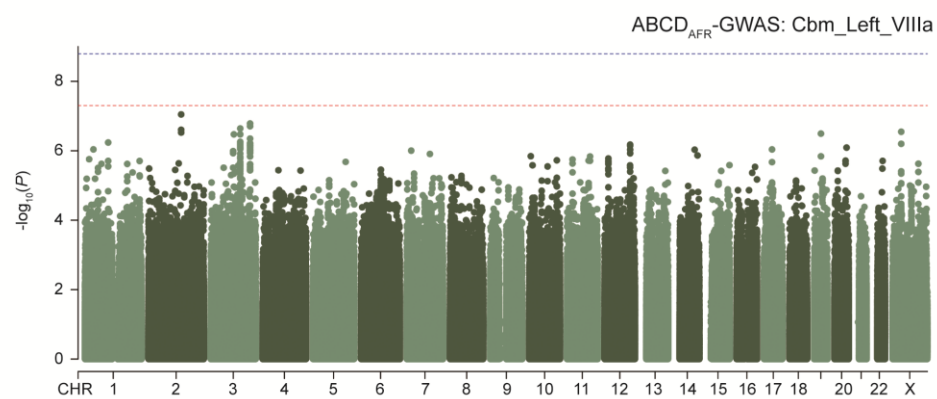
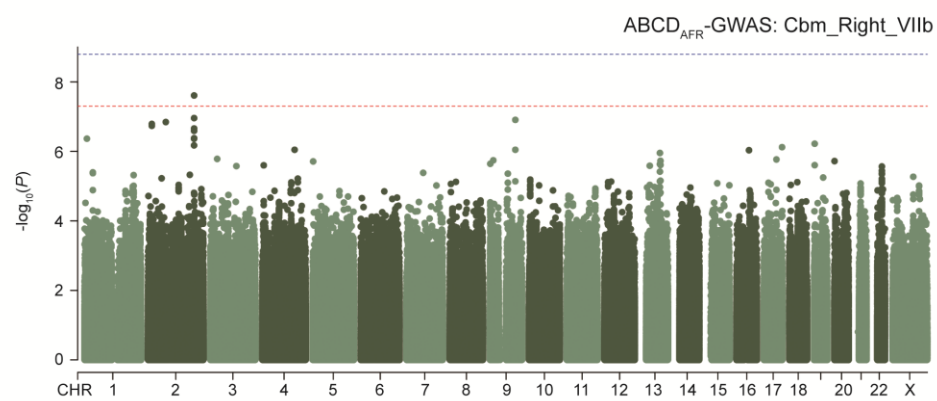
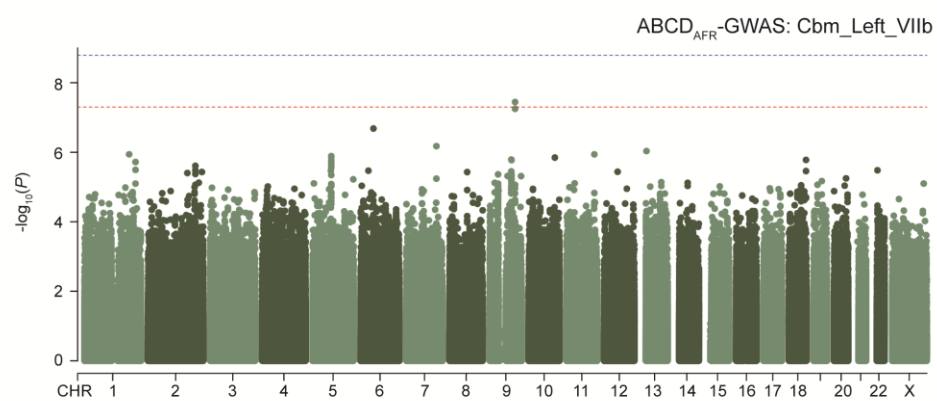
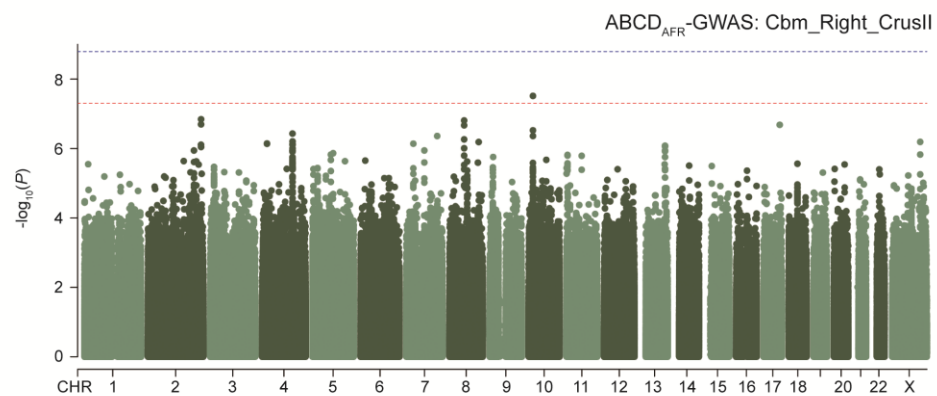


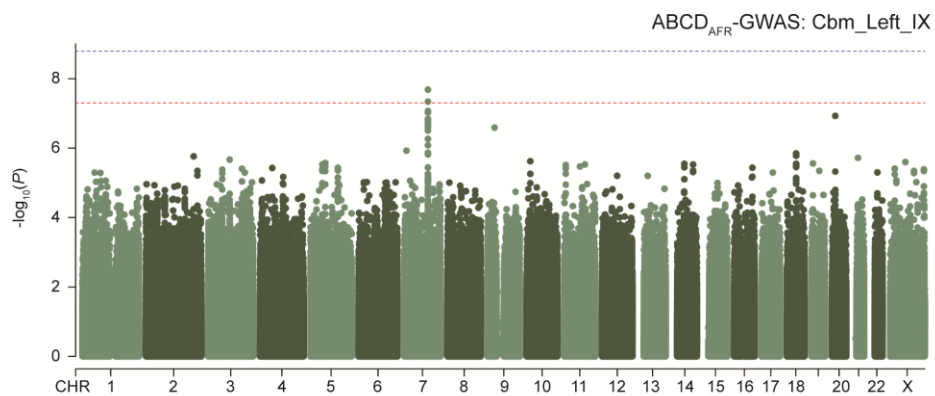
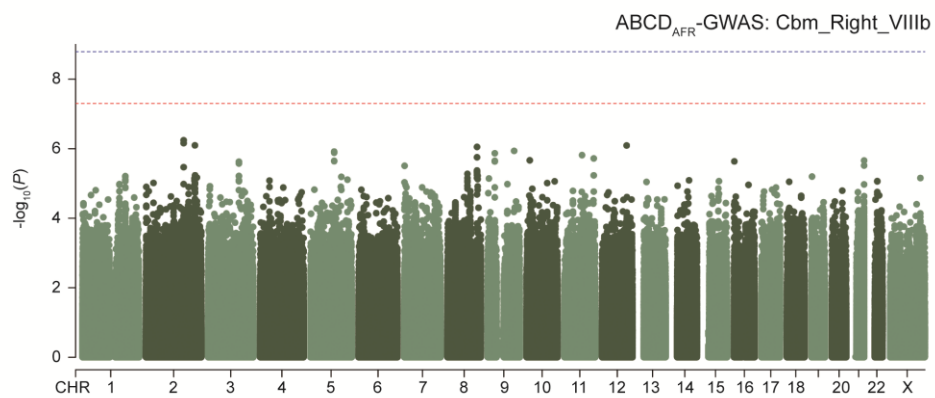
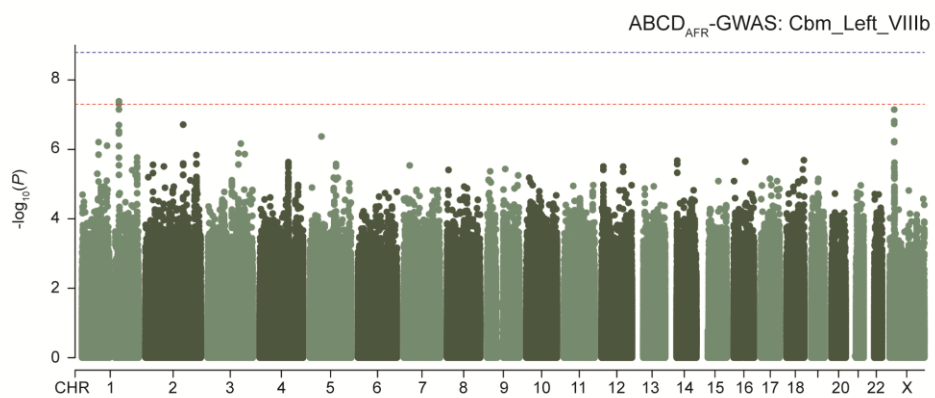
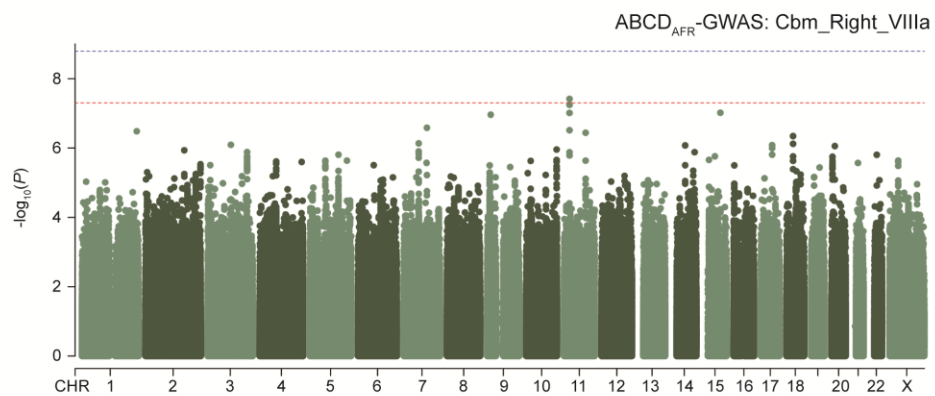


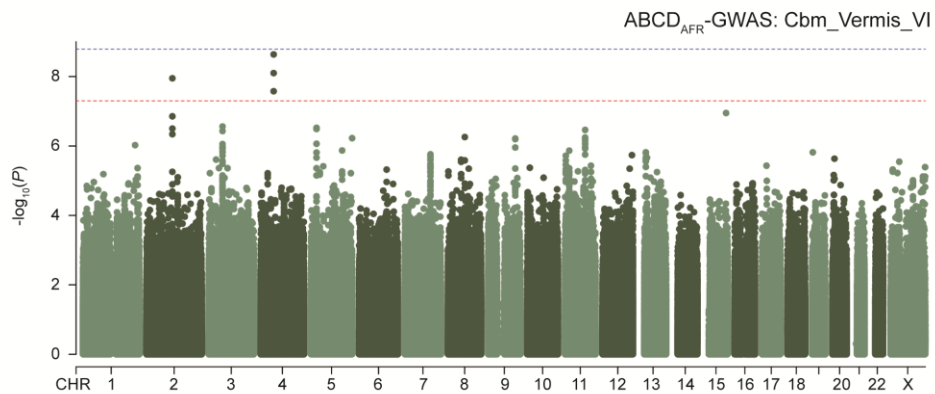
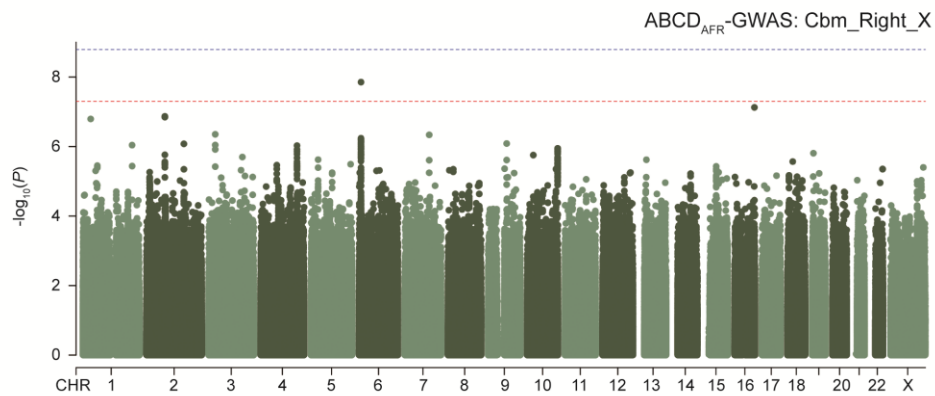
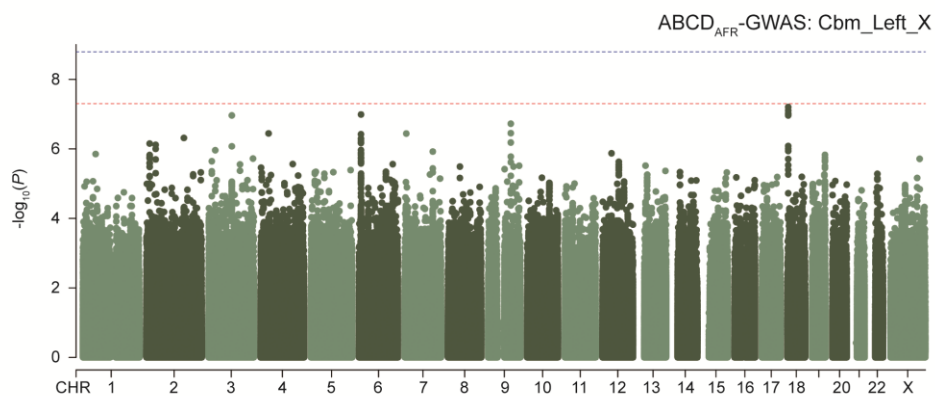
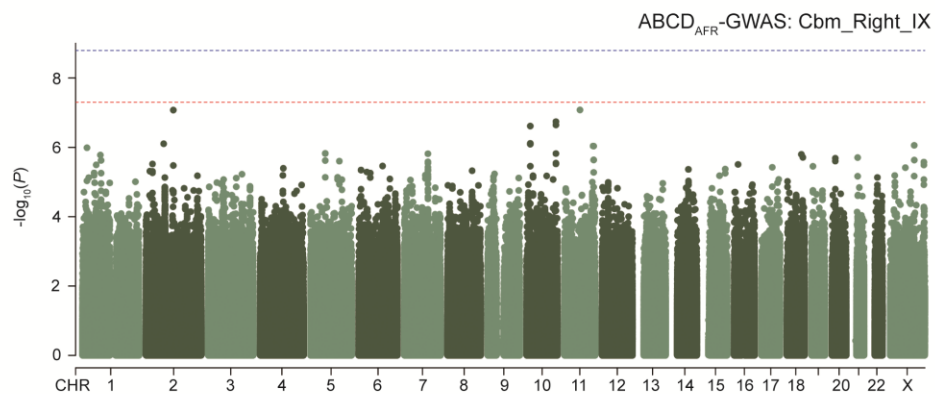


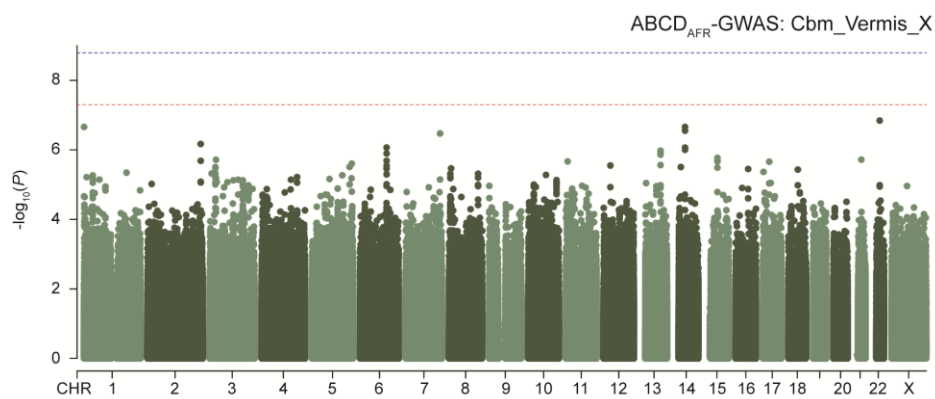
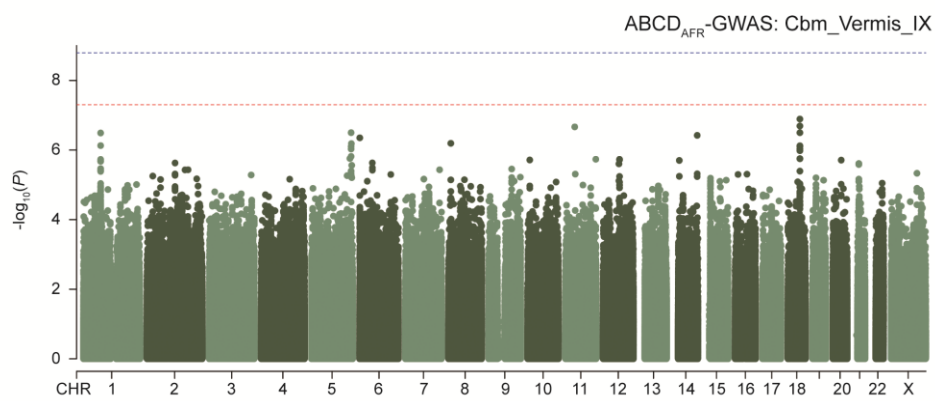
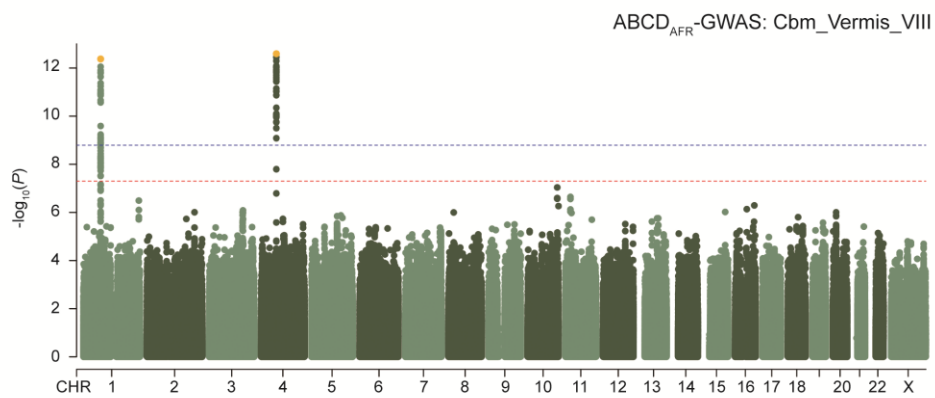
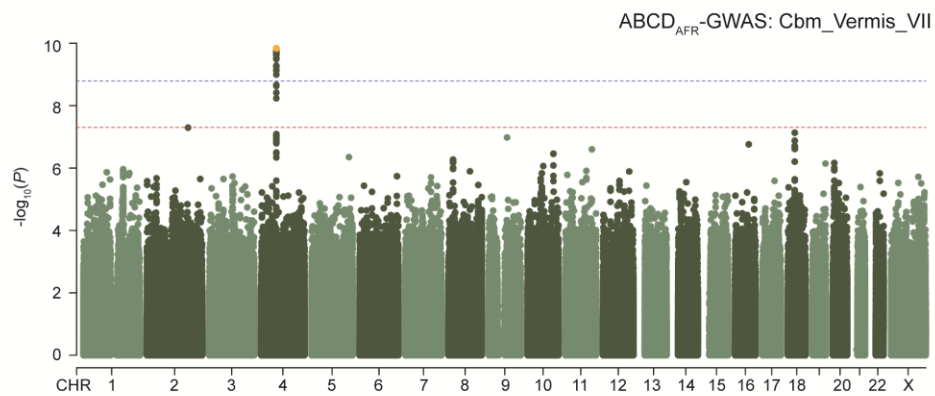


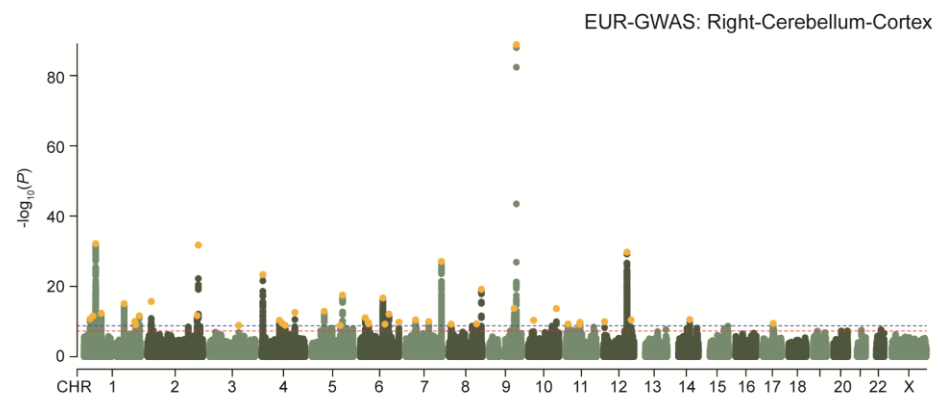
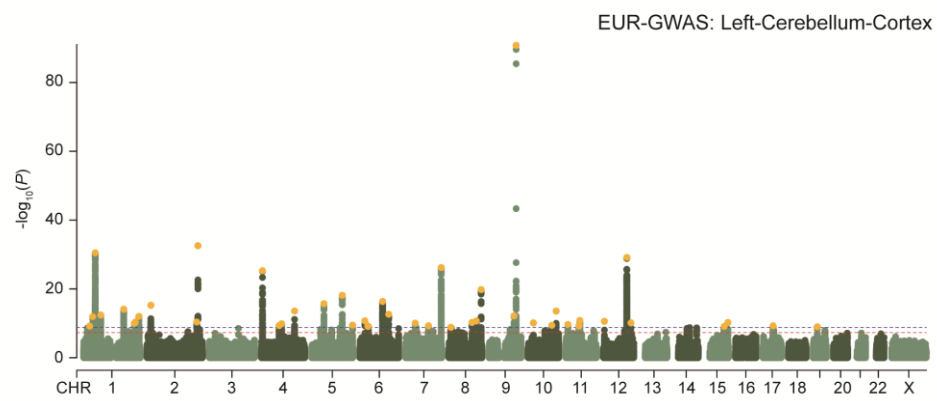
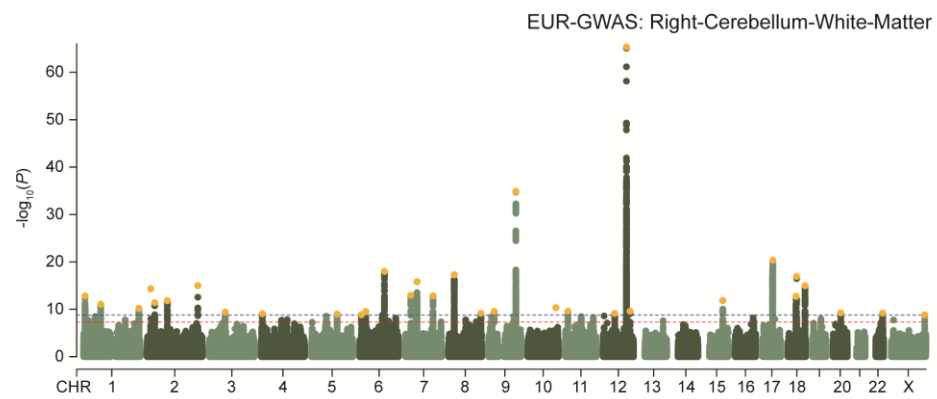
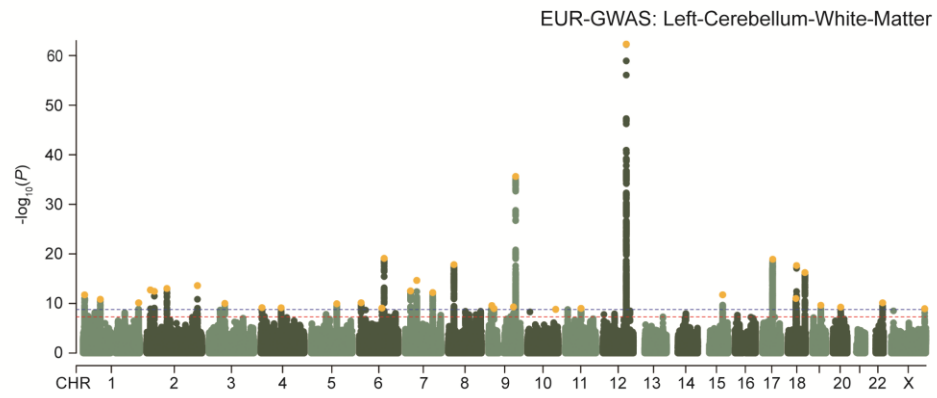


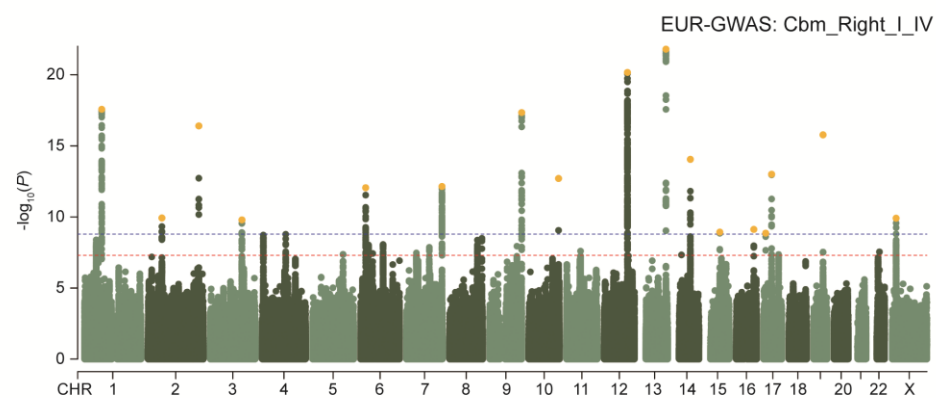
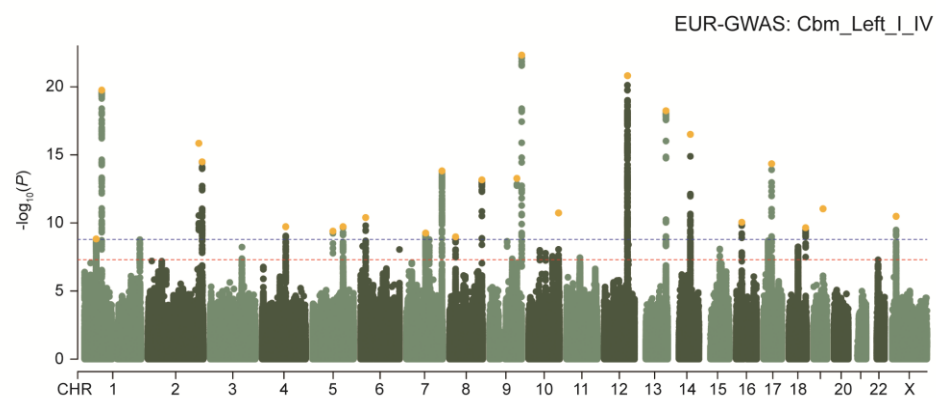
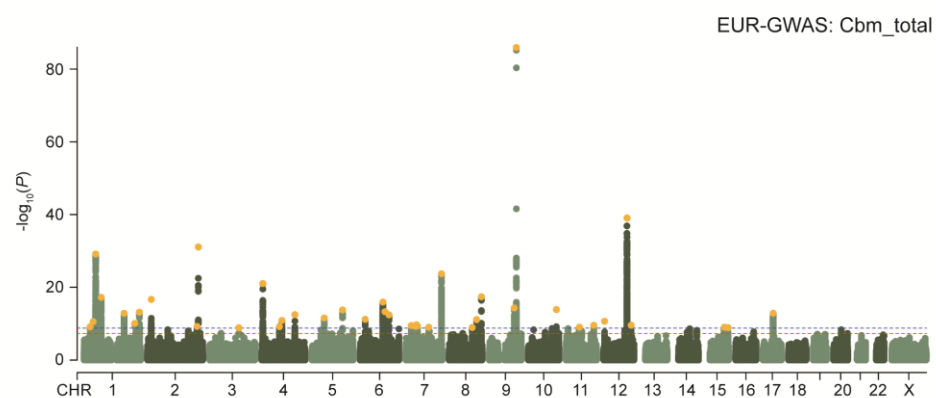
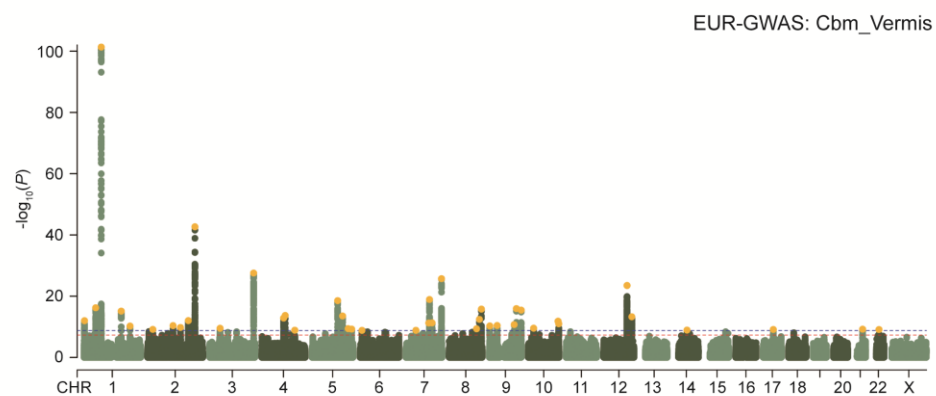


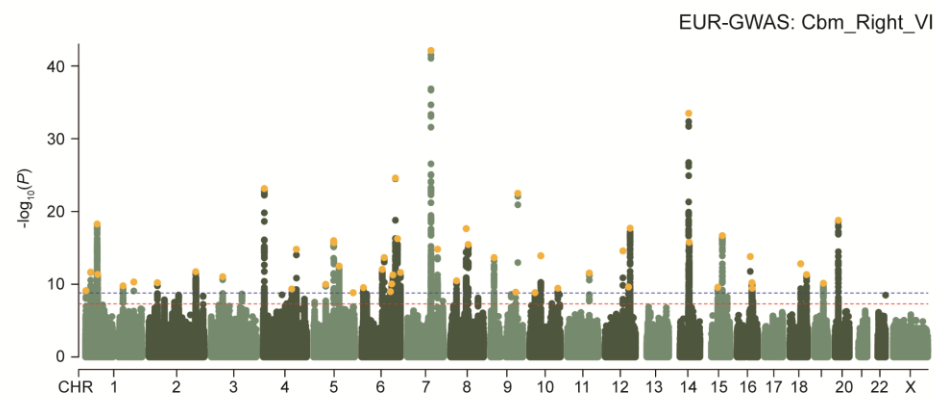
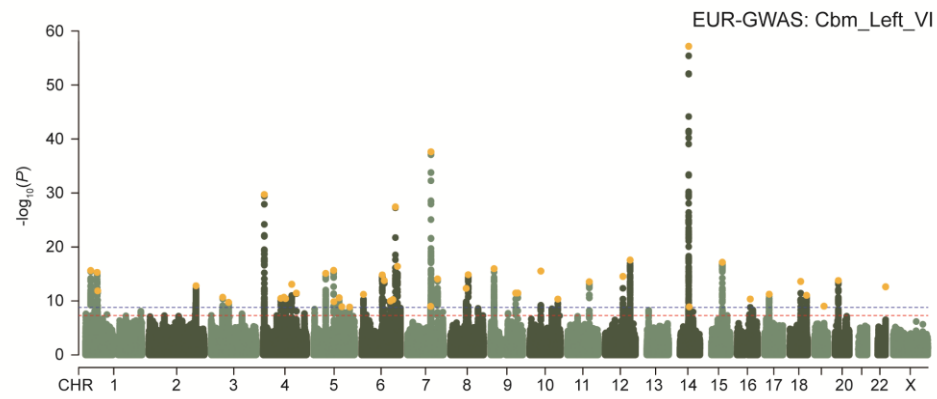
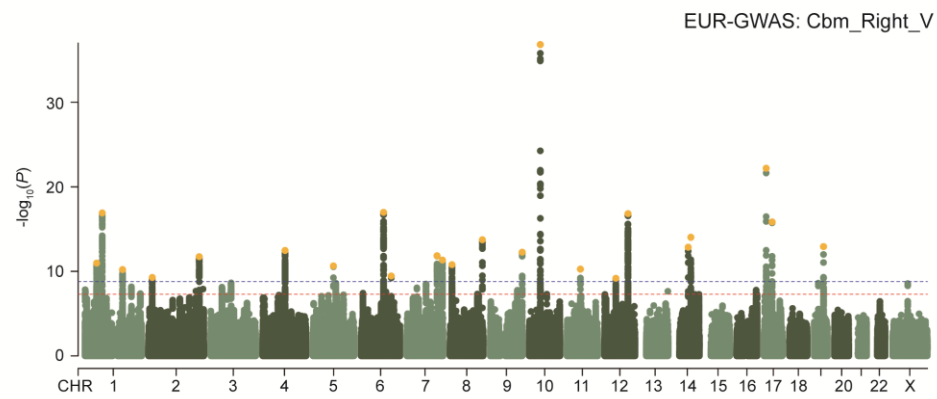
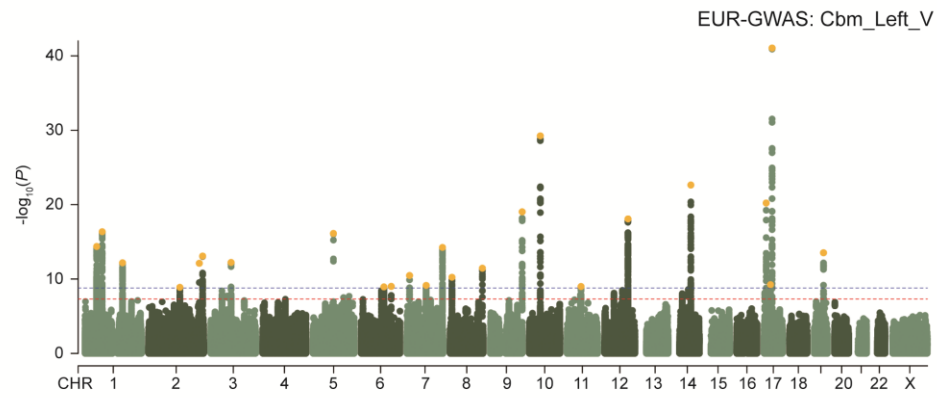


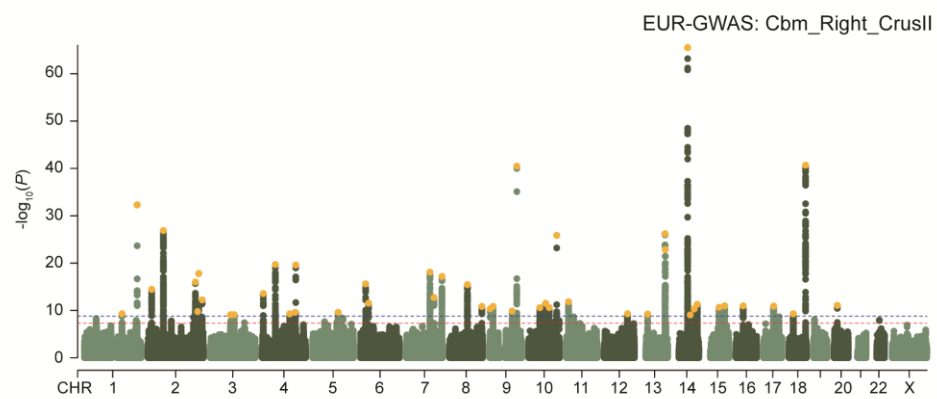
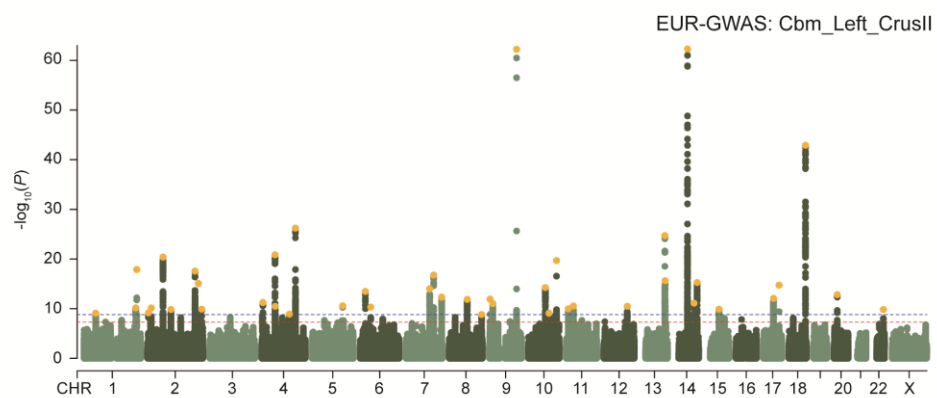
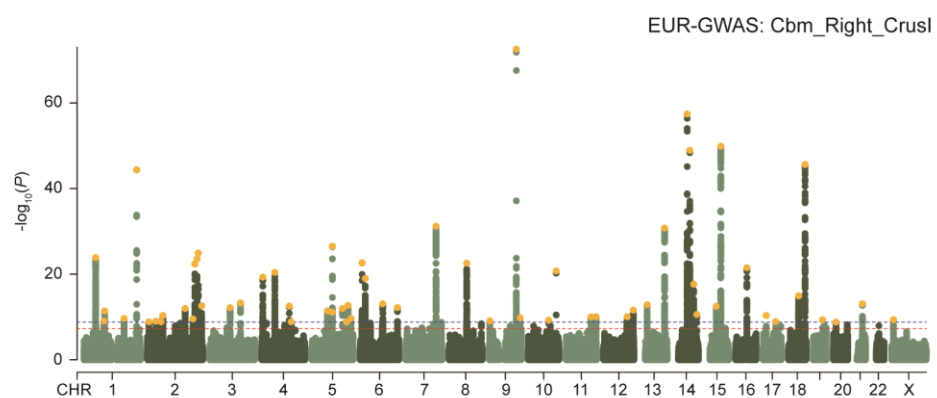
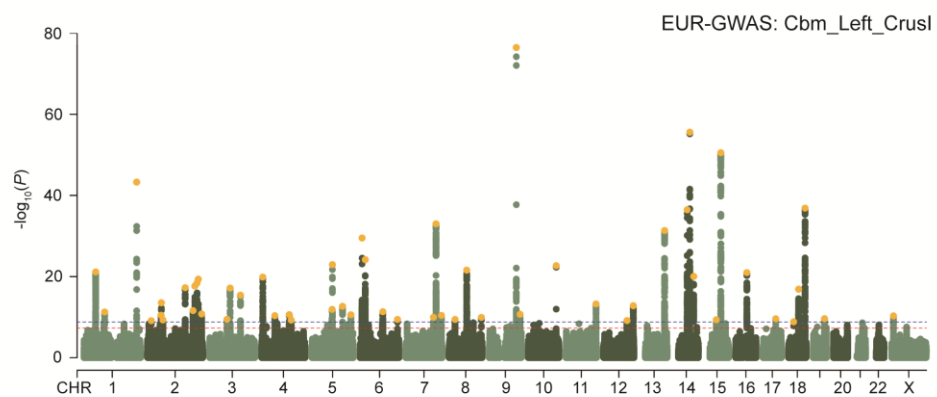


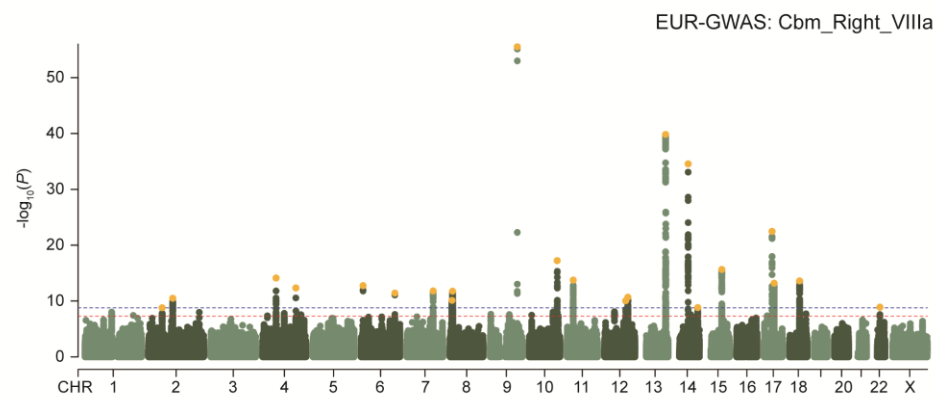
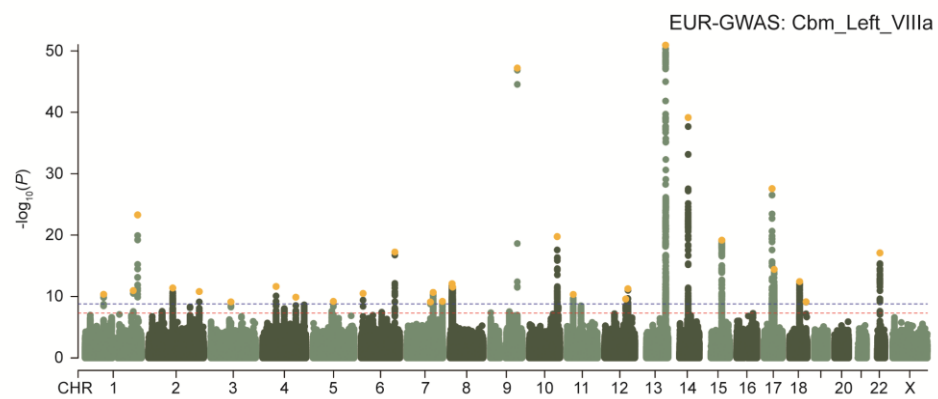
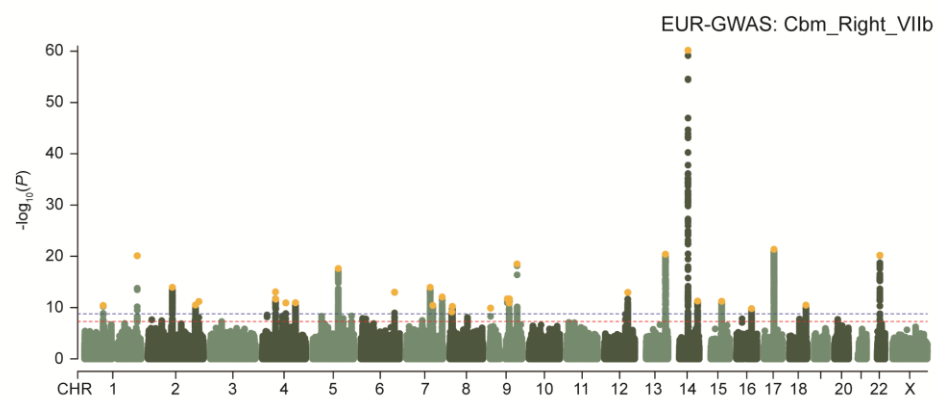
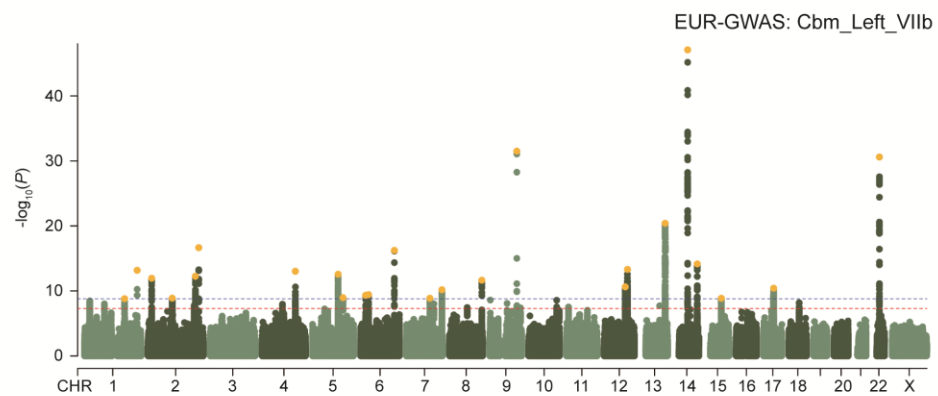


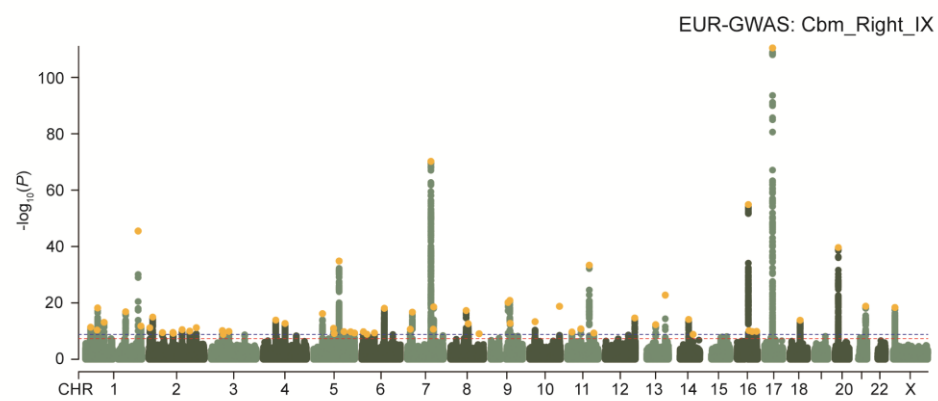
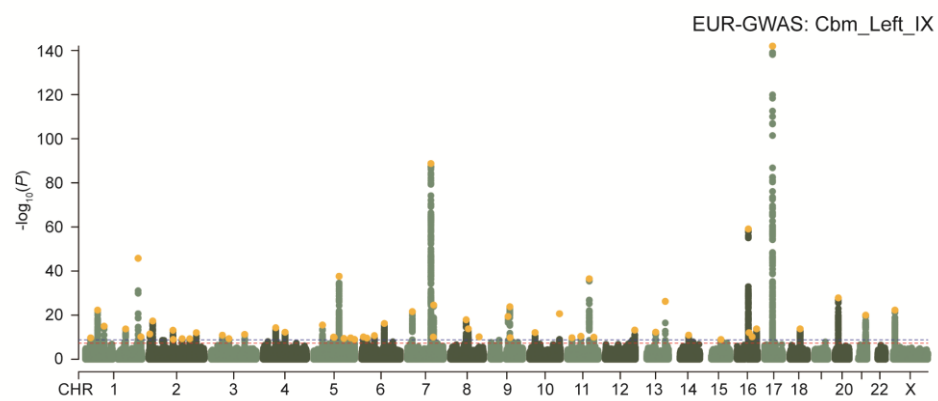
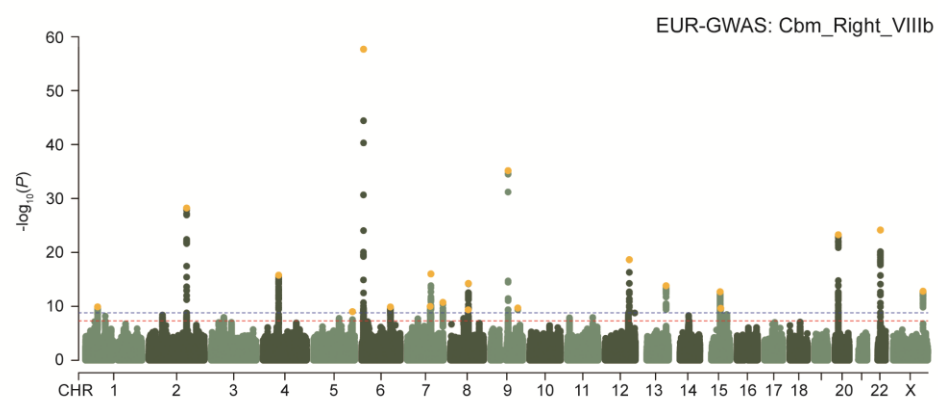
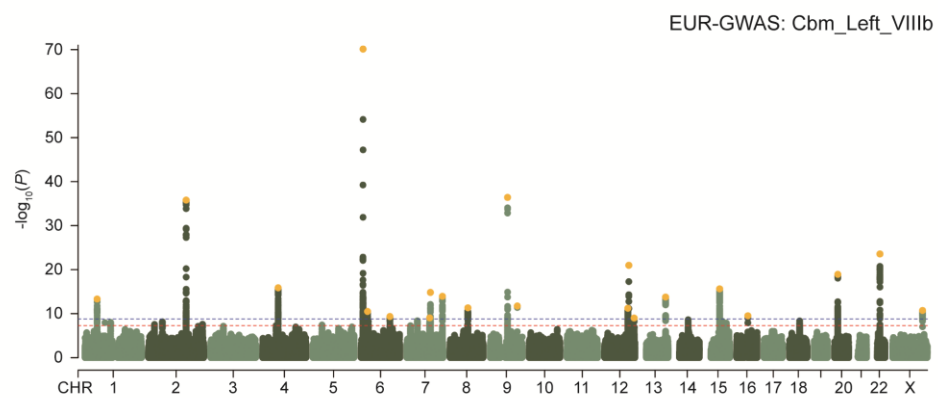


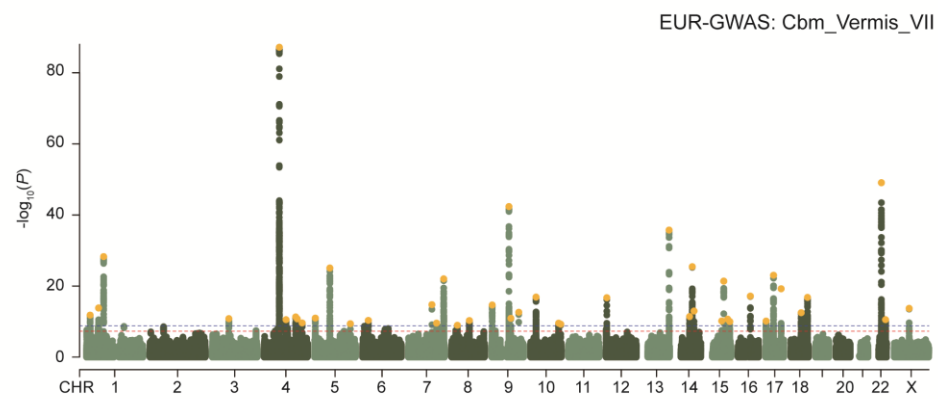
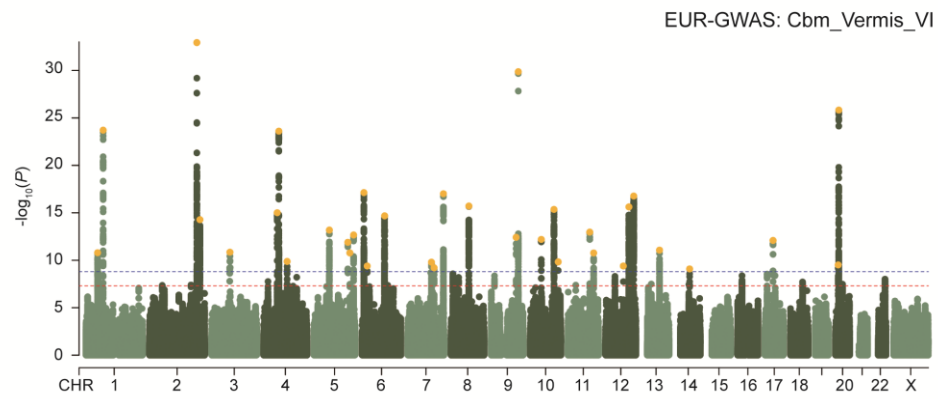
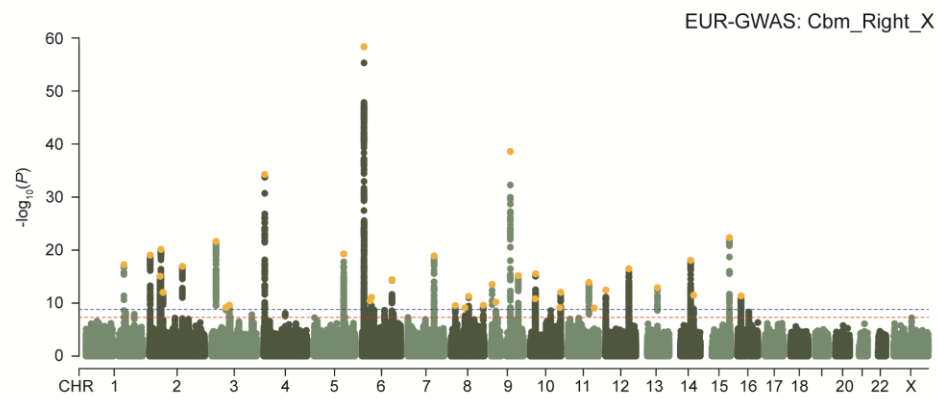
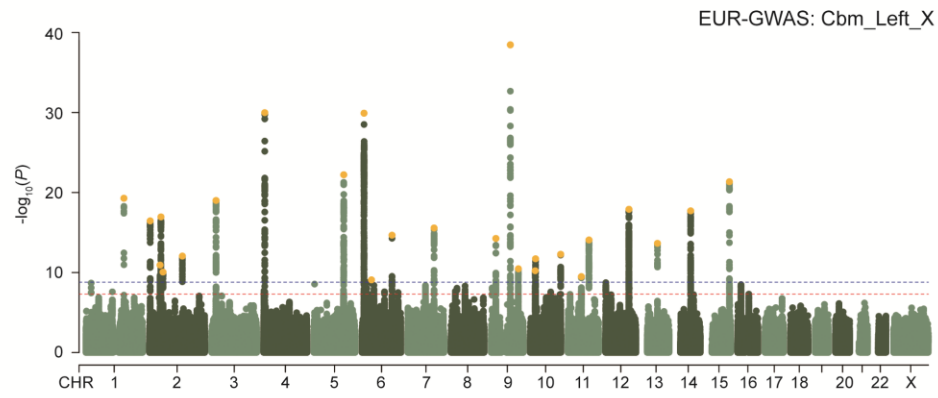




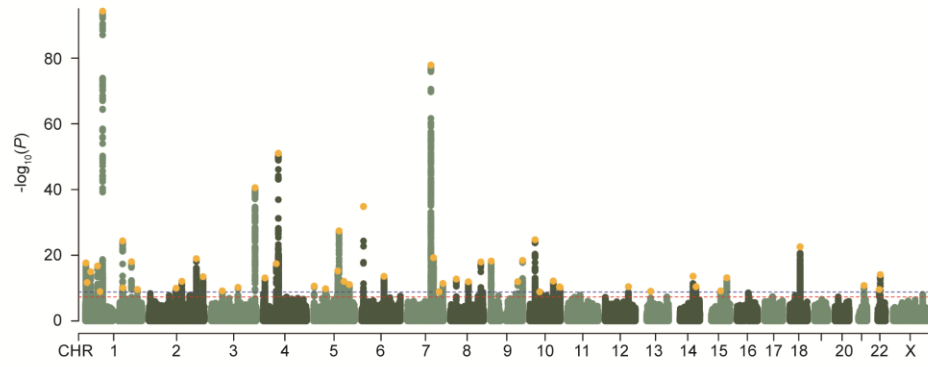




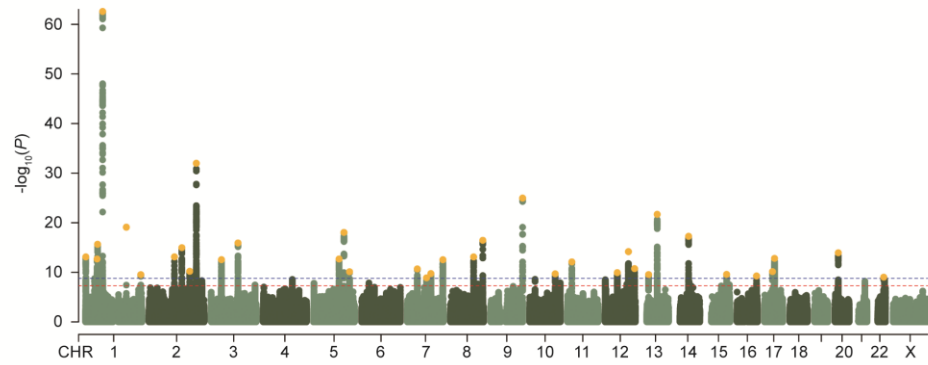




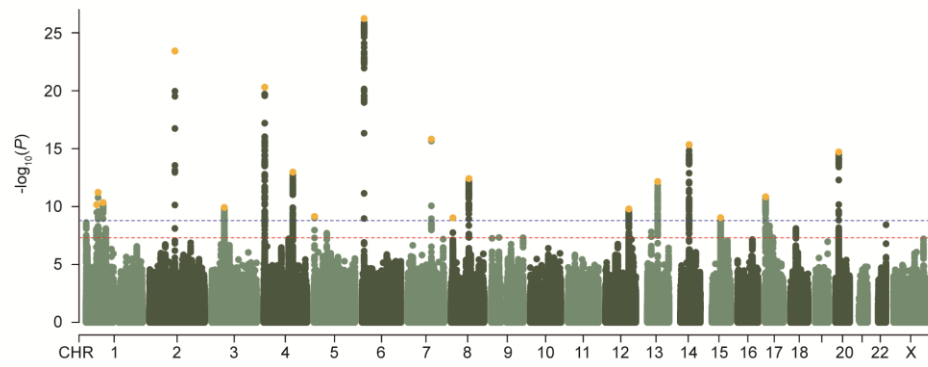
EUR-GWAS: Cbm_Vermis_VIII



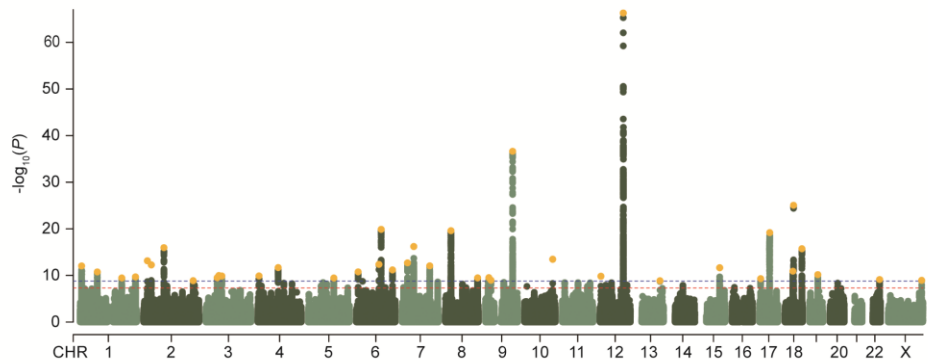
EUR-GWAS: Cbm_Vermis_IX

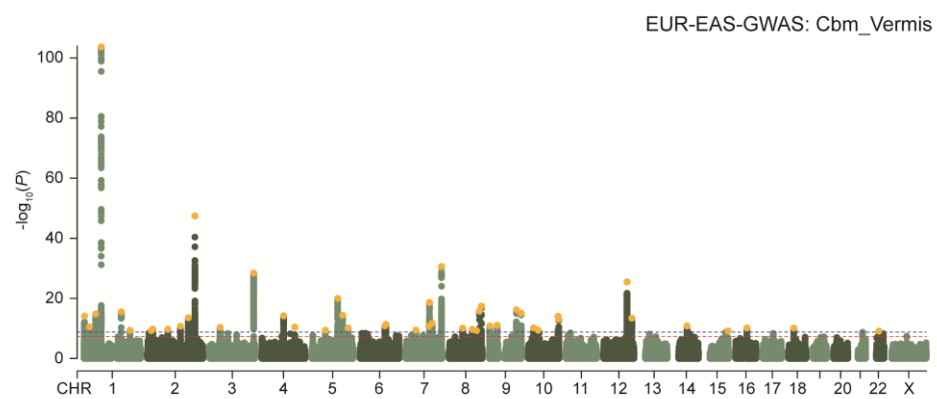
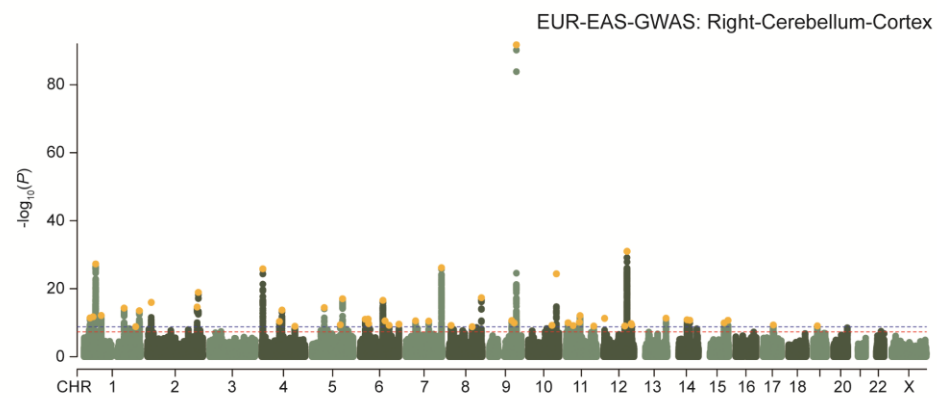
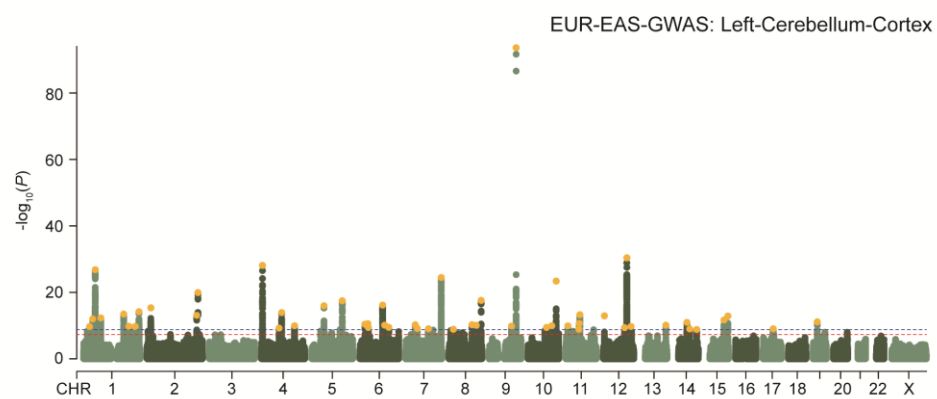
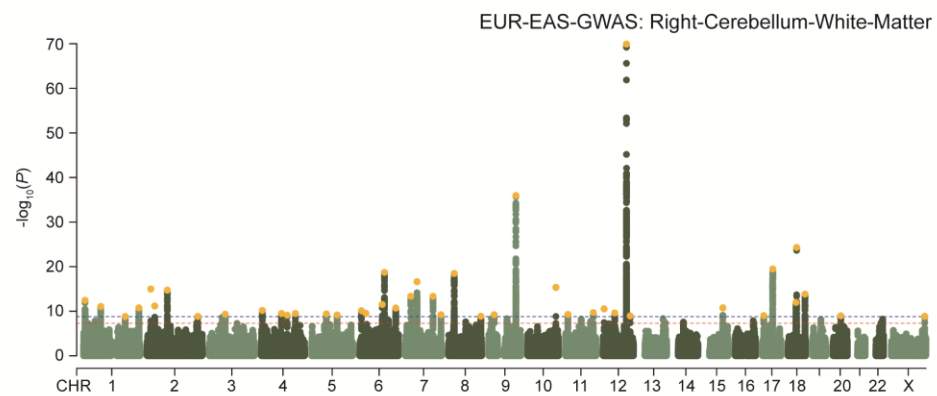


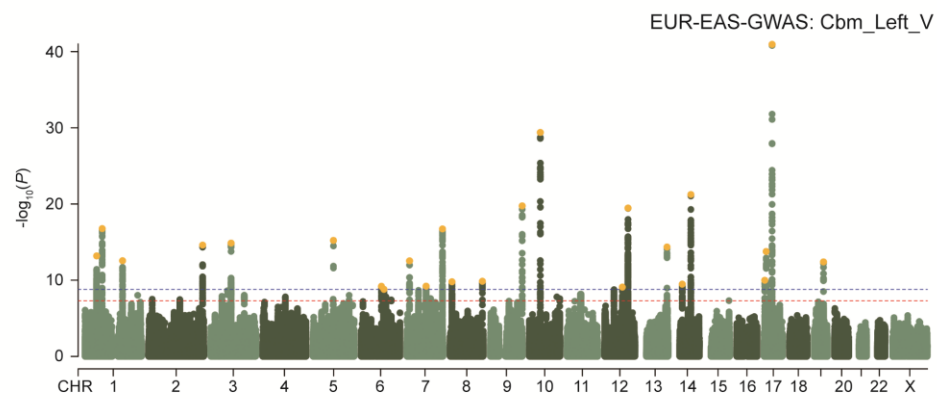
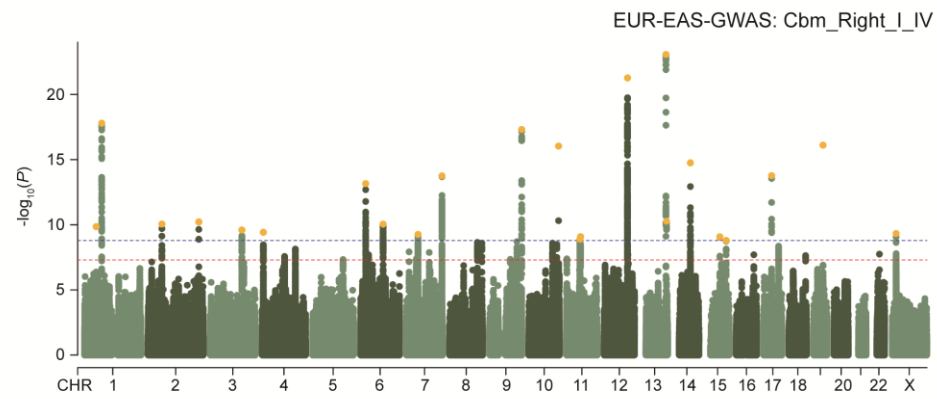
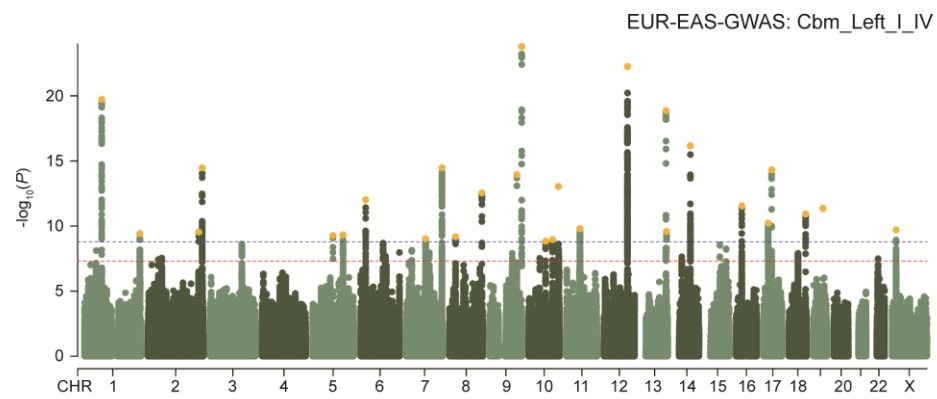
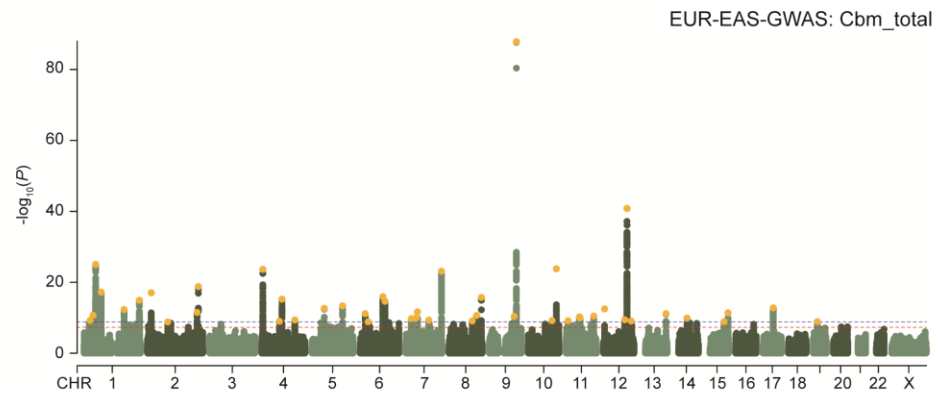
EUR-GWAS: Cbm_Vermis_X

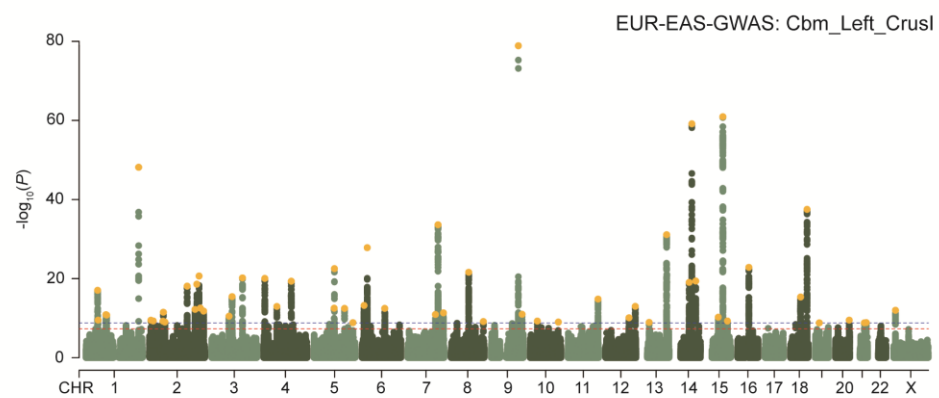
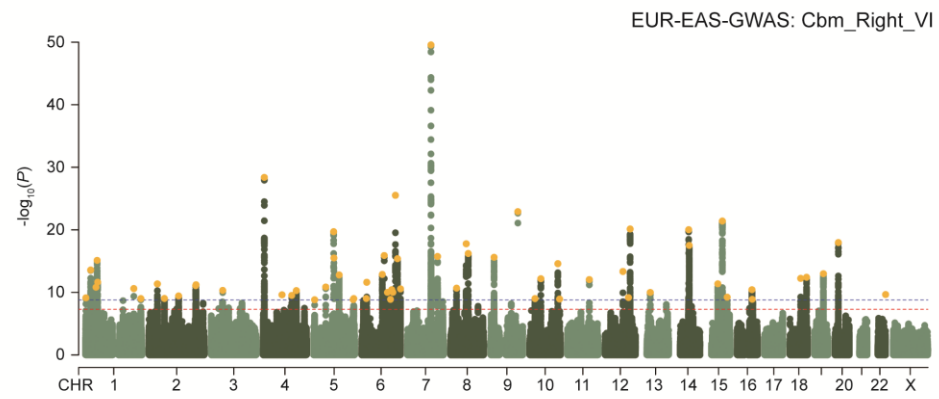
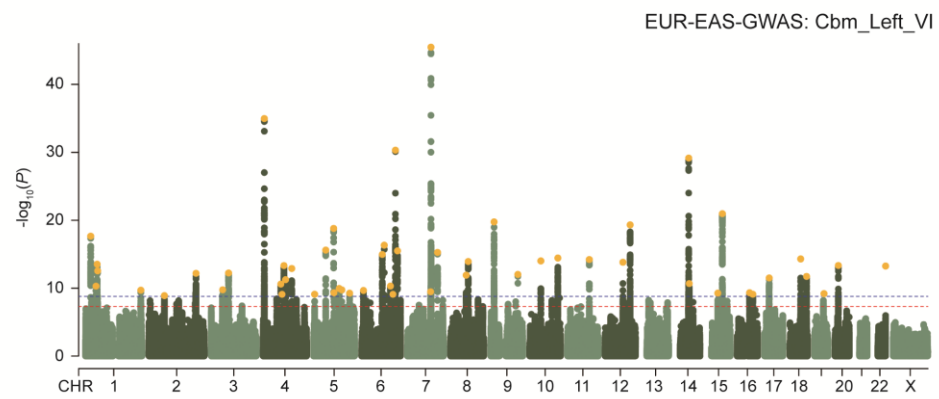
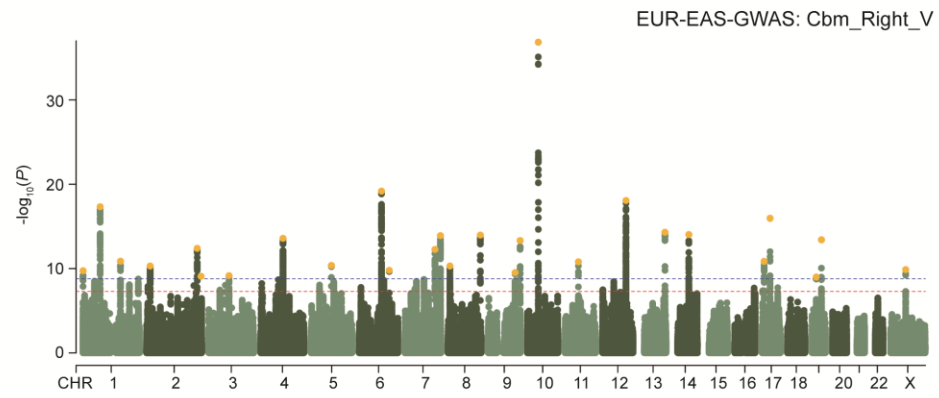


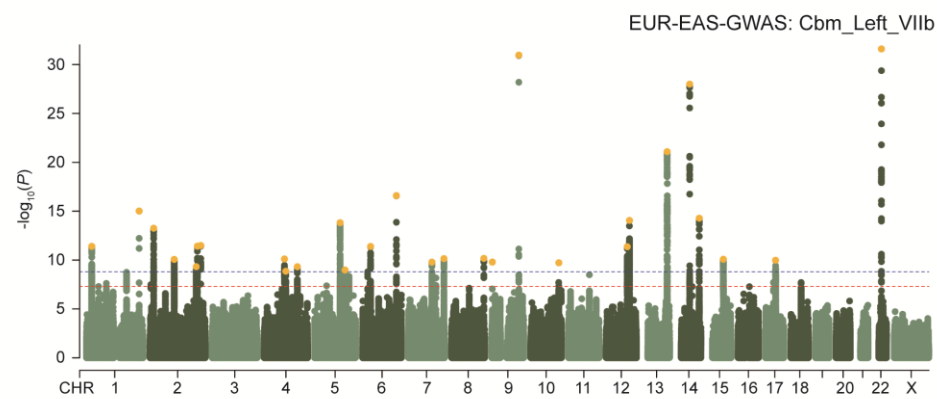
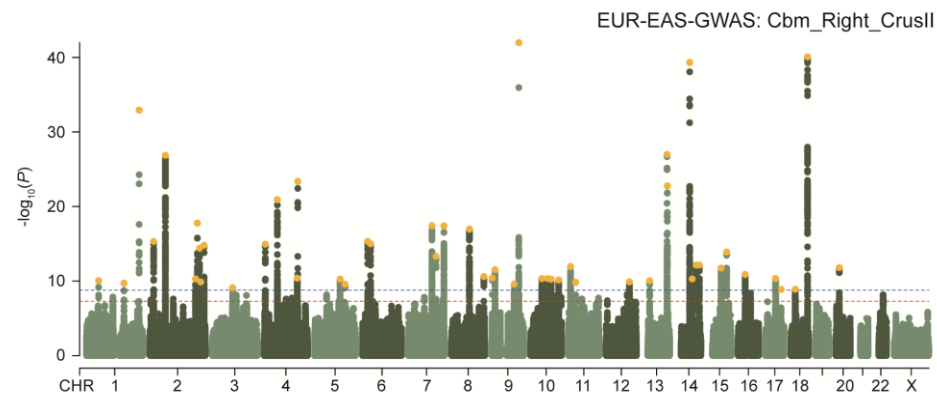
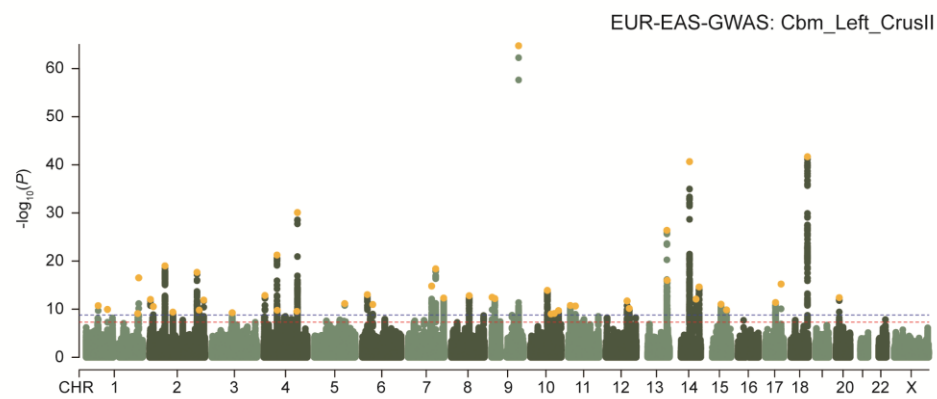
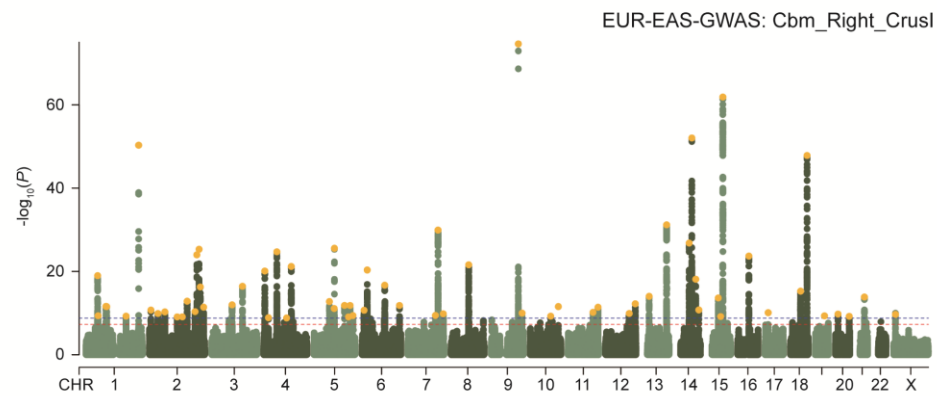
EUR-EAS-GWAS: Left-Cerebellum-White-Matter

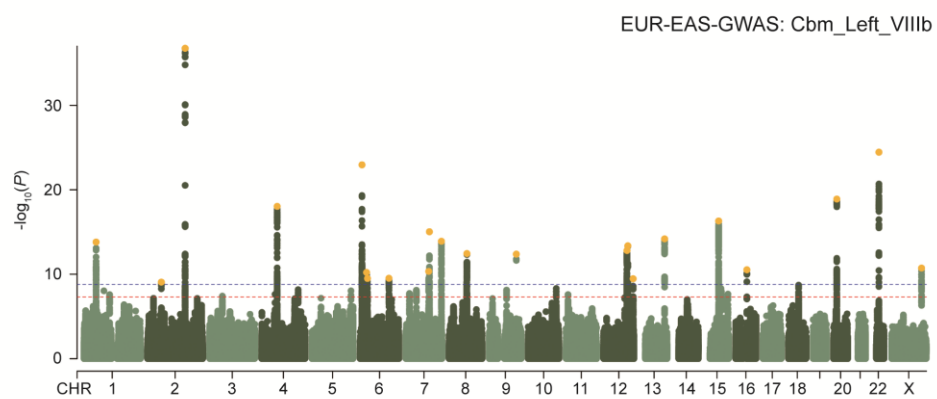
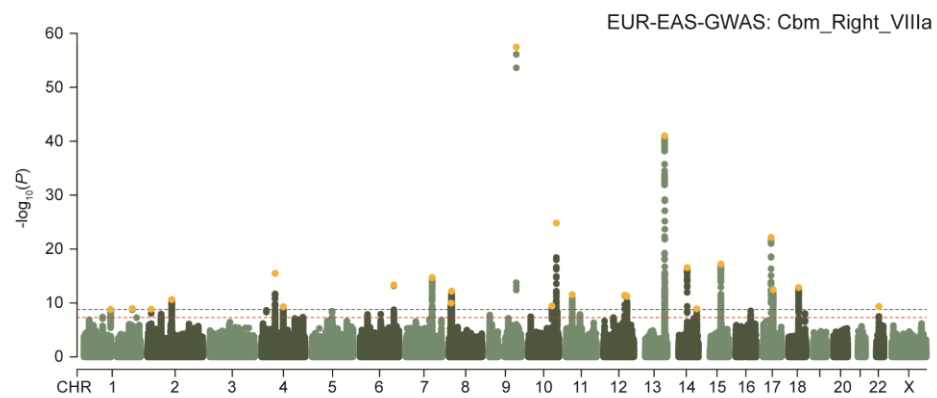
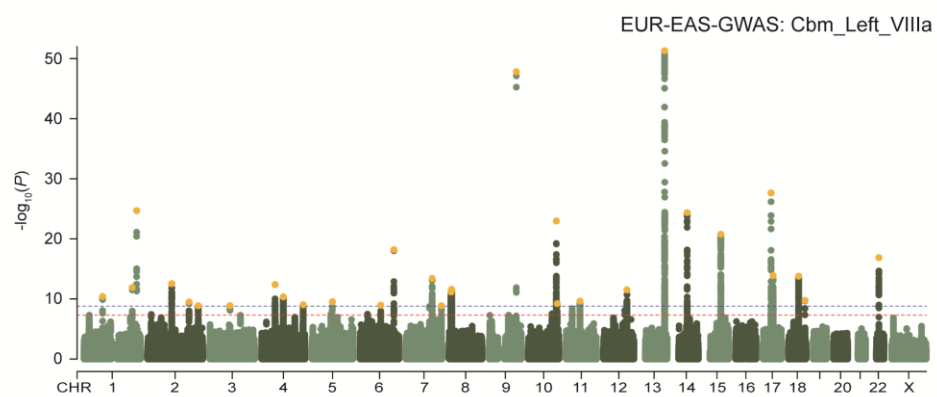
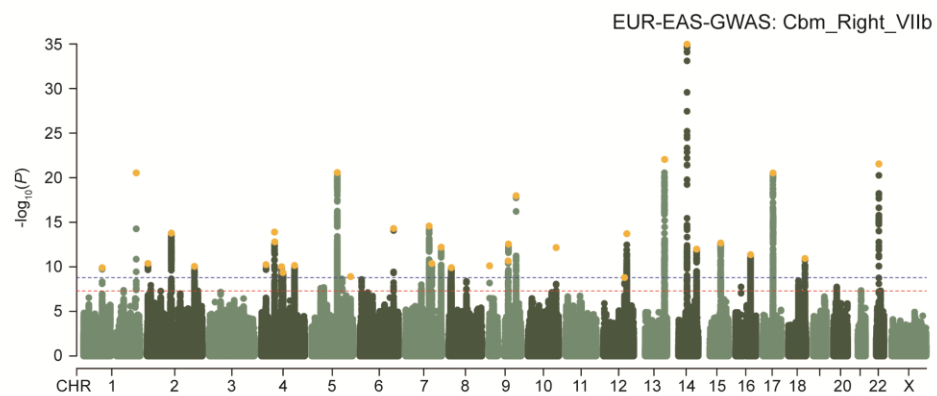


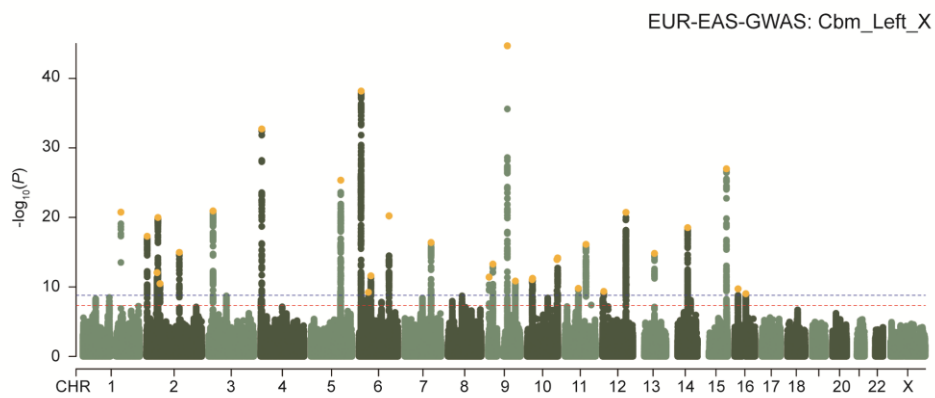
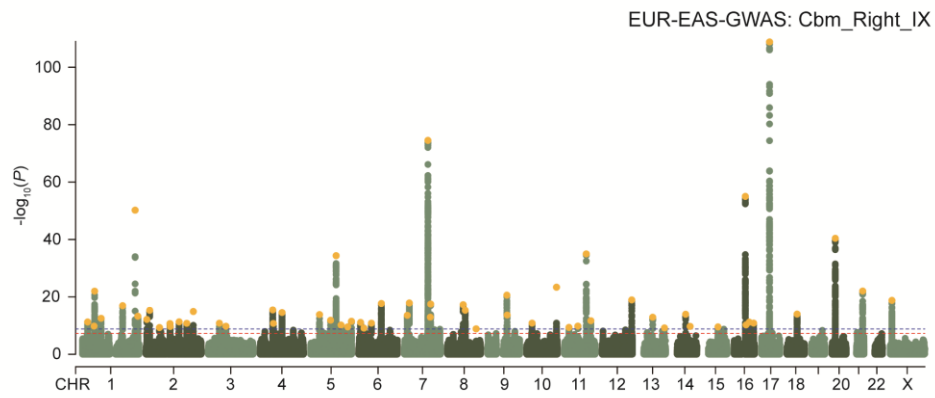
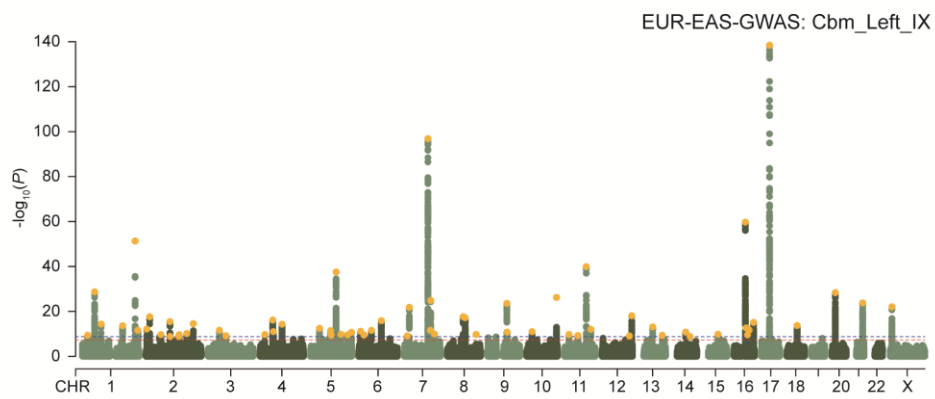
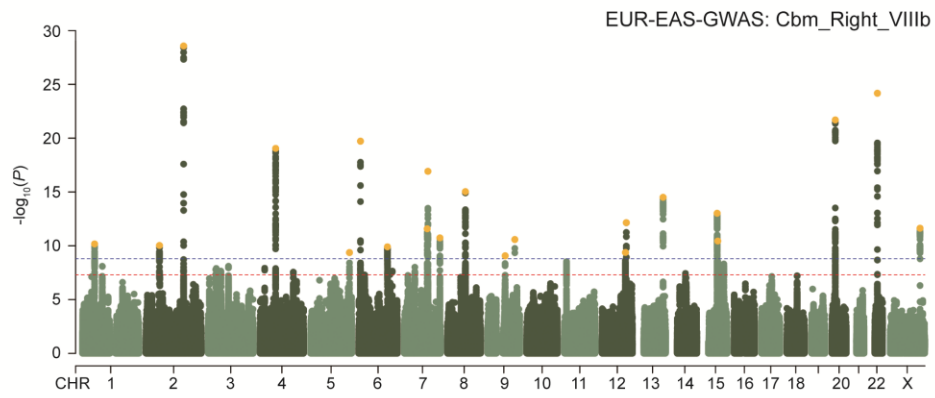


