Bruce Wayne - Dysautonomia/GI

June 20, 2018

PowerXomeGS + MitoPowerGS

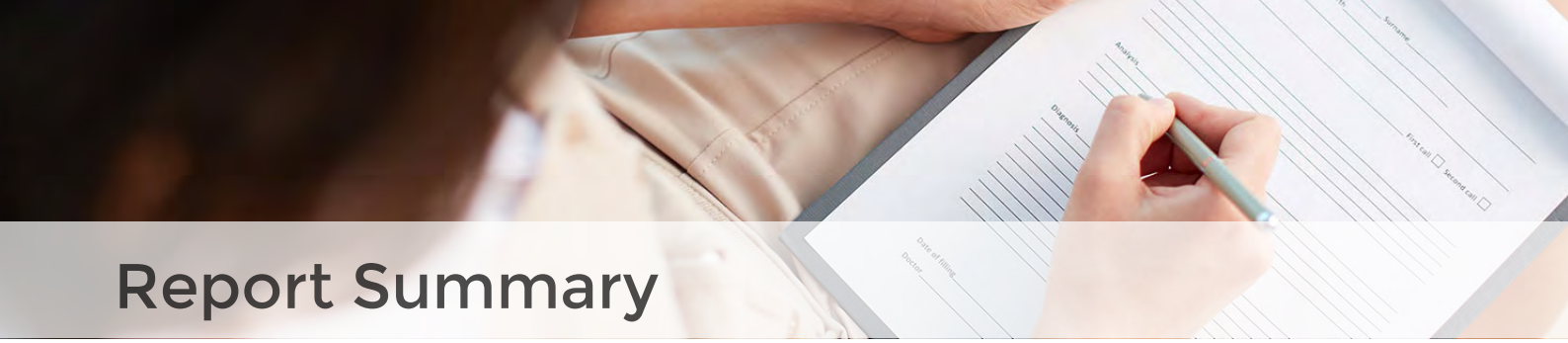
GeneSavvy

6016 NE Bothell Way,Suite G, Kenmore, WA USA

Phone: 425-686-0000 | Fax: 425-892-2548 | Email: info@GeneSavvy.com

Patient Information

Full Name:	Bruce Wayne - Dysautonomia/GI
Gender:	Male
Address:	1007 Mountain Drive, Gotham City, Metropolis 12345 United States
Phone:	123-456-7891
Email:	info@genesavvy.com
Date Of Birth:	1963-02-19
Marital Status:	Single
Accesession#:	BATMAN
Collected:	2018-04-01
Recieved:	2018-06-06
Reported:	2018-06-06
Tech:	GSTECH
Doctor:	Dr. Hugo Strange



Report Summary

Patient expressed being diagnosed with **Dysautonomia and Hashimotos Thyroiditis as well as dealing with severe headaches, fainting, and numerous stomach problems.**The results of this test were geared around finding the **underlying cause of Dysautonomia and GI concerns.**

After reviewing genetic info, found some interesting patterns that can correlate to both Dysautonomia and GI Issues with **variants related to Celiac Disease, IBS, and Autoimmune Inflammation (HLA-DQB1, HLA-DRB1, MGAM, IRF5).**

Liver function and Fat Metabolism/Transport/Absorption could also be disrupted by several genes (APOB, APIDOQ, ACADS).

There were also some signs of potential **Magnesium, Copper and GABA disruption (MGAM, ABAT, CLDN16, COMMD1, DBH)** with **DBH having specific mention of Autonomic Failure.** DBH (Dopamine beta hydroxylase)also **contributes to Dopamine beta hydroxylase deficiency which has many potential symptoms in Autonomic Dysfunction** and is a factor in the **conversion of dopamine to noradrenaline.**

PRSS3 and PRRS1 are both involved in Trypsin activity and pancreatitis.

MGAM also has a specific role in the digestion of malted dietary oligosaccharides used in food manufacturing.

Potential Next Steps

Testing to rule out celiac disease as a potential underlying cause of the dysautonomia and GI issues.

