Bruce Wayne - EHS/EMF

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E-SensitivityGS

GeneSavvy

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Patient Information

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Accesession#:	BATMAN
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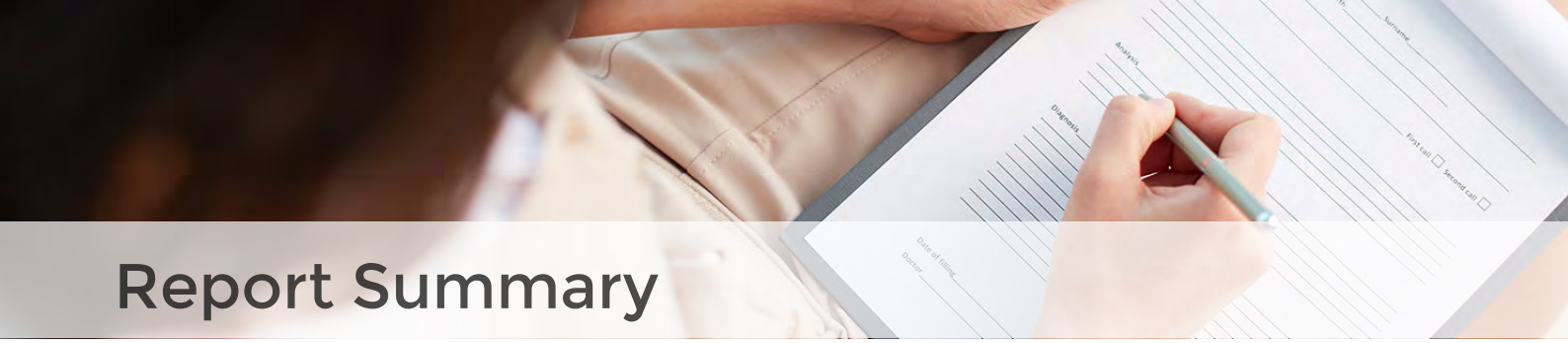
Tech:	GSTECH
Doctor:	Dr. Hugo Strange



Report Summary

After reviewing your results, there are very possible **patterns of mitochondrial ETC disturbances** with possible significant variants in NDUFS, ATG3, and SCN5A genes along with **autophagy/apoptosis/cell homeostasis disturbances** due to possible significant variants in HLA-DQB1, HLA-DRB1, IL3, and SCN5A.

The NDUFS genes can also contribute to **inefficient oxidoreductase processes and higher susceptibility to damage from oxidative stress.**

A few PER gene variants are showing some patterns of susceptibility to sleep pattern/circadian rhythm disturbance.

HLA and IL genes are showing **patterns of immune system inefficiencies** and histamine. This combined with the cell homeostasis disturbances can lead to weak viral and bacterial infection defense.

Heres an interesting article on the relation between EMF exposure and poor mitochondrial ETC activity: **https://www.ncbi.nlm.nih.gov/pubmed/24597749**

Potential Next Steps

Possible next steps should include supporting inefficient mitochondrial ETC processes and enhanced protection against oxidative stresses. **Removing unnecessary EMF UHF exposure** and mitoDNA sequencing to look for other possible disturbances in mitochondrial process efficiency. Immune system support would also be beneficial to help against viral and bacterial exposures.

Using this Report

This report was designed to visualize genetics in a polymorphic, gene network arrangement. Here at GeneSavvy we strongly believe that genetic susceptibilities are created by compounded genetic and environmental influences. The goal is to find genetic and environmental patterns that can show us possible biological processes that are more susceptible to environmental hits. If we find these susceptible processes we can adjust our environment to reduce toxic effects and increase biological efficiency.

Gene Networks: Our GeneSavvy gene networks are built using a Boolean model to find genes related to the functional health terms used in your report. After collecting the relational genes, we use a practical scoring function-based algorithm to calculate relevance and extract the top relevant genes for your report.

