Report Number:

R16441705080001

Comprehensive Personality





## Comprehensive Personality



Report Date	Feb. 06, 2022	
Name	Issac Lee	





Report Number: R16441705080001



There's probably dozens of people that look like you across the world, but it is your personality that makes you one of a kind. Personality has to do with the way different people behave, think, and feel in response to various situations. This complex trait facilitates the defining moments of our existence and is so pervasive in many aspects of our lives - the choices we make, how we interact with friends and loved ones, the music we like, our professional and financial growth, and even our health.



Comprehensive Personality

## It's Nature, Not Nurture

Many aspects of our personality is hard wired into our DNA. Contrary to popular belief, our genetics determine key personality traits like empathy, self- control, social skills and learning abilities more than our environment or childhood experience does.



Certain traits are strongly linked to a certain gene variations. This app takes key genotypes that are associated with 16 different personalities and cognitive traits and identifies which gene variation you have.

- ▶ Response to Stress
- Socio-emotional Sensitivity (Empathy, Loneliness and Parenting Ability)
- Suicidal Behavior
- Smoking Behavior
- ▶ Avoidance of Errors
- Pain Sensitivity
- ▶ Short Term Memory

- ▶ Intelligence/ IQ Performance
- Ability to Recognize faces
- Substance Abuse and Addiction Sensitivity (Alcohol dependence, cigarette smoke risk, Heroin addiction, Nicotine dependence)
- ▶ ADHD
- Depression
- Social Interaction

Don't worry too much if you didn't score perfectly in the personality department though- you can acquire and hone better traits through awareness and effort.





Report Number : R16441705080001

## **Overview of Your Results**

Phenotypes	GENES	Genotypes	Note
Warrior vs Worrier	СОМТ	AG	Balanced; Medium pain threshold, Normal stress resistance, Normal processing of infomration under most conditions.
Socio-emotional Sensitivity	OXTR	AA	Less empathetic, Less parental sensitivity, Have less psychological resources, Low sociality
Suicidal Behavior	HTR2A	CC	More anger and aggression related behavior. Increased risk for non-violent and impulsive suicidal behavior.
Smoking Behavior	CHRNA3	GG	Smokes normal (lower) number of cigarettes if a smoker.
Avoidance of Errors	DRD2	AG	Much less efficient at learning to avoid errors.
Pain Sensitivity	СОМТ	GG	Decreased sensitivity to pain
	WWC1	СТ	Slightly increased short-term memory
Episodic Memory	SORCS1	AG	-
		СТ	-
		AG	-
	Haplotype	AGCTAG	Typical short-term memory retention
Intelligence: IQ Performance	SNAP25	AG	IQ performance was typical
Recognize Faces	MET	СТ	Better facial emotion perception
Alcohol Dependence	DRD2	AG	Normal Alcool dependence
Cigarette Smoke Risk	ALDH2	AG	One working copy of ALDH2. Increase risk to cigarette smoke.
Heroin Addiction	OPRM1	AA	Typical odds of heroin addiction
Nicotine Dependence	CHRNA4	GG	Increased risk of Nicotine dependence
Social Interaction	OXTR	AA	Typical social interaction

Phenotypes	GENES	Genotypes	Note
ADHD	DRD2	AG	- Typical risk of ADHD
	CLOCK	AA	





Comprehensive Personality

Report Number: R16441705080001

Phenotypes	GENES	Genotypes	Note
	SLC6A3	CC	
ADHD	SLC6A2	CC	Typical risk of ADHD
	HTR2A	TT	

Phenotypes	GENES	Genotypes	Note
Depression	BCR	AA	- Typical genetic predisposition to depression
		AG	
		AA	
	MTHFR	AG	
	SLC6A15	AG	
		-	





Comprehensive Personality

Report Number: R16441705080001 Comprehensive Personality



 Hung RJ et al. (2008) . "A susceptibility locus for lung cancer maps to nicotinic acetylcholine receptor subunit genes on 15q25." Nature 452(7187):633-7.

- · Kim HS et al. (2010) . "Culture, distress, and oxytocin receptor polymorphism (*OXTR*) interact to influence emotional support seeking." Proc Natl Acad Sci U S A. 107(36):15717-21.
- Stein DJ et al. (2006) . "Warriors versus worriers: the role of COMT gene variants." CNS Spectr. 11(10):745 8.
- · Klein TA et al. (2007) . "Genetically determined differences in learning from errors." Science. 318(5856):1642-5.
- · Vargas-Alarcón G et al. (2007) . "Catechol-O-methyltransferase gene haplotypes in Mexican and Spanish patients with fibromyalgia. "Arthritis Res Ther. 9(5):R110.
- Xu W et al. (2013) . "The genetic variation of SORCS1 is associated with late-onset Alzheimer's disease in Chinese Han population." PLoS One. 8(5):e63621.
- Gosso MF et al. (2006) . "The SNAP-25 gene is associated with cognitive ability: evidence from a family-based study in two independent Dutch cohorts." Mol Psychiatry. 878-86.
- · Lin MT et al. (2012). "MET and AKT genetic influence on facial emotion perception." PLoS One. e36143.
- Blum K et al. (1996) . "Increased prevalence of the Taq I A1 allele of the dopamine receptor gene (*DRD2*) in obesity with comorbid substance use disorder: a preliminary report." Pharmacogenetics. 6(4):297-305.
- · Yokoyama A et al. (2005) . "Genetic polymorphisms of alcohol and aldehyde dehydrogenases and risk for esophageal and head and neck cancers." Alcohol. 35(3):175-85.
- Zhang H et al. (2006). "Association between two mu-opioid receptor gene (*OPRM1*) haplotype blocks and drug or alcohol dependence." Hum Mol Genet. 15(6):807-19.
- Feng Y et al. (2004) . "A common haplotype of the nicotine acetylcholine receptor alpha 4 subunit gene is associated with vulnerability to nicotine addiction in men." Am J Hum Genet. 75(1):112-21.
- Anitha A et al. (2008). "Genetic analyses of roundabout (ROBO) axon guidance receptors in autism." Am J Med Genet B Neuropsychiatr Genet. 147B(7):1019-27.





Report Number: R16441705080001 Comprehensive Personality



The reports from Kiragen are based on standard analysis from Whole genome, Exome, Targeted Sequencing or genotyping data that do not provide any medical advice, diagnosis or treatment. Analyses and reports provided by (Kiragen) are for informational purposes only and are subject to change. You should consult your physician if you have questions regarding any medical condition. The results and analysis presented in the report have not been clinically validated. Any report from Kiragen have not been cleared or approved by the FDA or similar government institutions.

Whole genome sequencing covers minimum 95% of your entire genome with an accuracy greater than 99.9% with 30X of genomics sequencing depth. The sequencing process is a minimum of 24X depth of data to assure the quality of the data and result. Exome sequencing roughly covers only 2-4% of your genome, mostly areas that are well known from a genetics perspective, with an average of 100X sequencing depth.

We welcome your feedback.

Please email mklee@kiragen.com with comments or suggestions.





