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Infinium® Neuro Consortium Array

Interrogation of genomic variants associated with common neurodegenerative diseases.

Introduction

The Infinium Neuro Consortium Array is a new neurogenomic tool with expertly-selected content for the interrogation of genomic variants associated with common neurodegenerative diseases. This FAQ addresses the most common questions about this array.

1. What are the general product specifications?

The Infinium Neuro Consortium Array features a 24-sample BeadChip. In addition to Infinium Core-24 BeadChip content, the array includes ~180,000 markers focused on characterization of neurodegenerative diseases.

2. What sources did the consortium use to choose the content for the array?

The Neuro Consortium Array includes content from the following sources:

- Infinium Core-24 BeadChip backbone
- Content from the NeuroX Custom Array[1]
- Known neurodegenerative disease genes for all coding/splice site variants reported in the Exome Aggregation Consortium (ExAC)[2]
- Tagging SNPs to capture all common variation in these genes
- Additional novel content based on current and ongoing exome sequencing and whole-genome sequencing (WGS) studies
- Full list of all genome-wide association studies (GWAS) hits in the National Human Genome Research Institute (NHGRI) database[3]

3. What neurodegenerative diseases are represented on this array?

The consortium gathered previously identified markers found in known neurodegenerative disease genes. The specific disease focus includes:

- Alzheimer's Disease
- Parkinson's Disease
- Amyotrophic Lateral Sclerosis (ALS)
- Multiple Sclerosis (MS)
- Progressive Supranuclear Palsy (PSP)/Corticobasal degeneration (CBD)
- Multiple System Atrophy (MSA)
- Frontotemporal Dementia (FTD)
- Dementia with Lewy Bodies (DLB)

4. Can I get the marker list to review?

A preliminary marker list is available under a confidential disclosure agreement (CDA). Contact a sales representative for the list.

5. What reagents and other consumables will I need to use this array?

BeadChip purchase includes all necessary reagents to run the arrays. The assay requires at least 200 ng of DNA per sample at a minimum concentration of 50 ng/µl, as measured by fluorescence quantification. Access to an Illumina iScan® or HiScan® System is required to process the array. If an Illumina scanner is not available, a local account manager can recommend a suitable service provider to run the arrays.

6. What is the minimum number of samples that I can order?

Orders must be for a minimum of 288 samples.

7. Will Illumina provide a cluster file for faster genotype calling with this array?

No, consortium products do not have a cluster file. Self-clustering samples using GenomeStudio® software is recommended. Generally, 100–200 samples are sufficient to generate a cluster file for analysis. For detailed information about generating a cluster file, refer to the Infinium Genotyping Data Analysis Technical Note[4] or contact Illumina Technical Support at 1-800-809-4566 or techsupport@illumina.com.

8. Will Illumina provide support files such as LIMS Product Descriptor File, Gene Annotation File, sample files?

The LIMS Product Descriptor files and sample files will be the same as those supplied with an Infinium Core-24 BeadChip. Both can be found on the Illumina website at www.illumina.com. Unfortunately, the Gene Annotation files will not be available.

9. How do I order the array?

Contact your local account representative or email consortiamanager@illumina.com, and an Illumina representative will contact you to answer any questions and help you place your order.

10. Is the custom neurodegenerative content available separately?

The neurodegenerative content on the Neuro Consortium Array is modular and portable as an add-on focused content set to some other genome-wide backbone arrays. The Neuro Consortium content is not available separately.

References

1. Nalls MA, Bras J, Hernandez DG, et al. NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. *Neurobiol Aging.* 2015;36(3):1605e7-12.
2. The Exome Aggregation Consortium (ExAC). exac.broadinstitute.org. Accessed 21 June 2016.
3. The National Human Genome Research Institute (NHGRI) database. www.ebi.ac.uk/gwas/home. Accessed 21 June 2016.
4. Infinium Genotyping Data Analysis Technical Note (www.illumina.com/Documents/products/technotes/technote_infinium_genotyping_data_analysis.pdf).

For more information, visit www.illumina.com/science/consortia/human-consortia.html

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