The Colors: We use colors to help you scan quickly for patterns within this report. Gene symbols in GREY mean there were no exome variants found in that gene. Gene symbols in GREEN mean there were variants found with only LOW predicted impact. Gene symbols in YELLOW mean there were variants found with MODERATE predicted impact. Gene symbols in RED mean there were variants found with HIGH predicted impact. Genes listed in RED should be the first genes to research as potentially causative to the health concern.

Low Predicted Impact: Low predicted impact variants are usually synonymous variants that don't cause any amino acid changes or variants in areas that don't usually lead to impact on gene efficiency.

Moderate Predicted Impact: Moderate predicted impact variants are usually non-synonymous variants that do change the amino acid. This category of impact also contains insertions or deletions in multiples of 3 that don't cause a disruptive frameshift.

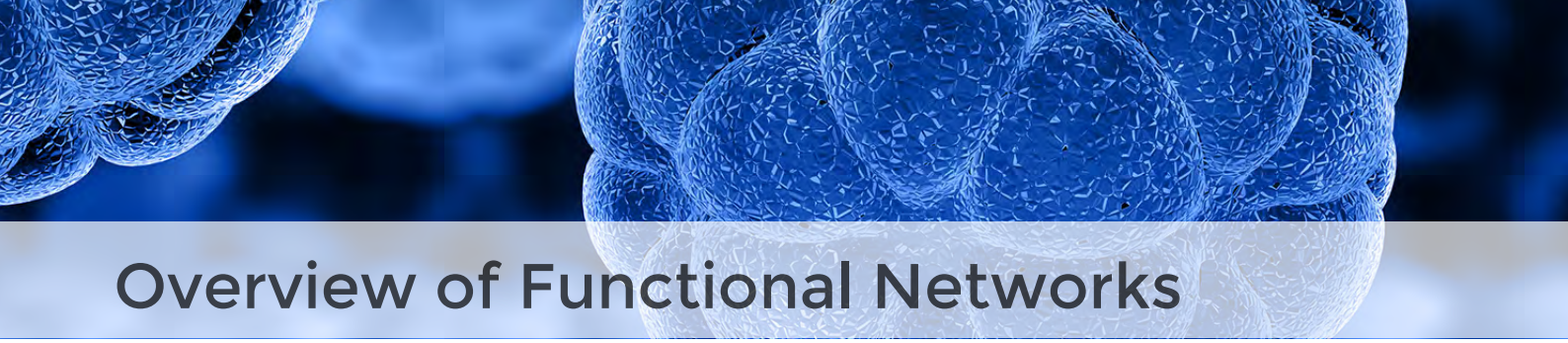
High Predicted Impact: High predicted impact variants are usually start or stop loss variants as well as disruptive frameshifts, major deletions or insertions or variants in splice site donors and splice site acceptors. These variants have high potential to impact gene functionality and efficiency.

Rarity: Rare genetic variants are usually given higher predicted impact compared to common variants. If the variant is found in 99% of our population then it has less chance to be a variant that directly leads to a health condition.

- **Very Rare:** Less than .01% of Population
- **Rare:** Less than 1% of Population
- **Uncommon:** Less than 5% of Population
- **Common:** Greater than 5% of Population
- **Unknown:** No Population Frequency Data

Significant Variants: Significant variants have high predicted impact. These variants should be first to research.

Common SNPs: Technically SNPs (Single Nucleotide Polymorphisms) are only classified as SNPs as they become commonly found in the population. These tend to have less impact on specific health conditions but they can still be key to finding patterns.



Overview of Functional Networks

The pathway and gene network overview below gives a quick view of the systems reviewed in this report. In general, networks with likely susceptibility should be addressed with priority for optimal health.