CD4/CD8/Immune system testing due to the HLA and immune gene variants present.

Serum Adiponectin to test the potential disruption of ADIPOQ.

Hepatic function testing would be recommended to check hepatic function efficiency with several liver related genes potentially impacted.

MGAM's specific role in the digestions of dietary oligosaccharides used in food manufacturing **suggests possible benefit from FODMAP diet.**

Testing Copper, Magnesium, GABA, and Calcium levels/utilization/absorption etc..

GI-MAP test for gut function and **autophagy/apoptosis testing** recommended as well.

Better treatment options can be created after testing functionality and efficiency of above systems.

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.

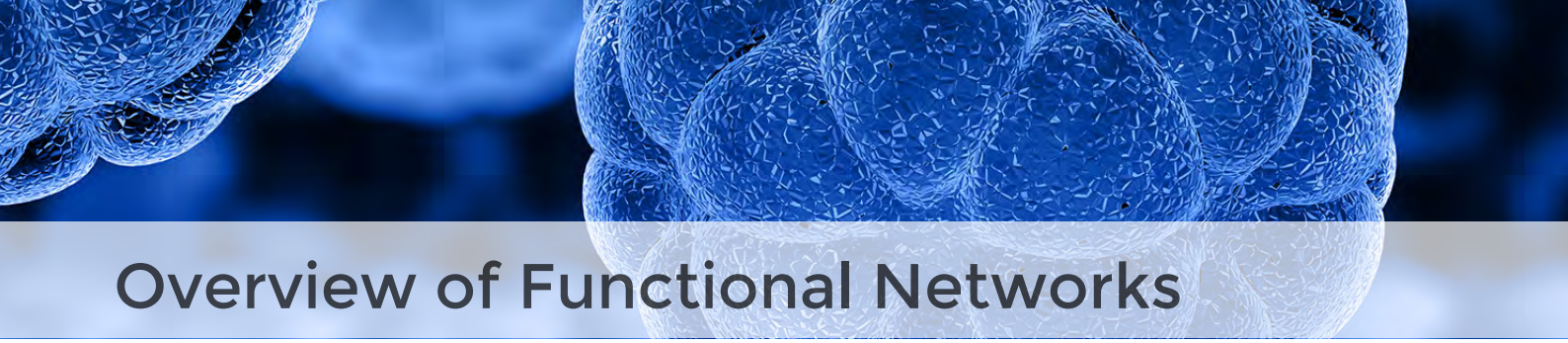
High Predicted Impact: High predicted impact variants are usually start or stop loss variants as well as disruptive frameshifts, major deletions or insertions or variants in splice site donors and splice site acceptors. These variants have high potential to impact gene functionality and efficiency.

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.

Autophagy	SUSCEPTABLE
Calcium Channel	LIKELY LESS STABLE
Celiac Disease	SUSCEPTABLE
Copper	SUSCEPTABLE
Diabetes Mellitus	LIKELY LESS STABLE
G6P	SUSCEPTABLE
GABA	SUSCEPTABLE
Lactic Acid	SUSCEPTABLE
Magnesium	SUSCEPTABLE

Mitochondrial Complex I	LIKELY LESS STABLE
Mitochondrial Complex II	LIKELY LESS STABLE
Mitochondrial Complex III	SUSCEPTABLE
Mitochondrial Complex IV	LIKELY LESS STABLE
Mitochondrial Complex V	LIKELY LESS STABLE
Mitochondrial Complex VI	LIKELY STABLE
Multiple sclerosis	SUSCEPTABLE
Trypsinogen	SUSCEPTABLE
Zinc	SUSCEPTABLE