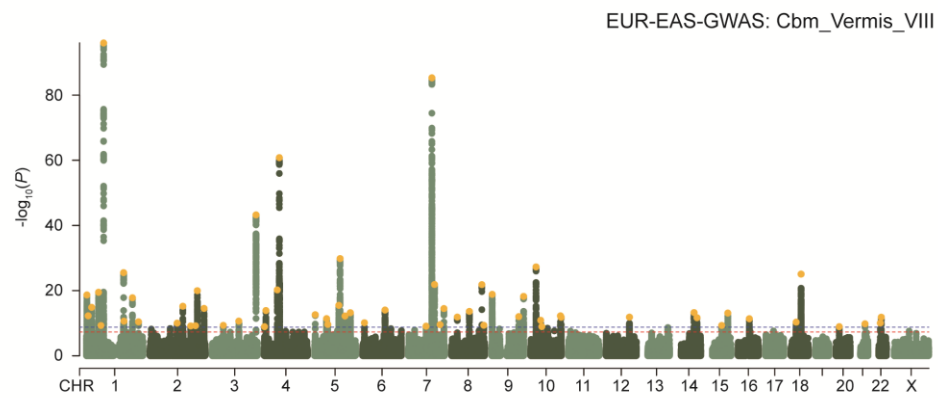
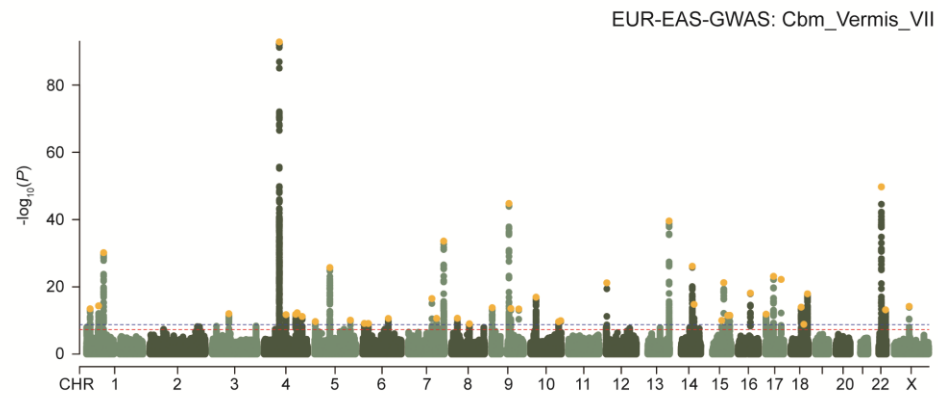
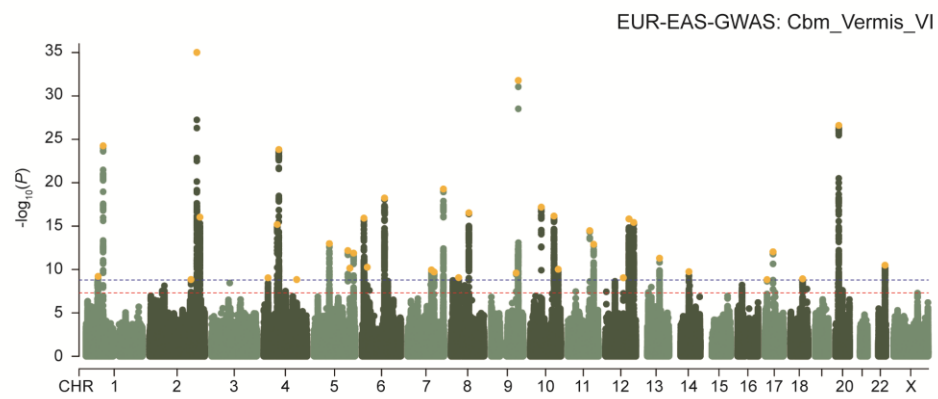
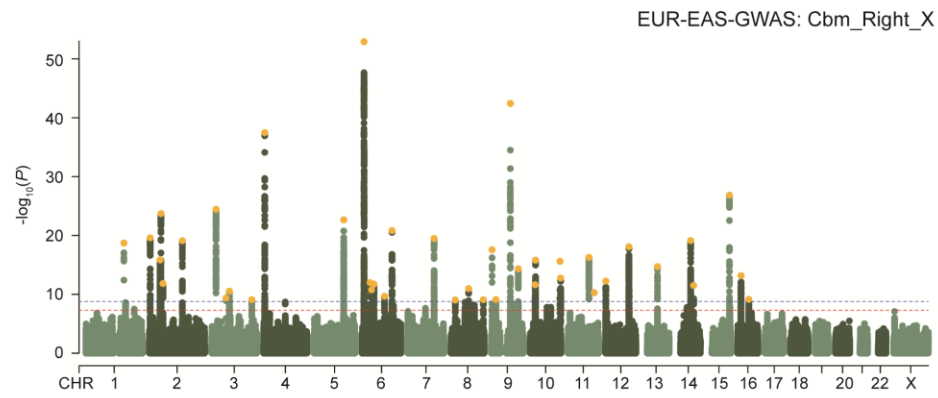


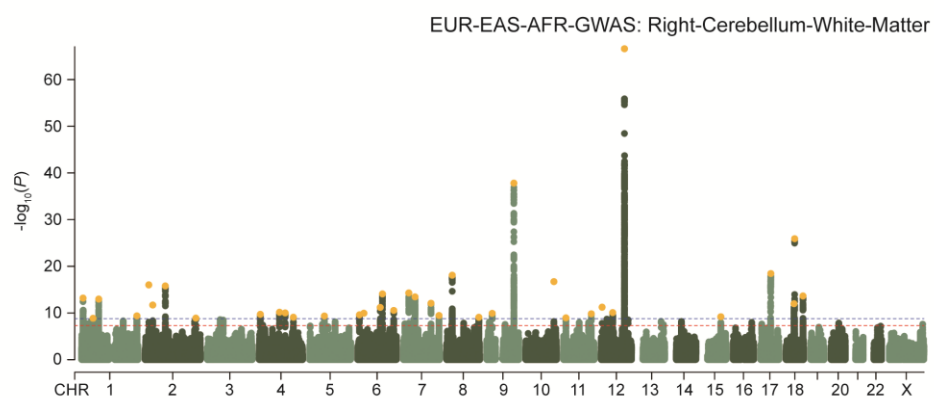
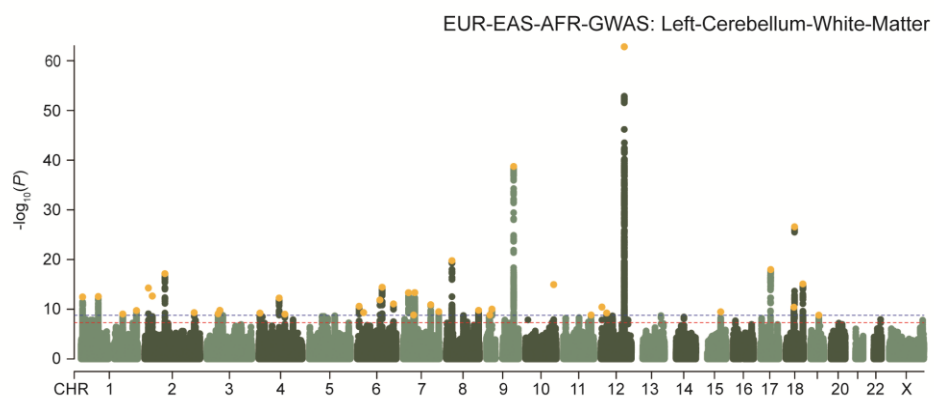
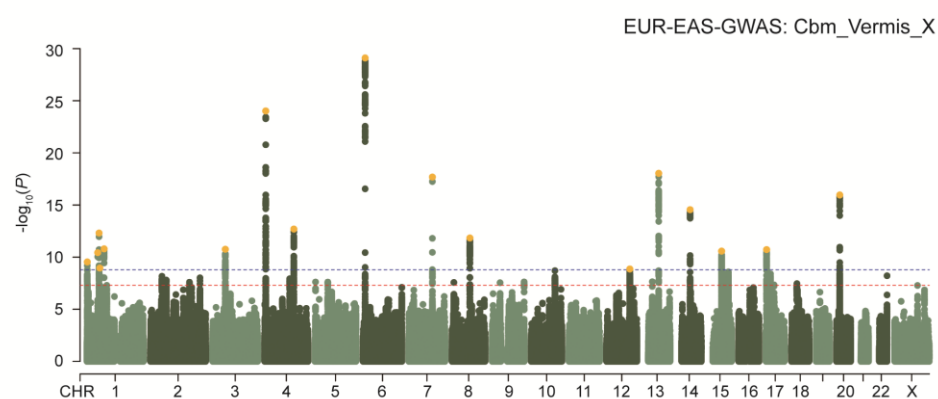
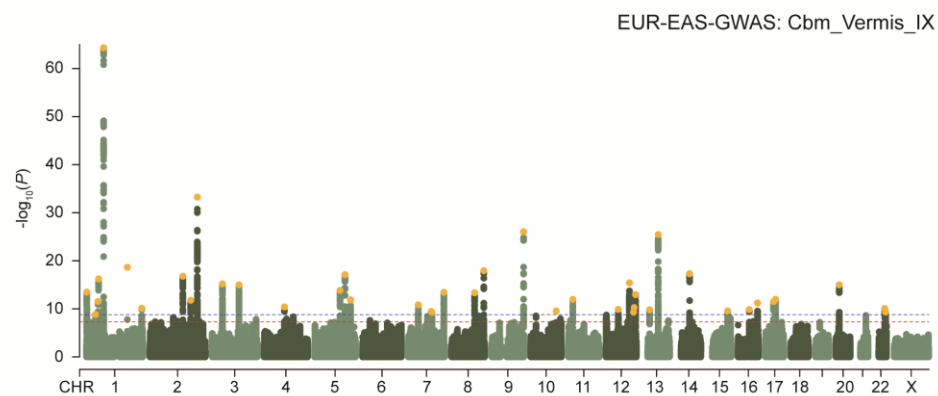


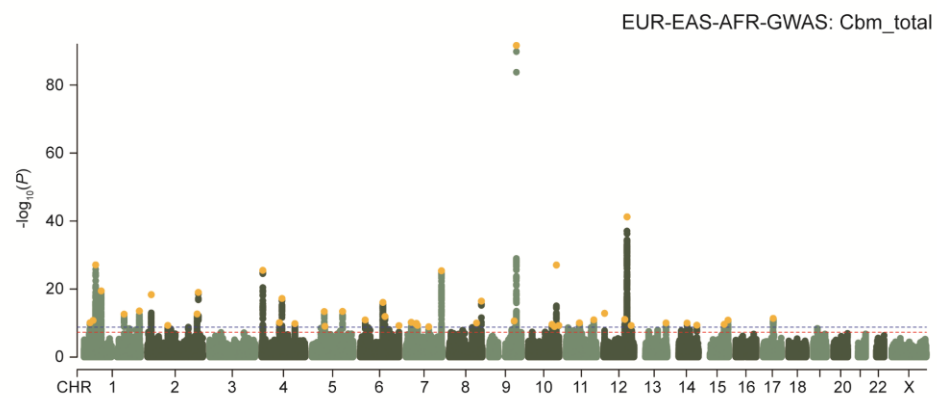
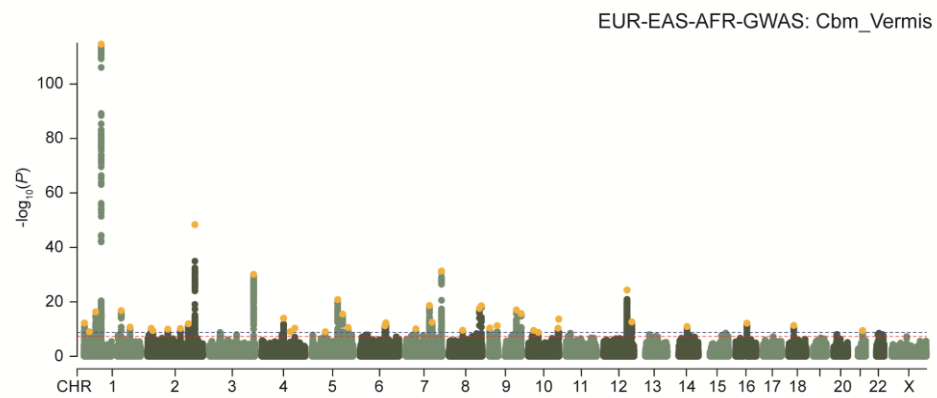
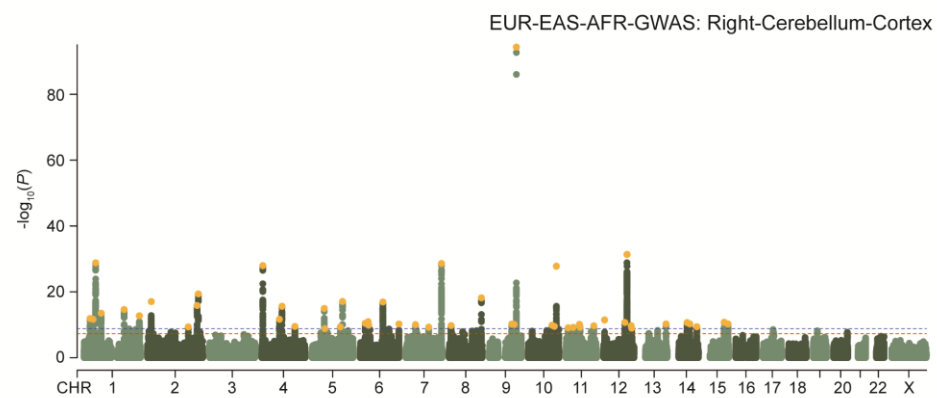
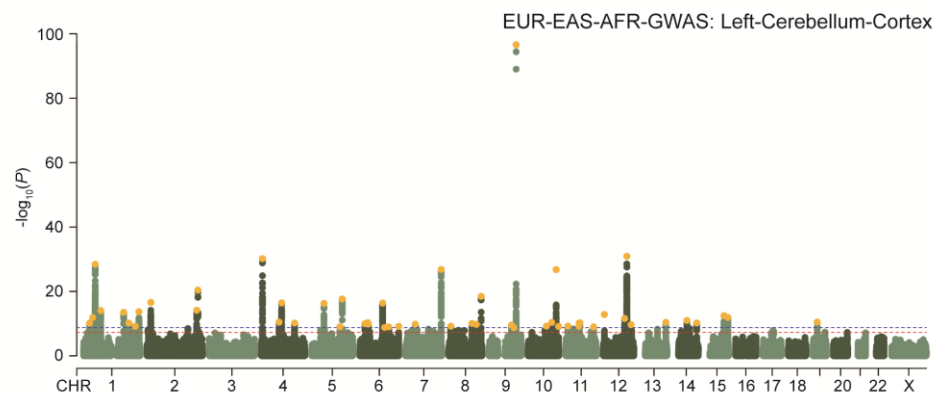


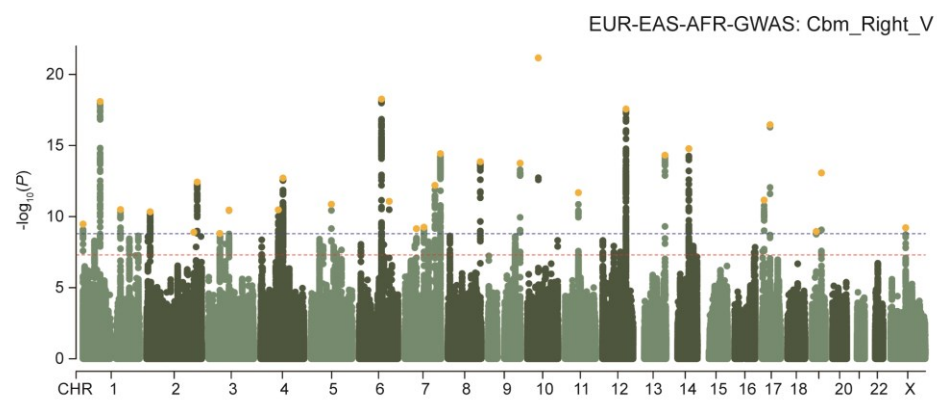
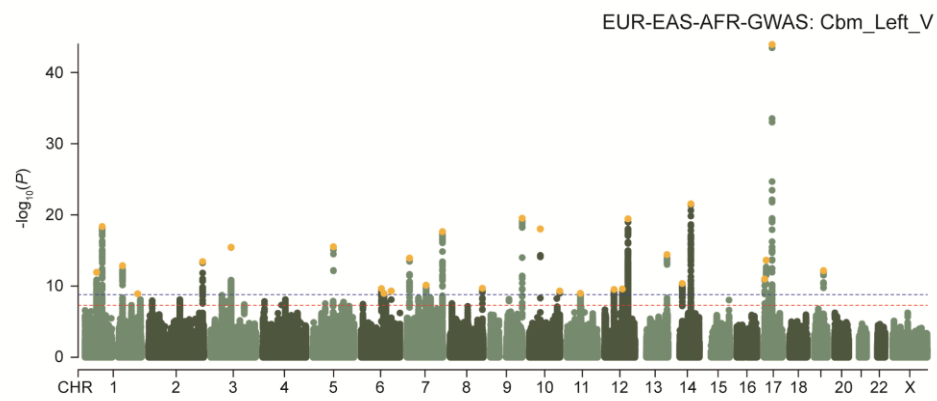
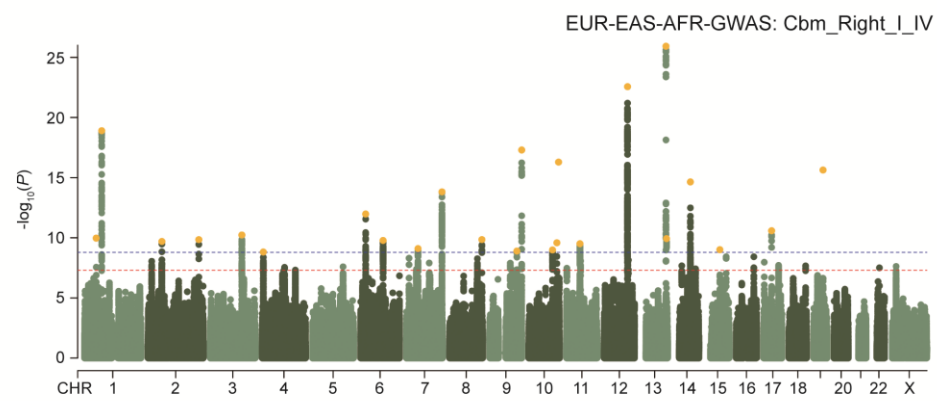
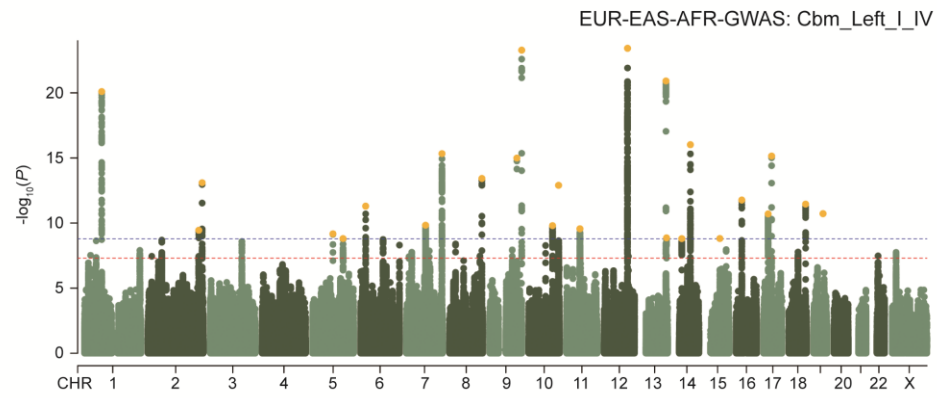


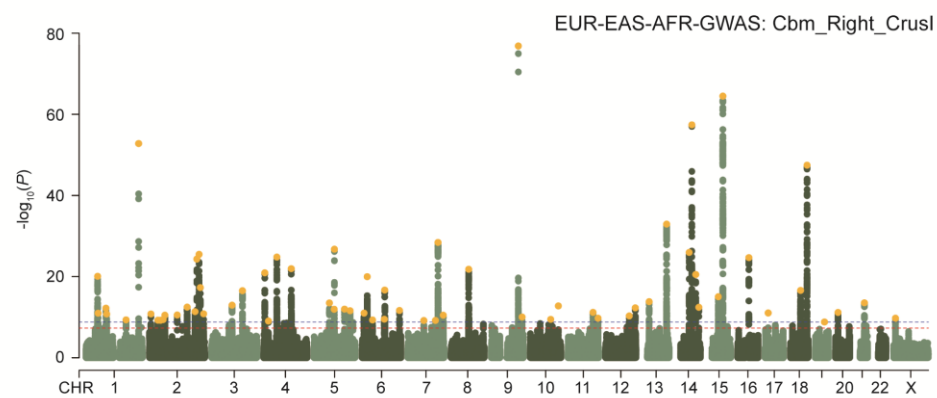
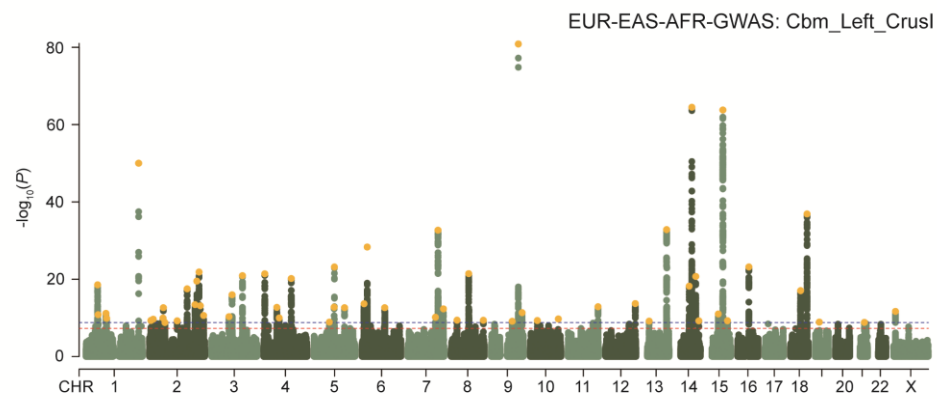
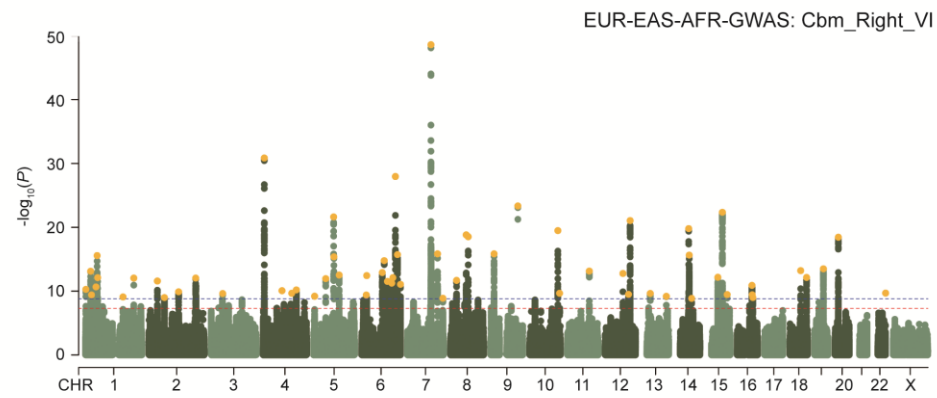
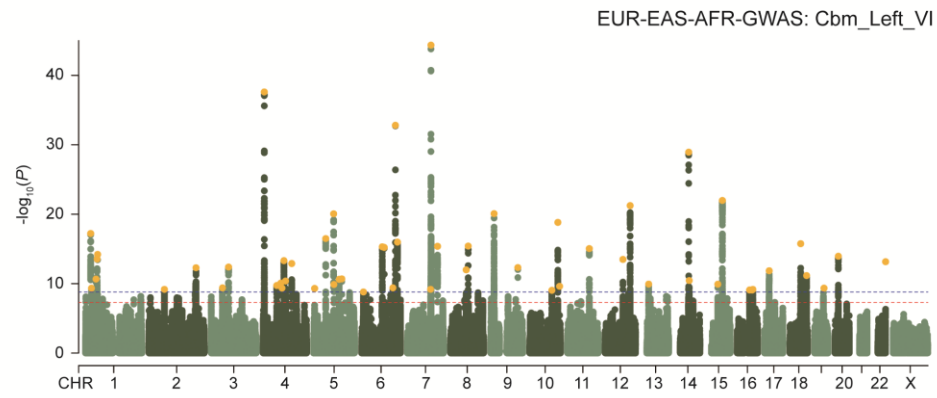


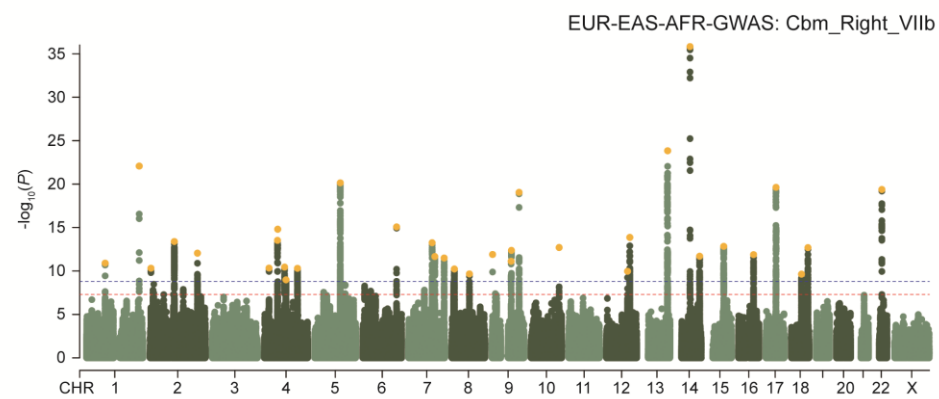
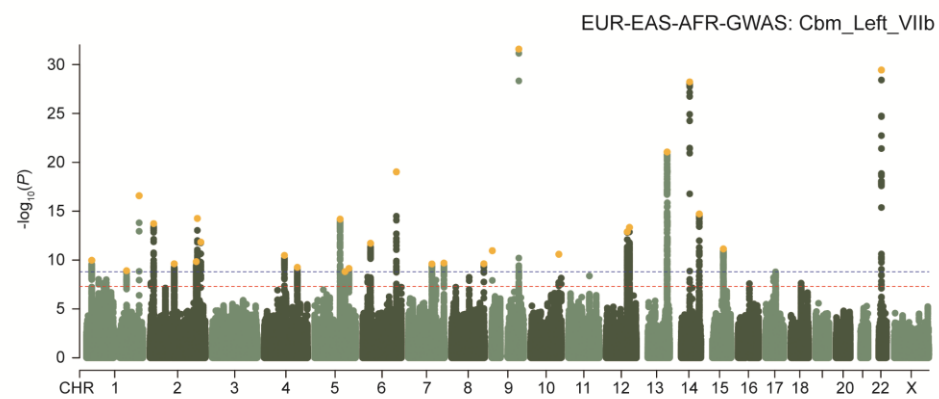
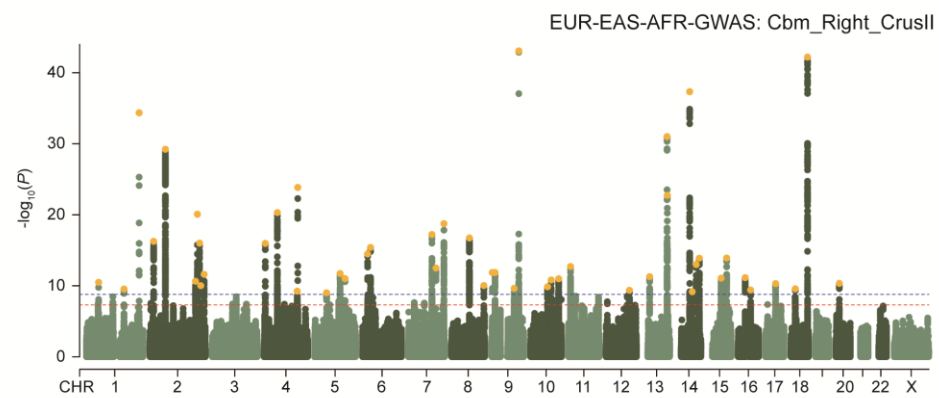
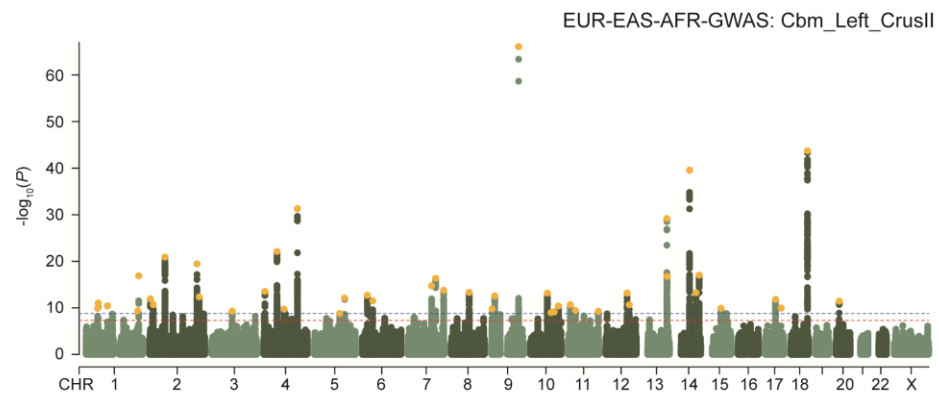


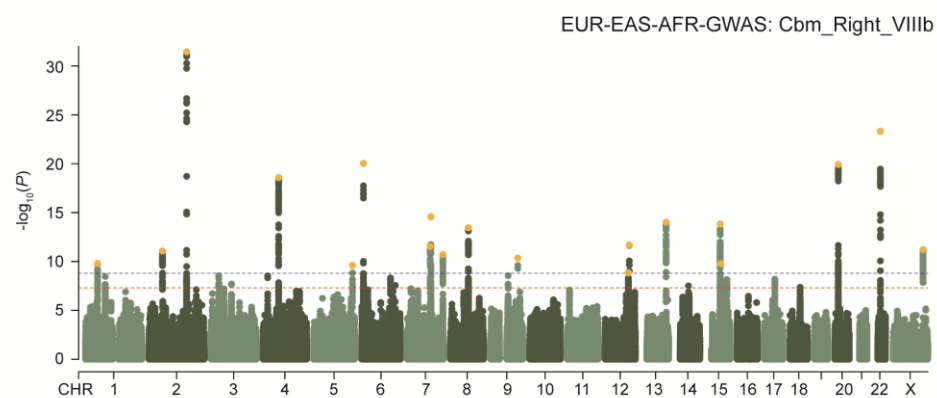
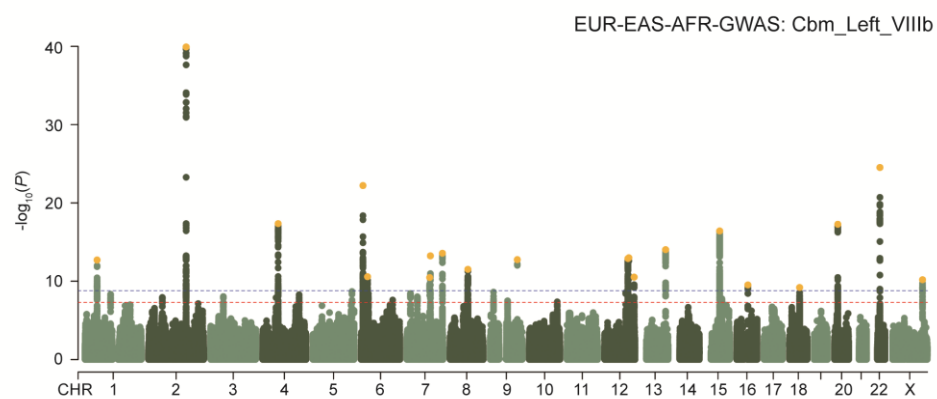
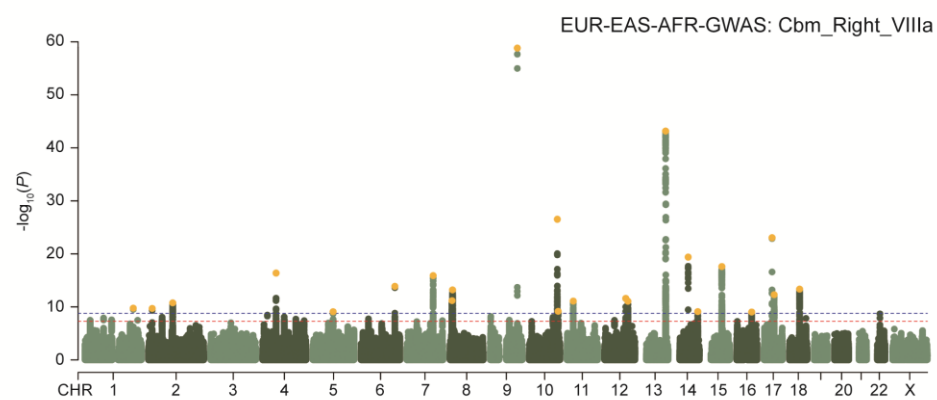
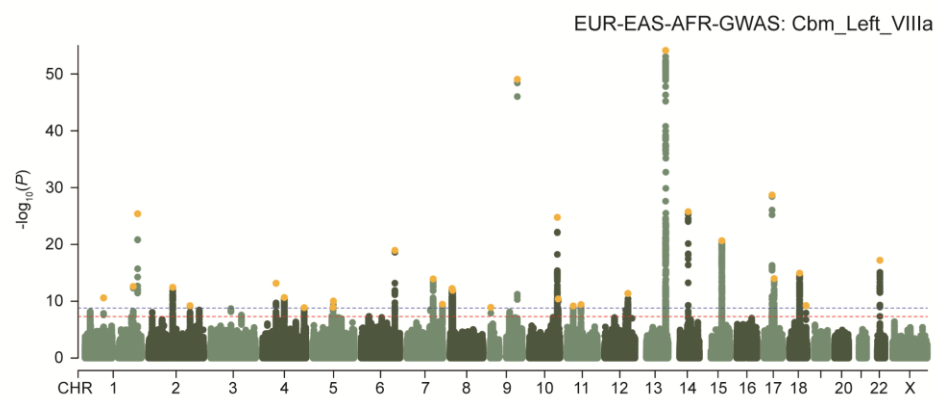


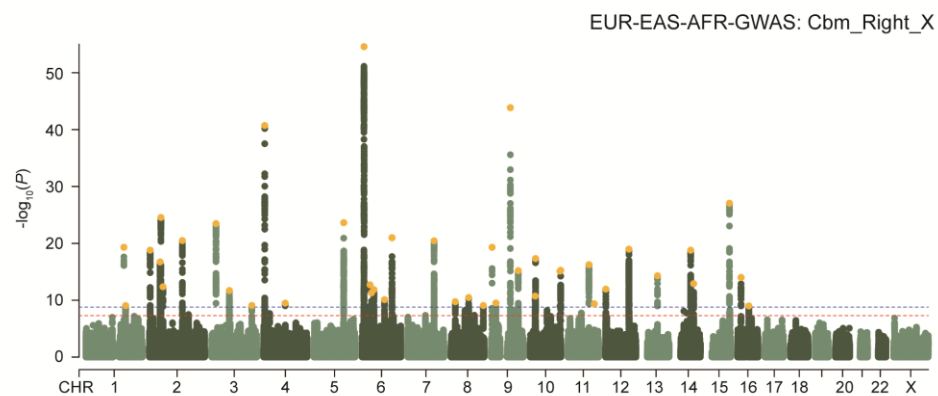
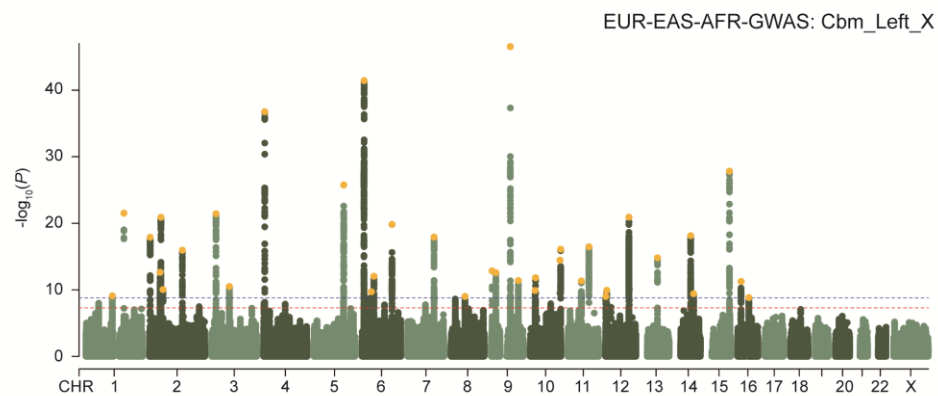
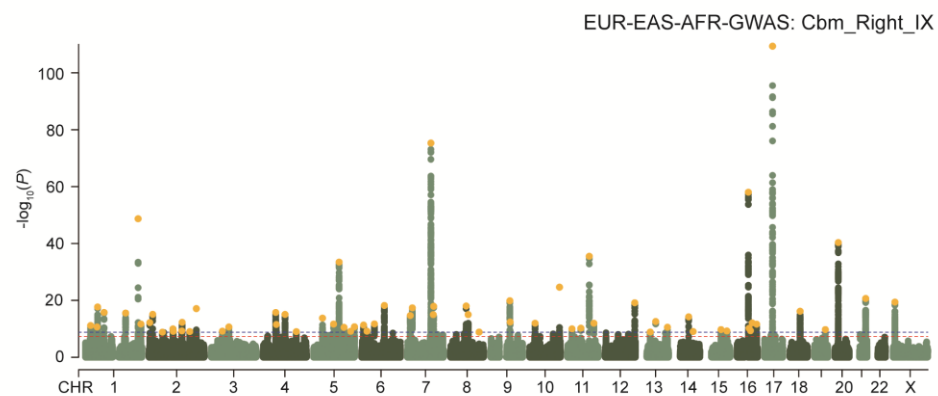
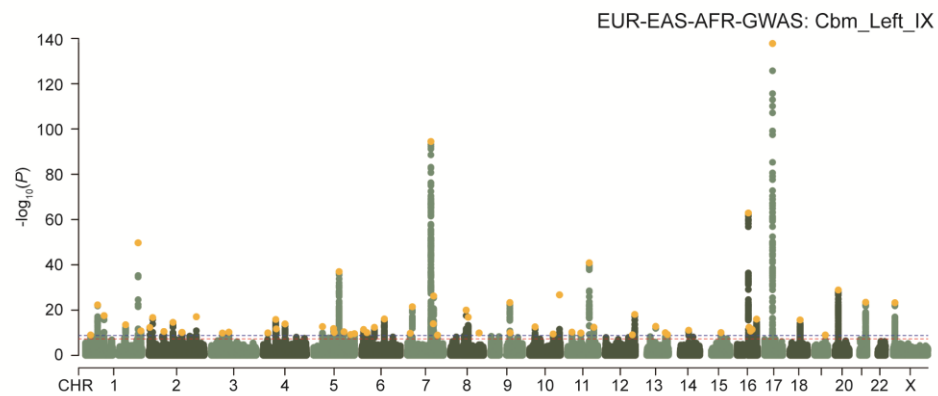


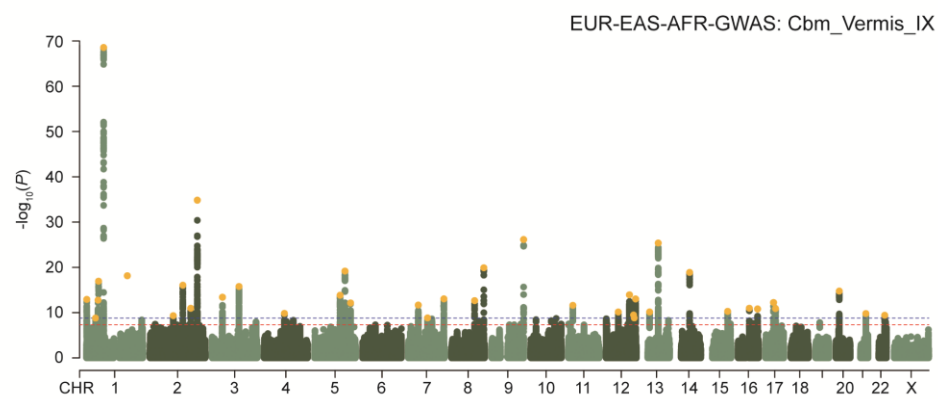
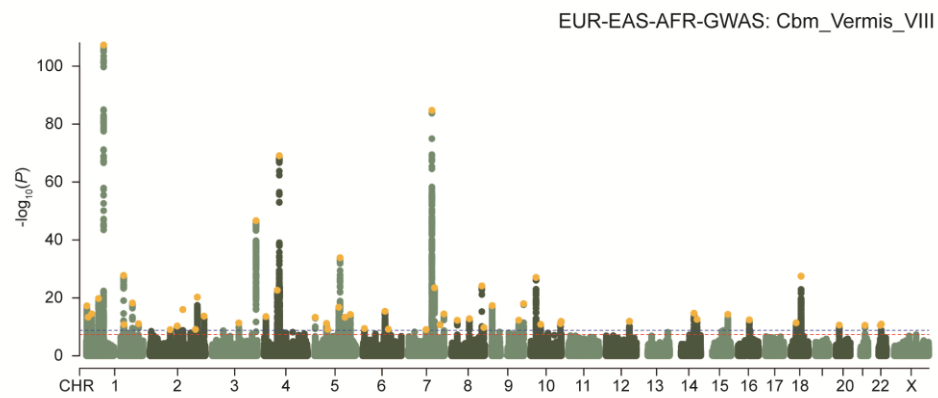
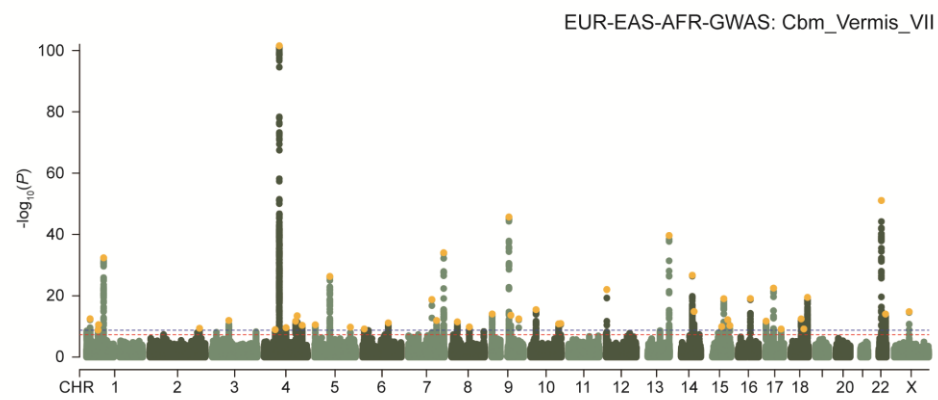
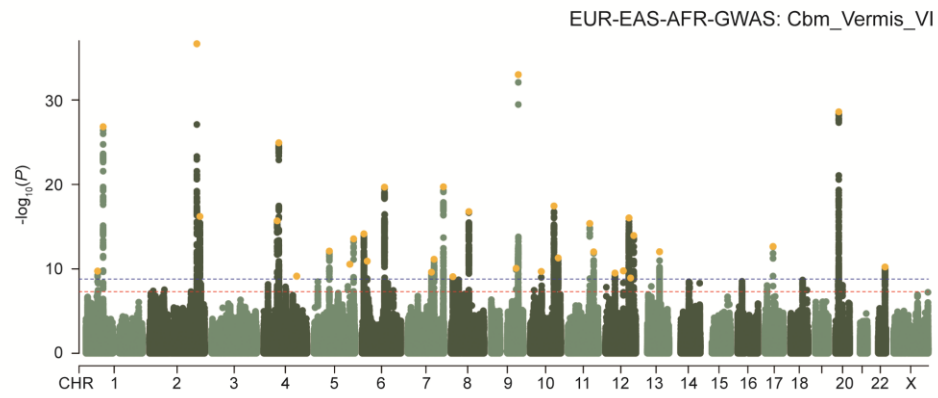












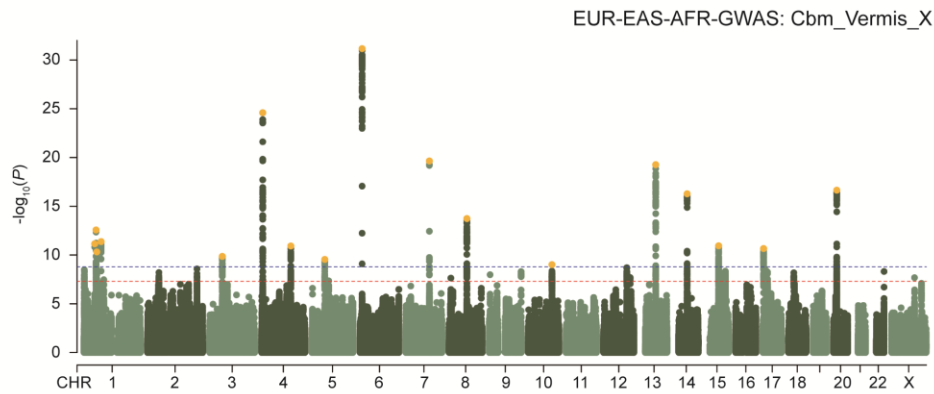
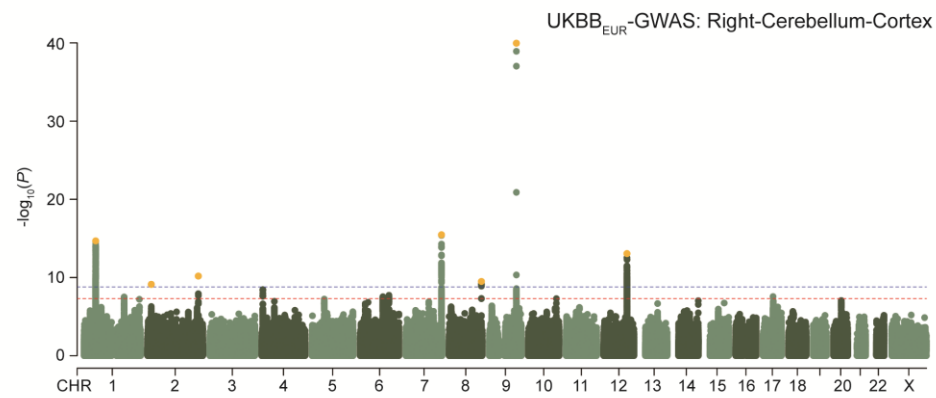
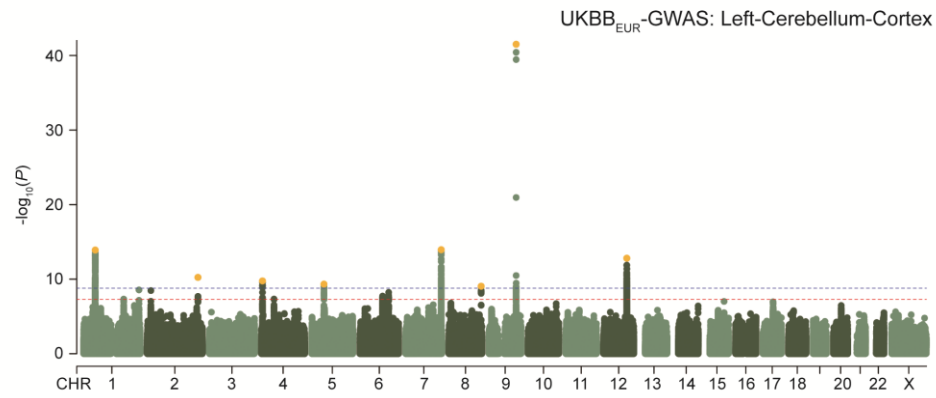
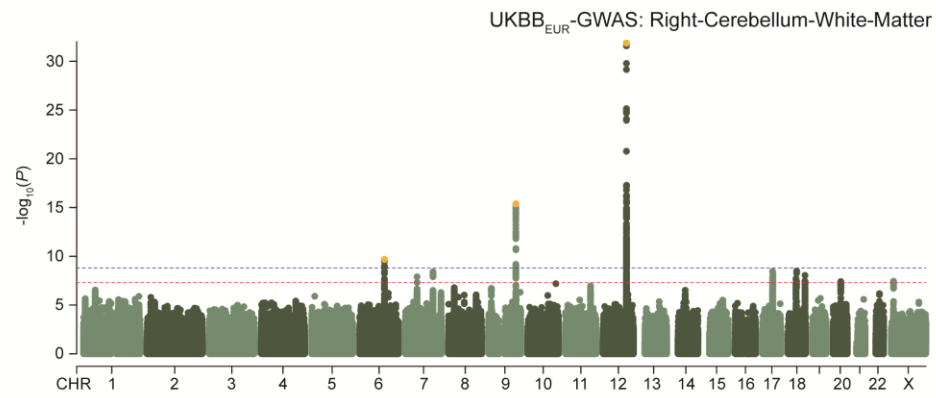
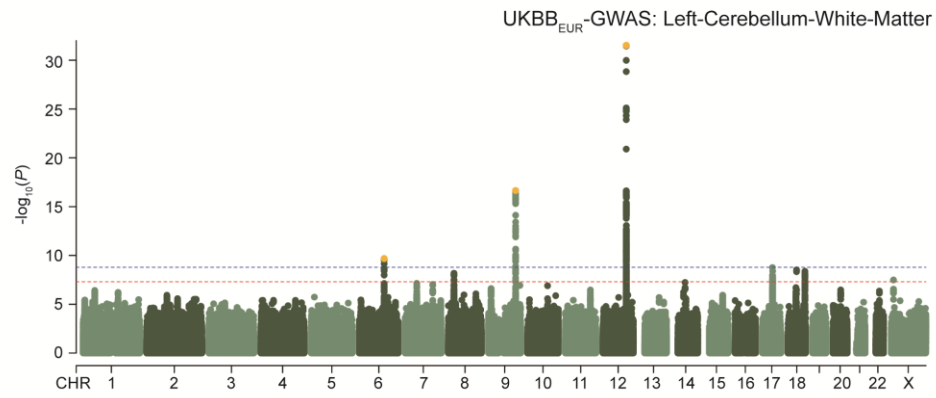
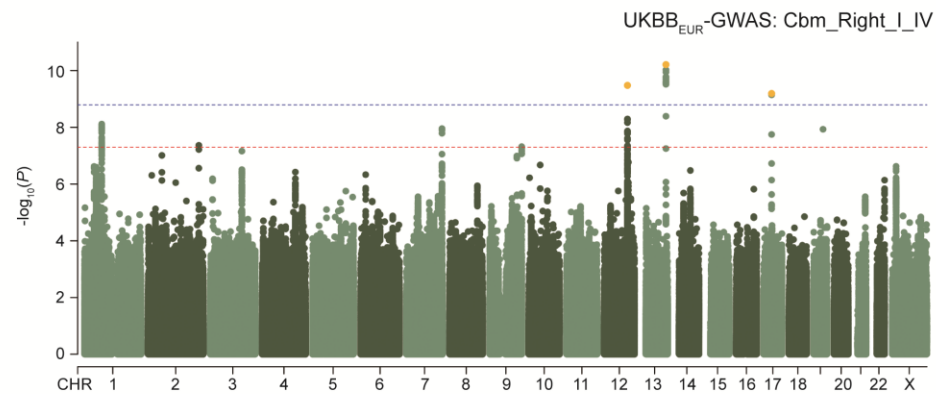
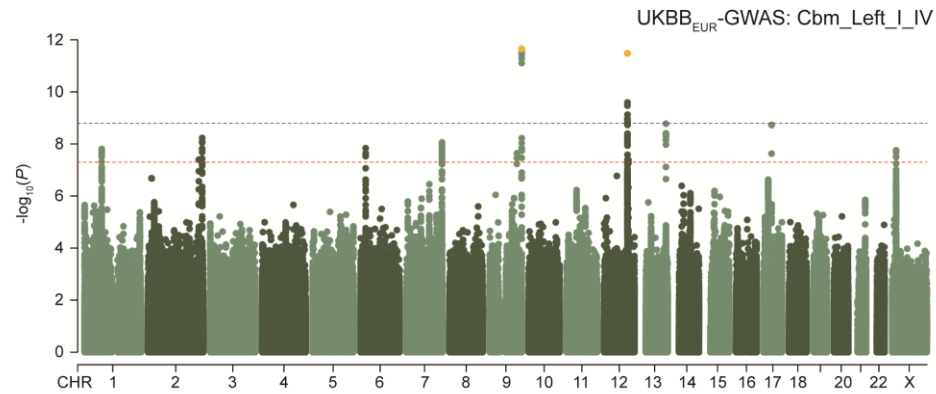
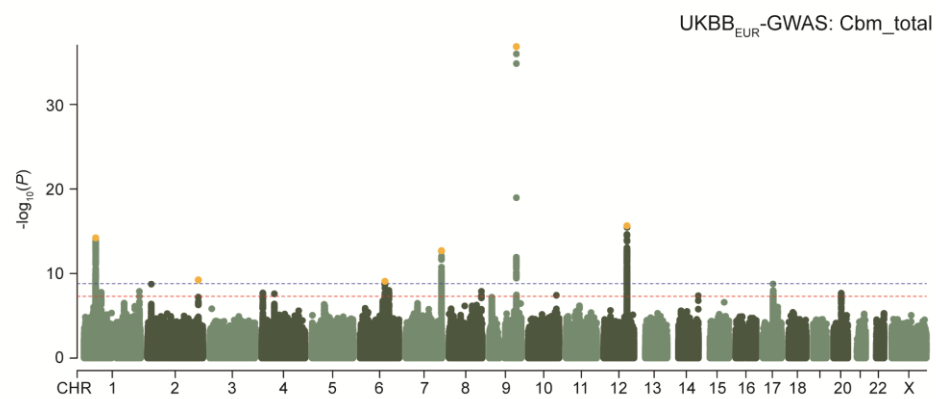
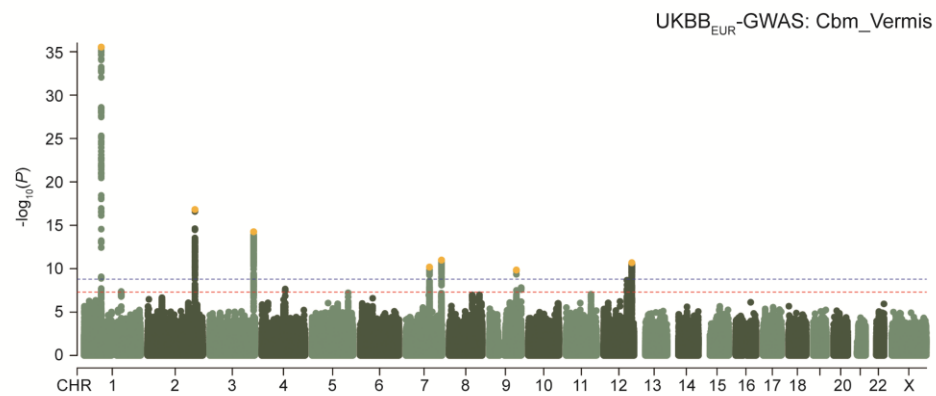
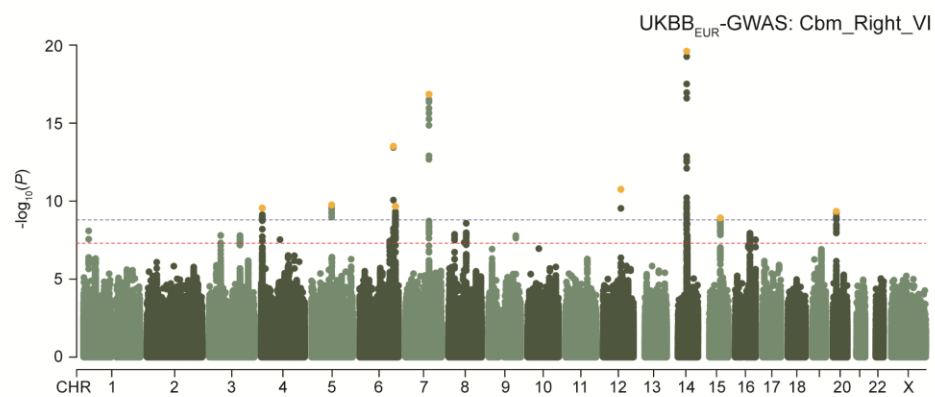
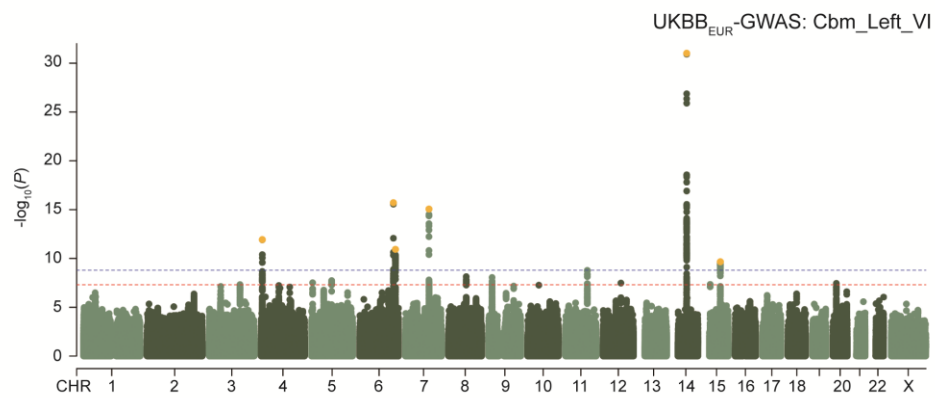
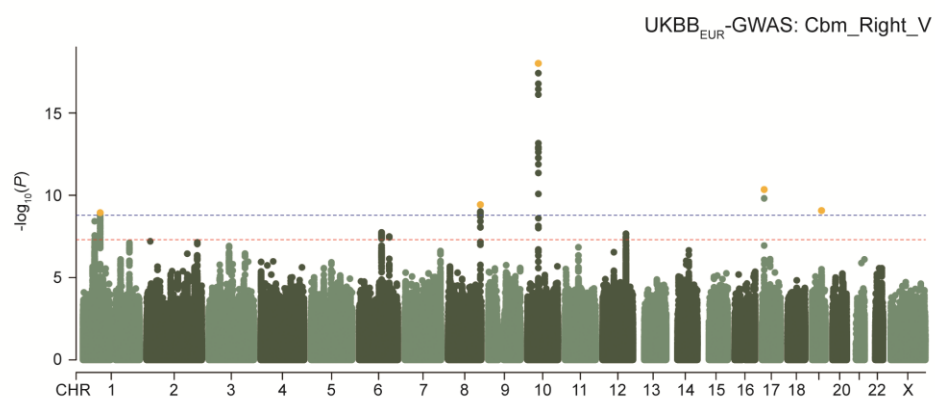
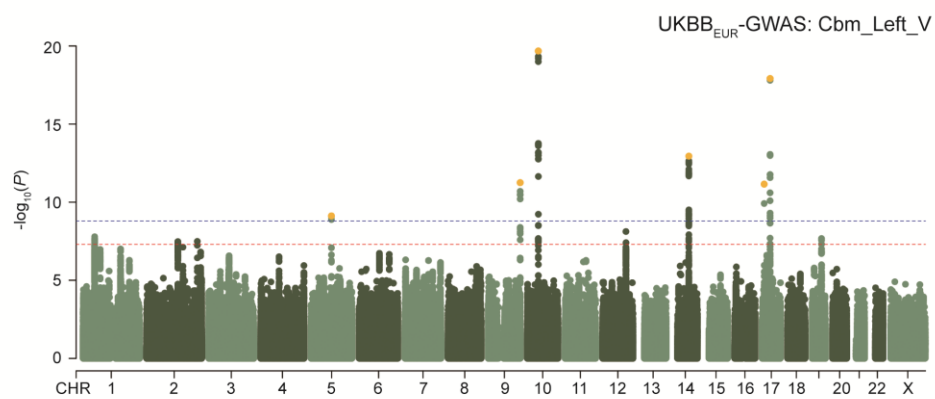
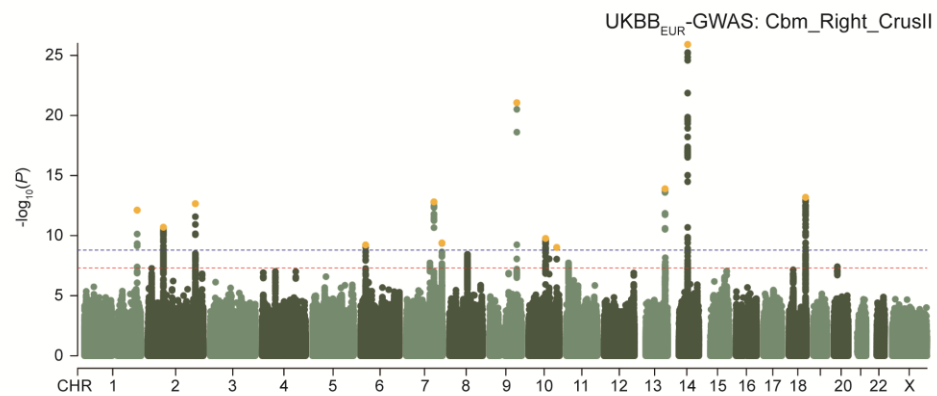
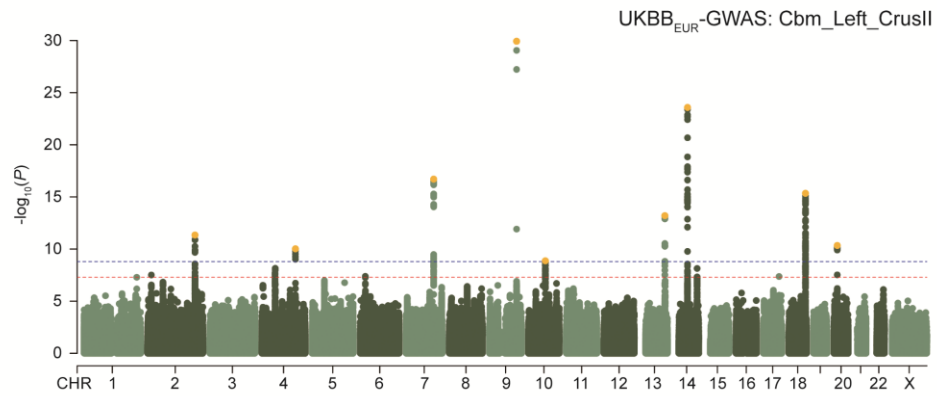
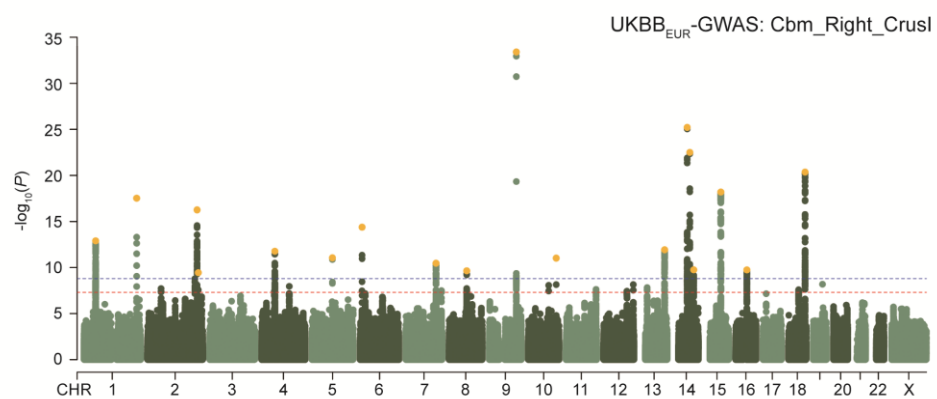
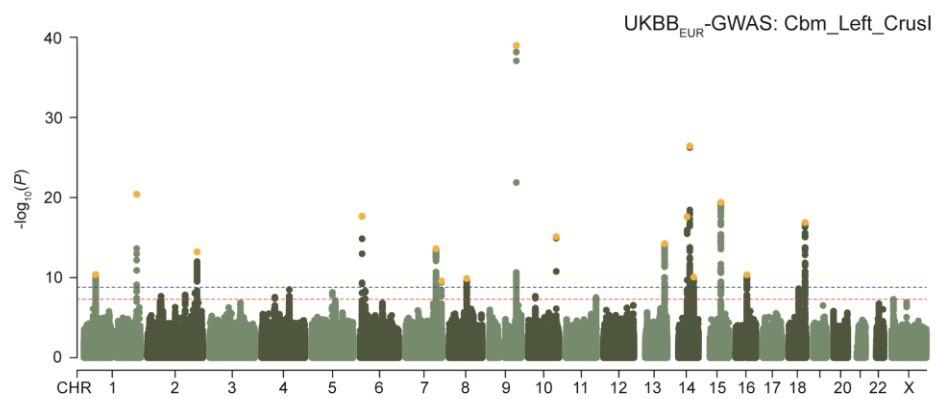


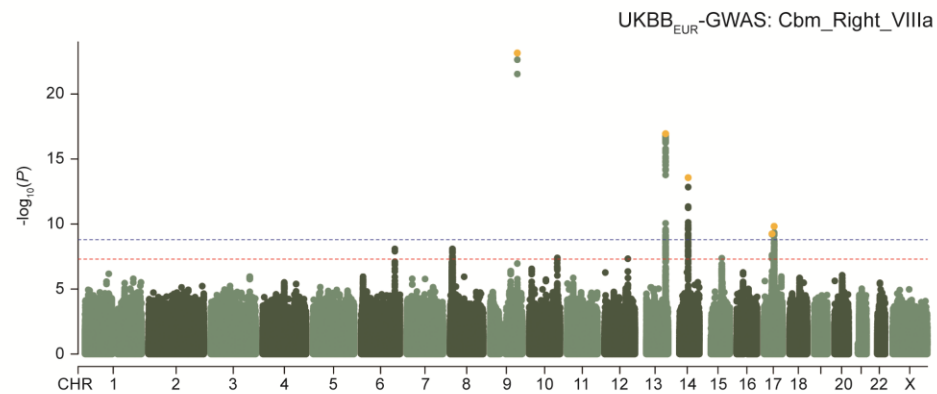
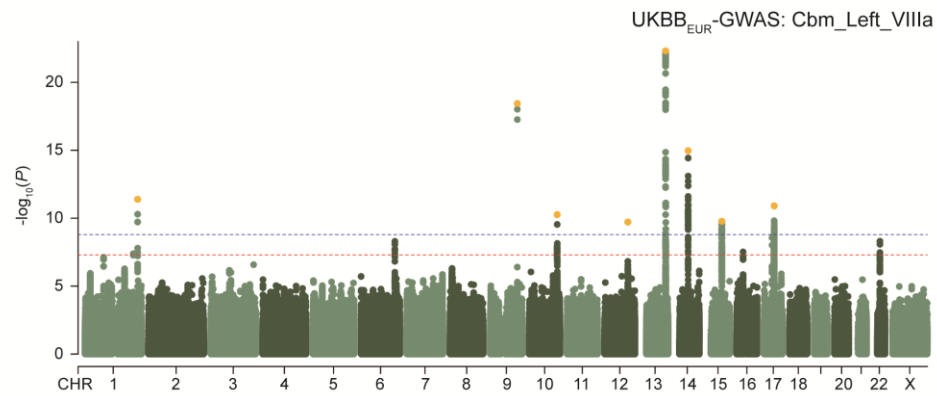
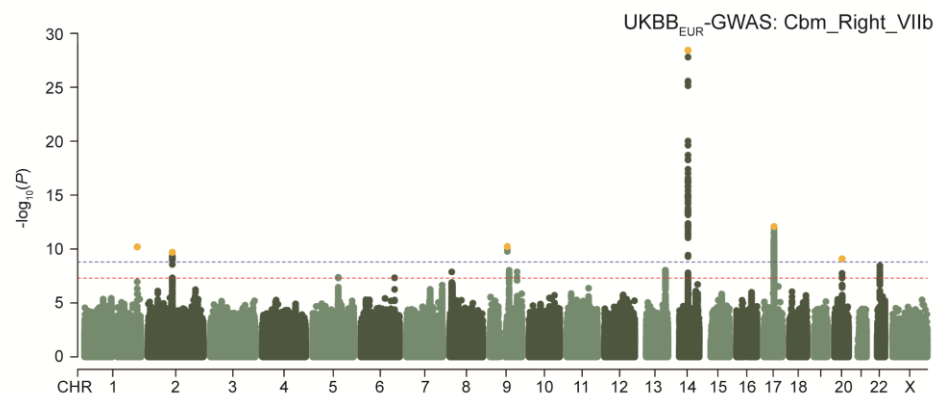
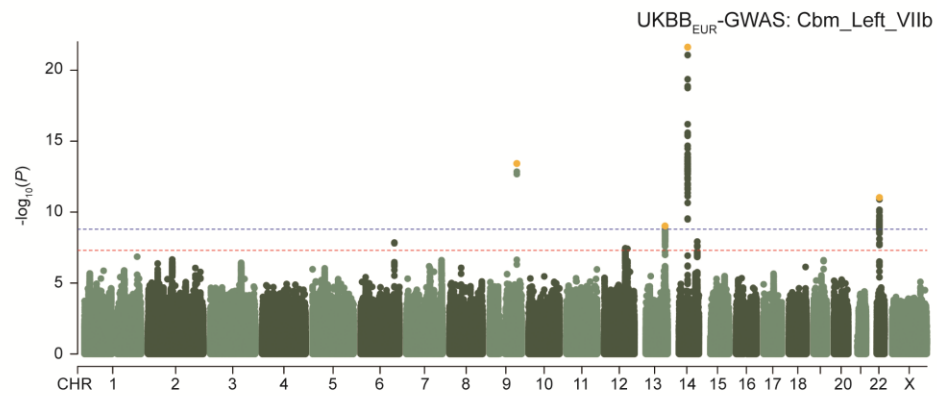
Fig. S3 | Genetic discovery of seven sets of sex-combined univariate GWAS. The Manhattan plots show the results from seven sex-combined univariate GWASs (UKBB_{EUR}-GWAS, ABCD_{EUR}-GWAS, CHIMGEN_{EAS}-GWAS, ABCD_{AFR}-GWAS, EUR-GWAS, EUR-EAS-GWAS, and EUR-EAS-AFR-GWAS) on the 31 cerebellar volumetric traits. Each plot shows genome-wide (red dashed line: $P = 5 \times 10^{-8}$) and study-wide (blue dashed line: $P = 1.61 \times 10^{-9}$) significant associations with 31 cerebellar volumetric traits. Each point represents a single genetic variant plotted according to its genomic position (x axis) and its $-\log_{10}(P)$ value for the association (y axis). Each yellow point represents an independent locus with study-wide significance ($P = 1.61 \times 10^{-9}$). Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; GWAS, genome-wide association study; UKBB, the UK Biobank study.

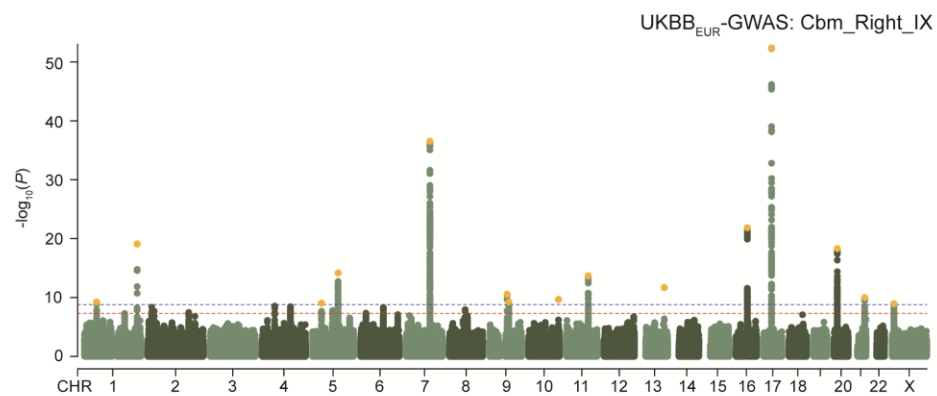
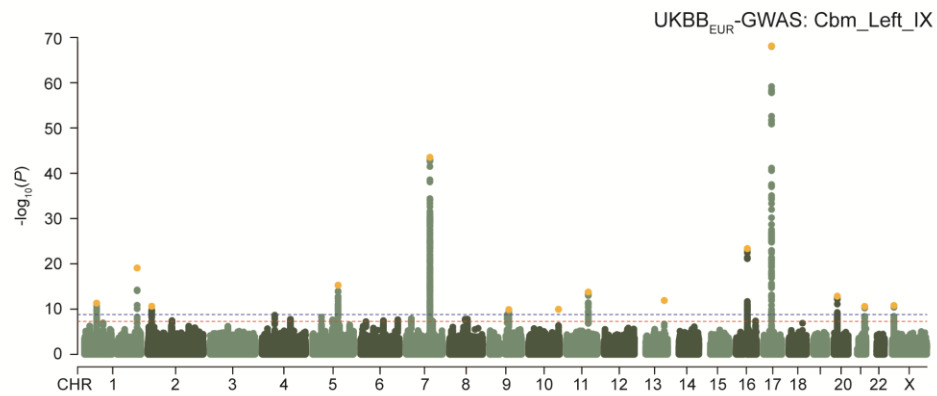
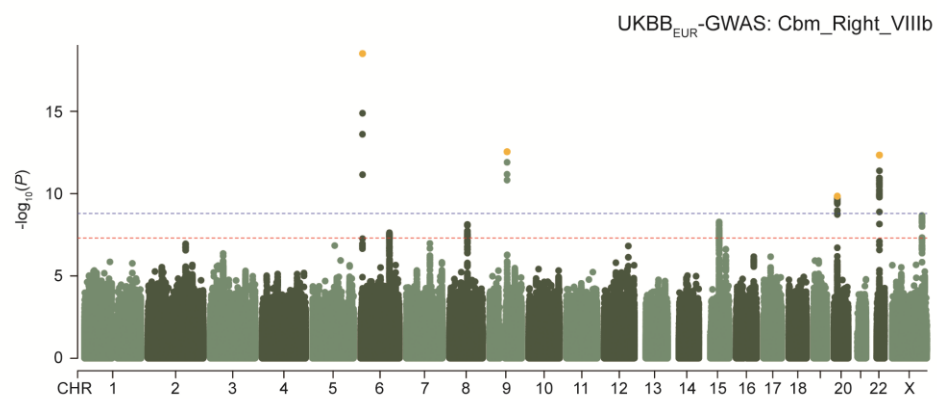
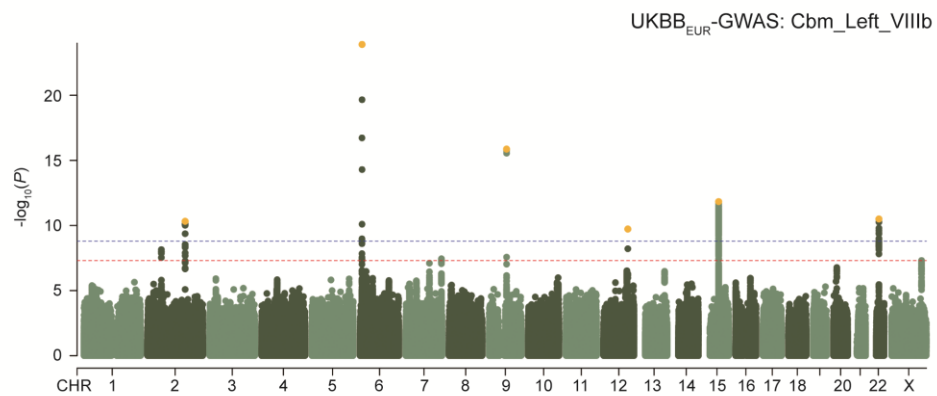


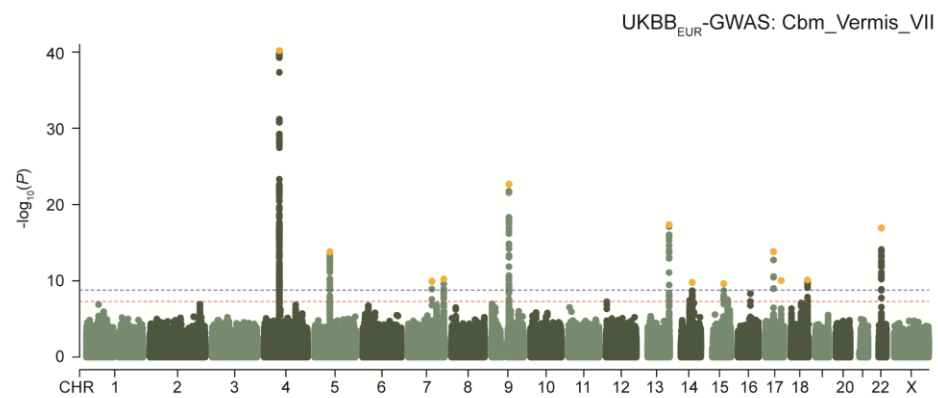
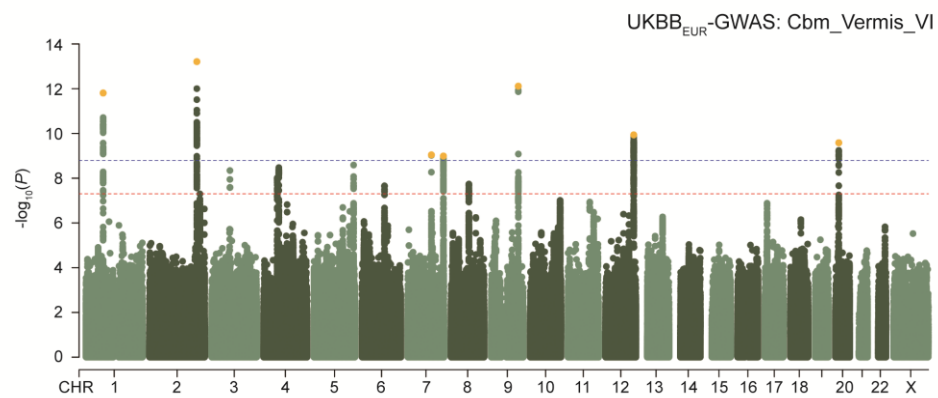
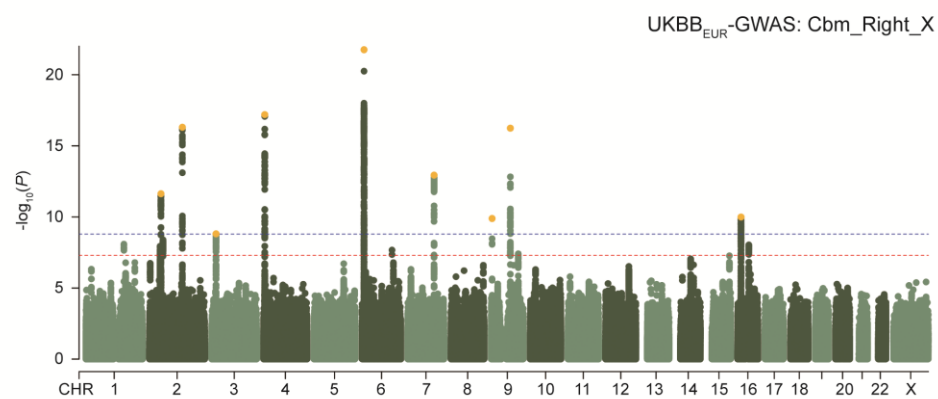
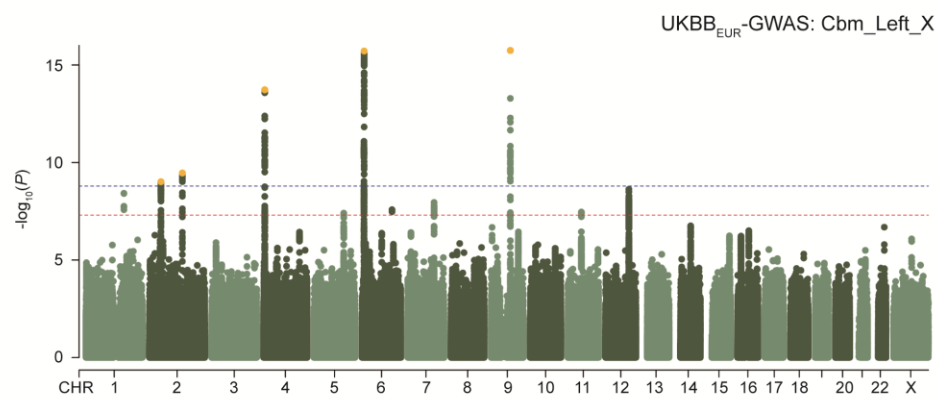


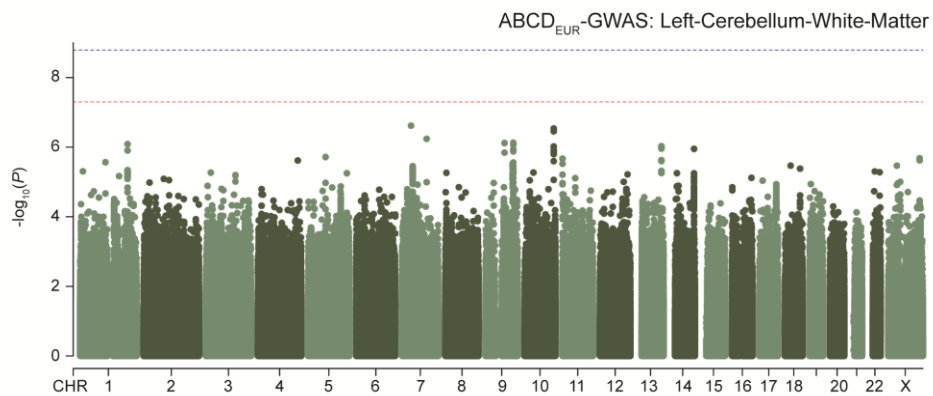
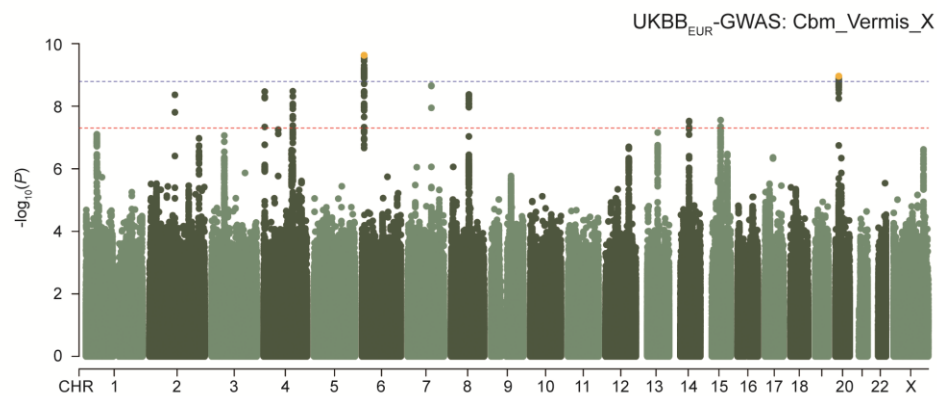
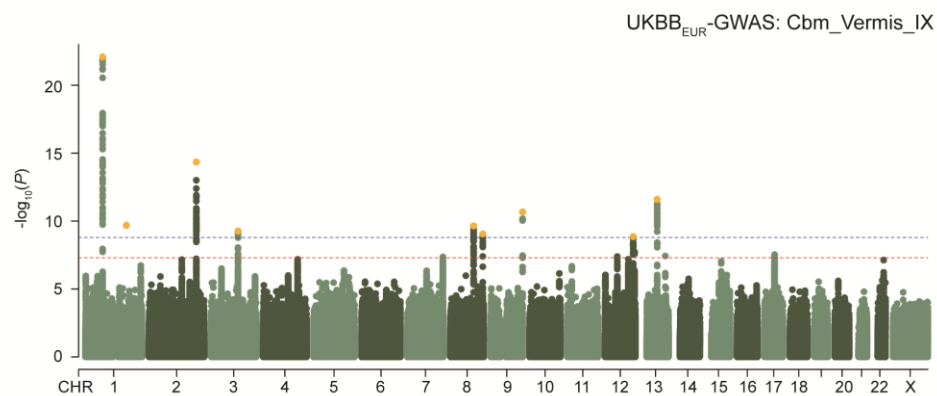
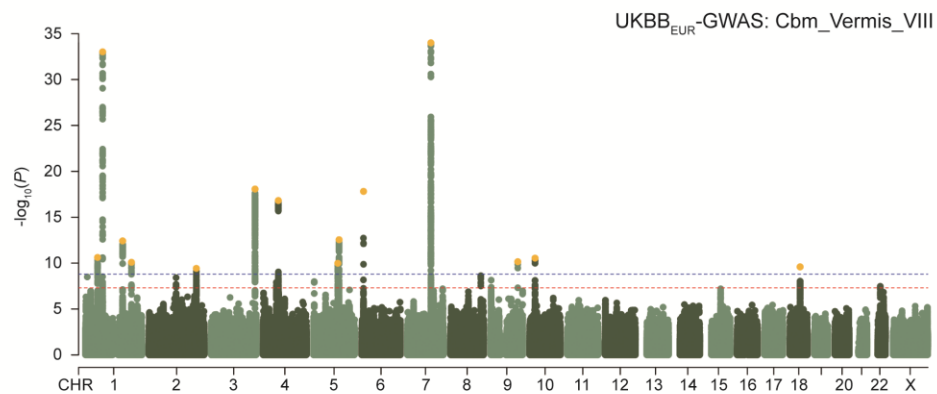


