Product Data Sheet

AddictID® Genotyping Array

A unified platform for genetic research on addiction and treatment approaches

Overview

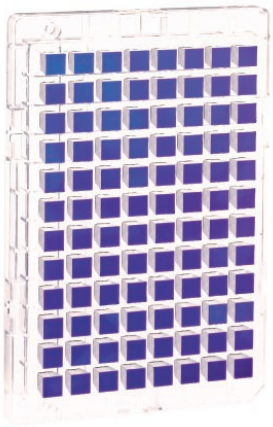
The AddictID array started through support from the National Institute on Drug Abuse (NIDA) in collaboration with leading scientists. Through the collaboration a list of genetic variants has been assembled and through validated research on smoking and addiction the Smokescreen Genotyping Array was developed. The array's content was designed to support a variety of research goals related to addiction, smoking cessation, drug response, and consequences of smoking. Subsequently, this same approach was leveraged to expand the set of biomarkers to include other addiction areas such as opioids, alcohol, and other drugs of abuse. As a result, scientists benefit from an end-to-end solution that provides the ability to incorporate genetics into addiction research.

Array Design

1000+ addiction-related genes

The NIDA Genetics Consortium identified 1,031 genes related to addiction. These genes (±20kb) are densely covered on the array in African, Asian and European populations. Over 296K SNPs and indels from the 1000 Genomes Project and Exome Sequencing Project were selected to cover both common gene variation (MAF≥5%, r^2≥0.9) and rare non-synonymous coding variation (majority with MAF<1%).

Figure 1: Smokescreen GenotypingArray



The Smokescreen Genotyping Array produces high-quality genotypes for over 646K markers in 96 individuals, which can be used for addiction research.

Product Information

Array Content

Category	No. of markers*
1000+ addiction-related genes	273,493
Genome-wide association markers	296,038
Fine-mapping of smoking-related loci	11,099
High-value addiction markers	20,451
Smoking comorbidity markers	16,301
General high-value markers	29,178
Total	646,247

Pairwise r^2 coverage of 1000+ addiction genes (±20kb)†

	r^2≥0.8		r^2≥0.9	
Population	MAF≥1%	MAF≥5%	MAF≥1%	MAF≥5%
African	63.6%	97.5%	61.1%	95.2%
East Asian	84.0%	98.1%	82.3%	97.0%
European	82.6%	98.1%	80.5%	97.0%

Genome-wide imputed coverage†

	r^2≥0.8		Average r^2	
Population	MAF≥1%	MAF≥5%	MAF≥1%	MAF≥5%
African	52.7%	65.7%	72.4%	82.3%
East Asian	71.7%	82.4%	80.2%	88.6%
European	78.2%	90.7%	85.2%	92.9%

*Markers in categories may overlap
†Based on 1000 Genomes Project Mar 2012 release (chr1-22)

Array Design (continued)

Genome-wide association markers
The panel of genome-wide association study (GWAS) markers from the Affymetrix Axiom Biobank Array and a 50K-SNP African booster panel were added to the Smokescreen design to enable discovery of new associations in European, Asian, African and Latino populations. This panel of SNPs was designed with a selection strategy aimed at maximizing the imputation efficiency to a larger variant set such as the 1000 Genomes Project.

Fine-mapping of smoking-related loci
Well-characterized loci related to smoking phenotypes, including the linkage disequilibrium (LD) block encompassing the nicotinic acetylcholine receptor gene cluster CHRNA5-A3-B4, and nicotine metabolizers CYP2A6-B6 were fine-mapped with all known rare and common markers from the 1000 Genomes Project and Exome Sequencing Project.

High-value addiction markers
Panels of SNPs related to addiction from peer-reviewed publications and research consortia, including the Pharmacogenetics of Nicotine Addiction Treatment (PNAT) Consortium and the NeuroSNP project are included on the array.

Smoking comorbidity markers
Smoking is a known risk factor and comorbidity of many diseases. For this reason, panels of SNPs related to lung cancer, psychiatric disorders, cardiovascular disease and others were included in the design.

