

Functional characterization of genes controlling mature mammalian adipocyte network.

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An elevated body mass index (BMI) and lipid abnormalities are associated with an increased risk for vascular disease. To support experimental investigation of genetic factors predisposing to high BMI, genes controlling lipid metabolism in adipose tissue were compiled and functionally characterized in our study. The set of genes, controlling metabolic and signaling pathways in mature mammalian adipocyte was collected using data on insulin signaling in adipocyte presented by [1] and data on metabolic pathways from Reactome. Genes were classified according to the functions of encoded proteins: insulin signaling, uptake and utilization of glucose, biosynthesis of fatty acids, triacylglycerols and cholesterol, regulation of gene expression, lipolysis. Genes were ranked according to their genic intolerance to functional variation using Residual Variation Intolerance Score values presented by [2]. Genes were prioritized according to their relevance to body mass abnormalities using two gene sets presented by [3]: (i) genes associated with obesity and extracted from OMIM; (ii) genes associated with elevated BMI and collected from GWAS meta-analysis papers.

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2. S.Petrovski et al. (2013) Genic intolerance to functional variation and the interpretation of personal genomes, *PLoS Genet*, **9**(8):e1003709.
3. E.V.Ignatieva et al. (2014) Human genes controlling feeding behavior or body mass and their functional and genomic characteristics: a review, *The Vavilov Journal of Genetics and Breeding*, **18**(4/2):667-875.