

Tables

Table 1. Causal exons for alcohol use disorder.

Skipped exon (SE)				Exon function			Predictive modeling				Discovery		Replication
SE	Host gene	Exon	Chromosome	Effects host gene expression	Protein coding	Functional domain (Pfam)	Num. of samples (CMC)	Num. of variants	P-value	R ²	Phenotype	FDR	FDR
1	<i>LINC00665</i>	ENSE00002438745	chr19	No	No	N.A.	380	3	3.42E-87	64.4%	SXCT	0.021	0.005
2	<i>NSUN4</i>	ENSE00001875548	chr1	Yes	No	N.A.	737	2	3.75E-42	22.1%	SXCT	0.031	0.005
3	<i>SRRM2</i>	ENSE00002674786	chr16	No	Yes	No	380	6	4.86E-06	3.1%	DSM-IV	0.032	0.029
4	<i>ELOVL7</i>	ENSE00002079807	chr5	Yes	No	N.A.	380	11	9.13E-42	39.5%	SXCT	0.031	0.033
5	<i>DRC1</i>	ENSE00003572542	chr2	Yes	Yes	PF14772	338	15	5.99E-39	38.9%	SXCT	0.031	0.033
6	<i>TBC1D5</i>	ENSE00001693995	chr3	N.A.	No	N.A.	376	14	1.66E-27	26.4%	SXCT	0.031	0.033

Genome assembly: GRCh38/hg38. PF14772: Dynein regulatory complex protein 1/2, N-terminal domain.

DSM-IV: alcohol dependence diagnosis. SXCT: symptom count.

Sample numbers for SXCT and DSM-IV in discovery cohort are 7,421 and 4,760, respectively.

Replication sample number is 2,856.