

Supplementary Table 16. Most associated gene sets for the GWAS meta-analysis of AUDIT total scores

| FULL_NAME | NGENES | BETA | BETA_STC | SE | P | ' bonferroni |
|--|--------|-------|----------|-------|----------|--------------|
| Curated_gene_sets:mikkelsen_dedifferentiated_state_dn | 7 | 1.740 | 0.034 | 0.437 | 3.35E-05 | No |
| Curated_gene_sets:reactome_adherens_junctions_interactions | 27 | 0.750 | 0.029 | 0.194 | 5.46E-05 | No |
| GO_mf:go_transcriptional_activator_activity_rna_polymerase_ii_distal_enhance | 25 | 0.636 | 0.024 | 0.175 | 1.38E-04 | No |
| Curated_gene_sets:howlin_cited1_targets_1_up | 32 | 0.559 | 0.024 | 0.158 | 2.04E-04 | No |
| GO_bp:go_dopaminergic_neuron_differentiation | 27 | 0.628 | 0.024 | 0.185 | 3.56E-04 | No |
| GO_cc:go_excitatory_synapse | 185 | 0.226 | 0.023 | 0.068 | 4.70E-04 | No |
| GO_mf:go_transcription_factor_binding | 484 | 0.140 | 0.023 | 0.043 | 5.42E-04 | No |
| GO_mf:go_nucleic_acid_binding_transcription_factor_activity | 1129 | 0.093 | 0.023 | 0.029 | 7.12E-04 | No |
| GO_mf:go_rna_polymerase_ii_distal_enhancer_sequence_specific_dna_bindin | 62 | 0.343 | 0.020 | 0.108 | 7.60E-04 | No |
| Curated_gene_sets:ikedamir30_targets_up | 112 | 0.284 | 0.022 | 0.090 | 7.79E-04 | No |
| GO_bp:go_adenohypophysis_development | 14 | 0.777 | 0.022 | 0.249 | 8.84E-04 | No |
| GO_mf:go_glucosidase_activity | 12 | 0.745 | 0.019 | 0.238 | 8.90E-04 | No |
| GO_bp:go_germ_cell_development | 201 | 0.202 | 0.021 | 0.065 | 9.62E-04 | No |
| GO_mf:go_protein_heterodimerization_activity | 442 | 0.142 | 0.022 | 0.046 | 9.97E-04 | No |
| GO_mf:go_enhancer_binding | 89 | 0.290 | 0.020 | 0.094 | 1.06E-03 | No |
| Curated_gene_sets:biocarta_pitx2_pathway | 15 | 0.728 | 0.021 | 0.238 | 1.09E-03 | No |
| Curated_gene_sets:lopez_mesothelioma_survival_overall_up | 7 | 1.060 | 0.021 | 0.349 | 1.14E-03 | No |
| GO_cc:go_postsynapse | 355 | 0.154 | 0.021 | 0.051 | 1.16E-03 | No |
| Curated_gene_sets:izadpanah_stem_cell_adipose_vs_bone_dn | 104 | 0.272 | 0.021 | 0.091 | 1.35E-03 | No |
| GO_mf:go_regulatory_region_nucleic_acid_binding | 782 | 0.100 | 0.020 | 0.034 | 1.37E-03 | No |
| Curated_gene_sets:kyng_response_to_h2o2_via_ercc6 | 17 | 0.594 | 0.018 | 0.199 | 1.40E-03 | No |
| Curated_gene_sets:lopez_mesothelioma_survival_up | 12 | 0.728 | 0.019 | 0.246 | 1.53E-03 | No |
| Curated_gene_sets:kyng_response_to_h2o2_via_ercc6_dn | 41 | 0.399 | 0.019 | 0.135 | 1.60E-03 | No |
| GO_bp:go_spermatid_differentiation | 121 | 0.245 | 0.020 | 0.083 | 1.61E-03 | No |
| Curated_gene_sets:kim_germinal_center_t_helper_up | 61 | 0.356 | 0.021 | 0.121 | 1.62E-03 | No |
| GO_bp:go_transcription_from_rna_polymerase_ii_promoter | 693 | 0.101 | 0.019 | 0.035 | 1.83E-03 | No |
| Curated_gene_sets:amit_egf_response_240_hela | 60 | 0.327 | 0.019 | 0.113 | 1.98E-03 | No |
| GO_bp:go_negative_regulation_of_alcohol_biosynthetic_process | 17 | 0.576 | 0.018 | 0.200 | 2.01E-03 | No |
| Curated_gene_sets:yao_temporal_response_to_progesterone_cluster_12 | 74 | 0.290 | 0.019 | 0.102 | 2.16E-03 | No |
| GO_bp:go_dna_damage_response_detection_of_dna_damage | 35 | 0.396 | 0.017 | 0.139 | 2.17E-03 | No |