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
ATG3	112253058	rs35560667 rs570214747 rs397767079	10	609606	Frameshift	HOM	High	Common (60.48%)
ATG4D	10659652	N/A	13	611340	Missense	HET	High	Uncertain
ATG9B	150713902	rs11393607 rs77573754	14	612205	Frameshift	HOM	High	Common (100%)
CACNA1B	140777306	rs4422842 rs4422842	19	601012	Missense	HET	High	Common (50%)
HLA-DQB1	32632638	rs1130385	7	604305	StopGain	HOM	High	Uncommon (16.99%)
COMMD1	62228013	rs55677935	14	607238	Missense	HET	High	Uncommon (2.22%)
DBH	136505114	rs1108580	9	609312	SpliceSite, Silent	HOM	High	Common (44.98%)
ADIPOQ	186572026	rs62625753 rs62625753	10	605441	Missense	HET	High	Very Rare (0.58%)
PGD	10477509	N/A	4	172200	StopGain	HET	High	Uncertain
PYGL	51378590	rs11356035	12	613741	Intron, SpliceAcceptor	HET	High	Common (43.94%)
SLC37A4	118898435	rs56966114 rs547203028	27	602671	Intron, SpliceAcceptor, SpliceDonor	HOM	High	Common (100%)
ABAT	8839954	rs1731017	16	137150	Missense, SpliceSite	HOM	High	Common (60.26%)
GABRR1	89913209	rs4590242	2	137161	Intron, SpliceAcceptor	HOM	High	Common (90.3%)

Gene	Variant Location	RSID	Depth	OMIM ID	Effect	Result	Severity	Frequency
ACADS	121176083	rs1799958	26	606885	Missense, SpliceSite	HET	High	Common (26.58%)
CLDN16	190106071	rs368234054	16	603959	Frameshift	HET	High	Uncommon (19.4%)
MGAM	141759274	rs2960758	6	154360	SpliceSite, Silent	HOM	High	Common (23.19%)
MGAM	141796131	rs6975672	11	154360	SpliceSite, Silent	HET	High	Common (72.94%)
SLC12A1	48580713	rs1552311	17	600839	Missense, SpliceSite	HOM	High	Common (100%)
BCS1L	219525876	rs121908576	23	603647	StopGain	HET	High	Very Rare (0.02%)
UQCRC2	21994411	rs7282	7	191329	SpliceSite, Silent	HET	High	Uncommon (11.7%)
HLA-DRB1	32549613	rs17882084	9	142857	Missense, SpliceSite	HOM	High	Uncommon (8.21%)
HLA-DRB1	32552127	rs17885011	4	142857	SpliceSite, Silent	HOM	High	Very Rare (0.69%)
HLA-DRB1	32549614	rs140866337	9	142857	SpliceSite, Silent	HOM	High	Uncommon (10.94%)
HLA-DRB1	32552130	rs9269951	4	142857	Intron, SpliceAcceptor	HOM	High	Common (29.92%)
FLNB	58112442	N/A	16	603381	Frameshift	HET	High	Uncertain
PRSS1	142460339	rs200973660	38	276000	Missense	HET	High	Uncommon (2.15%)
PRSS3	33797928	rs779080843	48	613578	Frameshift	HET	High	Uncertain
PRSS3	33796799	rs200709040	16	613578	Missense, SpliceSite	HET	High	Very Rare (0.17%)
PRSS3	33798079	rs144845866	33	613578	SpliceSite, Silent	HET	High	Very Rare (0.1%)
PRSS3	33797930	rs797012348	49	613578	Frameshift	HET	High	Uncertain
DNAH8	38800209	rs1678729	13	603337	SpliceSite, Silent	HET	High	Common (27.3%)