Acetylcholine	LIKELY LESS STABLE
Autophagy	SUSCEPTABLE
BBB Disruption	LIKELY LESS STABLE
Brain Trauma	LIKELY LESS STABLE
Chemical Sensitivity	LIKELY LESS STABLE
Circadian Rhythm	SUSCEPTABLE
Cryptochromes	LIKELY LESS STABLE
Dopamine	LIKELY LESS STABLE
Epstein-Barr	SUSCEPTABLE

Histamine	SUSCEPTABLE
Melatonin	LIKELY LESS STABLE
Neuro Histamine	LIKELY LESS STABLE
Neurodegeneration	LIKELY LESS STABLE
Neuroregeneration	LIKELY LESS STABLE
Neurotransmitter Regulation	LIKELY LESS STABLE
Nitric Oxide	LIKELY LESS STABLE
Noradrenaline	LIKELY LESS STABLE
Oxidative Stress	LIKELY LESS STABLE
Oxidoreductase	SUSCEPTABLE
Serotonin	LIKELY LESS STABLE

Potentially Significant Variants

This significant variant overview will show you the variants found with the highest predicted impact. In general, these variants will have high potential of affecting the output product of the gene its contained in. This data can be used to potentially super fine-tune treatment protocols by allowing you to increase or decrease enzyme activity to balance the impact of these variants.

Potentially Significant Variants Were Found in The Following Genes

Gene	Variant Location	RSID	Depth	OMIM ID	Effect	Result	Severity	Frequency
CHAT	50856652	rs4838544	60	118490	Missense, SpliceSite	HOM	High	Common (100%)
ATG3	112253058	rs35560667 rs570214747 rs397767079	16	609606	Frameshift	HOM	High	Common (60.48%)
ATG9B	150713902	rs11393607 rs77573754	20	612205	Frameshift	HOM	High	Common (100%)
F2	48549791	rs2305998	14	610465	SpliceSite, Silent	HOM	High	Common (25.59%)
POMGNT1	46655158	rs6659553	46	606822	Missense, SpliceSite	HOM	High	Common (99.94%)
PTEN	89623860	rs71022512	3	601728	Intron, SpliceAcceptor, SpliceDonor	HOM	High	Uncertain
VWF	6105387	rs216902	31	613160	SpliceSite, Silent	HOM	High	Common (74.4%)
VWF	6061559	rs7962217	42	613160	Missense, SpliceSite	HET	High	Uncommon (5.97%)
PER2	43925134	rs7169097	5	607249	Intron, SpliceAcceptor	HET	High	Common (42.31%)
PER3	7890064	rs12023156	67	603427	Intron, SpliceAcceptor	HET	High	Common (27.43%)
SCN5A	38647642	rs41312433	22	600163	Intron, SpliceSite	HET	High	Uncommon (17.21%)
HLA-DQB1	32632638	rs1130385	27	604305	StopGain	HOM	High	Uncommon (16.99%)
HLA-DRB1	32552130	rs9269951	6	142857	Intron, SpliceAcceptor	HOM	High	Common (29.92%)

Gene	Variant Location	RSID	Depth	OMIM ID	Effect	Result	Severity	Frequency
HLA-DRB1	32549613	rs17882084	19	142857	Missense, SpliceSite	HOM	High	Uncommon (8.21%)
HLA-DRB1	32549614	rs140866337	19	142857	SpliceSite, Silent	HOM	High	Uncommon (10.94%)
HLA-DRB1	32552127	rs17885011	6	142857	SpliceSite, Silent	HOM	High	Very Rare (0.69%)
PRF1	72360387	rs35947132	95	170280	Missense	HET	High	Uncommon (4.63%)
DST	56426931	rs9367689	27	113810	Intron, SpliceSite	HET	High	Common (36.26%)
IL3	24533474	rs117092113	33	614716	Missense	HET	High	Uncommon (4.28%)
CSF2	48549791	rs2305998	14	610465	SpliceSite, Silent	HOM	High	Common (25.59%)
ITGA5	54799450	rs1249378rs1249378	16	135620	SpliceSite, Silent	HOM	High	Common (99.9%)
NCAM1	112832339	rs11284059 rs11284059 rs796286007 rs796286007	17	116930	Intron, SpliceAcceptor, SpliceDonor	HOM	High	Common (99.99%)
ALDH3A2	19578873	rs7216	18	609523	SpliceSite, Silent	HOM	High	Common (98.6%)
NDUFS2	161182208	rs11576415	15	602985	Missense	HET	High	Uncommon (9.45%)
NDUFS7	1390925	N/A	26	601825	Frameshift	HET	High	Uncertain

