GENETICURE®

Find the right blood pressure treatment using your DNA.™

Kit ID:	#GCE123	Sample type:	Buccal swab
Patient ID:	123456	Collected:	3 Jan 2022
Patient name:	Sue Sample	Accessioned:	4 Jan 2022
Patient DOB:	1 Apr 1950	Genotyping assay:	5 Jan 2022
Indication:	Hypertension	Report created:	6 Jan 2022

HYPERTENSION GENOMIC MEDICINE PANEL RESULTS

Recommended Treatments

Do not start or stop taking any medications without first consulting your provider.

1. Primary recommendation: consider **a selective β-blocker**. If co-morbidity for **β-blockade** is present consider **a Ca^+ channel blocker**.
2. If the above recommendation is not effective or appropriate for the patient, consider **therapy with an ACE inhibitor**.
3. If the above recommendation is not effective or appropriate for the patient, consider **therapy with an angiotensin-II (AII) receptor blocker**.
4. If the above recommendation is not effective or appropriate for the patient, consider **thiazide or a thiazide-like diuretic**.

Functionality of Alleles in Organ Systems*

Cardiac System

The patient demonstrates the greatest functionality in the genes that encode receptors that control cardiac function, specifically the β_1-adrenergic receptors, and the genes that encode CYP2D6 (which metabolizes some β-blockers). The patient is most likely to respond to β-blockade, specifically a selective β-blocker. If co-morbidity for β-blockade is present consider a Ca^+ channel blocker.

Vascular System

Following this, the patient demonstrates functionality in the renin-angiotensin-aldosterone system, specifically the ACE gene and the angiotensin-II receptor. The patient is most likely to respond to therapy with an ACE inhibitor, and may respond to therapy with an angiotensin-II (AII) receptor blocker.

Renal System

The final line of therapy is informed by the patient's functionality in the genes that encode for channels/enzymes important in Na^+ reabsorption in the kidney. The patient is most likely to respond to a diuretic, specifically thiazide or a thiazide-like diuretic.

Nonfunctional allele ✗ Moderately functional − Functional allele ✓

Less ◀ Responsiveness to treatment ▶ More

Gene Name	SNP ID	HGVS ID	Result
ADRB1 49	rs1801252	NC_000010.11:g.114044277A>G	AA ✓
ADRB1 389	rs1801253	NC_000010.11:g.114045297G>C	CC ✓
ADRB2 16	rs1042713	NC_000005.10:g.148826877G>A	GA ✓
ADRB2 27	rs1042714	NC_000005.10:g.148826910G>C	CC ✗
CYP2D6	rs3892097	NC_000022.11:g.42128945C>T	TC −
ACE	rs1799752	NC_000017.11:g.63488543_63488544...	-/+ ✓
Angiotensin-I (a)	rs5051	NC_000001.11:g.230714126C>T	CT −
Angiotensin-I (b)	rs699	NC_000001.11:g.230710048A>G	CT ✓
Angiotensin-I (c)	rs7079	NC_000001.11:g.230702585G>T	GT ✗
A-II Receptor	rs5186	NC_000003.12:g.148742201A>C	CA −
Renin	rs12750834	NC_000001.11:g.204171656G>A	AA ✓
Alpha Adducin	rs4961	NC_000004.12:g.2904980G>T	TT ✓
SCNN1A	rs2228576	NC_000012.12:g.6347896T>C	CC ✗
SLC12A3	rs1529927	NC_000016.10:g.56870675C>G	GG ✗
WNK1(a)	rs1159744	NC_000012.12:g.825679C>G	GG ✓
WNK1(b)	rs2107614	NC_000012.12:g.793913T>C	CC ✓
WNK1(c)	rs2277869	NC_000012.12:g.907744T>C	TT ✗

This test was authorized by Dr. Sam Sample, NPI #1234567890.
Comments: *Thank you for using Geneticure!*

Sample Director, PhD
Laboratory Director
6 Jan 2022

Sample Consultant, MD
Clinical Consultant
6 Jan 2022

Analytical results were produced using tests developed and validated on behalf of Geneticure, Inc, CLIA ID 24D2145318, by the University of Arizona Genetics Core (UAGC), located at 1657 E Helen St. Tucson, AZ 85721. Genomic DNA was analyzed by Agena Bioscience™ MassARRAY® and/or Thermo Fisher TaqMan® methods to interrogate the variant locations listed in the Table of Assayed Variants. Less frequent haplotypes or novel alleles may be reported when appropriate. Genetic results are uploaded and analyzed by Geneticure's proprietary weighted algorithm through the secured patient/provider portal. This in silico assay is performed at the Geneticure laboratory located at the address below.

The test does not detect all known and unknown variations in the gene(s) tested, nor does absence of a detectable variant rule out the presence of other, non-detected variants. As with other common SNP genotyping techniques, these assays cannot differentiate between the maternal and paternal chromosomes. The variant detection methods validated by Geneticure provide >99.9% accuracy; however, PCR may be subject to general interference by factors such as reaction inhibitors and low quality or quantity of extracted DNA. When present, these interferents typically yield no result rather than an inaccurate one. Very infrequent variants or polymorphisms occurring in primer- or probe-binding regions may also affect testing and could produce an erroneous result or assay failure. Variant locations tested by the assay but not assigned a genotype call are reported as "No Call." Test results and clinical interpretation may be inaccurate for individuals who have undergone or are receiving non-autologous blood transfusions, tissue, and/or organ transplant therapies. Although extremely rare, results could also be impacted by other factors not addressed above, such as laboratory error.

These tests have not been cleared or approved by the U.S. Food and Drug Administration. UAGC and Geneticure are certified under CLIA-88 and are qualified to perform high-complexity testing. Due to the complexity of interpreting some genetic test results, such as those that may carry a probabilistic risk of disease, patients and providers should consider the benefits of consulting with a trained genetic counseling professional, physician, or pharmacogenomic specialist. For additional support, contact Geneticure using the information below.

* A system's functionality may not correlate to its responsiveness. "Functional" in this context refers to probable blood pressure reduction for the target therapy.

Geneticure
#4 3rd Street SW, Suite 305
Rochester, MN 55902
1-800-DNA-8109 · support@geneticure.com
For more detailed information, visit us online at Geneticure.com.