*Twin Research and Human Genetics*

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

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**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* | 2  2  2 | 1.34-6  1.97-6  5.51-6 |
| Nonsynonymous | ***SYNGAP1*** | **3** | **4.0-6** | ***SYNGAP1***  *HOXD1/ HOXD-AS1*  *CECR6*  *AC022201.5*  *CYP26C1*  *ZNF703*  *NFKBIL1* | **2**  2  2  2  2  2  3 | **1.23-6**  8.82-7  6.22-7  1.04-5  6.99-6  5.75-7  2.77-5 |
| Synonymous |  |  |  | *C9orf66*  *FAM110C*  *ID4/ RP1-167F1.2*  *TBC1* | 2  2  2  2 | 1.92-8  3.91-6  9.91-6  3.44-6 |

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**  2  2 | **9.94-7 8.05-7**  1.16-6  1.08-6 |
| 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**  2  2  2 | **2.85-7**  **2.4-7**  4.41-8  4.62-6  7.40-7 |
| Synonymous |  |  |  | *SOX17*  *FAM110C*  *ID4/RP1-167F1.2* | 2  2  2 | 2.61-7  4.16-6  9.35-6 |

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].