Functional Networks

Acetylcholine

LIKELY LESS STABLE

CHAT CHRM1 CHRM4 CHRNA1 CHRNA2 CHRNA3 CHRNA4 CHRNA9 CHRNB1 CHRNB4 CHRNE CHRNG RAPSN SLC18A3

Functional Network Summary

Acetylcholine is an organic chemical compound which functions in both the body and brain. It functions as a neurotransmitter and sends signals to other cells. The underlying processes related to acetylcholine include neuronal excitability, synaptic plasticity, synaptic transmission, and firing of groups of neurons. Moreover, the genes associated with acetylcholine include MUSK (Muscle Associated Receptor Tyrosine Kinase), CHRNE (Cholinergic Receptor Nicotinic Epsilon Subunit), RAPSN (Receptor Associated Protein Of The Synapse), and CHRNA (Cholinergic Receptor Nicotinic Alpha).

Autophagy

SUSCEPTABLE

ATG10 ATG2B ATG3 ATG4B ATG4C ATG4D ATG9A ATG9B SQSTM1 ULK1 ULK2

Functional Network Summary

Autophagy is the natural process that occurs in the body to destroy cells. It maintains the normal functioning of bodily processes while removing dead cells and turning over the cell contents for the formation of new cells. Processes such as protein stabilization, lysosome organization, and muscle cell cellular homeostasis are the underlying processes of autophagy. Genes such as LAMP2 (Lysosomal-Associated Membrane Protein 2), BECN1 (Beclin 1), and VMA21 (VMA21, Vacuolar ATPase Assembly Factor) have a direct relation to autophagy.

BBB Disruption

LIKELY LESS STABLE

APOE AR CFC1 COMT GFAP IL6 INS MAPT MMP2 MMP9 SPECC1L TP53

Functional Network Summary

Blood-brain barrier disruption refers to the process in which drugs are used to create an opening between the cells of the blood-brain barrier; a protective network of tissues and blood vessels in the brain. The procedure is primary used to treat brain tumors. BBB disruption can also take place due to diabetes mellitus. The underlying processes linked to BBB disruption include alteration in the size of the meshwork as well as changes in the electoral charges that surrounds the pores between the endothelial cells. The genes involved, on the other hand, include TNF (Tumor Necrosis Factor), APOE (Apolipoprotein E), INS (Insulin), TP53 (Tumor Protein P53), and ALB (Albumin).

Brain Trauma

LIKELY LESS STABLE

APOE BDNF COL4A1 DRD2 F2 F5 GFAP IL6 MAPT MTHFR PANK2 POMGNT1 PTEN TP53 VWF

Functional Network Summary

Brain trauma or intracranial injury takes place when an external force, usually a jolt or blow to the head, injures the brain. Numerous underlying processes are linked to the injury and some of them include negative regulation of apoptotic process, response to drug, axonogenesis, regulation of gene expression, neuron projection regeneration, and protein binding. Meanwhile, the genes linked with brain trauma include APOE (Apolipoprotein E), S100B (S100 Calcium Binding Protein B), ENO2 (Enolase 2), GFAP (Glial Fibrillary Acidic Protein), and BDNF (Brain-Derived Neurotrophic Factor).

Chemical Sensitivity

LIKELY LESS STABLE

ABCB1 ABCC8 ALB APOE BRCA1 CCL2 COMT CYP2D6 EGFR IL6 INS MTHFR NAT2 SLC2A1 TP53

Functional Network Summary

Multiple chemical sensitivity or chemical sensitivity is a disputed chronic condition that is characterized by those symptoms that are often attributed to low-level exposures to some commonly used chemicals. Some of the underlying processes of chemical sensitivity include lipid metabolic process, response to toxic substance, lipoxygenase pathway, oxidative demethylation, and drug metabolic process. Oxidoreductase activity, drug binding, and iron ion binding also play a role. Meanwhile, the associated genes include CYP2D6 (Cytochrome P450 Family 2 Subfamily D Member 6), POX (Paraoxonase), GSTT1 (Glutathione S-Transferase Theta 1), and NAT2 (N-Acetyltransferase 2).

