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| --- | --- | --- | --- | --- |
|  | Description | | Reference related to | |
| Gene Symbol | Location | Function (STRING or GENE CARD) | ASD | SCZ |
| ADIPOR1 | 1q32.1 | Adiponectin receptor protein 1; Receptor for ADIPOQ, an essential hormone secreted by adipocytes that regulates glucose and lipid metabolism. Required for normal glucose and fat homeostasis and for maintaining a normal body weight. ADIPOQ-binding activates a signaling cascade that leads to increased AMPK activity, and ultimately to increased fatty acid oxidation, increased glucose uptake and decreased gluconeogenesis. Has high affinity for globular adiponectin and low affinity for full-length adiponectin (By similarity); Belongs to the ADIPOR family | 37,38,39 | 40,41 |
| DCAF12 | 9p13.3 | DDB1- and CUL4-associated factor 12; May function as a substrate receptor for CUL4-DDB1 E3 ubiquitin-protein ligase complex; DDB1 and CUL4 associated factors |  |  |
| SNORD116-19 | 15q11.2 | SNORD116-19 (Small Nucleolar RNA, C/D Box 116-19) is an RNA Gene, and is affiliated with the snoRNA class. | 42,  43,  44,  45 | 45 |
| SCARNA17 | 18q21.1 | SCARNA17 (Small Cajal Body-Specific RNA 17) is an RNA Gene, and is affiliated with the snoRNA class. Diseases associated with SCARNA17 include Orofacial Cleft 11 and Exanthema Subitum. | 46,  47,  48 | 47,  48 |
| MALAT1 | 11q13.1 | This gene produces a precursor transcript from which a long non-coding RNA is derived by RNase P cleavage of a tRNA-like small ncRNA (known as mascRNA) from its 3' end. The resultant mature transcript lacks a canonical poly(A) tail but is instead stabilized by a 3' triple helical structure. This transcript is retained in the nucleus where it is thought to form molecular scaffolds for ribonucleoprotein complexes. It may act as a transcriptional regulator for numerous genes, including some genes involved in cancer metastasis and cell migration, and it is involved in cell cycle regulation. Its upregulation in multiple cancerous tissues has been associated with the proliferation and metastasis of tumor cells | 49,  50,  51,  52 | 53,  47 |
| RPS3A | 4q31.3 | 40S ribosomal protein S3a; May play a role during erythropoiesis through regulation of transcription factor DDIT3; Belongs to the eukaryotic ribosomal protein eS1 family | 54 |  |
| VNN2 | 6q23.2 | Vascular non-inflammatory molecule 2; Amidohydrolase that hydrolyzes specifically one of the carboamide linkages in D-pantetheine thus recycling pantothenic acid (vitamin B5) and releasing cysteamine. Involved in the thymus homing of bone marrow cells. May regulate beta-2 integrin-mediated cell adhesion, migration and motility of neutrophil; Vanins |  |  |
| RPS27 | 1q21.3 | 40S ribosomal protein S27; Component of the small ribosomal subunit. Required for proper rRNA processing and maturation of 18S rRNAs; Belongs to the eukaryotic ribosomal protein eS27 family. | 55 | 56 |
| HBE1 | 11p15.4 | The epsilon globin gene (HBE) is normally expressed in the embryonic yolk sac: two epsilon chains together with two zeta chains (an alpha-like globin) constitute the embryonic hemoglobin Hb Gower I; two epsilon chains together with two alpha chains form the embryonic Hb Gower II. Both of these embryonic hemoglobins are normally supplanted by fetal, and later, adult hemoglobin. The five beta-like globin genes are found within a 45 kb cluster on chromosome 11 in the following order: 5'-epsilon - G-gamma - A-gamma - delta - beta-3' |  |  |
| HCA112(TMEM176A) | 7q36.1 | Predicted to be involved in negative regulation of dendritic cell differentiation. Predicted to be integral component of membrane. is a Protein Coding gene. Diseases associated with TMEM176A include Hepatocellular Carcinoma. An important paralog of this gene is TMEM176B. |  | 57, 58 |
| TMEM176B | 7q36.1 | Predicted to be involved in negative regulation of dendritic cell differentiation. Predicted to be located in nuclear membrane. Predicted to be integral component of membrane. May play a role in the process of maturation of dendritic cells. Required for the development of cerebellar granule cells. Is a Protein Coding gene. An important paralog of this gene is TMEM176A. |  | 58, 59 |
| PLGLB1 | 2p11.2 | Plasminogen-like protein b; Plasminogen-like B1; May bind noncovalently to lysine binding sites present in the kringle structures of plasminogen. This may interfere with the binding of fibrin or alpha-2-antiplasmin to plasminogen and may result in the localization of activity at sites necessary for extracellular matrix destruction |  | 59 |

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| Genes | MST | | | OGF | | | Reference | |
| ASD | SCZ | Metanalysis | ASD | SCZ | Metanalysis | ASD | SCZ |
| ADIPOR1 | x |  |  | x |  | x | x | x |
| DCAF12 |  |  |  | x |  |  |  |  |
| SNORD116-19 |  |  |  |  |  |  | x | x |
| SCARNA17 |  |  |  |  |  |  | x | x |
| MALAT1 |  |  |  |  |  |  | x | x |
| RPS3A | x |  |  | x |  |  | x |  |
| VNN2 |  |  |  | x |  | x |  |  |
| RPS27 |  |  | x |  |  | x | x | x |
| HBE1 |  |  |  |  |  |  |  |  |
| HCA112(TMEM176A) |  |  |  |  |  |  |  | x |
| TMEM176B |  |  |  |  | x |  |  | x |
| PLGLB1 |  |  |  |  |  | x |  | x |

DCAF12, VNN2, and PLGLB1