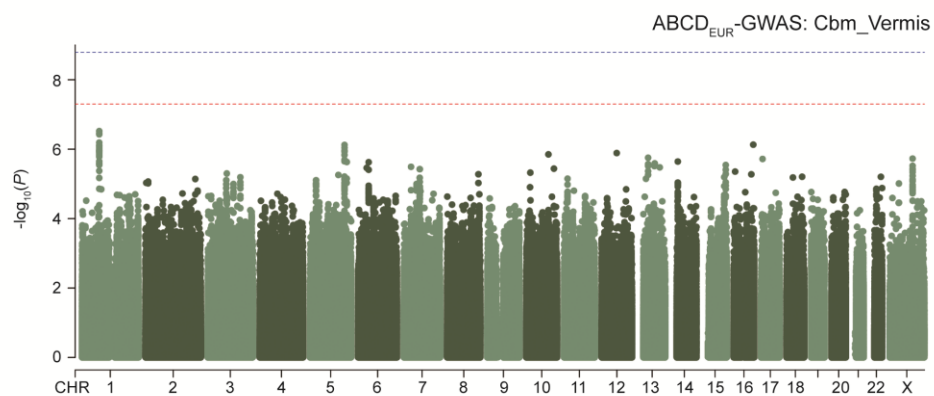
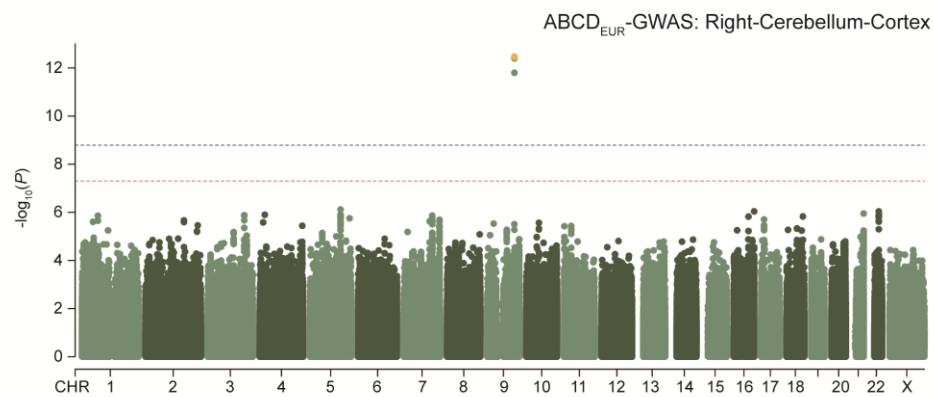
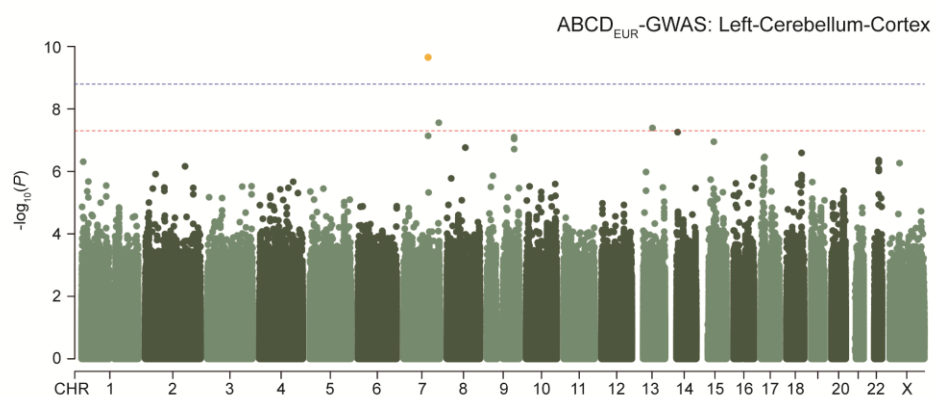
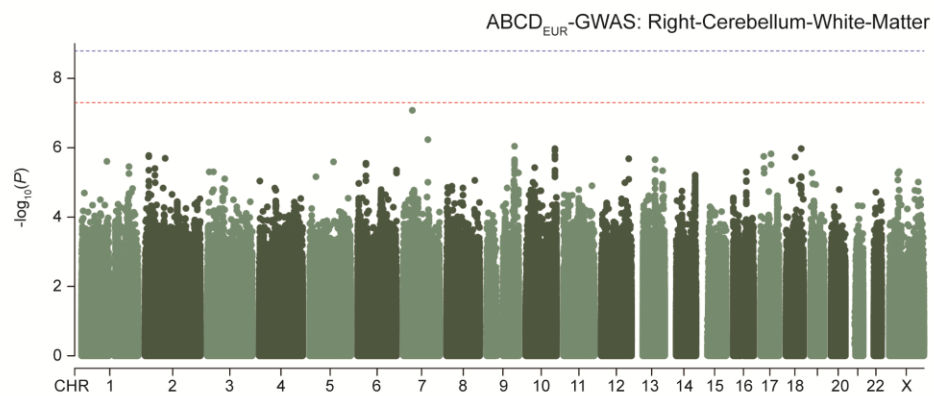


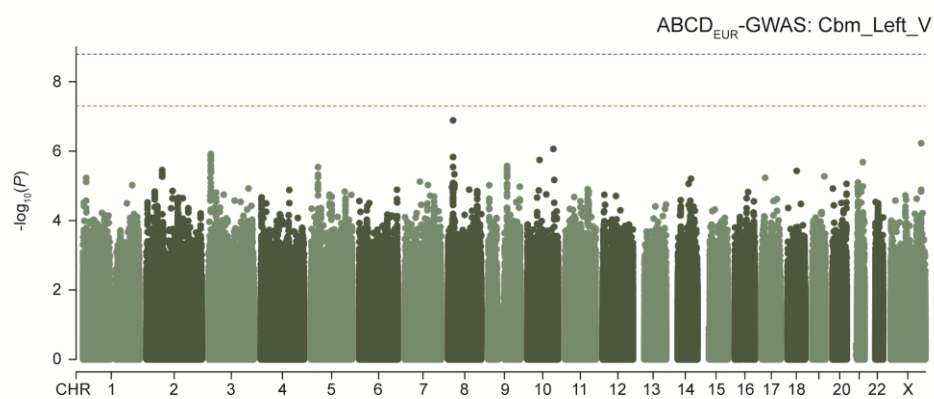
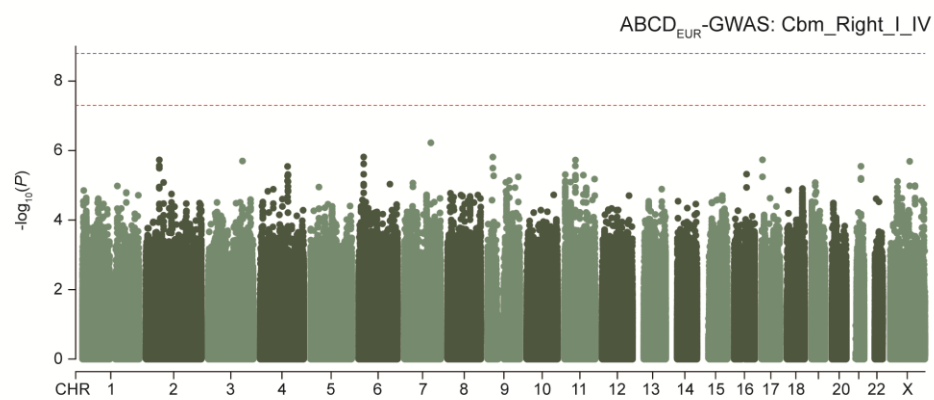
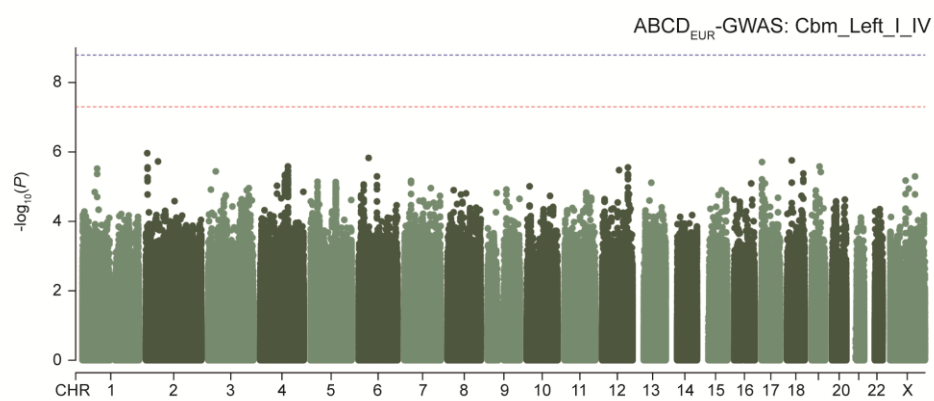
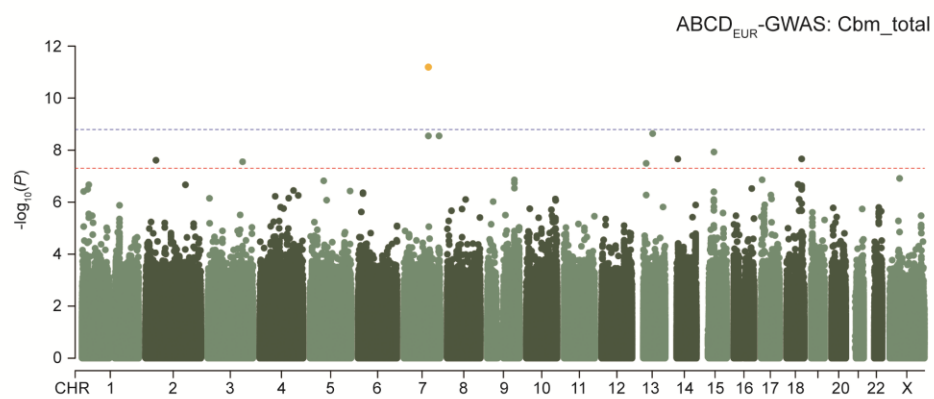


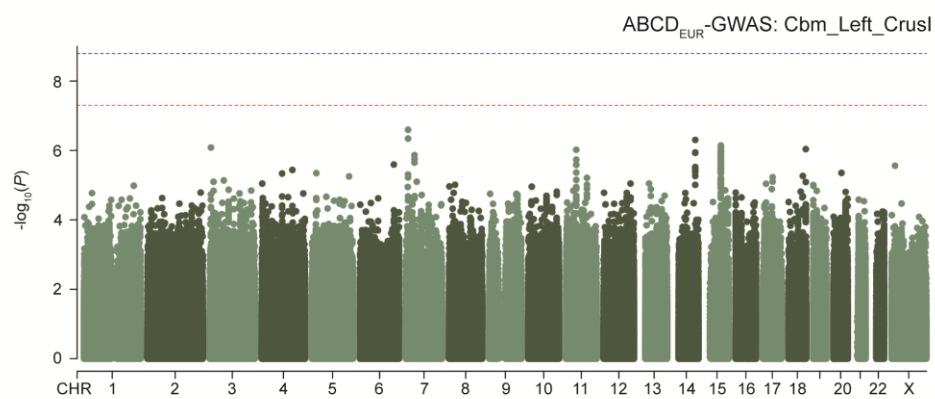
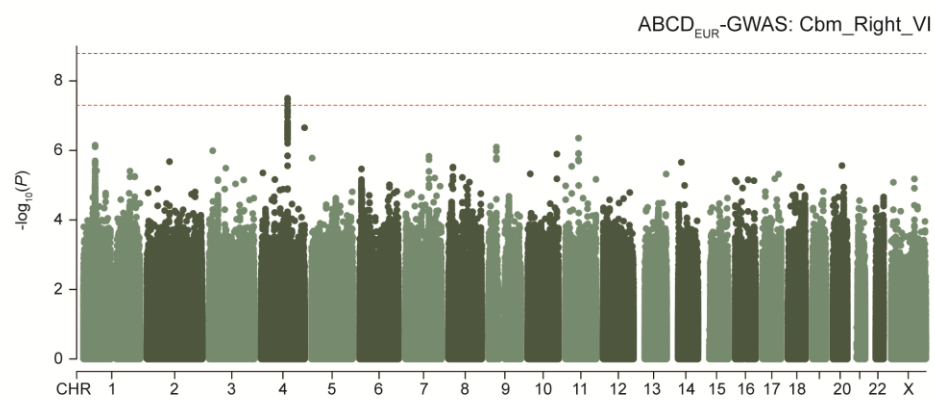
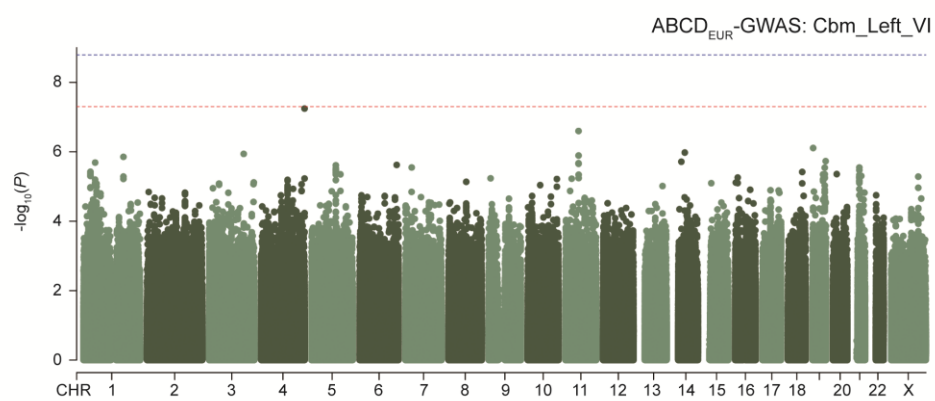
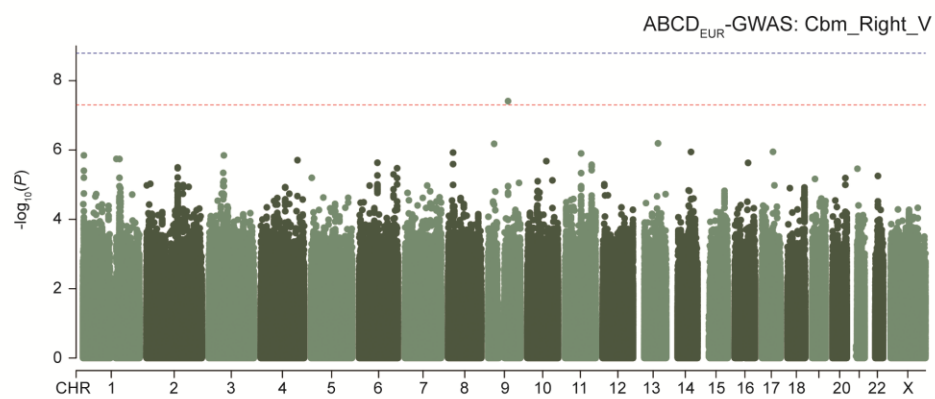


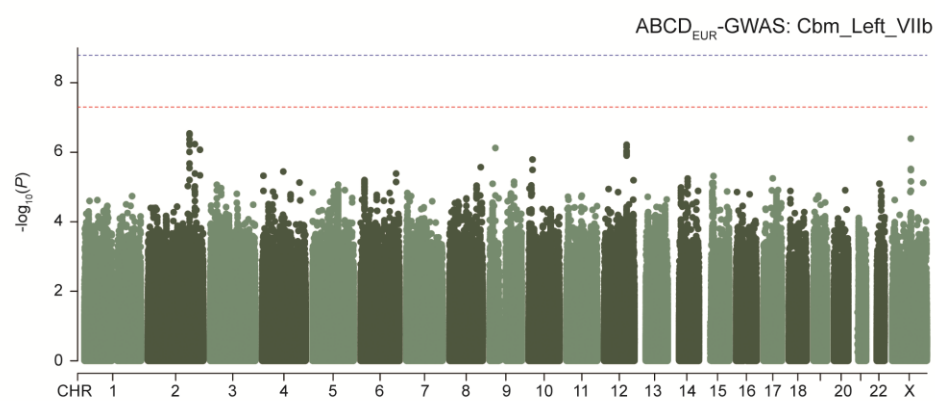
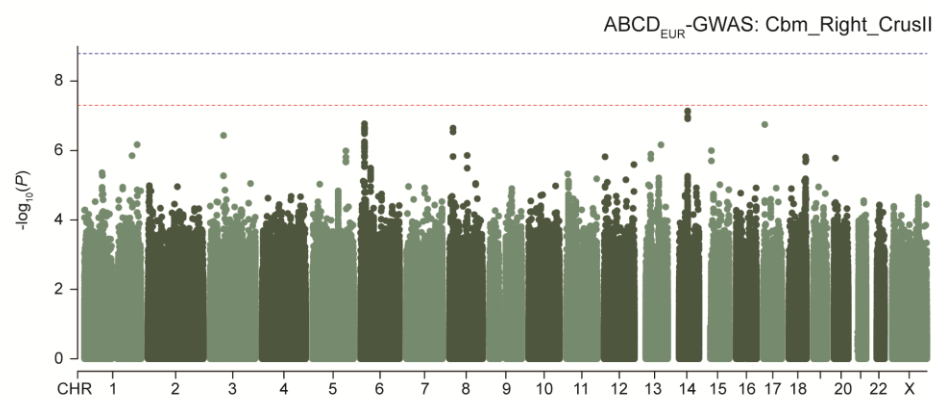
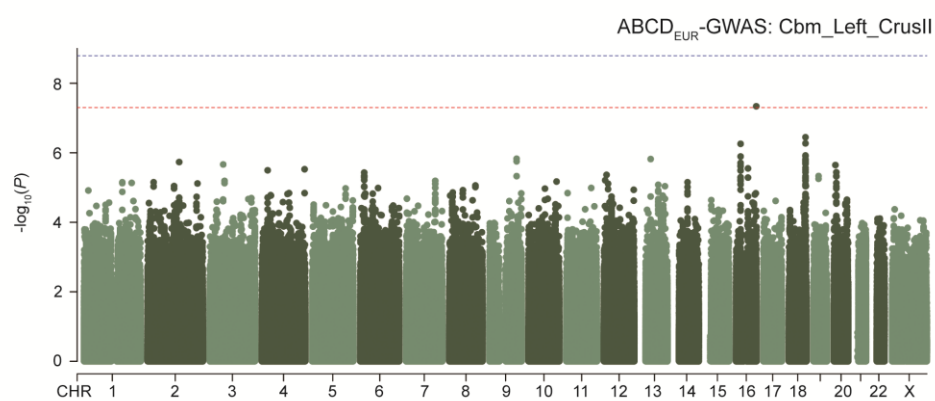
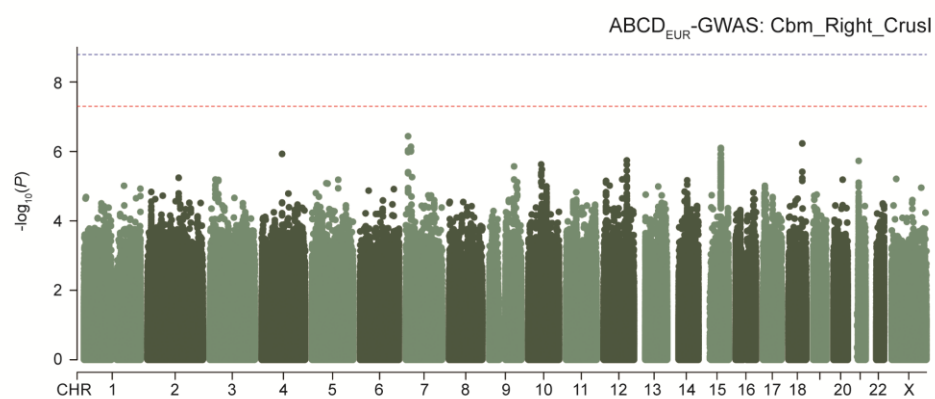


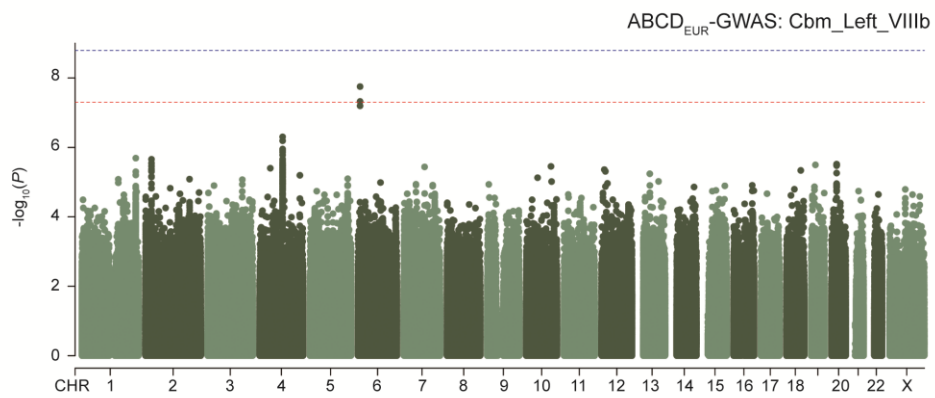
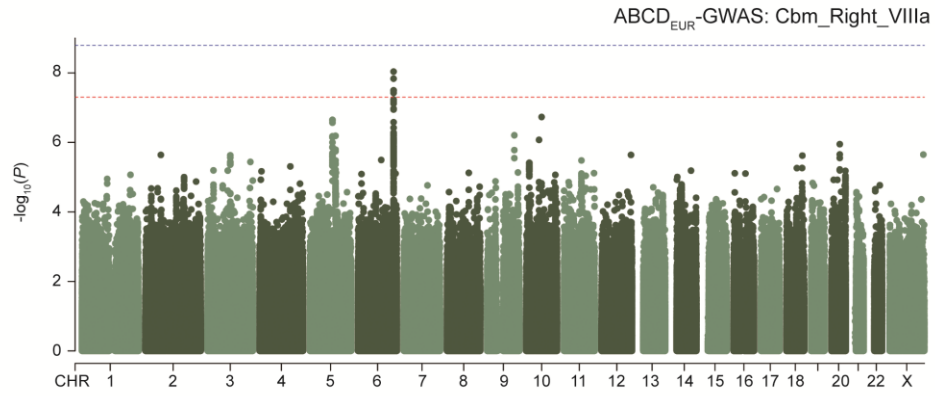
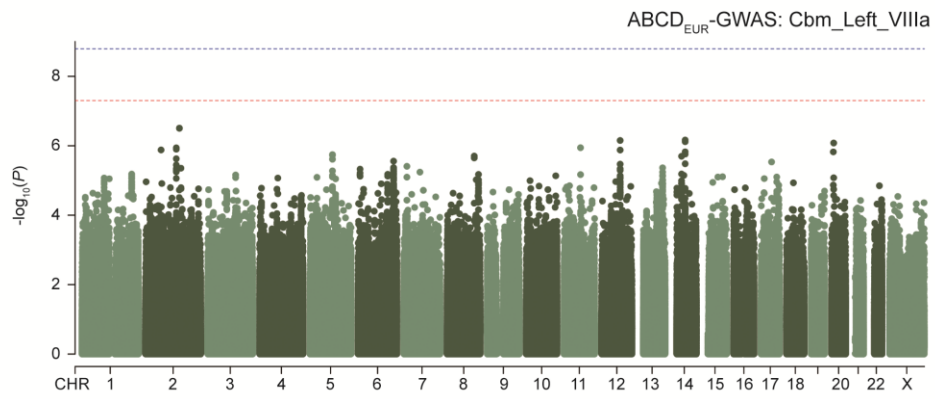
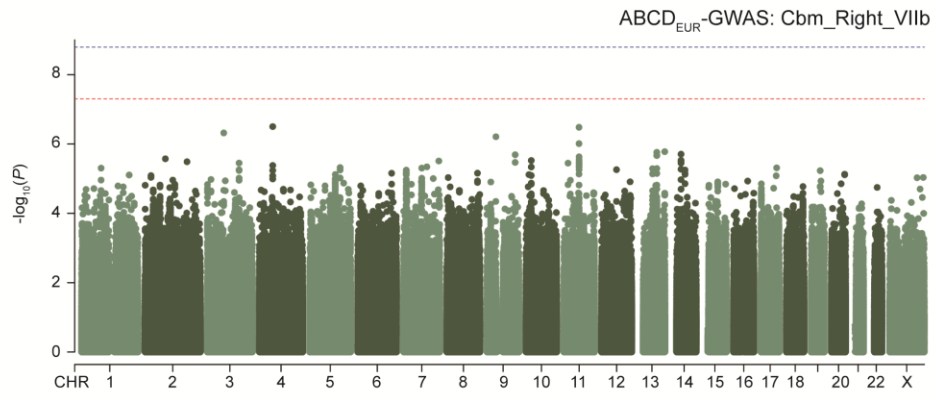


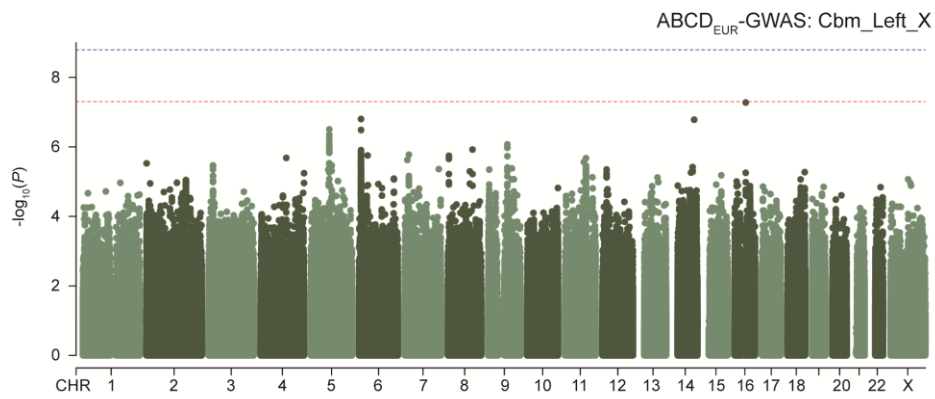
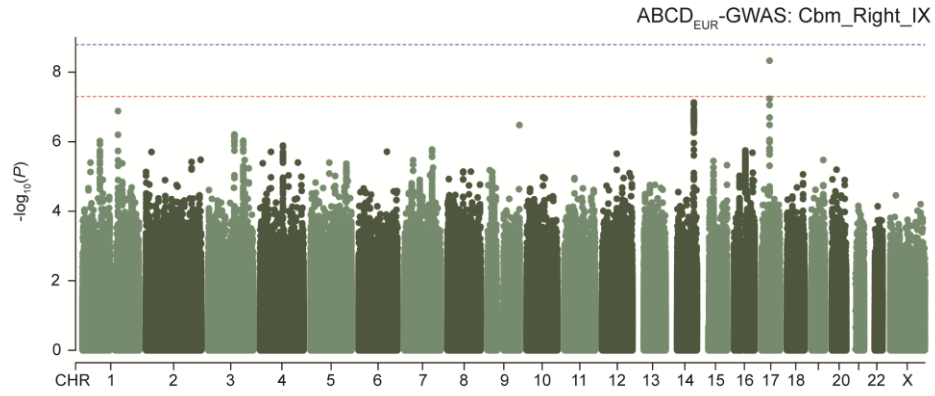
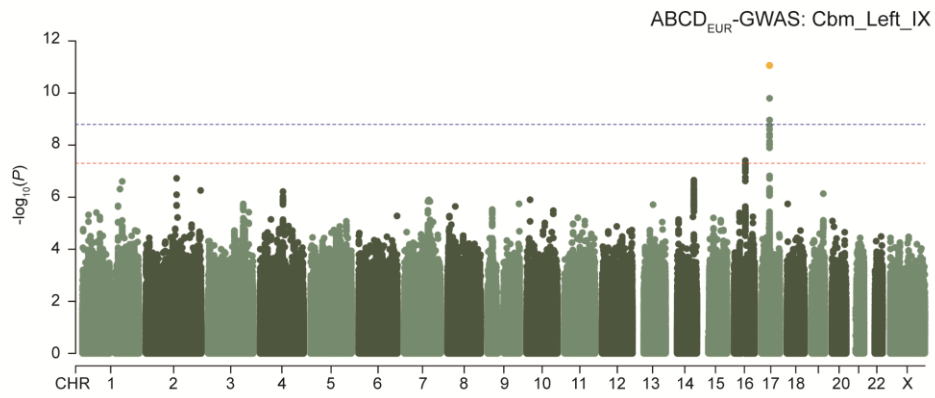
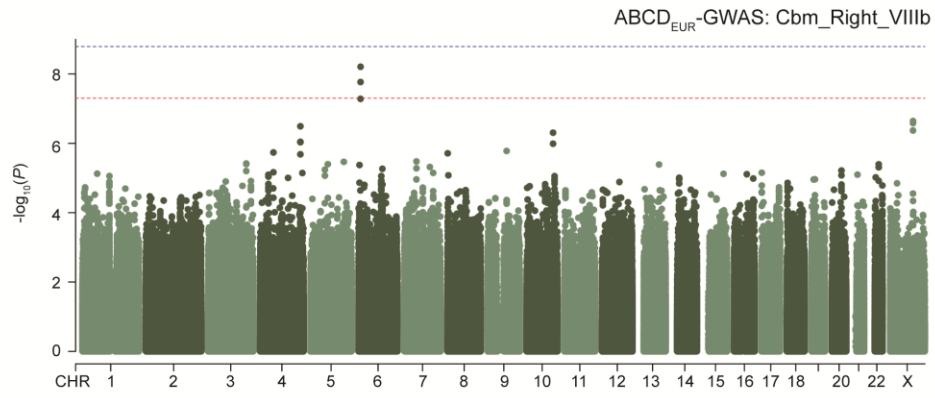


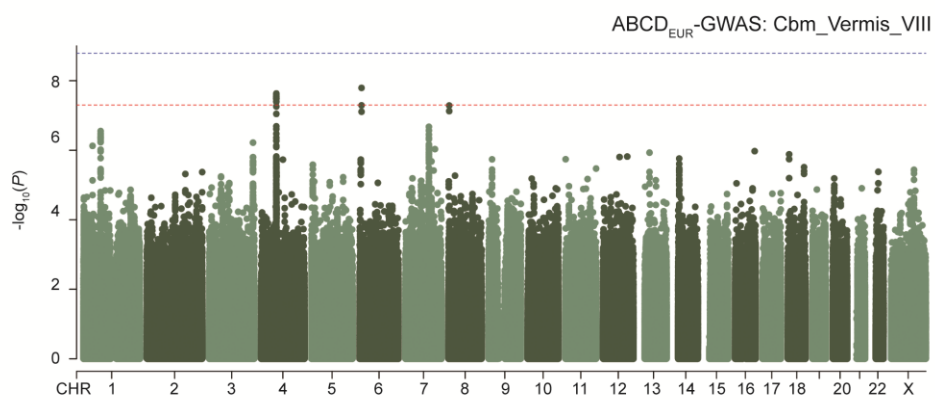
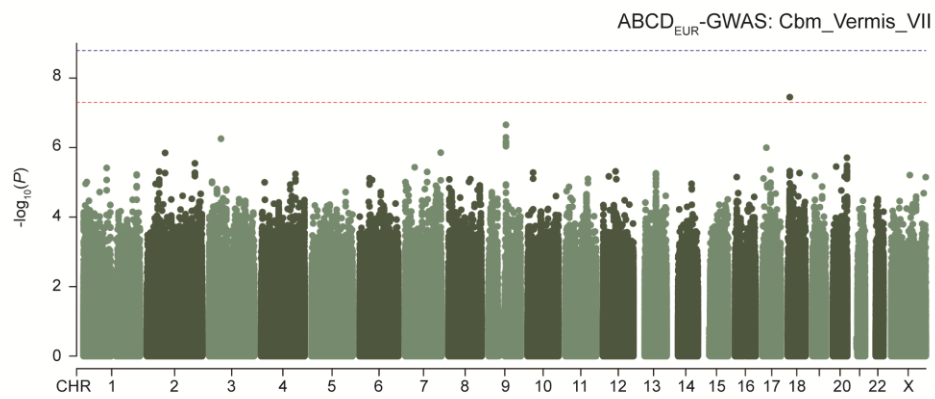
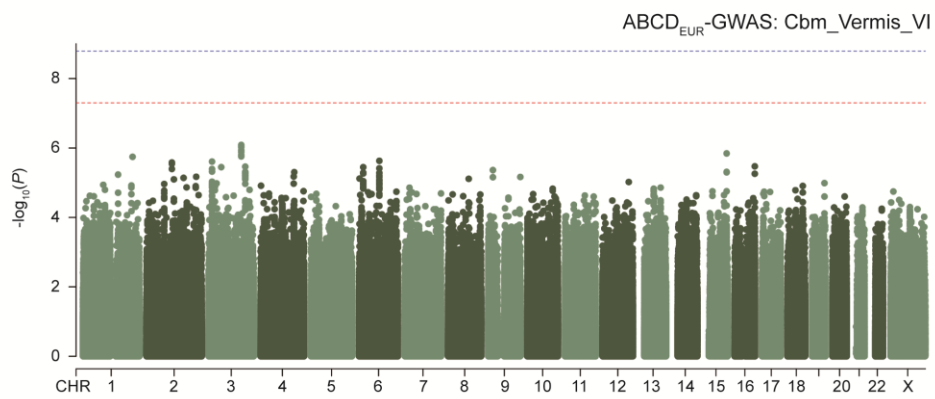
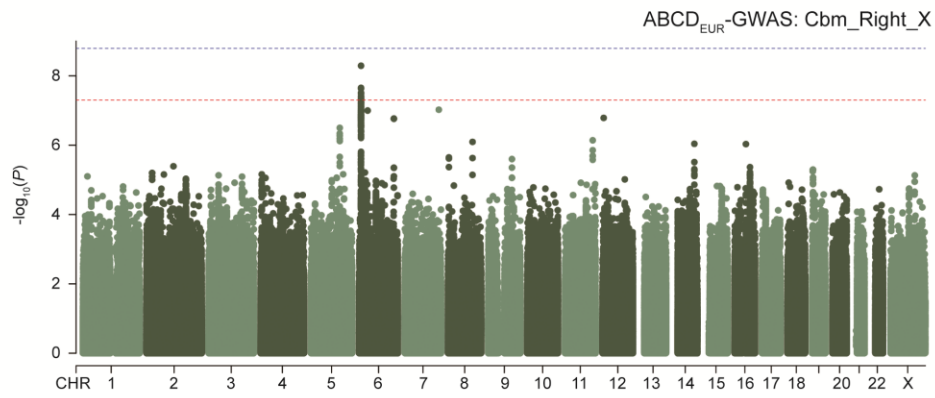


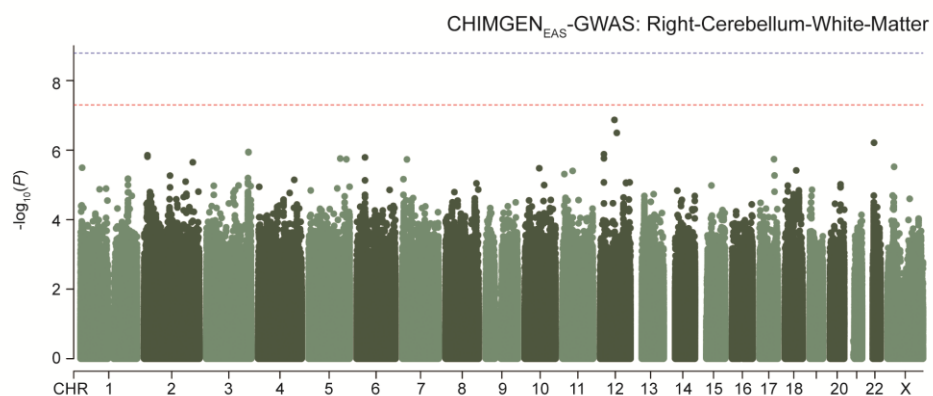
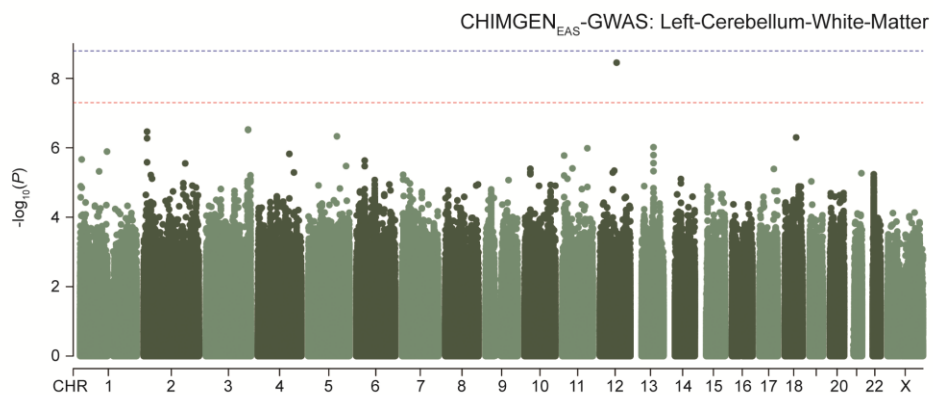
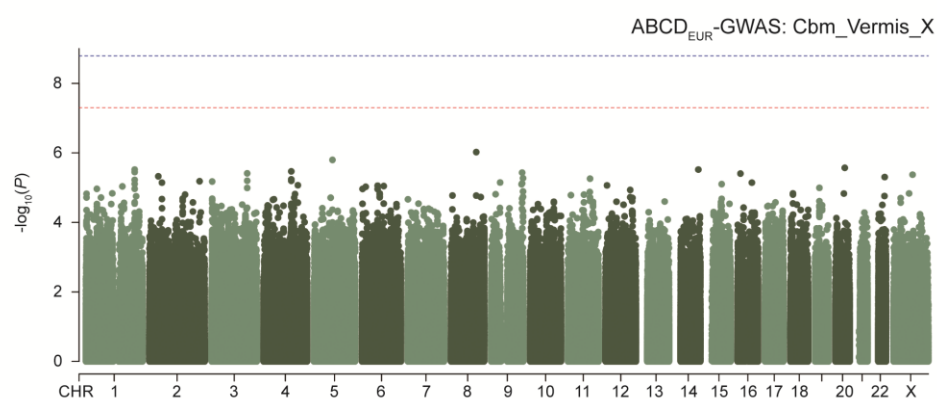
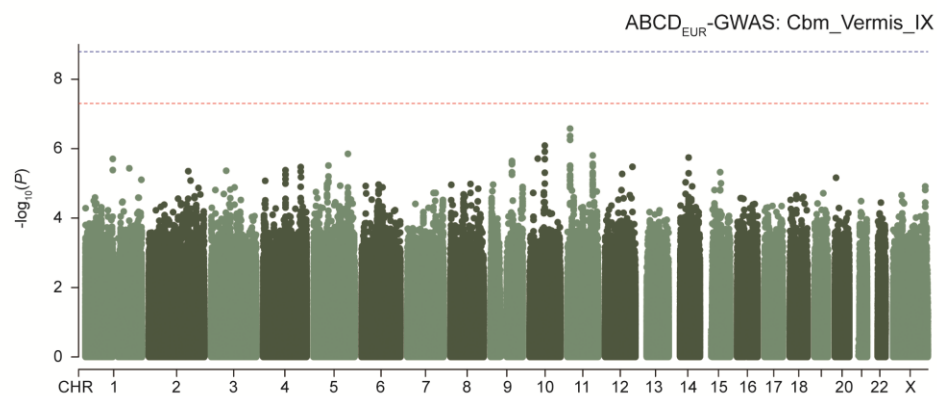


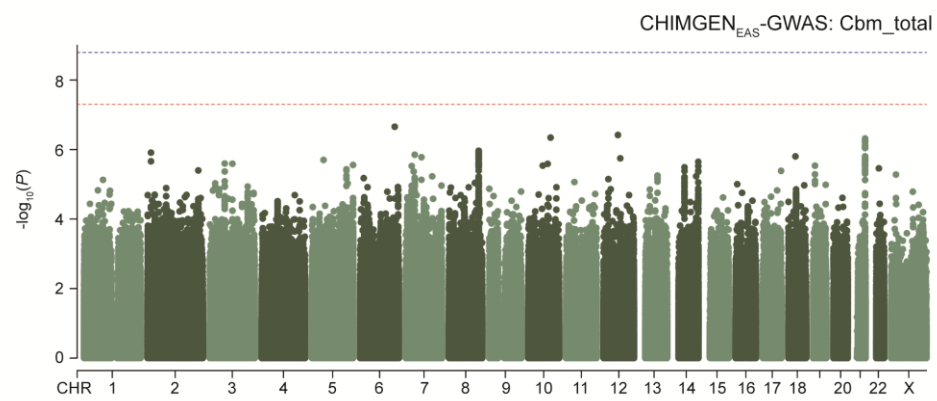
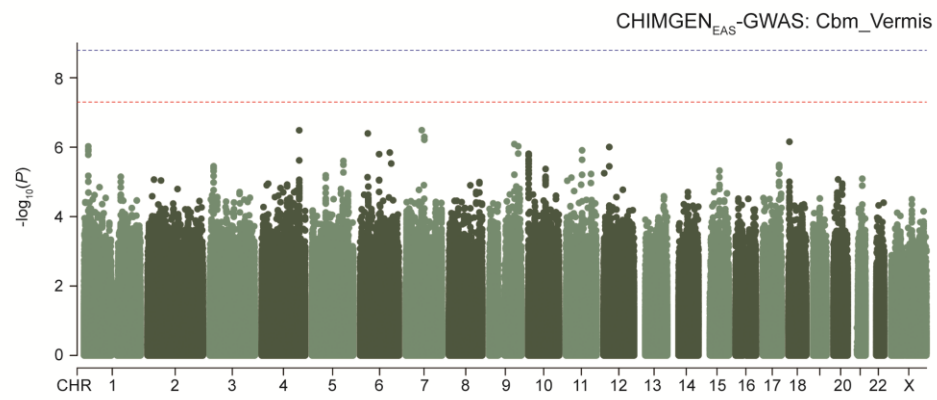
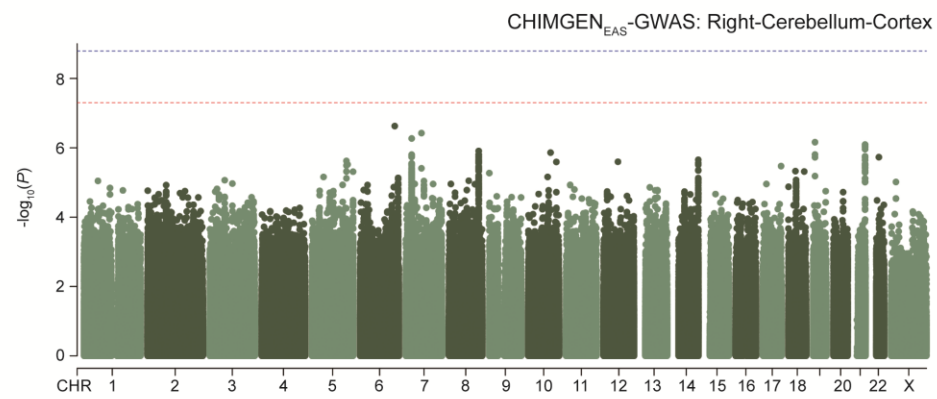
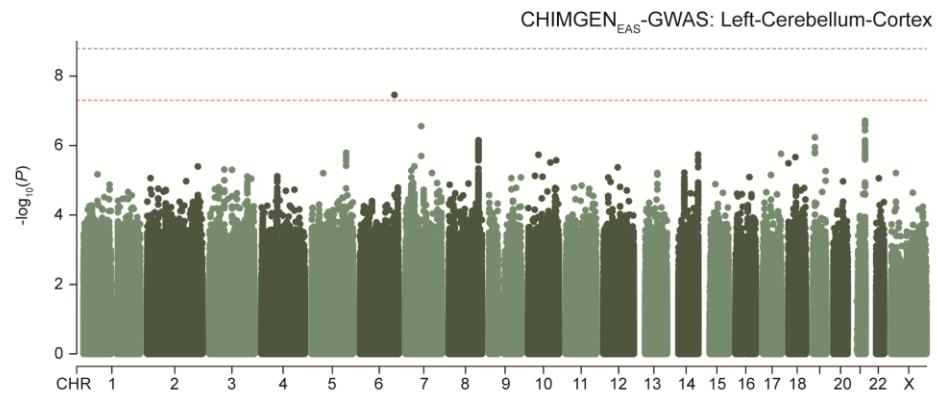


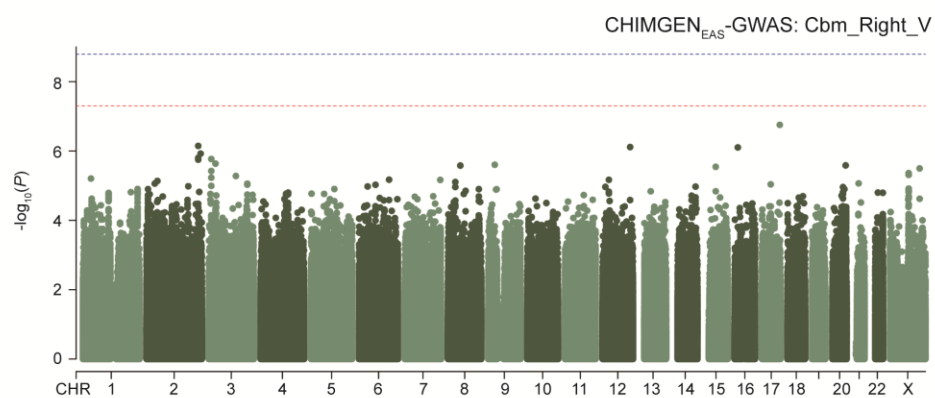
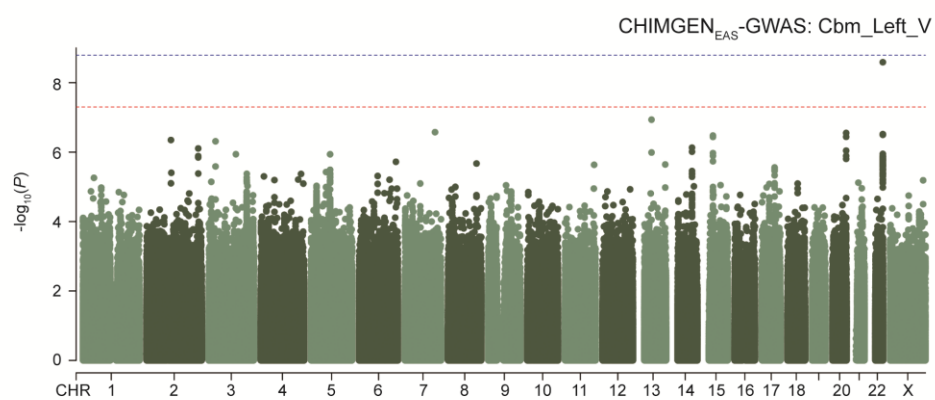
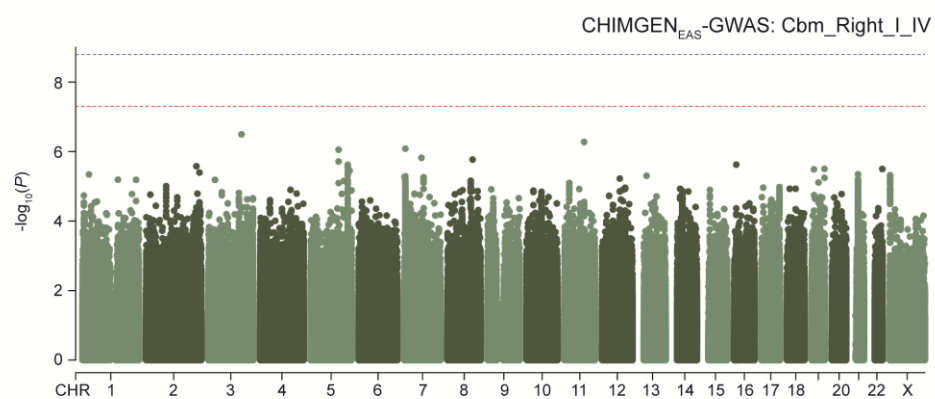
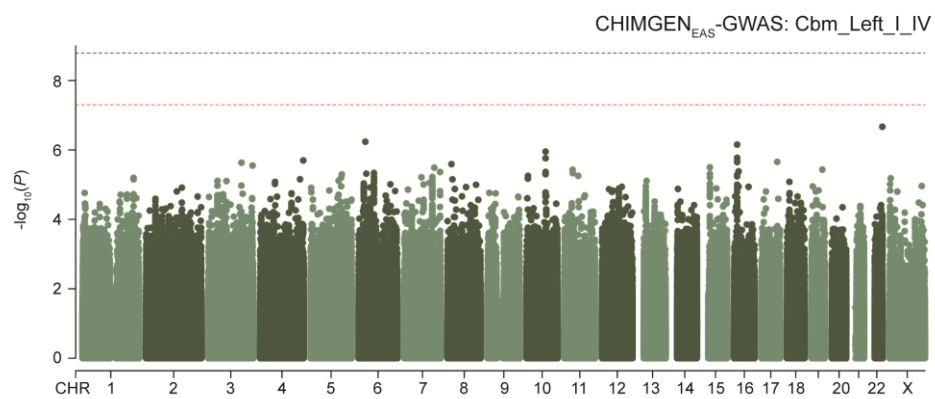


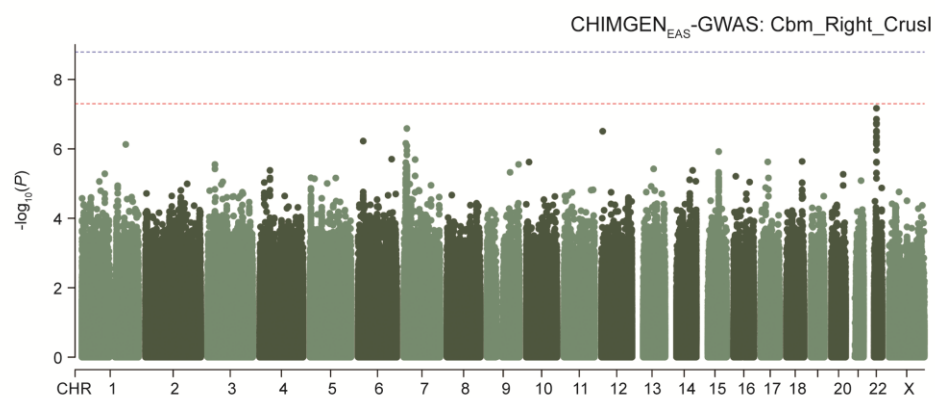
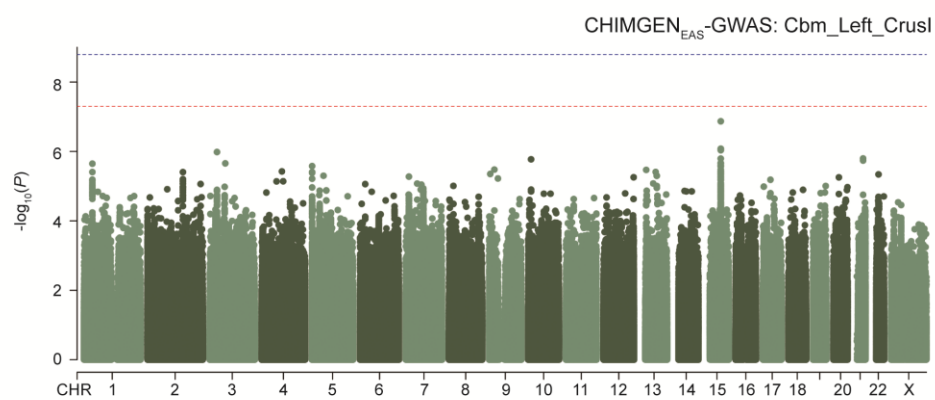
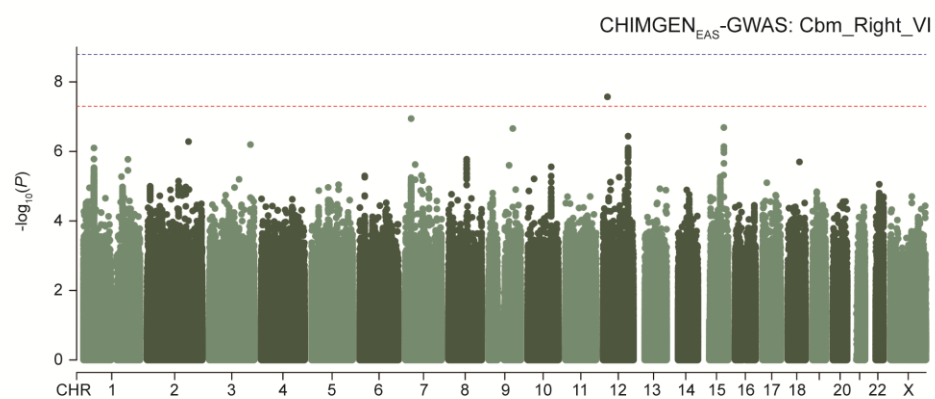
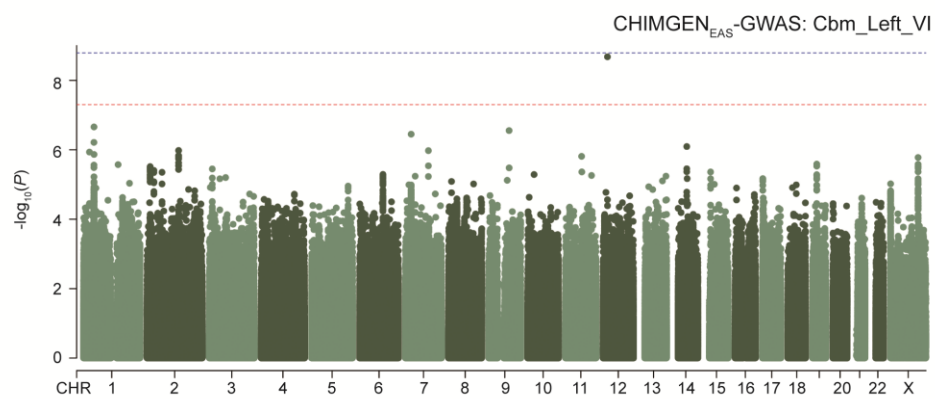


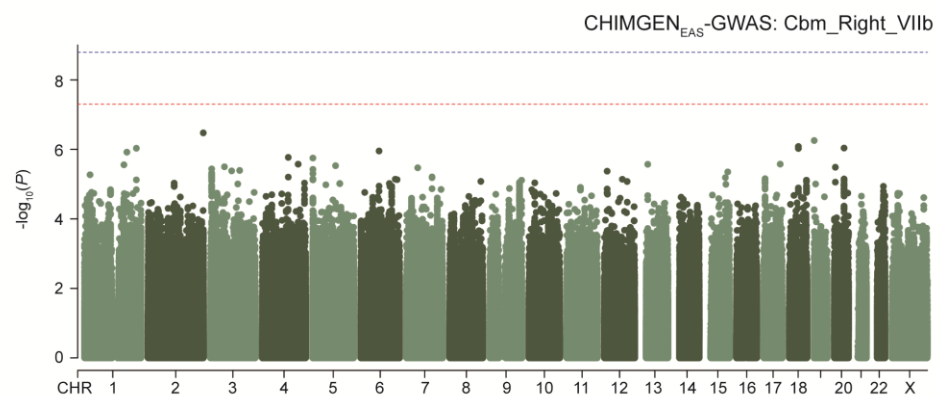
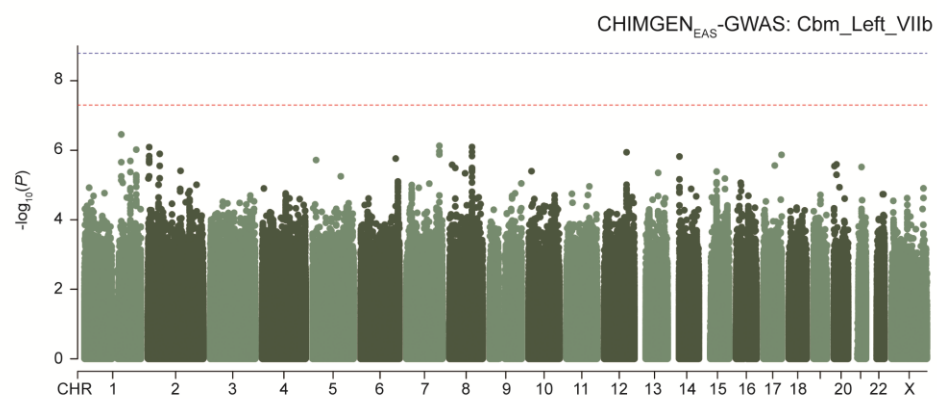
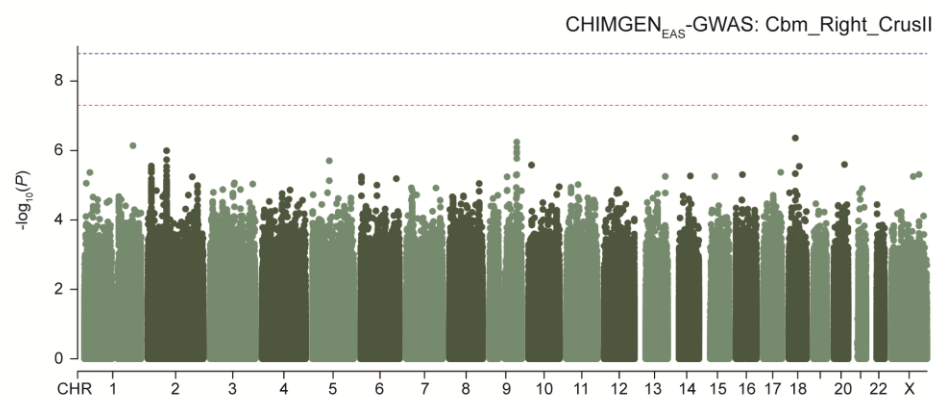
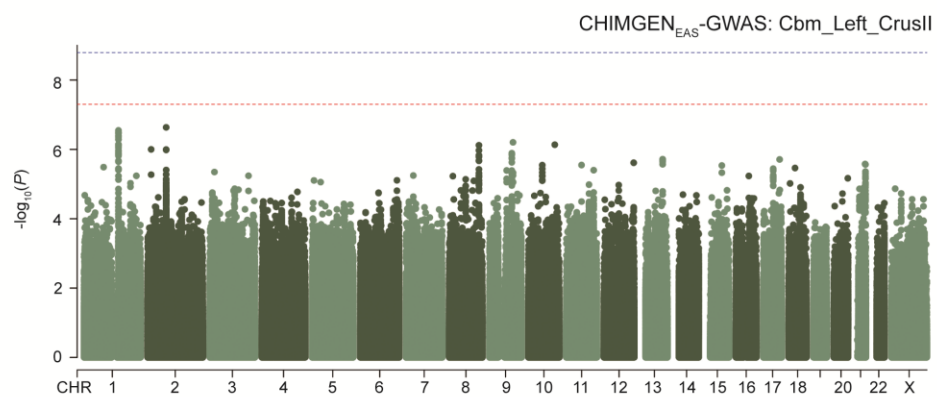


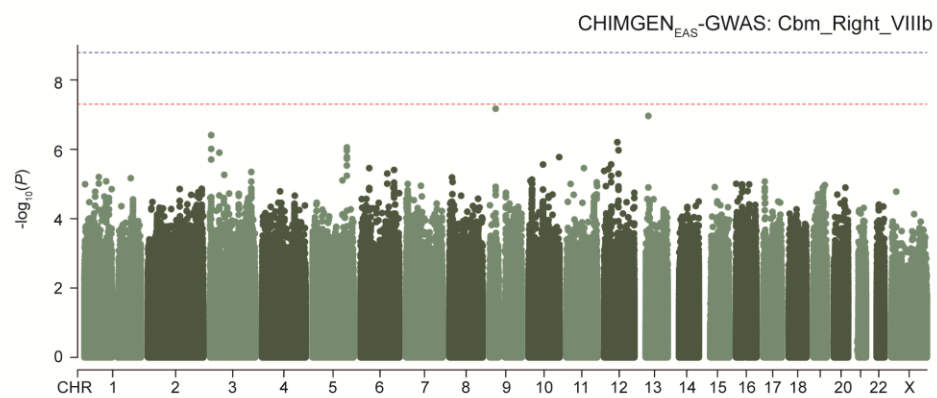
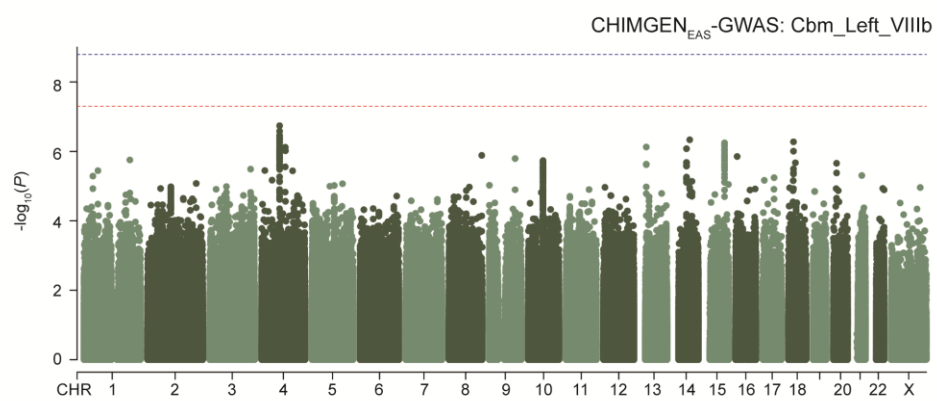
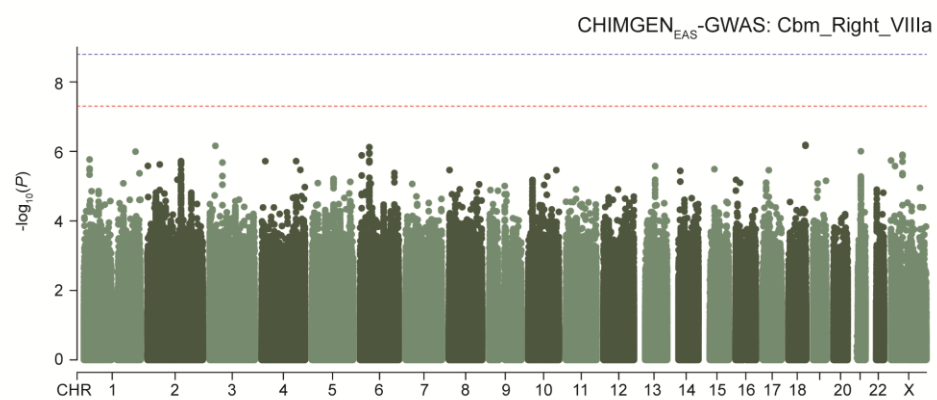
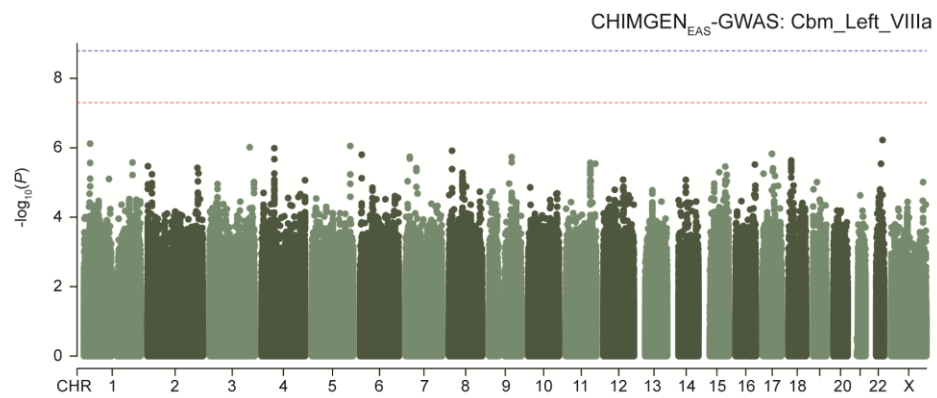


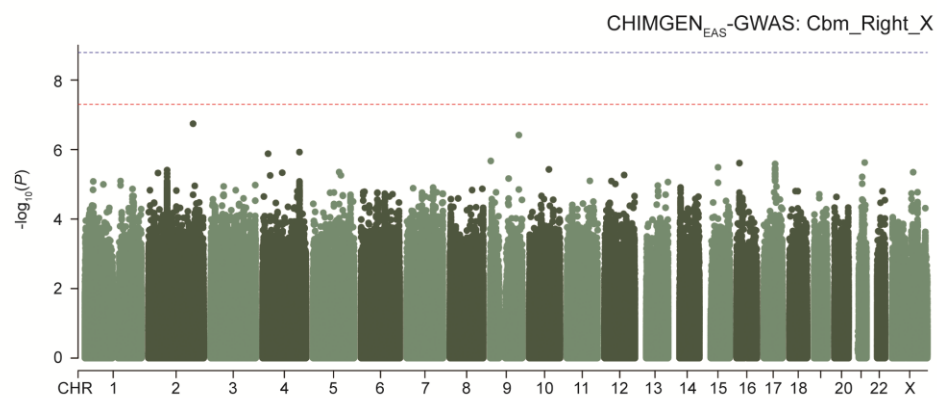
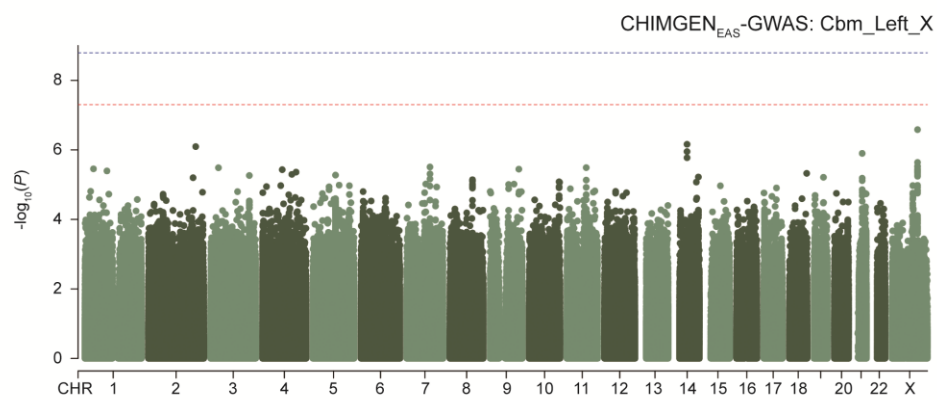
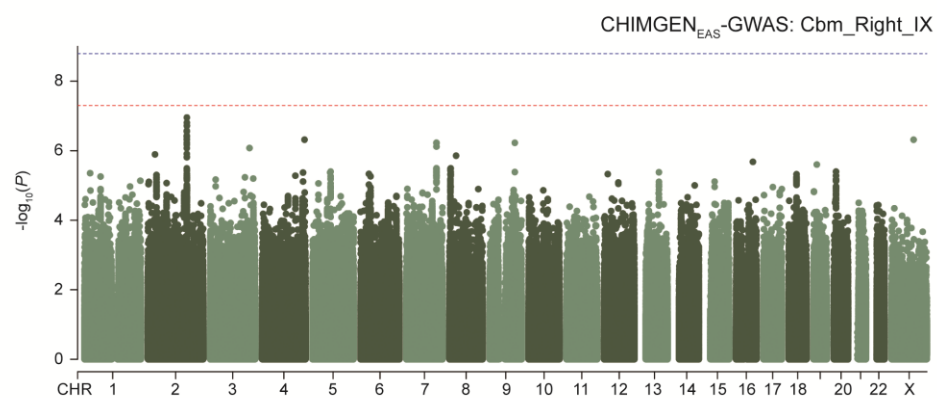
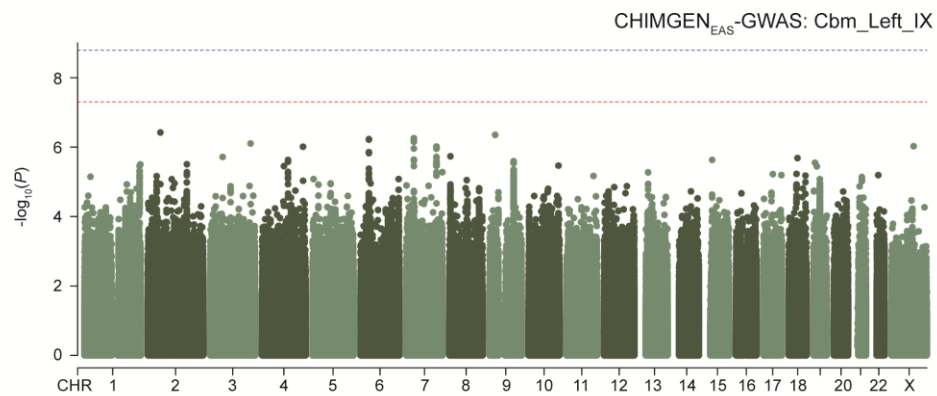


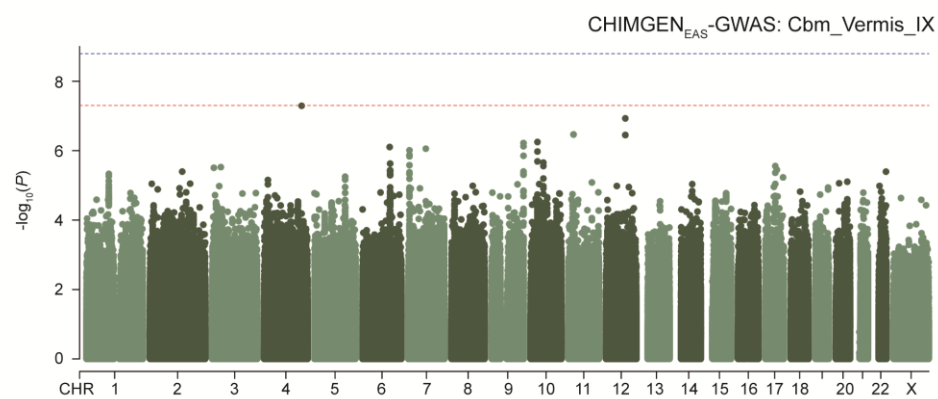
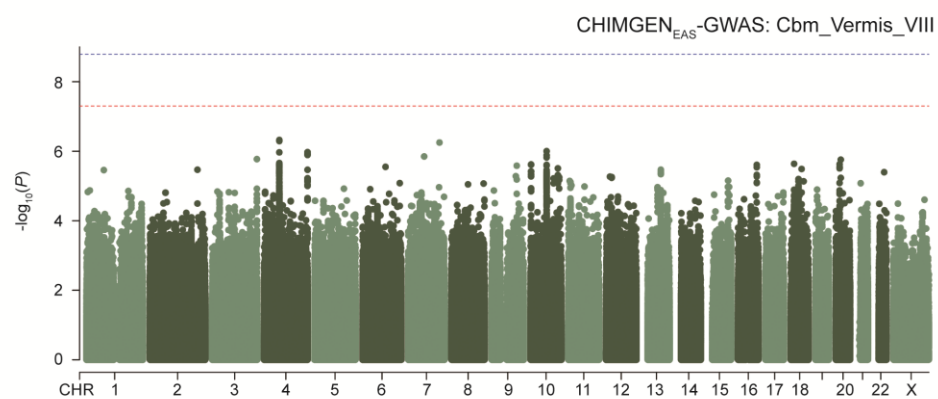
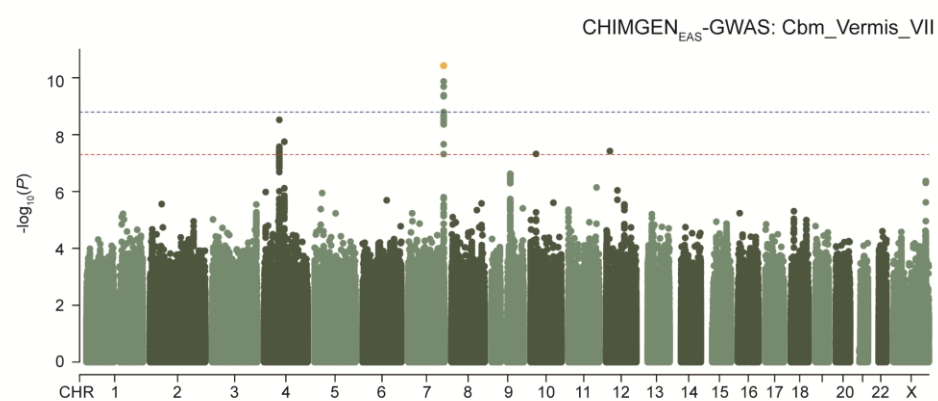
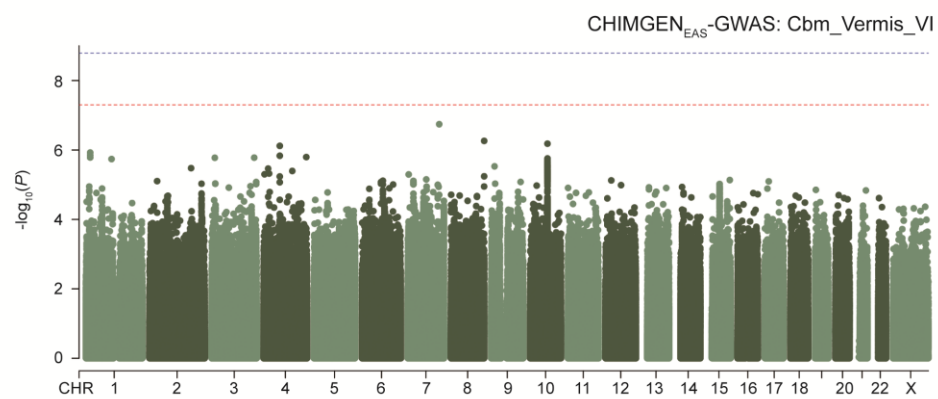


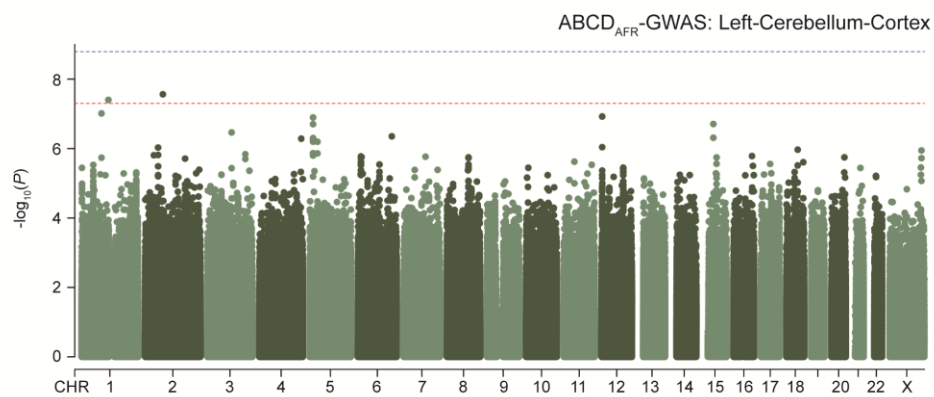
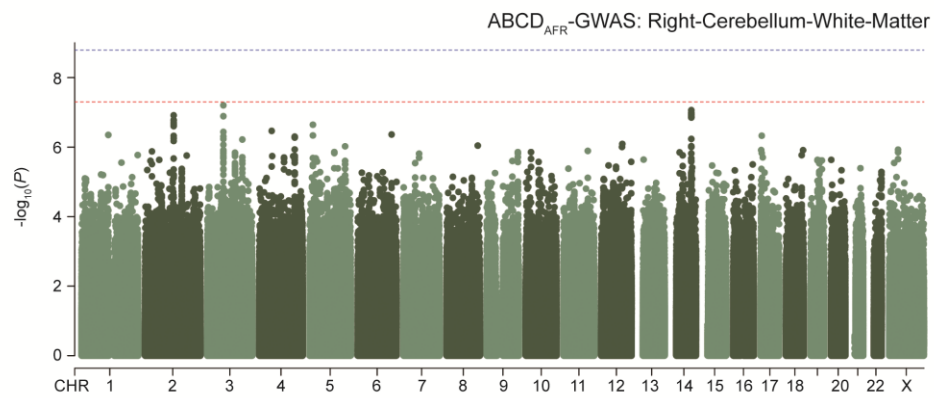
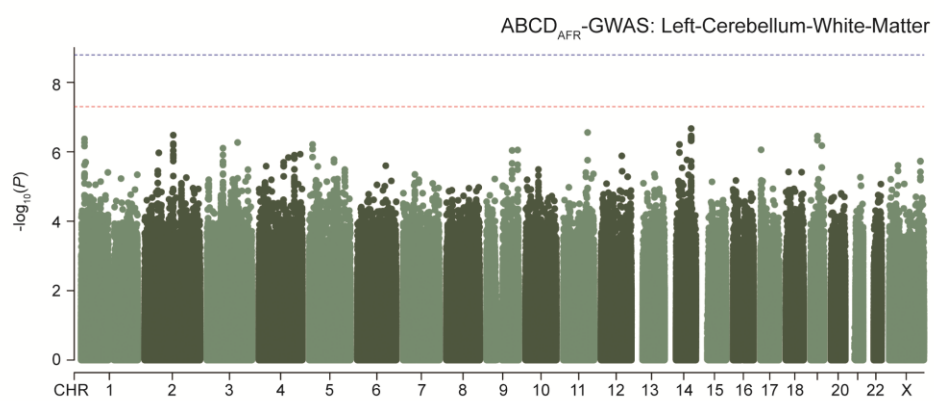
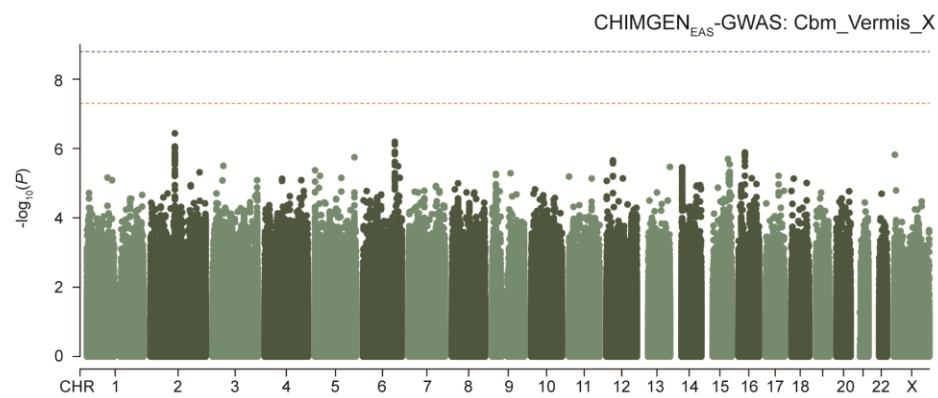


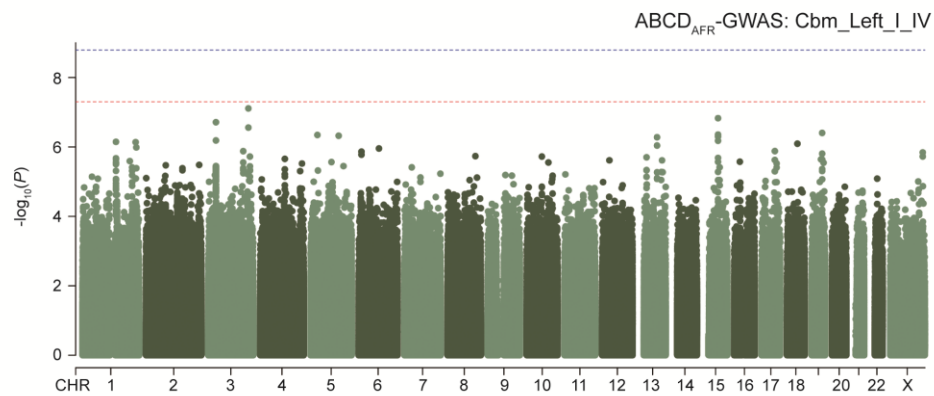
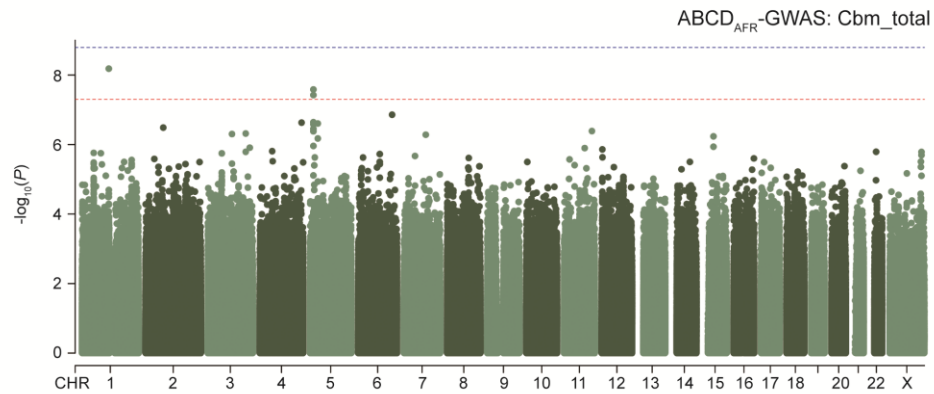
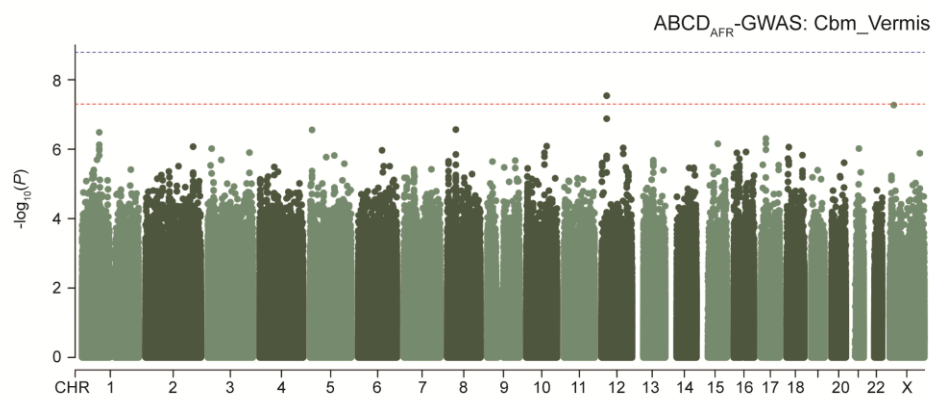
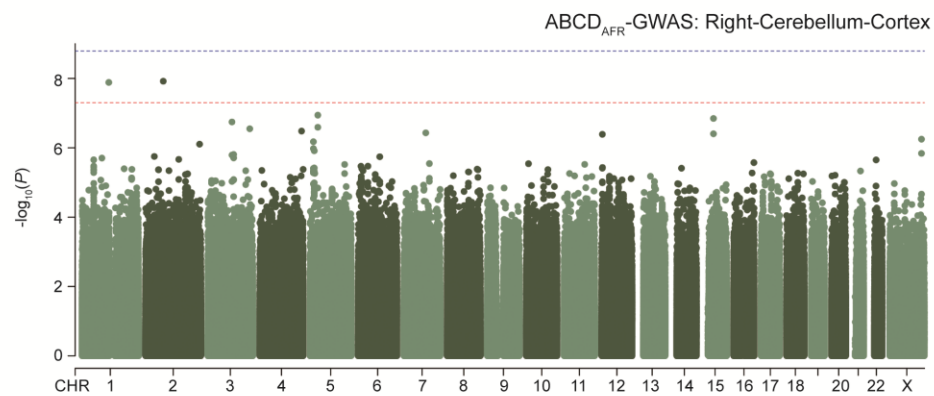


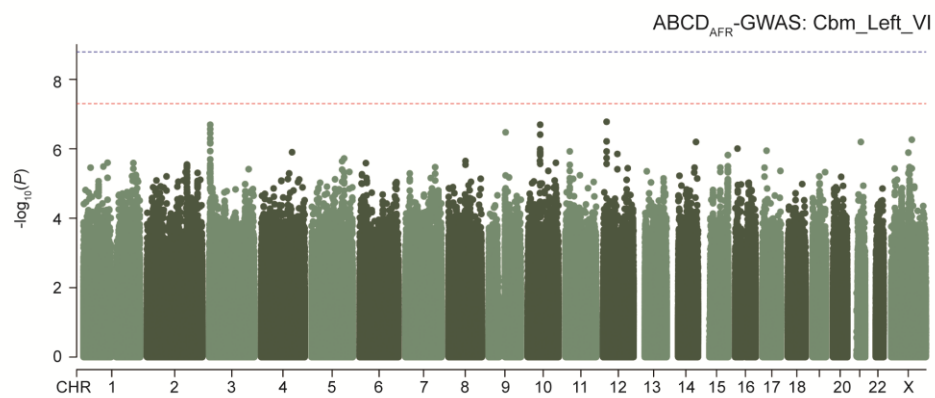
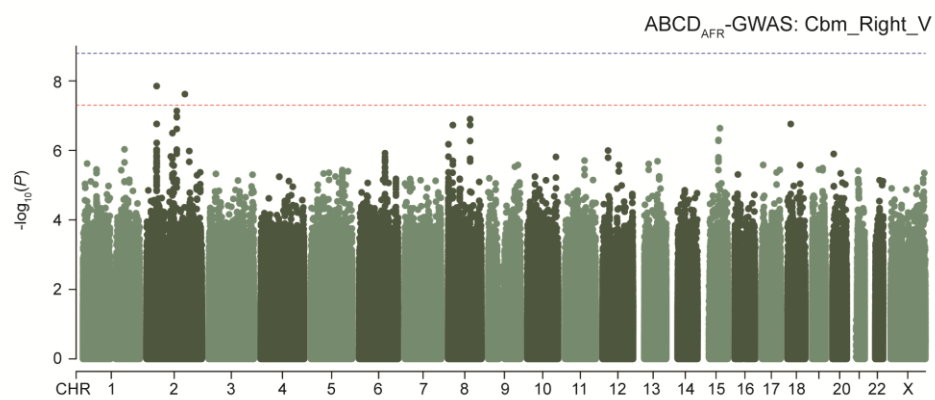
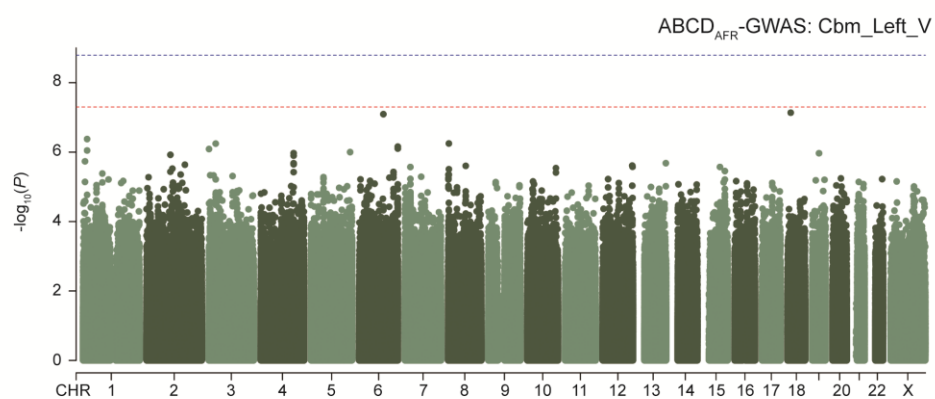
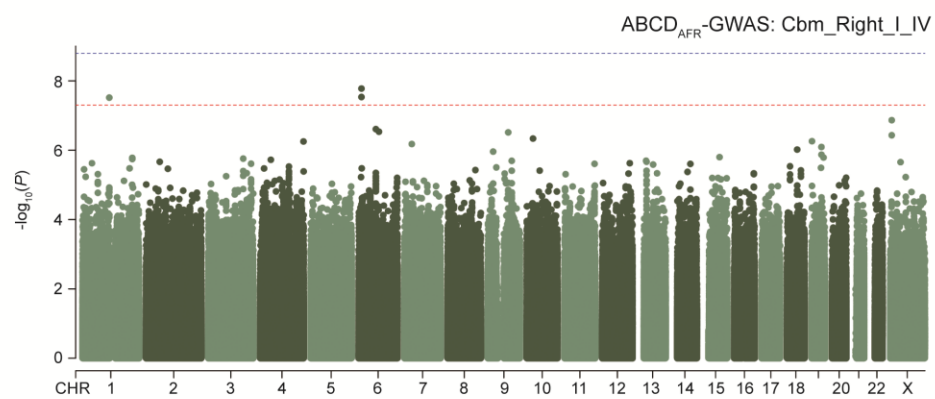