Circadian Rhythm

SUSCEPTABLE

ARNTL2 BHLHE41 CLOCK CRY1 CRY2 DBP MTNR1A NPAS2 NR1D2 PER1 PER2 PER3 RORA RORB SCN5A TIMELESS

Functional Network Summary

Circadian Rhythm is said to be the natural sleep and wake cycle of the human body. It is an internal 24-hour clock that controls the body and brain and signals them during different times of the day for sleep or being alert, appropriately during daytime and nighttime. Circadian rhythm is controlled by the hypothalamus in the brain. Rhythmic processes and gluconeogenesis are the underlying functions of the circadian rhythm. The genes CRY1 (Cryptochrome Circadian Regulator 1) and PER (Period Circadian Regulator) are the primary genes responsible for the regulation of the circadian rhythm cycle.

Cryptochromes

LIKELY LESS STABLE

AR CLOCK CRY1 CRY2 CUL1 DBP GNAS NPAS2 NR3C1 PER1 PER2 PER3 PPP5C RORA TIMELESS USP7

Functional Network Summary

Cryptochromes are defined as a class of flavoproteins that are quite sensitive o blue light and are found in both animals and plants. The underlying processes that are linked with cryptochromes include circadian rhythms and the sensing of magnetic fields. Meanwhile, the genes associated with cryptochromes are CRY (Cryptochrome Circadian Regulator), ARNTL (Aryl Hydrocarbon Receptor Nuclear Translocator Like), CLOCK (Clock Circadian Regulator), and PER (Period Circadian Regulator).

Dopamine

LIKELY LESS STABLE

COMT DBH DDC DRD1 DRD2 DRD3 DRD4 DRD5 HTR2A SLC6A2 SLC6A3 TH

Functional Network Summary

Dopamine is a chemical found in both the brain and the body. It is a part of the phenethylamine and catecholamine families. Primarily, it affects the movements, emotions, as well as sensations of pain and pleasure. The main process linked to dopamine is exocytosis while the genes linked to dopamine are DBH (Dopamine Beta-Hydroxylase), SLC6A3 (Solute Carrier Family 6 Member 3), DR (Dopamine Receptor), and DDC (Dopa Decarboxylase).

Epstein-Barr

SUSCEPTABLE

CD27 CD40LG CR2 FCGR3A HLA-DQB1 HLA-DRB1 IFNG IL2 PIK3CD PRF1 RPL22 TERT TP53

Functional Network Summary

Also called human herpesvirus 4, Epstein-Barr virus is one of the eight kinds of human herpesvirus in the herpes family. It is also described as one of the most common herpes viri in humans. The underlying processes related Epstein-Barr include full spectrum and titer of antibodies to EBV, variable deficiency of natural killer-cell activity, progressive bronchiectasis, and recurrent sinusitis, pneumonia, and otitis. Severe infectious mononucleosis and susceptibility to bacterial infections also play a role. Meanwhile, the major genes associated with virus include CR2 (Complement C3d Receptor 2), SH2D1A (SH2 Domain Containing 1A), MAGT1 (Magnesium Transporter 1), XIAP (X-Linked Inhibitor Of Apoptosis), and EBI3 (Epstein-Barr Virus Induced 3).

Histamine

SUSCEPTABLE

ADGRE2 ALB AOC1 DST GAST HAL HRH1 HRH2 HRH3 HRH4 IFNG IL2 IL3 IL6 KNG1

Functional Network Summary

Histamine is a chemical compound which has a number of functions in the body. It is linked with local immune responses, it is known for regulating the physiological function in the act. Plus, it also acts as a neurotransmitter for the uterus, spinal cord, and brain. While the underlying processes of neuro histamine are not clear, it is known that histamine is administered via G-protein-coupled H1-H4 receptors. Moreover, the genes associated with neuro histamine include HR (Histamine Receptor), HDC (Histidine Decarboxylase), CXCL8 (C-X-C Motif Chemokine Ligand 8), and AOC1 (Amine Oxidase, Copper Containing 1).

