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**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	<i>p</i> -value	Gene	Number of variants	<i>p</i> -value
All variants				<i>RP11-414H17.5</i>	2	1.34 <sup>-6</sup>
				<i>RP11-118B18.1</i>	2	1.97 <sup>-6</sup>
				<i>MESP2/SNORD113-9</i>	2	5.51 <sup>-6</sup>
Nonsynonymous	<b><i>SYNGAP1</i></b>	<b>3</b>	<b>4.0<sup>-6</sup></b>	<b><i>SYNGAP1</i></b>	<b>2</b>	<b>1.23<sup>-6</sup></b>
				<i>HOXD1/ HOXD-AS1</i>	2	8.82 <sup>-7</sup>
				<i>CECR6</i>	2	6.22 <sup>-7</sup>
				<i>AC022201.5</i>	2	1.04 <sup>-5</sup>
				<i>CYP26C1</i>	2	6.99 <sup>-6</sup>
				<i>ZNF703</i>	2	5.75 <sup>-7</sup>
				<i>NFKBIL1</i>	3	2.77 <sup>-5</sup>
Synonymous				<i>C9orf66</i>	2	1.92 <sup>-8</sup>
				<i>FAM110C</i>	2	3.91 <sup>-6</sup>
				<i>ID4/ RP1-167F1.2</i>	2	9.91 <sup>-6</sup>
				<i>TBC1</i>	2	3.44 <sup>-6</sup>

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	<i>p</i> -value	Gene	Number of variants	<i>p</i> -value
All variants	<b><i>RP11-673E1.4/ GYPB</i></b>	<b>14</b>	<b><math>2.74^{-12}</math></b>	<b><i>RP11-673E1.4/GYPB</i></b>	<b>11</b>	<b><math>9.94^{-7}</math></b>
	<b><i>/GYPA</i></b>	<b>/ 9</b>	<b><math>5.76^{-12}</math></b>	<b><i>/GYPA</i></b>	<b>/ 7</b>	<b><math>8.05^{-7}</math></b>
Nonsynonymous				<i>RP11-414H17.5</i>	2	$1.16^{-6}$
				<i>RP11-118B18.1</i>	2	$1.08^{-6}$
	<b><i>RP11-673E1.4/ GYPB</i></b>	<b>6</b>	<b><math>4.35^{-12}</math></b>	<b><i>RP11-673E1.4/ GYPB</i></b>	<b>5</b>	<b><math>2.85^{-7}</math></b>
	<b><i>/GYPA</i></b>	<b>/ 2</b>	<b><math>5.17^{-12}</math></b>	<b><i>/GYPA</i></b>	<b>/ 2</b>	<b><math>2.4^{-7}</math></b>
				<i>CECR6</i>	2	$4.41^{-8}$
				<i>FAM136A/AC022201.5</i>	2	$4.62^{-6}$
				<i>ZNF703</i>	2	$7.40^{-7}$
Synonymous				<i>SOX17</i>	2	$2.61^{-7}$
				<i>FAM110C</i>	2	$4.16^{-6}$
				<i>ID4/RP1-167F1.2</i>	2	$9.35^{-6}$

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

**Supplementary Table S3**

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

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

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].