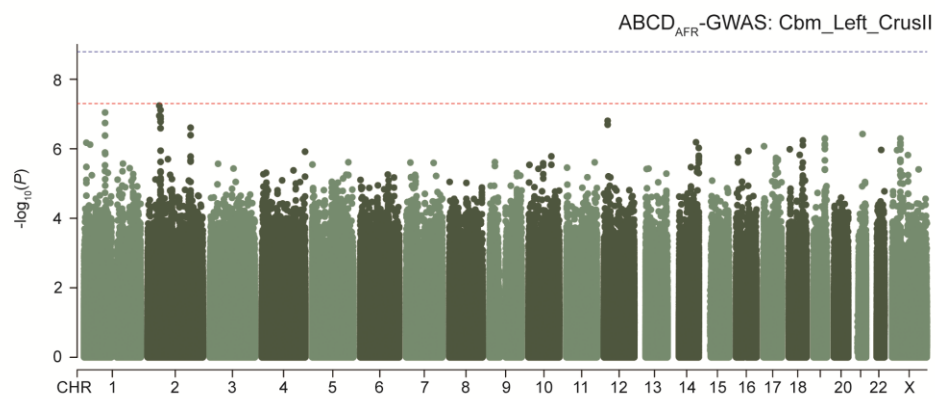
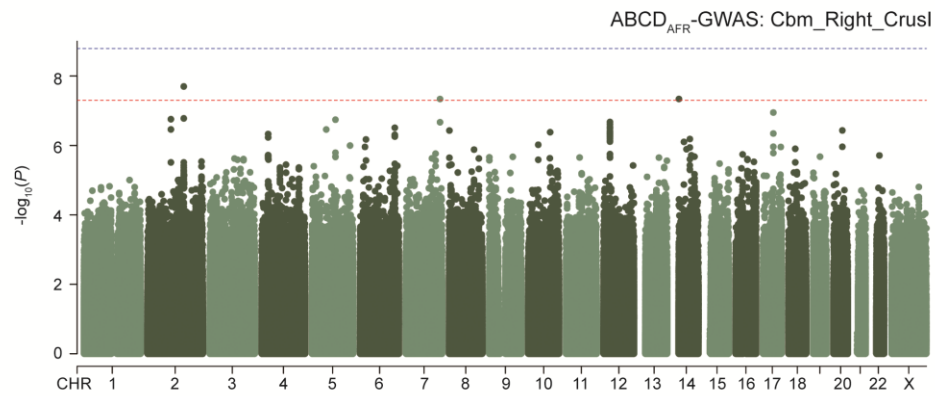
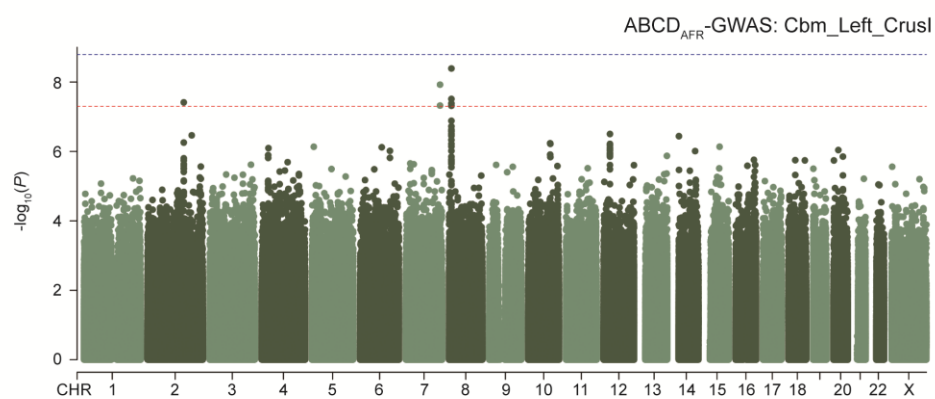
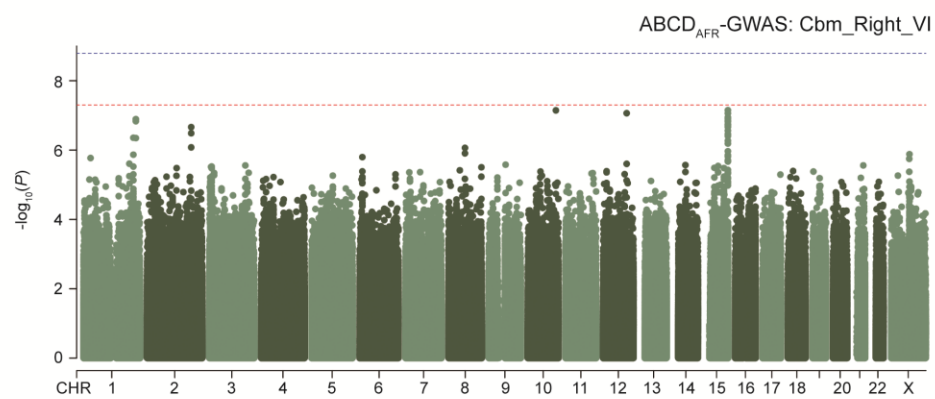


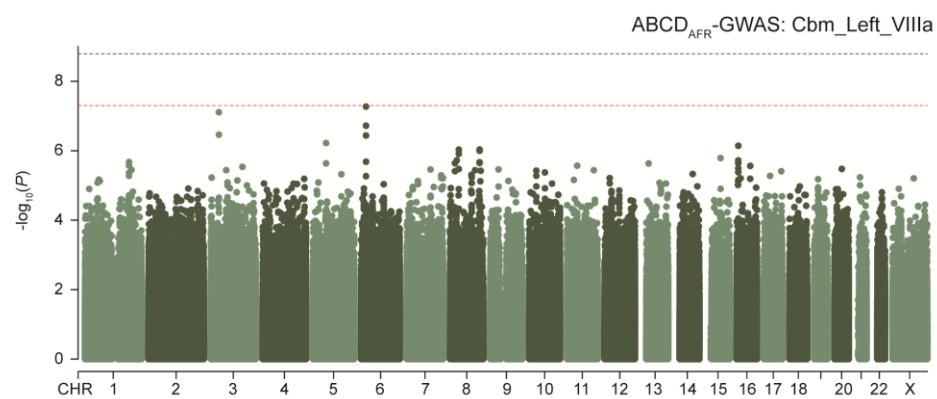
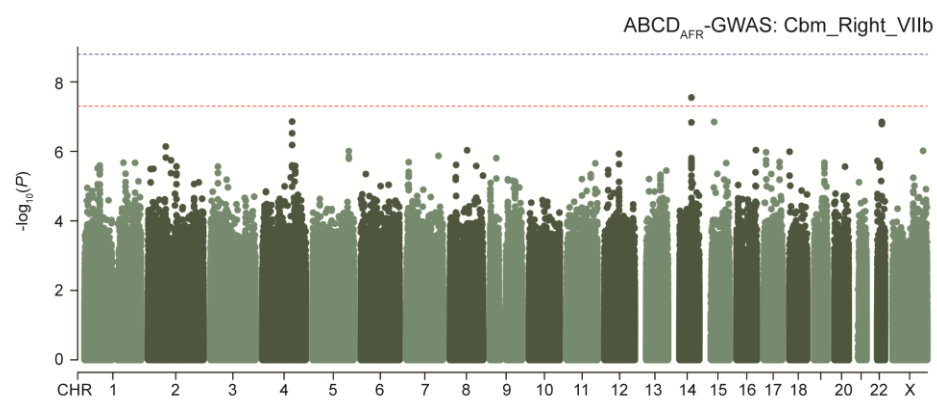
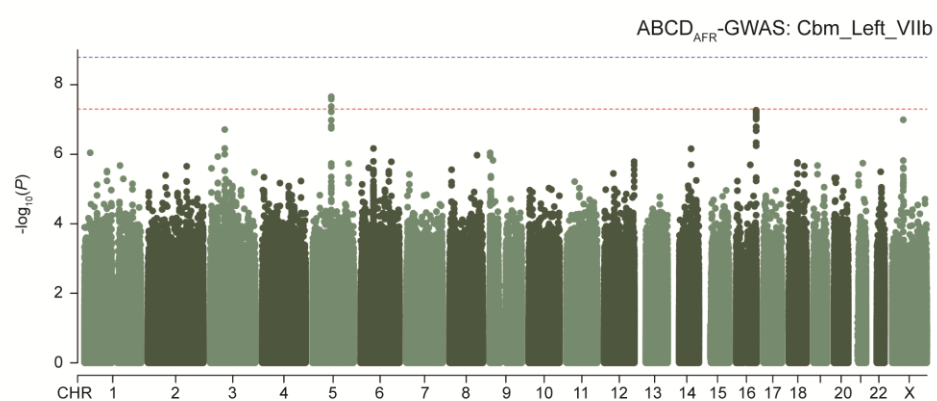
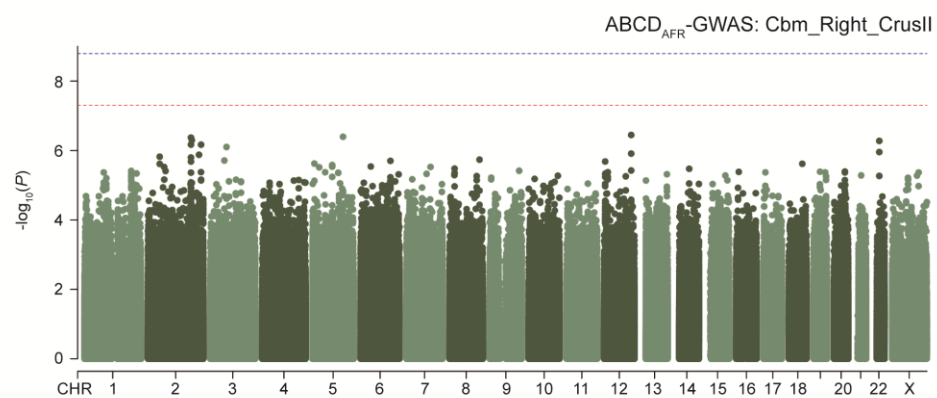


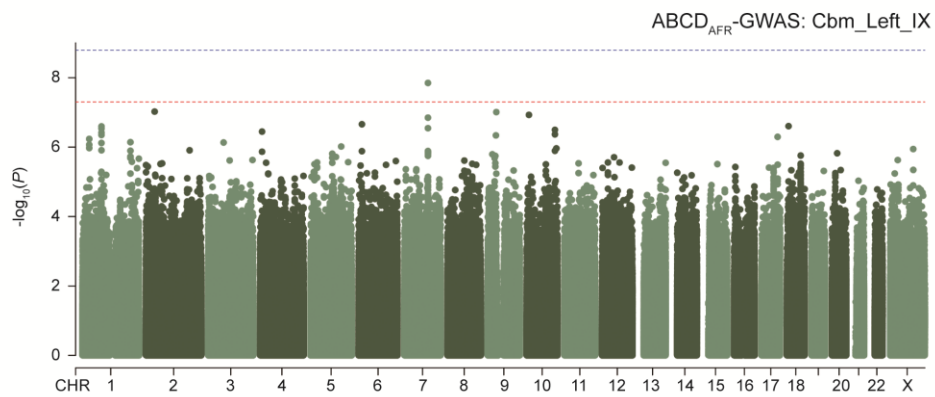
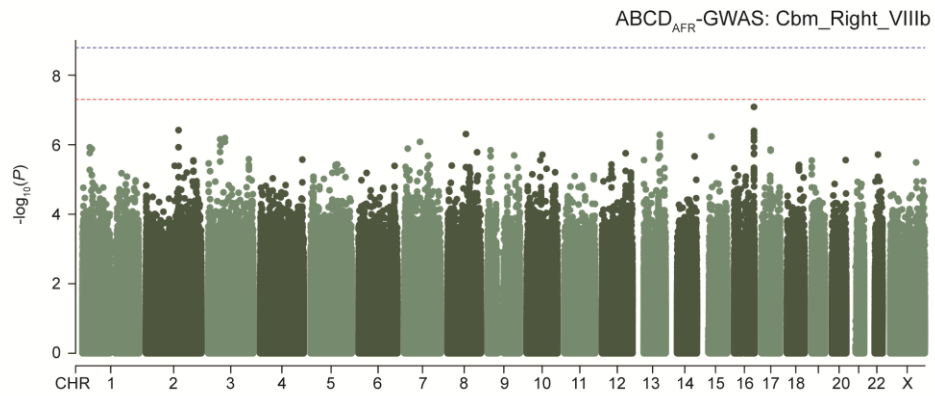
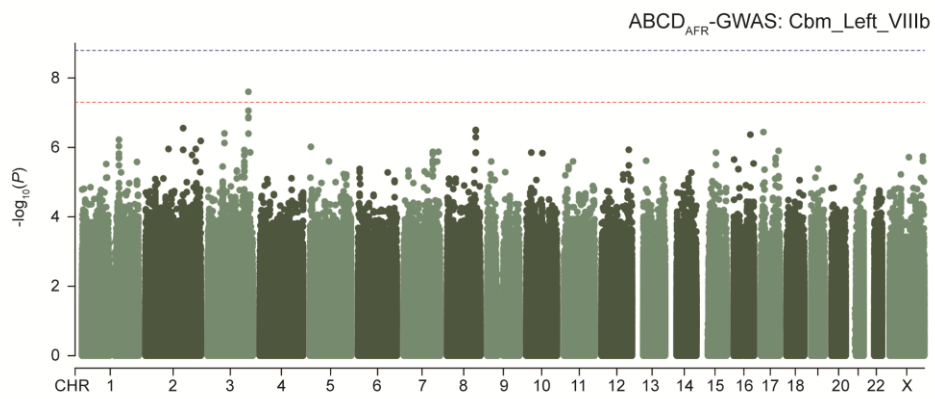
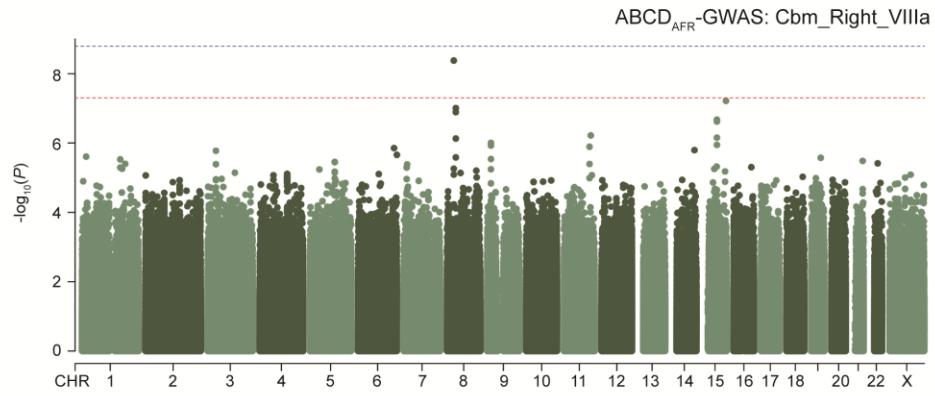


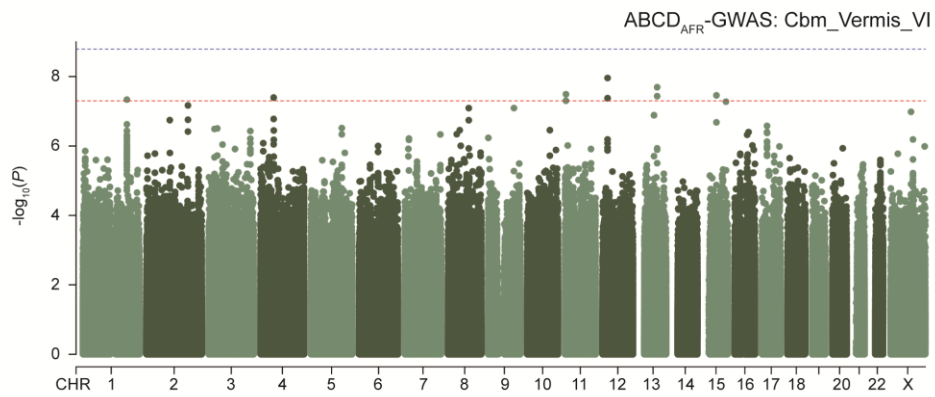
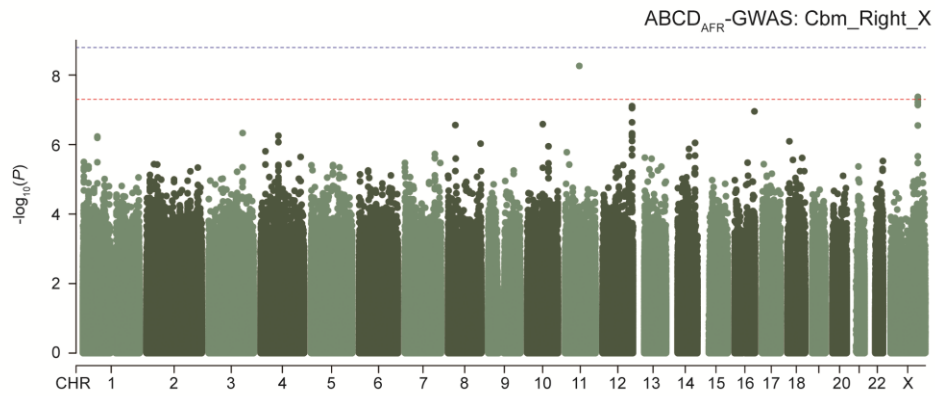
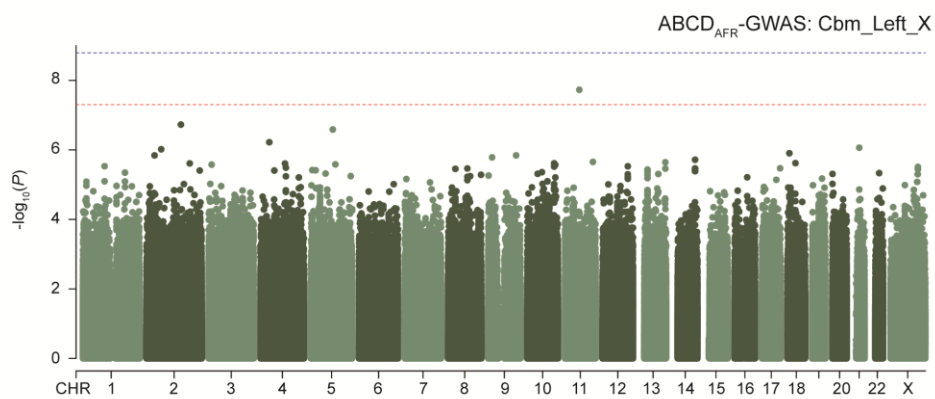
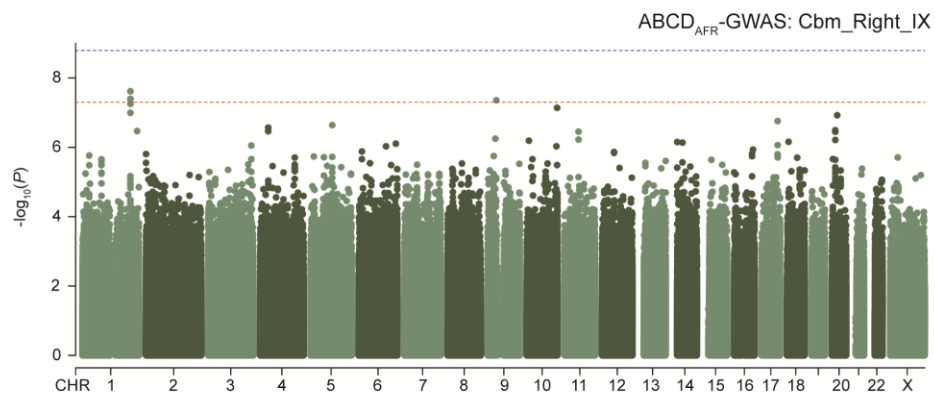


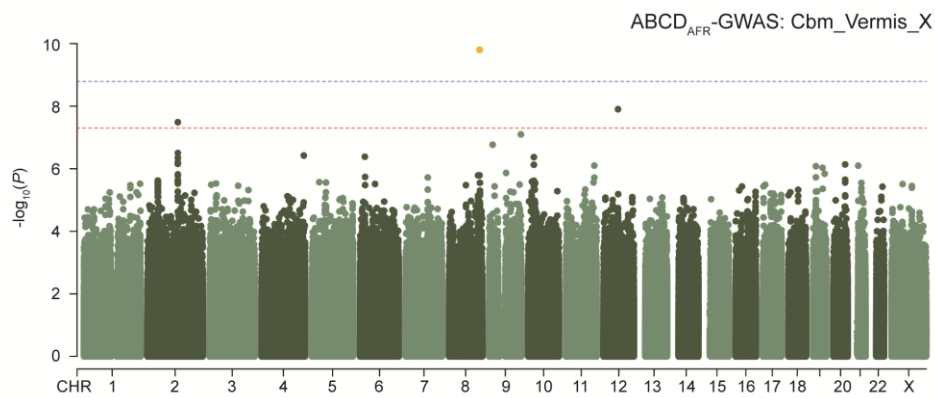
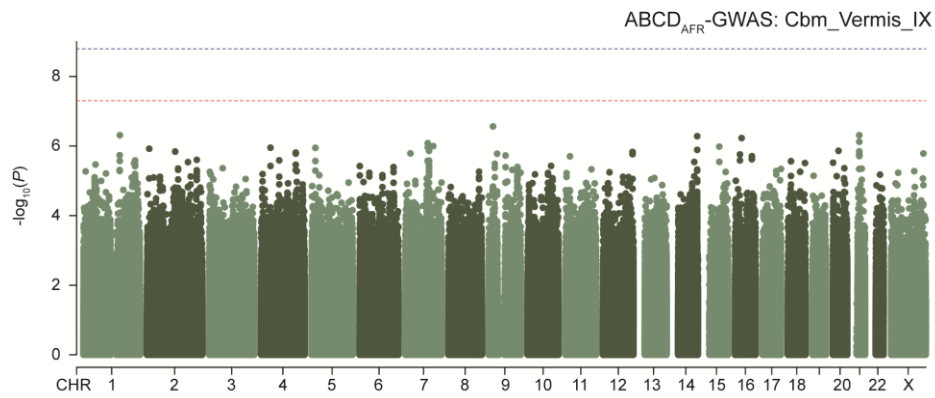
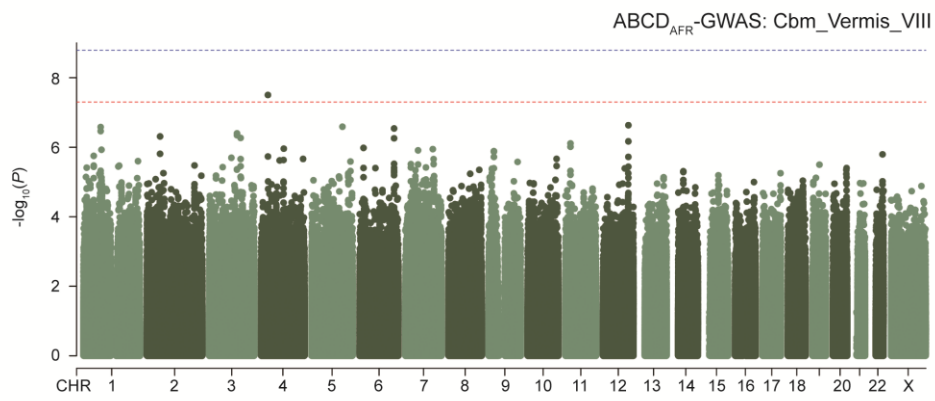
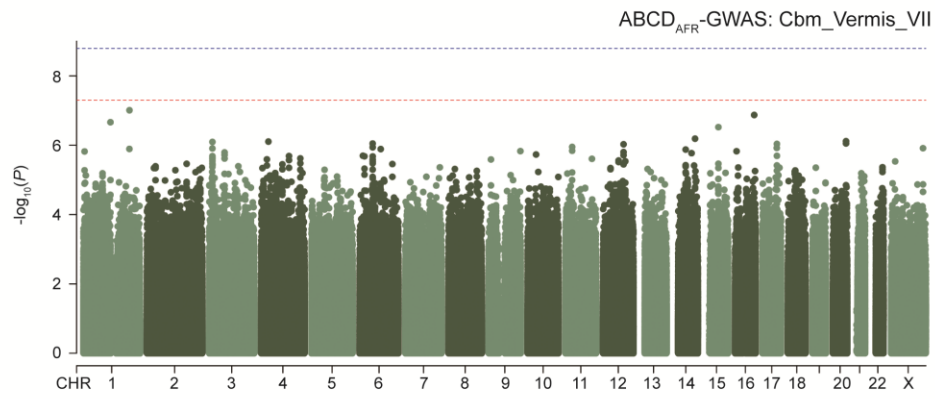


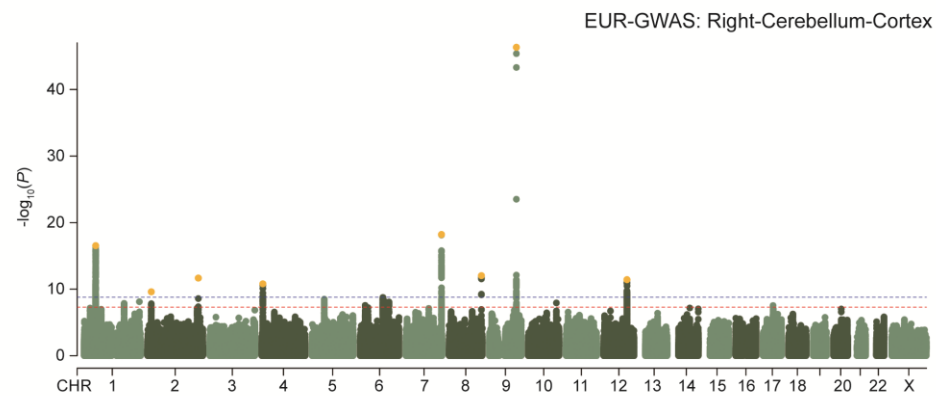
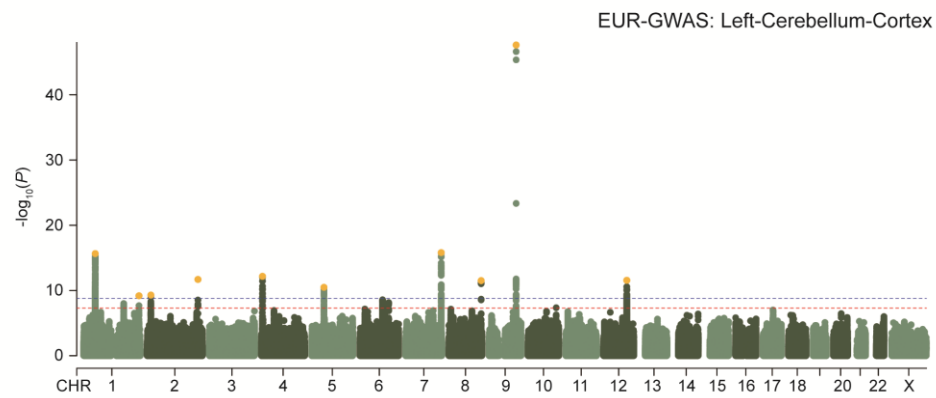
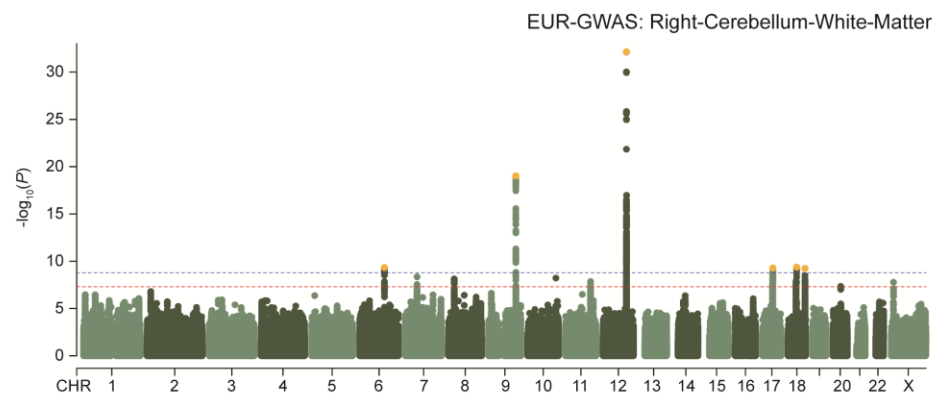
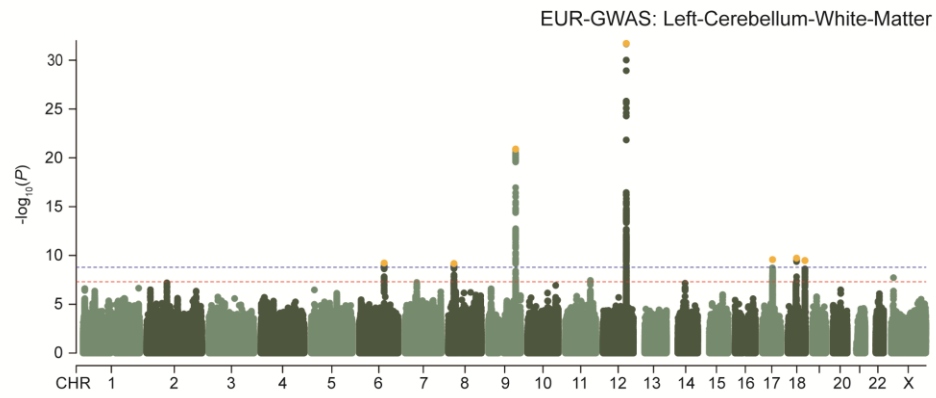




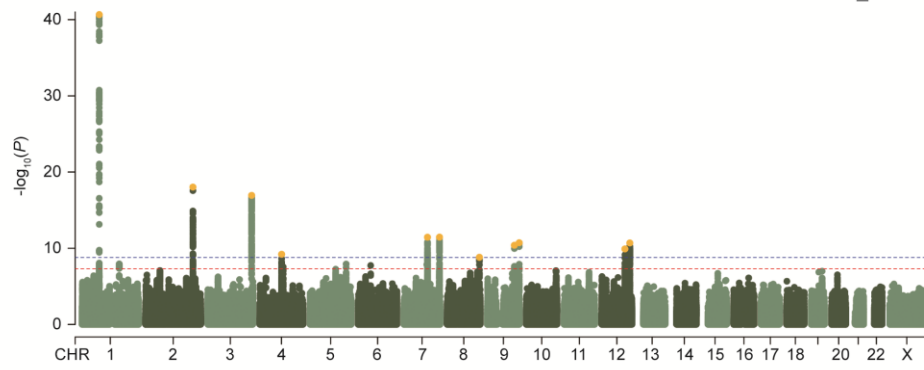




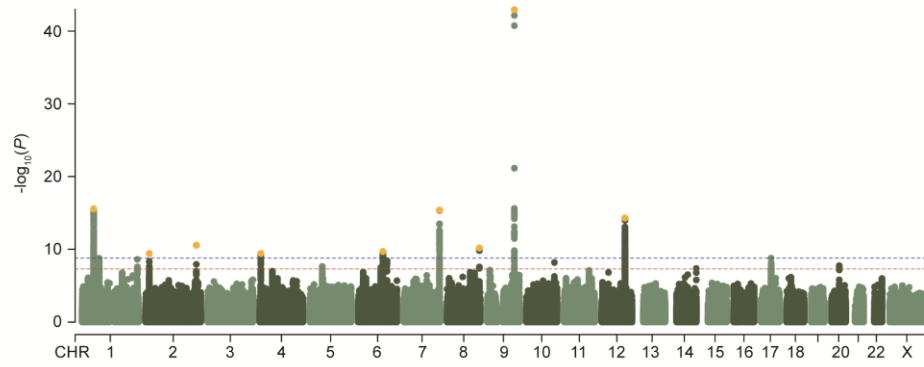




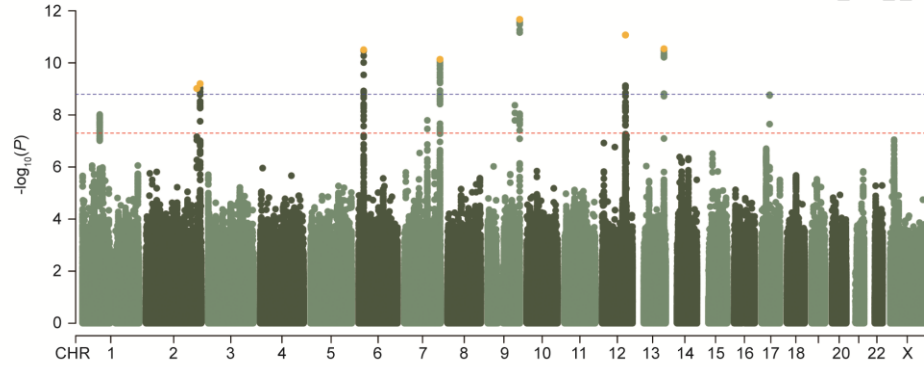
EUR-GWAS: Cbm_Vermis



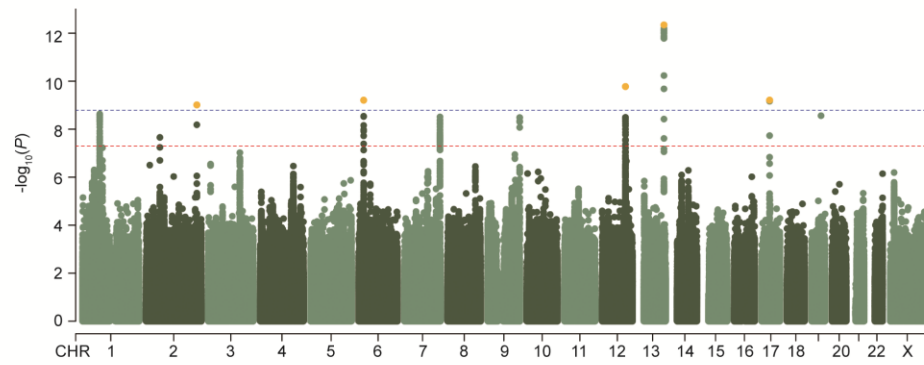
EUR-GWAS: Cbm_total

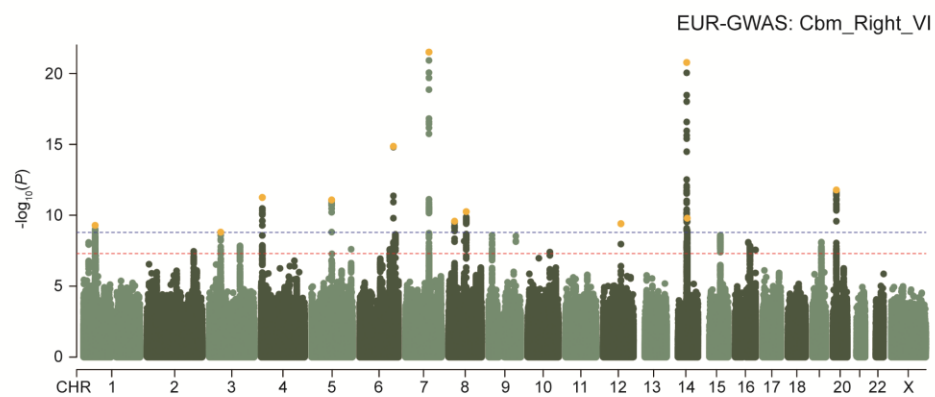
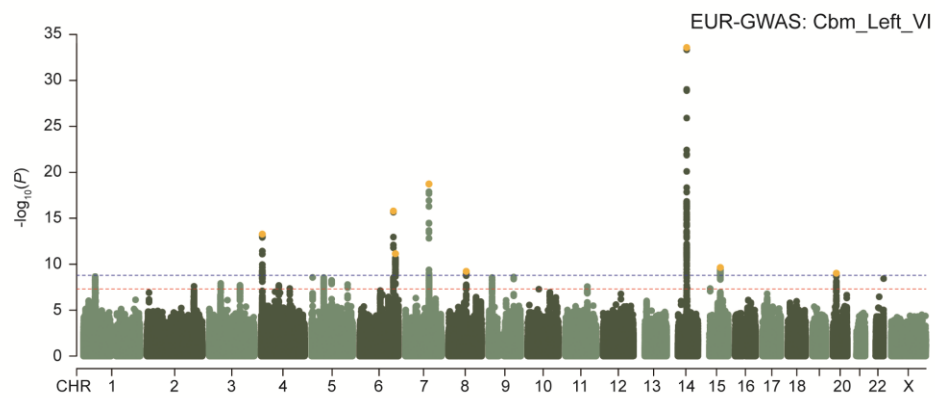
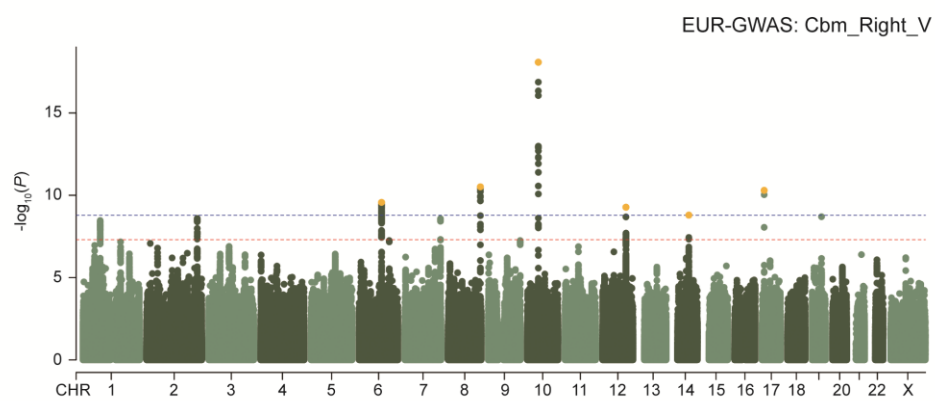
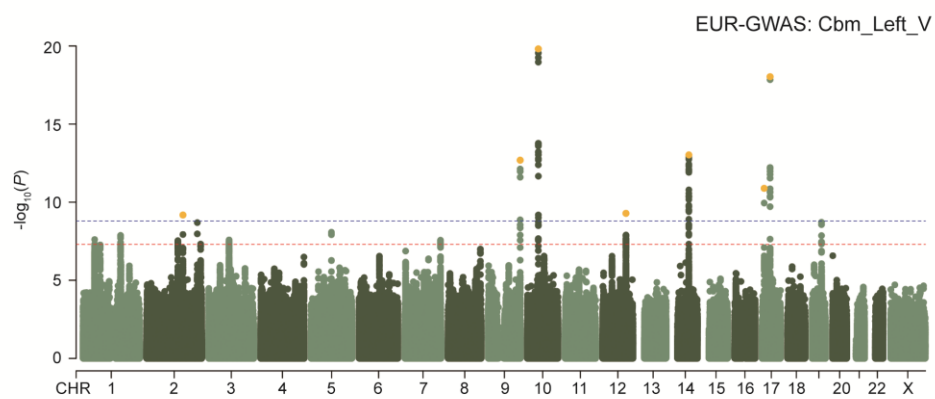


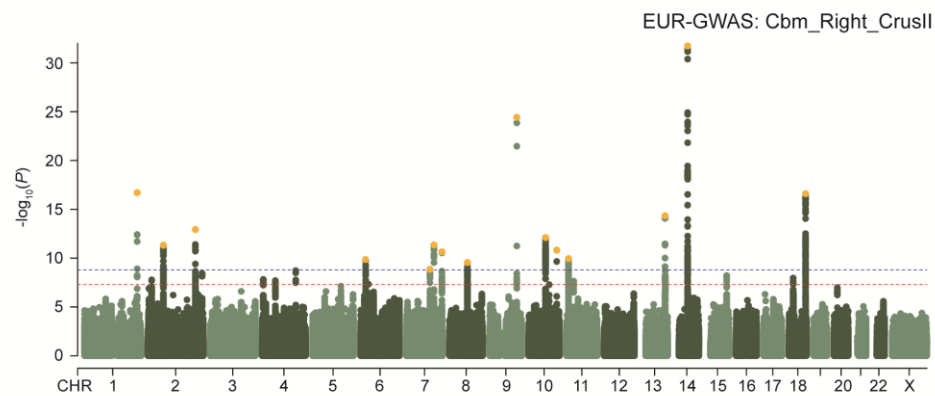
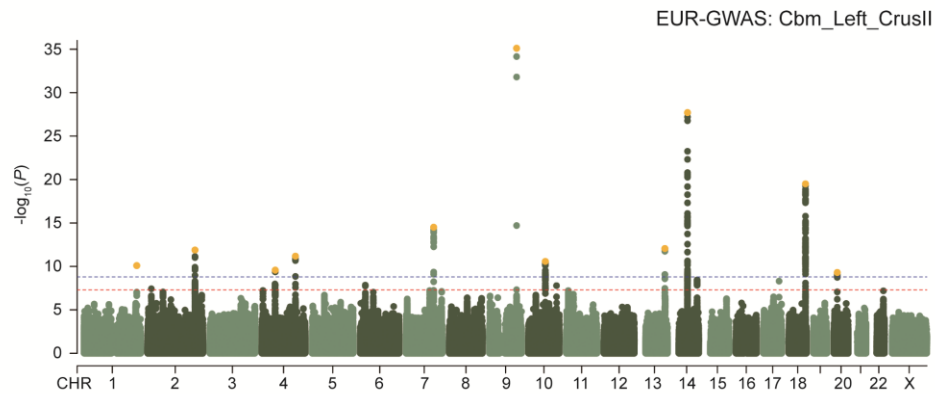
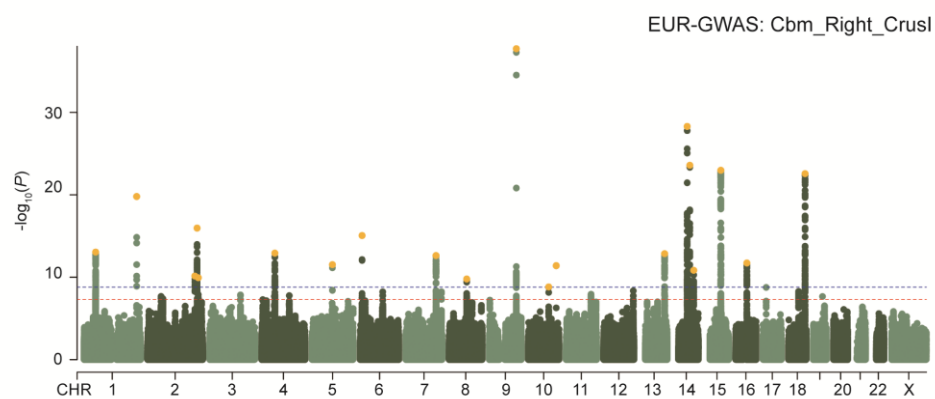
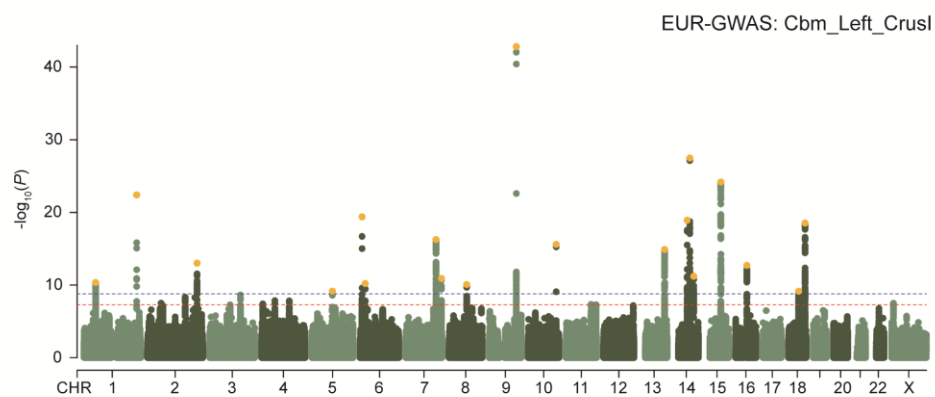
EUR-GWAS: Cbm_Left_I_IV

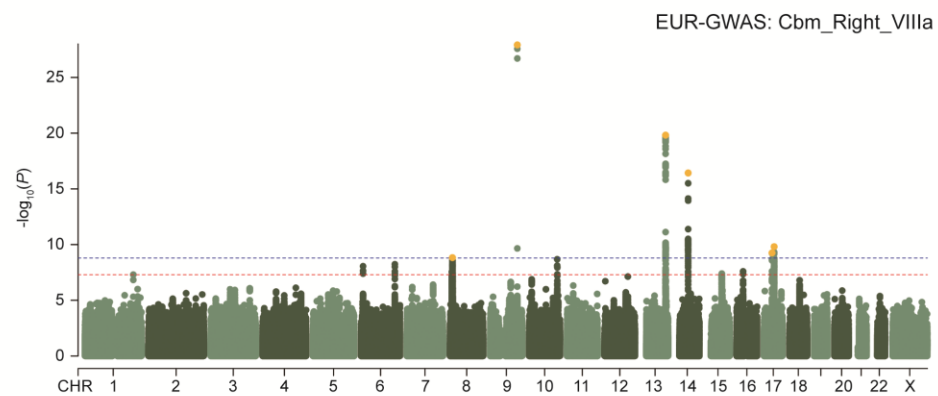
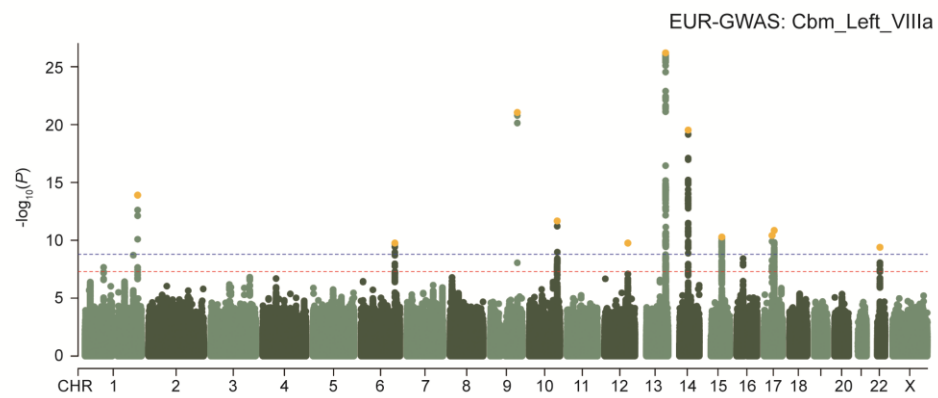
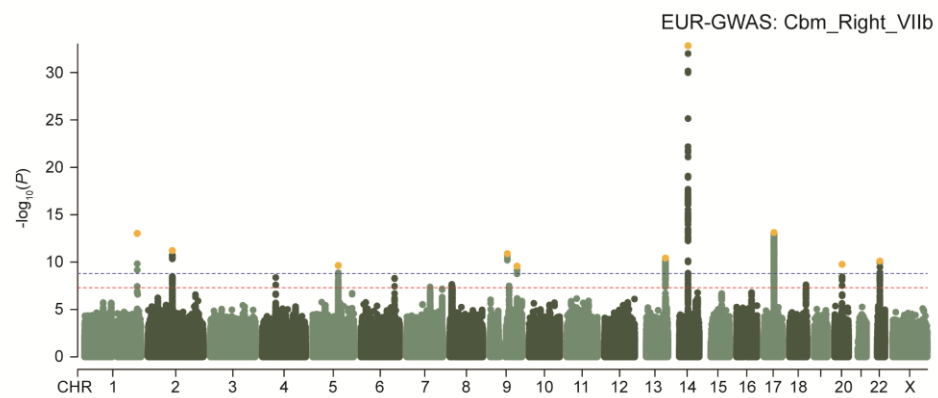
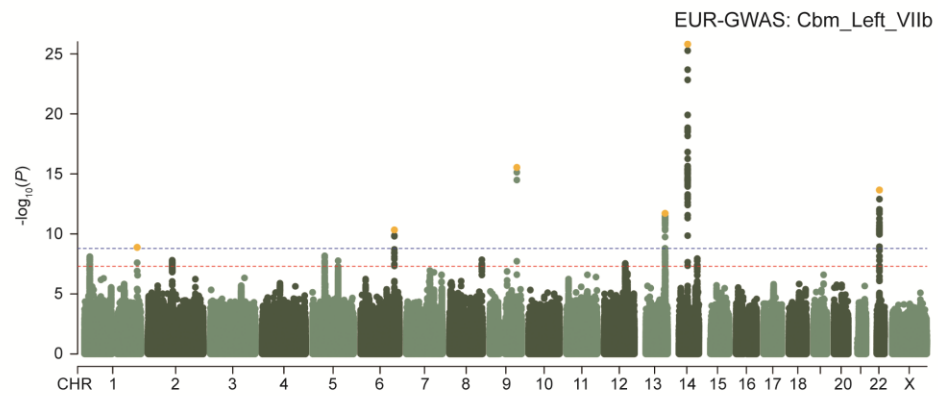


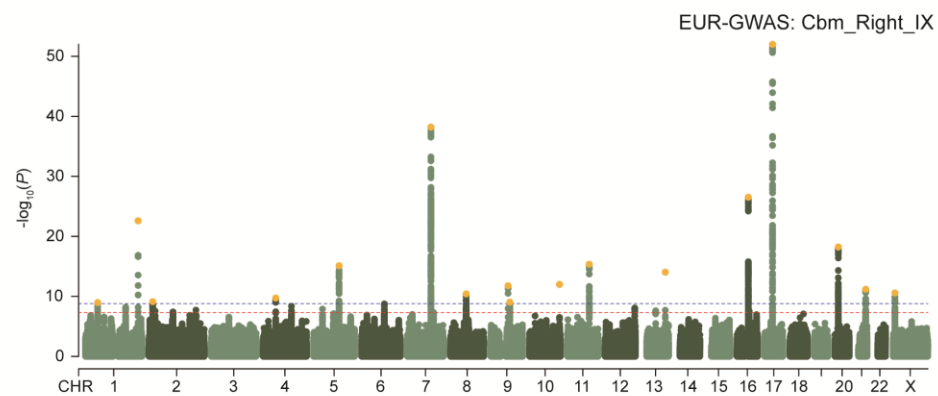
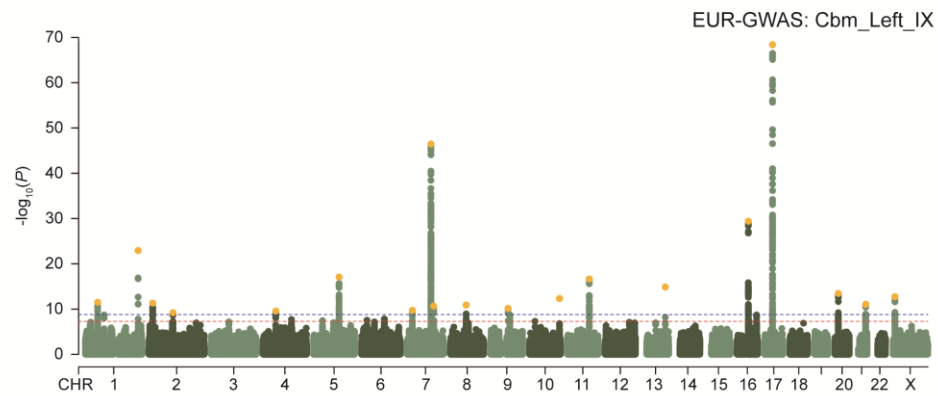
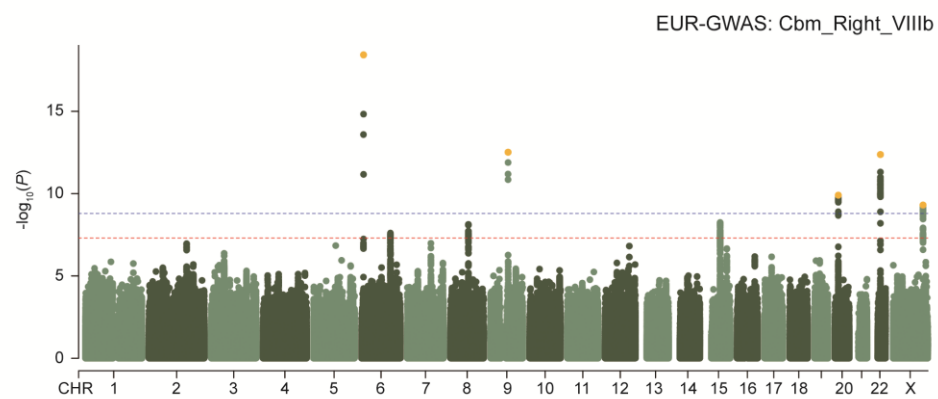
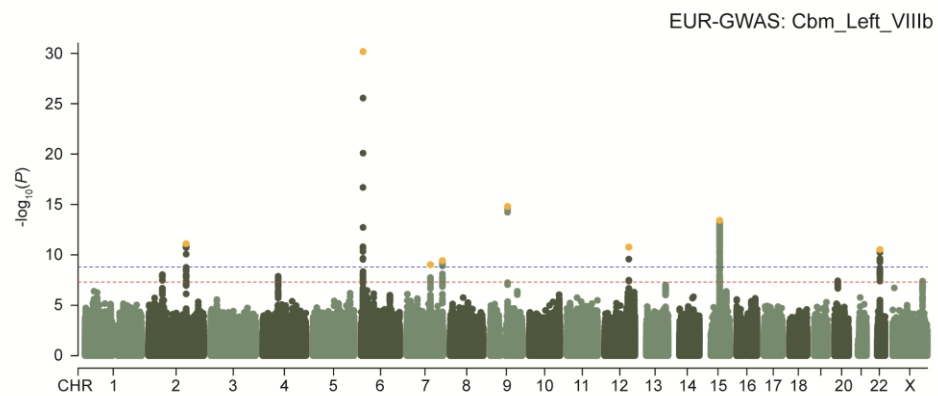
EUR-GWAS: Cbm_Right_I_IV

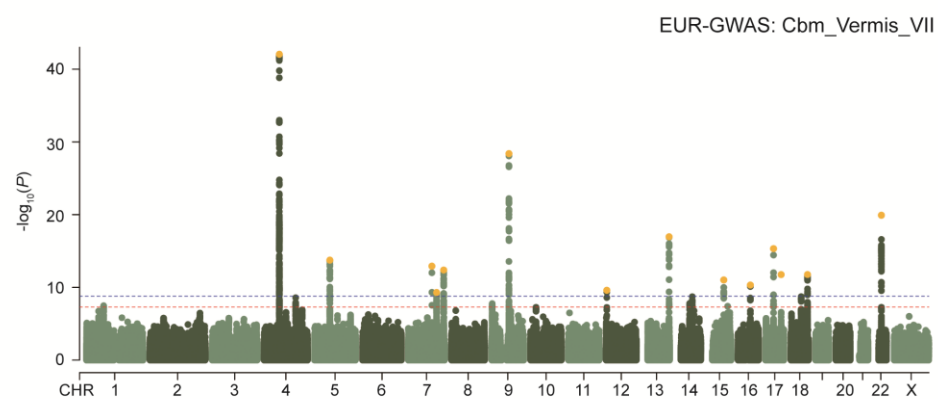
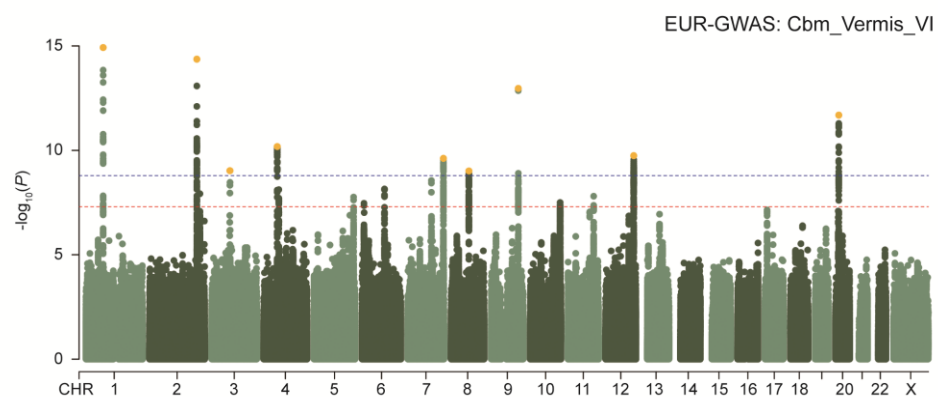
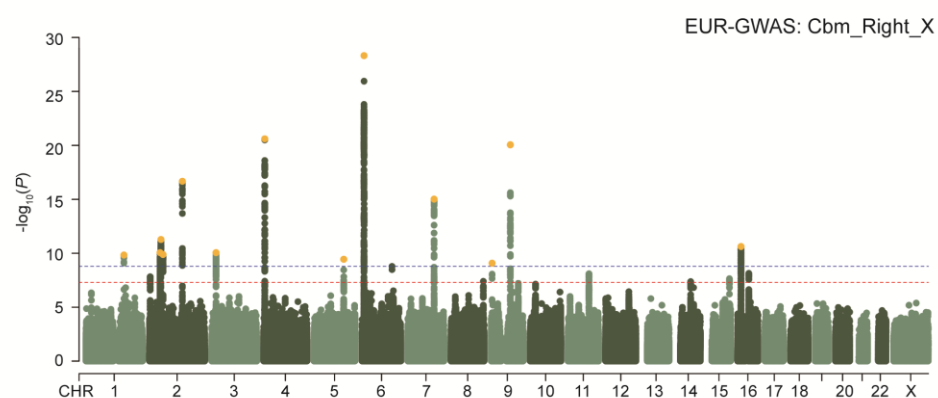
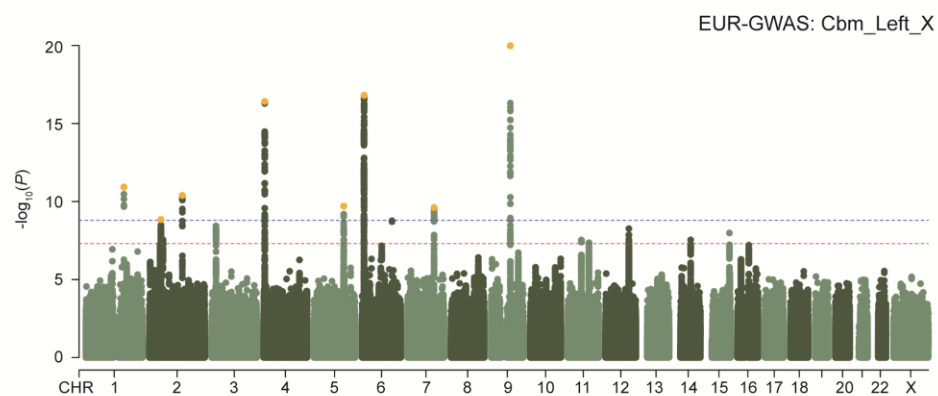


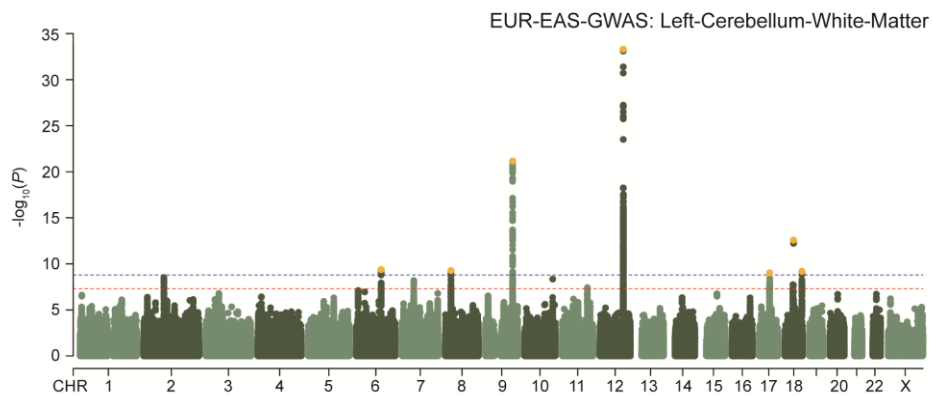
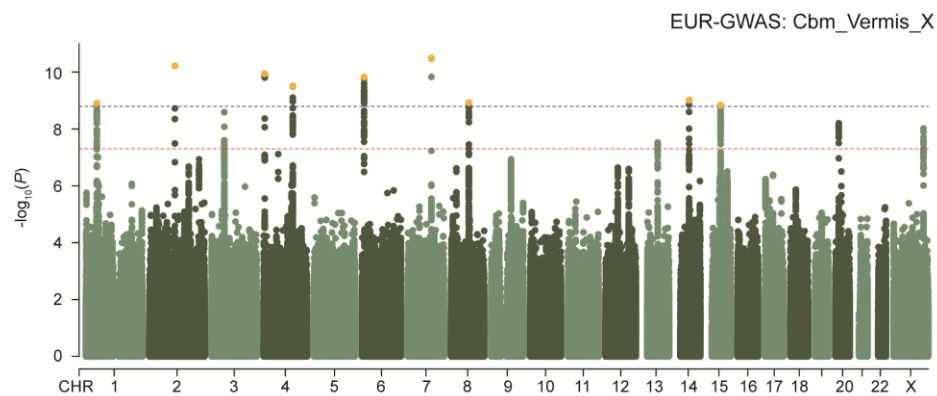
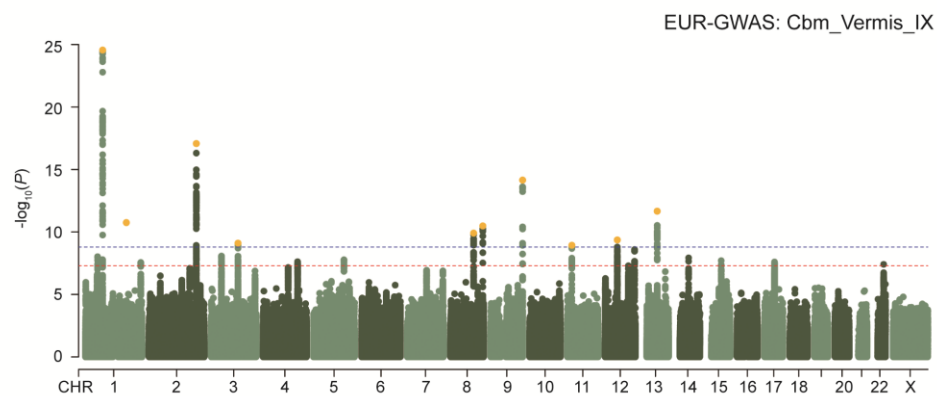
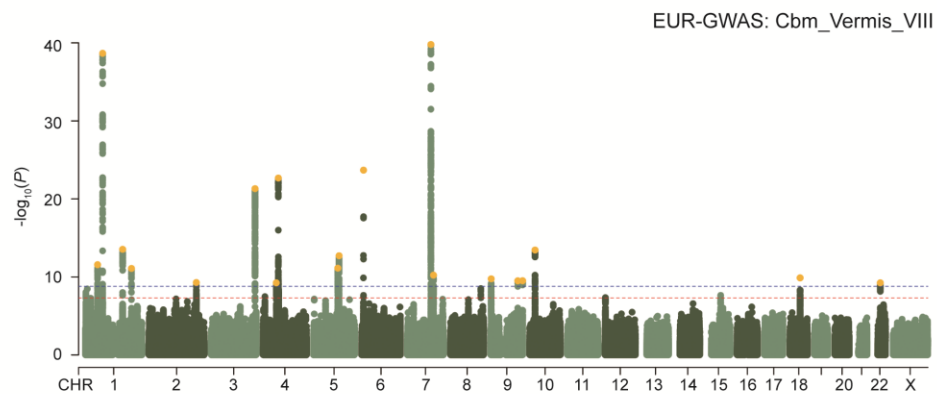


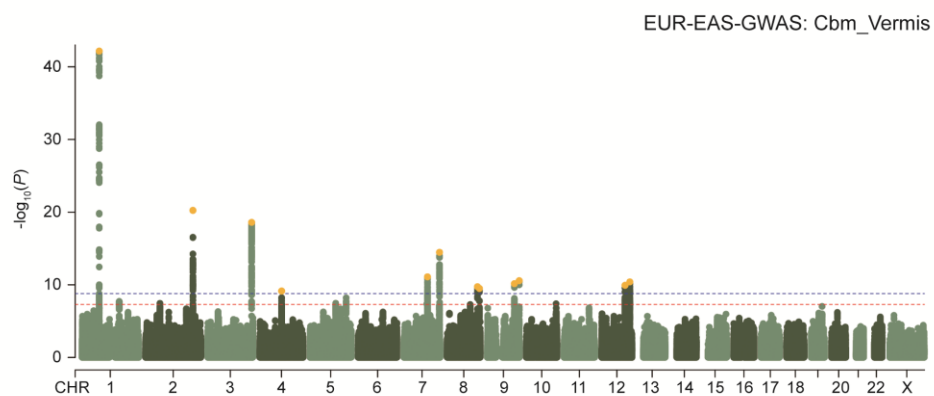
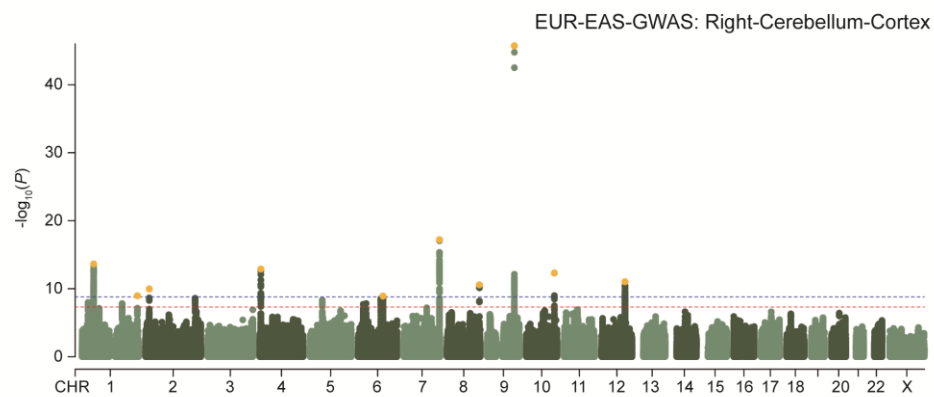
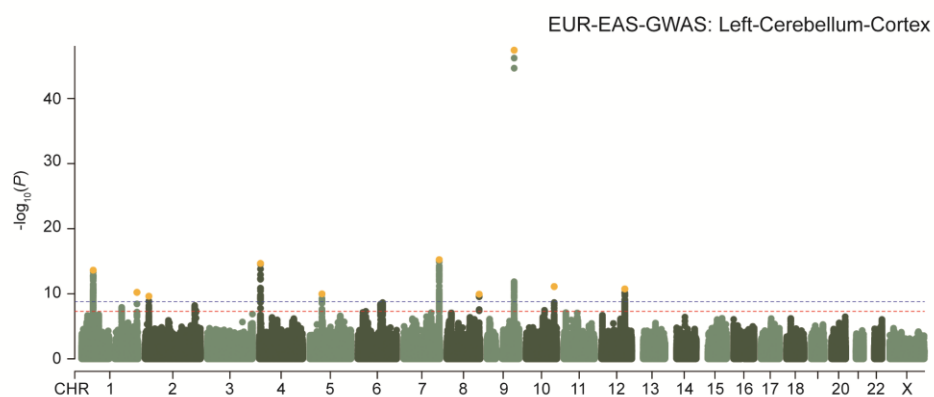
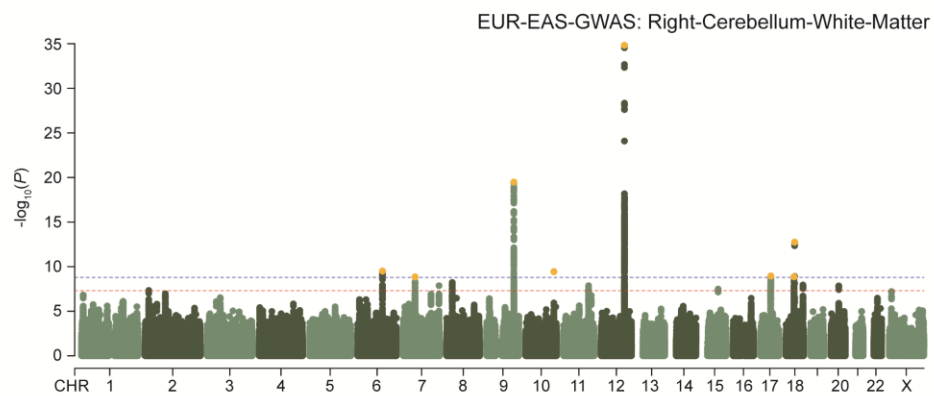


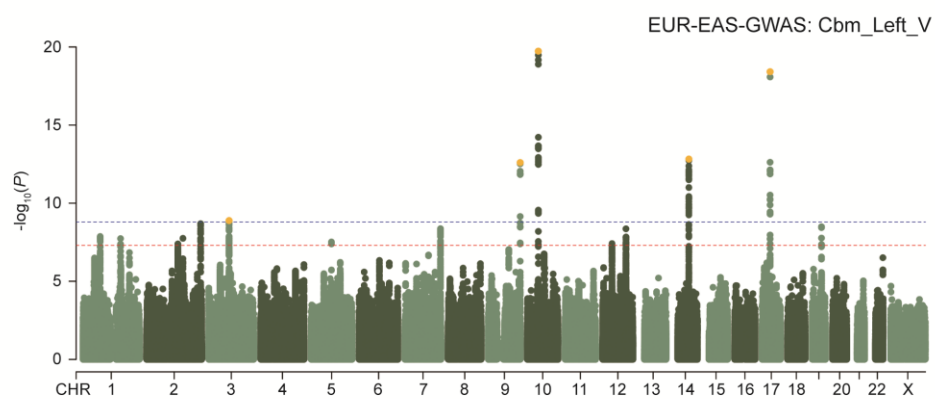
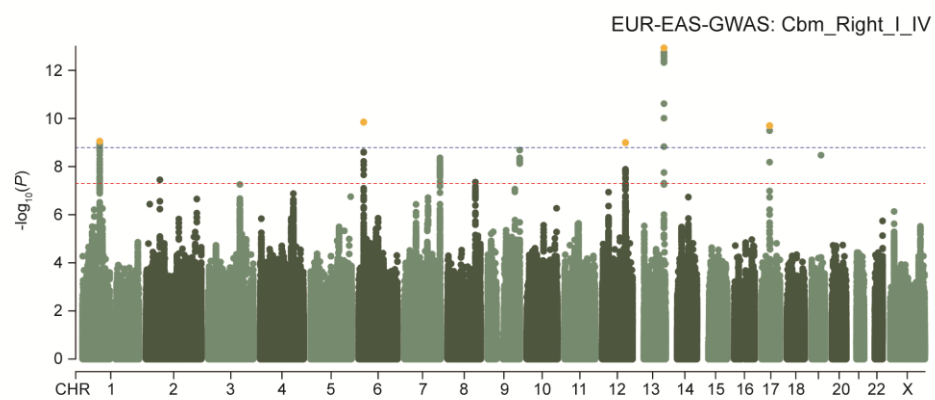
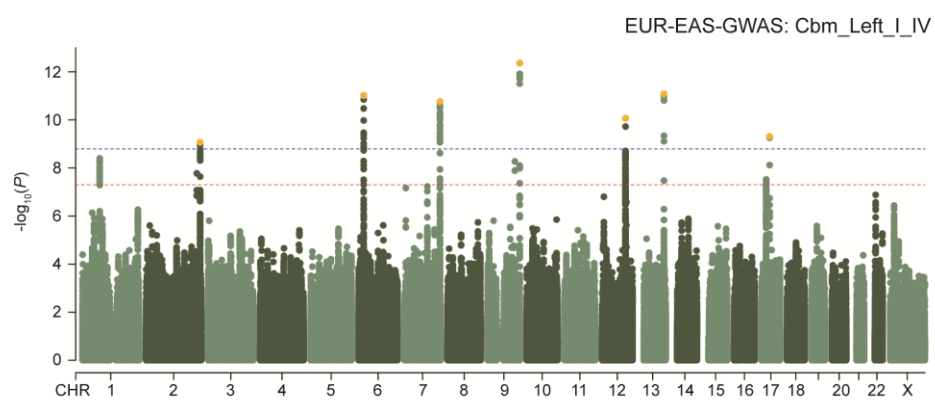
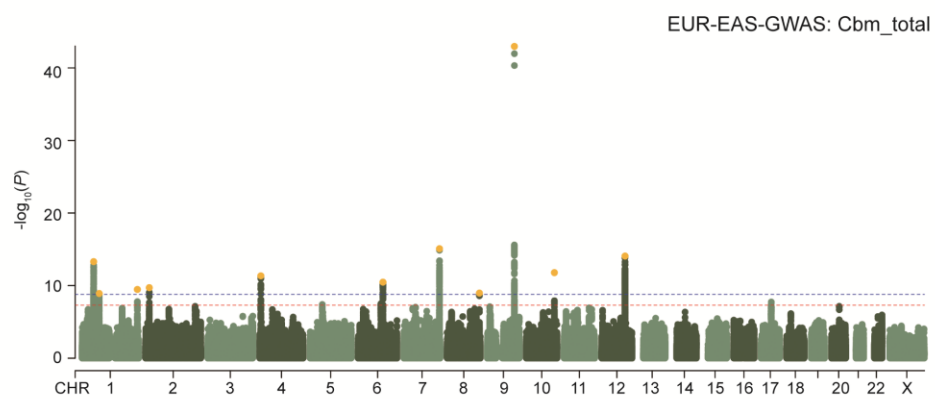


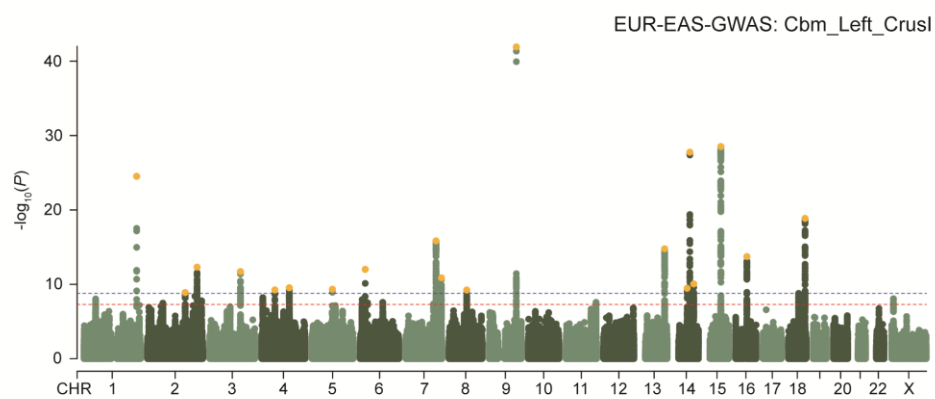
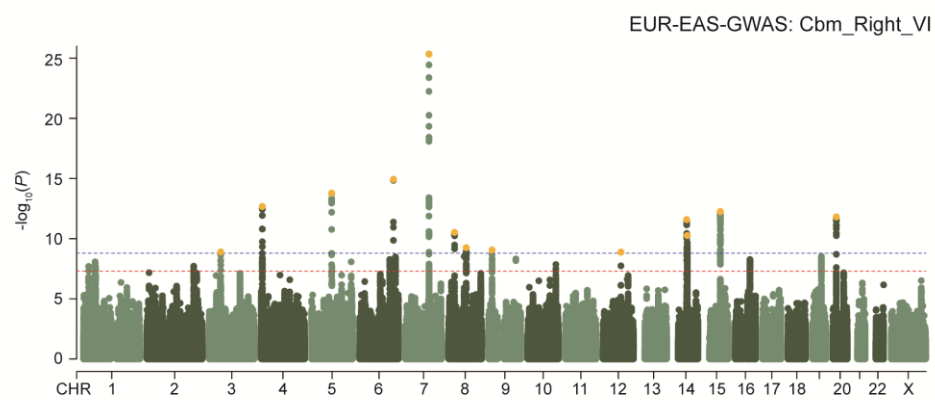
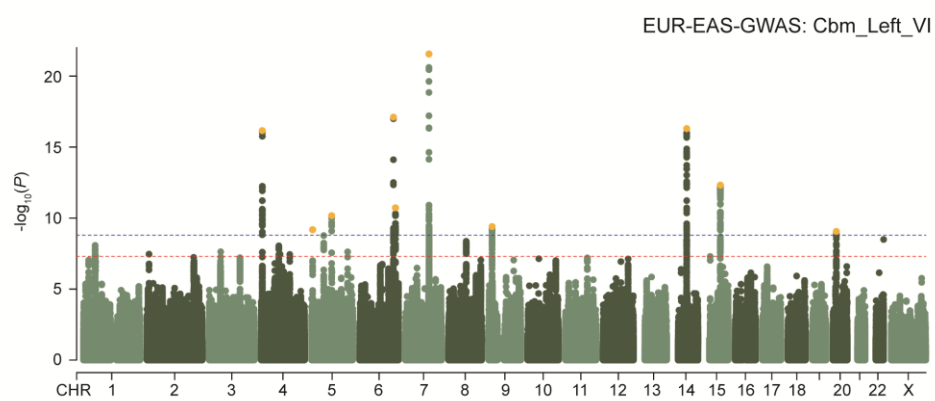
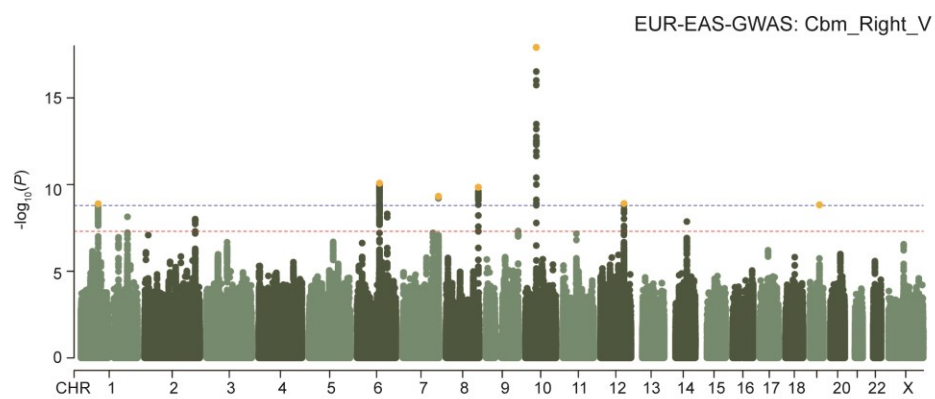


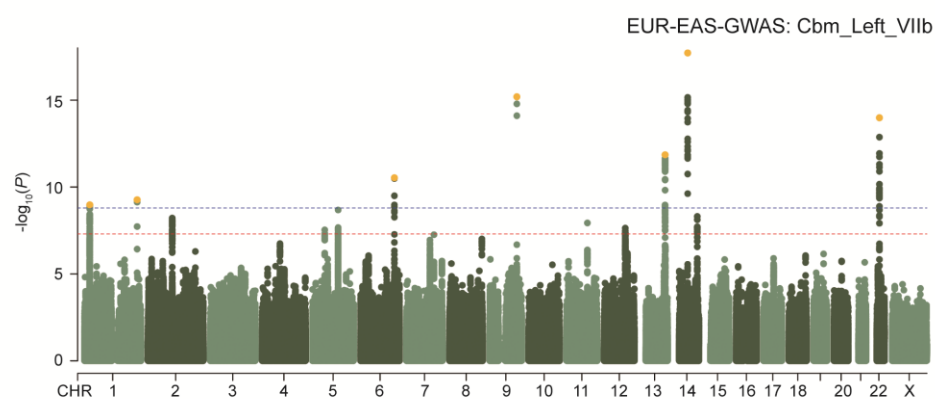
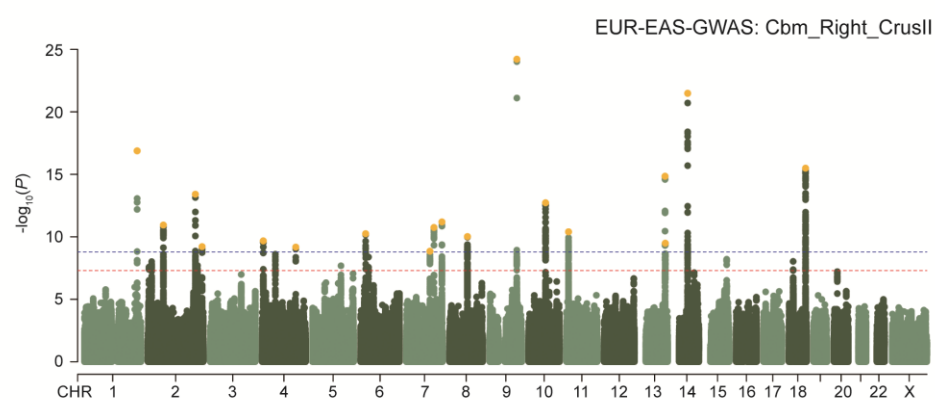
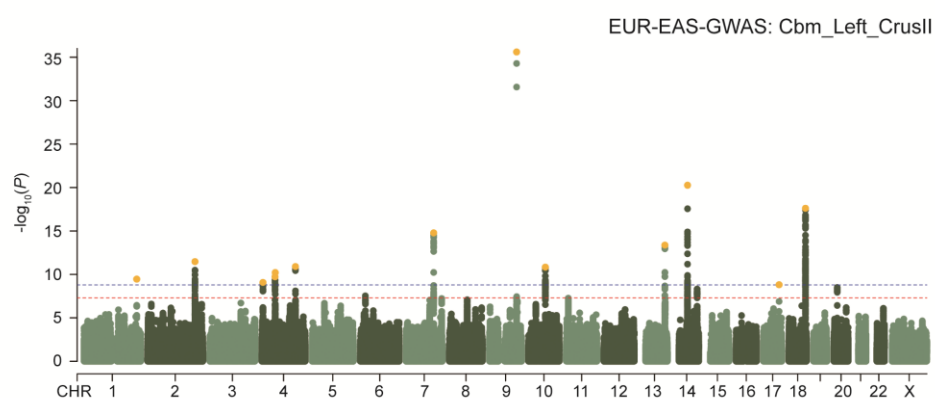
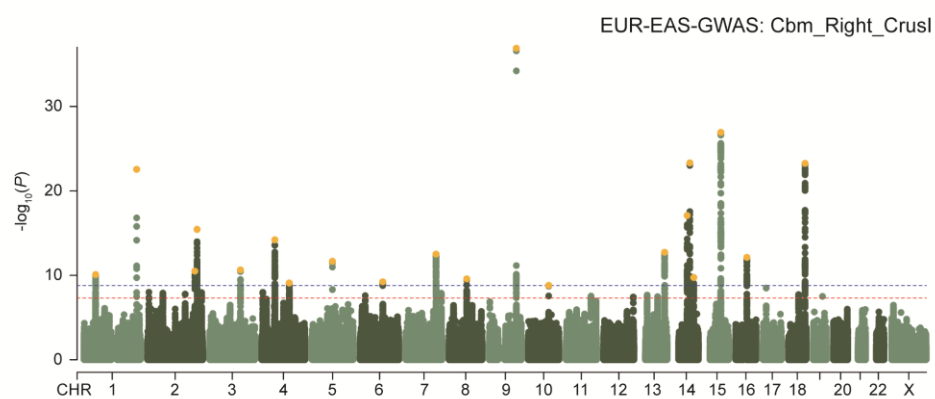


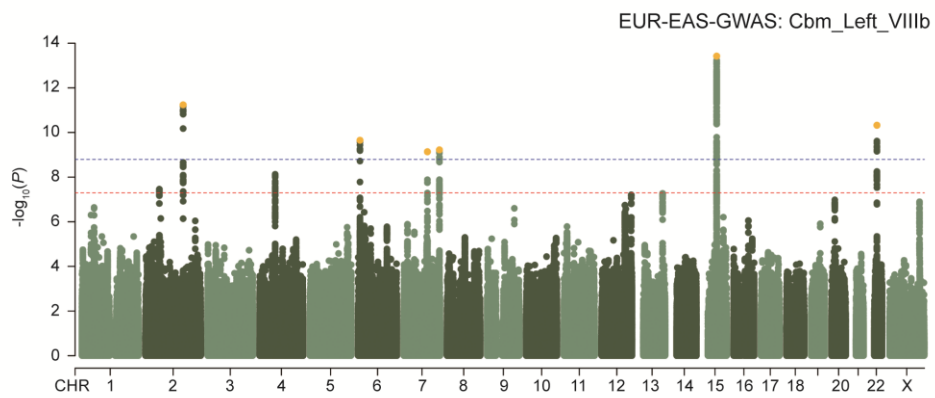
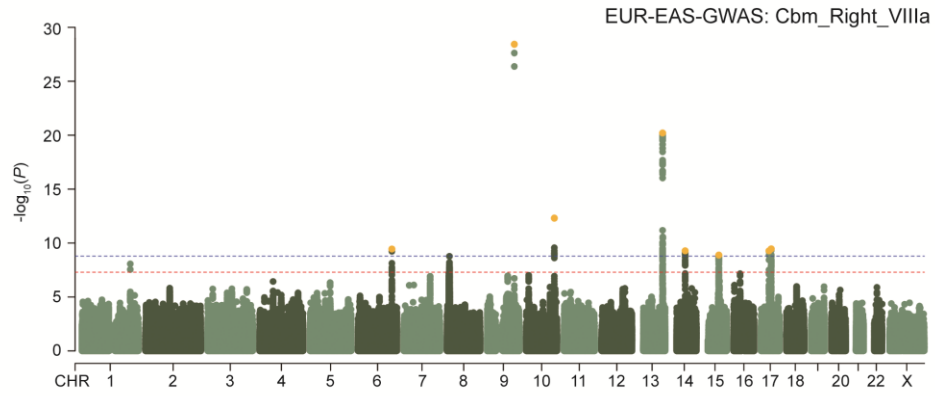
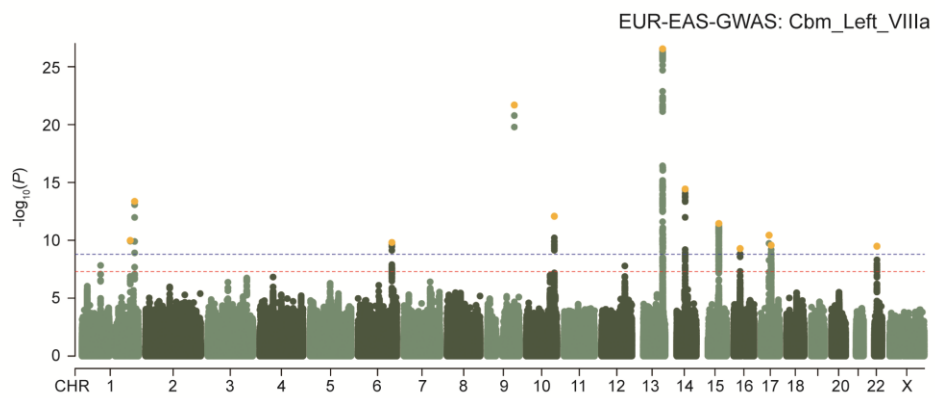
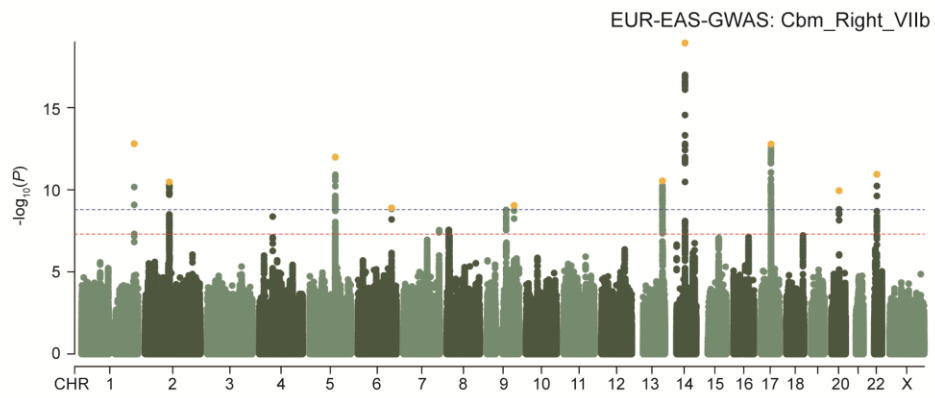