General high-value markers
Pharmacogenomic markers, expression quantitative trait loci (eQTLs), loss-of-function (LoF) markers, ancestry-informative markers (AIMs), HLA/KIR, and NHGRI GWAS Catalog SNPs are included on the array.

Full support to enable insightful discoveries
The AddictID array is paired with advanced analytical software. Furthermore, researchers can take advantage of bioinformatics and statistical genetics expertise with integrated quality control and data analysis. If processing support is needed, study sames can be sent to one of our partner labs and quality controlled genotype data is returned in a matter of weeks.

Ordering Information

For ordering and additional information, please contact:

AddictID Support
info@addictid.com

Detailed Array Content

Category	No. of markers
1000+ addiction-related genes[1,2]	
Tag SNPs (MAF >= 0.05)	255,862
Exonic markers[3,4,5]	17,632
Genome-wide association markers	
Affymetrix' Axiom® Biobank GWAS grid[3]	246,038
African (YRI) booster panel[3]	50,000
Fine-mapping of smoking-related loci	
CHRNA5-A3-B4 (552kb LD block)	8,913
CYP2A6 (±20kb)	573
CYP2B6 (±20kb)	1613
High-value addiction markers	
NeuroSNP Project[1,2]	4,994
Pharmacogenetics of Nicotine Addiction Treatment (PNAT) SNP panels[6,7]	2,271
v1.0 Quit Success Score[8]	12,058
Literature search for addition markers	1,329
Smoking comorbidity markers	
Lung cancer[9]	3,091
Psychiatric disorders[10]	1,200
Tobacco smoke constituent update and metabolic phenotypes[11]	1,907
Pulmonary diseases and traits[4,5]	7,945
Cardiovascular diseases and traits[4]	2,247
General high-value markers	
Pharmacogenomic markers (ADME)[2]	2,030
NHGRI GWAS Catalog[12]	7,612
eQTLs[3,4]	9,736
Loss-of-function markers[3,4]	4,680
Ancestry informative markers (AIMs)	5,545
HLA/KIR[4]	8,894
Mitochondrial[4]	180
Total	646,247

References

[1]Saccone SF, Saccone NL, Swan GE, et al. Systematic biological prioritization after a genome-wide association study: an application to nicotine dependence. *Bioinformatics*. 2008;24(16):1805-11.

[2]Saccone SF, Bierut LJ, Chesler EJ, et al. Supplementing high-density SNP microarrays for additional coverage of disease-related genes: addiction as a paradigm. *PLoS ONE*. 2009;4(4):e5225.

[3]http://www.affymetrix.com

[4]UK Biobank Array. http://www.ukbiobank.ac.uk.

[5]UK Biobank Lung Exome Variant Evaluation (UK BiLEVE)

[6]Conti DV, Lee W, Li D, et al. Nicotinic acetylcholine receptor beta2 subunit gene implicated in a systems-based candidate gene study of smoking cessation. *Hum Mol Genet*. 2008;17(18):2834-48.

[7]Bergen AW, Javitz HS, Krasnow R, et al. Nicotinic acetylcholine receptor variation and response to smoking cessation therapies. *Pharmacogenet Genomics*. 2013;23 (2):94-103.

[8]Uhl GR, Walther D, Musci R, et al. Smoking quit success genotype score predicts quit success and distinct patterns of developmental involvement with common addictive substances. *Mol Psychiatry*. 2014;19(1):50-4.

[9]Wang Y, McKay J, Rafnar T, et al. Imputation from the 1000 Genomes Project identifies rare large effect variants of BRCA2-K3326X and CHEK2-I157T as risk factors for lung cancer. 2013. Manuscript submitted for publication.

[10]Psychiatric Genomics Consortium. Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. *Lancet*. 2013;381(9875):1371-9.

[11]Hecht SS. 2013. Unpublished raw data.

[12]Hindorff LA, MacArthur J, Morales J, et al. A Catalog of Published Genome-Wide Association Studies. Available at: www.genome.gov/gwastudies. Accessed Oct. 13, 2013.