Mitochondrial Report

Mitochondrial Report

Gene	Result	AA Change	rsID	Clinvar	OMIM	MitoMap Disease	Conser-vation	Depth	Ref Allele	Alt Allele	Population Frequency	Disease Score	Hetero Fraction
MT-CO3	9380A	syn	NA	NA	NA	NA	-0.818346	169	G	A	NA	NA	Homoplasmy (98.80%)
MT-DLOOP	302C	NA	NA	NA	NA	NA	0.382307	156	A	ACC ACCCC	NA	NA	Multi-Het ACC (9.00%) ACCC (3.80%) C (3.70%)
MT-DLOOP	16482G	NA	NA	NA	NA	NA	-1.91705	136	A	G	NA	NA	Homoplasmy (94.90%)
MT-DLOOP	16193T	NA	NA	NA	NA	NA	0.580598	207	C	T	0.66%	NA	Homoplasmy (96.60%)
MT-DLOOP	16219G	NA	NA	NA	NA	NA	-2.96698	219	A	G	NA	NA	Homoplasmy (98.20%)
MT-DLOOP	239C	NA	NA	NA	NA	NA	-1.00551	166	T	C	0.62%	NA	Homoplasmy (97.60%)
MT-DLOOP	93G	NA	rs369034419	NA	NA	NA	-0.939425	92	A	G	3.93%	NA	Homoplasmy (100.00%)
MT-DLOOP	204C	NA	rs3135032	NA	NA	NA	-2.5255	175	T	C	4.68%	NA	Homoplasmy (97.70%)
MT-DLOOP	310C	NA	NA	NA	NA	NA	0.31622	115	T	TC C	26.63%	NA	Multi-Het TC (5.20%) C (76.10%)
MT-DLOOP	16362C	NA	rs62581341	NA	NA	NA	-4.62754	204	T	C	18.5%	NA	Homoplasmy (98.50%)
MT-ND1	3915A	syn	rs41524046	NA	NA	NA	-5.0315	209	G	A	1.07%	NA	Homoplasmy (99.00%)
MT-ND2	4727G	syn	NA	NA	NA	NA	-1.84798	172	A	G	NA	NA	Homoplasmy (100.00%)
MT-ND4L	10589A	syn	rs2853487	NA	NA	NA	-5.67109	245	G	A	1.81%	NA	Homoplasmy (98.80%)
MT-ND5	12825C	syn	NA	NA	NA	NA	-2.38194	211	T	C	NA	NA	Homoplasmy (2.40%)
MT-ND5	13748G	N471S	NA	NA	NA	NA	-1.67478	220	A	G	0.04%	Low	Homoplasmy (99.10%)

Functional Networks

Autophagy

SUSCEPTABLE

ATG13 ATG16L1 ATG2B ATG3 ATG4B 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.

Calcium Channel

LIKELY LESS STABLE

CACNA1A CACNA1B CACNA1C CACNA1D CACNA1E CACNA1G CACNA1H
CACNA1S CACNA2D1 CASR CFTR CHRNE KCNMA1 ORAI1 RYR1 RYR2 TRPV1

Functional Network Summary

Calcium channels are trans-membrane protein channels that are spread across the membrane. These calcium channels allow the movement of only calcium ions through it into the cell. There are two types of calcium channels that are voltage-gated and ligand-gated. Ion transport, muscle contraction immune responses are other processes related to calcium channels. The genes CASR (Calcium Sensing Receptor), CACN (Calcium Voltage-Gated Channel), KCNM (Potassium Calcium-Activated Channel Subfamily M), and RYR1 (Ryanodine Receptor 1) are associated with these calcium channels. Movement of ions, exocytosis of ATP and action potential are some of the related molecular pathways.

Celiac Disease

SUSCEPTABLE

APOE HLA-DQA1 HLA-DQB1 IFNG MTHFR MYO9B PTPN22 SH2B3 STAT3 TFRC TG TGFB1 TPO

Functional Network Summary

An autoimmune disorder, celiac diseases damages the small intestine while also inhibiting the absorption of nutrients. As a result, a person is unable to tolerate gluten in any form. The underlying processes related with celiac disease are immune system process, regulation of innate immune response, T cell costimulation, hormone biosynthetic processes, interferon-gamma-mediated signaling pathway, and MHC class II receptor activity. Meanwhile, the genes associated with the disease involved are HLA-DQ (Major Histocompatibility Complex, Class II, DQ) and CELIAC (Celiac Disease).