Melatonin

LIKELY LESS STABLE

BDNF CLOCK CYP1A2 CYP2C19 DRD4 GPR50 HTR2C HTR3A MTNR1A NQO2 NR1H2 PER2 PER3 RORA TPH1 TPH2

Functional Network Summary

Melatonin is a chemical hormone that is made by the pineal gland in humans and animals. It is responsible for regulating sleep and wakefulness. The primary underlying process related to melatonin is circadian rhythms. Meanwhile, the genes associated with melatonin include MTNR (Melatonin Receptor), AANAT (Aralkylamine N-Acetyltransferase), GPR50 (G Protein-Coupled Receptor 50), and ASMT (Acetylserotonin O-Methyltransferase).

Neuro Histamine

LIKELY LESS STABLE

ADCY10 ALB AOC1 CCL2 CSF2 GAST HRH1 HRH3 ICAM1 IFNG IL13 IL2 IL3 IL6 KNG1

Functional Network Summary

Neuro histamine is defined as an organic nitrogenous compound that is responsible for a number of functions in the body. Primarily, it functions as a neurotransmitter for the uterus, spinal cord, and brain. While the underlying processes of neuro histamine are not clear, it is known that histamine is administered via G-protein-coupled H1-H4 receptors. Moreover, the genes associated with neuro histamine include HR (Histamine Receptor), HDC (Histidine Decarboxylase), CXCL8 (C-X-C Motif Chemokine Ligand 8), and AOC1 (Amine Oxidase, Copper Containing 1).

Neurodegeneration

LIKELY LESS STABLE

ATP13A2 C19orf12 CAV1 COASY FA2H FTL GLB1 JPH3 MAPT PANK2 SNCB SQSTM1 VPS13A

Functional Network Summary

Neurodegeneration refers to the gradual damage to neuron structure and function resulting in neurodegenerative diseases such as Parkinson's, Alzheimer's, Huntington's, etc. Neurons form an important part of our nervous system and are responsible for transmitting signals and stimuli to the brain and then to the target organ to carry out a response. Underlying processes of neurodegeneration include coenzyme biosynthetic processes. C19orf12 (Chromosome 19 Open Reading Frame 12), PANK2 (Pantothenate Kinase 2), PLA2G6 (Phospholipase A2 Group VI), and COASY (Coenzyme A Synthase) are the major genes associated to neurodegeneration.

Neuroregeneration

LIKELY LESS STABLE

ANPEP BDNF CD34 CD44 CDH2 ENG FAS GFAP HMGB1 ITGA5 ITGB1 NCAM1 NES NT5E TP53

Functional Network Summary

Neuroregeneration is the repair or growth of nervous cells and tissue and all cell contents. As a result, it leads to the production of new neurons, axons, myelin sheaths that cover the axons, synapses, dendrites, etc. However, studies have also found that neuroregeneration may also lead to pathogenesis that is the pathway adopted for a disease to grow and spread. NT5E (5'-Nucleotidase Ecto), BDNF (Brain-Derived Neurotrophic Factor), and ANPEP (Alanyl Aminopeptidase, Membrane) are said to be the genes related to neuroregeneration and help in the growth and survival of the cells and tissues of the nervous system.

Neurotransmitter Regulation

LIKELY LESS STABLE

CHAT DDC EGFR HTR2A IFNG IL6 INS NOS3 QDPR SCN4A SLC6A3 TGFB1 TH TP53

Functional Network Summary

Neurotransmitter regulations refers to a development process where the nervous system has natural balance and checks in the form of neurotransmitters. The underlying processes of neurotransmitter regulation are believed to include transmission of signals between neurons and regulation of processes. Meanwhile, the DNA associated with neurotransmitter regulation include MAPK1 (Mitogen-Activated Protein Kinase 1), INS (Insulin), TNF (Tumor Necrosis Factor), and CHAT (Choline O-Acetyltransferase).

