

Table 1. GWAS summary statistics and individual-level genetic datasets used in the present study.

Dataset	Diagnosis	N _{cases}	N _{controls}	N _{effective}	SNP-h ² (%)	Associated loci	Ethnicity	Reference
GWAS summary statistics								
SCZ GWAS	SCZ	53,386	77,258	58,749	24.0	287	European	Trubetskoy et al., 2022
CanUD GWAS	CanUD	42,281	843,744	161,053	6.7	22	European	Levey et al., 2023
ODU GWAS	ODU	15,040	282,607	57,120	10.7	14	European	Kember et al., 2022
PAU GWAS	PAU	113,325	639,923	385,102	6.6	110	European	Zhou et al., 2023
TUD GWAS	TUD	174,021	565,874	532,367	11.7	88	European	Toikumo et al., 2023
AF gSEM*	PAU, PTU, CanUD, OUD	1,025,550	-	-	-	19	European	Hatoum et al., 2023
Individual-level genetic datasets								
CIBERSAM sample	SCZ	1,826	1,372	-	-	-	European (Spain)	Mitjans et al., 2024
PsyCourse Study	SCZ	553	404	-	-	-	European (Germany)	Budde et al., 2019
Galician sample	SUD**	1,176	1,001	-	-	-	European (Spain)	Gurriarán et al., 2019
AF: Addition Factor; CanUD: Cannabis use disorder; gSEM: Genomic structural equation model; GWAS: Genome-wide association study; h ² : heritability; OUD: Opioid use disorder; PAU: Problematic alcohol use; PTU: Problematic tobacco use; SCZ: Schizophrenia; SUD: Substance use disorder; TUD: Tobacco use disorder.								
*Summary statistics from a multivariate genome-wide association meta-analysis integrating published European GWAS of PAU, problematic tobacco use, CanUD and OUD.								
**Substances considered were alcohol, tobacco, cannabis, cocaine, opiates, hypnotics, stimulants and hallucinogens.								