Copper

SUSCEPTABLE

AOC1 ATP7A ATP7B CCS COMMD1 DBH SLC31A2 TF

Functional Network Summary

Copper belongs to a small group of metallic elements that are vital for the maintenance of human health. It is a micronutrient which is needed for maintenance, development, and proper growth of bone and other organs such as heart, brain, and connective tissue. Normal functioning of metabolic processes is often linked to copper. Meanwhile, some of the genes that are associated with copper include ATP (ATPase Copper Transporting), ATOX1 (Antioxidant 1 Copper Chaperone), SLC (Solute Carrier Family), and COMD1 (Copper Metabolism Domain Containing 1).

Diabetes Mellitus

LIKELY LESS STABLE

ABCC8 ACE ADIPOQ CAPN10 GLIS3 HNF1A INSR IRS1 KCNJ11 NEUROD1 PAX4 SLC2A4 WFS1

Functional Network Summary

Commonly referred to as diabetes, diabetes mellitus is a group of metabolic disorders characterized by high blood sugar levels over a long time period. Underlying processes include response to drug and insulin, liver development, carbohydrate metabolic processes, and cellular response to glucose and insulin stimulus. Sequence-specific DNA binding and ATP-activated inward rectifier potassium channel activity also play a role. Genes mostly associated with diabetes mellitus include KCNJ11 (Potassium Voltage-Gated Channel Subfamily J Member 11), MEN1 (Menin 1), INS (Insulin), and ABCC8 (ATP Binding Cassette Subfamily C Member 8).

G6P

SUSCEPTABLE

AGL GABRE GBE1 H6PD HK1 HK2 LPL MPI PCK2 PGD PPARGC1A PYGL SLC37A4

Functional Network Summary

Glucose-6-phosphate dehydrogenase is a cytosolic enzyme. Its primary responsibility is to catalyze a chemical reaction. This enzyme participates in the pentose phosphate pathway, a metabolic pathway that supplies reducing energy to cells such as erythrocytes by maintaining the level of the co-enzyme nicotinamide adenine dinucleotide phosphate (NADPH). GP6C (Glucose-6-Phosphatase Catalytic Subunit), SLC37A4 (Solute Carrier Family 37 Member 4), and LPL (Lipoprotein Lipase) are some genes linked with G6P. The dietary treatment of G6P deficiency aims at avoiding hypoglycemia. The diagnosis is based on clinical presentation, on abnormal basal values, and absence of hyperglycemic response to glucagon. It can be confirmed by demonstrating a deficient activity of a G6P system component in a liver biopsy.
https://ghr.nlm.nih.gov/gene/G6PC

GABA

SUSCEPTABLE

ABAT ALDH5A1 GABBR2 GABRA2 GABRA4 GABRA6 GABRB3 GABRD GABRG2 GABRP GABRR1 GABRR2 GABRR3 SLC6A13

Functional Network Summary

Lactic Acid

SUSCEPTABLE

ACADS CPT2 DBT HIBCH MT-ND1 MT-ND5 PDHB PDHX POLG SLC3A1 TYMP

Functional Network Summary

Lactic acid is found in the body naturally and is made from the glycogen present in the muscle cells. Its production starts when the muscle cells have insufficient supply of oxygen to support the production of energy. It also works to bring down the level of pH in the muscle cells. Two processes that are linked to lactic acid include the Krebs cycle and the aerobic energy system. Some of the genes linked to lactic acid include DLD (Dihydrolipoamide Dehydrogenase), PC (Pyruvate Carboxylase), PDHA1 (Pyruvate Dehydrogenase E1 Alpha 1), and LIAS (Lipoic Acid Synthetase). The molecular processes associated with lactic acid include anaerobic cellular respiration, glycolysis, and lactic fermentation.
http://www.lactic-acid.com/in_the_human_body.html /> http://www.lactic-acid.com/in_the_human_body.html

Magnesium

SUSCEPTABLE

ADCY10 CASR CLCNKB CLDN16 CNNM2 EGF MGAM MRS2 PTH SLC12A1 SLC12A3 SLC41A1 TRPM6 TRPM7

Functional Network Summary

Magnesium is an essential element that the body needs and is present abundantly in the body. In humans, magnesium is involved in more than 300 enzymatic reactions that take place in the body. While there are numerous underlying processes associated with magnesium, some of them include enzyme stabilization, regulation of vascular tone, and enables ATP-generating reactions. Meanwhile, some of the genes linked to the chemical element include CLDN16 (Claudin 16), TRPM6 (Transient Receptor Potential Cation Channel Subfamily M Member 6), MAGT1 (Magnesium Transporter 1), and FXYD2 (FXYD Domain Containing Ion Transport Regulator 2).

