*Twin Research and Human Genetics*

**Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study**

Michelle Luciano, Victoria Svinti, Archie Campbell, Riccardo E Marioni, Caroline Hayward, Alan F. Wright, Martin Taylor, David J Porteous, Pippa Thomson, James Prendergast, Nick Hastie, Susan Farrington, Generation Scotland, Malcolm Dunlop, Ian J Deary

**Supplementary Table S1**

**Results From Gene Set Analysis for Significant Variants With Frequency <0.01**

|  |  |  |
| --- | --- | --- |
|  | Obesity controls | Depression controls |
|  | Gene | Number of variants | *p-*value | Gene | Number of variants | *p-*value |
| All variants |  |  |  | *RP11-414H17.5**RP11-118B18.1**MESP2/SNORD113-9* | 222 | 1.34-61.97-65.51-6 |
| Nonsynonymous | ***SYNGAP1*** | **3** | **4.0-6** | ***SYNGAP1****HOXD1/ HOXD-AS1**CECR6**AC022201.5**CYP26C1* *ZNF703**NFKBIL1* | **2**222223 | **1.23-6**8.82-76.22-71.04-56.99-65.75-72.77-5 |
| Synonymous |  |  |  | *C9orf66**FAM110C* *ID4/ RP1-167F1.2**TBC1* | 2222 | 1.92-83.91-69.91-63.44-6 |

 Note: Significant genes containing a single variant are not shown. Bold indicates common results across case-control subgroup analyses.

**Supplementary Table S2**

**Results From Gene Set Analysis for Significant Variants With Frequency <0.05**

|  |  |  |
| --- | --- | --- |
|  | Obesity controls | Depression controls |
|  | Gene | Number of variants | *p-*value | Gene | Number of variants | *p-*value |
| All variants | ***RP11-673E1.4/ GYPB******/GYPA***  | **14** **/ 9** | **2.74-12** **5.76-12** | ***RP11-673E1.4/GYPB******/GYPA****RP11-414H17.5**RP11-118B18.1* | **11** **/ 7**22 | **9.94-7 8.05-7**1.16-61.08-6 |
| Nonsynonymous | ***RP11-673E1.4/ GYPB*** ***/GYPA*** | **6** **/ 2** | **4.35-12****5.17-12** | ***RP11-673E1.4/ GYPB******/GYPA****CECR6**FAM136A/AC022201.5* *ZNF703*  | **5** **/ 2**222 | **2.85-7****2.4-7**4.41-84.62-67.40-7 |
| Synonymous |  |  |  | *SOX17* *FAM110C* *ID4/RP1-167F1.2* | 222 | 2.61-74.16-69.35-6 |

Note: Significant genes containing a single variant are not shown. Bold indicates common results across case-control subgroup analyses.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Gene ontology | *p-*value | FDR *p-*value | Enrichment values\* | Genes in pathway |
| **Synonymous** |  |  |  |  |  |
| SNVs<.01 |  |  |  |  |  |
| Molecular Function GO:0008376 | acetylgalactosaminyltransferase activity | 1.23E-5 | .03 | 5.63 (6764,18,667,10) | *GALNT6* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 6 (galnac-t6)*GALNT12* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 12 (galnac-t12)*GALNT10* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 10 (galnac-t10)*B4GALNT3* — beta-1,4-n-acetyl-galactosaminyl transferase 3*GALNT18* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 18*GALNT3* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 3 (galnac-t3)*GALNT2* — udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 2 (galnac-t2)*CHPF* — chondroitin polymerizing factor*B3GALNT2* — beta-1,3-n-acetylgalactosaminyltransferase 2*B4GALNT4* — beta-1,4-n-acetyl-galactosaminyl transferase 4 |

**Supplementary Table S3**

**Significant Gene Ontology Pathways Enriched in the Varying Analyses Comprising the Depression Controls**

Note: *p-*value, FDR corrected *p-*value, enrichment values, and prominent genes in each pathway are listed.

SNV: Single nucleotide variants\* Enrichment is defined as (b/n)/(B/N) [*N*: Total number of genes; B: Total number of genes associated with a specific GO term,
n: Number of genes in the ‘target set’, b: Number of genes in the ‘target set’ associated with a specific GO term].