Nitric Oxide

LIKELY LESS STABLE

EDN1 IFNG KNG1 MPO NOS1 NOS1AP NOS2 NOS3 SOD2 XDH

Functional Network Summary

Nitric Oxide refers to a binary compound of nitrogen and oxygen and is known to be vital for numerous cellular processes in the body. While the exact underlying processes of nitric oxide are unknown, it is suggested that tight interplays among cyclic ADP ribose or cADPR, calcium ions, and protein kinases play a role. The genes associated with nitric oxide include NOS (Nitric Oxide Synthase), SOD1 (Superoxide Dismutase 1), CAT (Catalase), and XDH (Xanthine Dehydrogenase).

Noradrenaline

LIKELY LESS STABLE

ADRA1A ADRA1D ADRA2B ADRA2C ADRB1 ADRB2 COMT DBH EDN1 HTR2A INS KNG1 REN SLC22A2 SLC6A2

Functional Network Summary

Noradrenaline or norepinephrine is an organic chemical that belongs to the catecholamine family. It functions both as a neurotransmitter and a hormone and has various functions in the brain and the body. The underlying processes related to noradrenaline are regulation of synaptic mechanisms and changes in synaptic strength. Meanwhile, DBH (Dopamine Beta-Hydroxylase), SLC6A2 (Solute Carrier Family 6 Member 2), PNMT (Phenylethanolamine N-Methyltransferase), and NPY (Neuropeptide Y) are some of the genes associated with the chemical.

Oxidative Stress

LIKELY LESS STABLE

CPT2 EDN1 IL6 MPO NOS1 NOS2 NOS3 RYR2 SOD2 TP53 XDH

Functional Network Summary

Oxidative stress refers to the disturbance of the balance between free radicals and antioxidants in the body. Free radicals are the by-products of oxygen that contain an unpaired electron. As a result, they are highly reactive and react with structures in the cells such as DNA to gain electrons, making them unstable. This triggers a series of free radical reactions that can prove harmful for the body. Underlying process of oxidative stress can be lipid peroxidation as well as increased tissue damage in patients suffering from diabetes, DNA duplex unwinding, etc. Genes such as NOS (Nitric Oxide Synthase), CAT (Catalase), and SOD1 (Superoxide Dismutase 1) are said to be associated with oxidative stress.

Oxidoreductase

SUSCEPTABLE

ALDH3A2 ETFB ETFDH HSD3B7 MT-ND1 MT-ND3 MT-ND4 MT-ND5 MT-ND6 NDUFB9 NDUFS1 NDUFS2 NDUFS4 NDUFS7 WWOX XDH

Functional Network Summary

Oxidoreductase is an enzyme that catalyzes the removal of electrons and atoms of hydrogens from the compounds that they act on. There are numerous kinds of oxidoreductase with different mechanisms of catalytic activity; however, most revolve around the oxidation of a substrate to product output products that have different chemical properties. The primary genes that are associated with oxidoreductase include POR (Cytochrome P450 Oxidoreductase), ETFDH (Electron Transfer Flavoprotein Dehydrogenase), WWOX (WW Domain Containing Oxidoreductase), and FOXRED1 (FAD Dependent Oxidoreductase Domain Containing 1).

Serotonin

LIKELY LESS STABLE

COMT CYP2D6 DDC DRD2 HTR1B HTR2A HTR2C HTR3A HTR5A HTR6 SLC6A3 TPH1 TPH2

Functional Network Summary

Serotonin is a chemical made by the nerve cells. It is responsible for sending the signals between the nerve cells and is generally found in the digestive system. The process that is closely associated to serotonin is selective serotonin reuptake. Moreover, the genes associated to serotonin are SLC6A4 (Solute Carrier Family 6 Member 4), HTR (5-Hydroxytryptamine Receptor), and MAOA (Monoamine Oxidase A).

Thankyou!

Our team here at GeneSavvy thanks you for choosing GeneSavvy as your Genetic Testing!
We hope your experience with us was empowering.