Mitochondrial Complex I

LIKELY LESS STABLE

MT-ND1 MT-ND5 NDUFA10 NDUFA11 NDUFAF1 NDUFAF4 NDUFS1 NDUFS4 NDUFS7 NDUFV2 SDHA

Functional Network Summary

Mitochondrial Complex II

LIKELY LESS STABLE

BCS1L MT-CO3 MT-ND1 MT-ND5 NDUFS1 NDUFS4 POLG SDHA SDHAF1 SDHB

Functional Network Summary

Mitochondrial Complex III

SUSCEPTABLE

BCS1L CYC1 MT-CO3 MT-ND1 MT-ND2 MT-ND5 NDUFS1 NDUFS4 POLG SDHA UQCRB UQCRC2

Functional Network Summary

Mitochondrial Complex IV

LIKELY LESS STABLE

BCS1L COX10 MT-CO3 MT-ND1 MT-ND5 NDUFA10 NDUFAF4 NDUFS1 NDUFS4 POLG SDHA

Functional Network Summary

Mitochondrial Complex V

LIKELY LESS STABLE

BCS1L F5 MT-CO3 MT-ND1 MT-ND5 NDUFS1 NDUFS4 POLG SDHA

Functional Network Summary

Mitochondrial Complex VI

LIKELY STABLE

COL6A1 COX10 CYC1 MAPT MT-ND1 NDUFS4 OPA1 PDHX SDHB SERAC1 SLC25A46 TP53 TYMP UQCRB

Functional Network Summary

Multiple sclerosis

SUSCEPTABLE

ALS2 APOE FUS GFAP HLA-DRB1 IFNG MBP MEN1 OPTN PKD1 RET SETX SQSTM1 TNFRSF1A TSC1 VCP

Functional Network Summary

Multiple sclerosis is a disease of the spinal cord and brain which is characterized by the damage to the insulating covers of the nerve cells in the spinal cord and brain. The disease can also be potentially disabling. The underlying processes of the disease include cell surface receptor signaling pathway, viral entry into host cell, cellular response to exogenous dsRNA, T cell costimulation, B cell proliferation. MHC class II receptor activity and virus receptor activity are also the processes involved. Meanwhile, the genes involved include HLA-DRB1 (Major Histocompatibility Complex, Class II, DR Beta 1), PDCD1 (Programmed Cell Death 1), NR1H3 (Nuclear Receptor Subfamily 1 Group H Member 4), and MS (Multiple Sclerosis).

Trypsinogen

SUSCEPTABLE

BPI CFTR CLCA4 CTSB EFL1 FCGR2A FLNB PNLIP PRSS1 PRSS3 TGFB1 TMPRSS15

Functional Network Summary

Zinc

SUSCEPTABLE

DZIP1 SLC30A5 SLC39A14 SLC39A2 SLC39A4 SLC39A6 SLC39A8 WT1

Functional Network Summary

Zinc is a trace element crucial for a healthy immune system. In humans, this trace element is responsible for many functions. It also helps to stimulate the activity of more than a hundred different enzymes. The underlying processes that are most commonly linked to Zinc include synthesis and degradation of nucleic acids, proteins, lipids, and carbohydrates, stabilization of the molecular structures, maintenance of organ and cell integrity, and polynucleotide transcription. SLC (Solute Carrier Family), WT1 (Wilms Tumor 1), SOD1 (Superoxide Dismutase 1), and ZBTB16 (Zinc Finger And BTB Domain Containing 16) are some genes linked with zinc.

Thankyou!

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