Supplementary Table 15. Bonferroni significant results of gene-based association analyses for the GWAS meta-analysis of AUDIT total score (genes identified in the GWAS credible sets are highlighted in gray)

SYMBOL	CHR	START	STOP	NSNPS	NPARAM	ZSTAT	P
KLB	4	3.9E+07	3.9E+07	130	31	7.5328	2.48E-14
RFC1	4	3.9E+07	3.9E+07	122	15	6.2305	2.32E-10
CPS1	2	2.1E+08	2.1E+08	488	51	6.2095	2.66E-10
WNT3	17	4.5E+07	4.5E+07	106	22	6.1954	2.91E-10
SNX17	2	2.8E+07	2.8E+07	14	6	5.9324	1.49E-09
CADM2	3	8.5E+07	8.6E+07	3059	93	5.9167	1.64E-09
GCKR	2	2.8E+07	2.8E+07	60	13	5.7272	5.11E-09
SLC39A13	11	4.7E+07	4.7E+07	20	4	5.6963	6.12E-09
STH	17	4.4E+07	4.4E+07	1	1	5.5597	1.35E-08
RASIP1	19	4.9E+07	4.9E+07	46	7	5.5118	1.78E-08
NSF	17	4.5E+07	4.5E+07	55	6	5.4621	2.35E-08
GTF3C2	2	2.8E+07	2.8E+07	24	9	5.425	2.90E-08
FNBP4	11	4.8E+07	4.8E+07	120	17	5.3927	3.47E-08
CRHR1	17	4.4E+07	4.4E+07	901	12	5.3841	3.64E-08
MAPT	17	4.4E+07	4.4E+07	654	8	5.3806	3.71E-08
KANSL1	17	4.4E+07	4.4E+07	645	7	5.3789	3.75E-08
SPI1	11	4.7E+07	4.7E+07	71	10	5.3521	4.35E-08
SPPL2C	17	4.4E+07	4.4E+07	17	2	5.3433	4.56E-08
NUP160	11	4.8E+07	4.8E+07	141	17	5.3345	4.79E-08
DRD2	11	1.1E+08	1.1E+08	183	29	5.3323	4.85E-08
AGBL2	11	4.8E+07	4.8E+07	113	15	5.3167	5.28E-08
PSMC3	11	4.7E+07	4.7E+07	15	5	5.287	6.22E-08
FUT2	19	4.9E+07	4.9E+07	37	5	5.2157	9.16E-08
IFT172	2	2.8E+07	2.8E+07	80	15	5.1342	1.42E-07
NEGR1	1	7.2E+07	7.3E+07	1880	132	5.1336	1.42E-07
PPM1G	2	2.8E+07	2.8E+07	50	11	5.1223	1.51E-07
P11-766F14	4	1E+08	1E+08	58	15	4.8742	5.46E-07
WDR19	4	3.9E+07	3.9E+07	171	13	4.7935	8.20E-07
PLEKHM1	17	4.4E+07	4.4E+07	85	7	4.7902	8.33E-07
MAMSTR	19	4.9E+07	4.9E+07	19	4	4.7542	9.96E-07
NRBP1	2	2.8E+07	2.8E+07	26	7	4.735	1.10E-06
IZUMO1	19	4.9E+07	4.9E+07	25	2	4.7065	1.26E-06
ARHGAP27	17	4.3E+07	4.4E+07	96	8	4.6738	1.48E-06
TRIM59	3	1.6E+08	1.6E+08	144	25	4.6372	1.77E-06
ASXL3	18	3.1E+07	3.1E+07	434	49	4.6186	1.93E-06
LANCL1	2	2.1E+08	2.1E+08	126	14	4.5979	2.13E-06
NFKB1	4	1E+08	1E+08	275	24	4.5962	2.15E-06
FOXP1	3	7.1E+07	7.2E+07	1369	175	4.5937	2.18E-06
KPNA4	3	1.6E+08	1.6E+08	150	23	4.5929	2.19E-06
ATP2A1	16	2.9E+07	2.9E+07	32	7	4.5635	2.52E-06