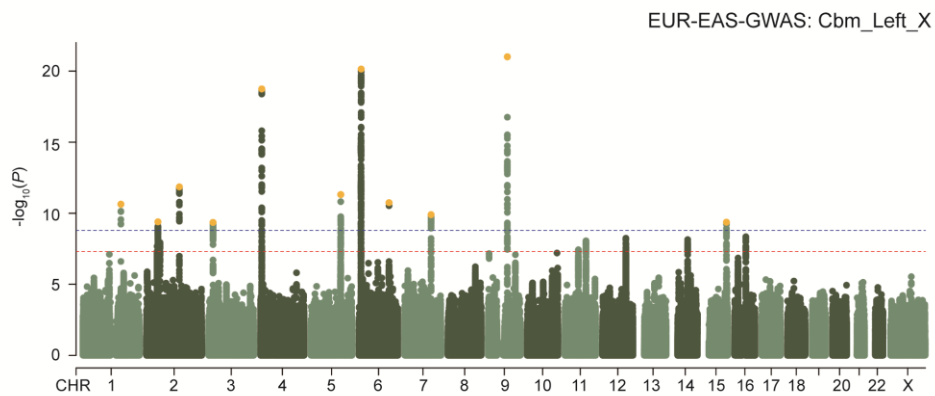
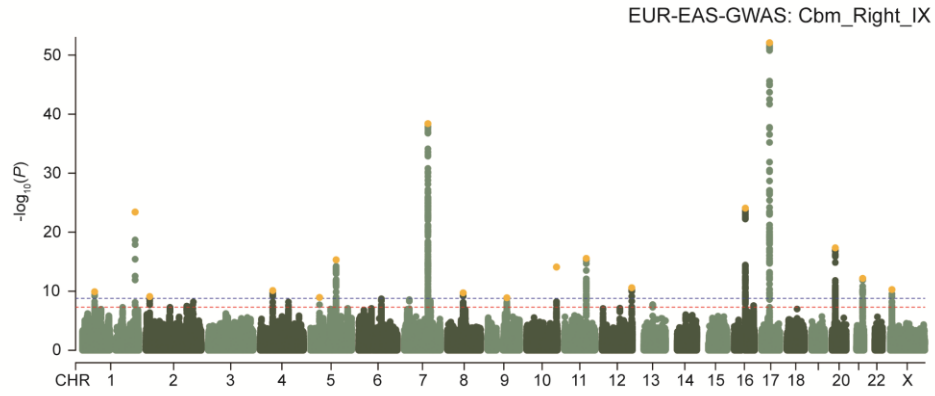
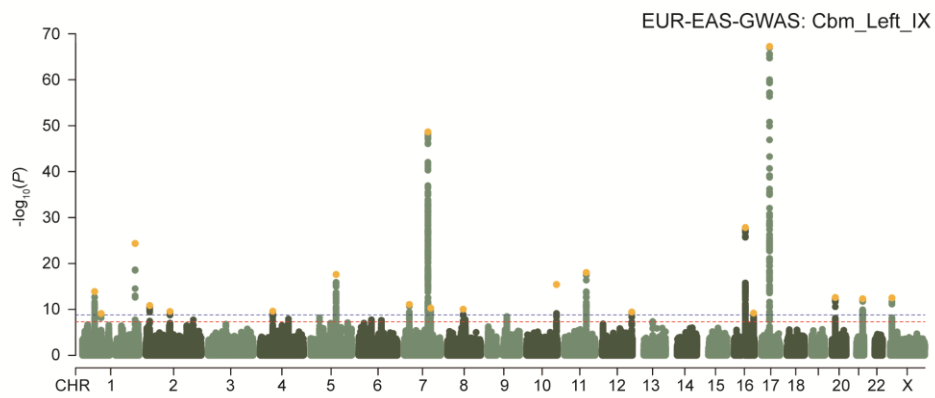
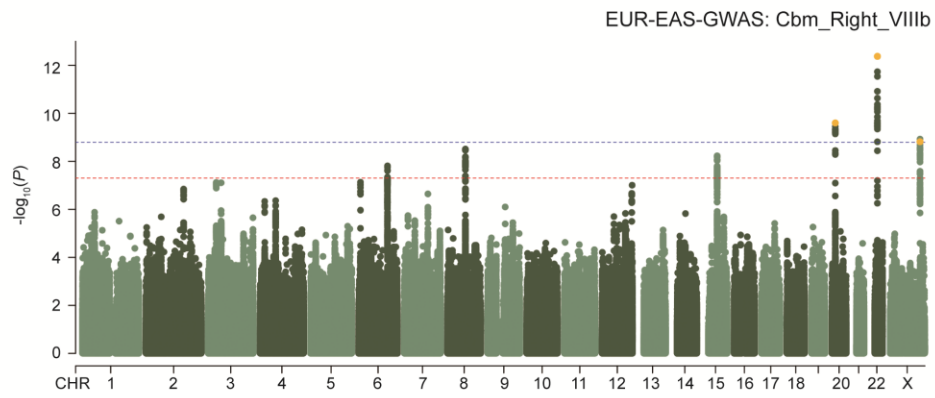


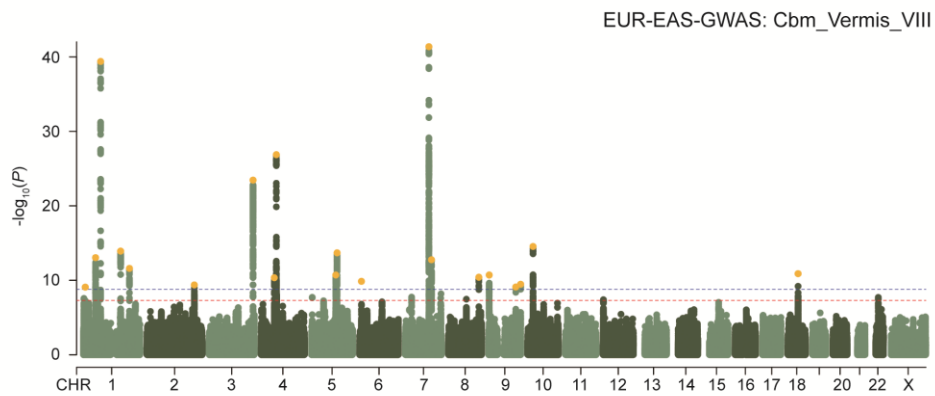
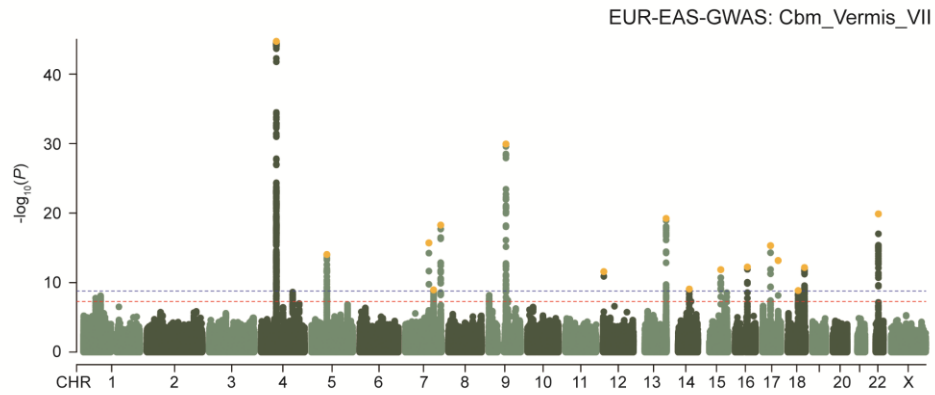
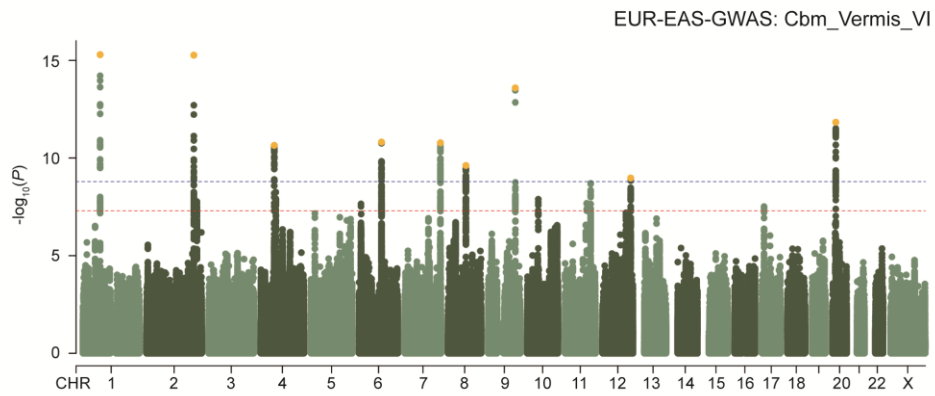
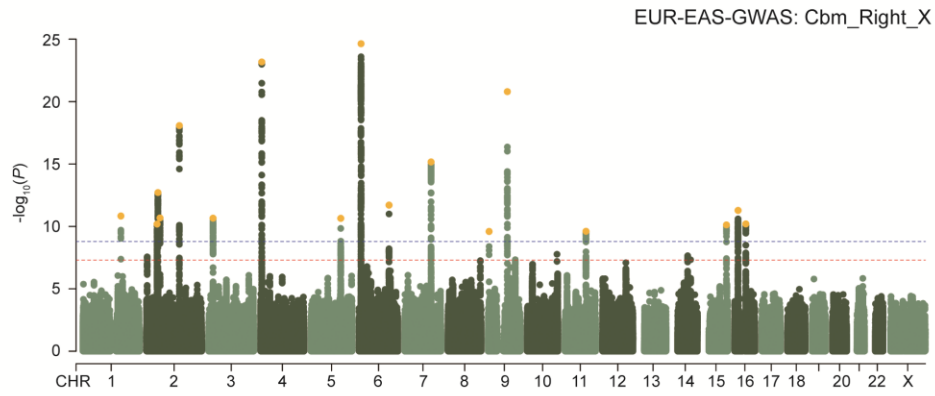


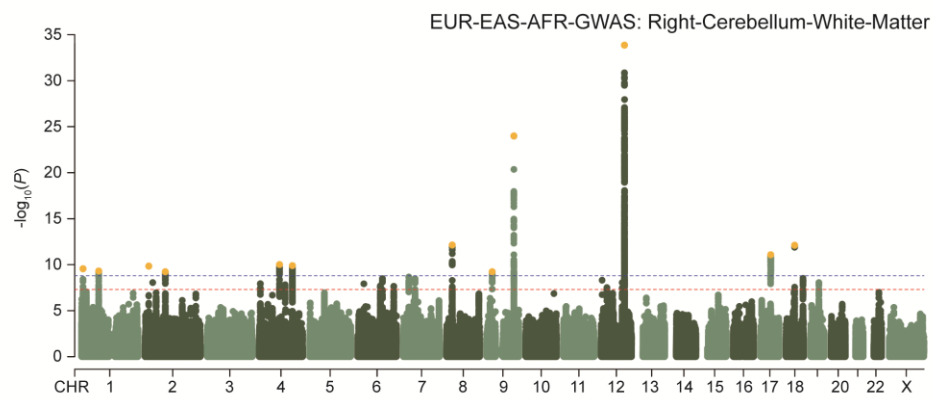
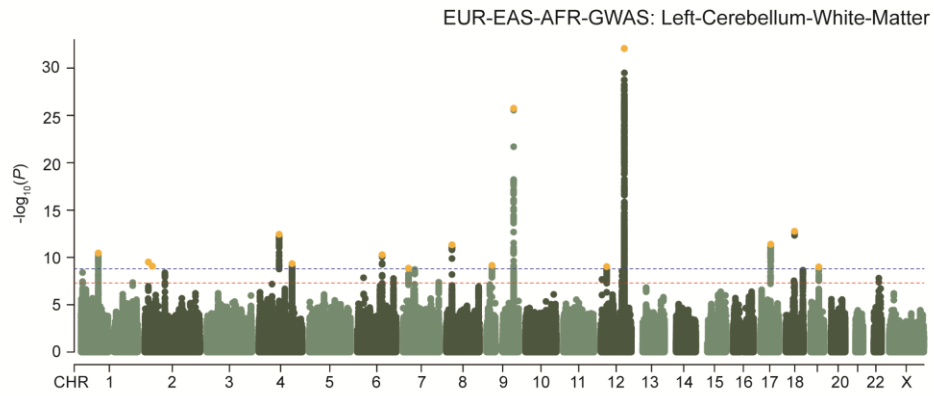
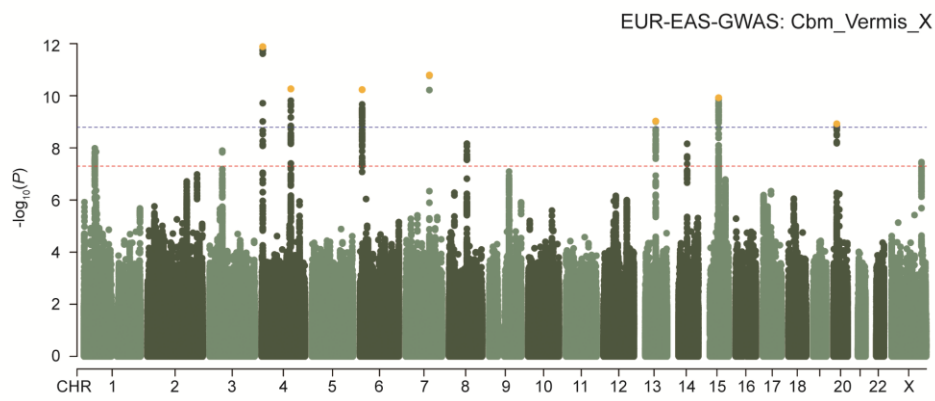
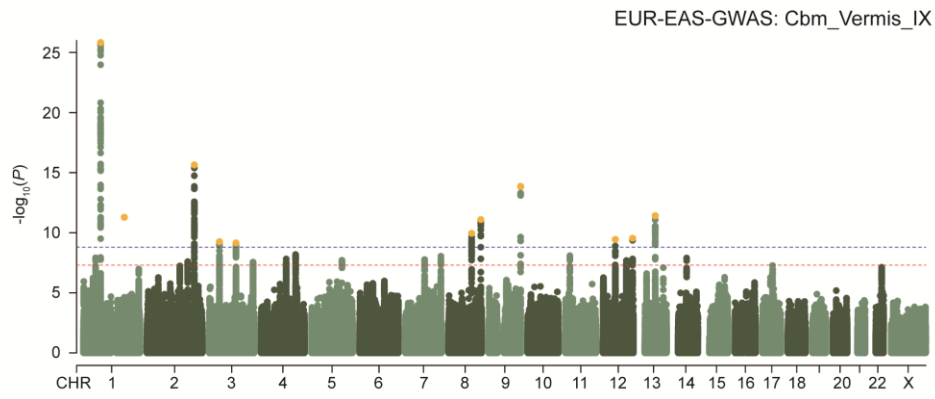


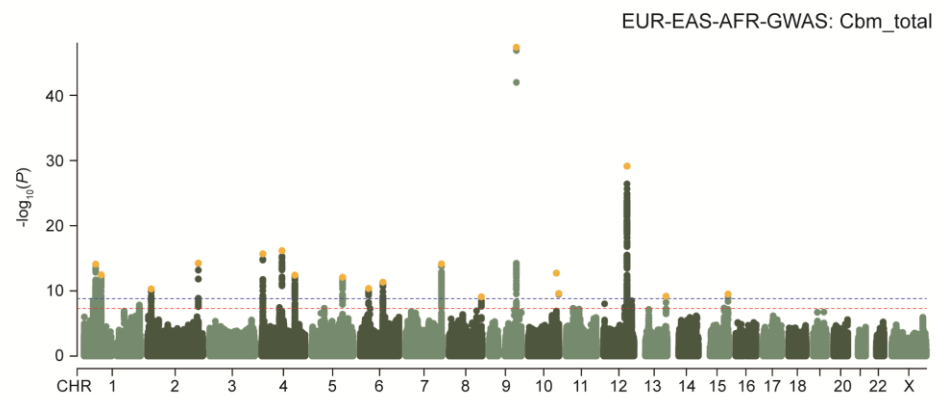
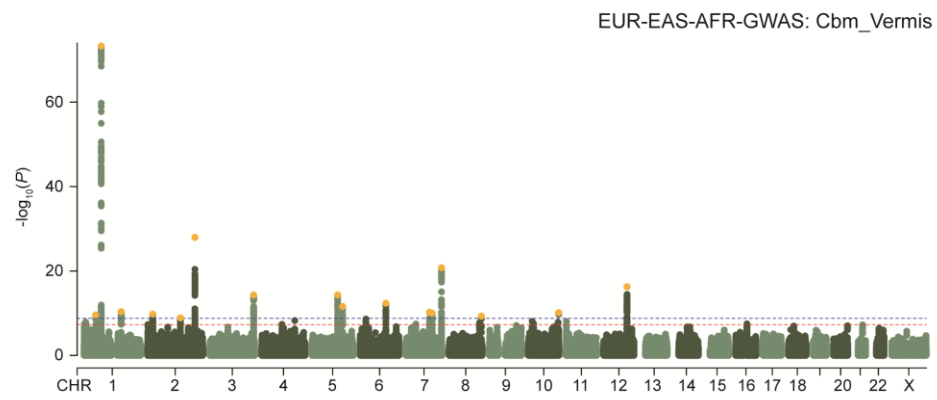
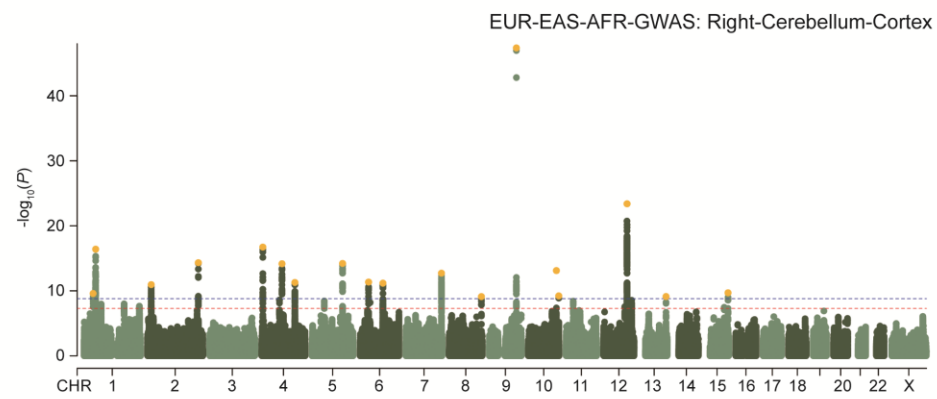
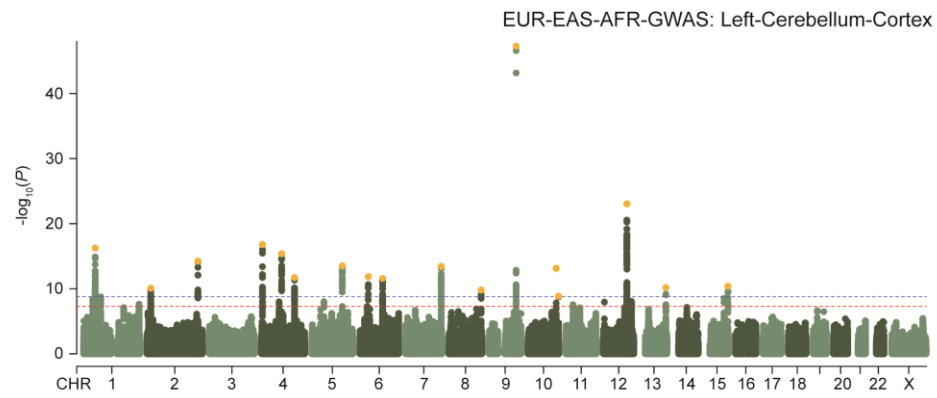


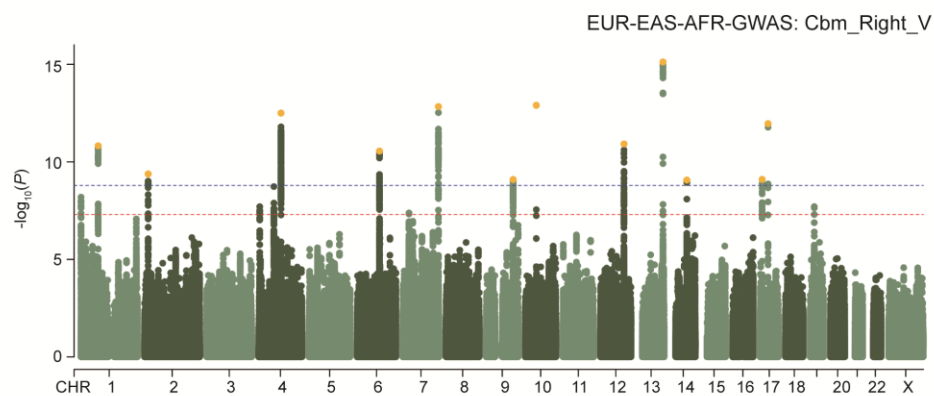
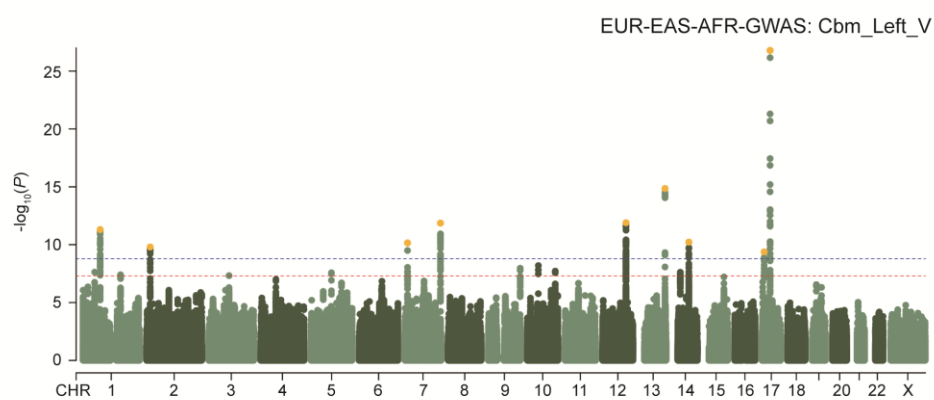
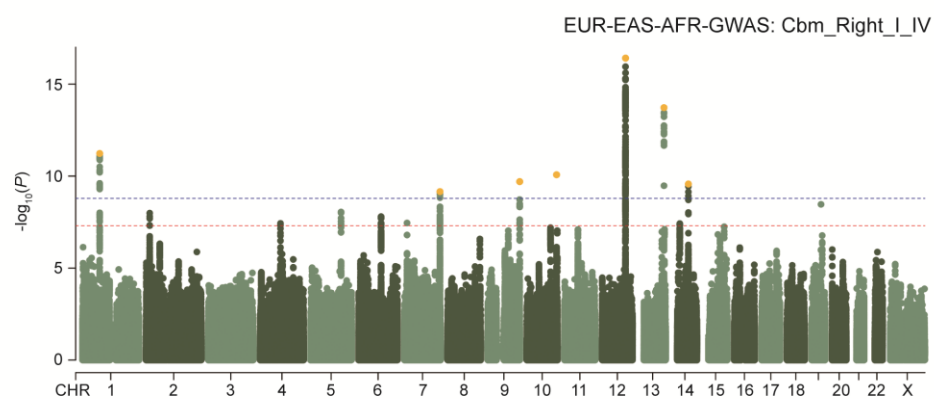
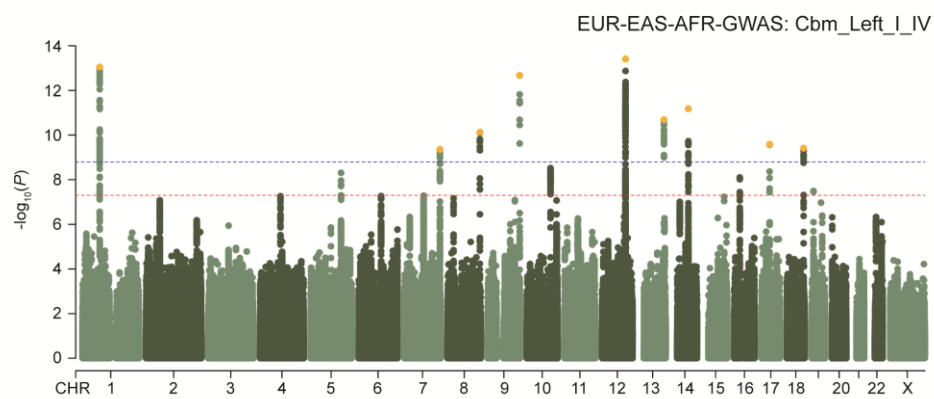


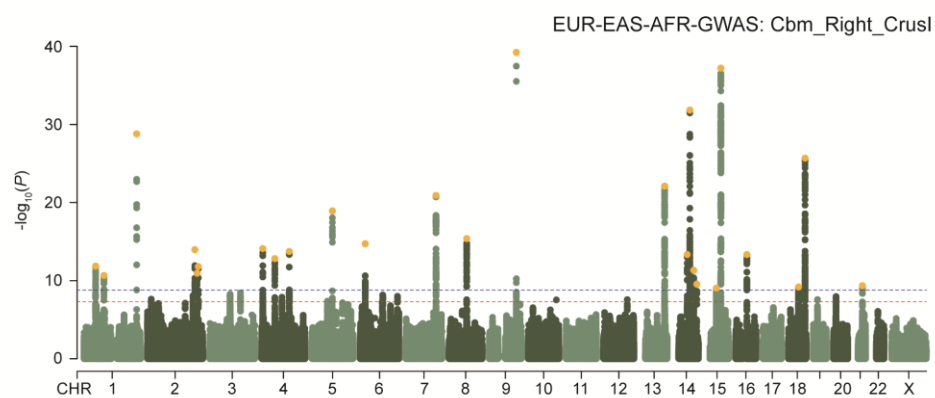
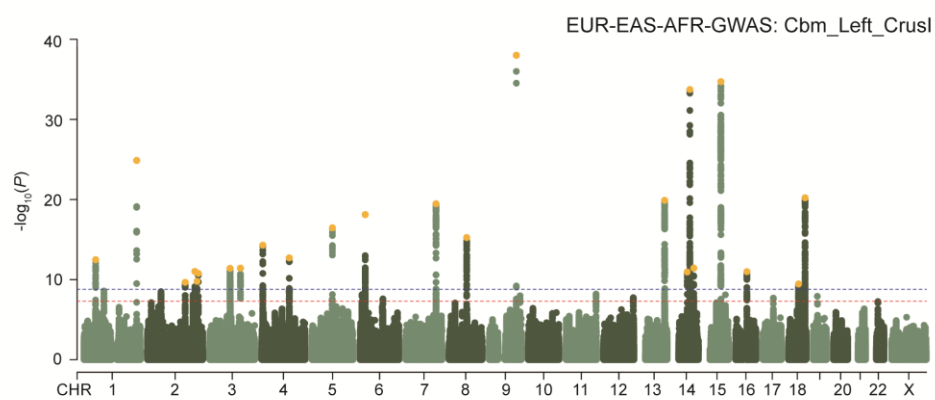
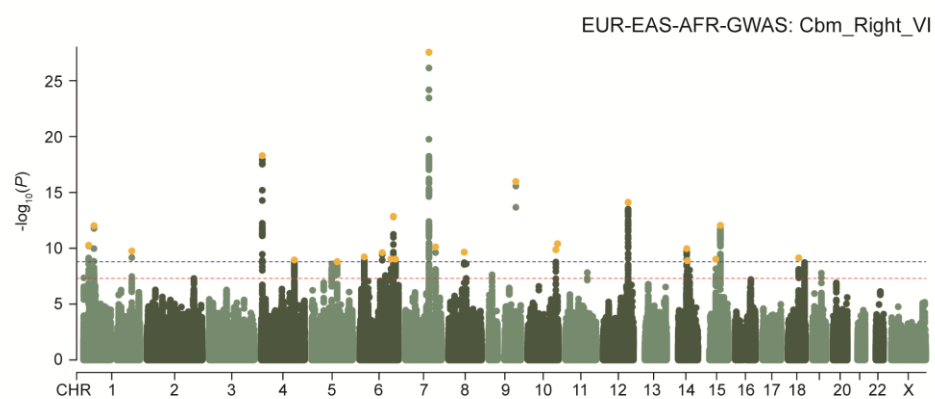
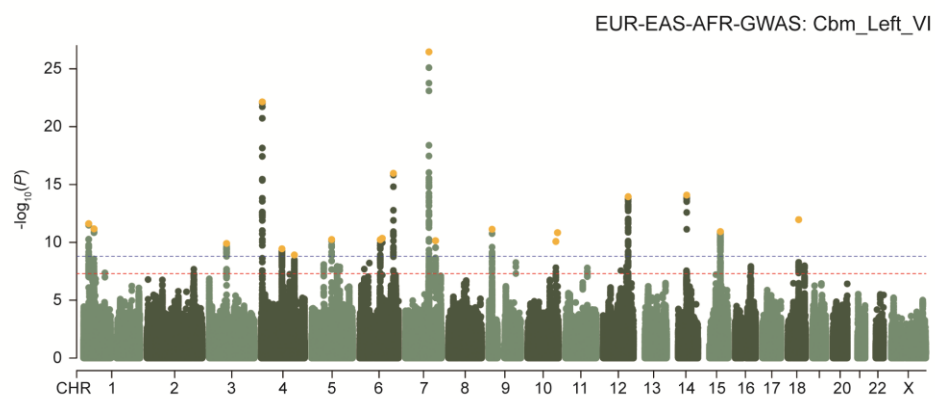


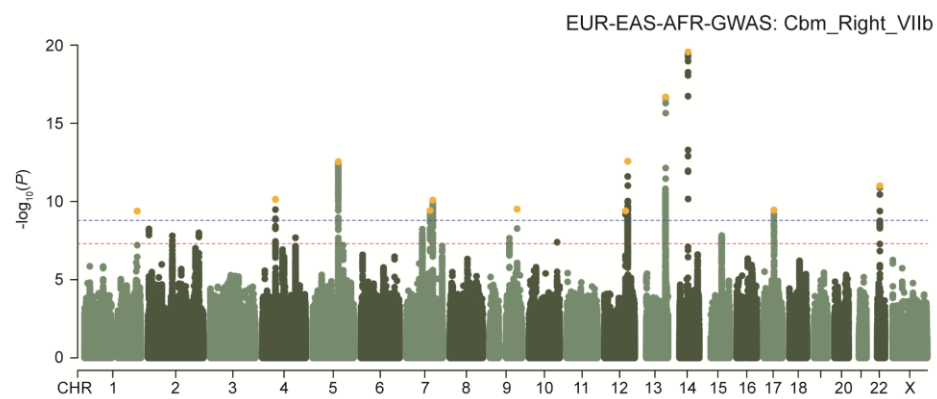
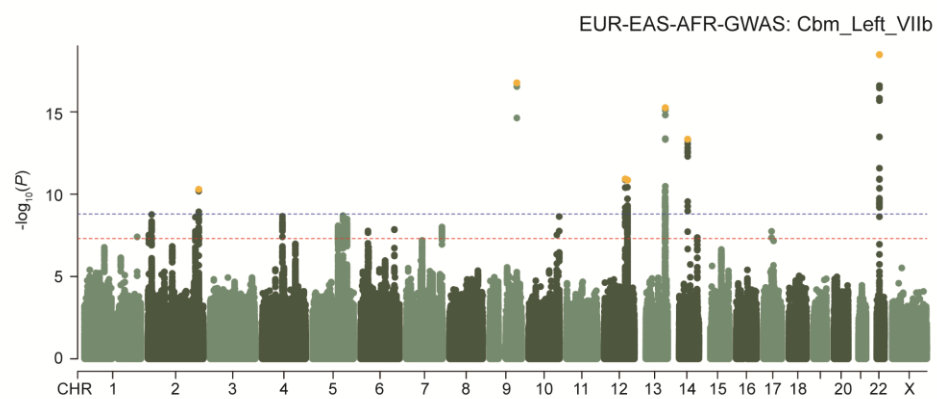
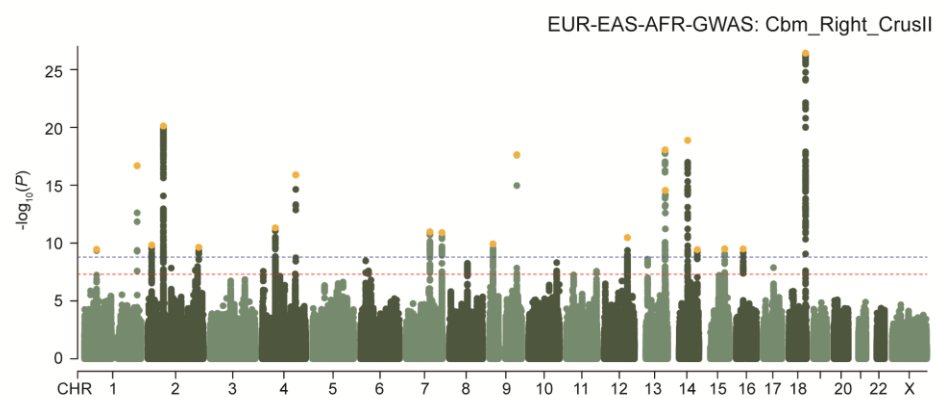
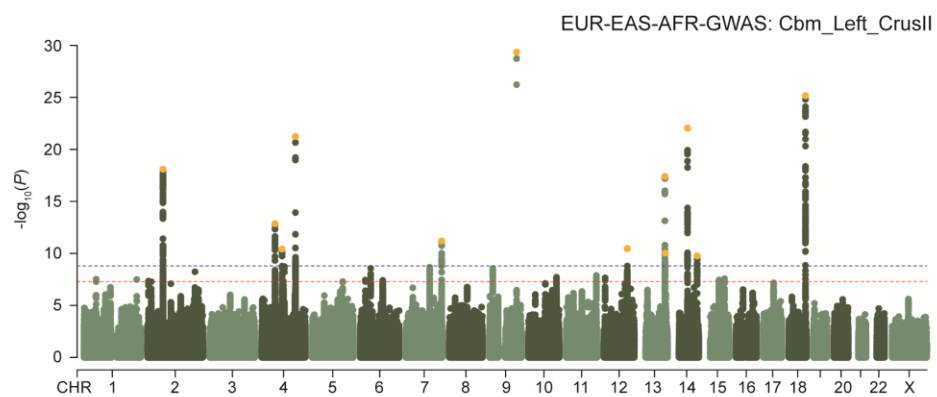


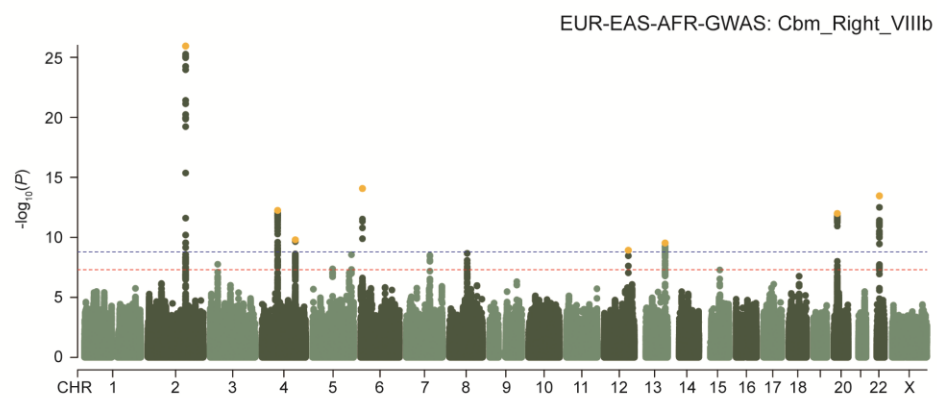
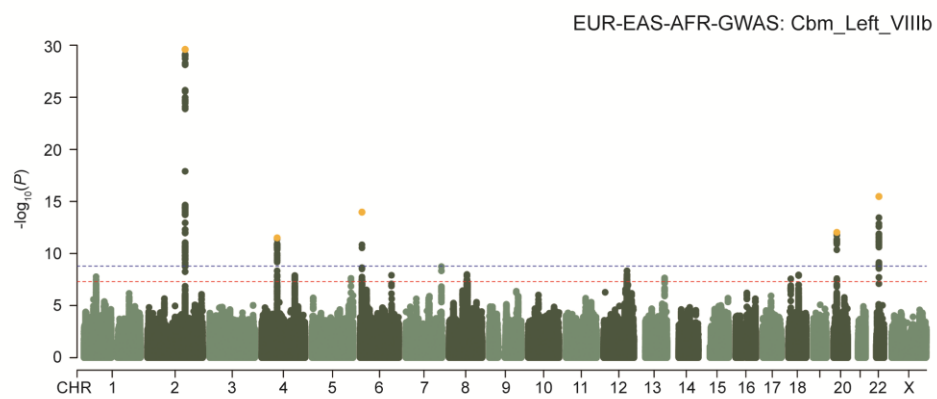
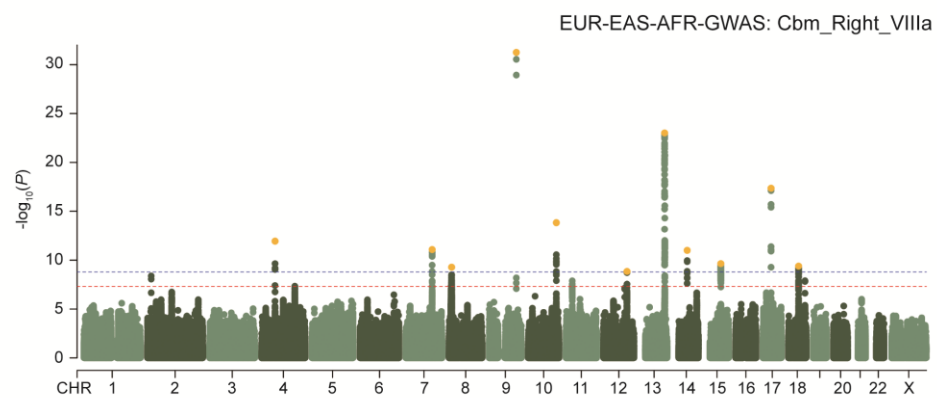
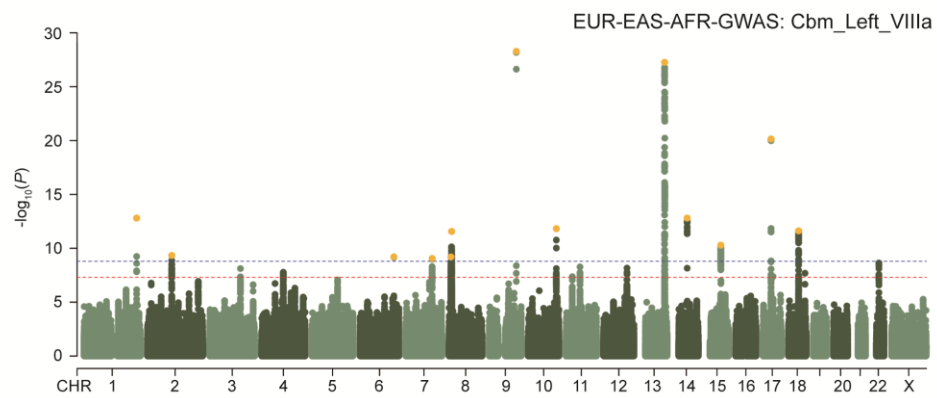


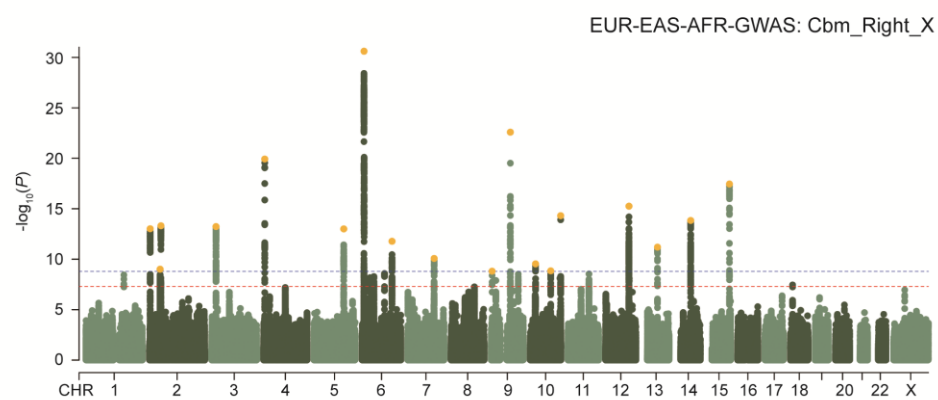
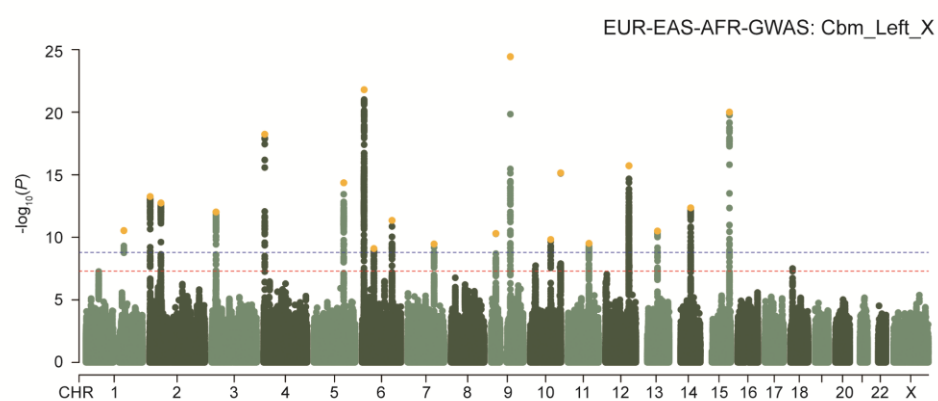
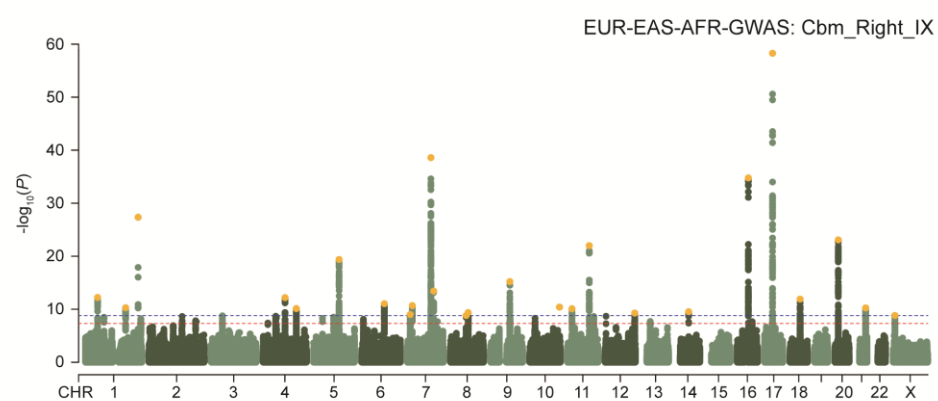
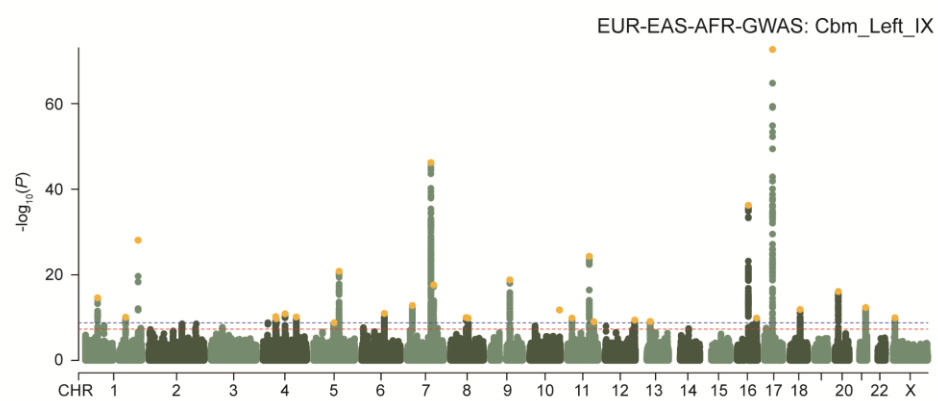


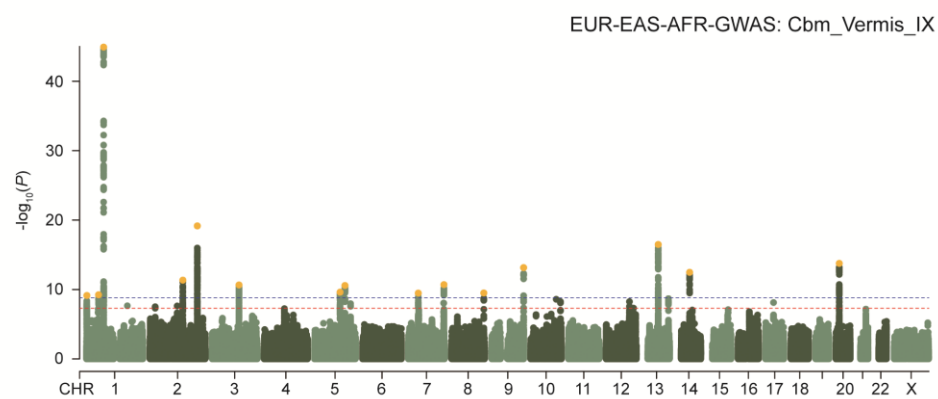
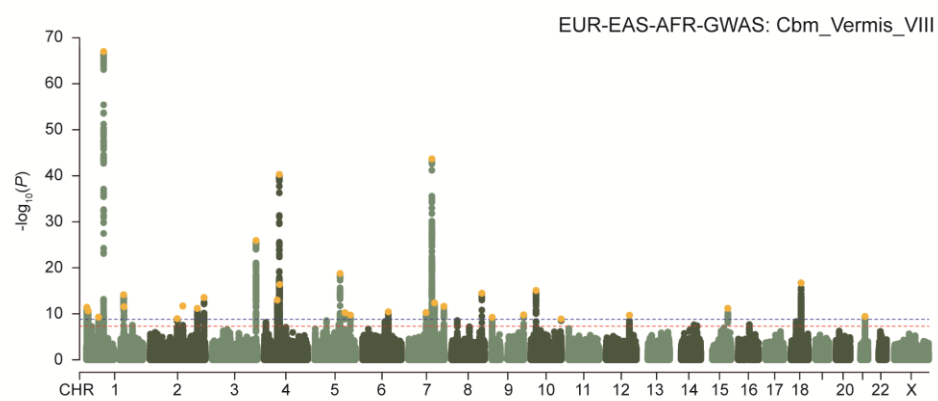
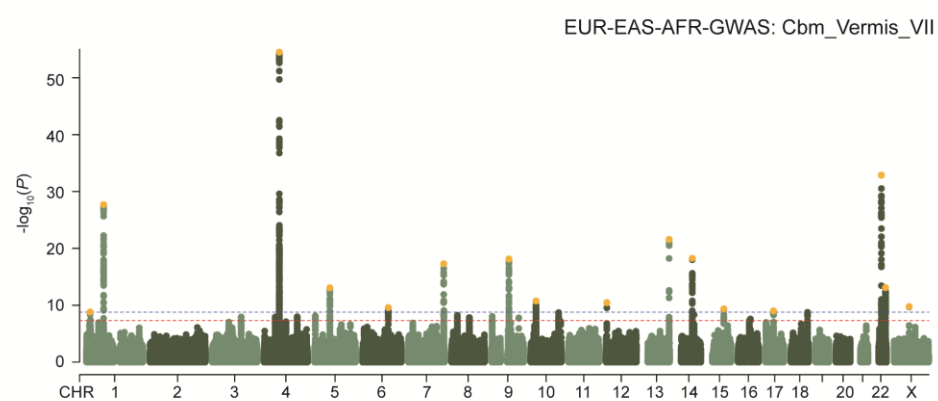
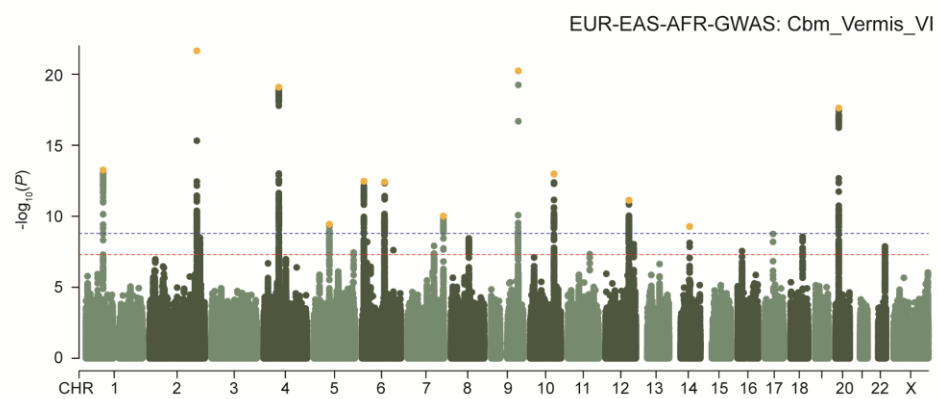












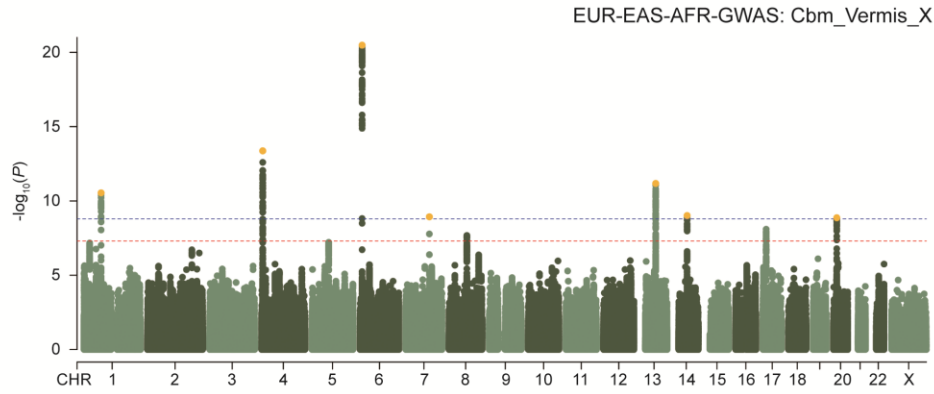
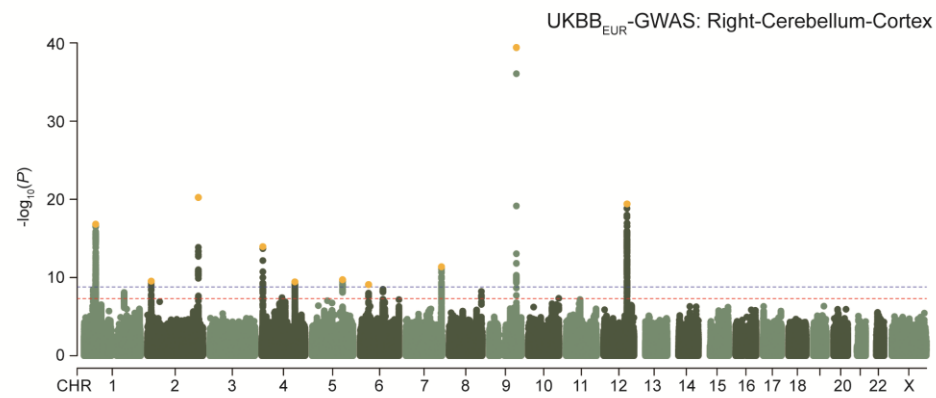
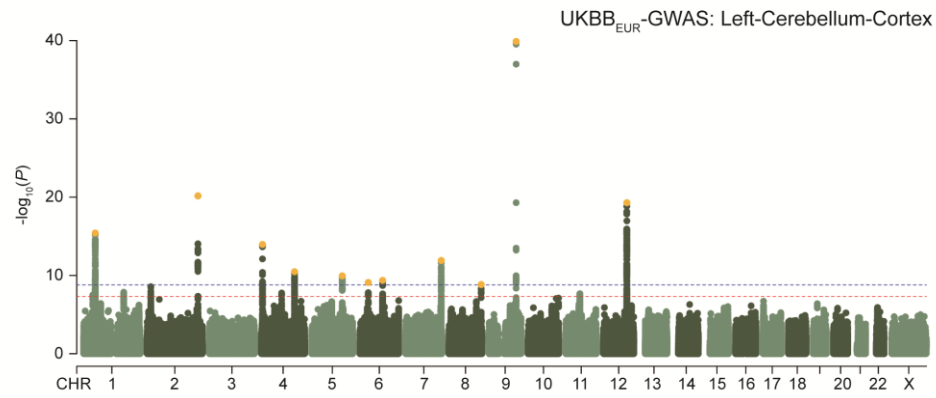
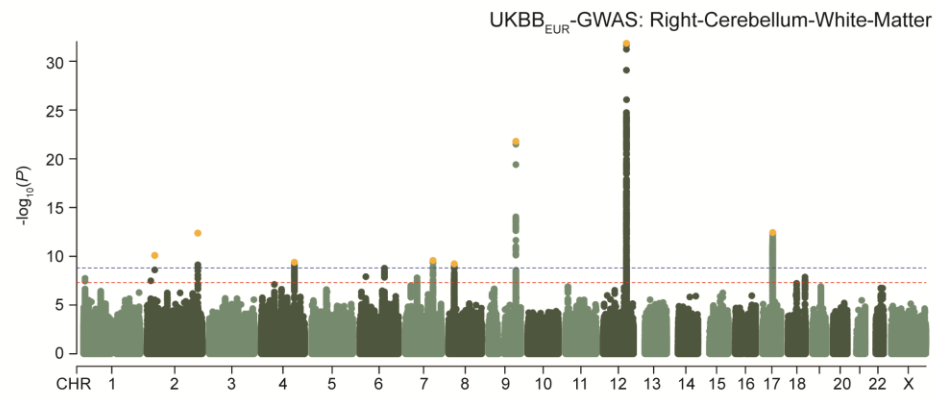
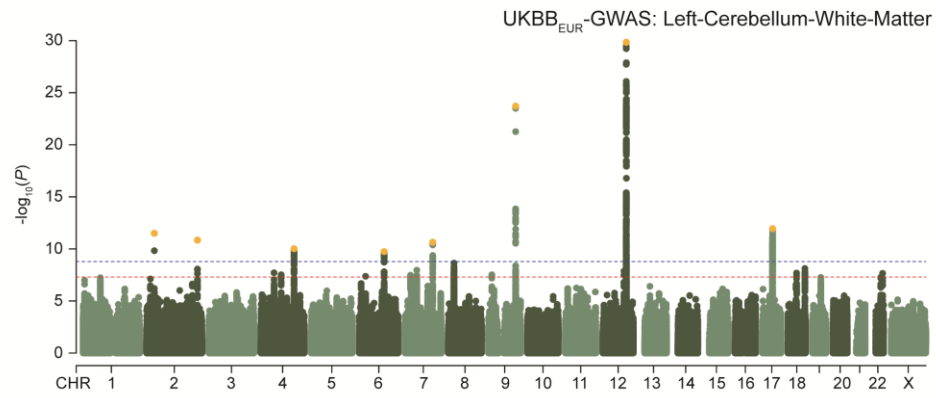
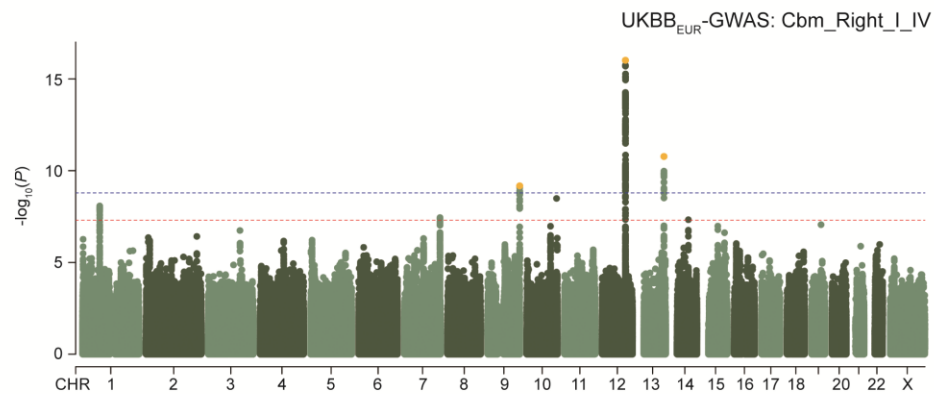
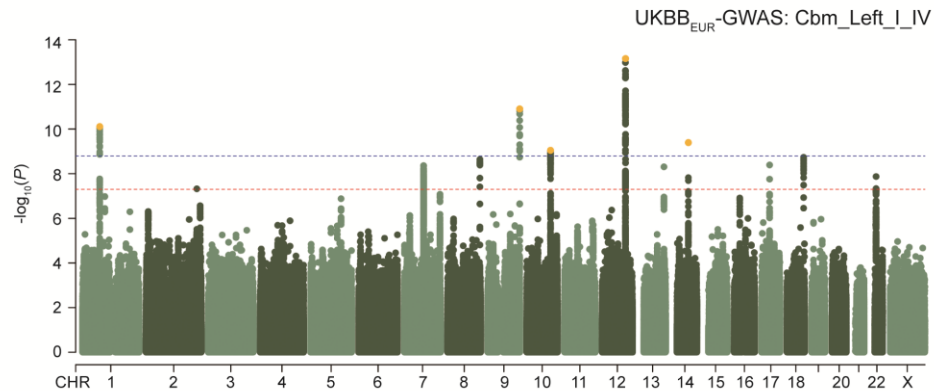
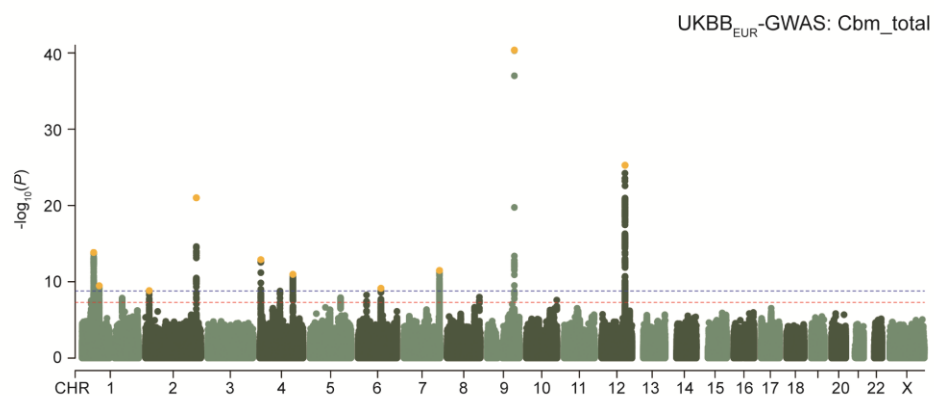
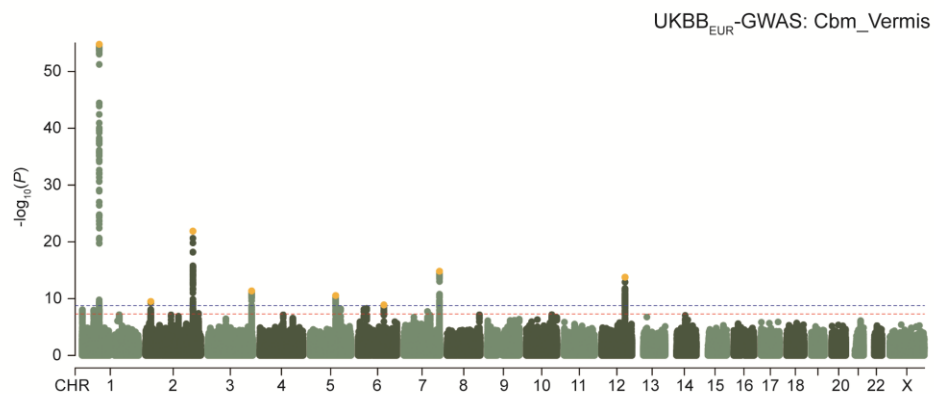
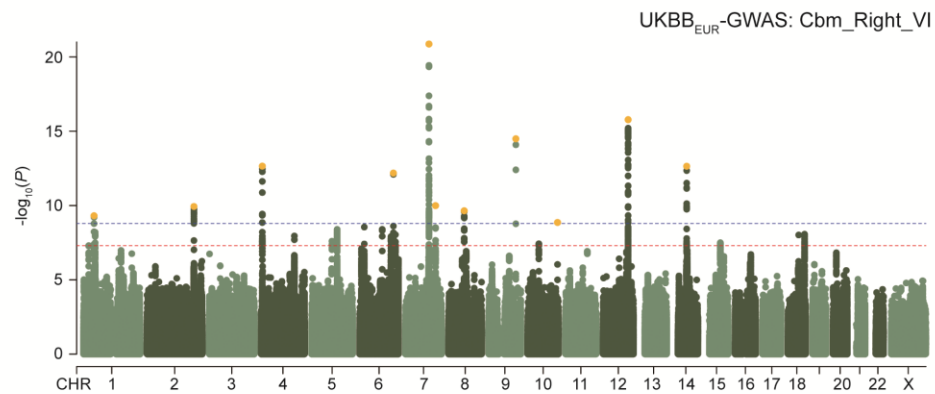
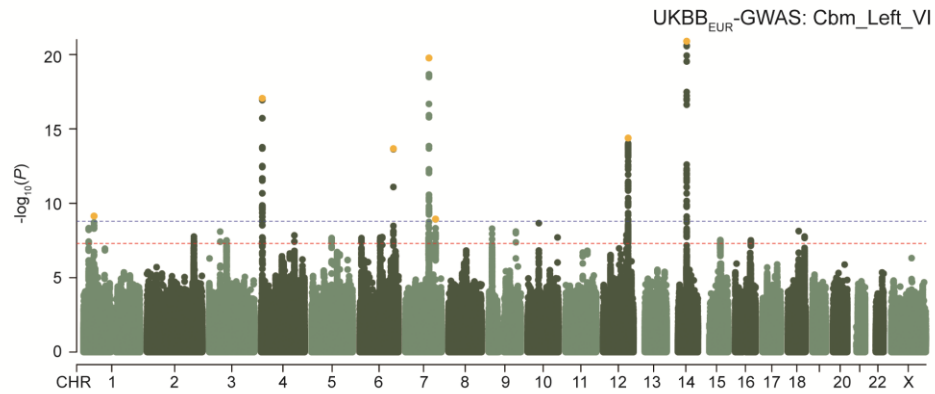
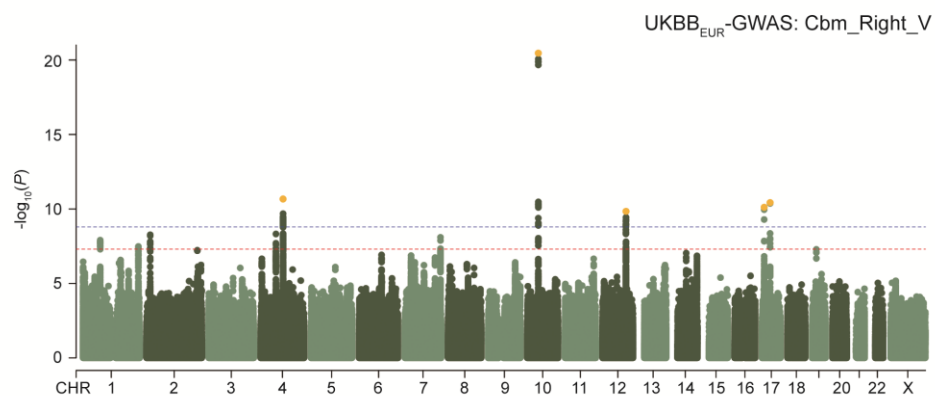
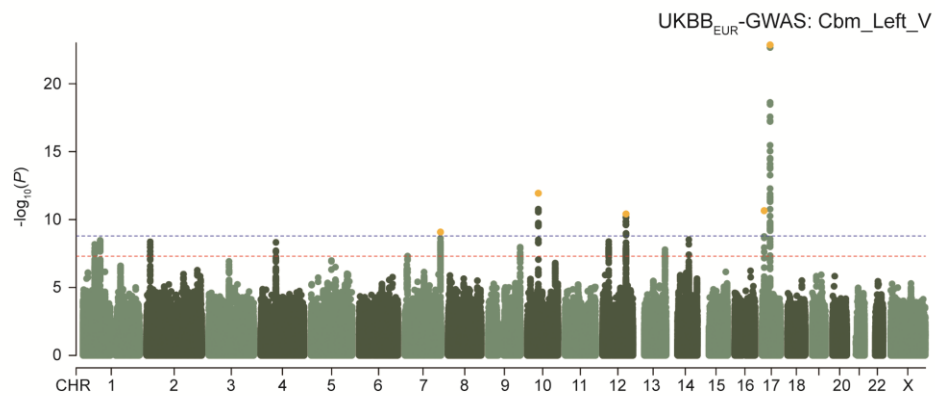
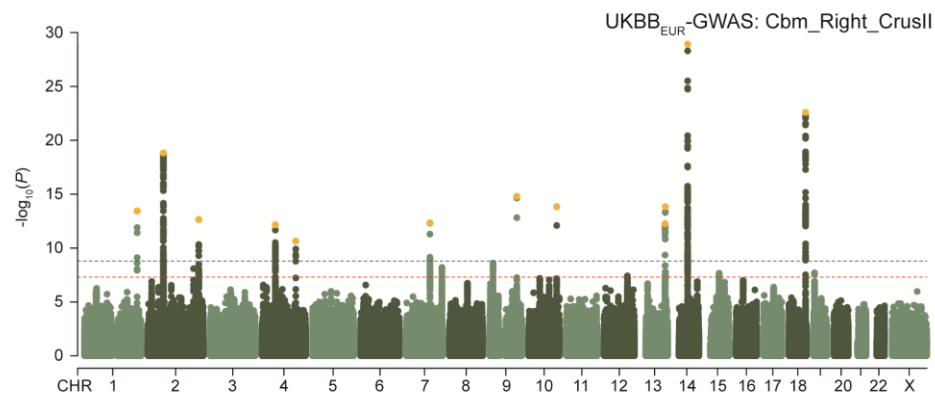
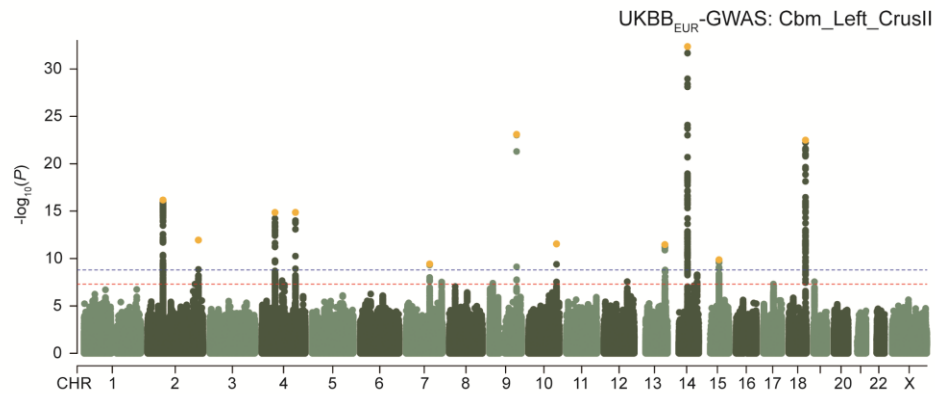
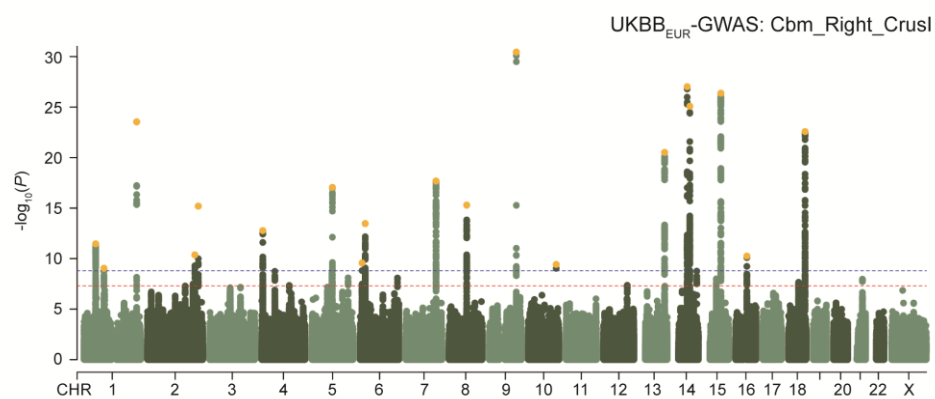
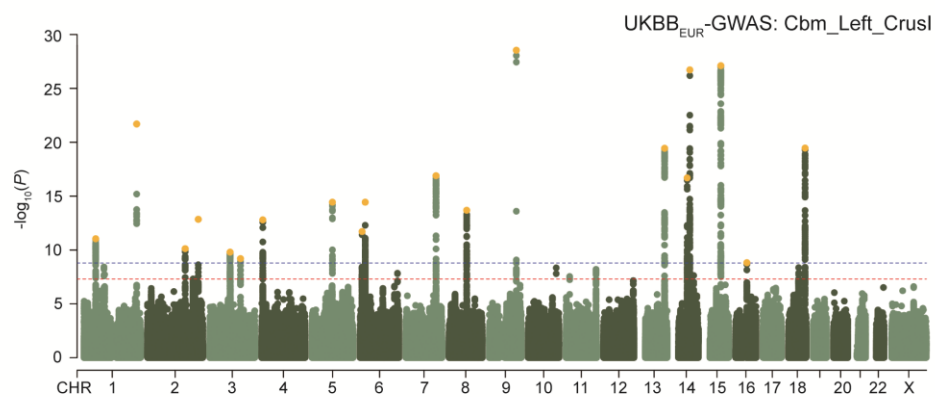


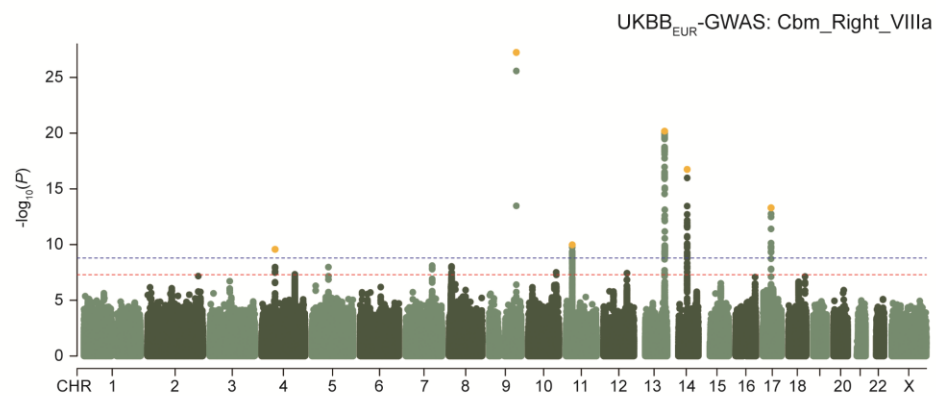
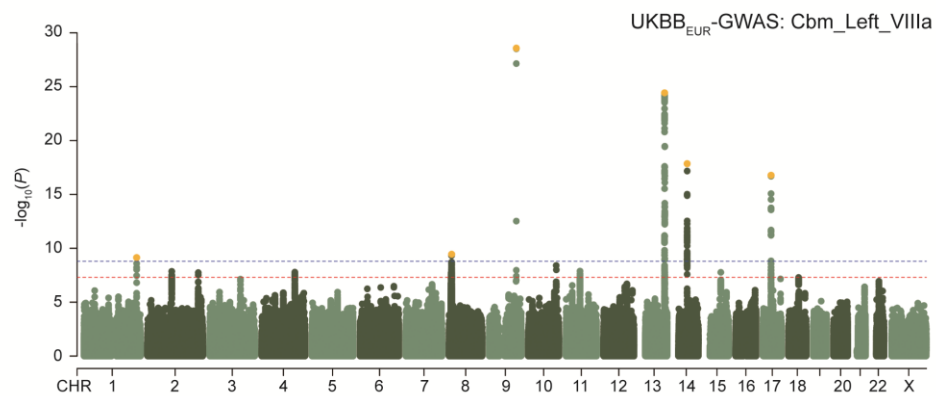
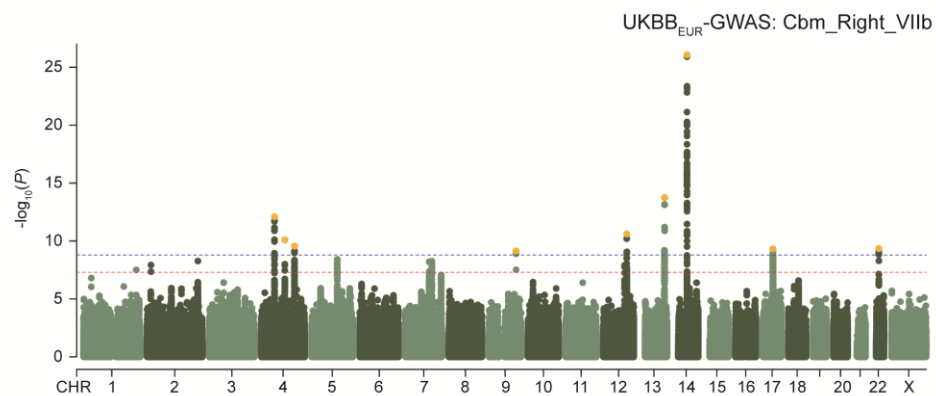
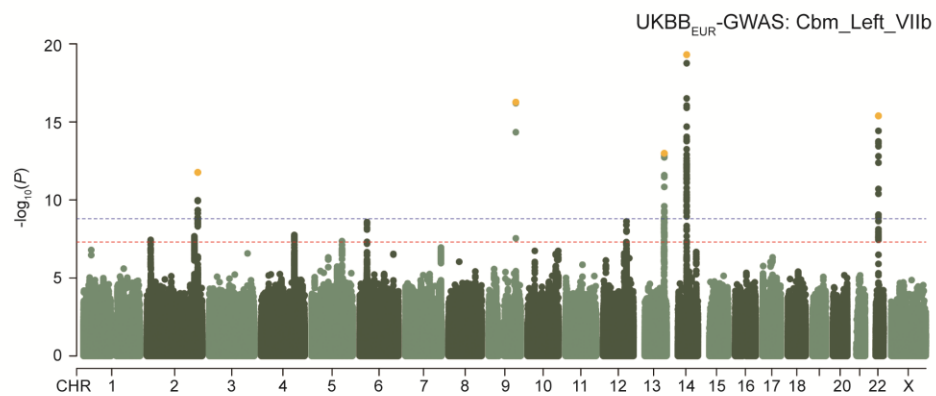
Fig. S4 | Genetic discovery of male-specific univariate GWAS. The Manhattan plots show the results from male-specific univariate GWASs (UKBB_{EUR}-GWAS, ABCD_{EUR}-GWAS, CHIMGEN_{EAS}-GWAS, ABCD_{AFR}-GWAS, EUR-GWAS, EUR-EAS-GWAS, and EUR-EAS-AFR-GWAS) on the 31 cerebellar volumetric traits. Each plot shows genome-wide (red dashed line: $P = 5 \times 10^{-8}$) and study-wide (blue dashed line: $P = 1.61 \times 10^{-9}$) significant associations. Each point represents a single genetic variant plotted according to its genomic position (x axis) and its $-\log_{10}(P)$ value for the association (y axis). Each yellow point represents an independent locus with study-wide significance ($P = 1.61 \times 10^{-9}$). Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; GWAS, genome-wide association study; UKBB, the UK Biobank study.

