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A Pilot Study

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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	<i>p</i> -value	Gene	Number of variants	<i>p</i> -value
All variants				<i>RP11-414H17.5</i>	2	1.34 ⁻⁶
				<i>RP11-118B18.1</i>	2	1.97 ⁻⁶
				<i>MESP2/SNORD113-9</i>	2	5.51 ⁻⁶
Nonsynonymous	<i>SYNGAP1</i>	3	4.0⁻⁶	<i>SYNGAP1</i>	2	1.23⁻⁶
				<i>HOXD1/ HOXD-AS1</i>	2	8.82 ⁻⁷
				<i>CECR6</i>	2	6.22 ⁻⁷
				<i>AC022201.5</i>	2	1.04 ⁻⁵
				<i>CYP26C1</i>	2	6.99 ⁻⁶
				<i>ZNF703</i>	2	5.75 ⁻⁷
				<i>NFKBIL1</i>	3	2.77 ⁻⁵
Synonymous				<i>C9orf66</i>	2	1.92 ⁻⁸
				<i>FAM110C</i>	2	3.91 ⁻⁶
				<i>ID4/ RP1-167F1.2</i>	2	9.91 ⁻⁶
				<i>TBC1</i>	2	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	<i>p</i> -value	Gene	Number of variants	<i>p</i> -value
All variants	<i>RP11-673E1.4/ GYPB</i>	14	2.74^{-12}	<i>RP11-673E1.4/GYPB</i>	11	9.94^{-7}
	<i>/GYPA</i>	/ 9	5.76^{-12}	<i>/GYPA</i>	/ 7	8.05^{-7}
Nonsynonymous				<i>RP11-414H17.5</i>	2	1.16^{-6}
				<i>RP11-118B18.1</i>	2	1.08^{-6}
	<i>RP11-673E1.4/ GYPB</i>	6	4.35^{-12}	<i>RP11-673E1.4/ GYPB</i>	5	2.85^{-7}
	<i>/GYPA</i>	/ 2	5.17^{-12}	<i>/GYPA</i>	/ 2	2.4^{-7}
				<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
Synonymous					
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].