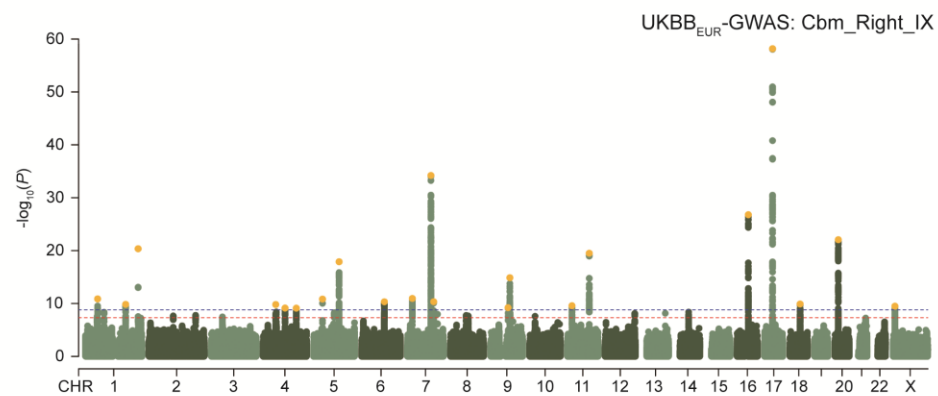
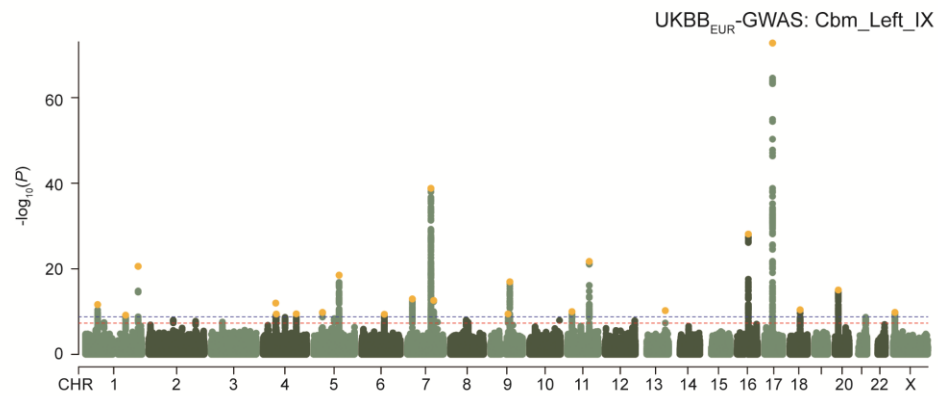
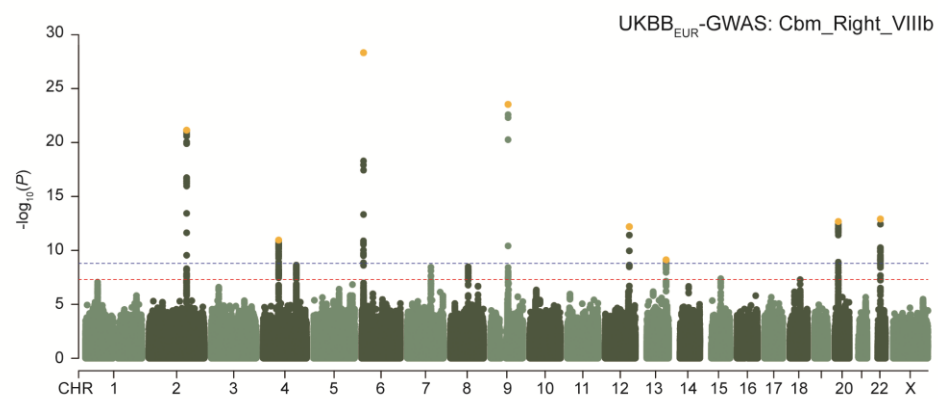
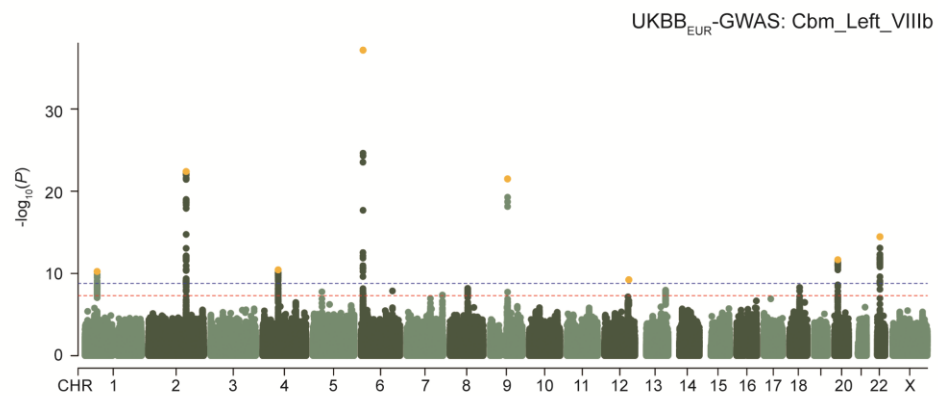


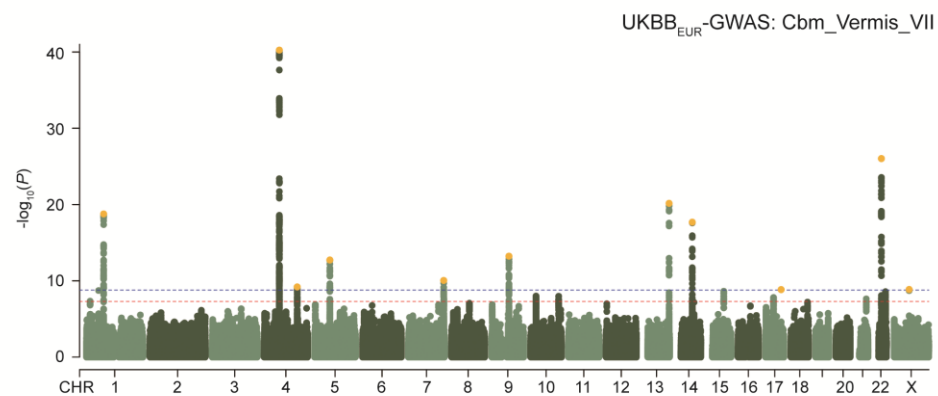
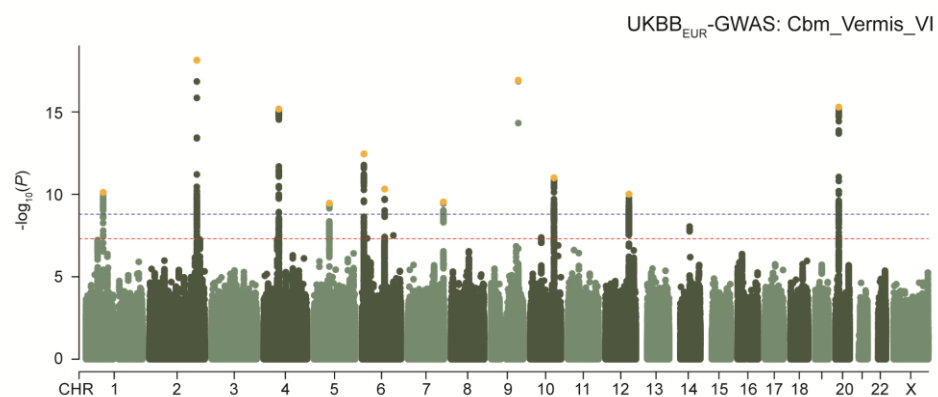
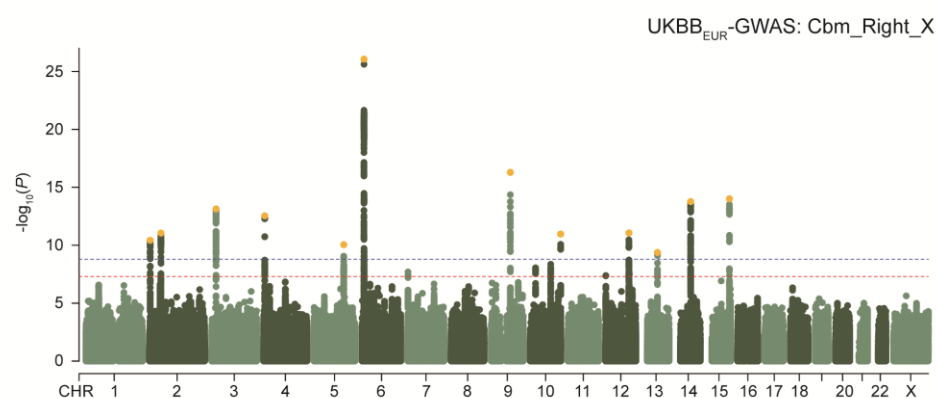
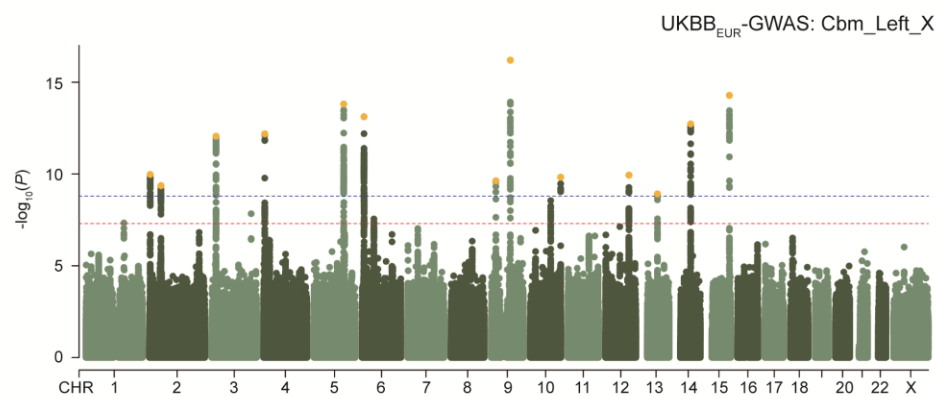


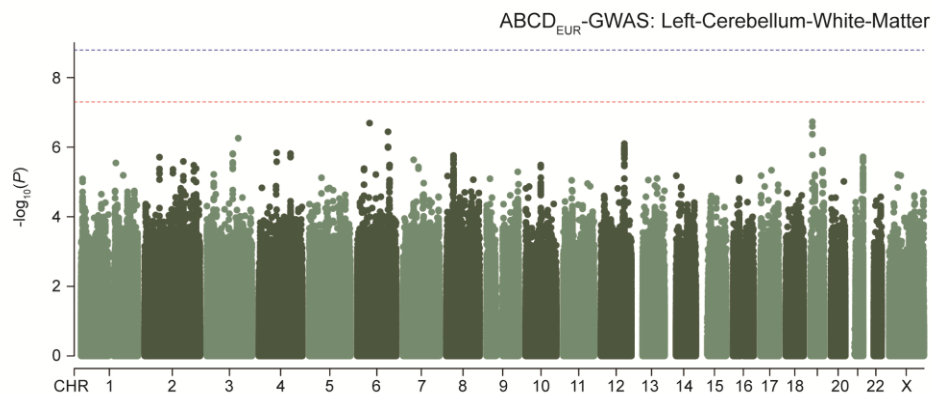
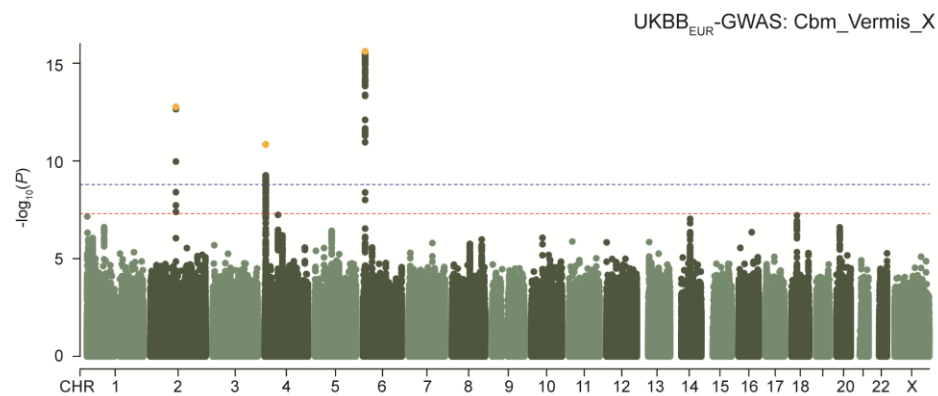
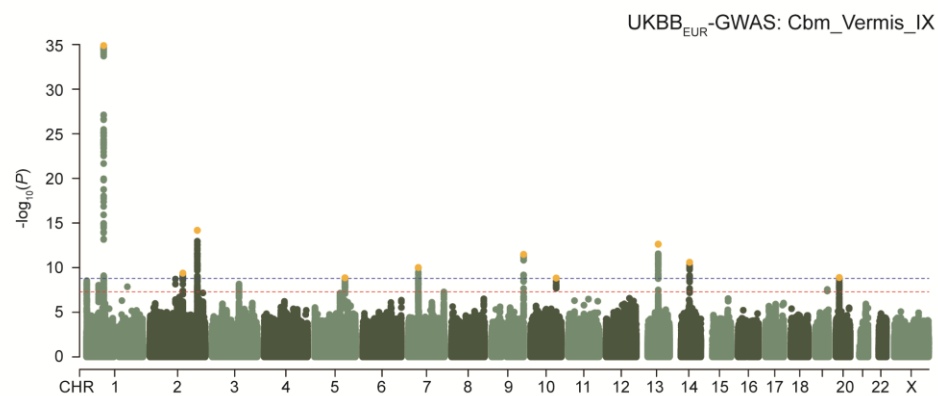
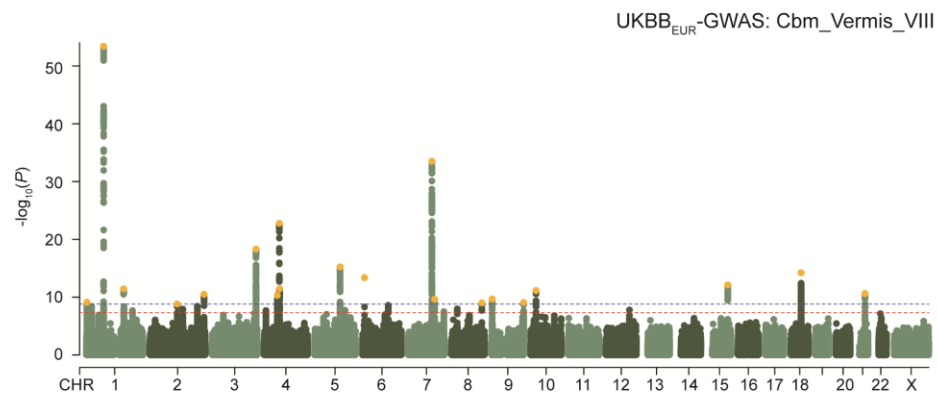


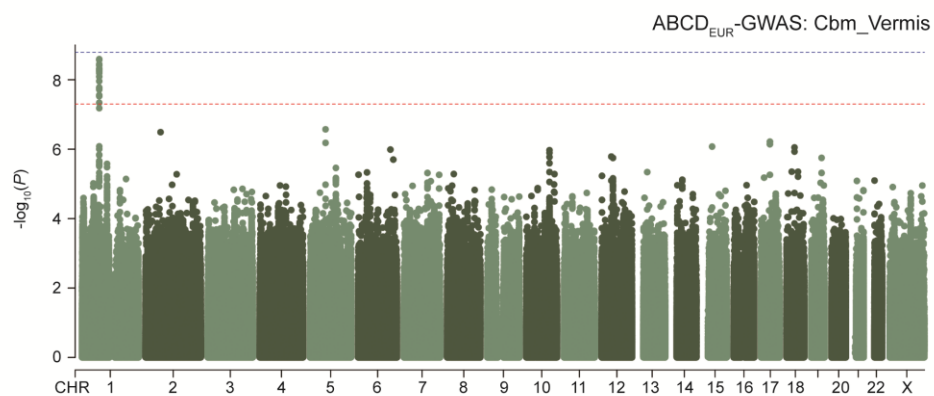
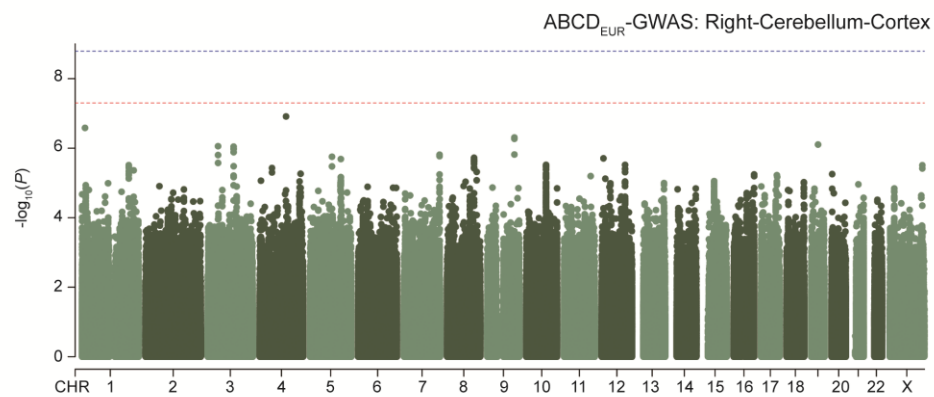
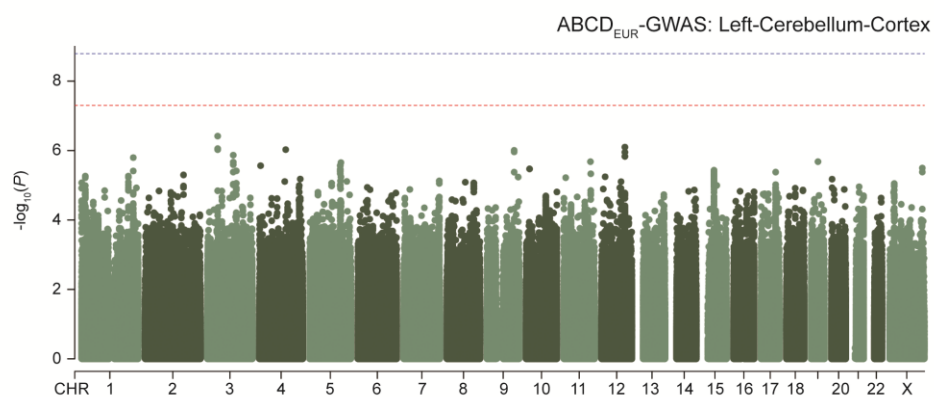
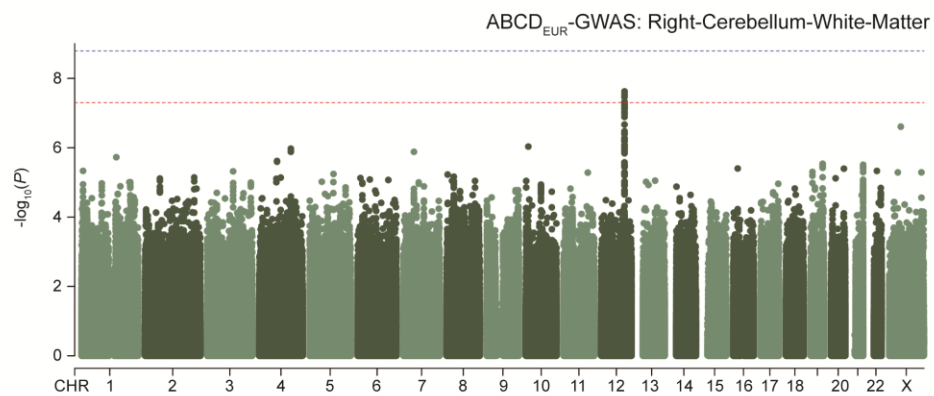


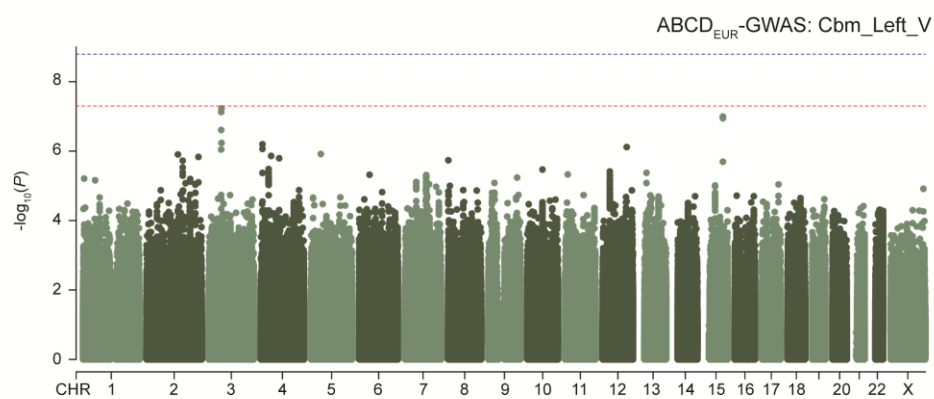
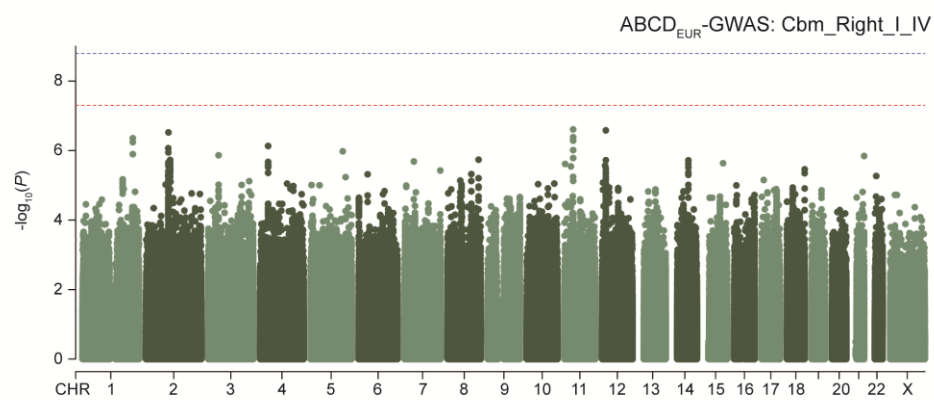
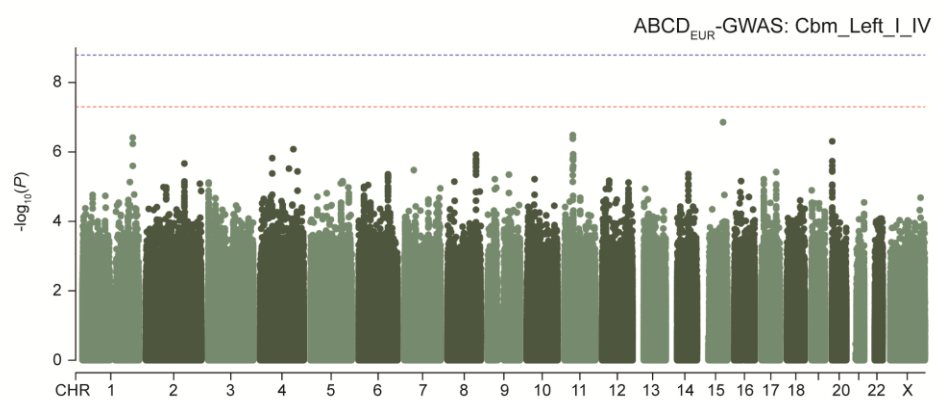
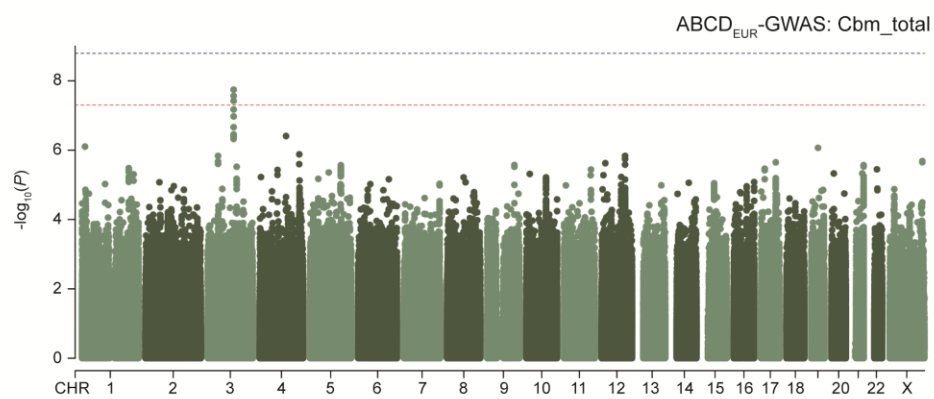


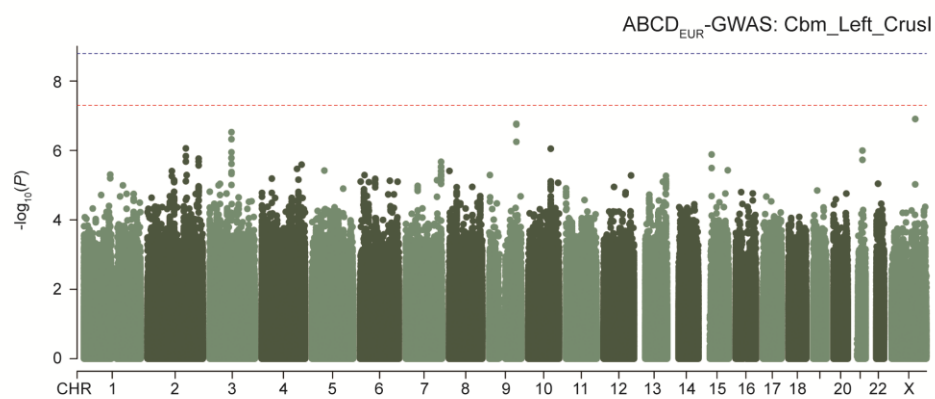
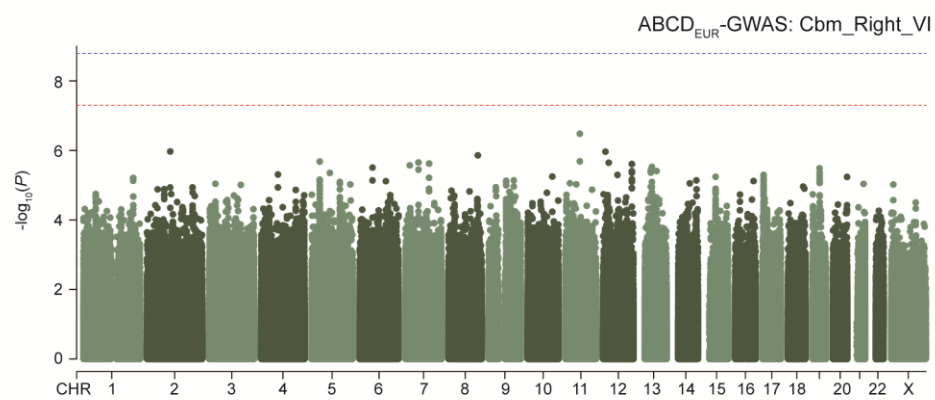
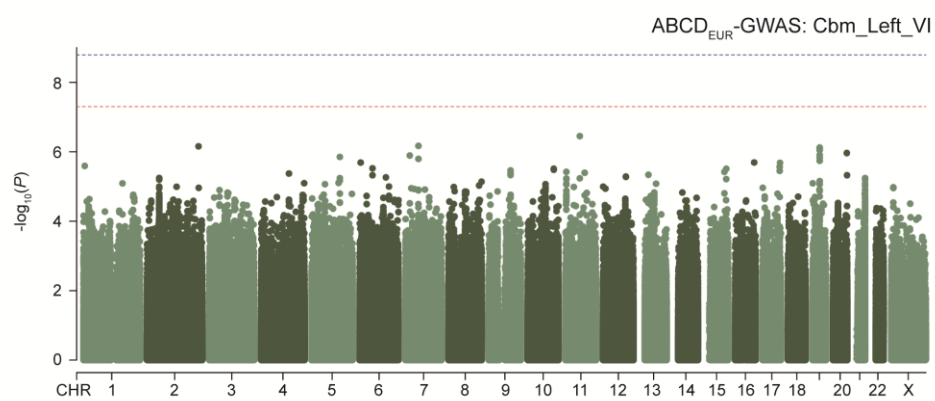
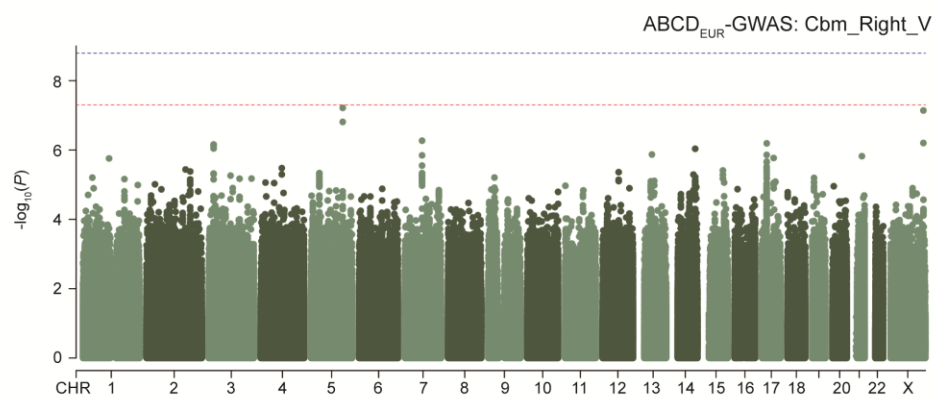


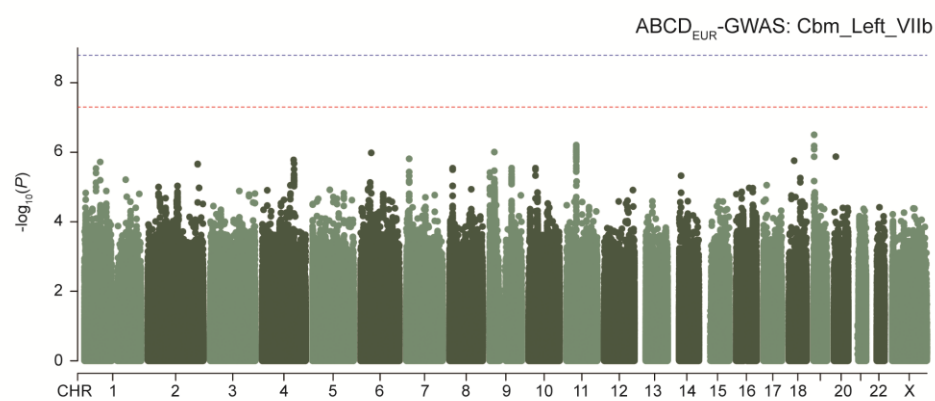
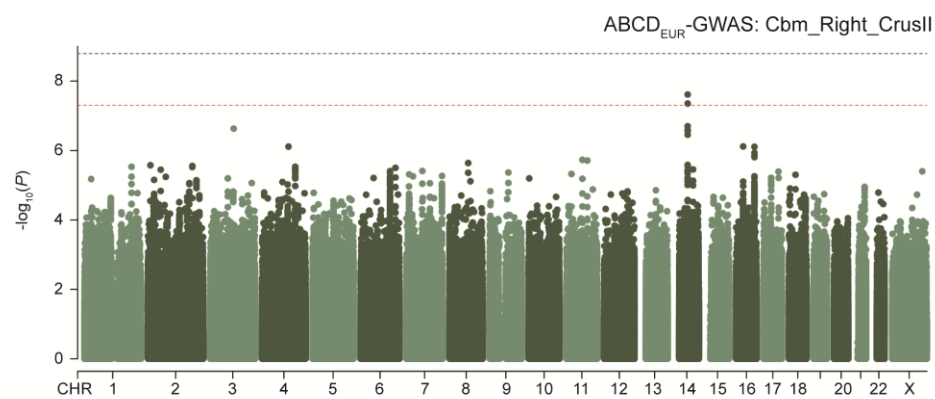
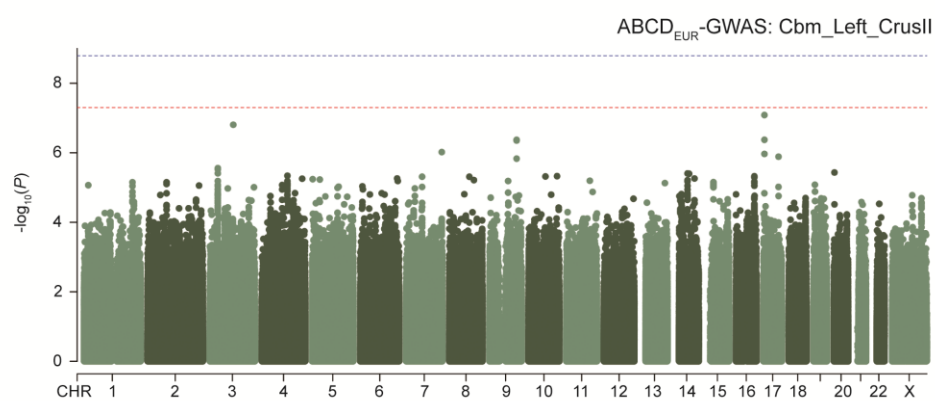
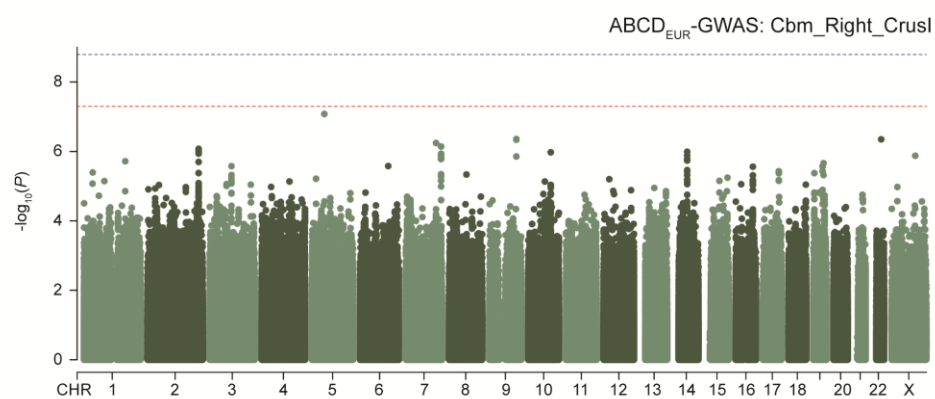


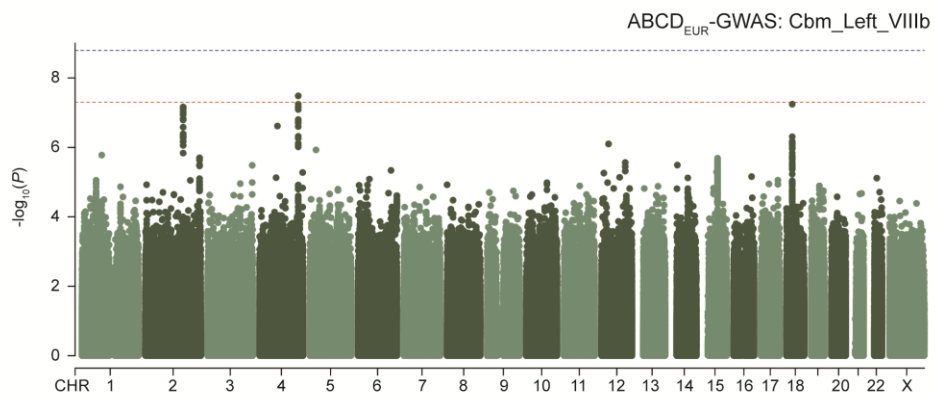
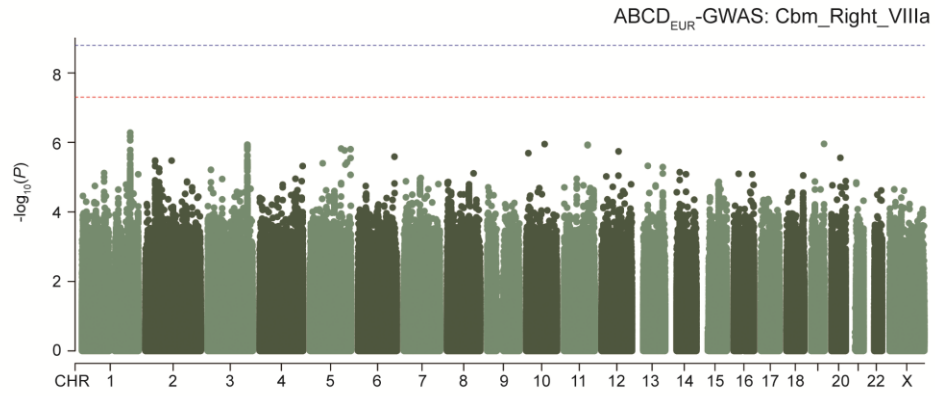
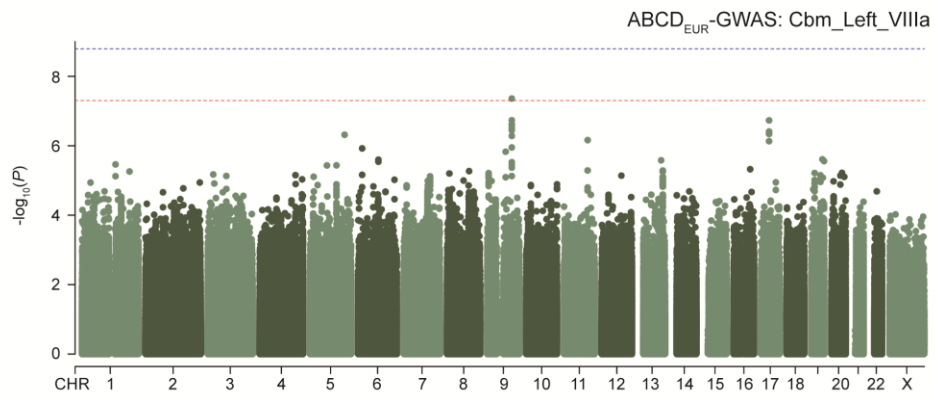
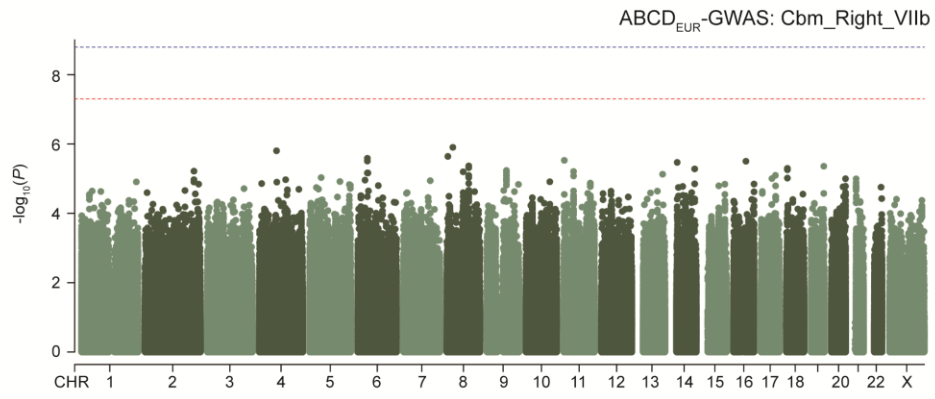


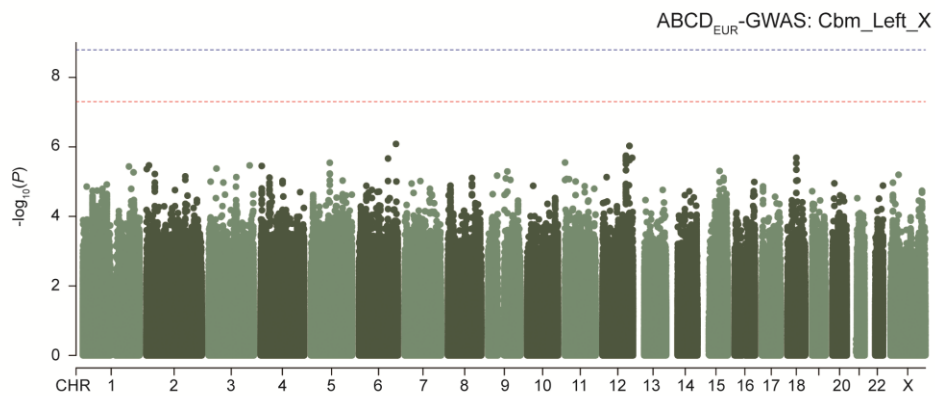
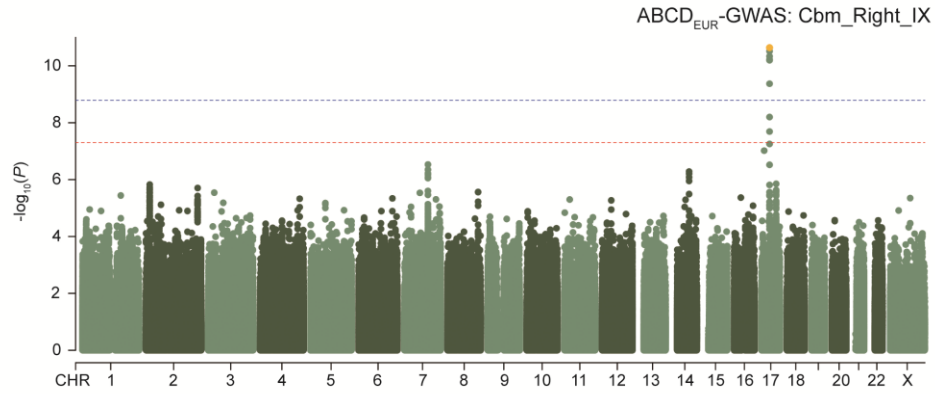
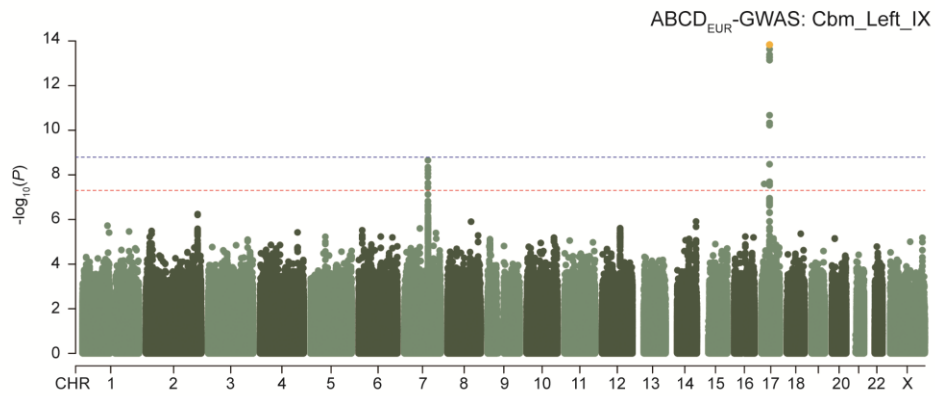
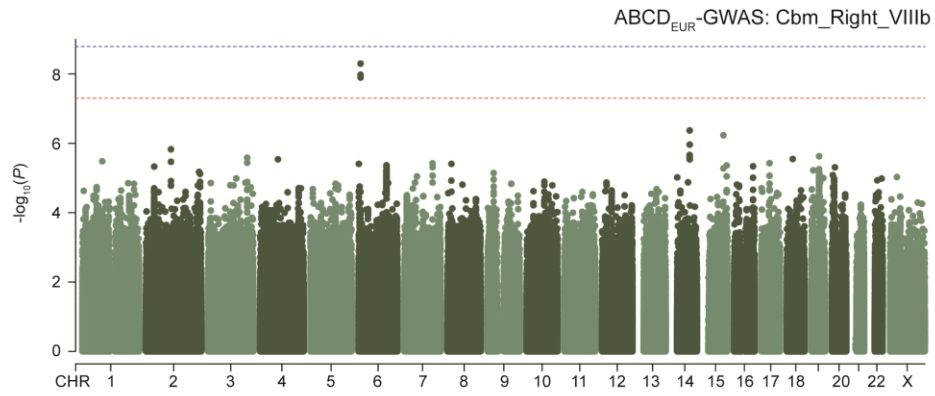


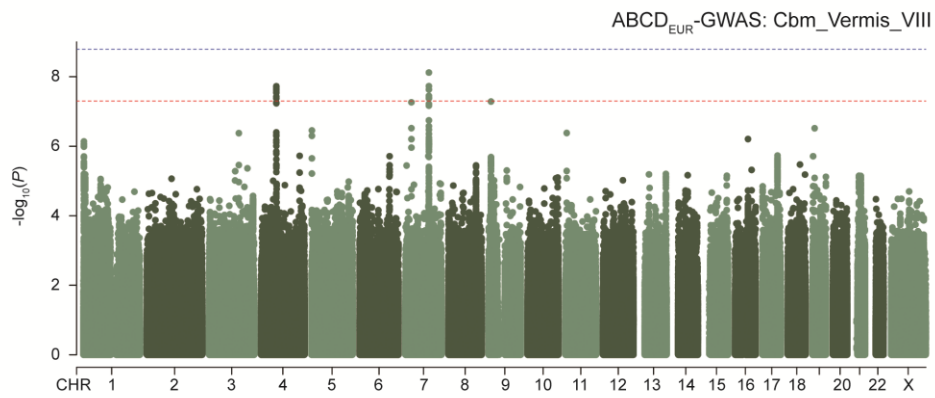
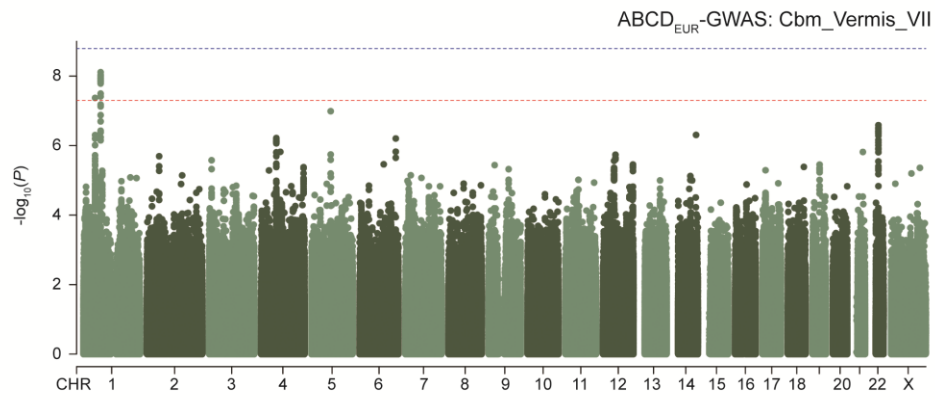
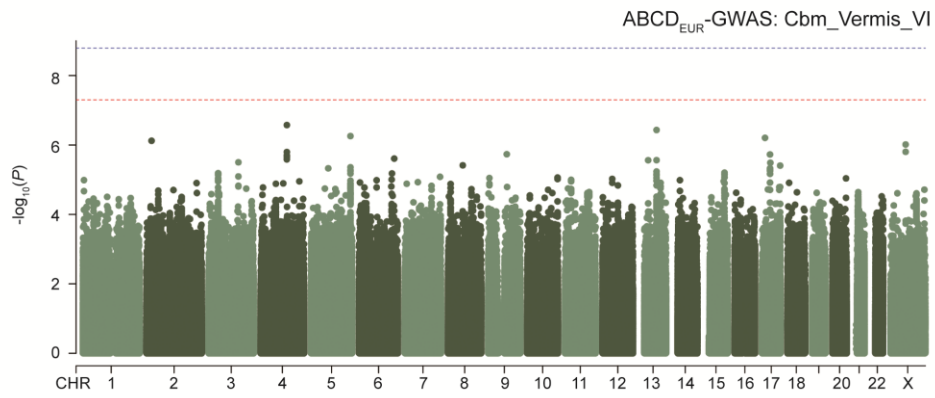
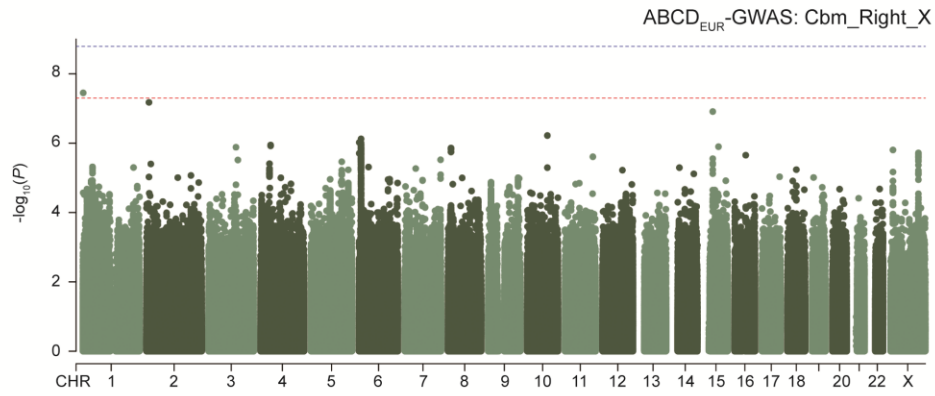


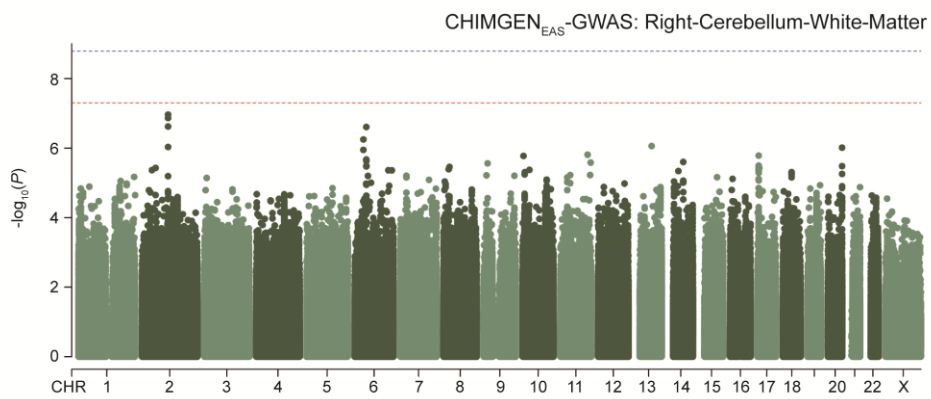
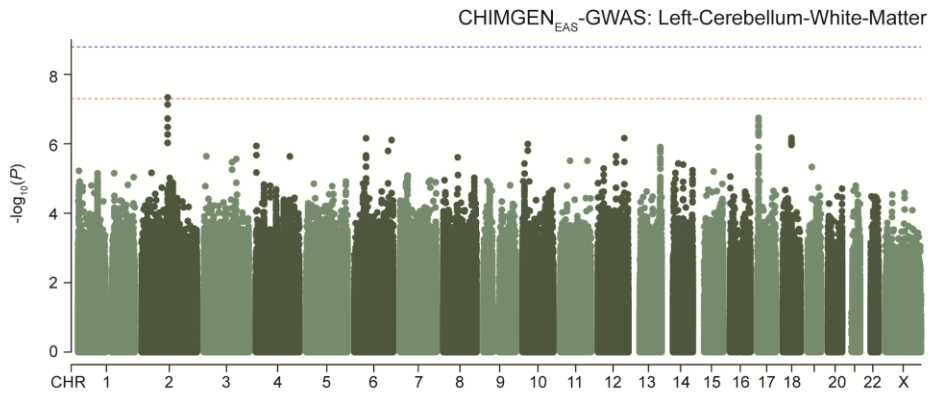
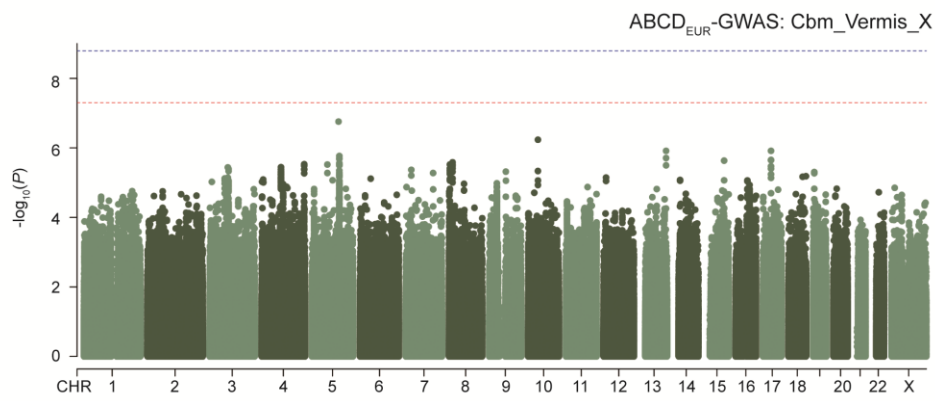
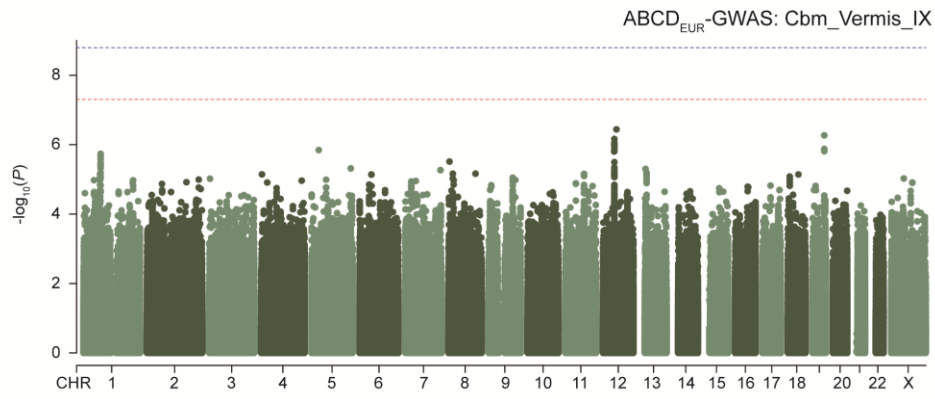


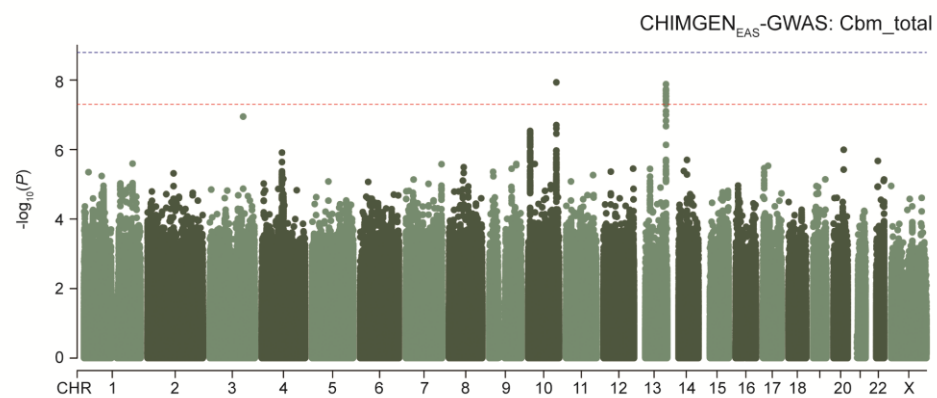
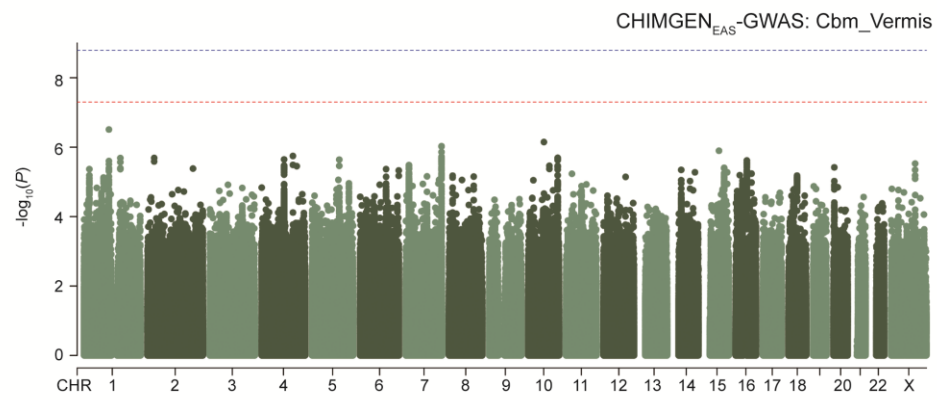
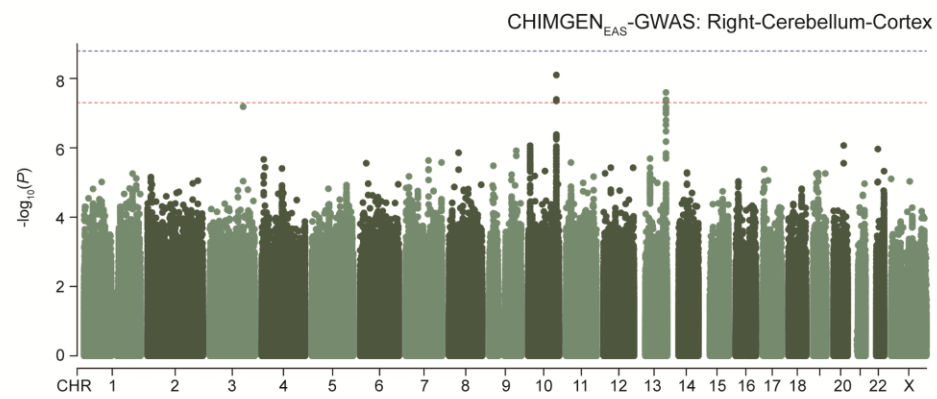
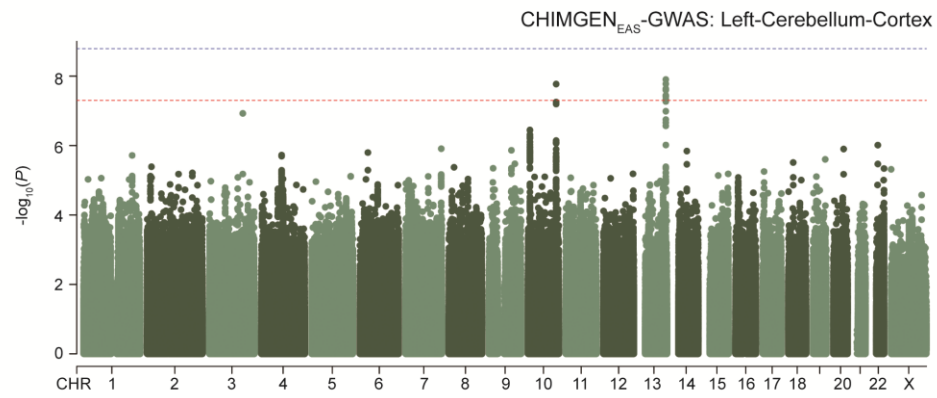


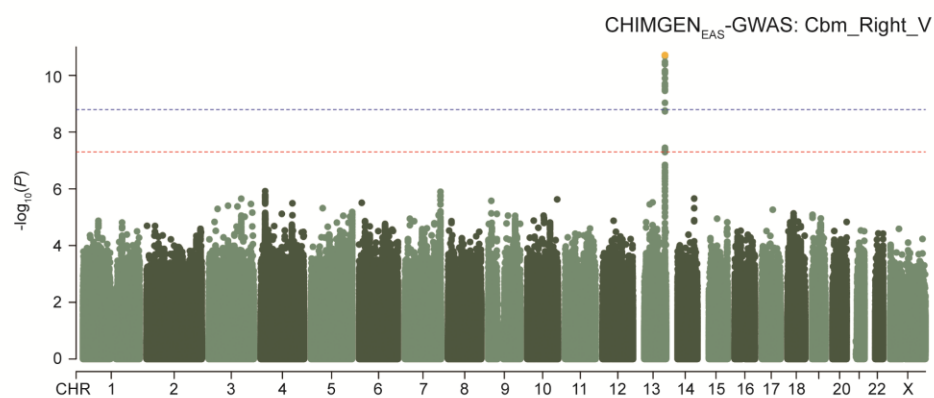
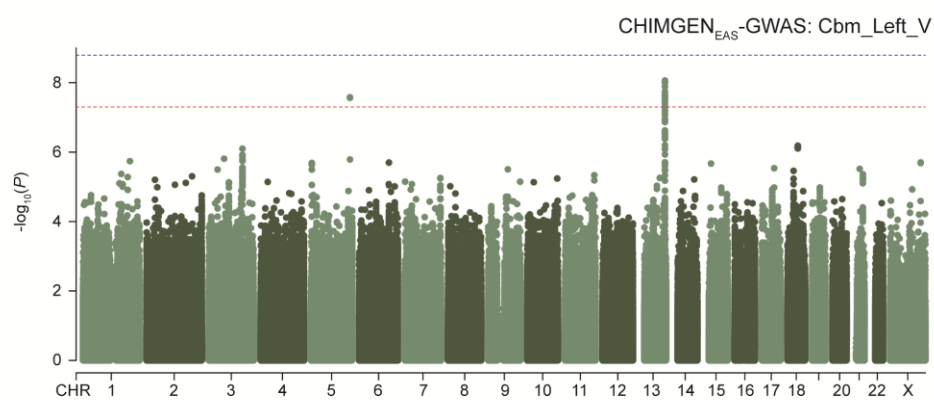
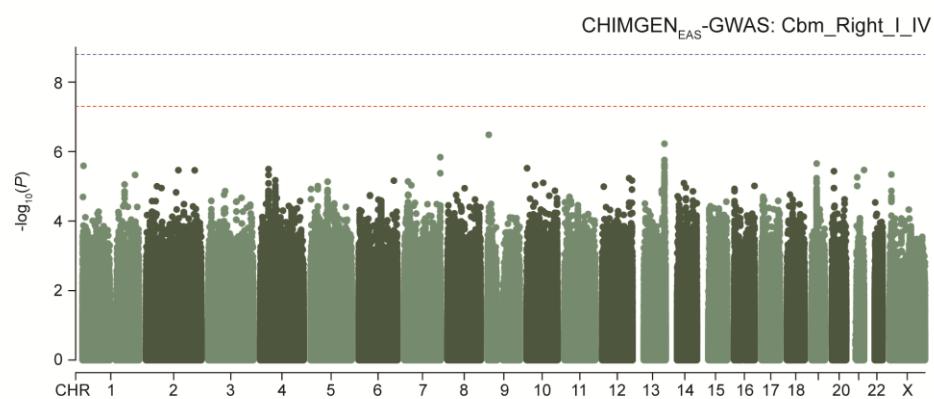
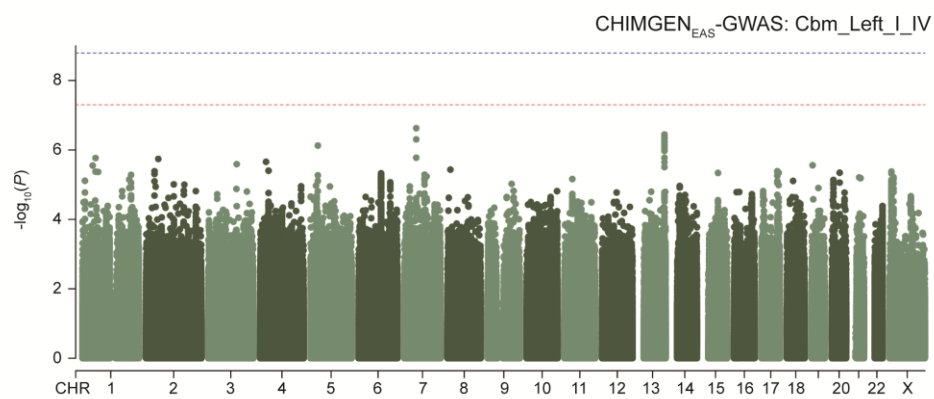


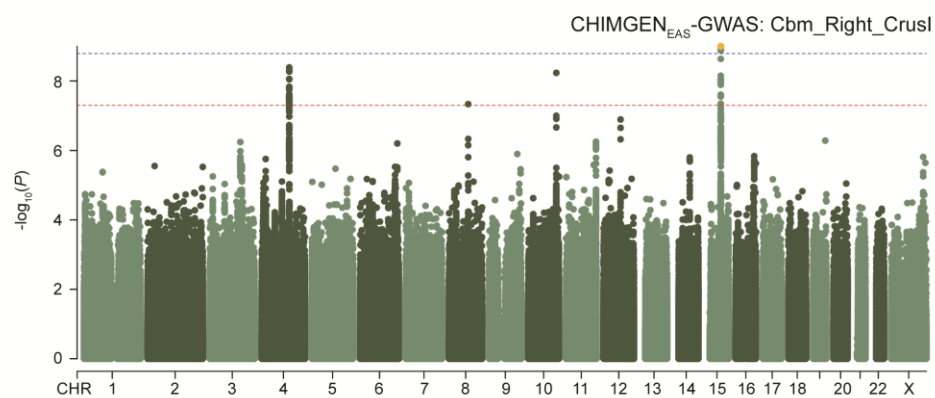
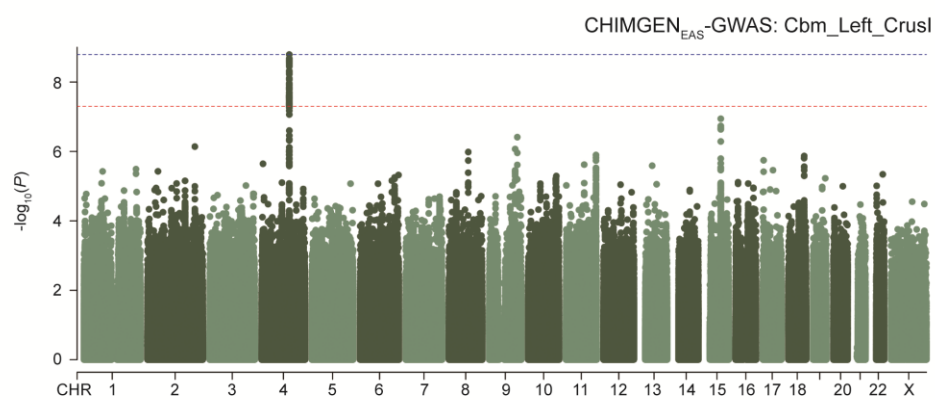
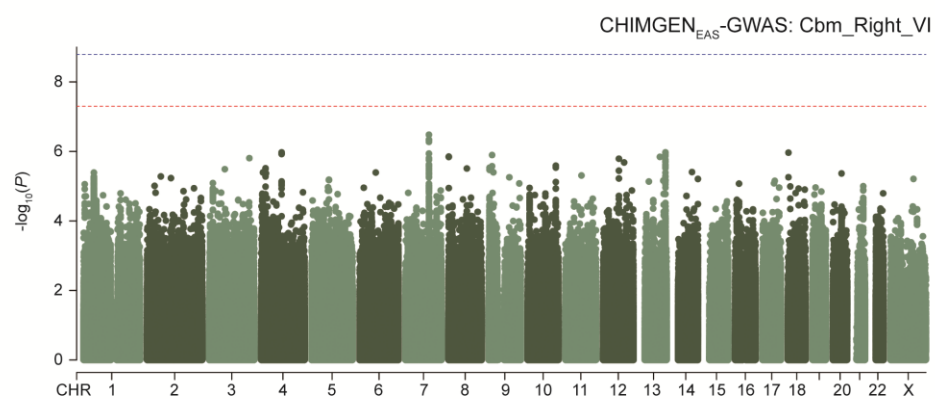
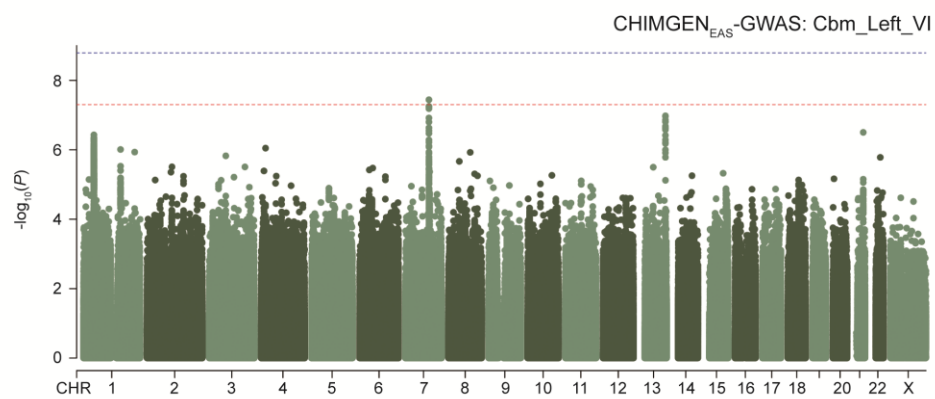


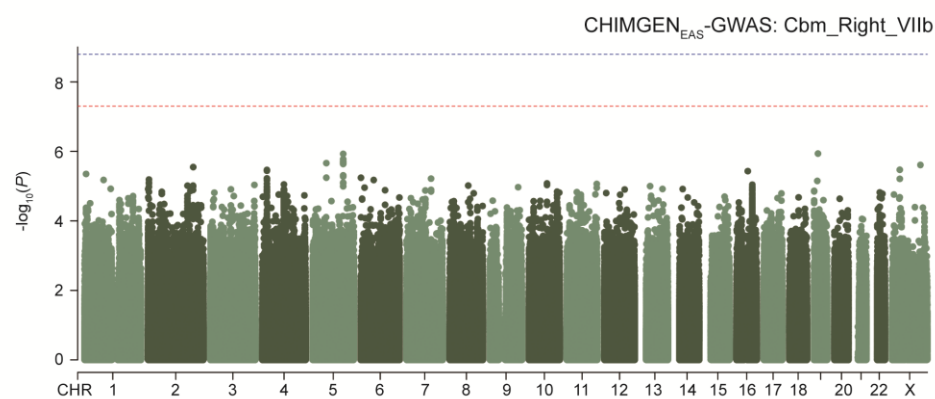
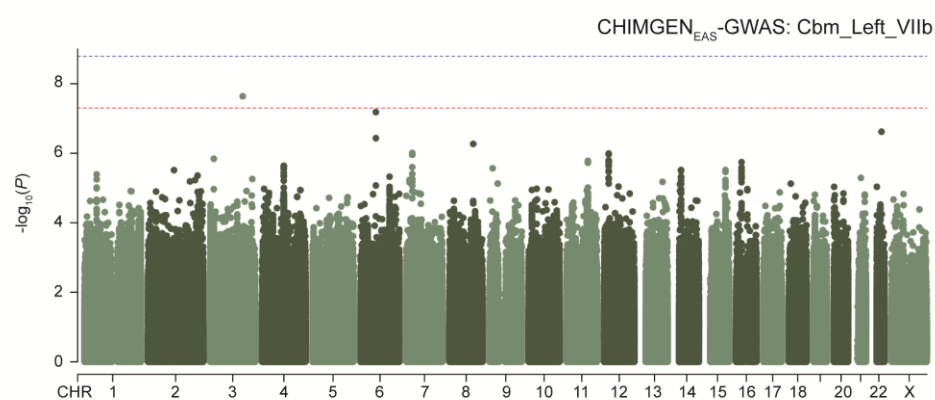
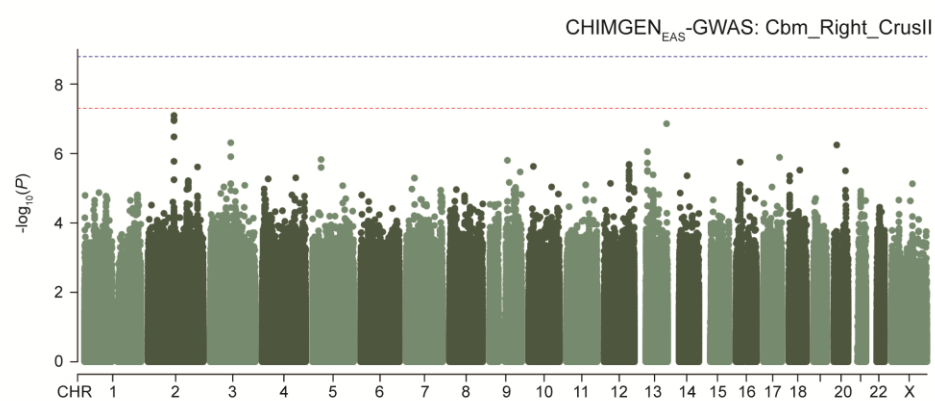
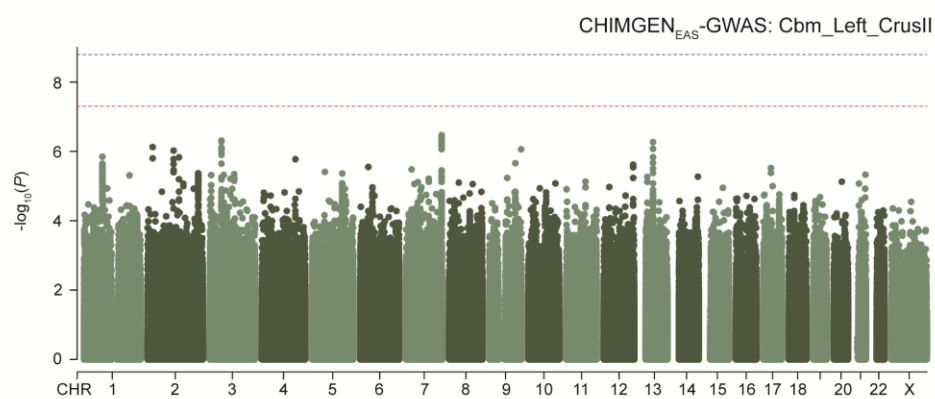


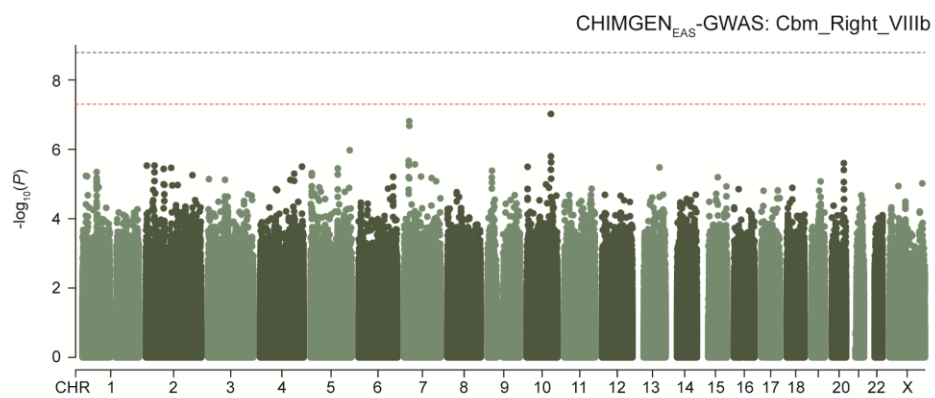
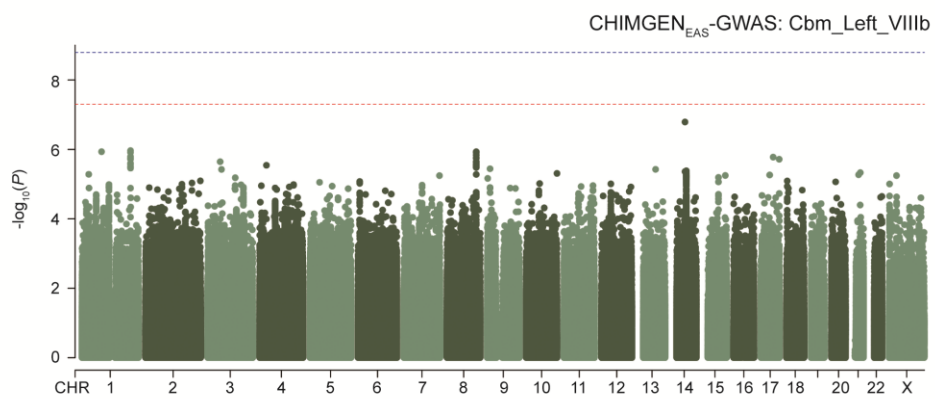
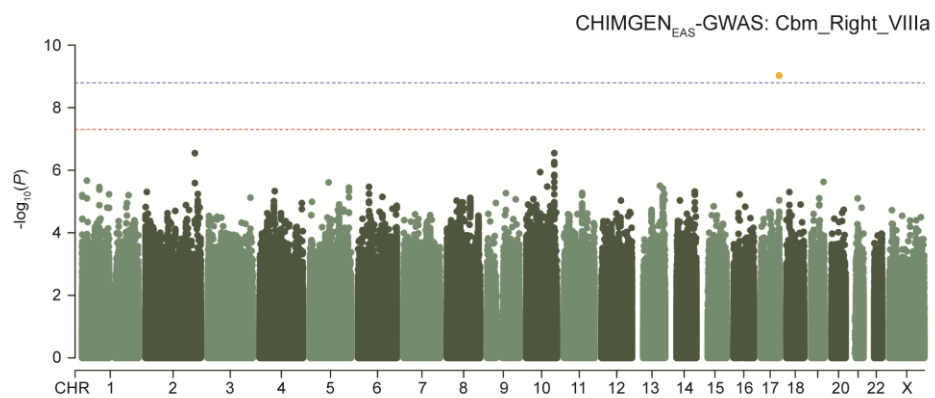
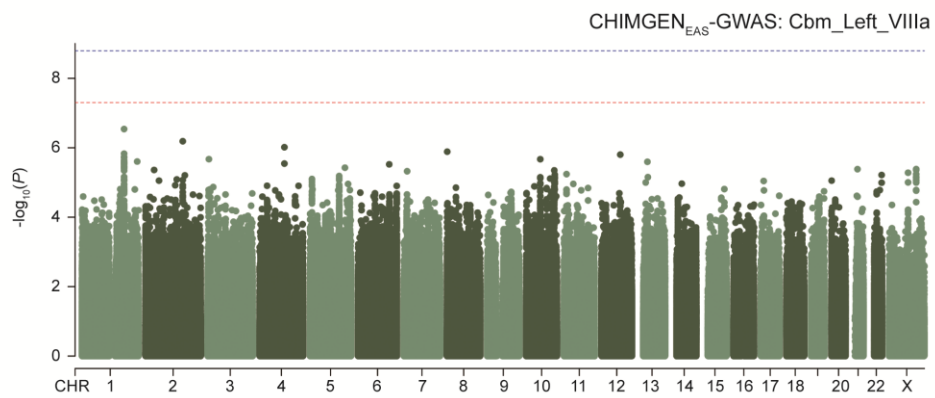


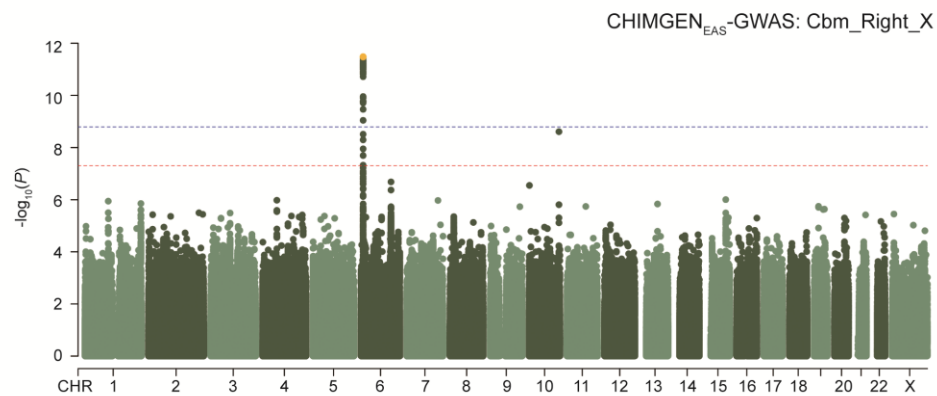
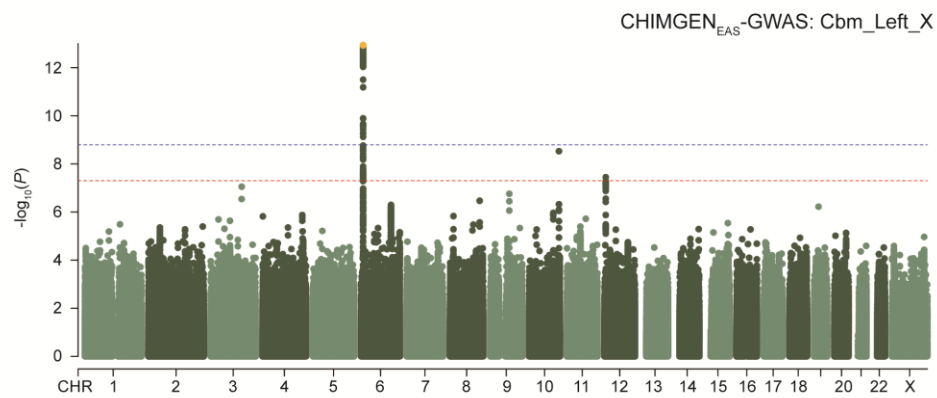
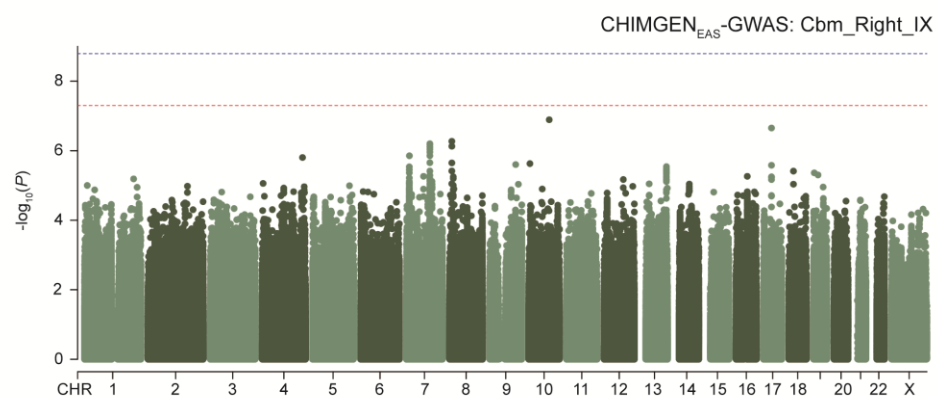
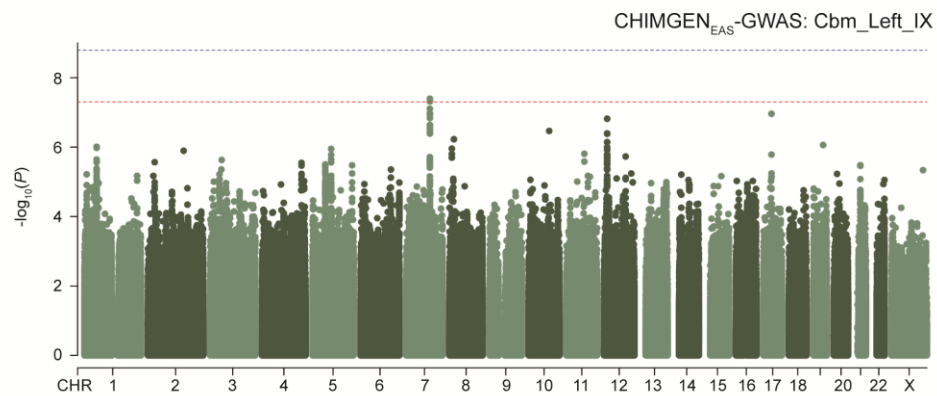


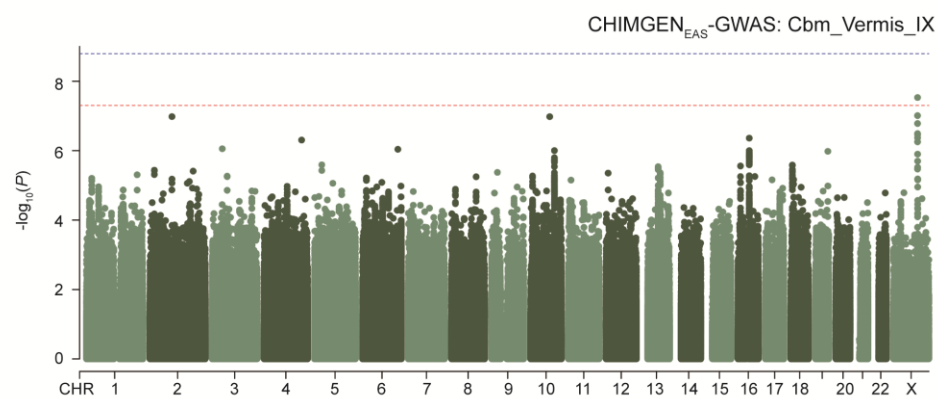
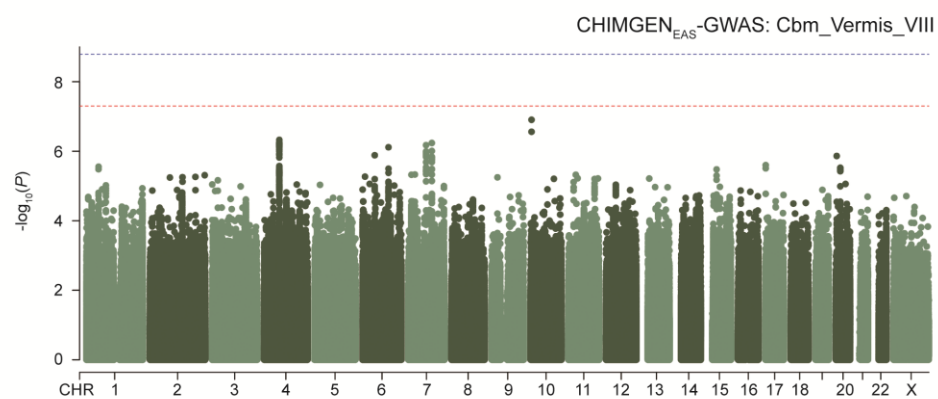
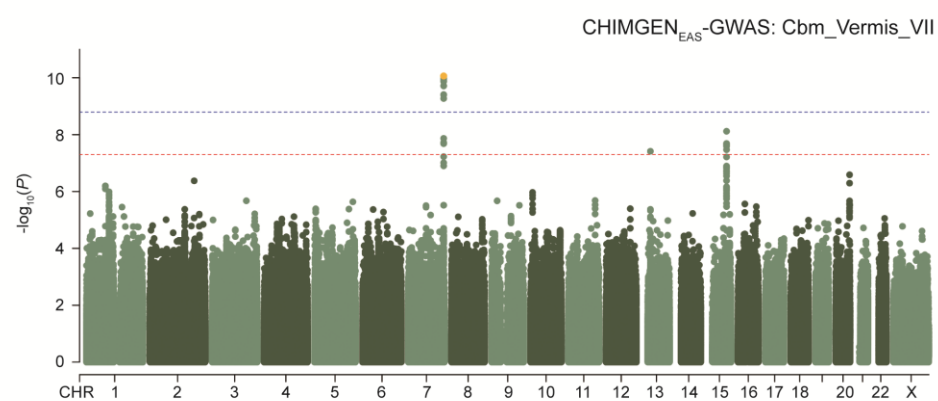
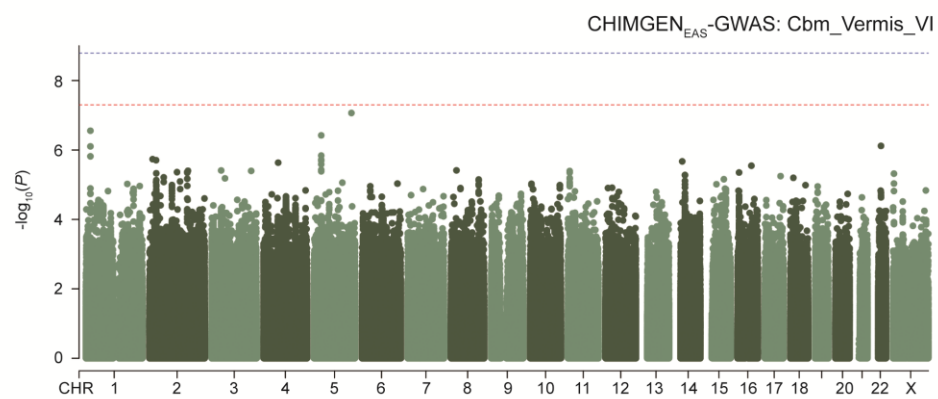


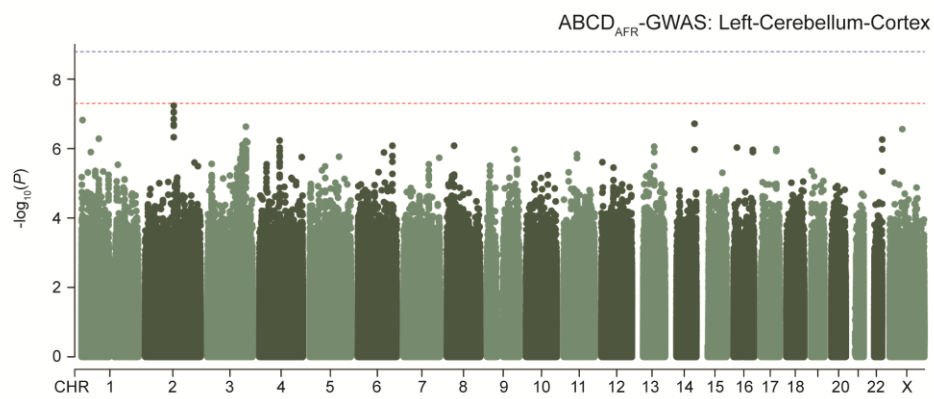
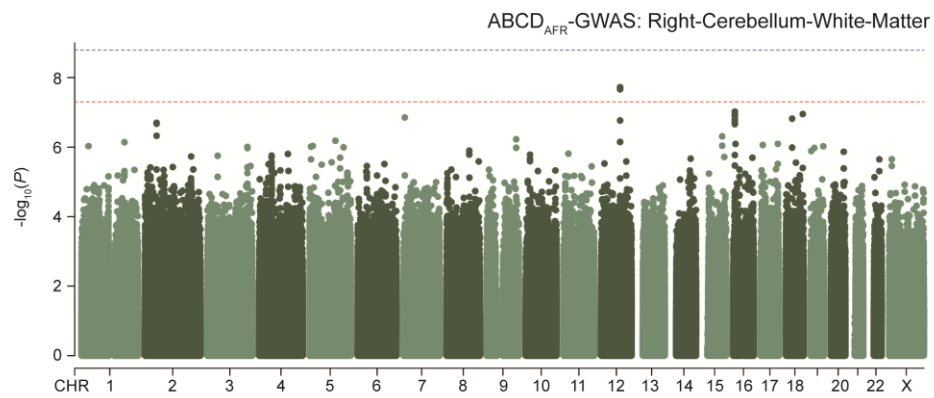
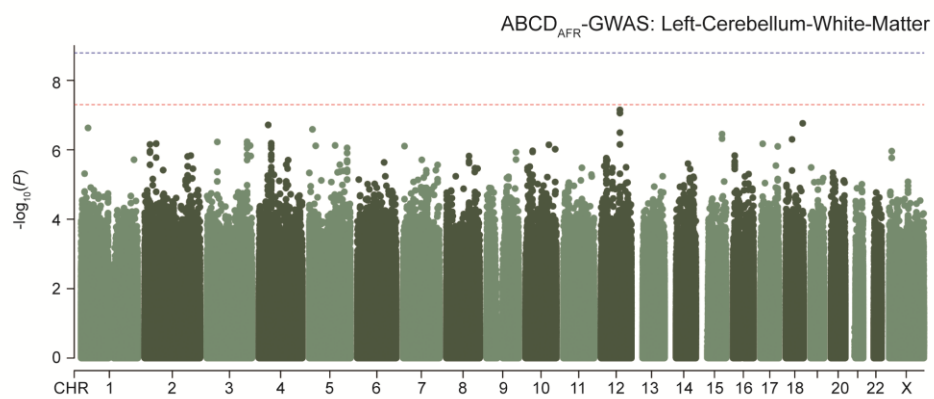
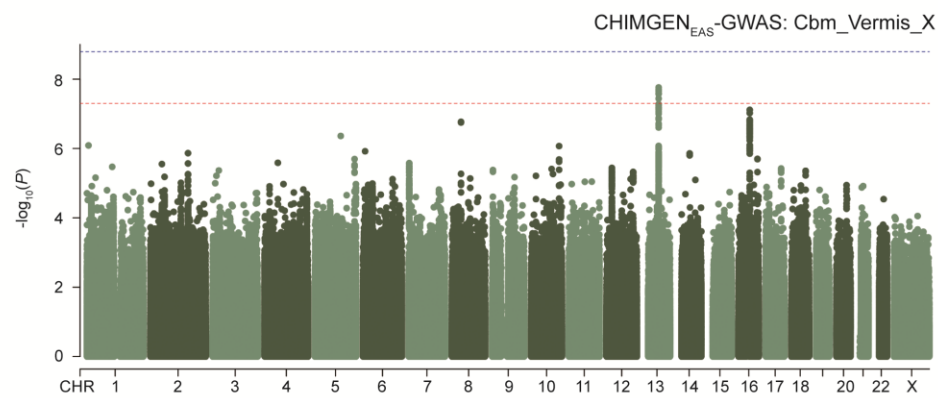


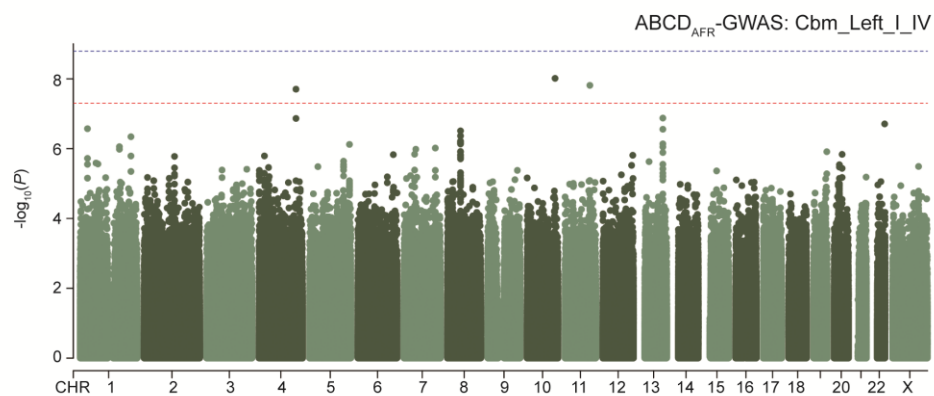
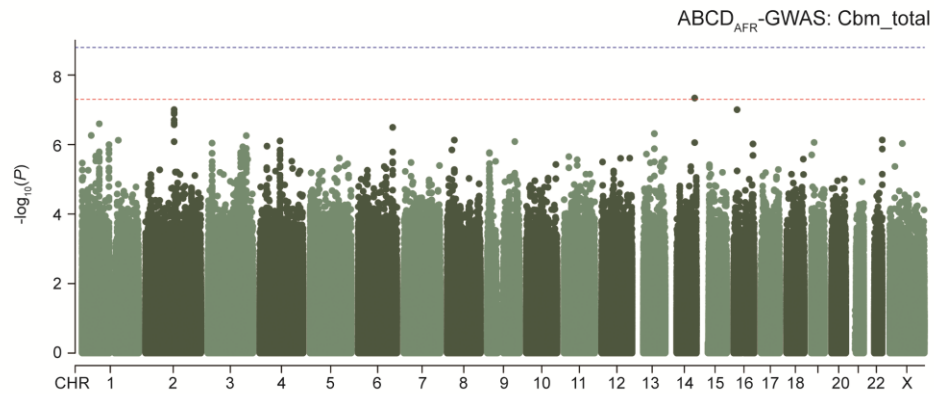
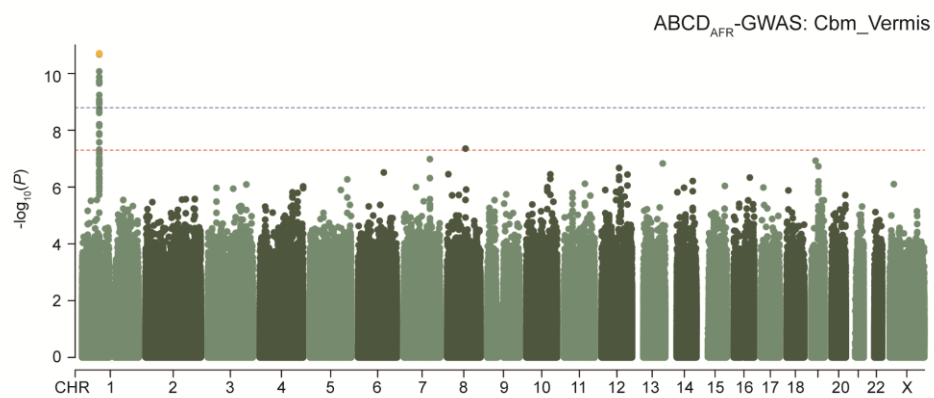
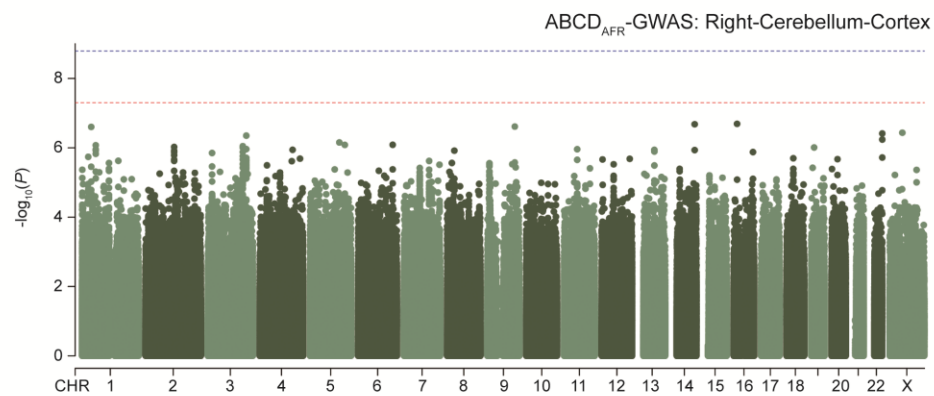


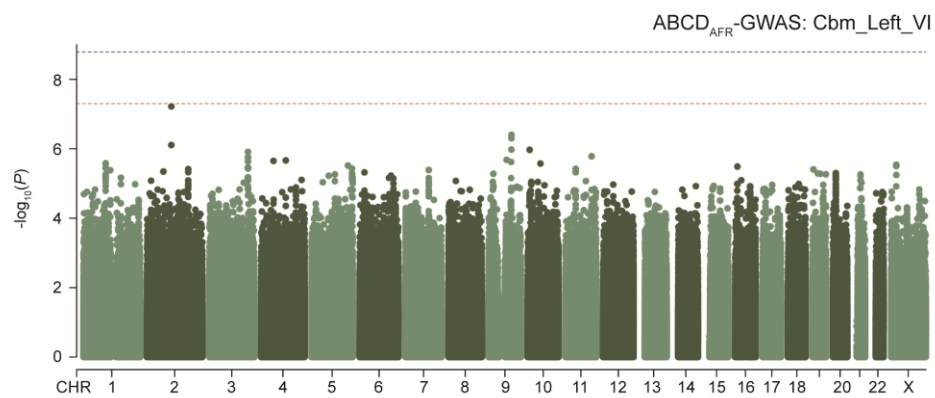
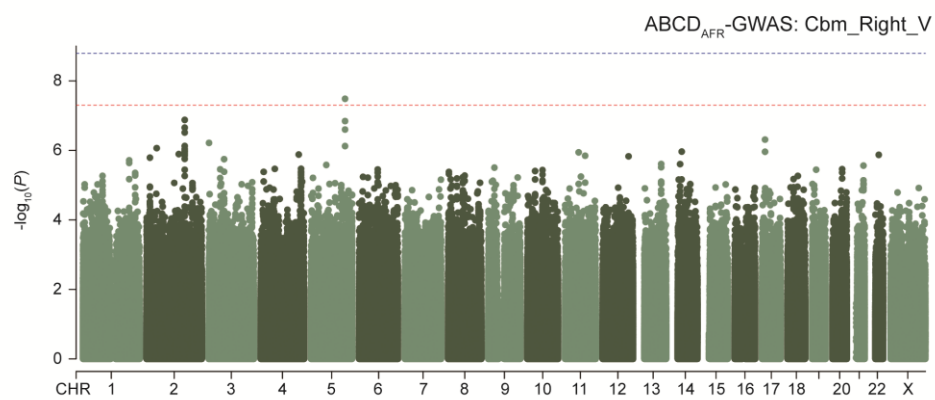
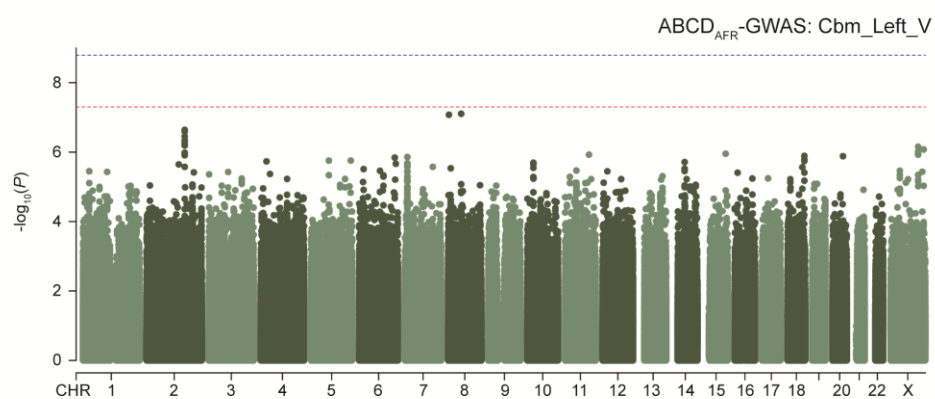
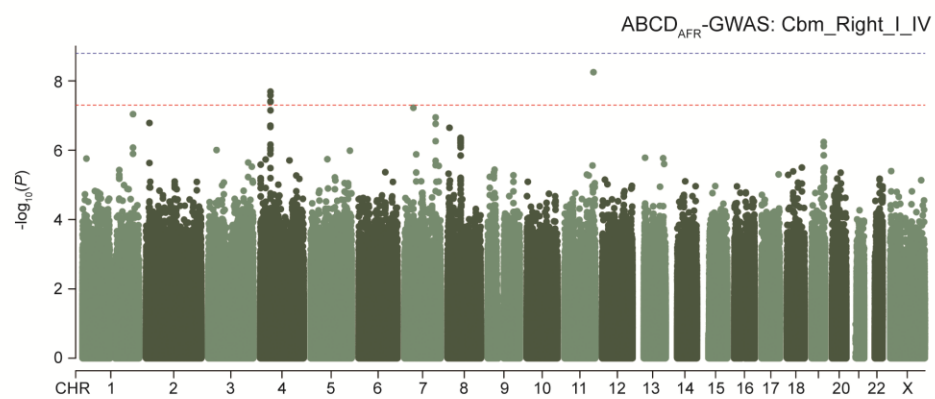


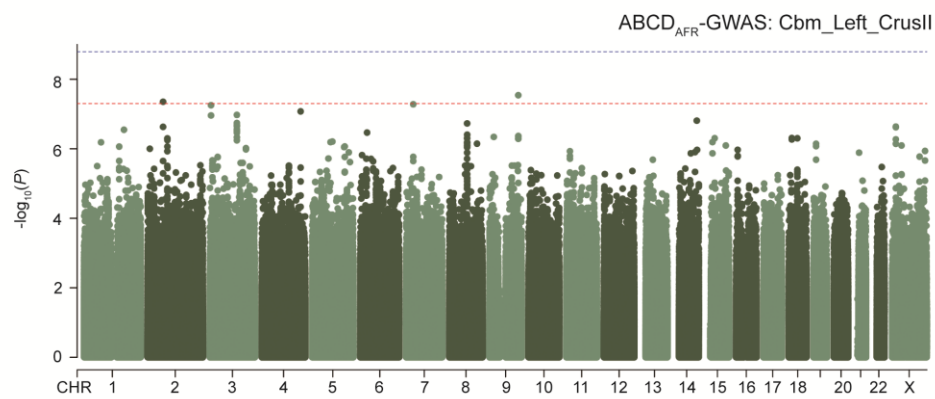
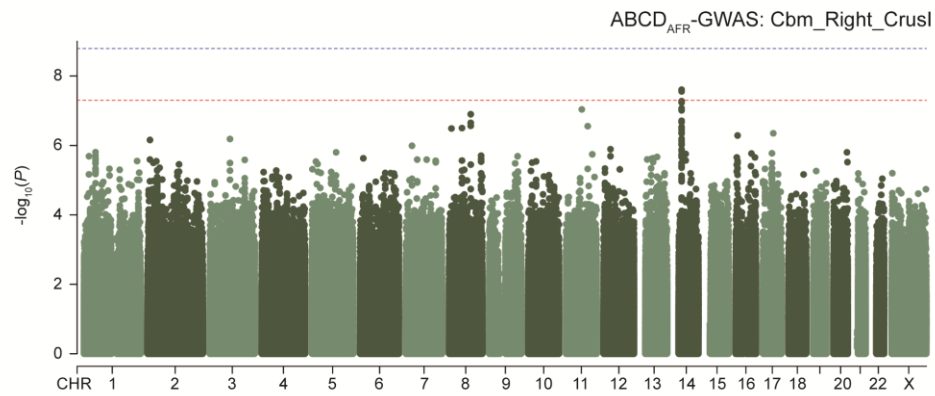
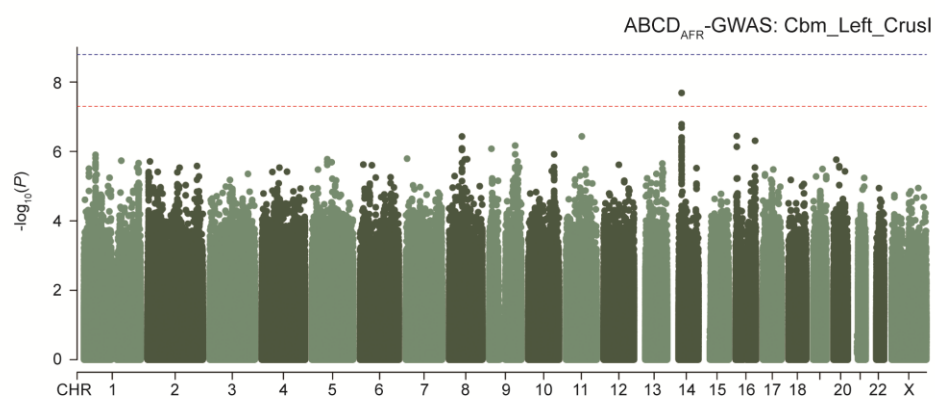
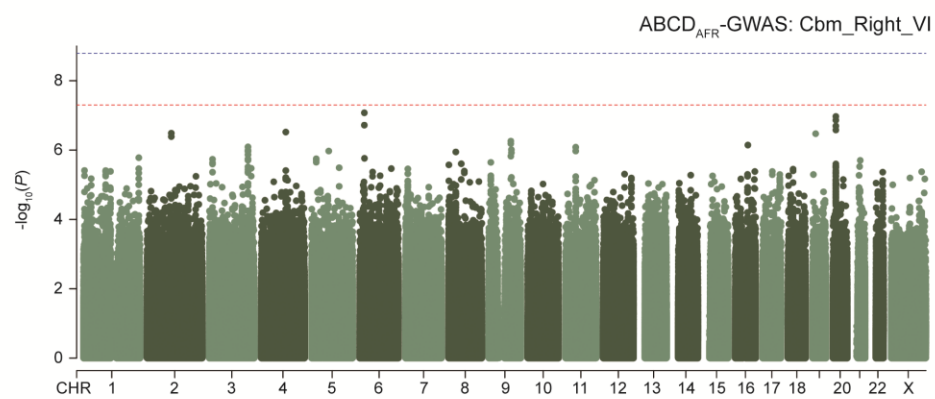


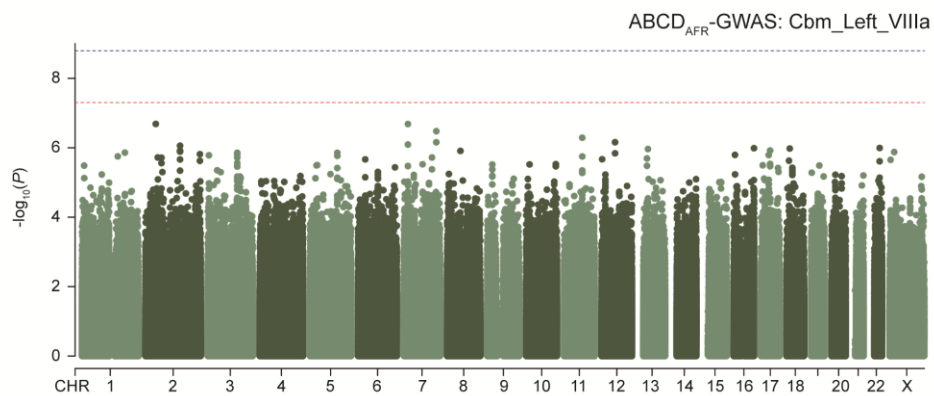
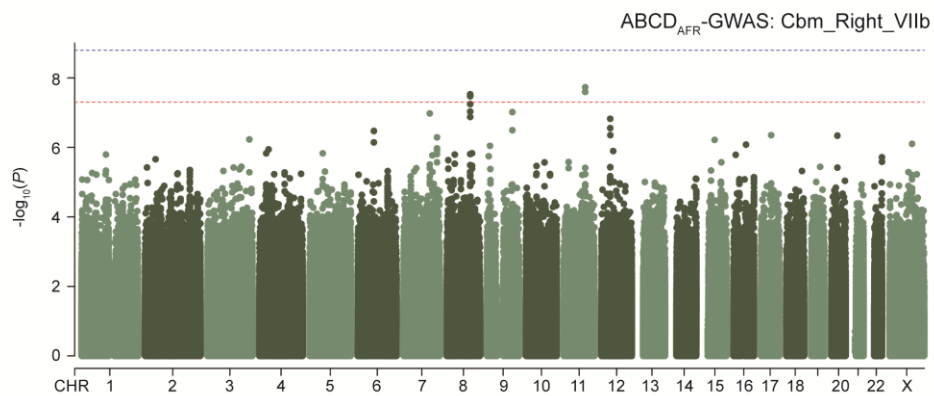
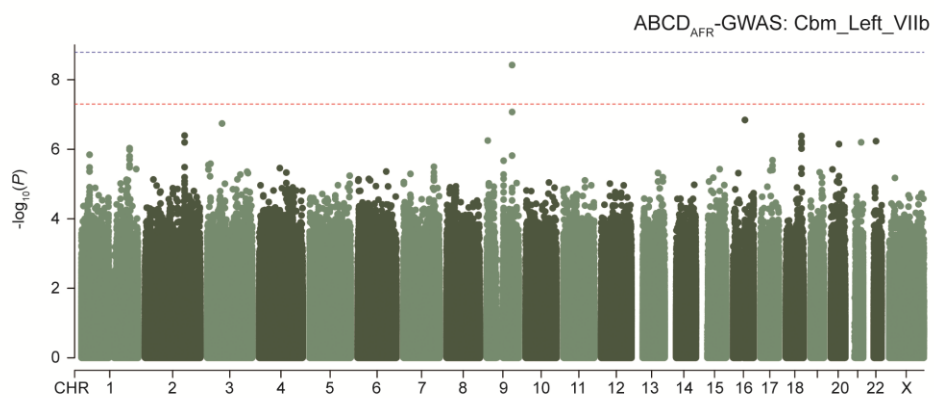
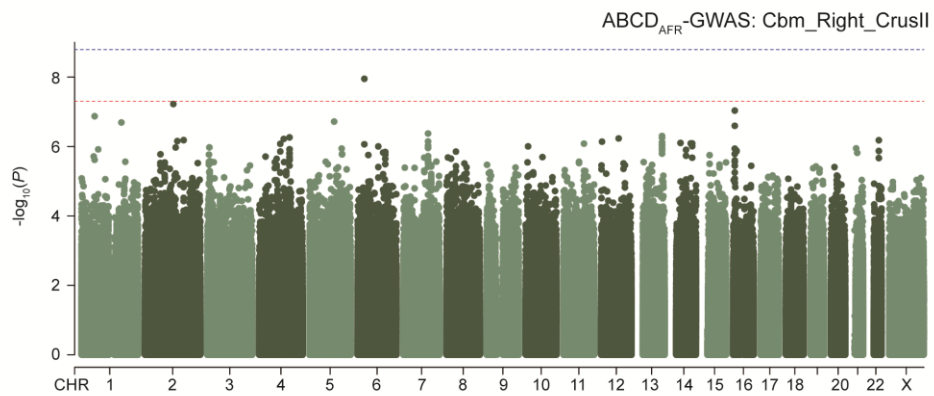


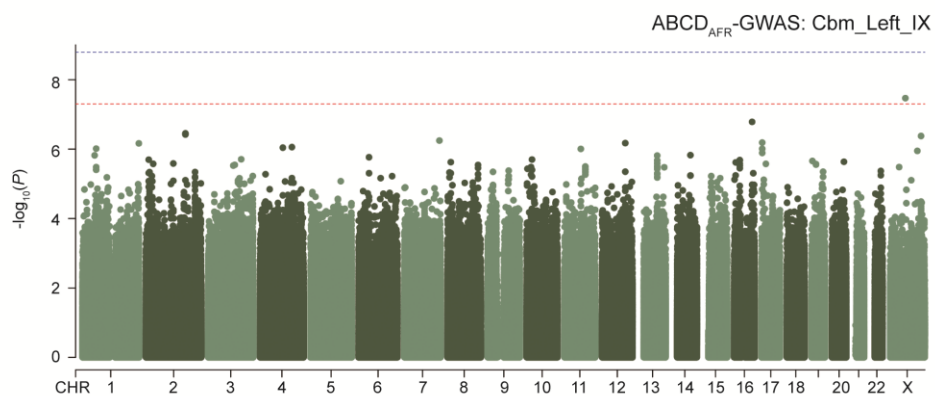
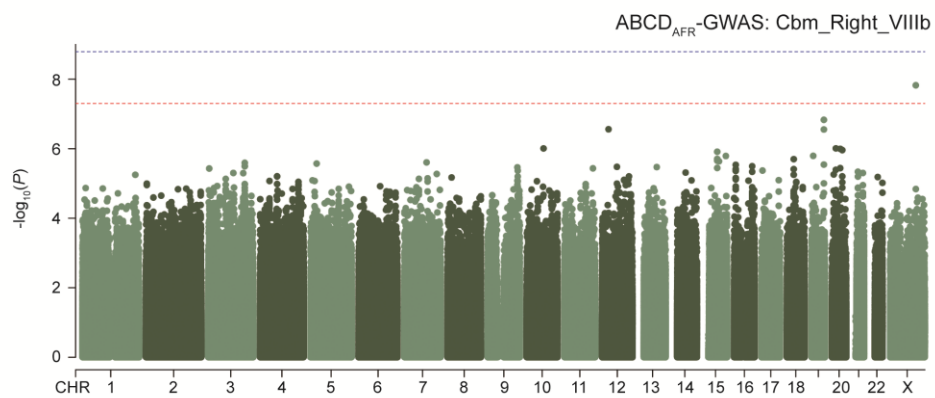
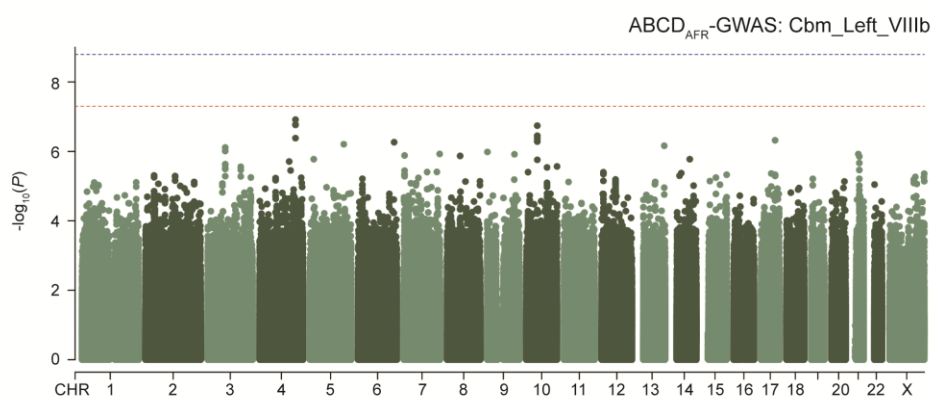
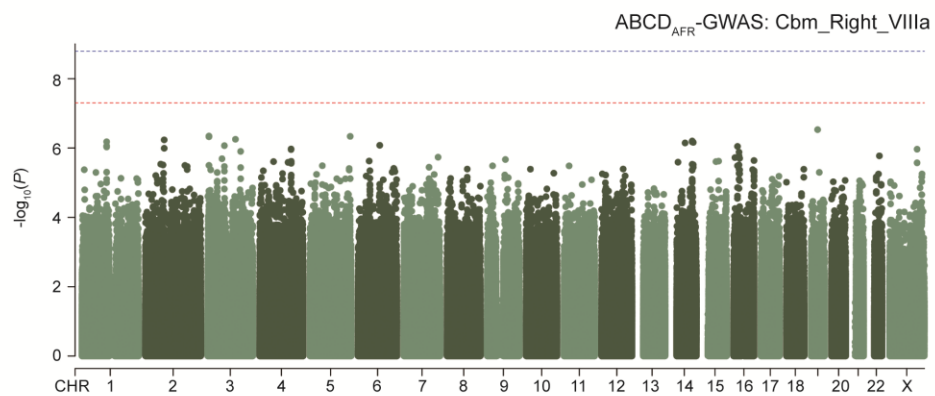


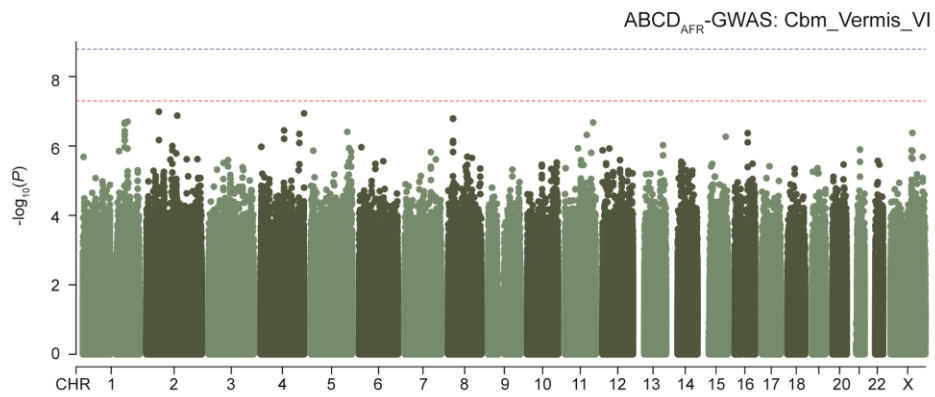
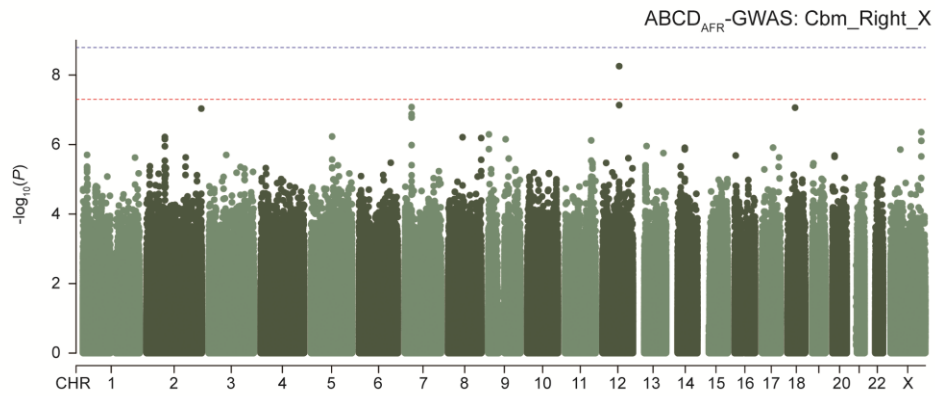
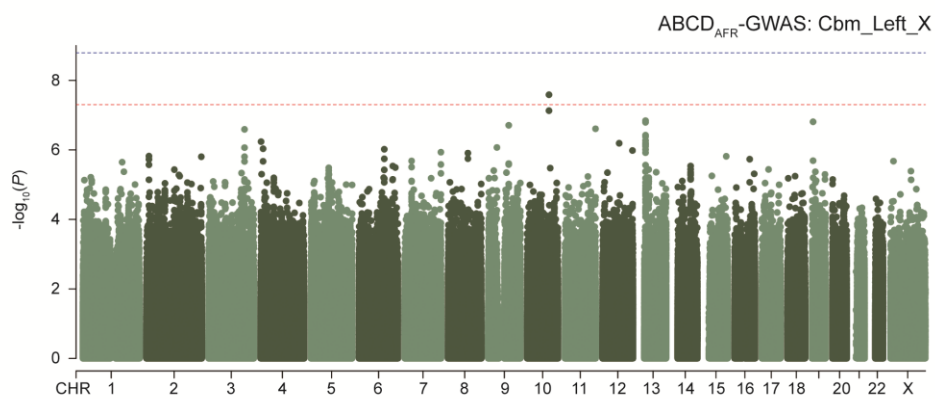
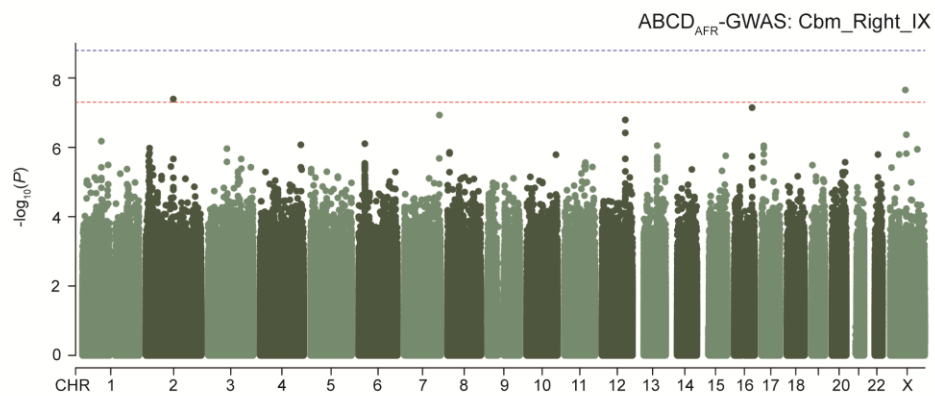


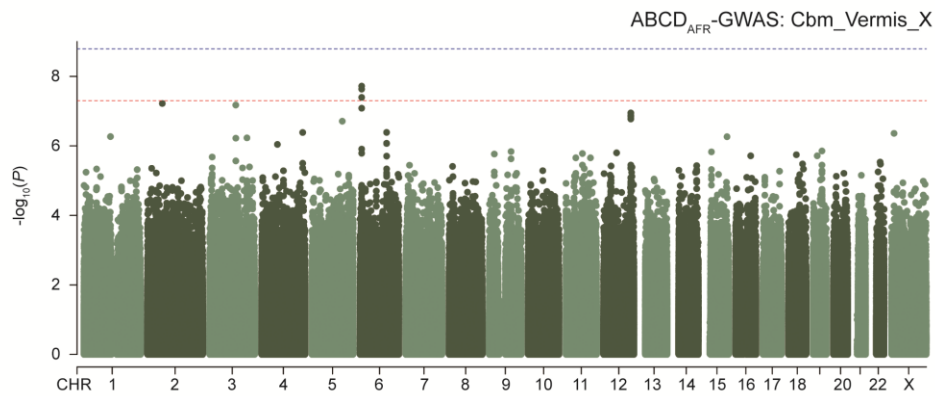
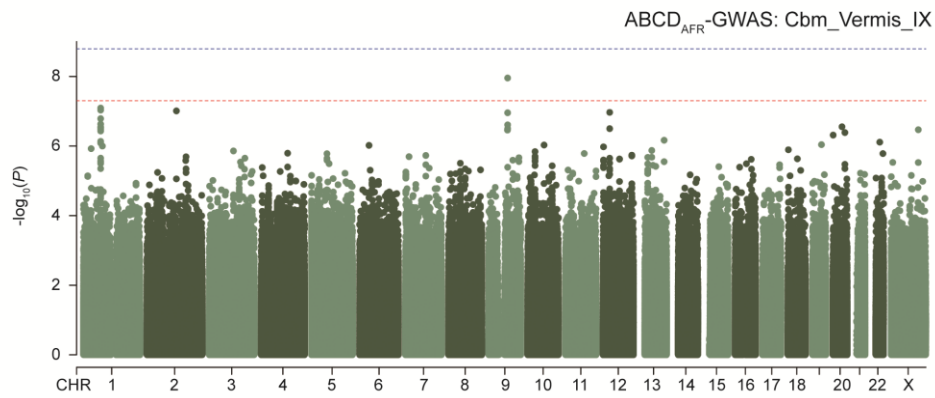
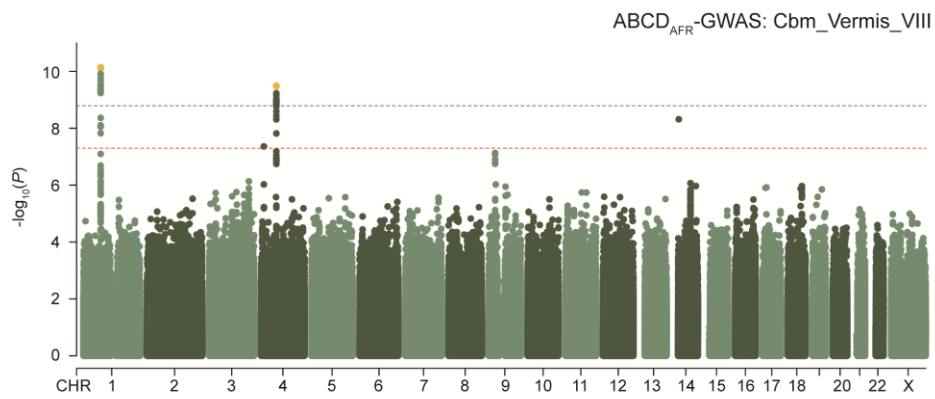
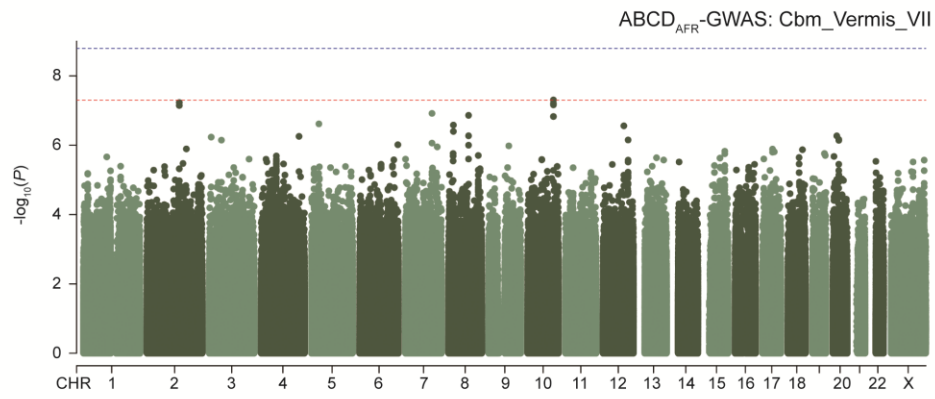


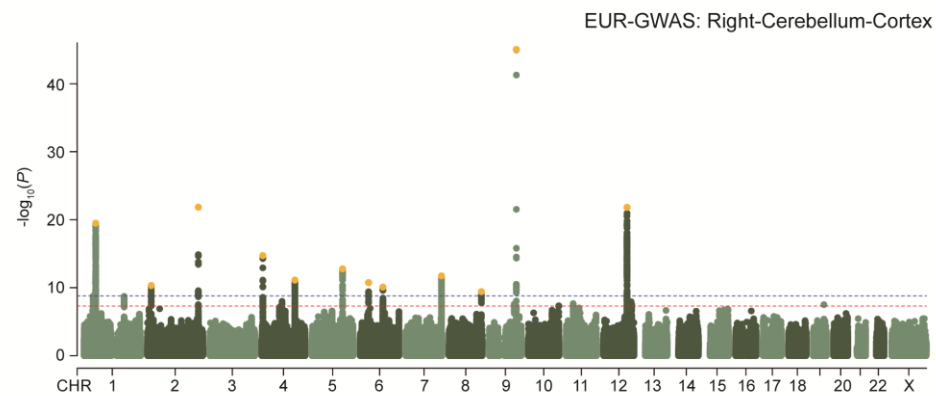
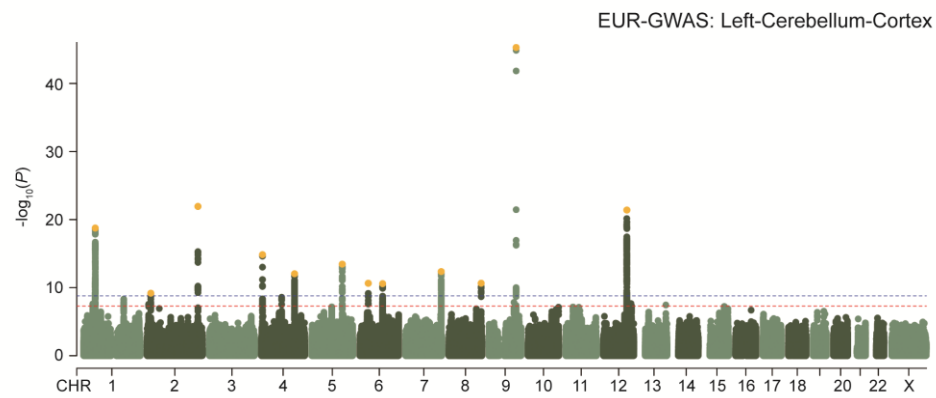
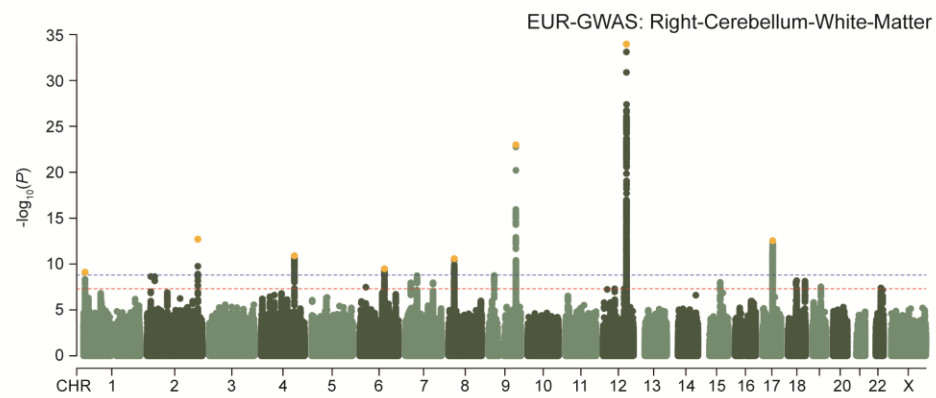
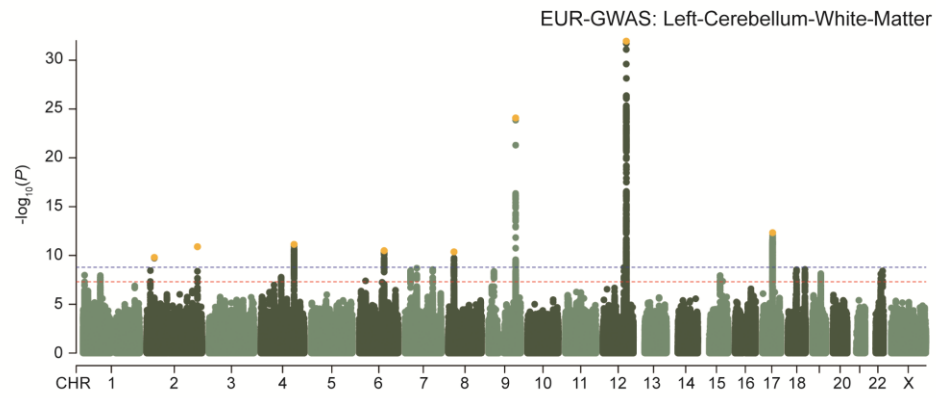


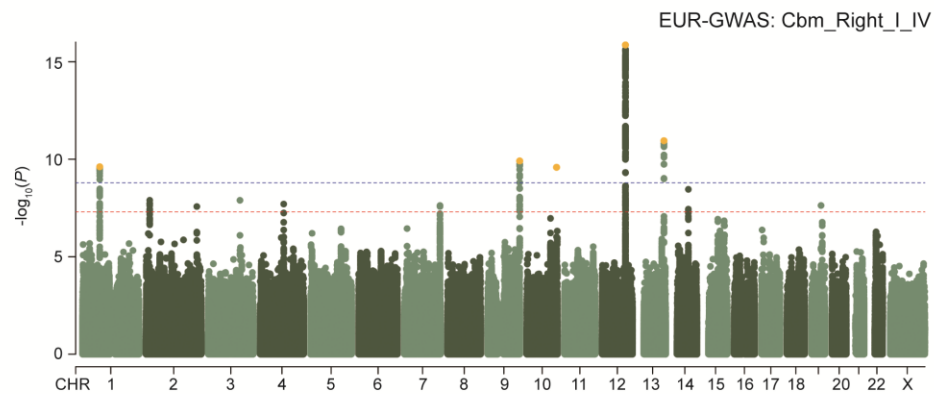
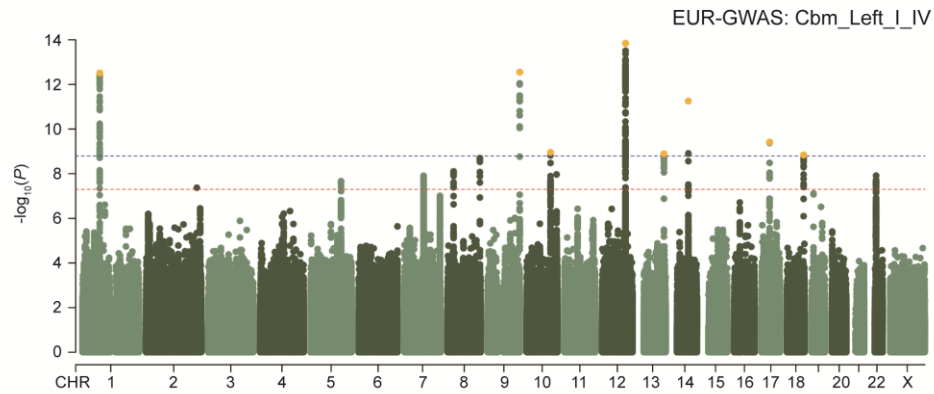
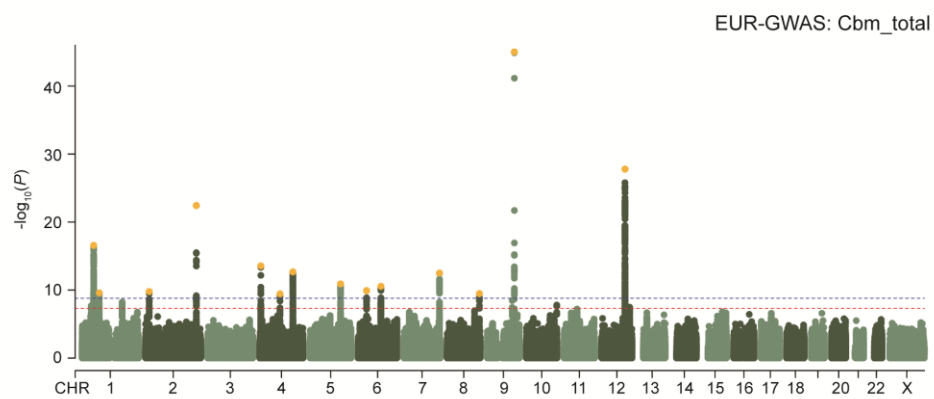
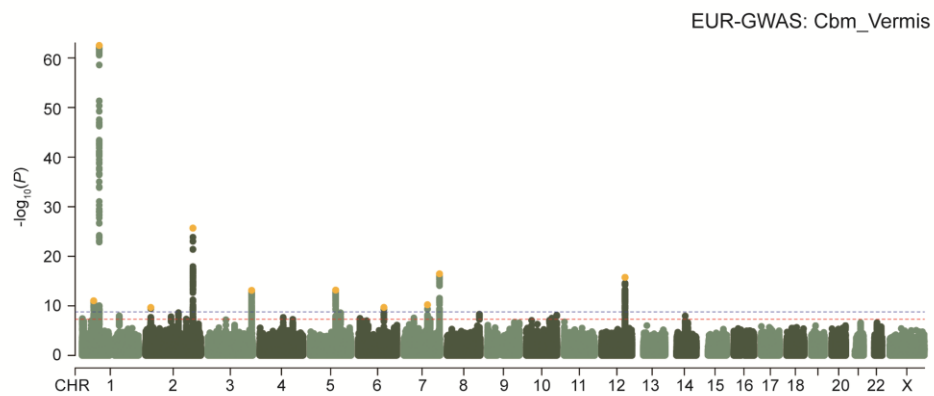


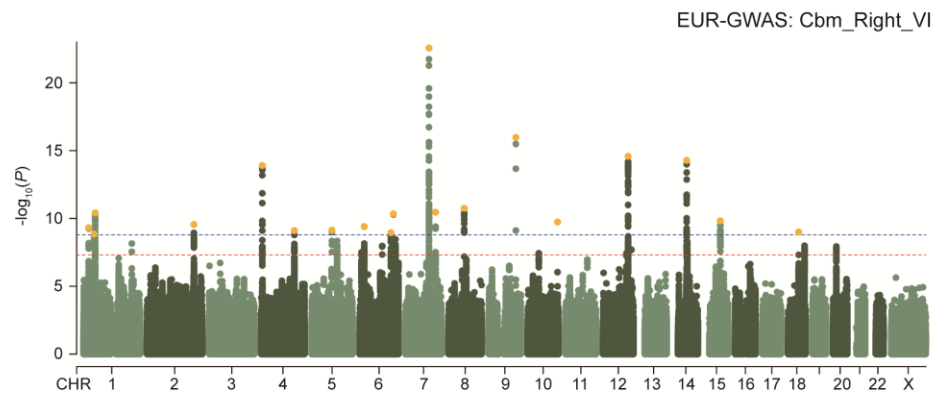
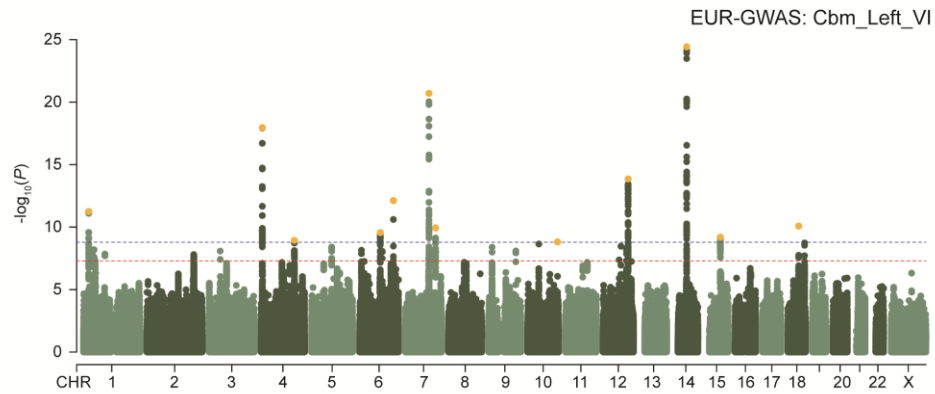
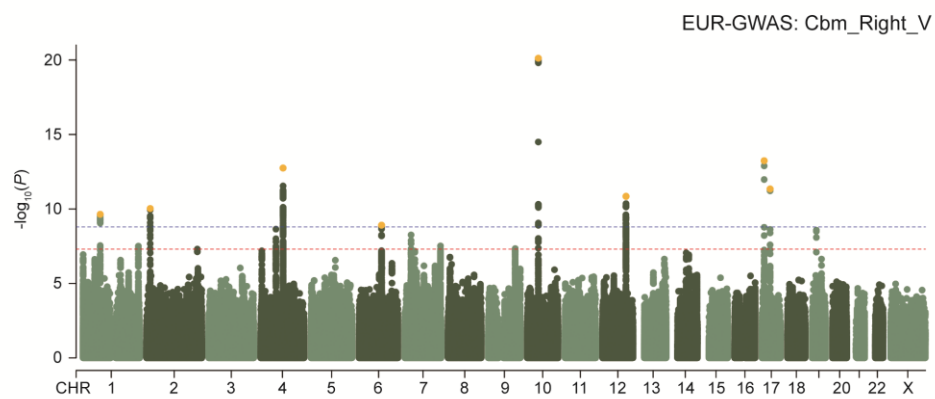
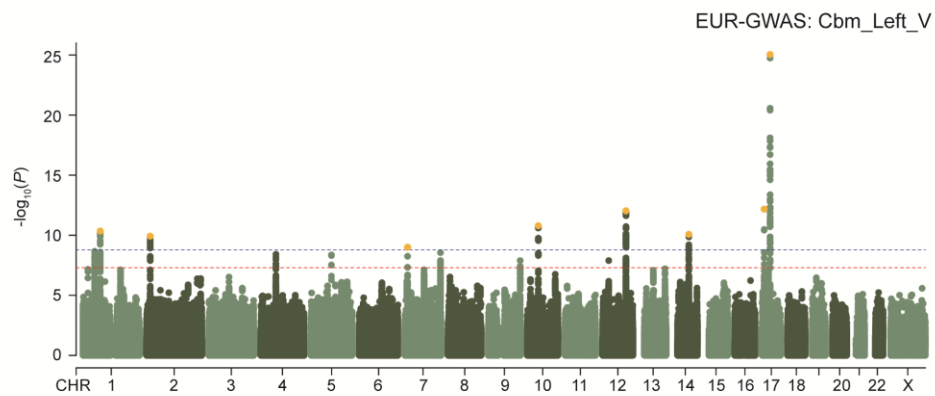


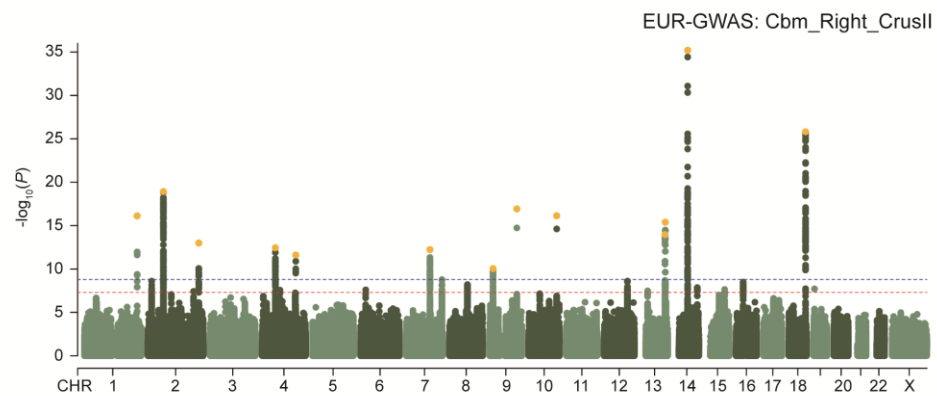
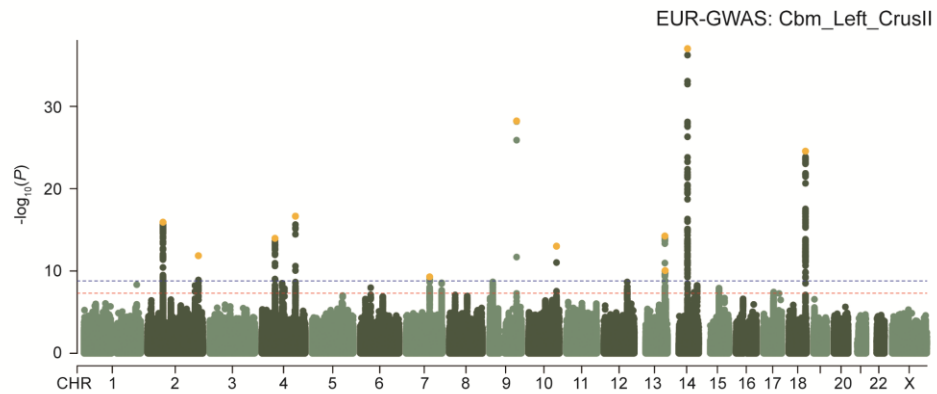
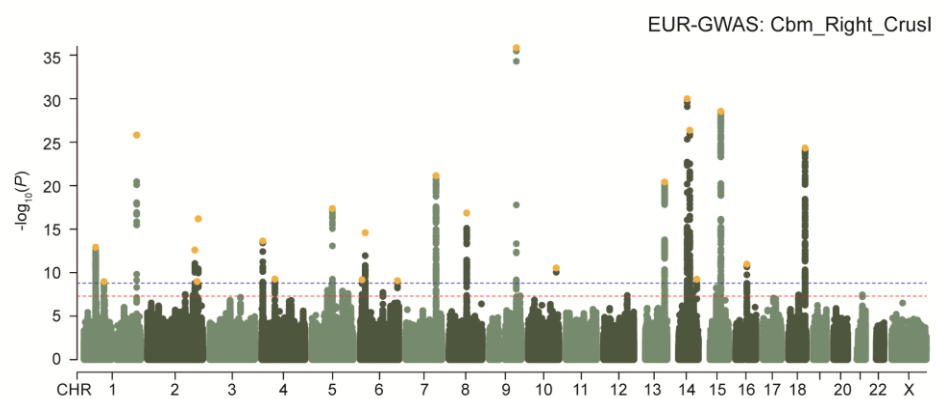
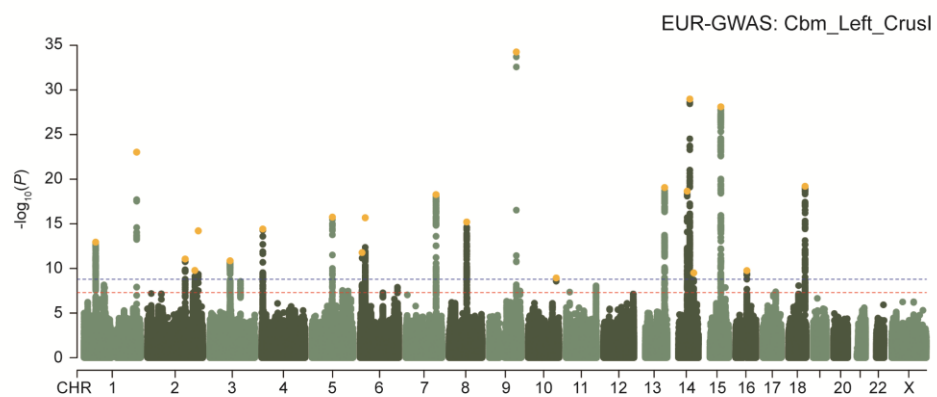


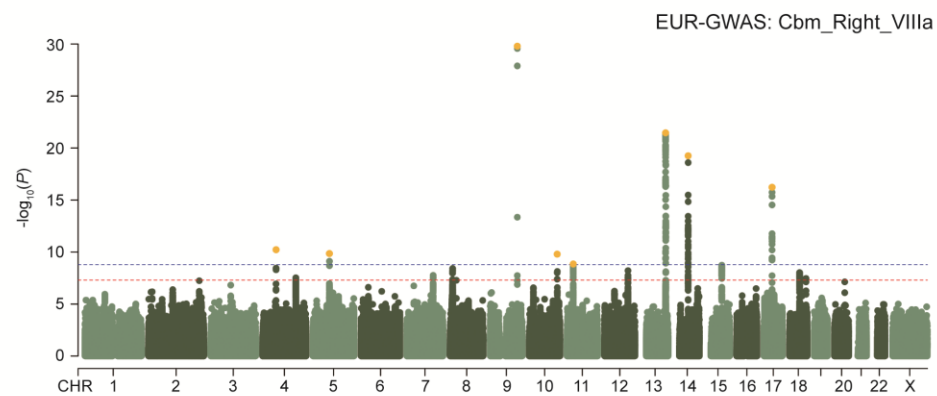
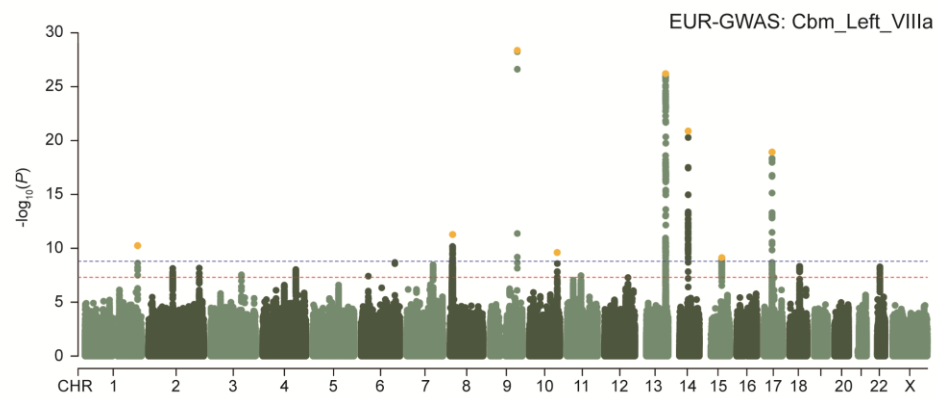
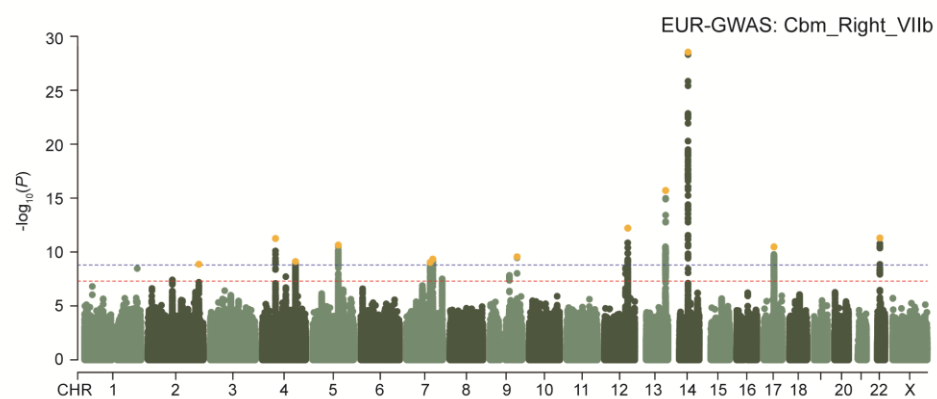
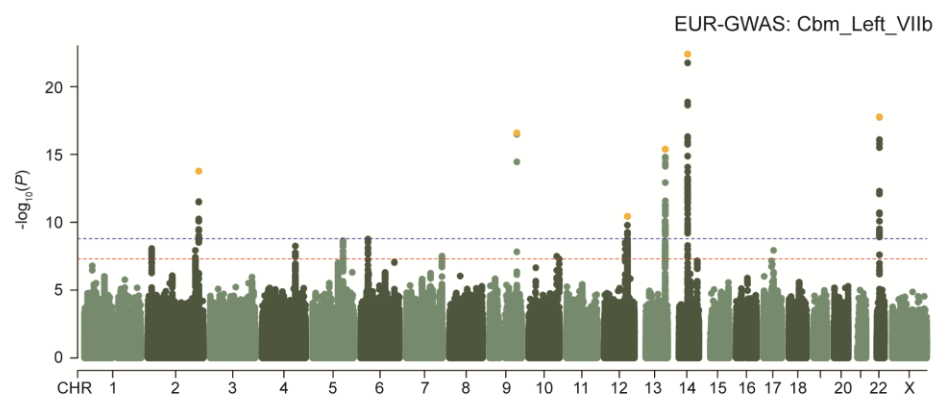


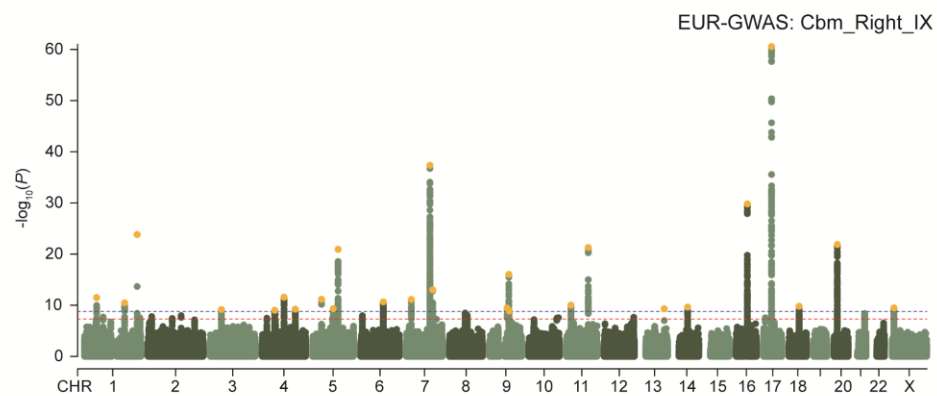
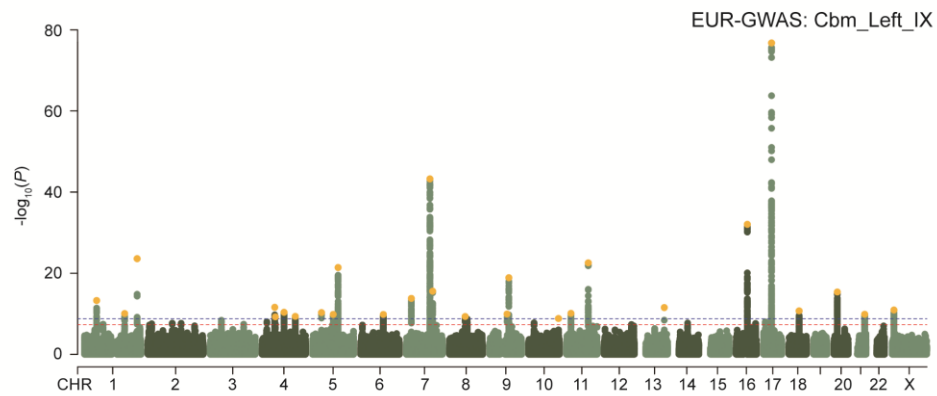
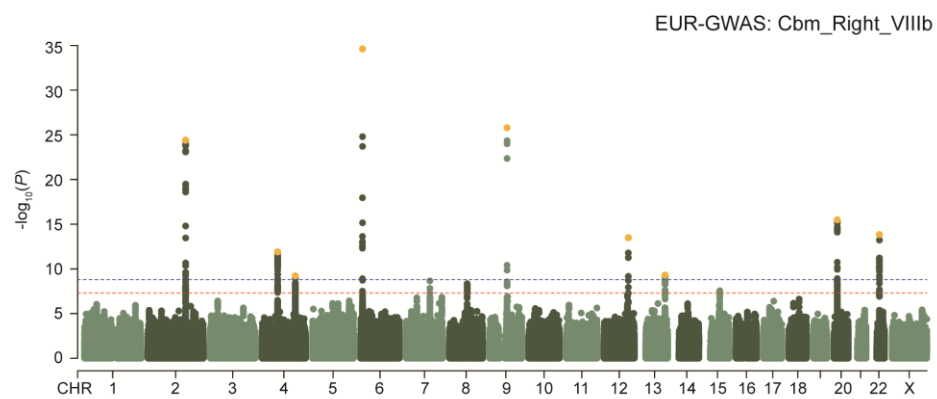
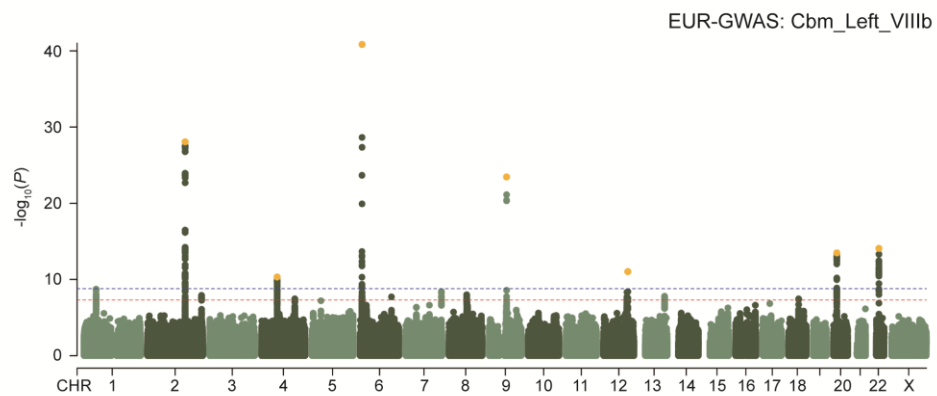


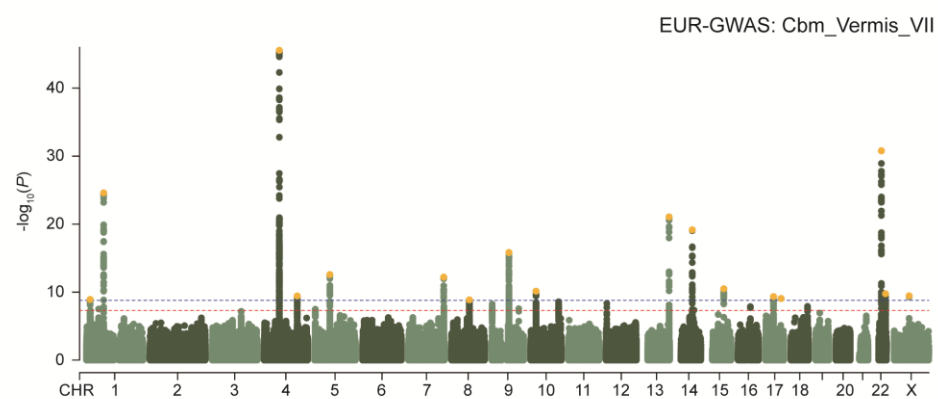
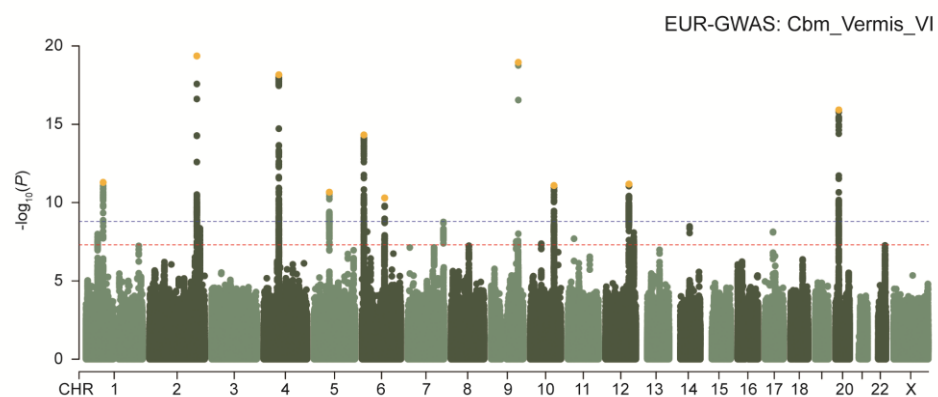
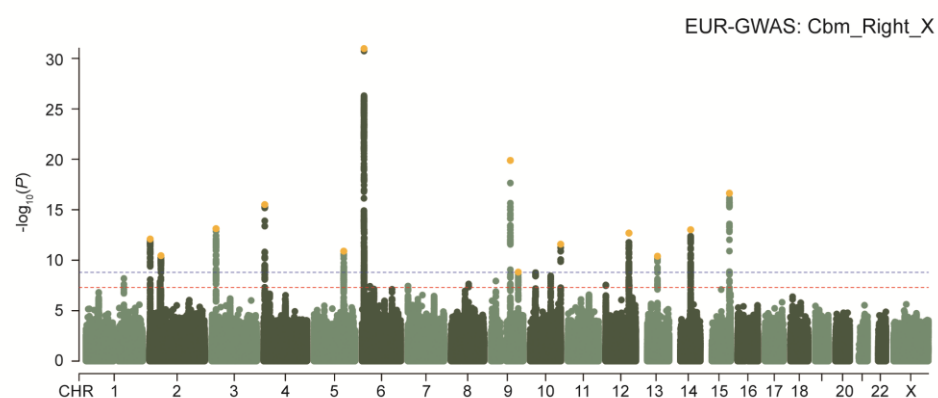
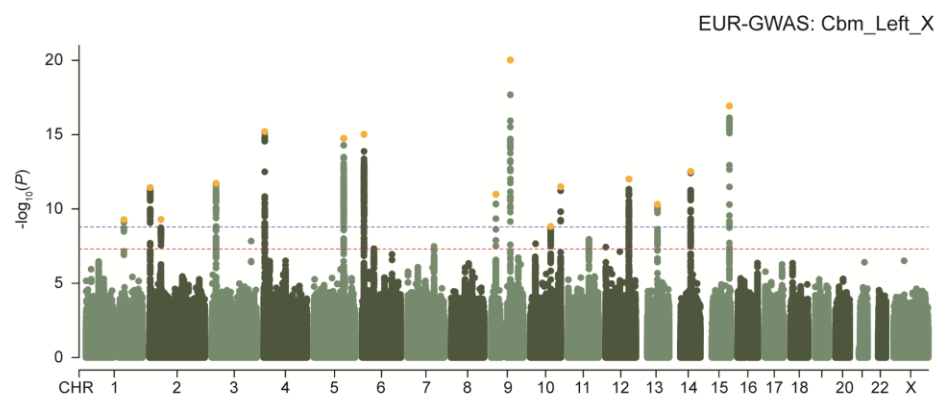


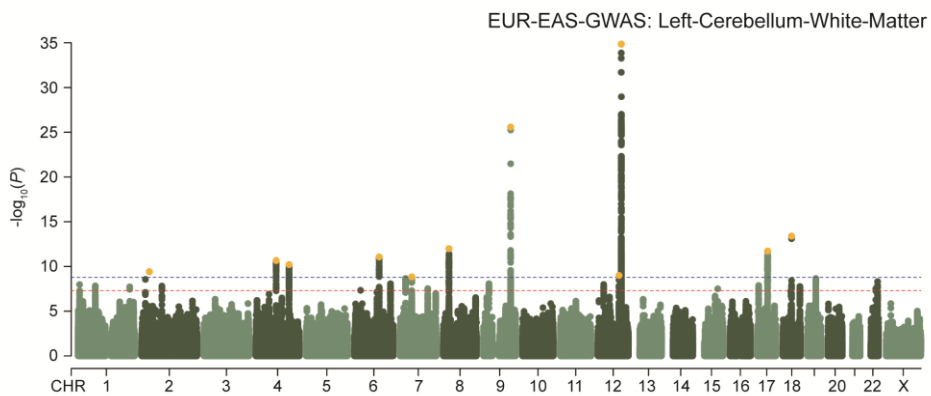
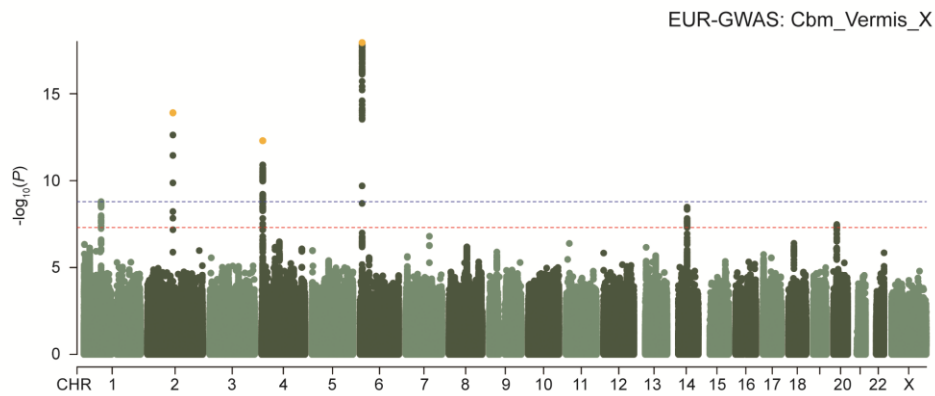
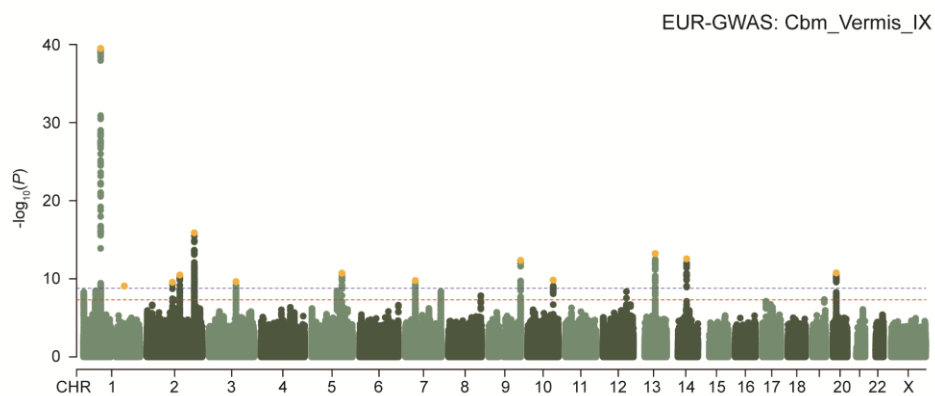
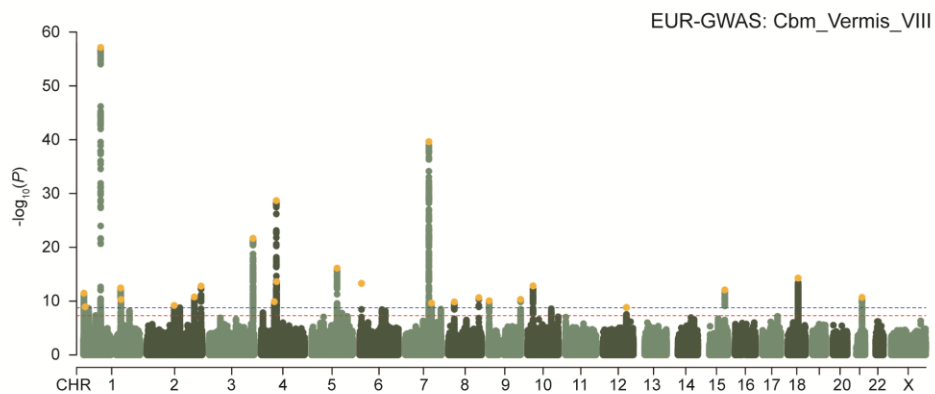


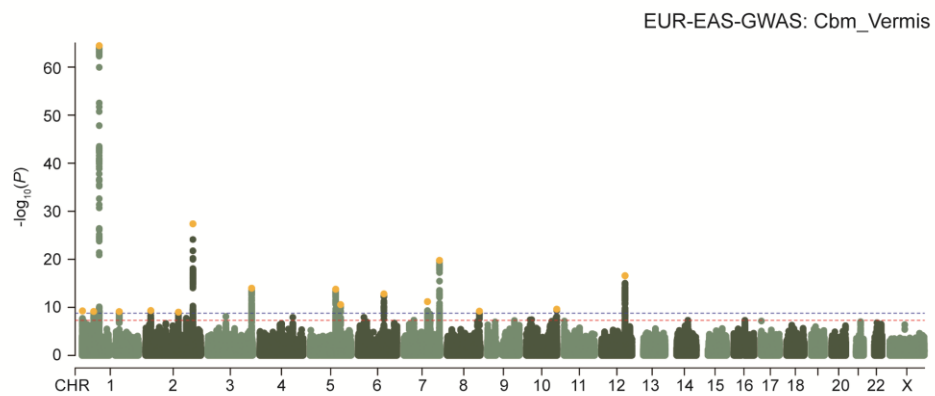
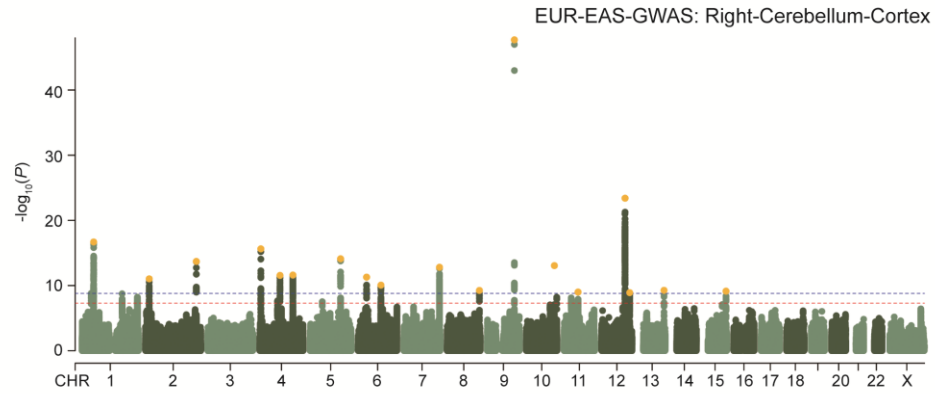
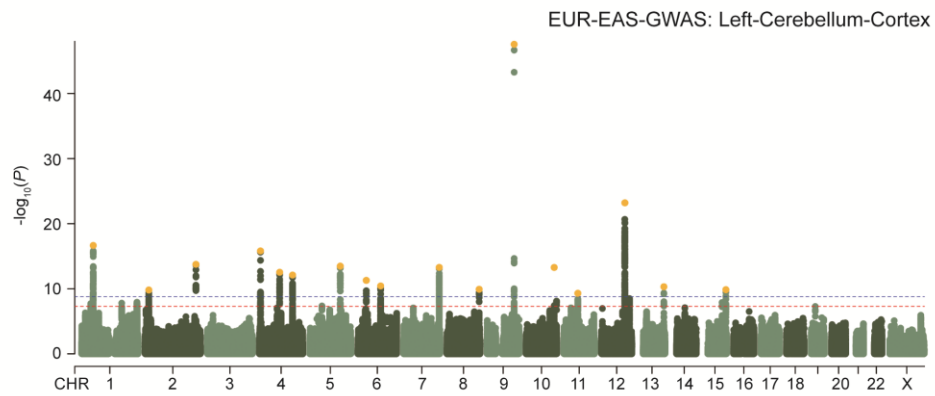
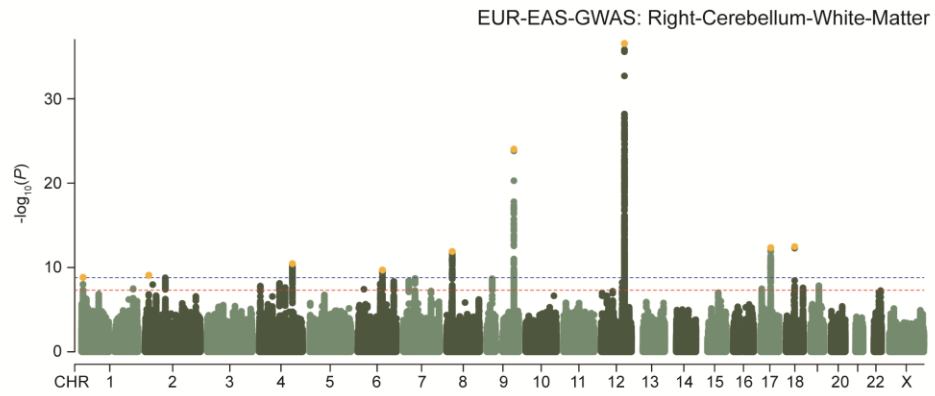


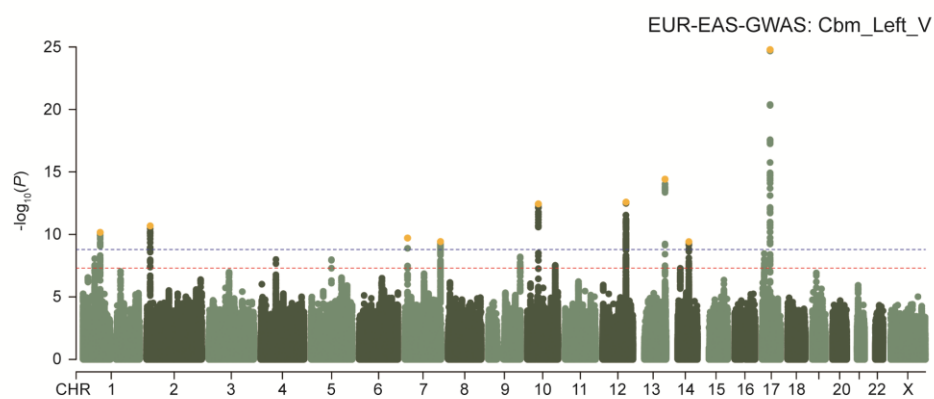
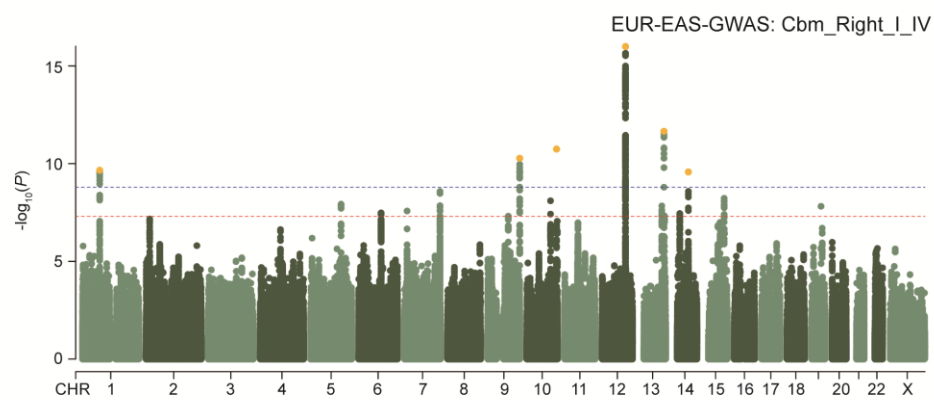
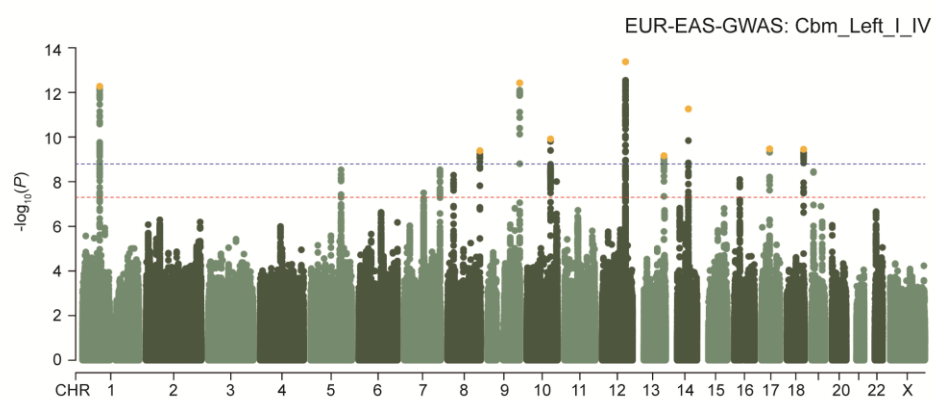
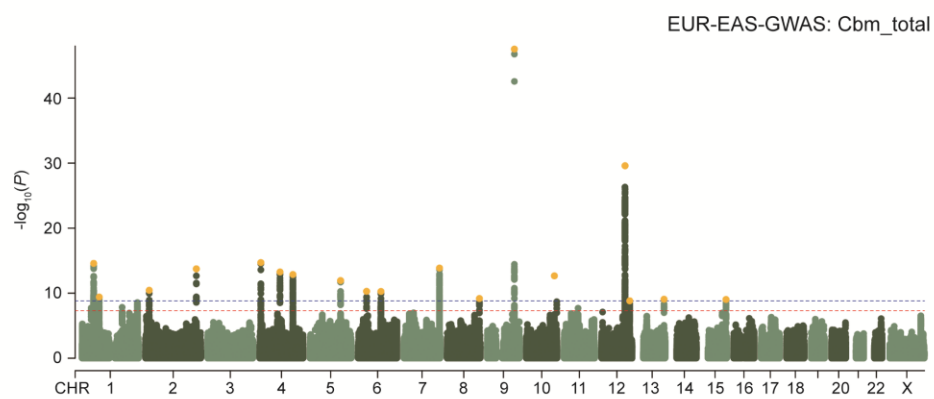


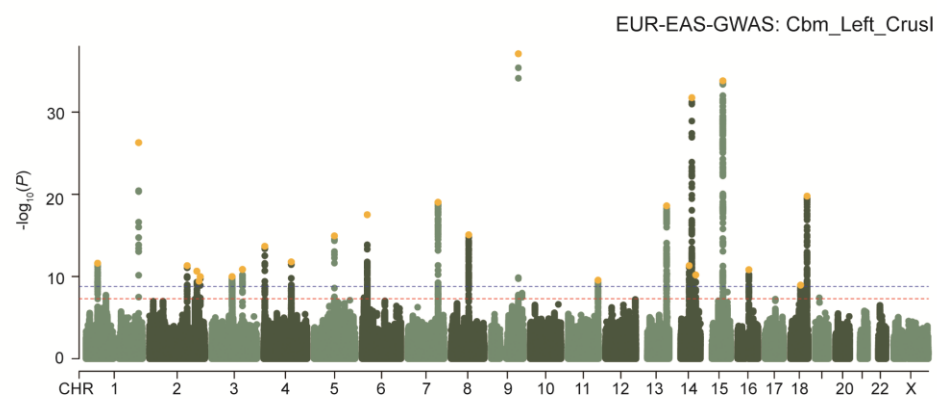
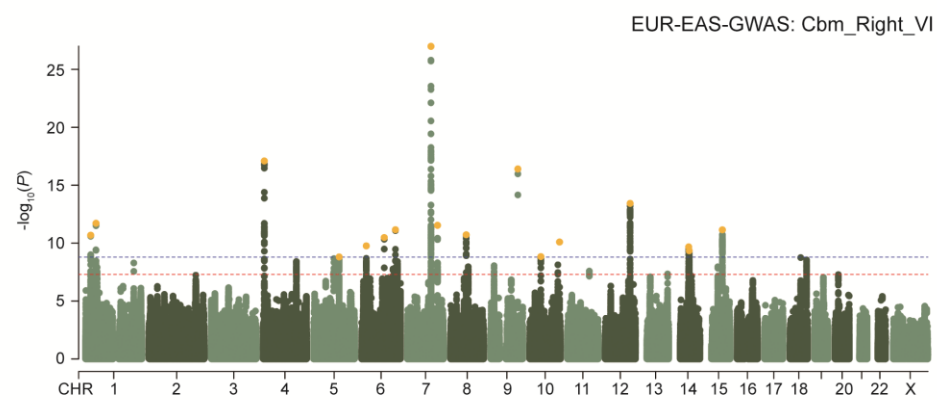
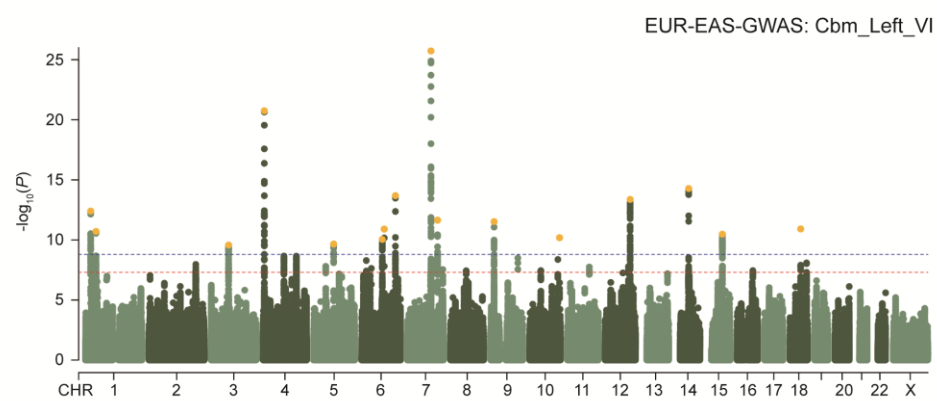
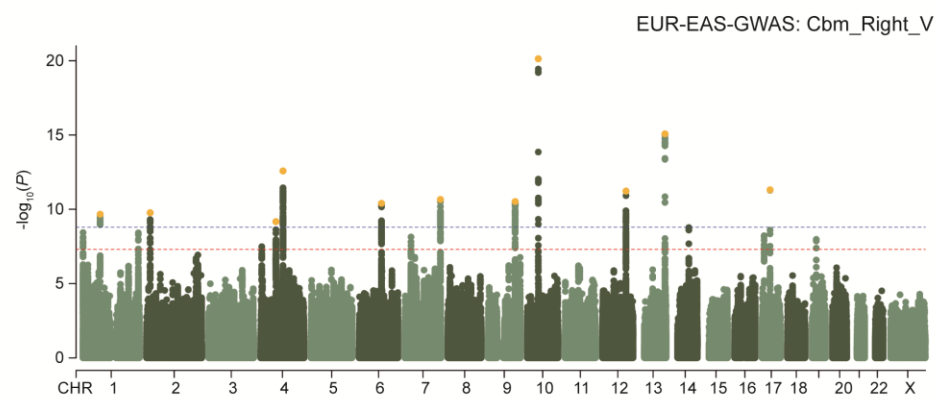


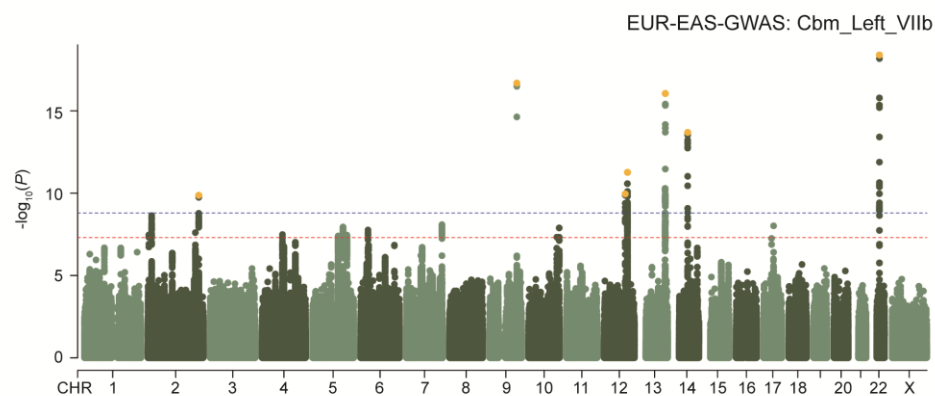
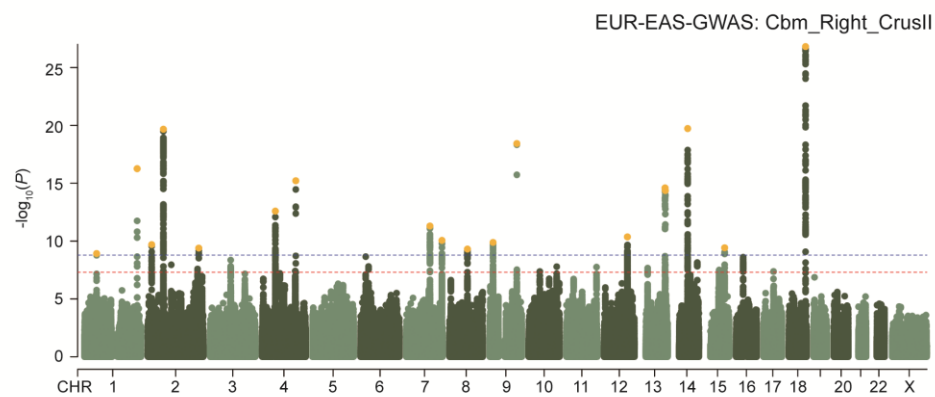
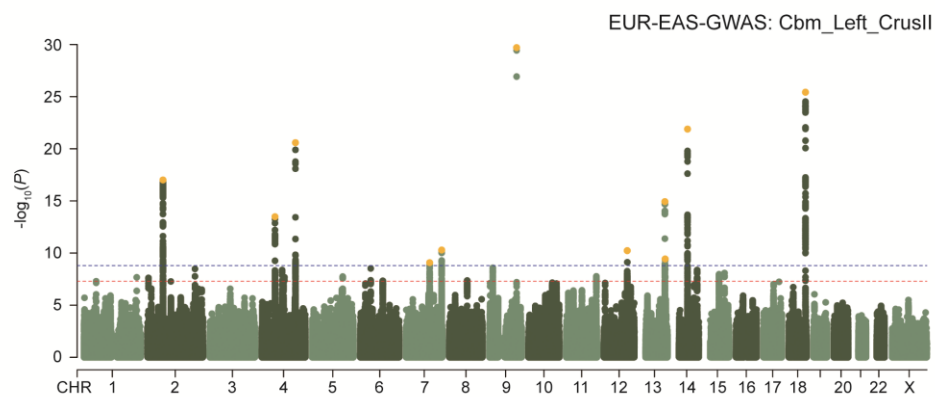
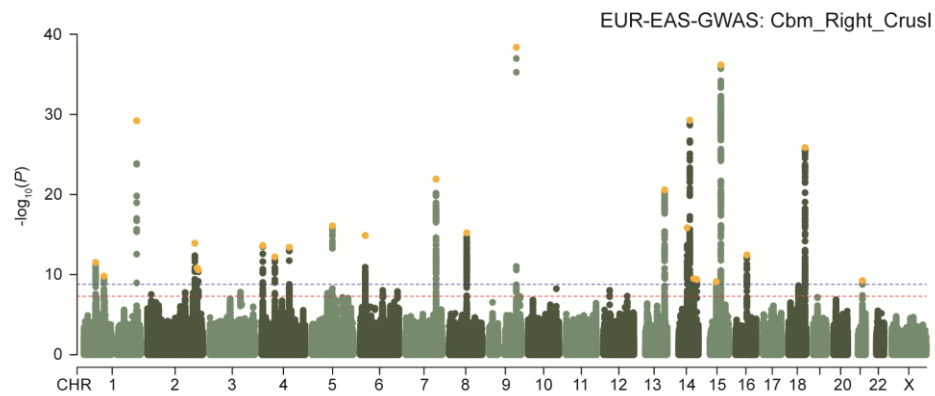


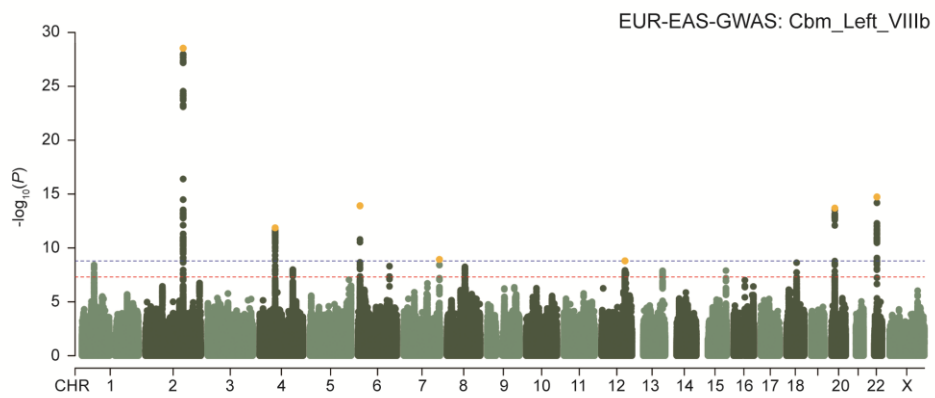
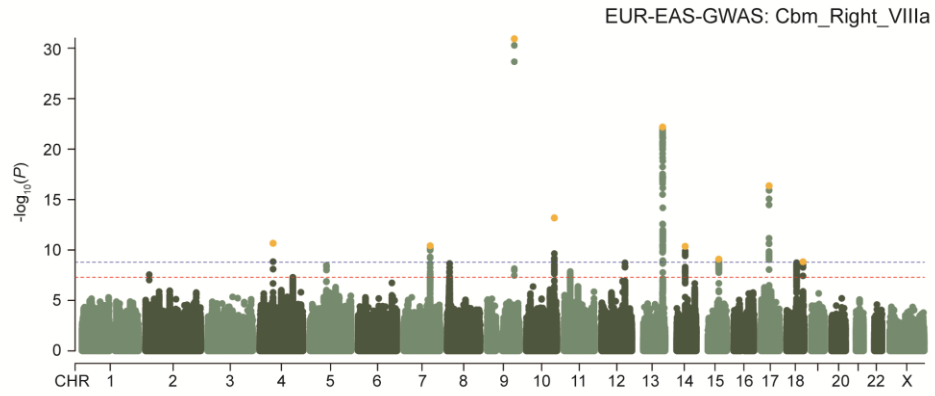
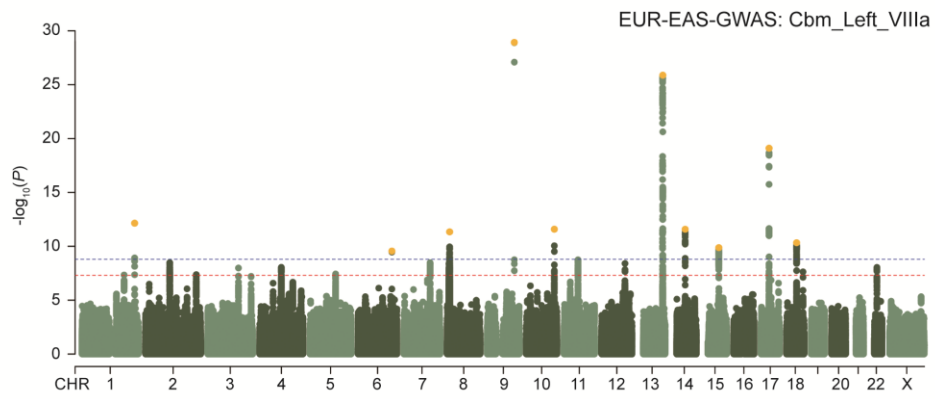
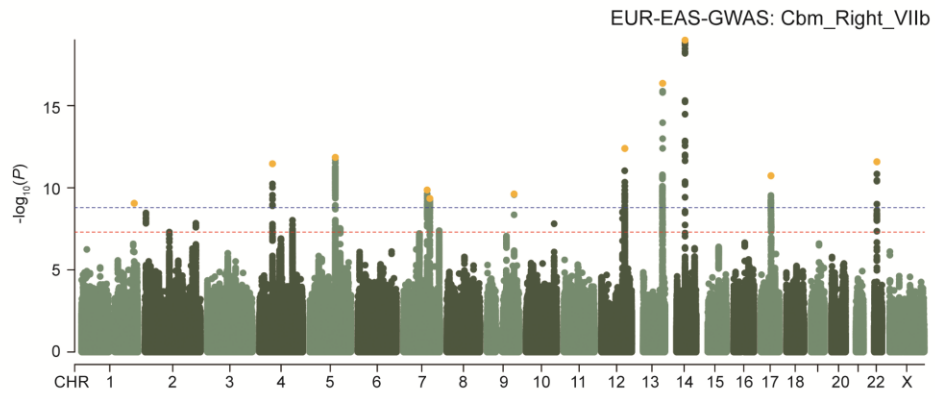


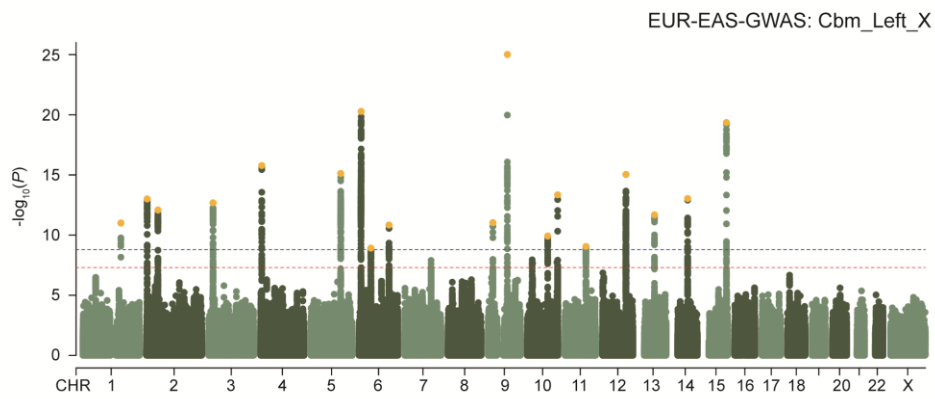
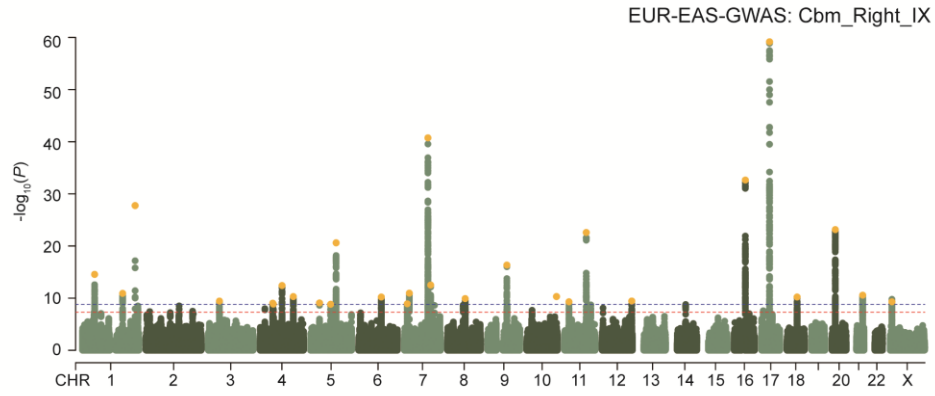
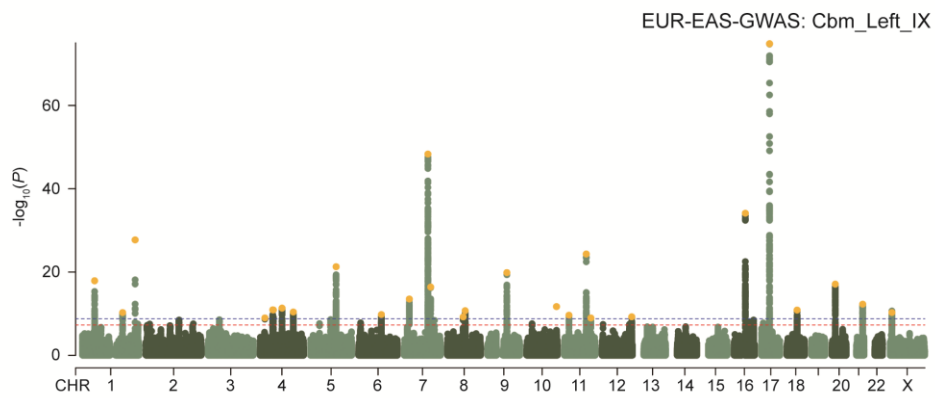
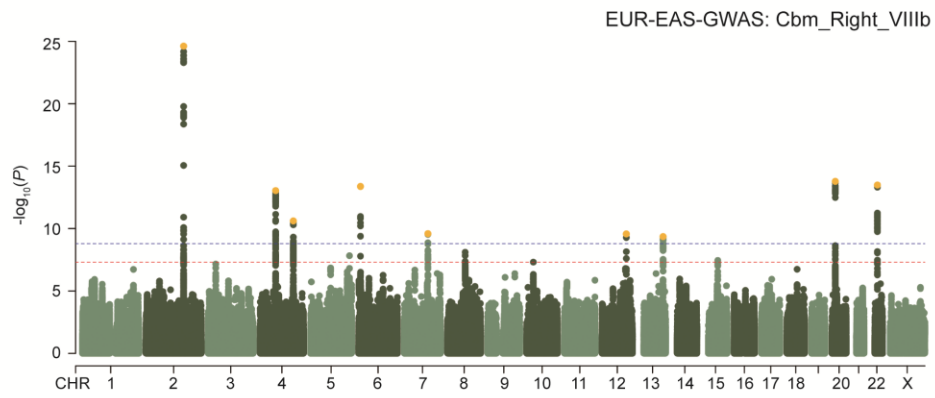


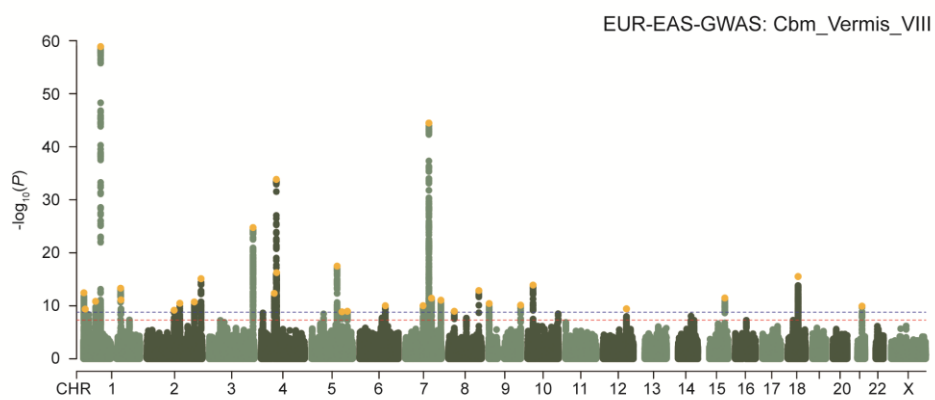
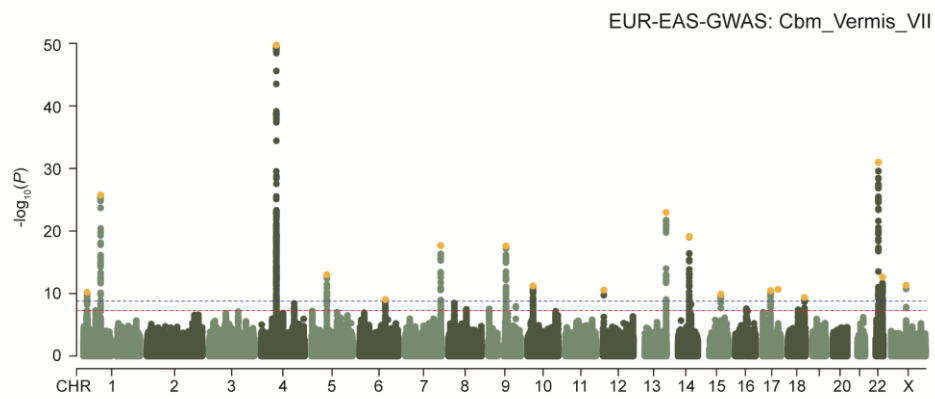
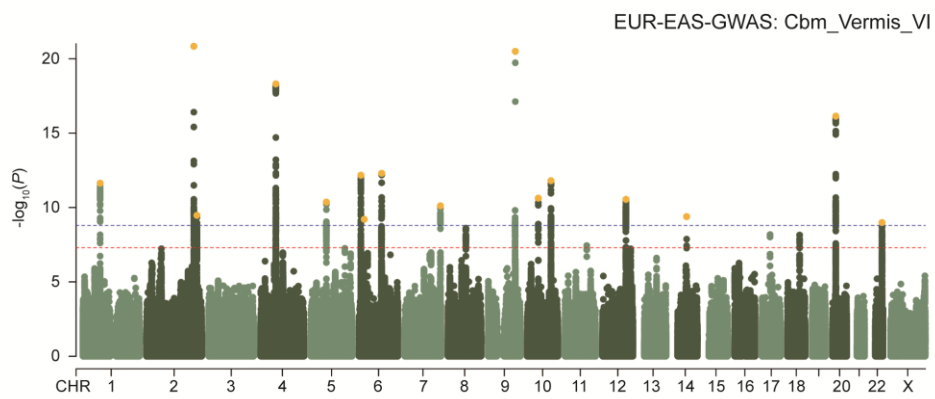
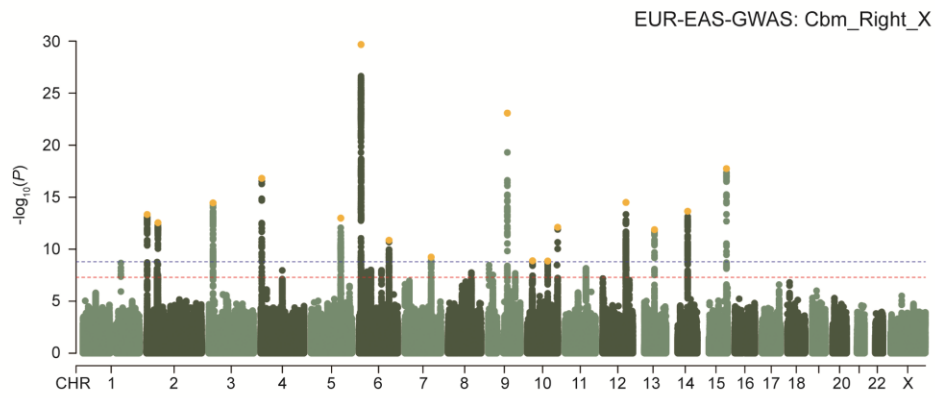


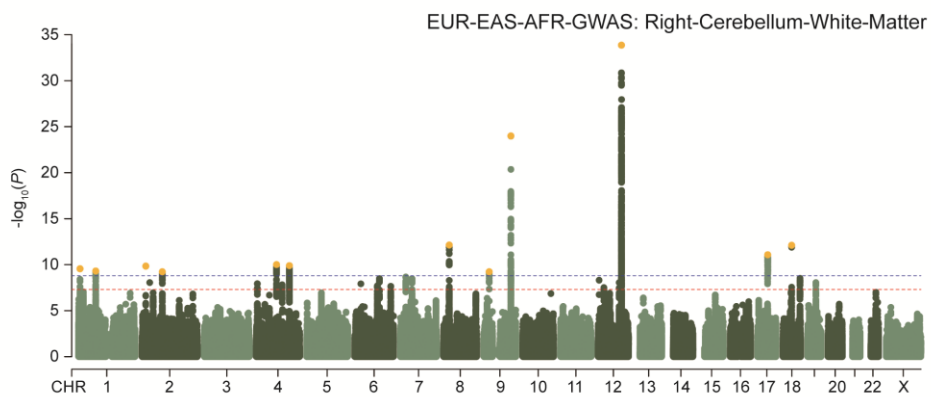
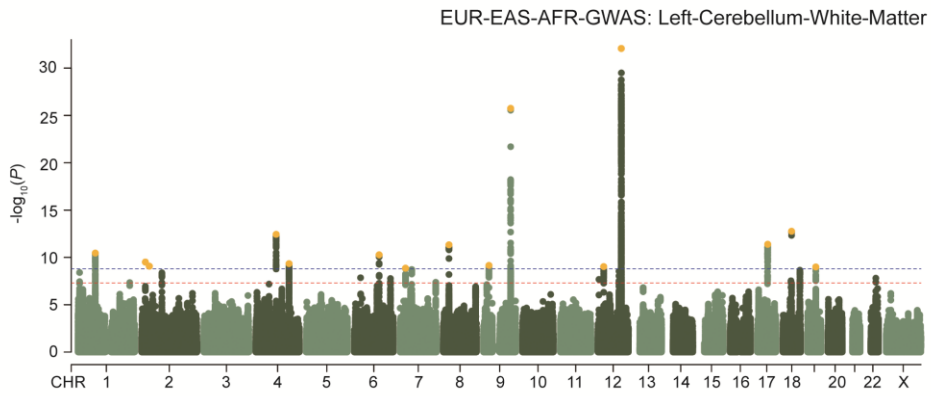
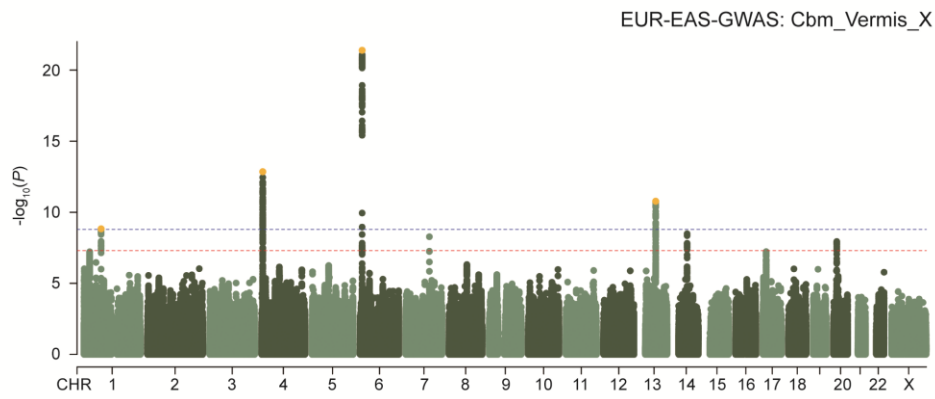
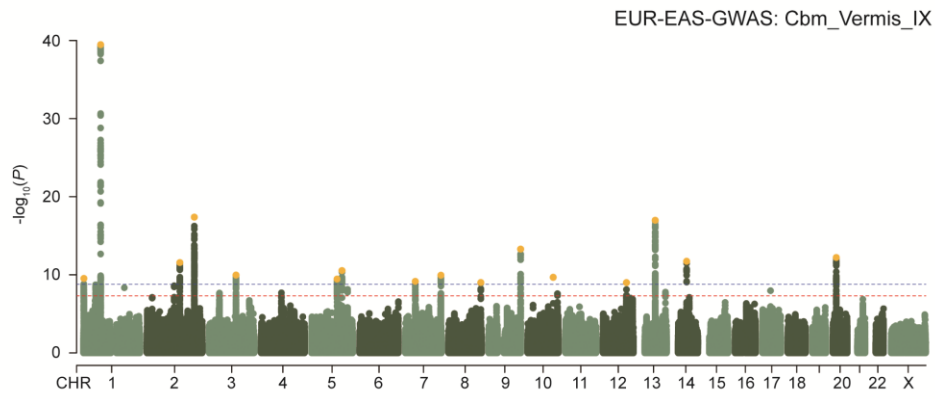


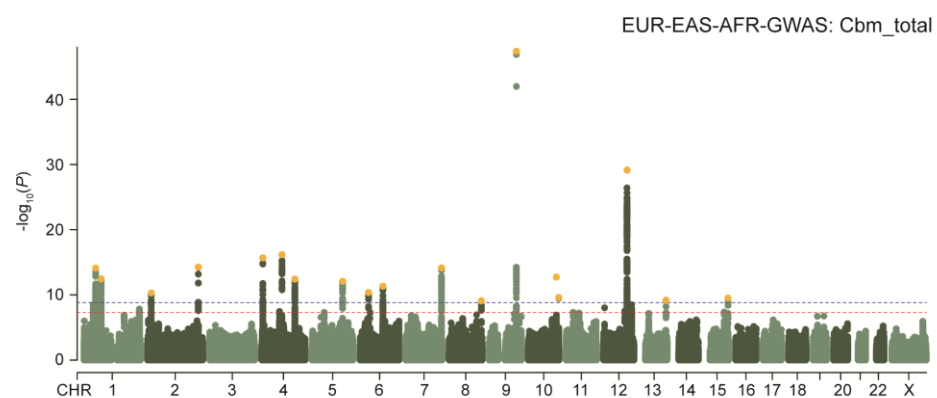
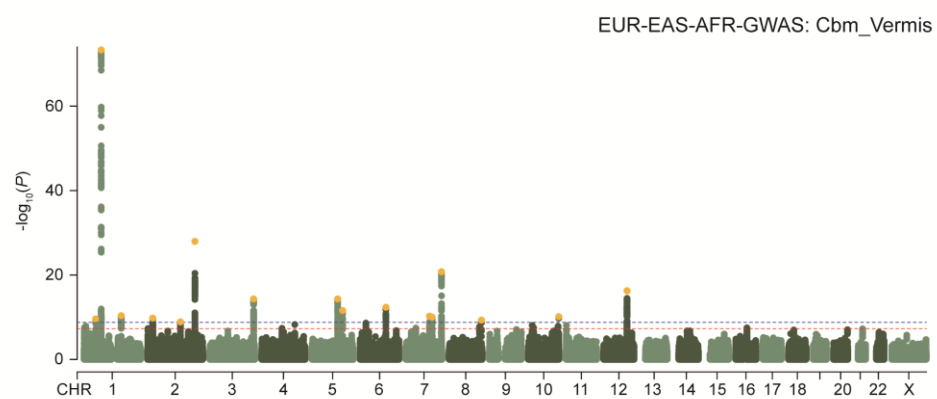
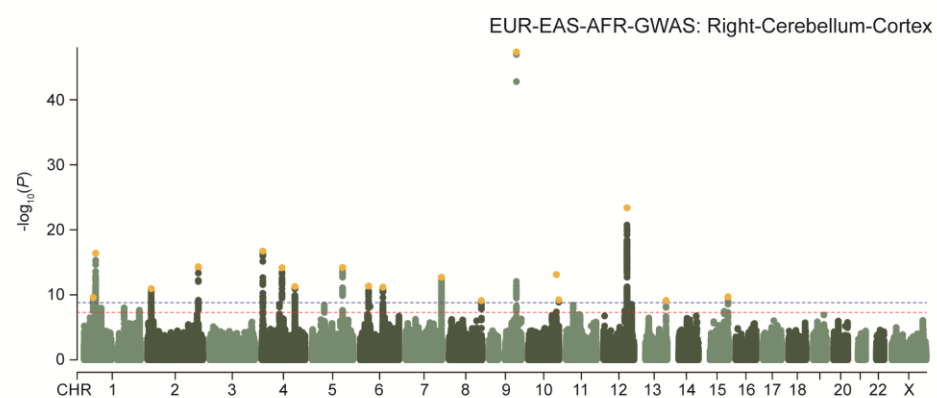
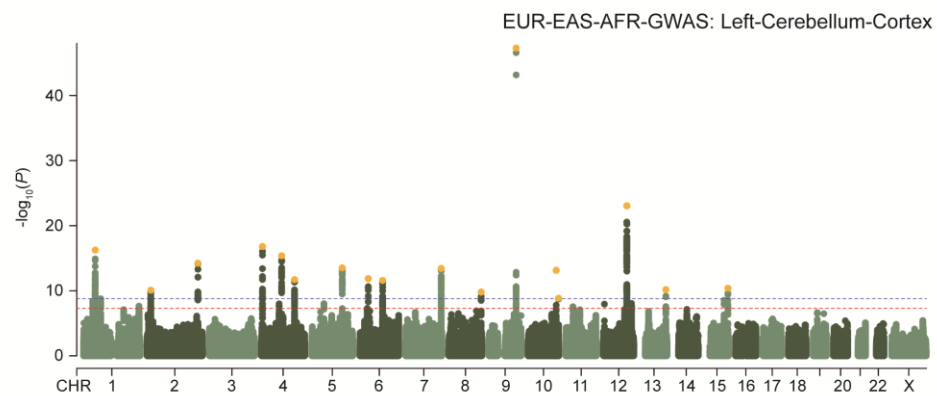


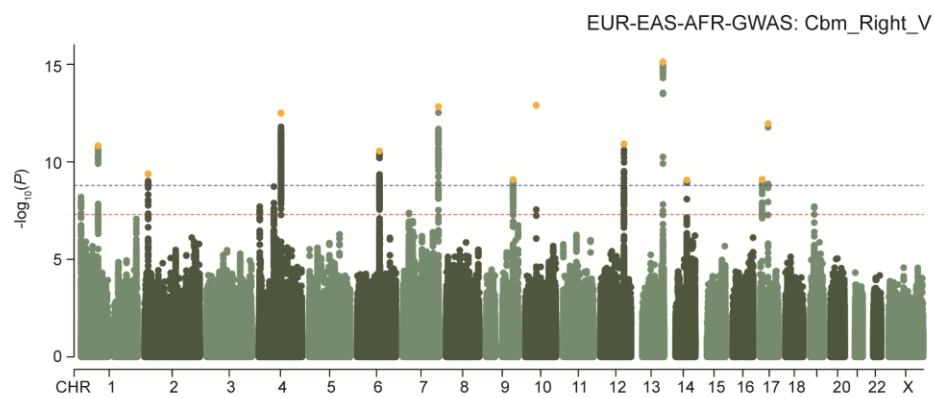
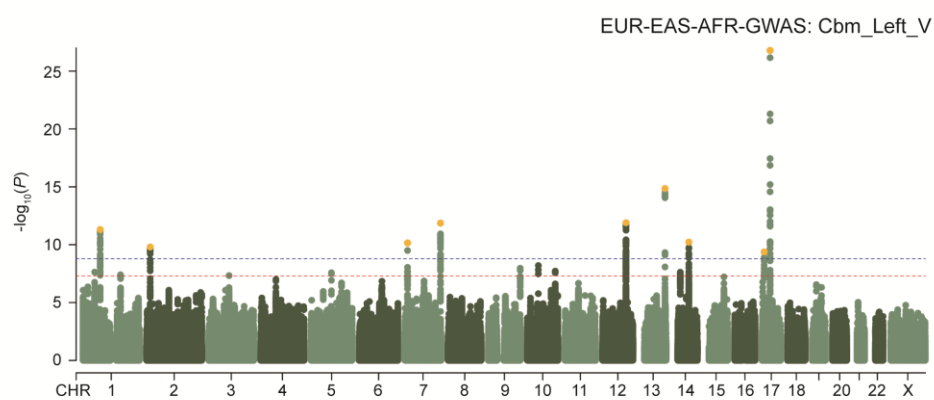
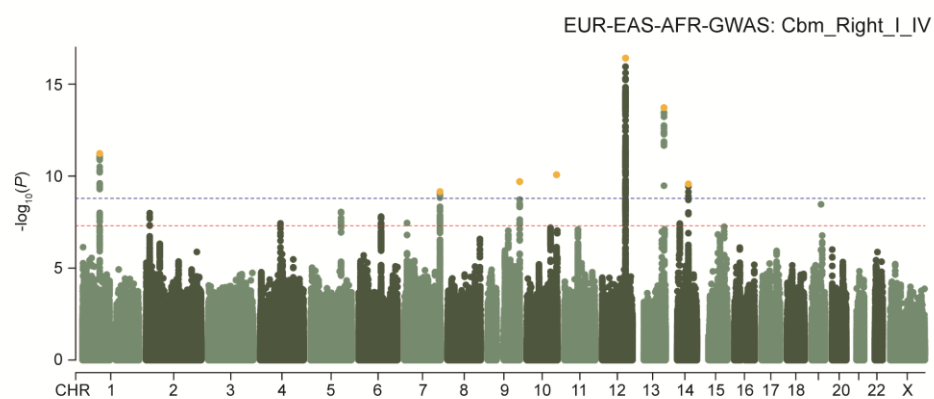
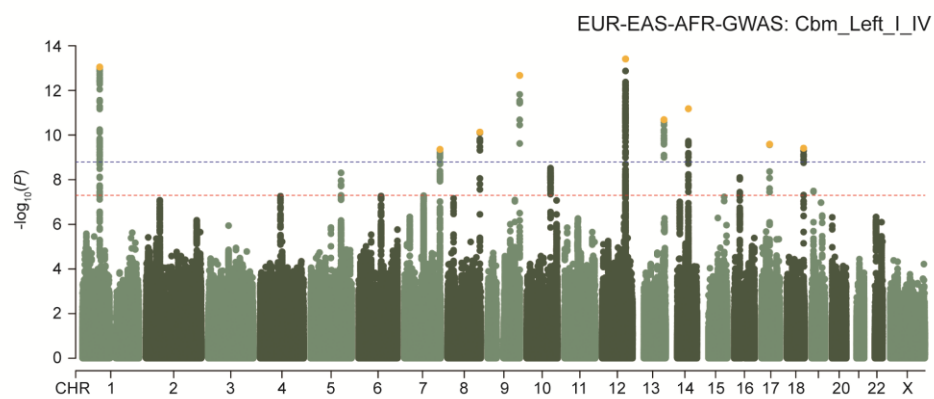


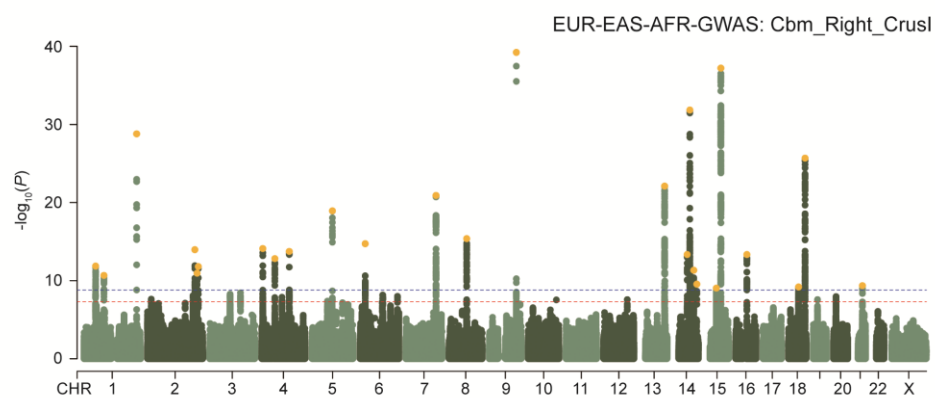
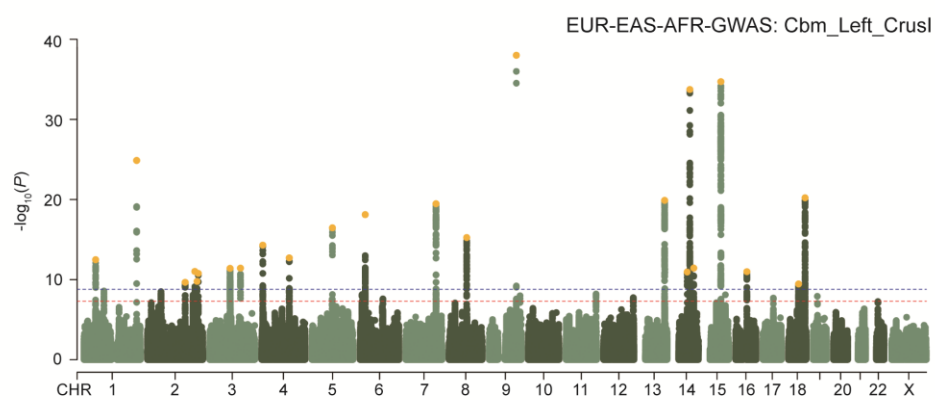
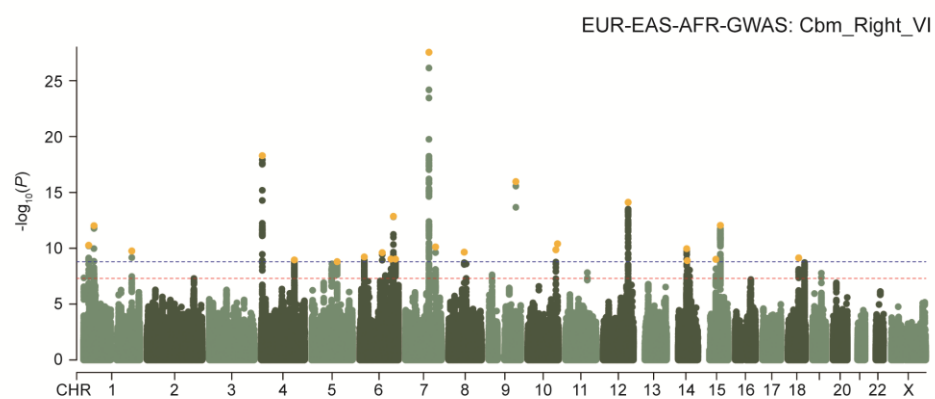
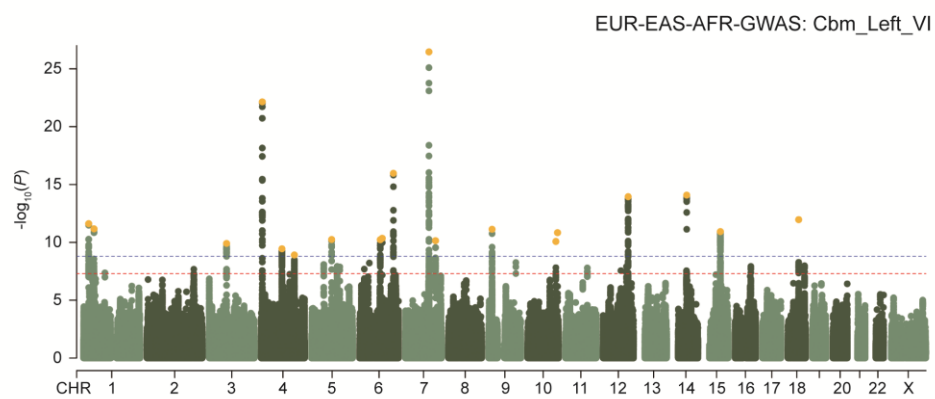


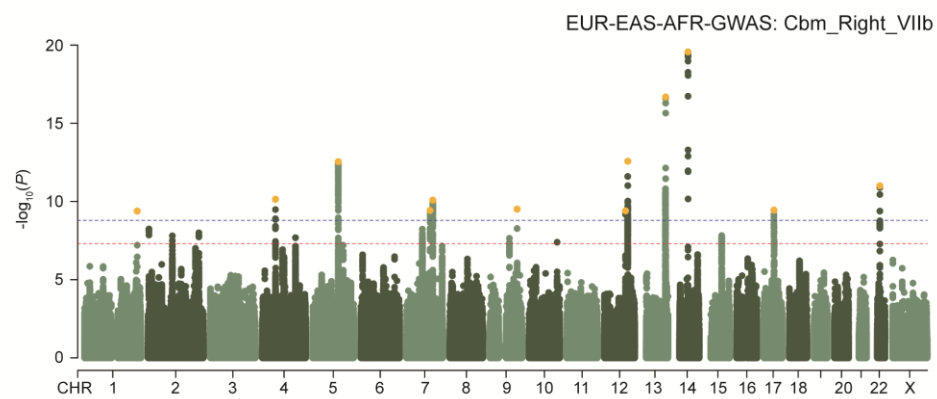
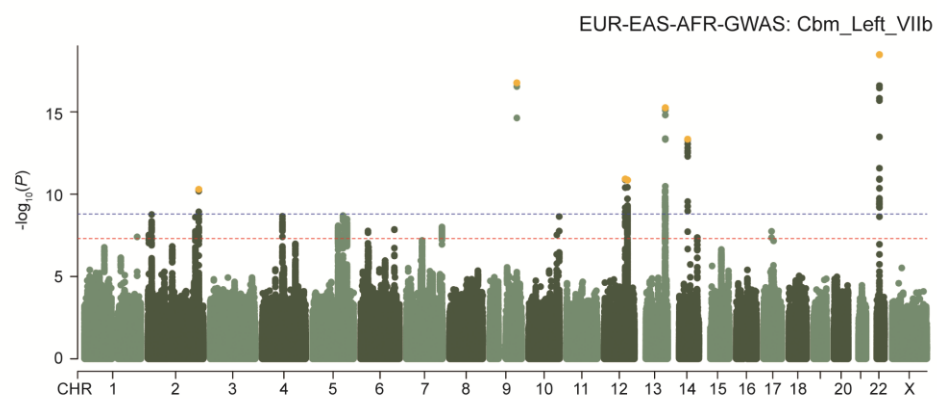
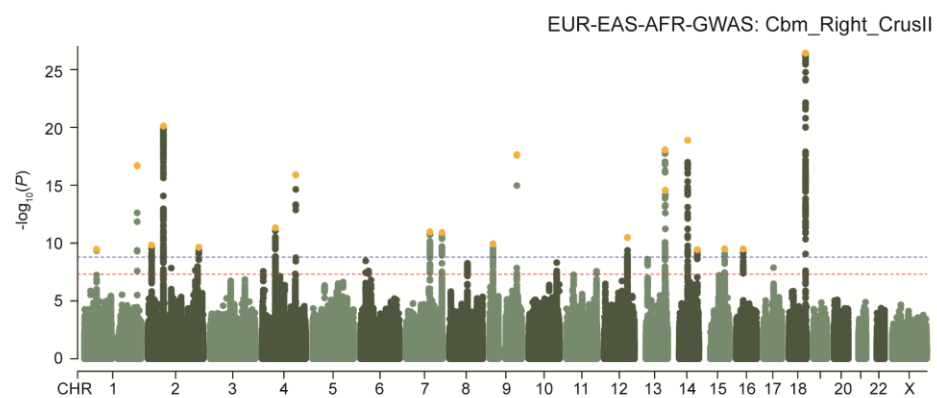
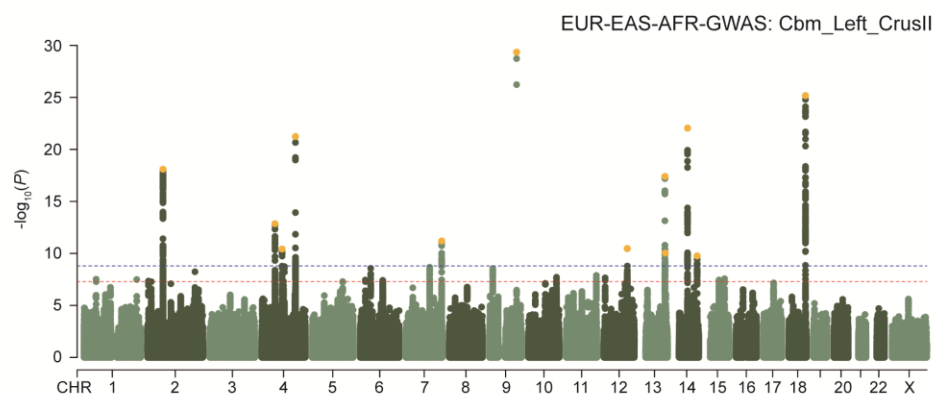


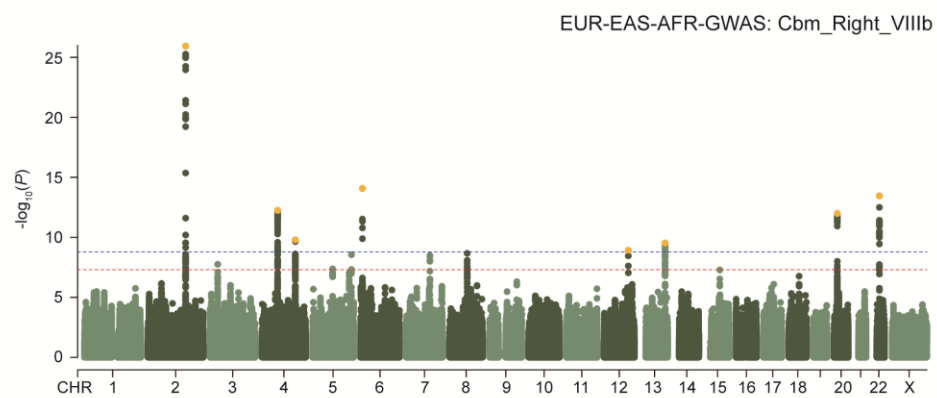
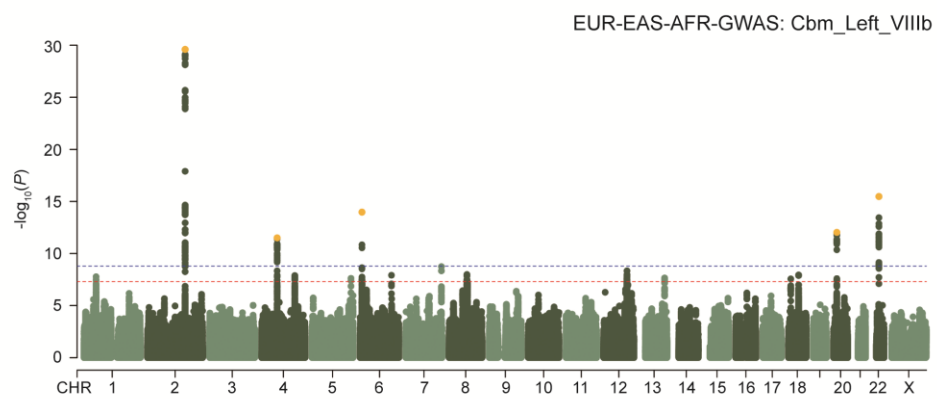
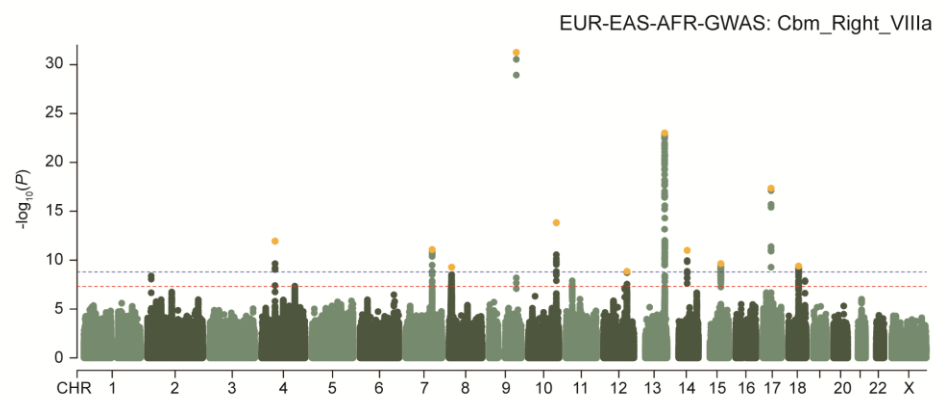
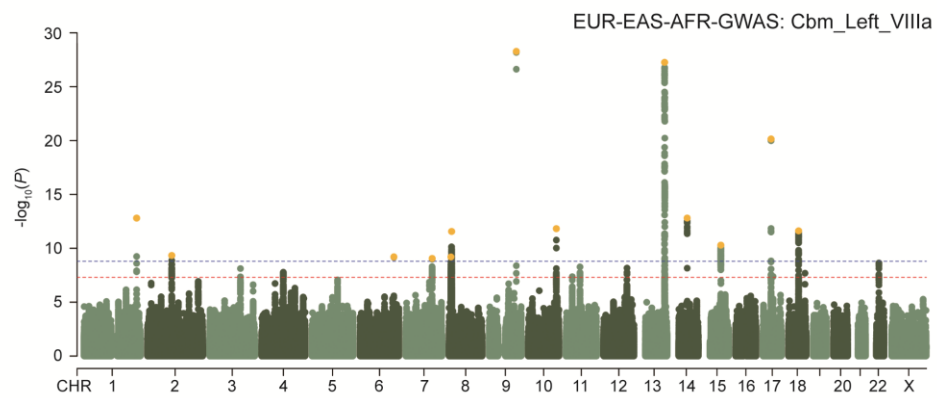


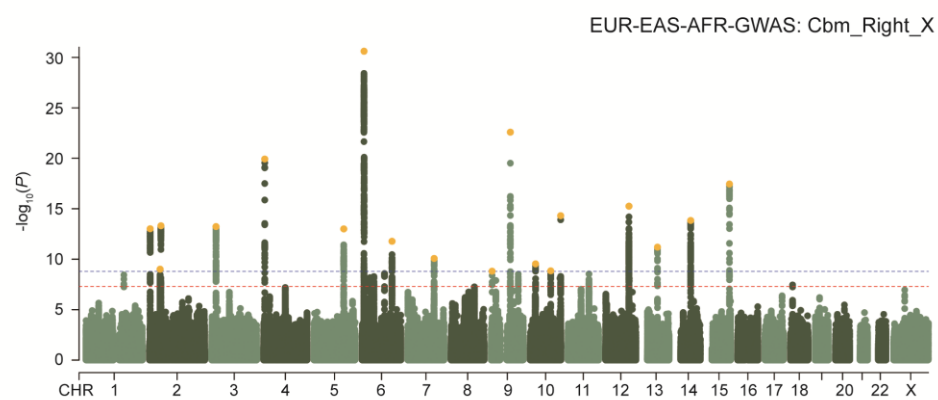
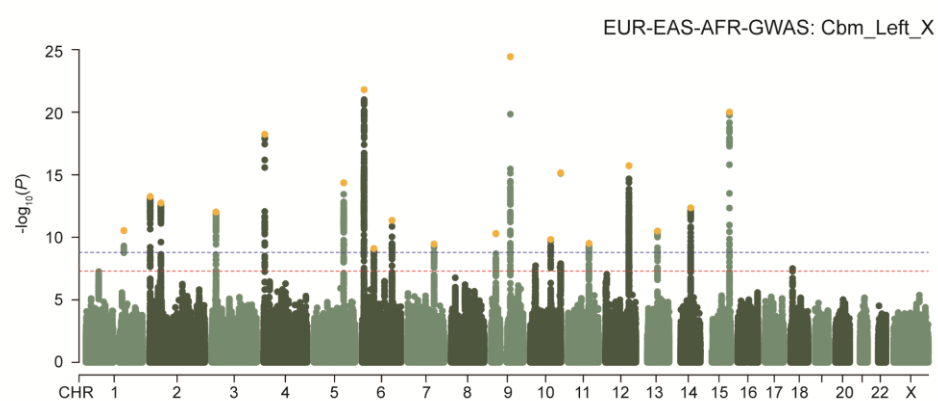
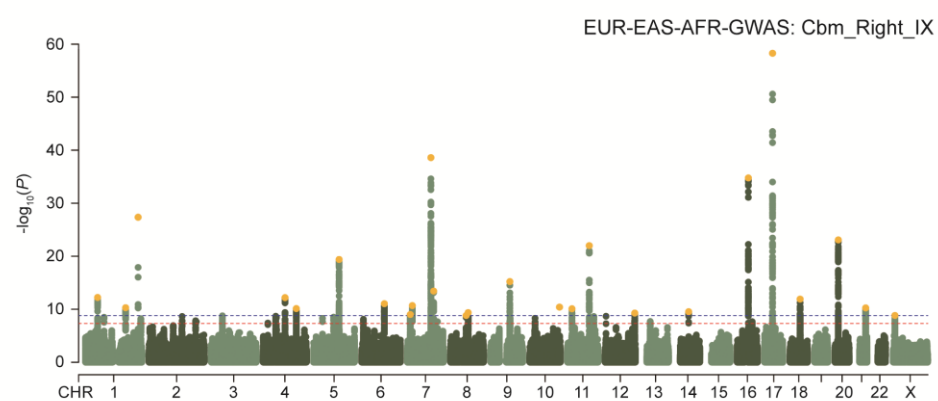
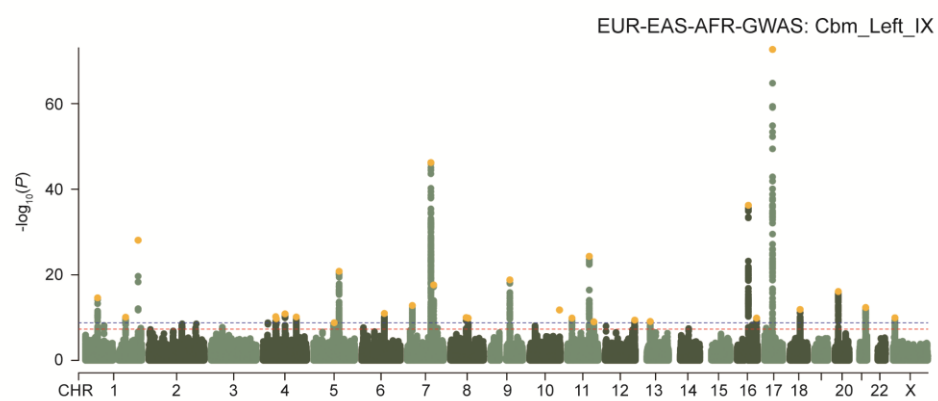


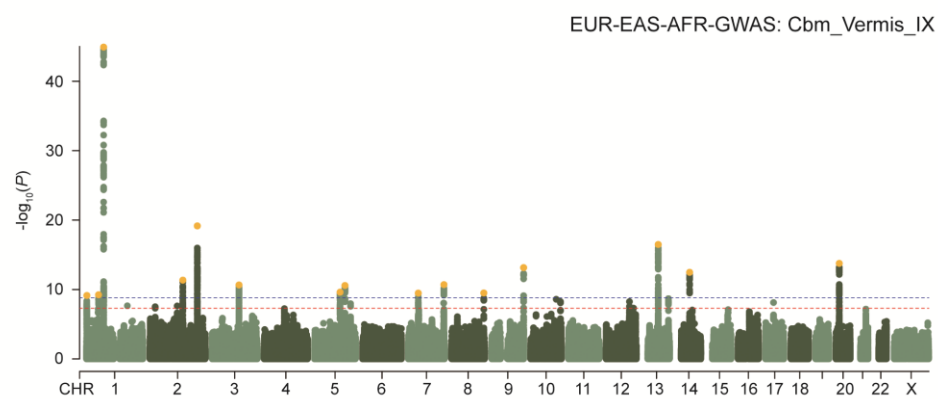
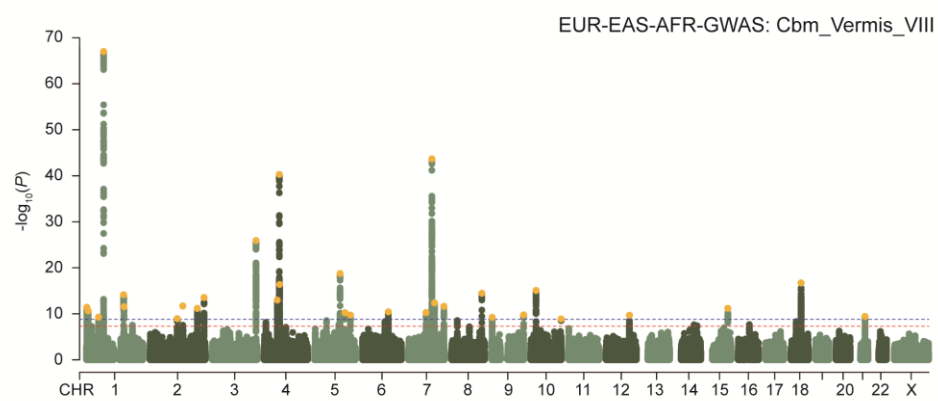
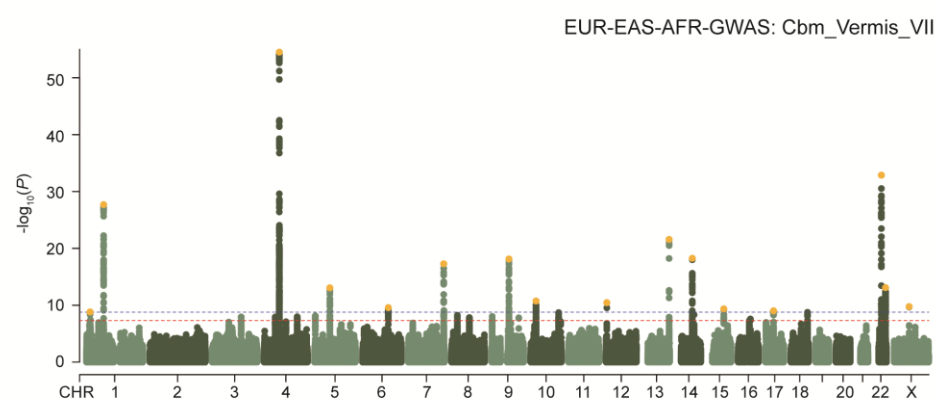
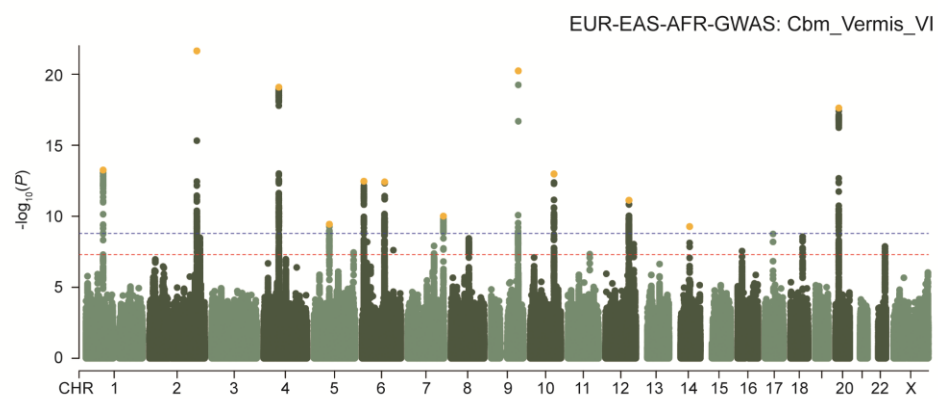












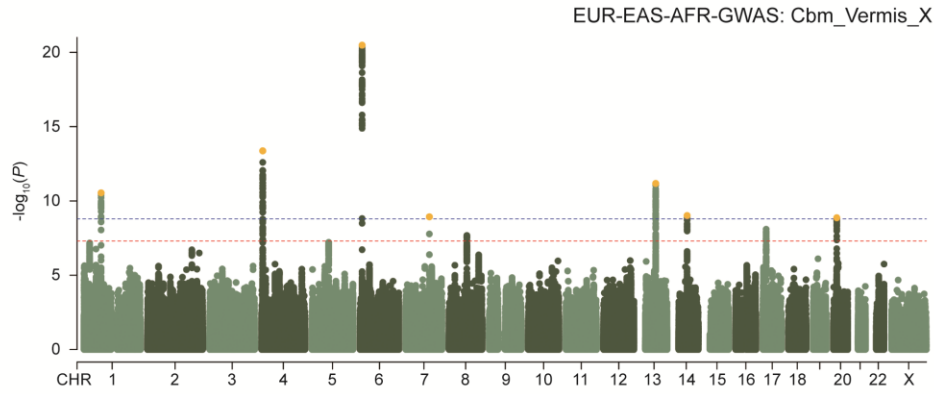
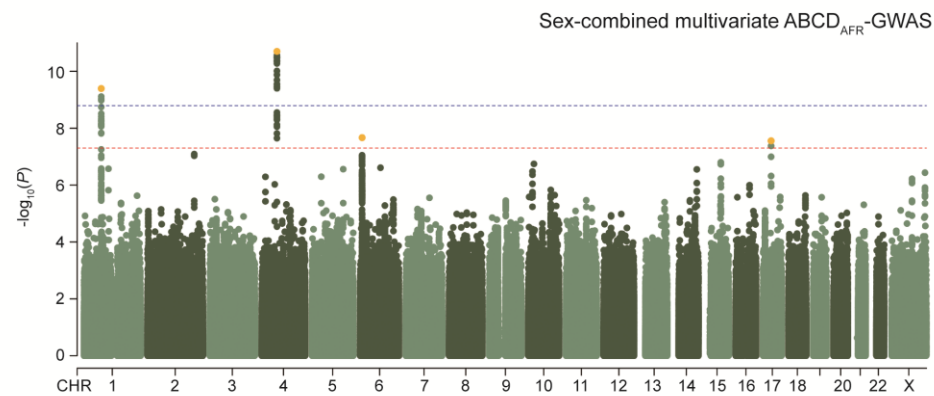
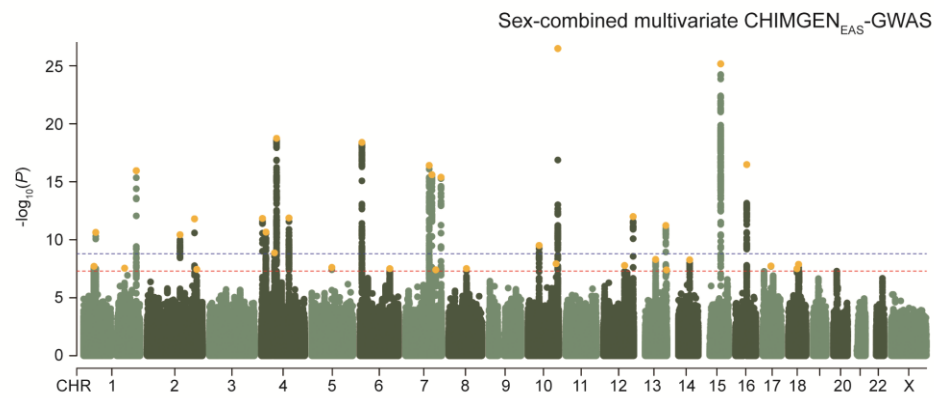
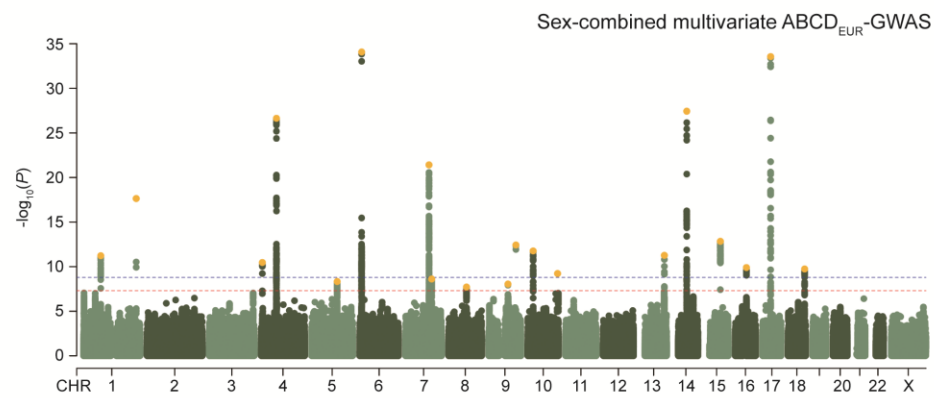
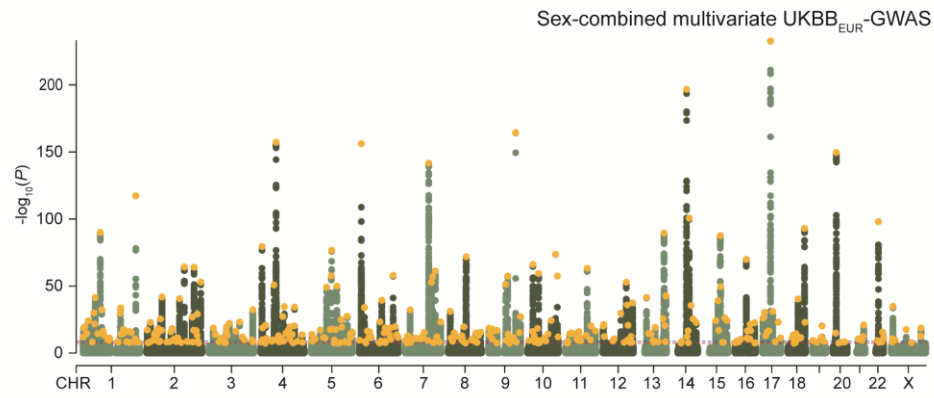
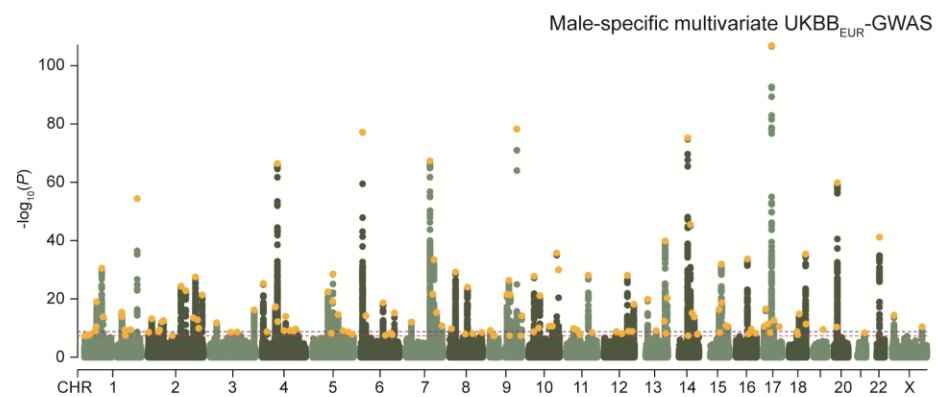
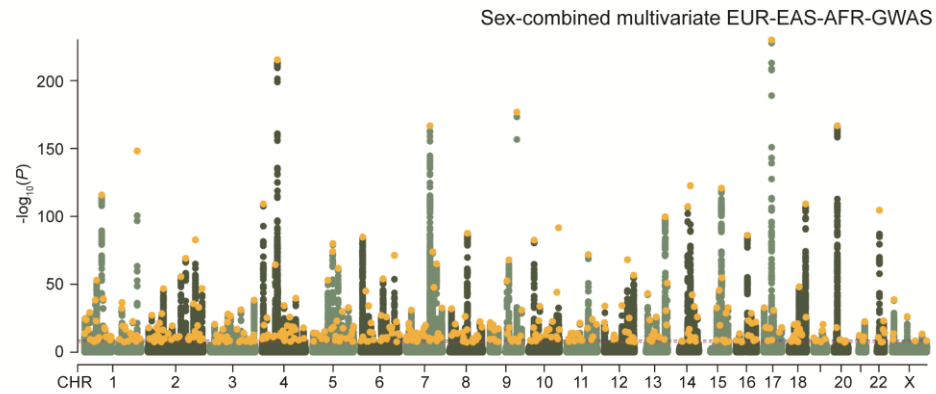
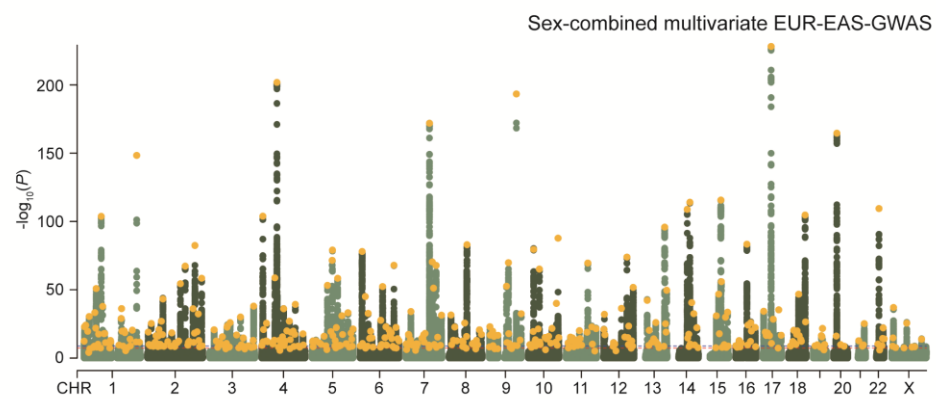
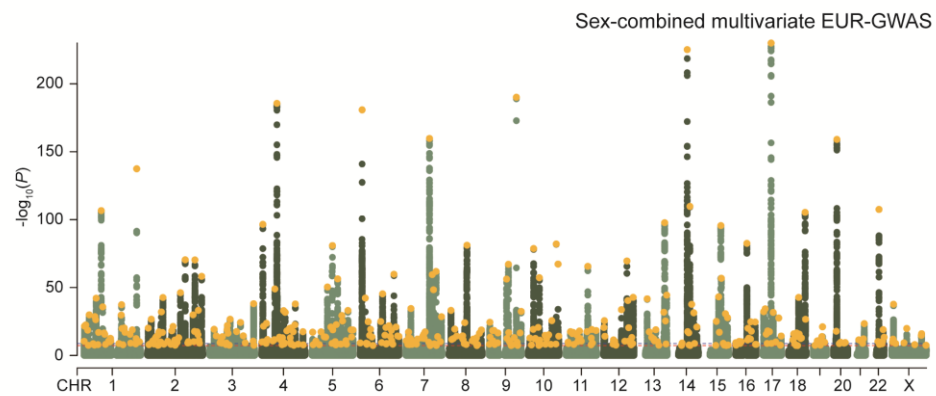
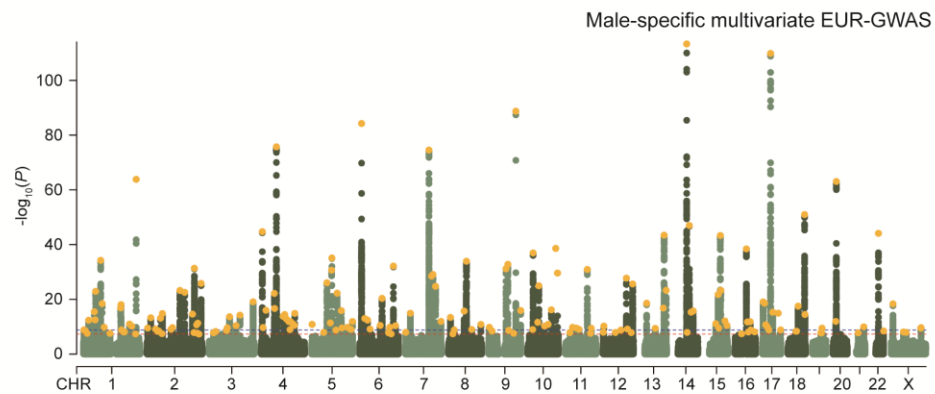
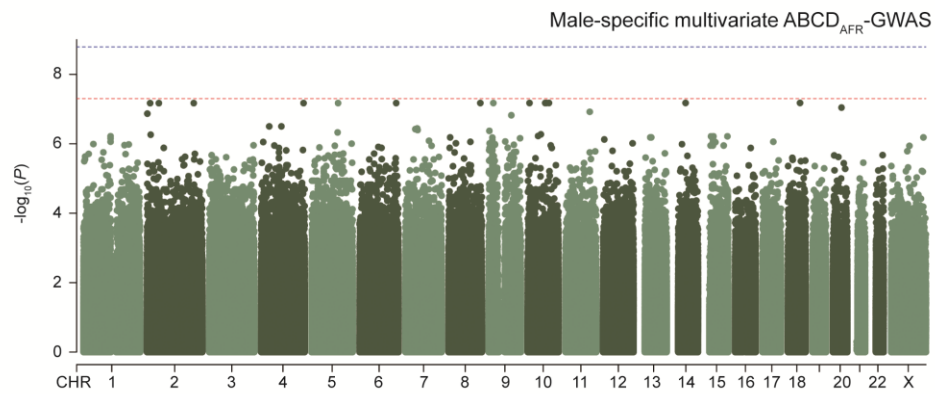
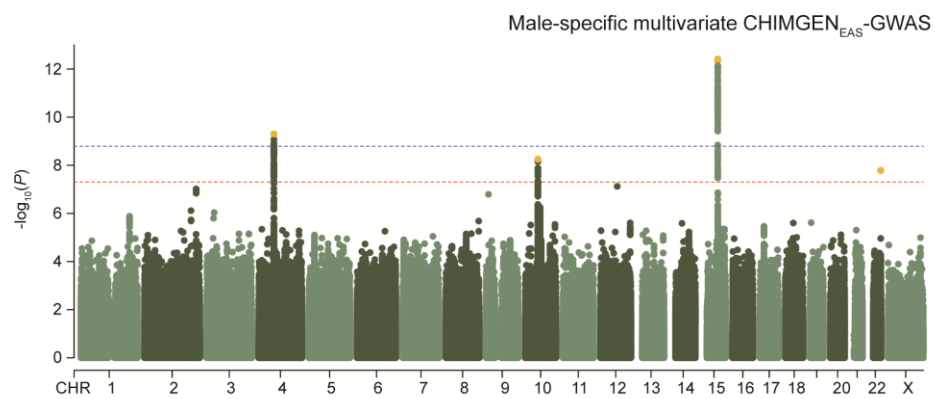
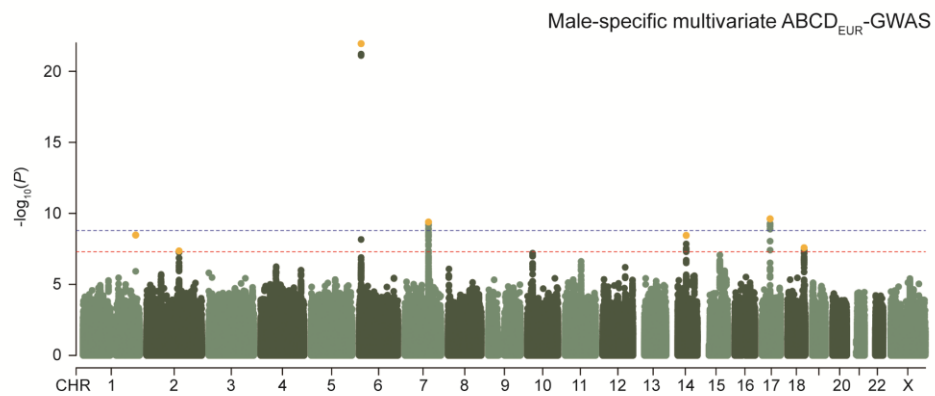
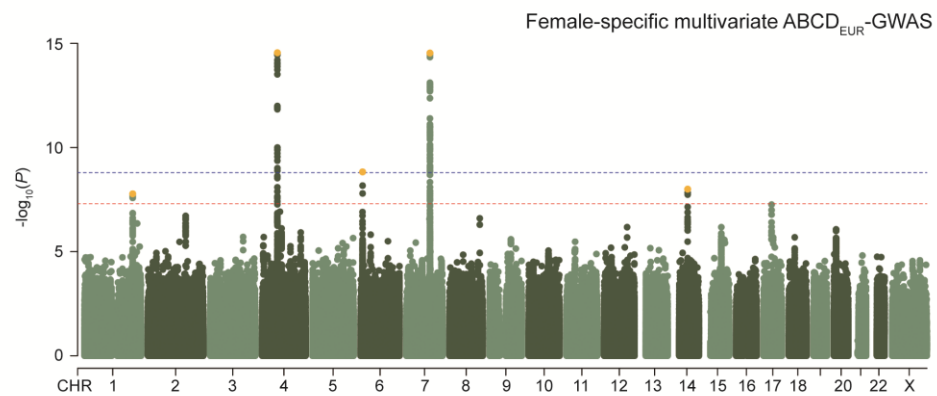
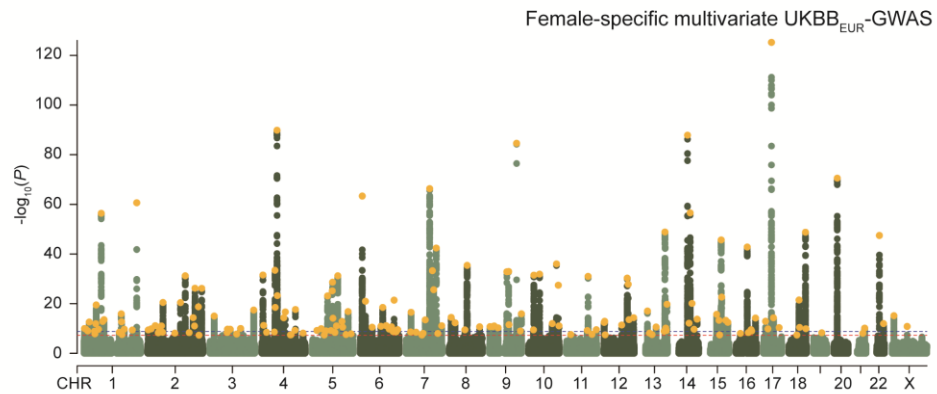
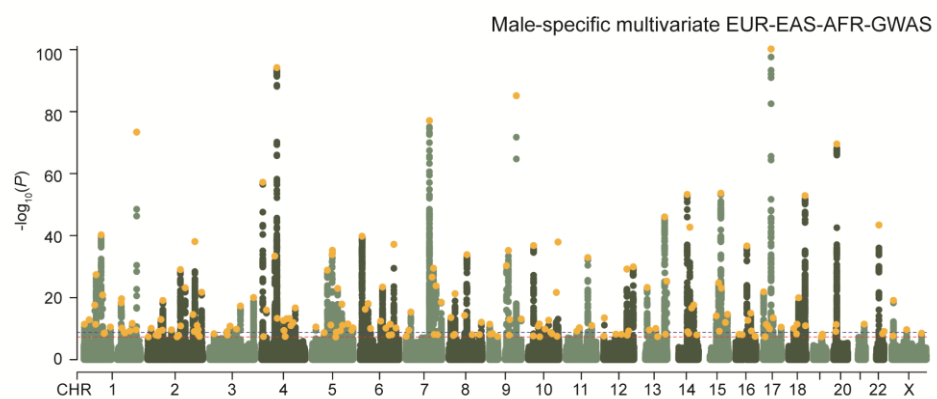
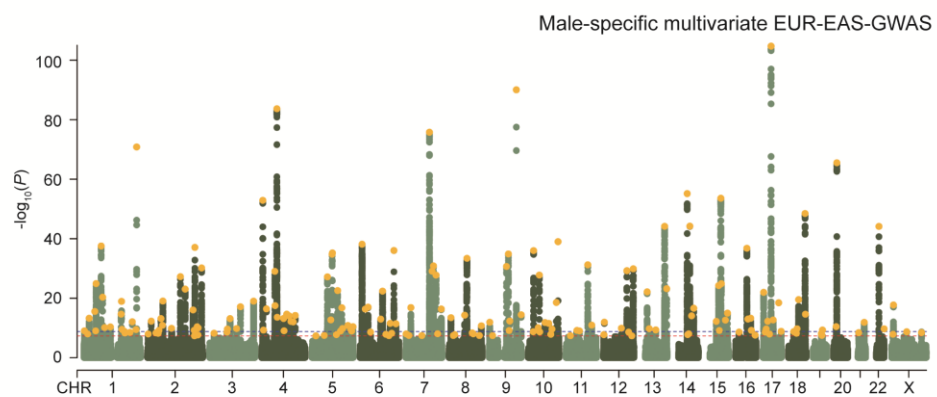


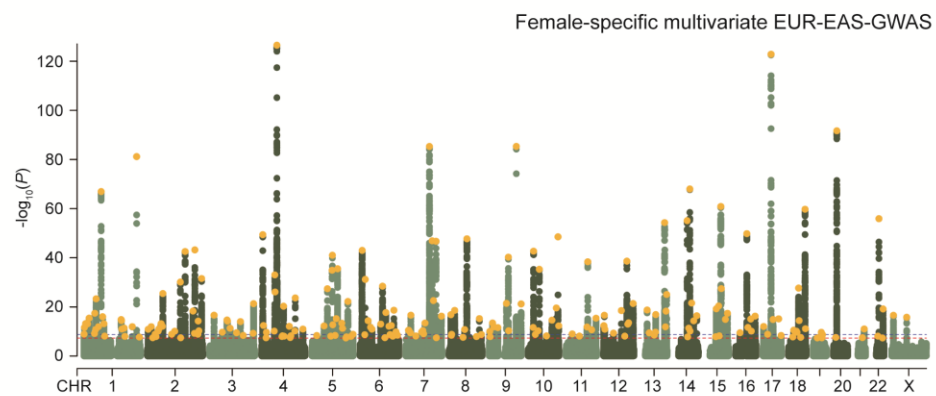
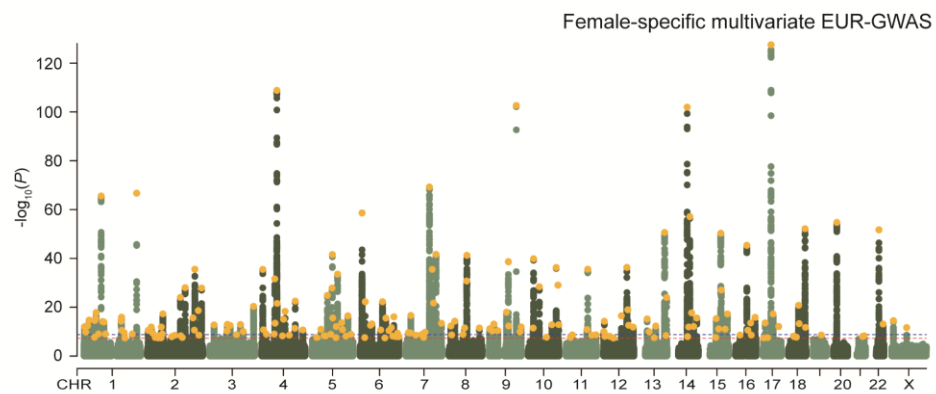
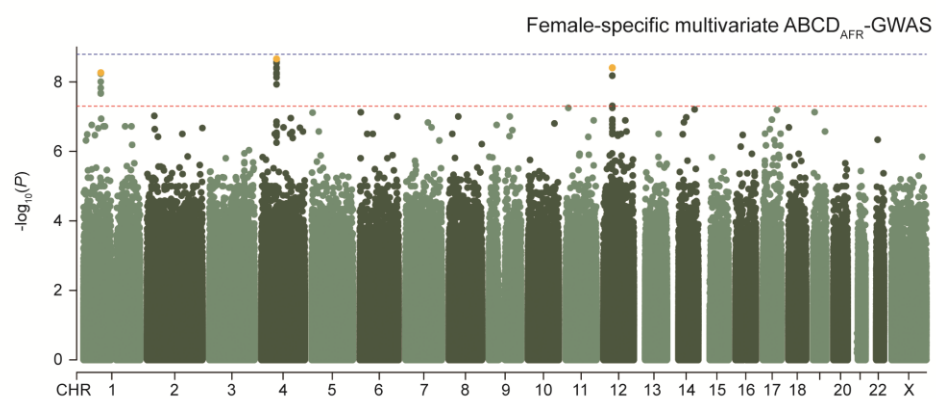
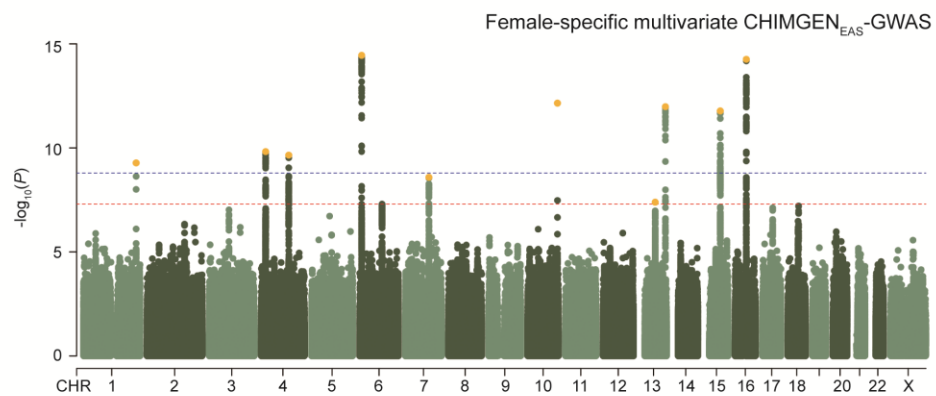
Fig. S5 | Genetic discovery of female-specific univariate GWAS. The Manhattan plots illustrate the results from female-specific univariate GWASs (UKBB_{EUR}-GWAS, ABCD_{EUR}-GWAS, CHIMGEN_{EAS}-GWAS, ABCD_{AFR}-GWAS, EUR-GWAS, EUR-EAS-GWAS, and EUR-EAS-AFR-GWAS) on the 31 cerebellar volumetric traits. Each plot shows genome-wide (red dashed line: $P = 5 \times 10^{-8}$) and study-wide (blue dashed line: $P = 1.61 \times 10^{-9}$) significant associations. Each point represents a single genetic variant plotted according to its genomic position (x axis) and its $-\log_{10}(P)$ value for the association (y axis). Each yellow point represents an independent locus with study-wide significance ($P = 1.61 \times 10^{-9}$). Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; GWAS, genome-wide association study; UKBB, the UK Biobank study.











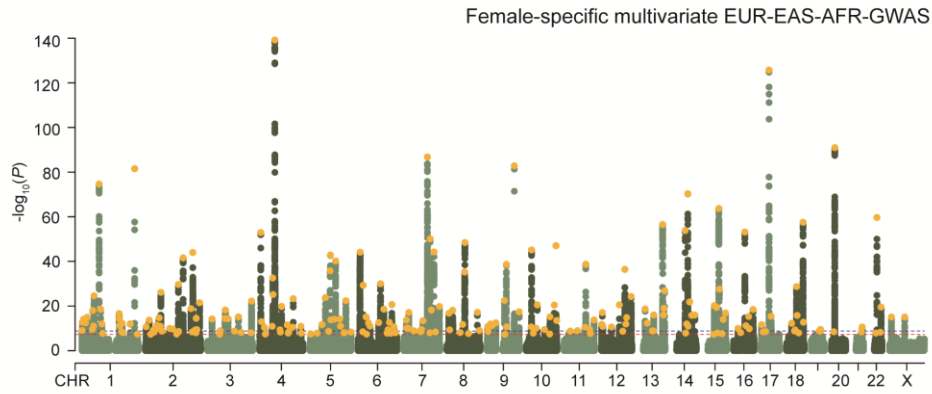


Fig. S6 | Genetic discovery of multivariate GWASs. The Manhattan plots show the results of multivariate GWASs on 27 non-overlapping cerebellar volumetric traits based on sex-combined, male-specific, and female-specific univariate GWASs. Each plot shows both genome-wide (red dashed line: $P = 5 \times 10^{-8}$) and study-wide (blue dashed line: $P = 1.61 \times 10^{-9}$) significance thresholds. Each point represents a single genetic variant plotted according to its genomic position (x axis) and its $-\log_{10}(P)$ value for the association (y axis). Each yellow point represents an independent locus with genome-wide significant association ($P = 5 \times 10^{-8}$). Abbreviations: ABCD, the Adolescent Brain Cognitive Development study; AFR, African ancestry; CHIMGEN, the Chinese Imaging Genetics study; EAS, East Asian ancestry; EUR, European ancestry; GWAS, genome-wide association study; UKBB, the UK Biobank study.

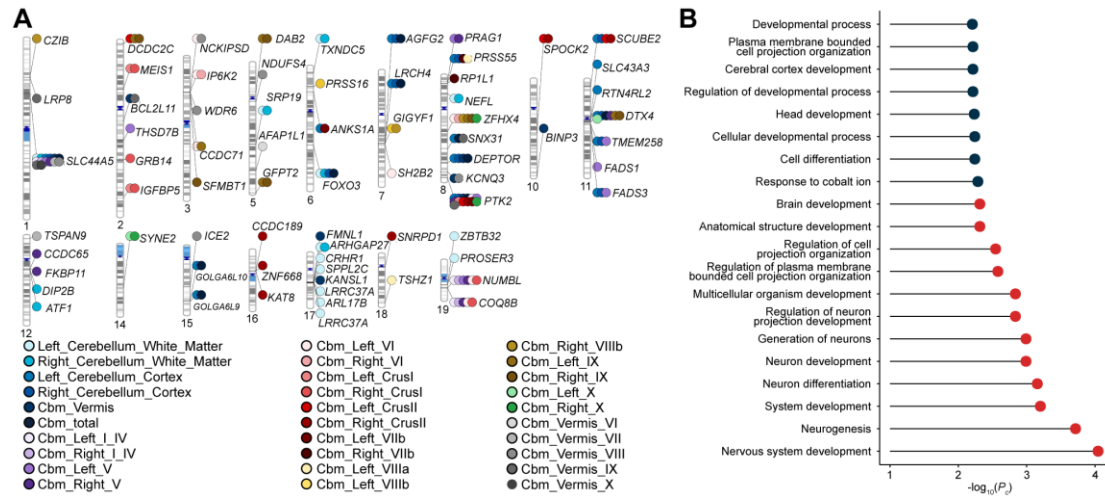


Fig. S7 | Prioritized causal genes and their enriched pathways. (A) The ideogram shows the prioritized causal genes identified by the genetic colocalization ($PP.H4 > 0.8$) analysis between locus-trait associations from EUR-GWASs and eQTLs in cerebellar tissue. (B) The Lollipop chart shows the top 20 pathways enriched by the 71 prioritized causal genes. The significant pathways are red colored ($P_c < 0.05$, Benjamini-Hochberg FDR corrected).

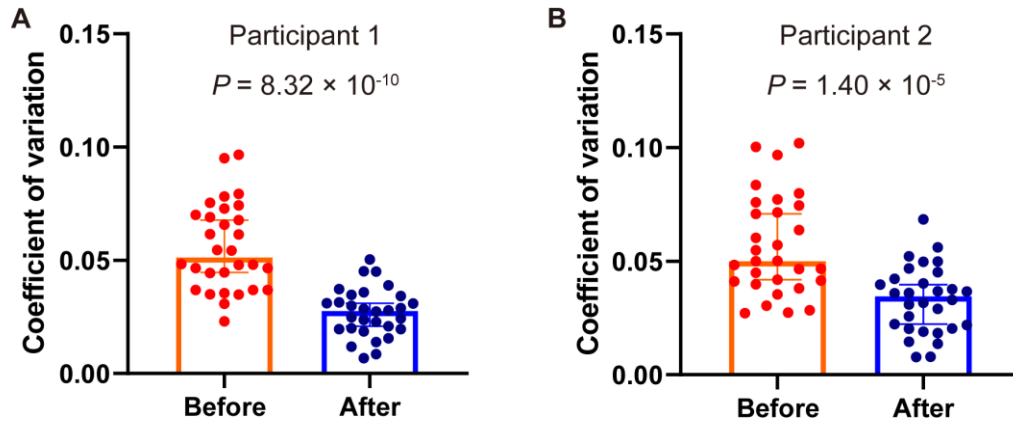


Fig. S8 | Inter-scanner consistency of 30 cerebellar substructure volumes calculated from CerebNet from the same participant before and after Combat harmonization. Two CHIMGEN participants travel to different centers and are scanned with 28 MRI scanners. In each subject, we calculate 30 cerebellar substructure volumes by CerebNet based on the structural MRI data acquired from each scanner and computed CV of each trait across scanners. After applying Combat harmonization to cerebellar substructure volumes, we re-calculate the CV. The Wilcoxon sum rank test is used to investigate the differences in CVs before (red dots) and after (blue dots) harmonization and we found that CVs of all traits before harmonization are reduced after harmonization in both two participants (Wilcoxon rank-sum test, Participant 1: $P = 8.32 \times 10^{-10}$; Participant 2: $P = 1.40 \times 10^{-5}$). The lines indicate the interquartile range of CVs and the box indicate the median of CVs. Abbreviations: CHIMGEN, Chinese imaging genetics; CV, coefficient of variation; MRI, magnetic resonance imaging.